ProbeName pvalues foldchange SI1_NS SI2_NS SI3_NS SI1_flags SI2_flags SI3_flags NC1_NS NC2_NS NC3_NS NC1_flags NC2_flags NC3_flags ProbeName Type ProbeSeq Accession Source Chromosome Strand Start End GeneSymbol Gene_ID Description GO Relation Associated_gene Associated_gene_description Associated_gene_strand circRNA_ID circ_chrom Hsa_hg19_circRNA_start Hsa_hg19_circRNA_end Hsa_hg19_circRNA_strand genomic_length spliced_seq_length best_transcript hostgene
LNCV6_136879_PI430048170 0.0612409354242023 0.822897007667521 11.0894562192215 11.0619762955544 11.3341798777439 P P P 11.3746968230214 11.4381014354332 11.5281784714012 P P P LNCV6_136879_PI430048170 mRNA TCCCGCAGCTCCTTCTGGCTTAGATTGAAAAATGGGCTTCCTAATGGGTTAAATCCTTTA NM_018715 RefSeq chr1 - 17406754 17439754 RCC2 55920 "regulator of chromosome condensation 2, transcript variant 1" GO:0005515|GO:0008017|GO:0030334|GO:0051987|GO:0005874|GO:0005730|GO:0030496|GO:0034506|GO:0051895|GO:0005829|GO:0048365|GO:0072356|GO:0007067|GO:0010971|GO:0007229|GO:0048041|GO:1900025|GO:0007032|GO:0000278|GO:0034260|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137316_PI430048170 0.893504217731354 1.00666623520573 0.507675753001255 0.642652903637605 0.607548422887322 A A A 0.350719461582272 0.800211451542286 0.546192661103785 A A A LNCV6_137316_PI430048170 mRNA ATTGCTGGGGTCTATTACTTCACCTACCACATCACTGTTTTCTCCAGGAATGTTCAGGTG NM_001007537 RefSeq chr13 - 23891098 23897006 C1QTNF9B 387911 "C1q and tumor necrosis factor related protein 9B, transcript variant 1" GO:0005581|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144182_PI430048170 0.357871873444783 1.02324474514133 0.370224182301532 0.275387225046888 0.332674120004747 A A A 0.28630296848331 0.289287081326491 0.304751023222701 A A A LNCV6_144182_PI430048170 mRNA ACTTAACTGAATGTTTATCTGACCAAAGGTGTGTCCCAGTTAAGTACTGTCAAATCTATT NM_020937 RefSeq chr14 + 45135938 45200890 FANCM 57697 "Fanconi anemia, complementation group M" GO:0005515|GO:0071821|GO:0090305|GO:0004386|GO:0003677|GO:0005524|GO:0043240|GO:0004518|GO:0006281|GO:0000712|GO:0003682|GO:0005654|GO:0031297 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131779_PI430048170 0.649871998235188 1.06810263887444 4.61514935750622 4.10888459771565 4.31786516008292 P P P 4.33979170020327 4.3582877087627 4.08844014820437 P P P LNCV6_131779_PI430048170 mRNA AGGGGCGCCCTCTGCCTTCCATACCCCACGCTTATAAAACATAACTAAGCCAAGAGTGGA NM_020427 RefSeq chr8 - 142740943 142742411 SLURP1 57152 secreted LY6/PLAUR domain containing 1 GO:0010839|GO:0050884|GO:0007626|GO:0005576|GO:0007155|GO:0005615|GO:0005125|GO:0001775|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100890_PI430048170 0.60175528856787 0.772092242272603 1.25098177920462 0.348087840276769 0.303832494346145 A A A 0.249407819401964 1.75685698553161 0.816924046077492 A A A LNCV6_100890_PI430048170 mRNA CAATGTTACGTGTTCTCCACGAAGAACTGGAACACACCAATTATATTTGATCTCAAAGAA NM_001190241 RefSeq chr3 - 160256985 160399532 IFT80 57560 "intraflagellar transport 80, transcript variant 2" GO:0005813|GO:0006996|GO:0050680|GO:0072372|GO:0001649|GO:0007224|GO:0005929|GO:0042384|GO:0045880|GO:2000051|GO:0005737|GO:0002062|GO:0060349|GO:0030992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137200_PI430048170 0.154087355706752 1.4747951900093 1.89253784626086 2.37354307333548 2.63474473185807 A A A 1.62995510264435 2.18749175297307 1.37427730168982 A A A LNCV6_137200_PI430048170 mRNA

ATCCAGAGGCCATGTTCCAATAAACAGGAGGTCGTGTATTTGGTCACGACATTTCTCTGA NM_000432 RefSeq chr12 - 110910819 110920600 MYL2 4633 "myosin, light chain 2, regulatory, cardiac, slow" GO:0005515|GO:0060047|GO:0030308|GO:0030049|GO:0055010|GO:0005509|GO:0006942|GO:0016459|GO:0009791|GO:0015629|GO:0030016|GO:0060048|GO:0030017|GO:0042694|GO:0005829|GO:0048747|GO:0003785|GO:0055003|GO:0005856|GO:0008307|GO:0031672|GO:0032036 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143434_PI430048170 0.139404541803039 0.779163391164106 1.89417853609995 2.31776313552179 2.4155688542016 A A A 2.55723929640299 2.63805093155955 2.56219088321092 P P P LNCV6_143434_PI430048170 mRNA
ACATGTTTGCACAGTTTCGGAAAAATGAGCGAGACAAGCAGAAACTCATTGACACCGTGG NM_015189 RefSeq chr2 - 72179314 72826048 EXOC6B 23233 exocyst complex component 6B GO:0000145|GO:0015031|GO:0006904 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54395_PI430048170 0.0970600453335671 0.818032657678525 6.71503116030886 6.69960204138967 7.02484748619474 P P P 7.10235211404126 7.06055651846465 7.16772354668084 P P P LNCV6_54395_PI430048170 mRNA
GCACCACAGATCGATTATACAGTGATGGTCTTCAAGCCAATTGTTGAAAAATTTGGTTTC NM_001130841 RefSeq chr1 + 100266157 100292769 RTCA 8634 "RNA 3'-terminal phosphate cyclase, transcript variant 1" GO:0006396|GO:0003963|GO:0003723|GO:0005654|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142392_PI430048170 0.148974112468267 0.785166040001728 0.276479692657681 0.28161665578406 0.310596302277173 A A A 0.809198469726099 0.728309185816706 0.335061607885717 A A A LNCV6_142392_PI430048170 mRNA
CCATGTTTGAATGCCAGTTTCTCTTCTTTGCTGAAGTACTTTATGATAAAAGTAAGCCTA NM_003643 RefSeq chr6 - 53126961 53148826 GCM1 8521 glial cells missing homolog 1 (Drosophila) GO:0005667|GO:0006355|GO:0003700|GO:0060706|GO:0060143|GO:0060670|GO:0005634|GO:0000978|GO:0003677|GO:0009653|GO:0006351|GO:0001077|GO:0060018|GO:0045944|GO:0008270|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130202_PI430048170 0.00609794426629914 0.501310164654498 7.63235898705462 7.47522826418528 7.8622891678695 P P P 8.46685180996322 8.55129355935806 8.92465605473509 P P P LNCV6_130202_PI430048170 mRNA
AGGAAGGTAAAGTTAGGGGACTAGAAGACTCTAAATTGGCTTCTACAGATCAATAATTTA NM_032833 RefSeq chr1 - 204403363 204411817 PPP1R15B 84919 "protein phosphatase 1, regulatory subunit 15B" GO:0005515|GO:0042542|GO:0006983|GO:0016311|GO:0000164|GO:0004722|GO:0006417 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142328_PI430048170 0.00447960810501206 0.520659261301128 4.01613999987299 4.34921900007718 4.41122939843487 P P P 5.02841554827034 5.24793270207431 5.33811808591232 P P P LNCV6_142328_PI430048170 mRNA
TGGGGGGTAATAACAGCTTTTTTGCACTATGTAAATACTAGTGGGGATTCTTCTGTACTA NM_001193489 RefSeq chr15 - 48988638 49046563 SECISBP2L 9728 "SECIS binding protein 2-like, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137833_PI430048170 0.91145948677744 1.00979801323844 0.255471506318251 1.30716250073295 0.400885446076228 A A A 0.368422507745714 0.953318139967681 0.776459458032974 A A A LNCV6_137833_PI430048170 mRNA
TAGCTGTATATACTATTTATTTCAGGGCTGGGCTATAACACAGACGAGCCCCAGACTCTG NM_015831 RefSeq chr7 - 100889993 100895920 ACHE 43 "acetylcholinesterase (Yt blood group), transcript variant E4-E5" GO:0005515|GO:0048471|GO:0003990|GO:0031594|GO:0030054|GO:0060041|GO:0005886|GO:0008283|GO:0004104|GO:0005518|GO:0050714|GO:0045202|GO:0007268|GO:0005634|GO:0044281|GO:0031225|GO:0043621|GO:0

005615|GO:0042803|GO:0031623|GO:0001540|GO:0042166|GO:0017171|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90688_PI430048170 0.0304858641445457 0.489890730677306 6.70594687787801 6.40796620800696 6.8000080430872 P P P 7.21801664809435 7.69751031778907 8.00810885926967 P P P LNCV6_90688_PI430048170 mRNA GCTCTCATTGCTTGTTTGCAAATGCTCTATGGACATTTGTGTGCTAAATCCTATTAAATA NM_006738 RefSeq chr15 + 85380615 85749358 AKAP13 11214 "A kinase (PRKA) anchor protein 13, transcript variant 1" GO:0045859|GO:0005515|GO:0051056|GO:0048471|GO:0048011|GO:0043065|GO:0007264|GO:0005634|GO:0097190|GO:0046872|GO:0005829|GO:0032947|GO:0005737|GO:0016020|GO:0032321|GO:1900169|GO:0006468|GO:0017048|GO:0004871|GO:0051018|GO:0005089|GO:0010611|GO:0051168|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_9915_PI430048170 0.04426703311204 0.701262810158046 6.66586921304832 6.27043983016163 6.6168167987316 P P P 7.03596988046927 7.24287906583007 6.80895583289037 P P P LNCV6_9915_PI430048170 mRNA GAAGCAACAAGATTGCTTGCAACAATTGTTATGCTTGTATAGCCTGTCGTACATCCCATA NM_145169 RefSeq chr6 - 166319727 166342606 SFT2D1 113402 "SFT2 domain containing 1, transcript variant 1" GO:0016021|GO:0016192|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137976_PI430048170 0.937924168120671 1.00162632832927 0.352834593094788 0.338099059757499 0.279278556938592 A A A 0.322234240761897 0.332622185604506 0.309272965509932 A A A LNCV6_137976_PI430048170 mRNA CAGCAAGTTAAACAAGCCTTCAAAGCTGTATTTAGAAAGATATTTTCTGCTTCAGACAAG NM_001005499 RefSeq chr12 - 55469199 55470138 OR6C70 NA "olfactory receptor, family 6, subfamily C, member 70" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141908_PI430048170 0.529068705058181 1.04564342093502 9.69440304510419 9.55723449879153 9.75588059941678 P P P 9.58470953728559 9.48345737616767 9.74150299714803 P P P LNCV6_141908_PI430048170 mRNA CGGAATAGGTTGCTTCTACCACCTGTTCTTAATGTAACAGTAAAAGTTTTCACATTTTTC NM_017896 RefSeq chr20 + 62938088 62948475 GID8 54994 GID complex subunit 8 GO:0030054|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135952_PI430048170 0.0669523861853958 0.663516639582681 3.26830939751099 3.10253938545324 2.66983945136927 P P A 3.65857101659356 3.68563764026673 3.53128301076703 P P P LNCV6_135952_PI430048170 mRNA AGTCCCCTGGTTCCTGTCTGTTATTTGTAAACTGAGGACCACAATAAAGAAATCTTTATA NM_001199951 RefSeq chr17_KI270857v1_alt - 169050 178242 LYZL6 57151 "lysozyme-like 6, transcript variant 1" GO:0008152|GO:0003796|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130988_PI430048170 0.00198160685396611 0.509804737949653 4.70725797881554 4.89070057688406 4.95346306436112 P P P 5.75074378299194 5.69204781955422 6.01489229785097 P P P LNCV6_130988_PI430048170 mRNA TCCCATGTTGGGGTTACTCAAGGTCCTTATTGGTTCTTCAGCATTTTGTGGCTATAAATA NM_012091 RefSeq chr16 - 75598348 75623323 ADAT1 23536 "adenosine deaminase, tRNA-specific 1, transcript variant 1" GO:0003723|GO:0008251|GO:0046872|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129407_PI430048170 0.289326082587722 1.02621651745424 0.34737563316594 0.269439488237596 0.269469640335442 A A A 0.252561632878397 0.271166816407785 0.251878878325931 A A A LNCV6_129407_PI430048170 mRNA TGTGTGTATCATCGGTGGGATGACAGAACAAACATATTTATGATCATGAATAATGTGCTT NM_001128205 RefSeq chr8 + 69492792 69660912 SULF1 23213 "sulfatase 1, transcript variant 1"

GO:0005886|GO:0051216|GO:0005783|GO:0048706|GO:0030177|GO:0008449|GO:0005615|GO:0032836|GO:0030513|GO:0002063|GO:0004065|GO:0030201|GO:0048010|GO:0030336|GO:0005794|GO:0005795|GO:0009986|GO:0001822|GO:0005509|GO:0006915|GO:0035860|GO:0010575|GO:0060686|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127304_PI430048170 0.901102266256476 0.996981877891917 0.376929340164465 0.349771643631272 0.253978861851675 A A A 0.321471746368047 0.344405187556342 0.330664098189051 A A A LNCV6_127304_PI430048170 mRNA GCTATGAAACCTGGTGTTATGAACTCAATTTAATTGCTGAGGGTCTTAAATCAACAGAAT NM_000036 RefSeq chr1 - 114673098 114695618 AMPD1 270 "adenosine monophosphate deaminase 1, transcript variant 1"
GO:0003876|GO:0010033|GO:0006144|GO:0032264|GO:0043101|GO:0055086|GO:0044281|GO:0046872|GO:0032036|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72433_PI430048170 0.00818155055458078 0.7596317989663 6.06159613743364 6.0606377544224 6.09515776701646 P P P 6.41378062379668 6.55290008952391 6.43697921044539 P P P LNCV6_72433_PI430048170 mRNA AGACAGTCCTCTCAGGACCTTGAAGAGGAAATCCAGCAACATGAAGCGCCTGTCCCCAGC NM_001199579 RefSeq chr22 - 38734713 38756019 SUN2 25777 "Sad1 and UNC84 domain containing 2, transcript variant 1"
GO:0005515|GO:0008017|GO:0031965|GO:0000794|GO:0030335|GO:0007097|GO:0090292|GO:0034993|GO:0090286|GO:0005635|GO:0042802|GO:0005639|GO:0051642|GO:0031022|GO:0006998|GO:0007052|GO:0000784|GO:0005521|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126755_PI430048170 0.545419797844673 0.539631965206097 1.31955945839639 0.427032019666625 0.453438736948818 A A A 2.74642779043118 0.698352886385578 0.401542183907022 P A A LNCV6_126755_PI430048170 mRNA CTCCTGGGTGTTCATTCATTTTGTTTGACACCAGGGTTCTTCAGCTATTGATGTTTGTGG NM_007227 RefSeq chr2 + 105241742 105243467 GPR45 11250 G protein-coupled receptor 45
GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139586_PI430048170 0.563751605635929 0.941890127174405 8.91574690168714 8.91337175025525 8.95105954953435 P P P 9.20635177331244 8.81568738793396 8.99093520089666 P P P LNCV6_139586_PI430048170 mRNA CGTGAGATGTTTATTCAGTGTTAAAGAGCCTGTTTTTCTACCAAACAATAAAACCAAGAG NM_015604 RefSeq chr14 + 72926331 72959649 DCAF4 26094 "DDB1 and CUL4 associated factor 4, transcript variant 1"
GO:0016567|GO:0080008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128625_PI430048170 0.879433505330329 0.992586220917486 9.54613211820538 9.76855195560232 9.48533424053325 P P P 9.63551912773827 9.65484731597045 9.55559576482334 P P P LNCV6_128625_PI430048170 mRNA ACTGTGGGTTGGGGGCCTTGGATCCCAAATAAATGAGTAGTTCCTCTGCAGTCTAAAAAA NM_014008 RefSeq chrX + 49235466 49250526 CCDC22 28952 coiled-coil domain containing 22
GO:0005515|GO:0008150|GO:0003674|GO:2000060|GO:0006878|GO:0007253|GO:0006893|GO:0005575|GO:0043123|GO:0043124 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116688_PI430048170 0.237774755717239 1.07597599092798 11.0306165628766 11.0127256729445 11.0835663074753 P P P 11.0527543755605 10.924646257562 10.8244097386041 P P P LNCV6_116688_PI430048170 mRNA CTGAGAAGTGTATATGGGGCCCAAGCTACTGGTGCCAGAACACAGAGACAGCAGCCCAGT NM_001042465 RefSeq chr10 - 71816297 71851325 PSAP 5660 "prosaposin, transcript variant 2"
GO:0005515|GO:0060736|GO:0044281|GO:0005765|GO:0005615|GO:0008289|GO:0043231|GO:0005739|GO:0043408|GO:0070062|GO:0043202|GO:0006665|GO:0005794|GO:0006687|GO:0071310|GO:0060742|GO:0005730|GO:0030168|GO:0005576|GO:0043085|GO:0019216|GO:0007596|GO:0006869|GO . NA - . NA NA NA

NA NA NA NA NA NA
LNCV6_145702_PI430048170 0.113544170615584 1.04276038426908 0.363719075634945
0.315995458561065 0.280691775698287 A A A 0.248947325607427 0.283189455772884
0.247971998385879 A A A LNCV6_145702_PI430048170 mRNA
CAGCATACTTTGGATCCATTTCATGCAGGATTGTGTTGTTTTAACTGTTGTTGAGGAAGC NM_021139 RefSeq chr4
- 69480164 69495908 UGT2B4 7363 "UDP glucuronosyltransferase 2 family, polypeptide B4,
transcript variant 1"
GO:0052696|GO:0006805|GO:0052695|GO:0009813|GO:0008152|GO:0001972|GO:0005789|GO:0015020|GO:0006
711|GO:0016021|GO:0032870|GO:0043231 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_68957_PI430048170 0.244227037626579 1.08282315900198 5.92797026910474
6.06850235744391 5.92328140560792 P P P 5.72876758498449 5.96396981109624
5.87765628703409 P P P LNCV6_68957_PI430048170 mRNA
AATCGATGAGTTTGAATCTAATGTCAATGAGGTGAAGGATCCCTACCCCTCAGCCGACTT NM_000069 RefSeq
chr1 - 201039511 201112566 CACNA1S 779 "calcium channel, voltage-dependent, L type, alpha 1S
subunit"
GO:0086010|GO:0005245|GO:0005886|GO:0006941|GO:0048741|GO:0030315|GO:0008331|GO:0007520|GO:0005
891|GO:0046872|GO:0070509|GO:0001501|GO:0005737|GO:0016529|GO:0006936|GO:0043501|GO:0007411|GO:0
007528|GO:0002074|GO:0070588|GO:0034765|GO:0006816|GO:0007029|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130875_PI430048170 0.632500085876089 0.664902694216562 0.276334828562495
1.13521219181964 0.403588861237136 A A A 0.373581213424675 0.327265836392258
2.19037850011688 A A A LNCV6_130875_PI430048170 mRNA
ATGCGTGAGGAAGGACAGCTGACTTGATTTACCTTCCAAGGCCAGCTCAACAACTTTTTT NM_199289 RefSeq
chr13 - 52064763 52129092 NEK5 341676 NIMA-related kinase 5
GO:2001056|GO:0004674|GO:0051155|GO:0006468|GO:0005634|GO:0005524|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135088_PI430048170 0.0558973757098607 1.47755667896237 9.46698289690206
9.48605193337398 9.52122708998789 P P P 9.05682220572449 9.0613069664346
8.62504377173545 P P P LNCV6_135088_PI430048170 mRNA
AGTAGCATTTCTTATTTGTTTGGTCACTGCTACACCTTAGCAGCTCTTCCCCTTTCCTGG NM_006005 RefSeq chr4
+ 6269849 6303265 WFS1 7466 "Wolfram syndrome 1 (wolframin), transcript variant 1"
GO:0005516|GO:0005215|GO:0034976|GO:0006983|GO:0051928|GO:0005783|GO:0007605|GO:0030176|GO:0030
425|GO:0043433|GO:2000675|GO:0055074|GO:0022417|GO:0030968|GO:0043069|GO:0043524|GO:0042048|GO:0
031398|GO:0051117|GO:0033613|GO:0031625|GO:0045927|GO:0051247|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145506_PI430048170 0.729896194019769 0.87538464299431 0.401411479219307
0.408037721345599 2.19265636398133 A A A 0.539397399693704 2.21234085513651
1.11049242749827 A A A LNCV6_145506_PI430048170 mRNA
GCCAGTGCCTTGATTTGGTTGTTTGTTGTTTGTTTGTTTTCCTACAAGTGATTTAGGGGC NM_145011 RefSeq chr10
- 37949866 37976525 ZNF25 219749 zinc finger protein 25
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_141534_PI430048170 0.1549989327381130.5125451946871971.8346921388308
0.3182024625415690.380967015625828A A A 2.48581454229718 1.3619566833863
1.91098402449896 A A A LNCV6_141534_PI430048170 mRNA
TCTCGGGAGAAATGGGACATTTTTATTTTCTCTGCTAAGTGAAATGCAACTTTTTGAAGA NM_178509RefSeq chr17
+ 54968764 55164088 STXBP4 252983 syntaxin binding protein 4
GO:0005515|GO:0008286|GO:0019905|GO:0010838|GO:0050821|GO:0006605|GO:0006974|GO:0005737|GO:0015

758|GO:0005654|GO:0045111|GO:0061178|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138943_PI430048170 0.11350889584957 1.11299246936728 0.571200281950571
0.3707293416958970.530423879539821A A A 0.2772012354538840.386482463783982
0.350880047954417A A A LNCV6_138943_PI430048170 mRNA
CACATGAAATGAGTTTACTGTGGAAATGAAAATGCAGAGTAAGTCCAACAGCTAGTTTAT NM_001278199 RefSeq
chr5 + 122774995 122834539 SNX2 6643 "sorting nexin 2, transcript variant 2"
GO:0005515|GO:0072673|GO:0005154|GO:0005158|GO:0051259|GO:0006886|GO:0030027|GO:0043231|GO:0006
897|GO:0043234|GO:0016050|GO:0005737|GO:0016020|GO:0034498|GO:0031901|GO:0042147|GO:0035091|GO:0
010008|GO:0070062|GO:0019898|GO:0030904 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58029_PI430048170 0.2076347368672180.5514824315516322.41324365558518 0.396242986103904
1.58812710550337 A A A 2.8935585049041 2.23956510384133 2.41780949774683 P A P
LNCV6_58029_PI430048170 mRNA
AACTGCCTGCAGCTAAAAAGCAGGAAAAACAAAAAGATGCCACAACAGATTGAGTGGGAG NM_012124RefSeq
chr11 - 90200429 90223364 CHORDC1 26973 "cysteine and histidine-rich domain (CHORD)
containing 1, transcript variant 1"
GO:0005515|GO:0061077|GO:0051879|GO:0008270|GO:2000299|GO:0010824|GO:0005575|GO:1900034 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138728_PI430048170 2.62936545170128e-05 2.77181995567376 9.24338739608752
9.26184125494095 9.22766278913149 P P P 7.81528786022148 7.76765060537672
7.73656349960528 P P P LNCV6_138728_PI430048170 mRNA
GTACTTGTGGCTTGCTAGTATGTTTTTATGATAATCTCGGGCATTGTTTGCATTGTGTTT NM_013412RefSeq chr2 +
113627228 113643398 RABL2A 11159 "RAB, member of RAS oncogene family-like 2A, transcript variant 1"
GO:0008152|GO:0003924|GO:0032482|GO:0019003|GO:0005525|GO:0006886|GO:0012505 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127601_PI430048170 0.299645654618786 1.02925924029147 0.33256751880991
0.2596417295326840.358836411855097A A A 0.2800416838258520.264897224778047
0.28304370273553 A A A LNCV6_127601_PI430048170 mRNA
TGAAGGAATCCCTTTGCAAGGTTGCATTACTGTACCCATCATTTCTAAAATGGAAGAGGG NM_002253RefSeq chr4
- 55078258 55125595 KDR 3791 kinase insert domain receptor
GO:0005515|GO:0030054|GO:0035584|GO:2001214|GO:0008360|GO:0051879|GO:0046777|GO:0030198|GO:0043
129|GO:0070374|GO:0045446|GO:0038084|GO:0038083|GO:0001945|GO:0038085|GO:0023014|GO:0005794|GO:0
030335|GO:0048286|GO:0014068|GO:0018108|GO:0010595|GO:0005178|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132659_PI430048170 0.0380039529689767 1.28554237621273 4.1371387053018
4.24447737499438 3.93615703902826 P P P 3.82191221900933 3.6532462480688
3.76717276012179 P P P LNCV6_132659_PI430048170 mRNA
TTACTGTGTAAGCAAGAGTAGAAGAATGTCTAATGTACAGTGGAACCTTGTACAGAATAA NM_004205RefSeq chr11
- 119355214 119381726 USP2 9099 "ubiquitin specific peptidase 2, transcript variant 1"
GO:0005515|GO:0016579|GO:0045475|GO:0048471|GO:0004843|GO:0005634|GO:0048512|GO:0046872|GO:0042
802|GO:0005737|GO:0005938|GO:0043153|GO:0031625|GO:0005813|GO:0030332|GO:0050821|GO:0000122|GO:0
048642|GO:0048643|GO:0032922|GO:0004197|GO:0007049|GO:0045931|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140768_PI430048170 0.297121237316406 1.02938508358644 0.321589675885429
0.2527651783561950.353137008667602A A A 0.2737990697579020.254098729462692
0.275963717949694A A A LNCV6_140768_PI430048170 mRNA
CCTTAACGTCAGACTTTCTCCAAGACCAAAACTCTAAGAACTTATTTCCATTCTTACAAA NM_016212RefSeq
chr16_KI270728v1_random + 17231 19833 TP53TG3 24150 "TP53 target 3, transcript variant 1"
GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121181_PI430048170 0.00508377099404899 2.39155688040089 7.26580223701078

7.42868720234919 7.38381011502552 P P P 6.26723611059497 6.16877656664202
5.83938588797796 P P P LNCV6_121181_PI430048170 mRNA
CCGCAAGCCCCCGGTATGAGATTGTCATCATCACTGTGGTAGCAGCCGCAGTCATAATGG NM_000201 RefSeq chr19
+ 10270840 10286615 ICAM1 3383 intercellular adhesion molecule 1
GO:0005515|GO:0014070|GO:0008360|GO:0007605|GO:0019221|GO:0050731|GO:0050900|GO:0005615|GO:0030
155|GO:0030838|GO:1900027|GO:0001618|GO:0030198|GO:0071356|GO:0031669|GO:0051926|GO:0070374|GO:0
070062|GO:0060333|GO:0009986|GO:0007569|GO:0071312|GO:0005178|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131925_PI430048170 0.0073876800373743 2.00379918683355 1.42925164049589
1.13711766052469 1.20271881976388 A A A 0.2669141417404530.242750065330095
0.267605788803252 A A A LNCV6_131925_PI430048170 mRNA
CTATGCTTCTTCAATGGTAACATCATCAAGTATCCTTGACCACTTTACTGGGGATTTTTT NM_001101357 RefSeq chrX
+ 134237046 134245778 CCDC160 NA coiled-coil domain containing 160 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_137164_PI430048170 0.4214453136669470.0854906123383742 0.549504234931398
0.4586493784591210.267619021544182 A A A 0.3948333031564755.47830022408009
0.46675352704051 A P A LNCV6_137164_PI430048170 mRNA
CGATTTGTACTTCATAGAGCACCAGACACAATGTCTCACCCAATTTGGAGTTCCATATTT NM_021649 RefSeq chr5
- 115578495 115602479 TICAM2 NA toll-like receptor adaptor molecule 2 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_124467_PI430048170 0.00105753331494405 0.5879524830357587.38421216994521
7.16247558841503 7.21545518028612 P P P 7.95325311172586 8.12886234131431
7.98189288611497 P P P LNCV6_124467_PI430048170 mRNA
ACCTGAGTGTGTTCTACCCCGGGACACTGCTGGAGACCGGTCATGACATCCTCTTCTTCT NM_006295 RefSeq
chr6_GL000252v2_alt - 3025293 3043709 VARS 7407 valyl-tRNA synthetase
GO:0005739|GO:0010467|GO:0004832|GO:0002161|GO:0006438|GO:0006450|GO:0005524|GO:0006418|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142102_PI430048170 0.2386057248997491.25764410672991 4.13068751803374
3.96220627659132 4.23349236888276 P P P 4.18417514367173 3.58809497554859
3.46912464962964 P P P LNCV6_142102_PI430048170 mRNA
AGTGTGCATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGATGCGCGT NM_000894 RefSeq chr19
- 49015979 49017090 LHB3972 luteinizing hormone beta polypeptide
GO:0007165|GO:0016486|GO:0006701|GO:0005179|GO:0007267|GO:0005102|GO:0005576|GO:0044267|GO:0008
584|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142482_PI430048170 0.33858079715278 0.92048090872865912.3070107810502
12.2441160302725 12.0877021103258 P P P 12.1813692868228 12.3337760043628
12.4760305847334 P P P LNCV6_142482_PI430048170 mRNA
CCATCTTCTGCACCCCACTCTTTGTTTCCAATAAAGTTATGTCCTTAGATAGCGAAAAAA NM_014389 RefSeq chr17
- 4671383 4704337 PELP1 27043 "proline, glutamate and leucine rich protein 1, transcript variant 1"
GO:0005515|GO:0005730|GO:0035327|GO:0005634|GO:0071391|GO:0006351|GO:0005737|GO:0016020|GO:0003
682|GO:0045944|GO:0071339|GO:0005654|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135640_PI430048170 0.0314831734307915 0.6127977913483655.47560082660916
5.65134890837525 6.04222983862373 P P P 6.29315019666752 6.44615125015233
6.59330194996573 P P P LNCV6_135640_PI430048170 mRNA
GGTATCTGACAATGTGTATTAGGTGTCATATACAATGGTAATATGCCTGTCTTTAAAGTG NM_182916 RefSeq chr3
+ 3126915 3149022 TRNT1 51095 "tRNA nucleotidyl transferase, CCA-adding, 1, transcript variant 1"
GO:0005739|GO:0005622|GO:0052927|GO:0000049|GO:0006626|GO:0001680|GO:0052929|GO:0004810|GO:0052
928|GO:0005524|GO:0042780 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128194_PI430048170 0.0514385628136198 0.5717440165973888.0922523735922

7.38509088806933 7.48310567299093 P P P 8.47175479748681 8.62737021168064
8.37563637499577 P P P LNCV6_128194_PI430048170 mRNA
CCTGGAAGGCGAGCCTTGATTGTCTGAACACATAAAGCAAACTGTCCAGAAGGGAAAAAA NM_022720 RefSeq
chr22 + 20080231 20111877 DGCR8 54487 "DGCR8 microprocessor complex subunit, transcript variant
1"
GO:0005515|GO:0003725|GO:0010467|GO:0005737|GO:0072091|GO:0031053|GO:0015630|GO:0005730|GO:0005
654|GO:0005634|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135503_PI430048170 0.0958672344614403 1.25939655696079 4.0276064450319
4.09472955382169 4.15243182575125 P P P 3.66420804222959 3.98874209050367
3.59499277469505 P P P LNCV6_135503_PI430048170 mRNA
GCACAAGGTCATGGCCTTTGTCATAGCAGTTGAATGTGCATTGACATATTTTTCTATGAT NM_001040446 RefSeq
chr5 - 32227006 32313008 MTMR12 54545 "myotubularin related protein 12, transcript variant 1"
GO:0005515|GO:0016791|GO:0005737|GO:0016311 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132580_PI430048170 0.00250819282652646 0.3437654180903664.38867988286173
3.850140987454 4.31994928442987 P P P 5.43461777570416 5.88551697591883
5.87326687674573 P P P LNCV6_132580_PI430048170 mRNA
CAGGAATGCTGGCAATAGCTTGTGCCAGATTACTGTATAAACTTGAAAGTAATAAAAATG NM_004094 RefSeq chr14
+ 67360316 67386516 EIF2S1 1965 "eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa"
GO:0005515|GO:0005851|GO:0005850|GO:0010467|GO:0010494|GO:0003743|GO:0005634|GO:0006412|GO:0006
413|GO:0030968|GO:0005829|GO:0043558|GO:0046777|GO:0016020|GO:0043022|GO:0006987|GO:0044267|GO:0
005844|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142068_PI430048170 0.130068639081527 1.05676379698568 0.443076239795614
0.467562947837716 0.487932706253895 A A A 0.327845170671899 0.383715718803898
0.445979488263083 A A A LNCV6_142068_PI430048170 mRNA
GCTTGAAACCAAAGCTTCAGATAAACTTGCAAGATAAGACAACTTTAAGAAACCAGTGTT NM_003151 RefSeq chr2
- 191029575 191151260 STAT4 6775 "signal transducer and activator of transcription 4, transcript variant
1"
GO:0043565|GO:0005515|GO:0005737|GO:0003700|GO:0008283|GO:0045944|GO:0019221|GO:0006468|GO:0005
654|GO:0004871|GO:0007259|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107289_PI430048170 0.695317493472212 0.908438822357076 0.487331129513748
0.568429176464915 0.569584092886669 A A A 0.337074110833222 1.08462762246723
0.511131657971443 A A A LNCV6_107289_PI430048170 mRNA
CAAAAGCCTATGGCTTCCAGGCACGAACCGATGCCCGTGGTGACATCATGGCTATTGCAC NM_152685 RefSeq chr5
- 139367195 139383350 SLC23A1 9963 "solute carrier family 23 (ascorbic acid transporter), member 1,
transcript variant 2"
GO:0005515|GO:0005886|GO:0070890|GO:0015882|GO:0030324|GO:0006767|GO:0044281|GO:0070837|GO:0005
737|GO:0016324|GO:0009925|GO:0043229|GO:0035725|GO:0015205|GO:0006814|GO:0070904|GO:0015229|GO:0
035461|GO:0070062|GO:0015851|GO:0009636|GO:0015081|GO:0005903|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_77090_PI430048170 0.782197654939644 1.01620187091425 7.41615431022515 7.61919546008314
7.46423532819786 P P P 7.55250874646475 7.4521957929333 7.43023787382312 P P P
LNCV6_77090_PI430048170 mRNA
GATCCAATGAGGCCCCCTAAATAATTGAGTTTTGGGTCCTGGTTGGTTGTTTTATTTTTTNM_002714 RefSeq
chr6_GL000253v2_alt - 1910628 1927536 PPP1R10 5514 "protein phosphatase 1, regulatory
subunit 10, transcript variant 1"
GO:0004864|GO:0005654|GO:0005634|GO:0006606|GO:0072357|GO:0043086|GO:0003677|GO:0000785|GO:0046
872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141526_PI430048170 0.293974954352198 1.02872220782183 0.318390890548467 0.2509398117086
0.348135575225955 A A A 0.271773973204220 0.251059831055255 0.273675378009059 A A A

LNCV6_141526_PI430048170 mRNA
TGAGACCCTACAACCCTTTCAACAAGAAGGACAAAGAAACCATAGACTACTAGAGGAGGC NM_001161834
RefSeq chr7 + 50096085 50159256 C7orf72 NA chromosome 7 open reading frame 72 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_129784_PI430048170 0.605983517139225 0.93311554824707 2.94250674838895
3.29459244606161 2.64217129262563 P P A 3.23180243049858 3.06434760347738
2.94204413354342 P P P LNCV6_129784_PI430048170 mRNA
AGGATGTGTAAGAAACCAGAGGTAAAGGTCTCGCGATATCTTAAGACATCCGGCGTAGTA NM_032356 RefSeq chr17
- 7856684 7857854 NAA38 84316 "N(alpha)-acetyltransferase 38, NatC auxiliary subunit"
GO:0043066|GO:0031417|GO:0005737|GO:0005654|GO:0005634|GO:0005844 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143842_PI430048170 0.226904849140004 1.08259733938868 0.620871793437919
0.821923644651624 0.627566217988698 A A A 0.538842065996126 0.605789985714556
0.590560024547023 A A A LNCV6_143842_PI430048170 mRNA
CTTTTGCTCACAAAACCTGGCACAATGGCTAATTCCCAGAGTGTGAAACTTCCTAAGTAT NM_000230 RefSeq chr7
+ 128241277 128257629 LEP 3952 leptin
GO:2000491|GO:0071298|GO:0033686|GO:0071300|GO:0045598|GO:0030300|GO:0001819|GO:0002021|GO:0005
615|GO:0050901|GO:0043270|GO:0033197|GO:2000486|GO:0032868|GO:0060587|GO:0007565|GO:0006635|GO:0
001542|GO:0046881|GO:0000122|GO:0001890|GO:0005179|GO:0048639|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142477_PI430048170 0.0831528378244092 0.978012458020461 0.328605587748583
0.363217343565266 0.347333439173415 A A A 0.389864130483635 0.386435006014421
0.359094314688459 A A A LNCV6_142477_PI430048170 mRNA
CCTCACAGGAACTAAAGCAACTTTAGTATGAAGTCTGACAAATTCTGTACAAAACTTAGA NM_001257268 RefSeq
chr14 - 103940425 103942308 RD3L NA retinal degeneration 3-like NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138250_PI430048170 0.656713746678407 1.0730026052457 3.23003663159835
0.455755323459584 0.526551966802064 P A A 1.58701847847076 2.33989536097864
1.72171096223942 A A A LNCV6_138250_PI430048170 mRNA
ACTAAAAACAGAAACAGGAAAATAAAATATGAATACAATCCAGCCCGGAGCTGGAGTGCA NM_007121 RefSeq
chr19 + 50376422 50383028 NR1H2 7376 "nuclear receptor subfamily 1, group H, member 2,
transcript variant 1"
GO:0005515|GO:0010467|GO:0032376|GO:2000188|GO:0090108|GO:0006367|GO:0090340|GO:0001133|GO:0090
187|GO:0003707|GO:0005634|GO:0010875|GO:0046965|GO:0060336|GO:0005737|GO:0034191|GO:0045944|GO:0
043401|GO:0051117|GO:0004879|GO:0044255|GO:0042632|GO:0010867|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132144_PI430048170 0.36413114673221 1.08885914473381 9.40351865371566
9.51888916009742 9.66878336580338 P P P 9.40626553284307 9.24229917370366
9.56810581774196 P P P LNCV6_132144_PI430048170 mRNA
GGCAGACAAGATGGCTGTCTGGTTTTGAGACACACTTTAATTTTATGTTAACTTGTTAAA NM_018428 RefSeq chr17
- 31863170 31901710 UTP6 55813 "UTP6, small subunit (SSU) processome component, homolog
(yeast)" GO:0000462|GO:0030515|GO:0032040|GO:0005730|GO:0034388 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144632_PI430048170 0.286668545632532 0.786881429617306 5.47838058867652
5.69581583078165 5.86293105272796 P P P 5.56111174292604 6.17173945159817
6.27028311510687 P P P LNCV6_144632_PI430048170 mRNA
CTGGGTGAATCATAGCTTAGTTTGCATGTCCAGCTAATTTGTTTCTATACATTTTGTTTG NM_001003699 RefSeq chr6
+ 7107852 7251980 RREB1 6239 "ras responsive element binding protein 1, transcript variant 1"
GO:0006355|GO:0003700|GO:0006366|GO:2000394|GO:0005730|GO:0005634|GO:0007265|GO:0007275|GO:0000

122|GO:0000979|GO:0046872|GO:0016604|GO:0005737|GO:1900026|GO:0016607|GO:0005654|GO:0045893|GO:0010634|GO:0033601|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136871_PI430048170 0.12800587008626 0.6432927323311133.50134544655749 2.63766144171011 3.03272279048747 P A A 3.25759932188455 3.86433292469991 3.9883241572976 P P P LNCV6_136871_PI430048170 mRNA
GGAGGGGGAGTTGGTTAATAGCAGATACTTTTCTTCTAGAAGCTTATGTTTTATGCTGTT NM_000112RefSeq chr5 + 149960736 149987400 SLC26A2 1836 "solute carrier family 26 (anion exchanger), member 2"
GO:0006805|GO:0050427|GO:0005886|GO:0050428|GO:0005975|GO:0044281|GO:0055085|GO:0001503|GO:0015116|GO:0016020|GO:0005887|GO:0008272|GO:0009405|GO:0008271|GO:0030203|GO:0070062|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140762_PI430048170 0.4613752590499130.7055834242904310.326688368777152 0.3202869714453260.270204715680522A A A 0.2604574761960480.271463705208295 1.51162582805248 A A A LNCV6_140762_PI430048170 mRNA
GTAGAGGGGGAAAAGGAGAATGATGATGATAGTTTCCTTCTGTCTATTGACCTTTTTTAT NM_080870RefSeq chr6_GL000255v2_alt + 2196153 2209373 DPCR1 135656 diffuse panbronchiolitis critical region 1
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145696_PI430048170 0.0675400269370493 0.4501575816506220.388542244687834 1.65319380614844 1.02332278296498 A A A 1.63132239733069 2.38996060825239 2.6019375397108 A P P LNCV6_145696_PI430048170 mRNA
CCAGGACTTTTCTCTTCCCCATGTCAAAATACAATCAATAATTGATGGTAAAAGTTTGGA NM_004897RefSeq chr10 + 87504465 87553461 MINPP1 9562 "multiple inositol-polyphosphate phosphatase 1, transcript variant 1"
GO:0034417|GO:0008969|GO:0052826|GO:0043647|GO:0005783|GO:0003993|GO:0006797|GO:0030282|GO:0044281|GO:0001503|GO:0016311|GO:0005788|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145418_PI430048170 0.3115361929149281.18478651142717 0.391412500544033 0.8829595272675890.369586807914507A A A 0.2993347965516020.311258828652719 0.359228010049927A A A LNCV6_145418_PI430048170 mRNA
CCTGCTAACTGTAGAAACTGGCATCTGCACTTTAATAATAATACTTTACTTCTGGACTTT NM_001040179 RefSeq chr6 - 99919909 99994223 MCHR2 84539 "melanin-concentrating hormone receptor 2, transcript variant 1" GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116070_PI430048170 0.7905875984232041.10261517156044 3.34475051457229 4.34656443713259 3.96327512314628 P P P 3.85509338043993 3.93717660160579 3.58761298034127 P P P LNCV6_116070_PI430048170 mRNA
CCATGATGATGGGTCTGAGCTCCCCCAGAAGTATTACTGGTGGTTCTTCCAGACCGTACC NM_017434RefSeq chr15 + 45129993 45165578 DUOX1 53905 "dual oxidase 1, transcript variant 1"
GO:0050661|GO:0042554|GO:0042335|GO:0005509|GO:0019221|GO:0050665|GO:0051591|GO:0016324|GO:0004601|GO:0042446|GO:0006590|GO:0016174|GO:0016021|GO:0042744|GO:0006979|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127398_PI430048170 0.2655849760114261.02978492731694 0.41849276066118 0.3431926101587450.37697192722617 A A A 0.3000431852739590.328052953868621 0.383272052736275A A A LNCV6_127398_PI430048170 mRNA
GCCAATGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCT NM_001184691 RefSeq chr4 + 105895439 105971671 NPNT 255743 "nephronectin, transcript variant 3"
GO:0001657|GO:0001658|GO:2000721|GO:0005509|GO:0010811|GO:0097195|GO:0005578|GO:0005576|GO:0033631|GO:0034678|GO:0045184|GO:0005604|GO:0030485|GO:0045669|GO:0005178|GO:0007160|GO:0045987|GO:0030198|GO:0071356|GO:0010694|GO:0070374|GO:0070062|GO:0030511 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135809_PI430048170 0.53591548477343 1.50236284109743 0.617130597541725

1.07638567399626 2.39992073578353 A A A 1.23989362188834 0.56847936010456
1.06539951789359 A A A LNCV6_135809_PI430048170 mRNA
CCTGTTTGTTCCTGCTTCTCATGATTTTCCTGTAAATAAACACACTCTTAATTTGCCAAA NM_001289162 RefSeq chr16
+ 57694800 57731455 DRC7 84229 "dynein regulatory complex subunit 7, transcript variant 1"
GO:0005737|GO:0031514|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144135_PI430048170 0.2057201474430370.8315433235226679.88922619696408
10.1198829064996 9.89146870572577 P P P 9.9417884300651 10.3798405980703
10.3496673335426 P P P LNCV6_144135_PI430048170 mRNA
CATTTCTCTTCTGTACAGGACCCAATAAAAACTTCCTTATGATTTGCACCTGGCAAAAAA NM_207370RefSeq chr1
- 6247345 6260975 GPR153 387509 G protein-coupled receptor 153
GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139896_PI430048170 0.7035291971470091.01925949851164 9.32950291181583
9.33427160905326 9.30810076098402 P P P 9.24270165763849 9.43184623954823
9.20448172698899 P P P LNCV6_139896_PI430048170 mRNA
CCTGGGGACTCATTACTTCTGGTAGCTGGCTTTCTATAAAAATGGGTCAAACCCAAAAAA NM_032222RefSeq chr7
+ 30771416 30892387 FAM188B 84182 "family with sequence similarity 188, member B" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_133324_PI430048170 0.0923820864380832.60346269553181 13.1026159791016
13.1473067782883 13.2410658354115 P P P 12.6208749542026 11.0117199522925
11.1154624782727 P P P LNCV6_133324_PI430048170 mRNA
GTTCAACTGCTTACTCCCAAAACAGCCTTTTTGTAATTTATTTTTTAAGTGGGCTCCTGA NM_006010RefSeq chr3 +
51385236 51389397 MANF 7873 mesencephalic astrocyte-derived neurotrophic factor
GO:0006986|GO:0008150|GO:0048471|GO:0005783|GO:0002014|GO:0005634|GO:0008083|GO:0005615 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127910_PI430048170 0.0364546510082273 0.8299971290319848.68638082288357
8.57515636817432 8.50186020150854 P P P 8.85581750765702 8.85370555333284
8.86631471594444 P P P LNCV6_127910_PI430048170 mRNA
CATGTCTTATTCTTGCCCTTCCCCCAACCAGTTTGTTAATCAAACAATAAAAACATGTTT NM_012339RefSeq chr10
+ 69451469 69507667 TSPAN15 23555 tetraspanin 15
GO:0051604|GO:0009986|GO:0005886|GO:0097197|GO:0016021|GO:0019899|GO:0090002|GO:0008593|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130155_PI430048170 0.32012017968673 1.34590685833191 0.484524173448405
0.4904854145490921.33586927972239 A A A 0.3553078193296680.409136727849467
0.434834048565925 A A A LNCV6_130155_PI430048170 mRNA
ATGCTCATGAAAACCACCAATGTGATTGTAAACTTCTCCAGACAAACTTAACCTTTTGTT NM_001184832 RefSeq
chr15 + 48206300 48304078 SLC12A1 6557 "solute carrier family 12 (sodium/potassium/chloride
transporter), member 1, transcript variant 2"
GO:0048878|GO:0006821|GO:0007588|GO:0005886|GO:0001822|GO:0055085|GO:0016324|GO:0034220|GO:0016
020|GO:0006810|GO:0016021|GO:0006814|GO:0006813|GO:0070062|GO:0006811|GO:0008511 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144194_PI430048170 0.4025305310580281.53779640849616 1.83760738105894
0.4242656066580020.572768266788911 A A A 0.4187127682983360.525842203921307
0.472511512915514 A A A LNCV6_144194_PI430048170 mRNA
GGCTTACTGTAGTAGAAACTTTAGTTTTGATGATGCACAAAATAAACAGCAGTGGTTCTC NM_001018113 RefSeq
chrX - 14843406 14873062 FANCB 2187 "Fanconi anemia, complementation group B, transcript
variant 1" GO:0005515|GO:0006281|GO:0005654|GO:0043240 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_59445_PI430048170 0.2721769521986160.7483599049708765.09281435435793 4.2562684555222
5.28347234131723 P P P 5.13297940863299 5.57805803819186 5.33346905577417 P P P

LNCV6_59445_PI430048170 mRNA
GAAGTCTCTTCAATCCATGTTATTCTGATGACTCTTTGAAGAAAGAACTTGAACCTAAGT NM_001177949 RefSeq
chr12 - 101728647 101739472 SYCP3 50511 "synaptonemal complex protein 3, transcript variant 1"
GO:0005694|GO:0005634|GO:0003677|GO:0035093|GO:0007141|GO:0051301 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130711_PI430048170 0.0274394483537544 0.7206217018723574.09964671672064
3.93578612456678 4.02744514496864 P P P 4.68948358631112 4.39120394252007
4.38333530699131 P P P LNCV6_130711_PI430048170 mRNA
ATGGGGAAGGTTGCCCTGATAAGCAACTTAAATGAAAATAATAAATGTATTGTTTGGCCT NM_145177RefSeq chrY
- 2219513 2500974 DHRSX 207063 dehydrogenase/reductase (SDR family) X-linked
GO:0016491|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141301_PI430048170 0.0111440625399356 0.6398850743731158.78478913915707
8.80484299460337 8.92557199441078 P P P 9.40360844153496 9.35981356888782
9.66847725601234 P P P LNCV6_141301_PI430048170 mRNA
TAGGGGGTTTTTCCCATGGGATTGTGGTAGTCTGATTTTTCATATCTATTCAAATGTTAA NM_145115RefSeq chr7
+ 99616947 99632407 ZSCAN25 221785 zinc finger and SCAN domain containing 25
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137764_PI430048170 0.5327790878499430.8492489387534984.44213901056063
3.66805916246805 4.58209219072416 P P P 4.26861167527151 4.23503055909938 4.93844137748 P
P P LNCV6_137764_PI430048170 mRNA
GTGTGTTATAGAGATTCAGAGCAGGGAGGAAAAGTTAGGGTAGATTATTATTAAAGGGTT NM_017681RefSeq chrX
- 107123426 107206440 NUP62CL 54830 "nucleoporin 62kDa C-terminal like, transcript variant 1"
GO:0005643|GO:0017056|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135950_PI430048170 0.00204421021136201 1.60354519097251 8.43213457558036
8.64126711576732 8.45768443559331 P P P 7.69709510350415 7.85961222498537
7.92994728516011 P P P LNCV6_135950_PI430048170 mRNA
AAGGGAATGAGGATGATCTTTGGCTGTTGCTGCTCTTTATGAAGAATCTTATTTGTAACT NM_080752RefSeq chr20
+ 45857580 45879130 ZSWIM3 140831 "zinc finger, SWIM-type containing 3, transcript variant 1"
GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103221_PI430048170 0.0328039354505171 1.41823750195627 8.17320457108537
7.99351737446481 8.13593915857312 P P P 7.3859439138432 7.79527624449217
7.58629037112476 P P P LNCV6_103221_PI430048170 mRNA
AACCAAATCAAAAATTGGGGCACCCCGAAGCTCTTTCTGCTGGCACAGGCTCCCCTCAAC NM_003461RefSeq chr7
+ 143381266 143391111 ZYX7791 "zyxin, transcript variant 1"
GO:0005515|GO:0001725|GO:0005886|GO:0043149|GO:0050727|GO:0007267|GO:0005634|GO:0007165|GO:0005
737|GO:0005913|GO:0007160|GO:0005887|GO:0007229|GO:0016032|GO:0008270|GO:0007179|GO:0007155|GO:0
005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127027_PI430048170 0.64923589164418 0.5128488819366552.18915172403554
0.5868388674382992.06643843828819 A A A 3.8271947376966 2.12267178021627
0.525242866144167P A A LNCV6_127027_PI430048170 mRNA
CATTGCAGCAGCTGCAATGTACACCATAGTGACTCCCATGTTGAACCCCTTTATCTATAG NM_012363RefSeq chr9
- 122526357 122527293 OR1N1 NA "olfactory receptor, family 1, subfamily N, member 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142228_PI430048170 0.13762734795197 0.6990740069653454.81417662781888
3.97791945286566 4.34572386860023 P P P 5.11744522260562 4.91192186746786
4.75749739766613 P P P LNCV6_142228_PI430048170 mRNA
GTATACTTCTGTAACACCCCTCCTCTTCATTATCTGGCATGTACATCGATATTAAAAATA NM_001010922 RefSeq
chr1 - 113876813 113887547 BCL2L15 440603 BCL2-like 15 GO:0006915|GO:0005634|GO:0005829

. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141116_PI430048170 0.473751490626475 0.586734133865101 0.266821474726406
0.996625560406852 0.292573338348595 A A A 0.463438577365172 0.449982654881189
2.26123256726707 A A A LNCV6_141116_PI430048170 mRNA
AGGAGAAAATATGCTTGATTTTTATTTGGCAGGGGGGCTAGGTTGTATGGGAGTAAAAAA NM_004764 RefSeq
chr12_KI270833v1_alt + 14812 49260 PIWIL1 9271 "piwi-like RNA-mediated gene silencing 1,
transcript variant 1"
GO:0005515|GO:0010467|GO:0051321|GO:0003727|GO:0019901|GO:0007286|GO:0007275|GO:0034584|GO:0031
047|GO:0003729|GO:0006417|GO:0033391|GO:0005737|GO:0034587|GO:0043186|GO:0005844|GO:0005845 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67115_PI430048170 0.122929134009821 1.20108548189046 6.28040731364606 6.34287364197571
6.20121373268295 P P P 6.09881278741775 6.1302484751086 5.7806621548741 P P P
LNCV6_67115_PI430048170 mRNA
TTATCAAGGCCTCCACCTTCTCTAAGGGCAGTGACGTCTGGAGTTTTGGGGTGCTGCTGT NM_002419 RefSeq chr11
- 65597754 65614249 MAP3K11 4296 mitogen-activated protein kinase kinase kinase 11
GO:0005515|GO:0008219|GO:0008283|GO:0046330|GO:0042803|GO:0042802|GO:0004706|GO:0000187|GO:0005
737|GO:0046777|GO:0043525|GO:0043507|GO:0007017|GO:0005813|GO:0005874|GO:0007254|GO:0031434|GO:0
007256|GO:0018108|GO:0031435|GO:0007257|GO:0005524|GO:0048365|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128206_PI430048170 0.0506064296013062 1.55613082203029 5.74723793923233
5.58734443658657 5.60820173425988 P P P 5.26235861044786 5.03207328531212
4.68144279959783 P P P LNCV6_128206_PI430048170 mRNA
TATTTTCTATGCAAAGGTGATTCAGAGAATTTATATAAAGGCGGGCGAGGGGCAGCCGAG NM_024029 RefSeq chr19
- 10922767 10929012 YIPF2 78992 "Yip1 domain family, member 2" GO:0030133|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135469_PI430048170 0.162582249408853 0.563759235565077 2.90306070757521
3.54604375453923 4.40110285175269 A P P 4.01011785502499 4.89520946042997
4.67774604089847 P P P LNCV6_135469_PI430048170 mRNA
ATGCTGGCCAAAATTACAAATTACAGTTTGTTGCATCAGTTTCAAAAGCCATGCTTTCAT NM_001300791 RefSeq
chr5 - 132692626 132737578 KIF3A 11127 "kinesin family member 3A, transcript variant 1"
GO:0005515|GO:0008017|GO:0005813|GO:0006996|GO:0016939|GO:0072383|GO:0030507|GO:0072372|GO:0003
777|GO:0005524|GO:0005829|GO:0042384|GO:0019886|GO:0007596|GO:0060271|GO:0008152|GO:0008574|GO:0
015630|GO:0061024|GO:0005876|GO:0016887|GO:0070062|GO:0022008|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145211_PI430048170 0.471082694114908 0.539715607058001 0.302612278955468
0.58406807319291 0.420177131635705 A A A 2.31484620052309 0.394161976756706
0.324591389268759 A A A LNCV6_145211_PI430048170 mRNA
TTTTGAAGGTTCACTCTCCGAAGTTTTATCTGAGAAAAGAATGTATAGAGACGTTGGGAG NM_012183 RefSeq chr1
+ 63323058 63325126 FOXD3 27022 forkhead box D3
GO:0005515|GO:0000790|GO:0000977|GO:0003700|GO:0001892|GO:0000122|GO:0001829|GO:0001227|GO:0001
701|GO:0006351|GO:0003690|GO:0045944|GO:0005654|GO:0035019 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129049_PI430048170 0.202156643415531 1.18394626573336 7.39923989369045
7.24514004121428 7.14011791674109 P P P 7.26134730123765 6.97612012984302
6.78839882205103 P P P LNCV6_129049_PI430048170 mRNA
GTTTTTAACACATAGCGCCGTGCTGTAAATAAGCCCAGTGCTGCTGTAAATACAGGAAGA NM_001202234 RefSeq
chr12 + 52037714 52059507 NR4A1 3164 "nuclear receptor subfamily 4, group A, member 1,
transcript variant 4"
GO:0005515|GO:0010467|GO:0035924|GO:0006367|GO:0035767|GO:0003707|GO:0002042|GO:0005634|GO:0005

737|GO:0007173|GO:0045944|GO:0043401|GO:0004879|GO:0048011|GO:0031965|GO:0048015|GO:0003677|GO:0
044344|GO:0043565|GO:0007165|GO:0001938|GO:0008543|GO:0045087|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142352_PI430048170 0.7703537708850940.8708828378900662.61669703862355
1.21291448608356 0.543398710641691A A A 0.5483665844674262.28159014900147
2.33726246932573 A A A LNCV6_142352_PI430048170 mRNA
CTTTCTGTCTGCTATTGTATGAAGAATACTGATGTTTACCTGTATTTGCTTTGCTGTACT NM_020932RefSeq chrX +
76427652 76431353 MAGEE1 57692 melanoma antigen family E1
GO:0005515|GO:0008150|GO:0048471|GO:0016010|GO:0005886|GO:0045211|GO:0005634|GO:0030425 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129155_PI430048170 0.1336417523206740.9447650869801260.243021977305844
0.2738660028789280.313749545990429A A A 0.4270515135069930.337237660172664
0.310539427574661A A A LNCV6_129155_PI430048170 mRNA
TTTATGTTCAGAAAGTGATCCTGGTTTCTAGGTCTTTGCTCTGCAGGATCGGGATCAGAG NM_000815RefSeq chr1
+ 2019328 2030753 GABRD 2563 "gamma-aminobutyric acid (GABA) A receptor, delta"
GO:0007165|GO:0005230|GO:0030054|GO:0005887|GO:0004890|GO:0045211|GO:0034707|GO:0006810|GO:0007
268|GO:0005254 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145293_PI430048170 0.00278112991871518 0.5421624461623926.11371518687883
5.83982844269906 5.80126067952072 P P P 6.91407441344836 6.87126866908118
6.62279226168976 P P P LNCV6_145293_PI430048170 mRNA
TTTGTGAAATTGACCAGCCCCCTCTATAAAACTTACAGTCCCCCATTGGGAAACTGACCA NM_001291291 RefSeq
chr19 + 14073008 14075062 LOC113230 113230 "uncharacterized protein LOC113230, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128141_PI430048170 0.1270203197858120.2414721428879831.1812618163433
0.5923104779215950.495633428962287A A A 1.10045876711791 3.51836041459176
2.97655830393695 A P P LNCV6_128141_PI430048170 mRNA
CTCAAAAGAGACTCCTGTTTGGAAGCAAATTGTTGGTTTAACAGGACATACTTTAGATAT NM_001013620 RefSeq
chr12 + 38316754 38329726 ALG10B 144245 "ALG10B, alpha-1,2-glucosyltransferase"
GO:0016758|GO:0005886|GO:0016021|GO:0006488|GO:0044267|GO:0043687|GO:0018279 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_72073_PI430048170 0.6908752088191841.06037920001485 10.0283681883657 10.5084461499628
10.4463124117304 P P P 10.3487008637293 10.2276306430261 10.1940208553172 P P P
LNCV6_72073_PI430048170 mRNA
TACCAATCGTTCCTGGAATACAGGGAGGTGGTGGACGGCCTGGAGAAGGCCATCTACAAG NM_000754RefSeq
chr22 + 19941739 19969975 COMT 1312 "catechol-O-methyltransferase, transcript variant 1"
GO:0005515|GO:0014070|GO:0030424|GO:0006805|GO:0005886|GO:0007268|GO:0044281|GO:0032259|GO:0050
668|GO:0005829|GO:0005739|GO:0048609|GO:0032502|GO:0043197|GO:0045211|GO:0045963|GO:0032496|GO:0
007612|GO:0016036|GO:0070062|GO:0007565|GO:0000287|GO:0042493|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139537_PI430048170 0.8237977281187271.04095465479259 0.298441875524793
0.8562689101567971.20091881815345 A A A 0.3141210534821511.39593601482125
0.32668069014317 A A A LNCV6_139537_PI430048170 mRNA
ACTGCCCATGACCTGAAGGCTCCAGGTGGCTTTAAAGCGCTATGTTTACCAACTAAAAAA NM_153230RefSeq chr17
+ 6776232 6787646 FBXO39 162517 F-box protein 39 NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141262_PI430048170 0.1721811082468280.9564791452867870.24550949542643
0.2678100288804550.339393948934466A A A 0.4009899760649280.325901033777093
0.318632738882513A A A LNCV6_141262_PI430048170 mRNA
TGTTGGTGACAGGACATTTATCTAAACCTTTCCTCCGAACCTACCAAAGGGGTACAGTGA NM_001135686 RefSeq

chr19_GL949747v2_alt - 44313 55747 TARM1 NA "T cell-interacting, activating receptor on myeloid cells 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138506_PI430048170 0.3403428257754012.44221499361545 2.22696844398264 4.68240680852397 4.47585489321098 A P P 2.64115929336988 2.63635525365885 3.18367200702033 P P P LNCV6_138506_PI430048170 mRNA
CGTGGTACAGTGTTTTGAATTGTGTACTAATATCATTAAAGCATGGGATTTTAGTGGCTT NM_018356RefSeq chr5 + 31532265 31555058 C5orf22 55322 chromosome 5 open reading frame 22 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65782_PI430048170 0.28807978954846 1.12793041478533 7.84392419099191 7.76458722465548 8.1211622194944 P P P 7.78995938095487 7.57140074224553 7.85683062989928 P P P LNCV6_65782_PI430048170 mRNA
TTGTCGTTTGGAAATTCGGTCCAGTCTAAAATCAGAACGTCTACGGTCTGACAGTTATAT NM_001201965 RefSeq chr2 - 53669979 53786848 ASB3 51130 "ankyrin repeat and SOCS box containing 3, transcript variant 3" GO:0035556|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129822_PI430048170 0.5395120924821350.9232587250182578.05506773276385 8.10786490031403 7.95565252268318 P P P 7.88930418790531 8.36593686120061 8.17368979365893 P P P LNCV6_129822_PI430048170 mRNA
GGGGACATTGAAATGGATGTTCTCAGGTTGTATTTATTTCGGACAAATAAACTAGAGAAT NM_001286499 RefSeq chr15 - 64815629 64825668 PIF1 80119 "PIF1 5'-to-3' DNA helicase, transcript variant 1" GO:0051974|GO:0043141|GO:0000287|GO:0010521|GO:0017116|GO:0042162|GO:0051880|GO:0006310|GO:0005524|GO:0005739|GO:0032211|GO:0006281|GO:0000723|GO:0032204|GO:0032508|GO:0000784|GO:0033682 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138970_PI430048170 0.9338127952195271.00813066094388 0.529841431403756 0.2682937104760920.314046591367374A A A 0.4329419523416250.345016394843347 0.310118774046911A A A LNCV6_138970_PI430048170 mRNA
GGGAACTGGTGAATAATAATTAACTATTGTGAACAGTACACTATACCATACTTCCTTAGC NM_015718RefSeq chr6 - 155395367 155455903 NOX3 50508 NADPH oxidase 3 GO:0042554|GO:0009590|GO:0005737|GO:0001659|GO:0048840|GO:0016175|GO:0043020|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132358_PI430048170 0.7383979219943310.9838068700119810.487556321448214 0.4344010255848360.270737432878109A A A 0.3743647644394860.459178906282862 0.437219037254836A A A LNCV6_132358_PI430048170 mRNA
TCCTTCAGGAATGCTGAAGTGAAAAATGCCATGAGGAGATTTATTGGGGGAAAAGTAATT NM_001004726 RefSeq chr11 + 48263860 48264778 OR4X1 NA "olfactory receptor, family 4, subfamily X, member 1 (gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88772_PI430048170 0.0391471675106405 1.37781212573329 6.64407767455112 6.93538116750401 6.56632354446591 P P P 6.09955351677299 6.21583398078296 6.44795351368383 P P P LNCV6_88772_PI430048170 mRNA
ATCAAATCTCATTGCTTTGTAACGTACTCAACAGTAGAGGAAGCTGTTGCCACCCGCACA NM_014977RefSeq chr14 - 23058564 23095614 ACIN1 22985 "apoptotic chromatin condensation inducer 1, transcript variant 1" GO:0005515|GO:0006397|GO:0008380|GO:0048025|GO:0043065|GO:0005886|GO:0005730|GO:0006915|GO:0005634|GO:0003676|GO:0006921|GO:0005829|GO:0005737|GO:0016607|GO:0000166|GO:0045657|GO:0030218|GO:0030263|GO:0005654|GO:0019899|GO:0016887|GO:0035145 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137381_PI430048170 0.4189358038520951.0328178284909 0.618474542795602 0.5031366832760530.512312358289458A A A 0.4260050909630560.535747746260118 0.532602893020518A A A LNCV6_137381_PI430048170 mRNA
TGGCAGGTCTTTTCAACTTTCTGATTCATGAGAACAACCTTGTGAAGCTTTTCCCACCTC NM_022131RefSeq chr3 + 139935184 140568077 CLSTN2 64084 calsyntenin 2

GO:0000139|GO:0045211|GO:0005509|GO:0005789|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130695_PI430048170 0.1515739884015462.23816921151992 7.24187147847311 7.08452106007117 7.06110310686827 P P P 6.95969597875237 5.00431216655111 4.97098023730285 P P P LNCV6_130695_PI430048170 mRNA AGACGCTCACGCTGGCCAAGAACTACATCAAATCGCTGACGGCCACCATCCTGACCATGT NM_177455RefSeq chr7 + 98212253 98212959 BHLHA15 168620 "basic helix-loop-helix family, member a15"
GO:0048312|GO:0000977|GO:0019722|GO:0006851|GO:0007267|GO:0005634|GO:0010832|GO:0042593|GO:0001228|GO:0042803|GO:0006351|GO:0030968|GO:0007186|GO:0045944|GO:0007030|GO:0048469|GO:0042149 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127134_PI430048170 0.0559797265411206 0.7176087444948511 1.5508757405265 11.1451589147144 11.1041891019267 P P P 11.6082174679232 11.9478746891128 11.7021837263568 P P P LNCV6_127134_PI430048170 mRNA GGTCCTGGGCCAGCCAGGATACCTGATAATAAAAGATCATTGGGTGAACAGCGGAAAAAA NM_001199196 RefSeq chr19 + 19033577 19058178 ARMC6 93436 "armadillo repeat containing 6, transcript variant 1"
GO:0002244 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132624_PI430048170 0.2827367314471481.02928781258474 0.363335573297934 0.3646155724345980.447749859084848A A A 0.3507389018369360.324287778913597 0.376887677691979A A A LNCV6_132624_PI430048170 mRNA CCATTATGTTGTTTGGGGAACAAAGTGCTCATTAAACTTCTGTGGAATAAATCAAACGAA NM_001242589 RefSeq chr6 - 41279538 41286719 TREM1 54210 "triggering receptor expressed on myeloid cells 1, transcript variant 2"
GO:0072672|GO:0070945|GO:0005886|GO:0030593|GO:0005576|GO:0050900|GO:0035556|GO:0050755|GO:0007596|GO:0006959|GO:0045087|GO:0097110|GO:0004872|GO:0016021|GO:0002374 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143827_PI430048170 0.0928058231357879 0.7592550551329656.08890206008349 6.49724291643336 6.50378554334259 P P P 6.80858697693012 6.77668103842477 6.73354370450833 P P P LNCV6_143827_PI430048170 mRNA ACAGGATGCACAATGTTGTCAATCCTGGAAATGGTCTTTCTTTTTTGTAAGATATGTGAA NM_019843RefSeq chr22 - 31439358 31489888 EIF4ENIF1 56478 "eukaryotic translation initiation factor 4E nuclear import factor 1, transcript variant 1"
GO:0005515|GO:0005737|GO:0016607|GO:0016020|GO:0016605|GO:0008565|GO:0005634|GO:0015031|GO:0043231|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135591_PI430048170 0.1290614681280431.05988317965886 0.44856868787487 0.4753471044025170.49987360356589 A A A 0.3280809765454010.389162029465205 0.452599475859789A A A LNCV6_135591_PI430048170 mRNA AACTCTGTAACCCTCAGCAAGTTTCATTTTTGTCATGACAATGTAGGAATTGCTGAATTA NM_053276RefSeq chr2 + 36696689 36814794 VIT 5212 "vitrin, transcript variant 1"
GO:0030198|GO:0010811|GO:0005539|GO:0005614 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138098_PI430048170 0.3104543928468361.0898310535074 8.05083296630265 8.11358903433338 8.31314984430164 P P P 7.91180261558991 8.04046891645991 8.15585487387233 P P P LNCV6_138098_PI430048170 mRNA GAGTTTGTTTAACCACCTTAGGAGAAACATACTACAAAGTCATCAAGAATAAAGGTTCCA NM_003134RefSeq chr15 - 40035689 40039188 SRP14 6727 "signal recognition particle 14kDa (homologous Alu RNA binding protein), transcript variant 1"
GO:0005515|GO:0005786|GO:0010467|GO:0042493|GO:0003723|GO:0006614|GO:0030942|GO:0006613|GO:0008312|GO:0005730|GO:0005634|GO:0045047|GO:0006412|GO:0045171|GO:0005829|GO:0005737|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128671_PI430048170 0.6145533431604470.9003853564488180.371799524029549

0.4270463270981170.356634139887409A A A 0.9164670901342860.308970500472802
0.294118596285184A A A LNCV6_128671_PI430048170 mRNA
GAAAAATGAACTCCCTGAGAATGGCTGGATGGGAATCAGATAGTCTGCTTCCATTCAGGA NM_020754RefSeq chr3
+ 119294372 119419476 ARHGAP31 57514 Rho GTPase activating protein 31
GO:0043547|GO:0051056|GO:0017124|GO:0007264|GO:0005925|GO:0030027|GO:0005829|GO:0005096 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133431_PI430048170 0.0820924323241162 0.5977454106288815.6615609291074
5.65023105960324 5.96918342163633 P P P 6.3638203365518 6.11410430475716
6.92932177731666 P P P LNCV6_133431_PI430048170 mRNA
GTGTCCTATAAATTGTCACTACTTTTCCTGATCTGTATAACTGACTGCAAAGTGTTTGTT NM_001134363 RefSeq chr10
+ 110644396 110839471 RBM20 282996 RNA binding motif protein 20
GO:0008380|GO:0007507|GO:0006397|GO:0000166|GO:0003723|GO:0008270|GO:0005634|GO:0033120 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141836_PI430048170 0.00259959197069021 2.92017371288117 3.88164553333704
4.26608838219268 4.45239468037723 P P P 2.90934381530662 2.36969860835769
2.68985991322068 P A P LNCV6_141836_PI430048170 mRNA
GGGTGCACTGACAAAGTATAGAAGGTTCTAGGTATCTTAATGTGTGGATATTCTTAATTA NM_012240RefSeq chr12
+ 120302320 120313242 SIRT4 23409 sirtuin 4
GO:0005515|GO:0006342|GO:0034983|GO:0046322|GO:0070403|GO:0006974|GO:0003950|GO:0034979|GO:0005
739|GO:0006471|GO:0046889|GO:0072350|GO:0005759|GO:0008270|GO:0046676|GO:0006541 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_50007_PI430048170 0.5958440961333340.9254220919219694.82338881130751 4.6231072614818
4.96739428002631 P P P 4.62504882653258 4.97685033335669 5.12361688366777 P P P
LNCV6_50007_PI430048170 mRNA
GACCAGTACTTGGAGCTGTTAGAAAAGCAGAGGCTATACTTTAAGACTGTGAAAGAGTTC NM_019044RefSeq chr2
- 117915477 118014163 CCDC93 54520 coiled-coil domain containing 93 GO:0005515|GO:0006893
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144967_PI430048170 0.0954121964450765 0.54036563812431 2.53919678606479
1.98081567082999 2.61503414906145 A A A 2.67086536986694 3.2597498409217 3.7498225990905
P P P LNCV6_144967_PI430048170 mRNA
CACTGGAAGGATATTCTATAAGTGTATGGAATGTGGGAAAGCATTCATTGGTTTTATCAC NM_001164276 RefSeq
chr19 - 12271809 12294899 ZNF44 51710 "zinc finger protein 44, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144940_PI430048170 0.00978210378256826 1.36024607599307 14.4275568523441
14.5352774019662 14.5700418653215 P P P 14.179965314642 14.0787287375589
13.9360187415303 P P P LNCV6_144940_PI430048170 mRNA
CGTCTCGTTTTTGGCTAATTGATTGTCATTGGCTTTTTCCATAAAGTTTAGAAATCGTTC NM_031287RefSeq chr6 -
144094880 144095617 SF3B5 83443 "splicing factor 3b, subunit 5, 10kDa"
GO:0008380|GO:0010467|GO:0000398|GO:0005654|GO:0005634|GO:0005689 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127003_PI430048170 0.8276112031818240.9825727582930633.22542417444359 2.494767600406
2.20627375173345 P A A 1.26118236005654 2.66459676478084 3.48728629703054 A P P
LNCV6_127003_PI430048170 mRNA
TCCATACTAGAAGCTTCTTTTGGGTTCAATTAAAAAGAAAATAAGCTAGTCATTCTGGGC NM_018335RefSeq chr14
+ 102319750 102343174 ZNF839 55778 "zinc finger protein 839, transcript variant 1" GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127107_PI430048170 0.2709973616334461.30099498063968 0.61688006568865
0.7393400463751541.35179414658942 A A A 0.5625197207057840.563815452486892

0.554557419000713 A A A LNCV6_127107_PI430048170 mRNA
ATATTCCAACTCAGATTGAGCCCTACATTGTGCTGCACCTGGTCATACGGAGTTGAATCA NM_007329 RefSeq chr10
+ 122560664 122643736 DMBT1 1755 "deleted in malignant brain tumors 1, transcript variant 2"
GO:0005515|GO:0001833|GO:0005578|GO:0005576|GO:0015031|GO:0005615|GO:0035375|GO:0006898|GO:0051
607|GO:0030858|GO:0002221|GO:0005737|GO:0042589|GO:0045087|GO:0030855|GO:0030670|GO:0016032|GO:0
043152|GO:0070062|GO:0048306|GO:0005044|GO:0008329|GO:0019898 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132973_PI430048170 0.450772900602238 1.06108324811859 0.730035726891929
0.559118630246415 0.432518872759468 A A A 0.540491059853362 0.469353417619909
0.469559553467498 A A A LNCV6_132973_PI430048170 mRNA
CTGTGTTTCCTCATGGTGCTATAAATATTACCAAGACATGTCTAAGAAACAAAAGCACAT NM_001198815 RefSeq
chr6_GL000256v2_alt + 2306661 2336137 MUC22 100507679 mucin 22
GO:0022408|GO:0005886|GO:0010812|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136582_PI430048170 0.310825996770314 1.16816133829824 6.84221769737982
7.08024833009212 7.28578781081078 P P P 6.60596887722103 6.80011025579577
7.11681871607634 P P P LNCV6_136582_PI430048170 mRNA
CCTGTTGCCAGAAGTTCAGTCTCAGCAGATAGTAGAATTTGCACAGAATAAAAACCATAT NM_001031721 RefSeq
chr19 + 51927434 51945758 ZNF613 79898 "zinc finger protein 613, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144293_PI430048170 0.0510680195484842 0.653225564462288 4.27318078846965
3.83270844252128 4.35079777724685 P P P 4.76390336678258 4.86698559878342
4.71685064080741 P P P LNCV6_144293_PI430048170 mRNA
AACTTCTCTCAAGAATACCTTTTCCAGGAGCAGTACCTGTCCAAGGATTTGACACCAGCA NM_021937 RefSeq
chr3 + 128153456 128408646 EEFSEC 60678 "eukaryotic elongation factor, selenocysteine-tRNA-
specific"
GO:0005739|GO:0035368|GO:0000049|GO:0030529|GO:0001514|GO:0043021|GO:0003924|GO:0005634|GO:0005
525|GO:0003746 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130606_PI430048170 0.498269585896284 0.766878610837466 0.468683576701378
0.541918367583691 0.539237738329311 A A A 1.51528714220164 0.422199445072338
0.484846197340666 A A A LNCV6_130606_PI430048170 mRNA
GGCATGAGAAGCTGAAAAGAATGGGATCATTGGACTTAAAGCCTTAAATACCCTTGTAGC NM_033277 RefSeq
chr12 - 54630838 54634879 LACRT 90070 lacritin
GO:0070075|GO:0050679|GO:0008284|GO:0019722|GO:0051047|GO:0005518|GO:0033173|GO:0051533|GO:0050
731|GO:0005576|GO:0005615|GO:0001948|GO:0047485|GO:0034067|GO:0043237|GO:0001968|GO:0030141|GO:0
051281|GO:0008083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132536_PI430048170 0.601142138317316 1.05033620081136 9.45424702111348
9.39965187643519 9.52059645234028 P P P 9.11587854120423 9.51576198583018
9.49854976887941 P P P LNCV6_132536_PI430048170 mRNA
TGAAAGTCACTTTTATGAGCATCTGCCTTAATAAACAGACATTGATTCCCTTATCAGAAG NM_001145437 RefSeq
chr21_KI270872v1_alt - 50493 80944 LSS 4047 "lanosterol synthase (2,3-oxidosqualene-lanosterol
cyclase), transcript variant 4"
GO:0005811|GO:0006695|GO:0016020|GO:0005789|GO:0000250|GO:0044281|GO:0008202 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_110619_PI430048170 0.206100145740889 1.39524413670959 0.58274834953003
1.28154751953492 0.541150030870739 A A A 0.285027947555881 0.389018630353213
0.41225384046271 A A A LNCV6_110619_PI430048170 mRNA
CAAAATGGGAAAGAAAAACTGATTGCTTATCAACGAGAATTCCTTGCTTTGAAAGAACGT NM_012214 RefSeq

chr2 - 98619105 98731126 MGAT4A 11320 "mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A, transcript variant 1"
GO:0000139|GO:0006491|GO:0016021|GO:0044267|GO:0046872|GO:0070062|GO:0043687|GO:0018279|GO:0008454 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128661_PI430048170 0.0116278166612017 0.560448067582979 11.8781025917661 11.5661142285127 11.9548802285759 P P P 12.4826835260548 12.4949661818727 12.9132514611103 P P P LNCV6_128661_PI430048170 mRNA
ACCTCCCGTTGCGTCAAGTCTAAACCAAGATTATGTGACTTGCAATAAAGTTATTCAGAA NM_201555 RefSeq
chr2 - 105360825 105399224 FHL2 2274 "four and a half LIM domains 2, transcript variant 2"
GO:0005515|GO:0043066|GO:0030018|GO:0003713|GO:0005634|GO:0050681|GO:0044281|GO:0000122|GO:0015629|GO:0031430|GO:0001649|GO:0006351|GO:0042802|GO:0060347|GO:0055015|GO:0005654|GO:0008270|GO:0055014|GO:0009725|GO:0045893|GO:0005925|GO:0044255|GO:0030521|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_20395_PI430048170 0.340984522847473 0.907386955589239 5.61996071596483 6.02592141478021 5.7665775386936 P P P 5.86878305370691 6.03915908935344 5.94972004365983 P P P LNCV6_20395_PI430048170 mRNA
ATTGACTAAGGAAAGGAGAAAATGGAAGAAGAACCCCCTCCTGCTTAGATGCAGTCATTT NM_001291913 RefSeq
chr7 + 155962631 155966343 LOC389602 NA uncharacterized LOC389602 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94526_PI430048170 0.0113467263757434 0.583904352857148 5.65241617496701 5.67142019724021 5.86446990868859 P P P 6.2497908031864 6.62893387764746 6.6166544782695 P P P LNCV6_94526_PI430048170 mRNA
CTGTCGAAGAACTCAAGAAAAGATACGGTGGTTGATTTCCATTTTTGCTGAAATAATTGT NM_024604 RefSeq
chr12 - 47661931 47706061 RPAP3 79657 "RNA polymerase II associated protein 3, transcript variant 1" GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134932_PI430048170 0.223916789860857 0.944202694035667 9.5910328879298 9.74817392108268 9.72442420769971 P P P 9.72415566444636 9.78424748500981 9.80736933283453 P P P LNCV6_134932_PI430048170 mRNA
AATAGGCTTTCTAAGATGCTGCGATCCCGTTCTGCTGCCCGTAATAAAAATGCTCTCAGA NM_003347 RefSeq
chr22 + 21567546 21624034 UBE2L3 7332 "ubiquitin-conjugating enzyme E2L 3, transcript variant 1"
GO:0000209|GO:0005515|GO:0006511|GO:0004842|GO:0006355|GO:0016567|GO:0008283|GO:0016874|GO:0003713|GO:0000151|GO:0005634|GO:0005524|GO:0006351|GO:0097027|GO:0071385|GO:0005737|GO:0070979|GO:0071383|GO:0031398|GO:0051443|GO:0019899|GO:0031625|GO:0006464|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128325_PI430048170 0.016689910970819 1.52524026237688 4.51726151818867 4.84722709687583 4.59250836540135 P P P 4.23274222583224 3.83419847654706 4.05656878921914 P P P LNCV6_128325_PI430048170 mRNA
CACTCTTAATGGACAAAAAGAAAGAAAGGGGAGGGAGTAACAGGGATATGAGCTCTAGCC NM_001033930 RefSeq chr19 + 18571803 18577460 UBA52 7311 "ubiquitin A-52 residue ribosomal protein fusion product 1, transcript variant 1"
GO:0005515|GO:0002474|GO:0010467|GO:0006367|GO:0007220|GO:0019221|GO:0007249|GO:0019058|GO:0005765|GO:0006412|GO:0006413|GO:0006414|GO:0002756|GO:0007173|GO:0007219|GO:0002755|GO:0007179|GO:0006977|GO:0000209|GO:0005975|GO:0034134|GO:0005978|GO:0000122|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142732_PI430048170 0.124009767659449 1.05384887944409 0.435958340629114 0.463056880690512 0.477767978804178 A A A 0.329675571557632 0.379340934498101 0.438995218054578 A A A LNCV6_142732_PI430048170 mRNA
AAATTGAATTCTACTATTTATGTGATCCTTTTGGAGTCAGACAGATGTGGTTGCATCCTA NM_005099 RefSeq chr1

- 161189747 161199055 ADAMTS4 9507 "ADAM metallopeptidase with thrombospondin type 1 motif, 4"
GO:0005515|GO:0005578|GO:0005576|GO:0002020|GO:0005615|GO:0031012|GO:0001501|GO:0022617|GO:0030198|GO:0006508|GO:0008233|GO:0008270|GO:0004222|GO:0042742|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141711_PI430048170 0.000502897181715803 0.5814226218424898.5375451543476 8.53921575507073 8.6897162166563 P P P 9.26520077375523 9.39365709004306 9.45362124930557 P P P LNCV6_141711_PI430048170 mRNA
CCACCCCCAGTCGTCAGCTCCTTCCCTCATTTATTTTTGTTAAGTTGTGTGAATTATTTT NM_001270680 RefSeq chr10 + 72692618 72887694 MCU 90550 "mitochondrial calcium uniporter, transcript variant 3"
GO:0005515|GO:0005262|GO:0035786|GO:0019722|GO:0006851|GO:0005743|GO:0034704|GO:0042593|GO:0042802|GO:0005739|GO:0051561|GO:0031305|GO:0032024|GO:0015292 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110404_PI430048170 0.0496349737579952 0.7837350316155138.0175679627324 7.90464495705726 7.74468754282299 P P P 8.16919821105836 8.42681998757898 8.1192880389416 P P P LNCV6_110404_PI430048170 mRNA
CTGCCCAGACCTGCACCAGGGACCCCCGCCAGCCAGCTGCTGCAGGAGTTGCATGCTAAG NM_174905 RefSeq chr19 + 38403134 38409088 FAM98C 147965 "family with sequence similarity 98, member C" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74105_PI430048170 0.195008194682116 1.75361340093961 0.4728908032898811.74675998273365 1.36005987839045 A A A 0.5615845477960920.4243373692858950.434236606484222 A A A LNCV6_74105_PI430048170 mRNA
AGACGTCTCTTCAGGCAGTTCTGTGATACCAAACCCACTCTAAAGAGGCACATTGAATTC NM_182982 RefSeq chr4 + 2963615 3040747 GRK4 2868 "G protein-coupled receptor kinase 4, transcript variant 1"
GO:0038032|GO:0050254|GO:0005524|GO:0002031|GO:0030425|GO:0005829|GO:0031623|GO:0007165|GO:0004703|GO:0008277|GO:0043025|GO:0006468|GO:0005938 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138366_PI430048170 0.65231017714216 0.9694170246842630.549106438673392 1.49842074657005 3.11936929238952 A A P 2.53386776046439 1.77586127195137 2.06087441858535 A A A LNCV6_138366_PI430048170 mRNA
GGGTTTGGTTCTTGACTTTGTATTCCTTCCAATACAGCAATAAACTTTGTCTCCCTTTTT NM_003578 RefSeq chr12 + 53103489 53124539 SOAT2 8435 sterol O-acyltransferase 2
GO:0042632|GO:0033344|GO:0016746|GO:0005783|GO:0010742|GO:0034379|GO:0005903|GO:0030299|GO:0034736|GO:0015485|GO:0005789|GO:0016021|GO:0034435|GO:0000062|GO:0008203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139591_PI430048170 0.3096108530867830.9683237291348450.255014173334716 0.2714233951109850.362630911743059 A A A 0.3831972040463020.316896984130847 0.329776350646614 A A A LNCV6_139591_PI430048170 mRNA
TCTAACTCTCCTGTGCTAATCTCAGAGGGGTCACCCTCAATATATCTGGATTATCCGTGT NM_021189 RefSeq chr1 + 159171586 159203142 CADM3 57863 "cell adhesion molecule 3, transcript variant 1"
GO:0008104|GO:0005886|GO:0005911|GO:0034329|GO:0016021|GO:0007156|GO:0045216|GO:0042803|GO:0007157|GO:0034332 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135489_PI430048170 0.5727773658185590.9745797633183790.474865348259912 0.4926659061247080.335566185426985 A A A 0.4030326175267920.524055147999679 0.489842780907331 A A A LNCV6_135489_PI430048170 mRNA
TGTTGTTTAAGAAGTTCAGAAAGGTTGGAAGATGGGTTTATAAATAAAGAAGTGGAGTCC NM_203451 RefSeq chr13 + 36673911 36697838 SERTM1 400120 serine-rich and transmembrane domain containing 1 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143459_PI430048170 0.0848044631281261 0.6723459903663043.54419924230362 3.60495365650458 3.27060603355857 P P P 3.64533799965333 4.27757171052757

4.16139702890638 P P P LNCV6_143459_PI430048170 mRNA
CTCAGAGATGCTGCTTCATTTACCCAGGAGGTCATATTCTTTATATATATTTTTTGTTGC NM_003632 RefSeq chr17 +
42682613 42699993 CNTNAP1 8506 contactin associated protein 1
GO:0005515|GO:0017124|GO:0002175|GO:0030913|GO:0033270|GO:0009967|GO:0019227|GO:0007165|GO:0005
887|GO:0007411|GO:0048812|GO:0005070|GO:0008076|GO:0050884|GO:0007010|GO:0050885|GO:0004872|GO:0
008088|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129659_PI430048170 0.449123068955752 1.05229259855883 0.756189685740964
0.5479864007176220.582340505924799 A A A 0.440414696225472 0.628608284213455
0.598633898927943 A A A LNCV6_129659_PI430048170 mRNA
TTTATTTATACCTTAAGAAACCAGCAGGTGAAACAGGCCCTTAGGGAATTCACCAAAAAA NM_001005518 RefSeq
chr12 + 55400528 55401467 OR6C65 NA "olfactory receptor, family 6, subfamily C, member 65" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139893_PI430048170 0.17645587145189 1.12832736413749 0.324018775649179
0.61324921536162 0.481337006423149 A A A 0.304992288212717 0.277145935764234
0.327940330929918 A A A LNCV6_139893_PI430048170 mRNA
ACAATAATGTAGTAAAGGTGGACTCCGTTTAAAAAAGCACCACGTTCCGGGTGAGATGGA NM_005958 RefSeq chr4
- 186533654 186555383 MTNR1A 4543 melatonin receptor 1A
GO:0043235|GO:0005515|GO:0005886|GO:0007617|GO:0007187|GO:0005887|GO:0042562|GO:0007623|GO:0097
159|GO:0030828|GO:0008502 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135243_PI430048170 0.203222040732487 1.25214951892958 3.69416275177021
3.92408198648056 4.24345316318223 P P P 3.57704853083833 3.43254303617088
3.89295034636263 P P P LNCV6_135243_PI430048170 mRNA
GGAATAATGTGTTCAGAATGCTCTTTCTTTCCCCCAATAAAGCCCTTTATAGTGTTAAAA NM_018112 RefSeq chr9
+ 105694524 105776611 TMEM38B 55151 transmembrane protein 38B
GO:0031965|GO:0033017|GO:0005267|GO:0005634|GO:0016021|GO:0071805 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129884_PI430048170 0.468744812769078 1.21329195430066 2.4497207555496
2.71635143218296 2.97158040063963 A A P 2.99719399627772 2.44584118580392
1.56148638626573 P A A LNCV6_129884_PI430048170 mRNA
ATTTACATTTCTGTTACAGTCAGCCCAGGAGGTTACAGTGAGCTCTCCACTAAGAATCTG NM_007072 RefSeq chr3
+ 108302484 108378284 HHLA2 11148 "HERV-H LTR-associating 2, transcript variant 1"
GO:0005515|GO:0042104|GO:0003674|GO:0031295|GO:0016021|GO:0005575|GO:0001819 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_92969_PI430048170 0.682855483308828 1.0257357724859 0.276687186076751 0.284364130961963
0.490018874562987 A A A 0.335905266511771 0.287961778804376 0.32708295336843 A A A
LNCV6_92969_PI430048170 mRNA
AGTTGACTGGGAAGAAGCTTTGGTCTTCTGAAGACTTTAGCACTTTAAATAGTGACATGG NM_000153 RefSeq chr14
- 87933013 87993271 GALC 2581 "galactosylceramidase, transcript variant 1"
GO:0006683|GO:0006665|GO:0006687|GO:0005975|GO:0004336|GO:0044281|GO:0005764|GO:0070062|GO:0043
202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129961_PI430048170 0.925051088031293 1.00262911693778 7.93835970497629
8.15229498423959 7.85961222498537 P P P 8.25875979346909 7.9914851877399
7.63861028189978 P P P LNCV6_129961_PI430048170 mRNA
CAGAGATTGCTGCAGAAATAAAGTCTGCTTGGCTCTTGGGATATGTTGAGCCAGCTCTGT NM_024712 RefSeq chr16
+ 67199124 67204024 ELMO3 79767 engulfment and cell motility 3
GO:0006909|GO:0017124|GO:0005737|GO:0006915|GO:0005856 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144386_PI430048170 0.989434416383811 0.956631582009498 0.910397145135222
1.76251026371179 0.402824209535734 A A A 0.760102544789926 1.9887963417463

0.299628993082372 A A A LNCV6_144386_PI430048170 mRNA
TACAGCCATGTAAATCCTCCTGTACAAGCGAACACGGAATATATACATATATAACTCAAT NM_018008 RefSeq chr3
- 62369671 62373515 FEZF2 55079 FEZ family zinc finger 2
GO:0021542|GO:0008285|GO:0005634|GO:0000122|GO:0000978|GO:0046872|GO:0006351|GO:0016358|GO:0021
853|GO:0007413|GO:0045666|GO:0007411|GO:0021797|GO:0007626|GO:0045893|GO:0021902 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_80678_PI430048170 0.2945863298461420.8684850044457135.7413101690625 5.438438023227
5.97997992960048 P P P 5.97264123218978 5.88440711187197 5.96189932457265 P P P
LNCV6_80678_PI430048170 mRNA
TTAGTCAAGATGAAAACTATCACCATCTCCCTTACGCACAGCAGCAAGCAATAGAGGAGC NM_194328 RefSeq chr9
- 36336400 36400923 RNF38 152006 "ring finger protein 38, transcript variant 2"
GO:0004842|GO:0016567|GO:0016874|GO:0036126|GO:0008270|GO:0005654|GO:0005634|GO:0008584 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127521_PI430048170 0.2694392725306513.99819208911048 0.295795774496334
3.43818000907159 1.30152599665408 A P A 0.2908969083925850.253536848402928
0.285719665624847 A A A LNCV6_127521_PI430048170 mRNA
ATCATTTACGGGGTGAGAACCCAAGAAATTAAGCAGGGAATGCAGAGGTTGTTGAAGAAA NM_001003443
RefSeq chr11 + 5947346 5948294 OR56A3 NA "olfactory receptor, family 56, subfamily A, member 3"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102153_PI430048170 0.0257203344133188 1.68096335331781 5.31610385621183
4.91611409389125 4.79859699664937 P P P 4.48743457552779 3.98539052384484
4.31815026492287 P P P LNCV6_102153_PI430048170 mRNA
TTCCAGTTTCCGAACAAAACATTTCGGCAATGGTGAGGGCTTCGATCCCTTCTCTGATTT NM_001244808 RefSeq
chr3 - 70954713 71583753 FOXP1 27086 "forkhead box P1, transcript variant 3"
GO:0005515|GO:2001182|GO:0006366|GO:0000981|GO:1900424|GO:0005634|GO:0050681|GO:0035926|GO:0046
872|GO:0072619|GO:0045655|GO:0002903|GO:0032496|GO:0006357|GO:0032680|GO:0030316|GO:0050727|GO:0
060766|GO:0048661|GO:0010595|GO:0043565|GO:0036035|GO:0042116|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_108377_PI430048170 0.0118828736680966 0.8790825644601789.71599955816243
9.76491669497942 9.73932824130828 P P P 9.92519900108759 9.87502641516554
9.97644008688198 P P P LNCV6_108377_PI430048170 mRNA
GGGCATCGTGGAGCTTTTGGTGTCCTTGGGTGCTGATGTCAATGCTCAGGAGCCCTGTAA NM_020529 RefSeq chr14
- 35401509 35404754 NFKBIA 4792 "nuclear factor of kappa light polypeptide gene enhancer in B-cells
inhibitor, alpha"
GO:0005515|GO:0042994|GO:0032403|GO:0042802|GO:0002756|GO:0031072|GO:0002755|GO:0042127|GO:0031
663|GO:0031625|GO:0000060|GO:0033256|GO:0045746|GO:0038124|GO:0010745|GO:0038123|GO:0034134|GO:0
070431|GO:0002224|GO:0043392|GO:0032270|GO:0045087|GO:0008139|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_102107_PI430048170 0.4421767414511881.09764258508565 4.55186193586023
4.66148492185219 4.6624517206268 P P P 4.74469904514868 4.48083349139338
4.19833345234939 P P P LNCV6_102107_PI430048170 mRNA
ATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTGTGTGTC NM_175739 RefSeq chr14 -
94462720 94476333 SERPINA9 327657 "serpin peptidase inhibitor, clade A (alpha-1 antiproteinase,
antitrypsin), member 9, transcript variant 1" GO:0010951|GO:0005737|GO:0016020|GO:0004867|GO:0005615 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60975_PI430048170 0.4204728130166941.17440678979011 11.1339856790273 11.5332306774746
11.8356630588942 P P P 11.2032882463497 11.2103867334643 11.4625114747333 P P P
LNCV6_60975_PI430048170 mRNA
TTTCTACTCCAGTCCAATGTAACTATTTAGCCCTGGATTATACATACTGTCCAATTTTCA NM_002788 RefSeq chr14 +

58244804 58272009 PSMA3 5684 "proteasome (prosome, macropain) subunit, alpha type, 3, transcript variant 1"
GO:0005515|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0004298|GO:0034641|GO:0005737|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0005839|GO:0000502|GO:0043066|GO:0006521|GO:0051437|GO:0042590|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141566_PI430048170 0.3489222483733020.8224170610622780.517506002033868 0.7029921389211540.625534218915567A A A 1.05650457102045 0.450673372772494 1.10387000111604 A A A LNCV6_141566_PI430048170 mRNA
AAGTTGGCAGTTTTGGTGCCAAACCCCAAATCTCCAAAGAGACATACCAGGCAAGACAAA NM_005220RefSeq chr17 - 49990004 49995224 DLX3 1747 distal-less homeobox 3
GO:0043565|GO:0001077|GO:0003700|GO:0001568|GO:0071895|GO:0045944|GO:0003682|GO:0042475|GO:0005634|GO:0001890 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131839_PI430048170 0.0535820000620966 0.6734191799147721 0.7996218803924 10.8693862786493 11.2335583649118 P P P 11.2965579734154 11.4725586792104 11.8310281664394 P P P LNCV6_131839_PI430048170 mRNA
TCAATGTTGGACCCTTTTTGTGAAGATTGGTCTCTGTGGTGTGATTCTCTTCCCAGGTGT NM_005687RefSeq chr2 - 222571442 222656355 FARSB 10056 "phenylalanyl-tRNA synthetase, beta subunit, transcript variant 1"
GO:0010467|GO:0005737|GO:0000287|GO:0016020|GO:0006432|GO:0003723|GO:0004826|GO:0006412|GO:0005524|GO:0006418|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135830_PI430048170 0.3062814363908241.10415778486011 9.49669235957042 9.83070388319935 9.73588339251484 P P P 9.47468784121988 9.5209443386692 9.65301853400842 P P P LNCV6_135830_PI430048170 mRNA
GGTTGGGGGGCACAAAGTTAACATATTCTTGGTTAACCATGGTTAAATATGCTATTTTAA NM_001253876 RefSeq chr2 - 106093302 106138881 UXS1 80146 "UDP-glucuronate decarboxylase 1, transcript variant 3"
GO:0005739|GO:0051262|GO:0032580|GO:0048040|GO:0033320|GO:0070403|GO:0016021|GO:0042803|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128552_PI430048170 0.0457081580977692 1.11484034726655 0.731962463028869 0.8266534252387470.707430551770906A A A 0.6060456101541190.606964251881138 0.585186421673088A A A LNCV6_128552_PI430048170 mRNA
GGAGCTGTATCCCCAGTAGAAAAAACATTTTAATCACTCTAATATAACTCTGGATGAAAC NM_001278939 RefSeq chr7 + 74027788 74069906 ELN2006 "elastin, transcript variant 13"
GO:0005515|GO:0022617|GO:0007585|GO:0030198|GO:0008283|GO:0008015|GO:0005578|GO:0009887|GO:0005576|GO:0071953|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128134_PI430048170 0.1726785435739990.875382053272048 3.44454844950147 3.30115767599737 3.62434406321872 P P P 3.64322341963422 3.7717470407515 3.53999227223307 P P P LNCV6_128134_PI430048170 mRNA
TTTGGGCAGAATATGTGCTGGTCAATAAATGTGTCAGAAAATGAGTAATTTTCTGACTGC NM_016153RefSeq chrX + 149774067 149776859 HSFX1 100506164 "heat shock transcription factor family, X linked 1"
GO:0043565|GO:0005515|GO:0006355|GO:0005737|GO:0003700|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70194_PI430048170 0.6034932583100881.0888244579545 9.51508225760486 9.54933398393934 9.9599080186415 P P P 9.25952868705252 9.47687028725038 9.89080742773923 P P P LNCV6_70194_PI430048170 mRNA
GGTGTTTTGCTTGCAGCAGAGAGACGCAACATCCACAAGCTTCTTGATGAAGTCTTTTTT NM_002789RefSeq chr15 + 78540404 78549221 PSMA4 5685 "proteasome (prosome, macropain) subunit, alpha type, 4, transcript variant 1"
GO:0005515|GO:0002474|GO:0010467|GO:0005886|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0043231|GO:0005829|GO:0004298|GO:0034641|GO:0005737|GO:0000082|GO:0000932|GO:0016032|GO:0090090|GO:0

070062|GO:0006977|GO:0000209|GO:0043066|GO:0000502|GO:0005839|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144301_PI430048170 0.0935024913539296 0.6552552346917156.63471416556109 6.63234960718789 6.85709168099532 P P P 7.01494866823622 7.16045737564971 7.69751031778907 P P P LNCV6_144301_PI430048170 mRNA GCTCACCTCCATGCAAAGACTTCAGTTTTAAAACATTATTTGCCTAAAATTAGCATTGTG NM_001011663 RefSeq chr10 - 103302795 103351134 PCGF6 84108 "polycomb group ring finger 6, transcript variant 1"
GO:0035102|GO:0031519|GO:0005515|GO:0003700|GO:0000977|GO:0008270|GO:0005634|GO:0000122|GO:0045892|GO:0003677|GO:0001227|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133934_PI430048170 0.8080376599803720.6309019591508362.35818247704941 0.9088456929800241.25701625215055 A A A 0.3453476791169883.41715688382716 1.55495428813467 A P A LNCV6_133934_PI430048170 mRNA AAGAGTGAACATGTACACAAAGTGCAATTGGAAGTGGGCTACAAATTTGGCCCCCAGCTT NM_005065 RefSeq chr14 - 81471546 81533861 SEL1L 6400 "sel-1 suppressor of lin-12-like (C. elegans), transcript variant 1"
GO:0005515|GO:0034976|GO:0007219|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68380_PI430048170 0.0155002216704351 1.97091912039524 2.65917885914225 2.91481946000528 3.11494226681021 A A P 1.940876112592 1.88130863232611 1.96474399971857 A A A LNCV6_68380_PI430048170 mRNA ATTTGGTGCAACAAAGACTGGGCCATCCCCGGCACTAATAGGGGCAAGGCCTCTGGGAATNM_001100873 RefSeq chr16 - 81053496 81077267 C16orf46 123775 "chromosome 16 open reading frame 46, transcript variant 1" GO:0005737|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134449_PI430048170 0.2785769710936221.31837048551311 3.60452848036147 4.12037101911783 4.42817422266657 P P P 3.84207623674933 3.85998445201843 3.30554484613604 P P P LNCV6_134449_PI430048170 mRNA GGTATTAATGAATCTAGTGCCTTTTAAATGTATCCCACGTTTTGTTCCCTACCATCTTTT NM_001193311 RefSeq chr7 + 40134975 40860767 SUGCT 79783 "succinyl-CoA:glutarate-CoA transferase, transcript variant 1"
GO:0005739|GO:0047369|GO:0008152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127511_PI430048170 0.2002865535129270.7277597742060482.83316782854335 2.36643478087087 1.88352026723316 A A A 2.95146911943944 2.93283344538384 2.71729951402007 P P P LNCV6_127511_PI430048170 mRNA TGCGACATGCCCTGCCTGAACAGGTGCTCAATAAATCCAAGTTTCCTTCTCTTGAAAAAA NM_152888 RefSeq chr8 - 138588234 138914006 COL22A1 169044 "collagen, type XXII, alpha 1"
GO:0005581|GO:0030198|GO:0005578|GO:0005788|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142023_PI430048170 0.8786118259637740.9029528385449070.581695910073423 1.23452799147347 1.3518626349554 A A A 0.5530580054067841.87555224078254 0.966084149399965 A A A LNCV6_142023_PI430048170 mRNA CGCCCATTCTGTATGGTGAGCACATAATAGGTACTTATTTAGTGTTTGTCGAATTAATAA NM_181657 RefSeq chr14 + 24313106 24318036 LTB4R 1241 "leukotriene B4 receptor, transcript variant 1"
GO:0006955|GO:0006954|GO:0006936|GO:0007186|GO:0005886|GO:0000166|GO:0005887|GO:0007200|GO:0006928|GO:0001632|GO:0004974 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142004_PI430048170 0.0417520792705067 0.6393392649319945.86555578628125 5.71106184959948 6.2027333663761 P P P 6.284276261678 6.58242199856084 6.84005541975754 P P P LNCV6_142004_PI430048170 mRNA GACACCCTGGAATAACCTTTTGGGAATGATGCCACAGAATAAAGTTCACTCTTAACTTTT NM_001286414 RefSeq chr15 + 43371058 43407095 TUBGCP4 27229 "tubulin, gamma complex associated protein 4, transcript variant 1"
GO:0005813|GO:0005874|GO:0005829|GO:0000922|GO:0006461|GO:0016020|GO:0000086|GO:0007020|GO:0015

630|GO:0005200|GO:0000278|GO:0055037|GO:0008274 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127319_PI430048170 0.0934379434526002 1.08419082585204 0.608737657998101
0.681805153660499 0.643687827057825 A A A 0.612849904891853 0.480462121797467
0.488123176129508 A A A LNCV6_127319_PI430048170 mRNA
GCTGCAAACCACACCTTCTCTTTCTTATGTCTTTTTACTACAAACTACAAGACAATTGTT NM_002411 RefSeq chr11 +
62270154 62273157 SCGB2A2 4250 "secretoglobin, family 2A, member 2"
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143079_PI430048170 0.0719900481568060 .73829202960154 8.43737396109365
8.62039091007338 8.74518617301627 P P P 8.9674014085805 8.82525260470326
9.29841046088057 P P P LNCV6_143079_PI430048170 mRNA
GTAACAAATTTATACAGGACAGTGGTACAGAAATACATCTTTGCTCTGAGAATACAGCAA NM_003943 RefSeq chr4
+ 76306025 76311130 STBD1 8987 starch binding domain 1
GO:0005515|GO:0006936|GO:0016020|GO:0005887|GO:2001070 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132294_PI430048170 0.0378069642006666 1.15745311976928 9.89485284522404
9.79859322214948 9.93135328315646 P P P 9.73133925690199 9.55723449879153
9.70068323907585 P P P LNCV6_132294_PI430048170 mRNA
TTCAGCTTCAAAGAAGACACTTTGCTGTTGATAGCTGAGGTTATGGGAGAAGATATCCCA NM_032847 RefSeq chr8
- 123219955 123241398 C8orf76 84933 chromosome 8 open reading frame 76 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_129225_PI430048170 0.809550235592782 1.30074232042267 2.16349159393038
0.399025039194405 0.305794994566587 A A A 0.615991094832815 1.39388018268988
0.319339714617279 A A A LNCV6_129225_PI430048170 mRNA
TAGTCCAAGAGGAGAGAGAGGAATAGGTTGCAAGCTAGAAAATGGATTTCTGCAGGACAG NM_003696 RefSeq
chr11 - 6794524 6795908 OR6A2 8590 "olfactory receptor, family 6, subfamily A, member 2"
GO:0050911|GO:0007608|GO:0007165|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145706_PI430048170 0.0932303640998895 0.778711356044453 9.27432153931442
9.00221165732059 9.383185073607 P P P 9.3656356778252 9.5992094498687
9.77463740242204 P P P LNCV6_145706_PI430048170 mRNA
GTTCTGCTGTGTGTGTGTGTATTTTACAAAATATGTATGGTTTCTGTTCAGCTCTTTTCA NM_024654 RefSeq chr1 -
6521346 6554598 NOL9 79707 nucleolar protein 9
GO:0051731|GO:0016310|GO:0000460|GO:0016020|GO:0003723|GO:0005730|GO:0005524|GO:0000448 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136754_PI430048170 0.118317841433791 0.963345230869503 0.413312267228652
0.417724359627504 0.349238517186543 A A A 0.42824925331984 0.469340392040369
0.445028137092358 A A A LNCV6_136754_PI430048170 mRNA
TGGACAAAGTTGAAGGCCTTCTGTCTGAATTGGCCAGGGGCCAATGAAAGCCAAAAAGCT NM_207511 RefSeq chr9
+ 137027463 137036782 C9orf139 401563 chromosome 9 open reading frame 139 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145114_PI430048170 0.0277624399039761 .07242205538255 0.348482215426182
0.406961271251265 0.333974581572645 A A A 0.248923651582461 0.285725484435684
0.252906324435095 A A A LNCV6_145114_PI430048170 mRNA
GGCCTGTGATTATCTTGGGAAGCAGAGTGATTCATGCTAGAAAACATTTAATATTGATTT NM_000015 RefSeq chr8
+ 18391244 18401213 NAT2 10 N-acetyltransferase 2 (arylamine N-acetyltransferase)
GO:0006805|GO:0004060|GO:0044281|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131106_PI430048170 0.655724345461113 1.07804807053037 3.89392584554792 4.0226014367237
4.26402892142778 P P P 3.34717215508423 3.95338444969003 4.39368996345259 P P P
LNCV6_131106_PI430048170 mRNA

GATCTGTGCAATAAAGTGTTTGCAGTCTTATTTTCTCTAAGAAATTCCTTATGGACGTCA NM_001164664 RefSeq chr5 + 66596347 67169595 MAST4 375449 "microtubule associated serine/threonine kinase family member 4, transcript variant 3" GO:0005737|GO:0000287|GO:0004674|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140012_PI430048170 0.0269123728761484 0.4930248728900898.71261274567798 9.02834081238841 8.8406405175241 P P P 9.46152132917256 9.93465549719704 10.1751998849795 P P P LNCV6_140012_PI430048170 mRNA
ACCCCACTTTAGAAAGGGTCGTCACTCCTTTAATCCTCTACTCAACAATGTACTCTTTTA NM_004925 RefSeq chr9 - 33441153 33447633 AQP3 360 aquaporin 3 (Gill blood group) GO:0005215|GO:0005886|GO:0034219|GO:0009992|GO:0033280|GO:0002684|GO:0070295|GO:0016323|GO:0045616|GO:0005737|GO:0034220|GO:0005911|GO:0015250|GO:0015793|GO:0006810|GO:0042476|GO:0015204|GO:0006833|GO:0015254|GO:0032526|GO:0007588|GO:0055085|GO:0003091|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142560_PI430048170 0.3969689409065071.67660789029256 0.407077692765496 0.4243816256064541.95573151362136 A A A 0.3698740380307920.366124665167458 0.404743843016727 A A A LNCV6_142560_PI430048170 mRNA
GCAGCTAATGTAATAAGCACTCATGTTATTAAAGGTTTTGCCTTGTCGTAACCAACCGAA NM_006539 RefSeq chr16 + 24255552 24362416 CACNG3 10368 "calcium channel, voltage-dependent, gamma subunit 3" GO:0030666|GO:0005886|GO:0005245|GO:0032281|GO:2000311|GO:0070588|GO:0007268|GO:0006816|GO:0005891 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111484_PI430048170 0.3865716646143661.58040745166881 1.74471151150338 0.4143746089751590.3267662360613 A A A 0.30593901183051 0.32997590786461 0.338189237988607 A A A LNCV6_111484_PI430048170 mRNA
CCCCTCTTTGAAGAGTCTAAAATATCAGATGTATCCCTTGTTTCTAACAGTTTTTCTATC NM_001102609 RefSeq chr5 + 170232916 170246231 C5orf58 133874 chromosome 5 open reading frame 58 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_5540_PI430048170 0.0709412354224229 0.7430281991423438.04115781698478 8.09420545026133 8.49109280947887 P P P 8.50625937474045 8.61927965932548 8.81276501581661 P P P LNCV6_5540_PI430048170 mRNA
TAAAAAGGCAGATACTGATCTGTGCCTTGCTACGTGGGAGTCATTCCTTACATCACAGAC NM_015976 RefSeq chr1 + 98661679 98760500 SNX7 51375 "sorting nexin 7, transcript variant 1" GO:0005515|GO:0016050|GO:0035091|GO:0015031|GO:0030659|GO:0019898|GO:0006897|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132867_PI430048170 0.4157264497777610.3350136788609960.345551916141075 0.3740518032727080.331228815393044 A A A 3.14354076656381 0.381385086764254 0.352850276925042 P A A LNCV6_132867_PI430048170 mRNA
TGTTCTACTTCACACAGTGGTCGAGAGGCTAAAATAAAATGAAAAGCATAAAACTCTCTG NM_176822 RefSeq chr11 + 7020468 7071526 NLRP14 338323 "NLR family, pyrin domain containing 14" GO:0007275|GO:0007283|GO:0005524|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116644_PI430048170 0.0128534402457487 0.5665584895936795.9300834041359 5.59918283231126 6.09855683365281 P P P 6.58804362011818 6.6154246597925 6.90539542949012 P P P LNCV6_116644_PI430048170 mRNA
TTGCTGGAATTGTTGTGGATAAGCCACCTTCTACTATGCAATTTGAAGATGATGATCATG NM_016824 RefSeq chr10 + 110007952 110135565 ADD3 120 "adducin 3 (gamma), transcript variant 1" GO:0005516|GO:0005737|GO:0000794|GO:0016020|GO:0005886|GO:0005911|GO:0005200|GO:0005654|GO:0003779|GO:0005856|GO:0005938 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143773_PI430048170 0.4890808726409461.02290637393325 0.337173165798253 0.3386299003976550.448183829254973 A A A 0.3490646659370320.312818185594228 0.366398503108302 A A A LNCV6_143773_PI430048170 mRNA

ATTTCCCTAAAGTGAATGGTCATTGTCTAATGATTCGATGCGCTACAGTCTACAGTGTTA NM_003604RefSeq chrX - 108732496 108736377 IRS4 8471 insulin receptor substrate 4 GO:0008286|GO:0005515|GO:0007165|GO:0005886|GO:0005158|GO:0005070|GO:0009967|GO:0004871|GO:0043548|GO:0019216|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_83348_PI430048170 0.00217956460595542 0.67343323932358 3.90791454562829 3.99262055903217 3.8924431627719 P P P 4.50294952158849 4.40474613607078 4.59239314863266 P P P LNCV6_83348_PI430048170 mRNA

GTCCCAGAGACAACGAGATGAACTAATGAAGAATTAGATAAAAAGTATGCTGGTCTTTTG NM_000430RefSeq chr17 + 2593628 2685615 PAFAH1B1 5048 "platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)" GO:0051219|GO:0008017|GO:0000235|GO:0005515|GO:0008090|GO:0009306|GO:0034452|GO:0017145|GO:0000132|GO:0019226|GO:0042803|GO:0007405|GO:0046329|GO:0047496|GO:0043274|GO:0031023|GO:0050885|GO:0043025|GO:0007611|GO:0032319|GO:0005938|GO:0021895|GO:0070062|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_139014_PI430048170 0.0560090585481827 0.482111489742355 9.81291854904619 9.71089824907779 10.0747887904741 P P P 10.3272633275855 11.0225705621707 11.2737584048602 P P P LNCV6_139014_PI430048170 mRNA

GAATGGGTGATTGGAGATTATTAGATTCTAGGTTAACTTCTACCACTTTACCCTAATACA NM_005914RefSeq chr8 + 47960202 47978159 MCM4 4173 "minichromosome maintenance complex component 4, transcript variant 1" GO:0005515|GO:0042555|GO:0005634|GO:0005524|GO:0006260|GO:0000082|GO:0006271|GO:0004003|GO:0003697|GO:0016020|GO:0006270|GO:0006268|GO:0005654|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135375_PI430048170 0.14131761059688 1.08542621127609 0.504901362208121 0.652950377289971 0.58290599674933 A A A 0.370305659587007 0.479436670415631 0.535182709329323 A A A LNCV6_135375_PI430048170 mRNA

CCCACCTTCTACTGGGCATAATTATATCTTAATCATATATGGAAATGTGCAACATATGGT NM_024021RefSeq chr11 + 60280540 60308972 MS4A4A 51338 "membrane-spanning 4-domains, subfamily A, member 4A, transcript variant 2" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135234_PI430048170 0.00015174052116944 4.47900207349512 4.70704506437444 4.60591967970117 4.32894043656359 P P P 2.57525818826365 2.2558981371161 2.32745455993872 P A P LNCV6_135234_PI430048170 mRNA

TACTGTAATTGGCTCTTAAGGCTTGAAGTAACCTTATAGGTTACTCATAAGGCATATACA NM_000433RefSeq chr1 - 183555561 183590604 NCF2 4688 "neutrophil cytosolic factor 2, transcript variant 1" GO:0045730|GO:0005515|GO:0002474|GO:0006801|GO:0045777|GO:0032870|GO:0005829|GO:0005737|GO:0043525|GO:0032496|GO:0032010|GO:0090382|GO:0042554|GO:0048010|GO:0014823|GO:0051701|GO:0001669|GO:0042493|GO:0007568|GO:0005730|GO:0042590|GO:0009055|GO:0008022|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_129866_PI430048170 0.0335875095448330 0.392154769905758 9.3474945505063 9.51794182773371 9.81187747516275 P P P 10.3867757464446 10.7699689416895 11.4187384597151 P P P LNCV6_129866_PI430048170 mRNA

GAGAGGTGTCTTAAGCTGTAGGCTTTTCTTTGTACTGCATTTATAGAGATTTAGCTTTAA NM_001113546 RefSeq chr12 - 50175779 50283570 LIMA1 51474 "LIM domain and actin binding 1, transcript variant 1" GO:0005515|GO:0001725|GO:0005886|GO:0015629|GO:0032154|GO:0031529|GO:0003785|GO:0030835|GO:0005737|GO:0051015|GO:0008270|GO:0005925|GO:0051017 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_66279_PI430048170 0.0122820460855992 0.647308426138143 5.19029852820723 5.00187511100204 4.81599256835992 P P P 5.64279758467133 5.51934778982623 5.74395337918626 P P P LNCV6_66279_PI430048170 mRNA

TAAAGGAAATGTGCATAGTTGACGAACCTTTAGAGGAATTCACTTCAAGGCATAGCTTGG NM_002518RefSeq chr2

+ 100820150 100996825 NPAS2 4862 neuronal PAS domain protein 2
GO:0005515|GO:0045475|GO:0003700|GO:2001020|GO:0051879|GO:0005634|GO:0044281|GO:0045739|GO:0046872|GO:0005829|GO:0042745|GO:0045944|GO:0060548|GO:0046983|GO:0004871|GO:0044255|GO:0005667|GO:0001047|GO:0007417|GO:0003677|GO:0006974|GO:0006351|GO:0032922|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128742_PI430048170 0.4091536329435230.9268787388157731.8050899440121 11.8136509420353 11.7458242293415 P P P 11.7159420479891 12.059631416373 11.8981545538253 P P P LNCV6_128742_PI430048170 mRNA
GTCTCCTCTCTGGGAAACGTCCCTTGTCAGGAGACGGCTCTTCTTTGAAATGAGGTCATT NM_003249RefSeq chr19 + 2785507 2813601 THOP1 7064 thimet oligopeptidase 1
GO:0035556|GO:0005515|GO:0042277|GO:0005737|GO:0006508|GO:0004222|GO:0046872|GO:0006518 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127772_PI430048170 0.1005749865049850.7818581417616029.71511745487387 9.6268632979875 9.95894351927194 P P P 10.2160741414469 9.86388676469233 10.2737222001398 P P P LNCV6_127772_PI430048170 mRNA
GTGGCAAAGATAACCAAATGTCTGGCTGTTTGCTTTTTGACCATATCAATAAACTTTTAC NM_032121RefSeq chrX - 77826364 77895568 MAGT1 84061 magnesium transporter 1
GO:0015693|GO:0050890|GO:0016020|GO:0005886|GO:0005887|GO:0015095|GO:0006487|GO:0008250|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132719_PI430048170 0.0764573819818584 0.61012459104777 10.7455613070636 9.9190153729705 10.1240577077426 P P P 11.2540669446287 11.0287510062057 10.7297452109891 P P P LNCV6_132719_PI430048170 mRNA
GGGTGTGATTTTTATACTGCTGCTGCTTGTCACAATTATTATAACTTCTCTGTAATTTCC NM_152381RefSeq chr2 + 166888486 167259751 XIRP2 129446 "xin actin-binding repeat containing 2, transcript variant 1"
GO:0030018|GO:0030054|GO:0030036|GO:0051393|GO:0003779|GO:0003281|GO:0055008|GO:0045216 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118490_PI430048170 0.0103600064144291.76090733216233 9.46299307350375 9.87400944180824 9.80736933283453 P P P 8.77360074034031 8.93047745166858 9.01388749625912 P P P LNCV6_118490_PI430048170 mRNA
GGTGGGAGCAGTTTGAAGGAGTAAGCCTGGTTTTATACTTTTAAATAAAGTGTTTTTATC NM_032305RefSeq chr1 + 145964702 145978848 POLR3GL 84265 polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like
GO:0010467|GO:0006386|GO:0000790|GO:0006385|GO:0001056|GO:0045087|GO:0005666|GO:0032481|GO:0005654|GO:0006384|GO:0006383|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139156_PI430048170 0.6782963835328251.02291109209116 0.371343998887443 0.5581544674596890.443240627261678A A A 0.5192854138435810.384234599956618 0.372706614628289A A A LNCV6_139156_PI430048170 mRNA
GGACTCTGTTGTGTGTAAAGTTAATGTGATTATTTTTCAAAGCAGTGTTTCTAAGGGGTA NM_001025077 RefSeq chr10 + 11005295 11336673 CELF2 10659 "CUGBP, Elav-like family member 2, transcript variant 3"
GO:0006397|GO:0006396|GO:0005737|GO:0000166|GO:0003723|GO:0008016|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76022_PI430048170 0.5963560658217981.10897435385172 4.13845557953635 4.01271019488547 4.19270825082258 P P P 3.1190820832178 4.37841578720298 4.12424706385167 P P P LNCV6_76022_PI430048170 mRNA
TGATCACTGACACCCCGTACAACATATTGCATAGGTAAGATCCTCGATCTGGTGTTCTCT NM_001257194 RefSeq chr5 - 137617499 137721310 KLHL3 26249 "kelch-like family member 3, transcript variant 2"
GO:0005515|GO:0016567|GO:0042787|GO:0005198|GO:0031463|GO:0072156|GO:0050801|GO:0003779|GO:0070936|GO:0005856|GO:0070294|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90446_PI430048170 0.9063703503405180.9587398544446133.05521671364067 3.64633758676954 3.88199882779563 P P P 4.31214611556918 2.53537658208152 3.51677267825708 P P P

LNCV6_90446_PI430048170 mRNA
GTGTAGAAAAGGAAAACCCATGAAGCTGACCATTGACCATACTCCAGAAAGAAAAGATGA NM_152542 RefSeq
chr4 - 88257608 88284831 PPM1K 152926 "protein phosphatase, Mg2+/Mn2+ dependent, 1K"
GO:0006470|GO:0005759|GO:0004722|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127907_PI430048170 0.536394217174341 1.21122066642201 3.19774793962484
2.35962161958606 2.28088323720064 P A A 2.24224152026795 2.6675448226097
2.24490111062073 A P A LNCV6_127907_PI430048170 mRNA
AGATGTTAACTTAAATGTTCAGGGTGCCCCAGTCTGTTCAGCATGGCTGAAATCCACACT NM_012466 RefSeq chr19
+ 11296138 11326996 TSPAN16 26526 "tetraspanin 16, transcript variant 1" GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_71258_PI430048170 0.903028643552861 0.993956845105738 0.30774516443235 0.507230219375371
0.372965280779257 A A A 0.494998203293143 0.377895756975079 0.344122501827525 A A A
LNCV6_71258_PI430048170 mRNA
AAAGATGTATCCCAAAGCAGTATTTATAGCCAAACTGAAGAGAAAGCACAGGGCAAGTCT NM_003007 RefSeq chr20
+ 45206996 45209773 SEMG1 6406 semenogelin I
GO:0005515|GO:0007320|GO:0005198|GO:0005634|GO:0005576|GO:0030141|GO:0005615|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143314_PI430048170 0.1716080024917 1.2143641311162 10.3276600469514
10.7239518429389 10.7395471723925 P P P 10.3072041682138 10.2163737403701
10.4535230664066 P P P LNCV6_143314_PI430048170 mRNA
TTTATAAGATGGCCAGATCTACATTAGGAAAAGTATAAGCCCCCTCCCTAATGGCCGCTG NM_014426 RefSeq chr20
- 17941595 17968794 SNX5 27131 "sorting nexin 5, transcript variant 2"
GO:0005515|GO:0006907|GO:0034452|GO:0001891|GO:0001726|GO:0006886|GO:0031234|GO:0016050|GO:0070
685|GO:0031313|GO:0031901|GO:0042147|GO:0035091|GO:0030659|GO:0030904 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131490_PI430048170 0.0544826425404905 1.9289692889929 9.16016409177475
9.42655885557249 9.39320620261652 P P P 8.86631471594444 8.04793257645317
8.07992410335017 P P P LNCV6_131490_PI430048170 mRNA
GCCTTCACATCTTGAGGATATGCTTCTGTACTTTTTAAAAGCTTATAGTTGGTATGGAAA NM_018441 RefSeq chr2
- 216038387 216081816 PECR 55825 peroxisomal trans-2-enoyl-CoA reductase
GO:0005739|GO:0008670|GO:0019166|GO:0005102|GO:0006633|GO:0033306|GO:0005778|GO:0055114|GO:0043
231|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118507_PI430048170 0.181521494573737 1.6225562087694 0.446503099330782
1.53611873206363 1.06104424015322 A A A 0.322559683921853 0.379552947158208
0.445371282049992 A A A LNCV6_118507_PI430048170 mRNA
TTAGCATGCTGTCACCCTGAATCATAATCGCTCCTTTGCACCTCTAAAAAGATGCCCTTA NM_001199828 RefSeq
chr1 + 152984087 152985814 SPRR1A 6698 "small proline-rich protein 1A, transcript variant 1"
GO:0005515|GO:0005737|GO:0018149|GO:0008544|GO:0030216|GO:0005198|GO:0031424|GO:0030674|GO:0001
533 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133451_PI430048170 0.425289597293460 0.891462116655842 0.346451618968472
0.34879578760539 0.379640367892307 A A A 0.38260602105209 0.3333309288093
0.807836839102176 A A A LNCV6_133451_PI430048170 mRNA
GTAAAGCAATTTTAATGCTCAAAATAGTCAACCAAGTATGGCATGGTTCTGGTTCAGATT NM_033429 RefSeq chr15
- 68190704 68206110 CALML4 91860 "calmodulin-like 4, transcript variant 1" GO:0005509 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141043_PI430048170 0.318890168335488 1.0643573781126 11.7548776921378
11.8098022198478 11.654690322481 P P P 11.6320889127772 11.7677867843637
11.5450329125049 P P P LNCV6_141043_PI430048170 mRNA
GAGGGTCATCTTCACGAGCAAAGAGAACCAATAAAGTGACAACGAACGTCTGAGGCTTCC NM_030783 RefSeq

chr11_KI270832v1_alt + 3533 21028 PTDSS2 81490 phosphatidylserine synthase 2
GO:0016020|GO:0005789|GO:0044281|GO:0016021|GO:0006644|GO:0006659|GO:0003882|GO:0046474 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126814_PI430048170 0.395306391190881 1.18278396128034 5.05831829968013
4.71991665149795 5.31653460917633 P P P 4.40126842775305 4.97227073419455
4.98287876277358 P P P LNCV6_126814_PI430048170 mRNA
CAAAATGTACACCACCACCTTTAGTAGAATTGGGAAGTTTTAGCACATACCCATGGAGGG NM_033631 RefSeq chr1
- 23084022 23168858 LUZP1 7798 "leucine zipper protein 1, transcript variant 1"
GO:0021503|GO:0016020|GO:0005634|GO:0003281|GO:0060840|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133839_PI430048170 0.1643861189775940.8417675952189670.399565422151801
0.39148307482989 0.257345598454673 A A A 0.3590084896839720.733237040037969
0.67847039457886 A A A LNCV6_133839_PI430048170 mRNA
TATTGGATTCACATGTGAAAGCATGGGGTTAATTGTTGCTACATCAAAGAGAGAGATTCT NM_133473 RefSeq chr19
+ 21142036 21186002 ZNF431 170959 zinc finger protein 431
GO:0003682|GO:0005634|GO:0001046|GO:0000122|GO:0046872|GO:0043433|GO:0030154|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145306_PI430048170 0.199276178328983 0.969622315337027 0.446622372073466
0.3886759570840660.40881256541703 A A A 0.4794661614592370.484112001725105
0.413576211076132 A A A LNCV6_145306_PI430048170 mRNA
GATGACAGCATTTTTACTGGGTTCCTTTTGTACCCAGAGGAAACTTCTGGAATTTCACCA NM_001080440 RefSeq
chr3 + 161496807 161503942 OTOL1 131149 otolin 1 GO:0005581|GO:0005576 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_94613_PI430048170 0.2382717458767410.8557828339780971 2.9123342820059 12.9077318284819
13.0261328038161 P P P 12.9256761428179 13.186428827308 13.3761861787571 P P P
LNCV6_94613_PI430048170 mRNA
TTTGGAAAATAATCTGCAGAAACGAGCTGTGCTTGCAAAGACTTCATAGTTCCCAAGAAT NM_152862 RefSeq chr2
+ 218217093 218254348 ARPC2 10109 "actin related protein 2/3 complex, subunit 2, 34kDa, transcript
variant 1"
GO:0005515|GO:0034314|GO:0043005|GO:0005886|GO:0005885|GO:0006928|GO:0045202|GO:0015629|GO:0005
829|GO:0010592|GO:0005737|GO:0051015|GO:1900026|GO:0007411|GO:0031252|GO:0070062|GO:0035650|GO:0
005794|GO:0048013|GO:0071933|GO:0045087|GO:0005200|GO:0019894|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133465_PI430048170 0.1838195979955171.84418115939326 1.424437347221
0.4047729032341921.69711243274872 A A A 0.4006940309425440.367584658171961
0.401867255913652 A A A LNCV6_133465_PI430048170 mRNA
AGGACAGCCAGAGGAGCTGCGACTTGGTATTTTTTGGAATAAATAGACATTTTCCTGATC NM_001145176 RefSeq
chr19 - 55428737 55442863 SHISA7 729956 shisa family member 7 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_56454_PI430048170 0.24118056015756 0.926200896522438 10.0080696778493 9.98065192907314
10.2015745439814 P P P 10.1139544531612 10.197685513297 10.2185512893585 P P P
LNCV6_56454_PI430048170 mRNA
TTCAAGCAGTTTCATTTCAAAGACTTCAACAGGGCCTTTGGGTTCATGACAAGAGTGGCC NM_001289797 RefSeq
chr10 - 70883507 70888254 PCBD1 5092 "pterin-4 alpha-carbinolamine dehydratase/dimerization
cofactor of hepatocyte nuclear factor 1 alpha, transcript variant 3"
GO:0005515|GO:0043496|GO:0006559|GO:0006729|GO:0003713|GO:0004505|GO:0044281|GO:0051291|GO:0006
351|GO:0005829|GO:0042802|GO:0034641|GO:0005737|GO:0051289|GO:0005654|GO:0045893|GO:0008124|GO:0
070062|GO:0055114. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143354_PI430048170 0.123903925893096 0.637165357336242 2.47071528751883

3.21342331610993 3.41036116452136 A P P 3.57161080121931 3.7122120378284
3.90186672994286 P P P LNCV6_143354_PI430048170 mRNA
TGGGCCCTGAAATGACACCCAATTTGTTAATGGAATTATGAAGAACAGCAATATAATACA NM_001123 RefSeq chr10
+ 74176488 74709303 ADK 132 "adenosine kinase, transcript variant 1"
GO:0046085|GO:0055086|GO:0044209|GO:0044281|GO:0005524|GO:0046872|GO:0009156|GO:0032922|GO:0005
829|GO:0016310|GO:0005737|GO:0044342|GO:0004001|GO:0006144|GO:0042102|GO:0043101|GO:0016773|GO:0
005654|GO:0006175|GO:0010613 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137001_PI430048170 0.19694203913599 1.97029834767298 1.90935927384172
0.4461625178470531.63384377066799 A A A 0.5202966856378930.421730661568142
0.484705986593928 A A A LNCV6_137001_PI430048170 mRNA
TCCAAAAGGGGGAAGTACTGCTTAGAGAAATATCTGTAAGCATTAAATTCTCTCCTTTAT NM_001099412 RefSeq -
- 0 0 --- NA "K(lysine) acetyltransferase 6A, transcript variant 1" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135057_PI430048170 0.4607481794047410.8395652176490340.983418192960696
0.3978964009441840.251314121889023 A A A 0.88130843652541 1.13383704636395
0.384728432414603 A A A LNCV6_135057_PI430048170 mRNA
GATGGGAGAAGGAAAGGTTATTTATTCTATAGAAGAGACTGCGGACAATTAGTATTCAAA NM_145174 RefSeq chr22
- 40859549 40862126 DNAJB7150353 "DnaJ (Hsp40) homolog, subfamily B, member 7" GO:0051087 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144373_PI430048170 0.8896353799626290.97128415764895 8.77474934482004
8.44814260483597 8.47015321522688 P P P 8.32963064857677 8.90900909980382
8.54384918032691 P P P LNCV6_144373_PI430048170 mRNA
CTGAGAGGTTTGTGGAAAAGATGGCAAATGGGGAATAAAAAGATTTTGTGTCAACAGTAG NM_000431 RefSeq chr12
+ 109573694 109597270 MVK 4598 "mevalonate kinase, transcript variant 1"
GO:0016310|GO:0006695|GO:0050728|GO:0004496|GO:0019287|GO:0044281|GO:0008299|GO:0005524|GO:0070
062|GO:0042802|GO:0005829|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140787_PI430048170 0.00216035086172653 0.3781818002376435.70687654236409
5.59971967668286 6.0407608422687 P P P 6.9480412936585 7.14950546478064
7.45100376104503 P P P LNCV6_140787_PI430048170 mRNA
CTGGTCAATGAACAGGAAGACTTAGAGATGTTTCACAAGCCTTTGATTTTTGTTTCATTT NM_012073 RefSeq chr5
+ 10249920 10266412 CCT5 22948 "chaperonin containing TCP1, subunit 5 (epsilon)"
GO:0005515|GO:0005813|GO:0031681|GO:0005832|GO:0005874|GO:0048487|GO:0005730|GO:0007339|GO:0009
615|GO:0005524|GO:0044297|GO:0005829|GO:0005737|GO:0006457|GO:0051084|GO:0002199|GO:0051082|GO:0
044267|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143240_PI430048170 0.4632620471879981.11604403893958 5.81723831695209
6.13655962280552 5.69993903458758 P P P 5.86741231411166 5.87890489075351
5.42324524604039 P P P LNCV6_143240_PI430048170 mRNA
TTTGATCTCCCAGCACCTGCCAGCTGGGTTCCTCTCTCTGCAAGGGCTTTCAGGAGACTT NM_181624 RefSeq chr21
- 30348398 30348606 KRTAP23-1 NA keratin associated protein 23-1 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_123694_PI430048170 0.0111308034360109 2.35024411048017 9.24486224990729
9.51980000450579 9.33869597912001 P P P 8.47906331837976 7.87054576439572
7.99511409291688 P P P LNCV6_123694_PI430048170 mRNA
GGCCCGGCAGTATGGCTCCGAGGGCAGGTTCACTTTCACTTCCCATACCCCTGAGAGTTC NM_017510 RefSeq chr5
+ 177592211 177596098 TMED9 54732 transmembrane emp24 protein transport domain containing 9
GO:0005515|GO:0019905|GO:0005793|GO:0005794|GO:0005783|GO:0048205|GO:0010638|GO:0000139|GO:0034
498|GO:0033116|GO:0005789|GO:0007030|GO:0032527|GO:0016021|GO:0030140|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136033_PI430048170 0.3416266565267081.05085268452695 11.8041104456879

11.8204651323838 11.7429892150763 P P P 11.6248067244919 11.8264465973279
11.6954797405509 P P P LNCV6_136033_PI430048170 mRNA
ACGTGCCGACATATGGCCATTGAGCTCCAACCCACACATTCCCATTCACCAATAAAGGCA NM_001267552 RefSeq
chr17 - 17505562 17591703 PEMT 10400 "phosphatidylethanolamine N-methyltransferase, transcript
variant 5"
GO:0006629|GO:0031966|GO:0008283|GO:0044281|GO:0032259|GO:0005789|GO:0080101|GO:0004608|GO:0016
021|GO:0000773|GO:0006644|GO:0006656|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111496_PI430048170 0.165289971557767 1.15440394338497 6.92354332378936
6.93644358409406 6.90642090188522 P P P 6.81890604187377 6.79751446072444
6.50834236398374 P P P LNCV6_111496_PI430048170 mRNA
TGACTGCCAGCTGAAGGCGTATAATTTTTCCCTCCGTGTGCCCCACCTACCCGTCCAAGA NM_001190946 RefSeq
chr5 - 177519788 177554547 FAM193B 54540 "family with sequence similarity 193, member B,
transcript variant 3" GO:0005737|GO:0005730|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_102915_PI430048170 0.0337299222223416 1.39802920966679 8.51149591025807
8.81223609266857 8.89195205843714 P P P 8.38744411293408 8.08253468447717
8.30577342550838 P P P LNCV6_102915_PI430048170 mRNA
GCATTGCCATGAATTTCTACCAGATGTGCTTTTATTTAGCTTTACATATTCCTTTGACCA NM_001287140 RefSeq chr8
- 80034869 80080831 TPD52 7163 "tumor protein D52, transcript variant 4"
GO:0005515|GO:0048471|GO:0008284|GO:0005737|GO:0046982|GO:0005783|GO:0030183|GO:0005509|GO:0009
653|GO:0046903|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93747_PI430048170 0.0482433745898751 2.73486477728099 4.81285457662504
4.52737472356679 4.78083132808303 P P P 2.42979666354906 3.64246447216137
3.44426738177613 A P P LNCV6_93747_PI430048170 mRNA
TTTGTCTCAGTGTACAAGATCAACAAAATGGCCTTCTGGGTCGGAGAGACAGTGTTTCTC NM_024789 RefSeq chr10
+ 102461412 102477045 TMEM180 79847 transmembrane protein 180 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128529_PI430048170 0.676288253144454 1.24350585499577 1.043364338006
2.50761571378026 1.69299197941155 A A A 1.70948349689362 1.75468700705491 1.1281489702833
A A A LNCV6_128529_PI430048170 mRNA
ATTCCGTTAAGAGCAAAAGAGAATGTTGGAAGGTGGGGGAAAACATTTCTTTGTTTTCTA NM_000130 RefSeq chr1
- 169511953 169586531 F5 2153 "coagulation factor V (proaccelerin, labile factor)"
GO:0005515|GO:0005794|GO:0004252|GO:0005886|GO:0005507|GO:0005783|GO:0008015|GO:0030168|GO:0005
576|GO:0031982|GO:0005615|GO:0016020|GO:0007596|GO:0002576|GO:0006508|GO:0031093 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126645_PI430048170 0.0194798741479739 0.946831376720267 0.350972437824551
0.350340937224543 0.3257990915316 A A A 0.448037718214084 0.420455992206514
0.394730337945523 A A A LNCV6_126645_PI430048170 mRNA
TCAACGATGAGATGCTCAACAGGACCAAGGATGCAGAGACCTACTTCAACTACAAGTATG NM_145811 RefSeq chr17
+ 66877272 66885278 CACNG5 27091 "calcium channel, voltage-dependent, gamma subunit 5"
GO:0030054|GO:0005245|GO:0015075|GO:0045211|GO:0032281|GO:2000311|GO:0070588|GO:0006810|GO:0014
069 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145746_PI430048170 0.128786320500387 1.60970215243853 1.54876795437926
1.86113959080843 1.39209087897147 A A A 0.432530987921401 0.654183765231621
1.47590710586583 A A A LNCV6_145746_PI430048170 mRNA
TTCCCTTTTCTCTGTATTGGTCAGTGTAGTTGATGTAAAACCGTTTTGTGGATGGAAAAT NM_024430 RefSeq chr18
- 45983535 46072284 PSTPIP2 9050 proline-serine-threonine phosphatase interacting protein 2
GO:0016020|GO:0007010|GO:0003779|GO:0005856|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA

LNCV6_145139_PI430048170 0.0576141124814337 1.4574115675436 11.5801390447037
11.5605198469613 11.5559389078576 P P P 10.7523820404605 11.2356488862134
11.0380417231203 P P P LNCV6_145139_PI430048170 mRNA
ATCTCCTTCATGCAGAGTGACATGGGTCGGGAAGCAGCATATGGCTTCTTCCTGCTGGGC NM_017854RefSeq chr19
- 47045908 47048624 TMEM160 54958 transmembrane protein 160 GO:0005739|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139933_PI430048170 0.00259078103538218 0.8710791509052719.68899105213421
9.68255383913853 9.65587482406404 P P P 9.85071833299591 9.91258435258541
9.86093779394749 P P P LNCV6_139933_PI430048170 mRNA
TTTGCAGCCTTGCTAAACTGTCTGAATCAAGGATCACAAACTACAGCCTGCAGGCCAAAT NM_201400RefSeq chr16
- 5084299 5097820 EEF2KMT 196483 "eukaryotic elongation factor 2 lysine methyltransferase,
transcript variant 1" GO:0005515|GO:0005737|GO:0016279|GO:0018023 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_135281_PI430048170 0.000860116617709953 0.5374376360588351 1.3122093702477
11.1133467161942 11.2508150542175 P P P 12.0102673528999 12.0896668029442 12.259695163248
P P P LNCV6_135281_PI430048170 mRNA
AAGCTTCAGTTTAACTGTTTCCATGCTAAACATGATTTATAACCAGCTCAGAGCTGAACA NM_003000RefSeq chr1
- 17018725 17054170 SDHB 6390 "succinate dehydrogenase complex, subunit B, iron sulfur (Ip)"
GO:0048039|GO:0005515|GO:0051538|GO:0051539|GO:0006099|GO:0051537|GO:0005743|GO:0009055|GO:0008
177|GO:0044281|GO:0046872|GO:0005739|GO:0009060|GO:0022904|GO:0005749|GO:0006105|GO:0044237|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129231_PI430048170 0.0204341481449267 0.9469479287152170.398200127398345
0.3519854348386370.348283738075483 A A A 0.4574337208295630.451753221479734
0.425549358495473 A A A LNCV6_129231_PI430048170 mRNA
GTAGCGATGACATTGTTTTCAGAATTTCCAAGAGTTCTGTCTGTTCTGTTTTTTATTCAG NM_178537RefSeq chr11 +
369794 382117 B4GALNT4 338707 "beta-1,4-N-acetyl-galactosaminyl transferase 4"
GO:0032580|GO:0008152|GO:0016021|GO:0033842|GO:0008376 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129965_PI430048170 0.0120370510114475 0.4072219046948142.86805712779534
3.35126612591562 2.56683877262245 A P A 3.91622311548407 4.29321988904145
4.51325111871888 P P P LNCV6_129965_PI430048170 mRNA
GACTGGGTAGCCTAGGAGTCAAGGATCAGAAAGGGTACTTCATATATATGTGGCAGAATT NM_153369RefSeq chr6
+ 111259278 111269058 KIAA1919 91749 KIAA1919
GO:0016324|GO:0008643|GO:0016021|GO:0006814|GO:0055085|GO:0015293 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132961_PI430048170 0.2122352589847421.03267369106267 0.41733532429363
0.3607232901485490.3899035848445 A A A 0.30440736263125 0.332170793115566
0.391412500544033 A A A LNCV6_132961_PI430048170 mRNA
GAGAGGATGTGAACTCATGAAGTTGTCTGCTGCACCATCCGAAATAAAGACACAAGAAAA NM_178455RefSeq chr20
+ 45722348 45725696 SPINT4 NA "serine peptidase inhibitor, Kunitz type 4" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_138069_PI430048170 0.0713743150793996 0.4503391470190942.17851042416647
2.85972361333265 3.54997576730951 A A P 3.81360660386707 4.04633083915763
4.43267451366939 P P P LNCV6_138069_PI430048170 mRNA
CCTTTTTCTGGCCTTCATTCATAAGATCTGGTTGTTTGGGCTGTAGGTGGCATAATTCAT NM_015255RefSeq chr6
+ 42564021 42693505 UBR2 23304 "ubiquitin protein ligase E3 component n-recognin 2, transcript
variant 1"
GO:0005515|GO:0006511|GO:0004842|GO:0006342|GO:0032007|GO:0033522|GO:0005886|GO:0016874|GO:0070
728|GO:0000151|GO:0007283|GO:0071233|GO:0005654|GO:0008270|GO:0000785|GO:0007141 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_135346_PI430048170 0.0269517424726110.4448944684533583.29028534754992
2.78560530127361 3.5305470243827 P A P 4.40595447709171 4.31188560854451
4.48554479272298 P P P LNCV6_135346_PI430048170 mRNA
TGACCTTCCTTTCCTATAAAAATATGAAGCAGAAAACTCCCCCATGATTTCCTCATGTTG NM_033107RefSeq chr7
+ 90346664 90391455 GTPBP10 85865 "GTP-binding protein 10 (putative), transcript variant 2"
GO:0005739|GO:0000287|GO:0005694|GO:0042254|GO:0008152|GO:0005730|GO:0003924|GO:0005525 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144436_PI430048170 0.2147979999822681.23770937417334 0.315150209694809
0.8525434416044470.763498402692637A A A 0.30111533297393 0.470848493474627
0.284079423303633A A A LNCV6_144436_PI430048170 mRNA
CACCAGTAGCGTTGTGTGTGATTTCTGATAAAATTGTAGAATAGCTAATGACATTTGACA NM_001271983 RefSeq
chr11 + 130672955 130717352 C11orf44 283171 chromosome 11 open reading frame 44 GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143341_PI430048170 0.91628591907563 0.9964340623731218.95308681205611 8.6855862972675
8.73939960923419 P P P 8.7798825996806 8.81740107005623 8.81006135313297 P P P
LNCV6_143341_PI430048170 mRNA
CTACATCCGTCCTTGGAAGAGGAAAAGAAAAAACATAAAAAGAAACGCCTAGTACAAAGT NM_015920RefSeq
chr15 - 63153339 63157542 RPS27L 51065 ribosomal protein S27-like
GO:0005515|GO:0003735|GO:0006919|GO:0005634|GO:0008494|GO:0045727|GO:0006412|GO:0008656|GO:0046
872|GO:0006974|GO:0042771|GO:0006281|GO:0005840|GO:0031571 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_137360_PI430048170 0.0056203549181283 0.3831481111101195.27318912031582
5.11547707869925 5.57905636742064 P P P 6.70714050234866 6.6518923723166
6.79613202057595 P P P LNCV6_137360_PI430048170 mRNA
GGTCAGTACTATGAAGCTTCTGTGGTTTGTATGATGTTTTAACTTTCACTTTAAACTGCA NM_001135575 RefSeq
chr6 + 11094032 11138736 SMIM13221710 small integral membrane protein 13 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82787_PI430048170 0.3776858618892110.9307870688010111 1.3638222014413 11.5513334422212
11.4004741549226 P P P 11.6985549931402 11.4224055083052 11.4977207146902 P P P
LNCV6_82787_PI430048170 mRNA
AATCACCAACCCATCAACATCAAGCCTCCCCCAGGCCGGTTCAAATAAATGTATTTAAAT NM_022744RefSeq chr16
- 31489474 31508419 C16orf58 64755 chromosome 16 open reading frame 58
GO:0016020|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135181_PI430048170 0.2871998815165221.30189392192903 4.13620847908095
4.14017331659832 3.77684094326752 P P P 4.03340317811062 3.71290222430522
3.01638779871372 P P P LNCV6_135181_PI430048170 mRNA
ATTTGGACGCCCCGAAAGACCCCTACGACCTCTACTTTTATGCTCCGGATACCTGGGTCC NM_001195256 RefSeq
chr19 + 49426430 49428818 GFYNA "golgi-associated, olfactory signaling regulator" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_111402_PI430048170 0.8617459838155940.9861918716114888.46181746899006 7.6805959385029
7.73324755824627 P P P 7.76017225690544 8.06145166268925 8.21617044355453 P P P
LNCV6_111402_PI430048170 mRNA
GAAGTTCCCCGCCTGGCAGAACAGCATCCGCCACAACCTCTCGCTCAACGACTGCTTCGT NM_004472RefSeq chr5
- 73446255 73448527 FOXD1 2297 forkhead box D1
GO:0003700|GO:0090184|GO:0008301|GO:0005634|GO:0072210|GO:0072076|GO:0000978|GO:0003677|GO:0006
351|GO:0072213|GO:0060678|GO:0010628|GO:0043565|GO:0030513|GO:0001077|GO:0007411|GO:0045944|GO:0
072267|GO:0045892. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138540_PI430048170 0.1486108691462311.08315789498941 0.494544470038086

0.54918893167009 0.576893264697315 A A A 0.3282798012464960.427822650182238
0.514028981817268 A A A LNCV6_138540_PI430048170 mRNA
CTGCTGCTCTGGTTTTGAAACATGTTTGTATATAGATACAGGAGTTGGCATAAATTTTGT NM_053042 RefSeq chr4
- 10439879 10457408 ZNF518B 85460 zinc finger protein 518B
GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0003677|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_121381_PI430048170 0.1414242999360460.562139619650345 0.271644265083798
0.2954422544464210.443521077320107 A A A 0.9493736907745740.618641645380252
1.71518890575109 A A A LNCV6_121381_PI430048170 mRNA
GGTATTTAATCAGAAGCGATACCTTGCATGCCATCGTAGATCTCACATTGATGAGAAACC NM_006969 RefSeq chr19
- 52797407 52821669 ZNF28 7576 "zinc finger protein 28, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_62535_PI430048170 0.4468720433282021.10218167541736 10.5756851476708 10.437541598935
10.6523509968802 P P P 10.08173560474 10.6115322034141 10.5067003136398 P P P
LNCV6_62535_PI430048170 mRNA
TTGCTAGTGTGGTGGAAAGATAAACCTTTTGAGGTGAAGAGCCAGGGGGTCAGGAAATAT NM_016310 RefSeq chr16
- 46978 53632 POLR3K 51728 "polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa"
GO:0010467|GO:0006386|GO:0006385|GO:0003899|GO:0003677|GO:0006383|GO:0005829|GO:0051607|GO:0001
056|GO:0045087|GO:0005666|GO:0005654|GO:0008270|GO:0032481 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141272_PI430048170 0.1435312998906540.8275536361314258.74118802715595
8.54237839833016 8.30511515641554 P P P 8.93242329025261 8.81301347322419
8.68467674682491 P P P LNCV6_141272_PI430048170 mRNA
TGAAGAAATAAACCTATTTAAATCACCCCCTGGTGGCTCCCTCACAGCAAAAAAGCCTGG NM_001124758 RefSeq
chr17 + 4498833 4539933 SPNS2 124976 spinster homolog 2 (Drosophila)
GO:0006665|GO:0001782|GO:0046624|GO:0003376|GO:0072676|GO:0005765|GO:0055085|GO:0031982|GO:0048
535|GO:0040011|GO:0060348|GO:0048073|GO:0006869|GO:0002920|GO:0016021|GO:0043029 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127988_PI430048170 0.1298096125292940.7897573487189679.29040562633134 9.3533533249401
9.55174779662596 P P P 9.49126090211105 9.71612775056662 9.98099470423961 P P P
LNCV6_127988_PI430048170 mRNA
TGGGGATGAATAGAAAACCTGTAAGCTTTGATGTTCTGGTTACTTCTAGTAAATTCCTGT NM_001809 RefSeq chr2
+ 26786013 26794587 CENPA 1058 "centromere protein A, transcript variant 1"
GO:0005515|GO:0000780|GO:0046982|GO:0006334|GO:0000132|GO:0005634|GO:0071459|GO:0003677|GO:0005
829|GO:0034080|GO:0051382|GO:0003682|GO:0016032|GO:0005654|GO:0000778|GO:0000278|GO:0000786|GO:0
000775|GO:0000939. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79849_PI430048170 0.0178538226873011 1.81309800230019 5.48541265777436
5.26855728292303 5.40620818069111 P P P 4.21884612117379 4.59799124171937
4.72898847009407 P P P LNCV6_79849_PI430048170 mRNA
TTCCGTGAATTCCTCCGAACAGAATTCAGTGAGGAAAATATGCTCTTCTGGATGGCCTGT NM_170587 RefSeq chr8
+ 53851807 53959304 RGS20 8601 "regulator of G-protein signaling 20, transcript variant 1"
GO:0043547|GO:0005515|GO:0005737|GO:0008277|GO:0005886|GO:0038032|GO:0005634|GO:0005096 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141409_PI430048170 0.0697254456000007 1.03079005992978 0.397238001016757
0.4103650769623140.436558623625479 A A A 0.3616304454026470.353881909708599
0.397303179033375 A A A LNCV6_141409_PI430048170 mRNA
TGAATTTGCCTTGTTCGAGAGTAACGTTTGAAAACCAAAGAAATAAAGTGATGCAGTGCC NM_018228 RefSeq chr14
+ 74348462 74360008 VRTN 55237 vertebrae development associated

GO:0043565|GO:0006313|GO:0004803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121403_PI430048170 0.2384601912815230.5845556533154110.330967000591629
0.2499837759513480.277571958484274A A A 1.64731796372107 0.258532251111781
0.949373690774574A A A LNCV6_121403_PI430048170 mRNA
ATCAGAGAATTCATACAGGAGAGAAACCTTATGTGTGTAATGTGTGTGGGAAAGCCTTTA NM_152478RefSeq chr19
+ 56404324 56425031 ZNF583 147949 "zinc finger protein 583, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130561_PI430048170 0.00974453355449055 0.3824309127012237.56723638584052
7.31021892138153 7.81766695550262 P P P 8.55240301004385 8.92851018343108
9.31778635452023 P P P LNCV6_130561_PI430048170 mRNA
GATTTATAATCATGATACTCTTCGGTGGTAGTTTCAAAAGACACTACTAATACGCAGGAA NM_019063RefSeq chr2
+ 42169337 42332548 EML4 27436 "echinoderm microtubule associated protein like 4, transcript
variant 1"
GO:0072686|GO:0003674|GO:0007067|GO:0005737|GO:0016020|GO:0005874|GO:0007026|GO:0007017 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130992_PI430048170 0.4258469698978541.0936187849163 9.45246818188601
9.33164756146001 9.61301294381594 P P P 9.33624648677678 9.10890969029318
9.54557485783771 P P P LNCV6_130992_PI430048170 mRNA
AGAGACTATGATGGACCAGCCCTGAGAAAGAATGAGTATTTTTGAATTGAGATGATCAAT NM_004398RefSeq chr11
+ 108665024 108940930 DDX10 1662 DEAD (Asp-Glu-Ala-Asp) box polypeptide 10
GO:0003724|GO:0008152|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135124_PI430048170 0.00293938556090825 1.50515738123715 11.88067647064
11.9636631666781 11.7317418060165 P P P 11.284650137529 11.3533486563279
11.1720601205427 P P P LNCV6_135124_PI430048170 mRNA
CTCCAGATCCGTCTGGTTTTTTACACCGTTTGTTAATAAAGCCTGAAACCGCTGAAAAAA NM_020378RefSeq chr19
+ 55485189 55487568 NAT14 57106 "N-acetyltransferase 14 (GCN5-related, putative)"
GO:0006352|GO:0008080|GO:0005634|GO:0016021|GO:0045893|GO:0003677 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_132343_PI430048170 0.252793575249895 0.920125200561397 7.44312326877098
7.27870173355589 7.54744481634993 P P P 7.58275745043312 7.47522826418528
7.58158562589813 P P P LNCV6_132343_PI430048170 mRNA
AGACAGAAATCTTCTAGCACTTTGTAAACACAGTGAATAACCTCTTGGAGTATTTTTGGC NM_002657 RefSeq
chr20 - 32192503 32207743 PLAGL2 5326 pleiomorphic adenoma gene-like 2
GO:0043565|GO:0006629|GO:0001077|GO:0003700|GO:0045944|GO:2001244|GO:0005634|GO:0009791|GO:0046
872|GO:0006351|GO:0034378 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140645_PI430048170 0.138694431532786 1.2371415532354 8.70149297491832
8.58664184938145 8.59165510954532 P P P 8.26989637879315 8.56270015919184
8.08910959669454 P P P LNCV6_140645_PI430048170 mRNA
TCAAGGCTTTCGAGGAGGAGCAGAACCTGCGGGGTAACCTCACCAACATGGAGACCAATG NM_001171993
RefSeq chr12 - 121839526 121888611 HPD 3242 "4-hydroxyphenylpyruvate dioxygenase,
transcript variant 2"
GO:0034641|GO:0006559|GO:0003868|GO:0044281|GO:0006572|GO:0046872|GO:0070062|GO:0055114|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128957_PI430048170 0.614041899825349 0.921780473534828 3.77788081325467
3.26600280079907 5.14516549290674 P P P 4.17470867952227 4.42037774778945
4.59902116954802 P P P LNCV6_128957_PI430048170 mRNA
GGGATGAAAAATATGTCTTACTGGAAAAATCCCTCATAATAACCTAATAGGGCATTGCTA NM_018559 RefSeq
chr13 + 44989551 45028269 GPALPP1 55425 GPALPP motifs containing 1 NA . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_51393_PI430048170 0.0723509481554072 1.42901229167526 5.14422846301327
5.10202747926764 5.37500542042438 P P P 4.62768922269074 4.40483751471387
4.99627409162798 P P P LNCV6_51393_PI430048170 mRNA
TATACACAGATTGCAAAGGAACATGCATTGGCCCAAGCTGAACTTCTTAAGCGCCAGGAA NM_004866 RefSeq
chr5 + 78360502 78480739 SCAMP1 9522 "secretory carrier membrane protein 1, transcript variant
1"
GO:0005802|GO:0005515|GO:0042589|GO:0030136|GO:0019904|GO:0006892|GO:0030672|GO:0016021|GO:0015
031|GO:0006887|GO:0055038|GO:0006897 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_137175_PI430048170 0.974493675627478 0.972120299850648 4.59330107838061
4.81762231958882 4.50851189878944 P P P 5.09983008354047 4.50104917200927
4.34466152189033 P P P LNCV6_137175_PI430048170 mRNA
CAAAAAGCACTTCAAAGAATGTATCAACTTCATCCACTGCTGCCGCCTTAATGGGGGGAA NM_080611 RefSeq
chr20 - 31861066 31870676 DUSP15 128853 "dual specificity phosphatase 15, transcript variant 1"
GO:0005515|GO:0005737|GO:0006470|GO:0005886|GO:0042127|GO:0046330|GO:0007179|GO:0008138|GO:0035
335|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137329_PI430048170 0.276920554527284 1.0219137462319 0.378002521033424
0.349675619931328 0.401443337302812 A A A 0.306193107718773 0.369588203728754
0.359187435979434 A A A LNCV6_137329_PI430048170 mRNA
TTCTACCCACCACTGTGTCGGATTTTTCTTAAATAAATGGAAGCGGTCAGACTGGAGGTG NM_001304438 RefSeq
chr17 + 34580748 34639318 TMEM132E NA transmembrane protein 132E NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_67178_PI430048170 0.651240870688173 0.928620522977965 7.62414794038423
7.27684495231386 7.21104108085348 P P P 7.61515141786988 7.65125575947691
7.14885243895286 P P P LNCV6_67178_PI430048170 mRNA
TCAGGACCTTCCTTTCACCCTTCCACTCGCCCCAGTTTCCAGGAGCTAAGAAGGGAGACA NM_005480 RefSeq
chr12 + 49323187 49331731 TROAP 10024 "trophinin associated protein, transcript variant 1"
GO:0005515|GO:0005737|GO:0007155 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_139459_PI430048170 0.987015223993762 0.99934160165453 0.354532342555582
0.501828057754454 0.387220065827501 A A A 0.500867474140465 0.375958199204692
0.369963535697725 A A A LNCV6_139459_PI430048170 mRNA
GGCCCACAAGTGTAACTATGCTGTTAACAGCTGTCAATAGATAATTAAAATTCATACTGT NM_000322 RefSeq
chr6 - 42696594 42722620 PRPH2 5961 "peripherin 2 (retinal degeneration, slow)"
GO:0060041|GO:0009645|GO:0016021|GO:0007155|GO:0007601 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_134547_PI430048170 0.0550537858871481 0.472624938891982 3.68274950362096
3.64334578941013 3.90194313576851 P P P 4.22494373431233 5.04338891029113
5.06874310123055 P P P LNCV6_134547_PI430048170 mRNA
GTCACTTTAAACTGGATTACCAATATGGTTGGTGTGGTCGCTTTAAAGTTTGTTTTCATT NM_175907 RefSeq
chr18 - 75195109 75209348 ZADH2 284273 zinc binding alcohol dehydrogenase domain containing
2 GO:0005739|GO:0008150|GO:0003674|GO:0016491|GO:0008270|GO:0055114|GO:0005777 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127751_PI430048170 0.435436806657212 0.87421712798146 10.0053935544777
10.447997022542 9.80202391226063 P P P 10.532687255749 10.2901076874781
10.0516297449113 P P P LNCV6_127751_PI430048170 mRNA
AGGGAAGAAGGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGAGGATGGGGCTATTCAC NM_139161 RefSeq
chr19 + 6464248 6467219 CRB3 92359 "crumbs family member 3, transcript variant 2"

GO:0017124|GO:0030054|GO:0005886|GO:0034329|GO:0019904|GO:0072659|GO:0045216|GO:0043234|GO:0016324|GO:0070830|GO:0005923|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130_PI430053867 0.438743345248058 1.34934640037009 1.5293265566184 1.51909599409544 2.57780181593715 A A A 1.8262067081572 0.859911653787336 1.73417293720038 A A A LNCV6_130_PI430053867 mRNA
AAATATGTCACCTCCTAAGAGAAACCTTCCCAGACCACTCTTTCTAAAATGAATCTTCTA NM_001184714 RefSeq chr1 - 160485029 160523262 SLAMF6 114836 "SLAM family member 6, transcript variant 1"
GO:0005886|GO:0004872|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143161_PI430048170 0.201563448098701 1.4070818134095 3.96196652171388 3.42886250884745 3.12088389414405 P P P 3.08170556717923 3.31180691455125 2.70378687995237 P P P LNCV6_143161_PI430048170 mRNA
TAATGTATTGCCAAATAGCACCATTCTTCTTCTCTCACTCTCTTGCCATGGGGGCTCTTA NM_182767 RefSeq chr12 - 84859487 84912829 SLC6A15 55117 "solute carrier family 6 (neutral amino acid transporter), member 15, transcript variant 1"
GO:0005886|GO:0005328|GO:0005326|GO:0006865|GO:0005298|GO:0055085|GO:0015804|GO:0015820|GO:0005887|GO:0035524|GO:0015824|GO:0006836|GO:0016021|GO:0006814|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144274_PI430048170 0.378966483262845 1.06730199822797 0.565608873334161 0.333960179133756 0.318656992820738 A A A 0.324347868533739 0.324486819795531 0.300860419178989 A A A LNCV6_144274_PI430048170 mRNA
GACTTGGTCTTCAACCACCATTACCCCTCTAACTTTGCACAAATAAACCTGTGTAGAAAC NM_001281428 RefSeq chr9 + 34458751 34520989 DNAI1 27019 "dynein, axonemal, intermediate chain 1, transcript variant 2"
GO:0005515|GO:0005929|GO:0005737|GO:0003774|GO:0030286|GO:0030030|GO:0008152|GO:0005874|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143951_PI430048170 0.0149730450246723 2.01372316926861 1.76740083896181 1.69501610052487 1.17513269688195 A A A 0.507390586734424 0.802112685766752 0.327359070596112 A A A LNCV6_143951_PI430048170 mRNA
TAAGGAGGAAGGAATAACACCTGGTCCAACATGAAACAATTCTTATTGACTCATATACCA NM_006900 RefSeq chr9 - 21367371 21368076 IFNA13 NA "interferon, alpha 13" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144390_PI430048170 0.0109460857304926 1.41992776746585 7.77004462060815 7.94153507564729 7.97429708520561 P P P 7.53791207362287 7.3832244661955 7.24013461736991 P P P LNCV6_144390_PI430048170 mRNA
TTGAAAGTATTGTGTTTATGCATTTCAATTTCAATGGTGTTGGCTTCCCCTCCCCACCCC NM_000252 RefSeq chrX + 150568596 150673143 MTM1 4534 myotubularin 1
GO:0005515|GO:0044088|GO:0045109|GO:0005886|GO:0030175|GO:0044281|GO:0015031|GO:0035335|GO:0046716|GO:0005829|GO:0005737|GO:0006470|GO:0052629|GO:0004721|GO:0004725|GO:0070062|GO:0048311|GO:0006661|GO:0005770|GO:0008333|GO:0001726|GO:0019215|GO:0070584|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142680_PI430048170 0.22871814644436 0.562392838888252 1.13264428749791 1.13610485262004 0.579624122155157 A A A 1.27018953274467 2.51944889211615 1.21320997937012 A A A LNCV6_142680_PI430048170 mRNA
GGTGGGAAAGGCTTTATCAGGTATCATCAACAGGTTCTCAATTAAAGATTTGATTTATTC NM_032214 RefSeq chr20 - 36612520 36646216 SLA2 84174 "Src-like-adaptor 2, transcript variant 1"
GO:0005515|GO:0019724|GO:0005886|GO:0050869|GO:0005770|GO:0009967|GO:0000122|GO:0050851|GO:0005737|GO:0042110|GO:0047485|GO:0005070|GO:0050776|GO:0016023|GO:0030522|GO:0050849|GO:0010008 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133487_PI430048170 0.0351426555506471 0.19555025459645 1.88478128235625
0.454838643509559 2.11782124526424 A A A 3.77213903122135 4.04913715264905
4.15971757563081 P P P LNCV6_133487_PI430048170 mRNA
AATCCCATTCCAAATAATATTTGTGTAGTGTTAGCTGTGAATTTACCCTGTACAGCTGTA NM_012301 RefSeq chr7
- 78017056 79453574 MAGI2 9863 "membrane associated guanylate kinase, WW and PDZ domain
containing 2, transcript variant 1"
GO:0051898|GO:0005515|GO:0048471|GO:0008285|GO:0072015|GO:0005886|GO:0030159|GO:0045202|GO:0005
634|GO:0046332|GO:0031697|GO:0060395|GO:0051291|GO:0030425|GO:0005737|GO:0070699|GO:0016482|GO:0
004871|GO:0030336|GO:0003402|GO:0005770|GO:0019902|GO:0014069|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_76879_PI430048170 0.524509042338476 1.19391683986301 2.38484560301344 1.90434940796373
1.57333404703535 A A A 0.860362162203915 2.53736971183138 1.25201986884646 A P A
LNCV6_76879_PI430048170 mRNA
CAGACAAAGCTGCCATCCGAAAGGAGCTCAATGAATTCAAAAGCACTGAGATGGAAGTTC NM_030948 RefSeq
chr6 + 12716804 13287843 PHACTR1 221692 "phosphatase and actin regulator 1, transcript variant
1"
GO:0030054|GO:0031532|GO:0004864|GO:0043149|GO:0031032|GO:0045202|GO:0003779|GO:0005634|GO:0043
086|GO:0005829|GO:0008599|GO:0048870|GO:0008157 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136198_PI430048170 0.241042769518616 1.167314933619 0.307711032595433
0.735764483501682 0.414879154808794 A A A 0.28569059094384 0.252511355114246
0.285398855036043 A A A LNCV6_136198_PI430048170 mRNA
CAACACTGCACATGTTTAACACAAAACAAAACAAACAAACTCCTGCCAGCTACAACAGGG NM_001080500 RefSeq
chr2 + 214411736 214575929 VWC2L 402117 von Willebrand factor C domain containing protein 2-like
GO:0030514|GO:0030054|GO:0045666|GO:0032281|GO:0045202|GO:0005615 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_102954_PI430048170 0.343201269692659 0.832917776651168 4.86472782756816
4.25260160557908 4.54188339575942 P P P 5.11336982976979 4.51750667392413
4.82338881130751 P P P LNCV6_102954_PI430048170 mRNA
AATACAGTCTGTTCTCCTCCAGCTCCTTCTTTCTGCAACATGGGGAAGAACAAACTCCTT NM_000014 RefSeq chr12
- 9067707 9115962 A2M 2 alpha-2-macroglobulin
GO:0005515|GO:0007264|GO:0004867|GO:0072562|GO:0002020|GO:0019959|GO:0005829|GO:0019966|GO:0019
838|GO:0022617|GO:0030198|GO:0031093|GO:0070062|GO:0001869|GO:0051056|GO:0043120|GO:0005102|GO:0
030168|GO:0005576|GO:0010951|GO:0048863|GO:0007596|GO:0007597|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139356_PI430048170 0.913922146925394 1.00063595179054 1.3816127641112
1.98399835928379 0.705468243674646 A A A 1.66188076176022 0.9140020051396
1.65002395406851 A A A LNCV6_139356_PI430048170 mRNA
TACCTGTTTTAATCACATGAGTATATGTCCCAGTACACAAAAGGGCACTGGTTGGCATTC NM_018652 RefSeq chr15
+ 72654696 72667397 GOLGA6B NA "golgin A6 family, member B" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_142763_PI430048170 0.691870795466181 0.9259542178507423.59733925898454
3.31111632990141 1.49483355164692 P P A 3.15408709338166 3.54607747290945 2.6441716630675
P P P LNCV6_142763_PI430048170 mRNA
TGAAAACTCTGCCTCATGCCCCACTGGCTGCAGCACCTTGATGTAAAGACCATTAAAAAA NM_178495 RefSeq chr2
+ 96326196 96328353 ITPRIPL1 150771 "inositol 1,4,5-trisphosphate receptor interacting protein-like 1,
transcript variant 1" GO:0016020|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62082_PI430048170 0.562233644204569 0.977826155355778 0.469299404116144 0.481421486190229
0.363465848438999 A A A 0.401424404583712 0.516909744058545 0.493235027688977 A A A

LNCV6_62082_PI430048170 mRNA
AGACAACATGAAGCTCCATAAGGTGGACTTTATCTGGATCAACAGAGACCAGCGGTCTTT NM_001184780 RefSeq
chr15 + 68930499 69057161 NOX5 79400 "NADPH oxidase, EF-hand calcium binding domain 5,
transcript variant 3"
GO:0050661|GO:0042554|GO:0005515|GO:0050663|GO:0005783|GO:0008283|GO:0050660|GO:0043012|GO:0005
509|GO:0006915|GO:0001525|GO:0000910|GO:0016175|GO:0001935|GO:0015252|GO:0010155|GO:0016021|GO:2
000379|GO:0055114|GO:0020037|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133347_PI430048170 0.0866608826770382 1.31231607781979 6.98246650507642
6.81775543455251 6.83358132970686 P P P 6.69824091595913 6.50554124652884
6.21981497409542 P P P LNCV6_133347_PI430048170 mRNA
TTAATGTCTGCCAGGAGTTCTAATCCTGCCTCTGTTCCCTTTTCTCTCCTTGAAAGTCCA NM_020439 RefSeq chr1 +
209583699 209613939 CAMK1G 57172 calcium/calmodulin-dependent protein kinase IG
GO:0043005|GO:0005516|GO:0005886|GO:0000139|GO:0006468|GO:0004683|GO:0005524|GO:0005954 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140060_PI430048170 0.0452553287096075 0.6732102324601926.11624115797139
5.87483322950536 6.27340346227859 P P P 6.36087297566061 6.72717430210897
6.87010936873619 P P P LNCV6_140060_PI430048170 mRNA
GAACCCAAACTGTATGGGGATATTTGATGTTTTCAGAAAGAGGAAGAAAATATGGTCCAA NM_001134779 RefSeq
chr5 + 62418883 62628589 IPO11 51194 "importin 11, transcript variant 1"
GO:0005737|GO:0006610|GO:0008565|GO:0008536|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132433_PI430048170 0.00565046089146666 0.2843943875914552.25669211365347
2.68056789892055 2.98153196802544 A A P 4.40666183258387 4.36730862206997 4.6593576603979
P P P LNCV6_132433_PI430048170 mRNA
GGTGGCAAGAAGGTGAAGATTACTACCTCTTTTGATATAACTAGTTTCTGAGGTATTTAA NM_152292 RefSeq chr4
- 99546706 99563668 TRMT10A 93587 "tRNA methyltransferase 10 homolog A (S. cerevisiae),
transcript variant 1"
GO:0008150|GO:0000049|GO:0010960|GO:0008168|GO:0030488|GO:0005730|GO:0005634|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133848_PI430048170 0.5604831590536690.9664610338405470.480708721355802
0.4789412687429920.26328449137215 A A A 0.4033691710512050.513927446357183
0.461816126881307 A A A LNCV6_133848_PI430048170 mRNA
CCTCTGAAATATACTGTCACCTTAAAACCACATCAGACTGTAATGTGAATTTTTGTAGAG NM_001177479 RefSeq
chrX - 84317873 84502479 HDX 139324 "highly divergent homeobox, transcript variant 1"
GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136372_PI430048170 0.1306023433335880.7966445640098735.97826882293343
5.99442091191957 6.35301657999331 P P P 6.43125396566819 6.22778964996384
6.65143920491757 P P P LNCV6_136372_PI430048170 mRNA
TTGTTTCTCAGATTAAGACACTGTTAGAACCTAAAGTAGTAGCTGATGGGTATCTGTGAA NM_178169 RefSeq chr12
+ 64610512 64697567 RASSF3 283349 "Ras association (RalGDS/AF-6) domain family member 3, transcript
variant 1" GO:0005515|GO:0007165|GO:0005737|GO:0005886|GO:0005874|GO:0042802 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_132077_PI430048170 0.8366644632289381.0437913337882 6.38937989516241
6.53939319123033 6.99614910598794 P P P 6.56615300594021 6.38966770281888
6.82178067733533 P P P LNCV6_132077_PI430048170 mRNA
CAAATGATAACCGAAGGACGTATGAATGGATTTATTGACCAGATTGATGGAATAGTTCAT NM_016129 RefSeq chr4
+ 83035085 83075818 COPS4 51138 "COP9 signalosome subunit 4, transcript variant 1"
GO:0005515|GO:0000338|GO:0030054|GO:0008180|GO:0010388|GO:0005654|GO:0005634|GO:0070062|GO:0008
021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_129501_PI430048170 0.3535621283923521.38994792525521 2.74615082144753
2.11734152799546 1.90973605241597 A A A 1.07654575578435 2.64390239374803
1.19706007068163 A A A LNCV6_129501_PI430048170 mRNA
TTCCAGGCAACTTGTTACTAACCAGCCTTTGGGTCTCGCCTTTTTGGATCATCTTACTGA NM_181623RefSeq chr21
+ 30440327 30440780 KRTAP15-1 254950 keratin associated protein 15-1 GO:0005882 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143110_PI430048170 0.8349784068407581.05196640107246 1.07249023920532
0.4661521901040320.441544033258317A A A 0.8370406194158990.348894928398796
0.62606792108546 A A A LNCV6_143110_PI430048170 mRNA
CCACAGCTGCAGGGCCAACAGATTACATGGATTGGGAAGTCTTTAGTATAAATATATTTT NM_014334RefSeq chr9
- 109137300 109167291 FRRS1L 23732 ferric-chelate reductase 1-like
GO:0008150|GO:0003674|GO:0030054|GO:0005886|GO:0045202|GO:0016021|GO:0005575 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_53128_PI430048170 0.1025518217190870.6882358734405159.67802165411725 10.0619852931246
10.3934961081936 P P P 10.3910160131026 10.515636111276 10.885025704876 P P P
LNCV6_53128_PI430048170 mRNA
GAATAGAACTTTCTCATTCATCTTTGAATAACGTCTCCTTGTTTACCCTGGTATTCTAGA NM_014736RefSeq chr15 -
64365011 64381510 KIAA0101 9768 "KIAA0101, transcript variant 1"
GO:0051297|GO:0006260|GO:0005515|GO:0048471|GO:0005737|GO:0003682|GO:0051726|GO:0005634|GO:0019
985|GO:0009411|GO:0006974 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136350_PI430048170 0.1383355157822170.4400320656225920.450251590228249
1.89071056273134 0.287221747193628A A A 1.27117066188881 2.75072025817678 2.367676208112
A P P LNCV6_136350_PI430048170 mRNA
CATCCCTATGCTGTACTTAAATGTCGAACAAAATGAGAGACAAAAATGAAGGAATCAAAC NM_001040129 RefSeq
chr5 + 148268859 148286210 SPINK13 153218 "serine peptidase inhibitor, Kazal type 13 (putative)"
GO:0010951|GO:0004867|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132647_PI430048170 0.4318896626363060.7726953446506470.363606203467618
3.05107593307687 1.69857077290202 A P A 2.59114899897682 2.29688489080604
2.49888321664448 P A P LNCV6_132647_PI430048170 mRNA
CATTCAAGCAAAATATCACAGTGGTCTTTTGTTTTCTGACCAATCTAACAATACCTGTGA NM_001166160 RefSeq
chr7 + 94907636 95296415 PPP1R9A 55607 "protein phosphatase 1, regulatory subunit 9A,
transcript variant 1"
GO:0005515|GO:0051015|GO:0030054|GO:0019722|GO:0043197|GO:0045202|GO:0007015|GO:0030864|GO:0030
175|GO:0031175|GO:0030426 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112197_PI430048170 0.0421298609593162 1.56075503391062 9.7812710998181
9.76165228404189 9.66332967424336 P P P 9.26673130658881 9.18860475194031
8.78145895004316 P P P LNCV6_112197_PI430048170 mRNA
TGGACACGGCCTCCTCGGATGAGGAGAATGAGGACGGAGACTTCACGGTGTACGAGTGCC NM_015392RefSeq
chr9 - 137039456 137046224 NPDC1 56654 "neural proliferation, differentiation and control, 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139438_PI430048170 0.6371607418468591.17364170091759 1.30495848045492
0.2552217851413051.37393509794375 A A A 0.2595094864189190.250625127726668
1.55761415015626 A A A LNCV6_139438_PI430048170 mRNA
GTTAAGTGAGGCCAGGCCTTTCCTTGCAATATCGTTAATGGCCCTTTTCAGGGCCGCGTA NM_003547RefSeq chr6
- 26246610 26246977 HIST1H4G 8369 "histone cluster 1, H4g"
GO:0008150|GO:0003674|GO:0046982|GO:0005634|GO:0000786|GO:0003677 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130531_PI430048170 0.1225636248443450.7698422309565216.54793066791743
6.61325802763606 6.95358055155073 P P P 6.85210923302846 7.04064644594972

7.34454743281628 P P P LNCV6_130531_PI430048170 mRNA
GCCAATTGAAATCAGACATATGCGATCTTGGGTTTTTGCATGGAAATTAATGTAATGCTT NM_178496 RefSeq chr3
- 192796815 192918161 MB21D2 151963 Mab-21 domain containing 2 GO:0032403 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_68845_PI430048170 0.1336662637446430.580960372323016 1.83792205530479 2.35940108140168
3.12560569991162 A A P 3.62584671185892 3.09047399578921 3.19324583908334 P P P
LNCV6_68845_PI430048170 mRNA
TGTAACCTGGATTGCAGAAGGGGCCAGTTTGGGCCCAGCTGCACCCTGCACTGTGACTGC NM_001409 RefSeq chr1
- 3487941 3611495 MEGF6 1953 multiple EGF-like-domains 6
GO:0005515|GO:0008150|GO:0005509|GO:0005576|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142744_PI430048170 0.1933188508708661.04609233297471 0.351961301473889
0.3432264529970750.450364218410768 A A A 0.3101275013374760.295374874815862
0.346999916732833 A A A LNCV6_142744_PI430048170 mRNA
GCCACTGTGCTGAATTCTGCAATGTTTTCCTTTGTCATCATTGTATATATGTGTGTTTAA NM_000905 RefSeq chr7 +
24284187 24291865 NPY 4852 neuropeptide Y
GO:0008343|GO:0007631|GO:0021987|GO:0008283|GO:0008015|GO:0032100|GO:0007268|GO:0006928|GO:0032
098|GO:0005615|GO:0031175|GO:0007218|GO:0007610|GO:0006816|GO:0005184|GO:0005794|GO:0005246|GO:0
004930|GO:0007586|GO:0031841|GO:0005623|GO:0005102|GO:0021954|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_109738_PI430048170 0.6194319021384341.03242760047906 0.28000340488107
0.2887154066511350.501484665237907 A A A 0.3309545752733930.284579396543722
0.327169414580977 A A A LNCV6_109738_PI430048170 mRNA
GTTTACATCAAGTTTCTAAAAGGCAACAGGTGGATCAACTGCCTAGGATGCAAGAGAATC NM_001198910 RefSeq
chr13 - 36168207 36297855 CCDC169-SOHLH2 NA CCDC169-SOHLH2 readthrough NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135937_PI430048170 0.0255406880903697 0.7654196353628177.48205310846173
7.2512557906808 7.22445724942246 P P P 7.70465528577857 7.77749982648473
7.64366982962926 P P P LNCV6_135937_PI430048170 mRNA
TGGGCCTGAACTGGGCCATTGATCAGACTAAATAAATTAAGCAGTTAACATAACTGGCAA NM_016733 RefSeq chr22
+ 31248361 31280080 LIMK2 3985 "LIM domain kinase 2, transcript variant 2b"
GO:0005515|GO:0016310|GO:0005801|GO:0005737|GO:0046982|GO:0004674|GO:0008270|GO:0006468|GO:0005
634|GO:0007283|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144863_PI430048170 0.2627489972127940.939511843493071 0.261303536517218
0.3631505137780730.276211125703894 A A A 0.48901552941951 0.384388238462181
0.29272911443434 A A A LNCV6_144863_PI430048170 mRNA
ATGTAAAATCCTACAGTGAAATGAGCAGCCCTTACAGTATTGTTACCACCAAGGGCAGGT NM_002460 RefSeq chr6
+ 391738 411443 IRF4 3662 "interferon regulatory factor 4, transcript variant 1"
GO:0005515|GO:0003700|GO:0034122|GO:0045404|GO:0019221|GO:0005634|GO:0072540|GO:0005829|GO:0005
737|GO:0060337|GO:0045944|GO:0000788|GO:0045368|GO:0043011|GO:0060333|GO:0018022|GO:0042832|GO:0
000978|GO:0016279|GO:0006351|GO:0043565|GO:0045086|GO:0001077|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_59702_PI430048170 0.1015026470565180.8172612218868666.74551310061512 6.48788115741313
6.37329207526242 P P P 6.82432048384301 6.77742453764252 6.90116252009507 P P P
LNCV6_59702_PI430048170 mRNA
ATTTATCTGCAGAAGGAACTTTGGGGTGCAGCCAGGACCCGTCAGCACACTGGGAAACCGNM_003959 RefSeq chr12
+ 122835437 122862960 HIP1R 9026 "huntingtin interacting protein 1 related, transcript variant 1"
GO:0005515|GO:0048471|GO:0030036|GO:0030136|GO:0003779|GO:0006898|GO:0043231|GO:0030665|GO:0005
737|GO:0005905|GO:0005856|GO:0030674|GO:0035091 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_135925_PI430048170 0.0031556190278206 4.02430832055855 5.97427167082829
6.29376271816419 5.93907605402281 P P P 4.44610423153367 3.92165276960736
3.74533289899384 P P P LNCV6_135925_PI430048170 mRNA
GATGCTTCTGAATAGAAATAAAGTGGGTTTTCCCTGGAGGTACCCAGCAGCCTGAAAAAA NM_139317RefSeq chr20
+ 63235882 63240507 BIRC7 79444 "baculoviral IAP repeat containing 7, transcript variant 1"
GO:0005515|GO:0043066|GO:0004842|GO:0004869|GO:0005794|GO:0016567|GO:0016874|GO:0070247|GO:0005
634|GO:0007257|GO:0009966|GO:0005737|GO:0042127|GO:0005876|GO:0008270|GO:0090307|GO:0019899|GO:0
043027 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137050_PI430048170 0.000532278366897542 0.47171226254667 5.89413177454162
5.74984033861821 5.62366697755662 P P P 6.72186940045903 6.92339357152184
6.87946017114267 P P P LNCV6_137050_PI430048170 mRNA
CCACAGGGAAGCATGTACTGTACTTCCCAATTGCCACATTTTAAATAAAGACAAATTTTT NM_000196RefSeq chr16
+ 67431132 67437551 HSD11B2 3291 hydroxysteroid (11-beta) dehydrogenase 2
GO:0001666|GO:0032868|GO:0007565|GO:0005783|GO:0042493|GO:0006704|GO:0003845|GO:0051384|GO:0032
094|GO:0051287|GO:0002017|GO:0005496|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128654_PI430048170 0.00977971107327997 0.2453261720347331.53847120049872
0.4167491428627090.698377929080194A A A 2.5462840887881 2.97804277768748
3.34712045643831 A P P LNCV6_128654_PI430048170 mRNA
CATCACACACACCCAAAGGCAAAGAAGGCAACGGTTGCTCCAAAAGTCAAAAGAACTCTA NM_030955RefSeq
chr5 - 33527180 33892019 ADAMTS12 81792 "ADAM metallopeptidase with thrombospondin type 1
motif, 12"
GO:0071773|GO:0005515|GO:0005578|GO:0050727|GO:2001113|GO:0030167|GO:0031012|GO:0007160|GO:0016
477|GO:0051603|GO:0071347|GO:0071356|GO:0008270|GO:0032331|GO:0004222 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_106415_PI430048170 0.161998770280356 1.60025308901764 3.83370950213677
3.49617384990624 3.74914180839314 P P P 3.53835963666179 2.29314890274296
2.97158040063963 P A P LNCV6_106415_PI430048170 mRNA
AGGATGCTCCCTACAGTTCGCTACTGACCAACAAGGAGAAACATGCAAATGTTTTAGCCA NM_001204478 RefSeq
chr17 - 15436014 15563631 TVP23C-CDRT4 100533496 "TVP23C-CDRT4 readthrough, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144216_PI430048170 0.131446542011951 0.7896195653770987.30426886872457
7.19423121720755 7.44869643374674 P P P 7.53256853098486 7.47640693666987
7.92856703177654 P P P LNCV6_144216_PI430048170 mRNA
GGCATAGTTTCATAATTGTGTACTCGGAAATTAAAGTTTGCTTGTTTCTTGGTCTGGATT NM_004622RefSeq chr2
+ 121755544 121767852 TSN7247 "translin, transcript variant 1"
GO:0043565|GO:0005515|GO:0010467|GO:0005737|GO:0003697|GO:0006310|GO:0005634|GO:0004521|GO:0003
729|GO:0032403|GO:0003677|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135132_PI430048170 0.00479972842296465 0.2822713883387680.453017762222707
0.4750042696787440.408365500194226A A A 2.11782124526424 2.5280417334331
2.12670342673836 A A A LNCV6_135132_PI430048170 mRNA
CCCAGAGATATTAGAAGTATGCTACAGTGAATGTTAAAGTACCTTGAGATCCTTAAATCA NM_003839RefSeq chr18
+ 62325286 62387710 TNFRSF11A 8792 "tumor necrosis factor receptor superfamily, member 11a, NFKB
activator, transcript variant 1"
GO:0005515|GO:0008284|GO:0071848|GO:0007267|GO:0046872|GO:0060086|GO:0048535|GO:0051091|GO:0051
092|GO:0032496|GO:0071847|GO:0004872|GO:0043507|GO:0034097|GO:0070555|GO:0009314|GO:0071812|GO:0
030316|GO:0033209|GO:0002548|GO:0002250|GO:0007165|GO:0005031|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_68096_PI430048170 0.5972368975366470.8953395115797623.88155434126493 3.80491212426903
4.23320920917935 P P P 3.71796114162035 4.41678007866513 4.21408477311931 P P P

LNCV6_68096_PI430048170 mRNA
AAGATTCCAAGGAGCTTTTGCAGAACTCTCAGAGTAGACAAGCAAAAGGGCACAAGAGTG NM_017886RefSeq
chr3 - 41246598 41962168 ULK4 54986 unc-51 like kinase 4
GO:0003351|GO:2001222|GO:0000226|GO:0005524|GO:0046328|GO:0022038|GO:0004674|GO:0090036|GO:0010
975|GO:0021591|GO:0043408|GO:0060271|GO:1900744|GO:0006468 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145223_PI430048170 0.0278964771468117 0.3652990669466967.97664726989478
7.22179026033464 7.12866389924767 P P P 8.88127408124928 9.02674266571342
8.93109727660544 P P P LNCV6_145223_PI430048170 mRNA
CTCTCCCACCCTCAACTCCACCAAAGTAAATCCTTTCGATAGTAAAAGTTTAATAATTTC NM_016652RefSeq chr20
- 20034360 20056046 CRNKL1 51340 "crooked neck pre-mRNA splicing factor 1, transcript variant 1"
GO:0005515|GO:0000245|GO:0005737|GO:0016607|GO:0000398|GO:0003723|GO:0005681|GO:0071013 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139279_PI430048170 0.6357783417151011.0511092759068 8.19469768465801
8.29189244197404 8.21986444487431 P P P 7.83217365637111 8.31940003777649
8.29107651232535 P P P LNCV6_139279_PI430048170 mRNA
AAGCCTGTGGTCTAGGAGTGCTATTCAGTGTTTCTTTTCCTGATAAACACTTTGAATATT NM_014384RefSeq chr11
+ 134253539 134265852 ACAD8 27034 "acyl-CoA dehydrogenase family, member 8"
GO:0006629|GO:0034641|GO:0006355|GO:0005759|GO:0050660|GO:0006574|GO:0009083|GO:0003995|GO:0044
281|GO:0006351|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131025_PI430048170 0.5072695436660590.86517148629329 4.45665416333211
4.74104517239768 4.12644829215346 P P P 4.46792535278982 5.05492175281604
4.39952454499174 P P P LNCV6_131025_PI430048170 mRNA
GGATCAAGGTGTTCACTAGAAGTCACTGTTACTAATACTTGATGACAATGTAAAGAAACA NM_003017RefSeq chr6
+ 36594312 36604467 SRSF3 6428 "serine/arginine-rich splicing factor 3, transcript variant 1"
GO:0008380|GO:0005515|GO:0010467|GO:0006369|GO:0005737|GO:0006406|GO:0006366|GO:0000166|GO:0000
398|GO:0003723|GO:0031124|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134571_PI430048170 0.7941786259613820.8937946993173713.05797015525446
2.78461076772508 3.09056833454868 P A P 2.75705778398568 2.76153864481993 3.7022149899444
P P P LNCV6_134571_PI430048170 mRNA
AAGCCCTTTACAACCATTAAATAAAGAACACCAGCTGCATTATGTGTGTTTAGAACGAGA NM_138348RefSeq chr5
+ 14664673 14699733 OTULIN 90268 OTU deubiquitinase with linear linkage specificity
GO:0005515|GO:0005737|GO:0004843|GO:0050728|GO:0045087|GO:0006508|GO:0071797|GO:0070431|GO:0032
088|GO:0002040|GO:0008234|GO:0060070 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126484_PI430048170 0.6486516767282110.9146170301572019.86925668665223
9.41168126964585 9.80013295436333 P P P 9.51609248564904 9.75257352268329
10.1638936473589 P P P LNCV6_126484_PI430048170 mRNA
AATTTGGTTCTGAGCGAGATGAGTACCGGGAGAAGTCAGAGAGTGGGGGCAGTGAATATG NM_001005271
RefSeq chr17 + 7884804 7912757 CHD3 1107 "chromodomain helicase DNA binding protein 3,
transcript variant 3"
GO:0005515|GO:0006355|GO:0005813|GO:0006357|GO:0004386|GO:0005730|GO:0006325|GO:0005634|GO:0003
677|GO:0005524|GO:0006351|GO:0006333|GO:0051297|GO:0005737|GO:0004003|GO:0016581|GO:0008270|GO:0
005654|GO:0045111|GO:0032508|GO:0007051|GO:0016568 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_143666_PI430048170 0.5666284120175170.9639468379421334.84062209782245
4.90692033084987 4.99712595059428 P P P 4.96417595692833 4.85050424773687
5.08376757160855 P P P LNCV6_143666_PI430048170 mRNA
CTTGGGAGAGATCTGAAAAGAAGGTGAATATTTTGCACTTTTGATACTCTTAGGAACAAA NM_015291RefSeq chr1
+ 15526812 15571733 DNAJC16 23341 "DnaJ (Hsp40) homolog, subfamily C, member 16, transcript

variant 1" GO:0045454|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130783_PI430048170 0.0551118949755747 0.867641091002681 10.3068532261751
10.311592042956 10.303962823672 P P P 10.4170159733009 10.587409843162 10.527335108005
P P P LNCV6_130783_PI430048170 mRNA
GGCAACTGGGAGATTTGTGAGTGAACACTGTTTCATCTTAATATGCTTCTGAATTTATTT NM_032848 RefSeq chr12
+ 113185525 113192368 RITA1 84934 "RBPJ interacting and tubulin associated 1, transcript variant 1"
GO:0005515|GO:0045746|GO:0005813|GO:0005737|GO:0005794|GO:0015631|GO:0007219|GO:0005654|GO:0005
634|GO:0000122|GO:0051168|GO:0022008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145526_PI430048170 0.63362763984084 0.841485691530632 1.03729494304919
0.293360065683974 0.86245866512205 A A A 1.26878479396282 0.268990423691509
1.28771311820912 A A A LNCV6_145526_PI430048170 mRNA
CTGGTGTCGTATTTTGCCTGTTAAATCGTAACAAGCAATAAACAACTTTCACTTTGCAAA NM_024490 RefSeq chr15
- 25678712 25863202 ATP10A 57194 "ATPase, class V, type 10A"
GO:0005515|GO:0000287|GO:0005886|GO:0005783|GO:0008360|GO:0055085|GO:0005524|GO:0006886|GO:0045
332|GO:0034220|GO:0004012|GO:0008152|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_135200_PI430048170 0.809746772277665 0.988470976250471 0.314455021976433
0.487351026027905 0.360345171594619 A A A 0.489610068037794 0.372609022491428
0.351869624919391 A A A LNCV6_135200_PI430048170 mRNA
CATATGTGGGTGACAGAAGCATATGTTACAGTGAAACATTAAAACTACAGCAAAGTGAAA NM_145912 RefSeq chr22
- 42380407 42432395 NFAM1 150372 NFAT activating protein with ITAM motif 1
GO:0050853|GO:0045577|GO:0005886|GO:0009986|GO:0001819|GO:0050861|GO:0035556|GO:0007165|GO:0051
091|GO:0006954|GO:0030183|GO:0045121|GO:0016021|GO:0004888 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_136794_PI430048170 0.0930977331297147 0.925378778250502 0.316342491622115
0.31237484359382 0.29233142069921 A A A 0.485949022607037 0.411838204698054
0.356080672150578 A A A LNCV6_136794_PI430048170 mRNA
TTGCCAATTCATTTCTCTATCCTGTGTATGTATAAGTGTGTACAAGCATTCAAGAAACTG NM_032608 RefSeq chr22
+ 25742152 26031041 MYO18B 84700 myosin XVIIIB
GO:0005813|GO:0003774|GO:0016461|GO:0008152|GO:0005654|GO:0003779|GO:0030017|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114016_PI430048170 0.482210937290481 1.47831945255029 0.254651725495616
0.370530721327013 1.71633833418173 A A A 0.467320091014628 0.360250205006289
0.308210865795773 A A A LNCV6_114016_PI430048170 mRNA
TTGTTGGACTAATGGGCAAAAGAGCTTTAAATTCTGGGCTTATGAAAGGAGTGCAATGCA NM_003182 RefSeq chr7
+ 97731958 97740472 TAC1 6863 "tachykinin, precursor 1, transcript variant beta"
GO:0005515|GO:0030424|GO:0005886|GO:0007267|GO:0007268|GO:2000854|GO:0045778|GO:0007204|GO:0005
615|GO:0006954|GO:0002675|GO:0007218|GO:0031835|GO:0043025|GO:0032496|GO:0045760|GO:0009725|GO:0
008306|GO:0010459|GO:0007616|GO:0050671|GO:0007217|GO:0043278|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142071_PI430048170 0.820539169174854 0.982730705434113 0.304867952730495
0.515430383910834 0.35792325728702 A A A 0.532857525782413 0.443303936641918
0.273989230854313 A A A LNCV6_142071_PI430048170 mRNA
CAGCAGATGGAAAACTAAAGCAAATGTAATCACCTGCATTTTGAAAATAGGTGTGTTTCT NM_001162483 RefSeq
chr2 - 227610089 227633320 C2orf83 56918 "chromosome 2 open reading frame 83, transcript variant
2" GO:0016020|GO:0006810 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128650_PI430048170 0.0650418299450115 3.08144262375133 3.39237980081579
2.89624194172309 2.40427166868831 P A A 2.18052758505261 0.310550556463983
0.822296016647377 A A A LNCV6_128650_PI430048170 mRNA

TGTGCTGGTAGTGGACCCGGGAACCAGATGCCATTACAGCACGCTGGCCTTCTCGCTCCT NM_001289974 RefSeq
chr1 - 22953042 22965430 LACTBL1 646262 "lactamase, beta-like 1" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_133285_PI430048170 0.000114535197202779 4.25561492649914 7.91852935185541
8.0868309934244 8.16022608180119 P P P 5.86599401480291 6.15644397885981
5.86564502614121 P P P LNCV6_133285_PI430048170 mRNA
CTTGGCTGATGTTCTGTATCTTAACATGACCACAGTTTGTAAGTACAAAGGTAATTGGTA NM_152365 RefSeq chr1
- 26949555 26960410 KDF1 126695 keratinocyte differentiation factor 1
GO:0010839|GO:0060887|GO:0030054|GO:0010482|GO:0061436|GO:2000647|GO:0003334|GO:0005737|GO:0045
606|GO:0048589|GO:0016331|GO:0005938|GO:0031252 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145633_PI430048170 0.20752765638529 1.07269498248836 0.335642993883599
0.4608590928517520.277898916786005 A A A 0.25755771239004 0.261547684196288
0.257678308740174 A A A LNCV6_145633_PI430048170 mRNA
AACGTATGTGTGTGTGTTTAATTAGAATAAAATTCCTCTAGGCAGATTTCAGGAGCTCCA NM_001099 RefSeq chr3
+ 132317366 132358846 ACPP 55 "acid phosphatase, prostate, transcript variant 1"
GO:0033265|GO:0005886|GO:0003993|GO:0046085|GO:0005634|GO:0030175|GO:0005765|GO:0005615|GO:0042
131|GO:0042803|GO:0042802|GO:0005622|GO:0016791|GO:0006772|GO:0052642|GO:0060168|GO:0030141|GO:0
070062|GO:0012506|GO:0005771|GO:0031985|GO:0045177|GO:0006144|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130249_PI430048170 0.1279722651843790.9477562894704290.257872657626765
0.2688856068810870.329545232279958 A A A 0.4243373692858950.3458787828223
0.317218036710514 A A A LNCV6_130249_PI430048170 mRNA
GTCTAGACATGCTTTGTTCAACTAGGTAATCACACGGGGTAAATTGGATTTAAATGTAAT NM_020709 RefSeq chr19
- 46491190 46495912 PNMAL2 57469 paraneoplastic Ma antigen family-like 2 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_91306_PI430048170 0.3632332994018521.15801586281274 5.08299155634118 5.10211974947588
4.78262593137993 P P P 5.13370879893514 4.51643282493874 4.62668959095778 P P P
LNCV6_91306_PI430048170 mRNA
ATCCATTGAAGGCCCTCCCAGACTGACGAAGGCGTGACCTCAGGCCCACCGCATCCAAGA NM_001037163 RefSeq
chr7 - 6329408 6348959 FAM220A 84792 "family with sequence similarity 220, member A"
GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143845_PI430048170 0.5337329718294010.6267023470879780.491707921844659
1.79514796310945 0.822565919458746 A A A 2.68195114142875 1.47130956610724
0.499191079096978 A A A LNCV6_143845_PI430048170 mRNA
GCCATGGTCCCCAAGACCTCTATATTTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTA NM_001142797 RefSeq chrX
- 71615915 71618517 CXCR3 2833 "chemokine (C-X-C motif) receptor 3, transcript variant 2"
GO:0008284|GO:0019722|GO:0005886|GO:0006928|GO:0002685|GO:0007204|GO:0019958|GO:0010818|GO:0019
956|GO:0005737|GO:0006954|GO:0050921|GO:0006935|GO:0045944|GO:0004950|GO:0043950|GO:0030816|GO:0
004872|GO:0007155|GO:0051281|GO:0070098|GO:0006915|GO:0001525|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129232_PI430048170 0.9561804582331051.00537925511306 11.0197365425252
11.1383383648674 11.4084305878893 P P P 11.1961763856898 10.9439092425258
11.3958447045276 P P P LNCV6_129232_PI430048170 mRNA
AGCCTGTCAGATTCTAACAACAAAAGCTGAATTTCTTCACCCAACTTAAATGTTCTTGAG NM_016077 RefSeq chr17
- 59697305 59707598 PTRH2 51651 peptidyl-tRNA hydrolase 2
GO:0005739|GO:0005515|GO:0016020|GO:2000210|GO:0010629|GO:0008152|GO:0006915|GO:2000811|GO:0004
045|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92044_PI430048170 0.2549049748045391.14071532933563 6.73434287169149 6.50072606104537
6.42181164843146 P P P 6.56386290455303 6.32750468069085 6.18915730636594 P P P

LNCV6_92044_PI430048170 mRNA
TTAAGAACACCATCACAGTGTCCCCCTTCTCGGGCGAGAGTGACATCTGTCCGCAGGACA NM_020376 RefSeq chr11
+ 818900 825571 PNPLA2 57104 patatin-like phospholipase domain containing 2
GO:0005811|GO:0004806|GO:0005886|GO:0019915|GO:0010898|GO:0044281|GO:0034389|GO:0043231|GO:0005
829|GO:0010891|GO:0005789|GO:0036155|GO:0016021|GO:0019433|GO:0006644|GO:0046474 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_112262_PI430048170 0.833864495852527 1.04316858895704 7.22450451937537
6.67502795335303 7.25816210125028 P P P 6.66922152659015 7.06957829963153 7.2476232815255
P P P LNCV6_112262_PI430048170 mRNA
GGTCGCTGCCATCGTAGGATTTGTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAA NM_001278740 RefSeq
chrX - 100627107 100636732 TSPAN6 7105 "tetraspanin 6, transcript variant 2"
GO:0005515|GO:0007165|GO:0039532|GO:0016021|GO:0004871|GO:0043123|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142857_PI430048170 0.0668532426024281 1.0408281117236 12.4900362693464
12.4754484604218 12.5156549997291 P P P 12.3993993012793 12.4574536447505 12.450683143426
P P P LNCV6_142857_PI430048170 mRNA
CAAAGGGCAAGAGGTTGCTATGGTATTTGGAAACAATGAAAATGGACTGTTAGATGCCAA NM_144772 RefSeq chr1
+ 156591765 156594299 APOA1BP 128240 apolipoprotein A-I binding protein
GO:0005515|GO:0005576|GO:0006739|GO:0005615|GO:0052856|GO:0046872|GO:0044297|GO:0042803|GO:0052
857|GO:0006734|GO:0043231|GO:0005739|GO:0005929|GO:0008150|GO:0005737|GO:0000166|GO:0051289|GO:0
005654|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141708_PI430048170 0.41806351450907 1.05030695061977 0.310433369217497
0.316263451363781 0.513653871233768 A A A 0.317791599918448 0.281852782029404
0.337142311781517 A A A LNCV6_141708_PI430048170 mRNA
CTGATCAAGAAAAGGCCCACTTTTTAAAAAGTGAAACAAGTTTGCAGATACGGTTCTCTT NM_001135196 RefSeq
chr10 + 49299141 49327492 C10orf71 NA chromosome 10 open reading frame 71 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128995_PI430048170 0.339145076125075 1.04490138872661 0.304147538110772
0.277727894973014 0.438112902746746 A A A 0.290201415735762 0.254791568684767
0.289786049997816 A A A LNCV6_128995_PI430048170 mRNA
CCCAAATAAAAGCACAATCTTTGGAATCACTCTATCTTTGGTCAGGCAAATGTTTAAAGA NM_001130002 RefSeq
chr3 + 157543343 157601232 PQLC2L 152078 "PQ loop repeat containing 2-like, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138428_PI430048170 0.135441321644362 1.70403301331021 1.42303290043126
1.41638416739813 2.16979125206908 A A A 0.415401553502628 0.634665594983168
1.53320923400699 A A A LNCV6_138428_PI430048170 mRNA
CTCTATTGTTCTTAAGGGTACCCCTGCTAATTAATTCCCCAAATAAAATTTTTGGTGTTGNM_013373 RefSeq chr22 +
20131840 20148007 ZDHHC8 29801 "zinc finger, DHHC-type containing 8, transcript variant 2"
GO:0005739|GO:0018345|GO:0005794|GO:0016409|GO:0008270|GO:0007626|GO:0016021|GO:0030659|GO:0019
706 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133437_PI430048170 0.455206142642972 1.0451687678501 0.284006712057237
0.294110232457759 0.486809605777761 A A A 0.31223090578464 0.274908400350724
0.295522169387734 A A A LNCV6_133437_PI430048170 mRNA
CAATGCTCAAACCTTATTGCACAGGAAAGCCTTTATACTTGATGAGAACAAATGTACAAA NM_001098626 RefSeq
chr19 - 22391096 22422346 ZNF98 NA zinc finger protein 98 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142740_PI430048170 0.0150429764163536 0.325203187414981 4.2049002693966
4.19550981364458 4.38269549314338 P P P 5.43442390086468 5.8905879881575 6.2215810959262
P P P LNCV6_142740_PI430048170 mRNA

CACATTTTTAAAACCAAATGTTCAATCTGTATTACTCTTTGCCGTCTTGTATGTAGAGGC NM_001142393 RefSeq chr6 - 11183297 11382348 NEDD9 4739 "neural precursor cell expressed, developmentally down-regulated 9, transcript variant 3" GO:0005515|GO:0005794|GO:0005819|GO:0005634|GO:0030027|GO:0007165|GO:0000922|GO:0005737|GO:0007067|GO:0007229|GO:0007010|GO:0007155|GO:0051017|GO:0005925|GO:0005938|GO:0040008|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127320_PI430048170 0.364302426239157 1.26931317404798 0.38250900407326 0.363300619429266 1.1378314810027 A A A 0.3104133781858350.314198393308475 0.368134895318017 A A A LNCV6_127320_PI430048170 mRNA
TTGTGTTGTCTTTTTATGTGGAAACTGCTAGACAACTGTTGAAACCTCAAATTCATTTCC NM_002407 RefSeq chr11 + 62208667 62213939 SCGB2A1 4246 "secretoglobin, family 2A, member 1" GO:0046982|GO:0005615|GO:0030521 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143752_PI430048170 0.1130568772102860.7508340530175731 2.5999644712163 12.4091421558749 12.7395915424647 P P P 12.7310597823082 12.9417866208977 13.2811083790576 P P P LNCV6_143752_PI430048170 mRNA
TAGCACCTGCAATTGTTGGGATGTGGATGGATGTGTGCATAAGAGAGAGAGAGAATATGT NM_020151 RefSeq chr2 - 96184860 96208835 STARD7 56910 StAR-related lipid transfer (START) domain containing 7 GO:0005739|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130977_PI430048170 0.2577726644923520.7865533224073313.88982962944355 4.35378752805168 4.50524373077785 P P P 4.66978127990726 4.87417161336251 4.24286744566587 P P P LNCV6_130977_PI430048170 mRNA
TTAATTTATCTGCTATGTTAAGGCTCGAGGGGTGGGGCGTAGACTCTCAGCTGTATATTG NM_001164446 RefSeq chr6 - 42101118 42142977 C6orf132 647024 chromosome 6 open reading frame 132 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133819_PI430048170 0.367895811033455 1.06845679420865 13.1355535735034 13.0554296014199 13.000668300934 P P P 13.114233153271 12.8223154223769 12.9568929335975 P P P LNCV6_133819_PI430048170 mRNA
CGTTCAAGGCTATGACAGTCTGCTACGCAAAACATTTTTTCAAGTAAAAATAGTAAGAGA NM_032641 RefSeq chr12 - 6870935 6873357 SPSB2 84727 "splA/ryanodine receptor domain and SOCS box containing 2, transcript variant 1" GO:0035556|GO:0005515|GO:0008150|GO:0003674|GO:0005737|GO:0016567|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136013_PI430048170 0.9710160921970591.01379278924668 2.71268520789424 1.74147583130812 3.14660844020404 A A P 3.18500915534347 2.59137778683298 1.75633737652169 P P A LNCV6_136013_PI430048170 mRNA
TATGTTGACCTGTCTGAATTATAAACCAGCCTGACCTTTCCTTTAGCATTAGATGTAATA NM_001215 RefSeq chr1 + 8945833 8975089 CA6 765 "carbonic anhydrase VI, transcript variant 1" GO:0005737|GO:0015701|GO:0008270|GO:0005576|GO:0044281|GO:0004089|GO:0006730|GO:0005615|GO:0001580|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138405_PI430048170 0.0148092568616293 0.5530971616049758.18045853610587 8.08521589823658 8.26666217314835 P P P 8.75252153591937 9.14771016139385 9.16454545361318 P P P LNCV6_138405_PI430048170 mRNA
GAATTCCAGGTGCCTTAATATAAAGTTTGAAGCTTCATCCACCAAAGTTAAATAGAGCTA NM_194463 RefSeq chrX + 106726663 106797016 RNF128 79589 "ring finger protein 128, E3 ubiquitin protein ligase, transcript variant 1" GO:0042036|GO:0048471|GO:0004842|GO:0016567|GO:0005794|GO:0005783|GO:0005770|GO:0016874|GO:0008270|GO:0016021|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135023_PI430048170 0.0488483839523308 0.76438533582672 9.77435229163607 9.91152968399194 10.0460190592888 P P P 10.1054879012238 10.303962823672 10.4745682004171 P P P LNCV6_135023_PI430048170 mRNA

GCAGTTATCTCAGAATTGTTAACGTGAATATATCTGGATGGGGGGTTTTGTAAATAATGA NM_181573 RefSeq chr3 - 186789892 186806695 RFC4 5984 "replication factor C (activator 1) 4, 37kDa, transcript variant 2" GO:0005515|GO:0003689|GO:0005634|GO:0005524|GO:0006260|GO:0005737|GO:0006271|GO:0006281|GO:0000723|GO:0006283|GO:0000722|GO:0006297|GO:0005654|GO:0005663|GO:0006289|GO:0000278|GO:0032201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130206_PI430048170 0.7336372302055280.96267410080925 0.344608857411926 0.3473363781454650.490004065375024 A A A 0.669115229946039 0.29953439877601 0.354607085408435 A A A LNCV6_130206_PI430048170 mRNA
TAGAGAACATGGTGCTTAGGGTCTGAGACCTTTTGAAAGGTCTGAGAACTCTTTAAAAAA NM_001737 RefSeq chr5 - 39284275 39364553 C9 735 complement component 9 GO:0006957|GO:0030449|GO:0005737|GO:0005886|GO:0005579|GO:0005887|GO:0045087|GO:0019836|GO:0006958|GO:0072562|GO:0005576|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144516_PI430048170 0.0286279379509021 1.43664888159109 14.4972395676845 14.9048717431395 14.7374206792834 P P P 14.2533383360938 14.2803135736629 14.0563749468414 P P P LNCV6_144516_PI430048170 mRNA
CTGCTCCTGCTGGCCTGGAAGACTCTGTGGGGTCAGCACTGTACTCCGTTGCTGTTTTTT NM_006412 RefSeq chr9 - 136673142 136687459 AGPAT2 10555 "1-acylglycerol-3-phosphate O-acyltransferase 2, transcript variant 1" GO:0005783|GO:0001819|GO:0044281|GO:0003841|GO:0008544|GO:0001961|GO:0005789|GO:0016024|GO:0019432|GO:0016021|GO:0006644|GO:0006654|GO:0044255|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65031_PI430048170 0.2356369507255231.71502177809318 0.3591210191338461.74084849947124 1.16939901651188 A A A 0.4337645982153080.422969233248605 0.396988946403229 A A A LNCV6_65031_PI430048170 mRNA
AAGCTTGCGGGACGTCGTAGAGAAAACCATCCAAAAGTACGGCACCAACCCCGAGGAGAC NM_001774 RefSeq chr19 + 49335419 49340604 CD37 951 "CD37 molecule, transcript variant 1" GO:0050688|GO:0005515|GO:0001772|GO:0008285|GO:0030886|GO:0016020|GO:0002639|GO:0042832|GO:0002920|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127545_PI430048170 0.1553273766180171.26411216561392 10.686399412428 10.8155639549683 10.7943928501983 P P P 10.10084196394 10.4749857172312 10.6553452687244 P P P LNCV6_127545_PI430048170 mRNA
CAGGAAAGAAGCATTTCTGATACTTTCTGTCAAAAATCAATATGCAGAATGGCATTTGCA NM_000285 RefSeq chr19 - 33386948 33521893 PEPD 5184 "peptidase D, transcript variant 1" GO:0006520|GO:0030145|GO:0004177|GO:0030574|GO:0006508|GO:0016805|GO:0070062|GO:0004181 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131874_PI430048170 0.8133651263390590.9079182387288772.87404752706242 2.73845491275017 2.783371892227 A A A 2.27795068739624 3.23545730782503 3.12760469515308 A P P LNCV6_131874_PI430048170 mRNA
GTGCGACATTGTGTACAAATGTCCTTTATAAAAGTAAAGGCCACTCGCACCCCCAAAAAA NM_001145115 RefSeq chr6 + 5085485 5087221 PPP1R3G 648791 "protein phosphatase 1, regulatory subunit 3G" GO:2000467|GO:0005737|GO:0045725|GO:2001069|GO:0019903|GO:0042593 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137398_PI430048170 0.4714914535878250.6936588158979380.599579327903915 0.4954543522913790.472258828355244 A A A 0.4196248214443140.522963678113695 1.78336822502603 A A A LNCV6_137398_PI430048170 mRNA
TTCGTTGGCTGGGAATGGGGAAGAATGTGATTTTTAAAAATAAAGCATAATCAAACTCTG NM_001128933 RefSeq chr4 + 118888840 119038520 SYNPO2 171024 "synaptopodin 2, transcript variant 2" GO:0005515|GO:0071889|GO:0051371|GO:0030018|GO:0005634|GO:0003779|GO:0015629|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_141874_PI430048170 0.0102765875335090.3204607939794610.553812984750292
0.4694419884420791.30386567597778 A A A 1.96496025896715 2.79047276574248
2.53181095058062 A P P LNCV6_141874_PI430048170 mRNA
GCAACAGGAGGCTTTTTCAGTGATCTTCACTGTATATGTAAATTACAAATGTGGCTGTAA NM_015032RefSeq chr13
+ 32586426 32778020 PDS5B 23047 PDS5 cohesin associated factor B
GO:0005515|GO:0008285|GO:0005694|GO:0008283|GO:0005634|GO:0003677|GO:0005524|GO:0005829|GO:0042
127|GO:0005654|GO:0000278|GO:0000785|GO:0000775|GO:0051301|GO:0007064 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135509_PI430048170 0.0167158378996945 0.1258266868062920.342480750466607
0.2541855440904970.272230796756824A A A 2.42146546761144 3.60240313325407
3.54229094861777 P P P LNCV6_135509_PI430048170 mRNA
GCCAATGGCTATCCAATTCATTGCATTTGTGAATTGTGCTTTTAGAAAAATTGTGGACAT NM_198468RefSeq chr6
- 97142160 97283176 MMS22L 253714 "MMS22-like, DNA repair protein"
GO:0005515|GO:0042555|GO:0035101|GO:0000724|GO:0031297|GO:0005654|GO:0043596 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_102688_PI430048170 0.1453320932770370.8637856576036584.57455528201001
4.46263106989768 4.32951830959071 P P P 4.84092676890099 4.54732447835872
4.60559162043251 P P P LNCV6_102688_PI430048170 mRNA
TTTTGTTATCTGTGTGCCAGACTGTGAGCCAAGGAATTTTGTGTTTCTTGCCATCTTACA NM_032043RefSeq chr17
- 61679185 61863559 BRIP1 83990 BRCA1 interacting protein C-terminal helicase 1
GO:0005515|GO:0031965|GO:0051539|GO:0006357|GO:0005634|GO:0044281|GO:0003677|GO:0005524|GO:0046
872|GO:0006302|GO:0005737|GO:0004003|GO:0000077|GO:0032508 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132576_PI430048170 0.3460030858567761.17974390085161 0.318913350137831
0.8247358155229590.273204381148673A A A 0.2554001589434920.256115426937394
0.257170070456807A A A LNCV6_132576_PI430048170 mRNA
GTCAGGTTTCACAAGAAAATTTTCAAGTTTTGAAGGGAATTTGAGGTTGATCTGGTTTTC NM_000231RefSeq chr13
+ 23180920 23325165 SGCG 6445 "sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)"
GO:0048738|GO:0042383|GO:0005515|GO:0060047|GO:0005737|GO:0007517|GO:0005886|GO:0016012|GO:0061
024|GO:0055001|GO:0016021|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62606_PI430048170 0.0994263045094355 1.13989172863194 11.7429892150763
11.9798708923316 11.8251400601533 P P P 11.7365105240004 11.5722611781201
11.6778648873557 P P P LNCV6_62606_PI430048170 mRNA
TGTCAGCGGCTGCCCCGCCGTCATAGACTTAAAGGACTGCAATAAATGTAGAGTTGATGT NM_080861RefSeq chr16
- 1776711 1782580 SPSB3 90864 splA/ryanodine receptor domain and SOCS box containing 3
GO:0035556|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143418_PI430048170 0.73585749724667 0.9875659429847370.259214848398702
0.2673216400880550.409794245977372A A A 0.3636643225241910.306267704029492
0.324982660700485A A A LNCV6_143418_PI430048170 mRNA
GGAGGATAGACATTCTTAGCTCACATTTCAATGTATTCATTTCTGCATTCATCTGTGAAA NM_172347RefSeq chr16
- 84221134 84239750 KCNG4 93107 "potassium channel, voltage gated modifier subfamily G, member
4" GO:0005251|GO:0005886|GO:0008076|GO:0007268|GO:0051260|GO:0034765|GO:0016021|GO:0071805 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129433_PI430048170 0.70541772792214 1.0094417817907 0.33456065792637
0.3354661244174820.418281356223074A A A 0.3607096204267610.318718975396986
0.369312364598921A A A LNCV6_129433_PI430048170 mRNA
GCTCACATCCATTATTTAAGCCAGATCTTTTCTAAGTATTATAGAAGTGTAGAGGCACAT NM_025113RefSeq chr13
- 46341999 46387500 KIAA0226L 80183 "KIAA0226-like, transcript variant 1" NA . NA - . NA
NA NA NA NA NA NA NA NA

LNCV6_131036_PI430048170 0.7734908072446551.01474509089578 10.0898695896831
10.0936002721809 10.2018562840109 P P P 9.97919589887949 10.1759639202951 10.16143131088
P P P LNCV6_131036_PI430048170 mRNA
CAGTGGTCTTTCCTGTTGATCATGATGATAAAGTAATGATGGCTGATCCCTATTTGTGAC NM_199129RefSeq chr20
- 50123736 50153798 TMEM189 NA "transmembrane protein 189, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_133758_PI430048170 0.3168791749550932.1209798297712 2.28518557638777
0.28637502190811 2.21440471492898 A A A 0.8198169409812960.37747482237342
0.997812298463022A A A LNCV6_133758_PI430048170 mRNA
GTTTACAGCTTTGGTTAAATGCACCTTGTTCTTCCACATTAAACTTTATTACAAGCGTCA NM_001031746 RefSeq
chr10 - 49014244 49115532 VSTM4 196740 "V-set and transmembrane domain containing 4, transcript
variant 1" GO:0005886|GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131142_PI430048170 0.0294357056396887 0.4768121503111334.64552951467255
4.1801795616886 3.87011035536862 P P P 4.84394030802577 5.57765138371621 5.4822980807838
P P P LNCV6_131142_PI430048170 mRNA
CATGCTCAACCTTCCTCATCATGGAGTAAGAAAATTCTACATGATTAAAGAATCCATGTA NM_014606RefSeq chr4
+ 88592422 88708542 HERC3 8916 "HECT and RLD domain containing E3 ubiquitin protein ligase 3,
transcript variant 1" GO:0004842|GO:0042787|GO:0016874|GO:0016023|GO:0005634 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_142662_PI430048170 0.0932456547991714 0.8462649317663818.75364709736643
8.47506934124246 8.55267543690598 P P P 8.86146810976925 8.80993968803669 8.8464568030824
P P P LNCV6_142662_PI430048170 mRNA
CTGTAGCCAAAACTTGTTTCCACATTAAGAGTCAGCCAGCTCTGGAATGGTCTGGAAATG NM_001278408 RefSeq
chr10 - 80155123 80204491 ANXA11 311 "annexin A11, transcript variant e"
GO:0005515|GO:0006909|GO:0042470|GO:0008429|GO:0005509|GO:0042581|GO:0005819|GO:0042582|GO:0030
496|GO:0005635|GO:0007109|GO:0045335|GO:0005544|GO:0051592|GO:0044548|GO:0005737|GO:0016020|GO:0
023026|GO:0005654|GO:0070062|GO:0048306 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136118_PI430048170 0.4746825115707470.8548832929154013.59173396372219
3.28996491156159 3.38985740937158 P P P 3.19980398066397 3.9516126600786
3.71645138284603 P P P LNCV6_136118_PI430048170 mRNA
TTGTGGCAGATGACACGCTGAGTGAAAGAAGAGAAACCCTCAACTCCATAGATTCACAAG NM_176888RefSeq
chr12_GL877876v1_alt - 220324 221326 TAS2R19 259294 "taste receptor, type 2, member 19"
GO:0033038|GO:0007186|GO:0005886|GO:0016021|GO:0001580 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137084_PI430048170 0.1999606969084040.9015504039066899.74766893874405
9.74336716497663 9.9184825917913 P P P 9.81409013532338 9.96382326767785
10.0753200966289 P P P LNCV6_137084_PI430048170 mRNA
CTTGCTTCTGTCAAGTGTGACTCTATCTCAGTAATTAAAATAAGTGCTGATCTACTGAAA NM_018269RefSeq chr2
- 3497918 3519579 ADI1 55256 acireductone dioxygenase 1
GO:0005515|GO:0005794|GO:0005506|GO:0005886|GO:0005634|GO:0044281|GO:0005829|GO:0034641|GO:0005
737|GO:0000096|GO:0019509|GO:0006595|GO:0016491|GO:0005654|GO:0010309|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137824_PI430048170 0.1396160539851660.8630807589408651 2.7511186077434
12.7315701017624 12.8778508865453 P P P 13.0149106307849 12.8255694436143
13.1441175291465 P P P LNCV6_137824_PI430048170 mRNA
ATGATTTCTCTGCTAACAGCCGCCTGTATGTTTCAATAAATTTGTCCAAAGCTCAAAAAA NM_032412RefSeq chr5
+ 140175067 140243789 CYSTM1 84418 cysteine-rich transmembrane module containing 1
GO:0008150|GO:0003674|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142210_PI430048170 0.1332465084800240.5174084139817421.51312341376825 2.1171411830298

2.17453537321136 A A A 2.05324511270081 3.19627518187299 3.21877672553686 A P P
LNCV6_142210_PI430048170 mRNA
TGCCTTTTATTTGGATTGTCTGATTTCTTAGTTGTACACATGAACCTCATTATTTGCCTG NM_022894RefSeq chr2 +
60756229 60802086 PAPOLG 64895 poly(A) polymerase gamma
GO:0006378|GO:0004652|GO:0005737|GO:0016020|GO:0003723|GO:0043631|GO:0005654|GO:0005634|GO:0005
524|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132031_PI430048170 0.3495951454031280.8428857977314016.85642208399895
7.11028719610314 7.43059834710157 P P P 7.07820685955208 7.41708160607665
7.64409469563888 P P P LNCV6_132031_PI430048170 mRNA
CATATCCATAACGTTTACAGTTGTAGTACAGTTGTGGTTAGTTATTTGTAGTGGGATTGA NM_022909RefSeq chr5
+ 69189547 69210357 CENPH 64946 centromere protein H
GO:0034080|GO:0005515|GO:0051382|GO:0006334|GO:0000777|GO:0000776|GO:0043515|GO:0005654|GO:0005
634|GO:0051383|GO:0000278|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133358_PI430048170 0.1349002036912441.24527952612768 4.4601466684023
4.34233061066468 4.02652167200128 P P P 3.8211572800475 4.16196854625723
3.90844674459221 P P P LNCV6_133358_PI430048170 mRNA
CTCAATTTTGGAATTTCAAACACCAGCAAAAAATTGGAAATCGAGATAGGTTGCTGACTT NM_005978RefSeq chr1
- 153561108 153565830 S100A2 6273 S100 calcium binding protein A2
GO:0005515|GO:0043542|GO:0005509|GO:0005575|GO:0042802 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_101247_PI430048170 0.0621107678980606 1.3680235526146 4.07294526990051
4.50191136736902 4.43584213800295 P P P 3.99561551627281 3.67190135050852
3.99895216285526 P P P LNCV6_101247_PI430048170 mRNA
ATATCAGAAAACTATGCTGGTGATGTTTCCCAGGTACCCGAGCTTGGAGATCTGTGTGAT NM_001029976 RefSeq
chr8 - 144930357 144950888 ZNF16 7564 "zinc finger protein 16, transcript variant 2"
GO:0005515|GO:0033674|GO:0006355|GO:0008284|GO:0043066|GO:0003700|GO:0005634|GO:0003677|GO:0006
351|GO:0046872|GO:0007049|GO:0045654|GO:0045648|GO:0051781|GO:0072707|GO:0051301 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136951_PI430048170 0.2206742241515860.5967217439946192.06318779291782
0.3319472884795430.47891211202115 A A A 1.9402857326722 1.84056817163992 2.0104367253134
A A A LNCV6_136951_PI430048170 mRNA
CAGGAACACCTGCTACTGCACACTCCAAACCAATAAAGTTTTATATTTTGTTTACTTCAA NM_207348RefSeq chr1
+ 15736313 15741392 SLC25A34 NA "solute carrier family 25, member 34" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_131483_PI430048170 0.9869627088122411.00173810301098 0.314448921508109
0.5261354345877430.389360671523359A A A 0.4999205333285970.380753086938313
0.345203283960224A A A LNCV6_131483_PI430048170 mRNA
CTTTTCCCCCAAAGATGTGTATAGTTATTGGTTAAAATGACTGTTTTCTCTCTCTATGGA NM_002202RefSeq chr5 +
51383123 51394729 ISL1 3670 ISL LIM homeobox 1
GO:0032755|GO:0055010|GO:0001755|GO:0003139|GO:0021559|GO:0060913|GO:0043524|GO:0060379|GO:0032
024|GO:0032729|GO:0016922|GO:0001102|GO:0001105|GO:0032725|GO:0032760|GO:0030331|GO:0000122|GO:0
060037|GO:0071385|GO:0060384|GO:0043388|GO:0048880|GO:0008270|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133290_PI430048170 0.5703495134672420.6853599366060120.368346139570422
0.6583612486254890.278530686711505A A A 0.2518263655528540.284518180207417
1.82678336688675 A A A LNCV6_133290_PI430048170 mRNA
GCATTTCTACATGTTTGAGGTGGTTGTTTTTAAAGGGGATATGTGTAATGCAGATTTTCT NM_005086RefSeq chr12
+ 26195572 26234775 SSPN 8082 "sarcospan, transcript variant 1"
GO:0042383|GO:0030133|GO:0030054|GO:0006936|GO:0016010|GO:0005887|GO:0045211|GO:0007155 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126008_PI430048170 0.000406215441351298 2.38643428072467 1.8281516189221
1.64024354776329 1.56918766309986 A A A 0.3544006281194920.324971316263476
0.591171145184407 A A A LNCV6_126008_PI430048170 mRNA
TACAGTTTCTTCTGATTGAACGCAGCCTTTGAATACTGCCTGGCCTATCGCGAATACATC NM_033031 RefSeq chrX
+ 50284539 50351912 CCNB3 85417 "cyclin B3, transcript variant 3"
GO:0005515|GO:0051321|GO:0019901|GO:0010389|GO:0005654|GO:0000079|GO:0051301 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_106801_PI430048170 0.00853524187225618 0.3735651848108640.511988988699851
0.4494548467444560.288306149720644 A A A 2.15175449567219 1.752034630343
1.55077304860591 A A A LNCV6_106801_PI430048170 mRNA
ACTAAGTATCTTGGGATAATTAACATGTTTTTTATTCGAGAGACTACTTCTCTTCGGGAG NM_001286174 RefSeq
chr12 - 22448545 22544546 C2CD5 9847 "C2 calcium-dependent domain containing 5, transcript
variant 2"
GO:0032869|GO:0005815|GO:0005886|GO:0005509|GO:0090314|GO:0031340|GO:0032587|GO:0038028|GO:0072
659|GO:0006906|GO:0065002|GO:0010828|GO:0005544|GO:2001275|GO:0005737|GO:0005938|GO:0030659 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137120_PI430048170 0.6106125262361751.14340407840097 0.328526010179852
0.3142244817520811.07236446743554 A A A 0.2713998380340550.278780875425794
0.682242772961024 A A A LNCV6_137120_PI430048170 mRNA
AATGCTGCACTAGCAGGCGGATTTGTGCAGGGGGCCAACTGCACCTGCCTGGAACGCTGT NM_001013658 RefSeq
chr16 - 1485938 1488467 PTX4 NA "pentraxin 4, long" NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_141001_PI430048170 0.4760812387758081.21011084828697 1.17573089093301
2.05849377627356 1.83736483729014 A A A 1.58574983703451 1.29234053113961
1.49123228330984 A A A LNCV6_141001_PI430048170 mRNA
CATCCACAAACCATTAATAGCACTCCCTGTGGGAAAATGTTTATACATTTTTACAGTTTG NM_001124759 RefSeq
chr3 + 75664335 75667217 FRG2C NA "FSHD region gene 2 family, member C" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131760_PI430048170 0.9020799719526141.02720667416001 5.37029490549999
5.35194711045246 4.81723541714296 P P P 5.34052286615586 5.23110563245461
4.87748979302771 P P P LNCV6_131760_PI430048170 mRNA
GGTTGGTTTGAAGCTATCATGTAAAATTGGCCTCTCCAAATATAATCAGAAATAAACCGA NM_015206 RefSeq chr15
+ 79432515 79472300 KIAA1024 NA KIAA1024 NA . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_132369_PI430048170 0.0763502013190455 0.8505659849693341 3.1592809174638
12.9220662166419 13.089343328836 P P P 13.3959055833983 13.1615329258591
13.3142242251336 P P P LNCV6_132369_PI430048170 mRNA
AGTCCGAGCTCTGAAGAACAACAGTAATGATATTGTAAATGCGATTATGGAATTAACAGT NM_199290 RefSeq chr17
- 61590432 61591202 NACA2 342538 nascent polypeptide-associated complex alpha subunit 2
GO:0005737|GO:0005634|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100271_PI430048170 0.206502622512017 1.08804610617293 6.0271036866693
6.22066230790779 6.11087949303028 P P P 6.11289108957034 5.95619058196274
5.92371853005592 P P P LNCV6_100271_PI430048170 mRNA
AAGTATCCAAGCGGCATTCAAATTCTGCCCCTACTGTGGAAATTCTTTGCCTGTAGAGGA NM_016440 RefSeq chr19
- 49976466 50025548 VRK3 51231 "vaccinia related kinase 3, transcript variant 1"
GO:0005737|GO:0018105|GO:0004674|GO:0008360|GO:0032516|GO:0070373|GO:0005634|GO:0016055|GO:0005
524|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75560_PI430048170 0.4598717074769910.8866948705079228.7367595445671 9.14081878120293

9.32148548781043 P P P 8.99148669944226 9.29238751513824 9.45797985965166 P P P
LNCV6_75560_PI430048170 mRNA
CAGGTGGATAGTATATAGGTTTATGCCTGTGTTTCTTTTTCTCCATGAGAAAGCTAAACA NM_001015891 RefSeq
chr5 - 69351725 69370013 AK6102157402 "adenylate kinase 6, transcript variant 3"
GO:0005515|GO:0015030|GO:0016020|GO:0046939|GO:0005730|GO:0005654|GO:0004017|GO:0016887|GO:0005
524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129192_PI430048170 0.377505992531088 1.19186788081216 11.4980572683505
11.6383417073333 12.0488862617725 P P P 11.8356630588942 11.1239541080914
11.4355226853041 P P P LNCV6_129192_PI430048170 mRNA
GGTGCTTTGCCTTTAACTAGAGTGTGTGATGGTAGATTATTTCAGATATGTATGTAAAAC NM_001267818 RefSeq
chr4 + 108650584 108667822 OSTC 58505 "oligosaccharyltransferase complex subunit (non-catalytic),
transcript variant 3" GO:0004579|GO:0016021|GO:0008250|GO:0018279 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_106352_PI430048170 0.0495278779309385 1.28438642408999 9.78438905939527
9.89524151799384 9.8048740168027 P P P 9.64871235447389 9.4052490938178
9.33020599647707 P P P LNCV6_106352_PI430048170 mRNA
AAAGCGTGTCTGGCCCTAGGTGGGAAAAGAACTGGCTGTGACCTTTGCCCTGACCTGGAA NM_024531 RefSeq chr8
+ 144358615 144361286 SLC52A2 79581 "solute carrier family 52 (riboflavin transporter), member 2,
transcript variant 1" GO:0032217|GO:0005887|GO:0001618|GO:0032218|GO:0009615 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_144502_PI430048170 0.256409837571093 0.918087297982376 13.5213057776113
13.6309543653001 13.43178033503 P P P 13.7883580896906 13.6104108602219
13.5514026016838 P P P LNCV6_144502_PI430048170 mRNA
GGGACCGAGAGATCAGATAGTTGCTGTTTTGTAAAATGTAATGTATATGTGGTTTTTAGT NM_177543 RefSeq chr19
- 281039 291169 PPAP2C 8612 "phosphatidic acid phosphatase type 2C, transcript variant 3"
GO:0006665|GO:0016020|GO:0005886|GO:0030148|GO:0016311|GO:0004721|GO:0044281|GO:0016021|GO:0008
195 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138252_PI430048170 0.556283431484154 1.0393867785293 9.67660095790193
9.42747411243168 9.60095720954861 P P P 9.55213219724419 9.48506547080744
9.51102397465789 P P P LNCV6_138252_PI430048170 mRNA
GGGGTCAGTGTGTGAGTGAGAGCAGGAGTATTTATGAAAATAAAACGTCGTTTTTCCTGG NM_001172688 RefSeq
chr22 + 37609039 37633564 GGA1 26088 "golgi-associated, gamma adaptin ear containing, ARF
binding protein 1, transcript variant 5"
GO:0005515|GO:0003674|GO:0045732|GO:0030131|GO:0005794|GO:0016020|GO:0005654|GO:0016192|GO:0006
886|GO:0010008|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66893_PI430048170 0.35466442775972 1.42707649873313 1.52061803106511
0.472273040870003 0.437758263313119 A A A 0.542010190392937 0.312351413286355
0.303384755008309 A A A LNCV6_66893_PI430048170 mRNA
GGAAACAAAACCTTCACCGCTCTTTGTTTGTTGTTTTGTTGTATTTTGTTTTCCTGCTAG NM_002148 RefSeq chr2
+ 176116763 176119942 HOXD10 3236 homeobox D10
GO:0035137|GO:0008344|GO:0035136|GO:0003700|GO:0021520|GO:0048704|GO:0005634|GO:0009954|GO:0030
326|GO:0009952|GO:0006351|GO:0050905|GO:0043565|GO:0007338|GO:0007519|GO:0045944|GO:0003682|GO:0
048935 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117073_PI430048170 0.14534170116403 0.800363169393026 5.31186448265551
5.49820841592086 5.80652908632581 P P P 5.70934091225476 5.83028951305204
6.06202738751155 P P P LNCV6_117073_PI430048170 mRNA
ACATGATGCTGAAAATAGCTGAAGAACTGCCTAAGGAACCTCAGGGCATCATAGCTTGCT NM_001001998 RefSeq
chr1 - 11066612 11099910 EXOSC10 5394 "exosome component 10, transcript variant 1"
GO:0005515|GO:0000460|GO:0008408|GO:0071028|GO:0071035|GO:0000956|GO:0005730|GO:0035327|GO:0004

532|GO:0009048|GO:0005634|GO:0071034|GO:0000178|GO:0005737|GO:0016020|GO:0000166|GO:0000184|GO:0071044|GO:0000176|GO:0005654|GO:0071048 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127738_PI430048170 0.04951846105622 0.616277704526792 0.341663499864288 0.329816669876638 0.299416821246625 A A A 0.704158996653729 1.24424226777723 1.06656329267416 A A A LNCV6_127738_PI430048170 mRNA GCTTAACTTCCCAAGTGTTCTGCATTGAACCACTTAGGGAAAATTTTGTTTGTTTTTATG NM_004277 RefSeq chr6 + 46652914 46678190 SLC25A27 9481 "solute carrier family 25, member 27, transcript variant 1" GO:0008284|GO:0043066|GO:0048839|GO:0005743|GO:0045177|GO:0006091|GO:0035356|GO:0005739|GO:0010917|GO:0051562|GO:0046324|GO:0070997|GO:0006810|GO:0043025|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137821_PI430048170 0.160711778125061 1.04111058880025 0.372026025013425 0.398514187568294 0.307787463866721 A A A 0.29296096596555 0.312561284933516 0.29986937771628 A A A LNCV6_137821_PI430048170 mRNA AGTCATGATAGTGAGTATTCTTACACTGTTCCCAGTATTACAGGGAATGCTTAGAAATTT NM_053282 RefSeq chr1 - 162395265 162412138 SH2D1B 117157 SH2 domain containing 1B GO:0005622|GO:0005515|GO:0045089|GO:0002717|GO:0030674|GO:0002366 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109977_PI430048170 0.0475181977394164 2.98428378659277 4.8087209710431 4.82522806087969 4.61407992606647 P P P 3.74484549559419 2.37636091398801 3.08717404703402 P A P LNCV6_109977_PI430048170 mRNA TTTCTCTATAAAGCCTCAGCGTATAGAACAGATTTCACATGCCCAGAGGCTGTTGAGCAG NM_172095 RefSeq chr15 - 43630561 43648841 CATSPER2 117155 "cation channel, sperm associated 2, transcript variant 2" GO:0005515|GO:0035036|GO:0086010|GO:0005245|GO:0005886|GO:0031514|GO:0036128|GO:0007275|GO:0007283|GO:0030317|GO:0030154|GO:0007338|GO:0070509|GO:0070588|GO:0034765|GO:0005227|GO:0032504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130054_PI430048170 0.00621480667966923 0.447856892291943 8.49109280947887 8.3468104413101 8.32540642896419 P P P 9.29040562633134 9.5852163588993 9.73519142587209 P P P LNCV6_130054_PI430048170 mRNA GACGGCAATGCAATAGCCTATTTAAAGACACTACGTGATCTGATTGAGATGTACATAGTT NM_173354 RefSeq chr21 - 43414518 43427122 SIK1 150094 salt-inducible kinase 1 GO:0045721|GO:0005515|GO:0010868|GO:0000287|GO:0019901|GO:0032792|GO:0010830|GO:0005634|GO:0005524|GO:0035556|GO:0071889|GO:0007346|GO:0005737|GO:0007049|GO:0008140|GO:0046777|GO:0004674|GO:2000210|GO:0002028|GO:0045595|GO:0006468|GO:0048511|GO:0055007|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138361_PI430048170 0.221977573915218 1.8299275837936 1.70108893278258 2.91970199807242 2.54553734898974 A A A 0.362364961658932 1.8275314729367 2.09339532272299 A A A LNCV6_138361_PI430048170 mRNA ATTCTACTGATGAAGAGGTTGACCTTCTCCACAGGCACTGAGATTCCGCATTTCTTCTGT NM_001005191 RefSeq chr19 - 9213849 9214871 OR7D4 125958 "olfactory receptor, family 7, subfamily D, member 4" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140451_PI430048170 0.440093362847589 1.04806280178004 0.309337060159226 0.314919432609446 0.514093805861 A A A 0.328518140263587 0.280356491105846 0.335252068501287 A A A LNCV6_140451_PI430048170 mRNA CAGTGCCTTCACTACACTGCCTTACATAAACCAAATCACAATAAAGTTCATATTCAGTAC NM_014289 RefSeq chrX - 111245098 111270546 CAPN6 827 calpain 6 GO:0008017|GO:0048471|GO:0004198|GO:0051493|GO:0001578|GO:0006508|GO:0005876 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_145339_PI430048170 0.268710904492027 1.02545195549144 0.305303693000374
0.2505990559131 0.331789118115193 A A A 0.268276800430068 0.243331397196811
0.268344599135485 A A A LNCV6_145339_PI430048170 mRNA
CGAGGGCAGCCATGGTCTACTGACAGATGGCAAGTTACTTTGTAACCTGTAATTTTGTTT NM_002379 RefSeq
chr1 - 30711276 30723585 MATN1 4146 "matrilin 1, cartilage matrix protein"
GO:0005515|GO:0030500|GO:0006461|GO:0030198|GO:0005578|GO:0003429|GO:0005576|GO:0005201 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_138721_PI430048170 0.217225557466684 0.79361877444784 0.275802258012481
0.290954769093488 0.491074985366054 A A A 0.827845575380329 0.869013955050023
0.306443250721753 A A A LNCV6_138721_PI430048170 mRNA
CAAGAAATAAAGTCTTCCCTGAGAAAGTTAATCTGGGTTCGGAAAATTCATTCCCCTTAG NM_003555 RefSeq
chr17 - 3126609 3127551 OR1G1 8390 "olfactory receptor, family 1, subfamily G, member 1"
GO:0050911|GO:0007165|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004
888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139617_PI430048170 0.027288899043069 0.769342210542214 9.95313729098035
9.66190924050863 9.80778334637981 P P P 10.0903914240231 10.326107541445
10.1452483059181 P P P LNCV6_139617_PI430048170 mRNA
AATAAGATCTTAATAAAGTCTTCTAGGCTGTAGGGTGGTTCCTACAACCACAGCCATGAT NM_080670 RefSeq
chr5 + 140564564 140569104 SLC35A4 113829 "solute carrier family 35, member A4"
GO:0000139|GO:0008643|GO:0005351|GO:0016021|GO:0015992 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_133055_PI430048170 0.516710353410149 1.26863212806465 0.539902905040134
1.43667641184237 0.34521265333334 A A A 0.388544816196943 0.602673510473577
0.539559855608184 A A A LNCV6_133055_PI430048170 mRNA
AAGATTCTACCTTTCTAAGACATCTGGAGTCAGACAGACCTGAGTTCAAGTCGTGCCTTC NM_174943 RefSeq
chr14 + 77760829 77769742 C14orf178 283579 "chromosome 14 open reading frame 178,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57753_PI430048170 0.529314739014544 0.931583657719757 4.55779002458167
4.94031547668638 4.4810169761436 P P P 4.62936215768631 4.83719605861093
4.85181565783085 P P P LNCV6_57753_PI430048170 mRNA
TCTGCCACCTTCGACTACCAGCAGGCTTTTGGCAACAGCACTGGTGGCTTTGATGGGCAA NM_006328 RefSeq
chr11 + 66616581 66629926 RBM14 10432 "RNA binding motif protein 14, transcript variant 1"
GO:0005515|GO:0005667|GO:0016575|GO:0001104|GO:0006366|GO:0003723|GO:0005730|GO:0006310|GO:0006
260|GO:0030374|GO:0006281|GO:0000166|GO:0045944|GO:0042921|GO:0030529|GO:0016592|GO:0005654|GO:0
009725|GO:0030674|GO:0030520 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136976_PI430048170 0.410126410126086 2.37634809335291 2.68364069147501
0.409673337266874 0.313498954348158 A A A 0.313674300519353 0.341734557941795
0.35098500299313 A A A LNCV6_136976_PI430048170 mRNA
ATTTTGTATCTAACAGACAGTGCTCAGTGCAAATCAACATTCCAGCGGTCAGGACTGACC NM_152643 RefSeq
chr10 + 133160466 133226412 KNDC1 85442 kinase non-catalytic C-lobe domain (KIND) containing
1
GO:0007264|GO:0005575|GO:0030425|GO:0048814|GO:0021707|GO:0003674|GO:0008150|GO:0032320|GO:0008
152|GO:0043025|GO:0001934|GO:0005088|GO:0016772|GO:0032045|GO:0032318 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_142313_PI430048170 0.00627663399193404 1.35218564715967 11.000479409802
11.1622441353014 10.9582997987304 P P P 10.6491844601967 10.6620335153013
10.5069772778581 P P P LNCV6_142313_PI430048170 mRNA
TGAGAACAGCATTTCTATTTAGGAGCGCGCTTCCCGTCTCTCCTCTCCCCATTCTGTGCC NM_001139 RefSeq

chr17 - 8072635 8087703 ALOX12B 242 "arachidonate 12-lipoxygenase, 12R type"
GO:0005515|GO:0006665|GO:0019369|GO:0005506|GO:0019372|GO:0061436|GO:0044281|GO:0070257|GO:0005
829|GO:0043651|GO:0010628|GO:0004052|GO:0006497|GO:0051122|GO:0046513|GO:0016702|GO:0043410|GO:0
055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128140_PI430048170 0.00299425157195062 1.47330832601278 6.56021106943431
6.33897471021949 6.47049293933807 P P P 5.8042168702802 5.94001800894562
5.95217776304682 P P P LNCV6_128140_PI430048170 mRNA
GATTTTATACCGAAGAAGTCAGACAGGGAGGGAGAAGAATAGGATTCGATGTCGTCACGT NM_032324 RefSeq
chr1 + 232950623 232978473 NTPCR 84284 "nucleoside-triphosphatase, cancer-related"
GO:0017111|GO:0016020|GO:0016311|GO:0005524|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_143171_PI430048170 0.0537750046746186 0.689556317478762 7.85576799543585
7.81831491597126 7.59977005293154 P P P 8.4407695248002 8.42835458896812
7.9806773217379 P P P LNCV6_143171_PI430048170 mRNA
GCCCTCGCCGCGTGCTGCGCTCAGTTCTTTGTTGGATTTCTTGTTTGTGTTCTTAAAAAA NM_003833 RefSeq
chr20 - 45293445 45308529 MATN4 8785 "matrilin 4, transcript variant 1"
GO:0005515|GO:0030198|GO:0005576|GO:0048678 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_95808_PI430048170 0.167897919889673 0.96558902856714 0.451376949026425
0.364903513825299 0.405272465814149 A A A 0.447791816409889 0.478483491972533
0.447915213235282 A A A LNCV6_95808_PI430048170 mRNA
ATGCTACTGAAGGCTGAGTTGCCTCTTGTGTTTTCAGCTTTTCACATGTCTGGTTTTGCA NM_152730 RefSeq chr6
- 121079493 121334500 TBC1D32 221322 "TBC1 domain family, member 32, transcript variant 1"
GO:0003406|GO:0005929|GO:0005737|GO:0002088|GO:0060271|GO:0032851|GO:0060831|GO:0042733|GO:0005
097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142833_PI430048170 0.649906795308261 1.04311912616473 10.8008474691871
11.000479409802 11.1314283959604 P P P 10.90409680333 10.8155639549683
11.0404803779997 P P P LNCV6_142833_PI430048170 mRNA
AATACTTTACTTTAGGCATCCCTCCTGTTGCTAGCAGCCTTTTGACCTATCTGCAATGCA NM_001300901 RefSeq
chrX + 103576230 103587736 TCEAL4 79921 "transcription elongation factor A (SII)-like 4, transcript
variant 5" GO:0006355|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_101301_PI430048170 0.597829649464817 1.27327890267599 3.00992154389947
1.89863648525091 1.80408440664149 P A A 1.91600579679271 1.91285683431914
2.15638841821763 A A A LNCV6_101301_PI430048170 mRNA
TCTCAGAAGGATTTATACAGAGATGTCATGTTGGAGAACTACAGGAACTTGGTATGGCTT NM_032453 RefSeq
chr19 + 37371156 37393064 ZNF527 84503 zinc finger protein 527
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_135044_PI430048170 0.0781666671204409 0.396915242522811 1.38121192825485
1.62257587904952 1.3009706381814 A A A 3.24498957610966 2.85486323151065
1.93109350524878 P P A LNCV6_135044_PI430048170 mRNA
GTTTACCATACCAAAGCTTGCTTTCTCTGGCATGGGAAAAATAAATTTAAGCACCAAAAA NM_022346 RefSeq
chr4 + 17810812 17844864 NCAPG 64151 "non-SMC condensin I complex, subunit G, transcript
variant 1"
GO:0005515|GO:0000796|GO:0007076|GO:0005813|GO:0005737|GO:0016020|GO:0005634|GO:0015629|GO:0000
278|GO:0051301|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129975_PI430048170 0.205830775815551 0.494486415385055 2.63341555491757
0.289746681348483 2.07621753478806 A A A 2.99981180619157 2.89895244028464

3.01624476531025 P P P LNCV6_129975_PI430048170 mRNA
CACTGAAGAGAGAAATCCTGTCAATGTAAGTAATATAGAAAGCGAGATACAAGATGATTC NM_153358 RefSeq
chr19 + 12610917 12629862 ZNF791 163049 zinc finger protein 791
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_98149_PI430048170 0.3691094776029621.98800184254684 0.4153324101018772.32460541513372
2.59869657896332 A A A 0.8158508261741991.64927951916407 0.422724312583401 A A A
LNCV6_98149_PI430048170 mRNA
AGGAAAACTCATTAGAATTCTTAAGTGATCTTACACCGGGAGATCAGGACCCATCTCAGA NM_001278432 RefSeq
chr13 - 32432487 32538885 N4BP2L2 10443 "NEDD4 binding protein 2-like 2, transcript variant 3"
GO:0005515|GO:0003674|GO:0001106|GO:0017053|GO:0000122|GO:0019899|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_108768_PI430048170 0.2729181110726290.9293436771513478.56630081054358
8.74761453731051 8.51605718296005 P P P 8.63662866830044 8.7377469738355
8.77944386545443 P P P LNCV6_108768_PI430048170 mRNA
ACAAGAGTTCTACCAGGATGATGAACTCGGGAAGAAGCAGTTCAAGTATGGGAACCAGTTNM_001278595 RefSeq
chr7 - 100092727 100101940 MCM7 4176 "minichromosome maintenance complex component 7,
transcript variant 3"
GO:0005515|GO:0042555|GO:0008283|GO:0042493|GO:0003677|GO:0005524|GO:0006974|GO:0005829|GO:0006
260|GO:0042325|GO:0006271|GO:0000082|GO:0005737|GO:0004003|GO:0016020|GO:0003697|GO:0071364|GO:0
006270|GO:0006268|GO:0005654|GO:0000278|GO:0000785 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_96014_PI430048170 0.00992517092395206 0.55049407003591912.461897913104 12.345262744436
12.5027965068231 P P P 13.0879379153406 13.2875650007235 13.4940880008748 P P P
LNCV6_96014_PI430048170 mRNA
TTTGACTGTTTCCATGTTGGCATCTGCCCCTCAAGAGCAAAAGCAAATGTTGGGTGAATG NM_183353RefSeq chrX
- 74582975 74614626 RLIM 51132 "ring finger protein, LIM domain interacting, transcript variant 2"
GO:0006511|GO:0004842|GO:0016567|GO:0003714|GO:0016874|GO:0005634|GO:0000122|GO:0060816|GO:0006
351|GO:0043433|GO:0005737|GO:0017053|GO:0005654|GO:0008270|GO:0045892 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141046_PI430048170 0.0889839650810517 1.78521154691644 1.57537833166894
1.59303714814728 1.83895338002726 A A A 1.34345671674947 0.305383053837595
0.668922415868197 A A A LNCV6_141046_PI430048170 mRNA
GCCACACAGCGTGTAACCTGAAGTCATCTAGATTATGGGGAAACTGCTCAGCTTCAATAA NM_052960RefSeq chr1
+ 9997196 10016020 RBP7 116362 "retinol binding protein 7, cellular"
GO:0005215|GO:0005737|GO:0016918|GO:0006810|GO:0019841 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141926_PI430048170 0.2875794974969471.02766014488401 0.314326703679862
0.24895390165653 0.340681591444723 A A A 0.2695295037974110.246757859117915
0.270996728299885 A A A LNCV6_141926_PI430048170 mRNA
AGGAGACTGTTGGGATATTGGATATGCTGTAGAAAATATGACTTCAGATCTCTGTATTGA NM_001004491 RefSeq
chr1 + 247965331 247966339 OR2AK2 NA "olfactory receptor, family 2, subfamily AK, member 2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139728_PI430048170 0.0969631306993116 0.8784540719683551 0.557026774236
10.6051709755086 10.6514798903338 P P P 10.7195061884512 10.7231334523737
10.9238459304306 P P P LNCV6_139728_PI430048170 mRNA
TCAGAATTACTGTTTTTGTTTCCTTTTACCCCAGCTGCCATTAAAGCCCAAACCTCTAGC NM_016222RefSeq chr5
- 177511576 177516966 DDX41 51428 DEAD (Asp-Glu-Ala-Asp) box polypeptide 41
GO:0005515|GO:0006396|GO:0032479|GO:0035458|GO:0005783|GO:0004386|GO:0006915|GO:0007275|GO:0071

013|GO:0003677|GO:0005524|GO:0005829|GO:0051607|GO:0016020|GO:0000398|GO:0045944|GO:0045087|GO:0
032481|GO:0008270. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130749_PI430048170 0.1529309732392520.3854014453236460.306219691361526
3.14492333450545 1.17043017684886 A P A 3.04800903166825 3.42920431897812
3.69563829043718 P P P LNCV6_130749_PI430048170 mRNA
TTCAGTGTGTTTTTTCCTGGGGCAACTGAATGATTCTTGTTTTGAATGAGTGATAAAATG NM_000706RefSeq chr12
- 63142758 63152810 AVPR1A552 arginine vasopressin receptor 1A
GO:0005515|GO:0008284|GO:0019722|GO:0005886|GO:0030307|GO:0008015|GO:0031894|GO:0007202|GO:0006
091|GO:0051970|GO:0007204|GO:0021537|GO:0032870|GO:0001992|GO:0014049|GO:0003084|GO:0045907|GO:0
005000|GO:0005080|GO:0007625|GO:0051412|GO:0042711|GO:0042631|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_104372_PI430048170 0.2260449527373060.8561447459931668.23384828506962 8.0532622430142
7.88405632031463 P P P 8.44882670339606 8.33328895185109 8.05454869817986 P P P
LNCV6_104372_PI430048170 mRNA
TATACTCCAACTCCTACTTGAGTTCCTGCGGTCTCCCCGCATCCACAGGGAGGGTAAAAC NM_175738RefSeq chr17
+ 74671116 74747335 RAB37 326624 "RAB37, member RAS oncogene family, transcript variant 3"
GO:0005793|GO:0009306|GO:0005886|GO:0003924|GO:0005525|GO:0072659|GO:0006886|GO:0006904|GO:0006
184|GO:0017157|GO:0032482|GO:0019003|GO:0005768|GO:0030667 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_74921_PI430048170 0.3242145252092960.6316215081533311.30169260153212 3.27488525286541
3.71840692943086 A P P 3.44417687625364 3.90047881773274 3.83282606170397 P P P
LNCV6_74921_PI430048170 mRNA
ATTTGATAAGAGCAGCAAAATATCGTGACCACGTGACAGCAACTCAACTAATCCAGAAAA NM_001199282 RefSeq
chr4 - 150264658 151015267 LRBA 987 "LPS-responsive vesicle trafficking, beach and anchor
containing, transcript variant 1"
GO:0005794|GO:0005886|GO:0005783|GO:0005764|GO:0012505|GO:0003674|GO:0008150|GO:0005543|GO:0016
020|GO:0016197|GO:0016023|GO:0016021|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130639_PI430048170 0.2949626873930941.11725235115288 9.84799810671309
9.93255454022015 10.2082154149669 P P P 9.75036104961586 9.90128117117149
9.87777466358638 P P P LNCV6_130639_PI430048170 mRNA
GCTTAATACTCCAAAGTGTGAGTTCCTCTGATCTCTTGATTCCTTAGTTCTAATCTCACGNM_017443RefSeq chr9 -
113407238 113410749 POLE3 54107 "polymerase (DNA directed), epsilon 3, accessory subunit, transcript
variant 1"
GO:0043565|GO:0006260|GO:0005515|GO:0008622|GO:0071897|GO:0046982|GO:0043966|GO:0003887|GO:0005
671|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130786_PI430048170 0.5526615864433141.24675359860435 1.29594945014712
1.42120668933831 0.313085666008963A A A 0.2616727810840810.955216074902807
0.982741250167683A A A LNCV6_130786_PI430048170 mRNA
TAATAACATTGATGTCAAGAAAATGACGGTCACAGACCAGGTGAACTGCCCCAAGCTCTC NM_001647RefSeq chr3
- 195568701 195584205 APOD 347 apolipoprotein D
GO:0006629|GO:0005515|GO:0048471|GO:0005783|GO:2000098|GO:0042246|GO:0071638|GO:0005615|GO:0048
678|GO:0030425|GO:0051895|GO:0015485|GO:0014012|GO:0043025|GO:0006006|GO:0010642|GO:0070062|GO:2
000405|GO:0060588|GO:0042493|GO:0007568|GO:0005576|GO:0048662|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128077_PI430048170 0.4383745205665091.2678991590164 1.17006584434971
0.3273884481831770.264745128788435A A A 0.3087613093412850.317275246979277
0.295529339769142A A A LNCV6_128077_PI430048170 mRNA
CTTGTGGGTTAGAGGAACAAATATCTAGACATTCAATCTTCACTCTTTCAATTGTGCATT NM_031457RefSeq chr11
+ 60699573 60715811 MS4A8 83661 "membrane-spanning 4-domains, subfamily A, member 8"

GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88442_PI430048170 0.00708496492789156 4.4663385157499 3.93014910263008
3.58664002059003 3.67390499549093 P P P 1.02028587130072 1.87763929906387
1.70376148808764 A A A LNCV6_88442_PI430048170 mRNA
AGGGGAGAGGTCCTTACCTCTGATCCACTTAGAGCAATAACCACTTTTTAAATGTAAAAT NM_001171941 RefSeq
chr1 - 32862267 32872492 FNDC5 252995 "fibronectin type III domain containing 5, transcript variant
1"
GO:0008150|GO:0003674|GO:0005886|GO:0005179|GO:0014850|GO:0005783|GO:0005576|GO:0016021|GO:0090
336|GO:0005778 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134305_PI430048170 0.5895091589341991.06199313822196 0.819135554978861
0.5513849284216350.435044375401838A A A 0.5174468744650740.383379525714158
0.658572539851421A A A LNCV6_134305_PI430048170 mRNA
GTAATCCTTGCCATGCAACAAATGATTAGGGGAAAATCCTTTCATAAAATTGCAGTTTAG NM_001004740 RefSeq
chr11 - 56612554 56613502 OR5M1 NA "olfactory receptor, family 5, subfamily M, member 1"NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127222_PI430048170 0.0660509708537522 1.24647619296769 11.0778638416998
11.3316339403538 11.3784018888575 P P P 11.0068935999369 10.9470178463543
10.8960408329795 P P P LNCV6_127222_PI430048170 mRNA
AGTGTACAGCAAATCAATGTTTTCCTGCTTGGGGCTCTCTTCCCTCATCTCTAGCAGTAT NM_016581RefSeq chr19
- 11505915 11529172 ECSIT 51295 "ECSIT signalling integrator, transcript variant 1"
GO:0005515|GO:0051341|GO:0005667|GO:0001707|GO:0003700|GO:0005634|GO:0030509|GO:0005739|GO:0005
737|GO:0045087|GO:0016651|GO:0005654|GO:0004871|GO:0055114 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133614_PI430048170 0.3932917363773311.04999804259396 10.5636845572633
10.6891260069359 10.7605687406669 P P P 10.6811899403933 10.532687255749
10.5912926315357 P P P LNCV6_133614_PI430048170 mRNA
CTGCACCACATGCTACACCAGTTCAGCGTGAGAATTTTCTAATAAATCTTTTCTGATACT NM_001242498 RefSeq
chr17 - 75266229 75271230 MIF4GD57409 "MIF4G domain containing, transcript variant 1"
GO:0005515|GO:0005737|GO:0003723|GO:0005730|GO:0008022|GO:0006417 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145288_PI430048170 0.00210925277422147 0.5041919563319957.63756230918337
7.94260227639194 7.92180454698806 P P P 8.74598842817892 8.70071903986278 9.0179723253747
P P P LNCV6_145288_PI430048170 mRNA
CACAGATTTCTGCTATGTGTCATCAAAACATCTAGTTCTGAGTAACATTTTCACGATTGT NM_022151RefSeq
chr14_KI270847v1_alt - 296757 299466 MOAP1 64112 modulator of apoptosis 1
GO:0005515|GO:0008625|GO:0043065|GO:0008630|GO:0001844|GO:0005741|GO:0097190|GO:0005829|GO:0097
192|GO:0005739|GO:0005737|GO:0090200|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131302_PI430048170 0.2792330893975421.11733323129882 13.4588321643036
13.1948759713488 13.1486735622766 P P P 12.9492729514321 13.1892058048357
13.1903965415857 P P P LNCV6_131302_PI430048170 mRNA
AGTGGCTTCCTGAATGATGAGGACCAGAATAAAGGTTTTTGATCAACCTCAAAAAAGAAA NM_019896RefSeq chr2
+ 74958647 74969732 POLE4 56655 "polymerase (DNA-directed), epsilon 4, accessory subunit"
GO:0043565|GO:0005515|GO:0008622|GO:0071897|GO:0046982|GO:0043966|GO:0003887|GO:0005671|GO:0005
634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126698_PI430048170 0.2602895431257470.7709101782855970.31479451926165
0.2710447120741050.277581509744045A A A 0.6097904145966260.258798612599613
1.02047576937737 A A A LNCV6_126698_PI430048170 mRNA
CTTTCTGGGCATTCCTAGGGGAGAAAATAAAATTTGTAATGTTCTAGAGATCATTTGGAA NM_001258449 RefSeq
chr5 + 137889435 137940467 PKD2L2 27039 "polycystic kidney disease 2-like 2, transcript variant 3"

GO:0008150|GO:0005262|GO:0050982|GO:0005509|GO:0070588|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143792_PI430048170 0.00970637264799041 0.3205178941170712.75133331426486 2.27915379846534 3.2186840292463 A A P 4.23584472708716 4.18859187861918 4.81356111534859 P P P LNCV6_143792_PI430048170 mRNA CAGAGGAAGCAGCTTGTTTCTAAACAAATAGTGTTATCCTTTTACAATTAACTGCACATC NM_022782RefSeq chr12 - 123156395 123233238 MPHOSPH9 10198 "M-phase phosphoprotein 9, transcript variant 1"
GO:0005813|GO:0005737|GO:0005794|GO:0016020|GO:0005886|GO:0000139|GO:0005814 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105884_PI430048170 0.2625259789726651.30928327025589 4.90621180823169 4.60965293311267 4.96241383140585 P P P 3.83356901780824 4.60978657395942 4.73815469621872 P P P LNCV6_105884_PI430048170 mRNA ACTTCTGGAAGCTTTCGAAAGAATCTTGTCCCTCATGACAGCATTTTATCATGAAAGCAG NM_021215RefSeq chr20 + 38033545 38092364 RPRD1B58490 regulation of nuclear pre-mRNA domain containing 1B
GO:0005515|GO:0008284|GO:0070940|GO:0045944|GO:0016591|GO:0000993|GO:0005634|GO:0010564|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131735_PI430048170 0.0331271115188019 0.9552591040221420.388587429109142 0.3842192167830760.340584694950741A A A 0.4403370838373610.447724472547781 0.423820706218807A A A LNCV6_131735_PI430048170 mRNA TGGTTCTGCAACCAGAGACAGAAACAGAAACGAATGAAGTATTCGGCTGTCCACTGATTG NM_002700RefSeq chr5 + 146339023 146340520 POU4F35459 POU class 4 homeobox 3
GO:0031290|GO:0003700|GO:0042472|GO:0042491|GO:0007605|GO:0048675|GO:0051402|GO:0000978|GO:0021562|GO:0001077|GO:0045944|GO:0050885|GO:0005654|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128842_PI430048170 0.7299131727145860.9758580964337870.276183169234917 0.4953008403082420.329132860134458A A A 0.5150033924723880.411155217780588 0.27979470438987 A A A LNCV6_128842_PI430048170 mRNA TGAGATGTAGGCTCCACCTTAACTGTGCTCAGATACACAAGTGAGGGCTTTTTAACTTGA NM_012409RefSeq chr20 + 4721853 4728462 PRND 23627 prion protein 2 (dublet) GO:0005886|GO:0051260|GO:0031225 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139781_PI430048170 0.3158484031867570.8117647090612660.382805014552945 0.2766132874606970.280985493972686A A A 0.2590261054185410.965137073472063 0.532378971857686A A A LNCV6_139781_PI430048170 mRNA TCTAGCTGCTGTGGCTACCGACCACTTTGCTACAGAAGATGCTATTCCTCTTGCTACTAA NM_181617RefSeq chr21 - 30746950 30747202 KRTAP21-2 NA keratin associated protein 21-2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141753_PI430048170 0.00680471678795949 0.5187820399191065.2267284752266 4.74820671728909 5.04608137698612 P P P 5.73763750814285 6.08140684739545 6.05736795390219 P P P LNCV6_141753_PI430048170 mRNA GCAACCAGCTACCATTCTAAAACTGCCATATGATTTTAGGATTTTTAAAAAGGGCCAAAT NM_002759RefSeq chr2 - 37105140 37157047 EIF2AK2 5610 "eukaryotic translation initiation factor 2-alpha kinase 2, transcript variant 1"
GO:0005515|GO:0003725|GO:0017148|GO:0048471|GO:0033689|GO:0008285|GO:0019054|GO:0008601|GO:0035455|GO:0019058|GO:0032874|GO:0005634|GO:0001819|GO:1900225|GO:0006412|GO:0030968|GO:0005829|GO:0051607|GO:0005737|GO:0000186|GO:0051092|GO:0046777|GO:0045071|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132419_PI430048170 0.8168357826222050.5624929951597 0.39519261794523 1.52452259650646 0.904775016081844A A A 0.2623830022091293.06780533531863 0.25901356722013 A P A LNCV6_132419_PI430048170 mRNA

TATACTGGACTACTTTTACACCTTCTAATATCCTGTCCAAGTTTGGGCGCAGATGGTGGA NM_007030 RefSeq chr5 - 659861 693395 TPPP 11076 tubulin polymerization promoting protein GO:0008017|GO:0005515|GO:0048471|GO:0046785|GO:0005737|GO:0031334|GO:0015631|GO:0032273|GO:0001578|GO:0005874|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_142928_PI430048170 0.00719316120549841 1.90093370181265 5.36238560633986 5.68757757079284 5.24967471035169 P P P 4.72887086839761 4.50588987141454 4.28761031776863 P P P LNCV6_142928_PI430048170 mRNA

AACTCCTGTGACAGGGGAAGTGGTCAGCAAGGCGGGAGCTCCAGCTGTGGCCACAGTTCT NM_178431 RefSeq chr1 - 152622833 152623103 LCE3A 353142 late cornified envelope 3A GO:0031424 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_101210_PI430048170 0.571176655068475 0.963129133057167 0.431158298760277 0.288957941199955 0.339062843750143 A A A 0.321701670178355 0.546488370236191 0.346521042211029 A A A LNCV6_101210_PI430048170 mRNA

TGGATCTGTATAGATGGAGTTTGTATGAGTGGGGATAAACAATGTACAGACACATTTGGC NM_001464 RefSeq chr8 - 39743735 39838289 ADAM2 2515 "ADAM metallopeptidase domain 2, transcript variant 1" GO:0005886|GO:0009986|GO:0007339|GO:0007338|GO:0005178|GO:0005887|GO:0007342|GO:0008542|GO:0006508|GO:0030534|GO:0008270|GO:0004222|GO:0007155|GO:0008237|GO:0032504 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_114243_PI430048170 0.0911077450738964 1.69384093318847 2.06861245972142 2.64358178231873 2.97139217223752 A A A 1.5538956185458 2.16349159393038 1.75696000272031 A A A LNCV6_114243_PI430048170 mRNA

CAAAAGAAGTAAAAGGCCTACTGTACCTCATGATGAAGACTCTTCAGATGATATTGCTGT NM_001080481 RefSeq chr6 - 99432305 99515376 USP45 85015 ubiquitin specific peptidase 45 GO:0004197|GO:0016579|GO:0004843|GO:0061136|GO:0043161|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_128502_PI430048170 0.573639848770341 1.07993326339313 8.89512420242779 8.75644101350321 8.9713539602527 P P P 8.35401247689236 8.86455141603781 9.00221165732059 P P P LNCV6_128502_PI430048170 mRNA

CTTTGCCTCTTACCATGCCTCTGAATGTCTTTGGATCCAACCCAGATGAGACTGAAAAAA NM_001145860 RefSeq chr8 + 98117292 98159841 POP1 10940 "processing of precursor 1, ribonuclease P/MRP subunit (S. cerevisiae), transcript variant 1" GO:0005515|GO:0000171|GO:0000172|GO:0004526|GO:0005655|GO:0016078|GO:0001682|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_133690_PI430048170 0.0100406585617693 0.482164071731071 0.897947592376038 1.2318042989267 0.635277824718843 A A A 1.83224529760842 1.83726417469925 2.2698753207619 A A A LNCV6_133690_PI430048170 mRNA

TTTCCACTGCCTCCTTAGCAATGACACTAATAAAAGTCGTAACACCTGTTCACATGCACA NM_001042690 RefSeq chr4 + 3249039 3256615 MSANTD1 NA Myb/SANT-like DNA-binding domain containing 1 NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_106122_PI430048170 0.817784213387511 1.02815346305013 11.7074935875241 11.303961454197 11.4893517605852 P P P 11.3630313231427 11.4004741549226 11.6306681718752 P P P LNCV6_106122_PI430048170 mRNA

AAGAGGTTCCAATCTTCGTGTTCACTTTAAGATATCCCAGAAGAAACTGAAGAAACAAAA NM_000985 RefSeq chr18 - 49488480 49492565 RPL17 6139 "ribosomal protein L17, transcript variant 1" GO:0010467|GO:0003735|GO:0006614|GO:0019083|GO:0019058|GO:0005634|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0000184|GO:0016032|GO:0022625|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_129531_PI430048170 0.404354730000706 0.656846578255479 0.277039636148473 0.304472316318064 0.368220216385116 A A A 1.66070048311523 0.347916684182875

0.328309045184653 A A A LNCV6_129531_PI430048170 mRNA
CTCATCATGATCCAGATTTCATTATGGCATTTTGTCTATAAATCAGGCACGACCTCATAA NM_005422 RefSeq chr11
+ 121102665 121190806 TECTA 7007 tectorin alpha
GO:0007160|GO:0005886|GO:0007605|GO:0005578|GO:0031225|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_118466_PI430048170 0.00231145119982849 0.65204912162148 6.58985719720943
6.52749746690188 6.56660667357292 P P P 7.11803071138448 7.14333542100173
7.26951742433478 P P P LNCV6_118466_PI430048170 mRNA
AGCCCTTGTGATTCGAAATGGTGAGAAAATGAGCATAAATGCGGAGGAAGTTGTGGTTGG NM_001160233 RefSeq
chr1 + 116373866 116404776 ATP1A1 476 "ATPase, Na+/K+ transporting, alpha 1 polypeptide, transcript
variant 3"
GO:0005515|GO:0006883|GO:0060048|GO:0034220|GO:0086009|GO:0045822|GO:0045823|GO:0086004|GO:0005
391|GO:0070062|GO:0042470|GO:0005794|GO:0019901|GO:0019904|GO:0030506|GO:0010107|GO:0030955|GO:0
086064|GO:0005890|GO:0043234|GO:0060081|GO:0043531|GO:0002026|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144366_PI430048170 0.890674274514793 1.02455002971044 0.846823571916406
1.54224921607067 0.281572167630671 A A A 1.67556146157776 0.401160230824825
0.34428458175349 A A A LNCV6_144366_PI430048170 mRNA
TGGCTGAAGGCCCCAGTGTGGACACCAGGCCCAAGAAGATGGAAAAAGAGCCTGCCGCCA NM_144616 RefSeq
chr19 - 2252250 2256423 JSRP1 126306 junctional sarcoplasmic reticulum protein 1
GO:0003009|GO:0060314|GO:0033017|GO:0072657 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81717_PI430048170 0.000554602871013114 0.391253775628548 7.75144910364565
7.62352537405713 7.50000011170721 P P P 9.05244016783589 8.94353424559409
8.94879121648375 P P P LNCV6_81717_PI430048170 mRNA
TTGAGTGAGGTCTTACCTCTTCTTTAAACCTCTTCAGGAGTGTCCTGATTATGTCCAGAA NM_177439 RefSeq chrX
+ 48476020 48486364 FTSJ1 24140 "FtsJ RNA methyltransferase homolog 1 (E. coli), transcript variant 3"
GO:0005737|GO:0002181|GO:0002128|GO:0008175 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140452_PI430048170 0.0721397242981007 0.940007012314728 7.78786404348933
7.79071774466792 7.72890493942052 P P P 7.91475624824137 7.83934584561441
7.82025407422821 P P P LNCV6_140452_PI430048170 mRNA
ATCCTGACTTCCATGTAGCTCCAGTCATTGTGATCAGACATCCTTTATAAAACATGTTTT NM_016452 RefSeq chr1
+ 230747414 230802003 CAPN9 10753 "calpain 9, transcript variant 2"
GO:0005737|GO:0004198|GO:0007586|GO:0005509|GO:0006508|GO:0005575 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138309_PI430048170 0.187496404982317 8.21096574882473 0.369336190842235
4.22105976053276 3.5879698478474 A P P 0.39500209168093 0.346065900766584
0.386347628130766 A A A LNCV6_138309_PI430048170 mRNA
AGACCGTGAGCCTGTTTTTGATTTGAGTGTTCCACTAAACAAACAACAAAAGCCAAAAAA NM_001200049 RefSeq
chr10 - 132808391 132942585 CFAP46 54777 cilia and flagella associated protein 46
GO:0035082|GO:0005930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141764_PI430048170 0.110775610157371 0.691620737475653 11.1118409748074
10.6067310701241 10.3625770976866 P P P 11.3498831017207 11.352871790137
11.0583339726111 P P P LNCV6_141764_PI430048170 mRNA
GTCCTAGACAGCAGTTTCCAGTAAAAGCTGAACAAAAGACTACTTGGTACTCTCAAAAAA NM_001256456 RefSeq
chr1 - 1311584 1324687 CPSF3L 54973 "cleavage and polyadenylation specific factor 3-like,
transcript variant 1" GO:0005515|GO:0005737|GO:0016787|GO:0032039|GO:0072562|GO:0016180 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138670_PI430048170 0.402010646130723 1.31750642697615 0.362665788339286
1.24434000964178 0.271084564493984 A A A 0.294006263976246 0.309582409818415

0.292338646225631 A A A LNCV6_138670_PI430048170 mRNA
AGCATATCTCCAACCTTGCAATTTGATTGGCATAATCACTCCAGTTTGCTTTCTAGGTCC NM_032649 RefSeq chr18
+ 74534456 74585026 CNDP1 84735 carnosine dipeptidase 1 (metallopeptidase M20 family)
GO:0034701|GO:0006508|GO:0004180|GO:0005576|GO:0016805|GO:0046872|GO:0008237 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132986_PI430048170 0.000273360747541681 0.323874602962258 7.43440902696971
7.34531579167704 7.40902413380237 P P P 8.92379632226415 9.00586946845632
9.13233113759593 P P P LNCV6_132986_PI430048170 mRNA
GACCATTATTCACAGGTGGACAAATGTTGATGTTGTCCTGTTAATTTATAGGCGTTTTTT NM_001032282 RefSeq
chr8 - 102648776 102653964 KLF10 7071 "Kruppel-like factor 10, transcript variant 2"
GO:0005515|GO:0003700|GO:0008285|GO:0008283|GO:0007267|GO:0045672|GO:0005634|GO:0030282|GO:0000
122|GO:0046872|GO:0006351|GO:0001501|GO:0042752|GO:0007623|GO:0007179|GO:0001046|GO:0045892|GO:0
035019|GO:0009267. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131440_PI430048170 0.0162345169241838 0.301260104455915 3.13780673108185
2.39226855351906 2.41084760537342 A A A 4.33337352000311 4.45510437315941
4.47259542802175 P P P LNCV6_131440_PI430048170 mRNA
GTTTGCACCTCCACATTTTATTGCTTCTGGATGTGAAATCATGTAATTATTTCTGCTGTT NM_014363 RefSeq chr13 -
23328822 23433728 SACS 26278 "sacsin molecular chaperone, transcript variant 1"
GO:0070852|GO:0005739|GO:0090084|GO:0030424|GO:0005737|GO:0006457|GO:0070628|GO:0051087|GO:0030
544|GO:0005634|GO:0030425 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135074_PI430048170 0.377830768252163 0.826363886213748 0.372251190086285
0.445894054742022 0.357131220544232 A A A 0.526090351745243 1.0501468860833
0.326506687668347 A A A LNCV6_135074_PI430048170 mRNA
CTTATCACTGTATACCACTGGAGTTTTCTGGTTATCTCTCGTATAGCAAAATCTAACTGA NM_013252 RefSeq chr7
- 141927356 141946983 CLEC5A 23601 "C-type lectin domain family 5, member A, transcript variant 1"
GO:0043066|GO:0005886|GO:0009986|GO:0050715|GO:0009615|GO:0007165|GO:0006968|GO:0002076|GO:0001
618|GO:0005887|GO:0045087|GO:0016032|GO:0030099|GO:0030246|GO:0033033 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135571_PI430048170 0.163421914532622 0.54191026690434 0.502116872147525
1.29481931867549 1.06972565004092 A A A 1.02221616671227 1.96292924958224
2.34618587541606 A A A LNCV6_135571_PI430048170 mRNA
CAGGTGTTGTTAATTTGTTCAAAGGCAGGCAAACAATCTCTCTGGCAACACAATTTTCTT NM_173561 RefSeq chr6
- 41026900 41039199 UNC5CL 222643 unc-5 homolog C (C. elegans)-like
GO:0007165|GO:0005737|GO:0016020|GO:0046330|GO:0006508|GO:0008233|GO:0016021|GO:0043123 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135325_PI430048170 0.00130281004807829 2.29102406605239 7.04091379482141
6.95284103378194 6.80862509369832 P P P 5.94018629174096 5.65180714973633
5.60890152687595 P P P LNCV6_135325_PI430048170 mRNA
CCCCAAGACAAACGCTGATGTATCCCCGAATAAATAAAGACATCTTACATCTTCAAAAAA NM_014475 RefSeq chr19
+ 48933681 48944969 DHDH 27294 dihydrodiol dehydrogenase (dimeric)
GO:0005975|GO:0047837|GO:0047115|GO:0008746|GO:0009055|GO:0042843|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134564_PI430048170 0.560487519174813 0.570950515554851 0.64922670287869
1.17124078032108 1.34777657043799 A A A 1.66384850675465 0.265600880266883
2.76093246504462 A A P LNCV6_134564_PI430048170 mRNA
CCCTGTTACATCCATTTGGTAAAATTTATTTGTCCTGATTAACCAGCTCTCATTTTATGG NM_021244 RefSeq chr6 -
89364615 89412276 RRAGD 58528 Ras-related GTP binding D
GO:0005515|GO:0032008|GO:0046982|GO:0003924|GO:0005634|GO:0005525|GO:0005764|GO:0006184|GO:0005
737|GO:0071230|GO:0010506|GO:0034613|GO:0019003|GO:0009267|GO:0034448 . NA - . NA NA NA

NA NA NA NA NA NA
LNCV6_128128_PI430048170 0.0547850977921867 0.6102055883872157.50085887186222
7.511175723916 7.78561768065738 P P P 7.91548823498747 8.3703040900766
8.58887544652123 P P P LNCV6_128128_PI430048170 mRNA
GAATGACTCTTCTGTGCATTCTTCTTAAAGAGCTGCTTGGTTATCCAAAAATGAAAATTC NM_001010924 RefSeq
chr10 - 15211644 15371059 FAM171A1 221061 "family with sequence similarity 171, member A1"
GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127491_PI430048170 0.1306315144889420.7733446917926126.00292607728947
5.69908007742602 6.05639263030547 P P P 6.47791149828422 6.38618994939662
5.98596338006604 P P P LNCV6_127491_PI430048170 mRNA
AACACTGAATATTTCAACAGCAGAAATTGAATGGGGGGATTGATAGCGCTGGCGAGGGAA NM_001271938
RefSeq chr19 + 42325608 42378769 MEGF8 1954 "multiple EGF-like-domains 8, transcript variant 1"
GO:0005515|GO:0010468|GO:0005509|GO:0048842|GO:0005634|GO:0048704|GO:0030326|GO:0030509|GO:0061
371|GO:0003143|GO:0042074|GO:0060972|GO:0060971|GO:0004872|GO:0016021|GO:0055113|GO:0097094|GO:0
035108|GO:0097155|GO:0071907|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115658_PI430048170 0.274659154084433 2.00502502640627 0.642771182980976
2.09616692986909 2.54278124658954 A A A 0.3167321259607631.16534417964576
1.21976556291734 A A A LNCV6_115658_PI430048170 mRNA
ATGTTCCCGGGAAATGGCGACGAGCAGCCTCTGACCGAGAACCCCCGGAAGTACGTCATG NM_001035256
RefSeq chr2 - 25160852 25168690 POMC 5443 "proopiomelanocortin, transcript variant 1"
GO:0005782|GO:2000852|GO:0007267|GO:0032098|GO:0006091|GO:0070873|GO:0005615|GO:0005737|GO:0016
486|GO:0007218|GO:0031781|GO:0045944|GO:0031782|GO:0030141|GO:0005777|GO:0001664|GO:0033059|GO:0
005102|GO:0032720|GO:0005576|GO:0042593|GO:0070996|GO:0007165|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134915_PI430048170 0.0166148723176315 1.26636615756674 11.6270036437333
11.6221271104277 11.428393238449 P P P 11.2713710084172 11.2652268768784 11.12275456429
P P P LNCV6_134915_PI430048170 mRNA
AGTGGGTGCTGGTTGCTGTGTCTTGTCTGTAAATAAACTCCTATCATGCCTTTTAAAAAA NM_153213RefSeq chr1
- 16198103 16212609 ARHGEF19 128272 Rho guanine nucleotide exchange factor (GEF) 19
GO:0005515|GO:0032321|GO:0032956|GO:0042060|GO:0005089|GO:0005096 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134621_PI430048170 0.5537849692142870.8473329256572113.38769456789809
3.33957934453161 2.54734033547488 P P A 3.75352645236238 3.38166367973658
2.86551322632637 P P P LNCV6_134621_PI430048170 mRNA
GAGCTGTCTCTCTCAATCACTCCTCAATGTTCTATCTTAATTTTGTGGAAGTTTAAAGTT NM_001105528 RefSeq chr18
- 32937401 33440081 CCDC178 374864 "coiled-coil domain containing 178, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98760_PI430048170 0.7444266183951110.9591736404813834.31688802262377 4.19582382432648
4.19774628862878 P P P 4.43931162806385 4.3931021041481 4.02763725807463 P P P
LNCV6_98760_PI430048170 mRNA
TACACAGAAGAACAGACAGTTCTTCAATGAACCAGAAGAAAATTTCTGGATGGTCATGGT NM_198097RefSeq chr7
- 6798934 6826295 CCZ1B 221960 CCZ1 vacuolar protein trafficking and biogenesis associated
homolog B (S. cerevisiae) GO:0031988|GO:0016192|GO:0005765|GO:0043231 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_12098_PI430048170 0.6612628355574040.8407724746384522.56059484715058 0.382239314243531
1.92762488806663 A A A 1.77957253307289 1.38544640745115 2.81679334983532 A A P
LNCV6_12098_PI430048170 mRNA
AAGTTGACTGGAACTTCCACAAGGACAGCTTTTTCTGCGACGTTCCAAGTGACCGATATT NM_032890RefSeq chr1
+ 222815088 223005995 DISP1 84976 dispatched homolog 1 (Drosophila)

GO:0009880|GO:0007368|GO:0015833|GO:0060539|GO:0007225|GO:0008158|GO:0016021|GO:0009953|GO:0015197|GO:0007224 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135657_PI430048170 0.34810696759842 0.6900743407360260.484320336763353 0.4651739928108811.54043377614459 A A A 1.89067003532476 0.664599495215708 1.56057866633623 A A A LNCV6_135657_PI430048170 mRNA
CCAGAAATCTGGCTTCATAATTTTGTTCCTCCTCTTTCTATGAAAGACTTAGCTATCTGCNM_004732RefSeq chr17 - 7921858 7929435 KCNAB3 9196 "potassium channel, voltage gated subfamily A regulatory beta subunit 3"
GO:0005737|GO:0005886|GO:0005249|GO:0015459|GO:0007268|GO:0034765|GO:0016021|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69346_PI430048170 0.5532305477694720.9473962858890426.21415136334146 5.98212435048863 6.05671035828528 P P P 6.00143071433475 6.32354556106196 6.153682573448 P P P
LNCV6_69346_PI430048170 mRNA
TTGCCTATATCGATGGGCAGGTTCTGGTACCCCCGGGCTATGGACAGGATGTACGGAAGT NM_004341RefSeq chr2 + 27217389 27243792 CAD 790 "carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase"
GO:0017144|GO:0005886|GO:0031100|GO:0005634|GO:0044281|GO:0042995|GO:0014075|GO:0016363|GO:0042802|GO:0005829|GO:0007507|GO:0046777|GO:0046134|GO:0031000|GO:0070409|GO:0043195|GO:0018107|GO:0043025|GO:0006526|GO:0070062|GO:0007565|GO:0044205|GO:0004087|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_38416_PI430048170 0.3989748860149011.3795773685075 3.37988250306125 2.62338724909473 3.70680293151776 P A P 1.86967896821869 3.08375706393568 3.22409894427019 A P P
LNCV6_38416_PI430048170 mRNA
CAATAAGATATCCGAGCTGAAGAATGGCTCATTTTCTGGGTTAAGTCTCCTTGAAAGATT NM_145290RefSeq chr4 - 22387373 22516054 ADGRA3 NA adhesion G protein-coupled receptor A3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139474_PI430048170 0.4511630873420621.10390106979077 6.49257752136288 6.09718850917038 6.4802403174406 P P P 6.29770063008232 6.01677950776869 6.34065724095026 P P P LNCV6_139474_PI430048170 mRNA
TATCCTTCCTGTGTCAAGCCTTATAAATCATGTAATTTAGTGCCACTCATGTAAATCAGT NM_018706RefSeq chr10 + 12068916 12123228 DHTKD1 55526 dehydrogenase E1 and transketolase domain containing 1
GO:0005739|GO:0006099|GO:0002244|GO:0006091|GO:0045252|GO:0030976|GO:0004591|GO:0006096|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141974_PI430048170 0.25669162008621 1.04380571068111 0.5559453702592660.6563514454539 0.529096794214759A A A 0.5231358590216010.5154202910089390.520408334886264A A A
LNCV6_141974_PI430048170 mRNA
CGACACCCTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCAC NM_206998RefSeq chr11 - 62296281 62299064 SCGB1D4 NA "secretoglobin, family 1D, member 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126717_PI430048170 0.7044568295852781.03431303067232 11.4062415064529 11.1250049504234 11.1136723950396 P P P 11.2249904740074 11.1297650155433 11.1619501230902 P P P LNCV6_126717_PI430048170 mRNA
TTCCAAGAAATGGGCTGCTGGCCAGAACAAACAACATTCTATTACCAAGAACACGGCCAA NM_001281297 RefSeq chr9 - 136862113 136866336 EDF1 8721 "endothelial differentiation-related factor 1, transcript variant 3"
GO:0005515|GO:0005516|GO:0006355|GO:0003700|GO:0005669|GO:0008168|GO:0003713|GO:0005730|GO:0005634|GO:0007275|GO:0006351|GO:0019216|GO:0043565|GO:0005622|GO:0005737|GO:0043388|GO:0045446|GO:0045893|GO:0004402|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141453_PI430048170 0.4705907684621430.7214840058412680.449666486138972

0.5110869474297810.474283220676951 A A A 1.63050821790637 0.415981434314051
0.447095484242661 A A A LNCV6_141453_PI430048170 mRNA
CAGTTTTCTTCAGGTTACTTTTTAATAATGATTAAAACGGGGAACTTCATTATCAAAAAA NM_001296RefSeq chr3
+ 42809471 42867283 ACKR2 1238 atypical chemokine receptor 2
GO:0070098|GO:0005886|GO:0005884|GO:0007275|GO:0019957|GO:0006898|GO:0006955|GO:0006954|GO:0006
935|GO:0007186|GO:0016494|GO:0005887|GO:0004950|GO:0016493|GO:0042119|GO:0055037|GO:0005769|GO:0
005044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140792_PI430048170 0.456974805029938 1.05067664976449 10.8285809424961
10.9558098348965 10.7437157921434 P P P 10.885450438451 10.751471671472
10.6774057611416 P P P LNCV6_140792_PI430048170 mRNA
TATGAGTATCGCCGGGCCCAGGAGGCCGTGTGAGGATCCCGCAATAAAGATGCCTTAAGTNM_017570RefSeq chr8
- 144051265 144060703 OPLAH 26873 5-oxoprolinase (ATP-hydrolysing)
GO:0006805|GO:0017168|GO:0006750|GO:0044281|GO:0005524|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142041_PI430048170 0.210671694036959 1.67263158041736 1.07449858594356
0.308553718740921 1.54779799833302 A A A 0.347429722830894 0.31135011890523
0.303721432103397 A A A LNCV6_142041_PI430048170 mRNA
CACTGAGATACGTTACCCAATTAGGGAAATAAATTTGTTAATAAAATTGCTGAGGTCACC NM_001142883 RefSeq
chr6 - 33721665 33746985 IP6K3 117283 "inositol hexakisphosphate kinase 3, transcript variant 2"
GO:0008440|GO:0043647|GO:0046488|GO:0052724|GO:0005634|GO:0052723|GO:0044281|GO:0000831|GO:0000
832|GO:0005524|GO:0005829|GO:0005737|GO:0032958|GO:0006468 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127197_PI430048170 0.683098106245443 1.17432428868911 1.57028893896088
0.582053340555473 1.90959877995775 A A A 0.516125110476758 0.911233553351142 1.8844534163353
A A A LNCV6_127197_PI430048170 mRNA
GGATAGGAGTGGACATATGTTTCAAATATGGGGACCCTGAAGATTTTTTAGAATGAAATA NM_138779RefSeq chr13
- 102765887 102773821 TEX30 93081 "testis expressed 30, transcript variant 1" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_144259_PI430048170 0.157084925465618 0.826102797734605 8.37585346973338
8.41042951480836 7.99791522775394 P P P 8.51565496687983 8.69759974004704
8.41891558341361 P P P LNCV6_144259_PI430048170 mRNA
GTGAGGTGGCAATGGGATTTGCTCAGATGCCACCCAATAAAATGCCTGTTACTTAAAAAA NM_003748RefSeq chr1
- 18871429 18902799 ALDH4A1 8659 "aldehyde dehydrogenase 4 family, member A1, transcript
variant P5CDhL"
GO:0006537|GO:0004029|GO:0009055|GO:0044281|GO:0003842|GO:0042802|GO:0034641|GO:0019470|GO:0005
759|GO:0006560|GO:0010133|GO:0006562|GO:0006561|GO:0055114 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130586_PI430048170 0.943491965062725 0.917091885505782 2.58256664054262
2.35088196160932 2.62797536306704 A A A 3.23278373874262 2.49284797768847
1.92783420733058 P A A LNCV6_130586_PI430048170 mRNA
GTTTTTCCTGCTCCTGGTGTCCTACATAGTCATATTATCATTACCCAAGTCTCAGGCAGG NM_001004705 RefSeq
chr11 + 59477429 59478365 OR4D10 NA "olfactory receptor, family 4, subfamily D, member 10"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52461_PI430048170 0.465179235241456 1.4520064160764 0.342603953282056 1.73751111827856
0.486783009877457 A A A 0.317291968661756 0.614676867851686 0.441198382807203 A A A
LNCV6_52461_PI430048170 mRNA
TTTTGTTCTGTTTTTCTACAACACAGAGTACTGACTCTGCCTGGTTCCTGAGAGAGGCTC NM_000929RefSeq chr1
+ 20070207 20091901 PLA2G5 5322 "phospholipase A2, group V"
GO:0019370|GO:0048471|GO:0005794|GO:0005886|GO:0009986|GO:0036149|GO:0006663|GO:0005509|GO:0036

148|GO:0005576|GO:0044281|GO:0051591|GO:0016042|GO:0036150|GO:0047498|GO:0006644|GO:0034097|GO:0006654|GO:0008201|GO:0036151|GO:0050482|GO:0046474|GO:0036152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135061_PI430048170 0.5071085268016271.13073232871032 4.08415159509977 3.60240313325407 3.47488301693502 P P P 3.34452340668489 3.73232275227375 3.60006931901461 P P P LNCV6_135061_PI430048170 mRNA GGGCCATCCACTTGCCTACAGGCACTCTGCTTTTATTATTAAAAATAGTCACTTTGTTAC NM_138413RefSeq chr10 + 97584344 97612798 HOGA1 112817 "4-hydroxy-2-oxoglutarate aldolase 1, transcript variant 1" GO:0005739|GO:0008700|GO:0033609|GO:0019470|GO:0046487|GO:0042866|GO:0009436|GO:0042803|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140331_PI430048170 0.0249406873713176 0.3622227638030550.375726755236314 0.3973542969860550.303786942621499A A A 1.33800645049121 1.88452759155552 2.1393450083779 A A A LNCV6_140331_PI430048170 mRNA GGGAAGTGGCACCTCACTAGCATTTATCACTTTTTTCCTTCTCTTTTTAAAAATAAAACC NM_031890RefSeq chr22 - 17116298 17121323 CECR6 27439 "cat eye syndrome chromosome region, candidate 6, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103261_PI430048170 0.0867585712683963 1.09924146302188 8.9745056994782 8.9850103218201 8.84364342221299 P P P 8.82434600849964 8.79443384577086 8.77873637925236 P P P LNCV6_103261_PI430048170 mRNA AAAGTTTTACAGCACAATATATGTGCTCTGCTCTCCTCCCGCAATCCTGCTCCAAGAGAT NM_032017RefSeq chr1 - 36339618 36385927 STK40 83931 "serine/threonine kinase 40, transcript variant 3" GO:0005515|GO:0010468|GO:0043066|GO:0048286|GO:0060425|GO:0005977|GO:0005524|GO:0003016|GO:0005737|GO:0035264|GO:0004674|GO:0043408|GO:0005654|GO:0006468 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137530_PI430048170 0.00787215787146413 0.5847989186065489.14554071022865 9.06483090430386 9.10490281001279 P P P 9.71378117566907 9.91503868193274 9.99517674031585 P P P LNCV6_137530_PI430048170 mRNA TGGCTGCCTTTCTCCTGTGTATGTGTAAATTCCTTAATAAATATTGCAGGGAAGGACAAA NM_022733RefSeq chr1 + 40373705 40423326 SMAP2 64744 "small ArfGAP2, transcript variant 1" GO:0043547|GO:0008060|GO:0005737|GO:0032312|GO:0008270|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131485_PI430048170 0.0456067691450267 1.60124132667476 9.10396147712237 9.50424344967769 9.70172416206693 P P P 8.50393787701227 8.74541550633661 9.03626140818022 P P P LNCV6_131485_PI430048170 mRNA GGGTCTTTGGTGTTTTTAAATGATTGTTTCTTCTTCATGCTTTTGCTTGCAATGTAGTCA NM_002690RefSeq chr8 + 42338454 42371813 POLB 5423 "polymerase (DNA directed), beta" GO:0008017|GO:0005515|GO:0008630|GO:0045471|GO:0003887|GO:0005874|GO:0005634|GO:0051402|GO:0046872|GO:0016829|GO:0006974|GO:0003684|GO:0006261|GO:0005737|GO:0006281|GO:0006290|GO:0071897|GO:0006284|GO:0006287|GO:0006297|GO:0005654|GO:0005876|GO:0019899 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139021_PI430048170 0.5771079448027521.39484091249122 3.18332452969819 3.84445964061709 2.15589535103259 P P A 2.79357045067901 2.71042515373869 2.7065096293484 P P P LNCV6_139021_PI430048170 mRNA ACCTCACCATGTACGCCAGCAGCTTTACGCTGGCTGCTGTCTCCGTGGACAGGTACCTGG NM_003614RefSeq chr22 + 37823381 37825495 GALR3 8484 galanin receptor 3 GO:0007631|GO:0005886|GO:0007218|GO:0045944|GO:0007611|GO:0007268|GO:0004966|GO:0016021|GO:0017046|GO:0007194|GO:0007193 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123092_PI430048170 0.7642605626591521.03328846529056 2.53113255725535 2.46156780436519 2.30326942001983 A A A 2.33371453341572 1.94847183389123

2.76570531375211 A A P LNCV6_123092_PI430048170 mRNA
ACCTTCAAGGCTGCAAGTCGGGCCATAGTTCAGTTCCTAGAGATTAATCAGAGTGAAGAA NM_014991 RefSeq chr4
- 84669539 84966391 WDFY3 23001 WD repeat and FYVE domain containing 3
GO:0005515|GO:0031965|GO:0005776|GO:0016234|GO:0003831|GO:0005635|GO:0046872|GO:0035973|GO:0005
545|GO:0005737|GO:0016605|GO:0016197|GO:0034274|GO:0016239|GO:0019898 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_2572_PI430048170 0.0627147433085643 4.09680629179358 10.4478085251782
10.5528536648668 10.4728444748688 P P P 9.38063627750005 7.78147381307493
7.39139554959869 P P P LNCV6_2572_PI430048170 mRNA
CGAGTGCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAAACTGCTACAATACTCC NM_001135101 RefSeq
chr22 + 49918629 49927540 CRELD2 79174 "cysteine-rich with EGF-like domains 2, transcript variant 1"
GO:0005515|GO:0005794|GO:0005783|GO:0005509|GO:0005615 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127088_PI430048170 0.6377050173855681.06082230863556 4.42650171747237
4.85928480111551 4.748385464478 P P P 4.52057415830688 4.53023828926911
4.75012561567077 P P P LNCV6_127088_PI430048170 mRNA
ATATCAGAGTCATCATTTTTCTTCCTGTGGAATAAAATGCCTTGTGGACTTCCCAAAAAA NM_015378 RefSeq chr1
+ 12230038 12512046 VPS13D 55187 "vacuolar protein sorting 13 homolog D (S. cerevisiae), transcript
variant 1" GO:0005622|GO:0045053|GO:0006623|GO:0070062|GO:0019898 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137534_PI430048170 0.4772664193102341.01949265579966 0.353425640769512
0.2456417503533690.288723250666507 A A A 0.2663508134755870.272991451083153
0.26692974886192 A A A LNCV6_137534_PI430048170 mRNA
ATTGTTTACATTGCATCCTGGATGGGACGTTTTTCATATGCAACGTGCTGCTCTCAGGAG NM_019074 RefSeq chr15
+ 40929332 40939060 DLL4 54567 delta-like 4 (Drosophila)
GO:0035912|GO:0035924|GO:0060579|GO:0007220|GO:0008285|GO:0005886|GO:0008015|GO:0005112|GO:0061
314|GO:0050767|GO:0007219|GO:0003222|GO:0090051|GO:2000179|GO:0001569|GO:0005509|GO:0072554|GO:0
001525|GO:0000122|GO:0003208|GO:0044344|GO:0003344|GO:0003209|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_94367_PI430048170 0.1500197372747221.76095979039904 2.81536631856091 3.83786723777266
3.14527542794018 A P P 3.11308018696271 1.88302739080681 2.26330213116434 P A A
LNCV6_94367_PI430048170 mRNA
AAGAGGACAGACAGCTGATGGCCGACCTTGTTGTCTCCAAAATGAGCCAGCTCCCGATGC NM_001135774 RefSeq
chr22 - 32512552 33058391 SYN3 8224 "synapsin III, transcript variant IIIg"
GO:0030054|GO:0032228|GO:0008152|GO:0030672|GO:0003824|GO:0005524|GO:0007269|GO:0008021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62849_PI430048170 0.0185016289945577 0.5949878687669494.71341969339084 4.3179116968981
4.64620058694025 P P P 5.02180497820379 5.51214496077314 5.37765291796025 P P P
LNCV6_62849_PI430048170 mRNA
AACTTTGTAGAACGATACAAGTTACTAAGAAGGCTTCATCCTTGCACATCCTCTGGCCCC NM_001163735 RefSeq
chr17_KI270857v1_alt - 730658 770361 MYO19 80179 "myosin XIX, transcript variant 2"
GO:0005737|GO:0003774|GO:0008152|GO:0005741|GO:0003779|GO:0016459|GO:0005524 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137601_PI430048170 0.00111013533600949 2.09252096246955 12.3532261458086
12.2829111411346 12.0437932128455 P P P 11.2941548991343 11.1819300379717
11.0121568324802 P P P LNCV6_137601_PI430048170 mRNA
TTGTCAGGATTACCCTCGGGCTAAAGAGGAAAAATAAAGATGTTGAGCTACCACTCTGGA NM_033518 RefSeq chrX
- 48458536 48470256 SLC38A5 92745 "solute carrier family 38, member 5"
GO:0015816|GO:0005886|GO:0005887|GO:0006865|GO:0015187|GO:0055085|GO:0003333|GO:0006811 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134430_PI430048170 0.2498128027369651.04502981897115 0.332963123703124
0.3137017720036230.440683295000072A A A 0.2994766271661410.27750374894779
0.322654607038275A A A LNCV6_134430_PI430048170 mRNA
AGTAGGGCTTGGTGAATGCTGCTGAGTGAATGAGTAAATAAACTCTTCAAGGCCAAGGGA NM_000491RefSeq chr1
+ 22653188 22661536 C1QB 713 "complement component 1, q subcomponent, B chain"
GO:0005515|GO:0006956|GO:0048839|GO:0005581|GO:0045087|GO:0006958|GO:0072562|GO:0005576|GO:0005
602|GO:0042803|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143605_PI430048170 0.8071069703200730.9732276398825235.57297468187351 4.7774545221413
5.52506727089999 P P P 5.1711759301159 5.40715659382824 5.52173244191659 P P P
LNCV6_143605_PI430048170 mRNA
ATACACATATGCAACCAACTAAACAGTTATAATCTTGGCACTGTTAATAGAAAGGTGGGA NM_005842RefSeq chr13
- 80335976 80340951 SPRY2 10253 sprouty homolog 2 (Drosophila)
GO:0005515|GO:0051897|GO:0008285|GO:0071902|GO:0005886|GO:0007605|GO:0000132|GO:0005829|GO:0046
580|GO:0033138|GO:0007173|GO:0043407|GO:0015630|GO:0060437|GO:0070373|GO:0070374|GO:0034261|GO:0
043066|GO:0042472|GO:0019901|GO:0005874|GO:0042059|GO:0032587|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133855_PI430048170 0.0159774771725039 1.40794439210071 10.3991215929186
10.4532987604586 10.4671935352564 P P P 9.93985878896663 10.0728102815859
9.81559386695263 P P P LNCV6_133855_PI430048170 mRNA
TCCAGCACTTTTTATATTTACGTATTCTCCAAAGCAGTGTTCACACGGGAGCCAGCCTGT NM_001025237 RefSeq
chr11 + 844445 867116 TSPAN47106 "tetraspanin 4, transcript variant 1"
GO:0006461|GO:0005178|GO:0005886|GO:0016021|GO:0031982|GO:0005925|GO:0003823 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143637_PI430048170 0.0128426815004483 0.2457462084426054.13657544670011
3.70631670176754 3.63336097268668 P P P 5.1830914461817 6.2682407748327 5.9490136321904
P P P LNCV6_143637_PI430048170 mRNA
TGGAAAATACAGTGCCCTGCCTTCTTAGGGGCATCAGCCCTGAACGGTTGAGAGCGTGGA NM_000695RefSeq chr11
- 67662161 67674631 ALDH3B2 222 "aldehyde dehydrogenase 3 family, member B2, transcript variant
1" GO:0006629|GO:0006066|GO:0006068|GO:0004029|GO:0004028|GO:0055114|GO:0004030 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133214_PI430048170 0.0593192422306950.7197103903820287.3847533923914
7.39880952007673 7.66382325585566 P P P 7.71209177624656 7.93538686471976
8.19954737128174 P P P LNCV6_133214_PI430048170 mRNA
TTTGGAACCAGACAAGAATCCAAAGAAAATAAGAACACAGACCACCAGTGCAAAACAAGA NM_001034194
RefSeq chr4 + 121801316 121817021 EXOSC95393 "exosome component 9, transcript variant 1"
GO:0005515|GO:0010467|GO:0030307|GO:0071028|GO:0006364|GO:0003723|GO:0071035|GO:0000956|GO:0005
730|GO:0043928|GO:0004532|GO:0005634|GO:0000228|GO:0000178|GO:0005829|GO:0006955|GO:0005737|GO:0
000175|GO:0000176|GO:0017091|GO:0005654|GO:0045111|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127872_PI430048170 0.0677376411937065 1.19045492652357 12.3601374474792
12.3432315740591 12.4365471998193 P P P 12.0857485675546 12.0137586034465 12.274842377459
P P P LNCV6_127872_PI430048170 mRNA
TAGGAGAGACCCTTTTGCTGCTACTTCATTCGTTCTGACCTAATAATAAAAGTTAGAACC NM_033414RefSeq chr5
- 16451518 16465785 ZNF622 90441 zinc finger protein 622
GO:0005515|GO:0033674|GO:0005737|GO:0043065|GO:0005794|GO:0008631|GO:0046330|GO:0005730|GO:0008
270|GO:0043410 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131743_PI430048170 0.3674774196012862.03361802921505 1.27221663064422
0.5109646190550472.81203693414042 A A A 0.2894625225145211.53361637894875

0.292145036734758 A A A LNCV6_131743_PI430048170 mRNA
GATTCTGGTGGAGAGAAGTGAGAATAGGCAGCCCCCAAATAAAAAATATTCATGGAAAAA NM_021966 RefSeq
chr14 - 95709966 95714196 TCL1A 8115 "T-cell leukemia/lymphoma 1A, transcript variant 1"
GO:0005515|GO:0005783|GO:0019827|GO:0007275|GO:0045120|GO:0005938 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130285_PI430048170 0.0543113045396354 0.770851015434863 6.83874421548543
6.9103997876506 6.94065073968674 P P P 7.113614210165 7.23288663982558
7.45110957000801 P P P LNCV6_130285_PI430048170 mRNA
CTGCCATTGTCCCCAAGGCTTCTGTCTACTAATTCTATTGGTCTTGTGTTTTGCTTGCTT NM_133367 RefSeq chr6 +
52362127 52407777 PAQR8 85315 progestin and adipoQ receptor family member VIII
GO:0048477|GO:0005886|GO:0043401|GO:0003707|GO:0007275|GO:0016021|GO:0048545|GO:0005496 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107504_PI430048170 0.0499493158092261 .36633862922005 8.90725628246998 8.9257909878519
9.26789058395037 P P P 8.39164665698785 8.58562809081099 8.77641131782916 P P P
LNCV6_107504_PI430048170 mRNA
CTCTGAGATAGTAGATGTTGGAGATAAAGTGTGGGTGAAGCTTATTGGCCGAGAGATGAA NM_001282568 RefSeq
chr1 + 31296981 31364953 ZCCHC17 51538 "zinc finger, CCHC domain containing 17, transcript
variant 4" GO:0005515|GO:0030529|GO:0005730|GO:0008270|GO:0005634|GO:0045111|GO:0043231 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142986_PI430048170 0.108166985258471 3.13225815058791 3.65236786207472
4.97505172067306 3.11497923523042 P P P 2.29934372609787 2.26558301853343
2.82590659308472 A A P LNCV6_142986_PI430048170 mRNA
AGCTCCAAGTAAACTAGTTACCTGGGTAAAAGCGCTAACGACCCAAAGGCTCTTCTAAGA NM_003525 RefSeq chr6
+ 26272975 26273412 HIST1H2BI 8346 "histone cluster 1, H2bi"
GO:0046982|GO:0050830|GO:0019731|GO:0006334|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0005
615|GO:0003677|GO:0070062|GO:0002227 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104062_PI430048170 0.00256726871676277 1.61154683729542 9.16180397609874
9.2796361926277 9.4218283635361 P P P 8.70858007408987 8.47374200254141
8.61772769629417 P P P LNCV6_104062_PI430048170 mRNA
AATATAAGAGCTGGTACTCCTGGTTAATCAACAGCTTCGTCAACGGGGTCTATGCCTTTG NM_030782 RefSeq
chr5_KI270791v1_alt + 169121 195710 CLPTM1L 81037 CLPTM1-like
GO:0016020|GO:0006915|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66766_PI430048170 0.770056491804754 0.949353566779462 0.963457970632287 0.458570991127559
0.365805059663523 A A A 0.981043055991433 0.386404286393282 0.657930953663407 A A A
LNCV6_66766_PI430048170 mRNA
GGAAAAATGGGATTTAATGCATTCAAAGAGCTATGGGCAGCTCTTAATGCCTGGAAGGAA NM_012198 RefSeq chr2
+ 162344072 162362638 GCA 25801 "grancalcin, EF-hand calcium binding protein"
GO:0005737|GO:0004198|GO:0046982|GO:0005886|GO:0005509|GO:0006508|GO:0061025|GO:0042803|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_8306_PI430048170 0.0479727394004691 0.962620927173841 0.424388971665938
0.396964202926243 0.372484306660488 A A A 0.431318789530278 0.472214110017446
0.455360452600735 A A A LNCV6_8306_PI430048170 mRNA
TGATGAACCCCTTCAGGCTGGAGAACGTGACAGTCAGCGAATCGAGCCGGCAACTTCTCA NM_001146336 RefSeq
chr16 - 8569499 8589838 TMEM114 283953 "transmembrane protein 114, transcript variant 1"
GO:0016324|GO:0016021|GO:0016327 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133231_PI430048170 0.0356348758610852 1.63213663780656 5.23189399342776
5.18147503981983 5.54273412249076 P P P 4.24189915086723 4.79286315913271
4.76443896057548 P P P LNCV6_133231_PI430048170 mRNA
CTCTGTCACCAGATTACATTAAGAATTTGTCAGATAATGTGTAGAACTGCATAACAGGTA NM_145265 RefSeq chr5

- 204759 218182 CCDC127 133957 coiled-coil domain containing 127 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136034_PI430048170 0.3957152081619950.92376383651865 6.61654928485766 6.51506404519646 6.8255194640016 P P P 6.92827781226751 6.68999506040957 6.68605268529278 P P P LNCV6_136034_PI430048170 mRNA
CTTAGGAGACTGGAAGTTTAAAAATGTACAAGTCCTTTCAGTGATGAGGGAATTGATTTT NM_001142595 RefSeq
chr10 - 73007221 73096974 P4HA1 5033 "prolyl 4-hydroxylase, alpha polypeptide I, transcript variant 3"
GO:0005515|GO:0016222|GO:0031418|GO:0005506|GO:0005783|GO:0004656|GO:0043231|GO:0005739|GO:0016020|GO:0030199|GO:0018401|GO:0005788|GO:0016702|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136114_PI430048170 0.00705177090117223 0.22298363204834 4.20301356243651 3.66600968082483 4.0449837550942 P P P 5.51560617831993 6.41838486393145 6.36228962827891 P P P LNCV6_136114_PI430048170 mRNA
CTTGGCATCACTCAGCAGAGGTTTTTGTTTATAAAGATGAAGTCTTGAATACTGTTCAAT NM_006047 RefSeq chr20 - 35648924 35664956 RBM12 10137 "RNA binding motif protein 12, transcript variant 1"
GO:0000166|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134398_PI430048170 0.0215609109898435 1.87324010196063 5.70328512326154 5.55985718237781 5.30314454376459 P P P 4.85438079666725 4.72378716119637 4.22662046534579 P P P LNCV6_134398_PI430048170 mRNA
GCAAGTGCTCTCCAATAAAGTAGGGGGAGAAAGCAAACCCAAAAACCCGCTTCTAAAAAA NM_052841 RefSeq
chr1 + 32362260 32364323 TSSK3 81629 testis-specific serine kinase 3
GO:0000287|GO:0004674|GO:0007275|GO:0006468|GO:0009966|GO:0007283|GO:0005524|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130390_PI430048170 0.000410055620460701 0.165114275266644 1.55101858660702 0.97271985360341 1.32263570751124 A A A 3.66101054610408 4.05866485947342 3.95117590154057 P P P LNCV6_130390_PI430048170 mRNA
TTCTGATGGCACTGAGTTTTCATTGTTCTGGATGTATAAGTCTGTGTGTCAGGTACAGCT NM_001134831 RefSeq
chr6 - 135283971 135497765 AHI1 54806 "Abelson helper integration site 1, transcript variant 1"
GO:0005515|GO:0036038|GO:0070986|GO:0006903|GO:0001738|GO:0036064|GO:0042802|GO:0001947|GO:0035844|GO:0035845|GO:0005912|GO:0005911|GO:0045944|GO:0016192|GO:0039008|GO:0043066|GO:0005813|GO:0033365|GO:0071599|GO:0005814|GO:0039023|GO:0010842|GO:0031513|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57736_PI430048170 0.00285702133685115 0.739329938226165 8.72129951112445 8.87812261130616 8.82525260470326 P P P 9.25847837032793 9.31897016975403 9.1539353061734 P P P LNCV6_57736_PI430048170 mRNA
AACAACATCTTTTGGGGTACAATTAGAATCTAAGTGTTTGCAGCCATATGTGTCATGTAG NM_025128 RefSeq
chr11 + 65860400 65866443 MUS81 80198 MUS81 structure-specific endonuclease subunit
GO:0005515|GO:0006281|GO:0005730|GO:0048257|GO:0006310|GO:0005634|GO:0072429|GO:0003677|GO:0000737|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_46890_PI430048170 0.403885784319552 1.798176941836 0.550094072802997 0.508210583725686 2.24877668182823 A A A 0.411271120551656 0.579297310035161 0.510313151234945 A A A LNCV6_46890_PI430048170 mRNA
TGAGCTTCTGATTGATCTCGGGGTCCATCTGTGATATTTCTTTGTGCCAAAAAGAAAAAA NM_003654 RefSeq
chr11 - 45647688 45665656 CHST1 8534 carbohydrate (keratan sulfate Gal-6) sulfotransferase 1
GO:0006790|GO:0005976|GO:0005975|GO:0044281|GO:0042339|GO:0045130|GO:0006954|GO:0000139|GO:0018146|GO:0008146|GO:0009405|GO:0016021|GO:0006012|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142947_PI430048170 0.122623788110061 0.757517360012087 10.4019182223614

10.3334649187054 10.4402303655237 P P P 10.4935324241419 10.8203211236444 11.017945331193 P P P LNCV6_142947_PI430048170 mRNA CTGGCTCAGAGCCTGTTTGCCCTCTGTCTTAAACAATTGTAAATATCACTTAAATTATAA NM_006077 RefSeq chr10 - 72367325 72626191 MICU1 10367 "mitochondrial calcium uptake 1, transcript variant 1" GO:0005515|GO:0006851|GO:0046982|GO:0005509|GO:0005743|GO:0006952|GO:0034704|GO:0042802|GO:0005622|GO:0005739|GO:0005758|GO:0070509|GO:0051561|GO:0032592|GO:0051560|GO:0051260 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135260_PI430048170 0.00053121169988586 0.535929506338015 4.74126148884646 4.8665170922849 4.71263787219403 P P P 5.71169633760107 5.54757830496714 5.75716120473826 P P P LNCV6_135260_PI430048170 mRNA CCTGCCATGAATTTGAGTGTTAGGAAGGGAAAAATAAAATACTAATCTGGTCTTGAAGAA NM_001033503 RefSeq chr5 - 134601148 134632843 SAR1B 51128 "secretion associated, Ras related GTPase 1B, transcript variant 1" GO:0002474|GO:0012507|GO:0003924|GO:0048208|GO:0044281|GO:0005525|GO:0006886|GO:0046872|GO:0005829|GO:0006888|GO:0019886|GO:0032580|GO:0005789|GO:0061024|GO:0044267|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127296_PI430048170 0.694634705010716 1.01007070207914 0.358507648268282 0.337043140485256 0.258825862990184 A A A 0.302628450141451 0.314802290416792 0.295407242510068 A A A LNCV6_127296_PI430048170 mRNA GAGGAATATCTGCTGTTGTCATCAACAAGTGCTATTAAAGGATGTAAATCCATGAGTAAA NM_012274 RefSeq chrX + 37990816 37991317 HYPM 25763 huntingtin interacting protein M GO:0046982 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129806_PI430048170 0.412379095843885 0.826274940546283 5.99932729933849 5.69851502642443 5.28402378679207 P P P 6.23043895276032 6.05829517108426 5.51413841279281 P P P LNCV6_129806_PI430048170 mRNA TGTCGGGACTGCCCTGCTCTCGGATGAAAACAGAATGACACGTAAAGTCCGGGATTTTTT NM_001276687 RefSeq chr1 - 237004102 237004418 MT1HL1 645745 metallothionein 1H-like 1 GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130911_PI430048170 0.945385908909052 0.999844969435072 2.82049061897077 3.60713046321647 2.45336889033942 A P A 3.39999082676005 3.11497923523042 2.46229719833234 P P P LNCV6_130911_PI430048170 mRNA GAAAATAAGTAACTACATCTGCATCATTATCACTGCCACTCTCTTCAGCTACTGCTGCAT NM_001005466 RefSeq chr14 - 21633835 21634940 OR10G2 NA "olfactory receptor, family 10, subfamily G, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132182_PI430048170 0.349511665652968 1.14642016343493 3.2016291044499 2.86271137371544 2.94497557415012 P A P 2.89861559109117 2.47894898913723 3.00985718552556 P A P LNCV6_132182_PI430048170 mRNA TTTTTGGGGGGAGAAACCTCGGAATTTCTATGAGACCTCCCCCAGGGAGGGGGTCAGTTG NM_002088 RefSeq chr19 - 41998315 42065805 GRIK5 2901 "glutamate receptor, ionotropic, kainate 5, transcript variant 2" GO:0017124|GO:0030054|GO:0005886|GO:0005783|GO:0005234|GO:0007268|GO:0030425|GO:0042802|GO:0034220|GO:0043525|GO:0043195|GO:0045211|GO:0015277|GO:0043204|GO:0051649|GO:0071333|GO:0035249|GO:0060079|GO:0014069|GO:0030165|GO:0042734|GO:0035235|GO:0032983|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142454_PI430048170 0.358954721562323 1.02383405580294 0.335211243334176 0.257466453915169 0.348076421056994 A A A 0.293115571827379 0.265849481435962 0.281369411669913 A A A LNCV6_142454_PI430048170 mRNA CTACCTTAACCCACCTAAGTAAATGTGGAAACATCCGATATAAATCTCATAGTTAATGGC NM_001244438 RefSeq chr6 + 131573203 131584332 ARG1 383 "arginase 1, transcript variant 1"

GO:0043005|GO:0070301|GO:0030324|GO:0033189|GO:0071560|GO:0005634|GO:0044281|GO:0014075|GO:0048678|GO:0010043|GO:0005615|GO:0010042|GO:0005829|GO:0070207|GO:0034641|GO:0005737|GO:0010963|GO:0071377|GO:0043025|GO:0071353|GO:0033197|GO:0006527|GO:0043200|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144158_PI430048170 0.194527412789784 1.12454782970479 9.8767224903858 10.1072138056533 9.84050136742951 P P P 9.87839708223044 9.79169989126333 9.65208124768791 P P P LNCV6_144158_PI430048170 mRNA GAATACAGGAAAATCCCTTCTAGGCATCTCCTCTCCCCAACCCTTCCACACGTTTGATTT NM_002774 RefSeq chr19 - 50958630 50969673 KLK6 5653 "kallikrein-related peptidase 6, transcript variant A" GO:0005515|GO:0016540|GO:0004252|GO:0005783|GO:0042246|GO:0005615|GO:0005739|GO:0005737|GO:0016485|GO:0015630|GO:0030574|GO:0006508|GO:0031965|GO:0045745|GO:0042552|GO:0009611|GO:0005730|GO:0005576|GO:0042982|GO:0007417|GO:0045171|GO:0070997|GO:0010975|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141853_PI430048170 0.410120089533414 0.91236333331136 0.326677133608464 0.352088274995375 0.353746099774705 A A A 0.348747885679854 0.347465611395076 0.703489530907318 A A A LNCV6_141853_PI430048170 mRNA CAAGTACTTTTCTTTCTAAGCTAACCTTTGGGATACATCACAGAGGATACTTGAAAAACA NM_015688 RefSeq chr4 - 17632085 17781512 FAM184B 27146 "family with sequence similarity 184, member B" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144830_PI430048170 0.0304469007509438 0.687523372538854 6.0537606203745 6.44196860115838 6.439168012945 P P P 6.92813948913954 6.68387631217495 6.96225730035886 P P P LNCV6_144830_PI430048170 mRNA CCGCATGTTCTAAGTGTGCATTTTTGTCAATCTTTGCAACAGTTATTTCATACAGATGTT NM_012110 RefSeq chr4 - 54009790 54064648 CHIC2 26511 cysteine-rich hydrophobic domain 2 GO:0005515|GO:0008150|GO:0003674|GO:0005886|GO:0005798|GO:0006893|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133369_PI430048170 0.0168610527540925 0.780370444606346 7.36098809204326 7.48288928036045 7.27316493295783 P P P 7.78028975521987 7.70918182745014 7.7073880087022 P P P LNCV6_133369_PI430048170 mRNA AACAGCAAACCATCTAGATTAAACTCCTAAAGCCAGTGCCACGAGGCATTCCTGTTCCAA NM_174977 RefSeq chr22 - 30488905 30505711 SEC14L4 284904 "SEC14-like 4 (S. cerevisiae), transcript variant 1" GO:0005622|GO:0005215|GO:0006810|GO:0016021|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140028_PI430048170 0.0129215012411995 0.467533719641996 6.5993854680386 6.32973317362386 6.8266952067883 P P P 7.69737165599599 7.63791956485441 7.75144910364565 P P P LNCV6_140028_PI430048170 mRNA GCCACTTACCCAAGCTTTAGAGAATCCCTAGTGGAAGATTATATGATAAACTTTCAGTCC NM_001254738 RefSeq chr2 - 150468192 150487695 RND3 390 "Rho family GTPase 3, transcript variant 1" GO:0005515|GO:0030036|GO:0000139|GO:0007264|GO:0008152|GO:0003924|GO:0007155|GO:0005525|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142586_PI430048170 0.0087737497500268 0.574819944124773 3.87124289323589 4.10671319099937 4.21951272515423 P P P 4.93282788764679 4.8799410507872 4.7996125884246 P P P LNCV6_142586_PI430048170 mRNA GGTAGTACTAATATACAAGATGGCGTTTCTAGAATGTATGACACTGAAGTGACTTTTTGT NM_144978 RefSeq chr2 + 108786749 108876591 CCDC138 165055 "coiled-coil domain containing 138, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135966_PI430048170 0.284819879980638 1.12842012227897 5.24415760102018 5.16326208781008 5.31409890382218 P P P 4.85420315684999 5.29425307516796 5.01949354470197 P P P LNCV6_135966_PI430048170 mRNA

AGTTCTCTGATGCAATGTCCTTTGGGGTCCGGACTGTGGTGAAGGTTCGTCCAGCTCCAC NM_001290056 RefSeq chr19 + 36014498 36045997 LOC101927572 NA uncharacterized LOC101927572 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137798_PI430048170 0.334819249766439 0.812045167725766 0.27466811345812 0.303575576266466 0.386900043242623 A A A 1.01389265173211 0.335961445258238 0.420338309557441 A A A LNCV6_137798_PI430048170 mRNA
TGCCTTTAAGGTTCAAAGGAGCCTCTATGAAGAAACTAACAAGGAAACATGGGGACCTGC NM_015594 RefSeq chr17 + 30559565 30563491 TBC1D29 26083 "TBC1 domain family, member 29"
GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132754_PI430048170 0.375079101318191 1.2765692250402 10.3244556677615 11.0402733941376 10.1724193616877 P P P 10.4974373933754 10.0682991359136 10.0208600101836 P P P LNCV6_132754_PI430048170 mRNA
AACTGTATGGATCGTGTTCTACTTCATGTGGATGTGAACTACTTGAAGTCCCTGCCCTGA NM_144663 RefSeq chr11 - 4571422 4577820 C11orf40 143501 chromosome 11 open reading frame 40 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129450_PI430048170 0.40856226338111 0.985931757842116 0.361646913441033 0.368877652724899 0.354647120935899 A A A 0.414478166200872 0.347289722438555 0.383975919754818 A A A LNCV6_129450_PI430048170 mRNA
TGTTTGAAGCTTGAATGTCCTGCTCAAAATCTCAAAACACGAGCCTTGGAATTCAAAAAA NM_005535 RefSeq chr19 - 18058994 18087003 IL12RB1 3594 "interleukin 12 receptor, beta 1, transcript variant 1"
GO:0032729|GO:2000318|GO:0072536|GO:0004896|GO:0038155|GO:0005143|GO:0019221|GO:0042020|GO:0018108|GO:2000330|GO:0016517|GO:0042104|GO:0007165|GO:0071346|GO:0043382|GO:0042022|GO:0001916|GO:0002230|GO:0002827|GO:0009897|GO:0042019|GO:0035722 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94725_PI430048170 0.0630482066757049 0.878950504850985 6.53653721519906 6.64578976391197 6.44958976604406 P P P 6.70998123327092 6.81454899221602 6.66859121644991 P P P LNCV6_94725_PI430048170 mRNA
AACAGAAAGGTGTGCCAGTGAAACAGAACACAGCTGTAAATTCCAGCTCCAGAAACCACT NM_002926 RefSeq chr4 + 3314146 3432177 RGS12 6002 "regulator of G-protein signaling 12, transcript variant 2"
GO:0000794|GO:0005886|GO:0005730|GO:0038032|GO:0005634|GO:0006351|GO:0016363|GO:0043547|GO:0035556|GO:0050790|GO:0005737|GO:0008277|GO:0005057|GO:0005096|GO:0030695 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140232_PI430048170 0.00780511243329494 0.497698650075392 4.8781248291526 4.46945101888711 4.72219221431689 P P P 5.46114909710458 5.62886529147717 5.97951120664122 P P P LNCV6_140232_PI430048170 mRNA
CTGTGGTTGCCCCTGTTCTACACCAATTTCAGTTCAATAAAAATGTTAACTTTGCAAAAA NM_012081 RefSeq chr5 - 95885097 95962071 ELL2 22936 "elongation factor, RNA polymerase II, 2"
GO:0006368|GO:0006355|GO:0005813|GO:0005737|GO:0042795|GO:0005654|GO:0008023 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109337_PI430048170 0.116822456718393 0.904385674980449 13.8119726818629 13.6499600607219 13.7607419480508 P P P 13.8715889237898 13.7994684905107 13.9852045110456 P P P LNCV6_109337_PI430048170 mRNA
AGCATCTTGAGAGGAACAGAAAGATAAGGATGCTAAATTCCGTCTGATTCTAATAGAGAG NM_001017 RefSeq chr11 - 17074391 17077673 RPS13 6207 ribosomal protein S13
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0005730|GO:0005634|GO:0003729|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0016020|GO:0000184|GO:0033119|GO:0022627|GO:0016032|GO:0005840|GO:0044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142246_PI430048170 0.182702532223621 1.49176379085766 0.631466133366211

1.50575706783564 1.35688365917328 A A A 0.654388947337032 0.518444663471948
0.724808573910443 A A A LNCV6_142246_PI430048170 mRNA
AAACAGTTTTTTAGACTGGAAAAAAGCCAGTCTAAAGGCCTCTGGATACTGGGCTCCCCA NM_006522 RefSeq
chr2 + 218859822 218874232 WNT6 7475 "wingless-type MMTV integration site family, member 6"
GO:0060684|GO:0001658|GO:0009798|GO:0005886|GO:0009986|GO:0071300|GO:0005796|GO:0070172|GO:0005
578|GO:0005576|GO:0072079|GO:0005615|GO:0061303|GO:0005109|GO:0010628|GO:0045165|GO:0030182|GO:0
042475|GO:0005788|GO:0045893|GO:0016055 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_126823_PI430048170 0.234864014079006 1.05631189660008 0.555913312884626
0.690882646228974 0.546784347965753 A A A 0.502538868458758 0.523871203273449
0.534439330502504 A A A LNCV6_126823_PI430048170 mRNA
CCTGTCATCTTTGTTGAGTAATAGCTTTATTGAGCTTTATTTGGAGAAATACACATACCG NM_001008215 RefSeq
chr2 - 98599322 98608518 COA5 493753 cytochrome c oxidase assembly factor 5 GO:0005739 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124419_PI430048170 0.0947657637833844 0.952748688071507 9.06221311539705
9.02418663508379 8.99570822667429 P P P 9.05516699720072 9.14093416751373
9.09499879807217 P P P LNCV6_124419_PI430048170 mRNA
TGATGCCTACTCCACTTTCTACCTGAATTCCAGTGGCCTCATTTGTCGCCATCGTCTAGA NM_001161376 RefSeq
chr6 + 30647038 30653210 C6orf136 221545 "chromosome 6 open reading frame 136, transcript
variant 3" GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113673_PI430048170 0.0568917972553187 0.82705406662809 4.92619287225586
4.99340022666827 5.19445869946594 P P P 5.38775111585732 5.26456163915988
5.29437936061098 P P P LNCV6_113673_PI430048170 mRNA
ATGCTGCTCAAGTGGAAAGGGTATTGCTAAAAGGATGTTTCCAAAAATCTTGTATATAAG NM_002009 RefSeq
chr15 + 49423177 49487326 FGF7 2252 fibroblast growth factor 7
GO:0008286|GO:0005515|GO:0010838|GO:0008284|GO:0051549|GO:0010463|GO:0050731|GO:0031069|GO:0060
665|GO:0007173|GO:0060501|GO:0051781|GO:0008201|GO:0050679|GO:0048011|GO:0005794|GO:0031532|GO:0
048015|GO:0009611|GO:0005576|GO:0005104|GO:0042056|GO:0050918|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138657_PI430048170 0.287333263896746 1.02935991433588 0.310147593299076
0.250283205961182 0.34963652179342 A A A 0.270341494466729 0.244500787200578
0.271551333701324 A A A LNCV6_138657_PI430048170 mRNA
ATTTTTGTGCAAATGAACTTCTCCTTTTGACCAGTAACCACCTTCCTTCAAGCCTTCAGC NM_001297713 RefSeq
chr1 - 161983191 162024465 OLFML2B 25903 "olfactomedin-like 2B, transcript variant 1"
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131800_PI430048170 0.0051320853849678 0.509430051432057 4.17350485199086
4.26984331246429 4.31273172146264 P P P 5.02531721604973 5.25824471875837
5.37363875804388 P P P LNCV6_131800_PI430048170 mRNA
CAGATGAATGGGAGTATTCTGTACATGAATCATGCTGTATTTTAAATCAGGACATCACTT NM_024646 RefSeq
chr1 + 52726458 52827341 ZYG11B 79699 "zyg-11 family member B, cell cycle regulator" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133312_PI430048170 0.217313091971144 0.904145629955798 6.19563408764004
6.03513955793481 6.29164576248032 P P P 6.22679082445506 6.28697051278435
6.44723649924829 P P P LNCV6_133312_PI430048170 mRNA
AAGGAAGGAGAGGGAAGCCATTCTCCTCTAGGGACTCTTCAGTCTCATTTAGATGATAGT NM_000449 RefSeq
chr1 - 151340639 151347293 RFX5 5993 "regulatory factor X, 5 (influences HLA class II expression),
transcript variant 1"
GO:0005515|GO:0003700|GO:0006357|GO:0005634|GO:0000122|GO:0000978|GO:0003677|GO:0006351 . NA
- . NA NA NA NA NA NA NA NA NA

LNCV6_68862_PI430048170 0.091738825379138 0.741818054690756 4.38827358857342
4.25484910722818 4.04580202713155 P P P 4.88332926664153 4.70671168384199
4.36475252448921 P P P LNCV6_68862_PI430048170 mRNA
TATTGCCCTCATCAAGCTTGCAGAGCATGTGGAGCTGAGTGACACCATCCAGGTGGCCTG NM_007272 RefSeq
chr1 + 15438441 15446658 CTRC 11330 chymotrypsin C (caldecrin)
GO:0004252|GO:0006508|GO:0008233 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140799_PI430048170 0.135022716092875 1.04218714602134 0.360376825734946
0.344742406051501 0.428608470770517 A A A 0.307947879635733 0.298685429375062
0.349135417051749 A A A LNCV6_140799_PI430048170 mRNA
CACATATGCTTGGTTACTTGCATGCATTCATTGGTTGTTCAATAAGTGAGATGATTACAG NM_013352 RefSeq chr6
+ 116370946 116438281 DSE 29940 "dermatan sulfate epimerase, transcript variant 1"
GO:0005794|GO:0005783|GO:0005975|GO:0015012|GO:0044281|GO:0030208|GO:0030206|GO:0000139|GO:0047
757|GO:0009405|GO:0016021|GO:0030204|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132762_PI430048170 0.349296713032257 1.05798471162912 12.0984461182651
12.3042258623987 12.1458963857253 P P P 12.0532153296949 12.0766073040505
12.1797583350167 P P P LNCV6_132762_PI430048170 mRNA
TGAAGCTTGTAACGACCATGGATCTGAATAAACATGTCCTTGCTTCTGAGTCTTCTGGCA NM_017951 RefSeq chr2
- 130151391 130181757 SMPD4 55627 "sphingomyelin phosphodiesterase 4, neutral membrane (neutral
sphingomyelinase-3), transcript variant 2"
GO:0005802|GO:0006665|GO:0006685|GO:0005794|GO:0006687|GO:0005783|GO:0004767|GO:0044281|GO:0046
872|GO:0000139|GO:0071356|GO:0005789|GO:0050290|GO:0016021|GO:0046475|GO:0046513 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129059_PI430048170 0.747343102996111 0.971393199917581 0.297128541283709
0.266414564714348 0.410106425950773 A A A 0.285398016544419 0.250009403955412
0.549000439751359 A A A LNCV6_129059_PI430048170 mRNA
CCTGCACAGTAGTTTGTCCTGTGGTTTATTTTGTATTACCTGTAAATAAAGTGGCTTTATNM_000839 RefSeq chr3 +
51707064 51718609 GRM2 2912 "glutamate receptor, metabotropic 2, transcript variant 1"
GO:0051966|GO:0030424|GO:0030054|GO:0005886|GO:0004930|GO:0005246|GO:0001641|GO:0007268|GO:0007
196|GO:0007194|GO:0014047|GO:0030425|GO:0005622|GO:0042734|GO:0005887|GO:0008066 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142588_PI430048170 0.309079063508991 1.14423214949089 7.00830597377213
7.22372452789658 7.29376636535376 P P P 6.9240653147179 6.74415001512751
7.24444883229148 P P P LNCV6_142588_PI430048170 mRNA
AAAGCTGTCAGTGTGTATTGGTTTCACCAATAACCACTGCTTGATCCTTACAATTAAATT NM_003825 RefSeq chr15
+ 42495305 42533061 SNAP23 8773 "synaptosomal-associated protein, 23kDa, transcript variant 1"
GO:0005515|GO:0019905|GO:0043005|GO:0016082|GO:0005886|GO:0042581|GO:0006892|GO:0045202|GO:0042
582|GO:0031201|GO:0015031|GO:0042629|GO:0006903|GO:0005484|GO:0005737|GO:0002553|GO:0061024|GO:0
061025|GO:0031629|GO:0005654|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_64520_PI430048170 0.035631352963203 1.28302754587476 11.4855500152129 11.3233694122397
11.1842321426108 P P P 10.897077149935 11.0573517740165 10.9713933851478 P P P
LNCV6_64520_PI430048170 mRNA
TGGCAAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCCGATTTTTACAA NM_017814 RefSeq chr19
- 19119615 19138501 TMEM161A 54929 "transmembrane protein 161A, transcript variant 1"
GO:0034644|GO:0045739|GO:0034599|GO:0032526|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144927_PI430048170 0.164456221475559 0.683340150323888 7.55838754748421
6.89174545357537 6.95307924370378 P P P 7.67409502569237 8.0904430986456
7.26810840538692 P P P LNCV6_144927_PI430048170 mRNA

TCCCCTCCTTGCACCGGCCCTTCCTGGTCTTTGAATAAAGTCTGAGTGGGCAGCAAAAAA NM_000517RefSeq chr16
+ 172846 173710 HBA2 3040 "hemoglobin, alpha 2"
GO:0005515|GO:0042542|GO:0072562|GO:0044281|GO:0051291|GO:0005829|GO:0031838|GO:0004601|GO:0071
682|GO:0042744|GO:0010942|GO:0031720|GO:0070062|GO:0005833|GO:0005506|GO:0005576|GO:0006898|GO:0
015671|GO:0019825|GO:0016020|GO:0022627|GO:0005344|GO:0015701|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139716_PI430048170 0.5670903866548981.16774578836206 0.404515518317202
1.13841803364938 0.3213642756864 A A A 0.2536459224324940.309669538198173
0.728617425460705A A A LNCV6_139716_PI430048170 mRNA
AGTATTTTATAGGACATGTGGCTGGTAGATTCCATGAACTTCAAGGCTTCATTGCTCTTT NM_133497RefSeq chr9
+ 2717525 2730037 KCNV2 169522 "potassium channel, voltage gated modifier subfamily V, member
2" GO:0005251|GO:0005886|GO:0008076|GO:0007268|GO:0051260|GO:0034765|GO:0016021|GO:0071805 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139103_PI430048170 0.1145710347819881.16354306264022 13.032533461192
13.1650725139738 13.2331531069601 P P P 13.0636548609832 12.7609467972361
12.9417866208977 P P P LNCV6_139103_PI430048170 mRNA
CTTATGTGTAATTATTCCACCGTGGGAACAGAGAATACCTGTTTAGTGTTGCACTTTAGA NM_004718RefSeq chr2
- 42350504 42361216 COX7A2L 9167 cytochrome c oxidase subunit VIIa polypeptide 2 like
GO:0022904|GO:0005746|GO:0004129|GO:0005743|GO:0044281|GO:0055085|GO:0044237 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132368_PI430048170 0.0858159841825623 0.88800097510384910.006816548863
10.0202876772727 10.0045544108653 P P P 10.131345004497 10.2868309891817
10.1216050675415 P P P LNCV6_132368_PI430048170 mRNA
CAATCTAAAAAGCAATTGAAAAGGTCTATGCAATAAAGGCAGTCGCTTCATTCCTCTCAG NM_020126RefSeq chr19
+ 48619290 48630406 SPHK2 56848 "sphingosine kinase 2, transcript variant 1"
GO:0005515|GO:0006665|GO:0043066|GO:0008284|GO:0001568|GO:0008283|GO:0030148|GO:0006670|GO:0044
281|GO:0005765|GO:0005524|GO:0008481|GO:0007205|GO:0005829|GO:0017050|GO:0003951|GO:0016020|GO:0
007420|GO:0004143|GO:0046834|GO:0017016|GO:0006669 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_89534_PI430048170 0.867142828349565 1.07227896750642 1.1489766094587 0.388199733818524
0.291345818284709A A A 0.5145453045013890.422991472245795 0.731763389601837A A A
LNCV6_89534_PI430048170 mRNA
AAATATGACAATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCC NM_017563RefSeq chr3
- 57089981 57165375 IL17RD 54756 interleukin 17 receptor D
GO:0030368|GO:0005794|GO:0000139|GO:0005887|GO:0019221|GO:0005654 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140664_PI430048170 0.5476248215791830.9025152908758760.333974581572645
0.3211814705457410.27411792638037 A A A 0.78666814637986 0.269459706071787
0.251400639646016A A A LNCV6_140664_PI430048170 mRNA
CTGTTTGTCCTTTTACACTCTTAACATTTTAAAAAGCACATCTCTGTATAGCCCATTCCA NM_001001791 RefSeq chr10
- 73909968 73922777 C10orf55 NA chromosome 10 open reading frame 55 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_144929_PI430048170 0.0910166625519709 0.6751491349968736.17441247768705
5.8863985783472 6.39129406317666 P P P 6.34065724095026 6.76603854084841
7.01163663195166 P P P LNCV6_144929_PI430048170 mRNA
TTGAAGCATCTGTCTTCATATGATGGCATTAGAACACCTTGGTATAATAAAAAGTTACCG NM_015190RefSeq chr10
- 73241955 73247331 DNAJC9 23234 "DnaJ (Hsp40) homolog, subfamily C, member 9"
GO:0035176|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138217_PI430048170 0.4100645417586121.17590590923036 6.50343113542456

5.96169829308254 6.33462693878035 P P P 5.82538530375206 6.44971768561916
5.77278372683796 P P P LNCV6_138217_PI430048170 mRNA
AATAGCAGAGCCTATTTTGGTGAGGTTTTTTGTTTTTAAGTCAAAGAAGACTCAGTATGC NM_002660RefSeq chr20
+ 41137520 41175717 PLCG1 5335 "phospholipase C, gamma 1, transcript variant 1"
GO:0005515|GO:0050852|GO:0019722|GO:0043647|GO:0005886|GO:0019221|GO:0044281|GO:0042995|GO:0007
202|GO:0050900|GO:0005829|GO:0004629|GO:0005737|GO:0000186|GO:0007173|GO:0008180|GO:0005911|GO:0
007411|GO:0016032|GO:0051281|GO:0048010|GO:0030971|GO:0048011|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133373_PI430048170 0.0394510474749815 0.4352356807971514.28854141011055
3.31718371814494 4.23374595098534 P P P 4.87554221498926 5.3257320908926
5.37741022316527 P P P LNCV6_133373_PI430048170 mRNA
GCAGTGAGTTTAATGACTGACTTAGTAGCAGGTACAAGAAGCAAACTTGTTAATATAGAT NM_020242RefSeq chr3
+ 44761716 44853256 KIF15 56992 kinesin family member 15
GO:0008017|GO:0005813|GO:0005871|GO:0005873|GO:0008283|GO:0005874|GO:0005819|GO:0003777|GO:0003
677|GO:0005524|GO:0005829|GO:0019886|GO:0003774|GO:0007067|GO:0016020|GO:0007596|GO:0008152|GO:0
016887|GO:0007018. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140023_PI430048170 0.0952462557632622 0.483153219259397 0.402188251791601
0.985862880116616 1.08567641471053 A A A 1.36374280756642 2.52635698793526
1.53225003934179 A P A LNCV6_140023_PI430048170 mRNA
ATCCCACAAAGCCGCTGCCATTTTATTAAAGTGTTTTGATCCACTTTCCACTGGAAAAAA NM_001014448 RefSeq
chr4 + 8592659 8619761 CPZ8532 "carboxypeptidase Z, transcript variant 3"
GO:0006508|GO:0005578|GO:0008270|GO:0016055|GO:0070062|GO:0004181 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_75462_PI430048170 0.468443299998047 1.35314665391785 0.352299000002454 1.47196154671778
0.341396331920633 A A A 0.402011749291607 0.330938192805634 0.433596189866564 A A A
LNCV6_75462_PI430048170 mRNA
AGATTTCAGAGACACGGTGGATGATCTCATTTCAGACTCATCCTCTATGATGTCGCCTAC NM_001190787 RefSeq
chr5 - 55219596 55227315 MCIDAS NA multiciliate differentiation and DNA synthesis associated
cell cycle protein NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143584_PI430048170 0.184123491087772 1.31471771546777 4.32229569483724
4.19949737882849 4.15062005838124 P P P 4.23009987584322 3.62540103528841
3.53510123683835 P P P LNCV6_143584_PI430048170 mRNA
CTGTGCCTGCATAATGCTGACACCTGCTTGTTTCCATACAAATTGATATCAAAATAAAAT NM_004794RefSeq chrX
+ 130171798 130184870 RAB33A 9363 "RAB33A, member RAS oncogene family"
GO:0005515|GO:0005794|GO:0005886|GO:0019882|GO:0008152|GO:2000785|GO:0003924|GO:0032482|GO:0019
003|GO:0005525|GO:0006886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127461_PI430048170 0.456808046265445 1.1567067435769 0.278858270134846
0.293839612453703 0.881829694383098 A A A 0.324209499259589 0.28169071394464
0.303526002964086 A A A LNCV6_127461_PI430048170 mRNA
AATTTTGCTTTGAGAAGTTGCCTTTTCTCCACTGAGCACAGCCTGGTAGGGCTGGAATTA NM_001256615 RefSeq
chr1 - 231184098 231187627 LOC149373 149373 uncharacterized LOC149373 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_128505_PI430048170 0.53669555030157 0.933451815134239 8.89635622155382
8.67627663620694 8.45046800123632 P P P 8.61615757839054 8.90522943826942
8.81907162020748 P P P LNCV6_128505_PI430048170 mRNA
CACCCCAACCCCGGAAATGTGTGGGAAAAAGAAAACAAAAACTTTCCAAATTCCAAAAAANM_015080RefSeq chr11
- 64606173 64723188 NRXN2 9379 "neurexin 2, transcript variant alpha-1"
GO:0005246|GO:0007268|GO:0007416|GO:0071625|GO:0007269|GO:0046872|GO:0097104|GO:0097116|GO:0035
176|GO:0030534|GO:0016021|GO:0042297|GO:0050839|GO:0097119|GO:0097118|GO:0097109|GO:0007158 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141572_PI430048170 0.00221241107935514 0.436125935520636 3.22894246200896
3.08836930439695 3.49857467153863 P P P 4.22513299822637 4.59330107838061
4.58943073405973 P P P LNCV6_141572_PI430048170 mRNA
CAAACTCTGTAAAGCTTACTGAATTCATTTGTCATTTATTACATTGCTGAGTGGTGCTTG NM_017919 RefSeq chr9
+ 99906632 99974536 STX17 55014 syntaxin 17
GO:0030134|GO:0031201|GO:0005765|GO:0006906|GO:0006886|GO:0034497|GO:0005829|GO:0005739|GO:0097
111|GO:0033116|GO:0000149|GO:0007030|GO:0044233|GO:0048278|GO:0005791|GO:0000046|GO:0012507|GO:0
005793|GO:0019901|GO:0019903|GO:0000421|GO:0006888|GO:0005484|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_118522_PI430048170 0.398478965929324 1.14944217239644 0.309005621499349
0.889809937456445 0.513872887039074 A A A 0.315349742197415 0.513304943474614
0.33390479994003 A A A LNCV6_118522_PI430048170 mRNA
CTCACAGTGCTTACAGTGGAGAAAAGGAGACTTCGGCTACCCAGAGAAGTTCAGTGCCCA NM_001204286 RefSeq
chr1 - 155185823 155192915 MUC1 4582 "mucin 1, cell surface associated, transcript variant 10"
GO:0090240|GO:0003712|GO:0005515|GO:0000790|GO:0009986|GO:0005796|GO:0016266|GO:0043618|GO:0000
978|GO:0031982|GO:0005615|GO:0002039|GO:0016324|GO:0005737|GO:0010944|GO:0006493|GO:0005887|GO:0
006978|GO:0044267|GO:0070062|GO:0043687|GO:0036003|GO:0006977 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140736_PI430048170 0.00242707241367006 0.208044329578119 5.11778049932078
5.61284397925127 5.05236908463873 P P P 7.65453161133658 7.56230692422417
7.41890785534417 P P P LNCV6_140736_PI430048170 mRNA
CCTGTACCCTGGCCAGAACATCTCACTGATACTCGAATTCTTTTGGCAAACTTCAAAAAA NM_003568 RefSeq chr1
+ 150982022 150995638 ANXA9 8416 annexin A9
GO:0005544|GO:0005515|GO:0016337|GO:0005543|GO:0009986|GO:0015464|GO:0005509|GO:0001786|GO:0007
268|GO:0042803|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2182_PI430048170 0.0437120427084683 1.24481737553176 11.0299258290606
11.1592643061268 11.0218889160164 P P P 10.5846168136222 10.8609198746426
10.8072812557817 P P P LNCV6_2182_PI430048170 mRNA
CACCTGAGCATGCTGACCCCCTTCCTACCTCCAGAATAAAGAATCTCAACCTGGAAAAAA NM_001288723 RefSeq
chr11 - 62615295 62622175 B3GAT3 26229 "beta-1,3-glucuronyltransferase 3, transcript variant 4"
GO:0005515|GO:0005801|GO:0050650|GO:0050651|GO:0005794|GO:0005975|GO:0015020|GO:0090316|GO:0044
281|GO:0015012|GO:0072542|GO:0043085|GO:0046872|GO:0006024|GO:0015018|GO:0000139|GO:0016020|GO:0
009405|GO:0006486|GO:0016021|GO:0030204|GO:0030203|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142260_PI430048170 0.213723228928438 1.05289853688113 0.536980404187279
0.661078405080113 0.53645315113081 A A A 0.482780319089438 0.509246708393118
0.522706958214207 A A A LNCV6_142260_PI430048170 mRNA
AAACCACTAAGACAATTGAAAATAACATAAGCAAAGTGTTTGATGAGAAGCTCTGGGAAC NM_001163629 RefSeq
chr1 + 170935470 171064765 MROH9 80133 "maestro heat-like repeat family member 9, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132400_PI430048170 0.487685251135152 0.750145919027652 0.457155086813185
0.643430936023803 0.989540144372711 A A A 0.860204546619981 1.74889526434168
0.467782205561402 A A A LNCV6_132400_PI430048170 mRNA
TGTTCATCTAGTTTCTATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCATCATTTA NM_147199 RefSeq chr11 -
18933812 18935002 MRGPRX1 259249 "MAS-related GPR, member X1"
GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0006953 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139542_PI430048170 0.00123494409069227 2.32580168460407 9.26084369317716

9.56482186040854 9.45500446168044 P P P 8.42590711212861 8.07225169586044
8.11945466030384 P P P LNCV6_139542_PI430048170 mRNA
AATCTATATGTTTCAAAACCACTTGCCATCCTGTTAGATTGCCAGTTCCTGGGACCAGGC NM_198183RefSeq chr11
- 57551654 57568330 UBE2L6 9246 "ubiquitin-conjugating enzyme E2L 6, transcript variant 2"
GO:0005515|GO:0004842|GO:0016567|GO:0032020|GO:0045087|GO:0019941|GO:0016874|GO:0019221|GO:0032
480|GO:0006464|GO:0042296|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145215_PI430048170 0.215249694048114 1.12497659532436 9.07531307623739
9.19892991013593 9.38703408748359 P P P 8.94784618051871 9.04093433699856
9.17123748215992 P P P LNCV6_145215_PI430048170 mRNA
CCTATACTTGAGCTGGTTTTTGTTTTTGGTATTTGTGGCTGTGTTTTTGGTATGTGTTTA NM_018149RefSeq chr17 +
59210009 59215250 SMG8 55181 SMG8 nonsense mediated mRNA decay factor
GO:0045859|GO:0005515|GO:0010467|GO:0000184|GO:0005575|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135816_PI430048170 3.15398140334395e-05 2.81025909303081 10.2431801534014
10.189407912295 10.1166998904152 P P P 8.65130940335583 8.71277636967446
8.71497812910291 P P P LNCV6_135816_PI430048170 mRNA
CCCGATGTTCTTGATTTTCCCAGAGAAGCAAATAAACAGCGTGAACAGCCCCAGAAAAAA NM_002579RefSeq chr19
+ 708952 748330 PALM 5064 "paralemmin, transcript variant 1"
GO:0005515|GO:0060160|GO:0030424|GO:0005886|GO:0072661|GO:0008360|GO:0031527|GO:0051491|GO:0006
928|GO:0005634|GO:0007194|GO:0016327|GO:0060074|GO:0043231|GO:0016323|GO:0071257|GO:0032590|GO:0
032591|GO:0005887|GO:0007010|GO:0016023|GO:0005654|GO:0060999|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142186_PI430048170 0.00280028029885777 1.50677904931833 7.81534614713887
7.66046648972459 7.70298403808348 P P P 7.25720788748042 7.1114593054776
7.03102293875546 P P P LNCV6_142186_PI430048170 mRNA
CTGTACACACATTTGAAAAACTCACAAAATTGTCATCTATGTATCACAAGTTGCTAGACC NM_033309RefSeq chr16
- 67148101 67150999 B3GNT984752 "UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9"
GO:0000139|GO:0006486|GO:0016021|GO:0008378 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136208_PI430048170 0.171365377883562 0.544416700166373 5.48688928330243
5.43544174494488 5.50501469634437 P P P 5.66931902720509 6.94771282780225
6.14855789619573 P P P LNCV6_136208_PI430048170 mRNA
CCTGCATCTGTCTGCTCTGCATATATGTCTCTTTGGAGTTGGAATTTCATTATATGTTAA NM_198098RefSeq chr7 +
30911799 30925516 AQP1 358 "aquaporin 1 (Colton blood group), transcript variant 1"
GO:0005515|GO:0015079|GO:0020003|GO:0043627|GO:0070301|GO:0020005|GO:0048593|GO:0030157|GO:0031
526|GO:0035377|GO:0006884|GO:0034644|GO:0009925|GO:0015793|GO:0006833|GO:0033363|GO:0070062|GO:0
005223|GO:0031965|GO:0030950|GO:0015696|GO:0005267|GO:0042538|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135608_PI430048170 0.174091452247061 1.15149964275606 0.713722645202862
0.387859530578479 0.646985634312622 A A A 0.282399909167434 0.416839561801078
0.453348124479095 A A A LNCV6_135608_PI430048170 mRNA
TCTGTTCCCTTATTGGGTAAATGATTTTCCAACTCTGGGAATGTGTAGAATTCATTATGG NM_001164694 RefSeq
chr6 + 150368891 150404629 IYD 389434 "iodotyrosine deiodinase, transcript variant 1"
GO:0034641|GO:0005886|GO:0004447|GO:0016491|GO:0006590|GO:0044281|GO:0016021|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129890_PI430048170 0.791794187555629 1.03583719849789 2.9792959667512
3.23005784999279 3.68417689840626 A P P 2.30961820467938 3.41488359608506
3.75040427040597 A P P LNCV6_129890_PI430048170 mRNA
ACGTTAACAAAGGAAAACTCTTCCTATGAATCTTCATGATGATAGGCCATGTCTCTTCTT NM_015450RefSeq chr7
- 124822385 124929983 POT1 25913 "protection of telomeres 1, transcript variant 1"

GO:0051974|GO:0005515|GO:0000781|GO:0016233|GO:0010521|GO:0005634|GO:0051973|GO:0060383|GO:0032212|GO:0005737|GO:0032211|GO:0000723|GO:0051096|GO:0032203|GO:0017151|GO:0005654|GO:0032508|GO:0043047|GO:0007004|GO:0000783 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129236_PI430048170 0.0542498792652495 0.3714728837880250.529509307397912 0.5127711557070240.608892963860109A A A 2.5545638856751 1.48632170749596 1.65786527058592 P A A LNCV6_129236_PI430048170 mRNA
AAGTTCTTGAACTATTTTACCAGCTTTAACTTTGGGGCTCTTAGTTTCTTTTCTCCAGAT NM_001030055 RefSeq chr14 + 32077288 32159728 ARHGAP5 394 "Rho GTPase activating protein 5, transcript variant 1"
GO:0005515|GO:0051056|GO:0008361|GO:0030335|GO:0007264|GO:0003924|GO:0030879|GO:0002053|GO:0007266|GO:0005525|GO:0005100|GO:0005829|GO:0005737|GO:0016020|GO:0032321|GO:0008152|GO:0007155|GO:0042169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118206_PI430048170 0.0423838875907755 1.23399442222803 6.13709094414788 6.05382255028372 6.02312624927396 P P P 5.64623774755738 5.91147088697239 5.73602262010351 P P P LNCV6_118206_PI430048170 mRNA
GAACAAAGCAGAGAGGAGAACTTAATCCCGTATTCTCCAGATGTACAGATACACGCAGAG NM_015047RefSeq chr1 - 19215663 19251559 EMC1 23065 "ER membrane protein complex subunit 1, transcript variant 1" GO:0072546|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132526_PI430048170 0.0182616221969955 0.3955512926462146.21554154183398 5.70111739442202 5.88950453126181 P P P 6.76184674412897 7.34734985505115 7.62862124112685 P P P LNCV6_132526_PI430048170 mRNA
CCAAAGAGTTGTAACATTTTACAGTGTTACCATTTGAGTAGGGGTTTTATATGTTGTTGC NM_139169RefSeq chr10 + 114938192 114977680 TRUB1 142940 TruB pseudouridine (psi) synthase family member 1
GO:0009982|GO:0003723|GO:0001522|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79444_PI430048170 0.1035795841896220.6088733667126720.3114605082530970.268905213841112 0.290713090933456A A A 0.7823684429085481.4353227778498 0.679577833505791A A A LNCV6_79444_PI430048170 mRNA
CTGAAAAAGAAACAGCAAATTAAAAGGAAGAAAGCAGCCGGCTTGGCAGCAAAGGCTGCT NM_001303100 RefSeq chr8 - 614736 731239 ERICH1 157697 "glutamate-rich 1, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140242_PI430048170 0.3970773857707053.39625388126036 0.517358682537329 3.50363385341909 0.588418741588601A P A 0.58401995273221 0.431036135485391 0.439972001529118A A A LNCV6_140242_PI430048170 mRNA
GAGCATGTGTCATTGCTTTTATAAAACGCACTTAATAGCTTTCTTTCTAAAAGGCAACTG NM_021176RefSeq chr2_GL383522v1_alt + 87866 96627 G6PC2 57818 "glucose-6-phosphatase, catalytic, 2, transcript variant 1"
GO:0005975|GO:0006094|GO:0042593|GO:0044281|GO:0055085|GO:0008645|GO:0015758|GO:0050796|GO:0016311|GO:0004346|GO:0005789|GO:0009405|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130439_PI430048170 0.33159747803293 1.09601721066508 9.72875447000098 9.91794049177867 10.0617174339235 P P P 9.73741507017008 9.69626724363183 9.88984156676884 P P P LNCV6_130439_PI430048170 mRNA
TGGCCACATGCTTGCTGAAGAGACTTGTTTTCTTCTTCTAAGACAGTGGTTTTGTTTTTT NM_199342RefSeq chr1 - 42807051 42817388 CCDC23 374969 coiled-coil domain containing 23
GO:0010596|GO:0009306|GO:0045177|GO:0031397 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137251_PI430048170 0.0401157425268929 0.6722309283897996.49591902091546 6.27445900868889 6.69821632473926 P P P 7.09347355439506 7.07376918691383 7.05096561574723 P P P LNCV6_137251_PI430048170 mRNA
CCCATCTTGCTTCAGAGACTGACATTTCAGGGTGGATATTAATTAAAGCATTAATTTTGT NM_173872RefSeq chr4 + 169620520 169723187 CLCN3 1182 "chloride channel, voltage-sensitive 3, transcript variant e"
GO:0005515|GO:0005886|GO:0042581|GO:0005254|GO:0042803|GO:0006885|GO:0044070|GO:0016324|GO:0034

220|GO:0015297|GO:0006810|GO:0072320|GO:0034765|GO:0030141|GO:0030658|GO:0012506|GO:0005794|GO:0
046982|GO:0009986|GO:0005770|GO:0005247|GO:0031410|GO:0030165|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140102_PI430048170 0.2740971811342020.9480853694403420.253494551760973
0.3690833892316610.2855049844119 A A A 0.4691708751079990.36214498277355
0.305150650563975A A A LNCV6_140102_PI430048170 mRNA
TGCACTGGGAATGCAGTTTGTTTTGTTGCGAACACTTGCATACATTCCTACTCCAATCTA NM_030958RefSeq chr8
- 69672332 69835064 SLCO5A1 81796 "solute carrier organic anion transporter family, member 5A1,
transcript variant 1" GO:0005215|GO:0005886|GO:0006810|GO:0016021 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140414_PI430048170 0.00884017874679242 0.77895836408142212.6327708942297
12.5899476986209 12.6524302505851 P P P 12.8924844423516 13.0141163328667
13.0458965994459 P P P LNCV6_140414_PI430048170 mRNA
CCACCTGCCTGTATACCCCAGACTTGCCTCTGGGGCCTGATTAAATAAGGCTGTTTTGAT NM_152243RefSeq chr22
+ 37560463 37569403 CDC42EP1 11135 CDC42 effector protein (Rho GTPase binding) 1
GO:0005515|GO:0005794|GO:0005886|GO:0008360|GO:0007266|GO:0015629|GO:0005100|GO:0005737|GO:0030
838|GO:0032321|GO:0031274|GO:0017049|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89867_PI430048170 0.422147244393521 0.765249321431116 0.49641462540566 0.539770590911363
0.454208888753456A A A 0.558611325209159 1.43524293492582 0.439709829622124A A A
LNCV6_89867_PI430048170 mRNA
TCCAAACCAGCAGTCACAGGAACATGCTGCTTTTAGATTTGCTTTGTCGCAACTCACAGA NM_001258020 RefSeq
chr5 + 153490523 153813869 GRIA1 2890 "glutamate receptor, ionotropic, AMPA 1, transcript variant
4"
GO:0005515|GO:0030054|GO:0005886|GO:0005234|GO:0007268|GO:0060292|GO:0030425|GO:0031623|GO:0034
220|GO:0043197|GO:0045211|GO:0004971|GO:0032281|GO:0043025|GO:0009986|GO:0007616|GO:0035249|GO:0
014069|GO:0044309|GO:0030165|GO:0044308|GO:0008021|GO:0030666|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132080_PI430048170 0.5691939322173081.40736901546904 1.896488737359
0.6100210704296020.290399100447469A A A 0.4567677819669420.351912581366921
0.963595453225064A A A LNCV6_132080_PI430048170 mRNA
GATCTCACCAGCAGGGTGCTTCCCATGTTGATGACAATAAAATGAATGTGTTGCAAACCG NM_181880RefSeq chrY
+ 14056221 14056958 VCY1B NA "variable charge, Y-linked 1B" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129926_PI430048170 0.9226670632879560.9799832502069047.60878941040964 7.7238006285216
8.04778456424354 P P P 7.55403059464272 7.76809045830748 8.12417715700797 P P P
LNCV6_129926_PI430048170 mRNA
CTTGCTGGAGAGGAGGAATGTGTATAGTTACTCATTTAGATGACTCCAAAACTTTTATTA NM_152329RefSeq chr14
+ 49598696 49614672 LRR1 122769 "leucine rich repeat protein 1, transcript variant 1" GO:0016567
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130257_PI430048170 0.6086926468569290.7612706431558641.58999544986414
0.4709339366033730.535912769606221A A A 0.3161498173699791.31032964940047
1.98358284942862 A A A LNCV6_130257_PI430048170 mRNA
CACCTACAAATTTCTAAATGCACAGTTCAAATGTTAGTTCTTCAGATTCCTGTCTCTGTA NM_175736RefSeq chr12
- 49637940 49707414 FMNL3 91010 "formin-like 3, transcript variant 1"
GO:0032794|GO:0005737|GO:0030036|GO:0016477|GO:0008360|GO:0007010|GO:0017048|GO:0003779 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136526_PI430048170 0.9219610086372241.00573710884586 0.265512589543606
0.2809310417089230.438840013674532A A A 0.3524120257366230.303920428383995
0.310163069348994A A A LNCV6_136526_PI430048170 mRNA

CAAATGGGAGACTCTTTGAAATGACATGTTCCTTTAAGGTACTGAAGCTTTATTTGCATA NM_003222RefSeq chr20 + 56629301 56639282 TFAP2C 7022 transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)
GO:0005515|GO:0003700|GO:0021987|GO:0006366|GO:0060750|GO:0007267|GO:0045682|GO:0005634|GO:0003334|GO:0060598|GO:0042127|GO:0045944|GO:0046983|GO:0001942|GO:0030718|GO:0035019|GO:0000977|GO:0006357|GO:0021877|GO:0001047|GO:0000122|GO:0001829|GO:0003677|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141165_PI430048170 0.611532057440817 0.904988509688976 0.308741314539317 0.30817313282033 0.502239953009659 A A A 0.882689606091266 0.272178143510893 0.322467965762132 A A A LNCV6_141165_PI430048170 mRNA
GCATGCTACAGAGATTTAGCTAAACTTTGTTCATTTGGCTAGCAATATTCTTTTTGTACC NM_001111319 RefSeq chr4 - 183318066 183320774 CLDN22 53842 claudin 22
GO:0016338|GO:0070830|GO:0005886|GO:0005198|GO:0034329|GO:0016021|GO:0005923|GO:0045216|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92606_PI430048170 0.414406020612145 1.11635983072103 4.95411160773995 4.96426145720724 5.13376858888586 P P P 5.1834388076018 4.65401251590382 4.68170459112135 P P P LNCV6_92606_PI430048170 mRNA
GGATGCCAATTCATGAAGCAGCTTATCACAACTCTGTAGAATGTTTGCAAATGTTAATTA NM_001164165 RefSeq chr2 - 53670315 53860033 GPR75-ASB3 NA GPR75-ASB3 readthrough NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114171_PI430048170 0.160764189217877 1.17333583126728 3.49764033792035 3.74391739590097 3.7498225990905 P P P 3.22135928795437 3.55805450033171 3.51165917991101 P P P LNCV6_114171_PI430048170 mRNA
ACTGCATCAGATCCAAGGGAACGAGCTGGAGCCCCTGAACCGTCCGCAGCTCAAGATCCC NM_001122742 RefSeq chr6 + 151690495 152103273 ESR1 2099 "estrogen receptor 1, transcript variant 4"
GO:0005515|GO:0010467|GO:0043627|GO:0006367|GO:0003700|GO:0008013|GO:0003707|GO:0042802|GO:0002064|GO:0005496|GO:0032355|GO:0043124|GO:0005794|GO:0035327|GO:0000978|GO:0060687|GO:0001547|GO:0048386|GO:0051000|GO:0005654|GO:0008270|GO:0019899|GO:0008134|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144332_PI430048170 0.112110971454122 1.60455851716317 4.41280523140025 4.13826456321 3.56102263547377 P P P 3.24358683038304 3.39702167835823 3.5359654860261 P P P LNCV6_144332_PI430048170 mRNA
ATGCTGCTGAGCATTTCAGCAGTGACAGATTCAAATAATAAGCTAATTTTTGGAGAAAGG NM_020699RefSeq chr1_GL383518v1_alt - 121425 145051 GATAD2B 57459 GATA zinc finger domain containing 2B
GO:0043234|GO:0006355|GO:0000790|GO:0003700|GO:0016607|GO:0043044|GO:0031492|GO:0008270|GO:0005654|GO:0000980|GO:0000978|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131773_PI430048170 0.590811782135287 0.970178201657488 0.473269993973479 0.441864111047677 0.245833185173116 A A A 0.384476656083694 0.479921212894416 0.436385921251695 A A A LNCV6_131773_PI430048170 mRNA
ACTGGACTTGGTTGGCATTTTAGTTTAATGACTGAAAAAGTAGGTTGAAAGCTCTCTGTA NM_207359RefSeq chr3 - 30726199 30894661 GADL1 NA glutamate decarboxylase-like 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138871_PI430048170 0.0132302790343645 7.42884356029929 2.69215629535468 3.11312595681211 3.89142388564303 A P P 0.52162250722767 0.440414696225472 0.310043658983493 A A A LNCV6_138871_PI430048170 mRNA
AGCTCAGGGACTGAGCCCCAAGACGCCTCTGTAACCTCGCTGCAGCTTCAGTAGTAAACT NM_001289117 RefSeq chr19 + 3933102 3942416 NMRK2 27231 "nicotinamide riboside kinase 2, transcript variant 1"
GO:0005622|GO:0005515|GO:0016310|GO:0050262|GO:0009435|GO:0005524|GO:0046872|GO:0045662 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_131630_PI430048170 0.58240454014377 0.982627045599331 0.267258518296484
0.286938322315245 0.389301467301505 A A A 0.377434193696075 0.328936737239256 0.3152357076783
A A A LNCV6_131630_PI430048170 mRNA
AAACCATCCATCTATATTGTGTTCTAGTATAGCATGACATGACATTGCTAAGAACTTTGC NM_001099921 RefSeq
chrX + 35798341 35803735 MAGEB16 NA melanoma antigen family B16 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_139861_PI430048170 0.208660194122384 1.37889776773018 0.425158846292779
0.978732573588301 1.21460438027916 A A A 0.41518699080706 0.479513414857059
0.44179206433157 A A A LNCV6_139861_PI430048170 mRNA
TCTTTGTAAACGAGACTTTGACATTGTTAGCAGGCCCATCTGTTTGCTTTTCTTAAATAA NM_001025232 RefSeq
chr12 - 92420093 92428148 CLLU1OS NA chronic lymphocytic leukemia up-regulated 1 opposite
strand NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127081_PI430048170 0.594772169879686 0.897164103772558 0.287997523319056
0.290858621571504 0.499755932375888 A A A 0.307085152058315 0.267678512450575
0.89488513599732 A A A LNCV6_127081_PI430048170 mRNA
GCTTCAGACATTTAAAAATCACTTTTTACTCCTAGGGAGATGCCAATAAACAGAACTCTT NM_000523 RefSeq chr2
+ 176092803 176095938 HOXD13 3239 homeobox D13
GO:0006355|GO:0003700|GO:0006366|GO:0005634|GO:0007275|GO:0060571|GO:0009952|GO:0003677|GO:0060
687|GO:0043565|GO:0030539|GO:0001501|GO:0048619|GO:0045944|GO:0003682|GO:0042127|GO:0060602|GO:0
042733|GO:0060527. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107350_PI430048170 0.706707483819608 0.982636674666625 14.2542474396853
14.0628691433165 14.06471498149 P P P 14.1371448546917 14.1860724441228
14.1424228782556 P P P LNCV6_107350_PI430048170 mRNA
ATATACACACAGTGGATGGACGGACAAGACAGGCAGAGATCTATAAACAGACAGGCTCTA NM_005526 RefSeq
chr8 + 144291587 144314722 HSF1 3297 heat shock transcription factor 1
GO:0005515|GO:0003700|GO:0008285|GO:0007283|GO:0005829|GO:0034605|GO:0005737|GO:0045944|GO:0032
496|GO:0040018|GO:0090231|GO:0001162|GO:0060136|GO:0001892|GO:0032720|GO:0006952|GO:0000122|GO:0
000978|GO:0006351|GO:0001078|GO:0043234|GO:0003682|GO:0006468|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142882_PI430048170 0.000594650634692412 1.82499529776425 6.02440272279566
5.94400717638432 6.16166790315242 P P P 5.28584476242078 5.16434280809484
5.07700644763729 P P P LNCV6_142882_PI430048170 mRNA
TAAAAGTATGAGGTCAAAGGATCACGAAACCTAAGTTTAAAAACTGCTTAGAGACTGAAG NM_016401 RefSeq chr11
+ 86302210 86345943 C11orf73 51501 "chromosome 11 open reading frame 73, transcript variant 1"
GO:0034605|GO:0005622|GO:0030054|GO:0030324|GO:0008565|GO:0007030|GO:0030544|GO:0005634|GO:0015
031|GO:0006606|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132855_PI430048170 0.191420918876924 0.910035544539628 13.9494362927154
13.9464273369063 13.834941567572 P P P 13.9172780538237 14.0534719990836
14.1607183876545 P P P LNCV6_132855_PI430048170 mRNA
CCCCTTTATCGCATTGCTGTCCTTGGGTAGAATATAAAATAAAGGGACTTTTATTTCTTA NM_000784 RefSeq chr2
+ 218781748 218815293 CYP27A1 1593 "cytochrome P450, family 27, subfamily A, polypeptide 1"
GO:0006805|GO:0005506|GO:0030343|GO:0006699|GO:0008395|GO:0005743|GO:0044281|GO:0031073|GO:0047
749|GO:0005759|GO:0008206|GO:0016125|GO:0055114|GO:0008203|GO:0020037 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_70875_PI430048170 0.316437129317858 1.40198087251123 0.50994467164632 0.543247576634147
1.47285312129336 A A A 0.321117341810181 0.428909908557183 0.525521686065466 A A A
LNCV6_70875_PI430048170 mRNA
AACTCAGCCCACGACACAGACCAGAACCTGAGTGTGGACAAATACGTGGACTCCTTCGGG NM_198994 RefSeq
chr20 + 2380907 2432753 TGM6 NA "transglutaminase 6, transcript variant 1" NA . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_106066_PI430048170 0.0268740012071354 1.947662628091 7.13195828001814
7.5401661482231 7.76296763576007 P P P 6.53929384414684 6.43029366525407
6.64177822303463 P P P LNCV6_106066_PI430048170 mRNA
CTCATTGTGCTTTTGAATACGTTGGTGGTGTTGTCATGAGGTGACATTGTGATTGCAAAA NM_144981 RefSeq chr11
- 31432398 31509628 IMMP1L 196294 "IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae),
transcript variant 1" GO:0005739|GO:0008150|GO:0003674|GO:0006627|GO:0006508|GO:0005743|GO:0008236
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83706_PI430048170 0.00310891047603476 2.50907772532031 7.5055368799145
8.02631649845658 7.75308044177159 P P P 6.64280150686446 6.31264799160089
6.37324099674927 P P P LNCV6_83706_PI430048170 mRNA
GATGATTTAAAACATGAAAGTGTATTGTTGTCACTGTGGTAATTTCCTTGCCAGTTTCTG NM_001285486 RefSeq
chr2 - 96497642 96505385 NEURL3 93082 "neuralized E3 ubiquitin protein ligase 3, transcript variant
2" GO:0004842|GO:0016567|GO:0016874|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141324_PI430048170 0.519650475965815 0.96911398764997 0.462963381437664
0.482412053506451 0.301789473227504 A A A 0.408964876502872 0.51147731648528
0.467402960826966 A A A LNCV6_141324_PI430048170 mRNA
CTGGTATGTGTTATATGCCCTCAATGTATTCACTGACTGTTCTGTAATTTCAGTTTGTCT NM_001034853 RefSeq chrX
- 38284448 38327535 RPGR 6103 "retinitis pigmentosa GTPase regulator, transcript variant C"
GO:0005515|GO:0005813|GO:0005794|GO:0036126|GO:0006886|GO:0036064|GO:0005085|GO:0043547|GO:0042
384|GO:0042073|GO:0007601|GO:0042462|GO:0050896|GO:0001750 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133650_PI430048170 0.358828583357725 0.873497669556528 9.64716149213841 9.4000769808068
9.25548436740501 P P P 9.89336731787262 9.56922049290723 9.41029781627221 P P P
LNCV6_133650_PI430048170 mRNA
GGGTGGATCTCTGTCCCTCTATCCCCAGGGACTCTCTCCCCTCTTGTATAGAATAAAAAA NM_138360 RefSeq chr14
+ 24051996 24069728 LRRC16B 90668 leucine rich repeat containing 16B GO:0005737 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_141615_PI430048170 0.495703104085118 0.905645810540442 5.57985112530715
5.70926637000637 6.14315981494748 P P P 5.99506348295257 5.75850039878426
6.14377158810946 P P P LNCV6_141615_PI430048170 mRNA
TGATTAGTATCGTGAGTTTGAAAAGTCTAGAACTCCTGTAAGTTTTTGAACTCAAGGGAG NM_152720 RefSeq chr13
- 52132642 52159535 NEK3 4752 "NIMA-related kinase 3, transcript variant 2"
GO:0005515|GO:0030424|GO:0007067|GO:0005737|GO:0004674|GO:0006468|GO:0005634|GO:0005524|GO:0046
872|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95164_PI430048170 0.00485575830729706 1.27314288631452 11.1909553383947
11.2783842140951 11.3498831017207 P P P 10.8473425412686 10.9548735054734
10.9730342150763 P P P LNCV6_95164_PI430048170 mRNA
CGAAGCCACTTTCTCAGAGACACTTTAATCATTGAGTATTTGTACACTTTTCTTTAGAAC NM_002484 RefSeq chr16
+ 10743785 10769351 NUBP1 4682 "nucleotide binding protein 1, transcript variant 1"
GO:0005515|GO:0051539|GO:0005886|GO:0016226|GO:0051536|GO:0010826|GO:0044281|GO:0005524|GO:0072
697|GO:0046872|GO:0005829|GO:0006879|GO:0051642|GO:0005737|GO:0000166|GO:0016049|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81038_PI430048170 0.148863836823039 1.14860270352072 9.9780218571186 10.1902852501626
10.2819011341389 P P P 9.95015333456082 9.87361505713556 10.0386733536658 P P P
LNCV6_81038_PI430048170 mRNA
CTAAAAGTTTATAATCATCCCTTAAACACTCTGTGATGGGATCTTCAGGATCATCTTTTG NM_198841 RefSeq chr9
- 93446499 93453592 FAM120AOS 158293 family with sequence similarity 120A opposite strand NA .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_134378_PI430048170 0.0893361089489085 0.6879322671685456.26351750880493
5.85716912640232 6.54161511777722 P P P 6.76990561950889 6.6403714105595
6.93626928823023 P P P LNCV6_134378_PI430048170 mRNA
GCTTCTCCTACAAAACGTAACTTGCAATTTGCCAGTTTATTATTGTTGGATACAAAGTTC NM_003850RefSeq chr13
- 47942655 48001326 SUCLA28803 "succinate-CoA ligase, ADP-forming, beta subunit"
GO:0005515|GO:0006099|GO:0044281|GO:0005524|GO:0006781|GO:0046872|GO:0005739|GO:0006105|GO:0005
759|GO:0006104|GO:0004775|GO:0044237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143664_PI430048170 0.0470634081816831 0.7744701622806997.21899341765293
7.2651777572862 7.35116967030461 P P P 7.52331678161165 7.5717839868661
7.83029547172401 P P P LNCV6_143664_PI430048170 mRNA
GCCAGGGGATTATCTTTCTATAAATGTATAACTGGCAACCTGTATCTTCCCTCTTTGTTG NM_032364RefSeq chr12
- 55820959 55829636 DNAJC14 85406 "DnaJ (Hsp40) homolog, subfamily C, member 14"
GO:0016020|GO:0005789|GO:0005730|GO:0005654|GO:0016021|GO:0015031|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127728_PI430048170 0.1097010114138980.6589142166293724.48286462835797
4.15655909132803 3.63095092236925 P P P 4.92708000681531 4.65206959238208 4.5991333780286
P P P LNCV6_127728_PI430048170 mRNA
GCTTCCCCCATAGCCACCCCAGAAATGGTGAAAATAAAATAAAGCAGGTTTTTCTCCTCT NM_000915RefSeq chr20
+ 3071619 3072517 OXT 5020 oxytocin/neurophysin I prepropeptide
GO:0060406|GO:0042220|GO:0005615|GO:0051591|GO:0007507|GO:0070474|GO:0034695|GO:0009744|GO:0051
602|GO:0007613|GO:0032355|GO:0005185|GO:0045925|GO:0051965|GO:0007565|GO:0030431|GO:0042538|GO:0
051384|GO:0010701|GO:0002125|GO:0002027|GO:0050806|GO:0035176|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128504_PI430048170 0.3058424192200131.55996858996656 0.529929862770147
1.70360395996386 0.538231548007102A A A 0.2972502777141290.423324119552948
0.45902830714589 A A A LNCV6_128504_PI430048170 mRNA
GCTGCTATATGCATGACTAACCAGGACCAAAAAGTTAATAAAAATACGAAAGTTTGGCAC NM_004796RefSeq chr14
+ 78403730 79868290 NRXN3 9369 "neurexin 3, transcript variant 1"
GO:0051965|GO:0090129|GO:0005246|GO:0007268|GO:0001525|GO:0071625|GO:0007416|GO:0046872|GO:0007
269|GO:0005887|GO:0007411|GO:0035176|GO:0004872|GO:0030534|GO:0007612|GO:0016021|GO:0050839|GO:0
097109|GO:0007158. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80893_PI430048170 0.0429814201371411 0.6054342990883644.09749267394334
4.70855972777359 4.6307724864571 P P P 5.36063718512467 5.05297683798694
5.25160100892747 P P P LNCV6_80893_PI430048170 mRNA
GAAACGACTAGAGTTACCAGAACATTTGAAAATCAAAGAAGACAATTTCTTCCAGGTTTC NM_018339RefSeq chr9
- 76385516 76394528 RFK 55312 riboflavin kinase
GO:0072593|GO:0006767|GO:0006915|GO:0044281|GO:0005524|GO:0046872|GO:0005829|GO:0009231|GO:0005
739|GO:0008531|GO:0006771|GO:0016310|GO:0005737|GO:0006766|GO:0009398|GO:0033864 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144316_PI430048170 0.00275173065762496 1.19366219778345 13.6389319248368
13.7015089882626 13.6513778233186 P P P 13.4019779124999 13.4598696930366
13.3628973529158 P P P LNCV6_144316_PI430048170 mRNA
GCAGCATGCTGAGGTGTCCATGTTGTCTGCCTTTGTATAAAGAAACAGCCTCTGACCTGC NM_001040457 RefSeq
chr7 + 75878998 75888926 RHBDD2 57414 "rhomboid domain containing 2, transcript variant 2"
GO:0048471|GO:0005794|GO:0004252|GO:0000139|GO:0006508|GO:0005654|GO:0005634|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139556_PI430048170 0.00395057351744606 0.2741850283965276.2766667256399
6.31175279480637 6.43143497816403 P P P 7.92471968526006 8.19191930951214
8.45885558689899 P P P LNCV6_139556_PI430048170 mRNA

GTGGCATTGGCTTTTGAATATGAAATCTTCTCATAGCTGCCTAAAAAAGACTAGAATGTA NM_020464 RefSeq chr6 - 138422043 138572531 NHSL1 57224 "NHS-like 1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129795_PI430048170 0.7531186613391691.00345445175704 0.3740805606877610.3714715083836 0.387748163885846 A A A 0.3848550407025620.3455042848688630.387684390638184 A A A LNCV6_129795_PI430048170 mRNA
TACCACACTTTACACAGCATTTCAAAAAGCAATAAAATTGACACTGTCTTCTCAAAGACC NM_006557 RefSeq chr9 + 1050345 1057554 DMRT2 10655 "doublesex and mab-3 related transcription factor 2, transcript variant 1"
GO:0000987|GO:0006355|GO:0003700|GO:0048706|GO:0005634|GO:0005575|GO:0014807|GO:0006351|GO:0042803|GO:0046872|GO:0003674|GO:0008150|GO:2000287 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135989_PI430048170 0.1227839871330720.6993557234781579.57330237625545 9.2734200378703 8.79827694445791 P P P 9.95422571178561 9.73174600556805 9.58587041154556 P P P LNCV6_135989_PI430048170 mRNA
ACACCCTAACTGCACCTGTCTCCCTGGAGATGAAAATATATGACGCTGCCCTGCAAAAAA NM_001171976 RefSeq chr5 + 176542510 176595768 CDHR2 54825 "cadherin-related family member 2, transcript variant 1"
GO:0005903|GO:0005515|GO:0030308|GO:0016324|GO:0030054|GO:0005509|GO:0016021|GO:0007155|GO:0007156|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135687_PI430048170 0.0597545531888997 1.05816781120431 0.390900779542598 0.3456642795942410.306381380144806 A A A 0.2511206249246350.301420444264089 0.246292139972096 A A A LNCV6_135687_PI430048170 mRNA
GTTGTGGAATGATGCTGGGTCTCAAGAATGCTGTGAATCAATAAACATTTTATTCAGAAA NM_080819 RefSeq chr4 + 8580489 8590023 GPR78 27201 "G protein-coupled receptor 78, transcript variant 1"
GO:0005886|GO:0004930|GO:0016021|GO:0007189 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103128_PI430048170 0.6431560912645170.9572032015136879.1586006844903 8.91006888589468 8.99257655520173 P P P 9.05641201389704 9.25714536940099 8.92910337840969 P P P LNCV6_103128_PI430048170 mRNA
ACAAGGTGGAGCCCCACGCCACCATTGCGGAGATCAAGAACCTCTTCACTAAGACCCATC NM_138501 RefSeq chr19 + 14529566 14565980 TECR 9524 "trans-2,3-enoyl-CoA reductase, transcript variant 1"
GO:0005783|GO:0030497|GO:0019432|GO:0005789|GO:0030176|GO:0005634|GO:0044281|GO:0035338|GO:0042761|GO:0016627|GO:0044255|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143774_PI430048170 0.0299421351870329 1.85742092290585 3.8903803771221 4.39403618263516 3.90505415889347 P P P 2.94962815269452 3.57743311834761 2.94592698709723 P P P LNCV6_143774_PI430048170 mRNA
TAACTGTTCTCTTCTTTTCCTTATTAATAAAACACACAATGCCTAGCTGGGGGGTCGGAA NM_178172 RefSeq chr8 + 143213192 143217170 GPIHBP1 338328 "glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1, transcript variant 1"
GO:0042632|GO:0008035|GO:0071813|GO:0035478|GO:0050821|GO:0070328|GO:0008320|GO:0006886|GO:0031362|GO:0090321|GO:0008289|GO:0016323|GO:0045056|GO:0016324|GO:0071503|GO:0034364|GO:0034394|GO:0006869|GO:0017038|GO:0035473|GO:0071806|GO:0009897|GO:0051006 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142340_PI430048170 0.2783071277024621.28572047135698 11.9822714524846 11.6813573135338 11.7661955953972 P P P 11.961729427599 11.0818400177631 11.1383383648674 P P P LNCV6_142340_PI430048170 mRNA
AAGACCTTTTACAAATGATACCAATTAAACTGCCCTGGAAAGGGCATAGGTGGGCATCGG NM_133328 RefSeq chr19 - 42198592 42217792 DEDD2 162989 "death effector domain containing 2, transcript variant 1"
GO:0005515|GO:0008625|GO:0006396|GO:0016075|GO:2001238|GO:0019725|GO:0030262|GO:0005730|GO:0030159|GO:0003677|GO:0006351|GO:0035556|GO:0005654|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_69196_PI430048170 0.2091301853449950.8499154478560771 1.5684860591894 11.8035340108416 11.9530909600785 P P P 11.8035340108416 12.0462487799242 12.1800144899619 P P P LNCV6_69196_PI430048170 mRNA AGAAATAGAAGAAGTTCAAGCCTTGGATGACACCGAAAGGGGTTCAGGAGGTTTTGGTTC NM_001025248 RefSeq chr15 + 48331423 48343373 DUT 1854 "deoxyuridine triphosphatase, transcript variant 1" GO:0005515|GO:0000287|GO:0046081|GO:0055086|GO:0005634|GO:0044281|GO:0006226|GO:0005739|GO:0006260|GO:0006139|GO:0046134|GO:0004170|GO:0005654|GO:0006206|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_99775_PI430048170 0.6284584735227830.9393406708434384.85432975967041 4.49304149431291 4.51464399840089 P P P 4.7621801192575 4.89509851596455 4.47308216499716 P P P LNCV6_99775_PI430048170 mRNA AAGAAGCTGATGGAATTCATATATCTGTCTCTCTCCTGCAAGAATCTACCTGAGACCATG NM_004717 RefSeq chr7 - 137389638 137846863 DGKI 9162 "diacylglycerol kinase, iota" GO:0005515|GO:0048471|GO:0005886|GO:0045202|GO:0030168|GO:0046579|GO:0005634|GO:0043086|GO:0005524|GO:0046872|GO:0007205|GO:0035556|GO:0016310|GO:0005737|GO:0003951|GO:0043197|GO:0007596|GO:0004143|GO:0005654|GO:0005095|GO:0017016|GO:0032317|GO:0032045 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_112030_PI430048170 0.5328256998791270.9443884755089731 1.2667873213738 11.4804723154898 11.0822103723348 P P P 11.3911342820697 11.4434446900319 11.2642822918714 P P P LNCV6_112030_PI430048170 mRNA CCCCTGAGACTCGGAGCGGGGCTGACTGGAAACAACACGAATCACTCACTTTTCCCCACA NM_145201 RefSeq chr8_KI270816v1_alt - 64824 68391 NAPRT 93100 "nicotinate phosphoribosyltransferase, transcript variant 1" GO:0019358|GO:0005794|GO:0016874|GO:0019674|GO:0006767|GO:0005634|GO:0044281|GO:0006769|GO:0005829|GO:0004516|GO:0005737|GO:0006766|GO:0004514|GO:0005654|GO:0009435|GO:0006979|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139192_PI430048170 0.0593025074594509 0.513500165141754 6.36035052147406 6.24074309844378 6.4733352953511 P P P 6.77549301690134 7.51233830859196 7.55590662736022 P P P LNCV6_139192_PI430048170 mRNA ACTGCAGTTCTGAATTTTGGGTTAAAGGTTTTGGCTGCTGTAAGAATGTGAATTTGAATG NM_016121 RefSeq chr1 + 215567391 215621808 KCTD3 51133 potassium channel tetramerization domain containing 3 GO:0051260 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_131931_PI430048170 0.190682703671247 2.12376434434942 0.314430919658814 1.68692783778864 1.83944991985391 A A A 0.345954703684674 0.304206067457828 0.35718366922709 A A A LNCV6_131931_PI430048170 mRNA GGAAAGTGTGAGTTAATATTGGACACATTTTATCCTGATCCACAGTGGAGTTTTAGTAAT NM_001256370 RefSeq chr21 - 14485227 14583402 SAMSN1 64092 "SAM domain, SH3 domain and nuclear localization signals 1, transcript variant 2" GO:0050869|GO:0050732|GO:0005634|GO:0001784|GO:0002820|GO:0001726|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_140379_PI430048170 0.219151194330216 0.830673985759523 0.461978829373339 0.370200556748599 0.418738670505897 A A A 0.95492870327734 0.48385188448718 0.571920595531836 A A A LNCV6_140379_PI430048170 mRNA CCTGCAGGCAGAAATGTGAAAGCATTTGGTATGTTGAAGATACTTGCTTCTTTTTTAATA NM_003647 RefSeq chr17 + 56834098 56868675 DGKE 8526 "diacylglycerol kinase, epsilon 64kDa" GO:0005886|GO:0030168|GO:0008654|GO:0005524|GO:0046872|GO:0007205|GO:0035556|GO:0016310|GO:0005737|GO:0003951|GO:0016020|GO:0007596|GO:0004143|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_78122_PI430048170 0.239983667124364 0.715563597703662 2.96641976149478

2.39454345468978 1.92830538053916 P A A 3.32155992022781 2.59998601620357
2.91259609013564 P P P LNCV6_78122_PI430048170 mRNA
GGGTTGGCCTATATTAAACAAGGAATTCATTTCAGAGAAAAGCCCTATACATGTAATGAA NM_001083956 RefSeq
chr7 + 99558421 99576456 ZNF655 79027 "zinc finger protein 655, transcript variant 7"
GO:0005515|GO:0003674|GO:0006355|GO:0005737|GO:0003700|GO:0005730|GO:2000134|GO:0005634|GO:0003
677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126916_PI430048170 0.174865982964317 0.799505637866938 5.45522517308051
6.00149346805168 5.88037334014111 P P P 6.27186064024551 6.14222743858476
5.92560938733545 P P P LNCV6_126916_PI430048170 mRNA
TCCCCCTGCTTCAGGTTAATTTTTTGGATATTTCAGAAACCCATAGCAATTCAGTGATTT NM_030953 RefSeq chr5
- 149993122 150001167 TIGD6 81789 "tigger transposable element derived 6, transcript variant 1"
GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129153_PI430048170 0.214907234506078 1.75979415333625 0.362755827771355
1.7310454836918 1.00163136651048 A A A 0.312601032993176 0.303044900519966
0.355236449227802 A A A LNCV6_129153_PI430048170 mRNA
GCTGTGTTTTTGATACTGATATTTTCCTATGCTGAATAGTTTTCTTACTTTCAGGGAAGG NM_001291303 RefSeq
chr4 + 125316411 125492932 FAT4 79633 "FAT atypical cadherin 4, transcript variant 1"
GO:0005515|GO:0007009|GO:0001658|GO:0060122|GO:0021987|GO:0043931|GO:0005886|GO:0005509|GO:0045
177|GO:0048565|GO:0035329|GO:0003007|GO:0072307|GO:0016021|GO:0007156|GO:0007157|GO:0070062|GO:0
022008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144753_PI430048170 0.564091543860373 0.868757886566082 3.55459132779041
1.79814261198574 2.97359297004296 P A P 3.23515009619573 2.86030054185868
3.30623418867207 P P P LNCV6_144753_PI430048170 mRNA
GGCATGAGGGAGGATATTTTAAAGGGAAGTATAGCTGATTTTAAAAGAACCTATACATTC NM_014818 RefSeq
chr11 - 8612036 8658836 TRIM66 9866 tripartite motif containing 66
GO:0016235|GO:0008270|GO:0005654 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_135184_PI430048170 0.0949450060132684 0.595461210113684 2.19378540820303
2.14698669763265 1.44864568251731 A A A 2.99184246477224 2.19664696104282
2.84116908372751 P A P LNCV6_135184_PI430048170 mRNA
GAAGCTCAAACTTCCTGGTAACTCAAGGCTACCAAGTGAAGCTTGCAGGATTTGAGTTGA NM_152649 RefSeq
chr16 - 74671854 74700891 MLKL 197259 "mixed lineage kinase domain-like, transcript variant 1"
GO:0005515|GO:0070207|GO:0005737|GO:0070266|GO:0004672|GO:0019901|GO:0005886|GO:0006468|GO:0032
403|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129668_PI430048170 0.237540584322395 0.890223332552398 0.421116813066254
0.443473160648478 0.325352294652917 A A A 0.754767236942023 0.477041572851004
0.443473160648478 A A A LNCV6_129668_PI430048170 mRNA
TTACCTGGGTTTGGCACACCTGGTTAGGGCTCTGAGTGGGAAAGAGGGTCCTGAAACCAG NM_001098622 RefSeq
chr19 + 13877248 13880757 NANOS3 342977 nanos homolog 3 (Drosophila)
GO:0005515|GO:0017148|GO:0048471|GO:0048477|GO:0010494|GO:2001234|GO:0003723|GO:0005634|GO:0007
275|GO:0007283|GO:0007281|GO:0006417|GO:0005737|GO:1900153|GO:0000932|GO:0051726|GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133219_PI430048170 0.082391080691562 0.850247831944124 4.04993565293673
4.21094675658929 4.28687449600266 P P P 4.42898798183889 4.28341227078024
4.53641663739981 P P P LNCV6_133219_PI430048170 mRNA
CTGCAGGTGGGTATATGGTAATGGGATTAGAGAGCCTTTAATTTTCTGCTTTGTATATTT NM_033114 RefSeq
chr12 - 42312085 42326130 ZCRB1 85437 zinc finger CCHC-type and RNA binding motif 1
GO:0008380|GO:0006397|GO:0000166|GO:0008270|GO:0005654|GO:0005689 . NA - . NA NA
NA NA NA NA NA NA NA

LNCV6_144979_PI430048170 0.360762178519743 0.591306250961417 0.476049989446838
0.494010694350187 2.03517695691813 A A A 2.12925707568091 0.704587822913813
2.50108814221284 A A P LNCV6_144979_PI430048170 mRNA
CTGCACACGCTAGCATATCTGGAACCTACTATGAAAATGAAAGGACCCTTATAGGTACTC NM_003672 RefSeq chr1
+ 100352466 100520277 CDC14A 8556 "cell division cycle 14A, transcript variant 1"
GO:0005515|GO:0005813|GO:0008283|GO:0005819|GO:0005634|GO:0035335|GO:0005737|GO:0007049|GO:0004
721|GO:0005654|GO:0008138|GO:0004725|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65817_PI430048170 0.0197649227644357 1.05704082066896 0.405332743022581
0.4484012940400440.396552814684509 A A A 0.3120099847271480.340138807459859
0.358205071564361 A A A LNCV6_65817_PI430048170 mRNA
TTGAAGCTCTATAAATATGTTGCTTTACGTGGCAAAAAGGACTTTACAGATCTGAGTACA NM_001288837 RefSeq
chr2 + 57907650 58159920 VRK2 7444 "vaccinia related kinase 2, transcript variant 8"
GO:0005515|GO:0031966|GO:0005783|GO:0008360|GO:0005634|GO:2000659|GO:0005524|GO:0006897|GO:0005
737|GO:0046777|GO:0018105|GO:0004674|GO:0043408|GO:0005789|GO:0016032|GO:0006468|GO:0034599|GO:0
016021|GO:0016055. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142757_PI430048170 0.34146182141199 0.91110340460528313.5040474160954
13.8162623620446 13.8172078606696 P P P 13.9434310182657 13.7123315685144
13.8965179957739 P P P LNCV6_142757_PI430048170 mRNA
AACTTAATAGCAGCAGCTGCCCAATGCCATGTGAAGTAACAAACTGGTTTTTGGTTTTTT NM_005801 RefSeq chr17
+ 41688874 41691646 EIF1 10209 eukaryotic translation initiation factor 1
GO:0005737|GO:0006446|GO:0006950|GO:0003743|GO:0009048|GO:0008135|GO:0006413 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132577_PI430048170 0.0191132152285315 0.6565771939019268.33589878159765
8.29528106722083 8.63841449364159 P P P 8.85679940846911 8.97924825962211
9.25075681729027 P P P LNCV6_132577_PI430048170 mRNA
CAAGAAGTAATGTGGCCAAGTAGGTTTTTGTATCATATTAGCCTAAAGATGAAAGGCTTA NM_020395 RefSeq chr4
- 105682627 105708724 INTS12 57117 "integrator complex subunit 12, transcript variant 1"
GO:0005515|GO:0032039|GO:0008270|GO:0016180 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100816_PI430048170 0.461045915460811 1.04763404397458 0.301625084004978
0.3099458173487790.516210940054619 A A A 0.3201149887909530.280970602180321
0.33515229066915 A A A LNCV6_100816_PI430048170 mRNA
AAACTCTGCACCGTTATCATGAAGTCTAATGGGAGTTTCCCAGTGAACAGGCGGAGAGTG NM_000795 RefSeq chr11
- 113409594 113475279 DRD2 1813 "dopamine receptor D2, transcript variant 1"
GO:0005515|GO:0007608|GO:0001659|GO:0015459|GO:0043266|GO:0007409|GO:0042220|GO:0031223|GO:0042
803|GO:0042802|GO:0010039|GO:0030672|GO:0009416|GO:0016055|GO:0008306|GO:0030336|GO:0007616|GO:0
032467|GO:0035240|GO:0009636|GO:0014069|GO:0043278|GO:0007416|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135772_PI430048170 0.5385306090390320.9249363903347827.82938786414499
7.55568056377668 7.28862818093441 P P P 7.83828600938751 7.68031579949138
7.52655022976187 P P P LNCV6_135772_PI430048170 mRNA
CCCACCCCACTCTGTTTTACATCTTTTATAAATGTGCCAAACTGTGTGGCCTCTGCCAGG NM_001303098 RefSeq
chr2 + 219543662 219550596 TMEM198 130612 "transmembrane protein 198, transcript variant 1"
GO:0005886|GO:0090263|GO:0016023|GO:0007275|GO:0016021|GO:0016055 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140557_PI430048170 0.8111070512790561.13115478431196 3.97735533860286
2.77049635989702 3.13526219082878 P A P 2.88037142168144 3.3218468929163
3.37317031920411 P P P LNCV6_140557_PI430048170 mRNA
ATGTGTCAGAGCCATTTGGTCCATCATCTCCTGCAATAAACCCATCGCAAGAATGACCTT NM_001279 RefSeq chr18
+ 12254318 12277595 CIDEA 1149 "cell death-inducing DFFA-like effector a, transcript variant 1"

GO:0005811|GO:0006629|GO:0008219|GO:0035634|GO:0006355|GO:0050995|GO:0001659|GO:0019915|GO:0032720|GO:0006915|GO:0042981|GO:0005634|GO:0005740|GO:0050710|GO:0042803|GO:0006351|GO:0005739|GO:0005737|GO:0010890|GO:1900118|GO:0030512 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127593_PI430048170 0.2384846734024890.8552115478623489.93291279627664
10.0390830659519 10.3033508812441 P P P 10.1013159805345 10.3360248371986
10.5114520609877 P P P LNCV6_127593_PI430048170 mRNA
CATATGCTTGCTATTTAAAGCTGTGTGTTGGTTTTGTTTTTCTGCCACATTCACTAGTTT NM_005067RefSeq chr3 - 150741122 150763476 SIAH2 6478 siah E3 ubiquitin protein ligase 2
GO:0005515|GO:2001237|GO:0043005|GO:0006511|GO:0043066|GO:0004842|GO:0016567|GO:0007264|GO:0016874|GO:0003714|GO:0043231|GO:0005829|GO:0005737|GO:0007049|GO:0007411|GO:0043025|GO:0031396|GO:0005654|GO:0008270|GO:0044257|GO:0043154|GO:0090090|GO:0005769|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128512_PI430048170 0.000304607171413611 1.63728936696278 11.8148206925164
11.9600946927354 11.8955067432717 P P P 11.1881941212836 11.0987264980044 11.249277628469
P P P LNCV6_128512_PI430048170 mRNA
GGTTTATGGCCTCGTTTTCACTTGTATATTTTTCACACTGTAAATTTCTTGTACAAACCC NM_032429RefSeq chr10 + 100997106 101007836 LZTS2 84445 "leucine zipper, putative tumor suppressor 2"
GO:0005515|GO:0051255|GO:0005813|GO:0008285|GO:0001822|GO:0005874|GO:0030496|GO:1900181|GO:0000910|GO:0051013|GO:0005737|GO:0007067|GO:0016055|GO:0090090|GO:0051168 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68259_PI430048170 0.0860055975511 1.17846397836714 9.76067443463905 9.90787532462349
9.72689208285073 P P P 9.68984859992078 9.58455465004494 9.40226821527127 P P P
LNCV6_68259_PI430048170 mRNA
ATGACATCCCTGTTCCTTAAAGTGCGGGGTTCCTCGCTGCCTTCTCCTCCCTAACTGGCA NM_001256088 RefSeq chr11 - 128899564 128906069 C11orf45 219833 "chromosome 11 open reading frame 45, transcript variant 1" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130363_PI430048170 0.0667301708303493 0.6444225159551 4.88750829298045
4.65229278409071 4.56606967045483 P P P 5.00082352874947 5.28207062010333
5.66629668320871 P P P LNCV6_130363_PI430048170 mRNA
GATTACCTAAACTCTCCTTCCAGAGCTACTTTAATGATTATATTCAACCAAAGCACTCTA NM_004109RefSeq chr11 + 110429936 110464884 FDX1 2230 ferredoxin 1
GO:0006805|GO:0005506|GO:0051537|GO:0009055|GO:0044281|GO:0005739|GO:0005759|GO:0006700|GO:0042446|GO:0016125|GO:0008202|GO:0008203|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133811_PI430048170 0.5960276253444090.9656635742101414.66127882703293
4.96044629867666 4.81829882970133 P P P 4.92242463948664 4.83660358723443
4.84615729988978 P P P LNCV6_133811_PI430048170 mRNA
CCACATTTTTCCTACAATCCAACCACATCAAGAAATGATAACTGCTCAGAAAGTTTATCA NM_001185092 RefSeq chr1 + 161118071 161125445 NIT1 4817 "nitrilase 1, transcript variant 2"
GO:0005739|GO:0008150|GO:0006807|GO:0000257|GO:0005634|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129158_PI430048170 0.9603648679236881.01960889429183 1.49443694557013
0.2896899524121110.58079929367003 A A A 0.4238524317596430.733597155765311
1.27789709223722 A A A LNCV6_129158_PI430048170 mRNA
GATGCAGTAGGGAAGAGACGATGTAAAAATAATAAACAATATATACCTTCCTAGAGTGTG NM_022097RefSeq chr16 + 23754626 23758951 CHP2 63928 calcineurin-like EF-hand protein 2
GO:0005515|GO:0008284|GO:0005737|GO:0005886|GO:0045944|GO:0010922|GO:0005509|GO:0071277|GO:0042307|GO:0005634|GO:0070886|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59142_PI430048170 0.0121290614313352 0.7168411222900747.42732988676439
7.43984237841013 7.29403007256686 P P P 7.80669332046592 7.76296763576007

8.02317531126379 P P P LNCV6_59142_PI430048170 mRNA
GAACATGTCTAACAGTAACACTACTCAAGAGACCCTGGAAATAATGAAAGAATCAGAAAA NM_014925 RefSeq chr12
- 57253764 57310463 R3HDM2 22864 R3H domain containing 2 GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136408_PI430048170 0.0138204726561483 1.25350131361025 8.04371678628953
7.98475139382774 7.85945351279045 P P P 7.59352470985629 7.63607825040734
7.68506400384171 P P P LNCV6_136408_PI430048170 mRNA
GACCCCACACAGCAATACGAGTCCAACTTAATAAACACATTTCTGGGGTTCCTCAAAAAA NM_198317 RefSeq chr1
+ 960586 965719 KLHL17 339451 kelch-like family member 17
GO:0031208|GO:0016567|GO:0030036|GO:0030054|GO:0014069|GO:0032839|GO:0015629|GO:0005615|GO:0032
947|GO:0051015|GO:0007420|GO:0045211|GO:0043025 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144877_PI430048170 0.0197259916522405 1.36081584405964 7.85212829753111
8.10017400001094 8.09960336091005 P P P 7.53403228285027 7.65071382651234
7.54473845080788 P P P LNCV6_144877_PI430048170 mRNA
GACTTCTCAAAGACTTTAGACCTTGACTTCAGTGATTTGTTGTAGTCTTGTATGCTTCTC NM_024809 RefSeq chr12 +
123671112 123708403 TCTN2 79867 "tectonic family member 2, transcript variant 1"
GO:0042384|GO:0060170|GO:0005737|GO:0006996|GO:0060271|GO:0036038|GO:0016021|GO:0005856|GO:0007
224 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143343_PI430048170 0.4845712495101131.04667443624916 0.282666506299402
0.2932202422471920.506375979788276 A A A 0.31623338287222 0.275205156067488
0.304298145838185 A A A LNCV6_143343_PI430048170 mRNA
GCTGAGACAATGGAAAACAAGGAAGTGGGAATTTTTACAGTTCCTTTGTTTGTTTTTCTT NM_001144960 RefSeq
chr3 - 149761102 149792823 ANKUB1 389161 ankyrin repeat and ubiquitin domain containing 1
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132555_PI430048170 0.7578224192655121.05206963942861 6.80677418484143
6.27489644409244 6.65705757958741 P P P 6.8059708168279 6.25855337737506
6.45097542491188 P P P LNCV6_132555_PI430048170 mRNA
ACCCATGCAGGCACCCCACCAAAGTACATATCTTCCTTCCAGTAATAATTTTTAATTACA NM_001098398 RefSeq
chr1 - 160288586 160343564 COPA 1314 "coatomer protein complex, subunit alpha, transcript
variant 1"
GO:0030126|GO:0006890|GO:0030157|GO:0005615|GO:0006886|GO:0048205|GO:0005829|GO:0005737|GO:0005
179|GO:0016020|GO:0005198|GO:0061024|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136011_PI430048170 0.4568431334752542.19527365206577 0.338781191057653
2.60478897293425 0.290135521366766 A A A 0.4249430434054620.314889471402737
0.397932898941833 A A A LNCV6_136011_PI430048170 mRNA
AGCCTTCCCAGGTGGGACTTTAGGCATGATTAAAATATGGACATATTTTTGGAGAAAAAA NM_000717 RefSeq chr17
+ 60149940 60159545 CA4 762 carbonic anhydrase IV
GO:0005802|GO:0005515|GO:0048471|GO:0005886|GO:0031526|GO:0044281|GO:0048513|GO:0031362|GO:0016
323|GO:0016324|GO:0006730|GO:0070062|GO:0030658|GO:0005791|GO:0005793|GO:0005794|GO:0009986|GO:0
042493|GO:0004089|GO:0048545|GO:0042383|GO:0016529|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136465_PI430048170 0.00227243637502299 0.2803119397840523.38593954933766
3.06289519119851 3.41289765874378 P P P 5.05530340685563 4.82103879070647
5.44571064904134 P P P LNCV6_136465_PI430048170 mRNA
CCCACCTACATTACCTTCAGGAGACTGTTCTACCTTTTAATTTGAAAACAAGGAAATTAA NM_178815 RefSeq chr10
+ 18659383 18678011 ARL5B 221079 ADP-ribosylation factor-like 5B
GO:0005622|GO:0007264|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75467_PI430048170 0.6470305788648381.0551939553551 8.2922466199136 7.99371936036447
8.40545131848437 P P P 8.03736684606048 8.20228278096134 8.24188394859013 P P P

LNCV6_75467_PI430048170 mRNA
CGATGGTTACATTGAATACTACATATGTCGAGGGAATGCAGAAAGAGTTAAGGAAGGCAGNM_176895RefSeq chr5
- 55424841 55535078 PPAP2A8611 "phosphatidic acid phosphatase type 2A, transcript variant 2"
GO:0006629|GO:0006665|GO:0008354|GO:0008285|GO:0005886|GO:0030148|GO:0044281|GO:0008195|GO:0007
205|GO:0019216|GO:0006470|GO:0016020|GO:0030518|GO:0046839|GO:0005887|GO:0030521|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131733_PI430048170 0.1819756949192080.9798688284671030.360478526349275
0.3586305777147140.385247317725735A A A 0.3825449712047390.427150767049699
0.382369369326674A A A LNCV6_131733_PI430048170 mRNA
ACACCAAATTGAGCAATTTGACCAAGATTTCTAGTAGCAGAGCCGGTACCTGCTGAGTGT NM_175881RefSeq chr15
+ 75723977 75727686 ODF3L1161753 outer dense fiber of sperm tails 3-like 1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_144123_PI430048170 0.3467294143966720.9536960445127210.27341053579771
0.2845074606655440.378822231650798A A A 0.4818620614308740.313048011931256
0.343705711620813A A A LNCV6_144123_PI430048170 mRNA
CCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTAAAC NM_001001920 RefSeq
chr11 + 55554306 55555419 OR4C1581309 "olfactory receptor, family 4, subfamily C, member 15"
GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135380_PI430048170 0.1521383624716131.10164374061203 0.56788336732892
0.4691816441941350.621854642542609A A A 0.2998298633117750.415563626348416
0.520272879425326A A A LNCV6_135380_PI430048170 mRNA
TTTTCCACACATGCGTGGGAAAGGTATGATTTCTGCATGTAATTGCAGTTTAACCCTTAT NM_002239RefSeq chr2
+ 154698580 154858352 KCNJ3 3760 "potassium channel, inwardly rectifying subfamily J, member 3,
transcript variant 1"
GO:0005515|GO:0005242|GO:0005886|GO:0015467|GO:0008076|GO:0051602|GO:0030315|GO:0010107|GO:0007
268|GO:0034765|GO:0006813|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144049_PI430048170 0.00788185824156148 0.4272343499930895.24127021153113
4.64471308845752 4.92500754120797 P P P 6.19044001040836 6.02216082693073
6.32498936942456 P P P LNCV6_144049_PI430048170 mRNA
CCCTGTACCTGAACACTTGTTGCTGCCTCACAAGAAAATAGAACTTTTATGTTAAAAATA NM_173511RefSeq chr2
+ 202635177 202769757 FAM117B 150864 "family with sequence similarity 117, member B" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_127798_PI430048170 0.7975586501135031.00581250152339 0.300181782722025
0.3374898904716090.390117720624198A A A 0.3525355133208880.334656749096393
0.316708071308616A A A LNCV6_127798_PI430048170 mRNA
ACGTCATGTGCACCTTTACACTGTGGTTAGTGTAATAAAACATGTTCCTTATATTTACTC NM_024013RefSeq chr9
+ 21440453 21441316 IFNA1 NA "interferon, alpha 1" NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141922_PI430048170 0.3001832808170741.08637435748652 0.315802235691093
0.5420757509450340.276378763803932A A A 0.2641633938137440.262792824357421
0.263223226227725A A A LNCV6_141922_PI430048170 mRNA
TTTGAAAAGATGAATCAAACGCATCTGTCTGGGAGAGCTGATGAACACTGTGTGATGCCC NM_001083308 RefSeq
chr3 + 191461162 191461456 PYDC2 NA pyrin domain containing 2 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_142116_PI430048170 0.0213168450990147 1.43836271725265 7.39274301228582
7.46899337444022 7.66253308870189 P P P 6.97034195738522 7.00877663844103
6.98517174863665 P P P LNCV6_142116_PI430048170 mRNA
AGGATCGGCATGGTCATTCACCAAGTGGAAGCCAAACCCTCTGTGTATTTCATCAAGTTT NM_001006681 RefSeq

chrX - 57119681 57121546 SPIN2B 474343 "spindlin family, member 2B, transcript variant 1"
GO:0007049|GO:0007276|GO:0051726|GO:0006915|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140613_PI430048170 0.469612959028466 1.12316686284886 5.17437292624515
5.25761262158468 5.10202747926764 P P P 5.28073650378357 5.11508867784888
4.53973515347353 P P P LNCV6_140613_PI430048170 mRNA
CACCCCAAGAGAACTCGCGCTCAGTAAACGGGAACATGCCCCCTGCAGACACGTAAAAAA NM_005823 RefSeq
chr16 + 760764 768865 MSLN 10232 "mesothelin, transcript variant 1"
GO:0005515|GO:0005794|GO:0031016|GO:0016020|GO:0009986|GO:0005886|GO:0031225|GO:0007155|GO:0005
615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61238_PI430048170 0.3333909630819880 0.7816738664799033 11533541017478 2.56977850054807
2.88141008614871 A A A 2.69423152122084 3.37722443804634 3.49130256574085 P P P
LNCV6_61238_PI430048170 mRNA
TTCTACAAAAGAAACCAAACATCAGAAATACATCCAGCATGGCTGGAGAGCTCCGACCAG NM_001286470 RefSeq
chr14 + 91114012 91225396 C14orf159 80017 "chromosome 14 open reading frame 159, transcript
variant 6" GO:0005739|GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137401_PI430048170 0.00708411789995755 1.81209133372231 7.73253705654348
8.02430785765369 8.09798056975443 P P P 7.18166777393366 6.99728930227048
7.12210409355728 P P P LNCV6_137401_PI430048170 mRNA
AATGATTGAGTCTTCTTTATGGAAACAACTGGCCTCAGCCCTTGCGCCCTTACTGTGATT NM_022059 RefSeq chr17
- 4733528 4739928 CXCL16 58191 "chemokine (C-X-C motif) ligand 16, transcript variant 1"
GO:0008009|GO:0030335|GO:0005886|GO:0030307|GO:0005576|GO:0005615|GO:0006898|GO:0010818|GO:0005
041|GO:0071222|GO:0006935|GO:0016020|GO:0034612|GO:0034341|GO:0016021|GO:0034097|GO:0005044 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134580_PI430048170 0.00515250678427313 0.4686586157097164 2564840215578
4.24491407135691 4.51949451845562 P P P 5.31350992257322 5.37542462005472
5.75414904518481 P P P LNCV6_134580_PI430048170 mRNA
CAATTTCCTTTTATGTAGCTTGCTTTTTCATTTGCTATAATTGATCCTGCAGGTGTGTGA NM_152551 RefSeq chr6 +
7590198 7611967 SNRNP48 154007 small nuclear ribonucleoprotein 48kDa (U11/U12)
GO:0008380|GO:0006397|GO:0005737|GO:0005654|GO:0046872|GO:0005689 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_77009_PI430048170 0.2201077266057051 .07940156129309 0.4685032084998680.650829341102147
0.603294875231058 A A A 0.5692396029802150.40897574231542 0.41403808687653 A A A
LNCV6_77009_PI430048170 mRNA
TAATAGTAGATGTTGGATCTTCAGGAAGCTGAAGAGGGCAGTGCCCAGAAATACCTGTCT NM_001076781 RefSeq
chr6 + 27388744 27401448 ZNF391 NA zinc finger protein 391 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129571_PI430048170 0.0289258959790854 1.32509900386467 7.61868942736631
7.75996428185286 7.44059125771422 P P P 7.126889593925 7.30980116050833
7.17564169388787 P P P LNCV6_129571_PI430048170 mRNA
GCATAAATATTCCTATCAGCCCAAGAAGTCTGTCCAACCCCAAAAGGCTCTTTTCAGAGC NM_003533 RefSeq chr6
- 27871844 27872321 HIST1H3I 8354 "histone cluster 1, H3i"
GO:0005515|GO:0010467|GO:0046982|GO:0006325|GO:0006335|GO:0005576|GO:0005634|GO:0000228|GO:0003
677|GO:0032776|GO:0043234|GO:0060968|GO:0016020|GO:0000183|GO:0007596|GO:0045814|GO:0040029|GO:0
005654|GO:0000786|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127417_PI430048170 0.5941446034734411 .03323934103632 0.363385292315174
0.5808060456874470.466163677979082 A A A 0.52011754262689 0.385929060669584
0.366075413592579 A A A LNCV6_127417_PI430048170 mRNA

CTCCGCTGATGAAACCAATTGTTTATTGTGTAAAAACTAAACAGATTAGAGTGAGAGTTG NM_001004748 RefSeq
chr11 - 4954771 4955713 OR51A2 NA "olfactory receptor, family 51, subfamily A, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131714_PI430048170 0.432459933332826 1.22359373802778 0.325962533274015 1.16383918531357 0.52464946358348 A A A 0.513472553872208 0.431295965265319 0.32806021338395 A A A LNCV6_131714_PI430048170 mRNA
AAGCGCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAA NM_001302 RefSeq chr1 + 10449718 10452003 CORT 1325 cortistatin
GO:0001664|GO:0007268|GO:0005184|GO:0007193|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131448_PI430048170 0.284230621943978 0.83838327399156 5.6017765319441 5.67334497905031 6.10448679294011 P P P 5.96482755687123 5.86928385540528 6.32104167725498 P P P LNCV6_131448_PI430048170 mRNA
GGCTAATTGACAGTATTTCTCAGCATCACTATGTAGCATTCTGTTTTAGCATCTTTGAAT NM_001310 RefSeq chr12 + 12611832 12645108 CREBL2 1389 cAMP responsive element binding protein-like 2
GO:0003700|GO:0050821|GO:0005634|GO:0006351|GO:0030154|GO:0043565|GO:0007165|GO:0046889|GO:0007049|GO:0033138|GO:0046326|GO:0045600|GO:0045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129892_PI430048170 0.10675173692048 0.581953762654997 1.30926448532033 1.9217300069132 2.41353419451956 A A A 3.08423273950161 2.58176547539499 2.44785466196909 P P P LNCV6_129892_PI430048170 mRNA
CTGTGTGTGGTAGGACTTGGAGAGTGATCTTTATCAACGTTTTTATTTAAAAGACTATCT NM_001561 RefSeq chr1 - 7915870 7943165 TNFRSF9 3604 "tumor necrosis factor receptor superfamily, member 9"
GO:2001183|GO:0070207|GO:2001180|GO:0019955|GO:0008285|GO:0005887|GO:0006915|GO:0004872|GO:0005615|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126627_PI430048170 0.0105621282103911 1.48624311630012 9.63431282605358 9.75754374418234 9.7041988574786 P P P 9.19197053548213 9.2198904135315 8.95773345739439 P P P LNCV6_126627_PI430048170 mRNA
GGGTCATGGTCTCCTCCTGGATGCTGCTCCTTGAATCTTTTTTCTTGATAAACCTTTTAC NM_153271 RefSeq chr15 + 75649006 75658627 SNX33 257364 sorting nexin 33
GO:0005515|GO:0051044|GO:0000281|GO:0097320|GO:0006886|GO:2000009|GO:0042802|GO:0036089|GO:0005829|GO:0006897|GO:0016050|GO:0007067|GO:0044351|GO:0016020|GO:0045806|GO:0016197|GO:2000010|GO:0016023|GO:0017038|GO:0007032|GO:0035091|GO:0030659|GO:0019898|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137543_PI430048170 0.0696317200980585 0.651426509241522 0.353789865912624 0.352681097199326 0.427505341500882 A A A 1.28100034603243 0.690974248916732 0.957566106392515 A A A LNCV6_137543_PI430048170 mRNA
GACAGCCACTTTGAATAAACCAGACACCGCACATGTGTCTTGAGAATTATTTGGAAAAAA NM_016724 RefSeq chr11 + 72189557 72196323 FOLR1 2348 "folate receptor 1 (adult), transcript variant 7"
GO:0005886|GO:0009986|GO:0015884|GO:0030136|GO:0031526|GO:0008517|GO:0031362|GO:0006898|GO:0005542|GO:0016324|GO:0016020|GO:0005887|GO:0046655|GO:0004872|GO:0070062|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127994_PI430048170 0.0762320716375828 1.40353771748073 8.44277600083977 8.36163451856955 8.87612777569392 P P P 8.19815966656797 7.87795268551401 8.17055312164208 P P P LNCV6_127994_PI430048170 mRNA
GATTGCCCAAGAAACTAATTTTTTAAAGAGAACACTGGACAACATTTTACTACTGAGGGA NM_001799 RefSeq
chr5_GL339449v2_alt + 17974 60596 CDK7 1022 cyclin-dependent kinase 7
GO:0005515|GO:0010467|GO:0048471|GO:0006368|GO:0006367|GO:0006366|GO:0008283|GO:0006363|GO:0006362|GO:0006361|GO:0005634|GO:0006360|GO:0050681|GO:0000079|GO:0005739|GO:0000082|GO:0005737|GO:0045944|GO:0000086|GO:0016032|GO:0007050|GO:0008094|GO:0003713|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_145221_PI430048170 0.1271240725247810.398365736150825 3.22853863941491
1.10916829870326 1.53353535783195 P A A 3.63371164254949 3.53860346831281
3.60624679565316 P P P LNCV6_145221_PI430048170 mRNA
CTCCCCTCTTTAACCCTATTATTTACAGTCTTAGAAATAAGCAAATAAAGGTGGCCATCA NM_001001918 RefSeq
chr1 + 248348774 248349713 OR14C36 NA "olfactory receptor, family 14, subfamily C, member 36"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130473_PI430048170 0.0562994929275028 0.4572481106627142.64583666958243
2.23559725739095 2.53659559143748 A A A 2.96051847505293 3.70928015739564
3.98301562361999 P P P LNCV6_130473_PI430048170 mRNA
CGTCTTAGTTGATTTCAGCATAATTTACATTAGGGAGACCTAAAAAGCACCTTCAAAGTA NM_001973RefSeq chr1
- 205607942 205632872 ELK4 2005 "ELK4, ETS-domain protein (SRF accessory protein 1), transcript
variant a"
GO:0003712|GO:0005515|GO:0070932|GO:0003700|GO:0006366|GO:0000981|GO:0001047|GO:0000122|GO:0003
677|GO:0030154|GO:0043565|GO:0005737|GO:0003682|GO:0005654 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138686_PI430048170 0.000271553271162681 2.14040526721268 10.6997047448728
10.5714236866998 10.477196490745 P P P 9.36891538540299 9.5910328879298
9.49483358897294 P P P LNCV6_138686_PI430048170 mRNA
GGTTCATGTCCAATCTTGTTCGATCACTAGATGATTCTAACATCGAAATAAACCTCTTTT NM_014811RefSeq chr9
+ 135479801 135488893 PPP1R26 9858 "protein phosphatase 1, regulatory subunit 26"
GO:0005515|GO:0019902|GO:0010923|GO:0004864|GO:0005730|GO:0005654 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138892_PI430048170 0.43376504539044 0.8070355883864050.368066336743298
0.41170779688879 1.0540295021294 A A A 1.27764490549585 0.402224095537675
1.05265504821645 A A A LNCV6_138892_PI430048170 mRNA
TTACCTCCTGTCTCAGAAGCTTGTTAGTTATTGTGCCACCTAAATATTGTAATAAAAGTG NM_000856RefSeq chr4
+ 155666709 155737062 GUCY1A3 2982 "guanylate cyclase 1, soluble, alpha 3, transcript variant 1"
GO:0007263|GO:0052565|GO:0008015|GO:0004383|GO:0005525|GO:0060087|GO:0008074|GO:0007596|GO:0006
182|GO:0008217|GO:0004872|GO:0030828|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127359_PI430048170 0.3676773465108 361.49756276711 6.64128681970455
16.1170857646927 6.40779992635773 P P P 6.23633296915531 5.93968894507188
5.91543967317297 P P P LNCV6_127359_PI430048170 mRNA
ACTCTGACTTCCAAGATATCTTTGGGAAATCCAAGGAGGAATTCTACAGCATGGCCACGT NM_015873RefSeq chr3
+ 37993586 38007185 VILL 50853 villin-like
GO:0007010|GO:0005200|GO:0003779|GO:0015629|GO:0051693 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145515_PI430048170 0.0739492170895076 0.6790208116640471 1.2545101926391
11.4628974003636 11.6813573135338 P P P 11.862602490716 11.8050899440121
12.3689476873786 P P P LNCV6_145515_PI430048170 mRNA
ATATGGTAGGATATCCCTCACCAACTCCCGACACTCAGCAGACTTGTTTTTATATTTTTT NM_152740RefSeq chr7
- 27525439 27663001 HIBADH11112 3-hydroxyisobutyrate dehydrogenase
GO:0034641|GO:0004616|GO:0051287|GO:0005759|GO:0006574|GO:0009083|GO:0044281|GO:0008442|GO:0006
098 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126374_PI430048170 0.9494195954811790.984362919153653 2.35020584983575
2.48266477297664 2.345932011087 A A A 1.86142085279561 2.61274840896648
2.64900893984849 A P P LNCV6_126374_PI430048170 mRNA
ATCAAGAAACTACAACCCTAAACACAGGAGCATTCCAATAAAAGTTAACAGGTTGGCCAC NM_001270976 RefSeq
chr16 + 71894407 71930637 IST1 9798 "increased sodium tolerance 1 homolog (yeast), transcript

variant 3"
GO:0005515|GO:0019076|GO:0005793|GO:0005813|GO:0019904|GO:0030496|GO:0046745|GO:0032403|GO:0045862|GO:0048672|GO:0005829|GO:0009838|GO:0045184|GO:0000910|GO:0008104|GO:0016023|GO:0070062|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62558_PI430048170 0.0525280959105863 1.63546309770511 6.33162311801341
6.41904897741866 6.87332077578681 P P P 5.87908507135986 5.81161047232325
5.86378436315793 P P P LNCV6_62558_PI430048170 mRNA
AGAACCTGAGGAACATCTCAGAGCTGTTCTACTACGCCCAGAAGGCCGTCCTGCATCCCA NM_138769RefSeq chr16
+ 668082 674174 RHOT2 89941 ras homolog family member T2
GO:0005515|GO:0051056|GO:0019725|GO:0005886|GO:0007264|GO:0005509|GO:0003924|GO:0005525|GO:0005829|GO:0016020|GO:0047497|GO:0008152|GO:0031307|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138722_PI430048170 0.0854279388909476 0.7001838632167225.81161047232325
5.61822607503621 5.98554752508928 P P P 5.95676314743351 6.44276828896762
6.51981353226767 P P P LNCV6_138722_PI430048170 mRNA
AAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCATGGTGCCA NM_024769RefSeq chr11
- 123072324 123195299 CLMP 79827 CXADR-like membrane protein
GO:0005881|GO:0009986|GO:0005886|GO:0048565|GO:0016021|GO:0005923|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112664_PI430048170 0.57188746891493 0.9365617282529610.374643533958704
0.3361623297204320.390843380664286A A A 0.6985763289113070.303139771628119
0.351044999457318A A A LNCV6_112664_PI430048170 mRNA
TAGAAGGGAATCTGTTGTAGCAAATGGGAATAAACCTGGGTTTCTATAGACCCAGAACTG NM_006108RefSeq chr11
+ 13962636 14268133 SPON1 10418 "spondin 1, extracellular matrix protein"
GO:0031012|GO:0005515|GO:0006493|GO:0005578|GO:0005788|GO:0036066|GO:0007155|GO:0044267|GO:0005615|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100960_PI430048170 0.5986524667875780.9809772430211960.256788281165029
0.2655030380596950.39613518815415 A A A 0.3694903073489030.309459536473992
0.326200584122348A A A LNCV6_100960_PI430048170 mRNA
AAGTCTGAACTGGAAGCACAGACAGGGCTCCAAATCTTGCAGACAGGAGTGGGACAGAGG NM_002846RefSeq
chr2 - 219289622 219309573 PTPRN 5798 "protein tyrosine phosphatase, receptor type, N, transcript variant 1"
GO:0005515|GO:0032868|GO:0043627|GO:0019221|GO:0030507|GO:0051591|GO:0009749|GO:0006470|GO:0051020|GO:0016021|GO:0000302|GO:0030073|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130762_PI430048170 0.3296959962736861.3181711988353 0.373535649356602
1.22916930613833 0.470220309451159A A A 0.3363429228036450.323198761074199
0.376924896224722A A A LNCV6_130762_PI430048170 mRNA
ACTGAGGGAGACAGGAGGAATACCAGGTTATTCATGGAATAAAGTCTTTCCATCTTTAAA NM_006240RefSeq chrX
+ 18690925 18827916 PPEF1 5475 "protein phosphatase, EF-hand calcium binding domain 1, transcript variant 1"
GO:0005515|GO:0050906|GO:0030145|GO:0006470|GO:0007603|GO:0005506|GO:0005509|GO:0022400|GO:0004722|GO:0016056|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142419_PI430048170 0.4060350611304810.9682376235767290.418183649918121
0.4428920222246540.297404268094968A A A 0.40687059378187 0.467754387235997
0.427048920304885A A A LNCV6_142419_PI430048170 mRNA
GTGGCAAAGGTGTCTCAATTTTTCAGTGTTCTTTACTCTCATGATCCTTAGAACAAAAAA NM_173536RefSeq chr4
- 46035769 46124065 GABRG1 2565 "gamma-aminobutyric acid (GABA) A receptor, gamma 1"
GO:0043235|GO:0005230|GO:0030054|GO:0004890|GO:0045211|GO:0034707|GO:0007268|GO:0007214|GO:0050811|GO:0005254 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133944_PI430048170 0.0391271590317262 1.45511194312509 6.37333955548385
6.63574230106351 6.20507448364628 P P P 6.01256669955403 5.96925745732374
5.60885191191834 P P P LNCV6_133944_PI430048170 mRNA
AGTGGGCCTGGAAGCCATTCTTACTTTTCAGTCTCTCCCATTCTGTACTGTTTTTTGTTT NM_004536 RefSeq
chr5_KI270897v1_alt - 626937 654414 NAIP 4671 "NLR family, apoptosis inhibitory protein, transcript variant 1"
GO:0005515|GO:0004842|GO:0043066|GO:0016567|GO:0005634|GO:0009966|GO:0005524|GO:0046872|GO:0007399|GO:0016323|GO:0043524|GO:0005737|GO:0006954|GO:0045087|GO:0005876|GO:0090307|GO:0043154|GO:0043027|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95931_PI430048170 0.4956173120329370.7866097018215790.3953271779572930.409456110535621
0.446014260375705 A A A 0.3290697346712831.3352601876545 0.392805566508174 A A A
LNCV6_95931_PI430048170 mRNA
TCCTTGACGTGATCCGGGCAGAGAACGACAGGGACATTTACCTGGTGTTTGAGTTTATGG NM_139021 RefSeq
chr8_KI270816v1_alt + 193383 199510 MAPK15 225689 mitogen-activated protein kinase 15
GO:0017124|GO:0045732|GO:0005576|GO:0005634|GO:0000122|GO:0005524|GO:0005622|GO:0046777|GO:0000165|GO:0001934|GO:0031398|GO:0008156|GO:0032355|GO:0004707 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128097_PI430048170 0.0196849608430983 0.4056869907992514.31033769672732
4.419075671599 4.31214611556918 P P P 5.97561043146996 5.30314454376459 5.590779945243
P P P LNCV6_128097_PI430048170 mRNA
GAGGTGCAAACCTTCTGAATATAGCTTTCATTTTGGACCAAACAATTTGTTATGGCAATA NM_019072 RefSeq chr5
- 65665927 65722114 SGTB 54557 "small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143422_PI430048170 0.1272698228824660.9403638930388990.252647934581857
0.2692500232893320.311262026137659 A A A 0.4370144443744270.348631909985291
0.311373003541639 A A A LNCV6_143422_PI430048170 mRNA
CTGCCATCAGGGTGGATATATTTCAAGCTTTCTTCTGGTCATTTCGGAGCTGAAACCTAG NM_001012277 RefSeq
chr1 + 12916646 12920480 PRAMEF7 NA PRAME family member 7 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_141696_PI430048170 0.0201761610184606 0.2308749096566172.90127384408512
2.67456445075875 3.88519981372747 A A P 5.15382276178468 5.40015175888381
5.52931596694219 P P P LNCV6_141696_PI430048170 mRNA
CAGGCTTGTATGATCTATTCCTTACCACAAAAGAAGTAGACAATTGCCACTTTTATTTCT NM_199421 RefSeq chr14
+ 55027125 55049488 SOCS4 122809 "suppressor of cytokine signaling 4, transcript variant 1"
GO:0035556|GO:0005737|GO:0016567|GO:0007175|GO:0019221|GO:0032436|GO:0004860|GO:0046426|GO:0040008. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143583_PI430048170 0.19361649061112 1.09860304287849 0.569135397214132
0.8036837486698810.630401588254011 A A A 0.4527317735718360.562477551629232
0.587828691254012 A A A LNCV6_143583_PI430048170 mRNA
CTCATGTGTACCAAAGTAGAAAACCAAATCACAGAGAAATAAAAACATGCTTCAGAGAGA NM_018245 RefSeq chr10
- 49734640 49762379 OGDHL 55753 "oxoglutarate dehydrogenase-like, transcript variant 1"
GO:0005739|GO:0005515|GO:0006099|GO:0005759|GO:0045252|GO:0030976|GO:0004591|GO:0046872|GO:0006096|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91486_PI430048170 0.0328577244273329 0.9130156568637743.948083415236
4.01455317383687 3.91725399346172 P P P 4.11386340983725 4.03316894737114
4.12667419055434 P P P LNCV6_91486_PI430048170 mRNA
ACAAGTACCTCCCAGGTTACTACAGTGCAGGGCTGGCGTTAAGATCATCTTCCGGGTGGC NM_015527 RefSeq chr16
- 30357100 30370201 TBC1D10B 26000 "TBC1 domain family, member 10B"
GO:0005515|GO:0032313|GO:0005737|GO:0005886|GO:0042147|GO:0032851|GO:0005097 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_138949_PI430048170 0.4416966699211691.33977371705915 1.40975397436618
0.3270567993162950.395718537304021A A A 0.4761395329836690.335873775738792
0.319875758219314A A A LNCV6_138949_PI430048170 mRNA
GTTCCACGTGTTTTATTCCTGTATGTTGTCCAATTGTTGACAGTTCTGAAGAATTCTAAT NM_000222RefSeq chr4 +
54657927 54740715 KIT 3815 "v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog,
transcript variant 1"
GO:0005515|GO:0008360|GO:0019221|GO:0007286|GO:0007283|GO:0002020|GO:0005615|GO:0042803|GO:0035
234|GO:0043069|GO:0043552|GO:0007173|GO:0042127|GO:0031274|GO:0002327|GO:0038162|GO:0023014|GO:0
002320|GO:0043303|GO:0030335|GO:0006687|GO:0031532|GO:0032762|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140125_PI430048170 0.6262509508462891.01117359843514 0.343008815752753
0.3424760474263260.417992176754286A A A 0.3616862114094760.321918092167069
0.372604658083707A A A LNCV6_140125_PI430048170 mRNA
ATTTGAGCAGAACAAGATGGGATTGCAGATGTGCTTTAGGAGGACTTGCCTAGCAGATGT NM_181449RefSeq chr17
- 74609882 74623758 CD300E 342510 CD300e molecule
GO:0005886|GO:0045087|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99472_PI430048170 0.7264403087057681.13255939097538 1.39455474976522 0.269040190301796
1.33356398892521 A A A 0.3608332049843380.5234095659587911.53060674106089 A A A
LNCV6_99472_PI430048170 mRNA
CATTTTGGAACACATCCAGGAAAAGATAACTTTCGACACACCTGTAGACGTTCGCCAGGT NM_014682RefSeq chr8
- 52110831 52409879 ST18 9705 "suppression of tumorigenicity 18, zinc finger"
GO:0006355|GO:0003700|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136222_PI430048170 0.00212483931139262 0.7081995429879927.31005089210588
7.31427175014135 7.17183947600825 P P P 7.8654622310836 7.70025936998899
7.72263177915168 P P P LNCV6_136222_PI430048170 mRNA
GCAGCAACAGCAAATCACGACCACTGATAGATGTCTATTCTTGTTGGAGACATGGGATGA NM_000698RefSeq
chr10_GL383546v1_alt + 215006 286950 ALOX5 240 "arachidonate 5-lipoxygenase, transcript variant 1"
GO:0005515|GO:0019369|GO:0019370|GO:0031965|GO:0005506|GO:0019372|GO:0044281|GO:0005635|GO:0005
615|GO:0006691|GO:0016363|GO:0005829|GO:0004051|GO:0002540|GO:0005641|GO:2001300|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63860_PI430048170 0.4918684011326880.9059052119816790.3266316072725220.30750290221932
0.267124573877082A A A 0.27284975886683 0.2782405030567030.729395568129103A A A
LNCV6_63860_PI430048170 mRNA
CACAGATCGGAACGGAGGCCTGTGGATTTTAATATAATTGAGGAAGCTCTTATCCGAAGA NM_017831RefSeq chr18
+ 32018481 32073191 RNF125 54941 "ring finger protein 125, E3 ubiquitin protein ligase"
GO:0004842|GO:0016567|GO:0045087|GO:0016874|GO:0008270|GO:0032480 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_125571_PI430048170 0.0414664957513408 2.0909222904764 6.63952717058925
7.48679212546303 6.98358020841543 P P P 6.16859206367549 5.97405219742864
5.88749968217356 P P P LNCV6_125571_PI430048170 mRNA
ATGTCTCGGGAGATGCAGGATGTAGACCTCGCTGAGGTGAAGCCTTTGGTGGAGAAAGGG NM_001135242
RefSeq chr8 - 133237170 133297304 NDRG1 10397 "N-myc downstream regulated 1, transcript variant
1"
GO:0005515|GO:0008017|GO:0048471|GO:0045576|GO:0005813|GO:0017137|GO:0045296|GO:0043015|GO:0005
886|GO:0030330|GO:0005874|GO:0071456|GO:0005634|GO:0032287|GO:0090232|GO:0005829|GO:0005737|GO:0
005913|GO:0010038|GO:0015630|GO:0055038|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA

LNCV6_97864_PI430048170 0.0198959714984972 1.36724555495279 10.3932395654623
10.2409222617251 10.1141295019722 P P P 9.90280208099129 9.86805553664281
9.62116878345909 P P P LNCV6_97864_PI430048170 mRNA
GCCTGCGAGGAGATGTTACGGCAGCTGGGCCGCCGGCGCCCGGAGCCGGCTGGTGGCGGG NM_198446 RefSeq
chr1 + 37807800 37809454 C1orf122 127687 "chromosome 1 open reading frame 122, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141998_PI430048170 0.746993839995188 0.859158187192467 0.434752577586493
1.41900342195674 1.55148550230571 A A A 1.7894136251392 0.489680450944743
1.69440656944915 A A A LNCV6_141998_PI430048170 mRNA
AGTGGAAATACATGGTGTTTAAGCCAGGAGCAAGCAAAGATGCATGTGGGGTAAGATCCA NM_001256617
RefSeq chr10 - 133278629 133309156 TUBGCP2 10844 "tubulin, gamma complex associated protein 2,
transcript variant 1"
GO:0005515|GO:0005881|GO:0005813|GO:0000922|GO:0006461|GO:0016020|GO:0005815|GO:0007020|GO:0000
086|GO:0005654|GO:0000278|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51690_PI430048170 0.000277393221766716 1.90554705562781 6.44770208817109
6.44450802660927 6.54950704836188 P P P 5.65198987952023 5.48591183037608
5.51005045560114 P P P LNCV6_51690_PI430048170 mRNA
ACATCAAGTCATTTGTGAGTCATCAGATCTTCTCCTGAAAATGGGAGACACAGTAGGGCC NM_005895 RefSeq chr12
- 132768908 132828702 GOLGA3 2802 "golgin A3, transcript variant 1"
GO:0005515|GO:0005215|GO:0005793|GO:0005794|GO:0005730|GO:0006891|GO:0005634|GO:0005829|GO:0000
139|GO:0016020|GO:0032580|GO:0017119|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143888_PI430048170 0.492156300139831 0.878461965837391 0.364852166620388 0.3624109734085
0.415115042053348 A A A 0.365974946360412 0.33238675803399 0.92553502381211 A A A
LNCV6_143888_PI430048170 mRNA
GCTGGAGCTCTCAAACTAAAAGACATTTGTTATTTTGGAAAGAAGAAAGACTCTATTCTC NM_007289 RefSeq chr3
+ 155080289 155183729 MME 4311 "membrane metallo-endopeptidase, transcript variant 2b"
GO:0005515|GO:0030424|GO:0005886|GO:0002003|GO:0045202|GO:0030425|GO:0005737|GO:0006508|GO:0070
062|GO:0042277|GO:0044306|GO:0001822|GO:0071492|GO:0071493|GO:0046449|GO:0019233|GO:0050435|GO:0
008021|GO:0005903|GO:0004175|GO:0071345|GO:0005887|GO:0008270|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141837_PI430048170 0.00912427103286797 1.18924430745517 12.4155840859199
12.395196985258 12.3113340435209 P P P 12.1155170448771 12.1105224053868
12.1477589754317 P P P LNCV6_141837_PI430048170 mRNA
GAGCCTCGGCTCTATGCAGACCTTTTTATTTCTATTAAACGTTTCTGCACTGGCAAAAAA NM_016538 RefSeq chr17
- 81911938 81918182 SIRT7 51547 sirtuin 7
GO:0005515|GO:0070932|GO:0070933|GO:0007072|GO:0009303|GO:0005730|GO:0005634|GO:0070403|GO:0000
122|GO:0005731|GO:0046872|GO:0005737|GO:0003682 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136584_PI430048170 0.227231761491248 0.594293006367239 0.392322735550716
0.445419312300107 0.389671247356453 A A A 0.302191150205737 1.46176488576293
1.44191783395983 A A A LNCV6_136584_PI430048170 mRNA
GTACCTAAACTTAAGTTTGATTGTTTCAGTGTGTACTTGGTAAATATGTCAGTGGCCTTT NM_030972 RefSeq chr19
- 52702812 52729882 ZNF611 81856 "zinc finger protein 611, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136882_PI430048170 0.309605937841964 0.833670768589004 7.58293579447246
7.70033648314378 8.07243473661747 P P P 7.71895497742106 8.14578366665171
8.26886461641207 P P P LNCV6_136882_PI430048170 mRNA
CAAAGAACCATGATACACTGGAATGTTTTTCTCTGGAATCCTCTTTCTACTCTTGTATTA NM_016297 RefSeq chr2
+ 70258098 70281185 PCYOX1 51449 prenylcysteine oxidase 1

GO:0034361|GO:0001735|GO:0005886|GO:0008555|GO:0030329|GO:0030328|GO:0030327|GO:0005764|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131009_PI430048170 0.0896429941350136 1.03758073817994 0.33658393230828 0.3169362461680160.273726614212046A A A 0.2477615484092990.269930092192083 0.250497795796579A A A LNCV6_131009_PI430048170 mRNA
AAAGTTCTTCCAGGGTGATAAGGGTGCAGGTTGATTCAAGGCAACTTAATTCAGATGGAA NM_001001922 RefSeq chr11 - 5777633 5778667 OR52N5 NA "olfactory receptor, family 52, subfamily N, member 5" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93645_PI430048170 0.00668483884061658 1.63107587044723 5.54817888948435 5.19297114089193 5.37864357526324 P P P 4.77441002116737 4.51475381398982 4.72210749206567 P P P LNCV6_93645_PI430048170 mRNA
TTTCGAGCTCATGAAGGGGCAGATAAGAGTAGCCAAGAGGCGGGTCGTGATGGCATCCCT NM_024419RefSeq chr17 + 78378617 78424659 PGS1 9489 "phosphatidylglycerophosphate synthase 1, transcript variant 1"
GO:0005739|GO:0005783|GO:0005509|GO:0005743|GO:0044281|GO:0032049|GO:0006644|GO:0005524|GO:0008444|GO:0006655|GO:0046474|GO:0046339 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134364_PI430048170 0.371968165960575 0.9485768203711050.263287897140992 0.4021638702574550.28426756293612 A A A 0.4956720554439790.390385024632212 0.288644090095631A A A LNCV6_134364_PI430048170 mRNA
CATGATGTTCTGGAAGTAAACCTTGGTTGTCTTTCGTTGGCCAGAGGAATTGAATGTCCG NM_133460RefSeq chr19 - 57921883 57935372 ZNF418 147686 zinc finger protein 418
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144564_PI430048170 0.0396890722057601 1.14915454435683 0.651019535229611 0.76724135002442 0.795101403836933A A A 0.6356440473890770.478520250615988 0.496305706104025A A A LNCV6_144564_PI430048170 mRNA
TGTTCTTTCCTTTCATCCTCAGCAAGTGCTGAGTCTGTGAATAAAGCCACATAACCAGCG NM_000738RefSeq chr11 - 62908678 62921540 CHRM1 1128 "cholinergic receptor, muscarinic 1"
GO:0008284|GO:0030054|GO:0005886|GO:0008283|GO:0007205|GO:0030425|GO:0032279|GO:0040012|GO:0043270|GO:0008144|GO:0045211|GO:0043679|GO:0046541|GO:0014069|GO:0090316|GO:0007274|GO:0007213|GO:0016907|GO:0007399|GO:0007165|GO:0050890|GO:0007186|GO:0016020|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138736_PI430048170 0.1095163090542481.3756986948264 4.12105326429987 4.67730630344544 4.19128996146407 P P P 4.03367568965283 3.72093982250054 3.9033140530982 P P P LNCV6_138736_PI430048170 mRNA
ATTTGAAAGAAATTCTTCTCTTTGTCAATGCTGAGGCATTCTCTCAGCCCCAGCCCCACA NM_178463RefSeq chr20 + 62550452 62570764 MIR1-1HG 128826 "MIR1-1 host gene, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136713_PI430048170 0.0774935934054168 1.04557887115933 0.385275116462005 0.3942485167436870.448891262684361A A A 0.32631879895315 0.327074807232273 0.382225293421005A A A LNCV6_136713_PI430048170 mRNA
GGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATTTTTCTCTACTAGTTATGTTTGATT NM_019617RefSeq chr2 + 68974572 68980980 GKN1 56287 gastrokine 1
GO:0003674|GO:0008284|GO:0007586|GO:0051781|GO:0005576|GO:0005575|GO:0030141|GO:0008083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144750_PI430048170 0.16512846992509 0.96152667985202 0.279081205131126 0.3372363754523140.317855452265818A A A 0.4208229926165350.333542617584803 0.348701870389238A A A LNCV6_144750_PI430048170 mRNA
TTTTTTCCTTTGAGTGCTGTCTCTGGACATCTTCAGCCCAGAATCTTCTCAGGAGCAAAG NM_001145545 RefSeq

chr16 + 27066897 27069166 C16orf82 162083 chromosome 16 open reading frame 82 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_131260_PI430048170 0.0121047702006993 0.64243699769131512.6759040479058
12.6452247857505 12.7689064910944 P P P 13.1480617212299 13.3821699384506
13.4598696930366 P P P LNCV6_131260_PI430048170 mRNA
GACACAAATGTATATTTTGCTAACAGCAATTCCAGGCTCAGTATTGTGACCGCGGAGCCA NM_002819RefSeq chr19
+ 797391 812327 PTBP1 5725 "polypyrimidine tract binding protein 1, transcript variant 1"
GO:0005515|GO:0006397|GO:0008380|GO:0010467|GO:0048025|GO:0003723|GO:0005730|GO:0008187|GO:0000
166|GO:0016020|GO:0000381|GO:0000398|GO:0033119|GO:0005654|GO:0051148|GO:0036002|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52683_PI430048170 0.27303598399823 1.48755807353697 1.63994731261113 1.82039908641499
0.883985027999748A A A 1.61688163360774 0.3904994897203860.41352187364313 A A A
LNCV6_52683_PI430048170 mRNA
TAAAAGCAATGGCCTATCCAAGGACATGGAAGCTCTGCATATGTCAGCCAATTCAGACAT NM_133447RefSeq chr10
+ 86970740 87010203 AGAP11 119385 ankyrin repeat and GTPase domain Arf GTPase activating
protein 11 GO:0043547|GO:0008060|GO:0032312|GO:0008270 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133972_PI430048170 0.6073695663645 0.9860492071448130.277622253140949
0.3098470961823340.387078496076828A A A 0.3768416624074650.338150122137433
0.322013192149064A A A LNCV6_133972_PI430048170 mRNA
GCTGTGATGTGAATCAGACCAAACAATTTATCTGCTTCAAATCCATATTGTAAAGAGGTT NM_207444RefSeq chr15
+ 38696597 38700038 C15orf53 NA chromosome 15 open reading frame 53 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_128182_PI430048170 0.5282298665908881.25419558588993 1.35075860580447
0.3763424364948670.359638110570578A A A 0.4425070615762760.46020417167755
0.440268416428398A A A LNCV6_128182_PI430048170 mRNA
GAGTCCCTTCCAAGTGAGATTGTAAATGTAGAATTTTCCACTGTTGGATCTAGATTTTTT NM_020335RefSeq chr1
+ 160400573 160428678 VANGL2 NA VANGL planar cell polarity protein 2 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_107040_PI430048170 0.0481004988829197 0.7726197334475415.68847613298012
6.05160593336877 5.88210801188233 P P P 6.14937352826652 6.22451027527066
6.37810751379007 P P P LNCV6_107040_PI430048170 mRNA
GATGTGACAGAAGTCCTTATACTTCAGTTGTTCAGTCAGATTGGACCCTGTAAAAGCTGT NM_001033925 RefSeq
chr10 - 119573465 119597029 TIAL1 7073 "TIA1 cytotoxic granule-associated RNA binding protein-
like 1, transcript variant 2"
GO:0008284|GO:0006357|GO:0010494|GO:0003723|GO:0017145|GO:0006915|GO:0005634|GO:0006952|GO:0005
764|GO:0007281|GO:0005737|GO:0000166|GO:0017091|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138497_PI430048170 0.1764216040373481.0997818666515 0.551953333001668
0.7766841788001930.622163988907048A A A 0.4270023312936020.538511345641406
0.578631388330769A A A LNCV6_138497_PI430048170 mRNA
AGAGAGTGAAGAATGCAGTTAAATACCTGCAAAGCCTTGAGAGGTCTTGAAGCCTCCTCA NM_002987RefSeq chr16
+ 57404766 57416062 CCL17 6361 chemokine (C-C motif) ligand 17
GO:0008009|GO:0005102|GO:0007267|GO:0005576|GO:0007275|GO:0005615|GO:0045662|GO:0006955|GO:0006
954|GO:0006935|GO:0007186|GO:0031729|GO:0060326 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144152_PI430048170 0.3887569007437181.2901302115629 0.504397933286523
1.39947619269735 0.584452337683674A A A 0.3207483537350180.423279292851113
0.779585139417773A A A LNCV6_144152_PI430048170 mRNA
GAGGATAAACTTAAAGGGTCCAAATAACGGTCCGAATACAAAAGGCATTCCTTCAAAAAA NM_001004309 RefSeq

chr15 + 90352244 90361483 ZNF774 NA zinc finger protein 774 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132086_PI430048170 0.000437378768017215 1.17646500931496 0.824783464437771 0.871628279322482 0.847279120824209 A A A 0.645447739120949 0.600900556751797 0.593802805166309 A A A LNCV6_132086_PI430048170 mRNA GGTGCTTTCCTTTGATTTTGGACTTTTTTGTTTTCTCAAGAATAAAGAAGTTGGATGTGG NM_144584 RefSeq chr1 - 108648287 108661526 HENMT1 113802 "HEN1 methyltransferase homolog 1 (Arabidopsis), transcript variant 1" GO:0005515|GO:0010467|GO:0001510|GO:0003723|GO:0034587|GO:0043186|GO:0031047|GO:0008171|GO:0046872|GO:0008173 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_36629_PI430048170 0.0622594191555942 .80025508357166 11.5024705879522 12.6655813795102 12.699786427062 P P P 10.7547635152308 11.1011673471632 10.8197703537483 P P P LNCV6_36629_PI430048170 mRNA GGCTGGAGCGCGGCGGAGGTGAGCCGGCCGCCCGCCCGCAGACGCCCCAGCCTACTGCGC NM_001173464 RefSeq chr12 - 39293227 39443390 KIF21A 55605 "kinesin family member 21A, transcript variant 1" GO:0008017|GO:0005515|GO:0005871|GO:0005737|GO:0008152|GO:0005874|GO:0003777|GO:0016887|GO:0005524|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130560_PI430048170 0.501691336902383 0.92053798907116 5.92267624864895 5.81112607146051 5.89750364499355 P P P 5.99025409846728 6.21133002007736 5.75437209190707 P P P LNCV6_130560_PI430048170 mRNA ATGGGAATTTCATCATGTCCAATTCTGGGGACTATGAGATTCTTTACTGGGACGTGGCTG NM_153265 RefSeq chr11 - 62602218 62612765 EML3 256364 "echinoderm microtubule associated protein like 3, transcript variant 3" GO:0005737|GO:0005874 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135458_PI430048170 0.202589224213871 1.32027374683579 0.575514197044449 1.01426149094319 0.331841206689855 A A A 0.256457358307989 0.286980694253323 0.259752491888731 A A A LNCV6_135458_PI430048170 mRNA GGTAGCGGTAGTGAGTGTATAGAGGCAGGGAAATATATTTATAATAAATTCTATGTCATG NM_000415 RefSeq chr12 + 21372867 21379980 IAPP 3375 islet amyloid polypeptide GO:0005102|GO:0007267|GO:0006915|GO:0005576|GO:0005615|GO:0045779|GO:0019233|GO:0042802|GO:0007165|GO:0005179|GO:0031018|GO:0043025|GO:0042755|GO:0045596 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139931_PI430048170 0.80269124310538 0.968223145071686 7.77083510128743 7.73879868060603 7.84111687253378 P P P 7.86452211519179 7.58293579447246 8.01250517058119 P P P LNCV6_139931_PI430048170 mRNA AAACAGCAACCCTGCCTACCGTTTTGATGACCTTTTTCCATATTAAACAAGTTGAGAACA NM_152293 RefSeq chr4 + 7043428 7057950 TADA2B 93624 transcriptional adaptor 2B GO:0006355|GO:0030914|GO:0003682|GO:0006325|GO:0008270|GO:0003677|GO:0006351|GO:0070461 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139300_PI430048170 0.268882278491941 .19582948639203 0.316496967775133 0.829701833295724 0.403511150907531 A A A 0.285130443774836 0.257264144048666 0.28690318222448 A A A LNCV6_139300_PI430048170 mRNA GTTTTGCAGAGACAAAAATCCATGAGTGAATAGCTATCCTAAGTCCATATTTTGATGCAT NM_021957 RefSeq chr12 - 21536188 21604847 GYS2 2998 glycogen synthase 2 (liver) GO:0005975|GO:0005978|GO:0043265|GO:0044281|GO:0006091|GO:0004373|GO:0042803|GO:0005829|GO:0009749|GO:0005737|GO:0009405|GO:0006006|GO:0030864|GO:0005856|GO:0005938 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133374_PI430048170 0.801719547318071 1.07700865871047 2.37192569262354 0.315232335396771 2.92162474864226 A A P 2.26447352752343 1.78626785001181 2.24569553312485 A A A LNCV6_133374_PI430048170 mRNA

GAACTTTGCTATTCATGTGAGCCAGACATAAAGTGCCGTACCTTTATTGCTTCCAAAAAA NM_006851 RefSeq chr12 + 75480732 75501936 GLIPR1 11010 GLI pathogenesis-related 1 GO:0016020|GO:0005886|GO:0005576|GO:0044281|GO:0016021|GO:0044255 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132341_PI430048170 0.0925587054782744 0.5630874741441211.95193145695129 2.33323164784847 1.27975534933878 A A A 2.58429995121031 2.89605066382872 2.74225745657742 A P P LNCV6_132341_PI430048170 mRNA
ATGGGTTTGTGGAAGGTTGTGGTGTCAGCAAAATATATGATAGAATAAAGAGTTTTGTAC NM_004290 RefSeq chr5 + 141968885 141990291 RNF14 9604 "ring finger protein 14, transcript variant 1" GO:0005515|GO:0006355|GO:0016567|GO:0006357|GO:0016874|GO:0003713|GO:0060765|GO:0005634|GO:0050681|GO:0006351|GO:0007165|GO:0005737|GO:0019787|GO:0008270|GO:0045893|GO:0032355|GO:0030521 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142197_PI430048170 0.00507756248708414 4.03258771676763 3.85257902886004 4.36411258751605 4.20103378956706 P P P 2.58031575903176 1.69894468162957 2.00813253012278 A A A LNCV6_142197_PI430048170 mRNA
ACAACCAGAGGTCTCATCTCTGAACTTTCTTGCGTACTGATTACATGAGTCTTTGGAGTC NM_001105248 RefSeq chr16 + 19410734 19499112 TMC5 79838 "transmembrane channel-like 5, transcript variant 1" GO:0016021|GO:0070062|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142642_PI430048170 0.0477960526151831 2.87496471614462 1.34708506022749 2.03606855488152 2.60456866716148 A A A 0.7314789927089370.579475931445933 0.347447053017849A A A LNCV6_142642_PI430048170 mRNA
TACCATCTGTATAAAAACACCTTGGGGGCAGGCAGGGGCATTTAAAAATGTAGGACCTAT NM_001080425 RefSeq chrX + 103215091 103217200 BEX4 56271 "brain expressed, X-linked 4, transcript variant 2" GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144083_PI430048170 0.8104549011035681.02321990857383 9.2158485219184 9.19661437944138 9.45187710534706 P P P 9.00019967170643 9.30810076098402 9.43679585302015 P P P LNCV6_144083_PI430048170 mRNA
TTCTGAGGAAGTCCGCCTTCGTTCATTTACTACTACAATCCACAAAGTAAATAGCATGGT NM_002358 RefSeq chr4 - 120059423 120066858 MAD2L1 4085 MAD2 mitotic arrest deficient-like 1 (yeast) GO:0005515|GO:0072686|GO:0007094|GO:0048471|GO:0043066|GO:0007093|GO:0042177|GO:0060564|GO:0005634|GO:0090267|GO:0051436|GO:0031145|GO:0051439|GO:0042803|GO:0042802|GO:0005829|GO:0000070|GO:0000922|GO:0045930|GO:0005643|GO:0000777|GO:0000776|GO:0000278|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130621_PI430048170 0.6614570039614241.02742299230795 0.273725540179879 0.2850382488142330.488191917406704A A A 0.3350230361920890.288731468629336 0.315986592857685A A A LNCV6_130621_PI430048170 mRNA
CTTAAAGTGTGCTTCCAACAGGAAGGTCAGTGATAAATTTTCAAAAGCATAACCTTCAAT NM_174900 RefSeq chr4 + 187995770 188005049 ZFP42 132625 "ZFP42 zinc finger protein, transcript variant 1" GO:2000653|GO:0006355|GO:0003700|GO:0007286|GO:0005634|GO:0001701|GO:0006351|GO:0046872|GO:0043565|GO:0008585|GO:0043234|GO:0005737|GO:0007126|GO:0008584 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129936_PI430048170 0.0137498620630024 0.5238383875478778.28333310411725 7.73336428396643 7.93641376407143 P P P 8.77474934482004 9.05188362719039 8.96542943422513 P P P LNCV6_129936_PI430048170 mRNA
TGTGTCCAGCAGGGTCAGGAAGCAGGATGGAAAGATGCACTCAGACTGTTAATTTATTAA NM_003045 RefSeq chr13 - 29509413 29595688 SLC7A1 6541 "solute carrier family 7 (cationic amino acid transporter, y+ system), member 1" GO:0016020|GO:0005886|GO:0005887|GO:0015181|GO:0006865|GO:0006810|GO:0015809|GO:0055085|GO:0003333|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137315_PI430048170 0.00172160478126897 1.85231125469076 8.97284598963562
9.11346844468942 9.13509334827699 P P P 8.21541133420962 8.30389457658631
8.02559242174959 P P P LNCV6_137315_PI430048170 mRNA
AGACTCAGATCCCAATAAAGTGCTGTTGCAGCTATGATGCTAGGTGGTTTCTAAGCACAG NM_020524RefSeq chr1
- 154944082 154956091 PBXIP1 57326 pre-B-cell leukemia homeobox interacting protein 1
GO:0005515|GO:0003714|GO:0005874|GO:0007275|GO:0005634|GO:0045892|GO:0030154|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144100_PI430048170 0.169059262419839 1.08225551821589 7.53392771351095
7.61707608156323 7.64890052043379 P P P 7.39468319073114 7.47108406245313
7.58785488295464 P P P LNCV6_144100_PI430048170 mRNA
TGCCTATTTTGTGCGTAGTCCCTGCAAGGTGCTCTCTGAATAATAAAGTTAACAAACTGG NM_203298RefSeq chr10
+ 73782049 73783648 CHCHD1 118487 coiled-coil-helix-coiled-coil-helix domain containing 1
GO:0070124|GO:0005739|GO:0005515|GO:0070125|GO:0070126|GO:0005737|GO:0032543|GO:0006996|GO:0005
743|GO:0005730|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128888_PI430048170 0.00068622274553135 0.175931689442116 3.57180610880369
3.09952789099167 2.9939056755368 P P P 5.55809871780831 5.94713580111016
5.72185839805069 P P P LNCV6_128888_PI430048170 mRNA
TATAATACTCCTGCCTGAGAATAGAGACAGAGTGGTGGTGGGGAGAGTGAAGAAAGAGAT NM_145865RefSeq
chr16 + 21233694 21252429 ANKS4B 257629 ankyrin repeat and sterile alpha motif domain containing
4B GO:0034976|GO:0005886|GO:0005789 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139650_PI430048170 0.000313899601470636 0.12050617244021 1.99241580944357
2.28289992119579 2.17565201888774 A A A 4.93384610753936 5.18221926598475
5.46010908903575 P P P LNCV6_139650_PI430048170 mRNA
CATGGTTCTCTGATTATGTCCATGCTGTGTCCAAGGAGGAGTAGGTACATACAATCAGCA NM_001981RefSeq chr1
- 51354262 51519323 EPS15 2060 "epidermal growth factor receptor pathway substrate 15, transcript
variant 1"
GO:0005515|GO:0060170|GO:0017124|GO:0005886|GO:0008283|GO:0030122|GO:0032456|GO:0005509|GO:0042
059|GO:0015031|GO:0006895|GO:0043231|GO:0042802|GO:0005829|GO:0006897|GO:0016050|GO:0005737|GO:0
005905|GO:0007173|GO:0016020|GO:0031901|GO:0048268|GO:0031593 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_145531_PI430048170 0.321206458848576 1.31413644507213 4.98822628374915
4.70731725420076 5.61291114491255 P P P 4.56386181167351 4.72598476565334
4.96145934127361 P P P LNCV6_145531_PI430048170 mRNA
TACAAGATTGATTCTTGGGAGAATGCTGAGGACTTTCTTGAGAAGCTCGCTTTCCGGACT NM_013285RefSeq chr1
- 37566811 37595985 GNL2 29889 guanine nucleotide binding protein-like 2 (nucleolar)
GO:0008150|GO:0016020|GO:0042254|GO:0008152|GO:0005730|GO:0003924|GO:0005634|GO:0005525 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143512_PI430048170 0.000115427489509082 0.352416113756114 8.27980052919779
8.10502350641015 8.04944980240042 P P P 9.510698442548 9.68338167831635
9.75356773998319 P P P LNCV6_143512_PI430048170 mRNA
GCTCAGTTTTGCTTGCATTCCTTGAGAATGTATTTATCTGAAGATCAAAACAAACAATCC NM_052932RefSeq chr11
- 102396324 102453044 TMEM123 114908 transmembrane protein 123
GO:0004872|GO:0016021|GO:0070267|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136790_PI430048170 0.730580808002604 0.988269713628454 0.397210249258749
0.369278113684762 0.248135914672284 A A A 0.336702575090496 0.375754923340168
0.357284206181778 A A A LNCV6_136790_PI430048170 mRNA
CTTTCACTACAGCACAGATTTCACCTCTGTCTTGAATAAAGGTCCCACTTTGAAGTCAAA NM_002289RefSeq chr12
- 48567683 48570046 LALBA 3906 "lactalbumin, alpha-"
GO:0005989|GO:0007165|GO:0005509|GO:0007267|GO:0006915|GO:0004461|GO:0005615|GO:0042742 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131426_PI430048170 0.0245148300572094 1.90883060373706 10.1310923139382
10.0082167311033 10.0842270744975 P P P 8.98192355932369 9.4523016861302
8.93531957720094 P P P LNCV6_131426_PI430048170 mRNA
ATCTATGATGAAGTGGTGAAGCTGCTCAACAAAGTGTGGAAGACGGACTAAGCCTAGAGA NM_005984 RefSeq
chr22 - 19175574 19178863 SLC25A1 6576 "solute carrier family 25 (mitochondrial carrier; citrate
transporter), member 1, transcript variant 1"
GO:0005975|GO:0005743|GO:0006094|GO:0005634|GO:0035338|GO:0044281|GO:0055085|GO:0015746|GO:0015
137|GO:0009405|GO:0019432|GO:0006006|GO:0016021|GO:0044255|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130041_PI430048170 0.0505803108075859 0.8364413745390435.34732236127399
5.51932603350719 5.59497305504281 P P P 5.72760139313588 5.69129267195113
5.82350523959406 P P P LNCV6_130041_PI430048170 mRNA
CCCATTTCAATCATGCAGATGGTTTCTTTTTGTAAAGAGTTCCGTTTGCCTTTCAATTTT NM_152443 RefSeq chr14 +
67701885 67734451 RDH12 145226 retinol dehydrogenase 12 (all-trans/9-cis/11-cis)
GO:0005622|GO:0005515|GO:0007603|GO:0042572|GO:0045494|GO:0004745|GO:0007601|GO:0001523|GO:0060
342|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144686_PI430048170 0.0128384965884873 0.7507141852623648.89277072574227
8.84980066054245 8.6530019583557 P P P 9.31001107887546 9.21168075535756
9.11974989687791 P P P LNCV6_144686_PI430048170 mRNA
CCGGCCACTGTGTGATGGCATCTTGTGTTTTTGATATGATAATATAAAGTCTGAAAATTT NM_001080514 RefSeq
chr8 + 144266557 144268483 SCX642658 scleraxis basic helix-loop-helix transcription factor
GO:0071773|GO:0008284|GO:0048706|GO:0071560|GO:0005634|GO:0003188|GO:0035914|GO:0030154|GO:0035
989|GO:0060008|GO:0001894|GO:0002062|GO:0035990|GO:0045944|GO:0030199|GO:0035993|GO:0035992|GO:0
005667|GO:0043066|GO:0001707|GO:0046982|GO:2000543|GO:0043425|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132959_PI430048170 0.9608455787989111.00852496038006 9.92684632812589
10.2534686047128 9.87597534826311 P P P 10.1677674239255 10.0035523452374
9.86171661610767 P P P LNCV6_132959_PI430048170 mRNA
TGGTGTGTAAGGGGGAAAGGGTCTTTCCTGGTTTTATTTAAATAAAGTAGTTTATGTAAC NM_030645 RefSeq chr1
- 248810451 248825955 SH3BP5L 80851 SH3-binding domain protein 5-like NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_136172_PI430048170 0.0605752024039916 1.27362022551002 9.33644560010082
9.34861316183811 9.64490801184004 P P P 9.09383884465591 9.03185983189747
9.17547270465141 P P P LNCV6_136172_PI430048170 mRNA
TTAGAGGATGCTTCTCAATGCAAGAAGTTAAGAAGCTCTTTCGAATCAAGTTGTCCCCAA NM_001301733 RefSeq
chr1 + 234373700 234384049 COA6 388753 "cytochrome c oxidase assembly factor 6, transcript
variant 3" GO:0005739|GO:0008150|GO:0004129 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_120422_PI430048170 0.486470984480134 1.14144148200664 5.02161119855413
4.74058509991062 4.90558941943584 P P P 4.10723367804259 4.94097997567353
4.91579709607654 P P P LNCV6_120422_PI430048170 mRNA
ACTGGATCTATCACAGAAATGTTTGGAGAATTCCGAACTGGGAAGACCCAGATCTGTCAT NM_133487 RefSeq
chr15 + 40695128 40732158 RAD51 5888 "RAD51 recombinase, transcript variant 2"
GO:0005515|GO:0000793|GO:0048471|GO:0005634|GO:0010569|GO:0042802|GO:0006302|GO:0005739|GO:0005
737|GO:0003690|GO:0003697|GO:0000724|GO:0005759|GO:0051260|GO:0007131|GO:0043142|GO:0000794|GO:0
005815|GO:0070182|GO:0005730|GO:0006310|GO:0000800|GO:0000228|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_109490_PI430048170 0.00537098520827547 0.297381725017168 7.69423029985793

7.20231437436005 7.26398790370411 P P P 9.12725696999439 9.10440725508319
9.22608058370042 P P P LNCV6_109490_PI430048170 mRNA
TGGTGGAGAGGATTATCCCACACCCCCTCTACAGTGCCCAGAATCATGACTACGACGTCG NM_001288751 RefSeq
chr11 - 113687545 113706373 TMPRSS5 80975 "transmembrane protease, serine 5, transcript variant
4" GO:0005886|GO:0004252|GO:0043025|GO:0006508|GO:0008233|GO:0016021|GO:0006898|GO:0005044 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144569_PI430048170 0.00787620510222591 0.575615485219078 8.26925792647196
8.09334220333778 8.49719126531815 P P P 8.91056333633978 9.04993211446008
9.29219699267907 P P P LNCV6_144569_PI430048170 mRNA
GTTCTGAGTACTGTTAATATCTGGAAAGTATCTTGAGATATCAGTGGAAAGCTAAACAGT NM_001005386 RefSeq
chr2 + 65227694 65271256 ACTR2 10097 "ARP2 actin-related protein 2 homolog (yeast), transcript
variant 1"
GO:0034314|GO:0005885|GO:0006928|GO:0042995|GO:0015629|GO:0016344|GO:0005829|GO:0005737|GO:0051
015|GO:0007411|GO:0016482|GO:0070062|GO:0008356|GO:0033206|GO:0048013|GO:0030478|GO:0005524|GO:0
051653|GO:0042384|GO:0007163|GO:0016020|GO:0045087|GO:0005200|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140698_PI430048170 0.305119616765862 1.03367133935812 0.308914037190609
0.254931539371983 0.374441371145084 A A A 0.275101097817513 0.24625771886508
0.275883983228022 A A A LNCV6_140698_PI430048170 mRNA
CAGTGCTCTGCTTTTAGTCACGTGTATTTTCATTACCACTCGTAAAAAGGTATCTTTTTT NM_000055 RefSeq chr3
- 165772903 165837465 BCHE 590 butyrylcholinesterase
GO:0033265|GO:0003990|GO:0008285|GO:0042493|GO:0004104|GO:0072562|GO:0051384|GO:0005576|GO:0043
279|GO:0003824|GO:0014016|GO:0019695|GO:0042802|GO:0051593|GO:0001540|GO:0016020|GO:0050805|GO:0
005641|GO:0050783|GO:0005788|GO:0007612|GO:0019899|GO:0044267 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137307_PI430048170 0.528006518750433 1.01901521112898 0.381489377969851
0.379645357922384 0.276627539489486 A A A 0.305954319141216 0.327056214702163
0.325605239434168 A A A LNCV6_137307_PI430048170 mRNA
ATTTTTCCAATTCAGTTCTGGAGATCGTAGAGAATGCTGTTGTGCTGACCGTGGCATCCT NM_182658 RefSeq
chr20 + 33055330 33073637 BPIFB3 359710 "BPI fold containing family B, member 3"
GO:0005737|GO:0045087|GO:0005576|GO:0008289 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130965_PI430048170 0.0606207416499669 0.746623217338971 4.54159640484945
4.16791411348792 4.13331061548506 P P P 4.84563021554916 4.59475524539413
4.69242524518282 P P P LNCV6_130965_PI430048170 mRNA
GATGCCCTTCCTCTTTGATCTTTAACCCCAAGAAGCAACAGCCAGCTAATGCTTTATTAA NM_181721 RefSeq
chr11 + 118971706 118981285 FOXR1 283150 forkhead box R1
GO:0043565|GO:0006366|GO:0006357|GO:0000981|GO:0005634 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_133413_PI430048170 0.391064626367738 0.540865691316886 0.424421401383922
0.446431107459648 0.326669013939767 A A A 0.418479807407804 0.480299422281497
2.19781853759356 A A A LNCV6_133413_PI430048170 mRNA
TTCCCAGCACATCCTTCAAGGCGTGTGTGTCTCTATAATACACAAGAACTAAATAAAAAT NM_001037497 RefSeq
chr6 - 50018842 50021981 DEFB110 NA "defensin, beta 110, transcript variant 1" NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_143473_PI430048170 0.00071793773469576 0.536994583977263 8.79018795303541
9.01807083593825 8.92240218994806 P P P 9.70172416206693 9.7828979045582
9.9362307618407 P P P LNCV6_143473_PI430048170 mRNA
AGCACGTTTCCACCAGCTGTATTCAACACTACAATGCATTTTTTAAACTATATTTGCATC NM_014938 RefSeq

chr12 + 122078727 122147347 MLXIP 22877 MLX interacting protein
GO:0003700|GO:0006357|GO:0046983|GO:1900402|GO:0005741|GO:0005634|GO:0003677|GO:0006351|GO:0006
913 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_43658_PI430048170 0.263951530520453 1.15370732641129 6.97936141713058
6.59888521296533 6.85236887157057 P P P 6.39656499592731 6.62854092680117
6.78595704798636 P P P LNCV6_43658_PI430048170 mRNA
AAGAAAGAAATCAATCGAGTTTTATACTCCCTGGCAAAGAAGGGCAAGCTACAGAAAGAG NM_001193495
RefSeq chr1 - 154582057 154606300 ADAR 103 "adenosine deaminase, RNA-specific, transcript
variant 5"
GO:0005515|GO:0010467|GO:0003726|GO:1900369|GO:0019221|GO:0035455|GO:0005634|GO:0006606|GO:0046
872|GO:0006382|GO:0051607|GO:0005737|GO:0060337|GO:0044530|GO:0060339|GO:0002244|GO:0031054|GO:0
006611|GO:0035280|GO:0045070|GO:0045071|GO:0006397|GO:0043066|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144865_PI430048170 0.00771495895678149 0.342380350838862 4.91551978534781
4.78213410173808 4.94153572119278 P P P 6.09063194339291 6.47451167513596
6.6608937575146 P P P LNCV6_144865_PI430048170 mRNA
CCACATTAGAAAGCATTCAATGTCAGTCCTGTTTTAATGGAATATCTGACTATTCAATGG NM_152360 RefSeq
chr19 - 37738301 37779590 ZNF573 126231 "zinc finger protein 573, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_136387_PI430048170 0.00711208996767947 0.321665949116159 5.87245289590514
5.79142604512902 6.3024832307343 P P P 7.58675761391447 7.70060478630311
7.63969475111217 P P P LNCV6_136387_PI430048170 mRNA
GTTCATATTGCATGTTTATTTTGGACAGTCTTTTGTTAAGCATGGTGCTTGTACTGGTTT NM_004124 RefSeq chr14
- 54474490 54489026 GMFB 2764 "glia maturation factor, beta"
GO:0034316|GO:0071933|GO:0003779|GO:0043085|GO:0007399|GO:0005622|GO:0007165|GO:0004860|GO:0006
468|GO:0007626|GO:0004871|GO:0006469|GO:0007612|GO:0008047|GO:0008083 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_59070_PI430048170 0.362045229995151 1.61607829858486 0.336026993888773
1.79060489515649 0.511574807914826 A A A 0.34882029495227 0.312311484067427
0.365955822278469 A A A LNCV6_59070_PI430048170 mRNA
TCTCCAGGGATGTGGATGGAACAACAGCCCTGTTTGCACTGAGTGGGCAGCCAGTCATTG NM_001144996 RefSeq
chr12 - 55684569 55707902 ITGA7 3679 "integrin, alpha 7, transcript variant 1"
GO:0031594|GO:0046982|GO:0005886|GO:0009986|GO:0008360|GO:0048514|GO:0034677|GO:0035987|GO:0046
872|GO:0042383|GO:0005737|GO:0005178|GO:0007517|GO:0007160|GO:0016477|GO:0007229|GO:0007519|GO:0
030198|GO:0043236|GO:0034113|GO:0005927 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_75435_PI430048170 0.122148945235598 0.546668237036186 3.51745304769812
2.48131030944364 3.65985226965627 P A P 4.10879512836807 4.20945258579358
4.2117770916409 P P P LNCV6_75435_PI430048170 mRNA
GTCATGGAACCAGACAAATGATGTCTTCAAAACATGGAGTTCGTATTGATGTCTGAGGTA NM_022483 RefSeq
chr5 - 43444251 43483890 C5orf28 64417 chromosome 5 open reading frame 28 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138990_PI430048170 0.481142390269732 0.952014523534479 11.6302698556773
11.5342891007437 11.6442769144756 P P P 11.5684860591894 11.6240717187852
11.8193801255375 P P P LNCV6_138990_PI430048170 mRNA
CCATGTGGGCTACTCATGATGGGCTTGATTCTTTGGGAATAATAAAATGAAATAATACTT NM_021199 RefSeq
chr15 + 45634739 45691294 SQRDL 58472 "sulfide quinone reductase-like (yeast), transcript variant
1"

GO:0034641|GO:0070224|GO:0048038|GO:0000096|GO:0000098|GO:0005743|GO:0044281|GO:0070813|GO:0070
221 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131471_PI430048170 0.139433510414574 0.656882838969105 4.99693455019481
4.03588837957922 4.45280549397522 P P P 5.2008415988677 5.17120989709238 5.0920668073861
P P P LNCV6_131471_PI430048170 mRNA
CCCCATCCCTGTCTTTACTCCTCACACTTACTGTAAGACATTAGTAACATAATAAATTAA NM_032727 RefSeq chr10
+ 103277162 103290351 INA 9118 "internexin neuronal intermediate filament protein, alpha"
GO:0060052|GO:0031965|GO:0021762|GO:0005883|GO:0005200|GO:0005654|GO:0045111|GO:0005615|GO:0030
154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121207_PI430048170 0.2881272941321260.826500582904841 0.302385951059245
0.3072297790469360.288805191996194 A A A 0.9031282750173 0.405051488363893
0.34816766839371 A A A LNCV6_121207_PI430048170 mRNA
AAGATAGTTTCCTCCATACGTGCAATCTCATCAGCTCAGGGGAAGTACAAGGCATTTTCC NM_030901 RefSeq chr19
- 14880425 14881355 OR7A1 726333 "olfactory receptor, family 7, subfamily A, member 17"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132028_PI430048170 0.0372247632260629 0.5121548363828592.65798413800147
2.47059178667299 3.26133771586809 A A P 3.99235543947623 3.65823643211367
3.73632399323717 P P P LNCV6_132028_PI430048170 mRNA
GAAATGAATGCATTGTGGTAATTTAGAATGGTGATAGCAATACCTTCTTCTTGCATATGG NM_001813 RefSeq chr4
- 103105805 103198409 CENPE 1062 "centromere protein E, 312kDa, transcript variant 1"
GO:0005515|GO:0008017|GO:0005634|GO:0007079|GO:0005829|GO:0019886|GO:0051315|GO:0005737|GO:0051
382|GO:0007059|GO:0045860|GO:0015630|GO:0016887|GO:0007018|GO:0005871|GO:0005694|GO:0005874|GO:0
030496|GO:0007275|GO:0003777|GO:0005524|GO:0000940|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137166_PI430048170 0.0358078403687061 0.8206662253288761 0.9512629772264
11.1888676944696 11.0299258290606 P P P 11.4075952018603 11.3391808201496
11.2863512762648 P P P LNCV6_137166_PI430048170 mRNA
TTTACAATTCCAATCTCTCTATTTCTGGGTGAAGGGTCTTGGTGGTGGGGGTATTGCTAC NM_182919 RefSeq chr19
- 4815923 4831742 TICAM1 148022 toll-like receptor adaptor molecule 1
GO:0005515|GO:0032755|GO:0043496|GO:0034142|GO:0030890|GO:0007249|GO:0045429|GO:0005829|GO:0032
092|GO:0032816|GO:0002756|GO:0051607|GO:0051092|GO:0006954|GO:0002281|GO:0031398|GO:0004871|GO:0
043123|GO:0031663|GO:0034138|GO:0019901|GO:0032760|GO:0002224|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131554_PI430048170 0.1487476738428470.765271636948935 4.52874924862097
4.69397492870799 4.70624550324156 P P P 4.96611083538768 4.7463851502028
5.32190465090247 P P P LNCV6_131554_PI430048170 mRNA
GTGATTGTTTGCAGTATGAAGACACATTTCTACTTATGCAGTATTCTCATGACTGTACTT NM_024089 RefSeq chr13
- 102784280 102799054 KDELC1 79070 KDEL (Lys-Asp-Glu-Leu) containing 1 GO:0005788 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143896_PI430048170 0.3162613330403261.02501707030688 0.301139083079514
0.2849667107796680.37171887440538 A A A 0.2963061942384810.276720908630012
0.279257862024639 A A A LNCV6_143896_PI430048170 mRNA
CCTGCAGTTGATTCAAACAACATGTAGTCACTCAGACATAGCAAATAAAAATGTTTTGGT NM_001007122 RefSeq
chr15 - 82755364 82806070 FSD2 123722 "fibronectin type III and SPRY domain containing 2,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131679_PI430048170 0.0021964592311749 0.6099946848993141 1.3237136395654
11.1404437012937 11.2592847487947 P P P 11.809097595256 11.9886439802355 12.059631416373
P P P LNCV6_131679_PI430048170 mRNA

TTCCTGTTGAGTCTAGTTGGAATTTTTAGTATGAATGTGAGATTTTTCTCCTGCTTGTGA NM_001099415 RefSeq chr7
- 75416780 75486288 POM121C NA POM121 transmembrane nucleoporin C NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_140404_PI430048170 0.33836074968886 1.33775064012976 1.25791961196252
0.3239785725810920.48278358831616 A A A 0.3703852722156290.281121432604154
0.333676278668297 A A A LNCV6_140404_PI430048170 mRNA
TCAAGGAAAAACTTAGAATAAGAACAAAAGCAGCTGTAAAGATCCAGGCCTGGTGGCGGG NM_203424 RefSeq
chr3 + 51861628 51863424 IQCF2 389123 IQ motif containing F2 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143894_PI430048170 0.00511075759460896 2.8353985597018 6.00327742883861
6.52915102035789 5.97129453824158 P P P 5.04021182526466 4.57159399520001
4.36737106564853 P P P LNCV6_143894_PI430048170 mRNA
CTGGGGATTTTTCAACATGAAAGGTACCGAGTCTCCAAATGCTGGTTGTAGGGCCTAAAA NM_001242854 RefSeq
chr11 - 6474682 6481479 ARFIP2 23647 "ADP-ribosylation factor interacting protein 2, transcript
variant 1"
GO:0005515|GO:0030036|GO:0005886|GO:0007264|GO:0019904|GO:0030032|GO:0070273|GO:0006928|GO:0005
525|GO:0032588|GO:0001726|GO:0031529|GO:0048365|GO:0005737|GO:0030742|GO:0005938 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132340_PI430048170 0.41127461575445 0.9779182165497270.370488873660709
0.4014074741533160.336253029051347 A A A 0.4564047316003710.360866533552506
0.386554843073656 A A A LNCV6_132340_PI430048170 mRNA
AGCACTAGTGCTTTACCTCTCATTTTTAATTGAACTGTTAGGAATTGTGTGGGGAAAAAA NM_001184993 RefSeq
chr13 + 24764162 24879920 RNF17 56163 "ring finger protein 17, transcript variant 2"
GO:0005737|GO:0007286|GO:0008270|GO:0007275|GO:0005634|GO:0042803 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_79929_PI430048170 0.0906737846688651 1.33937181687208 0.668829250970497
1.09770528780993 0.654928728698069 A A A 0.2861117220908490.415777412063413
0.492665906124708 A A A LNCV6_79929_PI430048170 mRNA
CAAAACATCAAATCTGTGTGGGAATCGAGCATATGGAAAATCTCTGATACCGCCAGTGCC NM_152765 RefSeq chr8
+ 66493255 66518524 C8orf46 254778 chromosome 8 open reading frame 46 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_134275_PI430048170 0.00506351988822645 1.34850408005518 9.65972420981147
9.85479300073464 9.75625660555075 P P P 9.38574350099378 9.22133750779138
9.37055384600106 P P P LNCV6_134275_PI430048170 mRNA
ATTAAACCAATCTAGACTGAATATTGGTGTGGACATGGGGGGTGGGTGGGAGTAGAAAAT NM_002370 RefSeq chr1
- 53226891 53238610 MAGOH 4116 "mago-nashi homolog, proliferation-associated (Drosophila)"
GO:0005515|GO:0008380|GO:0006369|GO:0010467|GO:0006366|GO:0031124|GO:0005634|GO:0071013|GO:0006
417|GO:0005829|GO:0006406|GO:0016607|GO:0000184|GO:0000381|GO:0000398|GO:0005654|GO:0035145 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130072_PI430048170 0.0444037028055194 1.05980665849052 0.343083560877839
0.3825228376914830.306918255250666 A A A 0.2488095656632660.280656572200825
0.252435521386411 A A A LNCV6_130072_PI430048170 mRNA
ACAGTCTTGACACTTGAGTACTGTATTACTATGTGAGCTCCGTGTTAAATAATTTATGCA NM_176824 RefSeq chr4
- 121824328 121870497 BBS7 55212 "Bardet-Biedl syndrome 7, transcript variant 1"
GO:0005515|GO:0007368|GO:0060170|GO:0001654|GO:0032436|GO:0005634|GO:0015031|GO:0032402|GO:0036
064|GO:0051877|GO:0007224|GO:0005829|GO:0001947|GO:0045444|GO:0060021|GO:0001103|GO:0005813|GO:0
034464|GO:0006996|GO:0006357|GO:0005930|GO:0035058|GO:0048546|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130092_PI430048170 0.5068757772263861.53625782358103 0.296392972895827

1.86236959165288 0.304340137548249 A A A 0.46330751950084 0.392973859957215
0.354135460748181 A A A LNCV6_130092_PI430048170 mRNA
GTCATATGAAAAGAAAAGGTGTAACTGAAGAACACTCAAGCAAGCATAGCTTTTTAAGGA NM_001276367 RefSeq
chr9 - 86220264 86259657 C9orf153 389766 "chromosome 9 open reading frame 153, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131482_PI430048170 0.8805779820411950.9906507321283419.25866295618671
9.15095212160695 9.24844557256704 P P P 9.13914688065952 9.35045927123232
9.20333654131969 P P P LNCV6_131482_PI430048170 mRNA
ATTTTTGGAAGCAGGCGTGGTAGAGTCCTGTAAATGAATGCTCTGGGCTAGATACAGCTT NM_013400 RefSeq chr7
+ 150368789 150374044 REPIN1 29803 "replication initiator 1, transcript variant 1"
GO:0006260|GO:0005811|GO:0031965|GO:2001273|GO:0022626|GO:0005654|GO:0005634|GO:2000191|GO:0005
664|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138168_PI430048170 0.0537956402151015 0.9580785347095010.425284910386899
0.3694123204979810.377318687242474 A A A 0.4424156714092360.467740477872143
0.447724472547781 A A A LNCV6_138168_PI430048170 mRNA
AAAGATGTCACGGGTCACTTTGTAATGTCATATCGTTGCTGTTGATAAATAAAGGAAATG NM_001039580 RefSeq
chr4 - 155342659 155376970 MAP9 79884 microtubule-associated protein 9
GO:0000235|GO:0000910|GO:0007088|GO:0090307 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134785_PI430048170 0.0176991380088521 0.4664432363994073.95612884732948
3.70124222521783 3.22217218743443 P P P 4.54904758558238 4.97653907352515
4.71553750214143 P P P LNCV6_134785_PI430048170 mRNA
TTCCCAGTGGGGTGGACAGTATATCAGATGGTCAGAACAAATAAAGTTCAGTGTCAAATG NM_003637 RefSeq chr1
- 145891207 145910189 ITGA10 8515 "integrin, alpha 10, transcript variant 1"
GO:0008305|GO:0034680|GO:0007160|GO:0005886|GO:0030198|GO:0007596|GO:0007411|GO:0007229|GO:0005
518|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133258_PI430048170 0.0283077167343983 1.60710158271786 3.10115304165211
2.95210123772593 3.37790234900563 P P P 2.50454073479546 2.41877127244986
2.48581454229718 A A P LNCV6_133258_PI430048170 mRNA
TAAAATCTGCAAGTCAGGACAGGTTTTCTTTGGAAGACCCTACCCCTGACATCATCCTCT NM_032133 RefSeq chr17
+ 50508383 50531501 MYCBPAP 84073 MYCBP associated protein
GO:0005515|GO:0005737|GO:0016020|GO:0007268|GO:0007275|GO:0007283|GO:0030154 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141626_PI430048170 0.00591501565813996 0.64337440950346 9.87894967243416
9.6019666932164 9.64041064981928 P P P 10.2629082466865 10.5067003136398
10.2624008765114 P P P LNCV6_141626_PI430048170 mRNA
TGGCCAGACTCGATGTGTACTCTAACTTAAGAAATAAATCAGTAAGGCAGAACAAGAGAA NM_001905 RefSeq chr1
+ 40979298 41012565 CTPS1 1503 "CTP synthase 1, transcript variant 1"
GO:0006241|GO:0015949|GO:0042493|GO:0055086|GO:0044281|GO:0005524|GO:0005829|GO:0006139|GO:0016
020|GO:0042098|GO:0042100|GO:0003883|GO:0044210|GO:0006541 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138680_PI430048170 0.4143895064419610.64620772871897 0.349082523936356
0.35679618164985 0.308707769239393 A A A 0.3423286714088120.354135460748181
1.73270161753826 A A A LNCV6_138680_PI430048170 mRNA
CTCATGTACTCTTTGAGAAACAAGGATGTGAAGAAAGCTTTAATAAAGGTTTGGGGTAGG NM_001004731 RefSeq
chr14 - 21154936 21156025 OR5AU1 NA "olfactory receptor, family 5, subfamily AU, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76998_PI430048170 0.7668753003090020.9847433501651970.5336708195933140.461871817889816
0.300365549787917 A A A 0.3957655079131780.5007050204810140.47372683053386 A A A
LNCV6_76998_PI430048170 mRNA

GTGTCTGCAAACATCCTTATTCCCAACTTAAAGTGCTTTATTGCAGAGAGTTATGGAAAT NM_005865 RefSeq chr6 + 27247722 27256620 PRSS16 10279 "protease, serine, 16 (thymus)" GO:0030163|GO:0006508|GO:0016023|GO:0008236|GO:0005764|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132042_PI430048170 0.6877592871518691.32184353072828 2.48636998125655 0.70345793212351 1.92015010355722 A A A 1.1660600319508 1.77792028899543 1.41199137137438 A A A LNCV6_132042_PI430048170 mRNA
CGGTCCTCACCCATAAATAAACATGAGAAAATTCATAATGGAGAGAACACCTACAAATGT NM_001137608 RefSeq chr4 - 270674 296155 ZNF732 654254 zinc finger protein 732 GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129143_PI430048170 0.3955174924080070.9134717319820260.416583059849826 0.3854719935048730.246329925212308A A A 0.3448602094335880.696378925658234 0.377743831237136A A A LNCV6_129143_PI430048170 mRNA
CAAAGCAGGAGTTCATCCGAGGCCAAGATGTTAATTATTCATACTGCATGACTGAGGATT NM_001101341 RefSeq chr14 - 36473288 36513785 SFTA3 253970 surfactant associated 3 GO:0005737|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126672_PI430048170 0.8017054677760690.9780236301907511.30017859964131 0.5447204582880260.435235110437192A A A 0.9065712437632270.660353650704609 0.953751829799797A A A LNCV6_126672_PI430048170 mRNA
AGTACACCTTTCCTGGATGATATGCAATCGAATGCTATATTATTAAACGCATTTTTCTCC NM_001001557 RefSeq chr8 - 96142329 96160792 GDF6 392255 growth differentiation factor 6 GO:0010862|GO:0006915|GO:0042981|GO:0030509|GO:0032924|GO:0060395|GO:0005125|GO:0005160|GO:0005615|GO:0042803|GO:0045666|GO:0043408|GO:0060389|GO:0048468|GO:0045893|GO:0008083|GO:0040007 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127435_PI430048170 0.45444919480815 1.70887220447723 0.29566927261953 0.3791812112726692.05568092587111 A A A 0.4446068207874180.346220782996816 0.356182337933854A A A LNCV6_127435_PI430048170 mRNA
AACTTTTTAGTAACTCACACGTGCATTCTTTTTTCAACGCTATCCTTAGAGTGAAAGTCA NM_001277115 RefSeq chr7 + 21543214 21901568 DNAH11 8701 "dynein, axonemal, heavy chain 11" GO:0005929|GO:0005737|GO:0030286|GO:0008152|GO:0005874|GO:0003341|GO:0003777|GO:0016887|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137347_PI430048170 0.1883058394943991.03379465619949 0.349373393202831 0.29900696383213 0.384854396179415A A A 0.2922693150219680.285121721815563 0.313135298988212A A A LNCV6_137347_PI430048170 mRNA
GGGTTCCTTTCTAGCTGTCATTTTAGAGAAAAGAATAATTTGGGAAAGGATCCTGTACAA NM_181535 RefSeq chr17 - 40792195 40799959 KRT28 162605 "keratin 28, type I" GO:0005882|GO:0008150|GO:0003674|GO:0005737|GO:0005198|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145698_PI430048170 0.0037402033786112 0.7055550282447049.04341764730286 8.82805479793795 8.92699843945839 P P P 9.46633036833799 9.34152745900474 9.50325616509691 P P P LNCV6_145698_PI430048170 mRNA
CGTTTGAGTACTGTGTTTTTGGTGTTGTCCAAGGAAAATTAAAAACCTGTAGCATGAATA NM_000551 RefSeq chr3 + 10141634 10153670 VHL 7428 "von Hippel-Lindau tumor suppressor, E3 ubiquitin protein ligase, transcript variant 1" GO:0005515|GO:0043066|GO:0004842|GO:0006355|GO:0016567|GO:0008285|GO:0005783|GO:0045597|GO:0050821|GO:0071456|GO:0061418|GO:0005634|GO:0000122|GO:0061428|GO:0005829|GO:0005739|GO:0000902|GO:0016020|GO:0006508|GO:0005654|GO:0045111|GO:0045893|GO:0019899|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_131671_PI430048170 0.5459221357234950.96731215191931 0.46162058029584
0.4568923404578310.255597775674518A A A 0.3947510047318560.490321616374343
0.440725635494605A A A LNCV6_131671_PI430048170 mRNA
TTGTCTTACTCACTTCTGACACCACTGCTGAATCTGCTTATCTACAGTTTGCGAAATAGT NM_001004461 RefSeq
chr11_KI270829v1_alt - 159218 160163 OR10A6NA "olfactory receptor, family 10, subfamily A, member 6
(gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137188_PI430048170 0.6526386455053261.04890908219714 8.88783087688968
8.73226524176414 8.64732908178728 P P P 8.89307507115325 8.72765916926673
8.40930691792124 P P P LNCV6_137188_PI430048170 mRNA
TCTGCTGATGTCCCAGGCTGACAAGATGACGGCGGAAGAGGTGGACCAGATGTTCCAGTT NM_002477RefSeq chr4
+ 677921 682028 MYL5 4636 "myosin, light chain 5, regulatory"
GO:0006937|GO:0005509|GO:0005859|GO:0008307 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136049_PI430048170 0.0149308796377737 0.2828386758327062.67826158449874
1.5768341036191 2.53438994091225 A A A 3.69183488114931 4.18175813609924
4.49759341907833 P P P LNCV6_136049_PI430048170 mRNA
CTCATATTGGGGTTCGACAGGTAAACACAAACTGCTATTTCAGTAGAAAAAGTTATTGTT NM_003474RefSeq chr10
- 126012384 126388558 ADAM12 8038 "ADAM metallopeptidase domain 12, transcript variant 1"
GO:0005515|GO:0017124|GO:0005886|GO:0005576|GO:0007520|GO:0005739|GO:0007173|GO:0006508|GO:0005
654|GO:0008270|GO:0016021|GO:0004222|GO:0007155|GO:0008237 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133987_PI430048170 0.3702323466108770.635041237423065 0.390104510082153
0.4614260549855340.420469107388135A A A 0.2978682335019560.713755339447342
1.79492021022346 A A A LNCV6_133987_PI430048170 mRNA
TGGGTAAATTTTCTGACTTATGTGGCTGTTTTTGACTTCTGTTATAGGATATAAAGGGGA NM_198268RefSeq chr1
+ 113929373 113977869 HIPK1 204851 "homeodomain interacting protein kinase 1, transcript variant 1"
GO:0005515|GO:0008284|GO:0001654|GO:0005634|GO:0061072|GO:0009952|GO:0048596|GO:0007224|GO:0005
737|GO:0030182|GO:0006355|GO:0060235|GO:0072577|GO:0010842|GO:0060216|GO:0060059|GO:0097191|GO:0
010803|GO:0005524|GO:0006351|GO:0045766|GO:0042771|GO:0016607|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129620_PI430048170 0.0190756918143748 0.7383091348053261 0.3319992400168
10.2135291261629 10.2428464235668 P P P 10.5799235331159 10.6608958842682
10.8498735423835 P P P LNCV6_129620_PI430048170 mRNA
CTGCCTAAATAGGTAGCTTAAACTTATGTCAAAATGTCTGCAGCAGTTTGTCAATAAAGT NM_006559RefSeq chr1
+ 32013693 32043881 KHDRBS1 10657 "KH domain containing, RNA binding, signal transduction
associated 1, transcript variant 1"
GO:0005515|GO:0017124|GO:0008283|GO:0003723|GO:0005634|GO:0032403|GO:0042802|GO:0008266|GO:0005
737|GO:0031647|GO:0000086|GO:0008143|GO:0070618|GO:0007050|GO:0045948|GO:0006397|GO:0009967|GO:0
003677|GO:0006351|GO:0007165|GO:0016020|GO:0005070|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135398_PI430048170 0.2080279491008771.01834111393926 0.313874230674671
0.3209156410497490.36032325678292 A A A 0.3180129104937930.307711032595433
0.291033783330227A A A LNCV6_135398_PI430048170 mRNA
CGTCATTATAATTGTACTGGGAAAAGGATTCTTGCAAGAAGCCTTAAAATGAATTCAAGG NM_181756RefSeq chr19
+ 44259913 44275317 ZNF233 353355 "zinc finger protein 233, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141603_PI430048170 0.0141553010125229 0.5456767942867597.96217900918204
7.7942121200288 8.18432079855892 P P P 8.63516771772162 8.74459617118875
9.15565340697901 P P P LNCV6_141603_PI430048170 mRNA

GTGGTTGCCTTTGGGTTTTCTGTACAGATTGTTTTTGTTATTAAATGGAAAAGGCCTGAA NM_004869RefSeq chr18 - 63389191 63422519 VPS4B 9525 vacuolar protein sorting 4 homolog B (S. cerevisiae) GO:0005515|GO:0042623|GO:0006200|GO:0033993|GO:0019058|GO:0031122|GO:0005634|GO:0015031|GO:0005764|GO:0005829|GO:0005737|GO:0016197|GO:0060548|GO:0061024|GO:0016032|GO:0007032|GO:0007033|GO:0016887|GO:0006813|GO:0070062|GO:0005774|GO:0005813|GO:0006997|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72314_PI430048170 0.756292025519991 1.09890175208684 2.60117670403969 1.91445634920029 2.78786739463126 A A A 2.27032366142529 2.55758605073472 2.17796455282426 A A A LNCV6_72314_PI430048170 mRNA
TTTCTGCGACGAGCCCATTGCTATGGAAACCAAAGCGTTAGGCCAGCGGGGATTGAGGCT NM_001304794 RefSeq chr22 - 30661457 30667890 DUSP18150290 "dual specificity phosphatase 18, transcript variant 1" GO:0000188|GO:0005737|GO:0005654|GO:0005634|GO:0008138|GO:0035335|GO:0017017|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141038_PI430048170 0.68316513106353 1.02449774157228 0.271899165721796 0.2855664153413540.479128961816038A A A 0.3378741031772070.292284964412331 0.310767717423915A A A LNCV6_141038_PI430048170 mRNA
CAGGGCTATGTTTGTTTATGATGCTCTGCAAACATTTCATATTGGCCAATAAACAGAAAT NM_001199687 RefSeq chrX - 66595639 66639298 EDA2R 60401 "ectodysplasin A2 receptor, transcript variant 1" GO:0005515|GO:0051092|GO:0005031|GO:0072332|GO:0008544|GO:0005887|GO:0046330|GO:0004872|GO:0016021|GO:0010668|GO:0033209 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127116_PI430048170 0.00501306944240864 0.4550375522807964.81571127283439 4.83803353361526 5.14422846301327 P P P 6.32643287288239 6.04947045936943 5.80688008561878 P P P LNCV6_127116_PI430048170 mRNA
ACTTAGTGTTTTTAATAATATGGTGCCACTGCAGGATTTGGGGGCGGTGGGGAAGAACAA NM_016045RefSeq chr20 - 59033144 59042846 SLMO2 51012 "slowmo homolog 2 (Drosophila), transcript variant 1" GO:0005758|GO:0015914 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130826_PI430048170 0.00853377161643375 0.6752408963591136.50426295803611 6.29640322881118 6.59824008175753 P P P 7.02342392305298 6.92937149176699 7.15321726397751 P P P LNCV6_130826_PI430048170 mRNA
GACTGGTGGAACGAACCTAGGAAATAAAAACTAGCTGCTTTTTAAGTTACACAAGAAAAA NM_014828RefSeq chr14 + 21477175 21499177 TOX4 9878 "TOX high mobility group box family member 4, transcript variant 1" GO:0005515|GO:0006355|GO:0003682|GO:0006338|GO:0005654|GO:0072357|GO:0003677|GO:0000785 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133958_PI430048170 0.0986593346149319 1.75589855609165 2.38209831575437 3.13010209777072 2.73930086907009 A P A 1.57466151877017 1.58757245844982 2.52948140483377 A A P LNCV6_133958_PI430048170 mRNA
AAATGACCAGTGCTGACTCCCAGGCAGACCGTGGTGTTGACCCCACTGGATGTGTGGTAT NM_080823RefSeq chr20 - 63539923 63547504 SRMS 6725 src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites GO:0005515|GO:0030036|GO:0005102|GO:0005524|GO:0030154|GO:0031234|GO:0005737|GO:0016477|GO:0045087|GO:0042127|GO:0004713|GO:0004715|GO:0007169|GO:0038083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129831_PI430048170 0.5147332035837461.08224609563228 3.46494752256081 3.78231769464542 3.72780957147575 P P P 3.31787085067559 3.5124523347792 3.78396941669239 P P P LNCV6_129831_PI430048170 mRNA
GCAAATGTTATTTTGAGCTTCGCAAATACATGATACCGTGCAATAAGCCTTTTTTCCTTA NM_024090RefSeq chr4 - 110049072 110198664 ELOVL6 79071 "ELOVL fatty acid elongase 6, transcript variant 1" GO:0005515|GO:0016747|GO:0005783|GO:0042759|GO:0019367|GO:0019432|GO:0005789|GO:0030176|GO:0044281|GO:0035338|GO:0044255 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_138439_PI430048170 0.5597918760681271.02243014352063 0.444742503368592
0.4618456311629890.433960308166905A A A 0.3363765172512450.502077144496644
0.401375433225112A A A LNCV6_138439_PI430048170 mRNA
AAATGGCATAGGCAGAGATGATACCTAATTCTGCATTTGATTGTCACTTTTTGTACCTGC NM_014143RefSeq chr9
+ 5450502 5470567 CD274 29126 "CD274 molecule, transcript variant 1"
GO:0005515|GO:2001181|GO:0070232|GO:0005886|GO:0032693|GO:0046006|GO:0046007|GO:0031295|GO:0012
505|GO:0007165|GO:0006955|GO:0042102|GO:0016021|GO:0032689|GO:0007166|GO:0009897|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136149_PI430048170 0.83019940175675 1.01429649841187 0.819683713841067
0.8612082237908920.874690489043102A A A 0.6631053269743920.558269348632864
1.19085281415881 A A A LNCV6_136149_PI430048170 mRNA
GGTTATAGCTATACCTTCAGGTCTTTTGTTACTTAGGCAAGGAAAACCACATGTCTGACC NM_024560RefSeq chr12
+ 81078029 81255803 ACSS3 79611 acyl-CoA synthetase short-chain family member 3
GO:0005739|GO:0008152|GO:0003987|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142650_PI430048170 0.2372044306610650.7877030657731931 0.6177069762561
10.6901999811577 10.9772758682998 P P P 10.8461908423238 10.942728181387
11.4729017456378 P P P LNCV6_142650_PI430048170 mRNA
CCTCTCTTTGCCTGTAGGATGTACTGTATGTAGTCATGCACTTTGTATTAATATATTAGANM_001135811 RefSeq
chr12_KI270835v1_alt - 171379 216981 FAM60A 58516 "family with sequence similarity 60, member A,
transcript variant 1" GO:0005515|GO:0030336|GO:0016580 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_142772_PI430048170 0.4856637397174130.9461489983389671 0.9552580650324
11.1673638869327 11.2268354256163 P P P 11.1564303265523 11.1100296367271
11.3272943953973 P P P LNCV6_142772_PI430048170 mRNA
CGACCACCCCCCTTCGGGCTGCTATATATATATTTATTTGTAGGTATTTATATATTGAAA NM_003655RefSeq chr17
- 79833155 79839414 CBX4 8535 chromobox homolog 4
GO:0051219|GO:0035102|GO:0031519|GO:0005515|GO:0043066|GO:0032183|GO:0003727|GO:0044212|GO:0003
714|GO:0016874|GO:0016925|GO:0005634|GO:0035064|GO:0000122|GO:0006351|GO:0016607|GO:0003682|GO:0
005654|GO:0019899|GO:0045892|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99755_PI430048170 0.0772321747169719 2.05175158758246 3.30988753495019
3.73268418150073 4.31894970454112 P P P 2.86832976737871 2.75347524983728
2.80626417588137 P P P LNCV6_99755_PI430048170 mRNA
AAACTGAAGAAGGATTTGATTTTGGGGAGTGACCGCTTGAAAGCCTTCTTGTTGCAGGCT NM_001271466 RefSeq
chr2 + 231206199 231375879 ARMC9 80210 "armadillo repeat containing 9, transcript variant 1"
GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139435_PI430048170 0.0623116537163586 0.8242611890626159.88702765924225
10.0374245507604 10.047682541463 P P P 10.2139754682907 10.432434894798
10.1525173070791 P P P LNCV6_139435_PI430048170 mRNA
CGGTTTCGGTGGTTGAGCGTCCCTTTCTATCAATAAAAGGCCCTTTTCAGGGCCACCCTA NM_021968RefSeq chr6
+ 27824124 27824480 HIST1H4J 8363 "histone cluster 1, H4j"
GO:0005515|GO:0010467|GO:0006325|GO:0005634|GO:0045653|GO:0000723|GO:0000183|GO:0000786|GO:0070
062|GO:0035574|GO:0035575|GO:0046982|GO:0006334|GO:0006335|GO:0005576|GO:0006336|GO:0000228|GO:0
003677|GO:0032776|GO:0034080|GO:0043234|GO:0016020|GO:0045814|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129268_PI430048170 0.0195029531977618 1.28830786049162 13.5800070633848
13.4495234815336 13.4347703141135 P P P 12.9822435204721 13.143387279935
13.2354227920278 P P P LNCV6_129268_PI430048170 mRNA
TGTGAGCACCTCCACTGACAGAGGCGGCCCCTCCCACGGCTCCCAATAAAAATGTGAAAA NM_004542RefSeq
chr19_KI270938v1_alt + 77272 81394 NDUFA3 4696 "NADH dehydrogenase (ubiquinone) 1 alpha

subcomplex, 3, 9kDa"
GO:0022904|GO:0005739|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0016021|GO:0008137|GO:0044237. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145769_PI430048170 0.2738483738752941.23896605936257 1.1595511507427
1.22478037136207 0.891403372851501A A A 0.31236971219539 1.03944316468 0.917965832422276A A A LNCV6_145769_PI430048170 mRNA
AGTCCAGGATTCAGATCTGGTTTCAGAATCGAAGAGCCAGGCACCGGGGACAGTCTGGCA NM_012149RefSeq - - 0 0 --- NA - NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141579_PI430048170 0.000112849932511987 7.83977616612596 3.60846311201888
3.45107335398504 3.25999538615505 P P P 0.5302519835585880.367259131284087
0.524721834665564A A A LNCV6_141579_PI430048170 mRNA
ACTCCTGTGTACTTCACATCACTGAGCACTCATTTAGAAGTGAGGGAGACAGAAGTCTAG NM_001039803 RefSeq chr9 - 87966443 87974780 CDK20 23552 "cyclin-dependent kinase 20, transcript variant 3"
GO:0005515|GO:0005929|GO:0007049|GO:0005737|GO:0051726|GO:0007275|GO:0006468|GO:0005634|GO:0005524|GO:0051301|GO:0004693 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128451_PI430048170 0.0074769260371793 0.56769491936725 10.0928270720615
9.97780933932152 10.2349771164485 P P P 10.7102092042164 10.9062731854026
11.1217174039111 P P P LNCV6_128451_PI430048170 mRNA
GAAAGCTGCATCTGTCTGTATCTTTCTTTTGTAAATGACCTCACATGTAAATTCACCAAA NM_014820RefSeq chr3 - 100363458 100401398 TOMM70A 9868 translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)
GO:0005739|GO:0005515|GO:0016020|GO:0006626|GO:0005742|GO:0016021|GO:0008320|GO:0071806|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136095_PI430048170 7.27728753428425e-05 0.44706582888469210.7372342429254
10.8655506673996 10.900543573878 P P P 11.9021354619812 12.0302903220365
12.0556532874621 P P P LNCV6_136095_PI430048170 mRNA
CAGAATGCGGTGGTGGTGGGGGTCTTTTGTACTGTTGGATTAATAAAATGATTTTAAAAT NM_138300RefSeq chr1 - 154957025 154961782 PYGO2 90780 pygopus family PHD finger 2
GO:0005515|GO:0035034|GO:0001822|GO:0007289|GO:0035065|GO:0030879|GO:0009791|GO:0035563|GO:0001701|GO:0033599|GO:0042393|GO:0048589|GO:0002088|GO:0007420|GO:0003682|GO:0060021|GO:0005654|GO:0008270|GO:0060070|GO:0051569 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128195_PI430048170 0.4939026416163770.917045022765861 11.2701154164399
11.7382157168234 11.2877680665033 P P P 11.4673438510831 11.4933347711612
11.7440902992715 P P P LNCV6_128195_PI430048170 mRNA
CTGTCAAACAAACACCACTTTTCAATGGTTTGCTAGGAGTATTTCTGTATTGAAAGTTTC NM_006861RefSeq chr12 - 120095094 120116839 RAB35 11021 "RAB35, member RAS oncogene family, transcript variant 1"
GO:0005515|GO:0005886|GO:0032456|GO:0003924|GO:0048227|GO:0006886|GO:0031175|GO:0005739|GO:0000910|GO:0008104|GO:0019882|GO:0016197|GO:0032482|GO:0070062|GO:0031253|GO:0042470|GO:0005546|GO:0005525|GO:0045171|GO:0006888|GO:0006184|GO:0005905|GO:0045334|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138166_PI430048170 0.9611136751280040.9988341164990150.482364206498186
0.59835694680792 0.550292273834219A A A 0.3627519009351260.746393033365187
0.502882858593107A A A LNCV6_138166_PI430048170 mRNA
ACATTAAGGGGAGCGCTCAGGAATCAAATATGGCCCTCAGTATGAAATGAGAGTGAATGG NM_003980RefSeq chr6 - 136342280 136550819 MAP7 9053 "microtubule-associated protein 7, transcript variant 4"
GO:0016323|GO:0048471|GO:0005737|GO:0007163|GO:0005198|GO:0005875|GO:0015630|GO:0005874|GO:0005102|GO:0000226|GO:0006970|GO:0072659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144363_PI430048170 0.0045358074604675 0.1823674940581210.445331196756835
0.499388913463895 0.459611900534724A A A 2.5848463590956 3.16510240950075

2.96144398341756 A P P LNCV6_144363_PI430048170 mRNA
AAGCTGTAGTCACTCTTTAAATTGAACTGCTCTAAGATTTGCAGTTTTAGTGAGATCTGA NM_152594 RefSeq chr15
+ 38252850 38357249 SPRED1 161742 "sprouty-related, EVH1 domain containing 1"
GO:0005515|GO:0019901|GO:0019902|GO:0007275|GO:0090311|GO:0010801|GO:0030291|GO:0000188|GO:0005
737|GO:0005901|GO:0010923|GO:0043517|GO:0005654|GO:0005173 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129525_PI430048170 0.0122612168629017 1.17313224084959 13.1663199467999
13.1225950476043 13.0317119703667 P P P 12.9005948308093 12.9201007215573
12.8096955567794 P P P LNCV6_129525_PI430048170 mRNA
GCTGGAAGCACTGGCTCCCTGGTAGGGACAATAAAGGTTTTGGGTCTTTCTGAGAAAAAA NM_001297658 RefSeq
chr11 + 2400487 2403878 TSSC4 10078 "tumor suppressing subtransferable candidate 4, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145078_PI430048170 0.000360107821320989 0.334698793631497 3.06069849647646
2.8824432426402 2.71822958084586 P A A 4.27736539578129 4.50220413331789
4.61874237524022 P P P LNCV6_145078_PI430048170 mRNA
ACAGCAATCATGGATCCTGCCTATCGAGGTGATTCACAATACACTTTCCCATTTCAAAAA NM_001286819 RefSeq
chr8 + 38386440 38409524 LETM2 137994 "leucine zipper-EF-hand containing transmembrane
protein 2, transcript variant 5" GO:0005743|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_139765_PI430048170 0.578071272393534 1.17493679122402 0.29941049077878
1.12278899105235 0.315378650380691 A A A 0.451575823003407 0.390699231559424
0.357673270355321 A A A LNCV6_139765_PI430048170 mRNA
ACTACCTATGCAACACTGTGTATTAGGTTTATCATCCTCATGTATTTTTATGTGACCTGT NM_004967 RefSeq chr4 +
87799549 87812449 IBSP 3381 integrin-binding sialoprotein
GO:0003674|GO:0071363|GO:0016020|GO:0030198|GO:0031988|GO:0005576|GO:0007155|GO:0031214|GO:0005
615|GO:0001649 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102300_PI430048170 0.0370166414642768 0.643406997028995 10.0187482848856
9.51871602840218 9.627250272484 P P P 10.2562413247591 10.4166561006776
10.4426088664911 P P P LNCV6_102300_PI430048170 mRNA
TCAGTATTGATTGACTCTGCTATTGGCAAGACAAAGAAACAATGAATAAAGGAACTGCTT NM_001007027 RefSeq
chr11 - 78100941 78139653 ALG8 79053 "ALG8, alpha-1,3-glucosyltransferase, transcript variant 2"
GO:0006490|GO:0000033|GO:0005789|GO:0042281|GO:0016021|GO:0006487|GO:0006488|GO:0044267|GO:0043
687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127651_PI430048170 0.8224178270766211.02890658250419 4.1124782909074
4.53398147814771 4.44084691464668 P P P 4.0999996858653 4.16271504696664
4.66544081080438 P P P LNCV6_127651_PI430048170 mRNA
CTCCACAAATGCATGAAAGGACAAATTTGCATCTTCTATCAGTATTTAACTTCCTTTTGC NM_012463 RefSeq chr12
+ 123712317 123761754 ATP6V0A2 23545 "ATPase, H+ transporting, lysosomal V0 subunit a2"
GO:0005515|GO:0008286|GO:0070072|GO:0015986|GO:0051701|GO:0001669|GO:0005886|GO:0005765|GO:0055
085|GO:0000220|GO:0006879|GO:0033572|GO:0005737|GO:0006955|GO:0046961|GO:0007035|GO:0030670|GO:0
015991|GO:0051117|GO:0016021|GO:0090382|GO:0005925|GO:0016471|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133386_PI430048170 0.719842495903803 1.16081714204868 1.38868587481756
0.412252033609845 0.301834844241573 A A A 0.943385895792729 0.362529362750106
0.328001695670722 A A A LNCV6_133386_PI430048170 mRNA
ATGGGAGGCGTGTTCAGTAACTTATTCATAATGCATCTGAAATGATTGCTGTACTCAAAT NM_002392 RefSeq chr12
+ 68808171 68845544 MDM2 4193 "MDM2 proto-oncogene, E3 ubiquitin protein ligase, transcript
variant 1"
GO:0005515|GO:0071157|GO:0004842|GO:0034504|GO:0070301|GO:0016874|GO:0045202|GO:0071301|GO:0018

205|GO:0042220|GO:0042802|GO:0009743|GO:0007173|GO:0042787|GO:0010039|GO:0032026|GO:0046677|GO:0
031625|GO:0006977|GO:0071312|GO:0071391|GO:0043278|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129132_PI430048170 0.5649429236631 0.966389132269396 0.48466096505715
0.48146635059968 0.263363863730358 A A A 0.404022598853532 0.517338019649023
0.464834132550357 A A A LNCV6_129132_PI430048170 mRNA
CAATCCAATCTGTAATTTCACTTTAGAAGGTTGTATTACCTTCCACTTCCATGTTGTCTT NM_006174 RefSeq chr4 +
163343938 163351934 NPY5R 4889 neuropeptide Y receptor Y5
GO:0043005|GO:0060112|GO:0043066|GO:0005886|GO:0014050|GO:0007268|GO:0003214|GO:0048661|GO:0003
151|GO:0005737|GO:0004983|GO:0002675|GO:0007186|GO:0005887|GO:0007218|GO:0001602|GO:0032229|GO:0
001601|GO:0042755. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130655_PI430048170 0.794345721613973 0.943863850851594 0.424475688175303
0.858063508291166 0.247136517523366 A A A 0.366615410032184 0.995958404802341
0.396181597072447 A A A LNCV6_130655_PI430048170 mRNA
CCATAATGTACTAAGTACTTTGTCCCATGCTTCCAAGACACATTATATTTATGACCACAA NM_001256385 RefSeq
chr1 - 100148447 100178273 LRRC39 127495 "leucine rich repeat containing 39, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100099_PI430048170 0.633211346485535 0.947472854262942 6.59253482608484
6.62718523664397 6.59258248897293 P P P 6.4295235752038 6.81073431701377
6.77595014505294 P P P LNCV6_100099_PI430048170 mRNA
AACTGTGTGAGATTGTGAAGTGGTCTGAATTCTGGAATCACAAACCAAGCCATGCTGGTG NM_001218 RefSeq chr15
- 63323530 63382110 CA12 771 "carbonic anhydrase XII, transcript variant 1"
GO:0005886|GO:0015701|GO:0008270|GO:0044281|GO:0016021|GO:0004089|GO:0006730|GO:0055064 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131559_PI430048170 0.0189887754497746 0.454977067922193 10.1872600974288
9.62116878345909 9.71746342991743 P P P 10.9327110698445 11.019341570923
11.0454555987653 P P P LNCV6_131559_PI430048170 mRNA
CCCTACCCTTCCCCGTAGGATATACCCTGGAGAATGGCAAAATGATTTAAAGAGAAAAAA NM_014680 RefSeq chr17
- 28614439 28645159 KIAA0100 9703 KIAA0100 GO:0005576 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139026_PI430048170 0.253515231722705 1.02268195668006 0.305877411391923
0.251243841330122 0.317784954096355 A A A 0.266750286749459 0.245329336638482
0.26651827190534 A A A LNCV6_139026_PI430048170 mRNA
GGTGTCTTTTATTTATTTCAAACAAATGGCAGTAGTTTATTTCGAATGCCTTTGGGTGCA NM_001089584 RefSeq
chr5 - 7830378 7851490 C5orf49 NA chromosome 5 open reading frame 49 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140089_PI430048170 0.277139155071837 0.535701040317514 0.473732371256967
0.489893633688947 0.38838776205379 A A A 0.503248311276849 0.893863215955783
2.13147457775106 A A A LNCV6_140089_PI430048170 mRNA
GCTTTATGCTGTGTATGCTAGTCTTATTGTATATATGTACTGAAAGTACCTTTGACACTG NM_001141972 RefSeq
chr15 - 35520272 35546203 DPH6 89978 "diphthamine biosynthesis 6, transcript variant 2"
GO:0017178|GO:0044267|GO:0005524|GO:0017183|GO:0043687|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_72199_PI430048170 0.0280070268588974 .18613109526367 6.29302598075002 6.58062652873806
6.44677839539922 P P P 5.05688788699509 3.77973441117691 3.94602165706463 P P P
LNCV6_72199_PI430048170 mRNA
ATCCTACCCATGACCCCTACTTGGGGCAGAAAAAACCCATCCTAAAGGCTGGGCCCATGC NM_198440 RefSeq
chr22_KI270879v1_alt - 70864 75374 DERL3 91319 "derlin 3, transcript variant 3"
GO:0005515|GO:0030176|GO:0030433|GO:0030968|GO:0018279 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_134102_PI430048170 0.2453217690582270.553959758816155 1.85195827323287
1.97698744659365 0.382822164700617 A A A 3.00209753562848 1.59401524300643
2.30633554909727 P A A LNCV6_134102_PI430048170 mRNA
CTGTGTCTTTAACCACTGCACAATGCATTGCCTGTTTAATAAAAGGTTTCAAACATGAAA NM_207362 RefSeq chr2
- 98793845 98936221 KIAA1211L 343990 KIAA1211-like NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140276_PI430048170 0.00123512951247134 0.6492036886203327.5717839868661
7.43549733549981 7.52184106511432 P P P 8.08777433074172 8.06618115036374
8.24178791796542 P P P LNCV6_140276_PI430048170 mRNA
CTCAGAGATGCTATATTCTGTGAAAACACTGAACCTCGCTCTCTCCAAGATAAGCAAAAA NM_153816 RefSeq chr6
- 85505496 85594156 SNX14 57231 "sorting nexin 14, transcript variant 1"
GO:0038032|GO:0016021|GO:0035091|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134657_PI430048170 0.3313128287972910.8819240533495934.61460561299406
4.55993797219241 4.95056818310961 P P P 4.7637727342044 4.79637123369833
5.11399734946144 P P P LNCV6_134657_PI430048170 mRNA
CCCCAGAAATCTGCATTTACTAAATTTGTCTTAAGTCCAATTGTGTTTAAAGGTCATGCT NM_020117 RefSeq chr5
- 146113025 146182731 LARS 51520 leucyl-tRNA synthetase
GO:0005515|GO:0010467|GO:0002161|GO:0004825|GO:0005634|GO:0004823|GO:0005524|GO:0006429|GO:0005
829|GO:0006418|GO:0005737|GO:0006431|GO:0006450 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128125_PI430048170 0.0712224911858991 0.4528674820247550.977068129482494
0.7515222790274030.845398786096651 A A A 1.39164666557931 1.92333886448906
2.48928002744258 A A P LNCV6_128125_PI430048170 mRNA
CTTGTGCCTTTGGCACAAATGTGCAGAATAGATACATCAGTTGGTGCATAATCGAAAAAA NM_006699 RefSeq chr1
+ 117367462 117525698 MAN1A2 10905 "mannosidase, alpha, class 1A, member 2"
GO:0005794|GO:0007585|GO:0048286|GO:0004571|GO:0005509|GO:0000139|GO:0016020|GO:0006491|GO:0016
021|GO:0044267|GO:0018279|GO:0043687|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143718_PI430048170 0.0470809394801668 0.1897750850263940.973167348154071
0.3165568614535290.41271017903085 A A A 1.66193068527866 3.26930512270899
3.47445949307555 A P P LNCV6_143718_PI430048170 mRNA
CTTACCTTCTATTATCCTATATTAGCTTCAATACATCCAAACCAAATGGCTGTTAGGTAG NM_003667 RefSeq chr12
+ 71439769 71586308 LGR5 8549 "leucine-rich repeat containing G protein-coupled receptor 5,
transcript variant 1"
GO:0005515|GO:0048839|GO:0007186|GO:0005886|GO:0005887|GO:0004930|GO:0090263|GO:0032588|GO:0004
888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131006_PI430048170 0.1431092025580221.03339908424027 0.332572865287077
0.3394362427398320.274511418486938 A A A 0.2634234802775580.278031170595333
0.263702699726607 A A A LNCV6_131006_PI430048170 mRNA
GGTACGAGAAAGTGTCATTAGGTTCTTTCTTAAGGGAAAGGACAATTCTCATAACTTTTA NM_001001913 RefSeq
chr11 - 5787853 5788816 OR52N1 NA "olfactory receptor, family 52, subfamily N, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135939_PI430048170 0.00574801334142367 0.4800900833801768.36841027863217
8.57822592969825 8.41816112862111 P P P 9.74138479313909 9.47307909295114
9.30004720904983 P P P LNCV6_135939_PI430048170 mRNA
TAGCAAGGAGCCCGAGATCAGCCCTGAACTCACTGTGTATTCTCTTGGAGCCTTGGGTGG NM_001195381 RefSeq
chr2 + 240605407 240631259 GPR35 2859 "G protein-coupled receptor 35, transcript variant 2"
GO:0007186|GO:0005887|GO:0004930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78678_PI430048170 0.8616422892087141.01764291298526 6.41461116499115 6.25989453869133
6.02086844393787 P P P 6.51317459503267 6.22964726478635 5.82164011066398 P P P

LNCV6_78678_PI430048170 mRNA
ACCCTGGTGTCCATCCCAGCCTCATCTCATGGCAAGCGTGGACTTTCAGTCTCCATTGAC NM_002314 RefSeq chr7
+ 74083776 74122525 LIMK1 3984 "LIM domain kinase 1, transcript variant 1"
GO:0005515|GO:0043005|GO:0030036|GO:0045773|GO:0007266|GO:0005829|GO:0005737|GO:0007411|GO:0031
072|GO:0032233|GO:0051444|GO:0046982|GO:0048013|GO:0005524|GO:0007399|GO:0007165|GO:0004672|GO:0
004674|GO:0045087|GO:0051496|GO:0006468|GO:0005654|GO:0008270|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145016_PI430048170 0.0285835396283908 0.7740103022297 9.76377367460652
9.61240263241898 9.88424107458505 P P P 10.255561650636 9.98740273154701
10.1265409452335 P P P LNCV6_145016_PI430048170 mRNA
GCTACACTCGGTTACTCTGGCCTTGATTCTGATCTCCAAATACATTATATTTTTTATTTG NM_021187 RefSeq chr19 -
15912369 15934866 CYP4F11 57834 "cytochrome P450, family 4, subfamily F, polypeptide 11, transcript
variant 1"
GO:0006805|GO:0005506|GO:0044281|GO:0042377|GO:0042376|GO:0006954|GO:0007596|GO:0016709|GO:0005
789|GO:0016021|GO:0042361|GO:0020037|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110271_PI430048170 0.721904316636226 1.27719427392291 0.35935455183124 1.8073179611112
0.31670982812263 A A A 0.372293915464868 0.394058963620298 1.07821415502529 A A A
LNCV6_110271_PI430048170 mRNA
AACAGAAAGGGGCTCATACTCATCTTATGGGAGAGAATCAAACTTACAGGGTTGCCACCA NM_001083962 RefSeq
chr18 - 55222330 55588629 TCF4 6925 "transcription factor 4, transcript variant 1"
GO:0005515|GO:0005667|GO:0006352|GO:0003700|GO:0006367|GO:0046982|GO:0001093|GO:0070888|GO:0005
634|GO:0000978|GO:0008022|GO:0065004|GO:0003677|GO:0001087|GO:0001077|GO:0045666|GO:0045944|GO:0
045893|GO:0001011. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139133_PI430048170 0.0423171005665048 0.907980932441571 11.0803882964008
11.124291619941 11.2052396621857 P P P 11.2600971277392 11.2375395197619
11.3312079826611 P P P LNCV6_139133_PI430048170 mRNA
ATCCGTAAATAAACTTCCTTCACTACACTGTAATCTGTGAGCATGCTTCCTCTGCCCTGG NM_001199654 RefSeq
chr1 + 156212987 156240077 PMF1 11243 "polyamine-modulated factor 1, transcript variant 1"
GO:0005515|GO:0005667|GO:0006355|GO:0006366|GO:0003713|GO:0005634|GO:0005829|GO:0043522|GO:0007
067|GO:0007059|GO:0000444|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131410_PI430048170 0.886015592239399 0.671164818049651 1.35569590411731
1.99911000348347 1.12710947864581 A A A 0.292070433202267 0.26873262353011
3.40522997976256 A A P LNCV6_131410_PI430048170 mRNA
GCACCCTGCCATTTAAAAAGATGTGTAAAGCACATATTCTCAACATATGCACATTGATTT NM_001271010 RefSeq
chr11 + 128693915 128813267 FLI1 2313 "Fli-1 proto-oncogene, ETS transcription factor, transcript
variant 3"
GO:0003700|GO:0006357|GO:0006366|GO:0000981|GO:0008015|GO:0005634|GO:0000978|GO:0003677|GO:0030
154|GO:0007599|GO:0035855|GO:0001077|GO:0045944|GO:0003682|GO:0009887|GO:0000980 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140617_PI430048170 0.0145461758300603 1.21707739546664 8.42338151811106
8.46159506289426 8.58959022935763 P P P 8.24615287246945 8.1537410009823
8.22805626519085 P P P LNCV6_140617_PI430048170 mRNA
GGTCACTATTTTCTCTTAACACATAGGAAAAAAGTTCAGACATCGCTACAATAAATGTGC NM_006067 RefSeq chr16
- 85778624 85799542 EMC8 10328 "ER membrane protein complex subunit 8, transcript variant 1"
GO:0072546|GO:0005739|GO:0005737|GO:0016020|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139339_PI430048170 0.522294857409931 0.933272680031031 5.26875014194911
4.80646404048553 4.88232211590665 P P P 5.13702678182572 5.15965898603489
4.99825659220056 P P P LNCV6_139339_PI430048170 mRNA

CTCGTGCAGGCTAAAAGTTGGAAGGGAAATGATTAAGAAATTATTAAATGCAAGGACTGA NM_001199672 RefSeq
chr7 + 128739291 128773423 CALU 813 "calumenin, transcript variant 4"
GO:0005515|GO:0042470|GO:0008150|GO:0005794|GO:0016020|GO:0007596|GO:0005783|GO:0005509|GO:0002
576|GO:0033018|GO:0030168|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142866_PI430048170 0.0399532091940840.6948165234564075.1441047807193
5.21485859758349 5.16636061831247 P P P 5.48427693611128 5.72325082287862
5.86878305370691 P P P LNCV6_142866_PI430048170 mRNA
GCTGTTTAGTTTTGTACTATTGGTGTGTTGGTGAATTTTTAAACTGTGTGCTAACTGCAA NM_006352RefSeq chr1
+ 244053204 244057478 ZBTB18 10472 "zinc finger and BTB domain containing 18, transcript variant 2"
GO:0003700|GO:0021987|GO:0005634|GO:0021549|GO:0000122|GO:0000228|GO:0001701|GO:0003677|GO:0046
872|GO:0006351|GO:0045171|GO:0048872|GO:0043565|GO:0021766|GO:0048666|GO:0007519|GO:0015630|GO:0
005654|GO:0045892|GO:0051302 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132869_PI430048170 0.4272234787505062.62912958666426 3.04173810805756
0.4629456752064470.459829048233654A A A 0.3572538637557760.38074662334228
0.674949903752422A A A LNCV6_132869_PI430048170 mRNA
GGTCAGATAGTATTAATAGAAAGTTCAGGATGTTAAACAACTTGGAGTGGTGTTGCTTTT NM_001040274 RefSeq
chr6 + 10886830 10974308 SYCP2L 221711 synaptonemal complex protein 2-like GO:0005654 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131783_PI430048170 0.4309626028669180.9397022163727051 2.136636053516
11.9138019562042 12.1477589754317 P P P 12.0201450100987 12.2488696735584
12.2002839702099 P P P LNCV6_131783_PI430048170 mRNA
CTGCTTACATTCCAACAAATGTCATTTCCATCACTGACGGACAGATCTTCTTGGAAACAG NM_001257335 RefSeq
chr18 - 46084143 46098353 ATP5A1 498 "ATP synthase, H+ transporting, mitochondrial F1 complex,
alpha subunit 1, cardiac muscle, transcript variant 5"
GO:0006629|GO:0005515|GO:0042288|GO:0005886|GO:0005743|GO:0009790|GO:0044281|GO:0005739|GO:0006
754|GO:0008180|GO:0046961|GO:0005759|GO:0016887|GO:0044237|GO:0070062|GO:0022857|GO:0005524|GO:0
005753|GO:0022904|GO:0016020|GO:0001937|GO:0042776|GO:0046933|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128293_PI430048170 0.00162602113366962 0.2474554865120661 0.031528634102
9.51312170787034 10.0133343759357 P P P 11.5108024019611 11.881416211615
12.1886039895989 P P P LNCV6_128293_PI430048170 mRNA
GTTGGCAAAGAGTGCTACACCGTTTCAATGAAACAATGTATGTTTGTTTTAACTGAACTA NM_018976RefSeq chr12
- 46358187 46372862 SLC38A2 54407 "solute carrier family 38, member 2"
GO:0015171|GO:0005886|GO:0005887|GO:0006865|GO:0007268|GO:0006814|GO:0055085|GO:0014047|GO:0003
333|GO:0007269|GO:0015293|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135228_PI430048170 0.0809215246047292 0.7267173728921826.28890476078511
5.78443702029404 6.18252880002694 P P P 6.54055568728115 6.49703784487971
6.64339647389807 P P P LNCV6_135228_PI430048170 mRNA
TGAGATGCTGGGCCTTTGGATGTGTACGGTAACCAACTTAATGCTAATGTTCAAAGTAAA NM_001145365 RefSeq
chr17 - 49289205 49362114 ZNF652 22834 "zinc finger protein 652, transcript variant 1"
GO:0005515|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143302_PI430048170 0.2235809570197280.9810209928130180.352535513320888
0.3829588053682510.327539810886891A A A 0.3816215308625750.397828147210733
0.366884866332489A A A LNCV6_143302_PI430048170 mRNA
GGAGCGCTTCATTTTAGACAATCCTGACATTCTATTTATATTCAACAAGTCTGTATCACT NM_001304369 RefSeq
chr20 - 58216125 58228653 ANKRD60 140731 ankyrin repeat domain 60 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_136727_PI430048170 0.1980852284154010.8442432245879247.06679762379475

7.49176706639373 7.33272672793249 P P P 7.74449257229903 7.45580242304938
7.43405784729326 P P P LNCV6_136727_PI430048170 mRNA
TCCGGCACAAGGTTCTTTCATGTTGAGTGTTGTTTCCTTCAATGTTTCTGCCTTTTTTAA NM_152640RefSeq chr12 -
1946047 2004511 DCP1B 196513 decapping mRNA 1B
GO:0005515|GO:0010467|GO:0043928|GO:0000290|GO:0005634|GO:0003729|GO:0043231|GO:0005829|GO:0031
087|GO:0050790|GO:0005737|GO:0000184|GO:0016020|GO:0016787|GO:0000932|GO:0030234|GO:0000340|GO:0
000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138434_PI430048170 0.1065703259557610.6459450287242227.39386376969146
6.73697526469899 6.56318383809618 P P P 7.74296946053634 7.70477653764454
7.21955964112908 P P P LNCV6_138434_PI430048170 mRNA
AATACCCGCCCCACCGGCTGTGATGCTCCAATAAACTTTTTTATGCTTTTGCGGAAAAAA NM_013304RefSeq chr16
- 67394418 67416436 ZDHHC1 29800 "zinc finger, DHHC-type containing 1"
GO:0018345|GO:0005783|GO:0016409|GO:0008270|GO:0016021|GO:0003677|GO:0019706|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136039_PI430048170 0.9246627883447090.9976079285443477.18474313111925
7.25638845388012 7.34348199836868 P P P 7.27120496940225 7.26780262703077
7.26033700780672 P P P LNCV6_136039_PI430048170 mRNA
CTAGTTCCCAAAGGCGATGTCCAGACACAGACTTTATGATTATTATATTTTTCAATGCCA NM_032998RefSeq chr1
- 161120977 161132688 DEDD 9191 "death effector domain containing, transcript variant 1"
GO:0008625|GO:0005515|GO:0046697|GO:0005737|GO:0042177|GO:0005730|GO:0042981|GO:0007283|GO:0003
677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128561_PI430048170 0.0856000492378238 1.53601588335631 3.40883262394967
3.54736230068638 3.65716392494514 P P P 3.25023787240263 2.49448622861272 2.9238826096713
P P P LNCV6_128561_PI430048170 mRNA
AGAAGCTGGAGATTCCTTAATTTATTCTAAAGGGAAAGGGCTCCTGGGGCCTTGGAGTAA NM_138356RefSeq chr15
- 45167213 45201175 SHF90525 "Src homology 2 domain containing F, transcript variant 2"
GO:0006915 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141474_PI430048170 0.2128752360385491.03429219689296 0.508319791294588
0.4687813970361660.437973400338024A A A 0.3719682418409720.444751336427556
0.451937453693593A A A LNCV6_141474_PI430048170 mRNA
GTGCGTTGGTTTCTCTCATAGAGGCATTAACTATACTGCCAATGCATTGAATTATTTAAA NM_002025RefSeq chrX
+ 148500618 149000663 AFF2 2334 "AF4/FMR2 family, member 2, transcript variant 1"
GO:0008380|GO:0006397|GO:0016607|GO:0007420|GO:0002151|GO:0007611|GO:0043484 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145303_PI430048170 0.3381436079727880.7052832818209350.267209709143467
0.2790259080987750.345567641495902A A A 0.4149242432727780.34799038202778
1.39088024090922 A A A LNCV6_145303_PI430048170 mRNA
AATCCGTGAAGATCCCAAGTTCCTGATAACCAATTACCAAGGAGTCCTGACGCTGAACAT NM_004533RefSeq chr19
+ 50432902 50466326 MYBPC2 4606 "myosin binding protein C, fast type"
GO:0005515|GO:0032982|GO:0030049|GO:0003779|GO:0008307|GO:0007155|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131878_PI430048170 0.9475576615825580.9790786094846340.476112048203468
1.22383305720265 1.6835641169877 A A A 1.9823353579442 0.801657958811711
0.47789229124147 A A A LNCV6_131878_PI430048170 mRNA
TTTTGTCATATCTCTTCCCAAGTGTCATCACTATATGGATGTTGAGGGCCCCCGATGACA NM_024807RefSeq chr6
- 41189748 41201187 TREML2 79865 triggering receptor expressed on myeloid cells-like 2
GO:0005515|GO:0042110|GO:0009986|GO:0005886|GO:0004872|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134531_PI430048170 0.00119640377929928 5.72116474713309 6.99518547162526

6.88954651100682 6.8055983594813 P P P 4.51956486322423 4.07727775538484
4.50833166669673 P P P LNCV6_134531_PI430048170 mRNA
TGTGGGTTCTGCCGGTGGGGCTTCAGGAGTAATAAAGTGTCACCCTATCCTTGTAAAAAA NM_014427RefSeq chr16
+ 89575767 89597246 CPNE7 27132 "copine VII, transcript variant 2"
GO:0006629|GO:0005215|GO:0006810|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139124_PI430048170 0.432905623794265 1.06416924645133 10.0770561820098
10.1829100888353 10.0462284269838 P P P 10.1716800473575 10.006816548863
9.84345200758736 P P P LNCV6_139124_PI430048170 mRNA
AGTCCCAGGGCATGGCCCAGCGGCCAGATTCTTTTTCCCAGGATTAAAACTCTGACCCCA NM_017720RefSeq chr19
- 4324042 4338850 STAP2 55620 "signal transducing adaptor family member 2, transcript variant 1"
GO:0005515|GO:0005737|GO:0005886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139000_PI430048170 0.0633596412598162 0.967409061422587 0.313901601635957
0.346196099045866 0.347307129909342 A A A 0.408418401685252 0.384194345436953
0.358006632921698 A A A LNCV6_139000_PI430048170 mRNA
TACTGGCTGAGCAAAAGCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTGTTGCAAGGCG NM_001727RefSeq chrX
+ 136487965 136492439 BRS3 680 bombesin-like receptor 3
GO:0008343|GO:0043005|GO:0004946|GO:0031989|GO:0005886|GO:0043025|GO:0008217|GO:0006006|GO:0016
021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130548_PI430048170 0.0272045025478154 0.725695417636599 2.03291943144819
1.68870220119238 1.9522325369005 A A A 2.27431767799248 2.46842865667422
2.33390874885406 A P P LNCV6_130548_PI430048170 mRNA
CCGGTTTTGAATGTGGAGTGTTTGTGTGTGTTCCTTTTTTAAATTAAGTTATTCCCTCAA NM_022124RefSeq chr10 +
71396933 71815947 CDH23 64072 "cadherin-related 23, transcript variant 1"
GO:0005515|GO:0005886|GO:0051480|GO:0007605|GO:0005509|GO:0032420|GO:0045494|GO:0016339|GO:0016
020|GO:0050957|GO:0006816|GO:0016021|GO:0007156|GO:0007601|GO:0050953|GO:0050896 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135168_PI430048170 0.119133400054428 0.67117490858571 4.73962878414512
4.33675730437736 3.93829112473258 P P P 5.28611026038493 4.76815785306543 4.7269991039863
P P P LNCV6_135168_PI430048170 mRNA
TCCACTTACCTGGAGCTGCTCTCCTGTATTATCCTCCACAATAAAATTCTCCAGAAAATA NM_130388RefSeq chrX
- 64224191 64230631 ASB12 142689 ankyrin repeat and SOCS box containing 12
GO:0035556|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129065_PI430048170 0.83464789425248 1.17718626465822 1.89103804724859
1.31009169971625 0.319425677652255 A A A 0.942823873561764 0.923158817427431
1.32110263722057 A A A LNCV6_129065_PI430048170 mRNA
GCCTGTGTAATTCAGCCCGCCATTGCTCGGTGGATAATTAAAGCATGTCACCATAAAAAA NM_000841RefSeq chr6
- 34018642 34146137 GRM4 2914 "glutamate receptor, metabotropic 4, transcript variant 1"
GO:0051966|GO:0005516|GO:0005886|GO:0004930|GO:0001642|GO:0007268|GO:0007196|GO:0031410|GO:0007
269|GO:0005622|GO:0043523|GO:0042734|GO:0000187|GO:0043198|GO:0005887|GO:0043195|GO:0008066|GO:0
007612|GO:0043410|GO:0048787|GO:0048306 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110428_PI430048170 0.891271033124345 1.00891667109768 7.65749662407123
7.45910519928358 7.44280322701213 P P P 7.19134369400714 7.68037288662344
7.61239206517343 P P P LNCV6_110428_PI430048170 mRNA
AGTGACAATCAGTTTCATGAAGGAGCTCATGCAGTGGTACAAGGACCAGAAGAAACTGCA NM_006247RefSeq
chr19 + 46346993 46390975 PPP5C 5536 "protein phosphatase 5, catalytic subunit, transcript variant
1"
GO:0005515|GO:0043005|GO:0003723|GO:0043278|GO:0005634|GO:0051291|GO:0046872|GO:0006351|GO:0043
231|GO:0042802|GO:0008289|GO:0005829|GO:0007165|GO:0005737|GO:0007067|GO:0006281|GO:0006470|GO:0
016020|GO:0043025|GO:0004721|GO:0005654|GO:0004722|GO:0004871|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_139677_PI430048170 0.3256475978064061.38971000850545 1.34643501438543
0.3456345149172010.48781508583349 A A A 0.3192755617743670.297404268094968
0.352266508880226A A A LNCV6_139677_PI430048170 mRNA
CCCTAAGAGTGTGGTCTGCAGGGTCAAGAATAAAGATTACAGATTATATTTACTTGAAAA NM_001099287 RefSeq
chr5 + 157460018 157474722 NIPAL4 NA "NIPA-like domain containing 4, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131249_PI430048170 0.4221702105851420.6825813079750810.348597164556238
0.3298166698766380.276234346236972A A A 0.31496023683925 0.32260563694973
1.57840837992999 A A A LNCV6_131249_PI430048170 mRNA
GTGAACGAATCCTCTGTGTCTAATAAAGACAGGTCTTGTGCTTGTGCTCCATGCTATTAC NM_001004297 RefSeq
chr10_GL383546v1_alt - 127421 140376 OR13A1NA "olfactory receptor, family 13, subfamily A, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69943_PI430048170 0.0537600488428291 0.8362808927500338.80614830738606
8.86221683306002 9.0439980524944 P P P 9.03955188089893 9.23649935508811 9.2130705117987
P P P LNCV6_69943_PI430048170 mRNA
GCTACAGGCTTTCTACTTAACTTCTGGGTTTGCTATTACAAATCCTATTTACTCTCATAC NM_003342RefSeq chr17 -
4269216 4366674 UBE2G17326 ubiquitin-conjugating enzyme E2G 1
GO:0006511|GO:0070534|GO:0005737|GO:0004842|GO:0019787|GO:0016874|GO:0070936|GO:0044257|GO:0005
524|GO:0031625|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134930_PI430048170 0.1714496178818891.41412055103166 5.18279159854806
4.96396534273636 4.95441960058068 P P P 4.80175206746881 4.71164357366968
3.96229420758297 P P P LNCV6_134930_PI430048170 mRNA
GATGGAAAGTGGGTCAGTGGAGAAGGGATTCAGAAAATGACACATTCTTCCCCATTTAAA NM_145755RefSeq chr3
+ 39107660 39138903 TTC21A 199223 "tetratricopeptide repeat domain 21A, transcript variant 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137529_PI430048170 0.4125149872375361.50134162309421 1.72119574804052
0.4792528120701690.359645981201282A A A 0.48846290783975 0.370729341695897
0.359862968822861A A A LNCV6_137529_PI430048170 mRNA
GCAAAATCTTGGAAGTGGTTTCTAATAAAATTCATTTATGTTCTCCTGTGAACGTGCCTT NM_175878RefSeq chr22
- 16783415 16821694 XKR3 150165 "XK, Kell blood group complex subunit-related family, member 3"
GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135464_PI430048170 0.0153063941354512 2.12225384797147 3.06270095374731
3.5305470243827 3.00465709901647 A P P 2.24687386015474 2.07424292784339
2.07247823419155 A A A LNCV6_135464_PI430048170 mRNA
GGAAGTATTCTCTCAAATGGAGGCAACAGAGGTGATTGTTATTTTGTTTTAGTTTCTGTT NM_033409 RefSeq
chr20 - 760079 768584 SLC52A3 113278 "solute carrier family 52 (riboflavin transporter), member 3"
GO:0034605|GO:0006771|GO:0016324|GO:0032217|GO:0005886|GO:0006766|GO:0005887|GO:0007605|GO:0006
767|GO:0044281|GO:0032218 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132267_PI430048170 0.0265399280709656 1.08749169455921 0.387951962080073
0.472324603391415 0.44324451786237 A A A 0.294467049268578 0.319256473392237
0.327846023167096 A A A LNCV6_132267_PI430048170 mRNA
CCTTGACATTTAATCACAGGTTACTTTCCAGAAAGGTTTCTAAAGTTACAGATTCAGCTT NM_012471 RefSeq chrX
- 111774313 112082776 TRPC5 7224 "transient receptor potential cation channel, subfamily C,
member 5"
GO:0005515|GO:0005262|GO:0005886|GO:0034704|GO:0055085|GO:0007399|GO:0070679|GO:0034220|GO:0005
887|GO:0007411|GO:0070588|GO:0006816|GO:0015279 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127501_PI430048170 0.451524164334232 0.411592216790796 1.70800457875093

0.415005398957067 1.45589057519254 A A A 3.53236596274866 0.36716377984244 2.31667907391549 P A A LNCV6_127501_PI430048170 mRNA TTTGGAAAGTTGGGGCGGCTAAGATTCAGTGGACAAAGCTAAAACCTGCAGAGCAATGAA NM_001037144 RefSeq chr17 + 7932123 7949919 CNTROB 116840 "centrobin, centrosomal BRCA2 interacting protein, transcript variant 2" GO:0005515|GO:0005813|GO:0005737|GO:0007099|GO:0005814|GO:0051299|GO:0019904 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137818_PI430048170 0.784785153160726 1.59091028245215 2.81726134464117 0.520570261235188 0.321711597444006 A A A 0.397277254236593 1.49783050965019 0.98288335542584 A A A LNCV6_137818_PI430048170 mRNA AGGAGGAAGTTGAGCAACATCCCCCTGAAGCTCACATGTTACTTTATTTCCTGCCCATTA NM_001282442 RefSeq chr16 - 68013435 68015911 LOC100131303 NA uncharacterized LOC100131303 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126928_PI430048170 0.0253005867580687 0.727779422160279 7.53919681708968 7.46683019884208 7.79121249730582 P P P 7.96164406649327 7.98368073450742 8.2317509517925 P P P LNCV6_126928_PI430048170 mRNA AAGATGCATTCCCTTCCTGTTCACACTCTTACCATGTTTTTGTTCTTCCTTAAGAATGAT NM_005653 RefSeq chr12 - 51093755 51173143 TFCP2 7024 "transcription factor CP2, transcript variant 1" GO:0043565|GO:0003700|GO:0006357|GO:0005634|GO:0005575|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65746_PI430048170 0.0111058625468789 1.7656051782305 10.0549911778606 10.2559643651886 10.3390321325924 P P P 9.56333338370961 9.1176046203511 9.48506547080744 P P P LNCV6_65746_PI430048170 mRNA GACATCTAATAGTCCCTAAGTGCTATTAAATACCTTATTGGACAAGGGCTTGCTTCAAGC NM_001171508 RefSeq chr2 - 46901869 46941855 MCFD2 90411 "multiple coagulation factor deficiency 2, transcript variant 4" GO:0012507|GO:0005793|GO:0005794|GO:0005783|GO:0005509|GO:0016192|GO:0015031|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141517_PI430048170 0.335454414811065 1.16424542192818 7.67290745629358 7.72161623270346 7.84603670787526 P P P 7.12166767915041 7.65884127448849 7.73372140827609 P P P LNCV6_141517_PI430048170 mRNA GTACTGAAGCACAAACATATATCATCTCTGTACCATTCTGTACTAAAGCACTTGAGTCTA NM_003165 RefSeq chr9 + 127612206 127692716 STXBP1 6812 "syntaxin binding protein 1, transcript variant 1" GO:0005886|GO:0035542|GO:0007268|GO:0060292|GO:0044281|GO:0015031|GO:0007269|GO:0042802|GO:0006904|GO:0005829|GO:0005739|GO:0043524|GO:0007412|GO:0005737|GO:0000149|GO:0031091|GO:0017075|GO:0070062|GO:0019905|GO:0019901|GO:0019904|GO:0050821|GO:0010807|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128433_PI430048170 0.343923147514389 0.804469130833934 6.06863183387209 6.10769431986508 6.37614125268296 P P P 6.01058252120059 6.6748623564813 6.72467739476318 P P P LNCV6_128433_PI430048170 mRNA GGACTCAGTTCAGTCTTGTTTTTATCAGAGTGATAATCATCCTGTTTCACATCCCAATAC NM_001008708 RefSeq chr2 + 53767791 53775150 CHAC2 494143 "ChaC, cation transport regulator homolog 2 (E. coli)" GO:0008150|GO:0003674|GO:0016746|GO:0008152|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141318_PI430048170 0.250009188547093 0.672583591556624 3.43432938368887 2.25448953556282 3.57151892187853 P A P 3.44969905683311 4.01284053124647 3.7839107646558 P P P LNCV6_141318_PI430048170 mRNA ATAAAGCATTTGAGCTGCTGCTACAGAGGAACAATCACCAGATATTGTGACCCTTTCAGA NM_018157 RefSeq chr12 + 106774620 106889316 RIC8B 55188 RIC8 guanine nucleotide exchange factor B GO:0043547|GO:0005085|GO:0001965|GO:0005813|GO:0005737|GO:0008277|GO:0005886|GO:0005938|GO:0005

829|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_27652_PI430048170 0.028059721640019 0.651928050090946 3.7344663057849
3.99603767204667 4.22036001071316 P P P 4.49120373744457 4.49238957226012
4.83220604835791 P P P LNCV6_27652_PI430048170 mRNA
TAGAGTGGCCTTATTGACTGCTGGTGTGATGCCACTGTAATGTAATAAATTATTAAATTG NM_001282494 RefSeq
chr15_KI270905v1_alt + 4808040 4821891 GOLGA8N NA "golgin A8 family, member N" NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_43638_PI430048170 0.0210204137482638 1.61432803429895 8.29144462801516
7.86769840921299 7.87054576439572 P P P 7.13767343343711 7.29826621895112
7.53543933938111 P P P LNCV6_43638_PI430048170 mRNA
ACTGCACAGAACAGTTGAATAGCTTAATGAATAACTACAGTAAAAGCTATGGTAACCACT NM_032357 RefSeq
chr2 - 130337932 130342383 CCDC115 84317 "coiled-coil domain containing 115, transcript variant
1" GO:0016020|GO:0005764|GO:0005768 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_127050_PI430048170 0.435910789832211 0.924797816456172 9.03293265887283
8.85581750765702 8.84607020086259 P P P 9.20506829931908 9.01117851238367
8.84177629433184 P P P LNCV6_127050_PI430048170 mRNA
GGTACTTGTCCTTGTTTAGGCCTCACCTCCCTGCTCCTGTGTCTTACCAATAAACTTATA NM_175068 RefSeq
chr12 - 52607569 52618559 KRT73 319101 "keratin 73, type II"
GO:0008150|GO:0003674|GO:0005198|GO:0005634|GO:0045095|GO:0070062 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_136140_PI430048170 0.649572752253278 0.916835628979671 0.41718551501515
0.42824925331984 0.440039974093731 A A A 0.324271051699616 0.355730948766224
0.904684856985169 A A A LNCV6_136140_PI430048170 mRNA
GGGTTGTGTGGGAAGAGTACTTATTATTGTGTTTTCTTCAGTGTAATTGTTCTTGGTAAT NM_021637 RefSeq chrX
+ 101078846 101096366 TMEM35 59353 transmembrane protein 35
GO:0008150|GO:0003674|GO:0016023|GO:0016021|GO:0005575|GO:0005778 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_145498_PI430048170 0.15290224595894 1.19173935827834 6.85946599919669
6.99146426939582 7.24650658189908 P P P 6.74297406247038 6.75025400544598
6.8686742555902 P P P LNCV6_145498_PI430048170 mRNA
GAAGACCTTTTGTCTGAAAACCAGCCAAGCTTTATTCAGGACACACTTCTTGCCTTCACT NM_007237 RefSeq
chr2 + 230225729 230313215 SP140 11262 "SP140 nuclear body protein, transcript variant 1"
GO:0005515|GO:0006355|GO:0003700|GO:0005634|GO:0006952|GO:0005635|GO:0003677|GO:0005737|GO:0003
682|GO:0016605|GO:0005654|GO:0006338|GO:0008270 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_94467_PI430048170 0.0907291618985043 1.44982896510445 8.80189337841595
8.78570349432781 9.08768488604578 P P P 7.93992882716345 8.5798529979145
8.48906968511913 P P P LNCV6_94467_PI430048170 mRNA
TTTATTGACATTGCTGAAGTGGAGACAGGGGACAAACTATGGGAGGTACAGTGTGAGTCT NM_032361 RefSeq
chr5 - 175959530 175968315 THOC3 84321 THO complex 3
GO:0008380|GO:0006397|GO:0006406|GO:0005794|GO:0016607|GO:0003723|GO:0000346|GO:0005654|GO:0000
445|GO:0046784|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143369_PI430048170 0.00498644813199191 0.733357408767405 11.8132276511906
11.6458217244785 11.6292925595973 P P P 12.0377184725651 12.1894491169949
12.2048372948951 P P P LNCV6_143369_PI430048170 mRNA
AACCCACCTTAGCATGTATCACTCTGTGGAGAATAAAGCACCCTATGTACACAGCCAAAA NM_014623 RefSeq
chr6 - 43012228 43013880 MEA1 4201 male-enhanced antigen 1
GO:0005515|GO:0005737|GO:0007283|GO:0030154|GO:0008584 . NA - . NA NA NA NA NA

NA NA NA NA
LNCV6_144137_PI430048170 0.180594945505655 0.653570022980833 0.343527449685359
0.331498006461249 0.317390056290259 A A A 1.37849747367529 0.417971480294646
0.87756130069264 A A A LNCV6_144137_PI430048170 mRNA
TGAAGAAACGAGTGCTCTGAAGAGCCAGTTACCCTGTGTTGGCTGCAATAAAGGTCATTA NM_032572 RefSeq
chr14 + 21042225 21044233 RNASE7 84659 "ribonuclease, RNase A family, 7"
GO:0050830|GO:0042834|GO:0004540|GO:0005576|GO:0003676|GO:0001530|GO:0009617|GO:0050829|GO:0004
519|GO:0045087|GO:0051673|GO:0019731|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134059_PI430048170 0.247585580859156 1.42907208566432 1.81244619838213
1.45957570607374 1.81909569190481 A A A 0.392812617280623 1.24112231758781
1.66661935893209 A A A LNCV6_134059_PI430048170 mRNA
CTTTAATACAAATCCTTGTCCTGACACTCTGTAGCTTTAATAATCCTATTACCAATCTGG NM_001039656 RefSeq
chr11 - 68736131 68751520 MTL5 9633 "metallothionein-like 5, testis-specific (tesmin), transcript
variant 2"
GO:0005737|GO:0010038|GO:0007275|GO:0005634|GO:0007283|GO:0006875|GO:0046872|GO:0030154 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_142372_PI430048170 0.0272032953840492 0.319726149833598 1.62510493237352
1.57799987117521 0.499706786508738 A A A 2.82916697590883 3.28308976098252
2.7152153055899 P P P LNCV6_142372_PI430048170 mRNA
GACACTGTGGCTGTCTAATGTAATCCTTTAAAAATTCTCTGCATTGTCAGTAAATGTAGT NM_014616 RefSeq chr3
+ 182793502 182921633 ATP11B 23200 "ATPase, class VI, type 11B"
GO:0005515|GO:0000287|GO:0005794|GO:0005886|GO:0005783|GO:0015075|GO:0005637|GO:0055085|GO:0005
524|GO:0045332|GO:0034220|GO:0016020|GO:0004012|GO:0008152|GO:0016021|GO:0015917|GO:0055037|GO:0
055038|GO:0005769|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143710_PI430048170 0.00225913642203304 0.501779996202796 6.05671035828528
6.01474492871418 6.25429581265798 P P P 7.12225908557498 6.90899757513306
7.2682009061717 P P P LNCV6_143710_PI430048170 mRNA
GATGGTCTAAGTTTTCTTCATGCTGGAACAAATGTTAAAGAAGCAGTGATTGCTTACAAT NM_001136200 RefSeq
chr10 + 102854209 102864961 C10orf32 119032 "chromosome 10 open reading frame 32,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140306_PI430048170 0.00203404238498764 0.31014007315283 4.86523977341345
4.27836185617118 4.6714783215288 P P P 6.01031027489288 6.31480381757917
6.56450842292496 P P P LNCV6_140306_PI430048170 mRNA
GGCTCAGAGAATCCTGCAAAATCCTTTTTTATTGTTTATTCTGCAGACAAAAATGTGACA NM_020456 RefSeq
chr13 - 49912701 49936501 SPRYD7 57213 "SPRY domain containing 7, transcript variant 1" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133625_PI430048170 0.0845221153696288 0.534394009723849 1.34016239862278
0.524466263279025 0.362379924990536 A A A 1.2737236506769 2.16535597227502
1.55156129723941 A A A LNCV6_133625_PI430048170 mRNA
GATGCCTGGTCTGCCATTGGCACTTAAATATTTGTTGTATTACGATTTATAATATGGTTC NM_000092 RefSeq chr2
- 227002710 227164559 COL4A4 1286 "collagen, type IV, alpha 4"
GO:0022617|GO:0030198|GO:0007411|GO:0030574|GO:0005605|GO:0005587|GO:0005788|GO:0005576|GO:0032
836|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134683_PI430048170 0.291946521500396 1.08300983853235 11.1810782148454
11.2300864025594 11.1057249962151 P P P 11.2041850494046 11.041269110433
10.9143260776265 P P P LNCV6_134683_PI430048170 mRNA
TGGAGTTCCCTCCCAAACACCAGACCACACAGTCCTCCAAAAATAAACATTTTATATAGA NM_001304814 RefSeq
chr17 - 44011187 44019447 TMEM101 84336 "transmembrane protein 101, transcript variant 3"

GO:0007165|GO:0016021|GO:0005575|GO:0004871|GO:0043123 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131749_PI430048170 0.000606575342757459 0.2806751778933312.42426484511285
2.27313450232269 2.73866217938438 A A A 4.10419378119613 4.44887056439111
4.39833999432478 P P P LNCV6_131749_PI430048170 mRNA
GAATGATATCTTGTAAATAAAGACATTCAGCACACTGTGAAAATGTATTTGTGCACCTGC NM_000522RefSeq chr7
- 27196879 27200106 HOXA13 3209 homeobox A13
GO:0048839|GO:0003700|GO:0044212|GO:0048844|GO:0045840|GO:0003281|GO:0005634|GO:0060847|GO:0003
677|GO:0006351|GO:0060442|GO:0043565|GO:0030539|GO:0001501|GO:0001894|GO:0001886|GO:0045944|GO:0
005654|GO:0045111|GO:0035115|GO:0030510|GO:0001570|GO:2001055 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_137941_PI430048170 0.6991581856617240.9947938884431560.352445643580691
0.3542561769604270.375366266143788A A A 0.3872356928057420.337061890283627
0.379966716472973A A A LNCV6_137941_PI430048170 mRNA
TATAGGGAGTGCGTACCACGCAGGCATCCAACAACCATAAGTGTGTTAAGTGTTAGTTCT NM_001166292 RefSeq
chr1 - 44819843 44842944 PTCH2 8643 "patched 2, transcript variant 2"
GO:0007165|GO:0042633|GO:0005119|GO:0008544|GO:0008158|GO:0045879|GO:0016021|GO:0097108 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126824_PI430048170 0.1766707069357261.09603651082559 0.580674054094305
0.3981744924003010.579487356026918A A A 0.2921821505060730.399439277979293
0.471729572491544A A A LNCV6_126824_PI430048170 mRNA
CTGCCGCTTGTGTTTCATAACTACGCTTGCTTTCCTTCAAAATATACCAAGTGTGTAATA NM_207361RefSeq chr13
+ 38687035 38887130 FREM2 NA FRAS1 related extracellular matrix protein 2 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_140347_PI430048170 0.00287291663844234 0.6035204980927774.70402110620979
4.54802184162928 4.55568171399197 P P P 5.34073363525832 5.30555107192172
5.35203047422864 P P P LNCV6_140347_PI430048170 mRNA
GCTCTCACCCTAACACTATAAGAAGCATGATCTCAATAGACCAATAATTCACCTTTTTAT NM_001164273 RefSeq
chr15 + 41660411 41769943 MGA 23269 "MGA, MAX dimerization protein, transcript variant 1"
GO:0005667|GO:0006355|GO:0005737|GO:0003700|GO:0071339|GO:0046983|GO:0005654|GO:0003677|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_20017_PI430048170 0.000455420767239965 0.6484743728128727.11862741679443
7.17708212218185 7.08024833009212 P P P 7.71622363012408 7.8309607019929
7.70154986552481 P P P LNCV6_20017_PI430048170 mRNA
CTTTCAACTCTTCTGAGCTTCCTAAGTGACGTTTTTGCAGGTATTTTCAATAAAAAGAAG NM_001195541 RefSeq
chr7 + 99598278 99610833 GS1-259H13.2 NA "transmembrane protein 225-like, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139946_PI430048170 0.0210406552902361 0.3388101310845170.410281217233856
1.27586118404662 0.343778109142624A A A 2.50013943370185 2.08513636039118
2.29701313560405 P A A LNCV6_139946_PI430048170 mRNA
TGTGGAAAATACCCTGCTAAATAGTCAGATGGTTTCAACTGATAACTCTTTGTCTTCTCA NM_054024RefSeq chr14
+ 39233920 39253371 MIA2 117153 melanoma inhibitory activity 2
GO:0042632|GO:0070328|GO:0005576|GO:0070971 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127743_PI430048170 0.38475771214695 0.8399096314772738.25791689101556
7.50394019521067 7.36169716435784 P P P 8.08661775086036 7.9773288712513
7.98037962593128 P P P LNCV6_127743_PI430048170 mRNA
CCAGGCCCCGCTCCTGGCCTTGTATTCTCTCTGCTCTGTTATTAAAAAGCAAGCAAGTGG NM_001167986 RefSeq
chr17 - 4988129 4997610 INCA1 NA "inhibitor of CDK, cyclin A1 interacting protein 1, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_128460_PI430048170 0.0964025871235668 1.03907635675824 0.38906526876029
0.40250135412467 0.454015116750957 A A A 0.3483691646842220.341265813616744
0.390369798623624 A A A LNCV6_128460_PI430048170 mRNA
GCTTTCTGAATATAGACTTTCTGGGAAAAGGTTTACTGCTCGTAAGGAAACATTTTATGT NM_000275 RefSeq
chr15_KI270905v1_alt - 5440 233611 OCA2 4948 "oculocutaneous albinism II, transcript variant 1"
GO:0005515|GO:0033162|GO:0005215|GO:0005302|GO:0006726|GO:0008283|GO:0007286|GO:0030318|GO:0005
765|GO:0055085|GO:0005737|GO:0042438|GO:0005789|GO:0015828|GO:0016021|GO:0010008 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145729_PI430048170 0.893544798950067 1.00598895182523 0.375825526499377
0.5155057420132090.406104322984012 A A A 0.5117437999405090.380476603830198
0.379079341508238 A A A LNCV6_145729_PI430048170 mRNA
CCTGGGTCTTGAGGAGTTCAATGTATGTCTATTTCTCTTGATTCACTTGTCAATAAAGTA NM_205841 RefSeq chr5
+ 148202793 148215137 SPINK6 404203 "serine peptidase inhibitor, Kazal type 6, transcript variant 1"
GO:0010951|GO:0004867|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74872_PI430048170 0.6284690346171850.9014399791848183.79634181286144 3.07435828789462
3.29409559809442 P A P 3.77093191585743 3.13545790098924 3.72242139495693 P P P
LNCV6_74872_PI430048170 mRNA
AGCTGTTTCAGTGCAGGGCTTCCTAAAACAGAAGCCAACTGGGTGAATGTAATAAGTGAT NM_172175 RefSeq chr4
+ 141636595 141733987 IL15 3600 "interleukin 15, transcript variant 2"
GO:0005515|GO:0008284|GO:0007267|GO:0032819|GO:0005615|GO:0071305|GO:0048535|GO:0005737|GO:0006
955|GO:0006954|GO:0042102|GO:0045580|GO:0048469|GO:0001779|GO:0032740|GO:0005794|GO:0009986|GO:0
042517|GO:0007568|GO:0048662|GO:0005576|GO:0014732|GO:0032825|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_111266_PI430048170 0.0528337974931587 1.32403414120588 10.857793909395
11.0852513573575 11.1709528059258 P P P 10.5301548108663 10.5012546828418 10.857793909395
P P P LNCV6_111266_PI430048170 mRNA
GGACCCTAAAGTTTGTAACATCAGATATCGGGAATAAATTCTATCACGTTACCACTAATA NM_016067 RefSeq chr4
+ 83455931 83461723 MRPS18C 51023 "mitochondrial ribosomal protein S18C, transcript variant 1"
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0022627|GO:0005743|GO:0006
412|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127053_PI430048170 0.3087058701414841.19177617823897 0.492907182307612
0.3535425961370740.926915365636789 A A A 0.2946982982513280.362364961658932
0.417950243618735 A A A LNCV6_127053_PI430048170 mRNA
GTTGTACTGTCAAGGGGCAGCATTTCTGGTATTTCTATAATAAATTTTTCTGTGATCTCA NM_175078 RefSeq chr12
- 52689625 52703463 KRT77 374454 "keratin 77, type II"
GO:0008150|GO:0003674|GO:0005198|GO:0045095|GO:0005856|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143707_PI430048170 0.0404712136708686 0.5635497945160214.7606191853492
4.6857809611901 4.6774674621099 P P P 5.72238332215769 5.65410419775096
5.17092338826492 P P P LNCV6_143707_PI430048170 mRNA
TACCTCCCCCATCTGCTGACAGTAGCTGAAGATTATTCTAAACATTCATTCTTTTAGATT NM_152609 RefSeq chr1
+ 246566336 246668582 CNST 163882 "consortin, connexin sorting protein, transcript variant 1"
GO:0030133|GO:0005802|GO:0005515|GO:0043234|GO:0016020|GO:0005886|GO:0019902|GO:0042998|GO:0010
923|GO:0016021|GO:0071253 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126684_PI430048170 0.4883393786183611.32690446846444 0.833320834750948
1.96778171487325 1.94902207038911 A A A 0.3214009724844321.67446208280463
1.46419818198721 A A A LNCV6_126684_PI430048170 mRNA
AACCACAGTATAACTAAGAAATGGCATAGAGTGAGGGGCACTGAAAGAAACTGCCCGTTC NM_016484 RefSeq
chrX - 70286360 70289948 PDZD11 51248 PDZ domain containing 11

GO:0005515|GO:0015939|GO:0006768|GO:0045202|GO:0006767|GO:0005576|GO:0044281|GO:0006887|GO:0008022|GO:0055085|GO:0045199|GO:0007269|GO:0005829|GO:0016323|GO:0034220|GO:0008105|GO:0005911|GO:0006766 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132864_PI430048170 0.6169246004445420.356006053698399 1.65854908150198 2.29298017975601 1.10793845026314 A A A 4.46994489379937 0.330587674301156 2.39763536772341 P A P LNCV6_132864_PI430048170 mRNA
AAGGGCTTCCAATACTCTCTGGAGGATCCTGACTCGTTTGGAGTATTATCCTTGTAAAAG NM_145019RefSeq chr13 + 51222333 51284241 FAM124A 220108 "family with sequence similarity 124A, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138344_PI430048170 0.2651217423621080.7404870741662072.71247355152477 3.32433538607651 3.48068808684524 A P P 3.71990351283205 3.94628185826023 3.14771575718152 P P P LNCV6_138344_PI430048170 mRNA
ACCTCTTTTCCCCCACTGATGTGAGAGGCTGCATTTTTCATCTAATAAAATCGAATATAT NM_001042549 RefSeq chr1 - 212726152 212791797 NSL1 25936 "NSL1, MIS12 kinetochore complex component, transcript variant 2"
GO:0005515|GO:0007067|GO:0007059|GO:0005634|GO:0000444|GO:0000278|GO:0051301|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112280_PI430048170 0.0571840427774875 0.5729565430914284.04943023427824 4.43108658482157 4.80461145222669 P P P 5.21614143231154 5.2267284752266 5.34723464937436 P P P LNCV6_112280_PI430048170 mRNA
GGAATTATGTTTAGCACCTTTGAGTTCTGCAAGAGAATCTGTCTTTATCAAAATGGTTAC NM_145305RefSeq chrX + 119399294 119454474 SLC25A43 203427 "solute carrier family 25, member 43"
GO:0005743|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98574_PI430048170 0.3029899520203771.13758182471394 5.89678749509272 5.61843420310126 5.91543967317297 P P P 5.73506128789906 5.75874826461 5.36491567350937 P P P
LNCV6_98574_PI430048170 mRNA
AGACATGAAGTATAAGAACCGTGTACGGAGTCGTATCTCCAACCTGAAGGATGCCAAGAANM_003195RefSeq chr20 + 64062656 64072347 TCEA2 6919 "transcription elongation factor A (SII), 2, transcript variant 1"
GO:0005515|GO:0005813|GO:0006354|GO:0032784|GO:0045944|GO:0008270|GO:0005654|GO:0008023|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143960_PI430048170 0.00410246840466852 0.2263365370094773.95544749953655 3.95917261727781 4.19200763411801 P P P 6.49173251938884 5.79379576415238 6.18082114873424 P P P LNCV6_143960_PI430048170 mRNA
CTGAGCCTTGTAAGTGTACAAAAATTATTCTTATTTTGTTCTGTCTCGGGAAACTGCAAA NM_001220RefSeq chr7 - 44217149 44325631 CAMK2B 816 "calcium/calmodulin-dependent protein kinase II beta, transcript variant 1"
GO:0005516|GO:0090129|GO:0005886|GO:2001235|GO:0019221|GO:0007268|GO:0051233|GO:0042803|GO:0005829|GO:0034605|GO:0051823|GO:0000082|GO:0046777|GO:0018105|GO:0048169|GO:0051924|GO:0050885|GO:0006816|GO:0060998|GO:0004683|GO:0061003|GO:0060333|GO:0005815|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135029_PI430048170 0.000634070359542196 0.55356837712124 11.8588623296568 11.6772617907632 11.6823103698874 P P P 12.4771804657135 12.601796860042 12.6980044888725 P P P LNCV6_135029_PI430048170 mRNA
CGCTTGTTTTTCTCCTTTTGGTGTAATGTTTTACAAATCCTTTGGCCTGAGAACTAATAT NM_002224RefSeq chr6 + 33621378 33696571 ITPR3 3710 "inositol 1,4,5-trisphosphate receptor, type 3"
GO:0005515|GO:0060402|GO:0060291|GO:0070679|GO:0007173|GO:0043025|GO:0007613|GO:0051260|GO:0005220|GO:0030168|GO:0000822|GO:0043235|GO:0051592|GO:0043533|GO:0007186|GO:0008543|GO:0005887|GO:0045087|GO:0005789|GO:0070588|GO:0005654|GO:0038096|GO:0038095|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_141955_PI430048170 0.1725338902888451.07933169926154 9.18239203582027
9.29841046088057 9.13914688065952 P P P 9.14664440410606 9.13897885041655
9.00424921691634 P P P LNCV6_141955_PI430048170 mRNA
GCCCTAGGGATGACTGCTCCTTTATTTGTTGTTAATGAATCTTGACCTCCTTGTGTGAAA NM_199337RefSeq chr11
+ 62787401 62790400 TMEM179B 374395 transmembrane protein 179B GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136926_PI430048170 0.1046812276124750.7021075777804463.59656041032201 3.2735878486012
3.32390662012248 P P P 4.21897395330008 3.56100326090285 3.89145677679319 P P P
LNCV6_136926_PI430048170 mRNA
TTTCATTCAAGTTGGTGTAATCAGCTGGGGAGTAGTGGATGTCTGCAAAAACCAGAAGCG NM_001710RefSeq
chr6_GL000256v2_alt + 3247132 3253273 CFB 629 complement factor B
GO:0006957|GO:0030449|GO:0006956|GO:0005886|GO:0004252|GO:0001848|GO:0045087|GO:0006508|GO:0072
562|GO:0005576|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139261_PI430048170 0.5254978376942622.56488339972915 0.287131508547095
3.53122970701151 3.45700948745258 A P P 1.47796057219616 1.93437829566384
1.40984428980641 A A A LNCV6_139261_PI430048170 mRNA
AACAGCAATTAAAGAGGAAGTGATTTTGTCTAGGGGGTGAGCTGCTGGTCTGTTCTTGGA NM_001122772 RefSeq
chr12 - 57724292 57738246 AGAP2 116986 "ArfGAP with GTPase domain, ankyrin repeat and PH
domain 2, transcript variant 1"
GO:0005515|GO:0007264|GO:0042177|GO:0005730|GO:0005634|GO:0005525|GO:0015031|GO:0043547|GO:0005
739|GO:0008060|GO:0043524|GO:0016020|GO:0007411|GO:0032312|GO:0008270|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129556_PI430048170 0.15602821266714 0.7270355694918992.04830577238385
1.54087231467103 2.27260050003025 A A A 2.73490565087547 2.27685721990001
2.27321364302262 P A A LNCV6_129556_PI430048170 mRNA
GCAGTTTTTGCTAGTAAAAGACCAAGTTCCCCTCCTTTATAAGTAACTTAAAACAACACT NM_006529RefSeq chr4
- 174642010 174829315 GLRA3 8001 "glycine receptor, alpha 3, transcript variant 1"
GO:0034220|GO:0030054|GO:0022824|GO:0005886|GO:0005887|GO:0045211|GO:0034707|GO:0016594|GO:0055
085|GO:0016934 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142597_PI430048170 0.3058133113450490.78375329890651 1.30427388297142
0.4349069771995240.774941922515718A A A 0.8555517742340331.29369094940522
1.48441443864322 A A A LNCV6_142597_PI430048170 mRNA
ATCAGAACTAATCCAGAGTGTGGGAAAGTGACAGTCAAAACCCCACCTGGAGCAAATAAA NM_175629RefSeq
chr2 - 25232960 25342590 DNMT3A 1788 "DNA (cytosine-5-)-methyltransferase 3 alpha,
transcript variant 1"
GO:0005515|GO:0010467|GO:0000791|GO:0003886|GO:0006346|GO:0006325|GO:0010424|GO:0005634|GO:0007
283|GO:0046872|GO:0044027|GO:0016363|GO:0042802|GO:0045322|GO:0005737|GO:0071230|GO:0009008|GO:0
051718|GO:0043045|GO:0043046|GO:0001741|GO:0090116|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137199_PI430048170 0.000250991146995634 0.3300523840261596.11955915415831
5.89947362291601 6.08840293867741 P P P 7.61619434445351 7.48146215807541 7.7994253981056
P P P LNCV6_137199_PI430048170 mRNA
CTGGCTTGGTAATGAGCTCATTGTCCTTAACTTTTGCTTTATTGATTCACAATACACTTA NM_080664RefSeq chr14 -
31446035 31457474 DTD2 112487 D-tyrosyl-tRNA deacylase 2 (putative)
GO:0005515|GO:0008150|GO:0003674|GO:0006399|GO:0005737|GO:0002161|GO:0051500|GO:0005575|GO:0006
450|GO:0019478 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98356_PI430048170 0.6394372829523231.02466261117286 12.0008831572685 11.8994504558785
11.8412402618465 P P P 11.9495169381244 11.776282572508 11.9092318219945 P P P
LNCV6_98356_PI430048170 mRNA

TTGTTAGCAAGAGTGTTGAGCTAGTTCCTGGTGAAGTGTTTCCACAGAAGACATGTGGAG NM_024104RefSeq chr19
- 16646147 16660157 SMIM7 79086 "small integral membrane protein 7, transcript variant 2"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131636_PI430048170 0.9078549830259421.03506153654418 1.57502101889028
3.05073316018254 2.43997780635169 A A A 3.15497015266049 1.6586320218134
2.02228897313913 P A A LNCV6_131636_PI430048170 mRNA
AAATATGAATTGAATGGAGGGTCCTAATGCCTTATTTCAAAACAATTCCTCAGGGGGAAC NM_000313RefSeq chr3
- 93873036 93974090 PROS1 5627 protein S (alpha)
GO:0030449|GO:0004866|GO:0005886|GO:0005796|GO:0005509|GO:0030168|GO:0072562|GO:0005576|GO:0050
900|GO:0005615|GO:0010951|GO:0017187|GO:0000139|GO:0007596|GO:0045087|GO:0002576|GO:0005789|GO:0
006508|GO:0031093|GO:0044267|GO:0042730|GO:0070062|GO:0043687 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_108134_PI430048170 0.0639166663035559 0.76321882615523710.2752599836627
10.1569813515597 10.4833611693942 P P P 10.4981749770862 10.6784595890513 10.899469086214
P P P LNCV6_108134_PI430048170 mRNA
GAACCTATATACATGCACTCGACAATGGTCTTTTTACCCTGGGAGCTCCACACAAAGAAG NM_004477RefSeq
chr4_KI270896v1_alt + 278348 300735 FRG1 2483 FSHD region gene 1
GO:0005515|GO:0030018|GO:0015030|GO:0007517|GO:0000398|GO:0006364|GO:0005730|GO:0003779|GO:0071
013 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128954_PI430048170 0.7808330294907550.9017580623055487.63504428213895
7.53865416741501 7.29456500036284 P P P 7.05399283478026 8.07637301363646
7.62884150543028 P P P LNCV6_128954_PI430048170 mRNA
CACCAGCTCCAAATAAATGGACGCATGTTCAAACCCAAAGGCTCTTTTCAGAGCCACTTA NM_003524RefSeq chr6
+ 26251650 26252075 HIST1H2BH 8345 "histone cluster 1, H2bh"
GO:0046982|GO:0006334|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0003677|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145019_PI430048170 0.1523154744342731.09971083279036 4.5530959645113
4.63942203998857 4.61899514763963 P P P 4.59336542484926 4.3897626222998
4.40955760022002 P P P LNCV6_145019_PI430048170 mRNA
CCCAAAAAGCTACACCAAGCTAATAAACTGCGAGTTCCCACCCCACTTCCAGCTGGAATG NM_152533RefSeq chr3
- 126549675 126558965 C3orf22 152065 "chromosome 3 open reading frame 22, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136619_PI430048170 0.2034403855383590.9596072723425870.280241022886069
0.35846435322998 0.309147969841929 A A A 0.4366163641491210.341110322569228
0.347679393488937 A A A LNCV6_136619_PI430048170 mRNA
CCTTAAGTAATGACAGAAGATATATATGGCCAGACACATATGTATAAACTTTTCAGCAGC NM_014893RefSeq chrY
+ 14523745 14843968 NLGN4Y 22829 "neuroligin 4, Y-linked, transcript variant 1"
GO:0052689|GO:0005515|GO:0030054|GO:0009986|GO:0050804|GO:0045202|GO:0014069|GO:0071625|GO:0005
615|GO:0007416|GO:0042043|GO:0005887|GO:0045211|GO:0008152|GO:0035176|GO:0004872|GO:0007612|GO:0
050839|GO:0007158. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143129_PI430048170 0.1460149894500181.09333056459436 0.513687470973144
0.6822656244316010.599693258198942 A A A 0.37063226661735 0.489127056195515
0.548949820464311 A A A LNCV6_143129_PI430048170 mRNA
CTGAGACATGGATAGTGCCTACGTCTTTGGTTAAAGTGCAATAAACAAAGAACTATATAA NM_005159RefSeq chr15
- 34788095 34795726 ACTC1 70 "actin, alpha, cardiac muscle 1"
GO:0030240|GO:0042643|GO:0060047|GO:0005884|GO:0045471|GO:0031032|GO:0072562|GO:0060048|GO:0030
017|GO:0005615|GO:0005829|GO:0005737|GO:0055003|GO:0016887|GO:0055008|GO:0070062|GO:0030048|GO:0
043066|GO:0030049|GO:0042493|GO:0006915|GO:0005524|GO:0033275|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_142584_PI430048170 0.2859877313213310.9208870975375171 5.735272049113
15.4553387267963 15.5433777165739 P P P 15.7919821184331 15.678121251824
15.6301242801478 P P P LNCV6_142584_PI430048170 mRNA
GCAGTGAAGGAACTGAAATGAACCAGACACACTGATTGGAACTGTATTATATTAAAATAC NM_000999RefSeq chr17
+ 74203655 74209880 RPL38 6169 "ribosomal protein L38, transcript variant 1"
GO:0048318|GO:0010467|GO:0034463|GO:0003735|GO:0019083|GO:0007605|GO:0003723|GO:0006614|GO:0019
058|GO:0033291|GO:0006415|GO:0006412|GO:0006413|GO:0006417|GO:0005829|GO:0006414|GO:0001501|GO:0
000184|GO:0001503|GO:0016032|GO:0042474|GO:0022625|GO:0044267|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143777_PI430048170 0.4630958519446160.9287620661278446.05977025668107
6.23343925670351 6.37447417816023 P P P 6.34238309167587 6.15914291139844
6.48479011360325 P P P LNCV6_143777_PI430048170 mRNA
AGGAGTAGGATCATTCAGATTTACTCCAATAAAAGTATGCAACCCTTAAGCAAAGCTTTT NM_001160094 RefSeq
chr6 + 24667034 24705067 ACOT13 55856 "acyl-CoA thioesterase 13, transcript variant 2"
GO:0047617|GO:0005739|GO:0051289|GO:0008152|GO:0005819|GO:0005634|GO:0070062|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135102_PI430048170 0.1273024293945480.9456154622125 8.71967984062308
8.70014051285657 8.68259319419221 P P P 8.71729045337328 8.7954965621265
8.82960165988341 P P P LNCV6_135102_PI430048170 mRNA
TCCTCTTGGACTTGAGGGCATTGTGAAAAGCTTTGCTGTGATTTAAAAATGCCAGCAATT NM_058246RefSeq chr7
+ 157337016 157417439 DNAJB610049 "DnaJ (Hsp40) homolog, subfamily B, member 6, transcript variant
1"
GO:0005515|GO:0090084|GO:0048471|GO:0030018|GO:0045109|GO:0051087|GO:0005634|GO:0032781|GO:0005
829|GO:0005737|GO:0016020|GO:0006457|GO:0031072|GO:0005654|GO:0051082|GO:0043154|GO:0001671 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131992_PI430048170 0.0579902006174071 0.4527560340330694.09272895612604
3.17710367529378 4.08638182947651 P P P 4.96611083538768 4.97294449104543
5.02324078627131 P P P LNCV6_131992_PI430048170 mRNA
GAGACTAGACTCTAATGGATATGTTTATATAATTCCAAACACTCAGGTGTGTGAATGCAT NM_014639RefSeq chr5
- 95463894 95555005 TTC37 9652 tetratricopeptide repeat domain 37
GO:0005515|GO:0005737|GO:0035327|GO:0005654|GO:0005634|GO:0055087 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131893_PI430048170 0.1701382115323380.8752843058382028.30924812697624
8.30102474612555 8.12957264325059 P P P 8.36908364231139 8.61615757839054
8.32042751304262 P P P LNCV6_131893_PI430048170 mRNA
TCTCACTTATGGGACAGAAAGGCCACGCGCTGCTCATTGACTGCAGGTCCTTGGAGACCA NM_000154RefSeq chr17
- 75757936 75765199 GALK1 2584 galactokinase 1
GO:0005975|GO:0019388|GO:0044281|GO:0005524|GO:0005829|GO:0004335|GO:0005737|GO:0005534|GO:0016
020|GO:0019402|GO:0009405|GO:0046835|GO:0006012|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134582_PI430048170 0.1482950916507640.6768599661597964.37764863818642
3.87889336823492 3.41790277491835 P P P 4.65214887051203 4.60856808353403 4.2247610042191
P P P LNCV6_134582_PI430048170 mRNA
CTCCCCTCTTGTCTGTGGAAGATATCACATGAACTACCTAATTTTCAAGCATGGATCTCC NM_019117RefSeq chrX
+ 87517711 87670050 KLHL4 56062 "kelch-like family member 4, transcript variant 1"
GO:0008150|GO:0003674|GO:0005737|GO:0003779|GO:0005856 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138504_PI430048170 0.00323804625572907 0.3467098368611326.36158017461705
5.95953184978178 6.41434255592103 P P P 7.42747655681026 7.82528817395276

8.04283637027346 P P P LNCV6_138504_PI430048170 mRNA
GTGTGCAATTATGTGTATGGGAATGGAGTAGTGTTCATGATTTGTATCTACATCATCATA NM_001135586 RefSeq
chr5 + 134845967 134859735 C5orf24 134553 "chromosome 5 open reading frame 24, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142939_PI430048170 0.0295597674388325 0.5934396941392147.39139554959869
7.11641431798273 7.67101932593403 P P P 7.86756179321595 8.14341646404939
8.42565105941293 P P P LNCV6_142939_PI430048170 mRNA
TCTGCTCGTTCCGTGGTTATGTTTAAGACTATAGTATATGACTCTCTTCAAAGTATATCA NM_001025780 RefSeq
chr9 - 71865151 71911232 ABHD17B 51104 "abhydrolase domain containing 17B, transcript variant
2" GO:0016787|GO:0016020|GO:0008152|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119284_PI430048170 0.0101240023798947 0.7543404900424085.69745914074412
5.64605520003105 5.48075207871338 P P P 5.89839915912884 6.08946767770878
6.05812900232976 P P P LNCV6_119284_PI430048170 mRNA
TTGGGACACCTTGACTCCAAGCCCAGCAGTAAGTCCAACATGATTCGGGGCCGCAACTCA NM_001039469 RefSeq
chr11 + 63838927 63911020 MARK2 2011 "MAP/microtubule affinity-regulating kinase 2, transcript
variant 4"
GO:0005515|GO:0045180|GO:0005886|GO:0005884|GO:0050321|GO:0005634|GO:0030010|GO:0008289|GO:0005
739|GO:0032147|GO:0035556|GO:0046777|GO:0018107|GO:0016055|GO:0051646|GO:0000287|GO:0000422|GO:0
030295|GO:0005524|GO:0016328|GO:0045197|GO:0051493|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132842_PI430048170 0.0520227585318314 1.25305332755691 10.826012540945
11.1374228309859 10.9377994787231 P P P 10.7848657346204 10.5736747978626
10.5732657947935 P P P LNCV6_132842_PI430048170 mRNA
GGGGCTGCTCAGGCCGCCTAGCTGCCCCTTTGCCAGGTTAATAAAGCACTGACTTGTTAA NM_207340RefSeq chr11
- 66539263 66546200 ZDHHC24 254359 "zinc finger, DHHC-type containing 24"
GO:0008152|GO:0008270|GO:0016021|GO:0019706 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127141_PI430048170 0.1415279579593450.4872739055774110.263829712671681
0.4282512189409470.297589641317561A A A 0.4862376000187751.51235070936342
1.80503409580274 A A A LNCV6_127141_PI430048170 mRNA
AATGCTGCAAAATTCATCTTTTGGAGGGTGGGGGGAAAACCCAAAAACAACAACAAAAAA NM_152534RefSeq
chr3 - 27110902 27369460 NEK10 152110 "NIMA-related kinase 10, transcript variant 2"
GO:0004672|GO:0043406|GO:0004674|GO:0006468|GO:0070372|GO:0005524|GO:0046872|GO:0031954 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143312_PI430048170 0.6582025585767850.9386741382807010.396005089054826
0.3671479339286690.398866021591662A A A 0.3090422361273510.322775996470504
0.757777689691674A A A LNCV6_143312_PI430048170 mRNA
CTGGAGATTGAATTTGAGGCTGTTGATTAAAAGGAGACTTTAGCTTTGCTTGTAGTTTTT NM_198539RefSeq chr19
+ 36916328 36952743 ZNF568 374900 "zinc finger protein 568, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134307_PI430048170 0.3476524159689330.7865859930596090.299608461057556
0.2750748684701040.436240742872189A A A 0.5621144232495290.252773422094714
1.10793845026314 A A A LNCV6_134307_PI430048170 mRNA
CCTGCCAGAAAGTTGGTTCTTGCAAAATAGATTAACTTGATGACTATGTGTATATTGGAT NM_004744RefSeq chr4
+ 154743970 154753119 LRAT 9227 "lecithin retinol acyltransferase (phosphatidylcholine--retinol O-
acyltransferase), transcript variant 1"
GO:0005791|GO:0047173|GO:0048471|GO:0016746|GO:0007603|GO:0005771|GO:0032370|GO:0001523|GO:0019
841|GO:0042573|GO:0006776|GO:0001972|GO:0042572|GO:0005789|GO:0016021|GO:0007601 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_131366_PI430048170 0.5834750875933480.8632704958288170.460310957394068
0.4712618697902750.47368146506306 A A A 0.34437694988429 1.14112821889497
0.414784103710338A A A LNCV6_131366_PI430048170 mRNA
GGAGATAATTCCTACGGGGAATTCTTAAAACTGTGCTCAACTATTAAAATGAATGAGCTT NM_000397RefSeq chrX
+ 37780016 37813461 CYBB 1536 "cytochrome b-245, beta polypeptide"
GO:0045730|GO:0005515|GO:0002474|GO:0005886|GO:0050660|GO:0006801|GO:0050665|GO:0046872|GO:0030
425|GO:0005739|GO:0006954|GO:0016175|GO:0030670|GO:0043025|GO:0034765|GO:0090382|GO:0006811|GO:0
005791|GO:0042554|GO:0048010|GO:0005794|GO:0005244|GO:0051701|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144986_PI430048170 0.3228123088030511.84663851710585 1.23231508248422
2.13571390956057 0.278336731863592A A A 0.4977310632223680.403459887065377
0.654548275633792A A A LNCV6_144986_PI430048170 mRNA
ATCCTCAGAAAGTGCAGCATGGAGGAAAATCTGAACTCTAAGCAGAAGACTCTCCACTGA NM_012134RefSeq chr1
- 201896455 201946588 LMOD1 25802 leiomodin 1 (smooth muscle)
GO:0006936|GO:0016020|GO:0030239|GO:0005865|GO:0007015|GO:0003779|GO:0005523|GO:0051694|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74245_PI430048170 0.0112942766654948 0.4661541245587826.15318878317753
5.81188614808713 6.05955194880763 P P P 6.84900894271282 6.99260675664497
7.43992796055434 P P P LNCV6_74245_PI430048170 mRNA
CTCAGTTCCATATTTCATCCGTGAAAAACTTGCAATACGAGCAGTTTCAAGGAATAAATA NM_203284RefSeq chr4
+ 26320806 26435130 RBPJ 3516 "recombination signal binding protein for immunoglobulin kappa J
region, transcript variant 4"
GO:0060045|GO:0005515|GO:0010467|GO:0003700|GO:0006367|GO:0003139|GO:0007221|GO:0007219|GO:0060
716|GO:0042742|GO:0001103|GO:0048505|GO:0000122|GO:0000978|GO:0000979|GO:2000138|GO:0048733|GO:0
060486|GO:0005654|GO:0072602|GO:0045892|GO:0002437|GO:0003160|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134483_PI430048170 0.1085799458338780.8589330019650891 5.252233064197
15.0293452528596 14.9707277809481 P P P 15.339622940514 15.3348390843257 15.249759194271
P P P LNCV6_134483_PI430048170 mRNA
AAACCTGTTATGCCAAACAGTTGTACCACTGCTAATAAATGACCAGTTTACCTGAAAAAA NM_001861RefSeq chr16
+ 85799566 85807001 COX4I1 1327 cytochrome c oxidase subunit IV isoform 1
GO:0005515|GO:0007584|GO:0004129|GO:0005743|GO:0005634|GO:0006091|GO:0044281|GO:0055085|GO:0005
739|GO:0022904|GO:0016020|GO:0044237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136652_PI430048170 0.0850020078694803 1.5330031021093 3.15036253810883
2.60982669334213 2.54868301268018 A A A 1.77586127195137 2.35267087234644
2.33864205062937 A A A LNCV6_136652_PI430048170 mRNA
CCTTCTCTACTTATTTAAATTGCCACTGGAATAAATGTGCCTTTTGAAGCAAAGTCCAAA NM_198504RefSeq chr3
- 142961230 142963336 PAQR9 344838 progestin and adipoQ receptor family member IX
GO:0004872|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132436_PI430048170 0.0600703650409031 0.81116010147674 6.00212438154187
5.89724994668515 5.75640856519523 P P P 6.09981851423878 6.36187130097258
6.09385408801251 P P P LNCV6_132436_PI430048170 mRNA
TGCTCAATAATGAAATGGATGACTTCAGCTCTACCAGCATCACCAACGAGTTTGGGGTAC NM_178311RefSeq chr20
- 23985052 23988779 GGTLC192086 "gamma-glutamyltransferase light chain 1, transcript variant A"
GO:0019370|GO:0003840|GO:0006749|GO:0031362 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143373_PI430048170 0.0145433210551588 1.42275436525447 9.48660252953241
9.45681939111958 9.34899568444799 P P P 9.04802570096919 8.95369884387917
8.75265901105239 P P P LNCV6_143373_PI430048170 mRNA
CTTAAGAAGATGGGGGAGAAAACTTCCAAATGTTTATAAAGAAAGTCTGTCACCACAAAA NM_019103RefSeq chr22

- 29730955 29766980 ZMAT5 55954 "zinc finger, matrin-type 5, transcript variant 1"
GO:0008380|GO:0006397|GO:0008270|GO:0005654|GO:0005689 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128264_PI430048170 0.5819961317006031.11544647678605 4.99839373220373
5.26888672443508 4.85976386009245 P P P 5.47177084903432 4.69223459154589
4.24959450794014 P P P LNCV6_128264_PI430048170 mRNA
TTGACTCATGAGTATGACTTAGAGAAAACAGCTTTGCCTCAGTGTTCTCCACCCAGCTGA NM_012369RefSeq chr7
+ 143959926 143961015 OR2F1 26211 "olfactory receptor, family 2, subfamily F, member 1
(gene/pseudogene)"
GO:0050911|GO:0007165|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143781_PI430048170 0.0801768965499611 0.5020098685409448.12338564284201
8.22729367745512 8.18963729281557 P P P 8.54858997996023 9.37729322083975
9.43995042848788 P P P LNCV6_143781_PI430048170 mRNA
GACAATTTTGTGTAGGCTTTTTCTAAAGTCCAGTACTTTGTCCAGATTTTAGATTCTCAGNM_001290050 RefSeq chr19
+ 4903079 4962154 UHRF1 29128 "ubiquitin-like with PHD and ring finger domains 1, transcript
variant 3"
GO:2000373|GO:0005515|GO:0000987|GO:0000792|GO:0010467|GO:0004842|GO:0000790|GO:0008327|GO:0003
700|GO:0000791|GO:0008283|GO:0005657|GO:0016874|GO:0005634|GO:0035064|GO:0016363|GO:0042802|GO:0
042393|GO:0010216|GO:0042787|GO:0045944|GO:0016574|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132760_PI430048170 0.00298967623431192 1.69118491909131 4.21596670566622
4.0890558565663 4.18096747402931 P P P 3.47001146879199 3.48184637196145
3.25153795547978 P P P LNCV6_132760_PI430048170 mRNA
TCTCTGTTACTGCTTGGGCTATACCTGGGCATACTAATAAAGTATGGTATTGAAACTAAA NM_000412RefSeq chr3
+ 186665957 186678234 HRG 3273 histidine-rich glycoprotein
GO:0033629|GO:0005515|GO:0010468|GO:0014070|GO:0030308|GO:0004869|GO:0008285|GO:0005886|GO:0004
867|GO:0050730|GO:0050832|GO:0010543|GO:0072562|GO:0051894|GO:0046872|GO:0036019|GO:0010593|GO:0
006935|GO:0019865|GO:0032956|GO:0031093|GO:0008201|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142391_PI430048170 0.1382830436789391.14600297338374 6.71957765388451
6.52284429816478 6.4318162921842 P P P 6.27673728085378 6.36296957879207
6.45438133535578 P P P LNCV6_142391_PI430048170 mRNA
GGTAGTGAGCTGATCATCCACTTTCTTCTAAAATAAAGAGAAGAAAATGGCCAGTAAAAA NM_004375RefSeq chr17
- 54961205 54968703 COX11 1353 "COX11 cytochrome c oxidase copper chaperone, transcript variant
1"
GO:0005739|GO:0008535|GO:0007585|GO:0005507|GO:0004129|GO:0005743|GO:0009055|GO:0033132|GO:0016
021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145529_PI430048170 0.0248419457083455 0.5786980505423181 0.2298721744549
10.401096037694 10.4084854316103 P P P 11.4001421609437 10.8748147648873 11.090106684168
P P P LNCV6_145529_PI430048170 mRNA
GCCCAAAGAAAGAGCTACCTGGACCTTTTGTTTTCTGTTTGACAACATGTTTAATAAATA NM_001145RefSeq chr14
+ 20684176 20694186 ANG 283 "angiogenin, ribonuclease, RNase A family, 5, transcript variant 1"
GO:0005515|GO:0017148|GO:0090305|GO:0009303|GO:0050714|GO:0005634|GO:0019843|GO:0001556|GO:0007
202|GO:0005615|GO:0032431|GO:0030426|GO:0001541|GO:0007154|GO:0032311|GO:0032148|GO:0043025|GO:0
030041|GO:0006651|GO:0009725|GO:0008201|GO:0070062|GO:0042277|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131635_PI430048170 0.20504791974168 1.08312652432516 0.548878325913086
0.34274544244272 0.500246109030821 A A A 0.2841078985726310.376500807328901

0.391288758073353 A A A LNCV6_131635_PI430048170 mRNA
CCATGAAGATATGTATATTGTCATTGGATGTATGATGAGTGTTGTGATTGGAACTGATGA NM_017855 RefSeq chr4
+ 70196526 70204576 ODAM 54959 "odontogenic, ameloblast asssociated"
GO:0005737|GO:0042475|GO:0043205|GO:0005634|GO:0005576|GO:0031214 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144561_PI430048170 0.811395482517538 1.5742362972493 2.77172901402112
0.553531224435687 0.318182713877074 A A A 1.05865475897084 1.22090392598955
0.721163367836278 A A A LNCV6_144561_PI430048170 mRNA
CTGTTACGGACTGAGAAGTGTCCCTGCAAAATTCACAGACATAAATAAATAAATACGTAT NM_005773 RefSeq chr19
- 57940832 57947709 ZNF256 10172 zinc finger protein 256
GO:0005515|GO:0003700|GO:0007275|GO:0005654|GO:0005634|GO:0045892|GO:0003677|GO:0046872|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145429_PI430048170 0.00720688151237859 1.61235566113052 12.6544469532805
12.9266194713857 12.9568929335975 P P P 12.1274931369952 12.0877021103258 12.267789608561
P P P LNCV6_145429_PI430048170 mRNA
CTTCTGTGTAGACATGGTTCTGGTTTAACTAATATTTGTCTGTGTGCTACTAACAGATTA NM_178191 RefSeq chr1
+ 28236090 28238105 ATPIF1 93974 "ATPase inhibitory factor 1, transcript variant 3"
GO:0004857|GO:0005516|GO:0009986|GO:0051346|GO:0072593|GO:0045980|GO:0042030|GO:0001525|GO:0006
091|GO:0042803|GO:0005753|GO:0006783|GO:0005739|GO:0051289|GO:0001937|GO:0043532|GO:0030218|GO:0
051117|GO:0051260. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132796_PI430048170 0.108544039514017 0.899535669117123 0.262483441603027
0.269057929468385 0.412440837497675 A A A 0.361942744700114 0.548375791827747
0.490675205475556 A A A LNCV6_132796_PI430048170 mRNA
TCTTCTCCCTGGTGAAGGTAAAATACATAATAAAGCTGATCCTAAGGCTGATATCTGAAA NM_001195571 RefSeq
chr1 + 153217583 153219317 PRR9 NA proline rich 9 NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143069_PI430048170 0.813550167512328 1.08263454556122 1.39433953364481
0.479983794948476 0.517034761920944 A A A 1.22880514833487 0.420069040701756
0.43976159417899 A A A LNCV6_143069_PI430048170 mRNA
TAGGCTAGGTACCTAGGATGAGAAATCCCTGAACATGAGCCCAGTTATTCTTCCAGCAAA NM_001301851 RefSeq
chr11 + 125495213 125499526 LOC403312 403312 putative uncharacterized protein MGC39545 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132426_PI430048170 0.423578952911155 0.678503131602664 2.18891723346793
1.09347961104546 0.391444763503088 A A A 1.18308490712321 2.67684065579882
1.64763394727179 A P A LNCV6_132426_PI430048170 mRNA
TATGACTTTGCACATATTACAACTGCTCTAGGCCTCAGTTTTATCACCCATATAAATCAA NM_078470 RefSeq chr10
- 99708747 99732666 COX15 1355 "cytochrome c oxidase assembly homolog 15 (yeast), transcript
variant 1"
GO:0007585|GO:0004129|GO:0005743|GO:0044281|GO:0016627|GO:0006784|GO:0006783|GO:0005739|GO:0045
333|GO:0005746|GO:0006778|GO:0008535|GO:0006123|GO:0070069|GO:0016021|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130382_PI430048170 0.378336809293901 0.899792424424521 9.6719310694329
9.71362333578643 9.29603904622331 P P P 9.76855195560232 9.8358451168275
9.55505749156891 P P P LNCV6_130382_PI430048170 mRNA
TGTGGAGGGTCACCAGGTTGGGAACATGCTGGAAATAAAACAGCTGCAACCAAGAAAAAA NM_001258012
RefSeq chr17 - 74862496 74873031 FDXR 2232 "ferredoxin reductase, transcript variant 3"
GO:0005515|GO:0006694|GO:0006805|GO:0044281|GO:0006091|GO:0005739|GO:0006744|GO:0004324|GO:0005
759|GO:0015039|GO:0006700|GO:0016125|GO:0008202|GO:0055114|GO:0008203 . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_127963_PI430048170 0.000268284119087816 0.446159860600531 3.80056016885736
3.99713370546466 3.9052517253306 P P P 4.95696726761789 5.19610582455771
5.03936047053026 P P P LNCV6_127963_PI430048170 mRNA
GCCTTCCCATCAGGCCTATTTGTCTACCCAATAAAGCGTGTTTTTTCCAGAAACAAGAAG NM_005276 RefSeq chr12
+ 50103818 50111320 GPD1 2819 "glycerol-3-phosphate dehydrogenase 1 (soluble), transcript variant
1"
GO:0009331|GO:0004368|GO:0006094|GO:0004367|GO:0044281|GO:0042803|GO:0046168|GO:0005829|GO:0005
739|GO:0006127|GO:0051287|GO:0071356|GO:0006116|GO:0019432|GO:0071320|GO:0045821|GO:0006644|GO:0
006654|GO:0044255|GO:0070062|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126938_PI430048170 0.982025542835205 0.999621574070778 5.40257598106994
4.35279441779986 4.94216469735577 P P P 4.83410845025874 5.41762577177781
4.47526596527344 P P P LNCV6_126938_PI430048170 mRNA
GTGACAAACGCAATGCAAAAACAATCCTCTTTCTCTCTCTTAATGCATGATACAGAATAA NM_003836 RefSeq chr14
+ 100726864 100735130 DLK1 8788 delta-like 1 homolog (Drosophila)
GO:0010468|GO:0045746|GO:0003674|GO:0007219|GO:0048706|GO:0007275|GO:0016021|GO:0009791|GO:0005
615|GO:0030154|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133509_PI430048170 0.59079726029936 1.17160221462379 1.14651098884735
0.35600199459825 0.292895285841343 A A A 0.507040563659465 0.425765965718351
0.337067163025666 A A A LNCV6_133509_PI430048170 mRNA
CAGAAAGCCCGTATTTGTAAGATGCTTACCACCAAATAAATGTACATAGACTGTGAAAAA NM_032594 RefSeq chr14
+ 35534041 35537054 INSM2 84684 insulinoma-associated 2
GO:0006355|GO:0005737|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136651_PI430048170 0.301763974642377 0.947609751230194 0.3490372744324
0.402935509695621 0.317193121696447 A A A 0.519163191458341 0.446895991652978
0.331112560003591 A A A LNCV6_136651_PI430048170 mRNA
CAGAATCTAAGGTCACACGTTCGTTTCTGTTTATCCAGTTTAAGAAACAGTTTTGCTATT NM_001011543 RefSeq
chrX - 152133310 152138578 MAGEA10 4109 "melanoma antigen family A10, transcript variant 1"
GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140709_PI430048170 0.431824028807545 1.0365725189087 13.16333962154
13.0053085742043 13.0149106307849 P P P 12.9941124076829 13.0244089725752
13.0149106307849 P P P LNCV6_140709_PI430048170 mRNA
GAGAAGGGCCTCTCTAGCAGTCAACTCCATTTGTAATAAAGCCCTAGCACTCTGAAAAAA NM_024099 RefSeq chr11
- 62662816 62671769 LBHD1 79081 LBH domain containing 1 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142320_PI430048170 0.36234458854991 1.18191479661597 0.889089162043781
0.317685475309531 0.352124076117741 A A A 0.314802290416792 0.305288018791742
0.289153592433688 A A A LNCV6_142320_PI430048170 mRNA
CCTAGCCAAAGCTCTGACTCGTTACCTATGTGTTTTTTAATAAATCTGAAATAGGCTACT NM_001141945 RefSeq
chr10 - 88935073 88991390 ACTA2 59 "actin, alpha 2, smooth muscle, aorta, transcript variant 1"
GO:0019901|GO:0009615|GO:0015629|GO:0005524|GO:0005615|GO:0005829|GO:0014829|GO:0030485|GO:0043
234|GO:0005737|GO:0006936|GO:0008217|GO:0072144|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_80484_PI430048170 0.144713394593107 1.29978718449472 3.7695407908405 4.0697889387937
3.86896590165033 P P P 3.84441277107554 3.23340250525438 3.44413620545988 P P P
LNCV6_80484_PI430048170 mRNA
TAGTGTCTCTAACTCATTACCATCCTACCTTTTTGGCACGGAAAGTAGCCACTCTCCTTA NM_001042413 RefSeq
chr9 - 3824127 4300035 GLIS3 169792 "GLIS family zinc finger 3, transcript variant 1"
GO:0001078|GO:0001077|GO:0005794|GO:0006366|GO:0045944|GO:0005654|GO:0005634|GO:0000122|GO:0000

978|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130659_PI430048170 0.5030916643205511.01798459657869 0.299122014711472
0.2737919098879480.369926044107595A A A 0.3241413371908170.266179806706043
0.27643502595961 A A A LNCV6_130659_PI430048170 mRNA
CTATTCCTTGGGAAAGGTATTTTGTACCATATGGGACTGAAATCATTTATCTGGATGAAT NM_182703RefSeq chr15
+ 64911901 64958699 ANKDD1A 348094 ankyrin repeat and death domain containing 1A GO:0007165
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61093_PI430048170 0.16985082077297 0.3895457392112520.3047942962261 1.64797663865628
0.325148747633157A A A 0.8900713939928862.94574680368797 2.28514107975789 A P A
LNCV6_61093_PI430048170 mRNA
CATAACCACAGGCTGCTGTTTTCAAGAAGAGCAATCTGTTTGGATAAGAAAAACCTTTAC NM_173462RefSeq chr14
+ 73237496 73274639 PAPLN 89932 "papilin, proteoglycan-like sulfated glycoprotein"
GO:0010951|GO:0004867|GO:0006508|GO:0008270|GO:0004222|GO:0005604 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135229_PI430048170 0.0336157478143086 0.71097212326828 0.385913971574731
0.6394635625469930.289593150071446A A A 0.9924442108566960.898468162586201
0.921781221153995A A A LNCV6_135229_PI430048170 mRNA
CGTGGGGCTTGTAATCTGTCTCTTTCTACTATTTACATCTGATTTAAATAAACCATTCCA NM_013416RefSeq
chr22_KI270877v1_alt + 81781 101331 NCF4 4689 "neutrophil cytosolic factor 4, 40kDa, transcript
variant 2"
GO:0005515|GO:0048010|GO:0002474|GO:0051701|GO:0042590|GO:0032266|GO:0043085|GO:0005829|GO:0006
955|GO:0016020|GO:0016176|GO:0046983|GO:0002479|GO:0032010|GO:0043020|GO:0090382|GO:0010008|GO:0
055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141648_PI430048170 0.2877146542544081.04929431648832 0.345437500035662
0.3485052928550590.489958695240215A A A 0.3234767947606830.300636246747413
0.355773865557358A A A LNCV6_141648_PI430048170 mRNA
ATTTGAAAACACTGCTGTTCTTTAAATGCGTTCCTCATCCATGCAGATAACAGCTGGTTG NM_006272RefSeq chr21
- 46598617 46605122 S100B 6285 S100 calcium binding protein B
GO:0005515|GO:0048471|GO:0008284|GO:0008283|GO:0048708|GO:0008360|GO:0060291|GO:0005634|GO:0007
409|GO:0005615|GO:0042803|GO:0042802|GO:0043231|GO:0005737|GO:0050786|GO:0048168|GO:0007611|GO:0
043025|GO:2001015|GO:0007613|GO:0043123|GO:0043065|GO:0005509|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_84746_PI430048170 0.7937088077963010.9576442580140597.54029377589296 7.90253218934476
7.53482720308402 P P P 7.83977529292003 7.9060978974709 7.4002297927137 P P P
LNCV6_84746_PI430048170 mRNA
CACAAGCTCCGTGGACGGTGGCTTGGGGGCCCTGCCCCAACCTACCTCAGTGCTGTCCCT NM_001761RefSeq chr16
+ 2429393 2458858 CCNF 899 cyclin F
GO:0005515|GO:0007067|GO:0016567|GO:0005814|GO:0010826|GO:0005634|GO:0001890|GO:0031146|GO:0000
320|GO:0019005|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140484_PI430048170 0.5240790249890071.8379423468744 2.47876748424508
0.5275247979630450.300795361227591A A A 0.4002832495718940.795706834236648
0.517682698393917A A A LNCV6_140484_PI430048170 mRNA
TATCTGCTCTTACCACCTGTGCTGAACCCTATCATTTACAGCTTGAAGACCAAGACAATC NM_001004759 RefSeq
chr11 + 4881818 4882883 OR51T1 NA "olfactory receptor, family 51, subfamily T, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136732_PI430048170 0.9585796173099221.00002749872255 11.6606623236292
11.9133103102867 11.5924339888471 P P P 11.6616488134423 11.7579130408239
11.7645922142597 P P P LNCV6_136732_PI430048170 mRNA
GGAAGAAGTGTAACTCACCAGCCTCTGCTCTTATCTTTGTAATAAATGTTAAAGCCAGAA NM_002250RefSeq chr19

- 43766532 43781257 KCNN4 3783 "potassium channel, calcium activated intermediate/small conductance subfamily N alpha, member 4"
GO:0005515|GO:0005516|GO:0005886|GO:0030322|GO:0050714|GO:0007268|GO:0045332|GO:0016286|GO:0006884|GO:0016323|GO:0071435|GO:0016324|GO:0008076|GO:0043025|GO:0006816|GO:0006813|GO:0071805|GO:0046541|GO:0019903|GO:0022894|GO:0006952|GO:0050862|GO:0045121|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139180_PI430048170 0.1970964514849170.4660232781231480.325468813643501 0.3543936880234630.356060139000669A A A 0.35412516154642 1.47353765401825 2.04384444985736 A A A LNCV6_139180_PI430048170 mRNA GCAATACCAATCTAGAGAGTCCAAGCTGGTGAACTATTAAGCTGTTTAAAGATCACCCTT NM_153259RefSeq chr1 - 84925582 84997122 MCOLN2 255231 mucolipin 2
GO:0034220|GO:0005886|GO:0070588|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139701_PI430048170 0.3094842562034950.9430501978763831 2.3492627042509 12.5331561587721 12.4777944345373 P P P 12.6219999068274 12.539321969592 12.453896060737 P P P LNCV6_139701_PI430048170 mRNA GTGGGTTTTTGTATCTGAATTTGCTGTCTTGAACATAAAGAATCTATCTGCTGTTGGAAA NM_005716RefSeq chr19 - 14477758 14496149 GIPC1 10755 "GIPC PDZ domain containing family, member 1, transcript variant 1"
GO:0005515|GO:0007268|GO:0030139|GO:0006605|GO:0032435|GO:0042803|GO:0005829|GO:0005737|GO:0031647|GO:0043197|GO:0048167|GO:0043198|GO:0005938|GO:0070062|GO:0030511|GO:0012506|GO:0032467|GO:0005102|GO:0003779|GO:0030165|GO:0014047|GO:0008021|GO:0005903|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_50120_PI430048170 0.2890631257912361.023532922573 0.3150371837884750.245740310011407 0.316677896246064A A A 0.2653087441507550.2459706416063170.266541559021774A A A LNCV6_50120_PI430048170 mRNA ACTGTGTGTCTCATGGTATGTAACTCTTAAAGCAAATAAATGAACTGACTTCAACTGGGA NM_000566RefSeq chr1 + 149782693 149792518 FCGR1ANA "Fc fragment of IgG, high affinity Ia, receptor (CD64)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145154_PI430048170 0.0195546504809709 0.3813178625105370.30879892987766 0.3467172757636270.375181445806128A A A 1.92156435732797 1.89165417274906 1.31368372213663 A A A LNCV6_145154_PI430048170 mRNA GTGTGTGAACCTTACTCAAGGGTGTAGGTAAAAAATGGTAACAGTATACTTTTAGTAACA NM_001289930 RefSeq chr4 + 124475 164159 ZNF718 255403 "zinc finger protein 718, transcript variant 2"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92739_PI430048170 0.0567874834383901 0.5828157391174094.49867137950386 4.80175206746881 4.91339696382278 P P P 5.17338012289815 5.38042250612259 5.9214942916672 P P P LNCV6_92739_PI430048170 mRNA ATGATCCCCAAAGTCAACATATGACATTAAGCCAGGCATTTCACCTTAAAAACAATAGTA NM_001098525 RefSeq chr13 + 52455359 52476631 CKAP2 26586 "cytoskeleton associated protein 2, transcript variant 2"
GO:0005881|GO:0005813|GO:0005737|GO:0000922|GO:0000281|GO:0045944|GO:0015630|GO:0007026|GO:0006915 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130461_PI430048170 0.16560574678794 1.08149630361943 0.479902937732903 0.3017740241300880.427230343786934A A A 0.2949767633224120.272101743608859 0.308267978010424A A A LNCV6_130461_PI430048170 mRNA GCAGGTTGTCTTATTATGTGATCAACAGATGTCCAGGAACTAATGAGTGGAATTTAATAT NM_001251851 RefSeq chr17 - 8878915 8965712 PIK3R5 23533 "phosphoinositide-3-kinase, regulatory subunit 5, transcript variant 3"

GO:0051897|GO:0006661|GO:0030168|GO:0005634|GO:0044281|GO:0031683|GO:0014065|GO:0005829|GO:0005
737|GO:0046935|GO:0007186|GO:0016020|GO:0043551|GO:0007596|GO:0043406|GO:0006644|GO:0005944 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140054_PI430048170 0.0163851382753474 1.41583186048467 12.5438776568125
12.4851565984469 12.7177372836949 P P P 12.2659380833726 11.9441880648426 12.022110578842
P P P LNCV6_140054_PI430048170 mRNA
TTGTATCAGGGTTTTTCACGCTTTTGTAGAACTGAGGTTTCAATAAACAGTTTCAGTTGC NM_015680 RefSeq chr2
- 219171896 219176980 CNPPD1 27013 cyclin Pas1/PHO80 domain containing 1
GO:0019901|GO:0016021|GO:0000079 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139895_PI430048170 0.0424257955755124 0.812449568792228 10.1321142311422
10.0205641726963 10.294630569752 P P P 10.4307245123781 10.3604546323828 10.561082967973
P P P LNCV6_139895_PI430048170 mRNA
ATGGGAATCTTCTTGTCATTCTTTTTAAACGGATGATACCGATGGAAATAAAAGGTGGGA NM_001243351 RefSeq
chr7 + 151341760 151378461 NUB1 51667 "negative regulator of ubiquitin-like proteins 1, transcript
variant 1"
GO:0005515|GO:0006511|GO:0005737|GO:0016567|GO:0032436|GO:0005730|GO:0034612|GO:0005634|GO:0034
341 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79330_PI430048170 0.670665443540675 0.934367380281165 6.9192699364843 7.03957417877467
6.90513936374056 P P P 7.3540374625109 6.91608990335967 6.83594314336427 P P P
LNCV6_79330_PI430048170 mRNA
TCCTGCTCCGCTTCATGTCCCCTCCTGAGTAGTCATGTGATAATAAACTCTCATGTTATT NM_018487 RefSeq chr7
+ 150800765 150805120 TMEM176A 55365 transmembrane protein 176A GO:0016021|GO:2001199 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73315_PI430048170 0.0026817166572320 0.384075854083395 4.03805172197554 3.90768778492567
4.26162308058898 P P P 5.23152021887877 5.35870845339707 5.73298191270892 P P P
LNCV6_73315_PI430048170 mRNA
TCTCTTGGAGCTTTTTTGCATAGCAATTAAAGGTGTGCTATTTGTCAGTAGCCATTTTTT NM_001777 RefSeq chr3 -
108043093 108091088 CD47 961 "CD47 molecule, transcript variant 1"
GO:0005515|GO:0008284|GO:0022409|GO:0005886|GO:0050900|GO:0009617|GO:0050766|GO:0005887|GO:0007
229|GO:0007596|GO:0030198|GO:0050870|GO:0050729|GO:0007155|GO:0008228|GO:0070062|GO:0070053 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129793_PI430048170 0.0195757040670770 0.316683194063204 5.05154778714752
4.44250398731577 4.92834465908582 P P P 5.79040163083191 6.83823702657399
6.64045986610436 P P P LNCV6_129793_PI430048170 mRNA
ATCCAGTGTTACAATCAGTGTGAATGGCAAATAAACAGTTTGACAAGTACATACACCATA NM_001001890 RefSeq
chr21 - 34787800 34888690 RUNX1 861 "runt-related transcription factor 1, transcript variant 2"
GO:0005515|GO:0003700|GO:0071560|GO:0005634|GO:0042803|GO:0043231|GO:0031069|GO:2000872|GO:0071
336|GO:0005737|GO:0045944|GO:0030854|GO:0070491|GO:0030099|GO:0030853|GO:0035162|GO:0030097|GO:0
000975|GO:0000977|GO:0046982|GO:0005509|GO:0060216|GO:0009966|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_99541_PI430048170 0.225643781303557 1.20666881959421 6.07747662738245 5.87201169856893
5.82477782233182 P P P 5.31723013220608 5.8826337166434 5.7170939730202 P P P
LNCV6_99541_PI430048170 mRNA
TTTACTGCAAAGGATGTTATGCTAAAAACTTCGGGCCCAAGGGCTTTGGTTTTGGGCAAG NM_001193571 RefSeq
chr1 - 201483529 201506839 CSRP1 1465 "cysteine and glycine-rich protein 1, transcript variant 4"
GO:0070527|GO:0008270|GO:0005634|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139291_PI430048170 0.00324363227056742 4.85631175796808 2.30610014862806
2.83794250204723 2.72512868989196 A A A 0.278100138457385 0.416671147473128

0.383817261727282 A A A LNCV6_139291_PI430048170 mRNA
GAACACTTTCAGGACTTTTTAGCCAGTTTGCCTTTCTTGAAAAATGTTATGTTTTCAGCA NM_017413 RefSeq chrX
- 129645258 129654956 APLN 8862 apelin
GO:0007165|GO:0006955|GO:0001664|GO:0007595|GO:0005179|GO:0023052|GO:0005102|GO:0005576|GO:0005
615|GO:0031704 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69473_PI430048170 0.453499334438321 1.2464421543903 3.47168193340682 3.37838295408819
2.76177651462173 P P A 3.09149544491323 3.31790658515552 2.0665223071843 P P A
LNCV6_69473_PI430048170 mRNA
ACAAGATCTGAGCTTCAACAAGAACCTGAGGGCTGTGGTGTCAGTGCTGGGCTCCTGGCT NM_001161616 RefSeq
chr19 - 11394055 11419342 RGL3 57139 "ral guanine nucleotide dissociation stimulator-like 3,
transcript variant 1" GO:0005622|GO:0008321|GO:0007264|GO:0017016|GO:0032852 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_128934_PI430048170 0.0970606516587928 0.7120695578469398.9833761517787
8.73285979835042 8.91260790343146 P P P 9.67207028215081 9.29854204948916
9.07559266199073 P P P LNCV6_128934_PI430048170 mRNA
GAGGAGCCTTAGTGGAGATTCCAGGTGAATATTTATGAAAAAGTCAACATTAGAACTGAA NM_005858 RefSeq chr19
- 15353520 15379801 AKAP8 10270 A kinase (PRKA) anchor protein 8
GO:0034237|GO:0000793|GO:0007076|GO:0005794|GO:0005634|GO:0016363|GO:0005739|GO:0007165|GO:0007
067|GO:0001939|GO:0003690|GO:0016020|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_135563_PI430048170 0.00120912966318643 0.1791561272240233.12760469515308
3.06368611498188 2.43245228209348 A A A 5.04338891029113 5.54247670778761
5.52353278823199 P P P LNCV6_135563_PI430048170 mRNA
GAGCCTAAATTTAGTTCAGCTTACCTTTGAGAATAGCATCAATTCAGACTCTCTTTTCAT NM_020455 RefSeq chr6
+ 142301918 142446266 ADGRG6 NA "adhesion G protein-coupled receptor G6, transcript variant a1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132206_PI430048170 0.0227211638292526 0.692874042474908 8.33116357878114
8.36640148743169 8.68791025935671 P P P 9.06384373012805 8.8241547747678
9.09778424106526 P P P LNCV6_132206_PI430048170 mRNA
GCAAAACTGATTTACTGGTTTGCCTTTCAGTTTGTTGAAATGTATTGTCAAGTACTGTAC NM_022366 RefSeq chr1
- 246540560 246566263 TFB2M 64216 "transcription factor B2, mitochondrial"
GO:0042645|GO:0003712|GO:0010467|GO:0031167|GO:0006996|GO:0005759|GO:0006391|GO:0007005|GO:0006
390|GO:0045893|GO:0000179 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142215_PI430048170 0.0340812137550874 0.604929616922193 3.55777705883746
4.18130905185754 3.9185126555559 P P P 4.57943682973053 4.83448554533584
4.46041592214733 P P P LNCV6_142215_PI430048170 mRNA
GAGTTTCATCCAACATTCTTGTTCTGCAGGTTGCTTTTATAAAGAAGGTGAACTATTTTC NM_030763 RefSeq chrX
- 81113700 81201942 HMGN5 79366 high mobility group nucleosome binding domain 5
GO:0006355|GO:0006357|GO:0003682|GO:0031492|GO:0005730|GO:0005654|GO:0005634|GO:0045893|GO:0000
785|GO:0006351|GO:0043231|GO:0016568 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_135999_PI430048170 0.0271190715269793 1.31826608386029 9.81378752303138
9.55353595886281 9.54330863256475 P P P 9.34036164587545 9.27950518966508
9.10083865762428 P P P LNCV6_135999_PI430048170 mRNA
TAGAGACGTAGCTGACCAAAAAGTAGGGGAGGGGCTGGGTCTGCAAATTAATAAATAGAA NM_001099737
RefSeq chr19 + 12666803 12675832 WDR83 84292 "WD repeat domain 83, transcript variant 1"
GO:0005515|GO:0005737|GO:0000398|GO:0000375|GO:0005681|GO:0071013 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_129549_PI430048170 0.990812610670821 1.00099545398135 10.4016724160282

10.1432108924211 10.1047120725254 P P P 10.303962823672 10.268998440386
10.0809241383442 P P P LNCV6_129549_PI430048170 mRNA
ATAAGTCAATTCCTGGAATTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCAGAAAAAA NM_005514 RefSeq
chr6_GL000256v2_alt - 2656109 2659450 HLA-B 3106 "major histocompatibility complex, class I, B"
GO:0002474|GO:0005886|GO:0005783|GO:0019221|GO:0051087|GO:0006955|GO:0060337|GO:0042605|GO:0030
670|GO:0071556|GO:0016032|GO:0070062|GO:0060333|GO:0042270|GO:0012507|GO:2001198|GO:0002480|GO:0
005794|GO:0002486|GO:0009986|GO:0042612|GO:0042590|GO:0005102|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127189_PI430048170 0.4103498234878 0.864118120862544 5.64401329071069
5.34395121799468 4.90764853272197 P P P 5.5737005018525 5.71203774241691
5.30597118957395 P P P LNCV6_127189_PI430048170 mRNA
CCACTAAGAAAGCCCCAGCCCATCAGTGGCTAATGGCTTTAATAAATTGGTCATTTGGCT NM_001098213 RefSeq
chr3 + 11137092 11263253 HRH1 3269 "histamine receptor H1, transcript variant 1"
GO:0005886|GO:0004930|GO:0048016|GO:0007200|GO:0004969|GO:0005737|GO:0006954|GO:0045907|GO:0007
186|GO:0048167|GO:0005887|GO:0008542|GO:0048245|GO:0043114|GO:0032962|GO:0005654|GO:0007613|GO:0
071420 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67501_PI430048170 0.290857550092589 1.0303597405183 0.308545185784499
0.251268325776618 0.355416625155559 A A A 0.271209534543808 0.244077116683375
0.272206317069257 A A A LNCV6_67501_PI430048170 mRNA
CTTCTGAACCATATGGTTCTGATGTCAGAGCCAGTGTAGTAAAGAGCTTCTGCTGTTCCT NM_173635 RefSeq
chr19 + 51257709 51269328 SIGLECL1 284369 "SIGLEC family like 1, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126822_PI430048170 0.924880487846493 1.00359042381472 13.354658790055
13.2881211573614 13.2460961398435 P P P 13.4215628156958 13.3040995839297
13.1355535735034 P P P LNCV6_126822_PI430048170 mRNA
TGACTTGTGAAAACGCAAACATGAATATGGTTGGAGAGCCCTGGATTAGGAGGGTGACAT NM_080822 RefSeq
chr17 + 2041982 2043431 OVCA2 124641 ovarian tumor suppressor candidate 2
GO:0005737|GO:0016787|GO:0008152|GO:0005634|GO:0032526 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_136757_PI430048170 0.878698718355655 0.981001313363316 11.935521381234
11.5771774989921 11.339495129733 P P P 11.8465678145263 11.7247519378413
11.3889360827592 P P P LNCV6_136757_PI430048170 mRNA
CTGCAAGGCAGCTCATACTTGTACTGTATGTTCAGAAATTTTAGGAGAGAAAAAAGTAAA NM_007022 RefSeq
chr3 + 50350694 50354065 CYB561D2 11068 "cytochrome b561 family, member D2, transcript
variant 1" GO:0016021|GO:0046872|GO:0055114 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142416_PI430048170 0.151395002902168 0.820738797399413 5.59521684543272
5.52111257583562 5.8580335198788 P P P 5.84586175838626 5.79448345048069
6.18003338859151 P P P LNCV6_142416_PI430048170 mRNA
GAGGACTGCCCTTTGGATGTTTAATCTTCATTAATAAATACCTCAAATGGCCAGTAACTC NM_018418 RefSeq
chr14 + 88385643 88438461 SPATA7 55812 "spermatogenesis associated 7, transcript variant 1"
GO:0005515|GO:0005930|GO:0015630|GO:0032391|GO:0045494|GO:0007601|GO:0050896|GO:0036064 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_131544_PI430048170 0.437359007984299 0.733819729210248 0.280640964415293
0.556765208141826 0.380013278882043 A A A 0.515393208039915 1.47845691471736
0.283804811508743 A A A LNCV6_131544_PI430048170 mRNA
TTTACTGAGAATTCAAAACTTCGTTTCCATCAAAGAATTCACACTGGAGAAAAGCCTTAC NM_001037813 RefSeq
chr19 + 44072143 44087470 ZNF284 342909 zinc finger protein 284
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA

NA NA NA NA
LNCV6_136696_PI430048170 0.58314328459629 0.963704452326955 0.273787773058
0.461367814523788 0.307534202376649 A A A 0.51160398659459 0.407505216414168
0.281419366388789 A A A LNCV6_136696_PI430048170 mRNA
CAGCAGTTCAACATGTGTAGTAGCTTTCAGTCTCTGCTGTTTGTGCCAAATATATAAGAA NM_022103 RefSeq
chr19 - 56439323 56477401 ZNF667 63934 "zinc finger protein 667, transcript variant 1"
GO:0003712|GO:0006357|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_132545_PI430048170 0.0875684045846944 0.802108396520654 11.433364012718
11.2247162102749 11.0652092191037 P P P 11.3891333272588 11.7080583791976
11.5864320767679 P P P LNCV6_132545_PI430048170 mRNA
CTGGAATCAGTGTTACTGCATCTGATTAAATGTCTCCAGAAATAAAGAATAATTCTGCCA NM_018067 RefSeq
chr1 + 36155964 36180849 MAP7D1 55700 "MAP7 domain containing 1, transcript variant 1"
GO:0005737|GO:0005198|GO:0005874|GO:0005819|GO:0000226 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132899_PI430048170 0.608390221857161 0.864796753740502 3.79055415778065
3.75416722164266 3.71779905264433 P P P 3.40032544885804 4.30649059003217
4.04203009831211 P P P LNCV6_132899_PI430048170 mRNA
TATTCTCCTGGTTACTTTCCCCCTTAGAGTTCCAGATGTACATGGTATATTTTGAAGTAG NM_199280 RefSeq chr2
+ 28981297 29052230 FAM179A 165186 "family with sequence similarity 179, member A" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136254_PI430048170 0.0101403159846847 0.453715523187618 5.48003618162603
5.15923365245111 5.75779978435 P P P 6.49687009788738 6.58437763985368
6.78285758979269 P P P LNCV6_136254_PI430048170 mRNA
TACCCAGTTTGACTCTACAGCCAGTGAAGTGGTTTATTGCTTCAATAAAAATATACTTGA NM_001286657 RefSeq
chr8 - 55738743 55763980 TMEM68 137695 "transmembrane protein 68, transcript variant 1"
GO:0016746|GO:0008152|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_64134_PI430048170 0.00807824435903841 1.90050555259507 4.73194919835381
5.13370879893514 5.08012330395493 P P P 4.04022147112177 4.17896940717422
3.97168471274281 P P P LNCV6_64134_PI430048170 mRNA
AGTTCAACCTCGCAGAGATCCTGTCACAGAACTACAGTGTTAGGGGGGAGTGCGAGGAGG NM_017550 RefSeq
chr19 - 305574 344791 MIER2 54531 "mesoderm induction early response 1, family member 2"
GO:0006355|GO:0003682|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_143470_PI430048170 0.0863924802263595 2.26062028666569 4.25152002987245
5.32440673866705 5.25722476807619 P P P 3.83164403392512 3.87075760524388
3.82801746620228 P P P LNCV6_143470_PI430048170 mRNA
TGGGTGAATCACAGTAATTTCCCTGTAAAATGTGGTACCTGAAGTCATATTTGAGATTCT NM_015660 RefSeq
chr7 + 150685705 150693640 GIMAP2 26157 "GTPase, IMAP family member 2"
GO:0005811|GO:0005737|GO:0016021|GO:0005525 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142826_PI430048170 0.161219306722148 1.32712728263822 0.595518778008898
1.16845623168427 1.14046336575018 A A A 0.487178809176416 0.52522448786339
0.724640813791964 A A A LNCV6_142826_PI430048170 mRNA
GGGGAGGGTCCGAGAGCCACTGTTACTTTCTGTTGTTCAATGAAGATGCTTTTGAACTTT NM_001205271 RefSeq
chr3 - 46719582 46736431 PRSS46 NA "protease, serine, 46" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_135275_PI430048170 0.0934805728993801 0.66414018695248 3.32971983486834

3.32645144348536 3.95748547075185 P P P 3.85494083817661 4.11417570801718
4.44939519650655 P P P LNCV6_135275_PI430048170 mRNA
TCCCCCTTTGAACTACCTTTGAAGTCACTATGAGCACATGGATAGAAATTTAACTTTTTT NM_153267 RefSeq
chr9_GL383541v1_alt + 19468 152600 MAMDC2 256691 "MAM domain containing 2, transcript variant 1"
GO:0019800|GO:0016020|GO:0005783|GO:0005539|GO:0005614 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_128585_PI430048170 0.0443929885967813 0.64638387505843 3.80103497643276
4.34305255340001 4.29380746455852 P P P 4.7168888598928 4.63390340934852
5.00808689165322 P P P LNCV6_128585_PI430048170 mRNA
CATTGTCAAATGAGAGCAAACTTTAGGTGTTGGCTCCATTGTACACTCTACTTGCTCTGC NM_018994 RefSeq
chr1 - 16246839 16352491 FBXO42 54455 F-box protein 42 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_145714_PI430048170 0.159189489646811 0.915305858034235 8.0679106986468
7.94619327734557 7.85866165807742 P P P 8.11560093361904 8.06696324548081
8.08046740178641 P P P LNCV6_145714_PI430048170 mRNA
AATTTTAACCTGGTTTCTTGTATGTAAACTCCTTGAGGGCAAGAACATGTTTGAACATAG NM_022917 RefSeq
chr9 - 33461352 33473943 NOL6 65083 "nucleolar protein 6 (RNA-associated), transcript variant alpha"
GO:0005739|GO:0000794|GO:0006409|GO:0032545|GO:0006364|GO:0032040|GO:0005730|GO:0005634|GO:0034
456 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58447_PI430048170 0.368170985521286 1.24249888151961 1.01042108933094
0.25381842126237 0.35884456811008 A A A 0.274569085328625 0.253463509230441
0.276661620720019 A A A LNCV6_58447_PI430048170 mRNA
ATGATGAGTGGCTCAGATATCAAATCTACAGACAAGCCCACGCTGTAAAACTGTGTCTGA NM_001080407 RefSeq
chr11 + 134276380 134319564 GLB1L3 112937 "galactosidase, beta 1-like 3"
GO:0005773|GO:0004565|GO:0005975 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131481_PI430048170 0.43860575489914 1.01929484645334 0.351826686034178
0.351198094602599 0.431839548270651 A A A 0.356597398876858 0.322331666036344
0.374238994489229 A A A LNCV6_131481_PI430048170 mRNA
CAGCTCCTCAATACTACCTGGAAAAAGCATTGGCATTATTTTCAATAAATATCAAGCACT NM_012317 RefSeq
chrX - 141175745 141177214 LDOC1 23641 "leucine zipper, down-regulated in cancer 1"
GO:0005515|GO:0008285|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127785_PI430048170 0.00457349299040634 1.55113076099635 12.4835631743767
12.6342247794958 12.363377032094 P P P 11.9587618548037 11.8136509420353
11.8167782805097 P P P LNCV6_127785_PI430048170 mRNA
CTGTGGCCTCAGGGCGCCTCCCAGTGCCAGAAAATAAAGTCCTTTTGGATTCTGAAAAAA NM_001135054 RefSeq
chr11 - 405715 414999 SIGIRR 59307 "single immunoglobulin and toll-interleukin 1 receptor (TIR) domain, transcript variant 1"
GO:0005515|GO:0007165|GO:0016020|GO:0001960|GO:0045079|GO:0031665|GO:0016021|GO:0006953|GO:0043
433 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127290_PI430048170 0.214793240486332 1.4821477360798 3.08750244410005
3.95964714383489 4.00057275644732 P P P 2.9236371923114 3.37108680805734
3.18550400281627 P P P LNCV6_127290_PI430048170 mRNA
TTCAAGACGGAGAAGAGGCTGTGCAAGATGTTCTACGCCGTCACGCTGCTCTTCCTGCTC NM_018971 RefSeq
chr3 + 71754049 71755177 GPR27 2850 G protein-coupled receptor 27
GO:0007165|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA
NA NA NA NA

LNCV6_127023_PI430048170 0.275384932206205 1.07475938997726 14.0960133992678
14.0696101791714 14.1034580254554 P P P 13.9051011455652 13.9137855977107
14.1272252534719 P P P LNCV6_127023_PI430048170 mRNA
GGTACAGTCTCATTTCCAAGTCATGTATAATCTTTATGGCTTCCAAGGACAAGAATTAAA NM_001256510 RefSeq
chr7_GL383534v2_alt + 111206 118188 SSBP1 6742 "single-stranded DNA binding protein 1,
mitochondrial, transcript variant 1"
GO:0005515|GO:0042645|GO:0006996|GO:0005634|GO:0005739|GO:0006260|GO:0003697|GO:0070584|GO:0003
682|GO:0005759|GO:0051096|GO:0007005|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143764_PI430048170 0.033660389172774 1.05200649340637 0.433144452216686
0.457382411379399 0.419386883673347 A A A 0.329816669876638 0.369466111402317
0.390794598991767 A A A LNCV6_143764_PI430048170 mRNA
TAAAAGTGACACTGAGCAAATAACCTCATCAGGTTATATTTGCCCACATACCCTAAGCAC NM_198474 RefSeq
chr11 + 7485368 7511375 OLFML1 283298 olfactomedin-like 1 GO:0005576 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_134103_PI430048170 0.547376896452431 0.942064994837335 14.680894518958
14.5407800833518 14.5989512867424 P P P 14.4793111392845 14.7387166517941
14.8407157286467 P P P LNCV6_134103_PI430048170 mRNA
CTGTATTTCCTGCTTCCCTGTTGAATTGGTGAATAAAACCTTGCTCTTTACATACAAAAA NM_021077 RefSeq
chr15 - 84655128 84658571 NMB 4828 "neuromedin B, transcript variant 1"
GO:0031710|GO:0043005|GO:0008284|GO:0007267|GO:0005576|GO:0042593|GO:0007204|GO:0046888|GO:0007
165|GO:0005179|GO:0007218|GO:0046887|GO:0050482 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145275_PI430048170 9.04279273600402e-05 0.353351860984015 7.99948613623864
7.96572186270625 8.08575649984138 P P P 9.40377767052414 9.58782788634787
9.5578208688021 P P P LNCV6_145275_PI430048170 mRNA
CAGGTTTGTTTCTTGATAGTTACTCAGACACTAGGGAAAGGTAAATACAAGTGAACAAAA NM_003472 RefSeq
chr6 - 18224168 18264568 DEK 7913 "DEK proto-oncogene, transcript variant 1"
GO:2001032|GO:0042393|GO:0007165|GO:0006366|GO:0006357|GO:0043292|GO:2000779|GO:0005634|GO:0019
079|GO:0003677|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141263_PI430048170 0.359457900639511 0.744582472736736 1.75456116682404
0.428130953737081 1.72635517989799 A A A 1.58879601377824 1.72175659787562
2.16233030960715 A A A LNCV6_141263_PI430048170 mRNA
GGAGAGAAACCTTATGAATGTACTGTTTGTGGAAAGGCTTTTAGTTACTGTGGATCCCTT NM_144694 RefSeq
chr19 + 37469057 37485358 ZNF570 148268 "zinc finger protein 570, transcript variant 2"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_130521_PI430048170 0.495469159965608 1.37598388975557 0.288676992996417
0.318521306268915 1.52760194559964 A A A 0.412608481865718 0.367219518791537
0.342963394302506 A A A LNCV6_130521_PI430048170 mRNA
CACTTGCCAGAATGTAATATTTGCTGTGAAGTGCTGAAAAGAAAAGTAACTTCCTTTTCA NM_001145777 RefSeq
chr6 - 35580556 35688942 FKBP5 2289 "FK506 binding protein 5, transcript variant 4"
GO:0005515|GO:0000413|GO:0061077|GO:0016020|GO:0006457|GO:0031072|GO:0005789|GO:0003755|GO:0005
528|GO:0005654|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128532_PI430048170 0.325402632368506 0.513614025419164 1.74094540056585
1.77141967262517 1.90111667641469 A A A 1.57305122505441 2.504049005928
3.55810286185139 A P P LNCV6_128532_PI430048170 mRNA
CAACTCGTTTTCTTCCCACATATCTAGTGTGACCTTTAAAAACCACAACTTTATTTTGGA NM_020964 RefSeq
chr18 - 45847608 45967339 EPG5 57724 ectopic P-granules autophagy protein 5 homolog (C.

elegans) GO:0005737|GO:0032456|GO:0006914 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145468_PI430048170 0.0250933069757216 1.4094399256291 6.12006030128833 6.23536184100411 5.87974852215087 P P P 5.53760948681128 5.76520585927319 5.45095244777453 P P P LNCV6_145468_PI430048170 mRNA GAAAAAGGATTTTGTGGTGGCCATCACTTTCATTCAATTTGCGACTGCTCTGATGGCACA NM_198586 RefSeq chr6 - 18120486 18122620 NHLRC1 NA NHL repeat containing E3 ubiquitin protein ligase 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128806_PI430048170 0.8918327150222521.11003765801809 2.44176214707038 0.2777613948697930.403975896311483 A A A 0.3640512871560091.51027651853148 1.60545348140993 A A A LNCV6_128806_PI430048170 mRNA GGGGAAAGGGAAGGCTAAAAATACTTGGTCAAATTTTAACATTATACCAAAGTTATACCC NM_001205220 RefSeq chr6 - 49834265 49877096 CRISP1 167 "cysteine-rich secretory protein 1, transcript variant 3" GO:0060046|GO:0007342|GO:0005246|GO:0005634|GO:0007339|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88939_PI430048170 0.2447320752667110.9031584817830564.77188434634484 4.81566636291777 4.97327336736294 P P P 4.89118455159229 4.93822320786504 5.16502093026713 P P P LNCV6_88939_PI430048170 mRNA TTCATCGGTACTCCAAGGTTCTGGAGGCCCATTTGGGAGACCCAAAACCTCGGCCTCTAC NM_003791 RefSeq chr16 - 84053760 84116943 MBTPS18720 "membrane-bound transcription factor peptidase, site 1" GO:0006629|GO:0034976|GO:0005794|GO:0004252|GO:0005795|GO:0031293|GO:0044281|GO:0042990|GO:0030968|GO:0000139|GO:0005789|GO:0006508|GO:0005788|GO:0016021|GO:0006987|GO:0044267|GO:0007040|GO:0008203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136291_PI430048170 0.0186617493084255 0.6501741417855428.06154832880344 7.82920305990223 7.70785731656778 P P P 8.43981211878347 8.48933760961338 8.55315766128911 P P P LNCV6_136291_PI430048170 mRNA GCTCTCTGCTTCCTTAGTCGGAAGTGTTTTCAACTAATCAAATAAATGAATGAATGATGA NM_024956 RefSeq chr15 + 43133523 43185143 TMEM62 80021 transmembrane protein 62 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137779_PI430048170 0.9705136029218030.9480963511868685.21117934271741 5.18565263538134 4.99272364792568 P P P 5.80506458707498 4.98225519730771 4.5559002893727 P P P LNCV6_137779_PI430048170 mRNA CCTGCATCAATAAAATGGGGCAGTGATGGCCTCCCACATTTGTCCCCTTCTTGGAAAAAA NM_001220500 RefSeq chr19 - 7688756 7702146 FCER2 2208 "Fc fragment of IgE, low affinity II, receptor for (CD23), transcript variant 3" GO:0005886|GO:0051712|GO:0046872|GO:0002925|GO:0019863|GO:0005178|GO:0007219|GO:0005887|GO:0051000|GO:0030246|GO:0051770|GO:0009897|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132065_PI430048170 0.36809195111258 0.6155557863824 0.284014078137935 0.3172660321204690.366314566484561 A A A 1.79223726907478 0.456365827927546 0.334206088199933 A A A LNCV6_132065_PI430048170 mRNA CGTGTGCCTTTGTACCCATTATAAGATGGTCATAAGACCCAAGAACTGATAAGCTTTGGT NM_003658 RefSeq chr11 + 129375985 129452279 BARX2 8538 BARX homeobox 2 GO:0005667|GO:0014902|GO:0000977|GO:0001502|GO:0045944|GO:0003682|GO:0005730|GO:0000122|GO:0001228|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127371_PI430048170 0.0685787172084260.7411813281030948.04778456424354 7.55972696617964 7.77227036029151 P P P 8.08046740178641 8.24414672073419 8.37786512676782 P P P LNCV6_127371_PI430048170 mRNA GGTACTACTGCCTCTGCAGCACAAATTTCTATTTCTGTCAATAAAAGGAGATGAAAATAT NM_001128620 RefSeq chr11 - 77322014 77474063 PAK1 5058 "p21 protein (Cdc42/Rac)-activated kinase 1, transcript

variant 1"
GO:0005515|GO:0030018|GO:0005518|GO:0060244|GO:0006887|GO:0046777|GO:0004702|GO:0007411|GO:0000165|GO:0023014|GO:0031965|GO:0032869|GO:0005794|GO:0019901|GO:0031532|GO:0016358|GO:0043234|GO:0045087|GO:0051496|GO:0042060|GO:0033148|GO:0000278|GO:0005925|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99425_PI430048170 0.905190429443963 0.991617254738104 13.661703697614 13.6286705164912 14.0232453878492 P P P 13.7086221236711 13.7143245917897 13.9480349938162 P P P LNCV6_99425_PI430048170 mRNA
TAAAGACAGCACTCTGATCATGCAGTTACTTAGGGACAATCTCACTCTGTGGACATCGGA NM_003404 RefSeq chr20 + 44885598 44908532 YWHAB 7529 "tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta, transcript variant 1"
GO:0051219|GO:0005515|GO:0008286|GO:0010467|GO:0048471|GO:0042826|GO:0007264|GO:0007265|GO:0005634|GO:0006605|GO:0051291|GO:0032403|GO:0050815|GO:0005829|GO:0005737|GO:0000186|GO:1900740|GO:0007173|GO:0000165|GO:0007411|GO:0017053|GO:0061024|GO:0030659|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127949_PI430048170 0.0451360488350624 0.403210412400739 4.57091876116464 4.71961853857441 4.70602350339126 P P P 5.3492193539923 6.21470407956744 6.20925634632015 P P P LNCV6_127949_PI430048170 mRNA
GAGACCCTGAAATGAACAATTATATTCTGACTCGACATCTTGTCCCCAATCCTTCCAAAA NM_006818 RefSeq chr1 + 151059674 151068497 MLLT11 10962 "myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11"
GO:0005622|GO:0003674|GO:0043065|GO:0051901|GO:0090200|GO:0097191|GO:0045893|GO:0097193 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140599_PI430048170 0.113593595977749 3.04046763615458 0.786876510247541 2.23933240284666 2.48987180316894 A A A 0.444713707220832 0.36768985857228 0.396831713104855 A A A LNCV6_140599_PI430048170 mRNA
TGACTTCTGGTGACATAGTAATAAAGTGAAGACTCAGAACCCACCAGCGATTGCAAAAAA NM_004711 RefSeq chr22 + 39349948 39385588 SYNGR19145 "synaptogyrin 1, transcript variant 1a"
GO:0042470|GO:0031594|GO:0030054|GO:0048169|GO:0030672|GO:0016021|GO:0006605|GO:0048172 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129481_PI430048170 0.273505350469288 1.65420081164763 1.87216447451804 0.938405744840989 0.450385071257997 A A A 0.280271672758957 0.767562428901875 0.356998128615795 A A A LNCV6_129481_PI430048170 mRNA
GGATTTTCTACAAGTGGACAGTCAAACTCCCCACACTAAAGTGGCAGTCATCGTTTACAC NM_022839 RefSeq chr15 + 88467452 88478630 MRPS11 64963 "mitochondrial ribosomal protein S11, transcript variant 1"
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0042769|GO:0005743|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70930_PI430048170 0.855438104307692 1.01221657839176 10.9651414208128 11.0691796424177 11.1441256303262 P P P 10.8786704282024 10.984853480409 11.2432204060813 P P P LNCV6_70930_PI430048170 mRNA
CCCTATTTTGGTGTTCAGCTTGAAAAAGGACTTGTCAGAATCAACTGTGTCATCAAAATT NM_019095 RefSeq chr20 + 6006092 6040051 CRLS1 54675 "cardiolipin synthase 1, transcript variant 1"
GO:0016780|GO:0036148|GO:0005743|GO:0044281|GO:0032049|GO:0016021|GO:0006644|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137810_PI430048170 0.144898880713929 0.645578007341056 9.8950787482884 9.91726900838822 9.84799810671309 P P P 9.97460230003961 10.6617604350394 10.7929023820924 P P P LNCV6_137810_PI430048170 mRNA
GACTAGCTGCTTGGCTGGATGTACAAAGAAATAGGCATTATTTTATTGCTGTAATATTGT NM_145804 RefSeq chr11 - 34150986 34358008 ABTB2 25841 ankyrin repeat and BTB (POZ) domain containing 2

GO:0003674|GO:0046982|GO:0097237|GO:0005654|GO:0005634|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140936_PI430048170 0.00924788717182869 2.00705716247164 6.59904279838683 7.13454730985612 6.84870755936615 P P P 5.99223921715476 5.68376143025614 5.92305352069173 P P P LNCV6_140936_PI430048170 mRNA TTCAGAGCCACCCACCTTTTCTGTAAAGTGCTGGAATACACATACGATGCCTGAAATCTC NM_021052RefSeq chr6 + 26216919 26217483 HIST1H2AE 3012 "histone cluster 1, H2ae"
GO:0008150|GO:0046982|GO:0005634|GO:0000786|GO:0003677|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131507_PI430048170 0.00991828290174842 0.819921105544251 9.52278113439431 9.47307909295114 9.36324278363662 P P P 9.72234699038877 9.68899105213421 9.80900730501259 P P P LNCV6_131507_PI430048170 mRNA TTATCCTTCCAGTTTCAAGTAGAATATATTCATAACCTCAATAAAGTTCTCCCTGCTCCC NM_147780RefSeq chr8 - 11842524 11868137 CTSB 1508 "cathepsin B, transcript variant 2"
GO:0005515|GO:0097067|GO:0048471|GO:0005518|GO:0005764|GO:0005615|GO:0043231|GO:0005739|GO:0005622|GO:0046697|GO:0022617|GO:0030198|GO:0051603|GO:0036021|GO:0030574|GO:0030855|GO:0006508|GO:0070062|GO:0042470|GO:0005730|GO:0043394|GO:0005576|GO:0042981|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127404_PI430048170 0.00134745619753685 0.651762434163786 10.4574699759083 10.4468537822497 10.2968272302959 P P P 10.9043676820855 11.0691796424177 11.0792808765186 P P P LNCV6_127404_PI430048170 mRNA CGGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTTAAACACAGATGTTTACAAAA NM_198686RefSeq chr14 - 64945813 64972157 RAB15 376267 "RAB15, member RAS oncogene family"
GO:0005515|GO:0048471|GO:0009306|GO:0005886|GO:0003924|GO:0072372|GO:0005525|GO:0072659|GO:0006886|GO:0006904|GO:0006184|GO:0005737|GO:0017157|GO:0032482|GO:0019003|GO:0010008|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138997_PI430048170 0.201298554498923 0.766484858185891 0.5331989557756 10.4851799162662 10.3932395654623 P P P 10.4522280251052 11.0969563520575 10.9414807411991 P P P LNCV6_138997_PI430048170 mRNA AAGGACTTCACCAAGCAGAAATACCCGGAGCACGCCATCCACAAGGTGCTGCAGCTCATG NM_006739RefSeq chr22 + 35400122 35424502 MCM5 4174 minichromosome maintenance complex component 5
GO:0005515|GO:0042555|GO:0005634|GO:0003677|GO:0005524|GO:0003678|GO:0006260|GO:0000082|GO:0006271|GO:0016020|GO:0006270|GO:0005654|GO:0032508|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140707_PI430048170 0.267180572924221 0.950380945892363 0.404765638234703 0.422935515405427 0.349226710688205 A A A 0.471230649528934 0.379079341508238 0.543222331091884 A A A LNCV6_140707_PI430048170 mRNA TTTACACGCTGAGAAACAGGGATGTAAAGGCAGCCATCACCAAAATCATGTCTCAAGACC NM_001005285 RefSeq chr11 - 75088750 75089713 OR2AT4 NA "olfactory receptor, family 2, subfamily AT, member 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143290_PI430048170 0.280647567019464 0.853346756086313 7.95818844332169 8.10721568041871 7.6142271475329 P P P 8.33044090439468 8.12091460570709 7.93013165299169 P P P LNCV6_143290_PI430048170 mRNA CAAAGCAACCCTGCCCACTCAGGCTTCATCCTGCACAATAAACTCCGGAAGCAAGTCAGT NM_000954RefSeq chr9 + 136977503 136981742 PTGDS 5730 prostaglandin D2 synthase 21kDa (brain)
GO:0005791|GO:0019369|GO:0019371|GO:0005215|GO:0048471|GO:0031965|GO:0005504|GO:0005794|GO:0045187|GO:0004667|GO:0051384|GO:0005576|GO:0044281|GO:0005615|GO:0001516|GO:0005501|GO:0005789|GO:0006810|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137099_PI430048170 0.684329794338837 1.18916692330186 1.14114871466456

0.4071786019444881.74555129840575 A A A 0.3687061521841571.4549432835531
0.813129655552881 A A A LNCV6_137099_PI430048170 mRNA
GTAAGGGTGGGGGTTGAAAGTTGTTATCTTTAAATACATGTACAAATCGTTGTCAAAAGT NM_014859 RefSeq chr17
+ 12789511 12991643 ARHGAP44 9912 Rho GTPase activating protein 44
GO:0005515|GO:0051056|GO:0031256|GO:0030054|GO:0007264|GO:0045202|GO:0006887|GO:0005829|GO:0043
547|GO:0005543|GO:0043197|GO:0055037|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133858_PI430048170 0.0116835665585191.44794469480483 11.12275456429
11.1094580731546 11.1018962483355 P P P 10.5983228638005 10.4610665318545
10.6653236281665 P P P LNCV6_133858_PI430048170 mRNA
CCTCTGTCTAGCATGCCAACAAGAATGCATTGATATTGTGAACATTTGTGATATATGTAT NM_004615 RefSeq chrX
+ 38561477 38688918 TSPAN7 7102 tetraspanin 7 GO:0005887|GO:0016032 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_134803_PI430048170 0.8903435431626651.00787596570165 0.265869359679761
0.2800173660210150.445173493582291 A A A 0.3502056234849150.301518095125198
0.311900141039496 A A A LNCV6_134803_PI430048170 mRNA
AATTTCTATAAGAAGACCCCCAAAGAAGACAAGGAGATGGACCCAAAGCGGATAAAGAAG NM_001304419
RefSeq chr7 - 151190873 151205496 IQCA1L NA IQ motif containing with AAA domain 1 like NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140752_PI430048170 0.0455098134867820.5199001327171 3.06384465028999
2.73662637668552 3.35152758096174 A A P 3.55475032216697 3.94194466511526
4.42066474299791 P P P LNCV6_140752_PI430048170 mRNA
GGCATCTTATTACTGTTACTCAAAAACATTGACTCTGCATCAAGAAAGAAACAAGAAAGC NM_015173 RefSeq chr4
+ 37891083 38139175 TBC1D1 23216 "TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1,
transcript variant 1" GO:0032880|GO:0005515|GO:0061024|GO:0032851|GO:0005634|GO:0005097|GO:0005829
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132805_PI430048170 0.6706625536555140.9719023156039930.340298809522041
0.4719707347644530.347882639457009 A A A 0.5321563461392060.455330990761887
0.289266716410882 A A A LNCV6_132805_PI430048170 mRNA
AACTTTTTTATTATTATTTTTATCTCCAACTGCAGGTGGTGTCTTTTGCCAAGGTCTCTG NM_080872 RefSeq chr8 +
35235456 35794663 UNC5D 137970 unc-5 homolog D (C. elegans)
GO:0021859|GO:0007165|GO:0009986|GO:0007411|GO:2001222|GO:0006915|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142623_PI430048170 0.0113399624250942 0.4803686998337435.58921678092997
5.56708971678079 5.77931904337521 P P P 6.47451167513596 6.60120751369482
6.99133053221786 P P P LNCV6_142623_PI430048170 mRNA
TGAGTTGAGAAAAGTAGTCCTACAAATAATGTGAAAGTTGTTACCACCACAGCATGAATG NM_153689 RefSeq chr2
+ 199911255 199928273 C2orf69 205327 chromosome 2 open reading frame 69 GO:0005576 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_143364_PI430048170 0.1688807424865681.16283467322942 5.16502093026713
5.29084962461075 5.32718919633518 P P P 5.25787620187781 4.9303254405782
4.92074617565024 P P P LNCV6_143364_PI430048170 mRNA
GGACATCAGTCTGATTAAAGGTGGTGCCAATTTATTTACATTTAAACTTGTCAGGGTATA NM_000211 RefSeq chr21
- 44885953 44921050 ITGB2 3689 "integrin, beta 2 (complement component 3 receptor 3 and 4
subunit), transcript variant 1"
GO:0005515|GO:0034142|GO:0005886|GO:0050730|GO:0008360|GO:0034687|GO:0007267|GO:0050900|GO:0035
987|GO:0032403|GO:0046872|GO:0045429|GO:0051092|GO:0006954|GO:0001948|GO:0030101|GO:0030198|GO:0
007159|GO:0034113|GO:0007155|GO:0050839|GO:0070062|GO:0008305|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134625_PI430048170 0.0310386444723762 0.8432743755441247.69996163060146

7.80525526117722 7.7118491127104 P P P 7.86855435829895 8.04241488571321
8.03942402699925 P P P LNCV6_134625_PI430048170 mRNA
CTTCTTTTGGTTCATTTCTGGCTTGACAACAATAAATAAACGTGGTATGTTCCTGAGAAA NM_001258RefSeq chr17
+ 76000905 76005999 CDK3 1018 cyclin-dependent kinase 3
GO:0007067|GO:0000082|GO:0008283|GO:0051726|GO:0006468|GO:0005524|GO:0051301|GO:0045023|GO:0004
693 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142425_PI430048170 0.1752220786226090.8564419244575018.52046029295123
8.33953686548932 8.63945111506996 P P P 8.57853484783779 8.66727827935705
8.91818922601306 P P P LNCV6_142425_PI430048170 mRNA
GCTTCAGTCATGTGTAAGTTTTGCAGTGTAATACATATGTAGTCTGGTCTGTATATATGA NM_078474RefSeq chr15
- 101641845 101652391 TM2D3 80213 "TM2 domain containing 3, transcript variant 1" GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127774_PI430048170 0.2490687422146281.1758135411917 5.0048075017427
4.74734442968917 4.76130930034665 P P P 4.30714190073732 4.65307081625199
4.82059400735182 P P P LNCV6_127774_PI430048170 mRNA
AGAATGCATGCTGGTGGCCTAATGCCAGGGCTGTTGAAACAATTTCAGATATAGCACTGT NM_024562RefSeq chr16
+ 68843605 69085182 TANGO6 79613 transport and golgi organization 6 homolog (Drosophila)
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136957_PI430048170 0.0465301401894781 0.3756056257348671.03973839749675
0.2452283956939690.979792572990978A A A 2.10509879418919 1.47269190053529
2.76597982691333 A A P LNCV6_136957_PI430048170 mRNA
AGTAACAAAGAGCACCAAGTTTTAATTTAAATAGGAGATTTAACACTAGGGATCAGGGAG NM_004272RefSeq chr5
- 79373823 79513836 HOMER1 9456 "homer scaffolding protein 1, transcript variant 1"
GO:0030424|GO:0030018|GO:0030054|GO:0051928|GO:0035418|GO:0007268|GO:0048148|GO:2001257|GO:2001
256|GO:0007206|GO:0042802|GO:0043198|GO:0045211|GO:0097110|GO:0043025|GO:0035591|GO:0048875|GO:0
046982|GO:0090279|GO:0045177|GO:0048741|GO:0009967|GO:0060076|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128246_PI430048170 0.0210182475953355 0.8192999583082911.1781520160098
11.0443778388538 11.1592643061268 P P P 11.3240597543018 11.3901022129893
11.5264075395037 P P P LNCV6_128246_PI430048170 mRNA
CCTATGGCTGCTGGTGTAAATAAACTGCATCTCCCCATTGGTAAACAGTAATAAAATTTT NM_001136262 RefSeq
chr12 + 74537770 74541452 ATXN7L3B 552889 ataxin 7-like 3B NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137669_PI430048170 0.1242241383626911.29245727239673 5.48634694951049
5.98801445417057 5.66724597440477 P P P 5.45318221735133 5.32937185963563
5.28890273114725 P P P LNCV6_137669_PI430048170 mRNA
GATGACAAACCGCAAGAGCCACAGACTTGCCAGTTCCTTCCCTCTTTCCTTCCTTTCTTT NM_001004318 RefSeq
chr19 + 39084304 39111488 PAPL 390928 iron/zinc purple acid phosphatase-like protein
GO:0016311|GO:0003993|GO:0005576|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130321_PI430048170 0.0586405334617231 0.7927004337920256.59854607183686
6.62586311187567 6.88615887663781 P P P 6.88598173235924 7.03624322663462
7.19505110793977 P P P LNCV6_130321_PI430048170 mRNA
ATAGTTCTAAACACATTCTTGATCACCAAACAACTTCAGAAAGACAGTGACTGTACAGTT NM_005872RefSeq chr1
- 114567559 114581644 BCAS2 10286 breast carcinoma amplified sequence 2
GO:0008380|GO:0005515|GO:0010467|GO:0030054|GO:0000398|GO:0000375|GO:0005730|GO:0005681|GO:0005
654|GO:0005634|GO:0005662 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107093_PI430048170 0.5743820297007331.14939574343036 2.29125438318587
2.33726246932573 1.89140654862662 A A A 0.5077197238034152.60944747432819
2.12381471776114 A P A LNCV6_107093_PI430048170 mRNA

GCTGCACAGTTAGCCTTCTGAACTTCTATAAGACTGAACTGAACAAGGAGGAGATGTATA NM_014705 RefSeq chr7 - 111726107 112206407 DOCK4 9732 dedicator of cytokinesis 4 GO:0005515|GO:0030971|GO:0017124|GO:0007264|GO:0032420|GO:0032421|GO:0030165|GO:0032855|GO:0005829|GO:0012505|GO:0005085|GO:0048365|GO:0016020|GO:0060326|GO:0030675 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134834_PI430048170 0.1014419308400790 0.9621391544872340 0.291529938237373 0.3218043640550020 0.349055897314163 A A A 0.4137144824891810 0.370109399414216 0.345355665948579 A A A LNCV6_134834_PI430048170 mRNA
GCTTATACCCAATGTGACAAAGAAGAACTGCTCTAATCAATAAATTCTTGAGTCAGGAAA NM_198692 RefSeq chr21 + 44646413 44647649 KRTAP10-11 NA keratin associated protein 10-11 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143313_PI430048170 0.00376696487796656 1.74372226129236 6.10102893142724 6.39635066752866 6.32332370798622 P P P 5.3992023176874 5.56585308733703 5.4603196410323 P P P LNCV6_143313_PI430048170 mRNA
GTGGGTGGGTACATATCTCTTCTTGATTCTGCATTTCATACTTAACTATATTAAAGCTTC NM_152869 RefSeq chrX + 47078354 47093314 RGN 9104 "regucalcin, transcript variant 2" GO:0050848|GO:0005737|GO:0004341|GO:0019853|GO:0005509|GO:0006874|GO:0030234|GO:0008270|GO:0005654|GO:0005634|GO:0032781 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53419_PI430048170 0.0665408462897462 0.7855761251884116 .18424808868382 6.27989573371436 6.23971995395496 P P P 6.44144015425822 6.77117615827056 6.51630947805064 P P P LNCV6_53419_PI430048170 mRNA
AGAATCAAGTGCCTTCTGCAAATCATGTTGGAAAAGTCCAAACCTGGAGATGTCCCTGTG NM_004285 RefSeq chr1 + 9234803 9271335 H6PD 9563 "hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase), transcript variant 2" GO:0050661|GO:0047936|GO:0004345|GO:0005788|GO:0017057|GO:0006098 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129037_PI430048170 0.00826712251352837 0.3484001087167150 .377382550126686 1.16456736913496 0.897835583945292 A A A 1.94373101699524 2.4227687977863 2.65573287114462 A P P LNCV6_129037_PI430048170 mRNA
TGTCCCACTGACTCATCACCCTTTTTTCTACTGTTTCAAGGTTCTCAGATGAGATTTTTT NM_001165252 RefSeq chr17_JH159146v1_alt - 208738 209590 KRTAP2-3 730755 keratin associated protein 2-3 GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136975_PI430048170 0.0123299284790229 0.4561048464842789 .43317096755532 9.39007865055465 9.95733395719405 P P P 10.3884046436111 10.7547635152308 11.0349273186757 P P P LNCV6_136975_PI430048170 mRNA
GCAAGTTTGTTCCAGGTGACCCATTGAGCTGTGTATGCATTTTTGTTTATTTCAATAAAA NM_006135 RefSeq chr1 + 112619452 112671619 CAPZA1 829 "capping protein (actin filament) muscle Z-line, alpha 1" GO:0005515|GO:0006928|GO:0003779|GO:0005576|GO:0015629|GO:0005829|GO:0051016|GO:0006461|GO:0007596|GO:0045087|GO:0071203|GO:0008290|GO:0005856|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104604_PI430048170 0.4011998820814191 .10539084519398 4.77646452902344 4.97535978553667 5.18289095893933 P P P 4.67905816093842 4.83472275961079 4.99822078169346 P P P LNCV6_104604_PI430048170 mRNA
AGGCAGTAATAGACATCACAAACTGCCATGGTTTTGCACTATGATTATAATACCTGCATT NM_001755 RefSeq chr16 + 67029146 67101055 CBFB 865 "core-binding factor, beta subunit, transcript variant 2" GO:0005515|GO:0003700|GO:0006366|GO:0003713|GO:0005634|GO:0060216|GO:0003677|GO:0001649|GO:0016020|GO:0045944|GO:0030098|GO:0030099|GO:0048469 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142890_PI430048170 0.0158236125072288 0.6017498151521937 .57114738087053 7.35543420501246 7.53780778513069 P P P 8.12744876995632 8.04175395941048 8.46685180996322 P P P LNCV6_142890_PI430048170 mRNA

AGACGACCCTGCAGTCCACCTGTTTGTAACTTTTTTAATAAAATAGACATCTGTATTACT NM_001271186 RefSeq chrX - 132203023 132219480 RAP2C 57826 "RAP2C, member of RAS oncogene family, transcript variant 1"
GO:0030336|GO:0005886|GO:0032486|GO:0061097|GO:0030033|GO:0003713|GO:0044291|GO:0005525|GO:0005829|GO:0006184|GO:0005737|GO:0005923|GO:0019003|GO:0055038|GO:0070062|GO:0031954 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127307_PI430048170 0.00981942551398502 0.64898046855243 4.23493325712015 4.54536794470193 4.24012182993107 P P P 5.09987783222218 4.84092676890099 4.96161345100852 P P P LNCV6_127307_PI430048170 mRNA
CCAAGCATTCATGTTCCCTCACCAGCTGTAGTAAGTTGATAATCCTAAAAAGCCTTGGCT NM_032773RefSeq chr3 + 197791225 197871585 LRCH3 84859 leucine-rich repeats and calponin homology (CH) domain containing 3 GO:0005737|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128318_PI430048170 0.0229229039531999 0.3386909707094924.66155171344103 3.80390860738158 4.61865311633322 P P P 5.92961092570732 6.11071794998732 5.86887123012451 P P P LNCV6_128318_PI430048170 mRNA
GGAGTATCCAACTTGTGCAAAAAGATAGAATCAATCATAAAGTGCACACCTTTATTCAGA NM_000186RefSeq chr1 + 196651877 196747504 CFH 3075 "complement factor H, transcript variant 1"
GO:0006957|GO:0005515|GO:0030449|GO:0006956|GO:0045087|GO:0072562|GO:0043395|GO:0005576|GO:0008201|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145470_PI430048170 0.1639448675534630.95649060583385 0.268770763614923 0.3351098424962060.308948257037258A A A 0.4288273878508290.336115092195442 0.339256768221743A A A LNCV6_145470_PI430048170 mRNA
CCTGATTGGGGAAAAGGTTGAATTTGTGAAACAATCTGCTCCAACCTTCTATTTTAATTA NM_153834RefSeq chrX + 136300962 136416888 ADGRG4 NA adhesion G protein-coupled receptor G4 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144417_PI430048170 0.7023948937466761.02022191167674 0.446696647896702 0.5038746589683840.506458582883009A A A 0.3442528377210230.427230343786934 0.588872191760649A A A LNCV6_144417_PI430048170 mRNA
TTACCTTTAACGTGAACTCACAGGCGGATTAAAGTGAAATAAAACCTACCATTTGAGTTA NM_130848RefSeq chr5 - 135444213 135447348 DCANP1 140947 dendritic cell-associated nuclear protein
GO:0006355|GO:0005737|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68169_PI430048170 0.0182482458989255 0.6539787148028452.45964341695258 2.68924286823582 2.27026330257002 A A A 3.28298220875615 2.96273557104147 3.02156974498227 P P P LNCV6_68169_PI430048170 mRNA
GGATACAGAGCTAAGCAAATGCTTCTTTAAGGGCCCTTAAAAGTGAAAAGTAACTTGCAA NM_013302RefSeq chr16 + 22206270 22288745 EEF2K 29904 eukaryotic elongation factor 2 kinase
GO:0008286|GO:0031952|GO:0005516|GO:0005737|GO:0046777|GO:0004672|GO:0005509|GO:0004686|GO:0005524|GO:0008135|GO:0006414|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104178_PI430048170 0.8678246796480311.01112843064374 6.82103732335105 6.83432988124093 6.6600660103416 P P P 6.72452774567197 6.94346787424276 6.58293677267011 P P P LNCV6_104178_PI430048170 mRNA
AATAAAATAACTCCTGCTCGTTTGGAATGTAACTCCTGGCACAGTGTTCCTGGATCCTGG NM_014742RefSeq chr20 + 32109505 32167258 TM9SF4 9777 transmembrane 9 superfamily protein member 4GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132879_PI430048170 0.3828858412231191 1.9983394588292 0.550407864846913 5.42346119096571 0.499388913463895A P A 0.28240552391118 0.376865642386752 0.38073932867769 A A A LNCV6_132879_PI430048170 mRNA
GAATCAAATCAGGAATCTTGTCTGAGCTACTGGAATGAAGTTCACAGGTCTTGAAGACCA NM_000212RefSeq chr17

+ 47253841 47312711 ITGB3 3690 "integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)"
GO:0005515|GO:0031527|GO:0050731|GO:0031528|GO:0050900|GO:0002020|GO:0042802|GO:0007411|GO:0006
457|GO:0030198|GO:0034446|GO:0034113|GO:0050839|GO:0070062|GO:0008305|GO:0042470|GO:0010745|GO:0
009986|GO:0031589|GO:0050840|GO:0003756|GO:0014909|GO:0030168|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127220_PI430048170 0.0943848933292021 0.42766547521328 3.42774185481976
2.585662518857 2.10820794913242 P A A 3.14492333450545 4.5045319425293
4.14863357953111 P P P LNCV6_127220_PI430048170 mRNA
CTGAGCCTGTAGCTAACGCATAAGCACAGTGTATTCAATAAAACATTTTTATTCTGTACA NM_006502 RefSeq chr6
+ 43576140 43620523 POLH 5429 "polymerase (DNA directed), eta, transcript variant 1"
GO:0005515|GO:0003887|GO:0006301|GO:0046872|GO:0003684|GO:0006260|GO:0005737|GO:0010225|GO:0006
281|GO:0006290|GO:0006282|GO:0000731|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_32031_PI430048170 0.00503162554393633 0.2728035349093269.35822305360031
8.74016769507041 8.78829821266452 P P P 10.9890797408428 10.8752164002206
10.7168687504255 P P P LNCV6_32031_PI430048170 mRNA
AGGGTGGACCAAAGCACCCCCTCTTTTCCTGGGCTTCCCGAGAGTTGATAATTGAAAAAA NM_001242901 RefSeq
chr19 + 4679281 4685948 DPP9-AS1 NA DPP9 antisense RNA 1 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128779_PI430048170 0.1760179189154260.8103180163702415.79252205061619
5.36063718512467 5.30175901133069 P P P 5.9420376725279 5.84888992383873
5.60496689677682 P P P LNCV6_128779_PI430048170 mRNA
ATTGGACCCATACCCTGTCTCCAACCCTGCCTTGAAGCAATTCAATAAAGAGGAAGCAAA NM_004803 RefSeq chr3
+ 38305953 38318368 SLC22A14 9389 "solute carrier family 22, member 14"
GO:0015695|GO:0005887|GO:0055085|GO:0015101 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136815_PI430048170 0.097070336289395 1.03649676057446 0.454165889061417
0.5088645223015920.453277175859752A A A 0.3946635803740980.420777279838793
0.445969427140158A A A LNCV6_136815_PI430048170 mRNA
TGTCACACCTGAAATGGCTTTGTTTTTATCAATAAATACTTGTTGATTGCGGTAAACAGC NM_153022 RefSeq chr12
+ 10178957 10191804 TMEM52B 120939 "transmembrane protein 52B, transcript variant 1"
GO:0008150|GO:0003674|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127041_PI430048170 0.0109550193860532 0.74474795402458 9.54393280424512
9.59171955439678 9.63293087404097 P P P 10.0338234957212 9.89720807451057
10.1066739898843 P P P LNCV6_127041_PI430048170 mRNA
GCTCTGTGTTAGAGATATGAAATGGTGTTTGATACTGTTTGAGACATTATGGAGAGATTT NM_003766 RefSeq chr17
- 42810131 42824292 BECN1 8678 "beclin 1, autophagy related"
GO:0005802|GO:0005515|GO:0008285|GO:0005634|GO:0032258|GO:0030425|GO:0000910|GO:0051607|GO:0045
324|GO:0048666|GO:0016032|GO:0071275|GO:0033197|GO:0000045|GO:0016239|GO:0006995|GO:0001666|GO:0
043066|GO:0042493|GO:0000407|GO:0050435|GO:0045335|GO:0050790|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_91729_PI430048170 0.0878914791171609 1.23730165955225 4.43098860493427
4.78556205977563 4.70473357046845 P P P 4.19854051400934 4.40544069556887
4.40923817210455 P P P LNCV6_91729_PI430048170 mRNA
TATCTTACATCACATCCAGAATTGCAGTGATGTCATTCCCAGCAGAAGGTGTGGAGTCAG NM_005255 RefSeq chr4
- 849276 932386 GAK 2580 "cyclin G associated kinase, transcript variant 1"
GO:0072583|GO:0005515|GO:0035622|GO:2000179|GO:0048471|GO:0005794|GO:0061436|GO:0005524|GO:0048
853|GO:0009913|GO:0043231|GO:0072318|GO:0007049|GO:0016020|GO:0004674|GO:0007030|GO:0006468|GO:0
048468|GO:0005925|GO:0007029 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132919_PI430048170 0.7773173188111431.17972089173084 0.33485534646727
1.95199024860251 1.24996730706468 A A A 1.47362060036813 0.262026531751035

1.25608111860437 A A A LNCV6_132919_PI430048170 mRNA
TTTGCTTATACCTATCTATGTCCAAGATCCCTGCGATCTCTGACAGAGGACAAGGTTCTG NM_001258284 RefSeq
chr1 + 248021947 248022886 OR2L5 NA "olfactory receptor, family 2, subfamily L, member 5" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129995_PI430048170 0.00154029572711521 0.626580181794511 10.0019908785876
10.0253237641225 10.0408489480966 P P P 10.6257496275377 10.7531026497233
10.7099687789772 P P P LNCV6_129995_PI430048170 mRNA
TTTCTCCTAGTGGTTCACAATTGAACTGAATTGAGATGGTGTCGGGTGGCTAAGGAGACA NM_133471 RefSeq
chr6_GL000253v2_alt - 1986641 1998148 PPP1R18 170954 "protein phosphatase 1, regulatory subunit 18, transcript variant 1" GO:0005737|GO:0019902|GO:0003779|GO:0005856 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_78425_PI430048170 0.00250161362935468 0.771852742488532 10.2314960507428
10.1179302699743 10.2085302247933 P P P 10.5130720503515 10.6411621480211
10.5234719481579 P P P LNCV6_78425_PI430048170 mRNA
AGTTTGTGACCAAAGTCAGAGTGGATCATGGTGGTTTGGCAGCAGGGAATTTGTCTTGTT NM_001122956 RefSeq
chr7 + 44044639 44061716 DBNL 28988 "drebrin-like, transcript variant 3"
GO:0005515|GO:0071800|GO:0030054|GO:0005886|GO:0002102|GO:0006921|GO:0030425|GO:0005829|GO:0005
737|GO:0051015|GO:0097178|GO:0005938|GO:0070062|GO:0019904|GO:0006915|GO:0014069|GO:0003779|GO:0
007257|GO:0008022|GO:0001726|GO:0007416|GO:0006898|GO:0030027|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142883_PI430048170 0.182852396350376 0.651808512928299 0.436852276801006
0.359591260689809 0.389333134978204 A A A 1.41340579047674 1.02332278296498
0.441952615602137 A A A LNCV6_142883_PI430048170 mRNA
TCAGGACAGCAGATTAGAGGCAGGAGGCAATGACAATAAAATAACGATAAAATCCTGAGA NM_178829 RefSeq
chr7_KI270803v1_alt + 962572 963937 C7orf34 135927 chromosome 7 open reading frame 34
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131826_PI430048170 0.315861312029118 1.36985432357724 1.47420818804027
0.655003173351279 0.536945768199386 A A A 0.469707668287697 0.503676251677643
0.520216882982281 A A A LNCV6_131826_PI430048170 mRNA
ATCCTAAGAAAGGGGACTATTTCGTAAGTACAAAGGAAACTTATCCTCCATGTTTTTTAC NM_001101320 RefSeq
chr13 + 51341031 51362103 SERPINE3 647174 "serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 3" GO:0010951|GO:0004867|GO:0005615 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139670_PI430048170 0.888173833529075 1.00936958119828 0.436699151144777
0.285671447491018 0.495465268077005 A A A 0.333034859739877 0.286184248451735
0.552101425902131 A A A LNCV6_139670_PI430048170 mRNA
ATCCTGACTTTCTAGCCATTAATAAAGAGAACTGCTCCTAGCACCTCAGCCTCTAAAAAA NM_001280558 RefSeq
chr14 + 24070836 24078100 CPNE6 9362 "copine VI (neuronal), transcript variant 1"
GO:0006629|GO:0030424|GO:0005215|GO:0016020|GO:0005509|GO:0001786|GO:0007268|GO:0016192|GO:0030
425|GO:0070062|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142312_PI430048170 0.0212342950667372 0.585096797394464 9.18129817583189
9.07041303269329 9.13809538887531 P P P 9.67318594501722 10.1133795370138
9.89163213634631 P P P LNCV6_142312_PI430048170 mRNA
CCCCTTGATTGCCAGGTCTGGTCTAAGTTTCTTTAATAAAGACAAAGGAGTGATTTTCCA NM_001278494 RefSeq
chr11 - 72109586 72112232 ANAPC15 25906 "anaphase promoting complex subunit 15, transcript variant 11" GO:0005622|GO:0007067|GO:0005680|GO:0090266|GO:0051301 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129785_PI430048170 0.301392870478986 0.516634685550158 0.445501065997037
0.507213132772587 0.842381791098908 A A A 0.350676262173618 1.46989266022517

2.26673822521559 A A A LNCV6_129785_PI430048170 mRNA
GGGAAATGTTAGTTTCAGCCAACCTCATTTTTTAGTTCATCTAGAAGAAAATCTAGCACA NM_006591 RefSeq chr11
+ 74592529 74643060 POLD3 10714 "polymerase (DNA-directed), delta 3, accessory subunit, transcript variant 1"
GO:0043625|GO:0005515|GO:0003887|GO:0005634|GO:0005739|GO:0006271|GO:0006281|GO:0000723|GO:0006283|GO:0006284|GO:0000722|GO:0000731|GO:0006297|GO:0005654|GO:0006298|GO:0006289|GO:0000278|GO:0032201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131795_PI430048170 0.9570357123182880.9973501621626796.84112500968537
6.61974872486081 6.78261180093485 P P P 6.49775259421083 7.02614531373322
6.68985497567198 P P P LNCV6_131795_PI430048170 mRNA
ATTTTCTGAAACAGGAGGTAAAATTTTTCTTTGGCAGAGGCCCCTAAGCAAGGGAGGGGT NM_005736 RefSeq chr10
- 102479228 102502755 ACTR1A 10121 "ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)"
GO:0019886|GO:0005813|GO:0005737|GO:0006996|GO:0005875|GO:0000086|GO:0016192|GO:0005869|GO:0000278|GO:0005524|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135587_PI430048170 0.4739776851178510.7500160373864362.07776289082894
0.2917028872292042.14894532725133 A A A 2.28787679586531 2.48510892692802 1.4285548752363
A P A LNCV6_135587_PI430048170 mRNA
AAGAAACGCTTTTGGAGTTAAGAAAAAGAACTGACCATCCTGGTCCGCCCACAGGAGAAA NM_016568 RefSeq
chr5_KI270794v1_alt + 137707 140240 RXFP3 51289 relaxin/insulin-like family peptide receptor 3
GO:0007186|GO:0005886|GO:0032467|GO:0005887|GO:0004930|GO:0051482|GO:0008528 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133672_PI430048170 0.1654439408832120.9844540965193590.331193409379962
0.3659390301926210.347882639457009 A A A 0.37882472808329 0.380513914596753
0.353540328446731 A A A LNCV6_133672_PI430048170 mRNA
GAAGTACACCCATCTGCATTGTTTTTAATTCCTTCCGGTTTTCTATCAATGTTACAGTTT NM_001007595 RefSeq chr15
- 62163537 62165283 C2CD4B 388125 C2 calcium-dependent domain containing 4B
GO:0005730|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134117_PI430048170 0.0136795153138558 0.4685991684079128.73073023473795
8.69017256305111 8.85783858414883 P P P 9.67412148547147 9.68785615181274
10.1502529265745 P P P LNCV6_134117_PI430048170 mRNA
GGTTTTGCAGAAGAAGGCATCGTCATGCACAGTATTTGTAATTAAAAGCAAATCATTTGT NM_001006610 RefSeq
chr16 - 48360535 48365873 SIAH1 6477 "siah E3 ubiquitin protein ligase 1, transcript variant 2"
GO:0005515|GO:0006511|GO:0004842|GO:0005886|GO:0016874|GO:0030877|GO:0005634|GO:0007283|GO:0051402|GO:0009653|GO:0005829|GO:0031648|GO:0030163|GO:0005737|GO:0042787|GO:0007411|GO:0043065|GO:0006915|GO:2001244|GO:0008022|GO:0007399|GO:0007049|GO:0008270|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130960_PI430048170 0.0495837187932534 1.07579848252129 11.7041672073519
11.6941510164478 11.612327001183 P P P 11.5761808796778 11.5975548396764
11.5213673324078 P P P LNCV6_130960_PI430048170 mRNA
GTTCCTTCCCTATGGGATCCATCTGTTTTGTAAACAATAAAGCGTCTGAGGGAGTGTAAA NM_138793 RefSeq chr17
- 78991715 79009817 CANT1 124583 "calcium activated nucleotidase 1, transcript variant 1"
GO:0007165|GO:0032580|GO:0045134|GO:0005509|GO:0005789|GO:0016021|GO:0004871|GO:0043123|GO:0070062|GO:0030166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_28587_PI430048170 0.1434254288109660.93628945948968 0.3758370154005110.396412157832805
0.327398489700019 A A A 0.5437317765360630.4332445340074680.404691896419638 A A A
LNCV6_28587_PI430048170 mRNA
TTTATCAACAATGAATGGCACGAATCCAAGAGTGGGAAAAAGTTTGCTACATGTAACCCT NM_000693 RefSeq chr15
+ 100879691 100916625 ALDH1A3 220 "aldehyde dehydrogenase 1 family, member A3, transcript variant 1"

GO:0043065|GO:0042472|GO:0001758|GO:0004029|GO:0070403|GO:0070324|GO:0042803|GO:0005829|GO:0005
737|GO:0042574|GO:0042573|GO:0060324|GO:0042572|GO:0060166|GO:0050885|GO:0002072|GO:0007626|GO:0
002138|GO:0060013|GO:0070062|GO:0055114|GO:0048048|GO:0004030|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138322_PI430048170 0.2595071536835890.7909272701315616.0605580974083
15.3853534567236 15.3536682329847 P P P 16.1649968239564 16.0195297026653 15.708873323373
P P P LNCV6_138322_PI430048170 mRNA
CTCCAGCTGTGGCTACAACATAGGGTTTTTATACAAGAAAAATAAAGTGAATTAAGCGTG NM_002952RefSeq chr16
- 1962060 1964826 RPS2 6187 ribosomal protein S2
GO:0005515|GO:0010467|GO:0019058|GO:0005634|GO:0003729|GO:0006412|GO:0006413|GO:0006414|GO:0005
829|GO:0005737|GO:0000184|GO:0016032|GO:0070062|GO:0003735|GO:0017134|GO:0006614|GO:0019083|GO:0
005730|GO:0051347|GO:0006415|GO:0016020|GO:0022627|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106646_PI430048170 0.0116220394647841.8068832343428 6.78693027317145
6.85955764569671 6.78970940940135 P P P 6.04414268233608 6.06946369528662 5.7406374904682
P P P LNCV6_106646_PI430048170 mRNA
CCAGAAGCCTCGAGGTCTCCTGTTTCTCTTCCTGAAAAATAAATATTTGCCTTTCGATCA NM_024307RefSeq chr16
- 30104809 30113557 GDPD3 79153 glycerophosphodiester phosphodiesterase domain containing 3
GO:0006629|GO:0016021|GO:0008889|GO:0006071|GO:0046872|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141632_PI430048170 0.0119328191538305 0.8093044148559228.78756083085475
8.92519237317964 8.80274042588714 P P P 9.03835199382057 9.19579689399618
9.19542294179895 P P P LNCV6_141632_PI430048170 mRNA
TGTTTTAATGGTCTTTCTGATTAAAGAAAGCCCCTGTGGCTTTGGAGGCATTGTGCCCAC NM_052875RefSeq chr11
+ 134224604 134247792 VPS26B 112936 vacuolar protein sorting 26 homolog B (S. pombe)
GO:0005770|GO:0008565|GO:0042147|GO:0006886|GO:0005769|GO:0043231|GO:0030904|GO:0005829|GO:0005
768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131588_PI430048170 0.02308592131834 0.6854704430633488.47450269794421
8.45266633175404 8.78884228985587 P P P 9.12649540886178 9.0413965955758
9.20318084135131 P P P LNCV6_131588_PI430048170 mRNA
CATGAAGAGACATAGCCTTTTAGTTTTGCTAATTGTGAAATGGAAATGCTTTACAGGAAG NM_016614RefSeq chr6
- 24649976 24666887 TDP2 51567 tyrosyl-DNA phosphodiesterase 2
GO:0005515|GO:0000287|GO:0030145|GO:0090305|GO:0070260|GO:0003714|GO:0005730|GO:0005634|GO:0045
171|GO:0006302|GO:0004518|GO:0005737|GO:0003697|GO:0016605|GO:0005654|GO:0007166 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_69121_PI430048170 0.1463820213503660.6570894582742013.64474104062711 2.95198126842604
2.75955417147382 P A A 3.35064919353052 4.09153313188253 3.79369303805661 P P P
LNCV6_69121_PI430048170 mRNA
GACCGAAACACCTTGGAAAATATGCTTGTACGGGTTCTTCTAGTAAAAGATATTTATGAT NM_003453RefSeq chr13
+ 19958669 20091845 ZMYM2 7750 "zinc finger, MYM-type 2, transcript variant 1"
GO:0008150|GO:0006355|GO:0016605|GO:0008270|GO:0006351|GO:0031624|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132151_PI430048170 0.0244845986185071 0.5329473098624335.50891844759476
5.40871718169342 5.50806613725606 P P P 6.13284876176789 6.3096650325231
6.65882659199886 P P P LNCV6_132151_PI430048170 mRNA
CAGTGTACCAATATGTTCACAACCTAGGATCATGATAATGGAGTGTGTTTTGGGTTTTTT NM_033637RefSeq chr10
+ 101354032 101557321 BTRC 8945 "beta-transducin repeat containing E3 ubiquitin protein ligase,
transcript variant 1"
GO:0005515|GO:0006511|GO:0004842|GO:0016567|GO:0008013|GO:0045309|GO:0016874|GO:0045879|GO:0031

146|GO:0031145|GO:0043433|GO:0005829|GO:0031648|GO:0006470|GO:0000086|GO:0051726|GO:0046983|GO:0
016032|GO:0016055|GO:0043122|GO:0000209|GO:0051437|GO:0051439|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134210_PI430048170 0.0301656832917635 0.3494831645338885.58223729237454
5.47520456199321 5.54661741526748 P P P 6.48291761485715 7.16273823883629
7.36968647147328 P P P LNCV6_134210_PI430048170 mRNA
GTTCATTCACCTGATTACTTTGGTTGCAGCACAACTGTATATATTGTATAACCGAAATTG NM_003887RefSeq chr2
+ 9206764 9405683 ASAP2 8853 "ArfGAP with SH3 domain, ankyrin repeat and PH domain 2,
transcript variant 1"
GO:0043547|GO:0005515|GO:0008060|GO:0005886|GO:0032312|GO:0032580|GO:0008270|GO:0043085|GO:0008
047 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128994_PI430048170 0.8009296268507460.9770905731972930.421700863899775
0.4639803835526880.466169595939621A A A 0.3494743249112270.662104606235591
0.422164991440716A A A LNCV6_128994_PI430048170 mRNA
TGCATTTAATGTTTGTAGTGTAAAGATATAACTACAATAAAAGAGGCCAGAGAGTCTGCA NM_152655RefSeq chr19
- 37147437 37172741 ZNF585A 199704 "zinc finger protein 585A, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003676|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143615_PI430048170 0.6431632115036990.95133467761148 0.35154509284593
0.35543510009232 0.484753927830841A A A 0.3310102780953520.689527289620999
0.363221549532241A A A LNCV6_143615_PI430048170 mRNA
TGTGCTGCAGGATTACATCATCTTACCCACCATCACCATTTTCACAGTCTAATCCTAAAT NM_001037732 RefSeq
chr20 - 187852 189681 DEFB128 NA "defensin, beta 128" NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_136334_PI430048170 0.1353842002714330.7126583404793044.67384894710765
4.07099790804558 4.60873286847799 P P P 4.61266280799486 4.97902132710768
5.23394128361894 P P P LNCV6_136334_PI430048170 mRNA
CTAAACCTTGTAGACAAGTGAGTCATCTGATATGTATAGAAGCTGTGATATATAGAGTAC NM_015310RefSeq chr8
- 18527302 19013686 PSD3 23362 "pleckstrin and Sec7 domain containing 3, transcript variant 1"
GO:0043547|GO:0005802|GO:0005086|GO:0030054|GO:0045211|GO:0030182|GO:0032012|GO:0014069|GO:0016
192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136755_PI430048170 0.7193130976646991.00256970231262 2.89309494115333
1.02539125414718 0.442911656710289A A A 2.27736827248778 1.15423181366063 1.8961371005468
A A A LNCV6_136755_PI430048170 mRNA
CCACTACACTATATGTGTATGTAACACAACTGCCCTTGTAACTTCCTAAACCTATAATTA NM_001037232 RefSeq
chr19 - 36888123 36916291 ZNF829 374899 "zinc finger protein 829, transcript variant 2"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137081_PI430048170 0.1663203062475060.8302931613043749.34710155040939
9.17547270465141 9.61835264661574 P P P 9.57581487042827 9.54920622281409
9.83773877204074 P P P LNCV6_137081_PI430048170 mRNA
AGCAGTGGACAACACATTTCAAAGAAGATCAAGTTTGTACATAACACTAGTGGCATTTCT NM_001286835 RefSeq
chr9 + 65675833 65734041 CBWD5 220869 "COBW domain containing 5, transcript variant 2"
GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138384_PI430048170 0.0338220386511358 1.61100505606727 7.50411981114365
7.51315395637072 7.48383565784106 P P P 7.05605076428326 6.73517071224498 6.6086076306804
P P P LNCV6_138384_PI430048170 mRNA
CTGCTGGGAAGTGGCTTAATAGTAATATCAATAAATAGATGAGTCCTGTTAGAATCTTGA NM_000447RefSeq chr1
+ 226870571 226896103 PSEN2 5664 "presenilin 2, transcript variant 1"

GO:0005515|GO:0030018|GO:0007220|GO:0031594|GO:0001756|GO:0048538|GO:0005765|GO:0015031|GO:0060048|GO:0007219|GO:0048167|GO:0007411|GO:0016485|GO:0007176|GO:0043025|GO:0007613|GO:0006509|GO:0005938|GO:0001942|GO:0005813|GO:0005794|GO:0048286|GO:0001708|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141763_PI430048170 0.0136350672401653 0.8263873147559748.44937951314708 8.43240827266211 8.37937800603642 P P P 8.78435456691619 8.64515907625379 8.65364005818132 P P P LNCV6_141763_PI430048170 mRNA
CCAGATAGATCTTGGCCCTGAGTTTGCCAATTAAAGATGCCGTGATTATTACCTAAAAAA NM_023931 RefSeq chr16 - 30530366 30534970 ZNF747 65988 "zinc finger protein 747, transcript variant 3"
GO:0005622|GO:0006355|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137338_PI430048170 0.1240700830342181.09375876822844 11.5332306774746 11.5677556871881 11.5737681958803 P P P 11.4488352362325 11.5057611149375 11.3268575130379 P P P LNCV6_137338_PI430048170 mRNA
CAACTTGCAAATGAGGTGCAAATAAAATGCAGATGATTGCGCGGCTTTGAATCGAAAAAA NM_001277864 RefSeq chr14 + 24007008 24051377 DHRS4L1 728635 "dehydrogenase/reductase (SDR family) member 4 like 1, transcript variant 1" GO:0016491|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81082_PI430048170 0.4806303270063960.8075390887222331.62121034863483 2.90999565044256 3.21370908968364 A A P 2.68714872589453 3.00449216375117 3.34199290851759 A P P LNCV6_81082_PI430048170 mRNA
AACACATTTCAGGCTACTGCTTTACAAAACCAGAACTGATCTTCACATTGGAACAAGGAG NM_001001662 RefSeq chr9 - 96816990 96854107 ZNF782 NA zinc finger protein 782 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143520_PI430048170 0.3651328464679831.60074286951207 0.422014426594144 1.77352723235477 0.402615407641602 A A A 0.28833960177805 0.434536248031253 0.293833218237543 A A A LNCV6_143520_PI430048170 mRNA
TATACACTGAGGAATGCAGAGGTGAAAAGTGCCATGAAGAAACTCTGGATGAAATGGGAG NM_001004704 RefSeq chr11 + 55665166 55666096 OR4C6 NA "olfactory receptor, family 4, subfamily C, member 6" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56511_PI430048170 0.1407708185331431.14424403289322 11.0237029595491 10.819191958708 11.1050457319613 P P P 10.7247453308276 10.885025704876 10.7649527055045 P P P LNCV6_56511_PI430048170 mRNA
GATGTTGACTTTGATTTTGCTGGACCTGCAATCCATGGTTCAGCTGTCTTTGGTTATGAG NM_001184783 RefSeq chr10 + 75210541 75231448 VDAC2 7417 "voltage-dependent anion channel 2, transcript variant 1"
GO:0005515|GO:0006820|GO:0042645|GO:0005743|GO:0005634|GO:0005741|GO:2001243|GO:0055085|GO:0005739|GO:0046930|GO:0044070|GO:0000166|GO:0032272|GO:0015288|GO:0008308|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134181_PI430048170 0.0103003927198262 0.270257439465154 2.62784847320306 2.58548454163941 2.9249268064378 A A P 4.05416660920182 4.90875303433279 4.72952775554737 P P P LNCV6_134181_PI430048170 mRNA
CATTTTGAGATTCTAGTTGCTTTATCTCAAAGCTTTCACTGAAGGGCTGTAACTGAAAAT NM_015235 RefSeq chr10 - 51695485 51699595 CSTF2T 23283 "cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant" GO:0006397|GO:0005622|GO:0000166|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132244_PI430048170 0.0393679712367205 1.19878601103589 12.0940967696864 12.161899646017 12.1284650432264 P P P 11.8363513455034 11.7750348985901 11.9813059392133 P P P LNCV6_132244_PI430048170 mRNA
ATTCAGGAAAAGGAAAAACTTCAAGAAGAAAAGAATCGTCACGACCCCGCAGACTGTCCT NM_181515 RefSeq chr11 - 68891277 68903835 MRPL21 219927 "mitochondrial ribosomal protein L21, transcript variant 1" GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0005840 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130055_PI430048170 0.000362644812188422 6.81042392589618 9.00118560339205
9.61946051515751 9.21932169781866 P P P 6.3315319085813 6.83641398202673
6.38279006563562 P P P LNCV6_130055_PI430048170 mRNA
TTCCCCAGAATGGATGGTATTGAATCTCAGCCACATGCAACACTGTGTCCAGCATTCTTT NM_004567 RefSeq
chr3 - 48517683 48556794 PFKFB4 5210 "6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4"
GO:0005975|GO:0044281|GO:0005524|GO:0006096|GO:0005829|GO:0004331|GO:0016311|GO:0009405|GO:0006
006|GO:0046835|GO:0006003|GO:0003873|GO:0006000 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_106008_PI430048170 0.191614652013553 1.01322266157731 0.317149504911636
0.283668226740612 0.292723726203363 A A A 0.28503128264566 0.278497224497221
0.273343651173341 A A A LNCV6_106008_PI430048170 mRNA
CATCTGGTAACAAACAGCAGCTACCTTTAGTCAATGAAACAAAAACAAAATCACAAGAGG NM_182496 RefSeq
chr12 - 95867047 95942650 CCDC38 120935 coiled-coil domain containing 38 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_126756_PI430048170 0.306324170410469 0.681305377125739 1.31758839175335
3.11654139505732 2.61684749178403 A P A 3.00786229467952 3.16433748428544
3.06746117966576 P P P LNCV6_126756_PI430048170 mRNA
CTGTTTTTAAGTATTTCAAAAGCTTGTGTGTTGACCCTTTGTAGCCTAAGTACGTAAACA NM_005738 RefSeq chr7
+ 12687285 12690933 ARL4A 10124 "ADP-ribosylation factor-like 4A, transcript variant 1"
GO:0005515|GO:0005737|GO:0005886|GO:0050873|GO:0007264|GO:0005730|GO:0005634|GO:0005525 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_144943_PI430048170 0.0767007513101941 1.25301754947151 12.6117735468047
12.705128075871 12.7074060491068 P P P 12.1949556934166 12.2858197654711
12.5459789437222 P P P LNCV6_144943_PI430048170 mRNA
GCAGTTCCCAAGGACTTGTCATTTCATGTTCTTATTTTAGACCTGTTTTGTAAATAAAGC NM_006842 RefSeq
chr11 + 66052344 66068911 SF3B2 10992 "splicing factor 3b, subunit 2, 145kDa"
GO:0008380|GO:0006397|GO:0005515|GO:0010467|GO:0000398|GO:0016032|GO:0005681|GO:0005654|GO:0071
013|GO:0005689 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142280_PI430048170 0.000160922330973704 0.323993183237627 3.19434371508229
3.43880584429632 3.17604112171492 P P P 4.79360937806832 4.83644082955143
5.05803842237565 P P P LNCV6_142280_PI430048170 mRNA
GGGAGGGCGAACTGTCGAATGTTGCGAATTTATTAAACTTTTGACAAAACTTAGAAAAAA NM_145064 RefSeq
chr12 - 57243454 57251193 STAC3 246329 "SH3 and cysteine rich domain 3, transcript variant 1"
GO:0035556|GO:0003009|GO:0048741|GO:0007274|GO:0046872|GO:0042802 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_93500_PI430048170 0.15580274706426 2.58485783862292 3.09675796127234
4.94689465878999 3.82018202654299 P P P 2.8779208956698 2.55834078753531
2.90020903056774 P P P LNCV6_93500_PI430048170 mRNA
ATTGTCTATCATCACTGGCTGCCCAGAATATTTGTACAAGTAAACTGCACTGCCCTGCTG NM_001252124 RefSeq
chr2 - 241113634 241149504 PASK 23178 "PAS domain containing serine/threonine kinase,
transcript variant 5"
GO:0005515|GO:0005794|GO:0005634|GO:0045727|GO:0005524|GO:0045719|GO:0007165|GO:0005737|GO:0043
576|GO:0046777|GO:0004674|GO:0006468|GO:0004871|GO:0035091|GO:2000505|GO:0070092 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138618_PI430048170 0.247893074656873 0.590981665604927 0.431981427344179
1.71665806704639 0.363009366571594 A A A 2.28051977812094 1.7077237772117
0.922594693554725 A A A LNCV6_138618_PI430048170 mRNA
GTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAACCCTATAATAAAT NM_004867 RefSeq

chrX - 79360383 79367552 ITM2A 9452 "integral membrane protein 2A, transcript variant 1" GO:0005515|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93477_PI430048170 0.0178049503136746 1.44741789997969 9.37651924517171 9.5446827546547 9.73778527416435 P P P 8.87812261130616 9.04247544407731 9.14791324914993 P P P LNCV6_93477_PI430048170 mRNA TCCCAAGCCTGGAAGAACTCGTCATGCTCTTTGTAGCGTGGTGCTTCTGTTGCTCACAGG NM_018224 RefSeq
chr7 - 43639246 43729541 COA1 55744 "cytochrome c oxidase assembly factor 1 homolog (S. cerevisiae), transcript variant 1" GO:0033617|GO:0005739|GO:0032981|GO:0005737|GO:0031305 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69835_PI430048170 0.237614324296696 1.1780986296349 7.95836218010758 8.24810965801289 8.43086056060633 P P P 7.93556061899335 7.92778507185558 8.09699014064962 P P P LNCV6_69835_PI430048170 mRNA ATTGCAAGATGTGGGCAATCGGGATTACTGTTCTGGTTATCTTCATCATCATCATCATCATCG NM_004781 RefSeq
chr1 + 7771268 7781432 VAMP3 9341 vesicle-associated membrane protein 3 GO:0070254|GO:0005515|GO:0043005|GO:0035493|GO:0030054|GO:0005886|GO:0043001|GO:0030136|GO:0031201|GO:0006887|GO:0006906|GO:0007269|GO:0043231|GO:0006904|GO:0005829|GO:0005622|GO:0016324|GO:0017156|GO:0000149|GO:0001921|GO:0042147|GO:0034446|GO:0061025|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139286_PI430048170 0.0284816446471544 0.2778574744163333.18784113073182 2.5462840887881 3.31256839532807 P A P 4.05758341567234 4.86022094639696 5.45543813777904 P P P LNCV6_139286_PI430048170 mRNA TATTTTTGGCTATTTGCATAGGTAACATTGGTTTAAGGAGAGAGACCTGTGATCGAACAG NM_001297568 RefSeq
chr1 - 247154988 247172017 ZNF124 7678 "zinc finger protein 124, transcript variant 4" GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129254_PI430048170 0.9306777022281261.01153194512534 7.08391769818505 8.22702779596629 7.42490361783471 P M P 7.33748974180318 7.50382322089477 8.00548635447054 P P P LNCV6_129254_PI430048170 mRNA GCAGTCTCCACGTGTGTTAATGTTTCAAACGTGTATCATAATGTGTATAATTGTGTAACA NM_018023RefSeq chr3 + 183697817 183812625 YEATS2 55689 YEATS domain containing 2 GO:0005515|GO:0072686|GO:0043966|GO:0006325|GO:0017025|GO:0005671|GO:0000122|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143261_PI430048170 0.0413514266231355 0.5586595094106024.59707294696407 5.22599587867901 5.27489215889368 P P P 6.05224237975566 5.71626483865217 5.92328140560792 P P P LNCV6_143261_PI430048170 mRNA GCCTTTTAGTCCTCTCAGAGTCTGTCACAGTTTCTTTGTGTAAATGATAAAAAAGTTTGA NM_001171796 RefSeq
chr8 - 92883529 92966144 TRIQK 286144 "triple QxxK/R motif containing, transcript variant 1" GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135576_PI430048170 0.7458046466627120.8101584690444651.51643049258263 1.70732069651632 0.40209436242825 A A A 0.3935493703995271.79507313497409 2.14046701962667 A A A LNCV6_135576_PI430048170 mRNA ACAGTCTGGAACTGACAATATGCAGGAGCAGTAAACTGGCAGAAAACCAGGAATCAGAGA NM_002033RefSeq
chr11 + 94543850 94549898 FUT4 2526 "fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)" GO:0046920|GO:0042355|GO:0005794|GO:0016020|GO:0009986|GO:0005975|GO:0032580|GO:0008417|GO:0006486|GO:0016021|GO:0036065|GO:0071944 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140464_PI430048170 0.0904051437008837 1.04899594051675 0.378758524930322 0.415287244239873 0.334263868459873 A A A 0.2951297031779260.316424423971698 0.310784078537812 A A A LNCV6_140464_PI430048170 mRNA

CTTTTGTTGTTGTTAATTTTTGTAAAGCAGACGCTACTCTCAAGCAGTTGACAAAACTGT NM_001965 RefSeq chr2 - 73290928 73293701 EGR4 1961 early growth response 4 GO:0043066|GO:0008284|GO:0006355|GO:0005737|GO:0071371|GO:0003700|GO:0005634|GO:0071320|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132783_PI430048170 0.0456421463800015 0.7442670735185528.91424563997438 8.59210298536838 8.5408032052485 P P P 8.95562414315727 9.24740784399839 9.13660236913703 P P P LNCV6_132783_PI430048170 mRNA
TGCTGCCGTGTGAGTTTTGAATGATTTTGCAGTAAAGACCTGATCTTTCTCATCAAAAAA NM_014798 RefSeq chr17_KI270908v1_alt - 126404 180935 PLEKHM1 9842 "pleckstrin homology domain containing, family M (with RUN domain) member 1, transcript variant 1" GO:0035556|GO:0005737|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131013_PI430048170 0.1409026325819850.4876360530917710.758614028856236 0.82525416743625 0.756924929323808 A A A 2.47936216404116 1.2357108255987 1.39892401398642 A A A LNCV6_131013_PI430048170 mRNA
GAAGATTCAGAGAAACAAAGGAATGTAACCTTATTGATTACATTTTTGGTGATCACCGAG NM_138459 RefSeq chr6 + 117675453 117710723 NUS1 116150 nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae) GO:0005515|GO:0003674|GO:0055092|GO:0005789|GO:0016765|GO:0006486|GO:0016021|GO:0001525|GO:0032367|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77046_PI430048170 0.5749155848167670.9709603081894720.4535618273305220.430039003455551 0.244827260102438 A A A 0.37877942178438 0.4632973168921580.421585077960951 A A A LNCV6_77046_PI430048170 mRNA
TAGTTCTCATTGTGAGATCACAAGTGGAGGCTCCAACCAGTCCAGAAGTTCCTTTCTATG NM_030883 RefSeq chr6_GL000252v2_alt + 723975 729845 OR2H1 26716 "olfactory receptor, family 2, subfamily H, member 1" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130087_PI430048170 0.0162003868847295 0.46269771068348 9.26725604279014 9.12582228378218 9.48998279295174 P P P 10.0953807143561 10.2954238284983 10.7669746783177 P P P LNCV6_130087_PI430048170 mRNA
CATTTCCCCATTTCTTGTTTTTAAAAGACCAACAAATCTCAAGCCCTATAAATGGCTTGT NM_005066 RefSeq chr1 - 35183599 35193142 SFPQ 6421 splicing factor proline/glutamine-rich GO:0008380|GO:0006397|GO:0005515|GO:0070932|GO:0000976|GO:0044212|GO:0042826|GO:0001047|GO:0005634|GO:0006310|GO:0000122|GO:0016363|GO:0006351|GO:0005737|GO:0042382|GO:0006281|GO:0000166|GO:0000380|GO:0042752|GO:0005654|GO:0048511|GO:0042754|GO:0045892|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135813_PI430048170 0.4002466958541540.63025388786587 0.424209968006731 0.4454745804254370.286385895166212 A A A 0.401124360636965 1.83194856367787 0.426586629909859 A A A LNCV6_135813_PI430048170 mRNA
GCTCTAGAACCCATGGTCTTAAGCACTGCAATATATCACCTTTCAGTATAAAAATATTTG NM_001258406 RefSeq chr13 + 76952488 76958641 IRG1 NA immunoresponsive 1 homolog (mouse) NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139872_PI430048170 0.19922928137942 0.6431040838327752.20523359506977 2.25441344291199 3.20197332500751 A A P 2.65264477158421 3.49489156576996 3.50297762390092 P P P LNCV6_139872_PI430048170 mRNA
TCCAAGATTTCAGATCTCTAAATCACAAAGAGAAATCTTGGCATGACCAGTGTGCACGTT NM_001134658 RefSeq chr10 + 93893972 93902734 SLC35G1 159371 "solute carrier family 35, member G1, transcript variant 1" GO:0005515|GO:0005886|GO:0051480|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143337_PI430048170 0.30542145568353 0.8524685729111017.06763674515638

6.60624581338953 6.44359988330171 P P P 6.93056308022441 6.97451789798607
6.97734572110662 P P P LNCV6_143337_PI430048170 mRNA
GAGAATTAGCTTAAATTCCCTCCTCCCTTTTGATAAATCCACAGGGATTCCTTCACTCTG NM_016848 RefSeq chr9
- 89005770 89178767 SHC3 53358 SHC (Src homology 2 domain containing) transforming protein 3
GO:0005515|GO:0008286|GO:0030971|GO:0048011|GO:0005886|GO:0019901|GO:0035249|GO:0007265|GO:0005
575|GO:0007417|GO:0005829|GO:0007173|GO:0007611|GO:0004871|GO:0007169 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132490_PI430048170 0.00837979917978969 0.635114228563946 10.937024936655
10.8672641942634 10.6978994726803 P P P 11.31703700437 11.6667463118177
11.4721526471235 P P P LNCV6_132490_PI430048170 mRNA
CGGGATGGGACAGGGCACGGGCTCTCAGAAAATAAACTGCTTTATTGGAATTACAAAAAA NM_016111 RefSeq chr16
+ 1493350 1510459 TELO2 9894 telomere maintenance 2
GO:0005622|GO:0005515|GO:0032006|GO:0032947|GO:0005737|GO:0000781|GO:0031931|GO:0016020|GO:0005
634|GO:0031932|GO:0032403 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138602_PI430048170 0.24188145134547 1.8618002635225 2.52761595683584
3.62947475107941 2.01080125826006 A P A 2.56083464429293 1.53551104163331
1.63674726132527 A A A LNCV6_138602_PI430048170 mRNA
CATTTCCTTAAACAAGCCTCACCATTGACCTTTCTTTTAAAACAATAAATTCCTTTTGCT NM_001242575 RefSeq chr2
- 213276552 213284205 LOC100130451 NA uncharacterized LOC100130451 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_138700_PI430048170 0.0211786313314034 0.40851249653638 7.11385691737256
7.05682229602249 7.30091991643067 P P P 8.07103029382807 8.34818276258463
8.83348358003519 P P P LNCV6_138700_PI430048170 mRNA
TGAGGAATAGTGTGAATTCCTTCCTTGCCTTATTGTTGACTGTTAATGAACATGTTTTGT NM_001004339 RefSeq chr1
+ 52842510 52894575 ZYG11A 440590 "zyg-11 family member A, cell cycle regulator" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141587_PI430048170 0.00116622340596951 1.18625352192843 0.836391157029723
0.876924461608739 0.867480987052494 A A A 0.653643552172871 0.594726884934464
0.592665288596694 A A A LNCV6_141587_PI430048170 mRNA
GATGTAAGAGAAACTTAAAAAGTAATAACTGTCTTTGGCGATCAAATGGCTATGGGGAAT NM_001007090 RefSeq
chr8 + 13566842 13568288 C8orf48 157773 chromosome 8 open reading frame 48 GO:0005515 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127249_PI430048170 0.968974542677882 0.999098230713144 0.588262175445023
0.488484673996195 0.37937531704609 A A A 0.417862054077711 0.533802199537418
0.513283548585258 A A A LNCV6_127249_PI430048170 mRNA
CAAATCATCAACAAGTTCGTGAATAGCGTGATCAACACGCTGAAAAGCACTGTATCCTCC NM_080574 RefSeq chr20
+ 33168153 33181417 BPIFA2 NA "BPI fold containing family A, member 2" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_145081_PI430048170 0.0580206454563415 1.36793924049809 9.93345166113254
10.3542343193515 10.145684650823 P P P 9.63720164356538 9.75883031831279
9.70935546293949 P P P LNCV6_145081_PI430048170 mRNA
CCTCACCAGCTGTGAGCCTGCTATCAGGCCTGCCCCTCCAATAAAAGTGTGTAGAACTCC NM_001039675 RefSeq
chr15 + 90930179 90954093 UNC45A 55898 "unc-45 homolog A (C. elegans), transcript variant 3"
GO:0048471|GO:0005737|GO:0007517|GO:0005794|GO:0061077|GO:0051879|GO:0005654|GO:0030154 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66826_PI430048170 0.0492131021382151 0.532088669529083 2.27535630235788
2.00860144378348 2.89213089636727 A A P 3.05557404014225 3.24773010382183
3.67806889949484 P P P LNCV6_66826_PI430048170 mRNA
GCAGCAGAAATTGCTTGCGGAGTTTGCTTCACGACAGAAAAGCTTTATGGAAACTGCAAT NM_172070 RefSeq chr2

+ 169827507 170084129 UBR3 130507 ubiquitin protein ligase E3 component n-recognin 3 (putative)
GO:0007608|GO:0006511|GO:0004842|GO:0016567|GO:0001967|GO:0042048|GO:0016874|GO:0008270|GO:0016
021|GO:0009790|GO:0001701 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128251_PI430048170 0.7484382978670051.05938137738573 8.53653553158273
8.09438519904838 7.97282014769355 P P P 8.30373866895809 8.11321481759352
7.98156652083718 P P P LNCV6_128251_PI430048170 mRNA
CTGCCTGTTCACATGTCGCCCAGGCGGGAAAAATGGAAAATAAAGTGTATTTACACAGTC NM_145245RefSeq chr19
+ 7830274 7864976 EVI5L 115704 "ecotropic viral integration site 5-like, transcript variant 2"
GO:0005515|GO:0017137|GO:0033126|GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132541_PI430048170 0.000714610695092852 0.4553714692176258.03051743392786
7.77721980226152 7.94573839312287 P P P 9.12710122394103 8.98239736566027
9.05641201389704 P P P LNCV6_132541_PI430048170 mRNA
GACTTTTTGCAAACCCAAGGATGAACTTTGTGTGCATTCAATAAAATCATCTTGGGGAAG NM_020946RefSeq chr9
- 123379653 123930138 DENND1A 57706 "DENN/MADD domain containing 1A, transcript variant 1"
GO:0017112|GO:0017124|GO:0030054|GO:0030136|GO:0032851|GO:0048488|GO:0015031|GO:0030425|GO:0006
897|GO:0030665|GO:0042734|GO:0032483|GO:0043025 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131010_PI430048170 0.175249902771912 0.857809251078712 6.93949623492643 7.2226709505218
7.03031179780334 P P P 7.45316923704421 7.09986430008372 7.29630306500872 P P P
LNCV6_131010_PI430048170 mRNA
GAGTCAGAAATGTTGCCAGAAAAAGTATCTCCTCCAACCAAAACATCTCAATAAAACCAT NM_032464RefSeq chr7
+ 74209756 74229834 LAT2 7462 "linker for activation of T cells family, member 2, transcript variant
1"
GO:0005515|GO:0050853|GO:0043303|GO:0019722|GO:0005886|GO:0042629|GO:0035556|GO:0042113|GO:0045
087|GO:0045121|GO:0016021|GO:0042169|GO:0038095|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140444_PI430048170 0.7504852334694890.9862486250515421 1.889740970803
12.0125569182243 11.9762045384777 P P P 11.9414774399853 12.066902663955 11.928714891136
P P P LNCV6_140444_PI430048170 mRNA
TATTAGTGATTTTAAAGGGGACTCTTCAGGGACTTGTGTACTGGTTATGGGGGTGCCAGA NM_001198868 RefSeq
chr11 + 65181214 65212006 CAPN1 823 "calpain 1, (mu/l) large subunit, transcript variant 1"
GO:0005515|GO:0008284|GO:0005886|GO:0005509|GO:0005829|GO:0005737|GO:0004198|GO:0016020|GO:0022
617|GO:0030198|GO:0032801|GO:0006508|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_131292_PI430048170 0.22989282354913 0.6199512103016020.42666945776997
0.4353106861096080.382199834210701 A A A 1.6997857701532 0.532364341797149
0.812902465582474 A A A LNCV6_131292_PI430048170 mRNA
GGAGCACTTCTTCCTTTGTTAGGCTGTGCTTTACTGATAAAACCAAGTATTGAATAAAGA NM_014839RefSeq chr1
+ 99264291 99309582 LPPR4 9890 "lipid phosphate phosphatase-related protein type 4, transcript
variant 1" GO:0048839|GO:0042577|GO:0046839|GO:0005887|GO:0008195|GO:0007409 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_143860_PI430048170 0.3746780670896431.05290318500954 0.418810978374145
0.6055180388013820.534659612388399 A A A 0.546420046394571 0.395878998676609
0.394345479272719 A A A LNCV6_143860_PI430048170 mRNA
GTGCTATTTTTATTTCCAATGGATATTTCTGTATTACTAGGGAGGCATTTACAGTCCTCT NM_197947RefSeq chr12 -
10116780 10130269 CLEC7A 64581 "C-type lectin domain family 7, member A, transcript variant 1"
GO:0042287|GO:0008037|GO:0005886|GO:0042832|GO:0006910|GO:0046872|GO:0002221|GO:0005737|GO:0009
756|GO:0042110|GO:0006954|GO:0045087|GO:0030246|GO:0016021|GO:0008329 . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_72751_PI430048170 0.0376325101992743 0.6164375843854315.79791688729155
5.86360139412339 6.10674661665398 P P P 6.27052489336046 6.71658291881659
6.83458547081024 P P P LNCV6_72751_PI430048170 mRNA
CTCTTGACAGGACCCTAGCTCATAAACATTTCTTCAGAACTATACTTCAAATGGGATGCT NM_001199251 RefSeq
chr3 - 20169479 20186233 SGOL1 151648 "shugoshin-like 1 (S. pombe), transcript variant A3"
GO:0005515|GO:0000780|GO:0010457|GO:0005813|GO:0030892|GO:0005829|GO:0007067|GO:0000922|GO:0005
737|GO:0007059|GO:0045132|GO:0000777|GO:0000776|GO:0000779|GO:0005654|GO:0019900|GO:0008608|GO:0
000278|GO:0000775|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129570_PI430048170 0.4624003677711470.8641285647759596.85284432432478
6.91686572949448 6.5105855883337 P P P 6.57069830104128 7.23702555812133
7.05739611594819 P P P LNCV6_129570_PI430048170 mRNA
GGGCTTGAGTCTCAAGGACTCACTGATTACATACCCAAAGGCTCTTTTCAGAGCCACCCA NM_003536RefSeq chr6
+ 27810063 27810536 HIST1H3H 8357 "histone cluster 1, H3h"
GO:0005515|GO:0010467|GO:0046982|GO:0006325|GO:0006335|GO:0005576|GO:0005634|GO:0000228|GO:0003
677|GO:0032776|GO:0043234|GO:0060968|GO:0016020|GO:0000183|GO:0007596|GO:0045814|GO:0040029|GO:0
005654|GO:0000786|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_50522_PI430048170 0.00533677718857492 1.76172906264516 7.09751950170355
6.95214627607185 6.72099527901435 P P P 6.17457483365063 6.19753321566194
5.96067028387362 P P P LNCV6_50522_PI430048170 mRNA
ATGCGCCGAGCACGAGACAATGATGCACATTTTAAAATAAAAGAATGATGCACATTTTAA NM_001167676 RefSeq
chr1 - 32361269 32362243 FAM229A NA "family with sequence similarity 229, member A" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82689_PI430048170 0.0975700081553685 1.15089655069343 7.98950444231148
7.86332408841961 7.85629863228369 P P P 7.65383856701152 7.84673817390472
7.59180057381978 P P P LNCV6_82689_PI430048170 mRNA
AGGACTTCATCAACAACATTAACAGTGTCTTGGAGTCCTTGTATATTGAGATAAAGAGAG NM_145080RefSeq chr16
- 27224993 27268792 NSMCE1 197370 non-SMC element 1 homolog (S. cerevisiae)
GO:0005515|GO:0000781|GO:0004842|GO:0016567|GO:0016874|GO:0030915|GO:2001022|GO:0006310|GO:0043
231|GO:0035556|GO:0005737|GO:0006281|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_72971_PI430048170 0.6201550441422890.8571302277028623.2903776354481 3.07457014268512
3.01999623452908 P P P 2.75914958281856 3.38784221049816 3.75160689807995 P P P
LNCV6_72971_PI430048170 mRNA
TATCTAGGCAACAGGGATGAGCCTGAACCTCCCTGAGGCCAGCTTACTGAGCAGAGCATC NM_001190316 RefSeq
chr3 - 48693450 48717278 IP6K2 51447 "inositol hexakisphosphate kinase 2, transcript variant 9"
GO:0008440|GO:0030308|GO:0043065|GO:0043647|GO:0019221|GO:0052724|GO:0052723|GO:0005634|GO:0044
281|GO:0000832|GO:0005524|GO:0046854|GO:0060337|GO:0006817|GO:0005654|GO:0045111 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136190_PI430048170 0.1578898479543041.16306784626006 9.80202391226063
9.76138085805099 9.59368582579321 P P P 9.64082072419571 9.55505749156891
9.29350260992936 P P P LNCV6_136190_PI430048170 mRNA
GACATGGGGTAATGTGAGAGAGTAGAACACCCCCGTACCTAATAAAAATCTTTATTTTTT NM_203413RefSeq chr17
+ 7252200 7259940 ELP5 23587 "elongator acetyltransferase complex subunit 5, transcript variant 2"
GO:0005515|GO:0033588|GO:0006355|GO:0005737|GO:0030335|GO:0006325|GO:0005634|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132282_PI430048170 0.3932479649878220.858753189545131 2.87638639824432 3.1733682357594
3.29875390560564 A P P 3.61673355572964 3.35055877247248 3.0085986054198 P P P
LNCV6_132282_PI430048170 mRNA
TAATATAACACGAGTTTGGGCCCGAATCAGTGTGTTCTCATCATTTTTCAGGCAGGGGAG NM_001136019 RefSeq

chr19 + 49512278 49526428 FCGRT 2217 "Fc fragment of IgG, receptor, transporter, alpha, transcript variant 1"
GO:0030881|GO:0006955|GO:0005886|GO:0019882|GO:0019864|GO:0002416|GO:0016021|GO:0019770|GO:0003823|GO:0038094 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140088_PI430048170 0.3249430527993630.9659110156548370.303005024728629
0.3959611414132580.315158036913488A A A 0.4545674036390950.350830678551102
0.358282203514859A A A LNCV6_140088_PI430048170 mRNA
GGAGATGTGCCAAACATGGCAAGAAGTTTTTGGATCTTTTTCTTACAAAGAAAAATGGAT NM_153692RefSeq chr8
+ 38974148 38988662 HTRA4 203100 HtrA serine peptidase 4
GO:0004252|GO:0004175|GO:0006508|GO:0005576|GO:0001558|GO:0030512|GO:0005520 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131216_PI430048170 0.4888176798838650.8097806231643425.10532342205473
5.42575983492807 5.0649354345161 P P P 6.03265666456703 5.13396129701707
5.18385124443667 P P P LNCV6_131216_PI430048170 mRNA
GATTTCTGCAACTGAGGACCTAATTATGCCTGTCTGCAAACTAATAATGTAAAAGGTAAT NM_171829RefSeq chr3
- 179242765 179259891 KCNMB3 27094 "potassium channel subfamily M regulatory beta subunit 3, transcript variant 2"
GO:0005513|GO:0005886|GO:0007596|GO:0005887|GO:0008076|GO:0015459|GO:0007268|GO:0001508|GO:0015269|GO:0006813|GO:0071805|GO:0019228 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131459_PI430048170 0.3176410540938020.8609160282989758.07278208394031 8.4325773235798
8.69426861208059 P P P 8.55592368611976 8.67681904138736 8.67814821752924 P P P
LNCV6_131459_PI430048170 mRNA
CTGTACAGGAAGCTTGCAAATTTTCTGTACAATGTGCTGTGAAAAATCTGATGACTTTAA NM_003642RefSeq chr2
+ 171922424 171983686 HAT1 8520 "histone acetyltransferase 1, transcript variant 1"
GO:0005515|GO:0000790|GO:0006348|GO:0007584|GO:0006325|GO:0006335|GO:0005634|GO:0006323|GO:0006336|GO:0016363|GO:0043231|GO:0043234|GO:0005737|GO:0043967|GO:0010485|GO:0005654|GO:0006475|GO:0004402 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140882_PI430048170 0.3786298726362450.9675418971144750.417570450276601
0.4431621940508810.303867789369615A A A 0.4111058523064740.469332402960066
0.43013894398218 A A A LNCV6_140882_PI430048170 mRNA
GAGAGGTAGATACTAACTTCCTCCATGAATTTTTTGAGGTATTCAAAGGAAAAGGAATTG NM_152585RefSeq chrY
+ 22308862 22417881 RBMY1F NA "RNA binding motif protein, Y-linked, family 1, member F, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145757_PI430048170 0.5172125120517110.9743489069824460.286673873595214
0.2737102848588760.397306100108035A A A 0.4264660469435550.307866435679738
0.336379088222663A A A LNCV6_145757_PI430048170 mRNA
TTCACCGCGACTGTTAAGCCAAGACCTGCCAGGAGTGTCTCTAAGAGATCCAGGAGGGAGNM_052890RefSeq chr19
- 15468645 15479504 PGLYRP2 114770 peptidoglycan recognition protein 2
GO:0016019|GO:0050830|GO:0044117|GO:0042834|GO:0050727|GO:0008745|GO:0032827|GO:0005622|GO:0009253|GO:0002221|GO:0016020|GO:0045087|GO:0001519|GO:0008270|GO:0016045|GO:0032689|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127071_PI430048170 0.00119569714758857 0.4338550071188233.21055428066813
3.57296557966247 3.31705725396286 P P P 4.38652644820068 4.71671494573237
4.61632044493147 P P P LNCV6_127071_PI430048170 mRNA
CCGGGAGGTGCACTTCTTTGAAGAACTTCCTAAAGTACCTGTATAGTAGTTTTCATCTTA NM_014875RefSeq chr1
- 200551496 200620734 KIF14 9928 kinesin family member 14
GO:0008017|GO:0005515|GO:0021846|GO:0008284|GO:0021987|GO:0005886|GO:0021695|GO:0005634|GO:0051233|GO:0031146|GO:0033624|GO:0030155|GO:0001558|GO:2000045|GO:0045184|GO:0032147|GO:0043523|GO:0043524|GO:0005737|GO:0015631|GO:0021772|GO:0008574|GO:0034446|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_130480_PI430048170 0.3775749443964751.2676543811485 0.367670384497489
0.2487961896214171.08291327916976 A A A 0.2687975269342760.281199552686181
0.270482037833365A A A LNCV6_130480_PI430048170 mRNA
GGTTTTACCTTGGAAATTGGCCAGACCCCAAAATATGTCTTTTACACATGCTGCTTTTTT NM_001205280 RefSeq
chr19 + 44613629 44636781 IGSF23 147710 "immunoglobulin superfamily, member 23" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131889_PI430048170 0.3350786658461471.31646301987421 1.28709438285331
0.5642742615118280.390937638321065A A A 0.5107953669732270.402237559455863
0.294622964085369A A A LNCV6_131889_PI430048170 mRNA
GAGAAAGGGAGACAAAAGGAGCTTTTTAATACCTAATCTACTTTGGAACATAACCGTATA NM_001278464 RefSeq
chr12 + 32679199 32745650 DNM1L 10059 "dynamin 1-like, transcript variant 5"
GO:0005515|GO:0003374|GO:0048471|GO:0030054|GO:0090149|GO:0032459|GO:1900063|GO:0050714|GO:0003
924|GO:0005741|GO:0001836|GO:0090141|GO:0042803|GO:0006921|GO:0043231|GO:0042802|GO:0005829|GO:0
008289|GO:0005739|GO:0005737|GO:0051289|GO:0090200|GO:0061025|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143394_PI430048170 0.00297706818371396 0.3889884002984976.4527659111766
6.35940991974187 6.04717787353561 P P P 7.55103196197569 7.71265538713433
7.70703247538808 P P P LNCV6_143394_PI430048170 mRNA
CCTCACCTGTGGTGGTTTATGGGTGTGATGGGGTTTTTAAGATTATTATAAACCAGTAAA NM_001288631 RefSeq
chr17 - 28755977 28842839 FAM222B 55731 "family with sequence similarity 222, member B,
transcript variant 3" GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55081_PI430048170 0.5243253554619551.22335896264353 0.2539524069683930.376646011622796
1.20075616384295 A A A 0.4777591729336150.3706216660695140.298027633984541A A A
LNCV6_55081_PI430048170 mRNA
GTTAACAAAAAGAATAAAGCTAATCATGTATTACAAACAGCAGTGTGCCCAGACTTGTGG NM_005149RefSeq chr1
+ 168281039 168314428 TBX19 9095 T-box 19
GO:0045165|GO:0003700|GO:0006357|GO:0045944|GO:0042127|GO:0021983|GO:0045595|GO:0005634|GO:0009
653|GO:0001158|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59523_PI430048170 0.77233481564427 1.03123048627876 5.70448666881198 5.6239194737783
5.46528341565302 P P P 5.1714050749239 5.87377424375494 5.54079335286398 P P P
LNCV6_59523_PI430048170 mRNA
TTGGAACTGACTTCATGGGTACCATAAGTACAGAGAACAAGGGATGCTGAGGCTTCTGAT NM_032300RefSeq chr12
+ 109900517 109918069 TCHP 84260 "trichoplein, keratin filament binding, transcript variant 1"
GO:0005739|GO:0005515|GO:0030308|GO:0005813|GO:0005737|GO:0045179|GO:0005886|GO:0006915|GO:0045
095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138622_PI430048170 0.0708343119676152 1.30931883867497 12.0204752892369
11.928714891136 11.8548294980022 P P P 11.3210492485205 11.752896927476
11.5361429363184 P P P LNCV6_138622_PI430048170 mRNA
TGGGACACGCCAAGCTCTTCAGTGAAGACACGATGTTATTAAAAGCCTGTTTTAGGGACT NM_020979RefSeq chr7
+ 102285061 102321711 SH2B2 10603 SH2B adaptor protein 2
GO:0005515|GO:0008286|GO:0030036|GO:0005886|GO:0005884|GO:0019221|GO:0019222|GO:0046578|GO:0050
851|GO:0005829|GO:0042802|GO:0035556|GO:0005737|GO:0008269|GO:0005068|GO:0004871|GO:0001922|GO:0
001725|GO:0046425|GO:0009967|GO:0001726|GO:0007399|GO:0007165|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_61844_PI430048170 0.1459605081669220.7010114487460113.83116010568741 3.38228543440895
4.15950661503881 P P P 4.42701666137523 3.96456682899488 4.55749413157973 P P P
LNCV6_61844_PI430048170 mRNA
GGAAAAGAGGTAAACCTTTTGAACAGTTGAATTTCATCAGAAGCTCTATAGCTTTTTGGT NM_012388RefSeq chr15

+ 45587218 45609711 BLOC1S6 26258 "biogenesis of lysosomal organelles complex-1, subunit 6, pallidin"
GO:0030133|GO:0005515|GO:0016081|GO:0048490|GO:0032438|GO:0031201|GO:0031175|GO:0032402|GO:0042803|GO:0005829|GO:0032816|GO:0042802|GO:0050942|GO:0005737|GO:0051015|GO:0033299|GO:0061024|GO:0061025|GO:0019905|GO:0006892|GO:0030318|GO:0031083|GO:0007596|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53947_PI430048170 0.2024198336434320.8642894328878887.32762045476809 7.58785488295464 7.73519032559156 P P P 7.78372357714176 7.71952526868225 7.80635832399806 P P P LNCV6_53947_PI430048170 mRNA
CCCAACTGGTTTAAAGCCCTGAGGATAGTAGTCACTTTATTGGCCACTTTTTCATTTATA NM_016486RefSeq chr1
+ 45688174 45694436 TMEM69 51249 transmembrane protein 69 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137069_PI430048170 0.0875586844833283 0.8457313275382979.36514721453869 9.60536058496111 9.63985709200627 P P P 9.70772680564237 9.80529181061888 9.83470881961078 P P P LNCV6_137069_PI430048170 mRNA
AAGGGACGTTTGTGTGAATAAAGTTATTTGATGGGGTCAAAGAAGCCATATGTGATTTGA NM_080836RefSeq chr20
+ 2101881 2148552 STK35 140901 serine/threonine kinase 35
GO:0005737|GO:0004674|GO:0005730|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131171_PI430048170 0.4316978487152511.42817319139295 0.495272524091441 0.6222672458310471.77803443301752 A A A 0.3640022449925540.799862201043922 0.524309120395753A A A LNCV6_131171_PI430048170 mRNA
CCCCCAGTCAGAACTGTGAAACAGGGAAATTTTGGGGTGGGAGTAAAAGCAAATTTGGAA NM_001013625 RefSeq chr1 - 161364730 161367883 CFAP126 257177 cilia and flagella associated protein 126
GO:0016324|GO:0005737|GO:0072372|GO:0036064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139804_PI430048170 0.00760158055196825 0.4235502665165548.75485733438231 8.47836165755386 8.57045375982419 P P P 9.5406018184384 9.82483071620894 10.1135615140424 P P P LNCV6_139804_PI430048170 mRNA
TACAGTATCTGTAGCATGCCGTTCTGGATTAATAAAAGCAACTTAGTATGTGCAGATAAA NM_001198525 RefSeq chr10 + 112950249 113167677 TCF7L2 6934 "transcription factor 7-like 2 (T-cell specific, HMG-box), transcript variant 7"
GO:0005515|GO:0000790|GO:0003700|GO:0044212|GO:0008013|GO:0045599|GO:0009791|GO:0010909|GO:0032993|GO:0030538|GO:0045444|GO:0032024|GO:0001103|GO:0045295|GO:0019901|GO:0005977|GO:0000122|GO:0000978|GO:0007420|GO:0043588|GO:0005654|GO:0045892|GO:0008134|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130489_PI430048170 0.10453637136413 1.25372334725012 12.7500898921101 12.8696061483772 12.4652282228976 P P P 12.5120396820002 12.4067392281493 12.199511934238 P P P LNCV6_130489_PI430048170 mRNA
GACTGCTTCTTTTGGCTCTCCGACAACTCCGGCCAATAAACACTTTCTGAATTGAAAAAA NM_138432RefSeq chr12
+ 113422389 113438276 SDSL 113675 "serine dehydratase-like, transcript variant 1"
GO:0005739|GO:0003941|GO:0008150|GO:0003674|GO:0005737|GO:0030170|GO:0004794|GO:0006565|GO:0070062|GO:0006567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144312_PI430048170 0.26048388937337 4.41879709076024 0.290778192352834 3.86144560122569 2.88168275892686 A P P 0.3785967027602320.318959303801198 1.42575710515175 A A A LNCV6_144312_PI430048170 mRNA
TCCAATTTGAATTTCAGGGCTGTAGTCACTGATGTGTCACATTTAGTGAAGGCTCTCGGC NM_203373RefSeq chr15
+ 63597352 63602421 FBXL22 283807 F-box and leucine-rich repeat protein 22 GO:0030018|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113918_PI430048170 0.000660185001200161 0.4234205676351925.42841852145439

5.42156488178728 5.56439183731427 P P P 6.70431390474 6.69493884170952 6.73880660533142 P P P LNCV6_113918_PI430048170 mRNA AAGTGATGTAACTATCAGACATTTGGAGAGAGATGGACAAAGGAAAGTGGCGATAGTGTA NM_001206938 RefSeq chr7 - 143851367 143902185 TCAF1 9747 "TRPM8 channel-associated factor 1, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80411_PI430048170 0.7301360092717681.04601683855852 4.67382200542919 4.74842500415806 4.32551725970788 P P P 4.69255171369522 4.38428793316239 4.49343865493922 P P P LNCV6_80411_PI430048170 mRNA ATAGCCTGGACCTACAGCACTCCATGTGGAGTCCACAGCTGTGGTGAGCTTCTTGGAGGA NM_012162RefSeq chr8 - 144355427 144358523 FBXL6 26233 "F-box and leucine-rich repeat protein 6, transcript variant 1" GO:0004842|GO:0016567|GO:0006508 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139268_PI430048170 0.0360086918772326 2.08586011036005 8.12304224822384 8.02368108488965 8.11847419711994 P P P 6.62122985945318 7.38552537301938 6.97728566755207 P P P LNCV6_139268_PI430048170 mRNA AAATATTAGTAACTATGACTGACGTCCCCAGAAGTTTCTGGGTCTACCACACTCCCCAAC NM_002084RefSeq chr5 + 151020437 151028993 GPX3 2878 glutathione peroxidase 3 GO:0004602|GO:0008430|GO:0006982|GO:0051289|GO:0005576|GO:0042744|GO:0005615|GO:0000302|GO:0070062|GO:0055114|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134830_PI430048170 0.3907025529558820.7838134573267611.10367667160893 0.3584294030494410.758676702777377A A A 0.80295404223385 1.60495747050591 0.806889887114769A A A LNCV6_134830_PI430048170 mRNA TCTAATTTGTGCGTGTGTGGACTCACTATGGAAATAAAATGCAGTAGAAAGAGCATGTAA NM_033337RefSeq chr3 + 8733799 8746765 CAV3 859 "caveolin 3, transcript variant 1" GO:0005515|GO:0030018|GO:0031594|GO:0008016|GO:0010831|GO:0051394|GO:0031122|GO:0060307|GO:0032403|GO:0030154|GO:0070836|GO:0060373|GO:0016010|GO:0051926|GO:0017015|GO:0071253|GO:0086005|GO:0051647|GO:0042632|GO:0009986|GO:0060762|GO:0007520|GO:0033292|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144975_PI430048170 0.1276934085892240.7610567166446023.72405120703328 3.300700052766 3.39057923386737 P P P 3.56170280116839 4.07960140362916 3.9425492234363 P P P LNCV6_144975_PI430048170 mRNA AACAGGACCAATGGATTAAACTGGCATTTCAGTCCAAGGAAGCTCGAAGCAGGTTTAGGA NM_032088RefSeq chr5 + 141391915 141512979 PCDHGA8 9708 "protocadherin gamma subfamily A, 8, transcript variant 1" GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92621_PI430048170 0.1276052215258780.6862210738474312.52441728334406 2.93258258590894 3.33364374702515 A A P 3.4471524408409 3.50300485611011 3.57982062031679 P P P LNCV6_92621_PI430048170 mRNA GGGATATTATCAAATCTACTACTGTTCATGGCAGAGTCCCTGTGAAGCAGGAAGAGTGAG NM_001278458 RefSeq chr2 - 164680184 164842168 COBLL1 22837 "cordon-bleu WH2 repeat protein-like 1, transcript variant 1" GO:0003779|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106901_PI430048170 0.000491858922863674 1.45954073027131 8.06269225921139 8.05820932863863 7.94428755883762 P P P 7.43440902696971 7.45168355144471 7.5432576829774 P P P LNCV6_106901_PI430048170 mRNA AACAATTCTGGGTGACTCAGCTTCGAGCTTGTGCCAAATACCACATGGAAATGAATTCTA NM_017784RefSeq chr3 - 31660824 31981850 OSBPL10 114884 "oxysterol binding protein-like 10, transcript variant 1" GO:0015485|GO:0006869 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145493_PI430048170 0.1958779345033280.62116477027167 1.87095640735803 1.66147910713228 0.517152376363242A A A 2.24485220879076 1.88666147473543 2.27724293204206 A A A LNCV6_145493_PI430048170 mRNA GCCCCTAATAGGACAATTCTATTTGTTGACCATTTCTACAATTTGTAAAAGTCCAATCTG NM_020665RefSeq chrX

- 15627315 15665031 TMEM27 57393 transmembrane protein 27
GO:0035543|GO:0005515|GO:0005737|GO:0045956|GO:0035774|GO:0008241|GO:0006508|GO:0031526|GO:0016021|GO:0051957|GO:0008237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129791_PI430048170 0.5006832372119471.31024090500742 0.693708032994114
1.96663626186142 1.58061641451317 A A A 1.43113333192469 0.852962443333745
0.998207781356672A A A LNCV6_129791_PI430048170 mRNA
AACAGGTACTTGAAAGGGGCTCTGAAAAAAGTAGTTGGCAGGGTGGTGTTTTCTGTCTGA NM_012360RefSeq chr16
+ 3204246 3205185 OR1F1 4992 "olfactory receptor, family 1, subfamily F, member 1"
GO:0050911|GO:0007165|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139120_PI430048170 6.08732825919548e-05 0.1901402535488677.77273387613853
7.45551710100183 7.68228967895948 P P P 9.87426860728401 10.0096398139321
10.2095991102702 P P P LNCV6_139120_PI430048170 mRNA
GAAGTAAGTGTGTTTGTTTTCATCTTATGGAAACTCTTGATGCATGTGCTTTTGTATGGA NM_014331RefSeq chr4
- 138164093 138242349 SLC7A11 23657 "solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11"
GO:0005515|GO:0005791|GO:0015327|GO:0070306|GO:0005886|GO:0009986|GO:0006865|GO:0009636|GO:0050900|GO:0055085|GO:0070527|GO:0007420|GO:0007596|GO:0016021|GO:0005856|GO:0006979|GO:0035094|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132382_PI430048170 0.00158922241452975 1.37730258699973 10.2098049593907
10.2954238284983 10.2342085971047 P P P 9.86050852273775 9.7184829873544
9.77268956540301 P P P LNCV6_132382_PI430048170 mRNA
AACTGAGGAGGGGAGGGGTGTGCTGGGGAATAAATCTTGTATGAGAACAATCTTTAAAAA NM_178126RefSeq
chr17 - 42579507 42609427 FAM134C 162427 "family with sequence similarity 134, member C, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135377_PI430048170 0.2486918866440371.18816418286605 0.819348003178053
0.3187364804137310.511450834111405A A A 0.32109366811719 0.285311205362782
0.341028185707077A A A LNCV6_135377_PI430048170 mRNA
CCAGCATGTACAAAAGTACCATAGAACAGAACTGCTAAATACTGTACATAGATGTATCAT NM_002240RefSeq chr21
- 37624222 37916438 KCNJ6 3763 "potassium channel, inwardly rectifying subfamily J, member 6"
GO:0005515|GO:0005242|GO:0005794|GO:0005886|GO:0015467|GO:0008076|GO:0010107|GO:0007268|GO:0034765|GO:0006813 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144414_PI430048170 0.8046348532142560.8835465114134540.542980248465177
0.5808607037127451.21231895947467 A A A 0.56708362046184 0.48843582822607
1.62290411986279 A A A LNCV6_144414_PI430048170 mRNA
CTGGGCCCACACTCACCTCTAGAATATTGTTTATTAGATAAAAGAAAAAGCTTTTCCTTA NM_001029881 RefSeq
chr2 - 26581204 26641343 CIB4 130106 calcium and integrin binding family member 4
GO:0005509 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136536_PI430048170 0.5217339817805140.8133677033357040.472343928029716
0.5374226442552940.461037799048962A A A 1.32439040409614 0.416804439579788
0.425731060140909A A A LNCV6_136536_PI430048170 mRNA
TGTGAAGTTTAGCATATATGGAGTATGCAGTATCAGCTTGAAGTGACTTCGCAGAAATAA NM_001164116 RefSeq
chr20 + 56412111 56459340 CASS4 57091 "Cas scaffolding protein family member 4, transcript variant 1" GO:0023014|GO:0005737|GO:0000160|GO:0016020|GO:0007155|GO:0005856|GO:0005925|GO:0000155 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136354_PI430048170 0.4354817523906191.85024641879414 2.79389588254888
3.97503872393494 1.68964819831971 A P A 1.8610694984044 1.92084867218402
2.71622761839267 A A P LNCV6_136354_PI430048170 mRNA
GTGGGGGAACACAAAGAGAAAATGGTTTGGAGGCTGAGCACCTTTTTTATTAATAGGTAT NM_001164310 RefSeq

chr9 - 35561829 35563899 FAM166B 730112 "family with sequence similarity 166, member B, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112500_PI430048170 0.0669992867913154 1.25500143117257 10.2967250581488
10.5797064181929 10.6197382357366 P P P 10.0721364459882 10.1323506969957
10.3180738293526 P P P LNCV6_112500_PI430048170 mRNA
TGCCAATGACAGATGCAAGCCCAACACCCTTTTGGTACGCAAAACCTGCTCTCAATAAAT NM_004853 RefSeq chr17
- 9250470 9575958 STX8 9482 "syntaxin 8, transcript variant 1"
GO:0019905|GO:0005802|GO:0048471|GO:0005770|GO:0005783|GO:0008333|GO:0031201|GO:0045022|GO:0005765|GO:0031982|GO:0006886|GO:0006906|GO:0019869|GO:0005484|GO:0005887|GO:0031902|GO:0006810|GO:0055037|GO:0031625|GO:0005769|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137555_PI430048170 0.2081849825132741.19471037769805 6.25153053910235
5.91864248407062 6.37401408728589 P P P 5.77418143976369 5.96482755687123
6.05837952913367 P P P LNCV6_137555_PI430048170 mRNA
GTTTTAAGTATGGGCAAAAATCTGGAAAACTTAGGATCCCTCTGACACCCCAGGATTAGG NM_001017392 RefSeq
chr19 - 18992367 19033571 SUGP2 10147 "SURP and G patch domain containing 2, transcript variant 1" GO:0008380|GO:0006397|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135686_PI430048170 0.4239210942929370.188555794955361 0.470413305584908
0.5358890538445720.457814894656977 A A A 0.5530426002397390.415938902020376
4.28687449600266 A A P LNCV6_135686_PI430048170 mRNA
GGTTTTCTTTCATCTGATGTGTCAGTATCTGTTGATTTGCTTTGTAGTTTGTTGACATCT NM_006794 RefSeq chr2 -
53852912 53860033 GPR75 10936 G protein-coupled receptor 75
GO:0070098|GO:0007186|GO:0005887|GO:0004930|GO:0016493 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60029_PI430048170 0.1072992162679440.760810044888013 7.68105517845783 7.43346693291622
7.77350178598753 P P P 7.83578473160728 7.90018604544156 8.30924812697624 P P P
LNCV6_60029_PI430048170 mRNA
TGGCAACAGGAACCTTAACAATAGTAATGGATGAGGAAGGCAAACTCTGTTGTCTTCACA NM_181503 RefSeq chr13
+ 37000540 37009616 EXOSC8 11340 exosome component 8
GO:0005515|GO:0010467|GO:0006364|GO:0005730|GO:0004532|GO:0043928|GO:0005634|GO:0000178|GO:0005829|GO:0008150|GO:0005737|GO:0017091|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143484_PI430048170 0.8001429466975720.954805291529776 6.23474932951504 6.2043524574916
6.71667044658154 P P P 6.26213826654794 6.29208676348732 6.79627712817662 P P P
LNCV6_143484_PI430048170 mRNA
CAAAGTCTTTCTTACACACTCTATCCTCTGCACTGTTAATAGTAACCTATGACATAATTG NM_025132 RefSeq chr4
+ 39182403 39285810 WDR19 57728 WD repeat domain 19
GO:0055123|GO:0042471|GO:0006996|GO:0031514|GO:0060830|GO:0031513|GO:0072372|GO:0060831|GO:0030326|GO:0048701|GO:0001701|GO:0061055|GO:0042384|GO:0005929|GO:0005737|GO:0031076|GO:0030991|GO:0050877|GO:0032391|GO:0005654|GO:0005856|GO:0035721 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127169_PI430048170 0.0206757010788968 1.3343365040361 10.8151644464491
10.7766274075644 10.5986939690035 P P P 10.4833611693942 10.2117022689641
10.2404501719503 P P P LNCV6_127169_PI430048170 mRNA
AGGGCGTTTTGTGTGATGACGACAGGCGCTTAAGGGAAATAAAAAACGAAGGTGAAAAAA NM_001014985
RefSeq chr17 + 4788958 4790589 GLTPD2 388323 glycolipid transfer protein domain containing 2
GO:0005737|GO:0051861|GO:0017089|GO:0046836 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138411_PI430048170 0.0158228055236614 0.6175536082217248.90076951836118
8.85811230342026 9.0928451267805 P P P 9.44188796632536 9.59835217729503
9.87486698252361 P P P LNCV6_138411_PI430048170 mRNA
TTAATGAATGGATGCCCAGCCAAGCTCAGAGTAGGCGCCCAAAGCATTGTGGATTATTTT NM_001276471 RefSeq

chr12 - 108645110 108730843 CORO1C 23603 "coronin, actin binding protein, 1C, transcript variant 3"
GO:0006909|GO:0007165|GO:0005737|GO:0051015|GO:0030036|GO:0005886|GO:0015629|GO:0005925|GO:0030
027 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131971_PI430048170 0.1076085304887690.7784572233755249.26769161033189
9.10633623522232 8.91370837688489 P P P 9.18860475194031 9.63050961697987
9.53762765623322 P P P LNCV6_131971_PI430048170 mRNA
TTGAGATTTTCTGGCATGTTTCTGGAGGTTTCAAAGGAAATAAAGGTTTCATAGAAATGG NM_015073RefSeq chr19
+ 37907220 38208372 SIPA1L323094 signal-induced proliferation-associated 1 like 3
GO:0043547|GO:0051056|GO:0002244|GO:0005615|GO:0005096 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_61869_PI430048170 0.28138740366812 1.03552319887664 0.5074414167599830.594855527488831
0.482797611494109A A A 0.4728332837089390.4767060522497030.486857648741975A A A
LNCV6_61869_PI430048170 mRNA
CACACCTATGGGAAAATGTTCCTCGAATATTTGAAGCACTTTTGATCATGGAATCAAAAT NM_152647RefSeq chr15
- 49328394 49620921 FAM227B 196951 "family with sequence similarity 227, member B" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_135898_PI430048170 0.8909381531732571.04224127040503 0.386056207627792
1.31434085869939 1.08424855957661 A A A 1.29834628435921 0.93365056183111
0.383733226714383A A A LNCV6_135898_PI430048170 mRNA
TTTTTCCGGACAGCAGATCTTCGCCCTGGAGAAGACTTTCGAACAAACAAAATACTTGGC NM_006168RefSeq chr4
- 84493282 84498234 NKX6-1 4825 NK6 homeobox 1
GO:0006366|GO:0008283|GO:0048709|GO:0072560|GO:0007224|GO:0030516|GO:0051091|GO:0045944|GO:0071
375|GO:0009887|GO:0032024|GO:0070062|GO:0042493|GO:2001222|GO:0045686|GO:0000122|GO:0045687|GO:0
000978|GO:0001078|GO:0051594|GO:0031016|GO:0071345|GO:0045666|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143999_PI430048170 0.0339463171135498 0.4245263342903554.56240912601655
4.27640708375534 4.6546758363382 P P P 5.16322410835998 5.84137099005197
6.07613056394958 P P P LNCV6_143999_PI430048170 mRNA
GCTCAATAGATTGCTCAAATCAGGTTTTCTTTTAAGAATCAATCATGTCAGTCTGCTTAG NM_001992RefSeq chr5
+ 76716042 76735770 F2R 2149 coagulation factor II (thrombin) receptor
GO:0005515|GO:0031594|GO:0051928|GO:0009653|GO:0043524|GO:0051482|GO:0045211|GO:0032496|GO:0070
374|GO:0043123|GO:0031681|GO:0051209|GO:0005794|GO:0030335|GO:0004930|GO:0030168|GO:0014068|GO:0
043280|GO:0007186|GO:0032967|GO:0005887|GO:0045893|GO:0051930|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144870_PI430048170 0.0657578570862896 0.8194109076986439.34611747317738
9.32911488596406 9.38926155758088 P P P 9.6719310694329 9.48484873434666
9.75711861382077 P P P LNCV6_144870_PI430048170 mRNA
TGCTGCCGCGCAGTGTGGAGGCCACTGTTTGGAAATAAATCTTCCTAACACTACAAAAAA NM_197966RefSeq chr22
- 17734139 17774042 BID 637 "BH3 interacting domain death agonist, transcript variant 1"
GO:0008625|GO:0005515|GO:2001238|GO:0006626|GO:0097284|GO:0005741|GO:0001836|GO:0051402|GO:2000
045|GO:0005829|GO:0005739|GO:1900740|GO:0008637|GO:0042127|GO:0090200|GO:0051260|GO:0032461|GO:0
032355|GO:0031625|GO:0070062|GO:0032464|GO:0034349|GO:0043065|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139051_PI430048170 0.2987190828602021.54214160340733 2.52070485077632
2.26443118998851 1.26537408183602 A A A 1.97655714309331 0.820310645949019
1.42989077533693 A A A LNCV6_139051_PI430048170 mRNA
TCTTACTGCCACCACCTTCATTCAGGTCCTTGTTCTACTAGTAAAACTTTATGAACTAAA NM_205548RefSeq chr5
+ 80487980 80542563 FAM151B NA "family with sequence similarity 151, member B" NA . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_143330_PI430048170 0.00437983283883541 2.10945532689309 11.1441256303262
11.160157052061 11.0909436048923 P P P 10.2226426774317 9.97090818758105
9.95612569081394 P P P LNCV6_143330_PI430048170 mRNA
GGAATTGTTTACACATGACCTACATTTTGGACGGTTTATCAATAAACATGTGTGAACAAC NM_013321 RefSeq chr7
- 2251769 2314475 SNX8 29886 sorting nexin 8
GO:0005515|GO:0016050|GO:0034498|GO:0031901|GO:0035091|GO:0006886|GO:0043231|GO:0042802|GO:0030
904|GO:0019898|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128309_PI430048170 0.0509131932841594 0.7603799267813725.62679183349275
5.8142190201223 5.79487767146452 P P P 6.14276491241418 5.94018629174096
6.32079495405656 P P P LNCV6_128309_PI430048170 mRNA
AGAGGGCTTCTGTTTCTTGGAATGTTTCCATATTGCTAAAAATAAATGTCTTCCACTATC NM_001001661 RefSeq
chr7 - 149102785 149126346 ZNF425 155054 zinc finger protein 425
GO:0005737|GO:0005634|GO:0045892|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128126_PI430048170 0.000814394064383767 1.46841755982665 13.3175713891066
13.3795694997691 13.415943588019 P P P 12.9009927804931 12.7791430784347
12.7680655429589 P P P LNCV6_128126_PI430048170 mRNA
GGTATTGGGTATACTTATACTCTATAGGGTCGTTGAATAAATGGCTTAGAATGTGGAAAA NM_014187 RefSeq chr16
+ 67227112 67229279 TMEM208 29100 transmembrane protein 208
GO:0006914|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143027_PI430048170 0.2089230196645840.8644132446664236.91153424284546
6.73895324992194 6.88674863836209 P P P 7.12035384133921 6.82653132738001
7.20066242662127 P P P LNCV6_143027_PI430048170 mRNA
GGAAGCTTTTTTATACATTGCCTAAATCTACGCCAACCAGAAAATAGTCTCATCTCTTTT NM_174902 RefSeq chr11
+ 35943980 36232136 LDLRAD3 143458 "low density lipoprotein receptor class A domain containing 3,
transcript variant 1" GO:0030054|GO:0001540|GO:0005886|GO:0070613|GO:0016021|GO:0006898 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131391_PI430048170 0.3502805867690030.7196422404512190.2591592366822140.4047914288173
0.289433719907526 A A A 0.4825714173479661.36401569672331 0.298345687994364 A A A
LNCV6_131391_PI430048170 mRNA
GCAGTGTCTTCATTCGAAGGGGACACTAACTGTGATGATCTCATATAATATTGTTTTCAT NM_033188 RefSeq chr17
- 41148923 41149802 KRTAP4-5 85289 keratin associated protein 4-5
GO:0042633|GO:0007568|GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127952_PI430048170 0.000203761333765326 3.05147519178668 5.2585558584376
5.56203982202542 5.38468015720147 P P P 3.95223477379191 3.77360835531352
3.65112245088398 P P P LNCV6_127952_PI430048170 mRNA
TTAAGCAGATAACCAAAGGGAGTTTCGTGATGGAGTGTCACACGTTTATGCAGGTGTGTG NM_001286732 RefSeq
chr13 - 113324842 113364148 GRTP1 79774 "growth hormone regulated TBC protein 1, transcript
variant 2" GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102642_PI430048170 0.0242706470677856 0.6610066728400594.33707926932075
4.0057932467038 4.14239478456133 P P P 4.6007682901122 5.00980772076096 4.6503639144026
P P P LNCV6_102642_PI430048170 mRNA
GCTAAACACTATTGCGGACATCCTTCAGGAGGAGAAGAAACAGGAAAAACAAAATGGAAA NM_001286768
RefSeq chr4 - 52590960 52659335 USP46 64854 "ubiquitin specific peptidase 46, transcript variant
4"
GO:0008343|GO:0005515|GO:0006511|GO:0016579|GO:0004843|GO:0048149|GO:0032228|GO:0001662|GO:0060
013 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141776_PI430048170 0.00399990264218089 4.41450146867919 3.40599322166318
2.76965133335598 2.78631933087692 P A A 1.23635260256178 0.313646954265306

0.933437741227121 A A A LNCV6_141776_PI430048170 mRNA
GGATCCCCTCGAGACTACTCTGTTACCAGTCATGAAACATTAAAACCTACAAGCCTTAAA NM_001615 RefSeq chr2
+ 73892965 73919653 ACTG2 72 "actin, gamma 2, smooth muscle, enteric, transcript variant 1"
GO:0006936|GO:0072562|GO:0005856|GO:0005615|GO:0005524|GO:0071944|GO:0070062|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143234_PI430048170 0.5359556218744511.06143193775705 9.2215291223084
9.22811857310133 9.44308216202678 P P P 8.99743341244191 9.25276527452921
9.37084830264441 P P P LNCV6_143234_PI430048170 mRNA
CCCAAAGTCACTGTAACAGTTAAGTGTGTCATTAACCTTTCTGTCTCTTTGCGCCATAAA NM_031954 RefSeq chr12
- 109448654 109477350 KCTD10 83892 potassium channel tetramerization domain containing 10
GO:0005737|GO:0004842|GO:0016567|GO:0031463|GO:0036038|GO:0051260|GO:0043161|GO:0005654 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134115_PI430048170 0.000673157292595432 0.3465263967534086.3974352262373
6.22574832006554 6.40533548335163 P P P 7.86483252947416 7.69398949004972
8.04257475793963 P P P LNCV6_134115_PI430048170 mRNA
CTCACCTCTTACCCCAGTACTATTCTCCAGAGGTAATCTATTAACAATTTCTTATGTAAT NM_014607 RefSeq chr2 +
135741618 135785063 UBXN4 23190 UBX domain protein 4
GO:0006986|GO:0005515|GO:0005737|GO:0005783|GO:0005789|GO:0005635 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126786_PI430048170 0.00533538615060286 0.3488949209699414.04151825157904
3.35736399630226 3.58715911414736 P P P 4.99163884418273 5.41887503166433
5.18681627110571 P P P LNCV6_126786_PI430048170 mRNA
AACCCTCCCAGGTTTGTAGGTTTTAGGGGTTTTCAGTTTTGTTTGGGTTTTTTGTTTTTT NM_001042492 RefSeq chr17
+ 31094926 31377677 NF14763 "neurofibromin 1, transcript variant 1"
GO:0001656|GO:0005515|GO:0048593|GO:0042992|GO:0007406|GO:0007507|GO:0046580|GO:0043525|GO:0000
165|GO:0030198|GO:0048745|GO:0030199|GO:0048169|GO:0021897|GO:0032318|GO:0030336|GO:0031235|GO:0
045685|GO:0014065|GO:0048485|GO:0046929|GO:0001649|GO:0043535|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133967_PI430048170 0.3960283826562270.85993096220208 7.33256189663364
7.43515253393204 7.78731959718152 P P P 7.3996319760754 7.80495702613169
7.98357291235384 P P P LNCV6_133967_PI430048170 mRNA
AAGTCCAAAGTCAAGTCCTTAGGGGATAATTTTGTTTTGGCTCAGTTGTTCCCTGCTTCC NM_000786 RefSeq chr7
- 92112148 92134526 CYP51A1 1595 "cytochrome P450, family 51, subfamily A, polypeptide 1,
transcript variant 1"
GO:0006695|GO:0006694|GO:0006805|GO:0005506|GO:0005783|GO:0070988|GO:0008398|GO:0044281|GO:0033
488|GO:0016020|GO:0005789|GO:0016021|GO:0016125|GO:0055114|GO:0020037 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141170_PI430048170 0.0294769299773356 0.7124800060235768.21093794380431
8.23786354757108 8.18317649095349 P P P 8.56591769260607 8.6502217234005
8.86668985373617 P P P LNCV6_141170_PI430048170 mRNA
GACACTGCTGAATCCTGTACAGCCTTACTCATAAATAAAGTACTTACTGAATTTCCACCA NM_003676 RefSeq chr1
+ 224183207 224193440 DEGS1 8560 "delta(4)-desaturase, sphingolipid 1"
GO:0006665|GO:0005739|GO:0006636|GO:0016020|GO:0005887|GO:0005783|GO:0030148|GO:0005789|GO:0009
055|GO:0044281|GO:0016705|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136440_PI430048170 0.0651933214493773 1.25716079716738 9.93956457181618
9.92519900108759 10.2047398970958 P P P 9.55388734974896 9.65116581030289
9.87272099447909 P P P LNCV6_136440_PI430048170 mRNA
GTTATTGCTATATGTGTTACAGACCTCGGTTCTCATTAAAGTATTTATTGGCAGAATCAC NM_001282197 RefSeq
chrX + 130339887 130373361 SLC25A14 9016 "solute carrier family 25 (mitochondrial carrier, brain),

member 14, transcript variant 3" GO:0009060|GO:0005739|GO:0005887|GO:0006810|GO:0005743|GO:0006839 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141013_PI430048170 0.0711678968907421 0.3942823979063551.31723015632942
0.2574984161582030.372932694739938A A A 1.16534417964576 2.19353852826742 2.5408066580866
A A P LNCV6_141013_PI430048170 mRNA
CCTCATTATCTTGCAGCTGTAAACATATTGGAATGTACATGTCAATAAAACCACTGTACA NM_015057RefSeq chr13
- 77044656 77327042 MYCBP2 23077 "MYC binding protein 2, E3 ubiquitin protein ligase"
GO:0005515|GO:0030424|GO:0004842|GO:0006355|GO:0016567|GO:0042177|GO:0016874|GO:0005634|GO:0021
952|GO:0042803|GO:0006351|GO:0032880|GO:0021785|GO:0051493|GO:0016020|GO:0015630|GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143589_PI430048170 0.2679467841835180.7986630158538467.99027352139293
7.43737437726466 7.20527601790871 P P P 8.08452088290942 7.91786622108549
7.69280273479813 P P P LNCV6_143589_PI430048170 mRNA
CCCTCGTCTCACCCCCTTTACACTCACATTTTTATCAAATAAAGCATGTTTTGTTAGTGC NM_021195RefSeq chr16 -
3014711 3018187 CLDN6 9074 claudin 6
GO:0016338|GO:0005886|GO:0005198|GO:0016032|GO:0016021|GO:0005923|GO:0045216|GO:0042802 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_46758_PI430048170 0.0287261425177512 0.7283666037770919.24995586548817
9.40838204061093 9.29219699267907 P P P 9.78931923531797 9.58711179194266
9.93015252845237 P P P LNCV6_46758_PI430048170 mRNA
ATTATGAGAAAGCTGTAAACGCTATGATCCTGGCAGGAAAAGCCTACTACGATGGAGTGG NM_018842RefSeq chr7
- 98291649 98401115 BAIAP2L1 55971 BAI1-associated protein 2-like 1
GO:0007009|GO:0005886|GO:0046626|GO:2000251|GO:0003779|GO:0015629|GO:0005829|GO:0009617|GO:0005
737|GO:0030838|GO:0005654|GO:0070064|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144084_PI430048170 0.4646043335946751.34988313726788 0.276415888337786
0.3088852029914781.40269471226861 A A A 0.3602844836082580.322520420802903
0.309618883706103A A A LNCV6_144084_PI430048170 mRNA
CCCTGAGGCTTTAAAACACTATGGACTTACCACTTTCTTGACAAAGAATTTGTAATTACA NM_001170574 RefSeq
chrX + 80335503 80445311 FAM46D 169966 "family with sequence similarity 46, member D,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142595_PI430048170 0.9064175051482181.0112696128819 3.78947034975202
3.82985885988823 3.53420187145779 P P P 3.88429688042899 3.63081218176732 3.5893629956564
P P P LNCV6_142595_PI430048170 mRNA
GGCACAGTATGCTCCTTACAGAAAAGTTGTCATTTTATTTCTAGAATAAATCTGTGAACC NM_004414RefSeq chr21
- 34516442 34615142 RCAN1 1827 "regulator of calcineurin 1, transcript variant 1"
GO:0005515|GO:0007165|GO:0006355|GO:0019722|GO:0003700|GO:0008015|GO:0005634|GO:0007417|GO:0003
677|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133229_PI430048170 0.9223165960871321.0046769863084 16.1012331354628
16.2322692955668 16.2516543479156 P P P 16.1985222261303 16.1617457049618
16.2088619900258 P P P LNCV6_133229_PI430048170 mRNA
CAAGAACAAGTGGTTCTTCCAGAAACTGCGGTTTTAGATGCTTTGTTTTGATCATTAAAA NM_000988RefSeq chr17
+ 42998428 43002954 RPL27 6155 ribosomal protein L27
GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0005634|GO:0006415|GO:0006412|GO:0006
413|GO:0005829|GO:0006414|GO:0000184|GO:0016020|GO:0030529|GO:0016032|GO:0005840|GO:0022625|GO:0
044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137085_PI430048170 0.3530676493182570.8809188299535959.98163075813703
9.81187747516275 10.2962645342047 P P P 10.0809241383442 10.1439865068326
10.4313779841056 P P P LNCV6_137085_PI430048170 mRNA
GTTTCCAAGAAGATCAAGTTTGTACATAACACTAGAGGCATTTCTTATCAAAAGGATTGG NM_001145355 RefSeq

chr9 - 121037 179075 CBWD1 NA "COBW domain containing 1, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92927_PI430048170 0.268361735249211 1.14537149745366 8.776182417127 8.43185957327106 8.53236423788994 P P P 8.17994300124119 8.57617618622372 8.39175519173451 P P P LNCV6_92927_PI430048170 mRNA
TTGGAAGAAGAACCAGGATGACTTTGAGTGTGTAACCACTCTCGAGGGCCATGAAAATGA NM_004804 RefSeq chr2 + 96266145 96274162 CIAO1 9391 cytosolic iron-sulfur assembly component 1
GO:0008284|GO:0007059|GO:0016226|GO:0006357|GO:0044281|GO:0071817 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143455_PI430048170 0.000508108888502459 1.16850181052273 0.817450123718289 0.870827360031295 0.831726209592061 A A A 0.639318305549903 0.609610149668617 0.597302009253122 A A A LNCV6_143455_PI430048170 mRNA
GAAGCGTTGTTTCCCAAGTTTCACAATGTGATTGTACATGACTTCTGAAATTAAAAAGAG NM_001739 RefSeq chr16 - 87888018 87936506 CA5A 763 "carbonic anhydrase VA, mitochondrial"
GO:0005739|GO:0005759|GO:0015701|GO:0008270|GO:0044281|GO:0004089|GO:0006730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130385_PI430048170 0.468483225357215 8.02007235408738 0.266243635476882 5.20480241336402 0.699655714833152 A P A 1.27939680648011 0.332944797799754 0.338092126395013 A A A LNCV6_130385_PI430048170 mRNA
GCATATAAGACAAAGTTCACTGCATAGACTACAATAGACTACATACGAAAACAAACCCAA NM_152569 RefSeq chr9 - 213107 215893 C9orf66 157983 chromosome 9 open reading frame 66 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127349_PI430048170 0.33590189970984 0.603480850334544 1.12483089499582 0.247178048810767 0.32871267354011 A A A 1.50626264674022 0.247466567087024 1.8613966333327 A A A LNCV6_127349_PI430048170 mRNA
TAGTTCCTTTTTCTGTATCAGAAGCCCTGTCTTCACAACACAGGCACACAATTTCAGTCC NM_000173 RefSeq chr17 + 4932274 4935030 GP1BA 2811 "glycoprotein Ib (platelet), alpha polypeptide"
GO:0005515|GO:0005886|GO:0009986|GO:0015057|GO:0030168|GO:0031362|GO:0000902|GO:0016020|GO:0030193|GO:0070493|GO:0005887|GO:0007596|GO:0007597|GO:0007155|GO:0042730|GO:0007166|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129134_PI430048170 0.00818159775629873 2.16306396426165 8.45565483791675 9.01117851238367 8.89046929034753 P P P 7.75869215322154 7.82888044153341 7.46194962785294 P P P LNCV6_129134_PI430048170 mRNA
TTGTAACCAGAGAACTATTACTAGGCCTTGAAGAACCTGTCTAACTGGATGCTCATTGCC NM_013332 RefSeq chr7 + 128455829 128458418 HILPDA 29923 "hypoxia inducible lipid droplet-associated, transcript variant 1"
GO:0005811|GO:0005515|GO:0008284|GO:0009986|GO:0006950|GO:0005102|GO:0010884|GO:0035425|GO:0016021|GO:0001819|GO:0030141|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136771_PI430048170 0.566746423353704 0.877512752267734 0.287022217545296 0.297334162441289 0.517850304787692 A A A 0.971742306467197 0.276590400551637 0.321900462203716 A A A LNCV6_136771_PI430048170 mRNA
CTGAGAATCCTGCAGCTTGGTTTAATGAGTGTGTTCATGAAATAAATAATGGAGGAATTG NM_024080 RefSeq chr2 + 233917397 234019522 TRPM8 79054 "transient receptor potential cation channel, subfamily M, member 8"
GO:0005262|GO:0005886|GO:0009409|GO:0006874|GO:0055085|GO:0042803|GO:0070207|GO:0034220|GO:0051289|GO:0070588|GO:0005789|GO:0050955|GO:0016048|GO:0045121|GO:0016021|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133294_PI430048170 0.119974357543772 0.80227931800549 7.04178927120423 6.59739890125166 6.93871404311131 P P P 7.18422722400936 7.08693004187903 7.28960272535366 P P P LNCV6_133294_PI430048170 mRNA

GGAACGACCTAGGTTTTGTTACTCGCAGTAGAATAAACAGCTACAGGAAGTTTCAAAAAA NM_033081 RefSeq chr20 - 62877737 62937952 DIDO1 11083 "death inducer-obliterator 1, transcript variant 4" GO:0005737|GO:0005819|GO:0008270|GO:0005634|GO:0097190|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133485_PI430048170 0.0279036452905701 0.674857939252535 1.90129730672273 2.34021135570295 2.08507476141206 A A A 2.8587906338826 2.69371256714031 2.48595636221851 P P P LNCV6_133485_PI430048170 mRNA
GAACAGACACAATATACATTCTGTAGCTAAAAAGGAGGGAAAAGTCTGTGAATGCTATTT NM_015520 RefSeq chr3 - 65354230 66038834 MAGI1 9223 "membrane associated guanylate kinase, WW and PDZ domain containing 1, transcript variant 1" GO:0005515|GO:0030054|GO:0005886|GO:0042995|GO:0008022|GO:0005524|GO:0005737|GO:0032947|GO:0006461|GO:0051393|GO:0005911|GO:0070997|GO:0005654|GO:0005923|GO:0007155|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138312_PI430048170 0.771057856974745 0.986642724987111 0.484251410761612 0.432718581782545 0.276589100373745 A A A 0.371503105204436 0.452982280224992 0.434033547947516 A A A LNCV6_138312_PI430048170 mRNA
CTGTATTCGACAGTTTATTTTGATTGCAAAGGTTTGAATCTCAGAACCTTCTTTTCCCTT NM_024423 RefSeq chr18 - 30989364 31042815 DSC3 1825 "desmocollin 3, transcript variant Dsc3b" GO:0030057|GO:0005886|GO:0045295|GO:0005509|GO:0050821|GO:0005576|GO:0001701|GO:0005737|GO:0016020|GO:0005911|GO:0016021|GO:0007155|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132572_PI430048170 0.00777746624640883 0.646543813901195 7.8094486375211 7.77456108555798 7.9720110608303 P P P 8.3631815923509 8.40626198915285 8.66330879825722 P P P LNCV6_132572_PI430048170 mRNA
CTGCTAAGACATTCAAGCAAATAGCTATTACACACTACTGCAGATTTTACAGGTTTCTAA NM_003848 RefSeq chr3 - 67374716 67654614 SUCLG2 8801 "succinate-CoA ligase, GDP-forming, beta subunit, transcript variant 2" GO:0004776|GO:0006099|GO:0046982|GO:0005886|GO:0044281|GO:0005525|GO:0005524|GO:0005739|GO:0045244|GO:0006105|GO:0005759|GO:0006104|GO:0019003|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60760_PI430048170 0.4646522814373 0.912424950222004 5.96199290595838 5.72500049018633 6.26035667483069 P P P 6.2785651479667 6.06725134783207 6.03603147948084 P P P LNCV6_60760_PI430048170 mRNA
AATCCTTTACAATATATCAAACAGTGGAAGGCTTTTACCAAGATGGCCTCAGCTCCGGCC NM_016106 RefSeq chr14 + 30622253 30735827 SCFD1 23256 "sec1 family domain containing 1, transcript variant 1" GO:0019905|GO:0005515|GO:0006909|GO:0001666|GO:0005801|GO:0005886|GO:0060628|GO:0006890|GO:0005798|GO:0006892|GO:0031201|GO:0009636|GO:0015031|GO:0051223|GO:0006904|GO:0000902|GO:0047485|GO:0032580|GO:0005789|GO:0017119 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137063_PI430048170 0.521774766178393 1.35974072529113 1.56654079266499 0.411602323323179 0.25966271779441 A A A 0.457936561927305 0.432056995426926 0.394279618642159 A A A LNCV6_137063_PI430048170 mRNA
GGGATTACACAGCTATGAATGTATTTGCTTCTAAAACCTCCCAAAGTGAATCTAATCTTA NM_014905 RefSeq chr2 + 190880820 190965544 GLS 2744 "glutaminase, transcript variant 1" GO:0005515|GO:0006537|GO:0007268|GO:0008652|GO:0044281|GO:0014047|GO:0007269|GO:0005829|GO:0005739|GO:0034641|GO:0002087|GO:0001967|GO:0051289|GO:0005759|GO:0004359|GO:0006543 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141551_PI430048170 0.160707664378323 1.08033427755082 0.501443901055216 0.503075267227 7 0.570804215139051 A A A 0.317270200524623 0.413550396537564 0.505054703222749 A A A LNCV6_141551_PI430048170 mRNA
TTCCTTCTGATGCACAAGAATGAAGCCGAGTTTCAGAGGTGGCTCATTTGCTGTTTTGGT NM_178477 RefSeq

chr20 + 17699947 17735872 BANF2 140836 "barrier to autointegration factor 2, transcript variant 1"
GO:0005737|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_108531_PI430048170 0.158997465504648 0.802430623399262 5.15886695220185
4.79055146447966 5.12583002243866 P P P 5.33820011282471 5.10184110065174
5.57682453203137 P P P LNCV6_108531_PI430048170 mRNA
GATGAAGATATCAGTCTTCTCCCAGAGAGTGAAGAACAGGAACGTGAAGAGGATGGTTCA NM_005791 RefSeq
chr2 + 71130313 71150102 MPHOSPH10 10199 M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
GO:0008380|GO:0005515|GO:0006396|GO:0005694|GO:0010923|GO:0006364|GO:0000375|GO:0005730|GO:0005
732 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144908_PI430048170 0.00443249158859417 0.601327671644372 9.32495394042245
9.64518069698292 9.54697421094526 P P P 10.3535442104528 10.0848722847609
10.2850924531643 P P P LNCV6_144908_PI430048170 mRNA
CCTGTAAATATATCTTAAGCAGGTTTGTTTTCAGCACTGATGGAAAATACCAGTGTTGGG NM_004417 RefSeq
chr5 - 172768089 172771200 DUSP1 1843 dual specificity phosphatase 1
GO:0005515|GO:0042542|GO:0090266|GO:0005634|GO:0051591|GO:0032870|GO:0035335|GO:0000188|GO:0035
556|GO:0043409|GO:0005737|GO:0006470|GO:0035970|GO:0051447|GO:0043407|GO:0070373|GO:0009416|GO:0
032526|GO:0032355|GO:0006979|GO:0017017|GO:0004726|GO:0001706|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129643_PI430048170 0.382953002651173 1.07119266940935 7.37258432743066
7.46754822151391 7.54543070651185 P P P 7.18456545244616 7.47243821858613
7.42009384033515 P P P LNCV6_129643_PI430048170 mRNA
TGCCAGTGAAGACTGTAAAGACAGAACACACTATTTTGGAGGGAGGATACTAATTGTTTA NM_016551 RefSeq
chr12 - 26971570 27014406 TM7SF3 51768 transmembrane 7 superfamily member 3
GO:0008150|GO:0003674|GO:0005886|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132939_PI430048170 0.00184631372749344 0.558927807759961 9.92792572954049
9.7307907947937 9.81957550562694 P P P 10.5233177291944 10.656760469833
10.8086364352266 P P P LNCV6_132939_PI430048170 mRNA
TGGAAAGTCTACAGTGCAGAAAGGCTTGAACCTGCCAGCTGATTTGAAATACTTTCCCCT NM_004454 RefSeq
chr3 - 186046316 186109112 ETV5 2119 ets variant 5
GO:0000977|GO:0003700|GO:0006357|GO:0006366|GO:0044212|GO:0060762|GO:0000981|GO:0005634|GO:0060
252|GO:0048133|GO:0007274|GO:0001228|GO:0003677|GO:0030154|GO:0050807|GO:0045666|GO:0045944|GO:0
007626|GO:0034599|GO:0071340 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137959_PI430048170 0.374686177099733 0.734023176921198 5.61809076589982
5.84684538018737 6.255854313758 P P P 5.68303038734791 6.39302688824107
6.83305277220042 P P P LNCV6_137959_PI430048170 mRNA
CTAAAAGATTTAGACCAAGTCACTGCCAGTTTTTGCCTTTGTTGCATTTTGTACAGTTTT NM_006951 RefSeq chr10
+ 103367966 103389066 TAF5 6877 "TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa"
GO:0005515|GO:0006352|GO:0010467|GO:0006355|GO:0006368|GO:0003700|GO:0005669|GO:0006367|GO:0044
212|GO:0016573|GO:0006366|GO:0005730|GO:0005634|GO:0015629|GO:0043231|GO:0033276|GO:0046983|GO:0
016032|GO:0005654|GO:0004402|GO:0016568 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_145359_PI430048170 0.599829336982262 1.14476283657951 1.31254126528177
0.470948595880336 0.784851109289738 A A A 0.478126038677384 1.10051427428143
0.431078046679682 A A A LNCV6_145359_PI430048170 mRNA
AAGATTAAGTCTCAAATGAGTAGGTTCTCTACAAAGACCAATAAAATCTGTGGACCCTGA NM_001005234 RefSeq

chr9 + 122675129 122676104 OR1L3 26735 "olfactory receptor, family 1, subfamily L, member 3"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_24367_PI430048170 0.0312214118823413 0.76989583965702 9.02081927565997
9.21056899200052 9.18540518401257 P P P 9.68860601347449 9.39947141035774
9.45100826151933 P P P LNCV6_24367_PI430048170 mRNA
CGGGTATAGGTTTGAGTTTTTTCCCCCTCATGCCAAGTATTTAAAACCTCTAGAAACCCA NM_207429 RefSeq
chr11 - 111293388 111299896 COLCA1 399948 "colorectal cancer associated 1, transcript variant 3"
GO:0016020|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128781_PI430048170 0.246968013658195 1.37712669625238 3.0346557770433
3.84352933021956 3.5094914139872 P P P 3.29041693281685 3.20243579759752
2.49959420385238 P P P LNCV6_128781_PI430048170 mRNA
CCTAATGCCTTTGTATTAGAGGAATCTTATTCTCATCTCCCATATGTTGTTTGTATGTCT NM_033125 RefSeq chr6
- 110424689 110476641 SLC22A16 85413 "solute carrier family 22 (organic cation/carnitine
transporter), member 16"
GO:0005886|GO:0015695|GO:0005275|GO:0007275|GO:0007283|GO:0030317|GO:0055085|GO:0015101|GO:0030
154|GO:0046717|GO:0007338|GO:0015837|GO:0016021|GO:0015879|GO:0015226 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_136682_PI430048170 0.224019583138716 0.564616422829252 0.277918669362131
0.300452787503027 2.21610414699453 A A A 1.66415057264789 1.95756424919238
2.46060711094845 A A P LNCV6_136682_PI430048170 mRNA
TGCAGAGGCAGCCCTCAATATGCAGTGGTTGAATAAATGAATGAAGAAACCACTATCAAA NM_005358 RefSeq
chr13 + 75620433 75859871 LMO7 4008 "LIM domain 7, transcript variant 1"
GO:0005737|GO:0004842|GO:0016567|GO:0023051|GO:0000151|GO:0008270|GO:0005634|GO:0030155|GO:0005
925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75980_PI430048170 0.602265804864582 1.02692701685676 0.393470385183233
0.55976531605825 0.463703708599243 A A A 0.52938969738114 0.387748163885846
0.384861577992492 A A A LNCV6_75980_PI430048170 mRNA
TTCATTTTTCTTTCTGATGTCAAAAATGTCTTGGGTAGGCGGGAAGGAGGGTTAGGGAGG NM_002188 RefSeq
chr5 + 132658172 132661109 IL13 3596 interleukin 13
GO:0005515|GO:0030890|GO:0043032|GO:0042526|GO:0045471|GO:0007267|GO:0050714|GO:0006928|GO:0005
615|GO:0071635|GO:0006955|GO:0005737|GO:0006954|GO:0002639|GO:0032496|GO:0010155|GO:0033861|GO:0
051281|GO:0001774|GO:0005144|GO:0005576|GO:0032723|GO:0005125|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135820_PI430048170 0.949082010866297 1.11439485837315 3.11879722505115
2.00083093334267 1.17971698320964 P A A 1.99731968940124 1.95272748886666
2.47392831736642 A A P LNCV6_135820_PI430048170 mRNA
TGGTCTTTGAGCAGTTTCTTCACAACAACGAGAACATTGAAAATGAGGACCTGGTGGCCT NM_001272072 RefSeq
chr7 + 150852476 150861291 AOC1 26 "amine oxidase, copper containing 1, transcript variant 1"
GO:0071280|GO:0097185|GO:0005886|GO:0005272|GO:0005615|GO:0032403|GO:0042803|GO:0008144|GO:0004
872|GO:0035725|GO:0008201|GO:0052600|GO:0046677|GO:0070062|GO:0005777|GO:0005261|GO:0048038|GO:0
005507|GO:0042493|GO:0005509|GO:0052599|GO:0052598|GO:0052597|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139433_PI430048170 0.638211432458877 0.937135811672882 9.24957843058064
9.46712453759542 9.14832586457721 P P P 9.16557609147879 9.63824052449297
9.31993580073157 P P P LNCV6_139433_PI430048170 mRNA
TGGCTAAGGCTCCTGCTTGCTGCACTCTTATTTTCATTTTCAACCAAAGGCCCTTTTCAG NM_003543 RefSeq chr6
- 26285125 26285499 HIST1H4H 8365 "histone cluster 1, H4h"
GO:0005515|GO:0010467|GO:0006325|GO:0005634|GO:0045653|GO:0000723|GO:0000183|GO:0000786|GO:0070

062|GO:0035574|GO:0035575|GO:0046982|GO:0006334|GO:0006335|GO:0005576|GO:0006336|GO:0000228|GO:0
003677|GO:0032776|GO:0034080|GO:0043234|GO:0016020|GO:0045814|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_106222_PI430048170 0.125595000065233 0.405212893279684 0.564819730708795
1.93903859504569 2.70941239934053 A A A 3.66442708845385 3.1420211501283
2.95368954068832 P P P LNCV6_106222_PI430048170 mRNA
AATGACCAACATGTATTAAGATGGACACCTACTCTACGAAACACGAAGTTCTATGGTCTC NM_032047 RefSeq chr3
+ 183253243 183273391 B3GNT584002 "UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5"
GO:0009247|GO:0047256|GO:0016266|GO:0008457|GO:0007417|GO:0008378|GO:0005622|GO:0000139|GO:0006
493|GO:0006486|GO:0016021|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83374_PI430048170 0.00492882173445668 1.28676808072735 7.06605473762751
7.06465834688438 7.14704173256994 P P P 6.8007766509764 6.73980263531187
6.64310819897416 P P P LNCV6_83374_PI430048170 mRNA
TGAAGACCTGGATGTGCTGGGCTTGTCCTTCCGCAAAGACCTGTTCATCGCCACCTACCA NM_001257328 RefSeq
chr17 + 4710493 4721500 ARRB2 409 "arrestin, beta 2, transcript variant 3"
GO:0005515|GO:0006366|GO:0051928|GO:0032715|GO:0034122|GO:0032691|GO:0050731|GO:0042699|GO:0015
031|GO:0032403|GO:0031623|GO:0031762|GO:0007219|GO:0045211|GO:0031398|GO:0007179|GO:0070374|GO:0
031397|GO:0031625|GO:0034260|GO:0051019|GO:0019904|GO:0060765|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137747_PI430048170 0.6228025213361870.8537985686064960.558024633374534
0.5048012157975450.587743738682821A A A 0.3903285224908720.466411863366676
1.29521716008583 A A A LNCV6_137747_PI430048170 mRNA
GATTTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAATTG NM_001004058 RefSeq
chr11 - 56159393 56160317 OR8K5 NA "olfactory receptor, family 8, subfamily K, member 5" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142725_PI430048170 0.0231615691883826 0.50153999989307 3.74209875746808
3.31377984523409 3.31856107845206 P P P 4.85620049007517 4.23749998462263
4.21494463878332 P P P LNCV6_142725_PI430048170 mRNA
TTTTCCCTGGAATTTTCCAAGTTGGCTTCAGCTGAAGAGCTGTTTTGTGAAGCATCCCAG NM_031449 RefSeq chr7
+ 44748930 44769880 ZMIZ2 83637 "zinc finger, MIZ-type containing 2, transcript variant 1"
GO:0005739|GO:0005515|GO:0030374|GO:0045944|GO:0008270|GO:0005654|GO:0005634|GO:0043596|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138175_PI430048170 0.00346095726509577 0.3465383852758676.69960204138967
6.41712721663516 7.05365170270589 P P P 7.98909604233742 8.24704422515111
8.53921575507073 P P P LNCV6_138175_PI430048170 mRNA
CCACCTTTGTTTTTCTGTTCGGTAATCCTGGTGTGGACAAATAAAGTTTTCACTTGTATGNM_001278205 RefSeq chr10
+ 14838159 14846999 HSPA1451182 "heat shock 70kDa protein 14, transcript variant 3"
GO:0005515|GO:0016020|GO:0005840|GO:0051083|GO:0005524|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128587_PI430048170 0.0139360258183897 1.34586768954679 9.08359939179392
9.13936627140295 9.09736889634699 P P P 8.75742595822325 8.55793708701486
8.71244686759594 P P P LNCV6_128587_PI430048170 mRNA
CTCTATCAATAGTTTGACATTTTTCCCTCTTTTACATTGAGATCATACCCTAGGTACTGT NM_138434 RefSeq chr7 +
150329848 150332721 ZBED6CL 113763 ZBED6 C-terminal like NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_128817_PI430048170 0.1560132478900340.9531748991986550.258696479343812
0.27004650822672 0.340955517165856A A A 0.4167694966239540.342504493000411
0.317514204863116A A A LNCV6_128817_PI430048170 mRNA
CTCCAAGTAAGCCTGCTAAGTAAACGTCATTTCTAACCCAAAGGCTCTTTTCAGAGCCAC NM_170610 RefSeq chr6

+ 25726908 25727345 HIST1H2BA 255626 "histone cluster 1, H2ba"
GO:0046982|GO:0006325|GO:0006334|GO:0051099|GO:0005634|GO:0006337|GO:0071674|GO:0003677|GO:0003
674|GO:0006954|GO:0031639|GO:0005654|GO:0000786|GO:0019897|GO:0035093 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140029_PI430048170 0.9492691811173011.52963920171475 0.301340630994257
3.67623411665547 2.9915162529053 A P P 2.31500731200504 2.00769754608322
2.42352358148801 A A P LNCV6_140029_PI430048170 mRNA
GGGATTACAGTGGGGGCATTTCTTTATATCACCTCTTAAAAACATTGTTTCCACTTTAAA NM_016134RefSeq chr8
+ 96645226 97143503 CPQ 10404 carboxypeptidase Q
GO:0005794|GO:0005783|GO:0042246|GO:0005615|GO:0005764|GO:0042803|GO:0046872|GO:0005737|GO:0070
573|GO:0004180|GO:0006508|GO:0006590|GO:0043171|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144067_PI430048170 0.5562246442201490.9511604114538015.14169293162689
5.40715659382824 5.45345228003887 P P P 5.33287546269224 5.53769318848653
5.35891160234166 P P P LNCV6_144067_PI430048170 mRNA
CACATGGGTAGAGATGATGTAAAAGCAGCCAATCTGGAAACAATACATTGTAAATAGTTT NM_001144382 RefSeq
chr3 + 16884958 17090606 PLCL2 23228 "phospholipase C-like 2, transcript variant 1"
GO:0006629|GO:0002322|GO:0002337|GO:0050859|GO:0007214|GO:0050811|GO:0035556|GO:0005737|GO:0004
435|GO:0032228|GO:0033135|GO:0004871|GO:1900122 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131894_PI430048170 0.1389756722860791.46618339277205 14.9800424870667
14.8989096307175 14.7571594910394 P P P 14.7942764099206 13.9852045110456 14.06471498149
P P P LNCV6_131894_PI430048170 mRNA
GGGTCCCAGATTGGCTCACACTGAGAATGTAAGAACTACAAACAAAATTTCTATTAAATT NM_004343RefSeq chr19
+ 12938599 12944490 CALR 811 calreticulin
GO:0005515|GO:0017148|GO:0002474|GO:0034504|GO:0050681|GO:0007283|GO:0005615|GO:0030968|GO:0005
622|GO:0001948|GO:0006457|GO:0006611|GO:0032355|GO:0031625|GO:0018279|GO:0005794|GO:0005506|GO:0
009986|GO:0045740|GO:0001849|GO:0005509|GO:0000122|GO:0045787|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137278_PI430048170 0.73112041851315 1.11950014223937 2.78311282520563
3.20673388443336 3.76830732362451 A P P 3.06103885250078 3.40838565552871
2.92675321958043 P P P LNCV6_137278_PI430048170 mRNA
TAAATGGCTACTAATTGCTGCTGTGTATGAAAACAAATGGCTATCAAGGCCGGGTGCAGT NM_176816RefSeq
chr5_GL339449v2_alt - 63866 115830 CCDC125 202243 "coiled-coil domain containing 125, transcript
variant 1" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127482_PI430048170 0.0297641987272672 0.5992119435214452.30257631959266
2.18217693455051 2.72067812469563 A A A 2.83965167222723 3.25978322869251
3.33213329485122 P P P LNCV6_127482_PI430048170 mRNA
AACCAGCCACTTTTTCAATCTGGCTTTTTGGAAGATTGTATTTAAAGTTCTTCAAGGATG NM_022133RefSeq chr8
- 81799582 81842286 SNX16 64089 "sorting nexin 16, transcript variant 1"
GO:0005770|GO:0031901|GO:0031313|GO:0031902|GO:0008333|GO:0006622|GO:0045022|GO:0035091|GO:0005
764|GO:0005769|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133163_PI430048170 0.00461999990835574 0.57548340181216 5.73743245588575
5.76769831499752 5.67123240958992 P P P 6.5054943775112 6.39250204158096
6.65905295225367 P P P LNCV6_133163_PI430048170 mRNA
GTGACTTTTTCTTCCTGTCCCCAAAGTGCCATATGCTACCTTAAAAAATATTAAAGTGAA NM_017694RefSeq chr2
+ 190408354 190502315 MFSD6 54842 major facilitator superfamily domain containing 6
GO:0016020|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132651_PI430048170 0.0287128089425467 0.2613236444729123.21722213241819
2.7601079043084 4.19007157455409 P A P 5.17209609244888 5.44254164102645

5.69538551174415 P P P LNCV6_132651_PI430048170 mRNA
CAGCACTTATCTTTTGAGTTTGTACTGTGGTCCATGTACTTACTAATATGTTGCTTTGTA NM_001278119 RefSeq chr6
+ 28141909 28159472 ZKSCAN8 7745 "zinc finger with KRAB and SCAN domains 8, transcript variant
1" GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145039_PI430048170 0.0673743513405591 1.18501402996309 7.14279530122312
7.23555714645572 7.18042140452037 P P P 6.85595272860469 6.86938674650653
7.08825080427517 P P P LNCV6_145039_PI430048170 mRNA
ATGTTGGCCATGGTGAAAGGGTTTGATATGGAGAAACAAAATCCTCAGGAAATTAGATAA NM_001226RefSeq chr4
- 109688628 109703473 CASP6 839 "caspase 6, apoptosis-related cysteine peptidase, transcript variant
alpha"
GO:0005515|GO:0004197|GO:0005737|GO:0030855|GO:0006508|GO:0006915|GO:0005654|GO:0008234|GO:0006
921|GO:0042802|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135596_PI430048170 0.0182936480984611 0.4079217921035284.73703763695101
4.21922635620473 5.00428025193525 P P P 5.65015909746336 5.75137681727466
6.41999696434732 P P P LNCV6_135596_PI430048170 mRNA
CGTTTTGTAAATGTTGTGCTGTTAACACTGCAAATAAACTTGGTAGCAAACACTTCCAAA NM_007300RefSeq chr17
- 43044294 43125483 BRCA1 672 "breast cancer 1, early onset, transcript variant 2"
GO:0005515|GO:0043627|GO:0004842|GO:0044212|GO:0016874|GO:0009048|GO:0050681|GO:0070531|GO:0042
127|GO:0044030|GO:0031398|GO:0006978|GO:0031625|GO:0005694|GO:0003713|GO:0031436|GO:0046600|GO:0
051865|GO:0043234|GO:0006281|GO:0005654|GO:0008270|GO:0045893|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136606_PI430048170 0.791381026623422 1.02608535771779 6.99376103707396
6.96827075120753 7.16212827939861 P P P 6.62521230008579 7.10999341069219
7.21884153708414 P P P LNCV6_136606_PI430048170 mRNA
GATTTTAGGGACATCTTCCATGGGCCTAGGCTAAAATAGTCATTGTGTTTTCTTTATATT NM_001039569 RefSeq
chr2 - 223755329 223837602 AP1S3 130340 "adaptor-related protein complex 1, sigma 3 subunit,
transcript variant 1"
GO:0006892|GO:0006605|GO:0005765|GO:0032588|GO:0030117|GO:0005829|GO:0050690|GO:0019886|GO:0005
905|GO:0000139|GO:0008565|GO:0061024|GO:0016032|GO:0030659 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_135356_PI430048170 0.0682311919046585 0.5709734856318942.39942916044721
1.58774413865957 2.26745294933919 A A A 2.86070878968189 2.85516861539035
3.07680964102345 P P P LNCV6_135356_PI430048170 mRNA
CACCTCTCCAGAATGTGTGTTATATACCAAATTTTGATGTATGTGAGATTGCTGACTATA NM_020207RefSeq chr9
+ 95875617 96018453 ERCC6L2 375748 "excision repair cross-complementation group 6-like 2,
transcript variant 1" GO:0008026|GO:0005739|GO:0006281|GO:0005815|GO:0005634|GO:0005524|GO:0003677
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103824_PI430048170 0.472087127324842 1.29801160245752 0.267748695982605
1.33827407570267 0.411265153865664 A A A 0.361586841620497 0.304333721551091
0.465012347068686 A A A LNCV6_103824_PI430048170 mRNA
GAGCAGTCTCTGGACAAGATGACCACACTCCAGGAATGCCAGTGCATCTTTTGCACAGCT NM_182757RefSeq chr6
+ 18387349 18468874 RNF144B 255488 ring finger protein 144B
GO:0005515|GO:0005737|GO:0004842|GO:0031966|GO:0042787|GO:0016874|GO:0006915|GO:0000151|GO:0008
270|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134709_PI430048170 0.0107979539564712 12.3946032407087 4.74193163015951
5.00004373103063 4.98642921534154 P P P 1.89303201652448 1.18190569780202
0.395528171882058 A A A LNCV6_134709_PI430048170 mRNA
CTGTAGTTCTAGAACCTGATTTTAACTCAGGAATAAAGACTTTCTGCGGTCAGTGGCAAA NM_198469RefSeq chr9

+ 122159907 122200088 MORN5 254956 "MORN repeat containing 5, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143812_PI430048170 0.0113747378560264 0.3731510602748595.8846295436983 5.71032664922027 5.9161719504228 P P P 6.98147557057926 7.11872188405728 7.60827342932758 P P P LNCV6_143812_PI430048170 mRNA
ACAGGCCCATGAATTACTTCCTCACTTTTGCAGTTGATTACTGAAATGTAAATCACAAGA NM_020412RefSeq chr18 + 11851389 11854449 CHMP1B 57132 charged multivesicular body protein 1B
GO:0005515|GO:0006997|GO:0019904|GO:0010824|GO:0015031|GO:0005829|GO:0045184|GO:0000920|GO:0000910|GO:0007034|GO:0031902|GO:0007080|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93813_PI430048170 0.443074422500941 0.797806665082777 0.3289640249170520.344446255243178 0.342863105652248 A A A 1.17088893396503 0.3357134726676530.312769887115584 A A A
LNCV6_93813_PI430048170 mRNA
CAGAAGTTCTAGAAATAGAATTCCTTTCCTACTCAAATGGAATGAATACCATCAGTGAAG NM_181723RefSeq chr8 + 17027237 17122639 MICU3 286097 "mitochondrial calcium uptake family, member 3"
GO:0005739|GO:0005509|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102645_PI430048170 0.240024312205037 1.78708585282247 1.80313546993273 0.321494413288937 1.28067516870137 A A A 0.4758217838762950.405496677028028 0.374359848858236 A A A LNCV6_102645_PI430048170 mRNA
ATTTTTCAGCCTTGGGAAGTGGAATGAGGCATTTGTTGCTGCCAAGGAATGTCTCCAATG NM_014831RefSeq chr3 - 36826816 36945057 TRANK19881 tetratricopeptide repeat and ankyrin repeat containing 1
GO:0016787|GO:0008152|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145263_PI430048170 0.0322416217955261 0.5886010268977457.40614419193645 7.96686119110801 7.71718367513427 P P P 8.39091397706482 8.48948520110365 8.55323325832962 P P P LNCV6_145263_PI430048170 mRNA
GTCTACTGTGTATTATGAAAATTACTGTTGTCCCCCCACCCTTTTTTCCTTAAATAAAGT NM_145686RefSeq chr2 + 101697702 101894690 MAP4K4 9448 "mitogen-activated protein kinase kinase kinase kinase 4, transcript variant 2"
GO:0046328|GO:0035556|GO:0023014|GO:0005515|GO:0050790|GO:0005737|GO:0005083|GO:0004702|GO:0004674|GO:0030033|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58073_PI430048170 0.413224683735609 1.14487038012241 4.40321044975475 3.87267496234392 4.30351141996472 P P P 4.04386386792965 3.77515153011412 4.1968665369618 P P P
LNCV6_58073_PI430048170 mRNA
GTTCCTACACATCTCATTATAGTTTGTCCTGAGGGAGTCTAACAAGTTAGCAGAAATGGA NM_001243571 RefSeq chr11 - 95832879 95924207 MTMR2 8898 "myotubularin related protein 2, transcript variant 4"
GO:0005515|GO:0030424|GO:0005634|GO:0044281|GO:0030425|GO:0035335|GO:0042803|GO:0005829|GO:0005737|GO:0006470|GO:0043197|GO:0048666|GO:0045806|GO:0052629|GO:0004725|GO:0031642|GO:0070062|GO:0005774|GO:0051262|GO:0006661|GO:2000643|GO:2000645|GO:0008021|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99654_PI430048170 0.0549372181823422 3.14898270051742 2.33698390094244 3.12832392431256 3.42485425039646 A P P 0.3218886606839751.1386832095678 2.1176948210576 A A A LNCV6_99654_PI430048170 mRNA
TCAGTTTCATGGCATTCTTCTTTACCTTCATGGCTCAGTTGGTCATCAGCATCATCCAGG NM_001178111 RefSeq chr15 + 74995534 75021495 SCAMP5 192683 "secretory carrier membrane protein 5, transcript variant 1"
GO:0005515|GO:0034976|GO:0030054|GO:0005886|GO:0031201|GO:0050715|GO:0006887|GO:0015031|GO:0032588|GO:0000139|GO:0045956|GO:0045806|GO:0030672|GO:0016021|GO:0055038 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115421_PI430048170 0.333229600822515 1.12580014463999 5.1398811222964 5.22782769962198 5.55413305176048 P P P 5.05695665318272 5.26297986542003

5.11489717904254 P P P LNCV6_115421_PI430048170 mRNA
GCATACAGATGTAGGTGATATTAAAATTGAAGTCTTCTGTGAGAGGACACCCAAAACATG NM_032472RefSeq chr2
- 200870955 200889126 PPIL3 53938 "peptidylprolyl isomerase (cyclophilin)-like 3, transcript variant
PPIL3a" GO:0005515|GO:0000413|GO:0006457|GO:0000398|GO:0003755|GO:0071013 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_131942_PI430048170 0.00951589240705379 0.60910809071196 8.96291638795888
9.02517477542254 8.73035578130886 P P P 9.57941723698905 9.6799168298454
9.61946051515751 P P P LNCV6_131942_PI430048170 mRNA
CATCTGTGTGCACTGATGCTTCCTCCCTTTTTTAATTTAAAATGGTTTTTATAAGCAACC NM_020812RefSeq chr19 -
11199292 11262492 DOCK6 57572 dedicator of cytokinesis 6
GO:0043547|GO:0005085|GO:0048471|GO:0005737|GO:0007596|GO:0007264|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_9584_PI430048170 0.111150958589401 1.18842464735151 7.18076566386973 7.28110844186117
7.08179764109786 P P P 7.09196282348394 6.94559925669279 6.74496039004526 P P P
LNCV6_9584_PI430048170 mRNA
AGCTGGCTGCTGGCCTCAGTTCTGCCTCTGTCCAGGTCCTTGTGACCCGCCCGCTCTCCT NM_145702RefSeq chr2
- 232547969 232550590 TIGD1 200765 tigger transposable element derived 1 GO:0005634|GO:0003677
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131012_PI430048170 0.0890026767135605 1.03845017391871 0.371701963428527
0.34902630635813 0.410061729541646 A A A 0.307062957275934 0.304999917718034
0.355523223976423 A A A LNCV6_131012_PI430048170 mRNA
TACCCAAATCACAGCTCCAAGCAGTACTTTTGAACAGAACTACAATAAAGTATGAATGTT NM_001039905 RefSeq
chr15 - 40250664 40252909 C15orf56 644809 chromosome 15 open reading frame 56 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_145699_PI430048170 0.0267540480122387 0.545352082141899 8.24810965801289
8.10376242072187 8.64418190152238 P P P 8.85125785859002 9.23985812735662
9.51001434519313 P P P LNCV6_145699_PI430048170 mRNA
CACTGTAGCTCATACTGGAAAAGTCGATCAATGTTTTGCAGTTTATTGAAAGTAGTTCTA NM_001358RefSeq chr4
- 24527464 24584561 DHX15 1665 DEAH (Asp-Glu-Ala-His) box helicase 15
GO:0003725|GO:0005515|GO:0006397|GO:0008380|GO:0003724|GO:0071008|GO:0005730|GO:0005634|GO:0005
524|GO:0004004|GO:0005737|GO:0000398|GO:0005654|GO:0005689 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144242_PI430048170 0.31676595659398 1.04701473114696 0.31357937477614
0.289849432937985 0.447389822131504 A A A 0.293937091319627 0.263215512805721
0.299606683294754 A A A LNCV6_144242_PI430048170 mRNA
CCCATGAATAATACACGACCTGTTATTTCCATGACTGCTTTACTGTATTTTTAAGGTCAA NM_015419RefSeq chrX
- 3308565 3346643 MXRA5 25878 matrix-remodelling associated 5
GO:0008150|GO:0003674|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136930_PI430048170 0.0429852858096972 0.702444950329983 13.1639078160911
13.6354354779672 13.4488610623782 P P P 13.8112293395464 13.9210000495271
14.0713076042075 P P P LNCV6_136930_PI430048170 mRNA
TGGGTCTTCCATCTAGAACTGTTTACATGAAGATAAGATACTCACTGTTCATGAATACAC NM_019058RefSeq chr10
+ 72273918 72276039 DDIT4 54541 DNA-damage-inducible transcript 4
GO:0001666|GO:0048011|GO:0032007|GO:0008283|GO:0072593|GO:0043241|GO:0010801|GO:0005829|GO:0005
622|GO:0005739|GO:0071889|GO:0042771|GO:0051607|GO:0005737|GO:0007420|GO:0033137|GO:0030182|GO:0
045820|GO:0001764. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131862_PI430048170 0.114660045714771 0.222907883142371 0.286566854369825
0.29037456337604 0.305546392857176 A A A 0.809784297520664 2.60556122031557
3.11494226681021 A P P LNCV6_131862_PI430048170 mRNA

GGTGAAACAAACAAAACAGTTTTTATCTGCTGTGACATTTAAGTTTGTTGTTAGCTGGAG NM_001252078 RefSeq chr12 + 62260339 62409721 USP15 9958 "ubiquitin specific peptidase 15, transcript variant 1" GO:0005515|GO:0016579|GO:0035616|GO:0004843|GO:0046332|GO:0005634|GO:0030509|GO:0005160|GO:0042802|GO:0004197|GO:0005737|GO:0061136|GO:0035520|GO:0043161|GO:0007179|GO:0060389|GO:0030512 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144161_PI430048170 0.0213554155769871 0.33827360663515 3.76524140391094 3.4607484821904 3.54631915991465 P P P 4.58507941439439 5.2684332706813 5.48331480376914 P P P LNCV6_144161_PI430048170 mRNA
CTGTAGAGGTGAGGTTTTGTTTTTAGTTGTTCTACTGATTATATCCTTTTCTGAGCTATG NM_033104 RefSeq chr14 - 81260649 81427212 STON2 85439 "stonin 2, transcript variant 1" GO:0005515|GO:0043005|GO:0030131|GO:0005737|GO:0030054|GO:0030100|GO:0002244|GO:0030136|GO:0005730|GO:0048488|GO:0006886|GO:0008021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135693_PI430048170 0.1238687453336470 0.9424614294019376 0.01256669955403 5.97936212219332 6.04881579094494 P P P 6.08706873366203 6.16480125921806 6.04357081968064 P P P LNCV6_135693_PI430048170 mRNA
ATTTTCACTATCTGGAAAATGGGCTCAATGCAAAGGTGGCAGACATTTATGGACACCCGC NM_012458 RefSeq chr19 - 2425623 2427916 TIMM1326517 translocase of inner mitochondrial membrane 13 homolog (yeast) GO:0005739|GO:0007605|GO:0006626|GO:0005743|GO:0005730|GO:0042719|GO:0008270|GO:0072321|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136901_PI430048170 0.0248971224732933 0.6439807483090824 .71466186975076 5.12935803513664 5.1467372836549 P P P 5.533328901604 5.8246791879677 5.55912849342318 P P P LNCV6_136901_PI430048170 mRNA
AAATGTGGACAAGGAGGGACATTTGCATACTCCTACTGTCTGTGTGGTCACAGCTAGTTT NM_001130143 RefSeq chr15 - 40815444 40828709 PPP1R14D 54866 "protein phosphatase 1, regulatory (inhibitor) subunit 14D, transcript variant 2" GO:0042325|GO:0005737|GO:0004864|GO:0043086 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136230_PI430048170 0.8272402017806540 .9867924627818027 .30585427286215 7.53256853098486 7.56859700410258 P P P 7.53468028802602 7.39946521522478 7.5398771357477 P P P LNCV6_136230_PI430048170 mRNA
ATCTAGGGAAATTTCATGTCACTTCCCTCCTTCACTGCATCACAATCATATTCCCTTTTT NM_014320 RefSeq chr6 + 138404198 138413445 HEBP2 23593 heme binding protein 2 GO:0005739|GO:0005515|GO:0005737|GO:0010917|GO:0035794|GO:0070062|GO:0010940 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77722_PI430048170 0.6312573807069511 .01482858428401 0.3286302394374150 .330642320565894 0.434212938555748 A A A 0.3538481936112650 .3128111780595310 .365141367580471 A A A LNCV6_77722_PI430048170 mRNA
TTACACCATTGTCACGGGCTTGTATCCAGAGTCACATGGCATCATTGACAATAATATGTA NM_005021 RefSeq chr6 + 131637301 131747410 ENPP3 5169 ectonucleotide pyrophosphatase/phosphodiesterase 3 GO:0048471|GO:0090305|GO:0004551|GO:0009143|GO:0006796|GO:0003676|GO:0006898|GO:0046872|GO:0030505|GO:0006955|GO:0004528|GO:0047429|GO:0005887|GO:0030247|GO:0035529|GO:0070062|GO:0005044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130146_PI430048170 0.39544942156695 1.26508381856762 0.39318223095336 0.3970190762634551 .19770427931547 A A A 0.3758107019756250 .354767841352362 0.395872054248647 A A A LNCV6_130146_PI430048170 mRNA
ACAGTGTGAAAACCAAGGAGATCCGCAAAGGGATTCTCAAGTTCTTCCATAAATCCCAGG NM_001005288 RefSeq chr11 - 5440541 5441553 OR51I1 NA "olfactory receptor, family 51, subfamily I, member 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142184_PI430048170 0.3568560736411951 .57863316205269 1.17442250520355 0.2906369389873581 .84358741682763 A A A 0.3540106896691850 .757811249264619

0.593622443430459 A A A LNCV6_142184_PI430048170 mRNA
GGGAAGCTCAATAAATCACTAGGTACAATCCTGGTATCATTGCCAATTATCATCATATTT NM_006588 RefSeq chr2
+ 108377964 108387814 SULT1C4 27233 "sulfotransferase family, cytosolic, 1C, member 4"
GO:0006805|GO:0050427|GO:0008146|GO:0051923|GO:0044281|GO:0005575|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133948_PI430048170 0.0159871139922768 0.558041610446445 5.95263025293717
5.47005203506553 5.64592511722384 P P P 6.4663287299333 6.51130847247922
6.65099496319894 P P P LNCV6_133948_PI430048170 mRNA
CCTCTGTTCAATTCCTAACGCAAACTACAATAAATGGTGACACACGTTCAGAAGAAAAAA NM_001105562 RefSeq
chr1 + 10032982 10181238 UBE4B 10277 "ubiquitination factor E4B, transcript variant 1"
GO:0005737|GO:0042787|GO:0016874|GO:0034450|GO:0000151|GO:0043161|GO:0005634|GO:0019899|GO:0008
626|GO:0009411 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106603_PI430048170 0.159395494589722 0.814776185572695 6.12767182948593
6.19828233720488 6.58590072380629 P P P 6.58912153061623 6.65258876584716
6.59924867778457 P P P LNCV6_106603_PI430048170 mRNA
GAAGATGCAGTCAGAGAGACTTTCGAAAGAATATGATCAACTCCTGAAAGAACACTCTGA NM_018844 RefSeq chr7
+ 107579976 107623317 BCAP29 55973 "B-cell receptor-associated protein 29, transcript variant 2"
GO:0006888|GO:0016020|GO:0005789|GO:0006915|GO:0016021|GO:0006886|GO:0001649|GO:0070973 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128405_PI430048170 0.0934327770493274 0.763172715328931 10.5059903087023
10.3068532261751 10.6848308616283 P P P 10.7013915192489 10.8046469264002 11.147450548095
P P P LNCV6_128405_PI430048170 mRNA
CCATCTCTTCCTCAGATGTAAATGATATCTGGTTAAGTGTTATATGGAATAAAGTGGACA NM_006826 RefSeq chr2
- 9583966 9631055 YWHAQ 10971 "tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
activation protein, theta"
GO:0005515|GO:0007264|GO:0019904|GO:0006915|GO:0006605|GO:0097193|GO:0005829|GO:0005737|GO:1900
740|GO:0047485|GO:0016020|GO:0021762|GO:0061024|GO:0005925|GO:0045892|GO:0030659|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137619_PI430048170 0.0203268726267343 0.854567119870779 9.77800244595129
9.86588570190499 9.70772680564237 P P P 9.98926387314066 9.98211985241823 10.063382834059
P P P LNCV6_137619_PI430048170 mRNA
TACTACTGCACTACTGTCCATTGTGGGATGATTAAACATGGTATTTAACTGTGCAAAAAA NM_024874 RefSeq chr1
- 35433489 35557436 KIAA0319L 79932 KIAA0319-like
GO:0005515|GO:0031410|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139621_PI430048170 0.297649800769068 0.926161201880542 0.522002166177397
0.492625148338117 0.261087117042399 A A A 0.587874765132556 0.544588255577956
0.487376753872154 A A A LNCV6_139621_PI430048170 mRNA
GGTTTTCTGAACCCTTAGCAGAAGGACTTTTAATGTTTTTACAACACACTATTGTATTGC NM_017934 RefSeq chr6
- 78934418 79078294 PHIP 55023 pleckstrin homology domain interacting protein
GO:0005515|GO:0008286|GO:2001237|GO:0010800|GO:0043066|GO:0008284|GO:0005158|GO:0008360|GO:0045
840|GO:0005634|GO:0006606|GO:0033138|GO:0043568|GO:0045944|GO:0007010|GO:0022604|GO:0070577|GO:0
001932|GO:0045893|GO:0040008|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129086_PI430048170 0.0233128421548355 1.80946565688935 4.66531563876754
4.11280450893269 4.62607462032508 P P P 3.44108218085693 3.79349311297202
3.64439721437325 P P P LNCV6_129086_PI430048170 mRNA
CAGGAGCAGCGGGGCAGTGTGGGGCTTTGTGTCATCACAACATTAAAGTATTTTATTCTA NM_005247 RefSeq chr11
- 69809967 69819424 FGF3 2248 fibroblast growth factor 3
GO:0005515|GO:0008286|GO:0048011|GO:0008284|GO:0005794|GO:0048015|GO:0030916|GO:0007267|GO:0048
538|GO:0005104|GO:0005576|GO:0048752|GO:0001759|GO:0009653|GO:0007165|GO:0007173|GO:0008543|GO:0

045087|GO:0051781|GO:0008083|GO:0055026|GO:0038095 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_106057_PI430048170 0.8520481273757820.9744176816543897.41842961807474
7.66996937459386 7.83402516251 P P P 7.42601617594478 7.73008853818006 7.8730763681081 P
P P LNCV6_106057_PI430048170 mRNA
CATGAGTAAGGTGGCTTTGATTGGTGTACAGTATTTCAAAGGACTAGTATTAAACTTGTG NM_017867RefSeq chr4
- 169729467 169757942 C4orf27 54969 chromosome 4 open reading frame 27 GO:0005634 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_130242_PI430048170 0.00547700030260258 0.5106952659789537.94216786501181
7.98431562929063 8.26910173769055 P P P 8.83092004492347 8.97654168927335
9.28166545066617 P P P LNCV6_130242_PI430048170 mRNA
GCTGGAAAGTCTGCAATAAACAGTATTTGCTGTCTGTTAATAAATGGTTTCTGTCTCATT NM_004447RefSeq chr12
- 15620140 15789576 EPS8 2059 epidermal growth factor receptor pathway substrate 8
GO:0005515|GO:0008344|GO:0030054|GO:0008283|GO:0008360|GO:0017146|GO:0030426|GO:0070358|GO:0030
832|GO:0051016|GO:0007173|GO:0051764|GO:0005938|GO:0051017|GO:0070062|GO:0010458|GO:0031532|GO:0
014069|GO:0032420|GO:0009967|GO:0003779|GO:0032587|GO:0031982|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140877_PI430048170 2.00455718960351e-05 2.04495826556241 9.27865159947467
9.2869383487981 9.37290872473157 P P P 8.33604172810993 8.22526753794116
8.28074981765498 P P P LNCV6_140877_PI430048170 mRNA
AGGGACTTAGTTATATCTTCAGACCAGTGCAGCTGGTACACACAAAGTTCTCCTGTCTCA NM_001081492 RefSeq
chr12 - 52168995 52192000 KRT80 144501 "keratin 80, type II, transcript variant 2"
GO:0030057|GO:0005882|GO:0005737|GO:0005198|GO:0045095 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138812_PI430048170 0.00515696786147602 0.6119138827456198.79559012335323
8.73712738108892 8.95949984670723 P P P 9.54920622281409 9.36634225153779
9.69326966568763 P P P LNCV6_138812_PI430048170 mRNA
CATTAGCCCACATACCAGTAACTTATACTTAAAGATGGGATGGAGTTATAAAGTGCTTTT NM_032144RefSeq chr2
+ 129979661 129982738 RAB6C 84084 "RAB6C, member RAS oncogene family"
GO:0005813|GO:0005794|GO:0007264|GO:0042493|GO:0006890|GO:0003924|GO:0006891|GO:0005634|GO:0010
824|GO:0022402|GO:0005525|GO:0006886|GO:0005622|GO:0008152|GO:0042147|GO:0032482|GO:0019003 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133511_PI430048170 0.0710545345942503 0.7944140877346177.55202156443003
7.85798213518786 7.51799909057878 P P P 7.92809174622026 8.07746635507783
7.93853339564022 P P P LNCV6_133511_PI430048170 mRNA
CAGAGGCCTTGCAGGTGACCAGCAGTGTCATTGTATTTATATACAGAGCTTATGACTTTA NM_015404RefSeq chr9
- 114402079 114505456 DFNB31 25861 "deafness, autosomal recessive 31, transcript variant 1"
GO:0010628|GO:0005515|GO:0005737|GO:0060122|GO:0002142|GO:0001895|GO:0007605|GO:0005884|GO:0032
420|GO:0032391|GO:0050953|GO:0030426 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143008_PI430048170 0.2299285535141510.9694340244173620.434677684265248
0.4379442912642250.363208370794738A A A 0.4190935198954160.487034192893339
0.464460559722617A A A LNCV6_143008_PI430048170 mRNA
GATGCATTTTTCAGTCCCTTTTCAGAGCAAATGCTTTTGCAATGGTAGTAATGTTTAGTT NM_000949RefSeq chr5
- 35055696 35230589 PRLR 5618 "prolactin receptor, transcript variant 1"
GO:0005515|GO:0042978|GO:0006694|GO:0042977|GO:0060736|GO:0005886|GO:0004925|GO:0060397|GO:0030
155|GO:0042803|GO:0046872|GO:0007171|GO:0060644|GO:0030856|GO:0043066|GO:0038161|GO:0009986|GO:0
007566|GO:0005576|GO:0031904|GO:0042110|GO:0007595|GO:0016021|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139754_PI430048170 0.3772675623887741.24591737599942 5.13165107685114

4.96448334915552 4.80764858365853 P P P 5.09798911738814 4.71247224921009
3.92680137835575 P P P LNCV6_139754_PI430048170 mRNA
ACAGAAAATGTGATTTTCACAGATTCAGCTCTTCTCTCCTTACATTTTACATTCATGCCANM_005212RefSeq chr4 +
70242615 70251428 CSN3 1448 casein kappa GO:0003674|GO:0007595|GO:0050821|GO:0005615 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129625_PI430048170 0.6029641590054180.962047417992951 0.520216882982281
0.5899996031295360.463236710165249A A A 0.5061342370025390.738645932024058
0.484959077709332A A A LNCV6_129625_PI430048170 mRNA
TTCTTTTTCCCTTGAACAGGGAGAGAGACACAATGGATCAGAGTGTCTCTGCCAGTTCTA NM_018085RefSeq chr1
+ 201829159 201884294 IPO9 55705 importin 9
GO:0005515|GO:0042393|GO:0005737|GO:0016020|GO:0008565|GO:0008536|GO:0005634|GO:0006606 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133233_PI430048170 0.1098489190989510.5093020898825780.317772115708926
0.3230015414446450.564038288280555A A A 1.12887361818925 1.94748606579925
0.817497331682745A A A LNCV6_133233_PI430048170 mRNA
CCATCGATTTCCCTAGCAGCATTCTAAAAGATAGCAAGTAAAATGATGTTTGTTATCCTA NM_001142683 RefSeq
chr2 - 27625638 27628878 CCDC121 79635 "coiled-coil domain containing 121, transcript variant 2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102327_PI430048170 0.6879056666762741.04025903006848 4.94966732961773
4.94075193363437 4.63847617131801 P P P 4.91182889498178 4.70297099817801 4.7562343682458
P P P LNCV6_102327_PI430048170 mRNA
AGGACGTGGAGATGGCCAAGCGTGAGATCCTGTCGGCGGCCGAACACTTCTCCATCATCC NM_203304RefSeq chr19
- 1554668 1568058 MEX3D 399664 "mex-3 RNA binding family member D, transcript variant 1"
GO:0061157|GO:0010609|GO:0048471|GO:0017091|GO:0008270|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126848_PI430048170 0.0131875404872113 0.48390088025447 6.07372745605056
6.14545417338902 6.12271291965426 P P P 6.89715106124349 7.24000005729746
7.31399116657538 P P P LNCV6_126848_PI430048170 mRNA
CATAGTTACCTGGATTGTCAGCCTTGGTAGCCTTTGTCTAAAGTCCTAAAGAGTTCCAAA NM_000390RefSeq chrX
- 85861179 86047562 CHM 1121 "choroideremia (Rab escort protein 1), transcript variant 1"
GO:0043547|GO:0017137|GO:0018344|GO:0005968|GO:0001568|GO:0006612|GO:0004663|GO:0007601|GO:0050
896|GO:0005829|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134229_PI430048170 0.1108961399689380.7224741923685053.39103106468766
2.81138800124656 2.89360357824155 P A P 3.52309130980976 3.48733130103659
3.56209227434617 P P P LNCV6_134229_PI430048170 mRNA
TTTGTTTTAATATCTAGTGATCTAATAAATTTGGATGATATCTTTTGACTATCAATTATG NM_015154RefSeq chr15 -
80975744 80989878 MESDC2 23184 "mesoderm development candidate 2, transcript variant 1"
GO:0003674|GO:0005886|GO:0006457|GO:0005783|GO:0034394|GO:0007498|GO:0005575|GO:0016055|GO:0050
750 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134835_PI430048170 0.000604366961891324 0.475173640215013 12.699786427062
12.5738283413186 12.8512575852592 P P P 13.7361115590168 13.6872025175611
13.9243694784902 P P P LNCV6_134835_PI430048170 mRNA
GCCTGGTTCCACCCTGGGCAGCACCCCCTCTAGTTCTAATAAAGCCGCCTCTGTCTCACA NM_181688RefSeq chr21
+ 44637355 44638455 KRTAP10-10353333 keratin associated protein 10-10 GO:0045095 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131524_PI430048170 0.1349265851521690.7326786334562572.76177651462173 2.8498882683938
2.93348712520263 A A P 3.33501821346649 3.55827169596729 2.9359136695726 P P P
LNCV6_131524_PI430048170 mRNA
AAAGTGTGGAGCATTCCTTGAGTTCCTGTTGTAGTGAGGTCTTGTCTGTCAGAGAAGTCT NM_001135178 RefSeq

chr18 + 35241029 35247189 ZNF397 84307 "zinc finger protein 397, transcript variant 1"
GO:0006355|GO:0005737|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126794_PI430048170 0.3336845042307880.5752681881574290.445401477724755
0.4524613672977170.927117453539812A A A 1.05706226646313 0.481447922776922
2.19353852826742 A A A LNCV6_126794_PI430048170 mRNA
CTGGCTCGAGGCCTTTGTTTCATTACTGTTTGATGAGGCATGATCCCTTACTTTAAAAAA NM_018452RefSeq chr6
- 157289021 157324259 TMEM242 729515 transmembrane protein 242 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134698_PI430048170 0.2289754065873561.0312422850809 0.34964918351683
0.3603200725518120.277697230679268A A A 0.2815470645500630.296404818404225
0.27788979401899 A A A LNCV6_134698_PI430048170 mRNA
GAACATGGTTTGACTCATCTTATATGGGAAACCATGTAGCAGTGAGTCATATCTTAATAT NM_000956RefSeq chr14
+ 52314297 52328604 PTGER2 5732 "prostaglandin E receptor 2 (subtype EP2), 53kDa"
GO:0007186|GO:0005886|GO:0005887|GO:0042127|GO:0032496|GO:0007189|GO:0071380|GO:0004957 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129084_PI430048170 0.0150633207570312 0.60070118150532 4.4110385145338
4.6644677648054 4.81556338927631 P P P 5.4620057882945 5.32163850490766
5.33771983246494 P P P LNCV6_129084_PI430048170 mRNA
CAGAGGCTTAGAATGATTCAGAATGTTCAATGCATAGTTCTCAATAAACAGGAGGCAGAA NM_001190972 RefSeq
chr8 - 90958477 90985257 C8orf88 100127983 chromosome 8 open reading frame 88 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_132435_PI430048170 0.4818619502480540.9739411117264280.404244097325092
0.4177646793631480.276616205366632A A A 0.38194835425167 0.436789216579182
0.39777576849285 A A A LNCV6_132435_PI430048170 mRNA
GGTGGATCCATTTCAAGTATTTATGCAAATGTGTCTCTGAACTAAAGTGTGATCTTATGC NM_007037RefSeq chr11
- 130404922 130428644 ADAMTS8 11095 "ADAM metallopeptidase with thrombospondin type 1 motif, 8"
GO:0031012|GO:0008285|GO:0005178|GO:0009673|GO:0035435|GO:0006508|GO:0005578|GO:0008270|GO:0004
222|GO:0008201|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144724_PI430048170 0.0209600258006938 0.6743311204788218.03012112596067
8.07278208394031 7.9458577592617 P P P 8.3872210712448 8.73415614231101
8.61443152188754 P P P LNCV6_144724_PI430048170 mRNA
TGGCATCGCGCACACTGTATGTACATACTGGCAACGATGTCAAATGTAATTTATTTTAAC NM_003740RefSeq chr6
- 39188970 39229475 KCNK5 8645 "potassium channel, two pore domain subfamily K, member 5"
GO:0007588|GO:0005244|GO:0005887|GO:0005267|GO:0034765|GO:0006813|GO:0071805 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136302_PI430048170 0.0199448212583438 0.7394008995078566.61933565490982
6.55851288463342 6.33124465822742 P P P 6.8516560647397 7.02393912469323
6.95074876837488 P P P LNCV6_136302_PI430048170 mRNA
TACAACACCTTCAAGTACTACTCCCACTTTCTCTTCAAAGTGGTGACCAAGCTGGTGAAC NM_020461RefSeq chr22
- 50217688 50244971 TUBGCP6 85378 "tubulin, gamma complex associated protein 6"
GO:0008017|GO:0005813|GO:0000922|GO:0016020|GO:0007020|GO:0000086|GO:0005874|GO:0000278|GO:0008
274|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_3694_PI430048170 0.00230757994781856 0.3555423518915721 0.4185099092067
10.1427932594419 10.0876450009389 P P P 11.7213395466342 11.7685845812759 11.654690322481
P P P LNCV6_3694_PI430048170 mRNA
TCAAGCCCCCAAAGAGCAAAGGCAACAGCAAGACCAGCGGGTTCTTGCAACACTGTGAGG NM_138387RefSeq
chr17 + 44070729 44076344 G6PC3 92579 "glucose 6 phosphatase, catalytic, 3, transcript variant 1"
GO:0005975|GO:0006094|GO:0015760|GO:0044281|GO:0055085|GO:0008645|GO:0015758|GO:0016020|GO:0016

311|GO:0004346|GO:0005789|GO:0009405|GO:0016021|GO:0051156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135309_PI430048170 0.8374303075074341.21982687700722 2.6586023192196
0.4472716709365181.58767046107202 A A A 0.3921558318849222.09004888674065 1.6726846643134
A A A LNCV6_135309_PI430048170 mRNA
GCTCAAAAGCCCAGTGTCTGTTTCCATTTATTTCCCTGGAATTTCATTTAAAATTGGTATNM_001080513 RefSeq chr3
- 194339764 194351328 CPN2 1370 "carboxypeptidase N, polypeptide 2, transcript variant 1"
GO:0050790|GO:0050821|GO:0072562|GO:0030234|GO:0005576|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138037_PI430048170 0.00508896419127148 0.3784633397385033.92371223203067
3.89716780486918 3.69675855787219 P P P 4.91493224586949 5.38847410950678
5.38102322781196 P P P LNCV6_138037_PI430048170 mRNA
GATCTAATGCTAAGTTTTCTCTGTGTACTGACTCAGTTGCCAGAATTATAATGAAAACTG NM_080546RefSeq chr9
+ 105244612 105397347 SLC44A1 23446 "solute carrier family 44 (choline transporter), member 1,
transcript variant 1"
GO:0015220|GO:0016020|GO:0005886|GO:0015871|GO:0005741|GO:0044281|GO:0016021|GO:0006644|GO:0055
085|GO:0070062|GO:0046474|GO:0006656 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141611_PI430048170 0.5103932261881271.20555230156079 0.264901587294874
0.3974870126430331.14073743533562 A A A 0.4695946300980160.361663194157833
0.320383642502855A A A LNCV6_141611_PI430048170 mRNA
TAAAAAGCAACTGCGGAAAAGCCAAGACGAACCCAAAGCACCAGACGGGCCAGAAAGCCC NM_001098169
RefSeq chr11 - 122977648 122981671 BSXNA brain-specific homeobox NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_143361_PI430048170 0.00763036360419492 0.4557429178368298.88270076619747
9.16293750238176 9.20259945920608 P P P 10.0181063843558 10.0619852931246
10.5317818827886 P P P LNCV6_143361_PI430048170 mRNA
AAGCGGTGTTCATGATTTCTTTTATTCTTTGCACAACAACAACAACAACAAATTCACGGA NM_002166RefSeq chr2
+ 8681982 8684453 ID2 3398 "inhibitor of DNA binding 2, dominant negative helix-loop-helix
protein"
GO:0001656|GO:0005515|GO:0043353|GO:2000045|GO:0071158|GO:0048541|GO:0046983|GO:0000785|GO:0071
285|GO:0005813|GO:2000178|GO:0007275|GO:0000122|GO:0045651|GO:0032922|GO:0071931|GO:0019216|GO:0
043392|GO:0044325|GO:0043234|GO:0033598|GO:0045648|GO:0045600|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143426_PI430048170 0.3814651477982741.61637186996898 0.341115447663313
1.73891335974685 0.300929241169132A A A 0.2585193870168480.28268241833262
0.260827599587672A A A LNCV6_143426_PI430048170 mRNA
GTGTATTAAACCTGTATGTGAAATCAGGTCCTAATACTGACAAGCAGTTTGTCTGTTAAA NM_139175RefSeq chr7
- 122697711 122699154 RNF133 168433 ring finger protein 133
GO:0016874|GO:0005789|GO:0008270|GO:0016021|GO:0051865 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_60093_PI430048170 0.3800880903952031.44000021914154 0.3828174622610580.382295765123892
1.51372898535985 A A A 0.31871666194276 0.3204912632773250.375861845938796A A A
LNCV6_60093_PI430048170 mRNA
CTCCAGCTGATGCAATCTAAATACAAGCAAAAGCTAAAAAGAGAAGAATCTGTAAGAATC NM_001002264 RefSeq
chr13 - 42886387 42992271 EPSTI1 94240 "epithelial stromal interaction 1 (breast), transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61885_PI430048170 0.2449855517457170.8341128438787227.09864343145549 6.90311276564402
7.46999122320177 P P P 7.47539162845229 7.2404019506772 7.57886967033451 P P P
LNCV6_61885_PI430048170 mRNA

ATATTGGGTTTTGGAGACATTATTGTACCAGGCCTGTTGATTGCATACTGTAGAAGATTT NM_032802 RefSeq chr15 - 50707539 50765713 SPPL2A 84888 signal peptide peptidase like 2A
GO:0005515|GO:0005886|GO:0031293|GO:0071458|GO:0005765|GO:0042803|GO:0030660|GO:0031902|GO:0050776|GO:0071556|GO:0004190|GO:0006509|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126681_PI430048170 0.6068673408274121.3341046855305 0.296973758177609
0.3171972227643641.66830440543343 A A A 0.3221235572058140.3021430504304490.8107023474864
A A A LNCV6_126681_PI430048170 mRNA
CCAAAAGAAGCATCTGGAGAAGGAAACGCCGGAGACCTCGGGAGACTTGTAGGCTGTGTG NM_005061 RefSeq chr16 - 1944578 1954678 RPL3L 6123 ribosomal protein L3-like
GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0000184|GO:0016020|GO:0005840|GO:0016032|GO:0022625|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141327_PI430048170 0.2819113688598151.36412049010065 1.42464695588404
0.5370670733744650.710046198268376 A A A 0.4299606523800220.509399757188426
0.546143260574234 A A A LNCV6_141327_PI430048170 mRNA
GTGGCAAAGCTTTTATTCAGTGCTCATACCTTATTAGACATAAAACAATTCATACCAGAG NM_001242680 RefSeq chr19 + 22286449 22317176 ZNF729 100287226 zinc finger protein 729
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132004_PI430048170 0.4643180254039170.9572103494339550.400316225697992
0.5213672237791640.421601414214595 A A A 0.5248998219982150.610790129347647
0.391362821508769 A A A LNCV6_132004_PI430048170 mRNA
TAGCAGGCTCAGAGTTATTAATGAATTGTACTTAAGCGTTGAGAGGCATATATTTATTGC NM_152791 RefSeq chr19 + 2841434 2860474 ZNF555 148254 "zinc finger protein 555, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136502_PI430048170 0.1738575053765250.6028759512395690.408365500194226
0.38057560453962 0.253591628476671 A A A 1.35368631903089 1.31871779939155
0.365381795256641 A A A LNCV6_136502_PI430048170 mRNA
AGCAGGTGAAGGGAAATCACAGGTTTAAAGGAAGATAAGCTGAAACAACACAAACTGTTT NM_130777 RefSeq chrX + 52369009 52375683 XAGE2 9502 "X antigen family, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132532_PI430048170 0.0115343022484099 0.1467692623281821.63108968844392
0.5299130429088670.654144039337583 A A A 3.93932124952462 3.75816137409429
3.67720508848029 P P P LNCV6_132532_PI430048170 mRNA
GGAGGAGTTTCTCCTCTGCTAACTATTCATATATGTAACTGTAACAAAAGTGTACTATGT NM_024921 RefSeq chrX - 85277388 85379743 POF1B 79983 "premature ovarian failure, 1B" GO:0003779|GO:0005923 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134332_PI430048170 0.8803268593838791.00628052070387 0.519933011289927
0.3900424923095290.51286839123293 A A A 0.4027190848332530.502998917665948
0.491614722043636 A A A LNCV6_134332_PI430048170 mRNA
AATTCTTTGAGCCAGCAAACTCCATCCAGTACATTCTTTCTTCTTTCATGAAAGAGCTTG NM_001098722 RefSeq chr1 - 235547684 235649993 GNG4 2786 "guanine nucleotide binding protein (G protein), gamma 4, transcript variant 1"
GO:0005515|GO:0030308|GO:0008277|GO:0006112|GO:0007186|GO:0005886|GO:0071377|GO:0005834|GO:0007268|GO:0044281|GO:0004871|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128816_PI430048170 0.0433367329463327 0.69461348360195 6.21705835169844
6.39945254004227 6.20039233495786 P P P 6.53426718593073 6.99015525876927
6.84146494641799 P P P LNCV6_128816_PI430048170 mRNA

TTGATGAGGTTCCTGGACGTGAGACCCTCACAAAGACCAACCATTCCTCTAATAGCCATT NM_032268RefSeq chr16 + 74999016 75110994 ZNRF1 84937 "zinc and ring finger 1, E3 ubiquitin protein ligase" GO:0005515|GO:0004842|GO:0030054|GO:0016020|GO:0016874|GO:0043161|GO:0030672|GO:0008270|GO:0070936|GO:0005764|GO:0005829|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_134840_PI430048170 0.6722916994913030.9685699133994140.301379879655627 0.3167439214742880.393441279459325A A A 0.5445330301604770.301862756654367 0.290551926729844A A A LNCV6_134840_PI430048170 mRNA GCCAGTGTATTTATGTAGGTCTGGAATTCATTCCGTGCATTACTCCAAACATTTTAATAA NM_152589RefSeq chr12 - 87980038 88029399 C12orf50 160419 chromosome 12 open reading frame 50 NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_143949_PI430048170 0.8222904463371090.9021865041385491.40929072475713 0.3009130021299041.15577491777394 A A A 1.54652952761525 1.39455474976522 0.297377149761614A A A LNCV6_143949_PI430048170 mRNA GACAAGGTGGTTTCTCTCTTCCACACAGTGATTTTTCCTTTGTTGAATCCTGTCATTTAT NM_001004723 RefSeq chr14 + 19803769 19828372 OR4N2 NA "olfactory receptor, family 4, subfamily N, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_127030_PI430048170 0.1766713039595891.32950223593959 3.44313785412952 4.03371914578643 3.44842865104444 P P P 3.11806469976267 3.13870873618492 3.48817516095088 P P P LNCV6_127030_PI430048170 mRNA GATTGGTGGAGATAAACAGATGCCAAACCTGACCTATTTCTTAAACTTTATGGAATAAAC NM_001283016 RefSeq chr10 + 73110374 73131828 NUDT13 25961 "nudix (nucleoside diphosphate linked moiety X)-type motif 13, transcript variant 4" GO:0005739|GO:0016787|GO:0008152|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_138723_PI430048170 0.6875655670245860.9854014128038060.256643217406553 0.2703097855915980.402391839710983A A A 0.3692969145589650.313963460029832 0.313554919236774A A A LNCV6_138723_PI430048170 mRNA GTTCTTGGTGTTGAAAATTAAAATAAAGCAAATCTGCAGAGTGCTGTGCAATGCCAAAAA NM_152676RefSeq chr18 - 74073352 74147764 FBXO15201456 "F-box protein 15, transcript variant 1" GO:0019005 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135717_PI430048170 0.2361791148775770.80210198760013 1.32369133679867 1.38775312595118 1.98431956030416 A A A 1.85752795092368 1.99967301218315 1.88478128235625 A A A LNCV6_135717_PI430048170 mRNA CAGGTGCAGCCTATATTATTAACAGACAAGGAAAGAATCCAAATAAAAGTTCTGTAAACC NM_018376RefSeq chr9 + 104763740 104777764 NIPSNAP3B 55335 "nipsnap homolog 3B (C. elegans), transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_134676_PI430048170 0.0524928544961176 0.6835839357333626.46218652879488 6.05050035516798 6.44643018658447 P P P 6.64498141365947 6.8071845365822 7.14417250471815 P P P LNCV6_134676_PI430048170 mRNA GTATTGTGAAGTGGTATAAGAAATGACTTTGAACCACTTTGCAATTGTAGATTCCCAACA NM_002526RefSeq chr6 + 85449583 85495791 NT5E 4907 "5'-nucleotidase, ecto (CD73), transcript variant 1" GO:0005886|GO:0009986|GO:0055086|GO:0046086|GO:0044281|GO:0006259|GO:0031225|GO:0046872|GO:0006196|GO:0046135|GO:0005737|GO:0006195|GO:0000166|GO:0016020|GO:0006144|GO:0050728|GO:0016311|GO:0008253|GO:0006206|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_143287_PI430048170 0.0833038104818585 0.8251325347555141 0.6876296710607 10.6687428936667 10.5975252771987 P P P 10.8079587363796 11.100595546022 10.8617010841003 P P P LNCV6_143287_PI430048170 mRNA GGCCCCTTCCCACCTGTCATACTGGTAACTGTAACAAGAAAAACGACATCACTTAAAAAA NM_014578RefSeq chr11 + 67056817 67072017 RHOD 29984 "ras homolog family member D, transcript variant 1" GO:0051056|GO:0030335|GO:0005886|GO:0019901|GO:0007264|GO:0030032|GO:0003924|GO:0006605|GO:0007

266|GO:0005525|GO:0051893|GO:0005829|GO:0045785|GO:2000249|GO:0048041|GO:0008152|GO:0051017|GO:0
005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99011_PI430048170 0.79531837194896 1.01679370040153 9.26789058395037 9.43858354064775
9.44386036602832 P P P 9.31838941870069 9.26275972599224 9.49376240141449 P P P
LNCV6_99011_PI430048170 mRNA
TTACTATCCCCAGCAATATGGACATTATGGTTACAACCAGCGGCCTCCTTACGGTTACTA NM_031452RefSeq chr15
+ 82986202 82991057 FAM103A1 83640 "family with sequence similarity 103, member A1"
GO:0005515|GO:0003723|GO:0036031|GO:0006370|GO:0005634|GO:0032259|GO:0005845 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141197_PI430048170 0.1885058920240450.8712674604770615.8301759832359
15.4933638265961 15.5403822520248 P P P 15.9276113167373 15.840848309637
15.7069315505974 P P P LNCV6_141197_PI430048170 mRNA
CATCGTCTCAAAGAACTTTTGACTGGAGAGAATCACAGATGTGGAATATTTGTCATAAAT NM_001024RefSeq chr20
+ 62387064 62388520 RPS21 6227 ribosomal protein S21
GO:0010467|GO:0000461|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0015935|GO:0006415|GO:0006
412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0047485|GO:0000184|GO:0022627|GO:0016032|GO:0
042274|GO:0000447|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140245_PI430048170 0.430871316353755 1.05290788537547 0.294400290696569
0.2997405563798390.513597533072614A A A 0.3097535962858930.27018498680502
0.315255110222314A A A LNCV6_140245_PI430048170 mRNA
GTGCTCAGAGACACTGTTGATAAAAACTCAGGCAAAGAAAATGAAATGCATATTTGCAAA NM_002427RefSeq chr11
- 102942991 102955734 MMP13 4322 matrix metallopeptidase 13
GO:0003417|GO:0005509|GO:0005518|GO:0005578|GO:0005576|GO:0030282|GO:0005615|GO:0001958|GO:0022
617|GO:0030198|GO:0060349|GO:0030574|GO:0006508|GO:0008270|GO:0004222|GO:0044267 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128442_PI430048170 0.29403251139285 1.51129340418073 2.76387968386779
2.63818472923638 2.74689137678174 A A A 2.66609878505281 2.2935025731443
0.85258685194633 P A A LNCV6_128442_PI430048170 mRNA
TCCTAAACTCAGAGTTTTAATAAAGGTGTGAGGAGGCTGGGGCCAGTTGACACCAAAAAA NM_152719RefSeq chr13
+ 45702303 45714559 SPERT 220082 "spermatid associated, transcript variant 1" GO:0016023 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141300_PI430048170 0.2098384152877610.7740533406178342.96325878258687
2.70716153145421 2.48617031050642 A A A 3.20199665857907 2.7019676106554
3.32784007963672 P P P LNCV6_141300_PI430048170 mRNA
GGTGGAAAAAGCATGTACTTTGATATAAAAATCATGCAGCCTCCTCAGTATGTGTATAAT NM_014892RefSeq chr6
+ 154733377 154834244 SCAF8 22828 "SR-related CTD-associated factor 8, transcript variant 4"
GO:0008380|GO:0006397|GO:0000166|GO:0003723|GO:0043175|GO:0005681|GO:0005654|GO:0016363 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134008_PI430048170 0.00127363614857431 0.3301995902129825.66206608557702
5.48206601976742 5.93224172533897 P P P 7.19529624602231 7.2507797097549 7.4494020751192
P P P LNCV6_134008_PI430048170 mRNA
CATTCTAATAATGTTCTCTGTTGAAAAAGCTGGCTTCAATTTATTGAGCAAGATGCTGGT NM_015659RefSeq chr16
- 11834195 11851585 RSL1D1 26156 ribosomal L1 domain containing 1
GO:0032880|GO:0016020|GO:0005730|GO:0042981|GO:2000772|GO:0001649 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_90887_PI430048170 0.0783916376506245 0.6026989900414243.50318940228741
2.74127648414624 2.77739955008414 P A A 3.87846639812705 3.62260537614894
3.83379145906399 P P P LNCV6_90887_PI430048170 mRNA
CTGTGTTAGTTTTGCTGGTGTTGATAGCCTGGATGATGTTAAAAATCATACATACAATGA NM_001112736 RefSeq

chr3 - 56620131 56683107 FAM208A 23272 "family with sequence similarity 208, member A, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140281_PI430048170 0.3726573900747281.45381616272277 2.54740174673414
2.68400782577269 1.64482404807338 A A A 2.12908316923067 2.233346283313
0.599978837778609A A A LNCV6_140281_PI430048170 mRNA
GCTAAGTATATGTGGGTCACAGGACAGCCAACTGCAAATTACTCTCCAGCCCTATTTTTT NM_001164484 RefSeq
chr10 - 49131155 49134020 FAM170B NA "family with sequence similarity 170, member B" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132418_PI430048170 0.9584238802940561.00071432307892 10.1262227198154
10.0166598560681 9.96869659706634 P P P 9.8350630181487 10.1607938495474
10.0969548371509 P P P LNCV6_132418_PI430048170 mRNA
TAGTGGCCTTGGATATCCTGTTTGTTAATAAAGACAATTCAACCAGCTCCCACCAAAAAA NM_153827RefSeq chr17
+ 4833339 4898061 MINK1 50488 "misshapen-like kinase 1, transcript variant 3"
GO:0005515|GO:0030424|GO:0030054|GO:0030033|GO:2000311|GO:0046330|GO:0007268|GO:0030425|GO:0005
829|GO:0035556|GO:0005737|GO:0005083|GO:0046777|GO:0004702|GO:0045211|GO:0070062|GO:0030334|GO:0
022407|GO:0005794|GO:0031532|GO:0007254|GO:0006950|GO:0014069|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138655_PI430048170 0.4266511939086340.9229523582475886.61597611189011
6.19044001040836 6.50787483173275 P P P 6.54530996869277 6.54902167610886
6.59944835347712 P P P LNCV6_138655_PI430048170 mRNA
GTGGCAAGATACTTTGGTTGGTTAAAATAATATGGAACAAAGGATCCACTGAAGTGAAAA NM_172016RefSeq
chr6_GL000251v2_alt + 1806907 1823410 TRIM39 56658 "tripartite motif containing 39, transcript variant 2"
GO:0005739|GO:0005515|GO:0016567|GO:0016874|GO:2001235|GO:0006915|GO:0008270|GO:2000059|GO:0042
802|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138467_PI430048170 0.9931812711231870.9784188701886191.00241113195672
0.2934599116519620.50201449482433 A A A 0.3152993060789940.275151627708458
1.19734823861688 A A A LNCV6_138467_PI430048170 mRNA
AGCATCGTGTGGGTCCCTAAGCACAATAAAAGACATCCACAATGGAAAAACTGCAAAAAA NM_001044RefSeq
chr5_KI270791v1_alt + 64344 121219 SLC6A3 6531 "solute carrier family 6 (neurotransmitter transporter), member 3"
GO:0005515|GO:0021984|GO:0007608|GO:0030424|GO:0005886|GO:0005329|GO:0045471|GO:0007268|GO:0042
220|GO:0002020|GO:0051591|GO:0032403|GO:0042053|GO:0042416|GO:0005737|GO:0008144|GO:0010039|GO:0
072488|GO:0043025|GO:0006836|GO:0007626|GO:0040018|GO:0005330|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130320_PI430048170 0.0340109589155771 0.5089492927002995.25425791922275
5.13226315537194 5.3375999009112 P P P 5.80722692013181 6.26966219294787
6.49515666275707 P P P LNCV6_130320_PI430048170 mRNA
GGACCCTGAGTCTATTAAAATGTAATTCAAAGTAGCATATGATTGACTGACAGTCATGTA NM_003657RefSeq chr20
- 53943539 54070765 BCAS1 8537 breast carcinoma amplified sequence 1 GO:0005737|GO:0070062
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133554_PI430048170 1.668830351164e-05 0.3096528818609434.6598862267947
4.55702893206949 4.707511907007 P P P 6.25656181264933 6.4273776888687
6.31311065326793 P P P LNCV6_133554_PI430048170 mRNA
GTCTTGAACTACTGTGTCTAGTGGGCAAATGTCATTGTTACCTCTGTGTGTTAAGAAAAT NM_000028RefSeq chr1
+ 99850488 99924023 AGL 178 "amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase, transcript variant 4"
GO:0005515|GO:0043033|GO:0016234|GO:0005975|GO:0007584|GO:0005978|GO:0051384|GO:0044281|GO:0005
829|GO:0005737|GO:0016529|GO:0004134|GO:0009405|GO:0004135|GO:0006006|GO:0030247|GO:0005654|GO:0

005980|GO:0031593|GO:0004133 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128790_PI430048170 0.0127981277053753 0.941987812012949 0.376712682168079
0.344122501827525 0.329929442949193 A A A 0.460901893517077 0.437920861583086
0.410560549810283 A A A LNCV6_128790_PI430048170 mRNA
GGGAGACTCCTCAGTAGGGCAACATTTTTTAATGGTGACATCACTGCAGGACTTTCATAA NM_198944 RefSeq chr19
- 14799173 14800136 OR7C1 NA "olfactory receptor, family 7, subfamily C, member 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129539_PI430048170 0.123741416872181 0.83661322260266 14.0572896309628
13.8516607243858 13.6971022294222 P P P 14.2897570322193 14.0493542396487
14.0481171558856 P P P LNCV6_129539_PI430048170 mRNA
GTCGGCTTAATCAGAGTGTGGCATAGAAGCTATTTAATGATTAAAGTCATTTGCAGTAAA NM_004793 RefSeq chr19
- 5691833 5720258 LONP1 9361 "lon peptidase 1, mitochondrial, transcript variant 1"
GO:0005515|GO:0042645|GO:0003727|GO:0006200|GO:0004252|GO:0010044|GO:0005739|GO:0005737|GO:0003
697|GO:0005759|GO:0051603|GO:0070407|GO:0051260|GO:0009725|GO:0051131|GO:0001666|GO:0032042|GO:0
070182|GO:0007568|GO:0051880|GO:0090296|GO:0005524|GO:0043565|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142862_PI430048170 0.216523873033064 0.603739714751204 1.45999398521084
0.531289624205288 1.24045874427567 A A A 1.09179132884472 2.36393956200988
1.84192281487582 A A A LNCV6_142862_PI430048170 mRNA
CACGCGCACAAAAGAGAGAAACGGACACCAGAGGAATGAACTAAAGAAAAACGTAAACTT NM_033400 RefSeq
chr14 - 23520854 23551649 ZFHX2 85446 zinc finger homeobox 2
GO:0043565|GO:0006355|GO:0030534|GO:0008270|GO:0005634|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138998_PI430048170 0.461104744779901 1.42436816895745 0.343158851823696
1.63674726132527 0.410364262813625 A A A 0.507230219375371 0.38073932867769
0.36007842509988 A A A LNCV6_138998_PI430048170 mRNA
TGACTAGCCAACTTTTCTGCATCTTCTTATTTCCTCATTAGAATGCTCTTGAAATAGCTG NM_019016 RefSeq chr17 -
40697990 40703750 KRT24 192666 "keratin 24, type I"
GO:0005882|GO:0008150|GO:0003674|GO:0005737|GO:0005198|GO:0045111|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_93577_PI430048170 0.702146055844026 0.78176111314058 0.309720132713584 1.32822123498294
0.37684332898262 A A A 0.324911233409256 0.521900520487254 1.91453620506402 A A A
LNCV6_93577_PI430048170 mRNA
TTTGGAAACTTCTCCTTCACACACCAGTTGAAGACTAGGCTTTGGAGGTTTTCAAAGCAG NM_001278359 RefSeq
chr4 + 40196906 40244764 RHOH 399 "ras homolog family member H, transcript variant 1"
GO:0001772|GO:0005515|GO:0051056|GO:0045576|GO:0006355|GO:0005886|GO:0007264|GO:0019210|GO:0005
525|GO:0043086|GO:0005829|GO:0042326|GO:0005737|GO:0030217|GO:0017048|GO:0005095|GO:0043124 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140847_PI430048170 0.0537756403617003 1.95188940501485 2.33486604152262
2.81833365252099 2.45460811041655 A A A 1.9789948102481 1.62039708829071
0.992737860776256 A A A LNCV6_140847_PI430048170 mRNA
GAATACATAAACAGTCTCAAACTCGCACAATTTTTTCCCCCTTTTGAAAGCCACTGGGGC NM_138284 RefSeq chr13
+ 20703342 20723098 IL17D 53342 interleukin 17D GO:0006954|GO:0005615|GO:0005125 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_133646_PI430048170 0.520572911813738 1.14528135867772 0.981675257854315
0.421014449652954 0.290350320811501 A A A 0.506722102537171 0.402942420206743
0.284597360212658 A A A LNCV6_133646_PI430048170 mRNA
CCTGAACGTGAAATTCTGTCAACACTCTCAATGATAAATCAGTCCTTAGATATCGTAAAA NM_173516 RefSeq chr6
+ 159800248 159820704 PNLDC1 154197 "poly(A)-specific ribonuclease (PARN)-like domain containing 1,

transcript variant 2" GO:0005634|GO:0016021|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131628_PI430048170 0.0432616419428364 0.61450984185836 0.44841785808534 0.5335915872193070.797645549133472A A A 1.19592886421122 1.62995510264435 1.0135417026217 A A A LNCV6_131628_PI430048170 mRNA AACAGCAGTGATGACAAGCCTCTCTACTTTCTTACTGGACGTCATGTATGAGCTTTTGAA NM_001142966 RefSeq chr18 + 21242241 21522830 GREB1L 80000 growth regulation by estrogen in breast cancer-like GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131225_PI430048170 0.699884817526084 0.916960695959647 4.408534343374 4.65725031822532 4.76399115655782 P P P 5.08411211281343 4.34548035509632 4.70377043803282 P P P LNCV6_131225_PI430048170 mRNA CTCTGCACTATGAACCCAAACCCAGCTCAAAAAGATAAAATCTAGTCATTTAAGATAATC NM_025218 RefSeq chr6 + 149964006 149973711 ULBP1 80329 UL16 binding protein 1 GO:0002474|GO:0030101|GO:0005886|GO:0005783|GO:0046703|GO:0042267|GO:0050776|GO:0042605|GO:0046658 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140049_PI430048170 0.0780065032020944 0.785595658898249 10.5451252061093 10.5410280292235 10.1833232393054 P P P 10.8939461243689 10.782207730674 10.6570626425818 P P P LNCV6_140049_PI430048170 mRNA AGGGAGGGTTGCCTGGGAACCCCAGGAATTGACCCTGAGTTTTAAATTCGAAAATAAAGT NM_144589 RefSeq chr10 - 75233970 75236012 COMTD1 118881 catechol-O-methyltransferase domain containing 1 GO:0005739|GO:0016021|GO:0032259|GO:0008171 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136336_PI430048170 0.113934116118555 1.16741273401576 9.68838751893653 9.67384994799073 9.49559380616663 P P P 9.54246600912336 9.40257190249559 9.23428810639147 P P P LNCV6_136336_PI430048170 mRNA CTGCTGACAGACACTAACTTTGTATCCGTTCAATAAGCATTTCATAAATAAAGGTGTAGA NM_002663 RefSeq chr17 + 4807100 4823432 PLD2 5338 "phospholipase D2, transcript variant 1" GO:0005515|GO:0005886|GO:0007264|GO:0004630|GO:0044281|GO:0031526|GO:0002031|GO:0016042|GO:0070290|GO:0045087|GO:0007010|GO:0005789|GO:0006644|GO:0035091|GO:0038096|GO:0006654|GO:0006655|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144999_PI430048170 0.469240061713369 1.10220291520217 11.7494601030591 11.8181697868239 12.193778569657 P P P 11.7572529704437 11.6628412482638 11.9462701132663 P P P LNCV6_144999_PI430048170 mRNA GAACCGTGTTGGTGCTGCTAAGTTTAGCCATTATGGTTTTTCCTTTCTCTCTCTTAAGCC NM_000310 RefSeq chr1 - 40072709 40097470 PPT1 5538 "palmitoyl-protein thioesterase 1, transcript variant 1" GO:0031579|GO:0030424|GO:0008344|GO:0030308|GO:0006907|GO:0005634|GO:0015031|GO:0005764|GO:0005615|GO:0030425|GO:0007269|GO:0005829|GO:0002084|GO:0030163|GO:0043524|GO:0048666|GO:0043025|GO:0007625|GO:0044257|GO:0051186|GO:0070062|GO:0008306|GO:0043066|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143679_PI430048170 0.661700387747076 0.980603919745647 0.518853856291279 0.538995730813021 0.57594333141148 A A A 0.498944045741059 0.544818036557338 0.6699143396583 A A A LNCV6_143679_PI430048170 mRNA TTGAGATACATCCTGTCATCAGTATATTTCAGAATACATGCAATGCACTAGCAAGTTACA NM_001289 RefSeq chrX - 155276206 155334681 CLIC2 1193 chloride intracellular channel 2 GO:0005515|GO:0005244|GO:0034707|GO:0051099|GO:0010881|GO:0005634|GO:0004364|GO:0005254|GO:0004602|GO:0005622|GO:0007165|GO:0005737|GO:0010880|GO:0060315|GO:0006810|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143150_PI430048170 0.226716091855706 0.563930924119475 0.85439973143263 0.903301454372074 0.976433416244932 A A A 1.9387041410169 2.14814531323069

0.803702757990616 A A A LNCV6_143150_PI430048170 mRNA
CAACTTAGTCTGATCCTTACTTAGTAGGAAATTGGGGATTACATCTGTCATTAACTTGTA NM_001287349 RefSeq
chr3 - 44498969 44510640 ZNF852 NA zinc finger protein 852 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_138821_PI430048170 0.428203860370086 0.985107217900538 0.375196832956428
0.382948387203597 0.351052247879271 A A A 0.428528523368511 0.355561157499367
0.389316429217992 A A A LNCV6_138821_PI430048170 mRNA
CCAAGACAAATGAAGACTGAAACCAAGAATATTGTTCTTATGCTGGAAATTTGACTGCTA NM_130467 RefSeq
chrX + 55220346 55224108 PAGE5 90737 "P antigen family, member 5 (prostate associated),
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140221_PI430048170 0.0285521532447749 2.15922500531406 3.51178222937133
4.04518170327213 3.94297875167416 P P P 2.26493605671737 2.64381929478178
3.16915682902586 A P P LNCV6_140221_PI430048170 mRNA
ATGCATTTGCATTGACTATGGGAGAAAAATTAGGGGGAAATGACAGTCATGGTGTTTTTT NM_001143912 RefSeq
chr1 + 27725978 27762912 FAM76A 199870 "family with sequence similarity 76, member A,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95094_PI430048170 0.0948711306415955 0.63848149162238 3.45090550291613
3.41541550348064 4.14530885522642 P P P 4.24959450794014 4.38188990609783
4.43840974418151 P P P LNCV6_95094_PI430048170 mRNA
CCTCGTGTTTGGTTTGTGAGTCTAAAGGAAACATGGATTTTATTTCTCAGGAACAAACAT NM_024943 RefSeq
chr4 - 38966745 39032421 TMEM156 80008 "transmembrane protein 156, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137878_PI430048170 0.941223491638613 0.941372076181784 0.695172786985551
1.3116653756283 0.669684599379031 A A A 0.615237989729448 1.61078784624475
0.546545990238121 A A A LNCV6_137878_PI430048170 mRNA
GAGATGAAGAGGACTTTGATAAAACTATGGCGAAGAAAAGTGATTTTACACACATTCTGA NM_001003745 RefSeq
chr11_KI270829v1_alt - 170076 171021 OR10A3 NA "olfactory receptor, family 10, subfamily A, member
3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129460_PI430048170 0.551961797100028 0.898311025336785 0.292723726203363
0.2783185017212 0.420407842298215 A A A 0.294218291727595 0.26263578622668
0.829927745980466 A A A LNCV6_129460_PI430048170 mRNA
GAGAAACCCATCAATTGCTCAAATACTCAGAAAGTACTGTCAAAAGCCTAATAAAAAACC NM_207032 RefSeq
chr20 + 59300426 59325992 EDN3 1908 "endothelin 3, transcript variant 2"
GO:0008284|GO:0008015|GO:0001755|GO:0007267|GO:0005615|GO:0019229|GO:0010961|GO:0043406|GO:0030
182|GO:0046887|GO:0042310|GO:0003100|GO:0014824|GO:0014826|GO:0048016|GO:0030593|GO:0006874|GO:0
005102|GO:0045840|GO:0007275|GO:0005576|GO:0030318|GO:0002690|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_56849_PI430048170 0.892253646727576 1.05654542685532 3.81662871714422
2.93004183823725 3.57867077350716 P A P 3.15499919894163 3.50485872457983
3.53589415359545 P P P LNCV6_56849_PI430048170 mRNA
TGTTCATTACCAACACTGCAGATTCCCATTGAGTTGGTGGGGGTTTTGTTACCTTTGTTT NM_014881 RefSeq
chr10 - 113834723 113854216 DCLRE1A 9937 "DNA cross-link repair 1A, transcript variant 2"
GO:0007067|GO:0005730|GO:0005634|GO:0006289|GO:0051301 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_128947_PI430048170 0.479556632817758 0.729924698604027 0.489420650752218
0.572359693851894 0.478738022052655 A A A 0.443438857699451 1.64131974250433
0.475331538496494 A A A LNCV6_128947_PI430048170 mRNA
TAATTTAATAACTAGGGACACCTGTGTGCCACAGCTGTGGCACAGACTCCCACTAAAGAA NM_058180 RefSeq
chr21 - 46301129 46323899 C21orf58 54058 "chromosome 21 open reading frame 58, transcript

variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104693_PI430048170 0.408458521150249 1.33083318926002 0.638192492519768
1.59683450791758 0.609419302721999 A A A 0.604457256243753 0.705817519618262
0.52329898523897 A A A LNCV6_104693_PI430048170 mRNA
CAATCTTAAACCCCGAAAAGAAGAAACCATTTCACAGTGCCTGAAGAAAATAACTCATAT NM_001013626 RefSeq
chr8 - 66988130 67028551 PPP1R42 286187 "protein phosphatase 1, regulatory subunit 42"
GO:0005813|GO:0005737|GO:0045502|GO:0015631|GO:0005815|GO:0002177|GO:0015630|GO:0010921|GO:0003
779 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102209_PI430048170 0.0518126237939642 1.49854919759189 4.23177043649084
4.37356608742722 4.5595507516204 P P P 3.45367101516111 3.99396942142771
3.92758914528351 P P P LNCV6_102209_PI430048170 mRNA
ATGATGTGGATGTGGGCTCATCAGTTTCCAACTCAGATGATGAGATCTCCAGCAGTGATA NM_030809 RefSeq
chr12 - 51061204 51083671 CSRNP2 81566 "cysteine-serine-rich nuclear protein 2, transcript variant
1"
GO:0043565|GO:0005515|GO:0003700|GO:0019902|GO:0045944|GO:0010923|GO:0006915|GO:0005634|GO:0001
228|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144379_PI430048170 0.000471023354035566 0.741994102671296 12.4524570450145
12.5545161875144 12.5070604724157 P P P 12.8995968485867 12.9142602925202
12.9918311727402 P P P LNCV6_144379_PI430048170 mRNA
GGTGTCCTTAGCCCAAAGCTTGTGCCAGTCTCTATCAGAAATAAATGCCCCCAAAACCTC NM_001097615 RefSeq
chr7 - 102537918 102572621 POLR2J3 548644 polymerase (RNA) II (DNA directed) polypeptide J3
GO:0003899|GO:0046983|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_106826_PI430048170 0.00610647081987595 1.33751200021893 12.4292890404169
12.603672085235 12.5770443807314 P P P 12.0050157545532 12.1494063018132
12.1961630632515 P P P LNCV6_106826_PI430048170 mRNA
TGCAGGTTGTGAACTCTGTAGACATCTTTATTGCTTGGCTAAGAGTAGATTTAATAAATG NM_015918 RefSeq
chr12 - 120579044 120581394 POP5 51367 "processing of precursor 5, ribonuclease P/MRP subunit
(S. cerevisiae), transcript variant 1" GO:0005515|GO:0004526|GO:0005655|GO:0008033 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_110438_PI430048170 0.522837292893689 0.988304559625176 0.393378489640095
0.39742969266036 0.357555795499585 A A A 0.435261251176456 0.366274181902255
0.397250416104089 A A A LNCV6_110438_PI430048170 mRNA
GCAGTGGGAGGAAGTCATCCATGAGACCAGTGAGGAAACTGAGTTTCCATCTGAAGCCCC NM_144688 RefSeq
chr19 + 49388217 49417999 CCDC155 147872 coiled-coil domain containing 155
GO:0005640|GO:0000781|GO:0048477|GO:0070840|GO:0000724|GO:0016021|GO:0007283|GO:0000800|GO:0090
220|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137243_PI430048170 0.00505765051017817 0.381411198741163 4.10063136496496
4.27675421359169 4.48532892668509 P P P 5.33349714280309 5.71881368195809
5.94338502053892 P P P LNCV6_137243_PI430048170 mRNA
GGACTGAGGGAACATCTGAAAGCTACCATCTTGAAAATTTTTGAGGAAGTGTTTCTGAAA NM_001010853 RefSeq
chr6 + 89146049 89165571 PM20D2 135293 peptidase M20 domain containing 2
GO:0016787|GO:0008152|GO:0005654|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131844_PI430048170 0.843544720563207 0.995102760151704 0.372547640991209
0.348808249020234 0.258056062442032 A A A 0.325510203252942 0.347286084042715
0.330286107475003 A A A LNCV6_131844_PI430048170 mRNA
GGAACCATTTCTCTCTACTAGGAGATTACCACATAATTGTACAGATAAAACATACCTGAA NM_178563RefSeq chr7
+ 134986507 135135778 AGBL3 340351 ATP/GTP binding protein-like 3

GO:0035610|GO:0006508|GO:0008270|GO:0005829|GO:0004181 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133106_PI430048170 0.2900590725571180.9493593815520490.407968042888279
0.4174185049404720.353591101274075A A A 0.461474601459781 0.379463303061004
0.558222564440464A A A LNCV6_133106_PI430048170 mRNA
ACAAGATCTTGGTTTGGCTTCATGTACTGTTTTCTAGAGAGAGTGCTACGAAAAACTTAT NM_016356RefSeq chr6
- 24171754 24358052 DCDC2 51473 "doublecortin domain containing 2, transcript variant 1"
GO:0035556|GO:0005515|GO:0048813|GO:0045880|GO:0006968|GO:0005737|GO:0008542|GO:0072372|GO:0001
764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142961_PI430048170 0.211403788967845 1.73126860293364 3.04130215862092
3.09275471704923 3.27534823135744 A A P 3.2401632328299 1.65412654431807
1.42174214966145 P A A LNCV6_142961_PI430048170 mRNA
TGAATACAAGTATGCCACATAACTCAGTTTTCGCCATCTTCCATTTCTTAACAGTGTAAA NM_001466RefSeq chr17
+ 44557443 44561262 FZD2 2535 frizzled class receptor 2
GO:0017147|GO:0007608|GO:0005886|GO:0090263|GO:0007267|GO:0005737|GO:0051091|GO:0030182|GO:0030
855|GO:0090103|GO:0060070|GO:0060022|GO:0042813|GO:0003150|GO:0004930|GO:0090179|GO:0060119|GO:0
030165|GO:0003151|GO:0007186|GO:0003149|GO:0030825|GO:0016021|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_88799_PI430048170 0.371065870694526 1.0716053043742 8.47877265246846 8.57559905850833
8.71393902691591 P P P 8.39769324134843 8.43771511167439 8.63223834083472 P P P
LNCV6_88799_PI430048170 mRNA
ATAGTTGAGAATTTATCCTCAAGAGTCAGCTGGCAGTAGGTCAAGAAGCAGGTCTCGATC NM_001039465 RefSeq
chr14 + 69767111 69772005 SRSF5 6430 "serine/arginine-rich splicing factor 5, transcript variant 1"
GO:0005515|GO:0006397|GO:0008380|GO:0010467|GO:0006369|GO:0006366|GO:0006376|GO:0031124|GO:0009
611|GO:0005730|GO:0005634|GO:0050733|GO:0005737|GO:0006406|GO:0016607|GO:0000166|GO:0000398|GO:0
051726|GO:0005654. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134577_PI430048170 0.0254502613095931 1.1870941899001 7.77599143767391
7.82202423995591 7.86621584095164 P P P 7.46754822151391 7.63354782155433
7.61653120052156 P P P LNCV6_134577_PI430048170 mRNA
GTTCTTGTTCTGCCATTTTTAAATCAAGGTTTCTGTTAACGAGGCATTCCATTTTCCATT NM_014649RefSeq chr19 -
5586998 5622927 SAFB2 9667 scaffold attachment factor B2
GO:0005515|GO:0006355|GO:0005737|GO:0000166|GO:0005654|GO:0003677|GO:0006351|GO:0070062|GO:0043
231|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61257_PI430048170 0.8784042075492930.985492245667553 4.96076305707554 4.49065099098045
4.92970571778457 P P P 4.64907928231943 4.83209361233617 4.9893213768421 P P P
LNCV6_61257_PI430048170 mRNA
ACATCAGGTACAAATCTTACTTCAGAAGAGCTTCGGAAGAGACGAGAAGCCTACTTTGAA NM_004993RefSeq chr14
- 92058551 92106621 ATXN3 4287 "ataxin 3, transcript variant reference"
GO:0005515|GO:0006511|GO:0004843|GO:0030036|GO:0045104|GO:0010810|GO:0007268|GO:0005634|GO:0016
363|GO:0005829|GO:0042802|GO:0034605|GO:0005737|GO:0070536|GO:0005759|GO:0035520|GO:0051117|GO:0
008242|GO:0071218|GO:0031625|GO:0071108|GO:0006355|GO:0031966|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135334_PI430048170 0.0197646057381719 0.3254531103264930.256134936417812
1.30292203433287 0.394176339460545A A A 2.03831747401597 2.63873137857049
2.30835480715979 A P A LNCV6_135334_PI430048170 mRNA
GATGTAGAACCTACAGATAAGGTGAGCCAACTGCATTAGGAAATAACTCTAATAATTCTG NM_024641RefSeq chr6
+ 95577496 95609452 MANEA 79694 "mannosidase, endo-alpha"
GO:0005794|GO:0000139|GO:0016021|GO:0044267|GO:0004569|GO:0043687|GO:0018279 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_143252_PI430048170 0.1382734273730850.6314425678264577.01714914678549
6.78858196750609 6.99810074230217 P P P 7.13729174899209 7.46882589071435
8.04836480511186 P P P LNCV6_143252_PI430048170 mRNA
CACAGATTCCTTGTTTAACCAAGTGTCCCAAAGCATGTACCTGAAGTTATATCATTTTTT NM_014611RefSeq chr6
- 89642774 89819794 MDN1 23195 "MDN1, midasin homolog (yeast)"
GO:0005515|GO:0005737|GO:0006461|GO:0016020|GO:0008152|GO:0005730|GO:0005634|GO:0051082|GO:0045
111|GO:0016887|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129322_PI430048170 0.1968753471323090.7684645464160610.3889312251835
0.3408902110697970.720069598662649A A A 0.4658117767776160.99480344226046
1.08526147699175 A A A LNCV6_129322_PI430048170 mRNA
GGATCCTACAAAGAAGGACACAATTATGAAAACAACCATCATTTTCATATGAATACTCCC NM_025087RefSeq chr4
+ 48986247 49062078 CWH43 80157 "cell wall biogenesis 43 C-terminal homolog (S. cerevisiae),
transcript variant 1" GO:0016021|GO:0006506 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134193_PI430048170 0.4421079104227870.8832937285737317.09227845315924
6.78638211970948 7.21983016875708 P P P 6.92799337265984 7.22079507293841
7.46988651880408 P P P LNCV6_134193_PI430048170 mRNA
ACAGGGAATCTGGTACCTGCAGAGACTGTCCAGCCATAAAATGTTACCACCTTAAGAGAA NM_019005RefSeq chr7
+ 7566984 7607479 MIOS 54468 "missing oocyte, meiosis regulator, homolog (Drosophila)"
GO:0005737|GO:0030054|GO:0005654|GO:0005634|GO:0005765 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_91866_PI430048170 0.2889292851022170.8508201860761524.03350464181704 4.56014438618739
4.56935953968568 P P P 4.63653491450532 4.73679760058182 4.54484556166622 P P P
LNCV6_91866_PI430048170 mRNA
ATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCCT NM_000391RefSeq chr11
- 6612765 6619461 TPP1 1200 tripeptidyl peptidase I
GO:0006629|GO:0005515|GO:0004252|GO:0045453|GO:0005764|GO:0046872|GO:0030968|GO:0005739|GO:0030
163|GO:0030855|GO:0006508|GO:0050885|GO:0008240|GO:0043171|GO:0043202|GO:0070062|GO:0042277|GO:0
042470|GO:0007399|GO:0004175|GO:0008236|GO:0008233|GO:0006987|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133919_PI430048170 0.3185924301424870.9453541688543190.258914352873353
0.3840695216501580.280288521991808A A A 0.4887078010079290.382589606090265
0.291568236714695A A A LNCV6_133919_PI430048170 mRNA
TTAGATGGTAGTCCTAGTAGAAGAATAGCTCTAGATGTGGAGTTGTCAAAAGAATTATAG NM_001282460 RefSeq
chr13 + 46211942 46276803 LRRC63 220416 leucine rich repeat containing 63 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137317_PI430048170 0.6661482666646540.9251708190632524.18992402894452
4.85601776050951 4.88912020771774 P P P 4.46164194766907 4.92452670689919
4.93815167994736 P P P LNCV6_137317_PI430048170 mRNA
TTTGGTAAGGAATACTTTTATTTCATGGATCCCAGGCAGGCATATAAAAGTTACGGAATT NM_145269RefSeq chr8
+ 93700506 93729250 FAM92A1 137392 "family with sequence similarity 92, member A1, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132085_PI430048170 0.2254324591945390.71238671556976 0.2947538897164721.3294565022272
0.475566306409512A A A 1.56095913236004 1.05845631304072 1.11653232938613 A A A
LNCV6_132085_PI430048170 mRNA
ACTGGATACTAGATCTTACATCTGCAGCTCTTTCTTCTTTGAATTTCCTATCTGTATGTC NM_001639RefSeq chr1 +
159587825 159588871 APCS 325 "amyloid P component, serum"
GO:0001849|GO:0005509|GO:0046790|GO:0072562|GO:0048525|GO:0005576|GO:0005634|GO:0006953|GO:0002
674|GO:0005615|GO:0031012|GO:0043234|GO:0045656|GO:0061045|GO:0046597|GO:0006457|GO:0045087|GO:0
030246|GO:0051082|GO:0051131|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_134451_PI430048170 0.0710051975021689 1.26985382240762 11.6706223203085
11.8356630588942 11.4590018029516 P P P 11.2120813910983 11.2567451266362
11.4732761913717 P P P LNCV6_134451_PI430048170 mRNA
AAGCAGTCCTCTTATTCCTAAGGTAATCCTATTAAAACACAGCTTTACAACTTCCATACT NM_003824RefSeq chr11
+ 70203162 70207402 FADD 8772 Fas (TNFRSF6)-associated via death domain
GO:0005515|GO:2000454|GO:0031265|GO:0031264|GO:0070236|GO:0032813|GO:0048538|GO:0097202|GO:0097
049|GO:0002020|GO:0048536|GO:0032403|GO:0032757|GO:0042802|GO:0048535|GO:0002756|GO:0051607|GO:0
043029|GO:0043123|GO:0060546|GO:0032729|GO:0005164|GO:0033077|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133168_PI430048170 0.5293457424707461.08186775727302 7.53307076380063
7.54383210705133 7.71881333954517 P P P 7.56624993702005 7.1405487863264
7.69894550092992 P P P LNCV6_133168_PI430048170 mRNA
CAGGAGTCATGCCAGACCAGAACTTGATGCTACTGTGTCTTGTGTTAAGAATCATTTCCT NM_032718RefSeq chr2
- 102717206 102736878 MFSD9 84804 major facilitator superfamily domain containing 9
GO:0005215|GO:0005886|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62642_PI430048170 0.4663099518042940.9466826756970699.46051282481331 9.31802431038199
9.58037641576265 P P P 9.4104708911796 9.56109363132453 9.62789253777064 P P P
LNCV6_62642_PI430048170 mRNA
ACAGCATCAAGCTGCACGTGGAAGCATCTCGCGGTTTTCTAGAAACAGGCATTTTCTTAT NM_015276RefSeq chr17
- 20999592 21043039 USP22 23326 ubiquitin specific peptidase 22
GO:0005515|GO:0016578|GO:0016579|GO:0004843|GO:0016574|GO:0003713|GO:0006325|GO:0009790|GO:0006
351|GO:0070461|GO:0004197|GO:0045931|GO:0007049|GO:0030374|GO:0061136|GO:0043967|GO:0000124|GO:0
043161|GO:0008270|GO:0010485|GO:0045893|GO:0019899 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_127769_PI430048170 0.6996642544989210.9537747372227734.92642575736246
4.47718900792091 4.71893301932514 P P P 4.61988453868551 4.72201547624281
4.99397689146492 P P P LNCV6_127769_PI430048170 mRNA
TCCTGACCCAGCCTGTGTATTCAAAACGAAAACAGTAAAACCAACATCAGGATGTCCGTC NM_006613RefSeq chr17
- 19020676 19047023 GRAP 10750 GRB2-related adaptor protein
GO:0005737|GO:0005070|GO:0007267|GO:0009967|GO:0007265|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_103873_PI430048170 0.8975531885990160.9749450171529380.411045454154125
0.3805564883274071.58111049668163 A A A 1.51013411483228 0.388678712016876
0.687465661407501 A A A LNCV6_103873_PI430048170 mRNA
GTCTCAGCATTTGAACCGAATGCTAATATAGTCACTTATTAAAGGATTATGCTGATGGAA NM_031898RefSeq chr17
- 15303811 15341641 TEKT3 64518 tektin 3
GO:0003674|GO:0080154|GO:0060271|GO:0005874|GO:0036126|GO:0005634|GO:0030317|GO:0002080|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131295_PI430048170 0.0256000668633008 1.57866909704197 10.4437900016566
10.8627691982617 10.7305943898524 P P P 10.0661943831361 10.0718218295081
9.95102916043988 P P P LNCV6_131295_PI430048170 mRNA
TTCAAATGCATTTTGGGGGTTTTTAATCTTTGTGACAGGAAAGCCCTCCCCCTTCCCCTT NM_005163RefSeq chr14
- 104769349 104793601 AKT1 207 "v-akt murine thymoma viral oncogene homolog 1, transcript variant 1"
GO:0005515|GO:0010467|GO:0009408|GO:0030307|GO:0006412|GO:0007281|GO:0030154|GO:0006809|GO:0010
907|GO:0030163|GO:0008637|GO:0018105|GO:0015758|GO:0007173|GO:0016301|GO:0010765|GO:0005080|GO:0
006979|GO:0000060|GO:0030334|GO:0005979|GO:0005978|GO:0007568|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140481_PI430048170 0.48321147992925 1.13893382161823 3.00738013302188
3.24167841777911 2.60533407818129 A P A 2.95439793232054 2.83477717435194

2.54171575044972 P P P LNCV6_140481_PI430048170 mRNA
AACAACATAAATTACATCACTGAGGGCATCAATGAGGCTGTCCTCCTCACAGAGAGCTCA NM_152413RefSeq chr8
- 37934280 37940129 GOT1L1137362 glutamic-oxaloacetic transaminase 1-like 1
GO:0006520|GO:0005737|GO:0009058|GO:0030170|GO:0008483 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132914_PI430048170 0.5235869671500891.27938399217937 0.4630283605718931.4219215494996
0.308158645270598A A A 0.4090219211057730.5123008949134010.47026942872222 A A A
LNCV6_132914_PI430048170 mRNA
CAGGCTCCAACTCACAAAATACGAGTTTAAAAACTGCGTTGTTATTTTTAGAGATTTGTG NM_002677RefSeq chr8
- 81440325 81447484 PMP2 5375 peripheral myelin protein 2
GO:0005215|GO:0005737|GO:0005504|GO:0015485|GO:0006810|GO:0061024|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137660_PI430048170 4.09086011313081e-06 0.4662308323942545.32006978938733
5.33523455308323 5.39507697040687 P P P 6.49195747421162 6.43167061978516
6.42962600612763 P P P LNCV6_137660_PI430048170 mRNA
CTGGCTTTTGTGCCCTGGAAGATCATAATAGTGACCAAAATATACATGCAGACTTGTTTT NM_006520RefSeq chrX
- 37838835 37847636 DYNLT36990 "dynein, light chain, Tctex-type 3"
GO:0007346|GO:0007067|GO:0003774|GO:0008152|GO:0005874|GO:0006810|GO:0000777|GO:0000776|GO:0005
634|GO:0005868|GO:0051301|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129375_PI430048170 0.0428829121079858 0.3442984602907510.3856909289855
0.3783801100578681.43158391683542 A A A 2.98584809855954 1.69244230048041 2.0876995369718
P A A LNCV6_129375_PI430048170 mRNA
GTAGCAAACATTTCTGTAAATTATCACAAGCTCTGTTACCTTTATATACACTGCCTCTTCNM_001301365 RefSeq chr1
- 235661030 235883708 LYST 1130 "lysosomal trafficking regulator, transcript variant 3"
GO:0005515|GO:0032438|GO:0042267|GO:0005829|GO:0032816|GO:0051607|GO:0005543|GO:0015630|GO:0033
299|GO:0007017|GO:0033364|GO:0042742|GO:0002446|GO:0030595|GO:0042493|GO:0042832|GO:0012505|GO:0
032510|GO:0007596|GO:0043473|GO:0055091|GO:0006644|GO:0007040|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_94685_PI430048170 0.9808122947807070.9959661634448377.31167793792058 7.46581615104557
7.74677876300034 P P P 7.39604386191495 7.36511932131584 7.77721980226152 P P P
LNCV6_94685_PI430048170 mRNA
TAATTTGATGCGAGTATTAGGAACAGAAGCTGTTCAAGACCCCACGAAGGTAGAAGCCCA NM_004698RefSeq chr1
+ 150321478 150353228 PRPF3 9129 pre-mRNA processing factor 3
GO:0000244|GO:0005515|GO:0006397|GO:0008380|GO:0015030|GO:0005634|GO:0042802|GO:0005737|GO:0016
607|GO:0000398|GO:0000375|GO:0005654|GO:0005681|GO:0046540 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143578_PI430048170 0.4986730107782861.04793779929385 11.5374445927282
11.3237136395654 11.2993265206129 P P P 11.3761474619434 11.3320746951467
11.2592847487947 P P P LNCV6_143578_PI430048170 mRNA
GCGGCGTCTCGACTGTTCTTAGAGTGTATTTCTAGTAAAATCAGAAGCTCACCAAAGCAA NM_024109RefSeq chr16
+ 8621669 8646222 METTL22 79091 methyltransferase like 22
GO:0008168|GO:0005634|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137478_PI430048170 0.4431727185087930.7062161613249210.321026667535857
0.2890863513841660.28370866033967 A A A 1.48509118978449 0.280693101874542
0.273389905743096A A A LNCV6_137478_PI430048170 mRNA
CGGGAAATTATTATGACTCAATAAAAGAATTCACACCTTAGGTGTGGGAGTAAGAACAAA NM_003356RefSeq chr11
- 74000280 74009237 UCP3 7352 "uncoupling protein 3 (mitochondrial, proton carrier), transcript
variant long"
GO:0005515|GO:0006629|GO:0032868|GO:0014823|GO:0001666|GO:0005215|GO:0007585|GO:0007584|GO:0007

568|GO:0009409|GO:0005743|GO:0051384|GO:0044281|GO:0032870|GO:0022904|GO:0005739|GO:0017077|GO:0006631|GO:0000303|GO:0016021|GO:0006839|GO:0044237|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131777_PI430048170 0.0823182962155855 0.762671051714778 10.5423306083822 10.3609926262998 10.5461891735334 P P P 10.70927354521 10.7597167802038 11.124291619941 P P P LNCV6_131777_PI430048170 mRNA
CTGCTGTGATACGATGCTTCAAGAGAAAATGCGGTTATAAAAAATGGTTCAGAATTAAAC NM_001904 RefSeq chr3 + 41199450 41240448 CTNNB1 1499 "catenin (cadherin-associated protein), beta 1, 88kDa, transcript variant 1"
GO:0005515|GO:0030018|GO:0001658|GO:0030054|GO:0003700|GO:0030877|GO:0016342|GO:0001711|GO:0010909|GO:0030539|GO:0016337|GO:0003690|GO:0000578|GO:0016055|GO:0005938|GO:0001102|GO:0005813|GO:0001708|GO:0005719|GO:0019903|GO:0030331|GO:0003713|GO:0000122|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135406_PI430048170 0.00179322156682893 0.533221444088255 7.61164847741891 7.39237080723254 7.35040987534545 P P P 8.34486577087107 8.51989816797586 8.20811898690445 P P P LNCV6_135406_PI430048170 mRNA
CCTCCTTCCCCCAACCCAACAGACTAGTTCAAATTTGGGTAAATAAATAAAATAAATAAG NM_001109660 RefSeq chr16 + 30023333 30024702 C16orf92 146378 "chromosome 16 open reading frame 92, transcript variant 2" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125074_PI430048170 0.641774328606914 1.08544895934869 6.20023900658687 5.60152359662213 5.78465111531462 P P P 5.79711979212982 5.74365983346814 5.75683431613825 P P P LNCV6_125074_PI430048170 mRNA
TGCTCTTTCTTCACCTGAAAAGAAGACTCCAGGAAGGGCAGCACATGCCGGAGAAAGATG NM_032164 RefSeq chr7 - 99493230 99500254 ZNF394 84124 zinc finger protein 394
GO:0006355|GO:0005737|GO:0003700|GO:0005654|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132414_PI430048170 0.0303812198305544 0.566497799886305 6.88187020584309 6.57673374992097 6.95451076036525 P P P 7.28934143555117 7.59379620332057 7.94260227639194 P P P LNCV6_132414_PI430048170 mRNA
GAAGTACTTTAAGTACTCCAAGGGGAAAATTAAAGTGGAAGTTTCTTCGGATCTTGTTTA NM_177966 RefSeq chr3 + 57556253 57562041 PDE12 201626 phosphodiesterase 12
GO:0006397|GO:0004535|GO:0005759|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137521_PI430048170 0.0180402333042534 1.13727698285694 0.722741858879521 0.780524982300916 0.757331529164387 A A A 0.635898924361415 0.526976722491995 0.539067964998788 A A A LNCV6_137521_PI430048170 mRNA
CCTCTTCATGTTTTAGACAGCAAACCCTATCCATTAAAGTACTTGTTAGAACACTGAAAA NM_138737 RefSeq chrX + 66162548 66267388 HEPH 9843 "hephaestin, transcript variant 1"
GO:0048471|GO:0005886|GO:0005507|GO:0055085|GO:0008198|GO:0005622|GO:0006879|GO:0004322|GO:0016323|GO:0006826|GO:0016021|GO:0006825|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140082_PI430048170 0.43990655849211 0.866115217238306 0.377214649475881 0.360852303471522 0.260284032857832 A A A 0.89522738204938 0.328435934411389 0.321471746368047 A A A LNCV6_140082_PI430048170 mRNA
CTGACCTGTGAAAATTAATCTGATTAGCTACTTTTGATTATATCCAAAGCTTGTGGGGTT NM_001009994 RefSeq chr6 + 83853265 83857516 RIPPLY2 134701 "ripply transcriptional repressor 2, transcript variant 1"
GO:0010468|GO:0007368|GO:0032525|GO:0007219|GO:0001503|GO:0060349|GO:0001756|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137308_PI430048170 0.431542710009208 0.807899624797196 4.63956356294887 4.19976734366773.4618467222861 P P P 4.82260821891808 4.42528607427963 4.1254443303086 P P P LNCV6_137308_PI430048170 mRNA

GCTGTATAGACCTGCCCTCTTGCATTAAACAACTTCTCTTGAGCTGCAACTTTCAAAAAA NM_025227 RefSeq chr20 + 33007577 33023709 BPIFB2 80341 "BPI fold containing family B, member 2" GO:0070062|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140631_PI430048170 0.6238654918873880 0.8209136262644370 0.529207264680183 1.82498442780052 1.7310454836918 A A A 0.9706380927280322 0.26605524000064 1.74331891882032 A A A LNCV6_140631_PI430048170 mRNA
AGGAGTGGAAAATATGCAGGTGACTCTTGCATGCCAAGCTGCTCAGAAAAATGCTTTGAT NM_001277339 RefSeq chr6 + 109236613 109270514 LOC100996634 100996634 transmembrane protein FLJ37396 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137812_PI430048170 0.8504929037278371 0.05063187112268 0.978365154696793 0.3660399663428680 0.33975415250416 A A A 0.4080282981879470 0.398977262811677 0.732130966266288 A A A LNCV6_137812_PI430048170 mRNA
GCTTTGAAAGCACAGTGTTCTCAAAGGATCTGGGAGTTGTCACAACCTCTTACACGTTAA NM_001256475 RefSeq chr4 + 56530608 56603323 THEGL NA theg spermatid protein-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140074_PI430048170 0.0656491648534597 1.39772078470936 9.79859322214948 9.53610540037738 9.52117165677021 P P P 8.81807909034065 9.23891401154282 9.31848865584197 P P P LNCV6_140074_PI430048170 mRNA
TTGGGAGCACGATGACTCTGAGTTTGAGCTATTAAAGTACTTCTTACACATTGCAAAAAA NM_002775 RefSeq chr10 + 122461524 122514908 HTRA1 5654 HtrA serine peptidase 1 GO:0050679|GO:0050687|GO:0004252|GO:0001558|GO:0005615|GO:0005829|GO:0030514|GO:0031012|GO:0097187|GO:0006508|GO:0008236|GO:0030512|GO:0005520|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132870_PI430048170 0.5649130389205160 0.9020549673256697 8.82992353580558 7.91940772208536 8.22470411334057 P P P 7.84248790102336 8.08388083265706 8.45694602123814 P P P LNCV6_132870_PI430048170 mRNA
CTAACTCATGTGAGCTTGATAACTGATGAACTCATTGGGAGCATTTTAAACTTTTCTACA NM_018230 RefSeq chr1 - 229441296 229508341 NUP13355746 nucleoporin 133kDa GO:0007077|GO:0005515|GO:0010467|GO:0019221|GO:0019058|GO:0044281|GO:0005635|GO:0015031|GO:0008645|GO:0005829|GO:0006406|GO:0015758|GO:0005643|GO:0016032|GO:0006999|GO:0048339|GO:0031965|GO:0005975|GO:0019083|GO:0055085|GO:0010827|GO:0000940|GO:0005487|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137920_PI430048170 0.9052644129249210 0.9915120219913390 0.283834971000944 0.2974523304688320 0.476285763953363 A A A 0.3143142115663880 0.278848697595584 0.49953892969534 A A A LNCV6_137920_PI430048170 mRNA
CTACTCTGCATCCATAAAATAAGCATGCAGTTCAGAAAATAGATTAAACGACTAATTGGC NM_004815 RefSeq chr1 - 94168906 94237751 ARHGAP29 9411 Rho GTPase activating protein 29 GO:0051056|GO:0032321|GO:0007264|GO:0007266|GO:0030165|GO:0046872|GO:0005100|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133959_PI430048170 0.1336060262988470 0.9665353828103570 0.290011983436754 0.3222808772500930 0.354461338430436 A A A 0.4055128334132820 0.366056943818509 0.342517274362409 A A A LNCV6_133959_PI430048170 mRNA
GGGGTCCAAAATCTGTTGAACATTTGTTCAGCTAGTTAGGTTTCAACATTAATCATATAC NM_000370 RefSeq chr8 - 63059488 63086053 TTPA 7274 tocopherol (alpha) transfer protein GO:0051180|GO:0006629|GO:0005215|GO:0005770|GO:0007584|GO:0043325|GO:0046909|GO:0001892|GO:0005546|GO:0009636|GO:0005829|GO:0090212|GO:0060548|GO:0006810|GO:0008431|GO:0051452|GO:0009268|GO:0042360 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142293_PI430048170 0.00111476360417917 1.65910024466929 11.8473505676856 12.0046757728895 11.9962827527354 P P P 11.2007535519411 11.2716071734842

11.1887119496077 P P P LNCV6_142293_PI430048170 mRNA
TGCTATTTGTTTATCCTATGAATACTGTTCTTGCAAACCTGGTTGTTTTGGGGTTCCTAA NM_006331 RefSeq chr12 +
6970780 6976003 EMG1 10436 EMG1 N1-specific pseudouridine methyltransferase
GO:0070037|GO:0031167|GO:0005737|GO:0006364|GO:0003723|GO:0005730|GO:0005634|GO:0042274|GO:0019
843 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112104_PI430048170 0.50477270777265 0.9286648188816768.27396021399001 8.0307326031407
8.54237839833016 P P P 8.33544789757455 8.39066919008568 8.48281944984893 P P P
LNCV6_112104_PI430048170 mRNA
GGTTGATGCTGAATTAGGGAGTGATATTTACCTTGATGTATCATAACTATTGTGGATTCA NM_201453 RefSeq chr9
+ 68241944 68300035 CBWD3 NA "COBW domain containing 3, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126985_PI430048170 0.0513557685910175 0.4563042495727145.48103974859122
4.79863423353243 4.53744455390002 P P P 6.12406674003842 6.1041438332531
6.15439166637206 P P P LNCV6_126985_PI430048170 mRNA
GGATAATCCATTTGGAAGAAGAAAAGAGTGAGGCTGAAAGTAAAGCCACATGACAAGCAT NM_001199922
RefSeq chr11 - 124635788 124676303 SIAE 54414 "sialic acid acetylesterase, transcript variant 2"
GO:0005975|GO:0002682|GO:0005764|GO:0005615|GO:0001681|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133551_PI430048170 0.000292506461394344 3.51442330440635 7.61732113743455
7.48544078174229 7.28657316259371 P P P 5.83417892075231 5.66324749702478
5.44488534937995 P P P LNCV6_133551_PI430048170 mRNA
CTCACAGGGCTCCCTCAGCCTGGGGAACATTAAAGGTTTTCTACAAATACAGTCAAAAAA NM_016948 RefSeq chr16
+ 67660947 67662778 PARD6A 50855 "par-6 family cell polarity regulator alpha, transcript variant 1"
GO:0005515|GO:0005886|GO:0034329|GO:0045177|GO:0005634|GO:0001726|GO:0045216|GO:0045217|GO:0005
829|GO:0043234|GO:0030742|GO:0007049|GO:0070830|GO:0005080|GO:0016032|GO:0007179|GO:0017048|GO:0
005923|GO:0005938|GO:0051301|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58184_PI430048170 0.568042103182014 1.1366143211779 1.05370370476945 0.325315755798047
0.507153920207092 A A A 0.7565688825335230.2876497004364960.343681249873039 A A A
LNCV6_58184_PI430048170 mRNA
GGACTAGGTCAAAGAATCTTAAGTCAAGGATGTCATCGAAGAGTATTTCAAATGTAAGAA NM_031938 RefSeq chr11
+ 112175484 112218926 BCO2 83875 "beta-carotene oxygenase 2, transcript variant 1"
GO:0007603|GO:0016119|GO:0051881|GO:0001523|GO:0046872|GO:0005622|GO:0005739|GO:0042574|GO:0005
759|GO:0042573|GO:2000377|GO:0016702|GO:0055114|GO:0016116|GO:0016121 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135372_PI430048170 0.2478613712256140.7468550855636993.56234539894757
4.01190393316904 4.58387766718105 P P P 4.46531422062657 4.34833287835283
4.75859100509935 P P P LNCV6_135372_PI430048170 mRNA
ATTTTTTAAACTAGATCCCTTCATTATTCTTTATGCCCCAGAGTAAATCCCAGATGGATC NM_005680 RefSeq chr2
+ 9843441 9934416 TAF1B 9014 "TATA box binding protein (TBP)-associated factor, RNA polymerase
I, B, 63kDa"
GO:0005515|GO:0010467|GO:0001164|GO:0003700|GO:0006363|GO:0006362|GO:0006361|GO:0005634|GO:0006
360|GO:0001187|GO:0046872|GO:0006351|GO:0001189|GO:0000183|GO:0045814|GO:0040029|GO:0017025|GO:0
005654|GO:0070860|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139900_PI430048170 0.776376900724764 1.08438819207022 0.287531889033631
1.19216922570056 1.41942814581219 A A A 1.61415613554608 0.382696668854097
0.416025226848608 A A A LNCV6_139900_PI430048170 mRNA
AGTTCTTGATGATTTCCAACAATGGCCTGGTCACTACCCTGTGGTTTATCTTCCTGCTTG NM_001004706 RefSeq
chr11 + 59503575 59504511 OR4D11 NA "olfactory receptor, family 4, subfamily D, member 11"
NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_128240_PI430048170 0.00394871812957676 4.30290463967941 8.17379446240198
8.77421673100199 8.66610491266047 P P P 6.5807747168636 6.39020074817578
6.38662732218917 P P P LNCV6_128240_PI430048170 mRNA
CTTCTCAACAAGAAAAACTTAAATCCGTCGTGCCCAAATATAGTTGTGCTTTTATTTCCA NM_004283 RefSeq chr19
- 11322045 11339668 RAB3D 9545 "RAB3D, member RAS oncogene family"
GO:0030133|GO:0009306|GO:0005886|GO:0003924|GO:0005525|GO:0072659|GO:0006886|GO:0016079|GO:0006
904|GO:0008021|GO:0042588|GO:0005739|GO:0031489|GO:0018125|GO:0051020|GO:0017157|GO:0032482|GO:0
019003|GO:0070062|GO:0030667|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74307_PI430048170 0.00984812090218368 1.20384928327786 0.814864835879045
0.862196653067861 0.897566108684811 A A A 0.672324859005906 0.535547702705118
0.561290613495744 A A A LNCV6_74307_PI430048170 mRNA
AGGTGCCACTACTGATAATGGCATCCAAATGAAAATTGCTGAGTTCCTGAATCGAGAAAC NM_024677 RefSeq chr4
+ 40749896 40809985 NSUN7 79730 "NOP2/Sun domain family, member 7"
GO:0003723|GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138383_PI430048170 0.00801209906677347 0.321507946982679 0.249145039130696
0.3469432587412 0.283550968820983 A A A 1.62952161221084 1.92783420733058
2.18253679160845 A A A LNCV6_138383_PI430048170 mRNA
CAGGGAACTGCAAGGTAGTTATTATTGATATTGTCATCACCACTTTGTATCTAGAGATTA NM_012086 RefSeq chr2
- 196763031 196799768 GTF3C3 9330 "general transcription factor IIIC, polypeptide 3, 102kDa, transcript variant 1"
GO:0005515|GO:0042797|GO:0010467|GO:0000127|GO:0005654|GO:0042791|GO:0006383|GO:0003677|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140850_PI430048170 0.0406950769881742 1.41139935106046 10.1969712666141
9.87982401052579 10.1850454238183 P P P 9.48948198984479 9.42766926556707
9.84001331814784 P P P LNCV6_140850_PI430048170 mRNA
CTCGTGAACCTAATTGTAAACTTTCAGGTATTTTTGTACAAATAAGGGACTGATGTTCTG NM_001001555 RefSeq
chr7 - 50590062 50793462 GRB10 2887 "growth factor receptor-bound protein 10, transcript variant 4"
GO:0005515|GO:0008286|GO:0030949|GO:0032868|GO:0005886|GO:0046627|GO:0005158|GO:0030178|GO:0045
719|GO:0005829|GO:0042326|GO:0005737|GO:0005070|GO:0046325|GO:0048009|GO:0042327 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_122282_PI430048170 0.116360503878905 0.771002870270296 4.66238079278508
4.72942234376675 4.7672259158147 P P P 4.94468059613881 4.93889078759101
5.36113657422328 P P P LNCV6_122282_PI430048170 mRNA
TATATTCAGAGTCGCTTTTATCGGTCTCCAGAGGTGCTACTGGGAATGCCTTATGACCTT NM_130436 RefSeq chr21
+ 37418904 37515376 DYRK1A 1859 "dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A, transcript variant 2"
GO:0005515|GO:0005634|GO:0043621|GO:0042802|GO:0046777|GO:0018105|GO:0000381|GO:0018107|GO:0048
156|GO:0018108|GO:0005524|GO:0007399|GO:0090312|GO:0004672|GO:0016607|GO:0004674|GO:0030529|GO:0
007623|GO:0043518|GO:0006468|GO:0005654|GO:0004712|GO:0004713|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142547_PI430048170 0.17482132014703 0.532411003988001 0.623689127602935
1.57079571639636 2.44703582456236 A A A 2.16306473139217 2.56499365218266
3.05649977332649 A P P LNCV6_142547_PI430048170 mRNA
GCATTGTATCATTTTGCTCTACAATGACTATATCCTCATTTGGGTTTATGGCCAGTTTAT NM_002790 RefSeq chr1 -
109399030 109426448 PSMA5 5686 "proteasome (prosome, macropain) subunit, alpha type, 5, transcript variant 1"
GO:0005515|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0004
298|GO:0034641|GO:0005737|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0

005839|GO:0000502|GO:0043066|GO:0006521|GO:0051437|GO:0042590|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71220_PI430048170 0.0453477708193148 1.38233439948208 5.56648000807313 5.55330499824205 5.90721672804718 P P P 5.00175781438726 5.23199361190086 5.39386542815623 P P P LNCV6_71220_PI430048170 mRNA TGAAACTGTGGATTACAGCTGGGCCAAGGGAAAAATTTACTGCAGCTGAGGGAAATTAGC NM_016004 RefSeq chr20 + 43590612 43647222 IFT52 51098 "intraflagellar transport 52, transcript variant 1" GO:0006996|GO:0005814|GO:0031514|GO:0070613|GO:0050680|GO:0044292|GO:0072372|GO:0009953|GO:0008022|GO:0001841|GO:0007224|GO:0001947|GO:0005929|GO:0042073|GO:0060271|GO:0030992|GO:0032391|GO:0042733 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129521_PI430048170 0.0270146856088426 0.593512638167466 9.01218114111672 8.70357105792569 9.18303589136938 P P P 9.53100029822894 9.56645440344621 10.0413143373449 P P P LNCV6_129521_PI430048170 mRNA CCTGGTTTTCGTTTGCAATTTGCTTGTGTAAATCAGGTTGTAAAAAGGCAGATAAATTGA NM_001498 RefSeq chr6 - 53497340 53545129 GCLC 2729 "glutamate-cysteine ligase, catalytic subunit, transcript variant 1" GO:2001237|GO:0050662|GO:0046685|GO:0006805|GO:0009408|GO:0006534|GO:0032436|GO:0051409|GO:0044281|GO:0005829|GO:0034641|GO:0043524|GO:0051900|GO:0050880|GO:0008637|GO:0004357|GO:0006750|GO:0009725|GO:0031397|GO:0006979|GO:0043066|GO:0000287|GO:0046982|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63844_PI430048170 0.00687802242030303 0.67927847438426 9.61301294381594 9.51626035042981 9.50151687104707 P P P 10.0109402023165 10.0439134825049 10.241352721422 P P P LNCV6_63844_PI430048170 mRNA ATCCGGATAAAGCAAGAGCCTCTGGACTAAATGGACATATTTCTTATGCAAAAAGGAAAA NM_001142730 RefSeq chr18 - 26454910 26548536 KCTD1 284252 "potassium channel tetramerization domain containing 1, transcript variant 3" GO:0003714|GO:0051260|GO:0005634|GO:0045892|GO:0006351|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135623_PI430048170 0.0500220380071023 1.53996166324766 5.077424962468 5.19467898946239 5.1867235184627 P P P 4.82029062864773 4.28703031218169 4.43188745184215 P P P LNCV6_135623_PI430048170 mRNA CCCCAAAAAATAATTAACTCCTTGTTGAGAATCTTGACTCTCCCCAATAAACGTTCTAAT NM_207416 RefSeq chr9 + 81943499 81950094 SPATA31D3 NA "SPATA31 subfamily D, member 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144674_PI430048170 0.4448870635598430.3153044215104080.386083438804398 0.3967635916170220.451704258866677 A A A 0.3281613256321633.3359687222366 0.383549843846904 A P A LNCV6_144674_PI430048170 mRNA AACACATCATCCATCCAGCTCAAGCACAAGAAACAGATGTGGAGCCTAACTGATAGTGCT NM_001277423 RefSeq chrX - 102460318 102471812 TCP11X2 NA "t-complex 11 family, X-linked 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135597_PI430048170 0.1606990190633311.61325262910199 1.20962429536918 1.57947569008057 0.547615822478921 A A A 0.3410891576360010.425414723403282 0.66221871859975 A A A LNCV6_135597_PI430048170 mRNA TTAAACAAGCCTCCGGAACCTTAAAGGCGGTGTTTCAAGGAAACTCTTATCACTACTATT NM_001914 RefSeq chr18 - 74253291 74292016 CYB5A 1528 "cytochrome b5 type A (microsomal), transcript variant 2" GO:0004129|GO:0006767|GO:0005741|GO:0044281|GO:0046872|GO:0019852|GO:0004033|GO:0016020|GO:0006766|GO:0005789|GO:0016021|GO:0019899|GO:0046686|GO:0070062|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130290_PI430048170 0.7257561956536080.7178970213537240.945854373456338 0.6136405581388591.76826980744043 A A A 0.5525864344193332.61143559081451 0.986880773791711 A P A LNCV6_130290_PI430048170 mRNA

TATTTCGACCTCTCAGTCGAGGCTGGGTCTCTAATATACCTTTCTCTATTAGCCATGCTG NM_001101340 RefSeq
chr19 + 49688684 49690990 ADM5 199800 adrenomedullin 5 (putative) GO:0005576 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131719_PI430048170 0.2548797907667730.8333768909564756.73686119787766
6.11064446157487 6.36975250489359 P P P 6.70487779589021 6.57996390471949
6.78324161792784 P P P LNCV6_131719_PI430048170 mRNA
CCACCCCCACAACCAGTACCAATGTACATAGTAATTGTAATGTTTTAGACTTTACAGAAA NM_001033561 RefSeq
chr17 - 28905252 28951490 PHF12 57649 "PHD finger protein 12, transcript variant 1"
GO:0005515|GO:0001106|GO:0005730|GO:0005634|GO:0000122|GO:0006351|GO:0001222|GO:0016580|GO:0017
053|GO:0005654|GO:0008270|GO:0035091|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143875_PI430048170 0.0778132337638253 0.7463056153260671 1.4667679801118
11.4760943128687 11.409373963155 P P P 11.6240717187852 12.0492130906327
11.9142367437133 P P P LNCV6_143875_PI430048170 mRNA
AAGCTTTATTTATATCATTCCAGTATCAATGCTACACAGTGTTGTCCCGAGCGCCGGGAG NM_007274 RefSeq chr1
- 6264271 6393766 ACOT7 11332 "acyl-CoA thioesterase 7, transcript variant hBACHa"
GO:0052689|GO:0005515|GO:0043005|GO:0016290|GO:0036116|GO:0015937|GO:1900535|GO:0044297|GO:0042
803|GO:0005829|GO:0009062|GO:0005739|GO:0036114|GO:0036042|GO:0005737|GO:0051792|GO:0005654|GO:0
000062|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142613_PI430048170 0.0541217693263592 1.14589673352468 10.5444874791913
10.3863010009541 10.557026774236 P P P 10.2085302247933 10.3556473140783
10.3360248371986 P P P LNCV6_142613_PI430048170 mRNA
TGGGCTTCAGAAGCATCTAAGAAAAGCAGTCATCAATTATAATTAACTTTCAAAGGGCAA NM_014161 RefSeq chr6
+ 159790459 159798429 MRPL1829074 mitochondrial ribosomal protein L18
GO:0070124|GO:0070125|GO:0070126|GO:0003735|GO:0006996|GO:0032543|GO:0005743|GO:0005761|GO:0005
615|GO:0006412|GO:0035928|GO:0005739|GO:0008097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132373_PI430048170 0.2815514196710240.8470331611831091 1.0309936366321
11.0258871377944 11.2462966392473 P P P 11.3788524240361 11.0377169284739
11.5673197268568 P P P LNCV6_132373_PI430048170 mRNA
GAGACCGACCTTGTTCACTCCAGATATTAACTGTATTGAACACAACAAAATACATTGAAT NM_032313 RefSeq chr4
- 56963349 56977660 NOA1 84273 nitric oxide associated 1
GO:0005739|GO:0005515|GO:0032543|GO:0031314|GO:0042254|GO:0003924|GO:0006915|GO:0043457|GO:0005
525|GO:0010941 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143453_PI430048170 0.5154781933705771.22196714708733 7.76938232297959
8.56622697357018 7.63939148097614 P P P 7.3574050885574 7.64091671169638 8.171579478174
P P P LNCV6_143453_PI430048170 mRNA
ATCCGAAAACTAAGCCAGGGAAGCGGTTAACTTATCTTTGCCAACATTTGAGGGAGCCTT NM_024876 RefSeq chr19
- 40691528 40716885 ADCK4 79934 "aarF domain containing kinase 4, transcript variant 1"
GO:0031966|GO:0005886|GO:0004674|GO:0006468|GO:0016021|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_68731_PI430048170 0.0938890740020335 0.8486554824624595.88302547587319
5.74005726571883 6.0281415622514 P P P 6.13937746817756 6.08577666115056
6.14987499215854 P P P LNCV6_68731_PI430048170 mRNA
CACTGGGTCCCTGTTTCCTTTAATCCTTCAGATAAGGAAATAATGACATTTCAACTTAAA NM_017761 RefSeq chr1
+ 23959810 23963459 PNRC2 55629 proline-rich nuclear receptor coactivator 2
GO:0031087|GO:0005515|GO:0006355|GO:0000184|GO:0000932|GO:0005634|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129888_PI430048170 0.3760671850092210.6581801759005270.4155382078957
0.4146928343333930.258244872051858 A A A 1.67723482404977 0.436621871586036
0.397677758605894 A A A LNCV6_129888_PI430048170 mRNA

CACCTGTCTCAGTCTCTAGAGCCCTGAAAAATAAAAACAAACTTATTTTTATCCAGTGAA NM_006507 RefSeq chr2 - 79085022 79088024 REG1B 5968 regenerating islet-derived 1 beta GO:0008283|GO:0030246|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_144036_PI430048170 0.0971525236435240.42249775398859 3.15347431576652 2.6413925033698 1.9218569285911 P A A 2.94483839782807 4.07108059675211 4.34259053744776 P P P LNCV6_144036_PI430048170 mRNA
GGCCTCATGTATAACCAGGGTTTTGAGGATAAAGAACTGTATTTTTAGAACTATCTCATC NM_007345 RefSeq chr18 + 76824159 76970726 ZNF236 7776 zinc finger protein 236 GO:0006355|GO:0005634|GO:0071333|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_142061_PI430048170 0.000386966029104866 1.93418541283123 10.5100929295179 10.4810254149117 10.6044573241979 P P P 9.52059645234028 9.52210375761458 9.69365421679357 P P P LNCV6_142061_PI430048170 mRNA
CTGACTCTTTTGCATTATGATCCAGTTGTGAAACAAAGAGTCCTCTTCGTGGAAAAGAAA NM_004891 RefSeq chr2 + 27771716 27779741 MRPL339553 "mitochondrial ribosomal protein L33, transcript variant 1" GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0005762 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_100808_PI430048170 0.93834770467037 0.9937313981594216.08260789800807 6.14401206304139 6.18150740690392 P P P 6.00399310101703 6.20453717123378 6.2187046210447 P P P LNCV6_100808_PI430048170 mRNA
TTTTGGAGACACAGTGAACACTGCTTCTCGAATGGAGTCTAATGGTCAAGCGCTGAAGAT NM_003995 RefSeq chr9 + 35792408 35809731 NPR2 4882 natriuretic peptide receptor 2 GO:0005886|GO:0042562|GO:1900194|GO:0004383|GO:0005525|GO:0005524|GO:0042802|GO:0035556|GO:0060348|GO:0007165|GO:0016941|GO:0004672|GO:0001503|GO:0051447|GO:0006182|GO:0008217|GO:0004872|GO:0006468|GO:0097011|GO:0016021|GO:0017046|GO:0007168|GO:0007166|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_93621_PI430048170 0.0853775533705822 1.25657681689394 6.76269981190343 7.03773381044788 7.07020969545112 P P P 6.83899129517916 6.54362726353237 6.49425918727686 P P P LNCV6_93621_PI430048170 mRNA
GTGGTATTTACGAGGAAATGAGAGTGAATAAGTCATCTCTAACCTCTCCCAGCCTTTTTT NM_001184889 RefSeq chr15 + 22838640 22868384 NIPA2 81614 "non imprinted in Prader-Willi/Angelman syndrome 2, transcript variant 5" GO:0015693|GO:0005886|GO:0015095|GO:0016021|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_145289_PI430048170 0.1944400631496 3.20828253979723 0.330754876170878 2.31523396839368 2.68118367853307 A A A 0.2673138586459670.617327637400412 0.268802775759704 A A A LNCV6_145289_PI430048170 mRNA
ATCAACCCAATCCTCTACAACCTCATTTCAAAGAAGTACAGAGCGGCGGCCTTTAAACTG NM_001507 RefSeq chr13 + 49220337 49222377 MLNR 2862 motilin receptor GO:0007186|GO:0005886|GO:0005887|GO:0004930|GO:0007586|GO:0016520 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_133276_PI430048170 0.0686686985056849 0.7019833828683111 11.3400797656844 11.3240597543018 11.2804341213415 P P P 11.5417972173804 12.0102673528999 11.8848955646722 P P P LNCV6_133276_PI430048170 mRNA
CGACTAGAACCTTAGGCATTGGGGAGTTTTAGATGGACTAATTTTATTAAAGGATTGTTT NM_002105 RefSeq chr11 - 119093874 119095467 H2AFX 3014 "H2A histone family, member X" GO:0005515|GO:0000790|GO:0005657|GO:0005634|GO:0007283|GO:0045739|GO:0006302|GO:0042393|GO:0000724|GO:0010212|GO:0000786|GO:0070062|GO:0001741|GO:0051321|GO:0000794|GO:0000781|GO:0046982|GO:0006334|GO:0035861|GO:0003677|GO:0006974|GO:0003684|GO:0006281|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_94937_PI430048170 0.8849374788763751.00870378510627 0.2695194103654630.276535831772843
0.454517834568276 A A A 0.3474253949763670.2959165657963140.326979206491223 A A A
LNCV6_94937_PI430048170 mRNA
GTTTCAGACTGTTCAGCCAATGGCTCTTCTACTTTTCCGAAGCAACAGGGATGTGTTTGT NM_001257965 RefSeq
chr1 + 197201461 197478455 CRB1 23418 "crumbs family member 1, photoreceptor morphogenesis
associated, transcript variant 3"
GO:0007009|GO:0005515|GO:0005902|GO:0016324|GO:0007163|GO:0005509|GO:0007267|GO:0005576|GO:0016
021|GO:0042462 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132464_PI430048170 0.2664401738898140.9454390961180821 6.7777793187243
16.6989250526366 16.7948016706969 P P P 16.938209663077 16.8011345049543
16.7712456725755 P P P LNCV6_132464_PI430048170 mRNA
AACATGTCTGTACACCTGTCCCCCTGCTTCAGGGACGTCCAGATCGGTGACATCGTCACA NM_001015 RefSeq chr19
+ 49496364 49499712 RPS11 6205 ribosomal protein S11
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0019843|GO:0006415|GO:0006
412|GO:0001649|GO:0006413|GO:0005829|GO:0006414|GO:0016020|GO:0000184|GO:0022627|GO:0016032|GO:0
005840|GO:0044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53725_PI430048170 0.8490741619428460.9922543755884 5.30906417000853 5.49639044313318
5.38920660927129 P P P 5.4616326172156 5.3628221032072 5.40830375291405 P P P
LNCV6_53725_PI430048170 mRNA
GATTTCCTGCCTGGAACAAGGGACCTGGAGAATGTTTTTGCGTGGGATGATGTGCTGGTC NM_175852 RefSeq chr1
+ 32179743 32198285 TXLNA 200081 taxilin alpha
GO:0019905|GO:0005515|GO:0042113|GO:0005737|GO:0016020|GO:0008283|GO:0030372|GO:0005576|GO:0006
887|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143072_PI430048170 0.00881776920619566 1.92819554288752 9.87740193730367
9.87575193634233 9.85843000553573 P P P 9.03123555092503 8.98457150263495
8.73712738108892 P P P LNCV6_143072_PI430048170 mRNA
TGTAGCCACCAGTTCATAGGTGCCAAGTCAATAAAGCATTGTCCCCCGTCTCTTATAACT NM_080744 RefSeq chr7
- 76389328 76409695 SSC4D 136853 "scavenger receptor cysteine rich family, 4 domains"
GO:0016020|GO:0006898|GO:0070062|GO:0005044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91125_PI430048170 0.0201583515003894 0.64599024823448 4.71239135665591 4.5402372749145
4.79254174549394 P P P 5.07047298174098 5.34366962755532 5.50123174947521 P P P
LNCV6_91125_PI430048170 mRNA
TCAGAGTGTAGCTGGGAAGATGAAGCCCTCATTGGAAAGAAATTCCAGAATTGCATTGAC NM_001271 RefSeq chr15
+ 92900320 93028007 CHD2 1106 "chromodomain helicase DNA binding protein 2, transcript variant
1"
GO:0006357|GO:0005730|GO:0005634|GO:0060218|GO:0003677|GO:0005524|GO:0006351|GO:0006974|GO:0043
231|GO:0042393|GO:0004003|GO:0007517|GO:0005654|GO:0001046|GO:0032508|GO:0070062|GO:0016568 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141876_PI430048170 0.3056320742778090.85728614603141 0.395077244680778
0.4022089939664180.421426014218056 A A A 0.5371822375652550.903247715712938
0.396426589491771 A A A LNCV6_141876_PI430048170 mRNA
CATGTTTTTTGTGTGTGTCATGTATTGTAAGTTGTAATATCTGTAGGAGTGAGTTGGACA NM_024744 RefSeq chr2
+ 202912217 202986485 CARF 79800 "calcium responsive transcription factor, transcript variant 2"
GO:0061400|GO:0001077|GO:0035865|GO:0003700|GO:0071277|GO:0005730|GO:0005654|GO:0005634|GO:0000
978|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134911_PI430048170 0.3699800672226438.6525617968308 0.874029684782064
4.91396311577597 0.273996409630822 A P A 0.2541971566125270.270388523196851
0.52303948040395 A A A LNCV6_134911_PI430048170 mRNA
AGCAAAGCCATGCATGGCAACAAGAAATCAGGGTATCAAAGAGATTTCATATCTACCCAA NM_175882 RefSeq

chr17_KI270908v1_alt + 547010 549193 SPPL2C 162540 signal peptide peptidase like 2C
GO:0031293|GO:0005789|GO:0071556|GO:0071458|GO:0006509|GO:0004190|GO:0042803 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_61880_PI430048170 0.10460897794537 1.41105451705347 4.33851165371449 4.63362388621008
4.97726396979988 P P P 4.23893420359535 3.93099589579848 4.3304519148816 P P P
LNCV6_61880_PI430048170 mRNA
ACAACAAAAAAGGCAGGAAACAGGAAGAGAGGATGGTGGCACATTGGCTAAAGGCTCTTT NM_001128610
RefSeq chr15 + 50424376 50501083 USP8 9101 "ubiquitin specific peptidase 8, transcript variant 2"
GO:0071108|GO:0005515|GO:0017124|GO:0016579|GO:0004843|GO:0005794|GO:0001669|GO:0000281|GO:0008
283|GO:0030496|GO:0007265|GO:0005829|GO:0004197|GO:0005737|GO:0070536|GO:0061136|GO:0031313|GO:0
043161|GO:0005654|GO:0007032|GO:0019897|GO:0005769 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131758_PI430048170 0.5686857208262151.04774285613054 9.81858177806357
9.60789744652491 9.51508225760486 P P P 9.62311538440504 9.61240263241898
9.51888916009742 P P P LNCV6_131758_PI430048170 mRNA
CATAAAGTCACTGGGGCTAGCTAAACAATAAAGAGTTTATTGTGAGAACATGGGGAAAAA NM_015324RefSeq chr11
- 6599913 6603650 RRP8 23378 "ribosomal RNA processing 8, methyltransferase, homolog (yeast)"
GO:0005515|GO:0010467|GO:0005886|GO:0006364|GO:0005730|GO:0033553|GO:0005634|GO:0008757|GO:0035
064|GO:0032259|GO:0071158|GO:0006351|GO:0005737|GO:0072332|GO:0000183|GO:0045814|GO:0040029|GO:0
005654|GO:0042149|GO:0046015|GO:0005677|GO:0016568 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_129223_PI430048170 0.65955468413079 1.04068499085677 10.8763002702415
10.7072821920461 10.6186392364196 P P P 10.8658668904906 10.6375423248831
10.5160969189489 P P P LNCV6_129223_PI430048170 mRNA
AAATAGAGCTGCCAGAGGTTCCCTCCGAGCCCCTTCCTGAGAAGATCCCAGAAAACGTCC NM_024591RefSeq chr17
+ 80991840 81000133 CHMP6 79643 charged multivesicular body protein 6
GO:0005515|GO:0006997|GO:0019058|GO:0015031|GO:0005829|GO:0000920|GO:0047485|GO:0007034|GO:0016
020|GO:0016197|GO:0031902|GO:0061024|GO:0016032|GO:0007080|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_2013_PI430048170 0.0288743212154990.3043989576296446.08364153829986 6.21932443283672
6.33563870316923 P P P 7.27239402055748 7.99304631008577 8.33773294287064 P P P
LNCV6_2013_PI430048170 mRNA
CAATTACGCTGTATTTTAACACGATGTATGTCTGTTTTTGTGGTGCTCTAGTGGTAAATA NM_001135599 RefSeq
chr1 + 218345333 218444619 TGFB2 7042 "transforming growth factor, beta 2, transcript variant 1"
GO:0005515|GO:0008219|GO:0030308|GO:0030307|GO:0001654|GO:0042704|GO:0009790|GO:0005615|GO:0042
803|GO:0031069|GO:0005114|GO:0007507|GO:0043525|GO:0004702|GO:0030198|GO:0007411|GO:0030199|GO:0
043025|GO:0007179|GO:0001942|GO:0023014|GO:0030593|GO:0030168|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134850_PI430048170 0.90820873684251 1.06256083585019 0.8030739400417111.7572069152197
0.838369463361415A A A 0.6501657623712511.30194266782271 1.30525993905737 A A A
LNCV6_134850_PI430048170 mRNA
TTTTCTCTCCTATGACTGTGGCAGTGACAAGGTCTTATCTATGGGTCACCTAGAAGAGCA NM_024518RefSeq chr6
- 150064606 150069066 ULBP3 79465 UL16 binding protein 3
GO:0002474|GO:0030101|GO:0005886|GO:0046703|GO:0042267|GO:0050776|GO:0042605|GO:0016032|GO:0046
658 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137281_PI430048170 0.3333217895810291.25904606419629 3.91862014453992
4.13558343486126 3.34220422167997 P P P 3.57148112082065 3.60646191008487
3.31580777022607 P P P LNCV6_137281_PI430048170 mRNA
ATGGGAAAAAGGACTTCCCTAGAAGTGAGTCTTGGGGAGTTGGGGGGAGAAAAGTGTCGA NM_001009812

RefSeq chr2 - 74497516 74503316 LBX2 85474 "ladybird homeobox 2, transcript variant 2"
GO:0006355|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145684_PI430048170 0.11875061374812 0.6370668685664584.56196902414575
5.29431674009905 5.47814045243834 P P P 5.479428640038 5.90620310786781
6.00128380291352 P P P LNCV6_145684_PI430048170 mRNA
GTCTTTTTGGGAAGTAGTTAAGATATGCCTGCTATCTTTAACTTTGGAGGTAGTATCAAA NM_018132RefSeq chr6
+ 49463382 49493107 CENPQ 55166 centromere protein Q
GO:0034080|GO:0006334|GO:0005654|GO:0015629|GO:0000278|GO:0000775|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134234_PI430048170 0.16382921908789 0.9277733722450191 0.3825055081817
10.4566549024954 10.3728786601149 P P P 10.4130522521958 10.5305199729024
10.5888777882957 P P P LNCV6_134234_PI430048170 mRNA
GTGCTGAGCGCTGTATCCCTGAATATAGTTTATTTTTTCTACATTTGAATTCTGTTGTAG NM_017588RefSeq chr9 +
134136087 134159972 WDR5 11091 "WD repeat domain 5, transcript variant 1"
GO:0005515|GO:0006325|GO:0035948|GO:0005634|GO:0042800|GO:0006351|GO:0043981|GO:0001501|GO:0035
097|GO:0043982|GO:0043966|GO:0043984|GO:0071339|GO:0048188|GO:0043996|GO:0043995|GO:0000123|GO:0
005671|GO:0046972|GO:0005654|GO:0051568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142896_PI430048170 0.9747661202227010.9856290981636414.4594333673575
4.40833053341787 4.44596832394259 P P P 4.62529026686564 4.56480839257635
4.14002889749965 P P P LNCV6_142896_PI430048170 mRNA
CCCTAGTTTCTTCCTGTGAACAACAGAGGTAATAAATAAACTCTGACATCGGTTGAACAT NM_001198961 RefSeq
chr1 - 52895909 52921774 ECHDC2 55268 "enoyl CoA hydratase domain containing 2, transcript
variant 1" GO:0005739|GO:0006631|GO:0016829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127843_PI430048170 0.7146187883319781.20289395819367 0.262608677857409
0.2723132919377511.43642145840889 A A A 0.7888282332137750.349929599940248
0.320936853774474A A A LNCV6_127843_PI430048170 mRNA
TTCAGGGCAAGCACACCAAGAGCCAGGAACTGCAGAACATGGTGGAGCAGATCTCGCTGT NM_001193282
RefSeq chr4 + 2418944 2462963 CFAP99 NA cilia and flagella associated protein 99 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_144251_PI430048170 0.2004064163251241 3.8421274767076 0.3364148718602935.2585558584376
4.04019077953438 A P P 0.3436878058895020.5746268070114340.364027747125606A A A
LNCV6_144251_PI430048170 mRNA
AGCTGAGTTCCTGCAGTACTTGTTGTCTGTACCACTCACCTGGCACTTATTTATTATTGTNM_001286633 RefSeq
chr6_GL000256v2_alt + 1435046 1447667 TRIM40 135644 "tripartite motif containing 40, transcript
variant 1"
GO:0005515|GO:0030308|GO:0045116|GO:0042177|GO:0008385|GO:0032088|GO:0008270|GO:1900181 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135735_PI430048170 0.3431928897006550.8070772266074215.36697853489588
5.33946333254878 5.55931442259772 P P P 5.33158609753165 5.65846705044341
6.10746808007602 P P P LNCV6_135735_PI430048170 mRNA
GAATCAGTGCTAGAGGGAACAGATTGTGAATTTTGTTTACAGCATCCAATATTTGGATTT NM_017633RefSeq chr6
- 81745729 81752711 FAM46A 55603 "family with sequence similarity 46, member A"
GO:0010468|GO:0030193 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141428_PI430048170 0.0088904036614091 0.7279060136881388.16358569457291
8.17542879082226 8.16155862239768 P P P 8.53710577661059 8.64860858611407
8.68532821145572 P P P LNCV6_141428_PI430048170 mRNA
GAAGGAGTGGACCCGCTGGTCTTTGGCATTTTGTATTTAGAATTATTCTAACTTTATACA NM_152558RefSeq chr7
+ 2558971 2614734 IQCE 23288 "IQ motif containing E, transcript variant 1" GO:0072372 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_84787_PI430048170 0.1406440495410740.7884293328489596.20207921145024 5.71630275311723
6.17371977116324 P P P 6.21646049156684 6.41544829891944 6.52207898178923 P P P
LNCV6_84787_PI430048170 mRNA
ATGGAACTAACTTTCCTGGACTGTGTTTCGCATTCGGCGTTATCTGGAAAGTGGACTGAA NM_032294RefSeq chr17
- 3860322 3893043 CAMKK1 84254 "calcium/calmodulin-dependent protein kinase kinase 1, alpha,
transcript variant 1"
GO:0005515|GO:0005516|GO:0007268|GO:0006468|GO:0005634|GO:0004683|GO:0005524|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101019_PI430048170 0.0284347874711976 0.7612561538379993.88853561573461
4.13151389614615 4.1837713994121 P P P 4.33678276911444 4.48949776508526
4.56571495864803 P P P LNCV6_101019_PI430048170 mRNA
TAGCCCTGGGCAGCCTTTTCCATGGCCTGGATGTGGTATTCCTTCAGCCAACCTCCTTGA NM_006122RefSeq chr15
+ 90904189 90922585 MAN2A2 4122 "mannosidase, alpha, class 2A, member 2"
GO:0004572|GO:0000139|GO:0030246|GO:0008270|GO:0016021|GO:0044267|GO:0016799|GO:0043687|GO:0018
279|GO:0006013 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139109_PI430048170 0.3215346959111661.10249785879409 5.43495759150624
5.60107867344464 5.7492617924679 P P P 5.29185793240085 5.50309782138762 5.5706658210488
P P P LNCV6_139109_PI430048170 mRNA
CCAGACTTGTATACTGGCTGAATATCAGTGCTGTTTGTAATTTTTCACTTTGAGAACCAA NM_017414RefSeq chr22
+ 18149990 18177395 USP18 11274 ubiquitin specific peptidase 18
GO:0005515|GO:0004197|GO:0019785|GO:0016579|GO:0060337|GO:0004843|GO:0060338|GO:0061136|GO:0019
221|GO:0043161|GO:0005634|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134344_PI430048170 0.0119850348338871 0.3578651448247020.286440467234717
0.2947918968936 0.461688151621885A A A 1.90206161309489 1.43325539655997
2.08615024046947 A A A LNCV6_134344_PI430048170 mRNA
AAAGAAAGAGTTGTCTCAACTCCTTGGTACAGGGTTCATTCAAACCCCCAAGCTGTGAGA NM_181501RefSeq chr5
+ 52788301 52953655 ITGA1 3672 "integrin, alpha 1"
GO:0005515|GO:0043005|GO:0008285|GO:0005886|GO:0005518|GO:0046872|GO:0000187|GO:0043525|GO:0006
936|GO:0007411|GO:0030198|GO:0042311|GO:0034665|GO:0043204|GO:0070062|GO:0008305|GO:0001669|GO:0
009986|GO:0019903|GO:0030593|GO:0045178|GO:0005102|GO:0042059|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_61114_PI430048170 0.4083128518836660.6770451831996110.2932147479258181.40578791802577
0.391831862745555A A A 1.37541047492198 0.3911589545651411.90898297308292 A A A
LNCV6_61114_PI430048170 mRNA
AAGGAACCAAGGAGAAAATTCAGAAGGAAAGAAAAAATTGCCTCTGCAGGTGTGCGAGCA NM_001249RefSeq
chr14 - 73966477 74019323 ENTPD5957 ectonucleoside triphosphate diphosphohydrolase 5
GO:0046034|GO:0004382|GO:0008283|GO:0005783|GO:0045134|GO:0051084|GO:0016049|GO:0006487|GO:0045
821|GO:0014066|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138914_PI430048170 0.0741592709175085 0.5286080851621964.87150724323426
3.9989105042452 4.83214257204133 P P P 4.98888596844784 5.65009632516074
5.84647451116212 P P P LNCV6_138914_PI430048170 mRNA
GTCTCATTTTAGTGACTCCTAAGGCTAGTCCTTTTATAAACAACTTTTTCTGACATAGCA NM_001170553 RefSeq
chrX + 108044969 108079184 VSIG1 340547 "V-set and immunoglobulin domain containing 1,
transcript variant 1" GO:0003382|GO:0030277|GO:0005886|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128418_PI430048170 0.383837182821894 0.908840982901767 12.8679742720601
12.7219101917821 13.0228780414838 P P P 12.8116716116618 13.0266733984724
13.1802592793506 P P P LNCV6_128418_PI430048170 mRNA
GCCACAGATACAGAATCTGTATTGTTCTTACTGAAACACAGCATGGAATTAACATTAAAC NM_006761 RefSeq

chr17_KI270862v1_alt - 286565 342288 YWHAE 7531 "tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon, transcript variant 1"
GO:0051219|GO:0005515|GO:0030424|GO:0021987|GO:0042826|GO:0060306|GO:0015459|GO:0006605|GO:0086091|GO:0050815|GO:0005829|GO:0035556|GO:0005739|GO:0034605|GO:0003064|GO:1900740|GO:0000086|GO:0061024|GO:0016032|GO:0030659|GO:0070062|GO:0042470|GO:0048011|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144775_PI430048170 0.198070286632436 1.25969337344431 3.25591590772516 3.08056847270338 3.31770711660488 P P P 3.1304469533363 2.49182321620296 2.96941742130854 P A P LNCV6_144775_PI430048170 mRNA
AGACTTAAGATGAAAGCAAATGATTCAGCTCCCTTATACCCCCATTAAATTCACTTTCAA NM_003125 RefSeq
chr1 + 153031202 153032900 SPRR1B 6699 small proline-rich protein 1B
GO:0005737|GO:0018149|GO:0008544|GO:0030216|GO:0005198|GO:0031424|GO:0030674|GO:0001533|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144276_PI430048170 0.708323809593157 0.976561740285528 0.272824861788601 0.482673462916769 0.325739321327157 A A A 0.498560992347992 0.391035557069022 0.295470134076805 A A A LNCV6_144276_PI430048170 mRNA
TAGCAAGTTTGCAAAAGCTGTGGAAGAAAGCCTCATTGACATGAGAGACCTCTGCAGTCT NM_001142934 RefSeq
chr10 + 49614036 49665104 CHAT 1103 "choline O-acetyltransferase, transcript variant S"
GO:0030424|GO:0004102|GO:0043179|GO:0007268|GO:0005634|GO:0044281|GO:0007274|GO:0016358|GO:0007269|GO:0005829|GO:0005739|GO:0005737|GO:0007517|GO:0007529|GO:0043025|GO:0007628|GO:0007622|GO:0042136|GO:0006644|GO:0046474|GO:0006656 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140594_PI430048170 0.8074818922592 0.983204525466815 7.10056528011773 6.67016695977448 6.87545059534204 P P P 6.94238317110559 6.87118152227819 6.93698078859669 P P P LNCV6_140594_PI430048170 mRNA
GGAAAATGAATCATTTGGACTCTTCAATGAAATGGAGTGAGCCCAGGAGAGCTCAGCCAA NM_152267 RefSeq
chr22 + 31160151 31207019 RNF185 91445 "ring finger protein 185, transcript variant 1"
GO:0016567|GO:0016874|GO:0006914|GO:0005789|GO:0008270|GO:0005741|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127466_PI430048170 0.0337208960445562 0.764665490434586 10.312588564045 10.063382834059 10.1122035779636 P P P 10.3825055081817 10.7003469457055 10.561381193783 P P P LNCV6_127466_PI430048170 mRNA
ATACAAACCTACCAAAATGGAATAAAAGGCTTGAAGCTGTGGCCTGAGTGCCTCACTGGA NM_005438 RefSeq
chr11 - 65892135 65900526 FOSL1 8061 "FOS-like antigen 1, transcript variant 1"
GO:0005515|GO:0043005|GO:0042542|GO:0008284|GO:0060674|GO:0003700|GO:0008285|GO:0006366|GO:0005634|GO:0051591|GO:0005829|GO:0051091|GO:0006935|GO:0031668|GO:0007612|GO:0034097|GO:0051412|GO:0007565|GO:0043065|GO:0000977|GO:0006357|GO:0042493|GO:0009615|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130023_PI430048170 0.434499064035949 9.10844340804107 0.26322841523387 5.01704749157327 0.342928929159419 A P A 0.392703372222766 0.321674292888317 0.337270006199129 A A A LNCV6_130023_PI430048170 mRNA
GCTTTCCATAAATTCATTGCTTATGTAAAGTTTTGTCCTGTTGTGACTATGCTGTTGAAC NM_198152 RefSeq chr3 - 191267154 191330536 UTS2B 257313 urotensin 2B
GO:0042312|GO:0001664|GO:0005179|GO:0008217|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140420_PI430048170 0.0100170494168169 1.32691500280349 11.9517778550782 11.9977939423881 11.7805984090859 P P P 11.5002074288465 11.6024600196863 11.4055075874299 P P P LNCV6_140420_PI430048170 mRNA
AAATGCGACGAACCTCTGAGCATCCTGGTGAGGAATAACAAGGGCCGCAGCAGCACCTAC NM_005101 RefSeq

chr1 + 1013466 1014539 ISG15 9636 ISG15 ubiquitin-like modifier
GO:0005515|GO:0032020|GO:0019221|GO:0005576|GO:0005829|GO:0032649|GO:0051607|GO:0060337|GO:0045
648|GO:0045087|GO:0019941|GO:0016032|GO:0031386|GO:0034340|GO:0031397|GO:0032480|GO:0042742|GO:0
045071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129905_PI430048170 0.125552522217536 0.722160248474378 14.357191033708
13.7331512919702 13.7344377840421 P P P 14.6223809501157 14.3488747396466
14.3375280605846 P P P LNCV6_129905_PI430048170 mRNA
GCCAGTTAAGCACAAAGGAAAACATTTCAATAAAGGATCATTTGACAACTGGTGGAAAAA NM_000976 RefSeq
chr9 - 127447673 127451432 RPL12 6136 ribosomal protein L12
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0006415|GO:0006412|GO:0006
413|GO:0005829|GO:0006414|GO:0000184|GO:0016020|GO:0016032|GO:0022625|GO:0044267|GO:0005925|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131056_PI430048170 0.132519605055682 1.463709698072 0.909097832683836
1.05807977950643 1.64927951916407 A A A 0.540999487397021 0.909463990653806
0.599483321157712 A A A LNCV6_131056_PI430048170 mRNA
ATAGATCAAATGCCCTAAAATGTAGTGACCCGTGAAAAGGACAAATAAAGCAATGAATAC NM_054023 RefSeq
chr5 + 147878710 147882193 SCGB3A2 117156 "secretoglobin, family 3A, member 2"
GO:0071682|GO:0005576|GO:0006898 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_130393_PI430048170 0.199413534787064 1.14607765183181 13.2240976697337
13.3276549950793 13.5301908678201 P P P 13.142203685908 13.0173574331304
13.3317560592411 P P P LNCV6_130393_PI430048170 mRNA
AAACATAAGGATGTTTCAGTTCCTCCATTTAACAGATATGAAGAGCATTTTAAGAGGTGC NM_001867 RefSeq
chr5 + 86617966 86620766 COX7C 1350 cytochrome c oxidase subunit VIIc
GO:0022904|GO:0005739|GO:0004129|GO:0005743|GO:0044281|GO:0016021|GO:0006091|GO:0055085|GO:0044
237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141264_PI430048170 0.0197042001900012 1.33393101324663 8.41414392104978
8.14359834787228 8.27509864132027 P P P 7.70595440933062 7.94072194808274
7.93937626289668 P P P LNCV6_141264_PI430048170 mRNA
GCTCCTACAAATCAGTAACATGAAGAACACTCAAAAATTGGCAAATGTCATCAGTGTTTT NM_001080843 RefSeq
chr22 - 23957413 23961181 GSTT2B NA glutathione S-transferase theta 2B (gene/pseudogene)
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145307_PI430048170 0.482989151540327 1.02703645281394 0.491479443364006
0.55751057167203 0.493306258859967 A A A 0.562979104682429 0.426280859114995
0.434444084633922 A A A LNCV6_145307_PI430048170 mRNA
GAAAGCACCGACAATCTTTGATTACTGAAAGTATTTAAATGTTTGCCAAAAACAACAGCC NM_000683 RefSeq
chr4 + 3766568 3768526 ADRA2C 152 adrenoceptor alpha 2C
GO:0005515|GO:0005886|GO:0032811|GO:0007267|GO:0051379|GO:0044281|GO:0031694|GO:0042803|GO:0005
737|GO:0045907|GO:0070473|GO:0032148|GO:0043679|GO:0071883|GO:0007565|GO:0046982|GO:0035625|GO:0
030168|GO:0010700|GO:0004938|GO:0006112|GO:0007186|GO:0050796|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_93808_PI430048170 0.22992958295496 1.26227514133128 7.62101959376992
7.80432229200708 8.03355404956236 P P P 7.05374889284509 7.71895497742106
7.62260633269601 P P P LNCV6_93808_PI430048170 mRNA
TTCATGCATTTGATCATTGTCGTGCCCATGTCGACTGGTTCACCAACATCAGACATTTGG NM_033276 RefSeq
chr12_GL383550v2_alt - 144645 160253 XRCC6BP1 91419 XRCC6 binding protein 1
GO:0004677|GO:0006508|GO:0006468|GO:0005958|GO:0006303|GO:0004222|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136145_PI430048170 0.467215602377697 0.728885612429019 0.324070002684575

0.298653428377915 0.268843967399691 A A A 0.253687065079773 1.41779185854912
0.255773333952723 A A A LNCV6_136145_PI430048170 mRNA
CCTTACACTGCCACCAGCAAGGATAAACATGTCCATCTTGCCCGTATTGGGAATTATCAT NM_032287 RefSeq
chr22 - 44492569 44498125 LDOC1L 84247 "leucine zipper, down-regulated in cancer 1-like" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99790_PI430048170 0.649156488818115 0.979097156453376 0.487986883863095
0.500961607325008 0.358536895361528 A A A 0.396073429089418 0.53638302405638
0.506948179945479 A A A LNCV6_99790_PI430048170 mRNA
TGACTTCCCAATTGCCCTTGAGCATGATTCGAAAGGAAACAAAATCGCCTGGAAGTTGGT NM_152410 RefSeq
chr6 + 162727131 163315492 PACRG 135138 "PARK2 co-regulated, transcript variant 1"
GO:0043005|GO:0001664|GO:0043014|GO:0097225|GO:0051879|GO:0051087|GO:0048487|GO:0007286|GO:0003
779|GO:0005634|GO:0031982|GO:0044297|GO:0005829|GO:0005739|GO:0031072|GO:0060548|GO:0030544|GO:0
034620|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133005_PI430048170 0.534453069927252 0.904439628188317 0.497968939925304
0.341038417477817 0.436761504736685 A A A 0.885582043106734 0.360734712693448
0.40808356775367 A A A LNCV6_133005_PI430048170 mRNA
CATGGTGAAAATCTAAGTGGAGAGGTTCTTTGTGGTTAACTTATACTATTGAGTGATGCA NM_001076678 RefSeq
chr19 + 21397118 21427494 ZNF493 284443 "zinc finger protein 493, transcript variant 3"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_139756_PI430048170 0.369957523620614 0.872056740220849 2.50712799279731
1.86694713506456 2.14435647220013 A A A 2.22385997753826 2.45958746500183
2.48522998891932 A A P LNCV6_139756_PI430048170 mRNA
CACTTTGGAGATAGACCCTATGAATGTAAACATGGGATAAAGCCTTAAGTAGTTTCAATT NM_001080493 RefSeq
chr19 - 11721264 11739009 ZNF823 55552 "zinc finger protein 823, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_135252_PI430048170 0.0327954376013166 2.41946234634343 2.08679519988514
3.08026572911866 2.7045710765855 A P A 0.993321357897002 1.18314600777748
1.8813691987343 A A A LNCV6_135252_PI430048170 mRNA
AGATCTGGTTTCAGAACCGCCGAGTGAAGCACAAGAAGGAGGGCAAGGGCAGCAACCATC NM_145657 RefSeq
chr13 + 27792642 27793952 GSX1 219409 GS homeobox 1
GO:0043565|GO:0021984|GO:0001077|GO:0045944|GO:0005634|GO:0048663|GO:0021854|GO:0000978|GO:0021
527|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139758_PI430048170 0.0766059255656575 1.37824520214754 4.07108059675211
3.91414766344761 4.0957515955923 P P P 3.84898958664898 3.4653684706133
3.3339770900622 P P P LNCV6_139758_PI430048170 mRNA
TGCTGTTAATCAGGACTTTATTAAATAAAAACATTGGCTCTTCCAACCCCCACTGCCAAA NM_207303 RefSeq
chr10 + 115093364 115948998 ATRNL1 26033 "attractin-like 1, transcript variant 1"
GO:0007186|GO:0030246|GO:0007275|GO:0004872|GO:0016021 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_131884_PI430048170 0.270936532978669 2.05016849138047 2.07014988934613
0.35045900101453 2.11657219573478 A A A 0.460161350307487 1.04515869082474
0.428805953128883 A A A LNCV6_131884_PI430048170 mRNA
CTCCTTACAAATATGATACTCTTTAGTGTTAAGCTAAGGCATTGATTCATGTATCTGTCC NM_020962 RefSeq
chr15 - 65381486 65423072 IGDCC4 57722 "immunoglobulin superfamily, DCC subclass, member 4"
GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131666_PI430048170 0.04393500127845 1.78069492879049 4.9329461227044
5.20034623025123 4.99542346309324 P P P 3.7604310358341 4.46089270021594

4.33209003192187 P P P LNCV6_131666_PI430048170 mRNA
GGGGGCCAGATTCTGTGTGTTTCTCTAACCTCTTTGTAAATAAATGCACAGTGTAACATA NM_145056 RefSeq
chr19 - 46647611 46661138 DACT3 147906 "dishevelled-binding antagonist of beta-catenin 3,
transcript variant 1"
GO:0030308|GO:0005737|GO:0070097|GO:0005080|GO:0030178|GO:0010719|GO:0051018|GO:0016055|GO:0090
090|GO:0035414|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68655_PI430048170 0.00397609352608743 0.652197945100355 7.54188158934051
7.36604691010791 7.27862167304989 P P P 7.88975754718937 8.04371678628953
8.10694246216882 P P P LNCV6_68655_PI430048170 mRNA
AAGCCAAGGGAAGGGACAGGGAAGTCACGAAGGGCACTACCTTTTTCAGAGAAGAAGAAA NM_194278 RefSeq
chr14 - 73715121 73760298 ELMSAN1 91748 "ELM2 and Myb/SANT-like domain containing 1,
transcript variant 1" GO:0006355|GO:0003682|GO:0005654|GO:0003677|GO:0006351 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_143924_PI430048170 0.858772893356657 0.958654092712526 3.61025090182125
3.55913548022425 4.0885732889643 P P P 3.49872828228327 3.712583491993
4.19908926045404 P P P LNCV6_143924_PI430048170 mRNA
CCTGTTTCACAGTTGATTATACTTCATGCTGTTTTCCAGCATGGTATTATTAAGGGATTT NM_003082 RefSeq chr14
+ 61762356 61796428 SNAPC1 6617 "small nuclear RNA activating complex, polypeptide 1, 43kDa"
GO:0010467|GO:0006355|GO:0005654|GO:0006383|GO:0003677 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_128684_PI430048170 0.00748362357049147 1.52106591525773 8.27260428197686
8.27962319345601 8.03122645143508 P P P 7.73037559609492 7.60982525067871
7.42537593739286 P P P LNCV6_128684_PI430048170 mRNA
CTGGGCACTGTGGTTTTATTTCCTAATTGATTTAAGAAATAAACCTGAAGACCGTCAAAA NM_198580 RefSeq
chr19 + 17470443 17506168 SLC27A1 376497 "solute carrier family 27 (fatty acid transporter),
member 1"
GO:0006646|GO:0001579|GO:0001676|GO:0071902|GO:0005886|GO:0005783|GO:0033211|GO:0009409|GO:0044
281|GO:0042803|GO:0000166|GO:0032049|GO:0031957|GO:0006654|GO:0006655|GO:0044255|GO:0006656|GO:0
015245|GO:0032868|GO:0006661|GO:0071072|GO:0055085|GO:0004467|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_95389_PI430048170 0.0099490012340564 0.484493440911225 2.69281850729289
2.33121821757094 2.84371704805536 A A A 3.3337019886415 3.82872668865689
3.83370950213677 P P P LNCV6_95389_PI430048170 mRNA
GCTTTCAATGTTGAGTGGCCTTTTATTAACATGTTTATGGTACTGCATAGATACGGGTAT NM_007375 RefSeq chr1
+ 11012621 11025492 TARDBP 23435 TAR DNA binding protein
GO:0008380|GO:0005515|GO:0006397|GO:0034976|GO:0003700|GO:0006366|GO:0035061|GO:0003723|GO:0001
205|GO:0005634|GO:0043922|GO:0042802|GO:0005726|GO:0005737|GO:0003690|GO:0016607|GO:0000166|GO:0
045944|GO:0032024|GO:0005654|GO:0003730|GO:0070935 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_134327_PI430048170 0.434690591354893 0.952547353211591 0.547908115154378
0.473178886441643 0.291116585920954 A A A 0.525521686065466 0.521123288729693
0.48761857318413 A A A LNCV6_134327_PI430048170 mRNA
CGGACGGTTAGCTTTGGAAAAAATGACTTGATTAATCTGATTCGCCAAATAAATAGATTC NM_005683RefSeq chr2
- 230907327 230925226 GPR55 9290 G protein-coupled receptor 55
GO:0007186|GO:0005886|GO:0005887|GO:0004930|GO:0045453|GO:0035025|GO:0045671|GO:0070374|GO:0007
202|GO:0004949 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137196_PI430048170 0.36320535008694 0.895270698799871 11.6764454177666
11.9330774161239 11.8273906080072 P P P 11.7378702353084 12.1661412139524 11.991382482751
P P P LNCV6_137196_PI430048170 mRNA

ATTTACGAGGAGACCCGCGGTGTGCTGAAGGTGTTCCTGGAGAATGTGATTCGGGACGCA NM_003548 RefSeq chr1 - 149860763 149861159 HIST2H4A NA "histone cluster 2, H4a" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130256_PI430048170 0.13380408457727 0.6316780764519567.23542822229354 6.87630877418562 7.45110957000801 P P P 7.30012006290183 7.93690270322463 8.22358931329442 P P P LNCV6_130256_PI430048170 mRNA
GGCATGTTCTTTTCTGTTTGTCTATTAATGGGCCTGCTTCTTAGCAATATTAGAATGTTT NM_052905 RefSeq chr2 + 152335236 152649834 FMNL2 114793 formin-like 2
GO:0005737|GO:0030866|GO:0022604|GO:0007010|GO:0017048|GO:0003779 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127496_PI430048170 0.2306915154855520.5446573864603690.351213324998621 0.3641460038725072.19818703749823 A A A 1.91543217562493 2.73597928323471 1.43103453035161 A P A LNCV6_127496_PI430048170 mRNA
CCTAGGAAAGAGGCTGTTATTCTCATTTATTTTGCTATACAGGATGTAATAGGTCAGGTA NM_001284259 RefSeq chr10 + 89701589 89774943 KIF20B 9585 "kinesin family member 20B, transcript variant 1"
GO:0008017|GO:0005813|GO:0007088|GO:0050699|GO:2001222|GO:0005874|GO:2000114|GO:0005730|GO:0005819|GO:0001843|GO:0003777|GO:0005524|GO:0005737|GO:0007067|GO:0070201|GO:0008152|GO:0005654|GO:0007050|GO:0016887|GO:0051301|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134185_PI430048170 0.0956508002495572 0.5788146844617738.25170552388801 8.1118061632386 8.44104311085742 P P P 8.57116388105705 8.9713539602527 9.49719196403792 P P P LNCV6_134185_PI430048170 mRNA
CTGGCTGGACAGTGTTCTATTAACTCATTGAATGTGTTTCCTTTGTCTTGTGTTAATAAA NM_173602 RefSeq chr12 + 50504984 50748667 DIP2B 57609 DIP2 disco-interacting protein 2 homolog B (Drosophila)
GO:0008150|GO:0003674|GO:0005737|GO:0016020|GO:0008152|GO:0005634|GO:0003824|GO:0070062|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101340_PI430048170 0.1761408133632690.4505079552599960.441697707785225 2.55375131343213 2.40645295046672 A A A 3.39339922156627 3.53343906926043 2.5184005147346 P P P LNCV6_101340_PI430048170 mRNA
GGCATTCAAGTCTTGCTAAACATAAGATAATTCACACTGGAGAGAAACCCTACAAATGTG NM_033273 RefSeq chr7 - 57119618 57139864 ZNF479 90827 zinc finger protein 479
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137977_PI430048170 0.38990324891372 1.1788554981285 4.68288000597836 4.18897595196439 4.42923922990837 P P P 4.45618529327045 4.32900396487719 3.75352645236238 P P P LNCV6_137977_PI430048170 mRNA
TGTCACCAAGGACACAGCGTCCGACTCCCCTGCAGGAATTGACAACCCTGTGTTTTCTCC NM_004174 RefSeq chr5 - 473218 524434 SLC9A3 6550 "solute carrier family 9, subfamily A (NHE3, cation proton antiporter 3), member 3, transcript variant 1"
GO:0005515|GO:0015385|GO:0005886|GO:0009986|GO:0031526|GO:0030165|GO:0055085|GO:0006885|GO:0005903|GO:0016324|GO:0035725|GO:0016021|GO:0070062|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111132_PI430048170 0.4388413876424770.9555929951788736.89063291527416 6.77922872258583 7.01736353486138 P P P 6.97106479865405 7.01494866823622 6.9055643297732 P P P LNCV6_111132_PI430048170 mRNA
GTTGGCAAAATTTCCAAGCACTGGACTGGAATTTTGAGAGAGGCATTTACAGACGCTGAT NM_021105 RefSeq chr3 - 146515179 146544841 PLSCR1 5359 phospholipid scramblase 1
GO:2000373|GO:0005515|GO:0017121|GO:0005154|GO:0017124|GO:0005886|GO:0017128|GO:0035456|GO:0005634|GO:0033003|GO:0005829|GO:0051607|GO:0042609|GO:0045944|GO:0070062|GO:0045071|GO:0005794|GO:0005509|GO:0005730|GO:0006915|GO:0030168|GO:0006953|GO:0003677|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_67547_PI430048170 0.5370025350844690.8147519221706610.4105988995425860.38943263121328
1.26246803687306 A A A 1.28218356673022 0.3374476632637181.31504630659096 A A A
LNCV6_67547_PI430048170 mRNA
AAGATCACTTTAGTCCTAGGGGACTAGAGAAGGAAAATGACATGAGGCAGTGGGGTATCT NM_138938RefSeq
chr2 - 79157005 79159753 REG3A 5068 "regenerating islet-derived 3 alpha, transcript variant 2"
GO:0045617|GO:0010838|GO:0005737|GO:0008283|GO:0090303|GO:0030246|GO:0007275|GO:0006953|GO:0005
615|GO:0007157 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129445_PI430048170 0.3537245292233870.7892687727136318.24314819248949
8.05525405137217 7.58794824232538 P P P 8.68259319419221 8.33618986855524
7.84930719766975 P P P LNCV6_129445_PI430048170 mRNA
GCCCACTGACCCTGCAGCTCCAGCCTTCTCCATACTTCAACAAAGAATGAGTTGTGGCAA NM_001145210 RefSeq
chr1 - 1418419 1421444 ANKRD65 441869 "ankyrin repeat domain 65, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135970_PI430048170 0.5989417571957230.9604567760552819.88061614755856
10.2103081893944 10.0780748229051 P P P 10.0599769040685 10.0837786942727
10.2139754682907 P P P LNCV6_135970_PI430048170 mRNA
GGTGTGGAATGTCGTCAGTGGCAAACATTTCACAGATTTTTATTTTGTTTCTGTCTTCAA NM_006079RefSeq chr6
- 139372254 139374650 CITED2 10370 "Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-
terminal domain, 2, transcript variant 1"
GO:0005515|GO:0043627|GO:0000790|GO:0007368|GO:0003700|GO:0008283|GO:0034405|GO:0005634|GO:0070
986|GO:0048536|GO:0030154|GO:0007530|GO:0007507|GO:0005737|GO:0035360|GO:0045944|GO:1900164|GO:0
060971|GO:0035802|GO:0030511|GO:0035035|GO:0001666|GO:0043066|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_77232_PI430048170 0.9411211234062721.00244010954413 9.71089824907779 9.67802165411725
9.53455300573734 P P P 9.84537734906023 9.53330948381229 9.51588985288346 P P P
LNCV6_77232_PI430048170 mRNA
TTTCTGGCTGGTTACTAAGGTGCCTGCTAGCCATTGTATAAAATTAAAACATGAAGAATA NM_021943RefSeq chr6
+ 37819530 38154623 ZFAND3 60685 "zinc finger, AN1-type domain 3"GO:0008270|GO:0003677 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134515_PI430048170 0.6913167843303781.0561856912057 5.86763145148924
5.37932423971943 5.64938792447333 P P P 5.63966967194441 5.46637234757472
5.58937620000051 P P P LNCV6_134515_PI430048170 mRNA
GCATCTTTGCTGTTGTTAATTATTATATGTGCCATTGTTACAGGAGATTATAGGCTAGTC NM_006377RefSeq chr9
+ 35161991 35405335 UNC13B 10497 unc-13 homolog B (C. elegans)
GO:0005515|GO:0016081|GO:0016082|GO:0030054|GO:0031594|GO:0005886|GO:0007268|GO:0007269|GO:0046
872|GO:0005829|GO:0035556|GO:0005737|GO:0007528|GO:0043195|GO:0004872|GO:0004871|GO:0097151|GO:0
048786|GO:0007588|GO:0005794|GO:0035249|GO:0006915|GO:0010808|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136199_PI430048170 0.1863639660379930.9749718093428190.298851834846436
0.33597377038066 0.360490138118102 A A A 0.3930577246623310.367629944669937
0.344589902463103 A A A LNCV6_136199_PI430048170 mRNA
GGTGGGATGCTGTTGTTTCTAATTATACCTATTTTTCAAGGCTTCTGTTGTATTTGAAGT NM_080617RefSeq chr20 -
55997356 56005472 CBLN4 140689 cerebellin 4 precursor
GO:0030054|GO:0009306|GO:0045202|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53588_PI430048170 0.0523022287835014 0.8761779749616147.75114745870499
7.58954653718958 7.73839698409379 P P P 7.83387857535324 7.97669461638011
7.84164170870382 P P P LNCV6_53588_PI430048170 mRNA
TACTTGCCTGTGGTCATCGATAACTTCCATAATGCCTTCCGTGGAGGGGGCTCCCTGCCT NM_000403RefSeq chr1

- 23795598 23800544 GALE 2582 "UDP-galactose-4-epimerase, transcript variant 1"
GO:0050662|GO:0003978|GO:0005975|GO:0003974|GO:0019388|GO:0009405|GO:0044281|GO:0042803|GO:0070
062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137483_PI430048170 0.8564189458761550.9765781049663794.98441899049516
5.48650227526382 5.49954663631544 P P P 5.10192841173891 5.51275257572949
5.48060641824322 P P P LNCV6_137483_PI430048170 mRNA
CAGATGCCTTATGGACCTCTTCAAAAATGTGGTTAGCCAATTGATTCAACTTTTATAGGT NM_138571RefSeq chr6
+ 125956714 125980243 HINT3 135114 histidine triad nucleotide binding protein 3
GO:0005739|GO:0005737|GO:0016787|GO:0000166|GO:0008152|GO:0005730|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132559_PI430048170 0.0610063149038452 0.4154232106443132.55249229026243
2.16049799616554 1.22618070074261 A A A 3.05563477164146 3.55669442679692
3.38312115306267 P P P LNCV6_132559_PI430048170 mRNA
CCATGTACCTAGGGGGAAATAACAATACTAGAAGTGTGCAGTTTTTGCTTTTATCTTTTT NM_001031855 RefSeq
chrX + 118974613 119018355 LONRF379836 "LON peptidase N-terminal domain and ring finger 3,
transcript variant 1" GO:0005515|GO:0004176|GO:0006508|GO:0008270 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140772_PI430048170 0.9111687323235640.8833266507071621.39522927582275
0.3561876351785161.49341523403715 A A A 2.12201946572059 0.373084292481786
0.975354924279444A A A LNCV6_140772_PI430048170 mRNA
ACAATTCCCTGCTGTCGTCTTAGCAAGAAGTAAAATGAGAAATTTTGTTGATATTCTCTC NM_002343RefSeq chr3
- 46436004 46465142 LTF 4057 "lactotransferrin, transcript variant 1"
GO:0005515|GO:0034145|GO:0071902|GO:0004252|GO:0033214|GO:1900229|GO:0042581|GO:0005634|GO:0005
615|GO:0001817|GO:0051092|GO:0001895|GO:0006959|GO:0006508|GO:0097013|GO:0031665|GO:0043123|GO:0
030141|GO:0033690|GO:0090382|GO:0008201|GO:0070062|GO:0043066|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135075_PI430048170 0.000658012614372113 0.1283249550489495.83490192954582
5.06007506100715 5.53367443228651 P P P 8.16221297410492 8.43665422180161
8.75759113365016 P P P LNCV6_135075_PI430048170 mRNA
GAATTAACAGTCTGTTCTTCCAGAGTCCAGAGACATTGTTAATAAAGACAATGAATCATG NM_025237RefSeq chr17
- 43753730 43758788 SOST 50964 sclerostin
GO:0005515|GO:0005794|GO:0005578|GO:0005576|GO:0005615|GO:0009612|GO:0030514|GO:0031012|GO:2000
054|GO:0030279|GO:0031333|GO:0001503|GO:0071374|GO:0045893|GO:0016055|GO:0090090|GO:0008201|GO:0
008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133376_PI430048170 0.16738579966876 1.58790261042994 3.44186692115074
2.70271021224845 3.12840391430075 P A P 2.27413063225355 3.01586956585938
1.81760531750411 A P A LNCV6_133376_PI430048170 mRNA
GTTAAGTGTGGGTTGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAAACATGAATAA NM_020997RefSeq chr1
- 225886281 225889146 LEFTY1 10637 left-right determination factor 1
GO:0007368|GO:0010862|GO:0042981|GO:0000122|GO:0060395|GO:0005125|GO:0005160|GO:0005615|GO:0003
007|GO:0043408|GO:0016049|GO:0007179|GO:0048468|GO:0008083 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145751_PI430048170 0.00700661504775274 0.5570142604947156.68778022291272
6.39193683314058 6.74455502403549 P P P 7.45828520436635 7.36968647147328
7.54770160323625 P P P LNCV6_145751_PI430048170 mRNA
GGAAACGGCAAATTGTGTTTTAAAGCTCTTTGTATTTCTCCAGTTTCTGACCTTGTAAAT NM_015308RefSeq chr11
- 47716516 47767441 FNBP4 23360 formin binding protein 4 GO:0005515|GO:0005654 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_70438_PI430048170 0.1578739332443160.7895464772497116.53588385042164 5.96853290334695

6.20048349368647 P P P 6.57811126529935 6.56030857889722 6.64468631807625 P P P
LNCV6_70438_PI430048170 mRNA
CGCCATCTTTAAGGTTCTAAATGAGAAGAAACTTCAAGAGGTTGATAGTTTATGGAAAGA NM_015934 RefSeq chr2
+ 202265791 202303661 NOP58 51602 NOP58 ribonucleoprotein
GO:0005515|GO:0015030|GO:0031428|GO:0006364|GO:0070761|GO:0005730|GO:0005634|GO:0005732|GO:0000
154|GO:0006608|GO:0005737|GO:0030515|GO:0016020|GO:0016049 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139917_PI430048170 0.2549136662190040.6243901654547182.6027892154113
1.17413632738517 2.91373897903721 A A P 3.27954407240006 3.14640750236517
2.77543138096937 P P P LNCV6_139917_PI430048170 mRNA
GGGGTTTCAGGAATATCATCAGTTGCTTTGCAGATGGAGATAACTTAAAATAAAAGATAC NM_016060 RefSeq chr17
- 6643312 6651634 MED31 51003 mediator complex subunit 31
GO:0005515|GO:0010467|GO:0006461|GO:0006367|GO:0001104|GO:0006357|GO:0016592|GO:0048147|GO:0060
173|GO:0005654|GO:0032403 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138072_PI430048170 0.3566865033431690.8145957975501737.6932162815901
7.72762269785711 8.21302156920137 P P P 7.77195620653093 8.20840630075658
8.50850167814022 P P P LNCV6_138072_PI430048170 mRNA
GTTGCTTTTAAGGAGTTCTGGCATTGTATGTGCATTTTTGTAGAAATTGTTACTGGACTT NM_175748 RefSeq
chr14_KI270847v1_alt + 321617 343777 UBR7 55148 "ubiquitin protein ligase E3 component n-recognin
7 (putative), transcript variant 2" GO:0008150|GO:0003674|GO:0016567|GO:0016874|GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145473_PI430048170 0.1033884770425531.0403420625135 0.395760025041528
0.3909244352847840.42040119461 A A A 0.3172284001489110.3299635313948240.387905471428834 A
A A LNCV6_145473_PI430048170 mRNA
ATACAGCAACGCTACATTGCAAATAAAAGTCCGATCCCAAAAGGAGAATGAGACAAAAAA NM_001098518
RefSeq chr6 - 46852505 46921977 ADGRF5 NA "adhesion G protein-coupled receptor F5, transcript
variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139644_PI430048170 0.1022468815266790.562690959150395 1.73007660620527
2.05516863527785 1.44389825502684 A A A 2.50833952722943 2.02335389464771
3.06375475919922 A A P LNCV6_139644_PI430048170 mRNA
AAGTAATCTGTCAATCAGAAACCATAGCTGAGGGCCAAACCAGTATTAAAGACCTTTCTG NM_032341 RefSeq chr1
+ 15617457 15661057 DDI2 NA DNA-damage inducible 1 homolog 2 (S. cerevisiae) NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_80649_PI430048170 0.0776527682581757 1.19637804199787 10.3311604803509
10.6025256693655 10.3764086898301 P P P 10.2489163776223 10.164322776657
10.1332282191272 P P P LNCV6_80649_PI430048170 mRNA
ATTAAGCAGAAAGGGCCTTGAATCCTGGCCTGGAATTTGGGCAGATATAGCATTAATAAA NM_000155 RefSeq chr9
+ 34646588 34650598 GALT 2592 "galactose-1-phosphate uridylyltransferase, transcript variant 1"
GO:0005794|GO:0005975|GO:0008108|GO:0019388|GO:0009405|GO:0006258|GO:0008270|GO:0044281|GO:0006
012|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_3865_PI430048170 0.0173472057213979 0.67039042891533 8.98096762784508
8.74524349575591 8.60183639209598 P P P 9.33020599647707 9.47825078279671
9.26782930721289 P P P LNCV6_3865_PI430048170 mRNA
AGGACTGGCTCCTTTCCCAGTGTCCTTAAAATAAAGAAATGAAAATGCTTGTTGGCACAT NM_009587 RefSeq chr17
+ 27631147 27649560 LGALS9 3965 "lectin, galactoside-binding, soluble, 9, transcript variant 1"
GO:0007165|GO:0005737|GO:0005534|GO:0030246|GO:0004871|GO:0043123|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126715_PI430048170 0.1989292314035781.11264788836975 10.1572427299394
9.99972777834049 10.110469215576 P P P 9.76400889417832 9.99517674031585

10.0361236669606 P P P LNCV6_126715_PI430048170 mRNA
ACCCAAGGTTTGGTTGGGGTGAAACATGATGACAACACATACACTTAAGAAGGTGGGAACNM_199287RefSeq chr17
+ 81666730 81673906 CCDC137 339230 coiled-coil domain containing 137 GO:0005730 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_54644_PI430048170 0.395409525075555 1.04526099113316 0.494955719848492 0.307934477535932
0.344983587844347 A A A 0.292475983250343 0.315215647801673 0.354773106187371 A A A
LNCV6_54644_PI430048170 mRNA
CTCATGAACAGAAACACCTAGGAAGGGAGAACTGGATTTATTTAATGGGGATGTGTTCAA NM_001178055 RefSeq
chr5 + 50665898 50846522 PARP8 79668 "poly (ADP-ribose) polymerase family, member 8, transcript
variant 1" GO:0005622|GO:0008152|GO:0003950 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135621_PI430048170 0.956778907774407 0.986287526819706 4.97580173989774
4.32182373617172 4.03588837957922 P P P 3.90909831284692 4.83459383448819
4.65856835088842 P P P LNCV6_135621_PI430048170 mRNA
CCTCCCAGTAGCTGTGCAACTACAACCAGTTTTATGAAAAAGCTTTATAAAAATAAGCTT NM_001267549 RefSeq
chr20 - 63698641 63708013 ARFRP1 10139 "ADP-ribosylation factor related protein 1, transcript variant
8"
GO:0005515|GO:0005802|GO:0005794|GO:0007369|GO:0007264|GO:0043001|GO:0003924|GO:0005525|GO:0007
165|GO:0016020|GO:0034067|GO:0008152|GO:0042147 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130933_PI430048170 0.0141650797084201 0.0862472732902865 2.14358704946481
0.336919842594124 0.483827297285926 A A A 4.32092976525574 4.88005733135464
5.02933611670481 P P P LNCV6_130933_PI430048170 mRNA
GGACAGTTGCACAGATGGCTAGTGTTAAATTTCTATAGACGATGGTAATAAAATCTGAAT NM_015458RefSeq chr8
+ 11284490 11328145 MTMR9 66036 myotubularin related protein 9
GO:0005515|GO:0016791|GO:0050790|GO:0005737|GO:0016311|GO:0030234 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141555_PI430048170 0.165746203770966 1.36559462222815 2.32404427414782
2.64593851499828 2.71725329841347 A A A 1.66869864361918 2.46984795529044
2.11990465105583 A P A LNCV6_141555_PI430048170 mRNA
TTGCCTATAAAAGGACCTTAGGATTTAAGGAAGGGGCTTCTTAATGTAGAAAGGGAAGAA NM_017821RefSeq chr1
- 38885805 38941830 RHBDL254933 "rhomboid, veinlet-like 2 (Drosophila), transcript variant 2"
GO:0005886|GO:0004252|GO:0006508|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144002_PI430048170 0.110380588285024 1.03895918734512 0.465620166474361 0.5303085075481
0.466079170335405 A A A 0.407135356017744 0.433628947364469 0.456370647133135 A A A
LNCV6_144002_PI430048170 mRNA
TTGTGTTCGCTCTTTTTAGGACCAAGAAAAAATTATTGGTTGCTGTTTTCTCAGTTTTGG NM_001242740 RefSeq chr6
- 138725210 138773679 LOC100507462 NA uncharacterized LOC100507462 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_130398_PI430048170 0.433219783413973 1.03209994094502 0.449069519948001
0.296380618220639 0.354275936400594 A A A 0.284852360965549 0.33122668436744
0.350251713441323 A A A LNCV6_130398_PI430048170 mRNA
TGACATTCCATACTTTTAACCTCCTAAAGCTAAAAACAATAGCTCGGAAACCATTCTTTC NM_020204RefSeq chr1
+ 197917386 197930143 LHX9 56956 "LIM homeobox 9, transcript variant 1"
GO:0043565|GO:0008585|GO:0035262|GO:0008045|GO:0008283|GO:0003714|GO:0008270|GO:0005634|GO:0045
892|GO:0008584 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136264_PI430048170 0.271621231652914 0.345402721102681 0.390708218374972
0.444643569413176 0.388036302955015 A A A 0.300936287137705 2.92712592594374
1.42584186005949 A P A LNCV6_136264_PI430048170 mRNA
CTTTGGTGTCTCAGAGAAGGAGTCTAGGTCTTTGATGTGTGATTTAATCTTTTATTTGTT NM_015432RefSeq - - 0
0 --- NA - NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_115153_PI430048170 0.00688613538280802 1.344082937279 14.687696623324
14.7504680697927 14.7183876717094 P P P 14.3524266080215 14.1939627895001
14.3260348877169 P P P LNCV6_115153_PI430048170 mRNA
GTTCAGGCATTATTTGGGGGGTTTTGTTTCCAAAGGAACTAAATAAAGTCATATTGCTTA NM_001136026 RefSeq
chr3 - 10300928 10321188 SEC13 6396 "SEC13 homolog (S. cerevisiae), transcript variant 3"
GO:0005515|GO:0002474|GO:0012507|GO:0048208|GO:0005635|GO:0006886|GO:0005829|GO:0006888|GO:0019
886|GO:0000139|GO:0031080|GO:0005789|GO:0061024|GO:0000776|GO:0051028|GO:0000278|GO:0044267|GO:0
070062|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_32612_PI430048170 0.0285035414526162 1.4365136631629 7.01463666992918
7.34868493173833 7.25170773275776 P P P 6.63689102329618 6.7149532264225
6.71422399157952 P P P LNCV6_32612_PI430048170 mRNA
ATTCTAGAAACATGGTCCATGGATCAGTGACATTCAGGGATGTGGCCATTGACTTCTCTC NM_001005851 RefSeq
chr19 - 40028259 40056208 ZNF780B 163131 zinc finger protein 780B
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132654_PI430048170 0.9217712998640451.01024123249665 8.48694493699801 8.5739030128281
8.81165576552937 P P P 8.67103389665826 8.42407710636823 8.73485100418503 P P P
LNCV6_132654_PI430048170 mRNA
CAAGGTGGAAACCTCTTATTCACATTTGCTTTGATTCCCCGATGGAGTAGACTGCCTTTG NM_138389RefSeq chr4
+ 38867732 38945744 FAM114A1 92689 "family with sequence similarity 114, member A1, transcript
variant 1" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55952_PI430048170 0.9395673044372481.01238981849972 8.68607197377352 8.467062331558
8.29119418754154 P P P 8.52708591362741 8.51196403592408 8.37434833659415 P P P
LNCV6_55952_PI430048170 mRNA
TTTCTGCAGCTTAGCTTGTGTCCTGCCCTCCGCCCGAGGCAAAACGTATCCTGAGGACTT NM_004566RefSeq chr10
+ 6202876 6235544 PFKFB3 5209 "6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3, transcript
variant 1"
GO:0005975|GO:0044281|GO:0005524|GO:0006096|GO:0005829|GO:0004331|GO:0007420|GO:0016311|GO:0009
405|GO:0046835|GO:0006006|GO:0005654|GO:0006003|GO:0003873|GO:0006000 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140166_PI430048170 0.3381050066410831.03147814189376 0.570163836305049
0.6202875187636380.56062545570102 A A A 0.5912459210383840.471230649528934
0.552586434419333A A A LNCV6_140166_PI430048170 mRNA
GCCTGCAACCAAATGAAAATTAATATAGTGAGTTCTTTCAGGAGCTTTCTCTGTTTTTCT NM_080764RefSeq
chr22_KI270875v1_alt - 120080 144844 ZNF280B 140883 "zinc finger protein 280B, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_62603_PI430048170 0.4803991850021691.07179349027785 8.3703040900766 8.4112143682326
8.10248312854558 P P P 8.03642805404014 8.27078276211945 8.28266296930731 P P P
LNCV6_62603_PI430048170 mRNA
TTGGATCAACAGCCCGCCAGCTGATTGGATGTCTAGGAATGACTGAAAGAAACCAAAACA NM_144570RefSeq chr16
+ 1678276 1702072 HN1L 90861 hematological and neurological expressed 1-like
GO:0005737|GO:0005886|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144116_PI430048170 0.00193250842929697 1.72931930500836 14.8508579788749
14.6661028483249 14.7602814248759 P P P 13.8312109025521 13.9650295277055
14.1034580254554 P P P LNCV6_144116_PI430048170 mRNA
GAAGCTACATCTCTCAACCTTGGGCAATGAAAATAAAGTTTGAGAAGCTGATGGCTGTGT NM_145662RefSeq chrX
- 141583673 141584738 SPANXA2 NA "SPANX family, member A2" NA . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_139892_PI430048170 0.2359482416639750.6307573101290820.246176000922016
0.2807387849331890.391355305343377A A A 0.84495214742172 1.51244923744849
0.306424079293056A A A LNCV6_139892_PI430048170 mRNA
TGTGGAAATTTTGCCTGAAGTCCTCCACCTAAAAACCTGATGCCATTGGTAATGATGTTT NM_152501RefSeq chr1
+ 158931546 158977059 PYHIN1 149628 "pyrin and HIN domain family, member 1, transcript variant 1"
GO:0007049|GO:0016607 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100846_PI430048170 0.00111197734048606 0.67762487348478410.6750697731462
10.5346509486064 10.686399412428 P P P 11.1167828766717 11.2740236971381
11.1902395210576 P P P LNCV6_100846_PI430048170 mRNA
GGAACAAAACACCAGCCCTTTTGTAGTGGATGCAGAATAAAATTGTTAATCCAATCACCT NM_004286RefSeq chr22
+ 38705801 38733587 GTPBP1 9567 GTP binding protein 1
GO:0006184|GO:0007165|GO:0006955|GO:0016020|GO:0000177|GO:0003924|GO:0061014|GO:0005525|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136808_PI430048170 0.1467485182374540.9419065101469021 4.8671745531053
14.7577415765617 14.7537683115909 P P P 14.9117337072935 14.8196999461825
14.9073238399979 P P P LNCV6_136808_PI430048170 mRNA
GTTTCAGTAATAGCTGAACCTGTTCAAAATGTTAATAAAGGTTTCGTTGCATGGTAGCAT NM_018955RefSeq chr17
+ 16380796 16382745 UBB 7314 "ubiquitin B, transcript variant 1"
GO:0005515|GO:0002474|GO:0010467|GO:0006367|GO:0007220|GO:0019221|GO:0007249|GO:0019058|GO:0002
756|GO:0034220|GO:0007173|GO:0007219|GO:0002755|GO:0007179|GO:0006977|GO:0000209|GO:0038124|GO:0
038123|GO:0005975|GO:0005978|GO:0034134|GO:0042059|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142157_PI430048170 0.3779727647806250.9120973860750420.408278896991057
0.3867962344018850.247672685684736A A A 0.3524256801375090.69241737773113
0.375750661096609A A A LNCV6_142157_PI430048170 mRNA
ACTAAAACCTAGGTCTTAGGTACATCCTATAGGGAGCACAGAACCCATCATTTCACACAT NM_001013407 RefSeq
chr1 + 13254197 13263435 PRAMEF5 NA PRAME family member 5 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_130837_PI430048170 0.1109391795667090.6196360002956247.13097581610365 7.390385523373
7.73372140827609 P P P 7.58637494890771 8.2012266572644 8.46751711098141 P P P
LNCV6_130837_PI430048170 mRNA
GGTTACAGATTGTCTTGATCTCTTGGATCTCCTCAGATCTTTGGTTTTTGCTTTAATTTA NM_018492RefSeq chr8 -
27809620 27838095 PBK55872 "PDZ binding kinase, transcript variant 1"
GO:0005515|GO:0034644|GO:0007067|GO:0004674|GO:0050728|GO:0001933|GO:0006468|GO:0032435|GO:0005
575|GO:0032873|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128336_PI430048170 0.0651274446393268 4.36370520434567 1.41377774716977
3.4228454328876 3.09015039689811 A P P 1.34203573323225 0.284879488782394
0.340688426930477A A A LNCV6_128336_PI430048170 mRNA
GAAAATAACATTTTCTGACTTCTTTCTATTTTCTTGCCCTGCACAGACCCTACCTGGTACNM_020645RefSeq chr11 -
8980575 9004049 NRIP3 56675 nuclear receptor interacting protein 3 GO:0006508|GO:0004190 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142057_PI430048170 0.0974016611025639 0.4676401887483330.395292899254276
1.48967377242219 1.16134822313909 A A A 1.98826531275885 1.49341523403715
2.76920678462788 A A P LNCV6_142057_PI430048170 mRNA
TTTGTTTTTGAATACAGCAAACTGGCTGTGGCCTGAAATATTAAAGCTCATTGTGAAAAG NM_001127358 RefSeq
chr7 + 77798791 77957504 PHTF2 57157 "putative homeodomain transcription factor 2, transcript
variant 3" GO:0006355|GO:0005783|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128276_PI430048170 0.6353839270051850.9403804830255768.91521577569331

8.90879014533171 9.01776744453043 P P P 8.85446953564811 8.92379632226415
9.29270649188752 P P P LNCV6_128276_PI430048170 mRNA
CATGTTTAGGGGGAAAATGAAAATCTCCCTTAAAATTTGTTTCAACTCCTCCTGCAAATA NM_005119RefSeq chr1
+ 36224415 36305356 THRAP39967 thyroid hormone receptor associated protein 3
GO:0051219|GO:0005515|GO:0008380|GO:0048026|GO:0006367|GO:0005634|GO:0046966|GO:0030374|GO:0030
518|GO:0000381|GO:0042809|GO:0045944|GO:0004872|GO:0048255|GO:0001046|GO:0035145|GO:0070062|GO:0
006397|GO:0003712|GO:0001104|GO:0003713|GO:0000956|GO:0005524|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133837_PI430048170 0.4159911401051431.03980078534794 0.288464365794601
0.2893624388523450.448992371780393A A A 0.3043023713519120.271505478309055
0.287895210901516A A A LNCV6_133837_PI430048170 mRNA
TAAAGTCTTTAGATGTTCTTCACAACTTCAAGTGCATGGAAGGGCTCACTGCATAGACAC NM_001080411 RefSeq
chr19 - 12014716 12035741 ZNF433 163059 zinc finger protein 433
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127589_PI430048170 0.4076947164529461.10261877799206 7.44612110877427
7.25162079540229 7.50394019521067 P P P 6.98426841831067 7.32987256251843
7.43868305735158 P P P LNCV6_127589_PI430048170 mRNA
GAGGGTATTTGGGGTGGGGTTGTTTTTTGAGATGTGTAATTCTTTTATGGAGTTTTTAAA NM_203327RefSeq chr20
- 4852355 5010293 SLC23A2 9962 "solute carrier family 23 (ascorbic acid transporter), member 2,
transcript variant 2"
GO:0005886|GO:0015882|GO:0070890|GO:0006767|GO:0044281|GO:0016323|GO:0005737|GO:0016324|GO:0009
925|GO:0015205|GO:0006814|GO:0015229|GO:0006979|GO:0035461|GO:0070904|GO:0015851|GO:0019852|GO:0
008520|GO:0006139|GO:0016020|GO:0006766|GO:0005887|GO:0008523|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_77304_PI430048170 0.5489755976732050.9522049453506434.16396680766274 4.22655553993886
4.4486574537903 P P P 4.4866578524256 4.31214611556918 4.25808569940489 P P P
LNCV6_77304_PI430048170 mRNA
AATCACTGTGGATTTTGGAAACCAGCAGAAAGAGGAAAGAGGTAGCAAGAGCTCCAGAGA NM_001171623
RefSeq chr6 + 43770208 43786486 VEGFA 7422 "vascular endothelial growth factor A, transcript
variant 1"
GO:0005515|GO:0008360|GO:0038033|GO:0005615|GO:0038084|GO:0030335|GO:0009986|GO:0030168|GO:0000
122|GO:0005161|GO:0042056|GO:0005125|GO:0001701|GO:0031077|GO:0002575|GO:0010595|GO:0038091|GO:0
040007|GO:0005172|GO:0008083|GO:0030949|GO:0035924|GO:0008284|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134387_PI430048170 0.0585264383551556 1.04334581935387 0.42416731921419
0.4667642271933610.459415530311985A A A 0.35967765068608 0.384221335433483
0.422459346084845A A A LNCV6_134387_PI430048170 mRNA
GTTCCTATTTCTTGTTGGCTGGCTGAGTAGAGAAAGCATATTTTACTACTTAAACCTTTTNM_018897RefSeq chr2 -
195737702 196068812 DNAH7 56171 "dynein, axonemal, heavy chain 7"
GO:0005929|GO:0001539|GO:0008152|GO:0005874|GO:0005509|GO:0005858|GO:0003341|GO:0003777|GO:0016
887|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135968_PI430048170 0.00078851253225419 5 0.6538228043350571 1.6347622789961
11.4683693173907 11.519008458754 P P P 12.066902663955 12.1990860286199
12.1963973152676 P P P LNCV6_135968_PI430048170 mRNA
CATCTGAGCATAACTGTACTAAATCCTTTTACCAGATCAGTATAATAAAGGAGTGATGTG NM_001029891 RefSeq
chrX - 77967960 77969638 PGAM4 NA phosphoglycerate mutase family member 4 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133108_PI430048170 0.4510188728754571.31223668342315 0.317966675920212

0.28305178514289 1.30409813052193 A A A 0.2751827236747420.273314902962286
0.422470559261987 A A A LNCV6_133108_PI430048170 mRNA
CTCGCTACTGTTCAATACTTGTACTATTCCTGGGTTTTGTTTCTTTGTACAGTAAACATT NM_003226RefSeq chr21 -
42311666 42315596 TFF3 7033 trefoil factor 3 (intestinal)
GO:0003674|GO:0007586|GO:0005578|GO:0043434|GO:0006952|GO:0005576|GO:0030141|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144245_PI430048170 0.7649687806394080.9626287716431190.472639051551403
0.5366043354962540.373922666136116 A A A 0.5349928762743950.711947540859952
0.272161358578195 A A A LNCV6_144245_PI430048170 mRNA
TAGACCACGAGACCTTCCTGATGCAAATTGACCAGGAGACAAAGAAGTGCACCTTCTATT NM_001077182 RefSeq
chr17 + 81528390 81537130 FSCN2 25794 "fascin actin-bundling protein 2, retinal, transcript variant 2"
GO:0005737|GO:0051015|GO:0030036|GO:0032420|GO:0003779|GO:0030674|GO:0015629|GO:0051017|GO:0042
462|GO:0009653|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142104_PI430048170 0.0847769248450349 1.38550338234195 7.36504654116501
7.8079754480185 7.66007221593361 P P P 7.40203924393272 7.15299004384407
6.84870755936615 P P P LNCV6_142104_PI430048170 mRNA
TTTGAGATCTGCGAGCCCTTGCTGCAGTTCAGATTCAACAAGGCCCTCTGCCCACCCTCT NM_001190707 RefSeq
chr3 - 46668994 46693656 ALS2CL 259173 "ALS2 C-terminal like, transcript variant 2"
GO:0017137|GO:0008104|GO:0032321|GO:0016023|GO:0007032|GO:0005089|GO:0042802|GO:0005096 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61805_PI430048170 0.5069539594690730.91041686207454 0.3089277019346030.282490908817684
0.329011277033869 A A A 0.7246793727010040.2780903229335630.276541191475117 A A A
LNCV6_61805_PI430048170 mRNA
CTCTACAGTAGAAGGAGATTGTGGGGAGAGAAATCTTAAGTCATAATGAATAAAGTGCAA NM_153700RefSeq chr15
- 43599562 43618800 STRC 161497 stereocilin
GO:0060091|GO:0009986|GO:0050910|GO:0060088|GO:0032420|GO:0032426 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129691_PI430048170 0.1266230407109470.6884824186886695.10138415413019
4.50530810376729 5.15336563883706 P P P 5.16207673826375 5.41261303174776
5.81101005315988 P P P LNCV6_129691_PI430048170 mRNA
GCTAAGCAGTATTCACAGGCCTAAAATAGGTTTGTATGGTGATCTACAAGATTTTACAAA NM_001105521 RefSeq
chr10 + 132104808 132184809 JAKMIP3 282973 Janus kinase and microtubule interacting protein 3
GO:0008017|GO:0005794|GO:0019900 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130631_PI430048170 0.6238779863084410.9683646107117530.52278863155944
0.5222379164204330.299446812437431 A A A 0.4010751970017040.575815169120598
0.512613070794917 A A A LNCV6_130631_PI430048170 mRNA
CTATGGGAAATCTTGTTTTGCCAATTTTCTTTGAAAATTCTGGCAGACCAAGGTTCTTTTNM_001282872 RefSeq chr1
+ 25272485 25330445 RHD 6007 "Rh blood group, D antigen, transcript variant 8"
GO:0005887|GO:0072488|GO:0008519 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127454_PI430048170 0.7537274745404060.9697962610687720.351224361280419
0.3453190245753170.288341984149255 A A A 0.5691707275396030.279689075145679
0.247365593266334 A A A LNCV6_127454_PI430048170 mRNA
GGTAGACAGTATATAACTAACAACCAAAGACTACATATTGTCACTGACACACACGTTATA NM_002416RefSeq chr4
- 76001341 76007523 CXCL9 4283 chemokine (C-X-C motif) ligand 9
GO:0005515|GO:0048248|GO:0007267|GO:0005615|GO:0010818|GO:0006955|GO:0051607|GO:0006954|GO:0006
935|GO:0042127|GO:0032496|GO:0030816|GO:0043950|GO:0051281|GO:0008009|GO:0070098|GO:0006952|GO:0
005576|GO:0005125|GO:0002690|GO:0007165|GO:0006968|GO:0007186|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143401_PI430048170 0.0156173330691447 0.7772807203484147.5320329956207 7

7.51215194176518 7.52204920837605 P P P 7.89759752505196 7.79604436912051 7.9584920097997
P P P LNCV6_143401_PI430048170 mRNA
CCAGCCACGCTCTTTATTCTGTTCTCAAATAAAGCAGTGTCACTAGTTTTTCCTAAAAAA NM_017880RefSeq chr2
- 70149884 70191019 C2orf42 54980 chromosome 2 open reading frame 42
GO:0031965|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136399_PI430048170 0.1081385089822040.7782966028264810.510432708811
10.6380389824932 10.9062731854026 P P P 10.9006984082766 10.9308649473615 11.301265158558
P P P LNCV6_136399_PI430048170 mRNA
TACTCCCTGATAACTTCATAGCTGCCTGTACAGAAAAGAAAATCCCCGTTGTTTTTCGAT NM_001984RefSeq chr13
- 46771255 46797232 ESD2098 esterase D
GO:0052689|GO:0008150|GO:0005737|GO:0046294|GO:0005794|GO:0005886|GO:0016788|GO:0016023|GO:0047
374|GO:0005654|GO:0018738|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134510_PI430048170 0.4117036926963511.05180435616882 0.308492695828701
0.3134373953004590.513860088875571A A A 0.3146995995359130.278758320181264
0.332867234654065A A A LNCV6_134510_PI430048170 mRNA
GGCAATCTCATGGTTAAATGACTTCCCTTTGAGCTCTTTAATTATTGGCAATAAACAACT NM_001007544 RefSeq
chr1 + 206052722 206102459 C1orf186 440712 chromosome 1 open reading frame 186
GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132278_PI430048170 0.5941505913758660.9387034700027343.48090176250654
3.55506699003099 3.024625764292 P P P 3.34595622660154 3.55007177964131
3.48585177996095 P P P LNCV6_132278_PI430048170 mRNA
TCTGTGCCTTACTGAGGCACCTTTCTAGAGATTAAAAGGGGCTTGATGGCTGTTAAAAAA NM_176786RefSeq chrY
+ 57184100 57197337 IL9R 3581 "interleukin 9 receptor, transcript variant 2"
GO:0007165|GO:0030307|GO:0008283|GO:0005887|GO:0004919|GO:0019983|GO:0005615|GO:0038113 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127865_PI430048170 0.000311444953855577 0.2486965179316735.47890818703283
5.31917370677238 5.37769779698597 P P P 7.223023301442 7.53516571207513 7.4275409472345
P P P LNCV6_127865_PI430048170 mRNA
TGCCCAGCCAAATCTTAATGTAAAGTAGCTAGAGCCATGGAAGTACAGTATGAATTAAAA NM_001286563 RefSeq
chr11 + 123525635 123627771 GRAMD1B 57476 "GRAM domain containing 1B, transcript variant 1"
GO:0016020|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140457_PI430048170 0.0883379802621299 0.9638664873077750.42040119461
0.4134669925636960.361017625886639A A A 0.4280912801037370.47349098377712
0.452957512570807A A A LNCV6_140457_PI430048170 mRNA
ATGGTAGTGGAATGTAAAATGAATAATATTGTCAGCACCAGAATCTACGAAAAGGTGTGA NM_001080526 RefSeq
chr8 - 81458382 81461523 FABP9 NA "fatty acid binding protein 9, testis" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_135048_PI430048170 0.0987595451412251 0.7240430162796577.68288646525759
8.0748549608497 8.29846235695089 P P P 8.56574624308636 8.34550948071849
8.59559615329031 P P P LNCV6_135048_PI430048170 mRNA
TTTGGGCCTAAAACCAAGTCACCTGTTGTGTATCAATTACCTTCTTTGATAAAAGGAAAT NM_001001660 RefSeq
chr12 + 25195215 25205015 LYRM5 144363 LYR motif containing 5 GO:0005739 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140190_PI430048170 0.5675889671341190.9499395880441827.09855816704574
6.89740465592231 6.75000264293463 P P P 7.13448946883531 6.93582116207381
6.90855558656774 P P P LNCV6_140190_PI430048170 mRNA
ACACCCTGACTCTACGCCCTGCCCCTGGGCATTGTCGTCTACTAGTCTATTCTGATGACT NM_001136537 RefSeq
chr1 + 44808481 44814129 BTBD19 149478 BTB (POZ) domain containing 19 NA . NA - . NA
NA NA NA NA NA NA NA NA

LNCV6_98564_PI430048170 0.1578410369367191.12366505114257 5.39588916397963 5.21960081235078
5.45755330810686 P P P 5.28153307864114 5.06442389076587 5.22421203178372 P P P
LNCV6_98564_PI430048170 mRNA
CTGATATCTGCCAATCTTAGTGATATTGACAATTTCAATGTCAAACCAGATAAATGTGCG NM_181659RefSeq chr20
+ 47501856 47656877 NCOA3 8202 "nuclear receptor coactivator 3, transcript variant 1"
GO:0005515|GO:0060713|GO:0060068|GO:0035257|GO:0005634|GO:0050681|GO:0032870|GO:0046966|GO:0005
737|GO:0048589|GO:0030374|GO:0045618|GO:0035264|GO:0045944|GO:0046983|GO:0004871|GO:2001141|GO:0
004402|GO:0070062|GO:0016922|GO:0060744|GO:0016573|GO:0003713|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128943_PI430048170 0.0190594845711733 0.3414416030045433.57139135703688
3.44955393552581 3.40531939873717 P P P 4.54971342008793 5.33909651748519 5.0850575477957
P P P LNCV6_128943_PI430048170 mRNA
CACGGAGCTGTTAGTGAACGAGGTAAAAATAATAAAGGTACAGCCAGTGCATCAGAAAAA NM_015074RefSeq
chr1 + 10210705 10381603 KIF1B 23095 "kinesin family member 1B, transcript variant 1"
GO:0005515|GO:0008017|GO:0043005|GO:0005871|GO:0006200|GO:0005875|GO:0005874|GO:0006915|GO:0031
410|GO:0007274|GO:0003777|GO:0005524|GO:0007270|GO:0030705|GO:0005739|GO:0047497|GO:0008574|GO:0
019894|GO:0008089|GO:0016192|GO:0016887|GO:0030659|GO:0007018 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129599_PI430048170 0.00943006943028525 0.2221867720465791.80616661388659
2.43911693095105 2.72637901455202 A A A 4.69919133944954 4.40640945600895
4.50774052490825 P P P LNCV6_129599_PI430048170 mRNA
TTGTTATTGCCTCTGGTGTTAATAAATGAACAAATGGCTATCTGGAGGAACAGCTACAAA NM_001162529 RefSeq
chr6 + 70426438 70561174 FAM135A 57579 "family with sequence similarity 135, member A,
transcript variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94690_PI430048170 0.9811486063587361.00249892308538 6.24953778210847 6.57276188625249
5.9877196895972 P P P 6.03874168598811 6.31471295827003 6.47258584323137 P P P
LNCV6_94690_PI430048170 mRNA
ATGATCTGAGGCAGACGGAAGGCTTTAAGAACGTGTCGCTGGGGAATGTGCTGGCTGTGG NM_130443RefSeq
chr11 + 66480012 66509659 DPP3 10072 "dipeptidyl-peptidase 3, transcript variant 2"
GO:0005515|GO:0005737|GO:0005886|GO:0006508|GO:0008270|GO:0005654|GO:0008239|GO:0008237|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135261_PI430048170 0.4257126715973091.19728337319454 0.34437694988429
0.36811458890585 1.03074557847341 A A A 0.3593202698703750.370556945245886
0.343866891094144A A A LNCV6_135261_PI430048170 mRNA
TTCCCATGATTTTACTTTTGAAATAATTCCAGCTATCTCTTCTGGATCTATCATTGTGGC NM_153445RefSeq
chr11_KI270829v1_alt - 45904 46840 OR5P3 120066 "olfactory receptor, family 5, subfamily P, member
3" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_83344_PI430048170 0.4786553739889290.8667901409301964.54363177411426 4.39210180390795
4.30828963481376 P P P 4.31998082616046 4.46857071889215 4.99429904717352 P P P
LNCV6_83344_PI430048170 mRNA
TGCTTTAAGATTCTAGGGTTGTACAGGCCCACGCCAGACACGACGTCTGGCAGGAACCTC NM_024086RefSeq chr17
- 2416053 2511906 METTL16 79066 methyltransferase like 16 GO:0008168|GO:0032259 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142408_PI430048170 0.5677179729865560.8196588171069331.53950021887673
0.4361717913523450.376766757125211A A A 1.47192071987816 1.41877500476334
0.415580391465743A A A LNCV6_142408_PI430048170 mRNA
AGCAGCAGGAATTATGTGACATCCTCGTGGCCTATTCTGCATATAACCCTGTGAGTATTC NM_001039397 RefSeq
chr17 - 18635528 18644427 TBC1D28 NA "TBC1 domain family, member 28" NA . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_133784_PI430048170 0.0120113557042960.5528284429776558.66772539975559
8.70688350504678 9.13620070188488 P P P 9.61946051515751 9.57124441948872 9.9099054561017
P P P LNCV6_133784_PI430048170 mRNA
CTTGGTCTTGAATTCATTGTACTGATATTAAACATGCATGCTGGATGTTTTCAAGTTGTG NM_001015892 RefSeq
chr5_GL339449v2_alt - 147937 153209 TAF9 6880 "TAF9 RNA polymerase II, TATA box binding protein
(TBP)-associated factor, 32kDa, transcript variant 4"
GO:0005515|GO:0010467|GO:0006368|GO:0006367|GO:0006366|GO:0044212|GO:0030307|GO:0006325|GO:0032
435|GO:0002039|GO:0000125|GO:0071339|GO:0045944|GO:0016032|GO:0033613|GO:0070555|GO:0004402|GO:0
043066|GO:0005669|GO:0046982|GO:0030914|GO:0060760|GO:0003713|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141234_PI430048170 0.4028573877619740.7872229066337650.353491002947424
0.3813236160268020.32369773452645 A A A 0.3739722071801451.19362962173758
0.360866533552506A A A LNCV6_141234_PI430048170 mRNA
CTTTGTCAACTGAACACATGTTCAATTCGGAGCTAATTGGGAAGACTTACATAAAATTCT NM_178011RefSeq chr10
+ 66926033 67101551 LRRTM3347731 "leucine rich repeat transmembrane neuronal 3, transcript variant
1" GO:0030054|GO:0045211|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99406_PI430048170 0.000660332662400749 0.3493378736768931.33329634728926
1.43094651278236 1.71727128757556 A A A 2.98898824936746 2.84002856385768
3.20853559771013 P P P LNCV6_99406_PI430048170 mRNA
GGAATTTATTGGAATTGTTTGGAATGCAGTGAAGCATCTCACACTACAGCTTGAAGTACA NM_017890RefSeq chr8
+ 99013265 99877586 VPS13B 157680 "vacuolar protein sorting 13 homolog B (yeast), transcript variant 5"
GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143013_PI430048170 0.0158409884647645 1.32970502820727 10.6428366256584
10.5660622857445 10.6653236281665 P P P 10.1854758863748 10.3428267555158
10.1041858688092 P P P LNCV6_143013_PI430048170 mRNA
TGCGTATTCAGTTTGTAAACGTATCCTCTGTATTCAGTAAACAGGCTGCCTCTCCAGGGA NM_006742RefSeq chr16
+ 67893271 67929678 PSKH1 5681 protein serine kinase H1
GO:0005515|GO:0005794|GO:0016607|GO:0005886|GO:0005815|GO:0004674|GO:0005789|GO:0006468|GO:0005
575|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128818_PI430048170 0.0798841464042011.2807811226367 9.20762125545621
9.38202074225999 9.39291838474707 P P P 8.93358812850215 8.76338307839414
9.18972948774388 P P P LNCV6_128818_PI430048170 mRNA
CAGGGAGAACATGAAACCAGAGGTTTCTTTCTTTCTCTGTAATCTGCTATGAAAGAAAAT NM_031899RefSeq chr3
- 39096598 39108363 GORASP1 64689 "golgi reassembly stacking protein 1, 65kDa, transcript variant
1" GO:0005794|GO:0000139|GO:0007030|GO:0050774|GO:0015031|GO:0000278 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143971_PI430048170 0.2442117847667670.6370191001842142.18766435441874
1.91039010906462 0.605720621209398A A A 2.43911693095105 2.35511867238093
2.29337720420884 A P A LNCV6_143971_PI430048170 mRNA
GCCCTTTCAGAACGTTCTCTTCAGTTTTATCTTTCAGTTTTACCATTGTTAGCAAAAAAG NM_031894RefSeq chrX -
31071240 31072053 FTHL17 53940 "ferritin, heavy polypeptide-like 17"
GO:0006879|GO:0006826|GO:0008199 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141016_PI430048170 0.4586326141067091.02140772349026 0.359079467215434
0.2504970479409360.276927057565907A A A 0.2611921709135550.276073254157735
0.259739719002755A A A LNCV6_141016_PI430048170 mRNA
GTGTTTTCCTTCGGCTTGTTACTGCCTTTTGTCAAATAATCTTGACAATGCTGTATAATA NM_001278065 RefSeq chr6
+ 146027781 146437598 GRM1 2911 "glutamate receptor, metabotropic 1, transcript variant 4"
GO:0005515|GO:0051966|GO:0005886|GO:0004930|GO:0007216|GO:0038042|GO:0014069|GO:0007268|GO:0005

634|GO:0038037|GO:0030425|GO:0019233|GO:0007205|GO:0038038|GO:0000187|GO:0071257|GO:0000186|GO:0
007186|GO:0005887|GO:0051482|GO:0008066|GO:0007626|GO:0051930 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_130056_PI430048170 0.3250383441592990.9129579480668870.311267607185302
0.2747851813025510.302505002574631A A A 0.3897967803142220.601998016952688
0.271538605091743A A A LNCV6_130056_PI430048170 mRNA
CCAACCTCCAATCACCCTGAGTCACCTGTAAATTCATTTGTCATTCAAAGCGGAATAACA NM_015980RefSeq chr5
+ 174045603 174109179 HMP19 51617 HMP19 protein
GO:0032051|GO:0032580|GO:0032585|GO:0016021|GO:0007212|GO:0030659|GO:0048268 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140422_PI430048170 0.00199910474242226 0.4024603754764466.720742094588
6.28705642360245 6.58159938363769 P P P 7.72189530020703 7.82958855292285
7.99709515657139 P P P LNCV6_140422_PI430048170 mRNA
CCTGCTTTGTTCATTCTCTGTATTCAAAATTAACAGATCATGCTGAAAACCACTCAAACG NM_006287RefSeq chr2
- 187464230 187554492 TFPI 7035 "tissue factor pathway inhibitor (lipoprotein-associated coagulation
inhibitor), transcript variant 1"
GO:0010951|GO:0009986|GO:0005886|GO:0004866|GO:0007596|GO:0005783|GO:0004867|GO:0031090|GO:0007
598|GO:0005576|GO:0031225|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91380_PI430048170 0.2798978355423682.14899822111011 0.2523356315655931.84590207598721
2.29960924249106 A A A 0.3954495691337650.9613945284667130.32820130697279 A A A
LNCV6_91380_PI430048170 mRNA
ACTACTACAGCCTCCTGCAGAGCTGTCTGCAGCAAGCTGGCCTTCCGGAGACTCAGGACC NM_001166222 RefSeq
chr11 + 67415677 67425607 CARNS1 57571 "carnosine synthase 1, transcript variant 1"
GO:0047730|GO:0035499|GO:0005575|GO:0016887|GO:0005524|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128427_PI430048170 0.4909250345811461.07336600963296 6.75163758018647 6.5958216914858
6.56559240341763 P P P 6.66520746659821 6.64365960918305 6.27190734690093 P P P
LNCV6_128427_PI430048170 mRNA
ATGTCTTCCCTTAATTTGATCTCCCTCTCCTTGATGCCTTTTAAAGTTTTAGAGACACAT NM_001199620 RefSeq chr6
+ 125781160 125932030 NCOA7 135112 "nuclear receptor coactivator 7, transcript variant 4"
GO:0005622|GO:0005515|GO:0030374|GO:0045944|GO:0035257|GO:0005634|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_98962_PI430048170 0.3022649795796620.5329179682431910.4539564885711460.480247023616056
0.383364962949377A A A 0.5223326744845152.17407463083439 0.753924814394153A A A
LNCV6_98962_PI430048170 mRNA
CAGTCGATTTGGGAAATTTGTAGAAATACATTTTAATGAAAAGGCTCAGTTGTTGGAGGA NM_004999RefSeq chr6
+ 75749191 75919537 MYO6 4646 "myosin VI, transcript variant 1"
GO:0005515|GO:0005516|GO:0007605|GO:0006605|GO:0005765|GO:0006886|GO:0071257|GO:0051015|GO:0048
167|GO:0043025|GO:0060001|GO:0005938|GO:0070062|GO:0031965|GO:0005794|GO:0042472|GO:0030330|GO:0
007416|GO:0016358|GO:0006897|GO:0043531|GO:0016591|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144029_PI430048170 0.0283661345466587 1.32984681767828 11.5312789410438
11.5457432681907 11.4971238206312 P P P 11.1100296367271 10.9777095908466
11.2410505369305 P P P LNCV6_144029_PI430048170 mRNA
CTGTCAGATGCTACTCCAAATGTTACCAGAACGATGACAAAAGGGGAGACGCTCTATTTT NM_015949RefSeq chr7
+ 876553 896434 GET4 51608 golgi to ER traffic protein 4 homolog (S. cerevisiae)
GO:0006810|GO:0071816|GO:0071818|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119707_PI430048170 0.1952367357434440.5527090108041791.46753329941034
0.4535295193167380.462198588265083A A A 0.82141253069452 2.17596662984317

1.88268432452104 A A A LNCV6_119707_PI430048170 mRNA
GAAGCTCAAAATCCGCAAAGATGAAGATAATTCAGATGAGCAAGAAAGTTCCGGAGCAAT NM_021150RefSeq
chr12 - 66347430 66679145 GRIP1 23426 "glutamate receptor interacting protein 1, transcript variant 1"
GO:0005515|GO:0043005|GO:0030054|GO:0005886|GO:0008013|GO:0005783|GO:0003713|GO:0007268|GO:0030159|GO:0050681|GO:0035259|GO:0008022|GO:0030425|GO:0016358|GO:0005829|GO:0035556|GO:0008104|GO:0045211|GO:0016023|GO:0045121|GO:0055037|GO:0045893|GO:0030521 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129578_PI430048170 0.0665843661160782 1.42426416542366 7.6087375495935
8.06109131283018 7.5978509431367 P P P 7.43917305620314 7.30956517898095
7.00448521238674 P P P LNCV6_129578_PI430048170 mRNA
GAAAGGGCATAAGTCTGCCCGTTTCTTCCTCATTGAAAAGGCTCTTTTCAGAGCCACTCA NM_003531RefSeq chr6
+ 26045410 26045869 HIST1H3C 8352 "histone cluster 1, H3c"
GO:0005515|GO:0010467|GO:0046982|GO:0006325|GO:0006335|GO:0005576|GO:0005634|GO:0000228|GO:0003677|GO:0032776|GO:0043234|GO:0060968|GO:0016020|GO:0000183|GO:0007596|GO:0045814|GO:0040029|GO:0005654|GO:0000786|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129498_PI430048170 0.377886487289738 0.69755490150248 2.93486733544272
2.80650805200768 2.30315293576824 A A A 3.78954407798152 3.12612164742297
2.46144578810198 P P P LNCV6_129498_PI430048170 mRNA
GAAAGACCCTTAGATGTCTTTTCACCCAACCCCAAACTCCCTGTACAGAAGGGAAACAAA NM_138568 RefSeq
chr19 - 45212620 45234211 EXOC3L2 90332 exocyst complex component 3-like 2
GO:0008150|GO:0003674|GO:0000145|GO:0051601|GO:0000149|GO:0005575|GO:0006887 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145074_PI430048170 0.823228623711042 0.943533990251628 2.94955731251408
3.14790818480848 3.06906077855136 A P P 3.4721502366544 3.12397569052907
2.7356971963486 P P P LNCV6_145074_PI430048170 mRNA
GGAGGAGGCCCCCCTGGGGCTCACATCCCAATAAATAAGTGTCTGACAATAAATAAAAAA NM_001013632 RefSeq
chr1 - 44805909 44807285 TCTEX1D4 NA Tctex1 domain containing 4 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143328_PI430048170 0.434795394723261 1.40218082897478 3.23947737437306
2.26507212535007 1.93244233626412 P A A 2.05013213908886 1.97965735694482
2.26316409227769 A A A LNCV6_143328_PI430048170 mRNA
TAAAATAAAAGAGTGTGAGTAAATCCAATTCCAGAGCATAACTGGCTCCAGATCTCAGAT NM_000100 RefSeq
chr21 - 43773664 43776375 CSTB 1476 cystatin B (stefin B)
GO:0010951|GO:0008344|GO:0005737|GO:0004869|GO:0004866|GO:0010466|GO:0005730|GO:0042981|GO:0002020|GO:0005615|GO:0070062|GO:0045861 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_140669_PI430048170 0.360158556295167 1.15292425705349 0.390932870571902
0.84272210641549 0.882456807418519 A A A 0.419107366784361 0.697803023012494
0.414376142542308 A A A LNCV6_140669_PI430048170 mRNA
GAATCCAGTGGTGTTGGGGCTTTTGTTTTTATTTTGTAAAGGTGATGACTTCTTATAAAC NM_001039360 RefSeq
chr18 - 48027267 48137309 ZBTB7C 201501 zinc finger and BTB domain containing 7C
GO:0003676|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_29184_PI430048170 0.700080394174398 0.861845240996916 5.34634778044974
4.85236937099051 4.47925740450225 P P P 5.63222923893763 5.14242113059293
4.43852008476984 P P P LNCV6_29184_PI430048170 mRNA
GCATTCTCCCACTTTTGATGGATATGTATCCAAATAAAAGTCATTCCCATGCTTTCTTTC NM_182493 RefSeq chr16
- 46702281 46748309 MYLK3 91807 myosin light chain kinase 3
GO:0002528|GO:0045214|GO:0015629|GO:0005524|GO:0005829|GO:0005737|GO:0060298|GO:0071347|GO:0004

687|GO:0055003|GO:0006468|GO:0004683|GO:0048769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134664_PI430048170 0.921851831972026 1.05670353663116 2.14130057052453 0.392601903351026 0.659274438259396 A A A 2.06841583749788 0.417950243618735 0.466169595939621 A A A LNCV6_134664_PI430048170 mRNA CCTCTCTTTTGTGACTCTTGTACAGCTTAATGTGCAATAAAGGAAAAGTTATATCTGTCT NM_003178 RefSeq chr3 + 12004359 12185732 SYN2 6854 "synapsin II, transcript variant IIb" GO:0030054|GO:0008152|GO:0045202|GO:0007268|GO:0030672|GO:0003824|GO:0005524|GO:0007269 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104807_PI430048170 0.8642912316032820.9823212305830879.30615915731736 9.33107502825016 8.93780104773881 P P P 9.31487964507874 9.32979308738905 9.01942092140534 P P P LNCV6_104807_PI430048170 mRNA TGAAAATGATGTTAAGACTGCTTTGGATCTGGCTGCCCTCTCCACAGAACATTCTCAGTA NM_001288781 RefSeq chr14 + 88824152 88877996 TTC8 123016 "tetratricopeptide repeat domain 8, transcript variant 4" GO:0001103|GO:0005515|GO:0007608|GO:0060170|GO:0005813|GO:0034464|GO:0006996|GO:0035058|GO:0015031|GO:0048560|GO:0036064|GO:0060219|GO:0005829|GO:0032880|GO:0042384|GO:0005929|GO:0050893|GO:0035264|GO:0021772|GO:0007411|GO:0045444|GO:0032391|GO:0061326 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143257_PI430048170 0.3266414953621980.9492818889252140.437173663473103 0.4754690315228540.380591488349365A A A 0.5183907783293260.401272205622862 0.593923405514012A A A LNCV6_143257_PI430048170 mRNA CCGTCTCAAGGCATTTACGGTTTAAAAAGACCTTTGTAATTACTAACGAAAATGCAAAGC NM_001144890 RefSeq chr2 - 219161458 219170095 SLC23A3 151295 "solute carrier family 23, member 3, transcript variant 3" GO:0005215|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139380_PI430048170 0.3781745603162391.31583291818084 1.85163185567784 1.60755733909335 1.97039188123042 A A A 2.16508482463691 0.43832461536383 1.13547905207765 A A A LNCV6_139380_PI430048170 mRNA CAGAATAAGGAGATAAAGGCAGCCCTGAGGAAAGTTCTGGGAAGTTCCAACATAATCTAA NM_001013354 RefSeq chr14 + 18601116 18602097 OR11H12 440153 "olfactory receptor, family 11, subfamily H, member 12" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110333_PI430048170 0.0492471940155823 1.28591887807047 3.35465716725309 3.02377868534949 3.11764285206644 P P P 2.71184753457575 2.8485233607832 2.8629791092503 P P P LNCV6_110333_PI430048170 mRNA AGTCTCAGTGGGTTTTATTGACTACATTGTGCACCCATTGTGGGAGACCTGGGCGGACCT NM_001111307 RefSeq chr19 + 10420656 10469631 PDE4A 5141 "phosphodiesterase 4A, cAMP-specific, transcript variant 1" GO:0005515|GO:0007608|GO:0048471|GO:0004115|GO:0010738|GO:0032587|GO:0035690|GO:0046872|GO:0005829|GO:0007165|GO:0030552|GO:0016020|GO:0043949|GO:0006198 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133023_PI430048170 0.00519590668652667 0.4023103190804398.10004904137435 8.03299820664732 8.28354247189361 P P P 9.18540518401257 9.42076743995149 9.71422917275472 P P P LNCV6_133023_PI430048170 mRNA AGCAGCCTTGGAAACCTAACCTGCCTCTTTTAGCATAATCACATTTTCTAAATGATTTTC NM_001943RefSeq chr18 + 31498063 31548851 DSG2 1829 desmoglein 2 GO:0030057|GO:0005886|GO:0009986|GO:0060135|GO:0005509|GO:0006915|GO:0086091|GO:0016328|GO:0006921|GO:0086069|GO:0016324|GO:0005911|GO:0032570|GO:0016021|GO:0007155|GO:0007156|GO:0086005|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57855_PI430048170 0.53547920488648 1.02008453703025 0.3862308094299740.258712055032081 0.304442332065842A A A 0.27911545632414 0.2956414360164790.291415174234638A A A

LNCV6_57855_PI430048170 mRNA
GCTGACTTCAGCATCTGCTGCAAACTGAAGATCATTCAAATTGATGGACAAAAGAAGTGG NM_001242853 RefSeq
chr11 + 71878452 71884561 LOC100129216 NA beta-defensin 131-like NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_68556_PI430048170 0.0421465061683575 0.6915763201344697.5017736385902
7.63607825040734 7.38835645824708 P P P 7.8510665664535 8.29846235695089
7.94391917828929 P P P LNCV6_68556_PI430048170 mRNA
ACGTGTTCATCTGGATCTCGTTCATAGACAGCTACTTTGAAATCCTCTTCCTGTTCCAGG NM_016113 RefSeq chr17
+ 16415541 16437003 TRPV2 51393 "transient receptor potential cation channel, subfamily V, member
2"
GO:0042470|GO:0005262|GO:0005261|GO:0005886|GO:0009408|GO:0009986|GO:0015075|GO:0045773|GO:0032
584|GO:0044295|GO:0090280|GO:0055085|GO:0044297|GO:0012505|GO:0009266|GO:0034220|GO:0005887|GO:0
070588|GO:0006810|GO:0005216|GO:0007600 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140956_PI430048170 0.0254730955589992 1.45993149245669 5.45558444373615
5.33686070745586 5.21604970507855 P P P 4.9510348204876 4.85054000200779
4.54958231072459 P P P LNCV6_140956_PI430048170 mRNA
AATGCCAACTCTGTAAAACACACTTACATTATCGGTTACAGAATGTCACTCTTACCGTCA NM_172364 RefSeq chr12
- 1791956 1918704 CACNA2D4 93589 "calcium channel, voltage-dependent, alpha 2/delta subunit 4"
GO:0005245|GO:0050908|GO:0070588|GO:0034765|GO:0005891|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141564_PI430048170 0.8758239222863960.98112190545011111.4313980085487
11.4831254121628 11.5930569453369 P P P 11.4459387441431 11.3833623857913
11.7398794577137 P P P LNCV6_141564_PI430048170 mRNA
AAGCATGTCTGTCAATCTCCCTTCTTGCTGATTAGCTTTCATATGACTATATTAAATGGA NM_017895 RefSeq chr20
+ 49219294 49244077 DDX27 55661 DEAD (Asp-Glu-Ala-Asp) box polypeptide 27
GO:0008152|GO:0004386|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144884_PI430048170 0.6649422778759731.02727167255633 0.273998398205254
0.2846171989497550.489127056195515 A A A 0.3350910482497380.288409240212262
0.317752052485521 A A A LNCV6_144884_PI430048170 mRNA
CTGTTGCTCATGACTTTCTTTTGTAAATATCTATAAATGGAGACAGATGGAGACACCAAA NM_152868 RefSeq chr22
- 38426327 38455199 KCNJ4 3761 "potassium channel, inwardly rectifying subfamily J, member 4,
transcript variant 1"
GO:0005515|GO:0005242|GO:0030054|GO:0005886|GO:0007268|GO:0010107|GO:0030165|GO:0016323|GO:0008
076|GO:0045211|GO:0034765|GO:0006813|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139205_PI430048170 0.3664076254913521.05146682562309 9.5436730259532
9.45773535268834 9.4897447542236 P P P 9.31721017753917 9.41168126964585
9.53784236549407 P P P LNCV6_139205_PI430048170 mRNA
GACCCTACCATTTATTTCTGCCTTTTTCTTCCGTTCATTGTGAGGAAAAATAAAACTGGT NM_015631 RefSeq chr10
- 95663395 95694143 TCTN3 26123 "tectonic family member 3, transcript variant 1"
GO:0060170|GO:0006996|GO:0060271|GO:0006915|GO:0016021|GO:0070062|GO:0007224 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131715_PI430048170 0.0751675475909424 0.5546396213168526.24360752040034
6.09959012424243 6.49591902091546 P P P 6.58466075554864 7.21228366369459
7.48146215807541 P P P LNCV6_131715_PI430048170 mRNA
GCTCCGCAGAGAATGTTAGCCTTTCTGTTGTAAATGTAATCTTCAAGTAGTCACTTTTTG NM_001130862 RefSeq
chr12 + 4538783 4560047 RAD51AP1 10635 "RAD51 associated protein 1, transcript variant 1"
GO:0005515|GO:0006281|GO:0003690|GO:0003697|GO:0000724|GO:0003723|GO:0005634|GO:0071479|GO:0010
569 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102673_PI430048170 0.2601267459088611.19507412338903 5.50790545394646

5.47580129547399 5.42723304842475 P P P 4.84907126413696 5.27019376962728
5.45636306782982 P P P LNCV6_102673_PI430048170 mRNA
TATCTGAAAAATGTCGCCTTGAAGCACATGCCCCCTAACTTACAGAAGGTGGACCTCTTT NM_032336 RefSeq chr8
+ 41529205 41545046 GINS4 84296 GINS complex subunit 4 (Sld5 homolog)
GO:0005515|GO:0006271|GO:0005737|GO:0001833|GO:0005654|GO:0000278 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143906_PI430048170 0.846864749201059 0.993114297888349 0.259495827569488
0.270572217599492 0.419881322404797 A A A 0.360475904324025 0.306100557038844
0.318336935273345 A A A LNCV6_143906_PI430048170 mRNA
GCTGTGCAAATCATCTTGAGGATTTCTTTCTTGATTTTATTGGGAATAGGAATATATGCC NM_001008740 RefSeq
chr1 + 40247900 40251693 TMCO2 127391 transmembrane and coiled-coil domains 2
GO:0005634|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137076_PI430048170 0.148625528602433 0.567514096938636 10.7943928501983 10.721839006956
10.8719618203732 P P P 10.9145662674669 11.693172713126 12.0244533574671 P P P
LNCV6_137076_PI430048170 mRNA
CTGAGTAACACCATCGATCATGATGTAGAGTGTGGTTATGAACTTTAAAGTTATAGTTGT NM_001071 RefSeq chr18
+ 657603 673499 TYMS 7298 thymidylate synthetase
GO:0046683|GO:0051216|GO:0045471|GO:0033189|GO:0031100|GO:0005743|GO:0005634|GO:0044281|GO:0003
729|GO:0032259|GO:0060574|GO:0042803|GO:0004799|GO:0005829|GO:0005739|GO:0019860|GO:0005737|GO:0
005542|GO:0000082|GO:0048589|GO:0046134|GO:0000083|GO:0000166|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138443_PI430048170 0.0648149906509114 0.666835521261815 8.71768784578476
8.62743052714349 8.90277726432157 P P P 9.1614144723348 9.12336292199157
9.66507255392411 P P P LNCV6_138443_PI430048170 mRNA
GGATGCCATCAGATTAAAGCATTGAAGTGTTTCATTGTTACCTGTACCTAATGGTTTTAA NM_001163280 RefSeq
chrX + 136497078 136512344 HTATSF1 27336 "HIV-1 Tat specific factor 1, transcript variant 1"
GO:0006357|GO:0000166|GO:0032784|GO:0005654|GO:0005634|GO:0019079|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140591_PI430048170 0.810173741413861 1.00899207778611 0.443763465318211
0.522837164758864 0.434698142446796 A A A 0.543345914534495 0.403795795699606
0.412780983481082 A A A LNCV6_140591_PI430048170 mRNA
TTTCGAAGAACATTAAAGTTCTACCAATGTAGAAGCATGAGGAATAAAAGATGGTCTGGA NM_001113561 RefSeq
chr5 + 64165843 64372869 RNF180 285671 "ring finger protein 180, transcript variant 1"
GO:0000209|GO:0004842|GO:0016874|GO:0032436|GO:0031227|GO:0005635|GO:0042415|GO:0042428|GO:0050
790|GO:0031398|GO:0008270|GO:0030534|GO:0016021|GO:0031624 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128533_PI430048170 0.154847185675273 1.71574028651218 4.09866237841778
4.86990158535818 5.25004084186841 P P P 4.0324511862177 3.7390505845236
4.28479467935402 P P P LNCV6_128533_PI430048170 mRNA
GTTTTGTTTTATAGCCCGGTAGAGGAGTTAACCCCAAAGGTGATATGGTTTTATTTCCTG NM_000132 RefSeq chrX
- 154835788 155022723 F8 2157 "coagulation factor VIII, procoagulant component, transcript variant 1"
GO:0005515|GO:0004252|GO:0005886|GO:0005507|GO:0030168|GO:0005576|GO:0006953|GO:0005615|GO:0007
596|GO:0007597|GO:0002576|GO:0006508|GO:0016491|GO:0031093|GO:0055114 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133514_PI430048170 0.0843168136347113 1.04715617333381 0.459781233088367
0.529774979408951 0.480385600158056 A A A 0.386178835865285 0.428114333834281
0.456257698245877 A A A LNCV6_133514_PI430048170 mRNA
GAAAAGGCTCATGTGCTGATGGATAATTTTGAGTCTTCTCCATTCTCTGTGAATGACCCC NM_001085437 RefSeq
chr2 - 240886047 240896156 C2orf54 79919 "chromosome 2 open reading frame 54, transcript variant

1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115961_PI430048170 0.0131611228415740.5923700059932954.72845088772532
4.65347682465324 5.05264434045698 P P P 5.53077592142625 5.68562698873012
5.50989294823607 P P P LNCV6_115961_PI430048170 mRNA
GCCCTGTGGGATCCACTCACTGTTCATCTTCTTGCTTGGGTGTCCACCAAGTGCCTGCTT NM_005121RefSeq chr17
- 61942604 62065282 MED13 9969 mediator complex subunit 13
GO:0003712|GO:0010467|GO:0001104|GO:0006367|GO:0003713|GO:0005634|GO:0046966|GO:0030374|GO:0016
020|GO:0030518|GO:0042809|GO:0045944|GO:0016592|GO:0004872|GO:0005654|GO:0045893|GO:0030521 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123237_PI430048170 0.3366356908439580.8105102891496730.265814823842785
0.2928643239808080.344437742576839A A A 0.3915152445601220.321386213055959
1.00005313828872 A A A LNCV6_123237_PI430048170 mRNA
ATGTCCCAGGTAAGGCAAGTGGGATTGCTGGCTGCTGGATGTCAGCCATGGAACAAGGATNM_170710RefSeq chr4
+ 176065833 176182828 WDR17 116966 "WD repeat domain 17, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126675_PI430048170 0.8166563696690020.9846447473627548.20884724141686
8.22152461118073 8.19107879588835 P P P 8.09578327224152 8.34137449092645
8.24092224185506 P P P LNCV6_126675_PI430048170 mRNA
ACTGAAGTCAAAAGCCCATTAACGAGAAAGTGCCTGCCCACTGCAACGGAGCCGCCAGCA NM_153340RefSeq
chr1 + 109483938 109492798 ATXN7L2 127002 ataxin 7-like 2 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132099_PI430048170 0.8556514283376 1.01559526102318 0.290913535720197
0.5771627634878350.405916412032215A A A 0.5103612618979060.398799819876526
0.304976464645776A A A LNCV6_132099_PI430048170 mRNA
TTGACTAGTGGGCCTATTGTGCCAATTTAAAAATAATGTATAGAATCAGCATCTCTGACT NM_001010940 RefSeq
chr9 + 69820804 69906235 C9orf135 138255 chromosome 9 open reading frame 135 GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128367_PI430048170 2.47034359658853e-05 0.1908010683546540.474290316987312
0.5183049944016840.426833310542601A A A 2.85597475218576 2.95036268107251
2.77900296155473 P P P LNCV6_128367_PI430048170 mRNA
GTTGGTCTTTTTGGAATGAGCCATAGGTAATGTTTATGTCCAATAAAATCTAGGAACCTC NM_017599RefSeq chr12
+ 95217745 95302790 VEZT 55591 "vezatin, adherens junctions transmembrane protein, transcript
variant 1"
GO:0016337|GO:0005737|GO:0005912|GO:0005886|GO:0001669|GO:0002142|GO:0017022|GO:0005654|GO:0016
021|GO:0043009 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132828_PI430048170 0.2035664895527181.02759741877332 0.337102758289053
0.2799671250885440.268143908918964A A A 0.2501029751610160.266702799497868
0.251470266209201A A A LNCV6_132828_PI430048170 mRNA
TAGCTCTCACATTCATGGCTGTTTAACCAATCTGAAAGTTACGGTTTGGGAATTAATAAA NM_173523RefSeq chrX
+ 26192439 26195646 MAGEB6 158809 melanoma antigen family B6
GO:0005515|GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131205_PI430048170 0.0595736733877628 1.18551454273629 8.82277735550149
9.06371329303297 8.98050382405473 P P P 8.81301347322419 8.60377524271581
8.71636998138348 P P P LNCV6_131205_PI430048170 mRNA
ATTTTTGTCATTGGCAATGGTAATAAACCTTGGATTTCCCTGCCCAGGGGAAAGGGCATC NM_001039567 RefSeq
chrY + 20756067 20781032 RPS4Y2 140032 "ribosomal protein S4, Y-linked 2"
GO:0008150|GO:0003674|GO:0003735|GO:0005840|GO:0019843|GO:0005575|GO:0006412 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138500_PI430048170 0.00543775218650536 2.93238218429764 7.17831510962959

6.66546265083807 6.70059225658123 P P P 4.97083739939407 5.6952248109245
5.18219807393263 P P P LNCV6_138500_PI430048170 mRNA
TGTACTGTATGTTTCTCTACTGTATGGAAAATAAAGTTTACAAGCACACGGTTCTCAGCC NM_053044RefSeq chr4
+ 8269764 8307111 HTRA3 94031 "HtrA serine peptidase 3, transcript variant 1"
GO:0030514|GO:0005515|GO:0004252|GO:0004175|GO:0006508|GO:0008236|GO:0005576|GO:0001558|GO:0030
512|GO:0005520 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140822_PI430048170 0.5112677742691580.98167862234614 0.476417462849743
0.4023601844945180.432252848047281A A A 0.4048075931023410.493976547835147
0.49146730015667 A A A LNCV6_140822_PI430048170 mRNA
GTCAAGATGCTATGTAAGGCTTTGAAAAAGTCGACATGCAGGCTGCAGAAACTCGGGTAA NM_176810RefSeq chr19
- 55895944 55932336 NLRP13 126204 "NLR family, pyrin domain containing 13" GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94290_PI430048170 0.1077116673843731.63015745879185 11.6703120559643 12.4271697811338
12.4277309503252 P P P 11.5796688675079 11.5885943279115 11.3537597671333 P P P
LNCV6_94290_PI430048170 mRNA
TGCATCTTCTATGGGATGATTGCAGATGGCACGCACACCAACCCCGCCGCCCTGCGGATC NM_001145815 RefSeq
chr16 + 2520361 2530954 AMDHD2 51005 "amidohydrolase domain containing 2, transcript
variant 2" GO:0005975|GO:0006044|GO:0008448|GO:0005634|GO:0019262|GO:0046872 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_115934_PI430048170 0.8080913118341650.9331629471709151.07507390786589
2.66781315887953 2.44754922273834 A A A 2.079064077774 2.89817206696587 1.6928623514122
A P A LNCV6_115934_PI430048170 mRNA
TCACGACCGACGTGGAAGATCTGTCCACGGCTCTCTTCTATGACACCGTGCCTGATACGT NM_173628RefSeq chr17
- 78423696 78577394 DNAH17 8632 "dynein, axonemal, heavy chain 17"
GO:0001539|GO:0008152|GO:0005874|GO:0005858|GO:0003777|GO:0016887|GO:0005524|GO:0007018 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144523_PI430048170 0.5428767390369570.9407555000776660.492574819000265
0.5412214137234170.429773770564242A A A 0.7861293270393510.455414464409385
0.463242291322795A A A LNCV6_144523_PI430048170 mRNA
CTGTTTAGTTACCCAGCTGTTTAATATTCCAGTCTTCCCAAAGTGAAAAGATTTGTATAC NM_001301206 RefSeq
chr15 - 83255902 83283457 BNC1 646 "basonuclin 1, transcript variant 2"
GO:0050679|GO:0008284|GO:0051276|GO:0003700|GO:0006357|GO:0006356|GO:0005634|GO:0003677|GO:0006
351|GO:0046872|GO:0005737|GO:0008544|GO:0042060 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138352_PI430048170 0.0030944630132427 0.27070965722986 4.9581204511439
4.61240056812593 5.03894056555869 P P P 6.32656931539794 6.89496750081642
6.99271868245736 P P P LNCV6_138352_PI430048170 mRNA
GGTGTCGATTTGGACTATGAATCAAAAGACCTTTTTCAGGTTCTTTCACTATTGTCTGGG NM_001267595 RefSeq
chr12 - 48042897 48105992 SENP1 29843 "SUMO1/sentrin specific peptidase 1, transcript variant 2"
GO:0005515|GO:0031965|GO:0006919|GO:0016926|GO:0016925|GO:0005634|GO:0016929|GO:0032435|GO:0097
190|GO:0010724|GO:0005737|GO:0004175|GO:0045944|GO:0006508|GO:0005654|GO:0044267|GO:0005925|GO:0
043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141403_PI430048170 0.8624778857979490.9552766452889195.66770037744709
5.49579566602513 5.31549975265739 P P P 5.80103161261186 5.68768930355554
5.12258064952662 P P P LNCV6_141403_PI430048170 mRNA
ACCCCGCCATCTCAATCAGTCACTGACTTTTGTTTATTCTGTCCTAGAAATACCTTTTTT NM_006261RefSeq
chr5_KI270898v1_alt - 127080 130957 PROP1 5626 PROP paired-like homeobox 1
GO:0005515|GO:0005667|GO:0043066|GO:0001568|GO:0008013|GO:0021979|GO:0005634|GO:0000122|GO:0009
953|GO:0007417|GO:0008022|GO:0060126|GO:0043565|GO:0048850|GO:0016477|GO:0045944|GO:0003682|GO:0
060070 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_136368_PI430048170 0.0222224195034649 0.6374226097898925.70066285621318
5.79682683394987 5.40416764876305 P P P 6.2246635537095 6.35706319421203
6.29431652564057 P P P LNCV6_136368_PI430048170 mRNA
TGACTTCAAAGGAAAGGAACAAATTTTCAAAGACTTGGGGGAGTGAAGGCAGAGCCTGGT NM_152486RefSeq
chr1 + 925740 944581 SAMD11 148398 sterile alpha motif domain containing 11
GO:0005634|GO:0000122|GO:0043621|GO:0042731|GO:0032093 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135778_PI430048170 0.6077425510667040.95992558590461 0.438468164752264
0.6125457888514510.39111385061213 A A A 0.6956189902485220.472651180997568
0.447252272054381A A A LNCV6_135778_PI430048170 mRNA
ATCCAGGGATTCTTCTACCCATGGAGCTGTGAGGGTGACATATGGGACCGGGAGAGCTGT NM_139172RefSeq chr19
+ 55376835 55378244 TMEM190 147744 transmembrane protein 190
GO:0002079|GO:0002244|GO:0005634|GO:0016021|GO:0043621 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_110123_PI430048170 0.0529517838639888 1.55785842470507 6.37527716674211
6.21739979637633 6.50804085499505 P P P 5.37571502222488 6.01448153814863
5.73630491400289 P P P LNCV6_110123_PI430048170 mRNA
TTCTGTGTCTGAAGATAACTCAGAGGATGAGATCAGCAACCTGGTGAAGTTGGACCTACT NM_198839RefSeq
chr17_KI270857v1_alt - 1320991 1645967 ACACA 31 "acetyl-CoA carboxylase alpha, transcript
variant 2"
GO:0005515|GO:0006768|GO:0006767|GO:0035338|GO:0044281|GO:0015629|GO:0046872|GO:0005829|GO:0005
739|GO:0005737|GO:0001894|GO:0051289|GO:0019432|GO:0006633|GO:0003989|GO:0044255|GO:0070062|GO:0
006853|GO:0055088|GO:0005730|GO:2001295|GO:0006084|GO:0005524|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132598_PI430048170 0.0162372686841489 10.7809409026736 10.1600954163237
10.7395471723925 10.5937771904833 P P P 7.97421217763456 6.36270026671927
6.21541078410278 P P P LNCV6_132598_PI430048170 mRNA
AAGAAAGTTTCTCAAAACAGGGAGTACTTCAAGATCACCCTCTACGGGAGAACCAAGGAG NM_005564RefSeq
chr9 + 128149452 128153455 LCN2 3934 lipocalin 2
GO:0005215|GO:0070301|GO:0002020|GO:0005615|GO:0042803|GO:0005829|GO:0006879|GO:0070207|GO:0031
669|GO:0071356|GO:0015891|GO:0006811|GO:0070062|GO:0005506|GO:0042493|GO:0036094|GO:0009635|GO:0
005576|GO:0009615|GO:0055085|GO:0097192|GO:0010628|GO:0071222|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140619_PI430048170 0.3664996283300571.22243933399298 0.952457824157187
0.2501415907217920.344094864786385A A A 0.2694379821123130.242554400049841
0.270112369458654A A A LNCV6_140619_PI430048170 mRNA
TCCTTAAGGGACAACATCCTTAAGTCAAAAGAGAGAAGAGGCACCACTAAAAGATCGCAG NM_003810RefSeq
chr3 - 172505507 172523507 TNFSF10 8743 "tumor necrosis factor (ligand) superfamily, member
10, transcript variant 1"
GO:0005515|GO:0032868|GO:0005164|GO:2001238|GO:2001239|GO:0043065|GO:0006919|GO:0005102|GO:0007
267|GO:0006915|GO:0005576|GO:0097190|GO:0005125|GO:0005615|GO:0046872|GO:0043280|GO:0007165|GO:0
006955|GO:0005887|GO:0090200|GO:0043123|GO:0008584|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142867_PI430048170 0.6943624669137741.02437138434677 0.272971829929378
0.2832245481224970.484418649451447A A A 0.33723894489187 0.28989866220334
0.318869573285905A A A LNCV6_142867_PI430048170 mRNA
CTTCTTCGGCTTGAAGGTAGCCCTAATATTTCCAGTACTTGTTTTACTTACTGTATTTAT NM_001009562 RefSeq chr12
+ 21015695 21090106 SLCO1B7 338821 "solute carrier organic anion transporter family, member 1B7
(non-functional)" GO:0005215|GO:0005886|GO:0006810|GO:0016021 . NA - . NA NA NA NA NA

NA NA NA NA
LNCV6_142452_PI430048170 0.0950248606415251 1.71467974087244 3.7524449656215
3.35981397144842 4.09242480717207 P P P 3.3894210206133 2.39459073793811
3.01048807817805 P A P LNCV6_142452_PI430048170 mRNA
GGGATAACACTGTCTACCTCACAGAAATGTTAAACTGAGACAATAAAAACCAAAGCATAA NM_001172RefSeq chr14
+ 67619861 67651719 ARG2 384 arginase 2
GO:0005739|GO:0034641|GO:0001657|GO:0005759|GO:0006941|GO:0000050|GO:0006525|GO:0044281|GO:0004
053|GO:0046872|GO:0006809 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127965_PI430048170 0.0230033227257001 1.40947412517915 6.94880221351581
7.09261568293278 6.80300198532588 P P P 6.4697927124005 6.62285386673384
6.25770293813849 P P P LNCV6_127965_PI430048170 mRNA
CTTCTTAAGAGGGTTTGGGGCAGTTTATAATAAAGGGGGCGTGTGCTCAACCCTAAAAAA NM_001288573 RefSeq
chr9 - 133152947 133163945 GBGT1 26301 "globoside alpha-1,3-N-acetylgalactosaminyltransferase 1,
transcript variant 5" GO:0009247|GO:0000139|GO:0047277|GO:0006486|GO:0016021|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139657_PI430048170 0.27722312560958 1.41493110901498 3.59211224428088
3.45132770985569 3.45050292377332 P P P 3.62746660820447 2.17140065785783
2.83119967059122 P A P LNCV6_139657_PI430048170 mRNA
CGTTTTGAGGAGAAATTTGATAATGACACTGTTTCCTGATAATAAAGGAACTGCATCAGA NM_005269RefSeq chr12
+ 57460150 57472264 GLI1 2735 "GLI family zinc finger 1, transcript variant 1"
GO:0005515|GO:0008017|GO:0008284|GO:0006366|GO:0044212|GO:0030324|GO:0003705|GO:0021696|GO:0021
983|GO:0005634|GO:0009954|GO:0007283|GO:0009953|GO:0046872|GO:0007224|GO:0005829|GO:0043231|GO:0
045880|GO:0005737|GO:0045944|GO:0090090|GO:0060032|GO:0021938|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_67579_PI430048170 0.2393241326371791.09730659500682 13.0706620213954 12.9313835231621
12.8399033098253 P P P 12.9454375873684 12.7878047716002 12.7058541378869 P P P
LNCV6_67579_PI430048170 mRNA
TCACCACTGGGGCAGTGGGGAGAGATGGCTATATTAATAAAATAACGTGTGTCTTTCAAA NM_001017964 RefSeq
chr22 - 21628089 21630051 YDJC 150223 YdjC homolog (bacterial) GO:0016810|GO:0005975 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134859_PI430048170 0.2959019948478060.7272602681708180.243452640167533
0.2832457098194010.301167506582632A A A 0.4394041681448250.34446202106097
1.24463867505244 A A A LNCV6_134859_PI430048170 mRNA
GCGGATGAATGGTACTTTCCACAAGTGCATTTGAGTAGAAGCATAACCTATTCTCAGTTA NM_001297550 RefSeq
chr4 + 164876987 164897527 APELA NA apelin receptor early endogenous ligand NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135213_PI430048170 0.9931171136471240.9939532051234570.447615252454677
0.5140584476527720.500569401848087A A A 0.3566042157054530.410047252675001
0.698726259002411A A A LNCV6_135213_PI430048170 mRNA
GGCTTGCTTTAGTTTCATGAATGAAGGGTACTTTAGAGACCACAACTTCTCTGTCAAAAA NM_138379RefSeq chr5
- 156919281 156963255 TIMD4 91937 "T-cell immunoglobulin and mucin domain containing 4, transcript
variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128005_PI430048170 0.0665562298651597 0.93397578211820910.2010087743572
10.1384306329633 10.0930291619344 P P P 10.2450087211485 10.2763190202403
10.2080008415465 P P P LNCV6_128005_PI430048170 mRNA
ATTATTTTTAAGCTCCGTGAGTGCGTGGGTCAGTGTCTGCATGAAGTGGAATAAACTGCC NM_015104RefSeq chr11
- 64894531 64917250 ATG2A 23130 autophagy related 2A
GO:0006995|GO:0005811|GO:0005515|GO:0034045|GO:0000422|GO:0000407|GO:0000045|GO:0019898 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_127117_PI430048170 0.3815748048221921.21558783431118 0.439203431762011
0.515870533959398 1.14068280007078 A A A 0.5404241046446580.401936410721351
0.411203858298887 A A A LNCV6_127117_PI430048170 mRNA
TGCTGTTACCAAATCTCAGTAGCTGATTCTGAACAATTTAGGGACTCTTTTAACTTGAGG NM_000862 RefSeq chr1
+ 119507202 119515058 HSD3B1 3283 "hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1"
GO:0006705|GO:0004769|GO:0006694|GO:0006702|GO:0006703|GO:0006704|GO:0005743|GO:0044281|GO:0003854|GO:0005758|GO:0030868|GO:0005789|GO:0016021|GO:0008202|GO:0055114 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129348_PI430048170 0.3165040090405911.05230787172958 0.327192797126706
0.3237777421526020.48827676808245 A A A 0.3089140371906090.281105246100676
0.334267043970698 A A A LNCV6_129348_PI430048170 mRNA
CATGTCAGAAACCATTAGCATTGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAA NM_004887 RefSeq chr5
- 135570680 135579279 CXCL14 9547 chemokine (C-X-C motif) ligand 14
GO:0008009|GO:0007165|GO:0048839|GO:0006955|GO:0005794|GO:0006935|GO:0060326|GO:0007267|GO:0005615|GO:0045662 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96742_PI430048170 0.895547074222991 1.02587007242837 0.4080012968761271.83131058844354
0.297728983257086 A A A 0.3333032369407761.3709485734423 1.08008342693864 A A A
LNCV6_96742_PI430048170 mRNA
CCAGACTTCAGGAAGAATAAAGGTCGCCAACTCAATAAAACCACCAAGCAAAAGAAGTAA NM_001025265
RefSeq chrX - 71103888 71106788 CXorf65 158830 "chromosome X open reading frame 65, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129432_PI430048170 0.1118091970880171.04728726788412 0.475685534857337
0.5596820389916910.488942030102953 A A A 0.4093338155985680.446526390049375
0.469265362412536 A A A LNCV6_129432_PI430048170 mRNA
CAGGCCCGGAATGGGAAAATCTATTCCAAAGAGACACACTAATAAATACTTCATTATAAA NM_001008723 RefSeq
chr10 + 104353763 104455090 CFAP58 NA cilia and flagella associated protein 58 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140152_PI430048170 0.23073956625711 2.44375785467883 2.08421465110293
0.2994978839490252.35272279614821 A A A 0.3191697197282690.277184985065332
0.902699672802443 A A A LNCV6_140152_PI430048170 mRNA
AACAAAGATGTCAAAGGGGCTCTCAGGAAACTAGTTGGGAGAAAGTGCTTCTCTCATAGG NM_001004684 RefSeq
chr11 + 6921001 6921994 OR2D3 NA "olfactory receptor, family 2, subfamily D, member 3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142449_PI430048170 0.56665456249745 1.05155153491531 8.9871748417613
9.03094231626374 8.95379568389535 P P P 8.68169223579822 9.08873065341298
8.95562414315727 P P P LNCV6_142449_PI430048170 mRNA
AATGACTGCCAGACTGTGGGGAGGCACTCTCCTCTGGACCTAAACCTGAAATCCCCCTCT NM_002659 RefSeq chr19
- 43648570 43670346 PLAUR 5329 "plasminogen activator, urokinase receptor, transcript variant 1"
GO:0005515|GO:0005886|GO:0006928|GO:0031225|GO:0030162|GO:0006935|GO:0071438|GO:0030377|GO:0004872|GO:0070062|GO:0006501|GO:0016255|GO:0019904|GO:0005102|GO:0007165|GO:0007596|GO:0005887|GO:0005789|GO:0005788|GO:0016021|GO:0019899|GO:0005925|GO:0042730|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128866_PI430048170 0.00221939772804367 1.13583083138992 7.95262128450849
8.00390791877806 7.94039288812955 P P P 7.75669207957738 7.80712035770248
7.78221524027572 P P P LNCV6_128866_PI430048170 mRNA
TTTTATAGTCACTATCCACATGCCAGTGTGAAATGGGCATCTATGACGTGGTCAGGGTGT NM_023015 RefSeq
chr1_GL383518v1_alt + 44791 90780 INTS3 65123 integrator complex subunit 3
GO:0005515|GO:0007093|GO:0006281|GO:0010212|GO:0032039|GO:0070876|GO:0005634|GO:0006974|GO:0016

180. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141687_PI430048170 0.00329649573570699 0.615742349076414 10.777540263848
10.5433827817853 10.5130720503515 P P P 11.1806236274776 11.3650546543647
11.3928123697602 P P P LNCV6_141687_PI430048170 mRNA
TTACATGTGGGTCTGAACTTGTAGACTCGGTCACAGTATCAAATAAAATCTATAACAGAA NM_001127244 RefSeq
chr9 + 128882501 128918038 LRRC8A 56262 "leucine rich repeat containing 8 family, member A,
transcript variant 1"
GO:0006820|GO:0005515|GO:0016020|GO:0009986|GO:0005886|GO:0034702|GO:0002329|GO:0006970|GO:0005
253|GO:0006884 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139325_PI430048170 0.439570943207482 0.718247929159247 0.491792053008086
2.27555828616844 2.67373927437553 A A A 2.75288917954095 1.8220973304751
2.86913092218388 A A P LNCV6_139325_PI430048170 mRNA
TGCTCACTTAGCAGAAGGACTGAAGGAACTAAGGAACTTGCTAAAGAGAAGAAGAAAACA NM_032839RefSeq
chr3 + 122795053 122881139 DIRC2 84925 disrupted in renal carcinoma 2
GO:0006810|GO:0016021|GO:0005765 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134846_PI430048170 0.0224146646504032 1.29553482034979 9.19087428924402
9.19197053548213 9.20549339990463 P P P 8.82203369683745 8.9198486429187
8.71886412990722 P P P LNCV6_134846_PI430048170 mRNA
TTCATATTTATTTTTGTAAATGATTCTGTGCCCAGGAGCAGCTGGGGGTTCCACCTCAGG NM_022338RefSeq chr11
- 68261334 68272001 C11orf24 53838 "chromosome 11 open reading frame 24, transcript variant 1"
GO:0005794|GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144832_PI430048170 0.342633970189475 0.697791330036292 2.87455072624333
0.353288282091342 0.352363932965849 A A A 2.43780224298288 2.00952609452794
2.24049130942507 A A A LNCV6_144832_PI430048170 mRNA
CAAGTCCTAGTCTATAGGATTGGCAGTTTAAATGCTTTACTCCCCCTTTTAAAATAAATG NM_006418RefSeq chr13
+ 53028740 53052061 OLFM4 10562 olfactomedin 4
GO:0048471|GO:0045296|GO:0005886|GO:0042581|GO:0042582|GO:0042981|GO:0003824|GO:0005615|GO:0042
803|GO:0050764|GO:0005739|GO:1900026|GO:0050777|GO:0008152|GO:0010939|GO:0051260|GO:0007155|GO:0
030141|GO:2000389|GO:0070062|GO:0043124 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127108_PI430048170 0.399606651727097 0.979928696167536 0.283901627759836
0.319294495735305 0.374192987402754 A A A 0.384544439257312 0.350420263577184
0.331107800643774 A A A LNCV6_127108_PI430048170 mRNA
CCTTTCTCTTATTGCTACAGTGTTTTGTACACGGTTAAAACACTAGTAAAGCTTTTTCGT NM_001002034 RefSeq
chr22_KI270928v1_alt + 0 1783 FAM109B 150368 "family with sequence similarity 109, member B"
GO:0005802|GO:0005515|GO:0001881|GO:0030136|GO:0042147|GO:0007032|GO:0055037|GO:0042803|GO:0005
769. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54824_PI430048170 0.21024998567442 0.958494272778055 14.7398912508191 14.6557056829228
14.6234457243636 P P P 14.711181459121 14.7656189142404 14.7276947499819 P P P
LNCV6_54824_PI430048170 mRNA
TGGGGCCATGTCAGTTTGTCACTCACCCAAACTGACCAATAAAACCTTTATTTATGCTAA NM_006118RefSeq chr1
+ 154272562 154275878 HAX1 10456 "HCLS1 associated protein X-1, transcript variant 1"
GO:0005515|GO:0051897|GO:0005667|GO:0031965|GO:0005783|GO:0019904|GO:0030136|GO:2000251|GO:0050
731|GO:0042981|GO:0014068|GO:0005635|GO:0015629|GO:0030027|GO:0005739|GO:0019966|GO:0033138|GO:0
016324|GO:0047485|GO:0030833|GO:0016529|GO:0071345|GO:0045944|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126942_PI430048170 0.159143804905988 1.07870190560299 0.499367481300229
0.49416844075832 0.564149530642923 A A A 0.316196515767535 0.409614870288715
0.499241943661733 A A A LNCV6_126942_PI430048170 mRNA
ATTTTCCACGGAACAAGGTGTGCTCTAAATGCAAGAGAGTCCGTATGCCAGTTGAGAATG NM_001195272 RefSeq

chrX + 125320119 125323101 LOC100129520 NA testis expressed sequence 13-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133556_PI430048170 0.3580559126661451.16218935255773 12.6291414673005 13.1465971008593 12.6953840747159 P P P 12.8255694436143 12.5576320221553 12.4698827126154 P P P LNCV6_133556_PI430048170 mRNA
GACTTACTACCAATAAGCATAAAACCTGACACGTTAAAATCCCTGCCCTTTGGTGAGCCC NM_015021RefSeq chr6 + 87155550 87263688 ZNF292 23036 zinc finger protein 292
GO:0001077|GO:0045944|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126770_PI430048170 0.4658524561581321.84615071336903 0.259754520276885 0.2674523600424592.19272279353044 A A A 0.3637326234389220.306106051124985 0.326227683867769A A A LNCV6_126770_PI430048170 mRNA
GAATGCAAACACATGGTAAAGCCTTAAGATGTTTCTTTTGAATATGGTTATCCCCTAACC NM_030824RefSeq chr19 - 12349370 12365661 ZNF442 79973 zinc finger protein 442
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134354_PI430048170 0.0173577680453097 1.32900457404938 9.69935098592621 9.83323835975764 9.6695573467714 P P P 9.27474880700267 9.47670314180272 9.21149886030119 P P P LNCV6_134354_PI430048170 mRNA
GCAGTGAGGACACGCGTGTTTGACAACTGCTCCCCTGAATAAATGCGAGGATAAATGTTT NM_001053RefSeq chr16 + 1078780 1081454 SSTR5 6755 "somatostatin receptor 5, transcript variant 1"
GO:0043005|GO:0008285|GO:0005886|GO:0032467|GO:0007268|GO:0042593|GO:0071385|GO:0004994|GO:0007186|GO:0042923|GO:0050796|GO:0005887|GO:0007187|GO:0007218|GO:0071392 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128982_PI430048170 0.5800023585834041.32011988486696 3.58369635107353 2.400644624959 2.26708559099752 P A A 2.45846320159189 2.61873748180287 2.34762800590964 A A A LNCV6_128982_PI430048170 mRNA
GGAGCTTCTACTGTACAATCAGAACTTGGAGATTTTAAGAAAAGGACAAACGGTAATTAA NM_032693RefSeq chr4 - 79317117 79326017 NAA11 84779 "N(alpha)-acetyltransferase 11, NatA catalytic subunit"
GO:0031415|GO:0005515|GO:0022626|GO:0004596|GO:0005634|GO:0018002|GO:0006475|GO:0017198|GO:0006474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126781_PI430048170 0.110019030109097 1.24816601685757 4.47395106131973 4.42552465246504 4.2007811907883 P P P 4.07424609672822 4.24249542395548 3.80528574777556 P P P LNCV6_126781_PI430048170 mRNA
AGGAAAATAAAGACCTGCACATCTGACCCCAAGGTGTCAGGCCGGTTTACTGGTAAAAAA NM_000159RefSeq chr19 + 12891128 12899999 GCDH 2639 "glutaryl-CoA dehydrogenase, transcript variant 1"
GO:0005739|GO:0034641|GO:0019395|GO:0005759|GO:0050660|GO:0005743|GO:0046949|GO:0044281|GO:0006554|GO:0000062|GO:0006568|GO:0004361 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58916_PI430048170 0.8359353187886131.01493757825444 5.00784806563922 5.02561842432184 4.88963294081886 P P P 5.27153449167512 4.89363426807503 4.62348023456309 P P P LNCV6_58916_PI430048170 mRNA
AAGGCTTCTTCAGCGAAGCATGAAGCGGAAGGCACTATTCACCTGCCCCTTCAACGGGGA NM_001017536 RefSeq chr12 - 47841536 47905031 VDR 7421 "vitamin D (1,25- dihydroxyvitamin D3) receptor, transcript variant 3"
GO:0060558|GO:0005515|GO:0010839|GO:0010467|GO:0006367|GO:0003700|GO:0008285|GO:0003707|GO:0005634|GO:0046965|GO:0046697|GO:0010980|GO:0045618|GO:0045944|GO:0043401|GO:0006816|GO:0008434|GO:0060745|GO:0060058|GO:0006874|GO:0000122|GO:0003677|GO:0010628|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142145_PI430048170 0.4684521563004351.21451412518115 0.32262092225593 0.4030989889692

1.14189661105151 A A A 0.4538202653976520.3518266860341780.366933158025846A A A
LNCV6_142145_PI430048170 mRNA
TGACGCAGCATTTATTGATAAAAATGGATTTTTCTGTCTGATTTCATGCTGTGGTCGTTTNM_182705RefSeq chr17 -
439979 445940 FAM101B 359845 "family with sequence similarity 101, member B"
GO:0005737|GO:0030036|GO:0031005|GO:0001837|GO:0015629 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140224_PI430048170 0.0020013044519570.466103119395655 2.30850271440309
2.33441586555255 1.99926848841548 A A A 3.13156119752666 3.30320971753503
3.50980928557299 P P P LNCV6_140224_PI430048170 mRNA
TAAGCTGTTCACATGTATAGACTATTGAAATACTGTACTTGTACACATCTGACTGTTGAC NM_144664RefSeq chr11
- 95768941 95789790 FAM76B 143684 "family with sequence similarity 76, member B"
GO:0019784|GO:0000338|GO:0031965|GO:0005737|GO:0016607|GO:0006508|GO:0005654|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69680_PI430048170 0.0431498741154212 0.3893909537574040.607128904395838
0.8864753606531811.82575931007967 A A A 2.27765373228041 2.53257027118321
2.83354958840655 A P P LNCV6_69680_PI430048170 mRNA
CACTCGTAGTGAAGAAAACCTTGAATCCTGTGTATAACGAAATACTGCGTATAAAATTGA NM_032943RefSeq chr11
- 85694220 85811159 SYTL2 54843 "synaptotagmin-like 2, transcript variant a"
GO:0005515|GO:0042470|GO:0017137|GO:0005794|GO:0005886|GO:0019902|GO:0005546|GO:0005634|GO:0006
887|GO:0042043|GO:0006886|GO:0070257|GO:0006904|GO:0005737|GO:0016020|GO:0010923|GO:0001786|GO:0
005654|GO:0016192|GO:0070382|GO:0019897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138471_PI430048170 0.841784792688045 1.09427654027595 2.70902939014822
1.37485503270759 0.500881152719261 A A A 1.88782099291448 1.63320868567635
1.50377435647062 A A A LNCV6_138471_PI430048170 mRNA
CCCCTTGTGTTCTATTGGTTCATTGTTAATAAATATCAAATGAGGTCACGCTCCTTAAAA NM_014228RefSeq chr5
+ 150189956 150211072 SLC6A7 6534 "solute carrier family 6 (neurotransmitter transporter), member 7"
GO:0016020|GO:0005886|GO:0005887|GO:0005328|GO:0015824|GO:0006836|GO:0006810|GO:0055085 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143268_PI430048170 0.000918637592805498 0.4306902938290455.3930705763145
5.22205566731935 5.3133658899549 P P P 6.34779195744764 6.61423892852821
6.60200194768764 P P P LNCV6_143268_PI430048170 mRNA
ACTTCTCATAAATGGAATTGATTTGAACTCAGGAAACCCTCAAATAGGCCAGAACAACTC NM_001288614 RefSeq
chr20 - 23627896 23638048 CST3 1471 "cystatin C, transcript variant 2"
GO:0005515|GO:0004869|GO:0010711|GO:0004866|GO:0010466|GO:0005576|GO:0006952|GO:0002020|GO:0005
615|GO:0010716|GO:0045861|GO:0010951|GO:0001540|GO:0034103|GO:0060313|GO:0060311|GO:0043206|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141775_PI430048170 0.0566227999397499 0.58867997805831310.9895386675268
10.9470178463543 11.0610706280153 P P P 11.358262181164 11.9403305447363
11.9223688990676 P P P LNCV6_141775_PI430048170 mRNA
CTTATTTTCTTGTTGAAGAAACACAAAACCCTCGAGATTCATGTACTGTATGTTGGAGAA NM_001145064 RefSeq
chr7 + 74964817 75031532 GATSL2 729438 GATS protein-like 2 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_96641_PI430048170 0.0172203206522558 1.61033651964295 9.56333338370961
9.97840470595138 9.84290646482576 P P P 9.17108958266147 9.17445914399772
9.00077542800731 P P P LNCV6_96641_PI430048170 mRNA
TTGGGTCAGCGGGTCTGGGACTGGTGGCACCGGCGGCGGCGTAGGACGGAGGCGTCGCTA NM_004169RefSeq
chr17 - 18327859 18363563 SHMT1 6470 "serine hydroxymethyltransferase 1 (soluble), transcript
variant 1"
GO:0051262|GO:0006767|GO:0005634|GO:0044281|GO:0004372|GO:0008732|GO:0042803|GO:0035999|GO:0005

829|GO:0019264|GO:0005739|GO:0034641|GO:0005737|GO:0051289|GO:0006766|GO:0045329|GO:0030170|GO:0
046655|GO:0005654|GO:0009113|GO:0006565|GO:0016597|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_93511_PI430048170 0.4149646675004471.50349564467905 1.41167562239392 2.63278780239534
2.93241874476422 A A P 1.21625390341567 2.04853253091237 2.17372789829042 A A A
LNCV6_93511_PI430048170 mRNA
TGTTTGGAGCTAAGGGAAGGGCAAAAGGCTCAGATATGATTCTCTATCTCTTGTGCCTGA NM_001178032 RefSeq
chrX - 64915801 65034744 ZC4H2 55906 "zinc finger, C4H2 domain containing, transcript variant 2"
GO:0005737|GO:0030054|GO:0021522|GO:0007528|GO:0045211|GO:0005634|GO:0046872|GO:0007399 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74972_PI430048170 0.745205732913681 1.04268285243081 0.46427739703277 0.496170269931931
0.867543586381524 A A A 0.5104811095553930.5138419018163420.653856452360535 A A A
LNCV6_74972_PI430048170 mRNA
CTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAA NM_016205 RefSeq
chr4 - 156761610 156971394 PDGFC 56034 "platelet derived growth factor C, transcript variant 1"
GO:0005515|GO:0009986|GO:0005886|GO:0050730|GO:0045740|GO:0005576|GO:0005634|GO:0048146|GO:0009
790|GO:0005161|GO:0007417|GO:0005615|GO:0042803|GO:0005737|GO:0007171|GO:0071230|GO:0000139|GO:0
009887|GO:0005788|GO:0051781|GO:0048008|GO:0008083|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_133821_PI430048170 0.6640378170960131.0694516979669 8.66677268484997 9.0394038288851
9.19804401881929 P P P 8.9033184622246 8.75141239181662 8.99841775669204 P P P
LNCV6_133821_PI430048170 mRNA
CAGAGGAAGCATTGATTTCTCATTGACCAGGGTTTGTTCTTGGTAGGGTTTTTCTTTTTC NM_032725 RefSeq chr11
- 116748169 116772998 BUD13 84811 "BUD13 homolog (S. cerevisiae), transcript variant 1"
GO:0005515|GO:0006406|GO:0000398|GO:0005654|GO:0005634|GO:0070274 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137707_PI430048170 0.00698212889238581 0.3734733884183464.20052527829464
4.40364027954297 3.74252637146167 P P P 5.3621704943743 5.57857854771461
5.72302801048177 P P P LNCV6_137707_PI430048170 mRNA
TTCCCTGCCGTCGTTTCTGGGAGGTTGAAAAATTGATCCAGAAAGACCTAAAACAAAAAA NM_006068 RefSeq chr4
- 38823707 38856817 TLR6 10333 toll-like receptor 6
GO:0034142|GO:0005886|GO:0042088|GO:0006955|GO:0006954|GO:0042498|GO:0002755|GO:0042496|GO:0030
670|GO:0004872|GO:0043507|GO:0043123|GO:0042742|GO:0071723|GO:0045410|GO:0071726|GO:0038124|GO:0
046982|GO:0007250|GO:0034150|GO:0038123|GO:0034134|GO:0002224|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140785_PI430048170 0.0718089397051954 0.875961802805619 15.1883644373571
15.3430010052477 15.38348582894 P P P 15.4318454061865 15.4614129385349
15.5966332491282 P P P LNCV6_140785_PI430048170 mRNA
AAAGACACTGACATGTAATTCTTCTCTATTGTAAGGTTTCCATTTAGTTTGCTTCCGATG NM_005998 RefSeq chr1
- 156308960 156338415 CCT3 7203 "chaperonin containing TCP1, subunit 3 (gamma), transcript variant
1"
GO:0005515|GO:0005886|GO:0005832|GO:0005874|GO:0007339|GO:0005524|GO:0044297|GO:0005829|GO:0046
931|GO:0005737|GO:0006457|GO:0051084|GO:0002199|GO:0051082|GO:0005856|GO:0044267|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131078_PI430048170 0.0517160751451824 1.18027166362184 8.01637272114154
8.14461244630837 8.10181690887437 P P P 7.76470973448928 7.79099201297367
7.98272477880071 P P P LNCV6_131078_PI430048170 mRNA
ACTCTAGAACTGTGTACCATCCAATTCGCCATCATAAAGGAATCTTCCTGCATCTCGAAA NM_021260 RefSeq chr14
- 72969444 73027212 ZFYVE1 53349 "zinc finger, FYVE domain containing 1, transcript variant 1"

GO:0005515|GO:0005545|GO:0048471|GO:0005776|GO:0005795|GO:0005783|GO:0043325|GO:0010923|GO:0005547|GO:0044233|GO:0008270|GO:0000407 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107082_PI430048170 0.0170906986728934 0.6684740199711972.92125309410718
3.10409194008757 3.30745393000245 A P P 3.50583782250459 3.7839107646558 3.7939967740599
P P P LNCV6_107082_PI430048170 mRNA
TGATATTACAACAGCAGCAACAGCAAATTCAGCCAATCACACTTCAGAATTCAACTCAAG NM_024947RefSeq chr3
- 170087579 170181749 PHC3 80012 polyhomeotic homolog 3 (Drosophila)
GO:0035102|GO:0031519|GO:0008270|GO:0007275|GO:0005654|GO:0005634|GO:0015629|GO:0003677|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134217_PI430048170 0.4057923141212031.18183552997933 3.72232921697769
3.48817516095088 3.83934070112951 P P P 3.49756746830117 3.80564706594716
2.90618359801316 P P P LNCV6_134217_PI430048170 mRNA
GGGGGGTGTTAATTTATGCACTTATAAGGTGTTTTCTGTGTAACCATTTTATAAAGTGCT NM_001195517 RefSeq
chr10 + 101131303 101137789 TLX1 3195 "T-cell leukemia homeobox 1, transcript variant 2"
GO:0048645|GO:0043565|GO:0005515|GO:0008284|GO:0045165|GO:0046982|GO:0045944|GO:0030182|GO:0005634|GO:0048536|GO:0007417 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99938_PI430048170 0.4460508937455881.06909859896328 6.86782239221735 6.99644716266282
6.95242167401102 P P P 7.0502419251045 6.70064572675744 6.75448462675981 P P P
LNCV6_99938_PI430048170 mRNA
ACTGTATTGATATCAATGAGTGTTTGAGTATCAGTGCCCCGTGCCCTATCGGGCATACAT NM_006486RefSeq chr22
+ 45502838 45601134 FBLN1 2192 "fibulin 1, transcript variant D"
GO:0007566|GO:0005509|GO:0005578|GO:0005576|GO:0005615|GO:0005604|GO:0016504|GO:0031012|GO:0010952|GO:0030198|GO:0016032|GO:0005201|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141937_PI430048170 0.2175979036706390.7885851640415947.38565996345794
7.27152325566347 7.58978670292477 P P P 7.41579725007792 7.74653010840177 8.059443070911
P P P LNCV6_141937_PI430048170 mRNA
CAGATGCTATTTAGAGGGAATCAGAAAAATGCCAAGCCTTTTCTCTTTGAATGTGCTATT NM_017553RefSeq chr15
- 40978880 41116246 INO80 54617 "INO80 complex subunit, transcript variant 1"
GO:0005515|GO:0043014|GO:0030307|GO:0005874|GO:0003779|GO:0005634|GO:0051225|GO:0003677|GO:0005524|GO:2000045|GO:0071479|GO:0003678|GO:0006302|GO:0031011|GO:0034644|GO:0000070|GO:0000724|GO:0045944|GO:0010571|GO:0070914|GO:0006338|GO:0032508|GO:0016887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_74941_PI430048170 0.00652892726858643 0.7408588172648785.63623351743293
5.63222923893763 5.57997232449132 P P P 6.0514123814711 5.96147994678344
6.12951819141751 P P P LNCV6_74941_PI430048170 mRNA
GCTCAAGAACTGTGGACCTTGAACTTGAAGCTCAGATTGATATATTAAGGGATAACAAGA NM_001287432 RefSeq
chr4 + 152779936 152911911 ARFIP1 27236 "ADP-ribosylation factor interacting protein 1, transcript variant 5" GO:0000139|GO:0019904|GO:0070273|GO:0050708|GO:0032588|GO:0006886|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138505_PI430048170 0.00470537160462178 0.3326358386214594.63403985817996
3.98750748244201 4.58261179898871 P P P 5.86574395056973 5.85927146403756
6.28544346455395 P P P LNCV6_138505_PI430048170 mRNA
GCTCAGAGCAACCCTTAAGAGAACTTTTGGCAGATTTTGTTGGCATTATTGAAATATATA NM_033426RefSeq chr14
+ 77098234 77117287 CIPC 85457 CLOCK-interacting pacemaker
GO:0005634|GO:0048511|GO:0042754|GO:0045892|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137144_PI430048170 0.3186575042733480.9047702987984029.98695824203311
10.3584634808338 10.2484596068426 P P P 10.3744684326392 10.4418493136627
10.2272144236586 P P P LNCV6_137144_PI430048170 mRNA

TGGCACGATGACGCATGAAGGAGATTATGTTGTGCTCTTTATTGCCAAAAATAAACACTT NM_018110RefSeq chr16 - 57471957 57486473 DOK4 55715 docking protein 4
GO:0005515|GO:0000165|GO:0005158|GO:0005057|GO:0007169|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137077_PI430048170 0.11429591075258 0.38863566593375 3.15364176733541 3.56024753115203 2.36090786552471 P P A 3.29621145523744 4.81534981934932 4.83237198521497 P P P LNCV6_137077_PI430048170 mRNA
CCACACTGACCCTGATACAGGCATGGCAGAAGAATGGGAATATTTTATACTGACAGAAAT NM_000758RefSeq chr5 + 132073791 132076170 CSF2 1437 colony stimulating factor 2 (granulocyte-macrophage)
GO:0005515|GO:0071803|GO:0008284|GO:0010744|GO:0045740|GO:0042523|GO:0001892|GO:0032747|GO:0005576|GO:0097028|GO:0005125|GO:0005615|GO:0010628|GO:0042045|GO:0006955|GO:0071222|GO:0042116|GO:0045918|GO:2001240|GO:0043011|GO:0008083|GO:0005129 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144045_PI430048170 0.135861740594021 1.20579928393794 9.35061827693133 9.36324278363662 9.24687108821717 P P P 9.25566296427389 9.02700711842731 8.84088464027355 P P P LNCV6_144045_PI430048170 mRNA
TCTACTCTCTCAAACGGAGCAGGTCGAAATTTCAGAAAAACACTGTTAGTTCGGGGCCAT NM_018217RefSeq chr20 - 35115356 35147358 EDEM2 55741 "ER degradation enhancer, mannosidase alpha-like 2, transcript variant 1"
GO:0006986|GO:0006457|GO:0005509|GO:0004571|GO:0005789|GO:0005788|GO:0005576|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134914_PI430048170 0.747433157448003 1.01100336568063 10.6223255027704 10.656760469833 10.6010014244574 P P P 10.5552120623495 10.5761715872539 10.6977468924616 P P P LNCV6_134914_PI430048170 mRNA
TATTTCTGACCCGCTTTAGAACTTAAGACCTGATTCTAGCAATAAACGTGTCCGAGATGA NM_001130955 RefSeq chr19 + 7439687 7472485 ARHGEF18 23370 "Rho/Rac guanine nucleotide exchange factor (GEF) 18, transcript variant 2"
GO:0051056|GO:0048011|GO:0030036|GO:0030054|GO:0043065|GO:0007264|GO:0008360|GO:0045177|GO:0097190|GO:0005829|GO:0005085|GO:0043547|GO:0005737|GO:0032321|GO:0007179|GO:0005089|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136763_PI430048170 0.877747744879834 0.992701528007559 1.98673530037058 0.451508303878097 0.368445603665979 A A A 0.368909678796987 1.01737975652402 1.74626553584451 A A A LNCV6_136763_PI430048170 mRNA
CTGTATGCCTTGCTTCTACCATGAGCAGAGACAATTAAAATCTTTATTCCAGTGAAAAAA NM_000906RefSeq chr1 + 153678687 153693992 NPR1 4881 natriuretic peptide receptor 1
GO:0030308|GO:0042562|GO:0008528|GO:0035556|GO:0042312|GO:0016941|GO:0050880|GO:0042417|GO:0007589|GO:0019901|GO:0048662|GO:0004383|GO:0005525|GO:0005524|GO:0043235|GO:0004672|GO:0007186|GO:0005887|GO:0006182|GO:0016525|GO:0035815|GO:0043114|GO:0008217|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138489_PI430048170 0.317165901953694 1.08956813903946 0.314845649601134 0.56993101122124 0.290469602883329 A A A 0.278192559741242 0.272205341456998 0.270492244137524 A A A LNCV6_138489_PI430048170 mRNA
TCAAAAGGAAACTTCCTTTCCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGA NM_207392RefSeq chr19 - 35487323 35490531 KRTDAP388533 "keratinocyte differentiation-associated protein, transcript variant 1" GO:0005576|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135831_PI430048170 0.156191747850431 1.26619415189489 4.47050270073243 4.35489558809114 4.25658046194351 P P P 4.25676738185445 4.06770596880401 3.68700748237864 P P P LNCV6_135831_PI430048170 mRNA
ACATGGCCCACAGCTCCTGTGCTGGCCAGACTCCCAGAAAATTCTCTATTTTTTAAGTAA NM_001199570 RefSeq

chr19 - 36014659 36032671 CLIP3 25999 "CAP-GLY domain containing linker protein 3, transcript variant 1"
GO:0005802|GO:0008017|GO:0031115|GO:0043065|GO:0005795|GO:0005886|GO:0035594|GO:0018230|GO:0044091|GO:0032588|GO:0010828|GO:0045807|GO:0031901|GO:0001934|GO:0045444|GO:0045121|GO:0072321|GO:0055038|GO:0090004. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57741_PI430048170 0.0222684073429431.42330363476874 6.1492595687648 6.07252245216528 6.18446415754511 P P P 5.64362572487991 5.77165870938084 5.44713420880119 P P P
LNCV6_57741_PI430048170 mRNA
AATGTTTCTTTTTTAAAGGCGGCTCTTGAAGCGACCCGGAAGCGGAAGTGGAAGAAAGTT NM_003860RefSeq chr11 + 66002078 66004146 BANF1 8815 "barrier to autointegration factor 1, transcript variant 1"
GO:0005515|GO:0007077|GO:0005694|GO:0007084|GO:0005634|GO:0015074|GO:0009615|GO:0003677|GO:0005829|GO:0005737|GO:0016032|GO:0005654|GO:0000278|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132364_PI430048170 0.2247505279742391.57448408075022 1.38691935141481 1.4313903804875 0.386776188964591A A A 0.41297965088345 0.630639688485641 0.405661681484159A A A
LNCV6_132364_PI430048170 mRNA
TTGATAACCCAGACTCAAATATCATTGCCTTCCTCCAGGAGTAATTAGGAACAGCTGAGG NM_175060RefSeq chr14 - 38253999 38256370 CLEC14A 161198 "C-type lectin domain family 14, member A"
GO:0030246|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140697_PI430048170 0.0278603614943902 0.46231271070395811.0943412097361 10.994998497909 11.4955993188354 P P P 11.8273906080072 12.3432315740591 12.6793255219922 P P P LNCV6_140697_PI430048170 mRNA
AATTTCCTATCTTGCAGCATCCTGTAAATAAACATTCAAGTCCACCCTTTTCTTGACTTC NM_002266RefSeq chr17 + 68035731 68046854 KPNA2 3838 "karyopherin alpha 2 (RAG cohort 1, importin alpha 1)"
GO:0005515|GO:0042826|GO:0019221|GO:0006259|GO:0006607|GO:0005829|GO:0005737|GO:0016020|GO:0008565|GO:0016032|GO:0005654|GO:0008139|GO:0000018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130325_PI430048170 0.0289976157377576 0.3075675526830381.60736969262143 0.486459358542197 0.447739986595738A A A 2.79864779754105 2.78399182951953 2.33650625036906 P P A LNCV6_130325_PI430048170 mRNA
AAGTTGATCCTTACATATGCCATCCTTCTGTGTCATTTTGTGGCTGTTCTGTGTTTTTCT NM_181671RefSeq chr17 + 67377280 67697263 PITPNC1 26207 "phosphatidylinositol transfer protein, cytoplasmic 1, transcript variant 2" GO:0005515|GO:0007165|GO:0005737|GO:0015914|GO:0008526|GO:0005654|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139819_PI430048170 0.309532395251814 0.869403360308157 11.3385828211457 11.0373071712073 10.9865386919222 P P P 11.5450329125049 11.0945613628024 11.3190916712714 P P P LNCV6_139819_PI430048170 mRNA
TTCAGACTGCCCCTCCCCTTTTTGTAAAAAGTCCATTTACTGTAAAATCGTTTTTTCCAG NM_001278698 RefSeq chr3 + 184362982 184368595 POLR2H 5437 "polymerase (RNA) II (DNA directed) polypeptide H, transcript variant 1"
GO:0008380|GO:0010467|GO:0006368|GO:0006386|GO:0006367|GO:0006385|GO:0006366|GO:0006363|GO:0006362|GO:0006361|GO:0005634|GO:0006360|GO:0006383|GO:0005829|GO:0005736|GO:0034587|GO:0005665|GO:0016032|GO:0005666|GO:0032481|GO:0035019|GO:0006370|GO:0003677|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127797_PI430048170 0.198505250556543 1.01677322609137 0.310820221596786 0.266792936004198 0.291415174234638A A A 0.26938599489041 0.261547684196288 0.266427218670311A A A LNCV6_127797_PI430048170 mRNA
ATCATGAGATCCTTCTCTTCATCAAGAAACTTGCAAGAAAGGTTAAGGAGGAAGGAATAA NM_021002RefSeq chr9 - 21350317 21350887 IFNA6 3443 "interferon, alpha 6"
GO:0005132|GO:0019221|GO:0005576|GO:0005575|GO:0033141|GO:0045343|GO:0005125|GO:0005615|GO:0002

250|GO:0051607|GO:0060337|GO:0060338|GO:0042100|GO:0007596|GO:0045087|GO:0006959|GO:0030183|GO:0
043330|GO:0002286|GO:0002323 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129848_PI430048170 0.4134311496743081.2029363596896 4.15533286529109
4.17288576448692 4.22160490714428 P P P 4.06988214862051 4.27042391334879
3.20529121005237 P P P LNCV6_129848_PI430048170 mRNA
TGAAGCCTCTGATGTTTGAGAAGGATGATGACAGCAACTTCCATGTGGACTTTGTGGTAG NM_003335RefSeq chr3
- 49805204 49813958 UBA7 7318 ubiquitin-like modifier activating enzyme 7
GO:0004842|GO:0016567|GO:0032020|GO:0019221|GO:0004839|GO:0005634|GO:0005524|GO:0005829|GO:0019
941|GO:0045087|GO:0032480|GO:0006464|GO:0019782 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64722_PI430048170 0.6750001893378190.9602429948190561 1.8789665520295 11.6754574559194
11.8224384516986 P P P 11.6597527478086 12.00648878459 11.8727972156231 P P P
LNCV6_64722_PI430048170 mRNA
TACTCAGATGAAAGTGGGAACATGGATTTTGACAACTTCATCAGCTGCTTGGTCAGGCTG NM_001749RefSeq chr19
+ 36139925 36150353 CAPNS1826 "calpain, small subunit 1, transcript variant 1"
GO:0005515|GO:0008284|GO:0005737|GO:0004198|GO:0022617|GO:0016020|GO:0005886|GO:0030198|GO:0005
509|GO:0006508|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65970_PI430048170 0.000780077690758018 1.89236758938942 9.82134599867318
9.67708379385444 9.93019703875658 P P P 8.95058816717699 8.94533736175003
8.77654406798391 P P P LNCV6_65970_PI430048170 mRNA
TAGGGATACTCACTCACCTGTATAGGGACTTTGATAAATGCAGGTTTGCTGGGTTTTGCC NM_017567RefSeq chr2
+ 71068277 71078868 NAGK 55577 N-acetylglucosamine kinase
GO:0005515|GO:0006051|GO:0006044|GO:0046835|GO:0045127|GO:0009384|GO:0019262|GO:0005524|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140355_PI430048170 0.0330128152226188 0.9348469003381191 2.5691501050993
12.5939059345464 12.5957711227955 P P P 12.7096101479619 12.6402041074955 12.699786427062
P P P LNCV6_140355_PI430048170 mRNA
CAGCTCCTTTGTGTGGCACCCTGATGAGTATTTAAAGCCCGTTTTGAAATGCCTAAAAAA NM_001167947 RefSeq
chrX - 48893446 48898143 TIMM17B 10245 "translocase of inner mitochondrial membrane 17
homolog B (yeast), transcript variant 1"
GO:0005744|GO:0015450|GO:0006626|GO:0005743|GO:0031305|GO:0071806|GO:0044267 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138637_PI430048170 0.8925497657409360.9909378195045664.45207888605518
4.94914323561184 4.92859054028136 P P P 4.71368362739094 4.73926837054421
4.95636159711351 P P P LNCV6_138637_PI430048170 mRNA
AAAGATTAACTTTTGACTAACCCTGGAATATCTCTTATCTCACTTATAGCTTCAGGCATG NM_001289758 RefSeq
chr10 + 89327818 89340968 IFIT3 3437 "interferon-induced protein with tetratricopeptide repeats
3, transcript variant 3"
GO:0005515|GO:0043066|GO:0008285|GO:0035457|GO:0019221|GO:0009615|GO:0005829|GO:0042802|GO:0005
739|GO:0003674|GO:0005737|GO:0051607|GO:0060337 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_42022_PI430048170 0.000661385062244327 1.75477428135593 6.912819294978
6.80650318004466 6.91079660973391 P P P 6.16796758673354 6.04890480902227
5.97535221847823 P P P LNCV6_42022_PI430048170 mRNA
ATTCTTGTAAGTGTTGCTGGTGTCAGAATAGGAACCTCCCTGCGCTTTGAAGGGATGAAT NM_001290221 RefSeq
chr6 + 2999815 3019876 NQO2 4835 "NAD(P)H dehydrogenase, quinone 2, transcript variant 1"
GO:0001512|GO:0005737|GO:0009055|GO:0007613|GO:0005654|GO:0046872|GO:0008753|GO:0070062|GO:0055
114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127276_PI430048170 0.11724724090025 2.50880164647732 3.03759073289245
1.65910931193367 1.706361905942 P A A 0.8446435553785261.09508015423138
0.926381302538319A A A LNCV6_127276_PI430048170 mRNA

GAGGTGCATGCATGGGGCCACCTTTGCAACATAACCGAAAGAATAAATGTTTTGTTCTGT NM_152591 RefSeq chr12 + 110846959 110907535 CCDC63 160762 "coiled-coil domain containing 63, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133598_PI430048170 0.3637009910939891 0.07516807267984 8.69932460885864 8.66256590285368 8.51568722450177 P P P 8.3530421123332 8.64307692403195 8.55902139223788 P P P LNCV6_133598_PI430048170 mRNA
ACCGTATTTATGGAATGACAAAATAAATAAAGCCCAAACCCATCGGTCTCTGTGAAAAAA NM_001199860 RefSeq chr1 + 6034287 6101193 KCNAB2 8514 "potassium channel, voltage gated subfamily A regulatory beta subunit 2, transcript variant 3"
GO:0005886|GO:0044224|GO:0005874|GO:0007268|GO:0015459|GO:0051291|GO:2000008|GO:0005829|GO:0031234|GO:0070995|GO:0004033|GO:0016020|GO:0002244|GO:0005249|GO:0008076|GO:0071805|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142686_PI430048170 0.285844173798335 0.663936691404768 1.98715839440133 3.62154020914292 1.83269811452532 A P A 3.00836607965149 3.50096797893415 3.39322090811001 P P P LNCV6_142686_PI430048170 mRNA
GCTCTACTGGACTTGACAGATCACATTTTGAGAGTGAATTCATTTAAACAATAAACCTCT NM_018383 RefSeq chr2 - 127704233 127811187 WDR33 55339 "WD repeat domain 33, transcript variant 1"
GO:0006379|GO:0006378|GO:0005581|GO:0005847|GO:0005730|GO:0005654|GO:0005634|GO:0007283|GO:0006301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140694_PI430048170 0.879074517144104 1.00376995788032 0.356319045702712 0.332239789667377 0.262538995486112 A A A 0.311977677488984 0.323049537047851 0.301339157807205 A A A LNCV6_140694_PI430048170 mRNA
AAACCTTAAGTAAGCAACAGCATAACAAGGTCCAAGATACCTAAAAGAGATTTCAAGAGA NM_000880 RefSeq chr8 - 78732771 78805523 IL7 3574 "interleukin 7, transcript variant 1"
GO:0005515|GO:0010468|GO:0043066|GO:0008284|GO:0046622|GO:0030890|GO:0045453|GO:0007267|GO:0005576|GO:0043086|GO:0005125|GO:0005615|GO:0048873|GO:0006959|GO:2001240|GO:0009887|GO:0002360|GO:0005139|GO:0008083|GO:0045582 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69168_PI430048170 0.0582875992130796 0.671470914848971 4.52373214221627 4.2735081813833 4.85515319653288 P P P 5.17522876638157 4.87339604238724 5.34765030337421 P P P LNCV6_69168_PI430048170 mRNA
TATGATGGGCATGCTGGTTCTCAGGTTGCCAAATACTGCTGTGAGCATTTGTTAGATCAC NM_021003 RefSeq chr14 + 60249247 60299087 PPM1A 5494 "protein phosphatase, Mg2+/Mn2+ dependent, 1A, transcript variant 1"
GO:0005515|GO:0008286|GO:0043005|GO:0010467|GO:0042347|GO:0006367|GO:0010991|GO:0030177|GO:0005634|GO:0005829|GO:0035970|GO:0006470|GO:0007050|GO:0007179|GO:0004871|GO:0004722|GO:0043123|GO:0016055|GO:0006499|GO:0030512|GO:0043124|GO:0033192|GO:0000287|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134892_PI430048170 0.737341230961509 0.858288881791621 2.51504087284423 1.89958601175569 2.13264785156777 A A A 2.78523456797012 1.58855802159833 2.63582267490574 P A P LNCV6_134892_PI430048170 mRNA
TATTGTGTGGAGTTGTCGATACCACGTGAATTCATACACAATAAAAAGCCTCACTCTCCC NM_052847 RefSeq chr19 - 2511219 2702748 GNG7 2788 "guanine nucleotide binding protein (G protein), gamma 7"
GO:0005886|GO:0005834|GO:0007268|GO:0044281|GO:0006112|GO:0008277|GO:0007186|GO:0071377|GO:0001662|GO:0007626|GO:0004871|GO:0045761|GO:0007168|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131936_PI430048170 0.166974447600896 1.04596419002324 0.592783273711753 0.634332738958836 0.551901997141482 A A A 0.587619100528013 0.497682018624445 0.498530016905047 A A A LNCV6_131936_PI430048170 mRNA
CGAGCAGACTTCTTTACTACACTGCACTGGATTGCTATATTTTTAACCAGAAATAAACTA NM_020655 RefSeq chr16

+ 87602886 87698155 JPH3 57338 "junctophilin 3, transcript variant 1"
GO:0060402|GO:0005886|GO:0030314|GO:0040011|GO:0003674|GO:0014701|GO:0048168|GO:0060314|GO:0070
588|GO:0050885|GO:0015278|GO:0007613|GO:0007612|GO:0016021|GO:0035640 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138267_PI430048170 0.3080845876304171.547876406593 0.292527734025728
1.58668172946692 0.648470811898391 A A A 0.3155880241814690.291146966313483
0.351931101230192 A A A LNCV6_138267_PI430048170 mRNA
TATTTTGAACCAGGTGGGAAAAGTTAATGAAAGCCCTACAGTCAGGAAATGTGACTGCGA NM_052845 RefSeq chr12
- 109553715 109573553 MMAB 326625 "methylmalonic aciduria (cobalamin deficiency) cblB type,
transcript variant 1"
GO:0009236|GO:0008817|GO:0009235|GO:0006766|GO:0005759|GO:0006767|GO:0044281|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136628_PI430048170 0.00314675478295938 0.6043566527947863.19199116349387
2.94996593408072 3.15905372592092 A A P 3.92319007368757 3.65871476696851 3.8960430083092
P P P LNCV6_136628_PI430048170 mRNA
GGCAGTTTCTAAACAGAGCTTTTTCTATACACTATTTGCAACTGGAGTGCAATATTGTAT NM_001077710 RefSeq
chr2 - 38813 46588 FAM110C 642273 "family with sequence similarity 110, member C"
GO:0005515|GO:0051897|GO:0005737|GO:0000922|GO:0030335|GO:0005815|GO:0043014|GO:0005874|GO:0060
491|GO:0005654|GO:0005938 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127278_PI430048170 0.0159012864074468 0.5816049254196738.19243954265853
7.93790342232593 7.70315723839138 P P P 8.59546891201595 8.82250725855877
8.79232282007694 P P P LNCV6_127278_PI430048170 mRNA
CATGCTGGGAGGGAGGATGTGTGCATTTTGTAAATAAACATATTTGCCCTGGGGAAAAAA NM_001267723 RefSeq
chr19 + 45995460 46018616 CCDC61 729440 coiled-coil domain containing 61 GO:0005813 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107876_PI430048170 0.0355981802276759 1.22557403153892 5.31914672474828
5.43164880943919 5.48180610369452 P P P 5.24546492181096 5.10990390564063
4.99032713638845 P P P LNCV6_107876_PI430048170 mRNA
TATGGGCATTACTTGGACGACTATCACACAAAAAGGACTTCATCCCTTGTCAGCCTGTCA NM_001174090 RefSeq
chr20 - 3227416 3238189 SLC4A11 83959 "solute carrier family 4, sodium borate transporter,
member 11, transcript variant 1"
GO:0046715|GO:0046713|GO:0035445|GO:0005272|GO:0030003|GO:0042044|GO:0016323|GO:0005452|GO:0005
887|GO:0015106|GO:0046983|GO:0051453|GO:0015252|GO:0015701|GO:0035725|GO:0006814|GO:0015293|GO:0
015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132775_PI430048170 0.0580850801170450.4657534150096671.05433785894027
0.6087551603067580.441568997630306 A A A 1.92258936579409 2.21367140450885
1.15016093075173 A A A LNCV6_132775_PI430048170 mRNA
CCCAAGGGGGAAGGGAGGACAGTTTTTCTTTGTTCTGCTTTTTGTTTTAATAAAAATTAT NM_001029883 RefSeq
chr2 - 29061689 29074261 C2orf71 NA chromosome 2 open reading frame 71 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140570_PI430048170 0.4144228187435721.23928093610535 0.4513164549521291.1069512708417
0.259147633895215 A A A 0.3642149357979220.3417319395754120.324874030694389 A A A
LNCV6_140570_PI430048170 mRNA
TATGCCTTTCAGGATGATGGTAGAGCAATATTAAACAAGCTTCCACTTTTGACTGCTAAA NM_001243509 RefSeq
chr1 - 216503245 217076970 ESRRG 2104 "estrogen-related receptor gamma, transcript variant 9"
GO:0005515|GO:0010467|GO:0006355|GO:0000977|GO:0006367|GO:0003707|GO:0050682|GO:0003708|GO:0001
228|GO:0048384|GO:0045944|GO:0043401|GO:0005654|GO:0008270|GO:0045893|GO:0005496 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128598_PI430048170 0.00708928819298389 0.3882379310282817.19801540224647

7.54640563520723 7.7597939972878 P P P 9.02674266571342 8.45806382563466
9.08934171762871 P P P LNCV6_128598_PI430048170 mRNA
CTGAATATTAAAACCTTACTTAGTGACTGGAATGGTATATGCTCCCTCCAAAAGTTTATC NM_004696 RefSeq chr1
- 110362850 110391082 SLC16A4 9122 "solute carrier family 16, member 4, transcript variant 1"
GO:0015718|GO:0034220|GO:0016020|GO:0005887|GO:0008028|GO:0016021|GO:0015293 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143217_PI430048170 0.322870181385888 1.03487516685711 0.309624199504234
0.258360666807427 0.387034459536034 A A A 0.278609224713234 0.252105193473489
0.278688917979367 A A A LNCV6_143217_PI430048170 mRNA
TTCCGCGCTGGCGTAAAATTGGAAAAGGCTGAGAAACAAAGTAAAACAGTATTTTGTTTG NM_144674 RefSeq
chr16 - 10627503 10694945 TEKT5 146279 tektin 5
GO:0005929|GO:0005737|GO:0005874|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143044_PI430048170 0.215375433133708 0.813511233198762 6.68021702286736
6.24953778210847 6.67282780246131 P P P 6.55327960036548 6.90894401221713
7.03253802404243 P P P LNCV6_143044_PI430048170 mRNA
TTCAAAATAATCTTTTAAGAAGCCAGGATTCTCCGGTCTGGAATTTCTGAGTGAGTCCTT NM_001244580 RefSeq
chr7 + 98878489 99013243 TRRAP 8295 "transformation/transcription domain-associated protein,
transcript variant 1"
GO:0003712|GO:0005515|GO:0016578|GO:0006355|GO:0007093|GO:0005794|GO:0016573|GO:0030914|GO:0003
713|GO:0006325|GO:0005634|GO:0000812|GO:0006351|GO:0033276|GO:0016310|GO:0006281|GO:0043967|GO:0
016301|GO:0000125|GO:0043968|GO:0035267|GO:0016773|GO:0005654 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_37716_PI430048170 0.564326429168341 1.07602664235943 5.41052410983652
5.13756602551926 5.33708985748691 P P P 4.92194064319143 5.10802583933684
5.49205890614142 P P P LNCV6_37716_PI430048170 mRNA
GTGTATATGGAAAAGTCTCATGCACCTGGATTAACTCAGAAAAAGTAAAGTCCTGAAACT NM_022081 RefSeq
chr22 - 26450882 26483863 HPS4 89781 "Hermansky-Pudlak syndrome 4, transcript variant 1"
GO:0005515|GO:0042470|GO:0042827|GO:0050821|GO:0030318|GO:0006605|GO:0005764|GO:0042803|GO:0007
599|GO:0005737|GO:0031085|GO:0016020|GO:0007596|GO:0046983|GO:0007040|GO:0048075 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130900_PI430048170 0.0199021128022254 6.82839206363578 4.16016536102098
4.71940753193081 4.12550163966145 P P P 1.81341160876842 2.06780172211074
0.406237324827837 A A A LNCV6_130900_PI430048170 mRNA
TTTCTGTGAAATAAAGACTTTTTGTATTTCTGGGGCTGAGGCTCAGCAACAGCCCCTCAG NM_005764 RefSeq
chr1 - 47183588 47190099 PDZK1IP1 10158 PDZK1 interacting protein 1
GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132798_PI430048170 0.00292018910790893 2.42847646327568 9.04630942770994
9.13762668892305 8.98528215569562 P P P 7.62175739174652 7.98377904988772
7.70209058969853 P P P LNCV6_132798_PI430048170 mRNA
TACTGGAATAGATTCCGAGGAGCAGGAGTGCTCAATAAAATGTTGGTTTCCAGCAAAAAA NM_001197 RefSeq
chr22 + 43110747 43129712 BIK 638 BCL2-interacting killer (apoptosis-inducing)
GO:0032464|GO:0005515|GO:0051400|GO:0031966|GO:0008637|GO:0046982|GO:0090200|GO:0006915|GO:0016
021|GO:0007283|GO:0008584|GO:0012505 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_134355_PI430048170 0.150517750773661 1.03245934450117 0.463225198959622
0.519786274844204 0.45092107074807 A A A 0.414202839138016 0.430340053307877
0.451826530436473 A A A LNCV6_134355_PI430048170 mRNA
TTTCTACGTGGTGCAGCTGCTGAACCTCTTCGTGACCAGCCTTGATGCCACCGTCAACCA NM_001052RefSeq chr20

+ 23035419 23036677 SSTR4 6754 somatostatin receptor 4
GO:0019369|GO:0043005|GO:0008285|GO:0005886|GO:0007268|GO:0071385|GO:0004994|GO:0005737|GO:0042
923|GO:0007186|GO:0016477|GO:0005887|GO:0007187|GO:0007218|GO:0030815|GO:0030900|GO:0043410 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133433_PI430048170 0.00463434794301018 0.7139885147294519.27596825999035
9.06293356978445 9.22031975607056 P P P 9.6161697112949 9.62631105775559
9.77746831962345 P P P LNCV6_133433_PI430048170 mRNA
CTGCTTCTGTTTGGTCTTAGAGTGTTTGGATATAACTGAATTGTAGATGGTAAAGGAAAT NM_018047RefSeq chr5
- 150690789 150701107 RBM22 55696 RNA binding motif protein 22
GO:0045292|GO:0005634|GO:0090316|GO:0071013|GO:0035690|GO:0033120|GO:0046872|GO:0005737|GO:0000
166|GO:0005487|GO:0000398|GO:0017069|GO:0005654|GO:0036002|GO:0048306|GO:0000060 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143830_PI430048170 0.00087876432263398 0.1272752058996274.50341785734806
3.75511671216654 4.18846317205906 P P P 6.89494145799164 7.31869705044948
7.21814019350233 P P P LNCV6_143830_PI430048170 mRNA
CGAAAACAAAGTTGGGGCTGTATTTCTTTAAAAAGATAAGCCTCTAAAAATGCTTGGCAA NM_015283RefSeq chr7
- 34928880 35038041 DPY19L1 23333 dpy-19-like 1 (C. elegans)
GO:0000030|GO:0016020|GO:0018406|GO:0005637|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_116997_PI430048170 0.9890073931727040.9998283038101551 1.8628730740512
11.9623653173708 12.0201450100987 P P P 12.0159673408848 11.934459678329
11.8975062920714 P P P LNCV6_116997_PI430048170 mRNA
CAAAAATTGGAGATATATTGTGCCTATGCTTACGGTGGATGGGAAGAGAGTCCCAAGGGA NM_006066RefSeq chr1
+ 45550782 45570051 AKR1A1 10327 "aldo-keto reductase family 1, member A1 (aldehyde reductase),
transcript variant 1"
GO:0046185|GO:0006081|GO:0042840|GO:0009055|GO:0005615|GO:0005829|GO:0004032|GO:0016324|GO:0019
853|GO:0006006|GO:0047939|GO:0055114|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95249_PI430048170 0.7993324973491180.9658087500145767.58469084272063 7.74468754282299
7.56911166929515 P P P 7.92192154726696 7.62414794038423 7.47294057341846 P P P
LNCV6_95249_PI430048170 mRNA
CCCTATGGTCAGCCACCTCCAAGTTCCTACGGTGCCCAGCAGCCTGGGCTTTATGGACAG NM_012392RefSeq chr1
- 31629861 31645237 PEF1 553115 "penta-EF-hand domain containing 1, transcript variant 1"
GO:0005515|GO:0051592|GO:0005737|GO:0004198|GO:0046982|GO:0016020|GO:0005509|GO:0046983|GO:0006
508|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131521_PI430048170 0.0249393976980095 1.36094546566373 8.77735390283485
9.05188362719039 8.93531957720094 P P P 8.50680092588457 8.49630728018712
8.43981211878347 P P P LNCV6_131521_PI430048170 mRNA
GGATTTCTAGGATTTCTAACTCCAGCTGTTCCCATACTGTCTAGTTTAAATTATGGCTGT NM_018641RefSeq chr7
+ 2403559 2434581 CHST12 55501 "carbohydrate (chondroitin 4) sulfotransferase 12, transcript variant
3"
GO:0005975|GO:0044281|GO:0050656|GO:0016051|GO:0030208|GO:0047756|GO:0030173|GO:0030206|GO:0000
139|GO:0016020|GO:0009405|GO:0030204|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133916_PI430048170 0.0746918845079614 0.4440838419220820.679095104261667
0.5641644924115081.85610593186731 A A A 2.43058212355789 2.52037007168385
1.98504295787627 A A A LNCV6_133916_PI430048170 mRNA
CCCGAGCAAAGTCTAAAGTTTACAGTAAATAAATTGTTTGACCATGCCTTCATTGCAAAA NM_000024RefSeq chr5
+ 148826592 148828634 ADRB2 154 "adrenoceptor beta 2, surface"
GO:0005515|GO:0005886|GO:0045453|GO:0004941|GO:0009409|GO:0002024|GO:0002025|GO:0015459|GO:0005
634|GO:0005764|GO:0042803|GO:0051380|GO:0042312|GO:0007190|GO:0031649|GO:0007171|GO:0016324|GO:0

045986|GO:0040015|GO:0045944|GO:0031398|GO:0030501|GO:0008179|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137296_PI430048170 0.0945786236878679 1.40291836977051 4.21559900547726 3.68040819277045 3.85541095890558 P P P 3.47435448508698 3.44356779896285 3.42019121520719 P P P LNCV6_137296_PI430048170 mRNA
TAAAACACACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGAC NM_001242 RefSeq chr12 + 6444884 6451718 CD27 939 CD27 molecule
GO:0005515|GO:0043066|GO:0016064|GO:0070233|GO:0045471|GO:0045579|GO:0046330|GO:0005576|GO:0097191|GO:0008588|GO:0005887|GO:0043154|GO:0007166|GO:0009897|GO:0043027|GO:0070062|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139695_PI430048170 0.2515312369787990.92257012628354 10.7803996467376 10.6419216820101 10.5720581490659 P P P 10.6710273486992 10.8838974753216 10.7882561177907 P P P LNCV6_139695_PI430048170 mRNA
ACAACTCTGTGTGGCTTTTGGACAAATTAAAGCTAGTTTTGGTATCCCCGGGCCAAAAAA NM_001281495 RefSeq chr20 + 37693954 37872129 CTNNBL1 56259 "catenin, beta like 1, transcript variant 2"
GO:0000974|GO:0005515|GO:0008380|GO:0010467|GO:0043065|GO:0006915|GO:0005634|GO:0016445|GO:0005737|GO:0016020|GO:0000398|GO:0005654|GO:0005681|GO:0019899 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136683_PI430048170 0.0796242024400247 0.4277136897135712.35962161958606 1.21489869898884 2.57901440732441 A A A 3.23751596929787 3.29841977710731 3.60014046266797 P P P LNCV6_136683_PI430048170 mRNA
GTGTAAACAGGGCCATTCTATTTCCTAAATCACAACTAATAAAGCAGAGGATGAAAATCA NM_006769 RefSeq chr1 + 87328467 87348923 LMO4 8543 LIM domain only 4
GO:0021514|GO:0050865|GO:0005667|GO:0042659|GO:0003700|GO:0021522|GO:0006366|GO:0001843|GO:0048538|GO:0003281|GO:0021527|GO:0031333|GO:0045944|GO:0008270|GO:0001158|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112413_PI430048170 0.00448993706838952 2.78510292277348 6.82050285152164 6.48729618130844 6.80993985947865 P P P 5.244402782207 5.2637830479291 5.19982380350799 P P P LNCV6_112413_PI430048170 mRNA
GTGATCTTGGAACTTCCATGATTATCCACTTAAAGATCAAAGTATTATATGCTGTGTGCT NM_012106 RefSeq chr16 + 57245125 57253633 ARL2BP 23568 ADP-ribosylation factor-like 2 binding protein
GO:0005515|GO:0005813|GO:0042517|GO:0003713|GO:0005819|GO:0030496|GO:0005634|GO:0005758|GO:0005929|GO:0007165|GO:0005083|GO:0050790|GO:0051457 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139919_PI430048170 0.126704186665861 1.46663803674853 11.1018962483355 10.9623998430264 11.2183162072469 P P P 10.9675619118149 10.1407125017777 10.401096037694 P P P LNCV6_139919_PI430048170 mRNA
GCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTGAATAAAATTGGACTTTGTTTA NM_016306 RefSeq chr3 + 186570675 186585800 DNAJB11 51726 "DnaJ (Hsp40) homolog, subfamily B, member 11"
GO:0005515|GO:0016020|GO:0016556|GO:0006457|GO:0005783|GO:0005788|GO:0005634|GO:0051082|GO:0006987|GO:0044267|GO:0030968 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_34144_PI430048170 0.00356948443017595 1.4483782496211 5.71958641498702 5.86310386199697 5.73805157977696 P P P 5.24572566084216 5.21132265370607 5.26414655541795 P P P LNCV6_34144_PI430048170 mRNA
ACAAAAGACCTCGGGGCCGGCCTCGCAAGGCGCTTCCCCTTTCCAGAGAGCCAGAAAGAA NM_170606 RefSeq chr7 - 152134924 152436005 KMT2C 58508 lysine (K)-specific methyltransferase 2C
GO:0035556|GO:0005515|GO:0035097|GO:0006355|GO:0006325|GO:0008270|GO:0005654|GO:0005634|GO:0042800|GO:0003677|GO:0051568|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144528_PI430048170 0.265401341517291 1.19757770136429 5.65851836800518 5.63131094905557 5.4333595438085 P P P 5.6343131528143 5.24843104002968

4.99847045871797 P P P LNCV6_144528_PI430048170 mRNA
GCCCCAATTTCCCCAAGCCCCATTTTTTCTTGTCTTTATCTAATAAACTCAATATTAAGA NM_033449 RefSeq chr5 -
141639301 141651419 FCHSD189848 FCH and double SH3 domains 1 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_99804_PI430048170 0.9299266982360760.9912316141482844.07164384110544 3.90929484618275
3.81610268126055 P P P 3.90354077922226 3.81160306602101 4.11474444746284 P P P
LNCV6_99804_PI430048170 mRNA
AAATCTTAAGGGACCTTTCCTTACTACAGATTCAAATGCGAGATCTTGAGGGTTACAGGG NM_057175 RefSeq chr4
+ 139301521 139390781 NAA15 80155 "N(alpha)-acetyltransferase 15, NatA auxiliary subunit"
GO:0005515|GO:0031415|GO:0005667|GO:0043066|GO:0008080|GO:0050821|GO:0005634|GO:0001525|GO:0006
351|GO:0030154|GO:0005737|GO:0016020|GO:0043022|GO:0016407|GO:0045893|GO:0006474 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_70655_PI430048170 0.0478330265531470.6235174616802447.82568367036035 7.73195707031075
8.16576533451537 P P P 8.2819705068267 8.53188800448685 8.91880873774453 P P P
LNCV6_70655_PI430048170 mRNA
CCCTCTGGAAGTACCAAAAGAAAAAGAAAAGGAAAAGGTTTCTACTGCTGTATTATCTAT NM_002807 RefSeq chr2
+ 231056863 231172826 PSMD1 5707 "proteasome (prosome, macropain) 26S subunit, non-ATPase, 1,
transcript variant 1"
GO:0010467|GO:0002474|GO:0090263|GO:0044281|GO:0031145|GO:0005829|GO:0034641|GO:0000082|GO:0016
032|GO:0030234|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0000502|GO:0043066|GO:0005838|GO:0
042176|GO:0006521|GO:0051437|GO:0042590|GO:0006915|GO:0042981|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128827_PI430048170 0.00306466101993146 0.2188557786700192.9948014815599
2.57819161815341 3.29381121583702 A A P 4.64803711531167 5.24819565262841
5.50588828393997 P P P LNCV6_128827_PI430048170 mRNA
GGCTGGGAATGCTATGTCTAGGTCATCAGCGGAGAAAGTTGGTTTGTAGAGAATGAACAA NM_032175 RefSeq chr5
+ 73565740 73583377 UTP15 84135 "UTP15, U3 small nucleolar ribonucleoprotein, homolog (S.
cerevisiae), transcript variant 1"
GO:0000462|GO:0005737|GO:0030515|GO:0030054|GO:0045943|GO:0032040|GO:0005730|GO:0005634|GO:0034
455 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121072_PI430048170 0.00366282114182521 0.6620552385287234.03961102434523
3.95069749145545 4.1662664741785 P P P 4.7781088531413 4.63198721164089
4.52863799301075 P P P LNCV6_121072_PI430048170 mRNA
ATGTGGCATCGGGGCTGTTCTGCAAGTGTGAACGGAGACGCTGCCTCCGGATTGTGGAAA NM_015846 RefSeq chr18
- 50268845 50281774 MBD1 4152 "methyl-CpG binding domain protein 1, transcript variant 1"
GO:0000792|GO:0005515|GO:0008327|GO:0003700|GO:0006366|GO:0003714|GO:0005634|GO:0003677|GO:0016
363|GO:0005737|GO:0016607|GO:0008270|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134291_PI430048170 0.0212667094068174 2.68626557593024 11.4198982213655
11.5012147018377 11.4452005179482 P P P 10.4382620048811 9.78174765889004
9.76377367460652 P P P LNCV6_134291_PI430048170 mRNA
AGGGCCACCTGTGACGTCTGCATCTTCTTGGAGAGAGAATAAAGTTTGTATTTAAGTGGT NM_178545 RefSeq chr1
- 1917589 1919301 TMEM52 339456 transmembrane protein 52 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137861_PI430048170 0.43253008831172 0.8795243054739419.58397390972322 9.510698442548
9.85233136255761 P P P 9.51888916009742 9.86114114824084 10.0892201214661 P P P
LNCV6_137861_PI430048170 mRNA
AATTGTACTAGTGTCTGCAGGGTTTGTCAGTACTCGTCAAAGCCAAGTCCAATTAAAAAA NM_015056 RefSeq chr21
+ 43659550 43696079 RRP1B 23076 ribosomal RNA processing 1B
GO:0000792|GO:0000791|GO:0010923|GO:0006364|GO:0005730|GO:0005634|GO:0030688|GO:0005829 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143973_PI430048170 0.8183922720623990.9598112208130054.49881602516123
4.63764869130642 4.57517555865106 P P P 4.38196948173092 4.53808419784018 4.9185647314706
P P P LNCV6_143973_PI430048170 mRNA
GTAGGGAATATATCAACCCGATTTCTTCCTCTCTTTTCCCTTTTATAGGATAAATAATCCNM_016063RefSeq chr6 -
125275349 125302136 HDDC2 51020 HD domain containing 2 GO:0005739|GO:0005515|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129103_PI430048170 0.0800570648450441 0.7513952302792866.26805580364452
6.35457504819417 6.62034591679877 P P P 6.80919910438725 6.59475676291179
7.06187266199409 P P P LNCV6_129103_PI430048170 mRNA
TCTATTTTTCAATGGTCAGTGTCCAGGCTGGGACACAGAACTTATGAACTTTTGCTACAG NM_018849RefSeq chr7
- 87402044 87475703 ABCB4 5244 "ATP-binding cassette, sub-family B (MDR/TAP), member 4,
transcript variant B"
GO:0006629|GO:0005886|GO:0042493|GO:0042626|GO:0042908|GO:0044281|GO:0055085|GO:0005524|GO:0046
581|GO:0008559|GO:0016020|GO:0005887|GO:0006855|GO:0006810|GO:0016021|GO:0044255|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138667_PI430048170 0.00460070474616281 1.91870656920298 6.15849955281973
6.14209534546518 5.9944551574172 P P P 5.10086897910196 4.99862502768662
5.35679673790649 P P P LNCV6_138667_PI430048170 mRNA
CTTCCCCACCGTAAACTATGGACTCTAGTTCAGTTTTATATGCAATGGATCACTATTTTA NM_173490RefSeq chr5
+ 73120560 73131817 TMEM171 134285 "transmembrane protein 171, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135396_PI430048170 0.0190928453442724 0.28031189718494 2.45132691849815
1.21731531048194 2.22407557946509 A A A 3.32873174251655 4.05779032688086
4.15155551805732 P P P LNCV6_135396_PI430048170 mRNA
GACGTGTTCCTTTATATATTTAAGTTCAGCACAGAAACTTTCCTACCTTTTTGTGGAAGA NM_003203RefSeq chr2
- 75662705 75710985 GCFC2 6936 "GC-rich sequence DNA-binding factor 2, transcript variant 1"
GO:0001078|GO:0000245|GO:0006355|GO:0071008|GO:0005730|GO:0005654|GO:0005634|GO:0000122|GO:0000
978|GO:0045892|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135451_PI430048170 0.00928922350962245 2.15259589967779 7.76593558662935
7.89336949218076 7.73016837658826 P P P 6.79623584961101 6.84299141970843 6.3968920929008
P P P LNCV6_135451_PI430048170 mRNA
TATCACTCTCCCCAACAACCTAGATGTGAAAACAGAATAAACTTCACCCAGAAAACACTT NM_022873RefSeq chr1
- 27666060 27672213 IFI6 2537 "interferon, alpha-inducible protein 6, transcript variant 3"
GO:0005739|GO:0005515|GO:0006955|GO:0060337|GO:0005886|GO:0051902|GO:0019221|GO:2001240|GO:0001
836|GO:0016021|GO:0043154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130835_PI430048170 0.0273548430621528 0.6656142201744697.53193880501019
7.25134716888086 7.38902524061285 P P P 8.23199593113148 7.82568367036035
7.85328688801703 P P P LNCV6_130835_PI430048170 mRNA
ATCCCTAGGCTGGCAGTGCAGCAGAAATACTGAATAAAATGTGACAAATCTCCCTGGAAA NM_001669RefSeq chrX
- 2903969 2929375 ARSD 414 arylsulfatase D
GO:0006665|GO:0006687|GO:0005788|GO:0004065|GO:0044281|GO:0044267|GO:0005764|GO:0046872|GO:0070
062|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98137_PI430048170 0.2218707589275030.4965202549267640.6305407566314241.88464701932231
3.5130580827557 A A P 3.12381080079072 3.35946166599503 3.8647032756766 P P P
LNCV6_98137_PI430048170 mRNA
ATAGAACTCGAGCTCTTCAGTGTCTCTTCTATTTGGCTGACAAGGAAACTATAGAATCTC NM_014708RefSeq chr12
+ 122527261 122626400 KNTC1 9735 kinetochore associated 1
GO:0005515|GO:0005828|GO:0007093|GO:0005886|GO:0007096|GO:0005634|GO:0015629|GO:0005829|GO:0000

922|GO:0005737|GO:0007067|GO:0006461|GO:0000777|GO:0000278|GO:0051301 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128991_PI430048170 0.3374687225198890.75378560913076 8.17551013015531
8.12091460570709 8.04338551977816 P P P 7.94446375852132 8.539453525152
8.92018108160025 P P P LNCV6_128991_PI430048170 mRNA
AAGGCACCACACCAGAAATGGGACCTAAATTAAGGCTTAAAGAATGAGCATGGCCACACT NM_024657RefSeq
chrX - 106940733 107000244 MORC4 79710 "MORC family CW-type zinc finger 4, transcript variant 1"
GO:0005515|GO:0008270|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129066_PI430048170 0.00632875216311841 0.29279572593193 0.336916701472686
0.3521107861967860.352496304286112A A A 1.83093161488043 2.18718138790886
2.29924807742675 A A A LNCV6_129066_PI430048170 mRNA
GAGAGGTCATCTAGCTCCAGTTCAAAAGATTATGTATATCTGATGTTTAAGAGGAAAAAC NM_020774RefSeq chr18
+ 21741328 21870957 MIB1 57534 mindbomb E3 ubiquitin protein ligase 1
GO:0005515|GO:0004842|GO:0005813|GO:0016567|GO:0001568|GO:0005886|GO:0016874|GO:0001756|GO:0014
069|GO:0031410|GO:0001701|GO:0001841|GO:0005829|GO:0006897|GO:0045807|GO:0001947|GO:0005737|GO:0
045665|GO:0007219|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92571_PI430048170 0.0153153165357079 0.6561442635520426.69339379495654
6.60220188618582 6.6909188597753 P P P 7.10820643640934 7.25910548134 7.42714450243057 P
P P LNCV6_92571_PI430048170 mRNA
GCAGACAATGAATGAAGTGTGCTCATTGAAATAAAATACAGAGTCAAATCGCTATTGTTG NM_013235RefSeq chr5
- 31400494 31532175 DROSHA 29102 "drosha, ribonuclease type III, transcript variant 1"
GO:0005515|GO:0010467|GO:0016075|GO:0050830|GO:0042254|GO:0005730|GO:0046872|GO:0010586|GO:0001
530|GO:0050829|GO:2000628|GO:0004525|GO:0031054|GO:0031053|GO:0005654 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143487_PI430048170 0.0398823402711743 0.6419789461593096.33880999713461
6.32161397395989 6.54378522859603 P P P 6.79355096491539 6.96458007442942
7.32345714218323 P P P LNCV6_143487_PI430048170 mRNA
GACCATAGGAGGTTTTAAGATTTATGTTTAGTCCGATAGGTGAGGTCTTTGATATTTTGA NM_018117RefSeq chr10
+ 120851174 120909526 WDR11 55717 WD repeat domain 11
GO:0005515|GO:0005929|GO:0005737|GO:0016020|GO:0015630|GO:0005634|GO:0016021|GO:0005765 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136816_PI430048170 0.4066204704233171.04955712844823 0.315559564577166
0.32104067998026 0.510531071272205A A A 0.3196073374428620.285225316341813
0.341072168518762A A A LNCV6_136816_PI430048170 mRNA
CAGAGATGTTCACCTTTTCCTTGCTGATTGCTAATGCTTATTATTTCTAATTCAGTTCTG NM_001271208 RefSeq chr2
- 151485338 151734487 NEB4703 "nebulin, transcript variant 4"
GO:0005515|GO:0030832|GO:0030018|GO:0030049|GO:0007517|GO:0003779|GO:0015629|GO:0008307|GO:0070
062|GO:0007525|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135209_PI430048170 0.3159115208181050.86125152906455 0.350681485392166
0.3719732584782320.340149368446831A A A 0.4276796464576230.853204974678881
0.380113235168497A A A LNCV6_135209_PI430048170 mRNA
CAAAAGGCATTTTGTAAATGACTTCTTTGAGCTATCCACAAATAAAAAGGCTGGGTGTCA NM_144605RefSeq chr16
- 4777613 4788521 SEPT12 NA "septin 12, transcript variant 2" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128568_PI430048170 0.0225009341322457 0.7535627863115671 3.6239283448425
13.8203977173397 13.5598657935896 P P P 14.0241035224678 14.1310816412582
14.0845566525336 P P P LNCV6_128568_PI430048170 mRNA
AACTACATGGCAGCTGACGGTGACTTCAAGATCAAATGTGTGGCCTTTGACTGAAATCAG NM_002305RefSeq chr22
+ 37675605 37679802 LGALS1 3956 "lectin, galactoside-binding, soluble, 1"

GO:0005515|GO:0031295|GO:0034120|GO:0010812|GO:0016936|GO:0005634|GO:0048678|GO:0005615|GO:0042803|GO:0005622|GO:0005737|GO:0001948|GO:0045445|GO:0004871|GO:0071333|GO:0043123|GO:0070062|GO:0030395|GO:0009986|GO:0042493|GO:0005578|GO:0006915|GO:0042981|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145630_PI430048170 0.2669827499804010.8747820387180874.91816175004553 4.70664197814694 4.51334566869626 P P P 5.04644704120067 4.95638088151759 4.72387196685037 P P P LNCV6_145630_PI430048170 mRNA CACTTCCCACCTCTCTGAATAGTGTGTATGTGTTGGTTTATTGATTCTGTAAATAAGTAA NM_001042747 RefSeq chr1 - 27612289 27626240 FGR2268 "FGR proto-oncogene, Src family tyrosine kinase, transcript variant 2"
GO:0045859|GO:0005515|GO:0005886|GO:0050830|GO:0008360|GO:0005743|GO:0050715|GO:0015629|GO:0030154|GO:0005829|GO:0050764|GO:0005758|GO:0046777|GO:0043552|GO:0042127|GO:0071375|GO:0005856|GO:0038083|GO:0070062|GO:0034987|GO:0034988|GO:0030335|GO:0019901|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105558_PI430048170 0.00104336085196179 0.4885862658796534.28526398479197 4.45551310088697 4.17513559849281 P P P 5.51430913547712 5.23979389837582 5.25908344267812 P P P LNCV6_105558_PI430048170 mRNA AAGAGATGCCGGGCTTGCCCCACAAAGTGTGTCGAAGGTGTGACGAGAACTGCTTGAGCTNM_002570RefSeq chr15 - 101303927 101489984 PCSK6 5046 "proprotein convertase subtilisin/kexin type 6, transcript variant 1"
GO:0032455|GO:0048011|GO:0007368|GO:0048406|GO:0004252|GO:0009986|GO:0005783|GO:0005796|GO:0007354|GO:0032902|GO:0005615|GO:0031012|GO:0009100|GO:0016486|GO:0004175|GO:0016020|GO:0016485|GO:0006508|GO:0030510|GO:0032940|GO:0008201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121329_PI430048170 0.263911597963521 1.68625054482586 0.612732291605646 1.92151205634369 0.78616056035555 A A A 0.4175677499659890.481332872729615 0.530392248887227 A A A LNCV6_121329_PI430048170 mRNA CTCTTCGTATTCACCAGAGAGTTCACTTGAGAGAGAAACTCTCTAAGTGTGACATGCGTG NM_006300RefSeq chr19 + 44002924 44013920 ZNF230 7773 zinc finger protein 230
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136746_PI430048170 0.00154009219360067 0.5658052495900063.51787018366318 3.47290340704837 3.6883109301966 P P P 4.34268167259518 4.35683728303997 4.4510671099408 P P P LNCV6_136746_PI430048170 mRNA CCTTAGAGGAGTTTTCAGTTCATCCTCTTCTTGAGAAACTATGTGTTGCTGTTACTAAAT NM_173601RefSeq chr12 - 42081845 42144871 GXYLT1 283464 "glucoside xylosyltransferase 1, transcript variant 1"
GO:0035252|GO:0000139|GO:0005975|GO:0009405|GO:0016266|GO:0044281|GO:0016021|GO:0030204|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145474_PI430048170 0.556690469499631 0.9660067286859030.476788039126771 0.4445262532167880.246357817544436 A A A 0.3861095655312330.500243389120427 0.439359838307795 A A A LNCV6_145474_PI430048170 mRNA TCACTATCTCCAGCTCAGAGTTTGATGGCTAAGACGGTAAGGGCAGAGAAGTTTCAAAGT NM_178471RefSeq chrX - 130384344 130385537 GPR119 139760 G protein-coupled receptor 119
GO:0043235|GO:0007186|GO:0005886|GO:0004930|GO:0031210|GO:0016021|GO:0030073 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144302_PI430048170 0.0589949134483298 0.36293178990618 3.43257325656837 1.99817792828809 2.80737147860569 P A A 4.20171592518395 4.29881310863338 4.45690939852784 P P P LNCV6_144302_PI430048170 mRNA TCTGTTGATCTATGGAATGTTCTGTACAAAGCTGTATAATTGTACTGTTGGGCTAGATAC NM_032373RefSeq chr10 + 91220601 91284331 PCGF5 84333 "polycomb group ring finger 5, transcript variant 1"
GO:0031519|GO:0005515|GO:0006355|GO:0005813|GO:0005730|GO:0008270|GO:0005634|GO:0006351 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141077_PI430048170 0.9346901493581681.05972792626285 0.455135966275232
0.4718323877935261.64563964302959 A A A 1.45512535492418 0.506552521228644
0.477585634517854A A A LNCV6_141077_PI430048170 mRNA
GTGAGAGAGGAAGAGAAAATAGATTTACCTGATTCCTCTTTAAAATTCAAGCCACTTTCT NM_014499RefSeq chrX
+ 78945331 78961941 P2RY10 27334 "purinergic receptor P2Y, G-protein coupled, 10, transcript variant
1" GO:0005886|GO:0045028|GO:0035589|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134623_PI430048170 0.00792321208037629 0.6394088039291856.34442058097402
6.40027554061051 6.23924113256482 P P P 6.78917589919076 7.04978666648703
7.06860543079548 P P P LNCV6_134623_PI430048170 mRNA
GGAAACACTTGTAGGACTTCCTTTACCAACATACTTTTTAAATGTTTTGCTATTGGTTCCNM_014793RefSeq chr15 -
43327775 43330622 LCMT2 9836 leucine carboxyl methyltransferase 2
GO:0005515|GO:0008168|GO:0032259|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137681_PI430048170 0.0169958466394255 0.3819545686046025.39076041874505
4.91278285621848 4.96915010625652 P P P 5.93604578255705 6.71957765388451
6.70183157092004 P P P LNCV6_137681_PI430048170 mRNA
CATTGCGCTGAACAGTATTTGAGTTACCATATAATATGGCTTTACACAAGGAAATGTGTG NM_138426RefSeq chr7
+ 7968742 8089079 GLCCI1 113263 glucocorticoid induced 1 GO:0005737 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_128400_PI430048170 0.51463182326073 1.1060144376106 7.78356600482374
7.66865266921119 7.59916601705331 P P P 7.73764485343025 7.72215586634752
7.06508325986645 P P P LNCV6_128400_PI430048170 mRNA
CCTCCCTGGCCGCGGGGCTACCTGCGATCCGCCCCCGGGATGGGCCATCCGCGCTCCTGA NM_001164405 RefSeq
chr17 + 1270563 1271271 BHLHA9 NA "basic helix-loop-helix family, member a9" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_127803_PI430048170 0.00296839015543315 0.3291330840832945.72321864352062
5.49814042691043 5.59126526277418 P P P 6.96358735028424 7.15938497577888
7.46384870479055 P P P LNCV6_127803_PI430048170 mRNA
GATGACAGGAGTAAGACTGTTTAGTGAATATCTGTTAAATTTTATTGTTGTGGCCAGAGA NM_006482RefSeq chr12
+ 67648731 67662664 DYRK2 8445 "dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2,
transcript variant 2"
GO:0005515|GO:0043130|GO:0030145|GO:0000287|GO:0045725|GO:0051534|GO:0000151|GO:0018108|GO:0005
634|GO:0005524|GO:0006974|GO:0007224|GO:0042771|GO:0005737|GO:0004674|GO:0030529|GO:0004712|GO:0
005654|GO:0006468|GO:0004713 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136667_PI430048170 0.1019530844709581.06732161207195 0.4721955636335
0.57377215001699 0.529588930852481A A A 0.3691965783455480.441030928594151
0.482856713819861A A A LNCV6_136667_PI430048170 mRNA
GACTTTGTGCCTTGAAAGGCTTCTCAGGAAAGCAGTAATAAAACAAAGTGTCCTTGTTTG NM_001291825 RefSeq
chr22 + 39946816 39973342 GRAP2 9402 "GRB2-related adaptor protein 2, transcript variant 2"
GO:0005515|GO:0050852|GO:0031295|GO:0007267|GO:0005634|GO:0007265|GO:0009967|GO:0005829|GO:0005
737|GO:0005070|GO:0045087|GO:0005654|GO:0038095|GO:0005768 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_63881_PI430048170 0.7658206382605291.03730715862762 4.83083756563426 4.58748851091032
4.98720397196753 P P P 4.93878158408813 4.52075957132696 4.78471850417764 P P P
LNCV6_63881_PI430048170 mRNA
GCCTGATAAGAATATGGAAGCTGTATATAAAGTCAACATCTTTAGAAACTCAGGATGACG NM_001242875 RefSeq
chr18 + 36129873 36174726 ELP2 55250 "elongator acetyltransferase complex subunit 2, transcript
variant 1"
GO:0033588|GO:0006368|GO:0005737|GO:0019901|GO:0006357|GO:0000123|GO:0006325|GO:0000993|GO:0046

425|GO:0008023 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137379_PI430048170 0.000782056869851406 0.5288406525486461 1.2529898052765
11.2508150542175 11.4680463062334 P P P 12.2164193963538 12.13905853928
12.3745560529706 P P P LNCV6_137379_PI430048170 mRNA
GAAGTGTGGAATTTGGGGTTGTCCTGTGTAAATTACACAATAAAGCAAAAGTCAGTTATT NM_014077 RefSeq chr19
+ 16185400 16192046 FAM32A 26017 "family with sequence similarity 32, member A"
GO:0005739|GO:0005515|GO:0008150|GO:0007049|GO:0005730|GO:0006915|GO:0005654|GO:0005634|GO:0043
231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128728_PI430048170 0.0280071962707099 1.22503669830344 9.51238911077891
9.69460612201747 9.67439623820865 P P P 9.36345806432746 9.30130290815123
9.34427974224235 P P P LNCV6_128728_PI430048170 mRNA
CACCAGGATAAGTGACACCTAGGACCCAGGAAATAAATGCCGATGATTTGTGTGAAAAAANM_001281444 RefSeq
chr20 + 44531780 44619037 PKIG 11142 "protein kinase (cAMP-dependent, catalytic) inhibitor
gamma, transcript variant 4"
GO:2000480|GO:0007165|GO:0005737|GO:0042308|GO:0005634|GO:0004862|GO:0000122 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130286_PI430048170 0.0253477402319176 0.4548386359192134.88597744273413
4.79425798441632 5.19806642859745 P P P 6.50175331379271 5.68731320321137
6.01282474255411 P P P LNCV6_130286_PI430048170 mRNA
GCAGTTCAGAATGCCATGCCTTGGTTGTCCTAGTGTGAATAATTTTCAGCTACTTTAAAA NM_001114752 RefSeq
chr1 + 207321471 207360966 CD55 1604 "CD55 molecule, decay accelerating factor for complement
(Cromer blood group), transcript variant 2"
GO:2000516|GO:0045730|GO:0005515|GO:0030449|GO:2000563|GO:0005886|GO:0009986|GO:0005576|GO:0031
225|GO:0009615|GO:0007204|GO:0008289|GO:0045916|GO:0001618|GO:0005887|GO:0045087|GO:0006958|GO:0
045121|GO:0035743|GO:0031664|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126943_PI430048170 0.0953363726994545 1.12125724207623 11.1057249962151
10.9683300770678 10.90409680333 P P P 10.8740727834334 10.8275713576444
10.7872561394402 P P P LNCV6_126943_PI430048170 mRNA
CAGCCACATCACTCACAGCTGATCACTGGTTGGTGGAAAATAAACTATGAGCAGCAGAAA NM_018146 RefSeq chr17
+ 782272 792501 RNMTL1 55178 RNA methyltransferase like 1
GO:0005739|GO:0001510|GO:0006364|GO:0008173 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133316_PI430048170 0.0821626765662465 0.8632194951073587.14149154636592
7.01257982812652 7.18230926251301 P P P 7.20127526637925 7.31680088390462 7.449579944653
P P P LNCV6_133316_PI430048170 mRNA
GTCACATCTGTTGATAGCTGGAGAACTTTAGTTTCAAGTACTACATTGTGAAAGCAATTA NM_001098208 RefSeq
chr10 - 43385616 43396831 HNRNPF 3185 "heterogeneous nuclear ribonucleoprotein F, transcript
variant 1"
GO:0005515|GO:0008380|GO:0006396|GO:0010467|GO:0003727|GO:0003723|GO:0005634|GO:0071013|GO:0000
166|GO:0016020|GO:0000398|GO:0005654|GO:0043484 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132396_PI430048170 0.1835729185486750.6478543895645478.23656516587679
7.85848812936933 8.39455587012213 P P P 8.23981489739128 8.71768784578476
9.27596825999035 P P P LNCV6_132396_PI430048170 mRNA
CCCTGAATGATGATTAGAGACATCACCGCTAAAAAACTACATTTATAAGCTAGGATTTGT NM_014000 RefSeq chr10
+ 73998113 74120156 VCL 7414 "vinculin, transcript variant 1"
GO:0005515|GO:0030055|GO:0002162|GO:0005886|GO:0008013|GO:0034333|GO:0030032|GO:0006928|GO:0048
675|GO:0015629|GO:0005829|GO:0043297|GO:0005916|GO:0005913|GO:0006936|GO:0005912|GO:0005911|GO:0
005856|GO:0007155|GO:0070062|GO:0090136|GO:0030336|GO:0045296|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139538_PI430048170 0.17324748766917 0.6583489799431493.03588761731895

2.45188256444728 2.19796265783636 A A A 2.96665576314107 2.83378832252653
3.67706486065773 P P P LNCV6_139538_PI430048170 mRNA
AGTCGGTTAGCCTGGGTTAGATAAGGCAAACTGAACAGATCTAATTTAGGAAGTCAGTAG NM_004333 RefSeq chr7
- 140734012 140924764 BRAF 673 "B-Raf proto-oncogene, serine/threonine kinase"
GO:0005515|GO:0043005|GO:0005886|GO:0031267|GO:0007264|GO:0043434|GO:0007268|GO:0060291|GO:0005
634|GO:0051591|GO:0051291|GO:0042802|GO:0005829|GO:0005739|GO:0043524|GO:0000186|GO:0033138|GO:1
900026|GO:0010764|GO:0000165|GO:0042127|GO:0071277|GO:0009887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131985_PI430048170 0.2197889033483040.418843923800175 1.34660927733789
0.2660857228472940.377449371741307 A A A 1.19550949868104 2.94178613975659
1.04999081575806 A P A LNCV6_131985_PI430048170 mRNA
TACTGGTGGTTCTCAATTGCCTAGTAAGTGAAGATCTGTAGGGGAGATGGCTTATATTCT NM_001077711 RefSeq
chr21 - 30337012 30337694 KRTAP27-1 NA keratin associated protein 27-1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_142750_PI430048170 0.0546012330904313 3.05236555198688 2.15070648390503
2.88373631197688 1.3785470428318 A A A 0.5290997935246280.317046199279531
1.02556855211989 A A A LNCV6_142750_PI430048170 mRNA
GCAGAGGGAATGGAAAGGAATGGAAAGATTTGTTGGCGTAATTTTTGAATATTTGTTATG NM_182522 RefSeq chr3
- 68731763 68932610 FAM19A4 151647 "family with sequence similarity 19 (chemokine (C-C motif)-like),
member A4, transcript variant 1" GO:0042391|GO:0005576|GO:0051930 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_70310_PI430048170 0.3896235888215311.02399039148841 0.3567935904768360.258396629641212
0.272138679693468 A A A 0.2564437309190620.2754783701129120.254688929661974 A A A
LNCV6_70310_PI430048170 mRNA
TCTCTTGCCTTTTTTATGCATAAATGGAGGTCAATTTGATTGTCCTGACCTACTGTATAA NM_080876 RefSeq chr2 +
183078558 183099994 DUSP19 142679 "dual specificity phosphatase 19, transcript variant 1"
GO:0046330|GO:0007254|GO:0008330|GO:0031435|GO:0030295|GO:0035335|GO:0000188|GO:0005737|GO:0008
579|GO:0046329|GO:0006470|GO:0045860|GO:0004860|GO:0043507|GO:0006469|GO:0043508|GO:0043410|GO:0
004725|GO:0005078. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143075_PI430048170 0.00702554465968089 0.5221318648332688.62519680852748
8.28266296930731 8.72462730883604 P P P 9.32868857639998 9.38667804390876
9.73213621358119 P P P LNCV6_143075_PI430048170 mRNA
GTCATGAGATAAAACAACACAATGCATGTTGCCTTTTTAATGTAAATACCCGTAGGTATC NM_005499 RefSeq chr19
+ 34428362 34469893 UBA2 10054 ubiquitin-like modifier activating enzyme 2
GO:0005515|GO:0046982|GO:0016925|GO:0031510|GO:0005634|GO:0043085|GO:0005524|GO:0046872|GO:0019
948|GO:0005829|GO:0019950|GO:0005654|GO:0008047|GO:0044267|GO:0008134|GO:0043687 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144367_PI430048170 0.0103168863315938 0.3701998784159 5.01035324689849
4.60935438773102 4.96778020886179 P P P 5.85411200092768 6.34744308192878
6.61847673545717 P P P LNCV6_144367_PI430048170 mRNA
GAGTGCTTGTCATCAGGTGTTTTCCTTAATAAGTAGGGATATGATCATTTACAGGAATTA NM_015055 RefSeq chr11
+ 9664076 9752991 SWAP70 23075 "SWAP switching B-cell complex 70kDa subunit, transcript
variant 1"
GO:0005737|GO:0005886|GO:0045190|GO:0005509|GO:0005634|GO:0005524|GO:0003677|GO:0030027 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127806_PI430048170 0.5346952048815511.26858581442943 2.46697482136671
3.53824773304714 2.5127041234153 A P A 2.1419481495237 2.83673591740893
2.69092051682585 A P P LNCV6_127806_PI430048170 mRNA
GCCCAGAGAGCAGCCTCACCAGAACCCCTACCCTAAGAGAGATTAAAATTTATTCTTTAC NM_080675 RefSeq chr20

- 32983774 33004433 SUN5 140732 Sad1 and UNC84 domain containing 5
GO:0003674|GO:0005637|GO:0006998|GO:0090286|GO:0016021|GO:0007283|GO:0005635|GO:0005575 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144463_PI430048170 0.0213729478624229 0.621332793649461 9.51821841314374
9.15111258847814 9.11816359834188 P P P 9.94424064997622 9.88351522900691
10.0496037695745 P P P LNCV6_144463_PI430048170 mRNA
CCACTCTGCTGCCTGTACAGAAGAAACTGAATCTTTTTCATATTCTAATAAATCAATGTG NM_003047 RefSeq chr1
- 27098808 27155130 SLC9A1 6548 "solute carrier family 9, subfamily A (NHE1, cation proton antiporter
1), member 1, transcript variant 1"
GO:0005515|GO:0005516|GO:0030346|GO:0030307|GO:0051492|GO:0006883|GO:0030011|GO:0071468|GO:0051
259|GO:0006885|GO:0071436|GO:0071257|GO:0086003|GO:0045760|GO:0030674|GO:0035794|GO:0055007|GO:0
030203|GO:0070062|GO:0032869|GO:0009986|GO:0005975|GO:0005546|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144493_PI430048170 0.0204723435529256 1.21409354497579 9.94227242308751
9.97665994191385 9.80614038416606 P P P 9.52642193469392 9.71167488814871
9.64682973376411 P P P LNCV6_144493_PI430048170 mRNA
CTGGCCTGGCCTTCGTGCCCTTTATTCATTGTCAATAAATCCGCTCAGACCATTAAAAAA NM_173828 RefSeq chr5
+ 141636949 141641064 RELL2 285613 "RELT-like 2, transcript variant 1"
GO:0005886|GO:0010811|GO:0005518|GO:0016021|GO:0005604 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142685_PI430048170 0.0824313006848881 0.704479111718316 0.314520588297448
0.321572744193011 0.359069887514743 A A A 0.989013144602982 0.957115479560552
0.519622583210182 A A A LNCV6_142685_PI430048170 mRNA
CATAGGAAACTTGAAAGGTCTGAGGATGATGTAGATTACTGAAAAATGCAAATTGCAATC NM_000348 RefSeq chr2
- 31524585 31580971 SRD5A2 6716 "steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-
steroid delta 4-dehydrogenase alpha 2)"
GO:0006706|GO:0003865|GO:0033218|GO:0018963|GO:0006702|GO:0007267|GO:0043434|GO:0018879|GO:0044
281|GO:0047751|GO:0030154|GO:0070852|GO:0030539|GO:0043025|GO:0031667|GO:0008202|GO:0032354|GO:0
008209|GO:0042493|GO:0009917|GO:0021854|GO:0033574|GO:0060348|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_59586_PI430048170 0.000106422874179109 4.50292638379954 7.37775857807982
7.52215738914763 7.19842670580738 P P P 5.13633906134221 5.39474883290429
5.05014620389299 P P P LNCV6_59586_PI430048170 mRNA
TGACTTATTTGACTGAGACTGGGGTCTCTACTTCACCAAACTGGCCTCTATCCATACCAA NM_004658 RefSeq chr12
- 113098818 113136239 RASAL1 8437 "RAS protein activator like 1 (GAP1 like), transcript variant 2"
GO:0035556|GO:0005099|GO:0046580|GO:0007165|GO:0005737|GO:0005543|GO:0032320|GO:0005886|GO:0031
235|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139092_PI430048170 0.238008875333712 0.82760227645631 8.10029947352947
7.52899058546568 7.60448317744573 P P P 8.10465929045129 8.09134916585846 7.9184188346604
P P P LNCV6_139092_PI430048170 mRNA
TATCACCCTCTCTTCCCCTTTTTAATGTAGAACTCATTCTTAATGATTTGTCAAAGGCAC NM_203458 RefSeq chr1 -
146151907 146229032 NOTCH2NL 388677 notch 2 N-terminal like
GO:0005737|GO:0007219|GO:0005509|GO:0007275|GO:0005576|GO:0030154 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142055_PI430048170 0.00153341941863355 0.292699521912007 0.38637172655981
0.380461827022237 0.264300075872999 A A A 2.25630222592512 1.89531419128746
2.17593454394469 A A A LNCV6_142055_PI430048170 mRNA
TCACCAAATGTATAAATCCGTATTAGTAAAAATTGGTTTTAACTGACCTCAGCACTGCCC NM_014267 RefSeq chr11
+ 16738600 16758354 C11orf58 10944 chromosome 11 open reading frame 58

GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133436_PI430048170 0.9662104596814960.9930605880986393.97950636697394
3.92069060602183 3.08540930232413 P P P 4.18264674915639 3.39659683563477
3.45827098464109 P P P LNCV6_133436_PI430048170 mRNA
ATAGTGGATGCTCTTCCAGTTTCTTTTTTCTATTAAACACCCCACTTCCTTTGGAAAAAANM_152456RefSeq chr16 +
70579894 70660682 IL34 146433 "interleukin 34, transcript variant 1"
GO:0008284|GO:0006954|GO:0045087|GO:0005157|GO:0001934|GO:0008083|GO:0005615|GO:0005125 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134197_PI430048170 0.2991608950545830.6594026950557512.70566891444003
4.50329371069623 4.30542022749362 A P P 4.62727919865665 4.54247216779752
4.71447697150322 P P P LNCV6_134197_PI430048170 mRNA
GTTTGTTTAAGTTAGTTACCCATGTCCCCAATCAAGGGAACCTAAATGAAGATATATCAT NM_019083RefSeq chr1
+ 100133149 100150498 TRMT1354482 tRNA methyltransferase 13 homolog (S. cerevisiae)
GO:0030488|GO:0008175|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51862_PI430048170 0.1633006205812091.83761528231642 1.21994539134622 2.35434702488491
1.72345932044388 A A A 0.5121385434993461.67991137035946 0.283517385787862A A A
LNCV6_51862_PI430048170 mRNA
AATATAGAGCAAAATTTCTGAGCCCAGCTCAGTATTTATATAAAGCTGGGGCTTGGACAC NM_017440RefSeq chr12
- 68294565 68332381 MDM1 56890 "Mdm1 nuclear protein homolog (mouse), transcript variant 1"
GO:0060041|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142443_PI430048170 0.1476044941551290.9533483656971260.2621584140318
0.2732873479108940.341012553167685A A A 0.4171900167225750.345582571908823
0.319959955724612A A A LNCV6_142443_PI430048170 mRNA
CCATAAGCCCAGAGGATTTTAGAGCTTCATGTGTGGCTTTTAAGAGCAGGTTTGAAAAAA NM_030632RefSeq chr18
+ 33578576 33747435 ASXL3 80816 additional sex combs like transcriptional regulator 3
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140136_PI430048170 0.0229841083977576 3.05944404648577 3.13253903380397
3.23564075591323 3.17404836371278 P P P 1.90579231880715 1.64185572828897
1.01975871981203 A A A LNCV6_140136_PI430048170 mRNA
AGCCTGCAGTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTCTTTCTTCCAGTTTTTC NM_031433RefSeq chr11
- 119338933 119346673 MFRP 83552 membrane frizzled-related protein
GO:0003674|GO:0016324|GO:0016021|GO:0009790 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141767_PI430048170 0.2518154581628910.70696709858018 4.51386642482268
3.28145231577247 4.06479564014855 P P P 4.20612639489504 4.68322352461162
4.67759806729554 P P P LNCV6_141767_PI430048170 mRNA
ATGGAAATTAAACAGGGACTTCAGAAAGCCGCACAGAAAGATCACCTTCCGATGGTGTGANM_144599RefSeq chr15
+ 22786631 22829789 NIPA1 123606 "non imprinted in Prader-Willi/Angelman syndrome 1, transcript
variant 1" GO:0015693|GO:0005886|GO:0015095|GO:0016021|GO:0005769 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_96869_PI430048170 0.5721528558131520.9157438037307578.15841672694508 8.213555796372
8.74817881399967 P P P 8.30136350361563 8.5009141618455 8.74138136597725 P P P
LNCV6_96869_PI430048170 mRNA
CCCTGGAGGAAGTGTTGACCTCAGACGCTCAGATTATGCTAAAGTGGCCAAAATATTTTA NM_003878RefSeq chr8
- 63015079 63039051 GGH 8836 "gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl
hydrolase)"
GO:0032868|GO:0042470|GO:0045471|GO:0042493|GO:0005634|GO:0005615|GO:0005764|GO:0010043|GO:0005
829|GO:0034722|GO:0006508|GO:0008242|GO:0070062|GO:0006541|GO:0008238 . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_136719_PI430048170 0.1229303738875330.7332056317393544.59076517713839 3.92362492827
4.16733705154614 P P P 4.88714464473245 4.56579699477478 4.63179945737603 P P P
LNCV6_136719_PI430048170 mRNA
CACAATTATTGGACTGTATTTTCTCCCCTCATCCAGTGCCTCCAGTGACAAGGACGTAAT NM_001004452 RefSeq
chr9 + 122519140 122520082 OR1J4 NA "olfactory receptor, family 1, subfamily J, member 4" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129238_PI430048170 0.7590740074089811.0360141334664 6.89174545357537
7.28101552817232 7.00602339642818 P P P 7.13695848237402 7.01477817454294
6.89168077717645 P P P LNCV6_129238_PI430048170 mRNA
GAGGGTCTATTCTTTACATTCACCATGGTCTGATGGTTGCTACATGTTTGTCTATGATTTNM_024293RefSeq chr2 +
219178216 219185475 FAM134A 79137 "family with sequence similarity 134, member A" GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143281_PI430048170 0.0110882738547842 1.08026039434622 0.370409266749107
0.4041358053564310.342067412269624A A A 0.2430381701176280.295364529540117
0.244119832435856A A A LNCV6_143281_PI430048170 mRNA
GGCTGAATTATGTAGACTTGTGTTTGACAGCTATGGGTTTATTTCTTAGAACATTGTTCA NM_015978RefSeq chr1
+ 74235386 74544432 TNNI3K 51086 TNNI3 interacting kinase
GO:0005515|GO:0005737|GO:0031013|GO:0004672|GO:0004674|GO:0006468|GO:0005634|GO:0008022|GO:0005
524|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128392_PI430048170 0.8710125089884840.8791516051830360.29406882442437
1.52689186479957 0.518028806016724A A A 0.45775537024016 1.87591456419727
0.330537634250945A A A LNCV6_128392_PI430048170 mRNA
TTTCAGAATCTCCAAAAATGTAACTGGGTTCCCTGCATTAAATGGTCAATAAACCTCCTT NM_003770RefSeq
chr17_GL383564v2_alt + 8365 12379 KRT37 8688 "keratin 37, type I"
GO:0005882|GO:0005198|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131711_PI430048170 0.319564163465651.01949543837191 0.333861990728981
0.3207936137016920.26523187955841 A A A 0.2786778081636820.285953523887567
0.272575708129503A A A LNCV6_131711_PI430048170 mRNA
GATGCAATGAAGGGAATATGACACTACAGTATACAGAGTTGTTGTTATATGATGCACAAA NM_001080512 RefSeq
chr10 + 58513143 58831437 BICC1 80114 BicC family RNA binding protein 1
GO:0005737|GO:0007275|GO:0090090 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138535_PI430048170 0.0847216062393946 0.8475526224881869.49600714792846
9.71183027476225 9.439209667789 P P P 9.86729691487531 9.83086148616967 9.6719310694329
P P P LNCV6_138535_PI430048170 mRNA
AATTTTTGGGTGACTCACTTAGATGTCGTTTCCTTCTTGCCCCCTCTTCCTCTCTGTAAT NM_016169RefSeq chr10 +
102503961 102633457 SUFU 51684 "suppressor of fused homolog (Drosophila), transcript variant 1"
GO:0005515|GO:0008013|GO:0045879|GO:0005634|GO:0042994|GO:0042992|GO:0043433|GO:0005829|GO:0001
947|GO:0021776|GO:0021775|GO:0005737|GO:0006508|GO:0004871|GO:0006355|GO:0019901|GO:0003714|GO:0
001843|GO:0007275|GO:0072372|GO:0000122|GO:2000059|GO:0007165|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126802_PI430048170 0.0523092665281479 0.5384881296412952.0804948535838
1.52599592367068 1.49989936411376 A A A 2.95587549853068 2.11018754550559
2.67313682062492 P A P LNCV6_126802_PI430048170 mRNA
TCATCATCAGCGTGGTCCTGGTCAGCTTCAGCTCCCTGAGAGAGGTGCAGAAGCAAGAGA NM_001280561 RefSeq
chr8 - 144353225 144355609 TMEM249 340393 "transmembrane protein 249, transcript variant 4"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133860_PI430048170 0.3663931595640921.04827509614478 0.298732364190098
0.2812331303577460.459865935617533A A A 0.2937705887264670.256569110118548
0.291939342367693A A A LNCV6_133860_PI430048170 mRNA

GACCCAAACATGCTTTTAAATGTCTCATGCCAAGGCACTGAATTAAGACTTCTTAATGTT NM_005725 RefSeq chr1 - 115048010 115089500 TSPAN2 10100 tetraspanin 2
GO:0006954|GO:0005886|GO:0048709|GO:0014002|GO:0007420|GO:0043209|GO:0042552|GO:0016021|GO:0014005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141469_PI430048170 0.5054453025061810.893701324750861 7.68652025321842 7.48104728549234 7.84118733706669 P P P 7.57596361029646 7.73228265572709 8.14747986742635 P P P LNCV6_141469_PI430048170 mRNA
CTTCACACTGTTATCACCTATCCTGAAGATGTGATACACTGAATGGAAATAAATAGATGT NM_005669 RefSeq chr5 - 112876383 112922334 REEP5 7905 receptor accessory protein 5
GO:0005515|GO:0008150|GO:0003674|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145562_PI430048170 0.000824886345972654 0.484518764082572 3.95971977744851 3.71848164022101 3.89692506380415 P P P 4.83340861621294 4.91023089280277 4.97486256836024 P P P LNCV6_145562_PI430048170 mRNA
CACCTGTGGAGTACTTTAGACTCCAACAAATAATAATGTAACTAAAACTGCTCACACATT NM_181837 RefSeq chr6 + 87590066 87667454 ORC3 23595 "origin recognition complex, subunit 3, transcript variant 1"
GO:0061351|GO:0006260|GO:0005515|GO:0000082|GO:0000808|GO:0005654|GO:0005664|GO:0003688|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_36076_PI430048170 0.974962949530225 1.00395568042457 6.67752783324256 7.13686212647352 6.81019230709855 P P P 6.99575938865833 6.82583446257757 6.81827733134666 P P P LNCV6_36076_PI430048170 mRNA
GGTGAGAATGGTATAAATTTCAAAAACAACGAAACCTTCTTTTGCCCCCTCCGCAGCAGT NM_001282275 RefSeq chr17 + 48723167 48724758 PRAC2 NA "prostate cancer susceptibility candidate 2, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127970_PI430048170 0.0033517030031299 0.610899328226783 10.9919900318737 11.0321974063296 11.1847994259012 P P P 11.8193801255375 11.7791322004947 11.7498584661124 P P P LNCV6_127970_PI430048170 mRNA
GGTCATCTGAATTGGGGGTAGCAATTGATACTGTTTTGTAAACTACATTTCCTACAAAAT NM_001042724 RefSeq chr19 + 44846135 44889228 PVRL2 5819 "poliovirus receptor-related 2 (herpesvirus entry mediator B), transcript variant delta"
GO:0005515|GO:0001675|GO:0005886|GO:0007289|GO:0007286|GO:0033005|GO:0030382|GO:0042803|GO:0042802|GO:0060370|GO:0005915|GO:0005911|GO:0001618|GO:0007010|GO:0042271|GO:0050839|GO:0007156|GO:0002891|GO:0070062|GO:0009986|GO:0034329|GO:0019064|GO:0009615|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129860_PI430048170 0.14670486961955 2.51520982182509 0.567325100198262 1.59843532139394 2.30271297794778 A A A 0.344427724268909 0.321526556219396 0.304936934164842 A A A LNCV6_129860_PI430048170 mRNA
ATGGCCCTTATACTGCAGTATTTTATGCTCCATGAGACTGTGGCACCTTCTGACATCATG NM_001282300 RefSeq chr18 + 11609557 11610612 SLC35G4 NA "solute carrier family 35, member G4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134602_PI430048170 0.0545929247677634 1.53098461149675 7.36832471268161 7.33718791329981 7.59734022249817 P P P 7.15021507283995 6.54826588540438 6.70594687787801 P P P LNCV6_134602_PI430048170 mRNA
TCAACCTGTGCTAGCAACATTCTGAAATTCCTTCAAAGAAGGCAGTCCTTTGGGAAGGTG NM_004892 RefSeq chr1 - 120155941 120176521 SEC22B 9554 SEC22 vesicle trafficking protein homolog B (S. cerevisiae) (gene/pseudogene)
GO:0019905|GO:0006888|GO:0005515|GO:0042470|GO:0045732|GO:0005793|GO:0000139|GO:0033116|GO:0005789|GO:0016021|GO:0033043|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127695_PI430048170 0.913960367573487 0.98756347753818 4.11465714518583

4.54796284148603 3.5911200288299 P P P 4.49088862626537 4.11361299479012
3.76931862237008 P P P LNCV6_127695_PI430048170 mRNA
AATTAATGTCCATTGTCTCTCCTAACAAATTCTCTCCCCAAGTCAACTGCAATTGCAGCT NM_001012709 RefSeq
chr11_KI270903v1_alt - 97514 98873 KRTAP5-4 NA keratin associated protein 5-4 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_125253_PI430048170 0.5107097905209530.978502604969301 0.263851861687051
0.2733816894482690.385116509197009 A A A 0.3728165487669050.310910899954832
0.335183130094107 A A A LNCV6_125253_PI430048170 mRNA
TTCCTGGACACCATCATCCGCAAGTTTGAGGGCCAGGCCGTAAGTTCATCATCGCCAACG NM_000238 RefSeq chr7
- 150944955 150978314 KCNH2 3757 "potassium channel, voltage gated eag related subfamily H,
member 2, transcript variant 1"
GO:0005515|GO:0005251|GO:0086010|GO:0005886|GO:0055075|GO:0060306|GO:0007268|GO:0005635|GO:0060
307|GO:0086091|GO:0000155|GO:0060048|GO:0042803|GO:0042802|GO:0003064|GO:0071435|GO:0005737|GO:0
000160|GO:0008076|GO:0005249|GO:0097110|GO:0042391|GO:0031625|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132035_PI430048170 0.97640619928699 1.00093306059152 0.483163800466925
0.5323483815619020.431595148456491 A A A 0.4631556065331460.448084249753361
0.53218860322585 A A A LNCV6_132035_PI430048170 mRNA
TGTGACAATGTATTGTAGTCCATCATCACTCAAACCTGAAACTTCAGCATATTTGTTCTA NM_133466 RefSeq chr19
- 36391958 36418648 ZFP82 284406 ZFP82 zinc finger protein
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_109530_PI430048170 0.4725672482289810.93858909708999 4.26756363796922
4.09979088777341 3.88253985629722 P P P 4.19525847712592 4.23569515274777
4.11634701125619 P P P LNCV6_109530_PI430048170 mRNA
AGCTCTTTGACTACTATGCGGCCAGTGGCATGTGCCTCCTGTTCGTGGCCATCTTCGAGT NM_016615 RefSeq chr12
- 220620 262873 SLC6A13 6540 "solute carrier family 6 (neurotransmitter transporter), member 13,
transcript variant 1"
GO:0005886|GO:0005887|GO:0005328|GO:0015812|GO:0007268|GO:0055085|GO:0005332|GO:0007269|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130001_PI430048170 0.1929289465016530.7696692287137574.0202123709537 3.3143491979133
3.85151486030653 P P P 4.14345083581182 3.93954724548383 4.30340559869493 P P P
LNCV6_130001_PI430048170 mRNA
CACTTTTGCATTCAGATACTTGGTCATTTACTTACCAAATTACAAACGCAATACTACAGC NM_024948 RefSeq chr10
- 15778175 15860520 FAM188A 80013 "family with sequence similarity 188, member A"
GO:0005515|GO:0031965|GO:0006915|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133899_PI430048170 0.0385431964298003 0.5789120011057155.50748017239397
5.27885945678837 5.86658645073027 P P P 6.41789714493689 6.3214371343703
6.33901994732965 P P P LNCV6_133899_PI430048170 mRNA
CAGTTATATTCATGTGATCGCGGCTAAAAAGTCAGTATTTTCTTTTTGTTCTAATGTGGC NM_001278594 RefSeq
chr14 - 74057664 74084493 ALDH6A1 4329 "aldehyde dehydrogenase 6 family, member A1,
transcript variant 3"
GO:0006210|GO:0004029|GO:0009083|GO:0019859|GO:0044281|GO:0005739|GO:0034641|GO:0050873|GO:0005
759|GO:0018478|GO:0006574|GO:0005654|GO:0006573|GO:0004491|GO:0000062|GO:0070062|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65735_PI430048170 0.5303724043290580.97021882745099 0.433843988990514 0.43488207515376
0.256921287063362 A A A 0.3845372558653240.4613163828358460.416788409153576 A A A
LNCV6_65735_PI430048170 mRNA
CCAAGCACTACCTATTCTGCATTGCAGCCATTTTGCTCTGTTTGATTAAAACTTTCTGGTNM_001145051 RefSeq chr2

+ 46479564 46484425 TMEM247 NA transmembrane protein 247 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91053_PI430048170 0.2429677842702360.8165397889301093.8439483455442 3.73711382346651 3.73352662210298 P P P 4.03413998594954 3.75889120889105 4.34243041481303 P P P
LNCV6_91053_PI430048170 mRNA
CTTAGAAAGAGATAACTCAGAAGAATTTTTAAAACGGGAAGCAAGGGCAAACCAGTTAGC NM_002973 RefSeq
chr12 - 111452213 111599676 ATXN2 6311 ataxin 2
GO:0005515|GO:0005802|GO:0048471|GO:0005154|GO:0033962|GO:0005794|GO:0016070|GO:0010494|GO:0003723|GO:0050658|GO:0008022|GO:0006417|GO:0050905|GO:0048872|GO:0034063|GO:0005737|GO:0040015|GO:0016020|GO:0021702|GO:0048812|GO:0030529|GO:0005654|GO:0005844|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118167_PI430048170 0.0366073322666992 0.7578309361443271 1.6259004287666 11.6243590332346 11.775521807016 P P P 11.959488834317 11.9874584903643 12.2642057970035 P P P LNCV6_118167_PI430048170 mRNA
ATCCTGTTTTCTGCAACATTCTATACAAAACTGTGCTGTGACCTTGCGGTAGGCCTGGAT NM_002074 RefSeq chr1 - 1785284 1891117 GNB1 2782 "guanine nucleotide binding protein (G protein), beta polypeptide 1, transcript variant 1"
GO:0005515|GO:0060041|GO:0005886|GO:0007603|GO:0042622|GO:0008283|GO:0003924|GO:0007200|GO:0007268|GO:0007265|GO:0044281|GO:0071380|GO:0005765|GO:0032403|GO:0031702|GO:0007204|GO:0030425|GO:0007191|GO:0005622|GO:0050909|GO:0071377|GO:0004871|GO:0070062|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129932_PI430048170 0.0526546989028325 0.7286036622826521 2.7537963715664 12.6759040479058 12.807655519296 P P P 12.959946496122 13.3487050818052 13.2733905369927 P P P LNCV6_129932_PI430048170 mRNA
GTAGGGTGTTCTGGCTTTTTTGTGGGGTTTTTATTTTTAAAGAAACACTCAATCATCCTA NM_003486 RefSeq chr16 - 87830022 87869494 SLC7A5 8140 "solute carrier family 7 (amino acid transporter light chain, L system), member 5"
GO:0006520|GO:0005886|GO:0005730|GO:0006865|GO:0005634|GO:0050900|GO:0055085|GO:0030154|GO:0043231|GO:0005829|GO:0007399|GO:0015804|GO:0016324|GO:0005737|GO:0016020|GO:0015171|GO:0007596|GO:0042605|GO:0006810|GO:0015175|GO:0016021|GO:0015179|GO:0070062|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134276_PI430048170 0.00240471569734011 0.1774697355604557.55298577689966 7.47651332910387 7.58767739600537 P P P 9.82375142985079 9.9258002334004 10.3068532261751 P P P LNCV6_134276_PI430048170 mRNA
CTGGTACAGTGTTCTGCTTGATTTACAACATGTAACTTGTGACTGTACAATAAACATAAG NM_002210 RefSeq chr2 + 186590062 186680902 ITGAV 3685 "integrin, alpha V, transcript variant 1"
GO:0005515|GO:0002474|GO:0031527|GO:0031528|GO:0034686|GO:0050900|GO:0002020|GO:0035987|GO:0007411|GO:0001618|GO:0030198|GO:0005080|GO:0034446|GO:0034113|GO:0070371|GO:0033690|GO:0070062|GO:0008305|GO:0030335|GO:0010745|GO:0009986|GO:0031589|GO:0050840|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121916_PI430048170 0.0817856590713291.13764073241868 10.5135802269626 10.574246135005 10.7168687504255 P P P 10.51863315908 10.3488795333835 10.380966046232 P P P
LNCV6_121916_PI430048170 mRNA
TTTCCTCTCTTCAGCGTGGGGCGCCCACAATTTGCGCGCTCTCTTTCTGCTGCTCCCCAG NM_001959 RefSeq chr2 + 206159593 206162929 EEF1B2 1933 "eukaryotic translation elongation factor 1 beta 2, transcript variant 1" GO:0005515|GO:0010467|GO:0005853|GO:0003746|GO:0044267|GO:0006412|GO:0006414|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120649_PI430048170 0.5577971815483531.27500631348513 2.92799954934249 2.20601341807358 3.52117610852238 A A P 1.73816592190636 2.91451965383239

2.94796619618927 A P P LNCV6_120649_PI430048170 mRNA
CAAGACAATTCCTGGGAAAGTTCAGTTCTTCTCAAGTGAGGGTTCTGACACATCTGTACC NM_014918RefSeq chr15
- 101175722 101251932 CHSY1 22856 chondroitin sulfate synthase 1
GO:0005975|GO:0005576|GO:0009954|GO:0044281|GO:0050510|GO:0046872|GO:0045880|GO:0030206|GO:0030
279|GO:0000139|GO:0002063|GO:0016020|GO:0060349|GO:0032580|GO:0009405|GO:0051923|GO:0031667|GO:0
016021|GO:0030204|GO:0047238|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132974_PI430048170 0.64618994574804 1.35528400587776 1.84936441402804
0.3761179090982960.330231524217899A A A 0.919547302009031 0.457377507991706
0.355559250041103 A A A LNCV6_132974_PI430048170 mRNA
TTACAGAAAAAGAGAGGAAGAAAGCAAGGGTAGTTAGTGGGTATTTGGTCTAACAGGAGC NM_001038705
RefSeq chr3 - 154337671 154429715 GPR149 344758 G protein-coupled receptor 149
GO:0043005|GO:0042923|GO:0007218|GO:0007187|GO:0005887|GO:0004930|GO:0060280|GO:0007268|GO:0001
546|GO:0001547 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143632_PI430048170 0.548586399656956 1.13351917558201 0.294325333117672
0.9454131834160550.346758882734511A A A 0.41632002594176 0.373234853283269
0.34811655321745 A A A LNCV6_143632_PI430048170 mRNA
CTCCATTTCTTAGAAGAACATGCTGAATTGTCTTTTCAGTGTCTTGCCCTGACAGCGTTT NM_001128598 RefSeq
chr21 - 30289144 30289514 KRTAP25-1 NA keratin associated protein 25-1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_80112_PI430048170 0.0197385812245349 0.490509365271506 2.22410856798957
2.83914569272694 2.69628822198649 A A A 3.38477817928709 4.0029850917339
3.43950649837217 P P P LNCV6_80112_PI430048170 mRNA
GCCCTCAGTAAATACAGCGAATGCTTAAAGATTAACAATAAGGAATGTGCCATATATACA NM_003114RefSeq chr8
+ 100158334 100241904 SPAG1 6674 "sperm associated antigen 1, transcript variant 1"
GO:0007338|GO:0005737|GO:0016787|GO:0015630|GO:0008152|GO:0005654|GO:0070286|GO:0005525 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128612_PI430048170 0.00945624765295224 1.27491437409248 11.3364797809995
11.4603955694395 11.5281784714012 P P P 11.0463281422787 11.0625867658907
11.1683757565456 P P P LNCV6_128612_PI430048170 mRNA
CAAGAGTGCTAATTTAGGTCTTTCTGTGGAATTTGGAACAATTCTAGTTTACACATGTGA NM_032346RefSeq chr19
+ 34404397 34426167 PDCD2L 84306 programmed cell death 2-like
GO:0007049|GO:0005737|GO:0016020 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143736_PI430048170 0.829118006788298 0.9925375881636 0.413846604146963
0.38491277039361 0.253669196407488A A A 0.336308070594183 0.381435479739434
0.371713113545417 A A A LNCV6_143736_PI430048170 mRNA
GGAGTCAGGACCAAGCAGATCCGAGAGCAAATTGTGAAAATATTTGTACAGAAAGAATAA NM_001005165
RefSeq chr11 + 5884292 5885231 OR52E4 NA "olfactory receptor, family 52, subfamily E, member 4"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128913_PI430048170 0.00104527029742892 0.223124888615893 5.7125254872428
5.64695215914672 6.22860586124968 P P P 7.78831376679034 7.93020509778443
8.36936643843583 P P P LNCV6_128913_PI430048170 mRNA
GGCATGTGCACGACTATGTTATTAGAAGCCACTTTATCATTTTCCTGCTTTAAATAGAAA NM_012234RefSeq chr3
- 72374592 72446623 RYBP 23429 RING1 and YY1 binding protein
GO:0031519|GO:0005515|GO:0035518|GO:0005737|GO:0003714|GO:0006915|GO:0008270|GO:0007275|GO:0005
654|GO:0000122|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128215_PI430048170 0.00225118436291824 0.217833549407448 1.97034880677212
2.29768421650477 2.76199658637332 A A A 4.18102831977183 4.52604647810795
4.93174096223538 P P P LNCV6_128215_PI430048170 mRNA
GGTGGGAGGGAATGTTTTCAAATTTCCCATTTCTCAAGAAATGTTCATATTAATTGAGGA NM_020361RefSeq chr8

- 67422169 67746385 CPA6 57094 carboxypeptidase A6
GO:0006508|GO:0005578|GO:0008270|GO:0004181 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143957_PI430048170 0.0264800064557684 0.7002896589191143.6412903365159
3.30099732798736 3.58823988457785 P P P 3.82862802774738 4.05039169900266
4.19299920859406 P P P LNCV6_143957_PI430048170 mRNA
ACCACTATTGACTGGGAAGACACACAAAGAACTTTGTCAAAGTTGTATGGCTGAGGCCCA NM_024026RefSeq chr13
+ 21176232 21179081 MRPL5778988 mitochondrial ribosomal protein L57
GO:0003735|GO:0005761|GO:0006412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88942_PI430048170 0.4307546608094240.90661484784159 4.38138582513557 3.84323668419906
4.25443417981699 P P P 4.29807601294772 4.32457289431092 4.33358366649775 P P P
LNCV6_88942_PI430048170 mRNA
GCCCACCCTTTCTTTTAAAGTATTCTTAACATGAAATCCACAAAAGCGGAAACAATGAAC NM_024731RefSeq chr16
+ 84648510 84667686 KLHL36 79786 "kelch-like family member 36, transcript variant 1" GO:0016567
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121582_PI430048170 0.2908640259899341.31701966731768 2.56352990398522
2.69409119239492 3.34155977630078 A A P 2.87098194592172 2.39129398297006
2.18183373387949 P A A LNCV6_121582_PI430048170 mRNA
TTTTAATGACTGCCCAGATTCCCACACTCAGTTCTGCTTCCATGGAACCTGCAGGTTTTT NM_003236RefSeq chr2
- 70447279 70554015 TGFA 7039 "transforming growth factor, alpha, transcript variant 1"
GO:0050679|GO:0005515|GO:0048471|GO:0043066|GO:0005154|GO:0005886|GO:0009986|GO:0008283|GO:0045
741|GO:0042493|GO:0045840|GO:0005634|GO:0031410|GO:0001525|GO:0005615|GO:0016323|GO:0000187|GO:0
001948|GO:0007173|GO:0005887|GO:0042060|GO:0008083|GO:0060749 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_126900_PI430048170 0.00221233289932624 2.73240884931712 7.06654256328884
7.08120521368206 6.93598429917082 P P P 5.66658277642149 5.69934109458239
5.34594753602174 P P P LNCV6_126900_PI430048170 mRNA
ATTTATTTGTTCAGAATACATTGGCAGCTGCTAGTGGTTTCCCTGGAAGTGGCAGCAGCA NM_001080496 RefSeq
chr9 + 35749279 35753267 RGP1 9827 RGP1 retrograde golgi transport homolog (S. cerevisiae)
GO:0005515|GO:0043234|GO:0017112|GO:0017137|GO:0016020|GO:0034066|GO:0042147|GO:0032851|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143713_PI430048170 0.0497870217274061.6412629134984 9.04887689839655
9.20135544741576 9.3049854964958 P P P 8.06823476944311 8.71944038966522
8.55788728947051 P P P LNCV6_143713_PI430048170 mRNA
GGCTACTTTATTGTTTAGGACAAGTGGTAGTGGCATTCTATTTATTGTGACCTTTTCAATNM_145306RefSeq chr10 +
69630246 69633599 C10orf35 219738 chromosome 10 open reading frame 35 GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_128335_PI430048170 0.782775244530551 1.06316359306675 3.74175801290497
4.44541319824404 4.02582938031505 P P P 4.20009167958962 4.1304497540235
3.64415246967526 P P P LNCV6_128335_PI430048170 mRNA
TGCAAAGACCCTGAGGAAGAGGAACTCTAACACTTCTCTCCTCCACTCTGAGCCCCCTGA NM_002621RefSeq chrX
- 47624212 47630305 CFP 5199 "complement factor properdin, transcript variant 1"
GO:0030449|GO:0005576|GO:0036066|GO:0005615|GO:0006957|GO:0031012|GO:0006956|GO:0006955|GO:0006
493|GO:0045087|GO:0005788|GO:0044267|GO:0042742|GO:0043687 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133462_PI430048170 0.0112549428308332 6.09600351614688 4.51071438303812
3.84759292878437 4.42626755062001 P P P 1.37405931736229 0.930165317788468
2.35909394912751 A A P LNCV6_133462_PI430048170 mRNA
GAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAGCTGAGCTACGATTCCGAAAAAA NM_020994RefSeq chrX
- 154651971 154653579 CTAG2 30848 "cancer/testis antigen 2, transcript variant 2"

GO:0008150|GO:0003674|GO:0005813 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128057_PI430048170 0.5841418080576150.9415343503548090.277585536528281
0.3001934018834310.474136440381546A A A 0.3304215048177890.66155215047396
0.300280181366483A A A LNCV6_128057_PI430048170 mRNA
TCACAATCAGGGAAATGATTGGCTTCTTGGTTGTTTGTTGAACTTTCTTTCTTTATATGG NM_178457RefSeq chr20 +
59191019 59259112 ZNF831 128611 zinc finger protein 831 GO:0003676|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142439_PI430048170 0.00778837465908419 1.25707061327383 14.4243698206359
14.4564630837737 14.5505496035866 P P P 14.1628242716263 14.1579250450377
14.1231116807654 P P P LNCV6_142439_PI430048170 mRNA
GGGGTGTTTGTGTGTGTGCGCGTGTGCGTTTCAATAAAGTTTGTACACTTTCTTAAAAAA NM_002087RefSeq chr17
+ 44345085 44353106 GRN 2896 granulin
GO:0050679|GO:0005739|GO:0005515|GO:0007165|GO:0007566|GO:0001835|GO:0008083|GO:0005615|GO:0005
125|GO:0070062|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129286_PI430048170 0.601045600127391 1.0682648125653 13.9859387121785
13.9375693788047 14.2378667136076 P P P 13.6971022294222 13.8972487779823
14.2454762021735 P P P LNCV6_129286_PI430048170 mRNA
TGAAATCTAGAGTAAAACCAAGCTGGCCCAAGGTGTCCTGCAGGCTGTAATGCAGTTTAA NM_021109RefSeq chrX
+ 12975106 12977227 TMSB4X 7114 "thymosin beta 4, X-linked"
GO:0005515|GO:0003785|GO:0042989|GO:0007596|GO:0002576|GO:0030168|GO:0031093|GO:0007015|GO:0005
576|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145713_PI430048170 0.135799634108579 0.821157592938316 12.2359469502968
12.3566576945771 12.660696561751 P P P 12.6939184237367 12.5806947181423
12.8523206780331 P P P LNCV6_145713_PI430048170 mRNA
AGAGGTTACCAGTGAAAAGAGCTGCTGTCCAGTTTTTGAATAATGCTTGGGGAATCCAAA NM_016167RefSeq chr6
+ 13615326 13620895 NOL7 51406 "nucleolar protein 7, 27kDa" GO:0005739|GO:0005730|GO:0005634
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73911_PI430048170 0.00142308285364419 0.443264450321069 8.86472968441691
8.55350636043875 8.79405834345153 P P P 9.9167309796234 9.82627687067504
10.0032577866013 P P P LNCV6_73911_PI430048170 mRNA
CAGCACTTGCTCAGTAGTTTTGTGAAAGTCTCAAGTAAAAGAGACACAAACAAAAAATTC NM_005524 RefSeq
chr3 + 194136141 194138612 HES1 3280 hes family bHLH transcription factor 1
GO:0005515|GO:0003700|GO:0006366|GO:0061106|GO:0021555|GO:0021558|GO:0045598|GO:0021557|GO:0046
331|GO:0048844|GO:0048538|GO:0003281|GO:0060675|GO:0021861|GO:0042803|GO:0007224|GO:0003143|GO:0
061009|GO:0007219|GO:0060716|GO:0045747|GO:0000122|GO:0001889|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131700_PI430048170 0.333781298158074 1.04138635802411 0.512652677916259
0.666961962513408 0.568055622373967 A A A 0.55185787636433 0.492255712360841
0.531659928371113 A A A LNCV6_131700_PI430048170 mRNA
CTTAACCAGATGTTGGTTTTCAATGTCTAATTTGTCATTAGTTTCACCACATTTGCTCAC NM_024837 RefSeq chr15
- 49858237 50119222 ATP8B4 79895 "ATPase, class I, type 8B, member 4, transcript variant 1"
GO:0005794|GO:0000287|GO:0005886|GO:0008152|GO:0004012|GO:0007030|GO:0016021|GO:0005524|GO:0045
332 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111746_PI430048170 0.0725644831598663 1.21945272728451 8.75252153591937
8.76730272100702 8.7849214477692 P P P 8.31060361805562 8.57996315070768
8.54123474597995 P P P LNCV6_111746_PI430048170 mRNA
GGGGTGATACTACTAGATCACTTGTCCTCTTGCCAGCTCATTTGTTAATAAAATACTGAA NM_006092 RefSeq
chr7 - 30424526 30478777 NOD1 10392 nucleotide-binding oligomerization domain containing 1
GO:0032755|GO:0005515|GO:0042228|GO:0050830|GO:0046330|GO:0051259|GO:0051403|GO:0042803|GO:0042

802|GO:0002756|GO:0002755|GO:0009595|GO:0070374|GO:0043123|GO:0042742|GO:0050700|GO:0038124|GO:0
032760|GO:0038123|GO:0034134|GO:0042834|GO:0006952|GO:0002224|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129431_PI430048170 0.127299857165776 1.16825923985667 6.61536536080831
6.90050904769205 6.85924418891506 P P P 6.56639253059307 6.60721960423629
6.54384303397098 P P P LNCV6_129431_PI430048170 mRNA
CCAAGAGAACCCAAACCAATAAAGTTTATGCTAAGTCGAGCCCATTGTGAAAATTTATTA NM_004123 RefSeq
chr17 - 48958555 48968593 GIP 2695 gastric inhibitory polypeptide
GO:0055123|GO:0014070|GO:0008344|GO:0033993|GO:0070328|GO:0043434|GO:0060291|GO:0048678|GO:0005
615|GO:0042594|GO:0043025|GO:0043950|GO:0007613|GO:0032024|GO:0043200|GO:0035640|GO:0007565|GO:0
042493|GO:0070094|GO:0010269|GO:0005576|GO:0019233|GO:0010828|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130265_PI430048170 0.574432326105543 0.924857907926656 9.19732605852056
9.84996718636637 9.20635177331244 P P P 9.50713834214043 9.52473468177236
9.65648865389726 P P P LNCV6_130265_PI430048170 mRNA
GGCAGGGCTGGGAGAACTTTGTACAGTGGAGAAATATTTATAAACTTAATTTTGTAAAAC NM_001291902 RefSeq
chr11 + 68312608 68449275 LRP5 4041 "low density lipoprotein receptor-related protein 5,
transcript variant 2"
GO:0005515|GO:0019534|GO:0017147|GO:0046850|GO:0090263|GO:0060042|GO:0048539|GO:0048596|GO:0042
074|GO:0046849|GO:0033690|GO:0016055|GO:0042632|GO:0060033|GO:0045840|GO:0060764|GO:0035426|GO:0
001702|GO:0006897|GO:0060828|GO:0043235|GO:0002076|GO:0060349|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138532_PI430048170 0.0689133865711906 0.5755640493203 8.9328197596146
8.75470097501783 8.87482380515287 P P P 9.18972948774388 9.72689208285073
9.94227242308751 P P P LNCV6_138532_PI430048170 mRNA
AAATATATTCCCAGATTATCCTTGTAATGACACGAATCTGCAATAAAAGCCATCAGTGCT NM_012098 RefSeq
chr9 - 127087348 127122765 ANGPTL2 23452 angiopoietin-like 2
GO:0005102|GO:0007275|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128022_PI430048170 0.120987514253165 1.16888098697497 10.2948163494573
10.4426088664911 10.2423116599753 P P P 10.1691061983239 10.2123881840748
9.91258435258541 P P P LNCV6_128022_PI430048170 mRNA
GCAGGGCTGCTCAGTGCCTGCCTCTGACAAAATTAAAGCATTGATGGCCTGTGGACCTGC NM_000355 RefSeq
chr22 + 30607082 30627060 TCN2 6948 "transcobalamin II, transcript variant 1"
GO:0015889|GO:0009235|GO:0031419|GO:0006767|GO:0005576|GO:0044281|GO:0005615|GO:0046872|GO:0006
766|GO:0005768|GO:0006824|GO:0043202|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139736_PI430048170 0.0855928372694873 1.05879442562074 0.461702992445321
0.545040694684917 0.508292743750479 A A A 0.3726102296657 0.429572582278659
0.465283197947686 A A A LNCV6_139736_PI430048170 mRNA
AAACCCTTCCAATAAGTCCTGATAATAAAGCACTTCAGGGTCCCATGTCTTGATAAAAAA NM_001289177 RefSeq
chr19 + 6135632 6193103 ACSBG2 81616 "acyl-CoA synthetase bubblegum family member 2, transcript
variant 1"
GO:0047617|GO:0005739|GO:0005737|GO:0001676|GO:0016020|GO:0006631|GO:0007275|GO:0007283|GO:0005
524|GO:0030154|GO:0005829|GO:0004467 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143292_PI430048170 0.201162616845756 4.22673959338452 0.365718849207075
2.10284795895544 3.34894671924922 A A P 0.301916180793819 0.297746568767531
0.344539474648408 A A A LNCV6_143292_PI430048170 mRNA
TAAAAAGCCAGCAAACTATCTTCAAACTCTTCCGTCCTTAATGTCTTCCATGGCTATTGC NM_030788 RefSeq chr8

+ 104339795 104356689 DCSTAMP 81501 "dendrocyte expressed seven transmembrane protein, transcript variant 1"
GO:0005515|GO:0030308|GO:0072675|GO:0036006|GO:0009986|GO:0030316|GO:0030176|GO:0045780|GO:0045657|GO:0005887|GO:0033116|GO:0071356|GO:0005789|GO:0071353|GO:0061025|GO:0016021|GO:0043011|GO:0010008|GO:0034241. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127541_PI430048170 0.9261997135054280.9735890019430523.842956043394
3.78328901120973 3.64265904500755 P P P 3.43600546334796 4.04491077396866
3.84605748302418 P P P LNCV6_127541_PI430048170 mRNA
CTTGATACTTCTGATTGTTTCCTGCACTTTAAGTTAAGCCTGGGCAACATGTTGAGATCC NM_198077RefSeq chr1
- 85249953 85259672 C1orf52 148423 "chromosome 1 open reading frame 52, transcript variant 1"
GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67776_PI430048170 0.384029872388795 1.83457923114443 0.6008789953818972.75844247882501
1.61231412074534 A A A 0.3984609216482111.7610664409251 0.559790681574948A A A
LNCV6_67776_PI430048170 mRNA
TTGATCTCTGTGAAGTTGGTCAGGAGGAAGTAATCCTGAAAACCGGGAAGCAAGCTAATC NM_001145418 RefSeq
chr22 - 27978013 28679865 TTC28 23331 tetratricopeptide repeat domain 28
GO:0007346|GO:0007067|GO:0005813|GO:0005737|GO:0000922|GO:0030496|GO:0051301 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134018_PI430048170 0.35427742188689 0.97102319211027 0.3957543593856
0.4205070149824890.302733387863525A A A 0.3995090961313430.442879639979201
0.406147872004668A A A LNCV6_134018_PI430048170 mRNA
GAGATGACAAGTGCTATGAAGAAGCTCTGGAGAAGAGACCTCATATCAAGTAGTACATAANM_001005512 RefSeq
chr11 + 48488792 48489722 OR4A47NA "olfactory receptor, family 4, subfamily A, member 47" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130120_PI430048170 0.0172961439981878 1.41375600361615 9.40831551544814
9.38667804390876 9.21773370540257 P P P 9.01807083593825 8.79559012335323
8.68805059134188 P P P LNCV6_130120_PI430048170 mRNA
ACACTGATGAAGCCCTGCCATACCCCTCCCGAGTCTAATAAAACGTATAATCACAAAAAA NM_205834RefSeq chr19
+ 35248655 35267964 LSR 51599 "lipolysis stimulated lipoprotein receptor, transcript variant 2"
GO:0034361|GO:0001889|GO:0005886|GO:0034362|GO:0042627|GO:0016021|GO:0070062|GO:0019216 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133998_PI430048170 0.0356807173320135 2.65977268487632 6.14209534546518
6.12448433578538 6.21043669500955 P P P 5.24900729553625 4.28359920355389
4.53108509271775 P P P LNCV6_133998_PI430048170 mRNA
GGAGTGGGGAAGTGTGTCAAATCAATAAATGAATAAATTCAATAAATGCCTATAACCAGC NM_005938RefSeq chrX
+ 71096148 71103534 FOXO4 4303 "forkhead box O4, transcript variant 1"
GO:0007095|GO:0005515|GO:0008286|GO:0003700|GO:0008285|GO:0006366|GO:0000981|GO:0005634|GO:0005829|GO:0005737|GO:0007173|GO:0007050|GO:0048011|GO:0006355|GO:0006357|GO:0051151|GO:0048015|GO:0070317|GO:0003677|GO:0048863|GO:0043565|GO:0007517|GO:0008543|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93174_PI430048170 0.9516606605092171.01630563249639 0.5283846148843591.44934390853675
0.25980283925453 A A A 1.25651001477845 0.5788503377699030.486944465183797A A A
LNCV6_93174_PI430048170 mRNA
AAAGATCAAGGACCGGTATCTTCTAAAGGCACTGGACAAATACTGGCATGAAGACTGCCT NM_018640RefSeq chr12
- 16548371 16606602 LMO3 55885 "LIM domain only 3 (rhombotin-like 2), transcript variant 1"
GO:0006355|GO:0005737|GO:0035360|GO:0045600|GO:0070373|GO:0008270|GO:2000324|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126578_PI430048170 0.6273348252568481.12411908494781 2.60694092590415
1.99094675466624 2.6916177241703 A A A 1.70061579017575 2.44822661108044

2.58369734379689 A A P LNCV6_126578_PI430048170 mRNA
GGCTCTGGCTACTGTGGCTACCGGCCATTTTGCTTTAGAAGATGCTATTCTTCCTGCTAA NM_181619RefSeq chr21
- 30755138 30755378 KRTAP21-1 NA keratin associated protein 21-1 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137047_PI430048170 0.0390575240170323 0.7362886554358737.12376412733897
7.44292843314946 7.26599830788559 P P P 7.72022464593952 7.74127663697523
7.71378985178019 P P P LNCV6_137047_PI430048170 mRNA
GGGTTTTGTTGTGTAAATATTCTATTTTATTCTTGGGGGGATCAAACCTTAGGAAAAGGA NM_005224RefSeq chr19
+ 926036 972803 ARID3A 1820 AT rich interactive domain 3A (BRIGHT-like)
GO:0005515|GO:0005737|GO:0005794|GO:0000977|GO:0045944|GO:0003682|GO:0005730|GO:0045121|GO:0005
654|GO:0001228|GO:0042803|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68620_PI430048170 0.7574018945314631.24249115170411 0.8645939878685651.11748759879198
2.37984619230615 A A A 1.09770528780993 1.13289232574312 1.61710998282729 A A A
LNCV6_68620_PI430048170 mRNA
GACTAACCTTTTAGGAGCAAGATTATATTTTGCTCCAAAAGTGTTGACACCCTATTGTTA NM_024091RefSeq chr5
- 7859158 7869037 FASTKD3 79072 "FAST kinase domains 3, transcript variant 1"
GO:0005739|GO:0045333|GO:0004672|GO:0006468 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137935_PI430048170 0.1699989860148080.6723807066712239.53072436476357
9.89336731787262 9.63461063169493 P P P 9.97577907898715 9.93367415778272
10.7412718891552 P P P LNCV6_137935_PI430048170 mRNA
GGTTGGGGGAAGCTTGACCTTGTGTCTTCGTCAATAAACTCACATTTACACAAAATGAAA NM_001030006 RefSeq
chr17 + 35587262 35726417 AP2B1 163 "adaptor-related protein complex 2, beta 1 subunit, transcript
variant 1"
GO:0072583|GO:0005515|GO:0048011|GO:0035615|GO:0048013|GO:0005886|GO:0030122|GO:0042059|GO:0007
268|GO:0006886|GO:0050690|GO:0043231|GO:0005829|GO:0030666|GO:0019886|GO:0007173|GO:0016020|GO:0
030276|GO:0007411|GO:0008565|GO:0016032|GO:0005048|GO:0030669 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142834_PI430048170 0.1103203334117541.03443606702137 0.328890947145645
0.3287490498833930.273591200296575A A A 0.2562144816303640.271289288946974
0.257848224680547A A A LNCV6_142834_PI430048170 mRNA
CAATCGCCTTTGGAAGGCAATGAAACACTTAATAAACTCTCAATAACAGAAGCGTAAAAA NM_152278RefSeq chrX
+ 103330185 103332323 TCEAL7 56849 transcription elongation factor A (SII)-like 7
GO:0032088|GO:0005634|GO:0045892|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93631_PI430048170 0.11265838478208 1.11534113950185 0.3418234088191120.372944670891215
0.529779309707356A A A 0.2481848065493790.2790871993963 0.251737813440617A A A
LNCV6_93631_PI430048170 mRNA
AGGTCTTCTTGATTATGCTACTGGTGCAATTGGATCAGTGTATGATATGGATGATGATGA NM_001302769 RefSeq
chr2 + 204545792 205620162 PARD3B 117583 "par-3 family cell polarity regulator beta, transcript
variant 1" GO:0007049|GO:0016020|GO:0005923|GO:0051301|GO:0012505 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144062_PI430048170 0.4322663927209170.8943747647534865.5332292139108 5.4711045258041
5.8105652084683 P P P 5.56043825856492 5.68569664274915 6.03265666456703 P P P
LNCV6_144062_PI430048170 mRNA
TGTGCAATGTTGTGGCTTTAACATTTTATGCAACTATTTATGAAGACCTCTGTTGTACCTNM_007118RefSeq chr5 +
14143719 14509349 TRIO 7204 trio Rho guanine nucleotide exchange factor
GO:0005515|GO:0051056|GO:0048011|GO:0043065|GO:0007264|GO:0097190|GO:0005524|GO:0005829|GO:0043
547|GO:0005085|GO:0004674|GO:0007411|GO:0032321|GO:0007185|GO:0006468|GO:0005089|GO:0019899 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57452_PI430048170 0.4184214800163831.09214273918113 5.86103407860334 5.74773858636656

5.56145027661998 P P P 5.72712884206732 5.6858135661136 5.36500021665583 P P P
LNCV6_57452_PI430048170 mRNA
AAGGACTTCGGGATGTCTGGGCTCCGCTTTGGCACGCTGTACACAGAAAACCAGGATGTG NM_032592 RefSeq chr11
+ 44066261 44084019 ACCS 84680 "1-aminocyclopropane-1-carboxylate synthase homolog
(Arabidopsis)(non-functional), transcript variant 1" GO:0009058|GO:0016847|GO:0030170|GO:0042803 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127162_PI430048170 0.7494008217272571.01107481787835 0.523778051407589
0.5675663772782850.437462663844036 A A A 0.5357983333122060.473553845381804
0.473914337555926 A A A LNCV6_127162_PI430048170 mRNA
CAAGCTCGAAGACAAACGAACAGAGATGTTTTGCTCACTTTAGTTAATAGATTTGATCAA NM_181745 RefSeq chr10
+ 93566664 93590072 FFAR4 338557 "free fatty acid receptor 4, transcript variant 1"
GO:0042277|GO:0005504|GO:0043066|GO:0005886|GO:0008527|GO:0030139|GO:0050710|GO:0010827|GO:0032
870|GO:0050912|GO:0046879|GO:0007186|GO:0005887|GO:0050728|GO:0070374 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144786_PI430048170 0.9070439657307571.01888775715362 11.2372407387178
10.8324267060096 10.8875985053551 P P P 11.0268095094816 11.0206215348656
10.8567309212212 P P P LNCV6_144786_PI430048170 mRNA
GATGTTTCTGTACTGGCATAGAAAAACCAAATAAAAGGCCTTTATTTTTATGGCTGAGGA NM_015963 RefSeq chr2
- 241584404 241637310 THAP4 51078 "THAP domain containing 4, transcript variant 1"
GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139372_PI430048170 0.2947260780931510.6017735545551350.330322386794592
0.3151530506902020.297474272518315 A A A 0.5301811381410961.7624255730583
0.446008965184224 A A A LNCV6_139372_PI430048170 mRNA
CAACTCAAGGGGCTCCTTTATTACTTTTGAATGTTTTTGCCCAAATGTCTATACCAAAGA NM_152367 RefSeq chr1
+ 116111754 116135240 MAB21L3 126868 mab-21-like 3 (C. elegans) NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137351_PI430048170 0.0722134365943902 0.7489862217072461 0.5371617660416
10.5456008228515 10.8464955359598 P P P 10.8998965108032 10.9490253962246
11.3164309796681 P P P LNCV6_137351_PI430048170 mRNA
GAAATTTTGGGTCTCAATTTTTACTGTGCCTTTGTTTTTACTAGTGTCTGCTGTTGCAAA NM_001277444 RefSeq chr1
- 149054032 149082311 NBPF9 400818 "neuroblastoma breakpoint family, member 9, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127457_PI430048170 0.38878857823329 0.9016331858253198.13834886132745
7.63084202532165 7.99175963023907 P P P 8.07160510543159 8.08022025524002
8.10318524226422 P P P LNCV6_127457_PI430048170 mRNA
CCAATCAGTGTATTGCTCATTTACTGACAAAAAGGGAAAATACGAAACACAGAAAGGGAA NM_207113 RefSeq chr7
- 140333751 140398550 SLC37A3 84255 "solute carrier family 37, member 3, transcript variant 1"
GO:0005215|GO:0008643|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_37714_PI430048170 0.1931236825870461.29727405421139 5.55025616000603 4.93765786802833
5.42629137162088 P P P 4.74939472889165 4.88801258540283 5.18526014246963 P P P
LNCV6_37714_PI430048170 mRNA
TATTGGAGGAGCTGGAGAAGTGTGATGCCAATCACTACATCATACTGTTTCGTGATGCTG NM_015447 RefSeq chr9
- 135808486 135907159 CAMSAP1 157922 calmodulin regulated spectrin-associated protein 1
GO:0008017|GO:0005516|GO:0005737|GO:0022604|GO:0007010|GO:0005874|GO:0030507|GO:0031175 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134875_PI430048170 0.4325793628254560.4393056596656890.393188455985862
0.2949821823424240.336099768238651 A A A 2.62185792383695 0.305512520257557
0.33848537324463 P A A LNCV6_134875_PI430048170 mRNA
AATTCTTAGCTGTGTGAGAGGTTCTGCATGCATTATCTCATTTATTCTCCTCGATAACCC NM_013411 RefSeq chr1

- 33007939 33036911 AK2204 "adenylate kinase 2, transcript variant 2"
GO:0046033|GO:0097066|GO:0015949|GO:0046060|GO:0097226|GO:0005743|GO:0055086|GO:0004017|GO:0044
281|GO:0005524|GO:0005829|GO:0006119|GO:0001889|GO:0005758|GO:0007420|GO:0046939|GO:0006172|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135160_PI430048170 0.0257532030593679 1.09003254248099 0.452568200524086
0.3808251079064760.390272751973545A A A 0.2609109600860690.337536074470412
0.251613407221139A A A LNCV6_135160_PI430048170 mRNA
ACTTTTCCCTCAAGTAGGTACCAATTTCCCTTGAATAAAATCTAGCCATGTCTATGTCTG NM_001206927 RefSeq
chr6 + 38715340 39030798 DNAH8 1769 "dynein, axonemal, heavy chain 8"
GO:0001539|GO:0008152|GO:0005874|GO:0005858|GO:0003777|GO:0016887|GO:0005524|GO:0007018 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127715_PI430048170 0.0797809194908354 0.818917948488051 0.620209462019229
0.5356125623193030.316424423971698A A A 0.7809382801018430.633533199051095
0.924526105162183A A A LNCV6_127715_PI430048170 mRNA
GGAAATCGTTTGATGGGGAAAAGTCTCTTGTAAGTAAAAGTAGTCAAATTCAAATGGCAA NM_006063 RefSeq chr2
+ 169509701 169526262 KLHL41 10324 kelch-like family member 41
GO:0005515|GO:0016567|GO:2000291|GO:0005886|GO:0031275|GO:0006941|GO:0033017|GO:0005634|GO:0035
914|GO:0001726|GO:0031430|GO:0045661|GO:0031143|GO:0005737|GO:0030239|GO:0031463|GO:0005789|GO:2
001014|GO:0005856. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132827_PI430048170 0.1348797078052650.613157752381072 0.372587757486704
0.3506465252947310.259572837685572A A A 0.4588694701169631.12796689876607
1.36933879681372 A A A LNCV6_132827_PI430048170 mRNA
CTATTGAAGTCTGAAGCTTTTTTCATCCAGTCAAGCAAATATAACATCACCAAAAGGGAT NM_001271752 RefSeq
chrX + 26216168 26218270 MAGEB5 NA melanoma antigen family B5 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_142413_PI430048170 0.3429340345254850.8949243981805857.63511709891935
7.36219969419774 7.78541029016857 P P P 7.60755656484534 7.76117688097327
7.91005893917534 P P P LNCV6_142413_PI430048170 mRNA
GTGTGCATCTTACTGGATGAGGTTGCTGTGATTGAGATAGTTAAATACATGCTAATTTAA NM_001135773 RefSeq
chr20 - 49903390 49913739 SPATA2 9825 "spermatogenesis associated 2, transcript variant 2"
GO:0003674|GO:0005737|GO:0005730|GO:0007275|GO:0005634|GO:0007283|GO:0030154 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_76847_PI430048170 0.2047239298637791.59359078912735 4.32478552641748 4.76715589470031
5.45948506294093 P P P 4.53067361248373 3.71561062292358 4.39391449497535 P P P
LNCV6_76847_PI430048170 mRNA
TTGGCCAATTTTAGTCTTGCTGTTTCTTGATGCTCACCTCTATATTAGTTTATTGTTAGG NM_001491 RefSeq chr6 +
10555715 10629368 GCNT2 2651 "glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood
group), transcript variant 2"
GO:0051897|GO:0008284|GO:0030335|GO:0010718|GO:0010812|GO:0007275|GO:0005575|GO:0008109|GO:0006
024|GO:0010608|GO:0000139|GO:0016020|GO:0034116|GO:0006486|GO:0007179|GO:0070374|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83439_PI430048170 0.00480237759739461 1.2255105955513 12.1010219277538 12.026900550322
12.0355589622507 P P P 11.7805984090859 11.8129079629158 11.6880795801183 P P P
LNCV6_83439_PI430048170 mRNA
CCCTTTGACCTTCATCTGATGGACATTTTTATACAGAAAACAATAAAGATTTCCCTCTCA NM_001142798 RefSeq
chr17 + 7014736 7017524 C17orf49 124944 "chromosome 17 open reading frame 49, transcript
variant 1" GO:0071339|GO:0003682|GO:0016589|GO:0003677|GO:0016568 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133632_PI430048170 0.00137652540281655 0.3682067311814987.4002297927137

7.09196282348394 7.46171830779679 P P P 8.55372099124585 8.70255262007739
9.01025744405637 P P P LNCV6_133632_PI430048170 mRNA
AACGTAAACACTGGTGACATAAACCATTCATTGCTACGTTGCTTATTGTGTTTTTATGCT NM_001146188 RefSeq
chr16 - 52438005 52547802 TOX3 27324 "TOX high mobility group box family member 3, transcript
variant 2"
GO:0051219|GO:0034056|GO:0005515|GO:0043524|GO:0003682|GO:0006915|GO:0006338|GO:0005634|GO:0045
893|GO:0042803|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144868_PI430048170 0.0496590935037245 0.415253503484161 2.61633252254852
2.0219527898545 3.2864157690949 A A P 3.66217871952081 3.69905573192895 4.4851580143022
P P P LNCV6_144868_PI430048170 mRNA
CCCTCCAGGTTATCTGAAAGAATTTCAATGCTTACCTTTAATCATGTGACATTGTTTATC NM_000254RefSeq chr1
+ 236795280 236903981 MTR 4548 "5-methyltetrahydrofolate-homocysteine methyltransferase,
transcript variant 1"
GO:0005515|GO:0006805|GO:0009235|GO:0031419|GO:0006767|GO:0009086|GO:0044281|GO:0042558|GO:0032
259|GO:0008705|GO:0005829|GO:0007399|GO:0034641|GO:0005737|GO:0000096|GO:0006766|GO:0008270|GO:0
008898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100470_PI430048170 0.0105609514169192 1.53745896833082 10.0439134825049
10.0098359870815 10.0417243041356 P P P 9.4880171783966 9.46576507628801
9.27053225166769 P P P LNCV6_100470_PI430048170 mRNA
GTCGGTGACCCTGTCCACGGTGTCTGTGTTCACTTTTGTTGCGGAGGTGAAGGGCTTTGT NM_000837RefSeq chr8
+ 143990057 143993415 GRINA 2907 "glutamate receptor, ionotropic, N-methyl D-aspartate-associated
protein 1 (glutamate binding), transcript variant 1"
GO:0005794|GO:0005783|GO:0032469|GO:0016021|GO:0044325 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141405_PI430048170 0.10150410355003 0.852757622407721 4.93817026813543
5.22166509396504 5.10091312014868 P P P 5.32868049167756 5.33548462555606
5.29966026674087 P P P LNCV6_141405_PI430048170 mRNA
CATTTGAAAGTGAAATGTTTCTCTTCGCAAAGGACTCTTATACCCTCCCCTAAAGAAATC NM_017856RefSeq chrX
- 14006725 14029916 GEMIN854960 "gem (nuclear organelle) associated protein 8, transcript variant 3"
GO:0005515|GO:0005737|GO:0032797|GO:0005654|GO:0005634|GO:0000387|GO:0034719|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115061_PI430048170 0.641007120245851 0.452509469832843 0.368753265655783
0.501086910473198 1.20662947205871 A A A 0.246713316456373 0.288373249945581
3.11665738626313 A A P LNCV6_115061_PI430048170 mRNA
TTAAGTTTAAAAAACAGAAAAACAGACAAAACAATCCCCATCAGGTAGCTGTCTAACCCC NM_001174051 RefSeq
chr3 - 50362612 50503597 CACNA2D2 9254 "calcium channel, voltage-dependent, alpha 2/delta
subunit 2, transcript variant 3"
GO:0046622|GO:0005245|GO:0005886|GO:0044281|GO:0005891|GO:0046872|GO:0048747|GO:0006112|GO:0050
796|GO:0007528|GO:0040014|GO:0070588|GO:0034765|GO:0060024 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_136994_PI430048170 0.361552747756139 0.910475651196113 6.59321050536512
6.18424808868382 6.47670200786075 P P P 6.49813132954627 6.65099496319894 6.5366851326504
P P P LNCV6_136994_PI430048170 mRNA
GGGCAGAAGGGGGAAAAACAGCAAAGAGGGATAAAATAGTTTTTGACTCTAATACTGTATNM_018288RefSeq chr6
- 169703905 169724010 PHF10 55274 "PHD finger protein 10, transcript variant 1"
GO:0006355|GO:0008270|GO:0071564|GO:0006351|GO:0007399 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137203_PI430048170 0.85401062166611 1.03339919904555 11.0302346766994
10.7234181997201 10.4990658770072 P P P 10.5868404133171 10.8054020983213

10.7588222696849 P P P LNCV6_137203_PI430048170 mRNA
ACCTACTCTCGGAGCTGCCTCCATGGGCACAGTAAAGGTGGCCCAAGGAAGGTGAAAAAA NM_024040 RefSeq
chr10 - 102423244 102432666 CUEDC2 79004 CUE domain containing 2
GO:0005515|GO:0031965|GO:0005737|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61432_PI430048170 0.00487870630948767 1.72952151678708 9.24009732035649
9.48049840191232 9.3070362239652 P P P 8.54906220920765 8.59577316596217
8.52148200955571 P P P LNCV6_61432_PI430048170 mRNA
ACACATTAGTGTCACATGGTTGCGTGTCCAGCCGAAGCAGTGTAATAAACATCTCCAATG NM_199165 RefSeq chr14
+ 104729890 104747311 ADSSL1 122622 "adenylosuccinate synthase like 1, transcript variant 1"
GO:0046040|GO:0000287|GO:0006531|GO:0009168|GO:0014850|GO:0003924|GO:0004019|GO:0055086|GO:0044
281|GO:0044208|GO:0005525|GO:0035690|GO:0042803|GO:0005829|GO:0006184|GO:0071257|GO:0005737|GO:0
006167|GO:0051015|GO:0042594|GO:0006144|GO:0042301|GO:0002376|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127783_PI430048170 0.9493104860787181.00490512563718 12.2390129992429
12.3292645710493 12.1057870788103 P P P 12.2651188760484 12.2507779040263
12.1426220692052 P P P LNCV6_127783_PI430048170 mRNA
CTAGGGCCGTGGCCTTTGCCGAGACTGTAGCAGAGAAAACGTATTTATTATTCCAAAAAA NM_001142467 RefSeq
chr1 - 998963 1000172 HES4 57801 "hes family bHLH transcription factor 4, transcript variant 1"
GO:0006355|GO:0046983|GO:0005634|GO:0003677|GO:0030154|GO:0006351|GO:0008134|GO:0007399 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136005_PI430048170 0.8519377121133460.9264610013616443.12575884245018 2.6397692336703
2.38329993564588 P A A 2.17315057186302 3.23529998238221 2.97317947377802 A P P
LNCV6_136005_PI430048170 mRNA
CTTCAGTACATTGATGTTTTGATGGCGGACTACATAAGCGTTAAAAATTGTGTTTTTCAG NM_001258272 RefSeq
chr14 - 63597038 63641923 WDR89 112840 "WD repeat domain 89, transcript variant 3" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_132326_PI430048170 0.0510733335754171 0.1205262947445550.289943386016479
2.70280442782775 2.94951311345129 A A P 5.03837794120899 5.59604605109386
5.55527821332739 P P P LNCV6_132326_PI430048170 mRNA
CCTGGACAGTTTGATGTGCTTATGGTTGAGATTTATAATCTGCTTGTACTTTGCTTTTTA NM_175884 RefSeq chr7 -
106656764 106661188 CCDC71L 168455 coiled-coil domain containing 71-like NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_135656_PI430048170 0.0733150733754811 0.3895227978801370.305951479423673
0.2685782366953330.320616204218607 A A A 2.28632830441162 1.23775102809643 1.1608997563088
A A A LNCV6_135656_PI430048170 mRNA
GGTCTCACCCAACTGCAGTTTACTATTGCTATCTTTTCTGGATGATCAGAAAAATAATTC NM_005814 RefSeq chr1
- 167052835 167090631 GPA33 10223 glycoprotein A33 (transmembrane)
GO:0005887|GO:0004872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145058_PI430048170 0.0275142176701425 1.10116624124659 13.0520703404547
13.0156335890321 13.0488392172873 P P P 12.8766301962386 12.9568929335975
12.8644448881039 P P P LNCV6_145058_PI430048170 mRNA
TTTTCCTTTGCCATTGATTTTTGAGACTCATGCATTAAATTCACTAGAAACCCAGAAAGT NM_001281 RefSeq chr19
+ 36114985 36125947 TBCB 1155 "tubulin folding cofactor B, transcript variant 1"
GO:0005515|GO:0005737|GO:0015630|GO:0005874|GO:0051084|GO:0005654|GO:0044267|GO:0030154|GO:0007
399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140233_PI430048170 0.37978978470378 0.9715369186181170.397771935829071
0.4217130702479820.298891747412677 A A A 0.3969159017059840.44324451786237
0.405689452655963 A A A LNCV6_140233_PI430048170 mRNA
TTTTGCTCTTTTGGGGATGGGACATCAAACAAAAGTCTCTTCGTGTATATCTCAGCTCCT NM_198153 RefSeq chr6

+ 41228323 41238382 TREML4 285852 triggering receptor expressed on myeloid cells-like 4 GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130374_PI430048170 0.593016287993097 0.968523946658975 0.490912366253971
0.457120407035494 0.24907188100141 A A A 0.393441279459325 0.499436709444034
0.452384576029461 A A A LNCV6_130374_PI430048170 mRNA
GTGTGGTGATGTCTTACCTGAATGTTGGTTGTTACTGATATATTACAATTTTCAAGGTGA NM_152638 RefSeq chr12
- 90952214 90955176 CCER1 196477 "coiled-coil glutamate-rich protein 1, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142489_PI430048170 0.513266028411558 1.53218666758244 2.04832635127526
0.471777513421831 0.469892052594571 A A A 0.77863627417739 0.534863928214401
0.426885360312465 A A A LNCV6_142489_PI430048170 mRNA
CTCGAGAAGTGAGGAGAGGCAGTTTGGAGCAGAATGGAGAGAATAAAATGTTTCTTGTCANM_033106 RefSeq chr19
+ 56176019 56185775 GALP 85569 "galanin-like peptide, transcript variant 1"
GO:0032868|GO:0008150|GO:0042595|GO:0005179|GO:0007218|GO:0032098|GO:0005576|GO:0005575|GO:0042
742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127712_PI430048170 0.453267831254155 0.876899542134113 10.3903474007354
10.6850089131159 10.7902219532973 P P P 10.6287099644256 10.6223255027704
11.1471013414872 P P P LNCV6_127712_PI430048170 mRNA
TGTTATCACTCTGCCTGTGTATAGTCAGATAGTCCATGCGAAGGCTGTATATATTGAACA NM_001289999 RefSeq
chr9 - 91409044 91424626 NFIL3 4783 "nuclear factor, interleukin 3 regulated, transcript variant 1"
GO:0000977|GO:0003700|GO:0006366|GO:0003714|GO:0005634|GO:0000122|GO:0000979|GO:0003677|GO:0010
628|GO:0001078|GO:0006955|GO:0007623|GO:0071353 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139085_PI430048170 0.158513898083507 0.939125150650153 0.244456743116726
0.298149411908881 0.293206849802183 A A A 0.449310097101101 0.349642314875894
0.305517753927711 A A A LNCV6_139085_PI430048170 mRNA
CACCTAGGTGTCTATGTTCTATCACATCTACAAACATGTCACTTCCTAATTAACAAAATG NM_001289036 RefSeq
chr18 + 596997 650293 CLUL1 27098 "clusterin-like 1 (retinal), transcript variant 3"
GO:0008219|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143990_PI430048170 0.446045604844684 1.40699804164675 2.67480474963459
2.45761272048475 1.33981894007922 A A A 1.8120252587353 2.31603768096726
0.807797692784105 A A A LNCV6_143990_PI430048170 mRNA
TCTGACTCTTAAACTAGAAGGCAAAAGGTCTCTCTCTTGAGATCAACAAAGGGCCTTCCA NM_001142935 RefSeq
chr5 - 177305499 177312291 MXD3 83463 "MAX dimerization protein 3, transcript variant 2"
GO:0046983|GO:0005634|GO:0045892|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_94171_PI430048170 0.426163821974813 0.939203689323439 0.538980919462133 0.488284224418445
0.262879047265595 A A A 0.410138092609036 0.546102750877719 0.612747701378808 A A A
LNCV6_94171_PI430048170 mRNA
TGAAGTCATCTTATTCTCGATCCTCAGCTGTTAAGTATTCTGGATCCAAAAGCCCTGGGC NM_001040261 RefSeq
chr4 + 150078273 150257456 DCLK2 166614 "doublecortin-like kinase 2, transcript variant 2"
GO:0035556|GO:0005737|GO:0004674|GO:0006468|GO:0005856|GO:0005524 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145496_PI430048170 0.20851850180727 1.54081153326222 3.43815232393135
3.65861614242587 3.63718558209663 P P P 3.598075493745 2.20765935764081
2.71742199284178 P A P LNCV6_145496_PI430048170 mRNA
GAAAATTCATAGCGCTGTGATTTTTAGATCGACCTCACATAAAACAGTCCCTGCACTCGC NM_012064 RefSeq chr12
- 56449501 56454651 MIP 4284 major intrinsic protein of lens fiber
GO:0005215|GO:0005516|GO:0005212|GO:0005886|GO:0046691|GO:0009992|GO:0055085|GO:0043231|GO:0016
324|GO:0034220|GO:0002088|GO:0005887|GO:0015793|GO:0015250|GO:0015722|GO:0005921|GO:0006833|GO:0

015254|GO:0007601|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131938_PI430048170 0.1092007080025021.83640165429102 4.75537081309244
3.73825028294713 3.85924835166642 P P P 3.45724924783823 3.56870723186139
2.81322247152209 P P P LNCV6_131938_PI430048170 mRNA
TTACTTCTCATAATGTGTGCATTGAGTTGTGTGGGCCGGTGGCTGTTGAGTATGCTTTCT NM_178554RefSeq chr3
- 134599922 134651022 KY 339855 kyphoscoliosis peptidase
GO:0030018|GO:0007517|GO:0007528|GO:0006508|GO:0008233|GO:0005856 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131616_PI430048170 0.1495304462741510.9548225387721190.265293899720346
0.2766917314227120.343687114288015A A A 0.41603531876687 0.347079559323171
0.322250068489571A A A LNCV6_131616_PI430048170 mRNA
ATCCATTGAAAGACTAGGCTATTTTTTCACTGTCCTCAGACATTTACTGAGTCCAGTTTG NM_207118RefSeq chr6
+ 158168346 158199344 GTF2H5404672 "general transcription factor IIH, polypeptide 5"
GO:0006355|GO:0000439|GO:0006364|GO:0000182|GO:0006294|GO:0006362|GO:0005730|GO:0071480|GO:0006
289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130226_PI430048170 0.0294730454034089 0.7157483768959715.87782640107761
5.52142502874907 5.84432342179391 P P P 6.38480415126118 6.13688775367099
6.18322136080499 P P P LNCV6_130226_PI430048170 mRNA
GGTAATTTGATTATGAAAGAGTGAATTTTTCTGGACAGAAAAGGGAGAGCTACCAAATTG NM_004090RefSeq chr17
- 43766120 43779000 DUSP3 1845 dual specificity phosphatase 3
GO:0033549|GO:0034142|GO:0005634|GO:0051403|GO:0035335|GO:0005829|GO:0000188|GO:0043409|GO:0002
756|GO:0005737|GO:0046329|GO:0002755|GO:0070373|GO:0034138|GO:0004725|GO:0070062|GO:0001772|GO:0
048011|GO:0038124|GO:0038123|GO:0050868|GO:0034134|GO:0002224|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140368_PI430048170 0.00718133296908674 0.21595959366896 1.14951702855108
0.4710218032944910.899162995562451A A A 2.4033776702386 3.45407648508906
3.18216996749329 A P P LNCV6_140368_PI430048170 mRNA
GGGCACTGCCTTGAGATCATCCTTCTCAAATAAAAAGAATGCATTTGAAGAAAGAAAAAA NM_178009RefSeq chr13
+ 42048707 42242897 DGKH 160851 "diacylglycerol kinase, eta, transcript variant 2"
GO:0031965|GO:0005886|GO:0030168|GO:0005634|GO:0051259|GO:0005524|GO:0046872|GO:0007205|GO:0035
556|GO:0016310|GO:0005737|GO:0003951|GO:0007596|GO:0004143|GO:0005768 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_142095_PI430048170 0.03403473216029 1.40140760206977 8.60542550086897
8.59780296990549 8.37898536327625 P P P 7.80284557867525 8.20866714258232
8.09169005043126 P P P LNCV6_142095_PI430048170 mRNA
AGAATTCGTAGATCATCCTCAGAAAAGCCTTGCCCTGGTGTTCTACCAGAAAAACGTCTC NM_013276RefSeq chr17
- 3608261 3636322 SHPK 23729 sedoheptulokinase
GO:0050277|GO:0016310|GO:0005737|GO:0071222|GO:0005975|GO:0043030|GO:0050727|GO:0071353|GO:0005
524|GO:0035963|GO:0009052 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127607_PI430048170 0.8797382287173251.00935870083647 12.2741000130404
12.3819479538558 12.4532112065109 P P P 12.3566576945771 12.1827330531416
12.5159621898074 P P P LNCV6_127607_PI430048170 mRNA
CGTCTGTGAGCCCCGTGCTGTATTTTGTAATAAAGTCTTTTGCAGATTGCTTCCCGAAAA NM_001015885 RefSeq
chr20 + 57351561 57378463 RAE1 8480 "ribonucleic acid export 1, transcript variant 2"
GO:0008017|GO:0007077|GO:0010467|GO:0003723|GO:0019221|GO:0019058|GO:0005634|GO:0005635|GO:0044
281|GO:0008645|GO:0005640|GO:0005737|GO:0006406|GO:0015758|GO:0005643|GO:0016032|GO:0005856|GO:0
005975|GO:0019083|GO:0005730|GO:0055085|GO:0010827|GO:0071407|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142238_PI430048170 0.6415127687393510.9706136937544289.61854123516875

9.72053596048987 9.47107444051229 P P P 9.74311604175887 9.63180957427818
9.56978454752253 P P P LNCV6_142238_PI430048170 mRNA
GGGAAGTGGGTTCTCAGGACTGGCATTCTTGGAATAAATTCACTCTGTCCTTGCAAAAAA NM_145059RefSeq chr16
+ 70454594 70480274 FUK197258 fucokinase GO:0016310|GO:0005737|GO:0050201|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141472_PI430048170 0.00762387897943535 3.7013732266423 5.17203700301352
4.72062714736928 4.59707294696407 P P P 2.91330129355167 2.99870772844679
2.97751287322442 P P P LNCV6_141472_PI430048170 mRNA
AGAGGGTGCCCATTGGACCTTTGGCACTGGATGAGCCAATAAACCAAACTCTGGCACCTC NM_001271803 RefSeq
chr5 + 138439000 138446969 REEP2 51308 "receptor accessory protein 2, transcript variant 1"
GO:0005881|GO:0032386|GO:0050913|GO:0005887|GO:0005783|GO:0071786|GO:0031883|GO:0005789|GO:0050
916|GO:0032596|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_31215_PI430048170 0.2937195344742160.79438040143933 7.00308341253546 7.01282252691011
7.06485142302987 P P P 6.90044031487673 7.53247645331709 7.55445161006326 P P P
LNCV6_31215_PI430048170 mRNA
TGTTGAGCCTCTAAGATGGTCTTTTCCTCTGATGTGATAATAAAGTGTTTATTCTGAACT NM_001012716 RefSeq
chr18 - 649619 658340 TYMSOS 494514 TYMS opposite strand NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131722_PI430048170 0.12402853128849 1.22172790248659 10.7054801908449 10.460719018251
10.3574480872465 P P P 10.0143630580807 10.3777867701536 10.2636235308095 P P P
LNCV6_131722_PI430048170 mRNA
AGTGAAGACATGGCCCCTGAAGGGCAATAAAGCTGCTAGTTTATTAATACAGTCAAAAAA NM_022830RefSeq chr11
- 62575044 62591637 TUT1 64852 "terminal uridylyl transferase 1, U6 snRNA-specific"
GO:0005515|GO:0006379|GO:0006378|GO:0003723|GO:0005730|GO:0005524|GO:0050265|GO:0046872|GO:0045
171|GO:0004652|GO:0016607|GO:0071044|GO:0005847|GO:0005654|GO:0003730|GO:0019899|GO:0016180 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142845_PI430048170 0.3635004714195891.08578358204928 6.21909473779554
6.20151686614194 6.09183736309841 P P P 6.20110690029256 5.84153411502508
6.09365063049723 P P P LNCV6_142845_PI430048170 mRNA
CCAACCCTTCTCACACATCAACTCATAAATCATCTTAAATAAAAGTCATTGGTATGACTC NM_001085451 RefSeq
chr3 + 100401192 100456326 LNP1 NA leukemia NUP98 fusion partner 1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_141019_PI430048170 0.2567953015219731.26638057189995 1.275567523011
0.7808631311308540.61256843465398 A A A 0.5715210050541050.589258375423553
0.570702307868187A A A LNCV6_141019_PI430048170 mRNA
GATGACTAATATCGTCCCATTTTGGAAATAAAGCAACAGACTTCTCAACAATCAATGAGT NM_001081450 RefSeq
chr19_KI270938v1_alt - 191260 217825 LILRB3 11025 "leukocyte immunoglobulin-like receptor,
subfamily B (with TM and ITIM domains), member 3, transcript variant 1"
GO:0005515|GO:0005887|GO:0045671|GO:0006952|GO:0004872|GO:0007166|GO:0004888|GO:0002376 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106539_PI430048170 0.0170030521605351 1.68291265162954 9.20814516784211
9.23946304399839 9.29207145960387 P P P 8.68943027160557 8.30675779845344
8.46609964768378 P P P LNCV6_106539_PI430048170 mRNA
TCATTAACCAGGGACTTTTGAACTCCTCTTTTTCTGGAACACTTCCCTGAGTCACGCTCA NM_001042432 RefSeq
chr16 - 28477278 28492302 CLN3 1201 "ceroid-lipofuscinosis, neuronal 3, transcript variant 1"
GO:0005802|GO:0005515|GO:0016242|GO:0005765|GO:0005764|GO:0030163|GO:0043524|GO:0007034|GO:0016
485|GO:0047496|GO:0050885|GO:0008306|GO:0006684|GO:0005794|GO:0005795|GO:0043086|GO:0006898|GO:0
006681|GO:0035235|GO:0035752|GO:0045121|GO:0051082|GO:0001508|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_141027_PI430048170 0.5495434477783471.0392777965448 12.3301710222188
12.5190612223211 12.348293565409 P P P 12.2283137590681 12.430754606097
12.3718948678987 P P P LNCV6_141027_PI430048170 mRNA
GAGGGTGTTTCCTCCCAGAGTTACTTTAATAAAGGTTGTTCATAGAGTTGACTTGTTCAT NM_006072RefSeq chr7
- 75769523 75789746 CCL26 10344 chemokine (C-C motif) ligand 26
GO:0008009|GO:0007165|GO:0006955|GO:0030335|GO:0006954|GO:0030838|GO:0006935|GO:0001938|GO:0060
326|GO:0007267|GO:0032855|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129604_PI430048170 0.2890411881383240.6276717096794832.20179641656125
0.3116348817979570.413859238097886A A A 1.26705112294059 1.97679576846733
2.34666614699052 A A P LNCV6_129604_PI430048170 mRNA
GCTGTGGTCTCAGCAATGCACCTGTTTTGTACATGATTGTGTAATTTAAAGGTATATAAA NM_020804RefSeq chr6
+ 34466060 34535223 PACSIN1 29993 "protein kinase C and casein kinase substrate in neurons 1,
transcript variant 1"
GO:0008092|GO:0005515|GO:0043005|GO:0048471|GO:0030054|GO:0030137|GO:0005886|GO:0097320|GO:0045
202|GO:0005829|GO:0005737|GO:0005543|GO:0030100|GO:0007010|GO:0045806|GO:0007015|GO:0043679|GO:0
030659|GO:1900006|GO:0031988|GO:0032587|GO:0048488|GO:0072657|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130034_PI430048170 0.00117988589281108 0.4588855845008 6.15842869415563
5.94693250680859 6.2818501454041 P P P 7.17401052063439 7.20274257219047
7.39167665520465 P P P LNCV6_130034_PI430048170 mRNA
CGTAAAGAACTCTGTTATATCCTAGAGGACTCTGTCTTTTATATTCGGGATAATAAAGAC NM_013262RefSeq chr6
+ 16129085 16148247 MYLIP 29116 myosin regulatory light chain interacting protein
GO:0042632|GO:0005515|GO:0008092|GO:0045732|GO:0004842|GO:0016567|GO:0005886|GO:0016874|GO:0006
928|GO:0007399|GO:0031648|GO:0005622|GO:0005737|GO:0042787|GO:0032803|GO:0008270|GO:0010989|GO:0
005856|GO:0019898. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136141_PI430048170 0.26372694347471 1.0202741767087 0.315708889130979
0.2508358474872270.287311467916456A A A 0.2587573743040710.24895390165653
0.259981270067988A A A LNCV6_136141_PI430048170 mRNA
ATGTTAGCCAAAGCATTAGACAGGTGTTTAAGTCGTACTTCTCAATAGTAGTTAAAACTG NM_001145720 RefSeq
chr1 + 32465056 32487858 ZBTB8B NA zinc finger and BTB domain containing 8B NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141991_PI430048170 0.5720713326470760.5741225557725870.246537361524169
0.2881383067361721.23558268100824 A A A 0.4511951074465712.50893224014863
0.305163086050349A P A LNCV6_141991_PI430048170 mRNA
TTGGTGGAAAAGTGCTGCTCACATTGTGGACTGAAATGTATGGACCCCAGACGTTGAATA NM_181510RefSeq chr20
- 45551151 45579326 WFDC8 90199 "WAP four-disulfide core domain 8, transcript variant b"
GO:0010951|GO:0004867|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137280_PI430048170 0.3911344874860691.17445109485008 0.342293356581887
0.9403901707724030.403651662667386A A A 0.3685567941716410.325287583402072
0.373882586743287A A A LNCV6_137280_PI430048170 mRNA
TCTTTCTTTGTGTTTAGTTTTCCTGAGGACTGACCTCTGGGGTAATGAGGCTGGAGTAGA NM_001109809 RefSeq
chr6_GL000255v2_alt - 937892 942657 ZFP57 346171 ZFP57 zinc finger protein
GO:0005720|GO:0007422|GO:0006349|GO:0000122|GO:0003677|GO:0046872|GO:0043045|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142881_PI430048170 0.5091807688680510.6717037702737430.286817220396903
0.8496363723594520.332260846089332A A A 0.4470270495749440.346863920580155
1.90237861996439 A A A LNCV6_142881_PI430048170 mRNA
TATTGCCATGGTGGCGGGGTATGCCGTCACCTCAGTAGTTTTACTGTAAAAGGGAAATTT NM_001406RefSeq chr17
+ 7705201 7711375 EFNB3 1949 ephrin-B3

GO:0005005|GO:0048013|GO:0046875|GO:0005886|GO:0007411|GO:0005887|GO:0016198|GO:0007628|GO:0007267|GO:0016032|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136581_PI430048170 0.2585999126105030.8883033860808377.72936140898171 7.68466143670187 7.48361977772519 P P P 7.95105648879123 7.84090881430654 7.60919142247283 P P P LNCV6_136581_PI430048170 mRNA GGGAAGGGGAAGGAAGAAAACTCTGAAAACAAAATCTTGTTCTATGCAAAAGCCTTGAAA NM_001286072 RefSeq chr1 + 112674311 112700746 MOV10 4343 "Mov10 RISC complex RNA helicase, transcript variant 3"
GO:0005515|GO:0048011|GO:0006355|GO:0048015|GO:0004386|GO:0005524|GO:0005615|GO:0035279|GO:0006351|GO:0005829|GO:0007173|GO:0007219|GO:0000932|GO:0008543|GO:0045087|GO:0038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141055_PI430048170 0.0294886328343022.43500802510369 4.9313421966373 5.0721768470302 4.80977275818679 P P P 3.73738553763493 3.99262055903217 3.10590398410484 P P P LNCV6_141055_PI430048170 mRNA TGTTGGCCTGCTGTGTTTATTGTAGAGACACTGTTTTAGTAAACATGCTGAGCATTCAAA NM_001127582 RefSeq chr12 - 6650537 6663142 ING4 51147 "inhibitor of growth family, member 4, transcript variant 9"
GO:0005515|GO:0043065|GO:0008285|GO:0003713|GO:0006325|GO:0006915|GO:0005634|GO:0035064|GO:0043981|GO:0006260|GO:0043983|GO:0043982|GO:0043966|GO:0043984|GO:0000123|GO:0005654|GO:0007050|GO:0008270|GO:0006978|GO:0045892|GO:0045926|GO:0006473 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143941_PI430048170 0.3846439991170721.53081487918287 0.386109565531233 0.3955182096776971.68507830956013 A A A 0.3266784469390130.32803485280719 0.383095986217983 A A A LNCV6_143941_PI430048170 mRNA AAGGACTCCATGGGAGCAGACAAAGAGGATCTTTCAGACAAACTCATCCCCCTTTTCTAT NM_019897 RefSeq chr9 - 35957107 35958154 OR2S2 56656 "olfactory receptor, family 2, subfamily S, member 2 (gene/pseudogene)"
GO:0050911|GO:0007608|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62177_PI430048170 0.00629981063556718 1.21472917483589 9.25583194218819 9.28626014377623 9.31778635452023 P P P 9.07414329177103 8.95397111410002 8.98784959423533 P P P LNCV6_62177_PI430048170 mRNA GAACTCTTGGCTTGCACTTCTACAGCTCTGTACATTTATAAGAATAAATGCAATCACACT NM_020447 RefSeq chr15 - 74899986 74907121 FAM219B 57184 "family with sequence similarity 219, member B" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128584_PI430048170 0.0330813184325972 0.4882802833848644.62510690061801 4.1950716853883 5.05249284394991 P P P 5.54037435119246 5.61548118529785 5.91768141264454 P P P LNCV6_128584_PI430048170 mRNA GGACTTGATGCAGTGATGACAAATCATTGCTTAGAATTAATGTTTTCAAATGTGCAACTC NM_145055 RefSeq chr18 + 46174021 46266992 C18orf25 147339 "chromosome 18 open reading frame 25, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142810_PI430048170 0.3224758617717341.27546421787444 5.04648633094509 5.66431325494569 5.81042827921198 P P P 4.8586683501696 5.1506331904125 5.49618445126616 P P P LNCV6_142810_PI430048170 mRNA TAGGCAAACTACACCCTGTTCATTGTTACCTGGAAAATAAATCCTCTATGTTTTGCACAA NM_021995 RefSeq chr1 - 7847611 7853491 UTS2 10911 "urotensin 2, transcript variant 1"
GO:0046005|GO:0045597|GO:0007268|GO:0048146|GO:0045776|GO:0045777|GO:0007204|GO:0005615|GO:0010763|GO:0006936|GO:0045909|GO:0046676|GO:0010459|GO:0001666|GO:0042493|GO:0005102|GO:0005576|GO:0010841|GO:0033574|GO:0003105|GO:0045766|GO:0032224|GO:0005179|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139087_PI430048170 0.1704651304067380.7231543319339699.10245456446086
9.09617012125668 9.29898938390635 P P P 9.26401684462951 9.54557485783771
10.0026015718826 P P P LNCV6_139087_PI430048170 mRNA
CAGCTCCTTCAGGTGTTTGATTCCAGCATGTAGTATACATTGTATGTGTTAAAAAGAAAT NM_001515RefSeq
chr5_KI270897v1_alt - 583509 616049 GTF2H2NA "general transcription factor IIH, polypeptide 2, 44kDa"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129048_PI430048170 0.0531913306724397 0.7322496098831164.9386473614247
4.73891426021444 4.53827927472619 P P P 4.96107472825492 5.2432065508746
5.35952989675712 P P P LNCV6_129048_PI430048170 mRNA
GTAATAAACTCTGCAAGAAGTTTAACCCACATAGGTTTGCGGCACTGCAAAATTGTTCAT NM_153498RefSeq chr10
+ 12349542 12835545 CAMK1D 57118 "calcium/calmodulin-dependent protein kinase ID, transcript
variant 2"
GO:0005516|GO:0043066|GO:0043065|GO:0071622|GO:0005634|GO:0060267|GO:0005524|GO:0032793|GO:0005
737|GO:0050766|GO:0006954|GO:0010976|GO:0090023|GO:0050773|GO:0006468|GO:0004683 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144998_PI430048170 0.00912554617492742 0.3949302375566957.03238722997652
6.53636431049314 7.09695229034764 P P P 7.86439995313959 8.19736513314013
8.59457641590729 P P P LNCV6_144998_PI430048170 mRNA
TACGGAAGTGTTCCAATATAATTTTTTCCTGTACTGGATGGCTAGGATTCTAGAGAATTG NM_002874RefSeq chr9
+ 107283235 107332194 RAD23B5887 "RAD23 homolog B (S. cerevisiae), transcript variant 1"
GO:0005515|GO:0000502|GO:0071942|GO:0032434|GO:0005634|GO:0007283|GO:0003684|GO:0005737|GO:0006
281|GO:0003697|GO:0000715|GO:0043161|GO:0005654|GO:0006289|GO:0000718|GO:0031593 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130493_PI430048170 0.8266627573610151.01357818036485 12.0352586996539
12.0361566665122 12.0829999006188 P P P 11.8059360172007 12.1433206023026
12.1231360711104 P P P LNCV6_130493_PI430048170 mRNA
CTGTCTATATCGACTTGTCCATGTACGTCTATTAAAACCATAGTCCGAGCGTGCTAAGCA NM_002653RefSeq chr5
- 135027733 135034274 PITX1 5307 paired-like homeodomain 1
GO:0005667|GO:0001190|GO:0051216|GO:0021983|GO:0005730|GO:0005634|GO:0000978|GO:0009653|GO:0006
351|GO:0001077|GO:0001501|GO:0005737|GO:0045944|GO:0035116|GO:0014707|GO:0048625 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_110275_PI430048170 0.5804790092177590.9732950160662270.312572185265383
0.4344841177209040.305044097988684A A A 0.4808527670034250.372012833560557
0.31513950276394 A A A LNCV6_110275_PI430048170 mRNA
GCAAATCTCTTTGGAAAGAGCACAATTGACCCTTCATCTGTAATGGTCCTGGTGAATGCC NM_080475RefSeq chr18
+ 63702303 63723893 SERPINB11 89778 "serpin peptidase inhibitor, clade B (ovalbumin), member 11
(gene/pseudogene), transcript variant 1" GO:0010951|GO:0005737|GO:0004867|GO:0005615 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140462_PI430048170 0.00781823744166455 0.3456098603237911.54609970437081
1.85267267008226 1.04812304918312 A A A 3.29875390560564 3.0512473470033
2.75553005297599 P P P LNCV6_140462_PI430048170 mRNA
CTAACGCAAAACCACTAACTGAAGTTCAGATAATGGATGGTTTGTGACTATAGTGTAAAT NM_000399RefSeq chr10
- 62811995 62816366 EGR2 1959 "early growth response 2, transcript variant 1"
GO:0005515|GO:0003700|GO:0044212|GO:0006366|GO:0016874|GO:0005634|GO:0035914|GO:0046872|GO:0014
037|GO:0005737|GO:0071371|GO:0021660|GO:0030278|GO:0048168|GO:0045944|GO:0035284|GO:0006611|GO:0
007611|GO:0045444|GO:0031625|GO:0001102|GO:0032868|GO:0043066|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136919_PI430048170 0.0414319764087112 0.6614672134385427.04332791629715
6.58743747894002 7.08301049716101 P P P 7.38955605689916 7.45567545280297

7.69026995026966 P P P LNCV6_136919_PI430048170 mRNA
GCTAAAGGGGAAATGGACTTTAAATTTTAAAGAGCTCATTTGCAATGCACTTGTATACAC NM_021229RefSeq chr12
- 95657806 95790758 NTN4 59277 netrin 4
GO:0016322|GO:0060668|GO:0005886|GO:0030198|GO:0007411|GO:0043237|GO:0005604 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137537_PI430048170 0.6529709709167631.0492914285767 4.36235614724877 4.581119617968
4.31946174456685 P P P 4.11041837076518 4.57429904243812 4.34666595790146 P P P
LNCV6_137537_PI430048170 mRNA
ACTGCCTTTATTGTCCTTTTTGATACGAAGATGTGCTTTTTCTAGATGGAAAAGATGTGT NM_005618RefSeq
chr6_KI270798v1_alt - 9443 17847 DLL1 28514 delta-like 1 (Drosophila)
GO:0005515|GO:0007368|GO:0007386|GO:0007220|GO:0005886|GO:0072014|GO:0001757|GO:0032693|GO:0007
267|GO:0005112|GO:0070986|GO:0030155|GO:0030154|GO:0001947|GO:0007219|GO:0045638|GO:0045944|GO:0
097150|GO:0030097|GO:0045747|GO:0048839|GO:0001709|GO:0005509|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141783_PI430048170 0.00456688066211899 2.64185306023968 6.46929750991618
7.03217432820669 6.54370435388133 P P P 5.30901140294587 5.55903618287474
4.98217691886359 P P P LNCV6_141783_PI430048170 mRNA
CCCAGGACTTGCGGTCTGAGCCTTTTTGGATAATTAATAAATATTTTACACAGCAAAAAA NM_001278720 RefSeq
chr16 + 675665 678268 RHBDL19028 "rhomboid, veinlet-like 1 (Drosophila), transcript variant 1"
GO:0007165|GO:0016020|GO:0004252|GO:0005887|GO:0006508 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134677_PI430048170 0.0186614563476433 1.07233651722726 0.382496645928802
0.3823612527567 0.326126436003358A A A 0.2453408989566190.299803337464269
0.24358504315781 A A A LNCV6_134677_PI430048170 mRNA
GTCATTTATTCAAGAAGTGTGTTGTGCAACTGGATAATATAAAGAATTGCTCCTGGTAAC NM_033328RefSeq chr12
+ 18738110 18739188 CAPZA3 93661 "capping protein (actin filament) muscle Z-line, alpha 3"
GO:0051016|GO:0016020|GO:0001669|GO:0007286|GO:0030863|GO:0008290|GO:0005634|GO:0003779 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126599_PI430048170 0.9123948734862681.01090598444248 15.3330418780697
15.5105331661868 15.6301242801478 P P P 15.5215859227363 15.4282967000549
15.4906825713001 P P P LNCV6_126599_PI430048170 mRNA
TGGAAGATGGACGTACTTTGTCTGACTACAATATTCAAAAGGAGTCTACTCTTCATCTTG NM_002954RefSeq chr2
+ 55232404 55235853 RPS27A 6233 "ribosomal protein S27a, transcript variant 1"
GO:0002474|GO:0010467|GO:0006367|GO:0007220|GO:0019221|GO:0007249|GO:0019058|GO:0006412|GO:0006
413|GO:0006414|GO:0002756|GO:0034220|GO:0007173|GO:0007219|GO:0002755|GO:0007179|GO:0006977|GO:0
000209|GO:0005975|GO:0034134|GO:0005978|GO:0000122|GO:0019068|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139528_PI430048170 0.6683970689685 0.9868804930531430.436237544163234
0.45654474109236 0.365923917148246A A A 0.4986981613158830.400799485428084
0.415989904578746A A A LNCV6_139528_PI430048170 mRNA
ATATTGCCCTAGGAATTGCCTTCATCGGCTACTTTGTAGAAAAGCCTCCAAATGCTGCAG NM_052891RefSeq chr1
- 153297861 153310718 PGLYRP3 114771 peptidoglycan recognition protein 3
GO:0016019|GO:0050830|GO:0044117|GO:0042834|GO:0008745|GO:0005576|GO:0032827|GO:0005622|GO:0009
253|GO:0002221|GO:0016020|GO:0045087|GO:0008270|GO:0016045|GO:0032689 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127395_PI430048170 0.1268831224067350.8088243770453218.19011504493619
8.19839191655474 8.59491810822262 P P P 8.60078779941121 8.55055640119622
8.77848238556897 P P P LNCV6_127395_PI430048170 mRNA
GATTTTTTGAGCTGTGCCATTTATGGTACTCTTTGCCTATGCATCCCCTTGTTAGATTTT NM_022130RefSeq chr5 -

32124717 32174319 GOLPH3 64083 golgi phosphoprotein 3 (coat-protein)
GO:0005802|GO:0005515|GO:0010467|GO:0009306|GO:0032008|GO:0005886|GO:0008283|GO:0043001|GO:0030032|GO:0070273|GO:0050714|GO:0050901|GO:0005829|GO:0005739|GO:0060352|GO:0005758|GO:0009101|GO:0032580|GO:0045053|GO:0007030|GO:0005794|GO:0010821|GO:0031985|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141951_PI430048170 0.0183220413498468 3.76275819423637 2.53929151226478 1.69640066401421 2.49255713068358 A A A 0.281348677480613 0.417607894062804 0.433816398521359 A A A LNCV6_141951_PI430048170 mRNA
TGTAACCTGCTGGCAGAAAAGCAATATGGCTTTTGTAAGGCAACACTCAGTGAGAAGCTT NM_001622 RefSeq chr3 + 186613060 186621318 AHSG 197 alpha-2-HS-glycoprotein
GO:0006907|GO:0030500|GO:0004869|GO:0019210|GO:0046627|GO:0050727|GO:0072562|GO:0005576|GO:0006953|GO:0030502|GO:0005615|GO:0010951|GO:0042326|GO:0050766|GO:0001501|GO:0001503|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133883_PI430048170 0.00124528063473271 0.632502278158487 11.3790343501574 11.2113288275066 11.4001421609437 P P P 11.8942298438055 12.0005369775666 12.0796495554357 P P P LNCV6_133883_PI430048170 mRNA
ATGGTTTTTGCTTCAGCGGCTTTAGGACAAATTAAAAGTCAACTCTGGTGCCAGAAAAAA NM_005381 RefSeq chr2 - 231454747 231464494 NCL 4691 nucleolin
GO:0005515|GO:0003723|GO:0042162|GO:0005730|GO:0005634|GO:0001525|GO:0008022|GO:0042802|GO:0000166|GO:0016020|GO:0030529|GO:0005654|GO:0005938|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134616_PI430048170 0.0941041406602076 1.16556304777114 9.06347022531619 9.14708634936594 9.26314499882207 P P P 8.81223609266857 8.90562196916327 9.08619179050037 P P P LNCV6_134616_PI430048170 mRNA
GATTTTTTGCGGGGCAGGGATGGGAATGTTTGTTCATAAATAATTAGACATTTTCTATAG NM_021243 RefSeq chr6 + 139028681 139043302 ABRACL58527 ABRA C-terminal like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140705_PI430048170 0.301186306839131 0.820347270210354 9.22632460079816 10.0243765459222 9.69645478590419 P P P 9.82789530065627 10.0645688271181 10.0103107411759 P P P LNCV6_140705_PI430048170 mRNA
ACCTCAGCTTTTTCCCTCACTTGCATCAATAAAGCTTCTGTGTTTGGAACAGCTAAAAAA NM_000607 RefSeq chr9 + 114323022 114326479 ORM1 5004 orosomucoid 1
GO:0005515|GO:0006954|GO:0006810|GO:0002682|GO:0072562|GO:0005576|GO:0006953|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130612_PI430048170 0.683787208594181 0.806316158962256 1.48230250216819 0.504759613172079 0.352175737050104 A A A 1.9086252747454 0.387284227282433 0.803600821022228 A A A LNCV6_130612_PI430048170 mRNA
CTGTAGTTCCTAATGGGCATGTTGTAAAGATGTTAAGACGTTTTCTATGCATTATAGGTA NM_024611 RefSeq chr15 - 60419608 60479160 ICE2 79664 "interactor of little elongation complex ELL subunit 2, transcript variant 1"
GO:0042796|GO:0005515|GO:0015030|GO:0035363|GO:0045945|GO:0042795|GO:0035327|GO:0008023 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107278_PI430048170 0.0853508185428319 2.73486966878699 2.51159428854396 1.0673816106665 1.76211072119397 A A A 0.475242636658964 0.427291319844465 0.440174226008074 A A A LNCV6_107278_PI430048170 mRNA
TCAGCCATGTCGACTGGTTTTCTGTCCACAAGGAGAAGCGGACGCTCATCTTCCGTGTGC NM_006500 RefSeq chr11 - 119308523 119317130 MCAM 4162 melanoma cell adhesion molecule
GO:0061042|GO:0030335|GO:0005886|GO:0003094|GO:0005634|GO:0016021|GO:0001525|GO:0007155|GO:0009653|GO:0005925|GO:0005615|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_134444_PI430048170 0.1295260762730480.7937456881069695.93302365508149
6.03603147948084 5.99658873025407 P P P 6.21900345637903 6.57064710171787
6.14033878756635 P P P LNCV6_134444_PI430048170 mRNA
GTAGACAGCACTCGATAATCTAAGGGACATTATCTTGTTGTGAAAAATTATCTCCCTCCT NM_198147RefSeq chr17
- 29560670 29567024 ABHD15 116236 abhydrolase domain containing 15
GO:0016787|GO:0016020|GO:0008152|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137927_PI430048170 0.6338400489236290.8335224726171530.701037683777011
1.13458271836866 0.404616879326495A A A 1.63445689130947 0.650733928323774
0.582921728418569A A A LNCV6_137927_PI430048170 mRNA
TGAAGTCCATGCTGTCTGTTAAATAAAATGCCATTCTGCAGAATTAACCATCCCACCAGA NM_001258415 RefSeq
chr11 - 110577034 110712050 ARHGAP20 57569 "Rho GTPase activating protein 20, transcript variant 2"
GO:0043547|GO:0051056|GO:0007264|GO:0005829|GO:0005096 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139928_PI430048170 0.0104315111585806 0.0810527118820793 1.81513872893526
3.12691588056895 2.20314977603433 A P A 6.07397885820021 6.10857191857344
6.16261324669488 P P P LNCV6_139928_PI430048170 mRNA
GCTGCGTTTCACACTTCTTTAGAGCTAGCTGACCTTTGGCCAAAAATAAACTTTGAAAAG NM_004132RefSeq chr10
+ 113553018 113589601 HABP2 3026 "hyaluronan binding protein 2, transcript variant 1"
GO:0004252|GO:0006508|GO:0005576|GO:0005539|GO:0007155|GO:0005615 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130888_PI430048170 0.00338195664646437 0.5507897367056338.12438767734389
8.06885573904741 8.32317631250798 P P P 8.9871748417613 8.8766848930948
9.22426807371835 P P P LNCV6_130888_PI430048170 mRNA
AACCCTTTGCTTCTTATAATGAGTGCGATATATGTTGTCGAGGCTGTTCTTCAAGAATTA NM_005654RefSeq chr5
+ 93583336 93594609 NR2F1 7025 "nuclear receptor subfamily 2, group F, member 1"
GO:0005515|GO:0010467|GO:0003700|GO:0006367|GO:0003713|GO:0003707|GO:0044323|GO:0005634|GO:0000
122|GO:0043565|GO:0007165|GO:0021796|GO:0045944|GO:0043401|GO:0010977|GO:0005654|GO:0008270|GO:0
004879|GO:0001764|GO:0030522 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144001_PI430048170 0.0411324537829288 0.3842115755909152.87080382392018
1.61810792991058 2.22329197034175 A A A 3.43683575706569 3.67436742929653
3.96212050014444 P P P LNCV6_144001_PI430048170 mRNA
GCTCTTGGGATATTTTTAAGCATAATAAGCTCATTGGATTCAGGTATTTTTCCCTTTGCANM_001277313 RefSeq
chr15_KI270905v1_alt - 4980140 5140748 FMN1 342184 "formin 1, transcript variant 1"
GO:0005737|GO:0005912|GO:0005886|GO:0005884|GO:0005634|GO:0003779|GO:0045010 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138016_PI430048170 0.6687107097136230.9686763225671460.332769620959341
0.3363889721367840.481183362852531A A A 0.3373071380485450.583104556359717
0.359673528070613A A A LNCV6_138016_PI430048170 mRNA
TATAAACTGAAGCAGATACCTGGAACCACCTAAAGAACTTCCATTTATGGAGGATTTTTT NM_000043RefSeq chr10
+ 88990530 89015785 FAS 355 "Fas cell surface death receptor, transcript variant 1"
GO:0005515|GO:0019724|GO:0031265|GO:0031264|GO:0097284|GO:0097049|GO:0048536|GO:0042802|GO:0045
619|GO:0051260|GO:0070062|GO:0032464|GO:0071285|GO:0009986|GO:0009636|GO:0051384|GO:0007623|GO:0
045121|GO:0009897|GO:0002377|GO:0004888|GO:0008625|GO:2001239|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143266_PI430048170 0.3206046672190331.02031760821357 0.322697557840277
0.2467762796801620.287516936610042A A A 0.2589455094248840.25200444284284
0.259972796333452A A A LNCV6_143266_PI430048170 mRNA
AACTGCAGAAGAAACAGTTGTGCTCTTTCGAGATCTACGAAGTTCCCTGGGAGAACAGAA NM_001898RefSeq chr20
- 23747552 23750937 CST1 1469 cystatin SN GO:0010951|GO:0004869|GO:0005615|GO:0001580 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126704_PI430048170 0.00947721340767081 1.35614212752935 7.75031585093126
7.96871862561886 7.76395632226742 P P P 7.39905670499226 7.48377534362435
7.28532191276863 P P P LNCV6_126704_PI430048170 mRNA
TTTTACGTTGAGTCCATTTTTAATGTTCTGATCACCTGACAGGGCACCCCAAACCCCCAA NM_001242898 RefSeq
chr22 + 50343316 50445089 PPP6R2 9701 "protein phosphatase 6, regulatory subunit 2, transcript
variant 1" GO:0005515|GO:0005737|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138144_PI430048170 0.2200530273876280.5610948638921780.39976828697231
2.42715537189066 0.542114392293085A A A 2.04684223272821 2.56380729880924
2.16579544698964 A A A LNCV6_138144_PI430048170 mRNA
GACTGGATTACTTCTTACTTAGTTACTAACTCAATGAGGAAAAATCCCTACAGGATCTTT NM_016227RefSeq chr1
+ 172532348 172611833 SUCO 51430 "SUN domain containing ossification factor, transcript variant 2"
GO:0045669|GO:0005791|GO:0046850|GO:0032967|GO:0016020|GO:0001503|GO:0030867|GO:0007275|GO:0016
021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67337_PI430048170 0.8904115760606 0.97902891995005 2.78299625257439 3.88113713336374
3.22586842310253 A P P 2.86926443216418 3.48680516601237 3.71359556311489 P P P
LNCV6_67337_PI430048170 mRNA
ACTCATTACGTGATCCCAGACTGGAAAGTTGTTCAAGATTATCTTGAGATCCTTGAGTTT NM_001143688 RefSeq
chr15 + 66293581 66333898 DIS3L 115752 "DIS3 like exosome 3'-5' exoribonuclease, transcript variant
1"
GO:0005515|GO:0016075|GO:0005813|GO:0005737|GO:0005886|GO:0000175|GO:0003723|GO:0000177|GO:0019
899 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138306_PI430048170 0.0337362189275117 0.7057783703507167.63986052791394
7.47841801871214 7.22118607524787 P P P 7.90825510031144 8.08309801541674
7.87816957373177 P P P LNCV6_138306_PI430048170 mRNA
TGAACCCTGATCTAGACTTATATGAATAAATGAAATTACATGCCAAGGGCCCTAAAAAGC NM_006767RefSeq chr22
+ 20982268 20999037 LZTR1 8216 leucine-zipper-like transcription regulator 1
GO:0006355|GO:0003700|GO:0009653 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131239_PI430048170 0.3516515924223990.4779909145992820.540502136094516
0.5097189789115230.271929575128279A A A 0.5645142608497070.57594333141148
2.47976203018831 A A A LNCV6_131239_PI430048170 mRNA
CACCATGATATTGGTGGTATTTATGCTGTTAAGTCCAAACCTTTATCTGTCTGTTATTCT NM_002126RefSeq chr17 +
55264959 55325065 HLF 3131 hepatic leukemia factor
GO:0043565|GO:0006355|GO:0003700|GO:0003690|GO:0006366|GO:0007275|GO:0005634|GO:0048511|GO:0035
914|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135090_PI430048170 0.4314025166710650.9216343862810487.30566856034921
6.98180813906931 6.86437308435455 P P P 7.21899341765293 7.19827837496879
7.12292926025077 P P P LNCV6_135090_PI430048170 mRNA
TGAATGTATAAGTACCGCAATCCCCGGCCCCTCAAGTGGAATAAATCTAACATGTATTGG NM_001302927 RefSeq
chr11 - 57386786 57390657 PRG2 5553 "proteoglycan 2, bone marrow (natural killer cell activator,
eosinophil granule major basic protein), transcript variant 4"
GO:0030133|GO:0032753|GO:0006955|GO:0032693|GO:0030246|GO:0005576|GO:0002215|GO:0008201|GO:0042
742|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138547_PI430048170 0.0559346877616055 0.7252328067783478.78570349432781
8.61624624428419 8.50531661338627 P P P 9.31645494646846 9.10656368196595
8.85125785859002 P P P LNCV6_138547_PI430048170 mRNA
AATCAAAGAACCTCAAAATTTAAACTGATGTGGATGGGAATATGGGAATTAGGGTGGGGGNM_001039690 RefSeq
chr16 - 69118008 69132590 CHTF8 54921 "CTF8, chromosome transmission fidelity factor 8 homolog
(S. cerevisiae), transcript variant 1" GO:0006260|GO:0007049|GO:0005634|GO:0003677|GO:0070062 . NA -

. NA NA NA NA NA NA NA NA NA
LNCV6_140069_PI430048170 0.00936166062137095 1.21216034598866 11.9669677107719
11.8617857844894 11.8247441893016 P P P 11.6116806562769 11.6754574559194
11.5339420014251 P P P LNCV6_140069_PI430048170 mRNA
CCCATCTTAAGTAATTACTTTCTGGAGTAATCAGGTGGAAATCCATAGACAAATGAAACA NM_016332 RefSeq chr16
- 1938232 1943293 MSRB1 51734 methionine sulfoxide reductase B1
GO:0030091|GO:0003779|GO:0005634|GO:0005575|GO:0015629|GO:0005737|GO:0045087|GO:0033743|GO:0030
041|GO:0008270|GO:0070191|GO:0006979|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144751_PI430048170 0.1277208278217141.04448164116563 0.357834679467625
0.3894969696824940.301987877990137 A A A 0.2812331303577460.300189008093902
0.280807940156025 A A A LNCV6_144751_PI430048170 mRNA
CCAGAGTCGATTTTTCTCCTAAATTTTTGGCAACTATAAGATGTTCATAATGCCACTTTC NM_001258025 RefSeq
chr4 + 165031998 165041744 TRIM60 166655 "tripartite motif containing 60, transcript variant 1"
GO:0005622|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145285_PI430048170 0.2408766038931381.03414632527705 0.431589086957569
0.3604998769489260.395156050555866 A A A 0.3027063695177690.339198284752921
0.399244206749033 A A A LNCV6_145285_PI430048170 mRNA
TTCAACAGAACGGGGCAAGTTCGTATTTGAATTCTGTTATATTTATCTAAGGGAAGCAAA NM_020844 RefSeq chr8
+ 12945673 13029775 KIAA1456 57604 "KIAA1456, transcript variant 1"
GO:0008168|GO:0032259|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144559_PI430048170 0.8751719340223710.9905750579058710.560654311103297
0.6408308238150470.52178412988909 A A A 0.5403478876500180.511951386801746
0.706749785742812 A A A LNCV6_144559_PI430048170 mRNA
CCTGATTTGTCAGCAGCATTCCACCTTTATTTTGGATTTGTTTTATTCAGAAGTCTGTAT NM_021061 RefSeq chr8 -
144876950 144901461 ZNF250 58500 "zinc finger protein 250, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141758_PI430048170 0.0238205914076285 1.49991402765643 12.9201007215573
12.9444427352714 13.029051159047 P P P 12.156272462363 12.4807926409209
12.4804986964338 P P P LNCV6_141758_PI430048170 mRNA
CAGTCAGTCTCTGGGGATGAAACTCTTAAATGCTTTGTATATTTTCTCAATTAGATCTCT NM_001287241 RefSeq
chr2 + 230864597 230879254 ITM2C 81618 "integral membrane protein 2C, transcript variant 5"
GO:0005515|GO:0048471|GO:2001238|GO:0005794|GO:0005886|GO:0005765|GO:0005524|GO:0005764|GO:0001
540|GO:0030182|GO:0010977|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128726_PI430048170 0.6430576953937291.01583774807556 0.531268327993834
0.5835425108079780.452277377721241 A A A 0.5381606794021490.481633998530372
0.481558486182904 A A A LNCV6_128726_PI430048170 mRNA
AGAGCCAAAAAACAGTAAAAAACAGATCATGCGTGTACGGCAGCAGTGCTGAAGCTGAGA NM_001166137
RefSeq chr9 - 88129304 88134985 SPATA31C2 645961 "SPATA31 subfamily C, member 2"
GO:0016021|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133232_PI430048170 0.9281567485079880.9789897780545625.18641927434294
5.17004201529458 5.65941665328927 P P P 4.54724210493161 5.59650311374678
5.75038595714311 P P P LNCV6_133232_PI430048170 mRNA
GCAGTCTTCTGTATTCCTGCATATTGTATATACCTGTATATGTTTTCCTGAGCAGTTAAA NM_002430 RefSeq chr22 -
27748276 27801498 MN1 4330 meningioma (disrupted in balanced translocation) 1
GO:0008150|GO:0003674|GO:0001957|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131912_PI430048170 0.0136609797473801 0.9436353707847830.385525649115181
0.3468599407957740.336747004120521 A A A 0.4604296183375080.44370512619533
0.416209213055278 A A A LNCV6_131912_PI430048170 mRNA

GCCGTAGAGAAATCCAATATCAGAATGTCTGAACATAGTAGAGAATGTCACTTTATGTAA NM_173806 RefSeq chr16 - 21983864 22001110 PDZD9 255762 "PDZ domain containing 9, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126809_PI430048170 0.4232414140024 1.0078006273005 0.411094279203654 0.416982023171522 0.393170787808835 A A A 0.405129751298975 0.375465432793015 0.406911852737092 A A A LNCV6_126809_PI430048170 mRNA
GGTAACTTCCACAGAAAACACAAACATGTATTTAAAGGCAAGTCTCATCTAAGATGAAAC NM_014932 RefSeq chr3 + 173398447 174283349 NLGN1 22871 neuroligin 1
GO:0052689|GO:0030054|GO:0017146|GO:2000311|GO:2000310|GO:0045202|GO:0051491|GO:0006605|GO:0005615|GO:0016339|GO:1900029|GO:0045211|GO:0046983|GO:0051260|GO:0050839|GO:0060999|GO:0097091|GO:0048789|GO:0051965|GO:2000463|GO:0009986|GO:0051968|GO:0050804|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127989_PI430048170 0.0242667747021952 2.50565326244362 9.49637273229102 9.50403003908747 9.85564438911563 P P P 7.71429795753279 8.4422751272718 8.60716143456151 P P P LNCV6_127989_PI430048170 mRNA
TTCACTTTCACATAGATGTCCCTTTCTTGGCCAGTTATCCCTTCCTTTTAGCCTAGTTCA NM_001145031 RefSeq chr10 + 73911103 73917500 PLAU 5328 "plasminogen activator, urokinase, transcript variant 2"
GO:0005515|GO:0033628|GO:0001666|GO:0010469|GO:0004252|GO:0005886|GO:0009986|GO:0014910|GO:0014909|GO:0005576|GO:2000097|GO:0005615|GO:0061041|GO:0007165|GO:0006935|GO:0007596|GO:0042127|GO:0006508|GO:0042730|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129655_PI430048170 0.0667062129888901 0.69983921790256 3.16618303832462 2.96956535743215 2.6469671693229 P P A 3.23292847466146 3.39087856754786 3.7090680008478 P P P LNCV6_129655_PI430048170 mRNA
ATAGAAGAACATTCCTTTGTGCAGCTTGTCCCCTGGAATAAAAATGGCCCATTTTCTCTA NM_138980 RefSeq chr4 - 86015122 86360222 MAPK10 5602 "mitogen-activated protein kinase 10, transcript variant 3"
GO:0005515|GO:0034142|GO:0005886|GO:0051403|GO:0005829|GO:0005739|GO:0051090|GO:0004705|GO:0002756|GO:0000187|GO:0005737|GO:0002755|GO:0009416|GO:0034138|GO:0004708|GO:0038124|GO:0038123|GO:0034134|GO:0007254|GO:0002224|GO:0007258|GO:0005524|GO:0007165|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144491_PI430048170 0.760909869841289 0.963538099115617 7.20186873736954 7.01197456053863 6.7733981101491 P P P 7.19967201769459 7.12910593243591 6.8239739573335 P P P LNCV6_144491_PI430048170 mRNA
TGATGATAGGTCTTCTCCTTGGGGCCTCCCCCAATAAATCTGTAATAAACCTGAAACCCA NM_153486 RefSeq chr16 - 75111859 75116772 LDHD 197257 "lactate dehydrogenase D, transcript variant 1"
GO:0005739|GO:0005515|GO:0004458|GO:0008762|GO:0050660|GO:0005743|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98999_PI430048170 0.307589817066007 1.02017167733708 0.367917844095126 0.366766460938889 0.425754688624142 A A A 0.36117300794098 0.331639815134037 0.381546411918164 A A A LNCV6_98999_PI430048170 mRNA
GTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAAT NM_014432 RefSeq chr6 - 136999970 137045180 IL20RA 53832 "interleukin 20 receptor, alpha, transcript variant 1"
GO:0042015|GO:0004896|GO:0005886|GO:0019221|GO:0045124|GO:2001244|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142360_PI430048170 0.202515255354811 0.684846594641587 0.345207504917664 0.242892814331879 0.2926170076028 A A A 0.264048724655177 0.979522615997304 1.13665219183553 A A A LNCV6_142360_PI430048170 mRNA
ACAATCACTGGGAAAATCAAACGCAACGTTTTAAGAGACCAAGAATGGAGAGGAAGATAG NM_001080454

RefSeq chr12 + 7304331 7328373 ACSM4 NA acyl-CoA synthetase medium-chain family member 4
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144608_PI430048170 0.958875135060199 1.00911250174561 3.42973382969172
2.66911027759315 3.26633335086208 P A P 3.34335800226404 3.00066396780562
3.06406555843535 P P P LNCV6_144608_PI430048170 mRNA
ATAAAGAGAGGATTAGGCAGCAGCACTGTGTGTGTCTTCCTGGGAGCCGAGCTGGGGGTT NM_001122636 RefSeq
chr12 - 132196371 132329319 GALNT9 50614 "polypeptide N-acetylgalactosaminyltransferase 9,
transcript variant A"
GO:0004653|GO:0006493|GO:0000139|GO:0030246|GO:0016266|GO:0016021|GO:0044267|GO:0046872|GO:0043
687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143385_PI430048170 0.00323553347169098 0.408697104580707 10.6088920794721
10.3134542303054 10.4765764452726 P P P 11.5665056027322 11.6498508148183
12.0274603252123 P P P LNCV6_143385_PI430048170 mRNA
CTGGCAGGCTCGTTTTACCTCATTCTAGAATATTTAAGAATCTAAAAATAAAGGGCAACT NM_001242307 RefSeq
chr10 - 3137726 3172841 PITRM1 10531 "pitrilysin metallopeptidase 1, transcript variant 1"
GO:0005739|GO:0005759|GO:0006508|GO:0043085|GO:0008047|GO:0004222|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_117_PI430053867 0.0768002240467407 1.41560039427831 4.16509203552926
4.02606332971783 3.63361520714737 P P P 3.58051377096601 3.39203810830204
3.39070810374757 P P P LNCV6_117_PI430053867 mRNA
GATGTTTCTAAGTCCCTAAACTGACTTGTCTCTCCTGCTTACAACCTTTCAGTGTCTTCC NM_001242791 RefSeq
chr17 + 49845909 49848837 FLJ45513 NA uncharacterized LOC729220 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129878_PI430048170 0.00750453135280845 0.505239546789749 9.08309256230666
9.04512675680467 9.31928934583093 P P P 9.91535228567577 10.0647491407927
10.3953190182716 P P P LNCV6_129878_PI430048170 mRNA
TATGTCTCGTATTTTACTGTCACTGGAGGCTCTGTGGGCTGTCATAGTTAATTGACCATA NM_014671 RefSeq chr7
+ 157138960 157269372 UBE3C 9690 ubiquitin protein ligase E3C
GO:0005622|GO:0005515|GO:0000209|GO:0005737|GO:0004842|GO:0000502|GO:0042787|GO:0016874|GO:0005
634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138088_PI430048170 0.508500574577473 1.07619880823142 5.69482096124635
5.84981344965671 5.6750994856992 P P P 5.79409488515427 5.33694203251856
5.73580294478606 P P P LNCV6_138088_PI430048170 mRNA
AATGGCACATGCTTCCACTCCATCCATACTGGCATCCTCAAATAAACAGATATGTATACA NM_080706 RefSeq
chr17 - 3565445 3592877 TRPV1 7442 "transient receptor potential cation channel, subfamily V, member
1, transcript variant 3"
GO:0051219|GO:0005516|GO:0005262|GO:0005231|GO:0030054|GO:0005886|GO:0007635|GO:0071312|GO:0031
226|GO:0055085|GO:0005524|GO:0071318|GO:0034220|GO:0032591|GO:0005887|GO:0045211|GO:0070588|GO:0
050955|GO:0006810|GO:0015278|GO:0016021|GO:0007166|GO:0004888 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_116502_PI430048170 0.867564390721356 1.03059608239206 9.33385043510047
9.26710474944864 8.83176157104648 P P P 9.29407389140774 9.03593442594913
9.00404813802086 P P P LNCV6_116502_PI430048170 mRNA
ATGAGTGGAAAATACCTGCACGATGACTTCGCCCTGCCCTGCCCACCGGGGCTGAAAATT NM_004716RefSeq chr11
- 117205070 117232525 PCSK7 9159 proprotein convertase subtilisin/kexin type 7
GO:0030173|GO:0016486|GO:0004252|GO:0016485|GO:0006508|GO:0008233 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135099_PI430048170 0.0705827528631389 0.741297407076782 11.633682085314
11.7122854563339 11.8876175432073 P P P 12.1164313651137 11.9597160685866

12.4254117904995 P P P LNCV6_135099_PI430048170 mRNA
GAAAGCCCTTTGACCCCAGCTTGCTAGTTGCATAATAATAAATTTTCTGTTCCTAATGGT NM_004284 RefSeq chr1
+ 147242640 147295766 CHD1L 9557 "chromodomain helicase DNA binding protein 1-like, transcript
variant 1"
GO:0005515|GO:0005886|GO:0005634|GO:0003677|GO:0005524|GO:0006974|GO:0005737|GO:0004003|GO:0006
281|GO:0000166|GO:0005654|GO:0006338|GO:0032508|GO:0016887 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_68961_PI430048170 0.1775772253252140.8781469253249864.10642802961036 4.3018665992014
4.43628301403342 P P P 4.45207888605518 4.50565839918077 4.46762619867781 P P P
LNCV6_68961_PI430048170 mRNA
TTGTGGCCAGCAACACAGGAAAATCCCAGCGCCCGTTGGAGTGCACCTAATTTCCACCAG NM_002646 RefSeq chr1
- 204422629 204490346 PIK3C2B 5287 "phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit
type 2 beta"
GO:0005515|GO:0005886|GO:0006661|GO:0036092|GO:0005783|GO:0048015|GO:0005634|GO:0030139|GO:0044
281|GO:0001727|GO:0005524|GO:0005829|GO:0046854|GO:0008150|GO:0016303|GO:0043491|GO:0035005|GO:0
035091|GO:0005942|GO:0006644 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131063_PI430048170 0.0142695787913448 0.5112592546299623.34561520917772
3.63250321603488 3.13169853833782 P P P 4.41834345386757 4.3737265030801
4.26085481669789 P P P LNCV6_131063_PI430048170 mRNA
TCATTACCCCCATGCTGAACCCCATCATCTATTCCCTGAGAAATCAAGAGATGAAGTCAG NM_001004708 RefSeq
chr11 + 59456960 59457905 OR4D6 NA "olfactory receptor, family 4, subfamily D, member 6" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130427_PI430048170 0.0183267405695878 1.38660605576536 2.88879964073646
2.57858779571688 2.67201408698605 A A A 2.32045266591071 2.0891312723138
2.32076245551451 A A P LNCV6_130427_PI430048170 mRNA
GGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCA NM_004465 RefSeq chr5
- 44304994 44388682 FGF10 2255 fibroblast growth factor 10
GO:0001656|GO:0005515|GO:0010838|GO:0000132|GO:0005111|GO:0048538|GO:0046579|GO:0001759|GO:0030
878|GO:0048536|GO:0005615|GO:0042693|GO:0031069|GO:0009880|GO:0031076|GO:0007173|GO:0030538|GO:0
032496|GO:0032355|GO:0045747|GO:0009986|GO:0031532|GO:0045740|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_68027_PI430048170 0.0584613009714813 0.82646750203160610.3331234764634
10.1280323325031 10.0795354061565 P P P 10.4512813556308 10.5797064181929
10.3371383211488 P P P LNCV6_68027_PI430048170 mRNA
AACACCAAGAAACCATGACTCCAGCCGGCTTGTCCTTCTTCCAGTGCCGCTGGGATGACT NM_032478 RefSeq chr17
- 75898642 75905100 MRPL3864978 mitochondrial ribosomal protein L38
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0005743|GO:0005840 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137842_PI430048170 0.00406906961778762 0.6355203882418059.38120707633284
9.53696210361472 9.26819310700902 P P P 9.94378004695836 10.2020920017256
10.0022447852836 P P P LNCV6_137842_PI430048170 mRNA
AACCGCCCCCAGTGATAACATCTGTGAAGCCAGCCATTACTCAATAAACTGCAAACTTGT NM_030971 RefSeq chr10
+ 101031238 101041241 SFXN3 81855 sideroflexin 3
GO:0005739|GO:0034220|GO:0031966|GO:0015075|GO:0016021|GO:0055072 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134429_PI430048170 0.2500203333700770.6864679554125430.372313048593783
0.3789761702412950.467100676070665 A A A 0.8758614334912961.41377774716977
0.372099226095306 A A A LNCV6_134429_PI430048170 mRNA
TCAAGTATTGGAAGGGGTGGGGAGATATATAAATAAATCATGAAATCAATACATAAAAAA NM_001114101 RefSeq

chr1 + 22643624 22648110 C1QC 714 "complement component 1, q subcomponent, C chain, transcript variant 1"
GO:0006956|GO:0006955|GO:0005581|GO:0045087|GO:0006958|GO:0030853|GO:0072562|GO:0005576|GO:0045650|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90819_PI430048170 0.993195552310788 0.999290689877342 9.90004701063555 9.86229076952781 9.77361700314922 P P P 9.94106326113571 9.86439296255723 9.72849707707246 P P P
LNCV6_90819_PI430048170 mRNA
AATGAGGACTGGGGCACCTGGAAAATGCCATTTTTTGGAAAATAAAATTTAAGAACAGCT NM_133450 RefSeq chr16 - 4696509 4734162 ANKS3 124401 "ankyrin repeat and sterile alpha motif domain containing 3, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141053_PI430048170 0.125204386275505 0.799459883200483 4.98713088947811 4.85898762841503 4.94906119371721 P P P 5.20171213570647 5.04672852131561 5.48395574144605 P P P LNCV6_141053_PI430048170 mRNA
CATTGGAGAAGGAAGGAAGAGCCTCAAAATAAGTGTGCACCCATGCACATATTCAGGAAC NM_000208 RefSeq chr19 - 7112254 7294000 INSR 3643 "insulin receptor, transcript variant 1"
GO:0005515|GO:0005159|GO:0043560|GO:0043231|GO:0046777|GO:0005899|GO:0046326|GO:0045821|GO:0038083|GO:0043559|GO:0070062|GO:0023014|GO:0032869|GO:0030335|GO:0005975|GO:0045740|GO:0018108|GO:0045840|GO:0043235|GO:0008544|GO:0007186|GO:0048639|GO:0005887|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144823_PI430048170 0.495341154908071 0.958736078188453 0.367259131284087 0.364276392650645 0.388920941874208 A A A 0.567413859807732 0.340744571625458 0.384659184490627 A A A LNCV6_144823_PI430048170 mRNA
CTGAGAAATAAGGATGTGAACAAAGCTCTCAGAAAAGTGATGGGCTCCAAAATTCACTCC NM_001004739 RefSeq chr11 + 55827218 55828154 OR5L2 26338 "olfactory receptor, family 5, subfamily L, member 2"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129818_PI430048170 0.24170982831728 1.0743276064151 0.472219483224326 0.654018437199112 0.54361317496122 A A A 0.347257165557279 0.52144243993528 0.490762819192903 A A A LNCV6_129818_PI430048170 mRNA
CCTCAAGCCCAGGTGACTCTGTGAGGTCTGCAGAGGGAGAAAAGAACCCACAAGGGAAGA NM_001123395 RefSeq chr1 - 42733092 42740254 CLDN19 149461 "claudin 19, transcript variant 2"
GO:0005634|GO:0019227|GO:0042802|GO:0043297|GO:0016323|GO:0043296|GO:0005737|GO:0016338|GO:0005198|GO:0005923|GO:0016021|GO:0007601|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145536_PI430048170 0.465398768526305 0.975174428760325 0.256734507843798 0.271239779175685 0.380679030860408 A A A 0.382001679783268 0.325011568456492 0.312701240483582 A A A LNCV6_145536_PI430048170 mRNA
CACAAGCAGATGACCAAGATATGATAGACTCTGTCTTTTATACAATCATAATTCCTTTGC NM_001005482 RefSeq chr3 + 98282887 98283832 OR5H2 NA "olfactory receptor, family 5, subfamily H, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143694_PI430048170 0.0320296110414386 0.525896492561492 8.24825532548195 8.04857850969058 8.18713123899703 P P P 8.69017256305111 9.21433770084453 9.29645518948594 P P P LNCV6_143694_PI430048170 mRNA
GAAGGCAGTAATGCAAGAGTCCTTTTGTGAAGAGTGTTTCTATGTAGAGATGTTTATATT NM_015221 RefSeq chr10 - 99875576 100009919 DNMBP 23268 dynamin binding protein
GO:0035556|GO:0005515|GO:0030054|GO:0005795|GO:0032321|GO:0045202|GO:0005856|GO:0005089 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122398_PI430048170 0.0259168695209071 1.41118090599287 5.49543118795316 5.86642877186233 5.74153884970072 P P P 5.3132767542553 5.2292374601124 5.08537083180029 P P P LNCV6_122398_PI430048170 mRNA

TCATTTGCTACTATGGGAACCGAGGGGAGCCTGATCCTATCGTTTTGACGCCAGGTGGCC NM_001283106 RefSeq chr22 + 20016999 20065926 TANGO2 128989 "transport and golgi organization 2 homolog (Drosophila), transcript variant 1" GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_40661_PI430048170 0.46049651770569 1.31438541663674 0.4667546579547251.67667083399433 1.09118358695809 A A A 0.5378178778948990.9660841493999650.764913971076892A A A
LNCV6_40661_PI430048170 mRNA
CTGCTAGCAGTTCCACCAATGAAAGAGGAGACCAGGATGTTTAAAACAGGCAAACACAAG NM_001278094 RefSeq chr5 + 37873424 37875798 GDNF-AS1 NA "GDNF antisense RNA 1 (head to head), transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102712_PI430048170 0.74293350133809 1.4063465604921 1.88692109693533 2.85857476579737 0.243829202294717A A A 2.26822157686853 0.434114525636769 1.29911167672837 A A A LNCV6_102712_PI430048170 mRNA
CCCCATACTCTTGGCTCTGTAGCATTTCCAAGTTCAGATAAACCCCTGAGTGCTCACCCA NM_020882RefSeq chr20 + 63293185 63330933 COL20A1 57642 "collagen, type XX, alpha 1" GO:0031012|GO:0005581|GO:0030198|GO:0005788|GO:0005576|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127624_PI430048170 0.0314175277878943 1.40801414090032 7.19523783671172 7.27942254257455 6.89543055627429 P P P 6.79156294484938 6.60378756672926 6.50666123030273 P P P LNCV6_127624_PI430048170 mRNA
ATTTAACTCAGTCAATAACATACTGGTTTTACTCATCTCCCCCTCCATTGATTAGCCAAA NM_001093729 RefSeq chr18 + 68715253 69055189 CCDC102B 79839 "coiled-coil domain containing 102B, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135265_PI430048170 0.3786418663191981.15802845697024 8.41190490366823 8.62632809504008 8.66015103176263 P P P 7.93835970497629 8.39395276650767 8.65471627546198 P P P LNCV6_135265_PI430048170 mRNA
CCAGTTATGGAGTGCTACTAAAACATTTTCTTCTCTCCTGGCCTCTGGAAGCATCTTTAG NM_014641RefSeq chr6 - 30699806 30717681 MDC1 9656 mediator of DNA-damage checkpoint 1 GO:0005515|GO:0006281|GO:0005694|GO:0000724|GO:0031573|GO:0070975|GO:0005654|GO:0005634|GO:0008022|GO:0005925|GO:0006302 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137899_PI430048170 0.00120345546616867 2.30063581313539 4.62870264442846 4.29328402880562 4.33346237682482 P P P 3.36035313202072 3.26892050010041 3.02311915049069 P P P LNCV6_137899_PI430048170 mRNA
ATGCAGAAAGCCGAAGAGTTAGAACTTTTGGATACAGCAGAAGAAACAGCGGCTCCACTA NM_145641RefSeq chr22 - 36140322 36166177 APOL3 80833 "apolipoprotein L, 3, transcript variant beta/a" GO:0007165|GO:0005737|GO:0006954|GO:0016020|GO:0006869|GO:0042157|GO:0005576|GO:0004871|GO:0043123|GO:0005319|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142046_PI430048170 0.72977167149201 1.10938700704187 1.07281799465113 0.3255354163690490.280433880526836A A A 0.4937581617591090.403633304210779 0.474623285086255A A A LNCV6_142046_PI430048170 mRNA
CTGTCAAGAGAAGCATGACAAACAAAATCATTTACCTGACTTTAGTGCTTTTTCCCATAA NM_001300790 RefSeq chr6_GL000252v2_alt - 4000853 4008312 HLA-DQB2 3120 "major histocompatibility complex, class II, DQ beta 2, transcript variant 1" GO:0050852|GO:0012507|GO:0005886|GO:0019221|GO:0031295|GO:0042613|GO:0005765|GO:0032588|GO:0030666|GO:0019886|GO:0006955|GO:0000139|GO:0071556|GO:0030669|GO:0032395|GO:0010008|GO:0060333|GO:0030658 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136370_PI430048170 0.000856299128411204 1.83275327507391 4.96241383140585 5.17262092182973 5.17883014775016 P P P 4.12376136881348 4.34941576348785 4.22007568069141 P P P LNCV6_136370_PI430048170 mRNA
CAACGCCTTGTTGAATTGGTGCTTTGTGGTTGCAATAAAGCATTGCTTCAGTTTAAAAAA NM_001010971 RefSeq

chr1 + 84298365 84350798 SAMD13 148418 "sterile alpha motif domain containing 13, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_30130_PI430048170 0.0626010902192914 1.80727980667471 5.00712394805674 5.353992605668 5.82573971586422 P P P 4.43382153839875 4.70523074966418 4.59142380735246 P P P
LNCV6_30130_PI430048170 mRNA
ATGTGGCAGTTTCAAAGGATTACTTGATGCAAAGTATGTTTCCTTTCAAAGGGATCTTGA NM_144775RefSeq chr17 + 18315279 18328056 SMCR8 140775 "Smith-Magenis syndrome chromosome region, candidate 8"
GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107555_PI430048170 0.0221614434131822 1.34407810450233 12.6169190803379 12.9251134975012 12.7404757762758 P P P 12.2571339637835 12.4716693724813 12.2809038904906 P P P LNCV6_107555_PI430048170 mRNA
TGAAGTGGCTTTACGCTTCAGGAAGCCACGCCTGTTGAATAAAGCTTTGGTGTGTTTGCA NM_002528RefSeq chr16 - 2039814 2047866 NTHL1 4913 nth endonuclease III-like 1 (E. coli)
GO:0003906|GO:0005515|GO:0051539|GO:0005634|GO:0046872|GO:0005739|GO:0019104|GO:0003690|GO:0004519|GO:0006281|GO:0006296|GO:0006284|GO:0045008|GO:0006285|GO:0005654|GO:0000737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101773_PI430048170 0.2750754906813490.8617634657622634.92752111777895 5.25414079922162 5.39485924904754 P P P 5.31345060609539 5.30733823248774 5.61646719289308 P P P LNCV6_101773_PI430048170 mRNA
AATAGCAAGGTGCTGGATCAAATACTGTTTGACTCTCATGCAGAATGCCCAACTCTCCAT NM_015634RefSeq chr10 + 68988720 69016983 KIAA1279 26128 KIAA1279
GO:0005739|GO:0005515|GO:0019894|GO:0005856|GO:0006839|GO:0030154|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106618_PI430048170 0.000805975487540214 0.2597592938245392.98974463650608 2.72289439757644 3.12781654867909 A A P 4.57755914308429 5.07796267123778 4.99964311425993 P P P LNCV6_106618_PI430048170 mRNA
GCAGAAGAAACAGAGTTTAGGTGAAGACCATGTGATTCTGGAGGAGCAAAAAACAATTCT NM_001100588 RefSeq chr9 - 122849452 122905283 RC3H2 54542 "ring finger and CCCH-type domains 2, transcript variant 1"
GO:0000209|GO:0004842|GO:0001782|GO:0048286|GO:0009986|GO:0048536|GO:0003729|GO:0009791|GO:0003677|GO:0048535|GO:0005737|GO:0010608|GO:0042098|GO:0035264|GO:0016020|GO:0000932|GO:0060173|GO:0005654|GO:0008270|GO:0043029 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133180_PI430048170 0.3878146975661071.07778838419462 12.112560432226 12.193778569657 11.8910777489238 P P P 11.8556779841971 12.0125569182243 12.0159673408848 P P P
LNCV6_133180_PI430048170 mRNA
AGCCAGGAGGTCTATGATGGTGACGATTTTTAAAATCAGGAAATAAAAGATCTTGACTCT NM_006579RefSeq chrX + 48521775 48528716 EBP 10682 emopamil binding protein (sterol isomerase)
GO:0030097|GO:0004769|GO:0006695|GO:0000247|GO:0005783|GO:0044281|GO:0047750|GO:0007165|GO:0001501|GO:0005887|GO:0006855|GO:0005789|GO:0015238|GO:0004888|GO:0008203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130273_PI430048170 0.5688108113270921.1581541050623 1.03202488509603 0.2709967282998850.3069627072359 A A A 0.4418743778543780.351760306295694 0.311729412511358A A A LNCV6_130273_PI430048170 mRNA
TCTGTATACTAGAAACCTCAACATCTCTAGAAGAGGAAATAAAAGCTGCTTTGCACTCTG NM_016298RefSeq chr3 + 121593322 121630292 FBXO40 51725 F-box protein 40
GO:0042692|GO:0003674|GO:0005737|GO:0004842|GO:0016567|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127149_PI430048170 0.000326097993245352 2.60086264781662 5.69934109458239 5.90307712559748 5.607344518677 P P P 4.49536301462955 4.36210992989341

4.21806881300154 P P P LNCV6_127149_PI430048170 mRNA
GAAAATGCCAGCCTAGTGTTTACAGTTTTCGGCCACAACATGAAGAGCAGCAATGACTTC NM_016524RefSeq chr16
+ 19168212 19268334 SYT17 51760 synaptotagmin XVII
GO:0005802|GO:0005215|GO:0016020|GO:0006887|GO:0008021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137005_PI430048170 0.5684814085371870.9613507660284530.291413739995215
0.4604296183375080.313451858962011A A A 0.5241762042771140.427190108906591
0.280032812231188A A A LNCV6_137005_PI430048170 mRNA
TATGGAATTTGTGAAAAGGAAATTACCTTGCAATAAAGTTGGTGGGACCAGGAAGTAGAG NM_002367RefSeq chrX
+ 30241939 30244191 MAGEB4 4115 melanoma antigen family B4 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_135327_PI430048170 0.0400452274025864 0.7465554802943018.260735157919
8.01414938623945 7.9853885692861 P P P 8.41837571333736 8.71729045337328
8.38181891862245 P P P LNCV6_135327_PI430048170 mRNA
CTGTTTGAAGTGATCATTGGCGTGTGTGTGTGTGCATAAATTTTTAGTGACATAAAACTT NM_173615RefSeq chr16
+ 22092537 22156966 VWA3A 146177 von Willebrand factor A domain containing 3A GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136616_PI430048170 0.2470112666167831.28792162344376 0.449091712492416
0.3860904305100581.03708674092249 A A A 0.2596464092385430.336404873860362
0.272879391999429A A A LNCV6_136616_PI430048170 mRNA
CAGAAGATAGTGTCTGAGTAGGGCTGATGTGTTTCCTGTTAGTCTGATTTTGCTTTTGCC NM_020678RefSeq chr3
- 54918353 54928074 LRTM1 57408 "leucine-rich repeats and transmembrane domains 1, transcript
variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130935_PI430048170 0.7720459666861561.03324732093668 4.6512183929744
4.28658511364536 4.53892816830411 P P P 4.66003298473046 4.38019170801009
4.29274555871975 P P P LNCV6_130935_PI430048170 mRNA
GTGTTTTACTCTTCAGTATTTTTCTATCAGACTTGTACAAATAAAGCCTTGTTCCAGGCT NM_001144072 RefSeq chr13
+ 99200424 99386499 UBAC2 337867 "UBA domain containing 2, transcript variant 1"
GO:0005783|GO:0016021|GO:0070972 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120764_PI430048170 0.0895299636829602 1.11111049778562 6.59556139459951
6.55425875905731 6.42211313560385 P P P 6.33740303576369 6.39835695508993
6.38509166482254 P P P LNCV6_120764_PI430048170 mRNA
AGAAGAAGGTGTATCTCAAAGTGCGGCCAGAGAGATCATGAGAGACTATATCCAGAAGCA NM_014233RefSeq
chr17 - 44205032 44219673 UBTF 7343 "upstream binding transcription factor, RNA polymerase I,
transcript variant 1"
GO:0005515|GO:0010467|GO:0006355|GO:0006356|GO:0006363|GO:0005730|GO:0006362|GO:0006361|GO:0006
360|GO:0003677|GO:0045943|GO:0045814|GO:0003682|GO:0040029|GO:0005654|GO:0006338 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136444_PI430048170 0.8719688740121421.01499360684399 8.64141964564351
8.53011139498437 8.33773294287064 P P P 8.53405680235518 8.52087910818948
8.40251058037981 P P P LNCV6_136444_PI430048170 mRNA
CGCTTCTCACTGTATGTTCTGGAACATAAAGCTAGCAATGAAGGTATTTCTTTGAAAAAA NM_024784RefSeq chr11
- 62750962 62754184 ZBTB3 79842 zinc finger and BTB domain containing 3
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144046_PI430048170 0.3454443153444250.9543733464694970.260520284039985
0.3943310267807320.291652177448593A A A 0.4722957459384430.36458307738504
0.310438342694953A A A LNCV6_144046_PI430048170 mRNA
TCATTTATTGCCTAAGAAACCGAGAGGTCAAGGAAGCTCTGAAGAAACTGGCATATTGCC NM_001005281 RefSeq

chr7 + 144003996 144004932 OR6B1 NA "olfactory receptor, family 6, subfamily B, member 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133201_PI430048170 0.4479014119417940.9243535101599460.329612565505714
0.3522069681768930.347533596893651A A A 0.670890780994561 0.347057215228129
0.325374190655592A A A LNCV6_133201_PI430048170 mRNA
ATGACATTGGGTGACATTGTCTTCAAGAGAATCAGCAAGAGAATTTAAACAAGTCTGCAT NM_001443RefSeq chr2
- 88122988 88128131 FABP1 2168 "fatty acid binding protein 1, liver"
GO:0043066|GO:0005504|GO:0008284|GO:0032052|GO:0070301|GO:0016209|GO:0051345|GO:0005782|GO:0005
324|GO:0071456|GO:0044281|GO:0005829|GO:0050892|GO:0005543|GO:0045179|GO:0003682|GO:0008144|GO:0
032000|GO:0005654|GO:0043154|GO:0015909|GO:0044255|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144168_PI430048170 0.00178353404698495 2.03973840937494 5.57259225871606
5.33374853015946 5.64496149582628 P P P 4.54412769745185 4.55429045920881
4.37917640451263 P P P LNCV6_144168_PI430048170 mRNA
TTAAGCAGTAATCCTACTTCATTAAGCCTTCCTGGGGTGCGGTACACACCGTTAATTCAG NM_018242RefSeq chr17
+ 19533853 19579033 SLC47A1 55244 "solute carrier family 47 (multidrug and toxin extrusion),
member 1"
GO:0015695|GO:0005886|GO:0006855|GO:0031988|GO:0005451|GO:0016021|GO:0055085|GO:0015238 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140386_PI430048170 0.4486103418176550.7744347533712962.89572437992227
2.26745294933919 2.37074463693396 A A A 2.346957220218 2.71378319494553
3.44062283806061 A P P LNCV6_140386_PI430048170 mRNA
ATAGTGATGGTAAGGCAAGATTCTAGCAAAGAGAGATGGGAGATAAATGGCTGAGAGTTC NM_153210RefSeq
chr17 + 9645536 9729686 USP43 124739 "ubiquitin specific peptidase 43, transcript variant 1"
GO:0004197|GO:0016579|GO:0004843|GO:0061136|GO:0043161 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131008_PI430048170 0.0443410466753531.06546878900104 0.346748899439871
0.4043138650262040.326759660210366A A A 0.2572332629962680.28671102982291
0.260359174123239A A A LNCV6_131008_PI430048170 mRNA
TTCAGGTTCTAAGGATACCAAATCCTACAGCATGTGAATGAACACTTGCCAGGAGTGAGA NM_001005175 RefSeq
chr11 + 5754692 5755729 OR52N4 NA "olfactory receptor, family 52, subfamily N, member 4
(gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144689_PI430048170 0.0106613662630870.5797146245778436.01917930239576
5.62594014271416 5.98939972277453 P P P 6.56310757823152 6.64992389076821
6.80315309986436 P P P LNCV6_144689_PI430048170 mRNA
CAACCATACTTTCCTGTGATGGAAGATGTTTCCTCTTGAAAAAATGCCAATACAGATTTT NM_001007024 RefSeq
chr17 + 30477407 30526814 GOSR1 9527 "golgi SNAP receptor complex member 1, transcript variant
3"
GO:0006888|GO:0005801|GO:0005484|GO:0005794|GO:0016020|GO:0000139|GO:0042147|GO:0031201|GO:0006
891|GO:0016021|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130780_PI430048170 0.0169848822582330.8645978164411058.5093846256555
8.47216293896891 8.53291750264761 P P P 8.67941036755993 8.78884228985587
8.67361271927938 P P P LNCV6_130780_PI430048170 mRNA
ACTGGGAGGAAATGGAAGATCAGAGAAGTTGAGGTGCTCAATAAATGGTGACCACTTGGA NM_145232RefSeq
chr19 - 51097605 51108390 CTU1 90353 cytosolic thiouridylase subunit 1
GO:0005739|GO:0005515|GO:0002098|GO:0000049|GO:0016779|GO:0034227|GO:0032447|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134882_PI430048170 0.1158998678342191.25713705803695 9.05404992354249
9.43844742172822 9.28676408266213 P P P 9.10836305931075 8.97999825326258

8.69587042920713 P P P LNCV6_134882_PI430048170 mRNA
AGGCCTGAGGACAAGGAAGAGCTTTGCCATCCCCTGCATGTGCCCCTGCCTCTACCTGTC NM_012284RefSeq chr12
+ 49539156 49558294 KCNH3 23416 "potassium channel, voltage gated eag related subfamily H,
member 3"
GO:0005515|GO:0023014|GO:0005886|GO:0007268|GO:0000155|GO:0000160|GO:0005887|GO:0005249|GO:0042
391|GO:0034765|GO:0016021|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108615_PI430048170 0.5595997184331681.13409327467308 3.14862067331209
3.76472300207799 3.53156734044709 P P P 2.81165861664203 3.77313234771896
3.21857985826616 P P P LNCV6_108615_PI430048170 mRNA
ATGGTTCTGGAATGAATTTGTTGCAGATACAGGATAAAGTCTGGTCCCAGGCTTGCCTTG NM_005108RefSeq chr3
+ 38346759 38414976 XYLB 9942 xylulokinase homolog (H. influenzae)
GO:0005998|GO:0005997|GO:0005975|GO:0004856|GO:0046835|GO:0006091|GO:0005524|GO:0070062|GO:0042
732 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131595_PI430048170 0.00121979507142328 0.3655226971411035.38337764777094
4.98870982958476 5.12759496966642 P P P 6.49974319436149 6.64709520054623
6.72765576606378 P P P LNCV6_131595_PI430048170 mRNA
GCTCCAATACCTAGGCCTTTTAAATAGACAATGCAAAGTGAAAACTGCAAATTTCACTTA NM_198450RefSeq chrX
+ 85003891 85093317 APOOL 139322 apolipoprotein O-like GO:0005743|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130627_PI430048170 0.0985959439756255 0.5551394445404087.77639168665803
6.83167924540362 6.72533812521008 P P P 8.23493092664451 7.9929961938254
7.87457362754984 P P P LNCV6_130627_PI430048170 mRNA
CGCCCCCATCCCTATAATATCTGTAACTACTCCTAAAAAGGTTTTGATTCAGGCTTTTTTNM_018649RefSeq chr10 +
70052600 70112284 H2AFY255506 "H2A histone family, member Y2"
GO:0001740|GO:0000790|GO:0046982|GO:0044212|GO:0006334|GO:0005634|GO:0000122|GO:0001558|GO:0031
490|GO:0071169|GO:0035098|GO:0007420|GO:0045814|GO:0005654|GO:0007549|GO:0000786|GO:0070062|GO:0
016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137174_PI430048170 0.4494311181779740.6954935232247941.4017198359167
0.2905023167307140.437221257070555A A A 1.48535374594547 1.7963169950537
0.300022073235836A A A LNCV6_137174_PI430048170 mRNA
GAAAGGAAGGATAATCCAAGAATATAGGAAATCTGTGTTCTCTTCCTTTCATTTTATCCC NM_001034850 RefSeq
chr5 - 16473037 16617058 FAM134B 54463 "family with sequence similarity 134, member B,
transcript variant 1" GO:0005801|GO:0005794|GO:0016021|GO:0019233 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_139288_PI430048170 0.1087003602759910.9291621707256170.259995898186909
0.3542714879638470.294994774380847A A A 0.4502484224334880.448330277945663
0.32682221585267 A A A LNCV6_139288_PI430048170 mRNA
GATTTCCGGAAGATTTACTTTACTCAAGGAACTTTAAAGGTTGTATCCCCCACCAAAAAA NM_152349RefSeq chr17
- 40655619 40665164 KRT222 125113 "keratin 222, type II" GO:0005882|GO:0005198 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_77555_PI430048170 0.1799577937195570.5897169057469116.20659419308426 5.41588365096885
6.06042916153712 P P P 6.97281143789767 6.97074279887221 5.9010434619133 P P P
LNCV6_77555_PI430048170 mRNA
GGACTGCTGAGAAAATAATGCAGGAATACCAGTTAGAACAGAAAGATGTGAATTCTCTTC NM_014165RefSeq chr6
- 96889310 96897891 NDUFAF4 29078 "NADH dehydrogenase (ubiquinone) complex I, assembly factor
4" GO:0005739|GO:0005515|GO:0032981|GO:0005516|GO:0031966 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_131713_PI430048170 0.5788800898478610.9575604073445599.80467330158458
9.88176776796123 9.8481837017622 P P P 9.72998431692895 9.9714760158491

10.0064911221872 P P P LNCV6_131713_PI430048170 mRNA
AATAAAAGAATCTTCTGAAGGATGGGTCCTCCTACCTACTGTGAGAGAGCTCTTCCCTGA NM_003076RefSeq chr12
+ 50085199 50100711 SMARCD1 6602 "SWI/SNF related, matrix associated, actin dependent regulator
of chromatin, subfamily d, member 1, transcript variant 1"
GO:0005515|GO:0071565|GO:0032947|GO:0006357|GO:0016514|GO:0003713|GO:0006338|GO:0006337|GO:0071
564|GO:0048096|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129420_PI430048170 0.23675909682967 1.53257348422846 3.20803063492896
3.51801396673979 2.83586608240583 P P A 1.64024354776329 2.87101422181238
2.95051211738063 A P P LNCV6_129420_PI430048170 mRNA
TTGTTTGAAAACCGTGGGCTTGGGACTGTGAATTATTGCATGACATTCAAAAAGAAAAAA NM_023035RefSeq chr19
- 13206442 13506460 CACNA1A 773 "calcium channel, voltage-dependent, P/Q type, alpha 1A subunit,
transcript variant 2"
GO:0005515|GO:0008219|GO:0086010|GO:0048791|GO:0042995|GO:0019226|GO:0017158|GO:0043524|GO:0017
156|GO:0050883|GO:0050885|GO:0043025|GO:0032353|GO:0019905|GO:0008331|GO:0007214|GO:0007274|GO:0
007416|GO:0005891|GO:0021590|GO:0070509|GO:0030644|GO:0070588|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133349_PI430048170 0.00225264304452512 0.5559478865288157.89247522114693
7.78616636423992 7.58309944523708 P P P 8.49663684097997 8.75082677322545
8.55984841500909 P P P LNCV6_133349_PI430048170 mRNA
CCACATACCAACGTACTGTGGATATTATAACCTGCATTAAAACAACTCTAAAGAACGCTG NM_001288951 RefSeq
chr2 + 46941173 47076136 TTC7A 57217 "tetratricopeptide repeat domain 7A, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140434_PI430048170 0.00720211396981132 0.4422287651640976.00983481166136
5.98095232398502 6.47757161455168 P P P 7.24583472121314 7.28351314834373
7.51150809952549 P P P LNCV6_140434_PI430048170 mRNA
CCGTGGTCCAAATGGCAATATAAATCCAGTCTTTATTCTCCCTTTGTTGTATTTATGCTGNM_019053RefSeq chr10 +
92848467 93059494 EXOC6 54536 "exocyst complex component 6, transcript variant 1"
GO:0006996|GO:0000145|GO:0005886|GO:0030218|GO:0061024|GO:0015031|GO:0044267|GO:0006904|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135849_PI430048170 0.3237609893619640.82822470349459 0.352164077004957
0.4372821674812140.320412132268935A A A 0.4593135751230150.995698329432919
0.394881582713987A A A LNCV6_135849_PI430048170 mRNA
CACGGCAACAACAACGACAACAACAAACATTTGGAATATTATTCTCAACTCACGTTTTAA NM_001254749 RefSeq
chr1 - 163142298 163203173 RGS5 8490 "regulator of G-protein signaling 5, transcript variant 4"
GO:0043547|GO:0007165|GO:0005737|GO:0008277|GO:0005886|GO:0038032|GO:0005096 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142932_PI430048170 0.0960414698280452 0.6921021798378244.01586415547291
3.55060589965426 4.23412854041993 P P P 4.31443829154961 4.39253964939852
4.73311775900371 P P P LNCV6_142932_PI430048170 mRNA
AAGGGTCTTTTACCTCCCTCACCAACTAAGATTTGGTCATGTTGCGTATAACTTCACCAC NM_207320RefSeq chrX
+ 70062490 70064179 OTUD6A 139562 OTU deubiquitinase 6A
GO:0004843|GO:0035523|GO:0006508|GO:0035871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141433_PI430048170 0.21686256556105 0.5559788077150392.33242609729555
0.6210429961363712.44850331848867 A A A 2.95388539937548 2.95579067747678
2.61730040298453 P P P LNCV6_141433_PI430048170 mRNA
GTGGAATGGTGTATCAGTTATCTTTGCACAACAAACCACACTAATAAGTTGCTTGAAAAG NM_003689RefSeq chr1
- 19302707 19312146 AKR7A28574 "aldo-keto reductase family 7, member A2 (aflatoxin aldehyde
reductase)"
GO:0044598|GO:0005794|GO:0006805|GO:0044597|GO:0005975|GO:0006081|GO:0009055|GO:0044281|GO:0005

829|GO:0005739|GO:0019119|GO:0004032|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101625_PI430048170 0.155211921192944 1.39366801537285 10.8617010841003 11.5963360685708 11.153536304262 P P P 11.0042154325633 10.6033036495972 10.6273060325295 P P P LNCV6_101625_PI430048170 mRNA TCTCATAAAGGTTGTCTGCAACTTCGGGACCAAAGTGGTTCCCTGCCCTGCCTGCTCCTG NM_025099 RefSeq chr17 - 8224820 8248095 CTC1 80169 "CTS telomere maintenance complex component 1, transcript variant 1"
GO:0005515|GO:0070188|GO:0010389|GO:0045740|GO:0005634|GO:0010833|GO:0048538|GO:0048539|GO:0048146|GO:0048536|GO:0006974|GO:0071425|GO:0000723|GO:0003697|GO:0035264|GO:0090399|GO:0000784 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134919_PI430048170 0.895200519272885 0.962580616414022 1.46162101681327 0.367895485032469 0.368747120507606 A A A 1.47084476335474 0.550757536947823 0.385825641999976 A A A LNCV6_134919_PI430048170 mRNA TGCAATGGAATCATGCTTGTCCATGTGAAATAAATATGGCTCTCTCGTGTCCTTAAAAAA NM_006043 RefSeq chr16 + 22814538 22916338 HS3ST2 9956 heparan sulfate (glucosamine) 3-O-sulfotransferase 2
GO:0000139|GO:0005975|GO:0009405|GO:0008146|GO:0033871|GO:0007623|GO:0044281|GO:0016021|GO:0030203|GO:0006024 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139816_PI430048170 0.551457334441694 1.09566727737996 11.1819300379717 11.4673438510831 11.7184571004821 P P P 11.1521127355106 11.3351873916379 11.5121881139589 P P P LNCV6_139816_PI430048170 mRNA TGATGCTCGATGAATGCTGGGAATTCAGAGGAATGTCTTCACTTATACTTGGATTTGCTC NM_005034 RefSeq chr8 + 100150610 100154002 POLR2K 5440 "polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa"
GO:0008380|GO:0010467|GO:0006386|GO:0006368|GO:0006367|GO:0006385|GO:0006366|GO:0006363|GO:0006362|GO:0006361|GO:0005634|GO:0006360|GO:0006383|GO:0005829|GO:0005736|GO:0034587|GO:0005665|GO:0016032|GO:0005666|GO:0032481|GO:0035019|GO:0006356|GO:0006370|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139399_PI430048170 0.456397959719849 1.01232829739122 0.364368106063646 0.361641486494604 0.410397552074209 A A A 0.368369609244809 0.333360414053316 0.381735955152913 A A A LNCV6_139399_PI430048170 mRNA CAGATAGATGGGTTGACATCAGTTTATTCCAGCAAGAAAGAAAAGATTGTTATGCAAGAT NM_053039 RefSeq chr4 + 69280498 69295050 UGT2B28 54490 "UDP glucuronosyltransferase 2 family, polypeptide B28, transcript variant 1"
GO:0052696|GO:0006805|GO:0009813|GO:0005783|GO:0008152|GO:0005789|GO:0015020|GO:0016021|GO:0032870 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141254_PI430048170 0.00917965781188139 0.308539902021389 2.91100589116594 2.87916455613115 3.02565648430363 A A P 4.34347557288787 4.52113503826398 4.97059278634096 P P P LNCV6_141254_PI430048170 mRNA CGAATTGGCAGTAAATGTTAGCCATTTACAGCAATGCCAAATATGGAGAAACATCATAAT NM_001018077 RefSeq chr5 - 143277930 143435512 NR3C1 2908 "nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor), transcript variant 5"
GO:0005515|GO:0010467|GO:0004883|GO:0003700|GO:0006367|GO:0006366|GO:0030325|GO:0038051|GO:0005634|GO:0005829|GO:0005737|GO:0043525|GO:0045944|GO:0005759|GO:0046983|GO:0043402|GO:0060603|GO:0005496|GO:0042711|GO:0006355|GO:0000978|GO:0006351|GO:1900170|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68194_PI430048170 0.112823263519221 0.603332673050411 1.8718309033329 2.69608728098764 2.84188592412335 A A A 3.07941950106588 3.34993693886575 3.32794330967513 P P P LNCV6_68194_PI430048170 mRNA TTTAACCGAAGGTTCTTTGCATGAGCCAGGGAGGCAAAGTGTCACACTGAGACAGAATAA NM_032139 RefSeq chr19

- 32597000 32675196 ANKRD27 84079 ankyrin repeat domain 27 (VPS9 domain)
GO:0005515|GO:0017137|GO:0005886|GO:0005770|GO:0045022|GO:0005764|GO:0005085|GO:0043547|GO:0035
544|GO:0005737|GO:0016020|GO:0005769|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134295_PI430048170 0.0109885504592019 0.4800356163064923.71962574803125
3.74010958547539 3.66600968082483 P P P 4.61023684361848 4.66512297958267
4.99672565232989 P P P LNCV6_134295_PI430048170 mRNA
TCCCCTCCATGAAAACCTTGGGATTTTCTTGTGCTAGAACACTACCACAATGTGGTGCAA NM_001199679 RefSeq
chr1 + 95092516 95197605 TMEM56 148534 "transmembrane protein 56, transcript variant 1"
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141030_PI430048170 0.0615369719494791 0.6780244186100095.82070049389316
5.74665687050444 5.70560898153225 P P P 6.24893066024721 6.07510729004174
6.58565733167053 P P P LNCV6_141030_PI430048170 mRNA
TATCTAGCCACAGATCACTTGGTCTAGCAAATTTTAGATGCTTTTCCTCAGATATCAATA NM_001018104 RefSeq
chr16 + 1827223 1840202 FAHD1 81889 "fumarylacetoacetate hydrolase domain containing 1,
transcript variant 1"
GO:0005739|GO:0005737|GO:0008152|GO:0005743|GO:0047621|GO:0005654|GO:0018773|GO:0046872|GO:0034
545|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_34057_PI430048170 0.0857688556493478 1.19638734991205 6.74780740840685
6.82985913466133 6.57792728998629 P P P 6.3857768858988 6.63033782900447
6.35896872733595 P P P LNCV6_34057_PI430048170 mRNA
TGTCTGCCTCCTTGGGACTGTGGAGTGGGTGCCCTCAGTAAAGCGCTTTGTTGGAATGGT NM_001271441 RefSeq
chr21 - 44328943 44339402 C21orf2755 "chromosome 21 open reading frame 2, transcript variant 3"
GO:0003674|GO:0005737|GO:0005886|GO:0008360|GO:0060271|GO:0007010|GO:0007224 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_50011_PI430048170 0.0141811417766866 1.51737608824693 3.80421639694079
3.74513906916595 3.78589958800958 P P P 3.22823569827391 3.27644673869421
3.01307001378723 P P P LNCV6_50011_PI430048170 mRNA
CTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCATCAG NM_016215 RefSeq
chr9 + 136662926 136672678 EGFL7 51162 "EGF-like-domain, multiple 7, transcript variant 1"
GO:0031012|GO:0045746|GO:0030336|GO:0001568|GO:0001938|GO:0005509|GO:0005112|GO:0005576|GO:0001
525|GO:0007155|GO:0005615|GO:0001570 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138806_PI430048170 0.590357268960001 0.8879182947877790.402600128267653
0.3545844814870040.320184708754517 A A A 0.25309195555536 0.308701887083856
0.929414055444633 A A A LNCV6_138806_PI430048170 mRNA
CAGAGCAGCACTTTGTGCTTTCCTTTGCATAGATATGAGCTAGAAATAAATGTTATTTTC NM_032110 RefSeq chr1
- 50417550 50423447 DMRTA2 NA DMRT-like family A2 NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_59661_PI430048170 0.2629691454078011.0920920689747 6.45024748199308 6.69696502324313
6.4640673728705 P P P 6.43826226829392 6.41685229339514 6.38799411590739 P P P
LNCV6_59661_PI430048170 mRNA
TACTTACCTCAAGTCGTGCATTTATGATGCTAAAACAGATCCCTTCTGCCCCATATTCCG NM_001256796 RefSeq
chr12 + 121209860 121234106 P2RX4 5025 "purinergic receptor P2X, ligand gated ion channel, 4,
transcript variant 1"
GO:0030054|GO:0051928|GO:0010524|GO:0034405|GO:0005765|GO:0019228|GO:0042803|GO:0006809|GO:0034
220|GO:0001894|GO:0006810|GO:0043025|GO:0001614|GO:0033198|GO:0051260|GO:0070062|GO:0045296|GO:0
004931|GO:0005507|GO:0060079|GO:0014069|GO:0071318|GO:0005887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_71759_PI430048170 0.0207362243808938 1.30857489618551 6.12406674003842
5.92504414739692 6.16119730047627 P P P 5.64486106154944 5.66052769531774

5.74969792471974 P P P LNCV6_71759_PI430048170 mRNA
TCTCTGCTAAGACAAGATGCTCAGTTGACACATTTGAAAAGTGTTTGAAAAATTCTTGTG NM_145858 RefSeq chr21
- 33589340 33641854 CRYZL1 9946 "crystallin, zeta (quinone reductase)-like 1"
GO:0050661|GO:0008270|GO:0003960|GO:0055114|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144623_PI430048170 0.0689924099045202 0.7675737370772287.04381455688612
7.15393011434803 7.26063590509682 P P P 7.29376636535376 7.59864707823685
7.68984985178283 P P P LNCV6_144623_PI430048170 mRNA
ATGCATCTGTGTGAGCAGATGATCATTGTATTACCTTTTATCGGTAGTAAGCTTGGAAAA NM_033393 RefSeq chr4
+ 152942982 152979696 FHDC1 85462 FH2 domain containing 1 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141471_PI430048170 0.0083604156710981 0.3469818516257965.90112425677621
5.80237664473069 6.04194693192466 P P P 7.12054358050368 7.37852217176665 7.7642035954428
P P P LNCV6_141471_PI430048170 mRNA
CTTTCCAAAGACAATGTGCCACAGATCTTTTGTTCTCTGTAATGAGGATTAATTGCTGTT NM_005935 RefSeq chr4
+ 87007000 87141039 AFF1 4299 "AF4/FMR2 family, member 1, transcript variant 2"
GO:0005515|GO:0003700|GO:0045893|GO:0008023 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108765_PI430048170 0.0967423146900277 0.9608836662134430.388717831495046
0.4021076455968540.333254836919705 A A A 0.4302288845371680.447567207099396
0.41976628907161 A A A LNCV6_108765_PI430048170 mRNA
TTTCTTCGATAACGACAGTAAATCATTCAGTGGTGTATTAGACTGTGGAAACTGTTCCAG NM_000722 RefSeq chr7
- 81946443 82443806 CACNA2D1 781 "calcium channel, voltage-dependent, alpha 2/delta subunit 1,
transcript variant 1"
GO:0016529|GO:0005245|GO:0070588|GO:0051924|GO:0030315|GO:0034765|GO:0006816|GO:0005891|GO:0046
872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142615_PI430048170 0.2121064253909870.7268127608114332.46456598535984
3.34103893475929 3.27525194704847 A P P 3.67105932133475 3.25967372395699
3.64864066882876 P P P LNCV6_142615_PI430048170 mRNA
GAGTTCATTCCATTGGGGAATTTTCTTTCCCTTTTATTCTACCCCCACTACCGCCTTTAT NM_024852 RefSeq chr1 +
35931081 36056462 AGO3 192669 "argonaute RISC catalytic component 3, transcript variant 1"
GO:0005515|GO:0010467|GO:0048011|GO:0048015|GO:0006402|GO:0016441|GO:0005829|GO:0016442|GO:0035
068|GO:0035278|GO:0035198|GO:0007173|GO:0007219|GO:0016020|GO:0000932|GO:0008543|GO:0072091|GO:0
045087|GO:0038095. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134872_PI430048170 0.0355745192272822 1.38112459027903 6.56891175178074
6.78063035614359 6.70452779896782 P P P 6.37249256605133 6.27691171574694
5.98784946162755 P P P LNCV6_134872_PI430048170 mRNA
AAGGTCAGGATGAGAACACACTGAGTGAGGAGTGGACGCTGTCCATTGCCACGGCCATGA NM_000476 RefSeq
chr9 - 127866479 127877743 AK1203 adenylate kinase 1
GO:0046033|GO:0046034|GO:0015949|GO:0005886|GO:0004550|GO:0055086|GO:0036126|GO:0044281|GO:0004
017|GO:0009142|GO:0005524|GO:0001520|GO:0005829|GO:0006165|GO:0005737|GO:0007050|GO:0006172|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136896_PI430048170 0.3975339201288550.7943640142039430.32636361602814
0.3304789492295370.397250416104089 A A A 0.3698788758844641.1609371786756
0.368517217293863 A A A LNCV6_136896_PI430048170 mRNA
GCTACCTACATACAATTCCAAACACATACAGGAAGGTAGAAATATCTGAAAATGTATGTG NM_001565 RefSeq chr4
- 76021115 76023536 CXCL10 3627 chemokine (C-X-C motif) ligand 10
GO:0045859|GO:0005515|GO:0008284|GO:0009306|GO:0008603|GO:0048248|GO:0008015|GO:0010996|GO:0009
409|GO:0007267|GO:0033280|GO:0005615|GO:0045662|GO:0010818|GO:0034605|GO:0051607|GO:0006955|GO:0
006954|GO:0006935|GO:0045944|GO:0042127|GO:0043950|GO:0030816|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_52194_PI430048170 0.0631370257173924 1.12967593975241 8.12957264325059
8.07824155720489 8.16402906205109 P P P 7.95433708263152 7.84930719766975
8.03572543728787 P P P LNCV6_52194_PI430048170 mRNA
ATGCTGAAAGGAATAACAAGGCTTATCTCTAGGATCCATAAGGCCAAGCATGGGGATCAG NM_001199849 RefSeq
chr1 + 155689090 155739009 DAP3 7818 "death associated protein 3, transcript variant 3"
GO:0005515|GO:0070124|GO:0070125|GO:0070126|GO:0006996|GO:0032543|GO:0005730|GO:0005743|GO:0005
761|GO:0015935|GO:0005634|GO:0097190|GO:0005739|GO:0008637|GO:0005654 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_95339_PI430048170 0.2038295896437 1.07216938797996 0.2942723820542710.37494700320031
0.480085851317875 A A A 0.2984418755247930.2601913606017530.294797738031643 A A A
LNCV6_95339_PI430048170 mRNA
GGGGTATGCTGACTTCAGCAGACAAAGACTTTTGAATAAATAAACTGAACTCACACCTGG NM_001278669 RefSeq
chr18 + 79395771 79529323 NFATC14772 "nuclear factor of activated T-cells, cytoplasmic, calcineurin-
dependent 1, transcript variant 6"
GO:0005515|GO:0000790|GO:0003700|GO:0006366|GO:0044212|GO:0003705|GO:0005634|GO:0001837|GO:0005
829|GO:0007507|GO:0035556|GO:0000082|GO:0005737|GO:0045944|GO:0001085|GO:0006816|GO:0048273|GO:0
005667|GO:0030316|GO:0005528|GO:0001205|GO:0000979|GO:0045087|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134824_PI430048170 0.1516044622835870.7461220500298063.19750517050482 2.5022308708497
2.9877343307398 P A P 3.36315081755684 3.21228479223896 3.45442592988224 P P P
LNCV6_134824_PI430048170 mRNA
TCCCACATAAACTACCTCAGGAGTCACTGTAAAATAAACTGGCCTTGTTGTCTTAAAAAA NM_001142470 RefSeq
chr6 + 107028171 107051586 C6orf203 51250 "chromosome 6 open reading frame 203, transcript
variant 3" GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129013_PI430048170 0.253972531198036 1.02001526442617 0.316400480047184
0.2542808305379320.28170779385965 A A A 0.2574088436534910.251073428577135
0.258795135927214 A A A LNCV6_129013_PI430048170 mRNA
TATGAGCATTGTTTCTGGAAGTTCAACTCCCATAAGCTTTTCAAGTATATTAACTCTACC NM_001145668 RefSeq
chr15 + 48191669 48203754 CTXN2 399697 cortexin 2 GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138849_PI430048170 0.0122364564953690.6340016823160495.96709300396533
5.61868404438676 5.89223549468086 P P P 6.47856915822165 6.29807589071893 6.6722396419677
P P P LNCV6_138849_PI430048170 mRNA
CAACGGCAGGAAAAAATAGTTTGTACCAGTTTCATGAAGTATGTCTTTGGGTTTTTGTAA NM_015045 RefSeq chr10
- 86435255 86521784 WAPAL 23063 wings apart-like homolog (Drosophila)
GO:0005515|GO:0000795|GO:0005694|GO:0009636|GO:0005634|GO:0071922|GO:0048146|GO:0045875|GO:0035
562|GO:0043231|GO:0005829|GO:0005737|GO:0007067|GO:0008278|GO:0015630|GO:0016032|GO:0005654|GO:0
008156|GO:0071168|GO:0000278|GO:0000785|GO:0000775|GO:0060623|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139603_PI430048170 0.46058334557861 0.7151312092348620.391679014942452
0.2710094816181850.285746984245049 A A A 1.48547508794713 0.296992077034542
0.260383444136597 A A A LNCV6_139603_PI430048170 mRNA
CACCGTTAGCCTGGACAGTTGCTTATGGCATCGATAGGGTTGGATAATATTCTGGGATTT NM_007250 RefSeq chrX
+ 56232388 56287889 KLF8 11279 "Kruppel-like factor 8, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128189_PI430048170 0.2454690244236150.9253577417443211.3905848446525
11.3752585891914 11.3259879406454 P P P 11.4713145802265 11.5913097757117

11.3561612376953 P P P LNCV6_128189_PI430048170 mRNA
AAACACACCTTCACCTTACAAGGTGCTGACCATATTAAATGTTCAGGTTCTCTCAAAAAA NM_032310RefSeq chr9
+ 93096167 93113283 C9orf89 84270 chromosome 9 open reading frame 89
GO:0050700|GO:0031966|GO:0005789|GO:0005634|GO:0016021|GO:0043124|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145453_PI430048170 0.2624527436583210.8066679681641451 1.6550209643389
11.5374445927282 11.7440902992715 P P P 11.600719097637 11.9467811721221
12.2531316215731 P P P LNCV6_145453_PI430048170 mRNA
CTGAACTGTGCCGACTCCACAAAACGATTATGTACTCTTCTGAGATAGAAGATGCTGTTC NM_003945RefSeq chr5
+ 172983759 173034897 ATP6V0E1 8992 "ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1"
GO:0008286|GO:0005215|GO:0051701|GO:0042625|GO:0055085|GO:0006879|GO:0033572|GO:0016020|GO:0046
961|GO:0007035|GO:0008152|GO:0015991|GO:0030670|GO:0016049|GO:0016021|GO:0090382|GO:0043200|GO:0
010008|GO:0033179|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95543_PI430048170 0.4443694829317131.09068931542136 4.45141302004884 4.3431818060611
4.57208585935891 P P P 4.11752120517345 4.25702935601679 4.58489336992751 P P P
LNCV6_95543_PI430048170 mRNA
GCTCTATTTTCTCTTGGCCCAGAAGAGCTTGGTTTGTTTGAAGATAAGGATAAACCCGAT NM_018218RefSeq chr2
- 233475518 233565590 USP40 55230 ubiquitin specific peptidase 40
GO:0004197|GO:0016579|GO:0005737|GO:0004843|GO:0061136|GO:0043161|GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129241_PI430048170 0.4814122640640981.33328139012392 1.55296573583134
0.5367399237861450.372822305222408A A A 0.3843462381936140.586577254863559
0.539080706965575A A A LNCV6_129241_PI430048170 mRNA
TAAATTCTTCAAGTGCCTTTATGAAGGGGAGATCACTCAGATCCAGTCCCACATCAGCGA NM_080747RefSeq chr12
- 52585588 52601538 KRT72 140807 "keratin 72, type II, transcript variant 1"
GO:0008150|GO:0003674|GO:0005198|GO:0045095|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145325_PI430048170 0.0288485836721818 0.7688104546536738.18515270039526
7.93641376407143 8.17542879082226 P P P 8.44660259229303 8.45178738774074
8.54773180289423 P P P LNCV6_145325_PI430048170 mRNA
ATAAGTAACTTGACTATAAAATAAAGCCGTCCGTGGGACGACTGACCTCGTTGCAAAAAA NM_002729RefSeq chr10
+ 92689923 92695651 HHEX 3087 hematopoietically expressed homeobox
GO:0005515|GO:0034504|GO:0044212|GO:0030878|GO:0030154|GO:0042803|GO:0060431|GO:0010944|GO:0006
406|GO:0032993|GO:0042127|GO:0022027|GO:0016055|GO:0071103|GO:0008301|GO:0000122|GO:0000978|GO:0
001701|GO:0002573|GO:0061017|GO:0016973|GO:0061010|GO:0071837|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144532_PI430048170 0.1397041204249650.8391155044106451 2.2966949499151
12.0949470445285 12.1800144899619 P P P 12.6567789758239 12.3335036799657
12.3220591149523 P P P LNCV6_144532_PI430048170 mRNA
AGGTTCTTGAAGATGTTTATTTATATTGTCCTTTTTTACTGGAAGACGTACGCATACTCCNM_001300829 RefSeq chr19
+ 1269265 1273172 CIRBP 1153 "cold inducible RNA binding protein, transcript variant 3"
GO:0005515|GO:0017148|GO:0010494|GO:0009409|GO:0005634|GO:0045727|GO:0030371|GO:0005737|GO:0034
063|GO:0000166|GO:0070181|GO:0005654|GO:0048255|GO:0003730|GO:0009411 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130277_PI430048170 0.1691451085766340.7760126935545793.33457559304411
3.14520452148216 3.5963041134638 P P P 3.73941717358559 3.99401861732501
3.41906234143005 P P P LNCV6_130277_PI430048170 mRNA
CAGGCTCTGCCTCCTGGTGTTACTCTTTGCCAACAGCTTTACGGACATTGGATGAAGCCG NM_001014765 RefSeq
chr1 + 11654856 11663327 FBXO44 93611 "F-box protein 44, transcript variant 4"

GO:0005515|GO:0019005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144759_PI430048170 0.7909289256854751.15238308333342 2.85519662810846
1.07604105021457 2.27004891102811 A A A 0.7449461100036342.52898560706418
2.27699023402527 A P A LNCV6_144759_PI430048170 mRNA
TGTAGCTGTTCTTGTCTTCCTTATTTCCCTGTGAATGCTTTAATAAATCCCCATCACTAA NM_001281463 RefSeq chrX
- 53374148 53422728 SMC1A 8243 "structural maintenance of chromosomes 1A, transcript variant 2"
GO:0005515|GO:0008380|GO:0010467|GO:0007093|GO:0030893|GO:0008280|GO:0032876|GO:0005634|GO:0005
829|GO:0005737|GO:0007052|GO:0009314|GO:0000794|GO:0046982|GO:0005694|GO:0005730|GO:0003777|GO:0
005524|GO:0042770|GO:0000070|GO:0006281|GO:0007126|GO:0036033|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128683_PI430048170 0.2025414148873710.5444162161476591.55073422811096
0.2833511283821470.319045964109461A A A 1.03676342325636 2.39172290994386
1.38335602244501 A A A LNCV6_128683_PI430048170 mRNA
GCCAAGAGCTCTAAACAGAAGTTTGAGAAGGTAAAAATTAAGTTGTAGTATCTGAGTTGT NM_001085487 RefSeq
chr1 - 58654738 58700075 MYSM1 114803 "Myb-like, SWIRM and MPN domains 1"
GO:0004843|GO:0003713|GO:0005634|GO:0003677|GO:0032403|GO:0046872|GO:0006351|GO:0042393|GO:0035
522|GO:0045944|GO:0003682|GO:0015630|GO:0006508|GO:0005654|GO:0006338|GO:0008237 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_81747_PI430048170 0.00690930201631625 1.76602402158055 10.5361356494347
10.3579194125508 10.4452845928924 P P P 9.45246818188601 9.81858177806357
9.58831971402821 P P P LNCV6_81747_PI430048170 mRNA
CCGTTCCTACCATGAGACTAGCAAGATGAAAGTGCTGAGATTCATTGCAGAGGTTCAGAA NM_001005333 RefSeq
chrX + 51893601 51902356 MAGED1 9500 "melanoma antigen family D1, transcript variant 1"
GO:0005515|GO:0048011|GO:0006355|GO:0043065|GO:0005886|GO:0006357|GO:2001235|GO:0003713|GO:0050
680|GO:0005634|GO:0042981|GO:0097190|GO:0032922|GO:0043234|GO:0005737|GO:0043406|GO:0042752|GO:0
045893|GO:0045892|GO:0000785|GO:0090190 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131961_PI430048170 0.2043756710507580.8923095730388260.5895467556537
10.6537404801973 10.7887115364853 P P P 10.8167219577715 10.7025911736448
10.9976109074064 P P P LNCV6_131961_PI430048170 mRNA
CAACTGTTCAGTTTCAGTGGAATCTTGTATTTCTGGTTCATTATAACAAACTGTTCGCTT NM_001206612 RefSeq chr1
+ 153633981 153646306 CHTOP 26097 "chromatin target of PRMT1, transcript variant 2"
GO:0005515|GO:0006355|GO:0006406|GO:0016607|GO:0000346|GO:0051096|GO:0005730|GO:0005654|GO:0032
781|GO:0006351|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83790_PI430048170 0.0531571067728214 1.12983245479796 0.622322542264567
0.7374519889324440.751174039026123A A A 0.6255342189155670.470665966531211
0.484721795349892A A A LNCV6_83790_PI430048170 mRNA
AATGTCTTAGTTCAAGGACATATTTTTCTGAATACCTCCCTTACTGAAGCATTCTGCATG NM_002641 RefSeq chrX
- 15319450 15335554 PIGA 5277 "phosphatidylinositol glycan anchor biosynthesis, class A, transcript
variant 1"
GO:0005515|GO:0006501|GO:0016254|GO:0008194|GO:0000506|GO:0017176|GO:0009893|GO:0016020|GO:0005
789|GO:0016021|GO:0044267|GO:0006506|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120855_PI430048170 0.0415339391207961 1.37784040419609 6.10863920571146
6.12781078577248 5.75917905276367 P P P 5.54290768383473 5.66423042250343 5.4199124944092
P P P LNCV6_120855_PI430048170 mRNA
AACCTGGCAAACAAGGTCCCTCTGGAGCAAGTGGTGAACGTGGTCCCCCTGGTCCCATGG NM_000088 RefSeq chr17
- 50184095 50201639 COL1A11277 "collagen, type I, alpha 1"
GO:0005515|GO:0042542|GO:0034504|GO:0034505|GO:0071300|GO:0007605|GO:0090263|GO:0048706|GO:0071
560|GO:0015031|GO:0050900|GO:0005615|GO:0051591|GO:0071306|GO:0042802|GO:0070208|GO:0030198|GO:0
030199|GO:0071356|GO:0030574|GO:0032355|GO:0030335|GO:0005794|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_131898_PI430048170 0.0224136646892453 1.4296959274839 8.01809073202938
8.22380262645265 7.85739436644835 P P P 7.40529707288162 7.56254085566004
7.60046267192739 P P P LNCV6_131898_PI430048170 mRNA
TTCTTCTGTGATGATTATAAGGTATACGAAGCTGGACAGATTAAACATTGAGCCCTGTGC NM_212551RefSeq chr1
- 151159747 151165894 LYSMD1 388695 "LysM, putative peptidoglycan-binding, domain containing 1,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135544_PI430048170 0.3431414631042340.8977183988600861 1.3897653142227
11.2841172281677 11.2642822918714 P P P 11.2433374479074 11.6541417701061
11.4816366568891 P P P LNCV6_135544_PI430048170 mRNA
GAGAGACAGACGGGCGGTTTGACTTGGACACAAAGAAAGCCTTGGTTTCTAAGCAAAAAA NM_017518RefSeq
chrX - 153447664 153470631 HAUS7 55559 "HAUS augmin-like complex, subunit 7, transcript variant 1"
GO:0051297|GO:0007067|GO:0005813|GO:0005737|GO:0005886|GO:0005874|GO:0005819|GO:0005730|GO:0070
652|GO:0031996|GO:0051225|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127517_PI430048170 0.2015313738955810.9383912782478090.249501409406107
0.3313261033936350.280546324372361A A A 0.4691449942335510.363936198911473
0.299593437916124A A A LNCV6_127517_PI430048170 mRNA
CTTGAAAACTGTGCTAAGGATTAAGGGTGAGGGAGATATGGCCAAAGCTCTAGGTACTTG NM_001146033 RefSeq
chr11 - 5967552 5968494 OR56A5NA "olfactory receptor, family 56, subfamily A, member 5" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144875_PI430048170 0.4221449591369220.88522371794714 7.88214708864478
7.52993088798431 7.66583935122721 P P P 7.63118687982339 7.79835871400376
8.14886311334646 P P P LNCV6_144875_PI430048170 mRNA
GCCATGTCTAGACACCATGTTGTATCAGAATAATTTTTGTGCCAATAAATGACATCAGAA NM_004958RefSeq chr1
- 11106530 11262551 MTOR 2475 mechanistic target of rapamycin (serine/threonine kinase)
GO:0045859|GO:0001156|GO:0005515|GO:0016242|GO:0010831|GO:0005765|GO:0005764|GO:0007281|GO:0031
529|GO:0034605|GO:0046889|GO:0030163|GO:0046777|GO:0032314|GO:0031931|GO:0007173|GO:0018105|GO:0
030838|GO:0016301|GO:0032956|GO:0018107|GO:0031669|GO:0046983|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_114725_PI430048170 0.0815716579452719 2.03150939887191 1.77846722885199
2.18174136255318 2.31144014392365 A A A 0.4104518263954510.858591772548033
1.68842597264461 A A A LNCV6_114725_PI430048170 mRNA
AGTAGAAGAGAGTTGGATGTGACAATGTCCTTGGATCTGATGCTGTTGAAGACGTCTGTG NM_139056RefSeq chr5
+ 5140329 5320299 ADAMTS16 170690 "ADAM metallopeptidase with thrombospondin type 1 motif,
16" GO:0001658|GO:0006508|GO:0005578|GO:0008270|GO:0004222 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142800_PI430048170 0.1103589096834411.20636400612188 7.31021892138153 7.2649501519225
7.36478018409829 P P P 6.83631538252004 7.07513913791474 7.19540780779634 P P P
LNCV6_142800_PI430048170 mRNA
GGAAAACTTTTGTATCCCTAAGCATATTATTTTATAGTGTCTGCCATGCCATGTGGAAAT NM_024513RefSeq chr3
- 45917898 45995824 FYCO1 79443 FYVE and coiled-coil domain containing 1
GO:0005515|GO:0005776|GO:0016020|GO:0005770|GO:0072383|GO:0031410|GO:0016021|GO:0005764|GO:0046
872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106707_PI430048170 0.0155328436658352 0.3533508151639564.50748640956459
4.85991986778434 5.06099683100238 P P P 5.746102134058 6.46150277578331
6.63264081512163 P P P LNCV6_106707_PI430048170 mRNA
CTGGTGGACCTGTAATATCCACATTGTGAAGCTGTGTATGAAATTCAACTATAATATGAA NM_002069RefSeq chr7
+ 80134823 80219409 GNAI1 2770 "guanine nucleotide binding protein (G protein), alpha inhibiting
activity polypeptide 1, transcript variant 1"

GO:0005515|GO:0005886|GO:0003924|GO:0007268|GO:0043434|GO:0005634|GO:0005765|GO:0007193|GO:0046872|GO:0005737|GO:0004871|GO:0070062|GO:0005813|GO:0005834|GO:0030168|GO:0030496|GO:0005525|GO:0031683|GO:0006184|GO:0007049|GO:0007186|GO:0007596|GO:0007188|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57546_PI430048170 0.0276756865211321 1.59372722986303 3.60466496860189 3.26930512270899 3.08976298219899 P P P 2.73321469254584 2.77484207859306 2.46766023561112 P P P LNCV6_57546_PI430048170 mRNA
GGCAATGCCACAGGGCAGGCTGATTTTTCTACACCACCGCCACACTCATCATAGCCTTCA NM_014096 RefSeq chr11 - 57406953 57427087 SLC43A3 29015 "solute carrier family 43, member 3, transcript variant 1"
GO:0008150|GO:0003674|GO:0016021|GO:0005575|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131183_PI430048170 0.0475176377082905 0.45322539483416 3.10266843229272 2.34087090343975 3.42722225219558 A A P 4.20877643989995 3.86472217448057 4.37895684792031 P P P LNCV6_131183_PI430048170 mRNA
ATAATAGATCATCTTGTATATACTTCTGCAATTATAAGATGTTTTTTGATGATGAAAAAA NM_001282777 RefSeq chr2 + 112541914 112577152 POLR1B 84172 "polymerase (RNA) I polypeptide B, 128kDa, transcript variant 6"
GO:0005515|GO:0010467|GO:0017126|GO:0007566|GO:0009303|GO:0006363|GO:0005730|GO:0006362|GO:0032549|GO:0006361|GO:0006360|GO:0003677|GO:0046872|GO:0005737|GO:0005736|GO:0045814|GO:0001054|GO:0040029|GO:0005654. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139262_PI430048170 0.0209993970334773 0.41334959957775 5.1178652584541 4.39905622063672 4.58442970724539 P P P 5.90406190532917 6.02965246099303 6.08487643818648 P P P LNCV6_139262_PI430048170 mRNA
GCTGTTGTGATCTAGGGAAGTCAACACATAGTGTAAAATAATTACATGCCTAATGAAAAG NM_015054 RefSeq chr12 - 100037084 100142864 UHRF1BP1L 23074 "UHRF1 binding protein 1-like, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108248_PI430048170 0.497059377858532 0.970025735918006 0.423433849441157 0.435517476476583 0.267246071420052 A A A 0.389201319435832 0.458740008502248 0.415142722011094 A A A LNCV6_108248_PI430048170 mRNA
AACAGCCATGTGGACAACTGCACCGTGTACCTCTGTGAGGCTGAGGGTGGAGTCCATTTG NM_002458 RefSeq chr11 + 1223064 1262176 MUC5B 727897 "mucin 5B, oligomeric mucus/gel-forming"
GO:0005515|GO:0006493|GO:0005796|GO:0043030|GO:0016266|GO:0044267|GO:0005615|GO:0042742|GO:0070062|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69188_PI430048170 0.101799962916144 1.29486164868666 4.050491974967 4.00675146940009 3.88711726178584 P P P 3.37992858314265 3.54229094861777 3.86564337665598 P P P LNCV6_69188_PI430048170 mRNA
TTCAGGAGCCAATTACAGGATGGAGGAAGACTGTGTGCCACAACGGGGTGCTAGGCCTGA NM_153613 RefSeq chr15 - 34358887 34367194 LPCAT4 254531 lysophosphatidylcholine acyltransferase 4
GO:0047184|GO:0047166|GO:0005783|GO:0036148|GO:0044281|GO:0036150|GO:0047192|GO:0016020|GO:0071617|GO:0005789|GO:0019432|GO:0016021|GO:0006644|GO:0006654|GO:0036151|GO:0044255|GO:0046474|GO:0036152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128901_PI430048170 0.533650805927655 1.02058947938216 0.38823803955513 0.258431556353649 0.304237176333975 A A A 0.278381389286935 0.296708226060518 0.290565196402785 A A A LNCV6_128901_PI430048170 mRNA
GGGTGGTTAAAAAACCTCTTGACCCTAGATAGAATCCTATCTGAATTTTTCTGTTCTTTA NM_003221 RefSeq chr6 + 50818725 50847613 TFAP2B 7021 transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
GO:0005515|GO:0035137|GO:0035136|GO:0003700|GO:0006366|GO:0000983|GO:0000981|GO:0042803|GO:0043524|GO:0043525|GO:0097277|GO:0097276|GO:0097275|GO:0046983|GO:0045444|GO:0043027|GO:0001105|GO:0

046982|GO:0001106|GO:0072044|GO:0003714|GO:0003713|GO:0055062|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99619_PI430048170 0.0623385758099841.25605867632435 12.3797452671529 12.439672566606 12.1434609698831 P P P 12.0182075406664 12.0213748093212 11.9522213125853 P P P LNCV6_99619_PI430048170 mRNA ACATGGGCCCGGCTTTCCTGGATATCAGGACTTCCAATAAATAAAGACTCTGTATACTGG NM_032309RefSeq chr2 + 112584436 112589040 CHCHD5 84269 "coiled-coil-helix-coiled-coil-helix domain containing 5, transcript variant 1" GO:0033617|GO:0009060|GO:0005758 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130100_PI430048170 0.000249887888687017 0.418406072675059 0.293763213446947 0.553026047696075 0.41319038903309 A A A 1.56559563242965 1.67790177729175 1.79048659784739 A A A LNCV6_130100_PI430048170 mRNA CTCGGCAGTACTGTGAATTTTGAAGTTAAACTAAATTTTGGTACCATACCAACTGGAATT NM_182588RefSeq chr2 + 107826931 107892544 RGPD4 NA RANBP2-like and GRIP domain containing 4 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142444_PI430048170 0.963708862341836 1.42871248272898 3.70656738840236 2.56179376027193 0.257701437308345 P A A 2.40245064561858 2.09438173977746 2.18583309342311 A A A LNCV6_142444_PI430048170 mRNA AAACTTCCTCCTAGTGCAGCCCTATGCTTTAAAAACAGTTCCTGGTGGCCTTTCTGAAAG NM_015689RefSeq chr7 - 140518419 140602542 DENND2A 27147 DENN/MADD domain containing 2A GO:0017112|GO:0005737|GO:0042147|GO:0032851|GO:0015629|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141210_PI430048170 0.0147099204521337 0.183797717131843 0.255033476075421 0.267321640088055 0.326021057029548 A A A 3.10976244082609 2.10475850255734 2.79239131145747 P A P LNCV6_141210_PI430048170 mRNA CATGTTGCACCTAAAGCTTTGGAGTTTTCCTGTGATTAGTGTTTTTGGTGTTGTTTTATT NM_030641 RefSeq chr22 + 35648376 35668409 APOL6 80830 "apolipoprotein L, 6" GO:0005737|GO:0006869|GO:0042157|GO:0005576|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139392_PI430048170 0.026138498986917 2.52908899247567 12.9549059698952 13.3175713891066 13.2733905369927 P P P 11.2469563929078 11.9868979024848 12.1679558676845 P P P LNCV6_139392_PI430048170 mRNA CTGGCCCTCTAGCTTCTACCCTTTGTCCCTGTAGCCTATACAGTTTAGAATATTTATTTG NM_001878 RefSeq chr1 - 156699607 156705667 CRABP2 1382 "cellular retinoic acid binding protein 2, transcript variant 1" GO:0005215|GO:0006355|GO:0005783|GO:0016918|GO:0055085|GO:0019841|GO:0005829|GO:0007165|GO:0005737|GO:0008544|GO:0042573|GO:0001972|GO:0005501|GO:0005654|GO:0035115|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140235_PI430048170 0.766314929600753 1.27779890423867 1.49447253193604 2.54190090242204 0.394514507797181 A A A 2.11163553702792 0.828389216725002 0.760223927678274 A A A LNCV6_140235_PI430048170 mRNA ATCTTCTTTGATGACCAGATGTTCCATGTGGCTGGGGCTCAGGAGATGGGCACTGTGGCC NM_032526 RefSeq chr1 - 39659120 39672038 NT5C1A 84618 "5'-nucleotidase, cytosolic IA" GO:0000287|GO:0046085|GO:0055086|GO:0044281|GO:0005829|GO:0006195|GO:0046135|GO:0000166|GO:0006144|GO:0016311|GO:0008253|GO:0009116|GO:0009128|GO:0006206 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57427_PI430048170 0.492277234093386 1.38018588461962 1.62382816477628 0.294359959571937 1.72401441457052 A A A 0.282848031424163 1.62772378973475 0.272872227563791 A A A LNCV6_57427_PI430048170 mRNA AGAAGAGACCCCACATTCTACAAGCACAAATAGGAATGATGTCACAGGTGGAAGAAGAGA NM_000610 RefSeq

chr11 + 35138869 35232402 CD44 960 "CD44 molecule (Indian blood group), transcript variant 1"
GO:0005515|GO:0001658|GO:0005886|GO:0051216|GO:0005518|GO:0019221|GO:0050731|GO:0044281|GO:0050
900|GO:0016323|GO:0033138|GO:0005737|GO:0016337|GO:0005540|GO:0022617|GO:0030198|GO:0034116|GO:0
070374|GO:0043154|GO:0016055|GO:1900625|GO:0030203|GO:0070062|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130420_PI430048170 0.119514251845961 0.790380544205951 4.02108361297473
4.15576852352283 4.1959749659875 P P P 4.7188920238982 4.29647043929049
4.3431818060611 P P P LNCV6_130420_PI430048170 mRNA
GACCTAGAACCCTTTCCCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATT NM_005117 RefSeq
chr11 - 69698237 69704338 FGF19 9965 fibroblast growth factor 19
GO:0005515|GO:0008286|GO:0048011|GO:0008284|GO:0048015|GO:0001755|GO:0046330|GO:0005104|GO:0005
576|GO:0070858|GO:0007399|GO:0007507|GO:0007173|GO:0008543|GO:0046326|GO:0045087|GO:0010629|GO:0
001934|GO:0070374|GO:0008083|GO:0038095 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_145042_PI430048170 0.876476938740404 0.992321397935733 4.33749583719633
4.15827508216577 4.57279772904243 P P P 4.37302067999865 4.37222964115446
4.38673129261119 P P P LNCV6_145042_PI430048170 mRNA
GGGCCCTGGATGTTAGGATGGATTTCTGAATTAATAATAATAATAAAACCCTCATCAAGA NM_001229 RefSeq
chr1 - 15491400 15524445 CASP9 842 "caspase 9, apoptosis-related cysteine peptidase, transcript
variant alpha"
GO:0005515|GO:0017124|GO:2001020|GO:0005634|GO:0005829|GO:0005739|GO:0034644|GO:0043525|GO:0043
293|GO:0007173|GO:0006508|GO:0032496|GO:0032025|GO:0032355|GO:0046677|GO:0030220|GO:0034349|GO:0
048011|GO:0043065|GO:0008635|GO:0008630|GO:0019901|GO:0048015|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_93323_PI430048170 0.129581192896857 1.27731905728098 8.46115171706326
8.8803404402454 8.86102609434215 P P P 8.40054653939172 8.4039970671064
8.37597680610877 P P P LNCV6_93323_PI430048170 mRNA
AGGTTCAAGACAAATGTTGAACTAAAAACTTTACACTCCCCACCCCCACTTCAGACAGGT NM_018328 RefSeq
chr2 + 148021010 148513475 MBD5 55777 methyl-CpG binding domain protein 5
GO:0010369|GO:0003682|GO:0040014|GO:0060399|GO:0005634|GO:0042593|GO:0003677|GO:0070062|GO:0007
399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133820_PI430048170 0.0386917913005878 0.39936797047405 8.50475239507916
8.43920935605756 8.87433160449158 P P P 9.43428603344291 9.71652149074737
10.4722447294456 P P P LNCV6_133820_PI430048170 mRNA
TAGGCCCAGTCGTCATCAGATGCTTGCGGCAAAAGGAAAGCTGTGTTTATATGGAAGAAA NM_000104 RefSeq
chr2 - 38067602 38076181 CYP1B1 1545 "cytochrome P450, family 1, subfamily B, polypeptide 1"
GO:0033629|GO:0019369|GO:0006725|GO:0070301|GO:0006805|GO:0008285|GO:0048514|GO:0044281|GO:0006
809|GO:0005739|GO:0004497|GO:0042574|GO:0030199|GO:0042572|GO:0016712|GO:0007155|GO:0008202|GO:0
030336|GO:0046466|GO:0043065|GO:0070330|GO:0005506|GO:0019373|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133196_PI430048170 0.335864243598327 1.44167883323407 0.511329211362004
0.480081369264032 1.54617882912602 A A A 0.311101852496467 0.407734518500745
0.500432240715345 A A A LNCV6_133196_PI430048170 mRNA
TACGAGGAACAGGGTCCCTATATCGTGTACCGCAAATGCTACTGACCAGGGCAGAGCTGG NM_178525 RefSeq
chr19 - 8697396 8698830 ACTL9 284382 actin-like 9 GO:0005737|GO:0005856 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_143456_PI430048170 0.389738460134446 0.969286237223054 0.409316344046979
0.434542830905775 0.298787898165206 A A A 0.404044950118892 0.45800027997203
0.418659703295867 A A A LNCV6_143456_PI430048170 mRNA

GCTTCTACCTTTATTGCAGTTCCCCAAATCGCCTAATAAACTTTCCTCTTGCAAAGCAGA NM_002279 RefSeq chr17_GL383564v2_alt + 70460 76767 KRT33B 3884 "keratin 33B, type I" GO:0005882|GO:0042633|GO:0005198|GO:0007568|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127867_PI430048170 0.0225710986296703 5.43484813377615 3.35357545842794 3.53749750428573 3.74355661610372 P P P 1.82128462184765 0.750520469341629 0.339683576334747 A A A LNCV6_127867_PI430048170 mRNA
ATTACAAATGAGCCCGAATCATGACAGTCAGCAACATGATACCTGGATCCAGCCATTCCT NM_003332 RefSeq chr19 - 35904400 35908309 TYROBP 7305 "TYRO protein tyrosine kinase binding protein, transcript variant 1" GO:0005515|GO:0005886|GO:0009986|GO:2001204|GO:0005102|GO:0042802|GO:0035556|GO:0007165|GO:0006968|GO:0002281|GO:0005887|GO:0007229|GO:0007411|GO:0045087|GO:0050776|GO:0002283|GO:0005057 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144818_PI430048170 0.960885015287784 0.99324667842676 11.6276646664802 11.5171103913393 11.575295940917 P P P 11.8691723851922 11.2850863057347 11.5374445927282 P P P LNCV6_144818_PI430048170 mRNA
TTTATTTTTAATTTATCTCTGTGACCTGCCAGGGAGAGGGGAGAGAGAGAGAGATGCTGT NM_003204 RefSeq chr17 + 48048323 48061545 NFE2L1 4779 "nuclear factor, erythroid 2-like 1" GO:0003712|GO:0001190|GO:0003700|GO:0006366|GO:0001205|GO:0005634|GO:0009653|GO:0006783|GO:0006954|GO:0045944|GO:0030218|GO:0005789|GO:0000980|GO:0034599|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142155_PI430048170 0.949334911422516 0.930259788099383 12.1821164754165 12.2416064431413 12.3845518247888 P P P 13.094961610019 11.9163646137632 11.7033102570053 P P P LNCV6_142155_PI430048170 mRNA
GTGGCCTTGGTCTAACTTTTGTGTGAAATAATAAACAACATTGTCTGATAGTAGCTTGAA NM_002133 RefSeq chr22 + 35381066 35394214 HMOX1 3162 heme oxygenase (decycling) 1 GO:0031670|GO:0008219|GO:0042542|GO:0043627|GO:0005615|GO:0042803|GO:0006879|GO:0043524|GO:0051260|GO:0042167|GO:0043123|GO:0006979|GO:0032764|GO:0043305|GO:0014806|GO:0006788|GO:0043392|GO:0006778|GO:0010656|GO:0005789|GO:0019899|GO:0071243|GO:0020037|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137953_PI430048170 0.243462876700572 0.699806532729877 1.55334968922635 1.51937357195013 0.435994599265 A A A 1.87743022514034 1.68418647572745 1.73800223083899 A A A LNCV6_137953_PI430048170 mRNA
GCTTCTCTCTGTTCCTCTGTACAGTATTAATAGACAATAAACTGCCTTTTCACTGCATCT NM_053016 RefSeq chr9 + 109780296 109951476 PALM2 114299 "paralemmin 2, transcript variant 1" GO:0005886|GO:0008360 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126871_PI430048170 0.7258771028765840.9031068175152871.27611378203551 0.5987083683807090.46987972631851 A A A 1.42794642633664 0.488784739264681 0.846569936732193 A A A LNCV6_126871_PI430048170 mRNA
CGCATATATTGTAATTTTAATGTCTGCTTAGCACCCCACTGATAACCAAATCACAGTTTA NM_016388 RefSeq chr3 + 108822783 108854867 TRAT1 50852 T cell receptor associated transmembrane adaptor 1 GO:0050852|GO:0048011|GO:0005886|GO:0048015|GO:0050862|GO:0050850|GO:0007165|GO:0006968|GO:0007173|GO:0005887|GO:0008543|GO:0042101|GO:0045087|GO:0001920|GO:0005068|GO:0038095|GO:0051051 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138391_PI430048170 0.3328471160936341.23343992174579 0.311717333770587 0.5916559621807121.04823781345098 A A A 0.4565748790305490.351516146533632 0.32938549703254 A A A LNCV6_138391_PI430048170 mRNA
AAGGGAAAGAAATCCATGAATGGATACCTCTGTGTCCTAAGTGTTTGTAATAATGCTGTG NM_002725 RefSeq chr1 + 203475754 203491351 PRELP 5549 "proline/arginine-rich end leucine-rich repeat protein, transcript

variant 1"
GO:0005796|GO:0005975|GO:0007569|GO:0005578|GO:0005576|GO:0044281|GO:0031982|GO:0042339|GO:0031012|GO:0001501|GO:0018146|GO:0042340|GO:0009405|GO:0008201|GO:0030203|GO:0070062|GO:0043202|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143291_PI430048170 0.154373337445755 1.09745878075444 0.526522755037093
0.7200180706726920.606991721583647 A A A 0.3857308657127850.506529333412801
0.559867509454256 A A A LNCV6_143291_PI430048170 mRNA
CCCATTGGGACTGTTATGGCCATATTCTACAGTATAGTAAATTTTAAATTGGCCACATTT NM_001293725 RefSeq
chr18 + 26226882 26391686 TAF4B 6875 "TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa, transcript variant 1"
GO:0010467|GO:0006355|GO:0006368|GO:0003700|GO:0005669|GO:0006367|GO:0051059|GO:0048477|GO:0046982|GO:0006366|GO:0005730|GO:0007283|GO:0003677|GO:0005737|GO:0016032|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81221_PI430048170 0.00780664227968161 0.5527785578338 11.05191640413
10.7610440670292 10.9883150908272 P P P 12.0345284032365 11.6116806562769
11.7015071833409 P P P LNCV6_81221_PI430048170 mRNA
CCTCTGCATTTCTGGAATGTGTGTGCATCAATGATGTTTGTATATTTGAGGCATTTAAAA NM_030767 RefSeq chr9
- 114334153 114394405 AKNA 80709 AT-hook transcription factor
GO:0001077|GO:0016020|GO:0045944|GO:0005634|GO:0000978|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93728_PI430048170 0.667118142910782 0.932817882051448 2.29708363847518 2.06837874569514
3.10734294251801 A A P 2.5145688267044 2.56059484715058 2.88550313890004 A P P
LNCV6_93728_PI430048170 mRNA
ATCCACATATGTCGAAGCAAGACAGAAACCAAAGACCGTCCAGCATGGTCAGTGAAACATNM_175058 RefSeq chr11
- 16787659 17014416 PLEKHA7 144100 "pleckstrin homology domain containing, family A member 7"
GO:0090136|GO:0005915|GO:0005813|GO:0005737|GO:0030054|GO:0070097|GO:0005634|GO:0045218|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126924_PI430048170 0.669765823851072 1.06413703971127 9.32219534441714
9.32460762766306 9.54674963663944 P P P 8.77084005556802 9.49341620413334
9.54948563945549 P P P LNCV6_126924_PI430048170 mRNA
ATTGCAAAGTAAAGGATCTTTGAGTAGGTTCGGTCTGAAAGGTGTGGCCTTTATATTTGA NM_003255 RefSeq chr17
- 78852976 78925390 TIMP2 7077 TIMP metallopeptidase inhibitor 2
GO:0005515|GO:0051045|GO:0008285|GO:0002020|GO:0005615|GO:0046872|GO:0030426|GO:0046580|GO:0022617|GO:0030198|GO:0043025|GO:0009725|GO:0034097|GO:0070062|GO:0009986|GO:0071310|GO:0042493|GO:0007568|GO:0032487|GO:0005578|GO:0005576|GO:0045762|GO:0007417|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139830_PI430048170 0.786540307570343 0.954328175153667 0.46545578442599
0.882783497445816 0.317390056290259 A A A 0.408192469783446 0.515238943173286
0.947452089726118 A A A LNCV6_139830_PI430048170 mRNA
CTACCTGGCTAGAGTTTCTTCTCATCAGAGCACTGGGACATTAAACCAACCTTTTACAAC NM_000835 RefSeq chr17
- 74842022 74859884 GRIN2C 2905 "glutamate receptor, ionotropic, N-methyl D-aspartate 2C, transcript variant 1"
GO:0005515|GO:0030054|GO:0005886|GO:0017146|GO:0005234|GO:0007268|GO:0030425|GO:0008104|GO:0034220|GO:0004972|GO:0045211|GO:0006810|GO:0050885|GO:0005261|GO:0033058|GO:0042177|GO:0009611|GO:0035249|GO:0060079|GO:0014069|GO:0007215|GO:0030165|GO:0035235|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138243_PI430048170 0.5937697634647 1.03308694655204 11.5074071611351
11.7091149815509 11.5178532396679 P P P 11.4638627845213 11.5367184029225
11.5988190191022 P P P LNCV6_138243_PI430048170 mRNA

GAAGGTTCTGGCTCCACGGGTGAATCTGACTTTTCGTAAAATTTTGCTTACTAAAAAATA NM_001145374 RefSeq chr12 - 109088187 109093488 ALKBH2 121642 "alkB, alkylation repair homolog 2 (E. coli), transcript variant 1"
GO:0006307|GO:0006281|GO:0015630|GO:0080111|GO:0070989|GO:0043734|GO:0035511|GO:0005654|GO:0005634|GO:0051747|GO:0008198 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142019_PI430048170 0.6066966002874020.9380819257710843.49160249446701 2.95607920983893 3.35457752817123 P P P 3.38901810244923 3.51284913844507 3.21348884814993 P P P LNCV6_142019_PI430048170 mRNA
GGACATTTCATCTTTACTCTCAGTGAATTTACTGAACTTTTTGCACTAGACTGATGTTGT NM_197964 RefSeq chr7 + 139341131 139346319 C7orf55 154791 "chromosome 7 open reading frame 55, transcript variant 1"
GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129463_PI430048170 0.00421009603686091 0.7730855481578564.77049924947353 4.90921122676125 4.77632002513251 P P P 5.13468813791109 5.21773815570859 5.2201833430924 P P P LNCV6_129463_PI430048170 mRNA
AATTGTTTCAGATCATCTCATGCCTCAGGCTTTGGCAGGTATCCTGCCCTCCATCTTATT NM_001002814 RefSeq chr8 - 37858946 37899497 RAB11FIP1 80223 "RAB11 family interacting protein 1 (class I), transcript variant 3" GO:0045055|GO:0017137|GO:0005737|GO:0030670|GO:0055037|GO:0015031|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133548_PI430048170 0.6612109230406270.9922308210208570.302912171840704 0.3429633943025060.376087895362994A A A 0.3698159825213050.353410565455932 0.333190574603427A A A LNCV6_133548_PI430048170 mRNA
GTAAGTCTCAATTTCTCTACCTCCTTTACTTGGAGAAAATTTGTAAATGTACCCTGTGAA NM_003034 RefSeq chr12 - 22193390 22334714 ST8SIA1 6489 "ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1, transcript variant 1"
GO:0003828|GO:0008284|GO:0008373|GO:0005975|GO:0006688|GO:0034605|GO:0030173|GO:0000139|GO:0016021|GO:0006488|GO:0044267|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131812_PI430048170 0.99740456604016 0.9730627281567785.89847586974258 5.56380172744189 5.88206479586817 P P P 5.36136804255377 5.73547831090205 6.25048672193505 P P P LNCV6_131812_PI430048170 mRNA
CCTTTTAGACATTCGTCAGCCTCTTCTAATAAACCTTTGTACTATGTAAACATCAGGAAA NM_006216 RefSeq chr2 - 223975047 224039319 SERPINE2 5270 "serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2, transcript variant 1"
GO:0005515|GO:0030308|GO:0061108|GO:0008285|GO:0031594|GO:0004867|GO:0060291|GO:0045879|GO:0005539|GO:0005615|GO:0042628|GO:0005829|GO:0010766|GO:0031091|GO:0033363|GO:0008201|GO:0030334|GO:0051966|GO:0048505|GO:0042177|GO:0021683|GO:0090331|GO:0005102|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134374_PI430048170 0.0026386519662222 0.2209060894576366.93871404311131 6.56067162712429 6.89450229587441 P P P 8.57778272329225 8.96425195421707 9.32116296309667 P P P LNCV6_134374_PI430048170 mRNA
TGTGCTGAGTGAGCTCCTGTGTGCTTCAGACAAAAATAAATGAGACTTTGTGTTTACGTT NM_001242506 RefSeq chr9 + 72149350 72252224 GDA 9615 "guanine deaminase, transcript variant 3"
GO:0006147|GO:0005622|GO:0006195|GO:0006139|GO:0006144|GO:0008892|GO:0055086|GO:0008270|GO:0044281|GO:0070062|GO:0007399|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66759_PI430048170 0.0449627667303783 1.14266018849152 0.638595662352182 0.7567723892595150.781919055986287A A A 0.6319964047656080.475173102610062 0.491750159037929A A A LNCV6_66759_PI430048170 mRNA
TACTTCTCTTTCTTGTAATGAAACTCTTCACCTTTAGGAGACCTGGGCAGTCCTGTCAGG NM_006593 RefSeq chr2 + 161416108 161425062 TBR1 10716 "T-box, brain, 1"
GO:0003700|GO:0007420|GO:0007411|GO:0045944|GO:0010975|GO:0010092|GO:0005634|GO:0021902|GO:0030

902|GO:0000979|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69822_PI430048170 0.531566749031686 1.0900730678081 3.16940096753171 3.02072255803572
2.99268937640616 P P P 2.97538164570474 3.21480660782523 2.54875554424462 P P P
LNCV6_69822_PI430048170 mRNA
TCCATCTGCCTGAGCATCTACCAGGACCCGGTGAGCCTGGGCTGCGAGCATTACTTCTGC NM_018207 RefSeq chr1
- 33145401 33182070 TRIM62 55223 tripartite motif containing 62
GO:0051091|GO:0051092|GO:0016567|GO:0046596|GO:0045087|GO:0016874|GO:0019221|GO:0032897|GO:0008
270|GO:0043123|GO:0060333|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129058_PI430048170 0.704625749082433 0.943657631463884 8.87769553567794
8.87273530548547 9.20318084135131 P P P 8.87400872433054 8.95058816717699
9.35734764500124 P P P LNCV6_129058_PI430048170 mRNA
GATTTTTGTTTTGTTGGCTTTAAAGGTCTACCCCACTTTATCACATGTACAGATCACAAA NM_003507 RefSeq chr2
+ 202034586 202038437 FZD7 8324 frizzled class receptor 7
GO:0005515|GO:0017147|GO:0048103|GO:0005886|GO:0071300|GO:0038031|GO:0010812|GO:0046330|GO:0042
666|GO:0035412|GO:0005109|GO:0030182|GO:0034446|GO:0014834|GO:0060070|GO:0042813|GO:0060054|GO:0
006355|GO:0033077|GO:0004930|GO:0060231|GO:0030165|GO:0007186|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140803_PI430048170 0.0254285610907795 0.763094351868581 7.54533494088289
7.43848554186494 7.28870738051598 P P P 7.92820359801035 7.85924155871274
7.65270637203823 P P P LNCV6_140803_PI430048170 mRNA
CCCTGTAATTTTCCAAGGAAAATAAAGAACAGACTAACTAGTGTCTTTCACCCTGAAAAA NM_203500 RefSeq chr19
- 10486119 10503378 KEAP1 9817 "kelch-like ECH-associated protein 1, transcript variant 1"
GO:0005515|GO:0016567|GO:0005815|GO:0005783|GO:0032436|GO:0030496|GO:0001701|GO:0043433|GO:0006
351|GO:0005829|GO:0005737|GO:0031463|GO:0071353|GO:0005654|GO:0045604|GO:0008134|GO:0010499 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144537_PI430048170 0.220660932281218 1.26375173464612 5.29075920965632
5.31215168351443 5.28968620515522 P P P 5.3468405001948 4.74929496067139
4.68780704512778 P P P LNCV6_144537_PI430048170 mRNA
AAGCTGCTCCACCCCCAGATTGCAATGCTACCAATAAAGCCGCCTGGTGTTTACAACTAA NM_006274 RefSeq chr9
- 34689569 34691277 CCL19 6363 chemokine (C-C motif) ligand 19
GO:0051897|GO:0042346|GO:0048020|GO:0071731|GO:0031295|GO:0046330|GO:0032735|GO:0097029|GO:0005
615|GO:2000147|GO:0045807|GO:0006955|GO:0007154|GO:0006954|GO:0050921|GO:0043552|GO:0034695|GO:0
050718|GO:0072610|GO:0045860|GO:0043089|GO:0042102|GO:0060491|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_52017_PI430048170 0.549088964380553 0.886589664297749 3.40134305022876 2.94910283795645
2.4650177036159 P A A 2.87888790930746 3.15295367854333 3.40667917760034 P P P
LNCV6_52017_PI430048170 mRNA
TGTGTGTGAAGCCGGGCCTCTGTCGATGCAAGCCTGGATTCTTTGGGGCCCACTGCAGCT NM_003693 RefSeq
chr17_KI270861v1_alt - 63885 75817 SCARF1 8578 "scavenger receptor class F, member 1, transcript
variant 1"
GO:0006707|GO:0005886|GO:0030169|GO:0006898|GO:0016358|GO:0016322|GO:0030666|GO:0007165|GO:0048
680|GO:0010976|GO:0016021|GO:0007155|GO:0004888|GO:0005044 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_68715_PI430048170 0.775225347465571 0.979248146818236 6.26914734905671 6.13662260976241
6.03134733209727 P P P 6.05781274168349 6.30161160596944 6.16796758673354 P P P
LNCV6_68715_PI430048170 mRNA
ACAGAAGGATACCTTCAGCCAGCAGATCCTTCGCGAGCGAGTGAACAAGAGGCGGGTGAA NM_014652 RefSeq
chr1 + 43946805 43968022 IPO13 9670 importin 13
GO:0005515|GO:0005737|GO:0008536|GO:0005634|GO:0006606 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_142266_PI430048170 0.1579470539940311.09300371805792 10.4181372292323
10.5924444229752 10.4091617840216 P P P 10.3912229998129 10.3180738293526
10.3319992400168 P P P LNCV6_142266_PI430048170 mRNA
CAAGCCCTTCAGTGAGGGATGTGCCCAATAAACTCATCTGCTCCCAGCGAGTGACTGACA NM_032450RefSeq chr8
+ 144148015 144261940 MROH1 727957 "maestro heat-like repeat family member 1, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135355_PI430048170 0.0544067585494548 0.6946043863179268.07036150779692
8.18292076241274 7.77721980226152 P P P 8.24314819248949 8.72883557241755
8.62171338111633 P P P LNCV6_135355_PI430048170 mRNA
CAGAGATTCAGAGTAGGATCACATGAATAGGGGAAAAAAGAGAGTCTATTTTTGTCTAAT NM_015319RefSeq chr12
+ 53048948 53064378 TNS2 23371 "tensin 2, transcript variant 1"
GO:0005515|GO:0019725|GO:0008285|GO:0005886|GO:0001822|GO:0014850|GO:0046872|GO:0035556|GO:0048
871|GO:0035264|GO:0016311|GO:0032963|GO:0004721|GO:0005925 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_137807_PI430048170 0.0264049218856081 1.41533899173486 8.08998905734633
8.21286330470304 8.43696903918027 P P P 7.67491396487788 7.60878941040964
7.95105648879123 P P P LNCV6_137807_PI430048170 mRNA
GAAGCAGCAGTCCTCTATCTTAGTGTAACCCAAATGTGAAGCTTTTAAAACTTGACATTA NM_001145715 RefSeq
chr7 - 99173573 99207466 KPNA7 NA karyopherin alpha 7 (importin alpha 8) NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135627_PI430048170 0.2235445328235570.9653760156403150.414508293823615
0.4324268476566980.335000962082856A A A 0.4230400740221970.471334020698241
0.44151375673818 A A A LNCV6_135627_PI430048170 mRNA
GTACCATTGTCACTGCAATAAGTGGGTTTTAGAAAATAAGTGTGAAAAGAATCAGGTGTT NM_171998RefSeq chrX
- 155258233 155264589 RAB39B 116442 "RAB39B, member RAS oncogene family"
GO:0005515|GO:0043005|GO:0005794|GO:0005886|GO:0003924|GO:0005525|GO:0006886|GO:0031982|GO:0005
622|GO:0006184|GO:0031489|GO:0050808|GO:0032482|GO:0016192|GO:0019003 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_112398_PI430048170 0.0166994259595332 2.15001359406192 3.6501799347742
3.5272471991499 3.97272879750371 P P P 2.27179750762072 2.50590172450282
2.99911896571445 A P P LNCV6_112398_PI430048170 mRNA
TTGAGAGGAGACTTACTGAATATATTCATTGTTTGCAACCTGCTACTGGACGCTGGAGAA NM_153261RefSeq chr16
+ 50025205 50037088 CNEP1R1 255919 "CTD nuclear envelope phosphatase 1 regulatory subunit 1,
transcript variant 1"
GO:0007077|GO:0006629|GO:0005515|GO:0034504|GO:0031965|GO:0005737|GO:0010867|GO:0035307|GO:0071
595|GO:0016021|GO:0005635|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145007_PI430048170 0.7070965320130291.04669530956953 8.18113452854885 8.2854417537135
7.95793113522123 P P P 8.34339627358439 8.0694625674573 7.77816049014339 P P P
LNCV6_145007_PI430048170 mRNA
CTCTGGCAGGAGTGCCTGTACCCCACCAAGCCATGTGAATAAAATAATCTGGAAGTAGCC NM_020956RefSeq chr19
- 40393763 40413364 PRX57716 "periaxin, transcript variant 1"
GO:0005515|GO:0003674|GO:0005737|GO:0005886|GO:0005634|GO:0005575|GO:0008366 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135045_PI430048170 0.0434342433863495 0.6677366927530188.08012563185721
8.17436039140787 8.5232915560772 P P P 8.88948261816089 8.86895282862702 8.8045909212242
P P P LNCV6_135045_PI430048170 mRNA
AGATTTGCTTAAAGTGAGGTTTTTTGGTGTGTGCTTTTTTGTTGTCTTTTGACCCTTCCA NM_001302836 RefSeq chr16
+ 20900297 20925011 LYRM1 57149 "LYR motif containing 1, transcript variant 5"

GO:0005739|GO:0005654|GO:0045171 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142418_PI430048170 0.14851060610243 1.85144907703261 2.19678542914777
1.69969724202334 2.53832368854602 A A A 1.07480556700263 0.406277966874442
1.97694969937797 A A A LNCV6_142418_PI430048170 mRNA
TGAACAAGAAAATCCATCCTCTGGTAGGTTAGACTTTACACTGTGGTTTATAATATAAGC NM_031952 RefSeq chr5
- 95658315 95683010 SPATA9 83890 "spermatogenesis associated 9, transcript variant 1"
GO:0007275|GO:0016021|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145712_PI430048170 0.155128041189089 1.01300393161984 0.317359702519309
0.287221747193628 0.29953439877601 A A A 0.289971352445736 0.282504667987164
0.275845137019984 A A A LNCV6_145712_PI430048170 mRNA
CCTGGAATAGGTGTTGCGTATCAAATACAGATGAAGAAGGAAAAGAGAAACCAGAGATGG NM_016512 RefSeq
chr8_KI270813v1_alt - 133664 146780 SPAG11B 10407 "sperm associated antigen 11B, transcript
variant A" GO:0003674|GO:0005576|GO:0007283 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139748_PI430048170 0.252310217563942 0.833434077422688 6.88372751573329 6.7358782490478
6.56760702391087 P P P 7.21605319832401 7.04249021847317 6.68484168848734 P P P
LNCV6_139748_PI430048170 mRNA
CCTGCTATTCTCTCCCAAATTAATTATTAATAAGTGTTGTTCATTTACTGCACTGCTGAG NM_015097 RefSeq chr3 -
33496245 33718213 CLASP2 23122 "cytoplasmic linker associated protein 2, transcript variant 1"
GO:0005828|GO:0005802|GO:0005515|GO:0005881|GO:0005886|GO:0034453|GO:0036065|GO:0005829|GO:0005
737|GO:0051010|GO:0007411|GO:0008107|GO:0031023|GO:0005938|GO:0005794|GO:0005815|GO:0031110|GO:0
005874|GO:0032886|GO:0032587|GO:0007067|GO:0007163|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130112_PI430048170 0.0527089190802421 1.17886184088058 0.635748510610205
0.804292886574371 0.851365804054342 A A A 0.638034592251721 0.461002863116772
0.48243391114406 A A A LNCV6_130112_PI430048170 mRNA
CTCAAGACTTCAAATGCATGGAAGCACTCACACTTGGCAGAAACTCTATGAATGTAAGCA NM_152262 RefSeq chr19
+ 11866028 11869491 ZNF439 90594 zinc finger protein 439
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136864_PI430048170 0.300895211941132 1.3241200691765 0.404972494785558
1.14125522256619 0.332819125463688 A A A 0.252029843164139 0.311121853371029
0.245358729086641 A A A LNCV6_136864_PI430048170 mRNA
AAGCTTCCAAAACCTGTTTGTTCCAGTGGACACAGAGTAGGAAATGCTGACTCGTTCAGA NM_001007534 RefSeq
chr3 + 127193130 127198184 C3orf56 NA chromosome 3 open reading frame 56 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132355_PI430048170 0.239506818792164 1.25449419466811 1.13748800376526
0.608997490270874 0.554330166567629 A A A 0.563351127794076 0.409469326096156
0.415920699257307 A A A LNCV6_132355_PI430048170 mRNA
ATGCTGAAATGAGGAAGGCCATGAAGAGGCTGTGGATTAGGACATTGAGACTAAATGAGA NM_001004727
RefSeq chr11 + 48245103 48246015 OR4X2 119764 "olfactory receptor, family 4, subfamily X, member
2 (gene/pseudogene)"
GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55009_PI430048170 0.180686093868101 0.765466621344408 4.76555233794158 4.97133707859518
5.47340817068829 P P P 5.55366246688202 5.37178227718907 5.52923156954662 P P P
LNCV6_55009_PI430048170 mRNA
AAATAATCAACAGAAAACCCGTATTCTTCAGGGTGCTCTGGAACAGGGCTCAAATTCTCA NM_007348 RefSeq chr1
+ 161766243 161964070 ATF6 22926 activating transcription factor 6
GO:0005515|GO:0000977|GO:0003700|GO:0005794|GO:0006357|GO:0035497|GO:0006990|GO:0005783|GO:0003

713|GO:0006950|GO:0030176|GO:0005634|GO:0005635|GO:0006351|GO:0030968|GO:0007165|GO:0016020|GO:0000139|GO:0006457|GO:0005789|GO:0005654|GO:0006987|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140395_PI430048170 0.00938743138960182 1.33535615279831 8.71452721644386 8.50421014049946 8.5342851121298 P P P 8.15511235508456 8.24670719249282 8.10502350641015 P P P LNCV6_140395_PI430048170 mRNA TTTTCGTTTTTCATCTTTTGAAGAGCAAAGGGAAATCAAGAGGAGACCCCCAGGCAGAGG NM_139343 RefSeq chr2 - 127048022 127107327 BIN1 274 "bridging integrator 1, transcript variant 1"
GO:0071156|GO:0005515|GO:0030424|GO:0030018|GO:0008283|GO:0005634|GO:0015629|GO:0032403|GO:0042802|GO:0042692|GO:0045807|GO:0043194|GO:0005737|GO:0043196|GO:0016032|GO:0043679|GO:0070063|GO:0043065|GO:0046982|GO:0044300|GO:0048156|GO:0030315|GO:0008021|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135051_PI430048170 0.191694178530223 1.09272138487842 14.3643257428906 14.2272893999474 14.1689992778355 P P P 14.0194430460902 14.1414849205329 14.2161403144614 P P P LNCV6_135051_PI430048170 mRNA GCCTGCCATTCTGACCTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAAAAAA NM_019056 RefSeq chrX - 47142215 47145210 NDUFB11 54539 "NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa, transcript variant 1"
GO:0022904|GO:0005739|GO:0005747|GO:0005743|GO:0044281|GO:0016021|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134298_PI430048170 0.172279115457577 1.22503367664152 7.7051617789373 7.57596361029646 7.59239686142721 P P P 7.11844417419297 7.61402341927326 7.217084629488 P P P LNCV6_134298_PI430048170 mRNA AGGATGGAGTGTCTGTAAAATCAACAGGAAATAAAACTGTGTATGAGCCCAGGCAAGTTG NM_021948 RefSeq chr1 + 156641947 156659532 BCAN 63827 "brevican, transcript variant 1"
GO:0005796|GO:0005975|GO:0005578|GO:0005576|GO:0044281|GO:0031225|GO:0007417|GO:0030208|GO:0030207|GO:0021766|GO:0030206|GO:0001501|GO:0005540|GO:0022617|GO:0030198|GO:0009405|GO:0030246|GO:0030204|GO:0007155|GO:0030203|GO:0043202|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130591_PI430048170 0.525421225312656 1.09647862100563 9.95671330334666 9.86729691487531 9.4796164192594 P P P 9.79602213626434 9.68415847895321 9.44619749512293 P P P LNCV6_130591_PI430048170 mRNA ACCACTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTCAGAGGAATCGTGAAAAAA NM_017636 RefSeq chr19 + 49157758 49211841 TRPM4 54795 "transient receptor potential cation channel, subfamily M, member 4, transcript variant 1"
GO:0005516|GO:0005262|GO:0008284|GO:0005794|GO:0005886|GO:0005783|GO:0016925|GO:0090263|GO:0002407|GO:0002724|GO:0055085|GO:0005524|GO:0034220|GO:0042391|GO:0042310|GO:0070588|GO:0005654|GO:0005227|GO:0016021|GO:0061337 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138235_PI430048170 0.238979601552781 1.23566933881316 4.51169626239338 4.83176469510656 4.67802512947608 P P P 3.96327512314628 4.62502592755092 4.45618529327045 P P P LNCV6_138235_PI430048170 mRNA GGGATATTTTGTACATTTTCAACACAGAATAAAAAATGTACTGTGCCTTGCCTCTCTTGT NM_001146015 RefSeq chr14 - 55148115 55191678 DLGAP5 9787 "discs, large (Drosophila) homolog-associated protein 5, transcript variant 2"
GO:0005515|GO:0005737|GO:0005815|GO:0008283|GO:0016311|GO:0045842|GO:0007267|GO:0031616|GO:0005634|GO:0004721|GO:0007079 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135723_PI430048170 0.0303367611224564 3.23464219683465 3.03977409855933 1.85163185567784 2.93238979819121 A A A 0.632665134722607 1.60222065591398 0.517612324775256 A A A LNCV6_135723_PI430048170 mRNA

ATGCCTACTTCAAGGGTATGGCTTCTGCCTAATAAAGAATGTTCAGCTCAACTTCCTGAT NM_000519RefSeq chr11 - 5232828 5234628 HBD 3045 "hemoglobin, delta"
GO:0019825|GO:0005833|GO:0005506|GO:0007596|GO:0005344|GO:0072562|GO:0020037|GO:0015671|GO:0005829. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142962_PI430048170 0.9369984008152931.04565967841526 1.39746757156655
0.3170534178863630.337729300508658A A A 1.25824915421092 0.325553548817142
0.34950623733852 A A A LNCV6_142962_PI430048170 mRNA
TCTGATGTGCTTTGCACTCTGCTCTTGTAGATTTATTTTGTTTACAGTAGACTGATGTCA NM_017412RefSeq chr8 + 28494204 28574268 FZD3 7976 "frizzled class receptor 3, transcript variant 1"
GO:0005515|GO:0001736|GO:0017147|GO:0030424|GO:0005886|GO:0071679|GO:0030425|GO:0016324|GO:0005737|GO:0033278|GO:0030182|GO:0043025|GO:0060070|GO:0001942|GO:0042813|GO:0048786|GO:0042472|GO:0009986|GO:0004930|GO:0002052|GO:0001843|GO:0030165|GO:0016328|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135815_PI430048170 0.2066810695579491.07656184369796 8.16560188358376
7.96673701435412 8.04549566634956 P P P 7.98646886565244 7.95262128450849 7.9257909878519
P P P LNCV6_135815_PI430048170 mRNA
ATTTCTGAGCTGCTACCACATGACAGACACAAGGCTCAGATGAAGAGGTGAATTGAACAC NM_001199142 RefSeq chr16 + 28688557 28735729 EIF3C 8663 "eukaryotic translation initiation factor 3, subunit C, transcript variant 3"
GO:0005515|GO:0010467|GO:0005852|GO:0016282|GO:0033290|GO:0001731|GO:0003743|GO:0006412|GO:0006413|GO:0005829|GO:0006446|GO:0031369|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127544_PI430048170 0.0485887706480944 0.7111226602171137.62249029793313
7.3065399254775 7.77333298199954 P P P 7.88863316564648 8.06109131283018
8.24469015890393 P P P LNCV6_127544_PI430048170 mRNA
CATGTGCTGATGTTTACAATGATGCCGAACATTAGGAATTGTTTATACACAACTTTGCAA NM_001105RefSeq chr2 - 157736445 157875111 ACVR1 90 "activin A receptor, type I, transcript variant 1"
GO:0005515|GO:0003289|GO:0001655|GO:0001755|GO:0003183|GO:0046332|GO:0007281|GO:0042803|GO:0003143|GO:0004702|GO:0018107|GO:0007179|GO:0009968|GO:0023014|GO:0002526|GO:0001707|GO:0030501|GO:0032926|GO:0030509|GO:0032924|GO:0001701|GO:0001702|GO:0060923|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132230_PI430048170 0.00926748744680544 0.5359702196199610.2237725055228
9.72276846120677 9.9571354234557 P P P 10.8155639549683 10.7017706780116 11.099684662943
P P P LNCV6_132230_PI430048170 mRNA
GTCTGGTGTTGTAGCCATCTCAAGAACAAATCAACAGCAACAAAAGAGAAAGAATAAATT NM_012470RefSeq chr7 - 128954179 129055173 TNPO3 23534 "transportin 3, transcript variant 1"
GO:0005515|GO:0035048|GO:0005737|GO:0005634|GO:0004872|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131315_PI430048170 0.1115408220016661.25080730542048 9.12843905116146
9.19114453135635 9.04872303523839 P P P 8.53484632817148 8.94679513247236
8.88819249488713 P P P LNCV6_131315_PI430048170 mRNA
TTTCTAAAACTAAACTATTTTGGTACCTGCTTCTGGGCCAGTCCCCAGCCTGTCATGAGT NM_004140RefSeq chr17 + 18225621 18244874 LLGL1 3996 lethal giant larvae homolog 1 (Drosophila)
GO:0005515|GO:0030424|GO:0019901|GO:0032851|GO:0006893|GO:0007409|GO:0006887|GO:0032588|GO:0000137|GO:0005737|GO:0006461|GO:0000139|GO:0030866|GO:0005198|GO:0031901|GO:0035090|GO:0030864|GO:0005856|GO:0005097|GO:0035748 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128238_PI430048170 0.3401563344543540.92215818388925 8.7435830718668
8.67086169314555 8.46480050526568 P P P 8.72964951786682 8.87253329685012
8.63188610037418 P P P LNCV6_128238_PI430048170 mRNA
TGTGAAAGGCGCTGGGAACCGGCTTTGAATGAATAAATGAATCGTGTCATCTGCAAAAAA NM_003311RefSeq

chr11_KI270831v1_alt - 160387 161535 PHLDA2 7262 "pleckstrin homology-like domain, family A, member 2"
GO:0045995|GO:0030334|GO:0010468|GO:0005737|GO:0016020|GO:0009887|GO:0006915|GO:0001890|GO:0070873. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115721_PI430048170 0.0082101616333603 2.11887417048706 4.58275278459692 4.69344002849158 4.99500783821646 P P P 4.00148596176994 3.47194200025401 3.51836041459176 P P P LNCV6_115721_PI430048170 mRNA
CGGACGACGCGGCCTTCCGGGAGCGCGCGCGGTTGCTGGCCGCCCTCGAGCGCCGCCACT NM_178449RefSeq
chr19 - 49422413 49423441 PTH2 113091 parathyroid hormone 2 GO:0007218|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138853_PI430048170 0.430827967206515 0.900937741399828 12.8488310365274 12.544814788068 12.8488310365274 P P P 12.6469488060689 13.0925648458333 12.9403582906321 P P P LNCV6_138853_PI430048170 mRNA
TACTGCTCCCTAAGAAGACGGAGAGTCACCACAAGGCAAAGGGCAAGTGAGGCTGACGTC NM_003516RefSeq
chr1 + 149851060 149851594 HIST2H2AA3 NA "histone cluster 2, H2aa3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134871_PI430048170 0.0299727732677424 0.595783485533106 3.9825170835188 3.64215359403616 4.24072417970268 P P P 4.58657371220128 4.67848662032444 4.88682893737847 P P P LNCV6_134871_PI430048170 mRNA
GGCTTGTTTGTGTTACTGCATACTGTGATTAGCATAATAATTGTTTCTTTGAGGTCATCT NM_003069RefSeq chrX - 129446500 129523505 SMARCA1 6594 "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1, transcript variant 1"
GO:0005515|GO:0070615|GO:0043044|GO:0004386|GO:0031491|GO:0005634|GO:0003677|GO:0005524|GO:0006351|GO:0000733|GO:0007420|GO:0030182|GO:0006338|GO:0045893|GO:0016589|GO:0008094 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129649_PI430048170 0.252285222079656 0.858902229637989 0.252010298282485 0.284958481211357 0.326883196845226 A A A 0.40655299634864 0.326456371636215 0.753546062876091 A A A LNCV6_129649_PI430048170 mRNA
GGGTGAACCCTAGCCCCAGCTTTGGGAGGATGTTCAATAAAGGACCAATGCCGGAAAAAA NM_080431RefSeq
chr1 + 3021481 3022903 ACTRT2 140625 actin-related protein T2 GO:0005737|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139100_PI430048170 0.000696832516693271 1.43810842091196 11.1424888528335 11.2713710084172 11.2573332298369 P P P 10.6734700040914 10.7666539588342 10.6596197143065 P P P LNCV6_139100_PI430048170 mRNA
CTTCCTGGGTTTTCTCATTGTCTTTTTGCATCAGTACTTTGTATTGGGATATTAAAGAGA NM_005133RefSeq chr11 + 66843411 66846532 RCE1 9986 "Ras converting CAAX endopeptidase 1, transcript variant 1"
GO:0004197|GO:0016020|GO:0005887|GO:0006508|GO:0005789|GO:0071586|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118511_PI430048170 0.113915812469326 0.900273162327036 13.4526686780574 13.6554956913876 13.5754021559301 P P P 13.6805569537952 13.8029454344239 13.6576887533345 P P P LNCV6_118511_PI430048170 mRNA
TCGACCGCTCGCGTCGCATTTGGCCGCCTCCCTACCCTCCAAGCCCAGCCCTCAGCCATG NM_014624RefSeq chr1 - 153534599 153536241 S100A6 6277 S100 calcium binding protein A6
GO:0005515|GO:0048471|GO:0015075|GO:0005509|GO:0005634|GO:0048146|GO:0005635|GO:0007409|GO:0001726|GO:0042803|GO:0005829|GO:0031234|GO:0044548|GO:0007165|GO:0005737|GO:0034220|GO:0008270|GO:0005523|GO:0070062|GO:0048306 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102763_PI430048170 0.255773662412505 1.22916755590275 4.99328608899621 4.88647633615645 5.42494022253159 P P P 4.77125412924827 5.08019765281021 4.57231419313818 P P P LNCV6_102763_PI430048170 mRNA

TACCCCCAGGTTCCAGATGAGAAGGACTTAATGACTCAGCTGCGCCAGGTCCTTGAGTCC NM_002319 RefSeq chr7 - 100574010 100586188 LRCH4 NA "leucine-rich repeats and calponin homology (CH) domain containing 4, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127554_PI430048170 0.4545923517903730.79977651380412 0.354710961106214 0.3424995055836360.262130133791889 A A A 1.15451840232211 0.306662605451799 0.287798938039643 A A A LNCV6_127554_PI430048170 mRNA
ATAAAGAACCATGGCGCTGTGTGTTTAAAGATCTACATCATTCCTAATGAAATCCAATTC NM_001010939 RefSeq chr10 + 88586761 88606976 LIPJ NA "lipase, family member J" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142487_PI430048170 0.1086128726162390.9390036265392950.375259121430187 0.3538793509252710.321079733176434 A A A 0.4973470062445960.447130582207173 0.376081410831985 A A A LNCV6_142487_PI430048170 mRNA
TTTGTACCTCATAGCACTATGGGCAAAATAATTGCTCAATAAATGCTTAAGATCAGGGTA NM_001198986 RefSeq chr20 - 45536279 45547426 EPPIN-WFDC6 NA EPPIN-WFDC6 readthrough NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128870_PI430048170 0.1381291363477821.08767233598919 0.499978853333868 0.62619052782489 0.588943490068458 A A A 0.3528115659858530.462957973646254 0.532828109019253 A A A LNCV6_128870_PI430048170 mRNA
ATCTGTTAAACAGCTTCGTGTCTAGTATGAGCTCAGTACTTGCCCTGTGAAAATCCCAGA NM_016267 RefSeq chrX + 136532151 136556807 VGLL1 51442 vestigial-like family member 1
GO:0006355|GO:0003713|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139986_PI430048170 0.1366229654926810.7307154869553256.67315138647209 6.44605050985212 5.96945068446696 P P P 6.71254772649384 7.06187266199409 6.73121540219599 P P P LNCV6_139986_PI430048170 mRNA
ACAATAAATGATGTTTTTATGTGCCTCCCCTAAGAATAATTAGCACCGGGGCGGAAAAAA NM_018380 RefSeq chr16 - 68021273 68023867 DDX28 55794 DEAD (Asp-Glu-Ala-Asp) box polypeptide 28
GO:0042645|GO:0005739|GO:0005737|GO:0008152|GO:0005730|GO:0004386|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77299_PI430048170 0.2711557440871170.87850798015614 8.30487049956948 7.97770570378335 8.3517285078729 P P P 8.22301372520199 8.49639224083809 8.48717164464293 P P P LNCV6_77299_PI430048170 mRNA
CCCTTGGGAGAGCAGTTCCGAAAAGAAGTTCACATTAAGAATCTTCCCTCACTTTTCAAA NM_020750 RefSeq chr6 - 43522329 43576075 XPO5 57510 exportin 5
GO:0005515|GO:0010467|GO:0005737|GO:0000049|GO:0003723|GO:0008565|GO:0008536|GO:0006611|GO:0005654|GO:0031047|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142112_PI430048170 0.0831099201591009 3.07721200474553 4.25586639614932 4.33725414255744 4.31118714014876 P P P 3.55267801107527 2.13058508663458 1.63926728461116 P A A LNCV6_142112_PI430048170 mRNA
CTGTTCTCTGAAGATGTTTTGTGACCAGGTTTGTGTTTTCTTAAAATAAAATGCAGAGAC NM_001204406 RefSeq chr13 + 30713477 30764428 ALOX5AP 241 "arachidonate 5-lipoxygenase-activating protein, transcript variant 2"
GO:0005515|GO:0019369|GO:0019370|GO:0031965|GO:0050544|GO:0005783|GO:0019372|GO:0044281|GO:0005635|GO:0043085|GO:0004364|GO:0004464|GO:0006691|GO:0004602|GO:0070207|GO:0047485|GO:0016020|GO:0071277|GO:0005789|GO:2001300|GO:0016021|GO:0008047 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136857_PI430048170 0.00256662806697319 0.51300999438419 7.0855712468814 6.88794814748316 6.726489730622 P P P 7.94887510322867 7.9756490046837 7.66699560128357 P P P LNCV6_136857_PI430048170 mRNA
ACATTCTGCTCTGCTAAGTTTGGAGAAAACAGAACAATAAACCAGATGCAGGTGGTGCCC NM_001110514 RefSeq

chr20 + 2692877 2760108 EBF4 57593 early B-cell factor 4
GO:0006355|GO:0046983|GO:0007275|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140593_PI430048170 0.3541857746208011.40587547623972 1.78483254775009
2.33270907920445 2.17680938735415 A A A 0.375958199204692 1.68036801965254
2.24717797790471 A A A LNCV6_140593_PI430048170 mRNA
GGGAAGCTCCTGTTCCTCTTATTCCAATGTTCTTGGTTTTTCTTTATATAACTTGATGAA NM_019062 RefSeq chr1 -
19814028 19815278 RNF186 54546 ring finger protein 186 GO:0008270|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139535_PI430048170 0.2027633286803961.476223170161 3.12667843011304
4.09690135333908 3.4721502366544 P P P 3.19627518187299 3.18648957046995
2.75609782512562 P P P LNCV6_139535_PI430048170 mRNA
CTTGATACATACCCAAGCTGAACAATCTTCCCTTCCCTAAATAAATTATATGACTGCAAA NM_022360 RefSeq chr14
+ 20768426 20770948 EDDM3B 64184 epididymal protein 3B GO:0003674|GO:0005576 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_133604_PI430048170 0.0713343687698006 1.15815003492606 6.57058800774982
6.80089043287694 6.73159858126521 P P P 6.58008964324409 6.44657911809718
6.44635080714094 P P P LNCV6_133604_PI430048170 mRNA
TGAGTTTGAACTTGGAAGGAGAATGGCATTATCTATAGAGGCTGATGCAGGAGAGACCCA NM_020160 RefSeq chr19
- 47403117 47419528 MEIS3 56917 "Meis homeobox 3, transcript variant 1"
GO:0043565|GO:0051897|GO:0001077|GO:2001234|GO:0045944|GO:0003682|GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_69160_PI430048170 0.4893045605086030.9233901055964175.65984860756418 6.02038344611715
6.15616861549554 P P P 6.11131187871572 5.95961128929881 6.1480168124747 P P P
LNCV6_69160_PI430048170 mRNA
TACGTGACTTTTTTGAACGAACCATTCTGTGCAACAGCCTTGTGTGGAGTTGTGCTGTGA NM_013448 RefSeq chr14
- 34752730 34875647 BAZ1A 11177 "bromodomain adjacent to zinc finger domain, 1A, transcript
variant 1"
GO:0005515|GO:0006261|GO:0008623|GO:0006355|GO:0016590|GO:0008270|GO:0006338|GO:0000228|GO:0006
351|GO:0004402 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145358_PI430048170 0.9295389913797771.00239686019395 8.84715216505983 8.9443759054133
8.99653958426068 P P P 8.85970301334783 8.73906251453872 9.15126259236626 P P P
LNCV6_145358_PI430048170 mRNA
CAGGTTAGGACATCTAGGTTCCAATTCATTCACATTCTTGGTTCCAGATAAAATCAACTG NM_018050 RefSeq chr12
- 12329283 12350235 MANSC1 54682 MANSC domain containing 1 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135420_PI430048170 0.5005111908796331.176157073541 1.04245803563201
0.3574511484990160.306084667829489 A A A 0.438754156307575 0.341944467158637
0.343460052124552 A A A LNCV6_135420_PI430048170 mRNA
GCTATTGTAACCATGTTTTATTGCAAAGATGTAAAATATGCCAGATGTGTGTGAGTTGGA NM_015678 RefSeq chr13
+ 34942286 35672736 NBEA 26960 "neurobeachin, transcript variant 1"
GO:0005802|GO:0008104|GO:0005543|GO:0019901|GO:0005886|GO:0016197|GO:0019898|GO:0012505|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135064_PI430048170 0.0498828988397452 0.6634073385002336.30830814308845
5.75791118568895 6.21766397676446 P P P 6.52011586593772 6.67986479034851
6.89359693705039 P P P LNCV6_135064_PI430048170 mRNA
CCACGGACCCTGACATTGATAAAAAAGAAAGAAAAAAGATGGTCAAGGAAGCCCAGAGAG NM_031480 RefSeq
chr6 + 7389828 7418037 RIOK1 83732 "RIO kinase 1, transcript variant 1"
GO:0004674|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_90882_PI430048170 0.00364482411052624 0.2364076148569087.84800901245213
7.94708585712971 7.73848424550783 P P P 9.64716149213841 9.82933267908704
10.2410676434031 P P P LNCV6_90882_PI430048170 mRNA
TGTTTTATGCACCTCGTCTGAGAATCAATAAGCGGATTTTGGCCTTATGTATGGGAAACC NM_002906RefSeq chr11
- 110229440 110296712 RDX 5962 "radixin, transcript variant 3"
GO:0005515|GO:0005886|GO:0030033|GO:0045177|GO:0032420|GO:0030315|GO:0045176|GO:0003779|GO:0030
175|GO:0032154|GO:0001726|GO:0005615|GO:0030027|GO:0071944|GO:0051693|GO:0010628|GO:0051286|GO:0
005737|GO:0061028|GO:0005856|GO:0005925|GO:0070062|GO:0019898 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144793_PI430048170 0.0172068756850759 0.2522406629215864.10591968003215
3.2982049341068 4.56025109828667 P P P 5.70727868866016 6.15616861549554
6.27107760409912 P P P LNCV6_144793_PI430048170 mRNA
ATGTGAATCCTGTTTTAAAGTGCTCAGATTTCAACTGTGTAAGCCATTGATATAACGCTG NM_003615RefSeq chr3
- 27372720 27456754 SLC4A7 9497 "solute carrier family 4, sodium bicarbonate cotransporter, member
7, transcript variant 1"
GO:0005886|GO:0061299|GO:0032420|GO:0055085|GO:0060117|GO:0016323|GO:0016324|GO:0005452|GO:0005
887|GO:0046666|GO:0051453|GO:0015701|GO:0035725|GO:0016021|GO:0021747|GO:0008510|GO:0006811 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133200_PI430048170 0.0041968458358950.4913092743301431 1.6780054219673
11.4204500318055 11.3849315729018 P P P 12.2578304154068 12.6208749542026
12.6650791585832 P P P LNCV6_133200_PI430048170 mRNA
GGTGTGAGCCAGCTTGAGAACACTAACTACTCAATAAAAGCGAAGGTGGACATGAAAAAA NM_202002RefSeq
chr12 - 2857680 2877155 FOXM1 2305 "forkhead box M1, transcript variant 1"
GO:0071156|GO:0005515|GO:0008284|GO:0003700|GO:0006366|GO:0044212|GO:0000981|GO:0090344|GO:0046
578|GO:0001558|GO:0032873|GO:0005737|GO:0045944|GO:0000086|GO:0042127|GO:0051726|GO:0006978|GO:0
006355|GO:0019901|GO:0000122|GO:0003677|GO:0001889|GO:0043565|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127086_PI430048170 0.0252693714967053 0.4043233640683142.52184488025407
3.04871334253583 3.54736230068638 A P P 4.01931391191007 4.6530207381079
4.47318652947612 P P P LNCV6_127086_PI430048170 mRNA
GTAACTGATGCCTTTCATTTTGTTCAACTTATACAAAACAAGCCAGCATCTGATCAAAAG NM_021033RefSeq chr13
+ 97434220 97467998 RAP2A 5911 "RAP2A, member of RAS oncogene family"
GO:0005515|GO:0030336|GO:0005886|GO:0031532|GO:0032486|GO:0030033|GO:0003924|GO:0030496|GO:0005
525|GO:0072659|GO:0035690|GO:0045198|GO:0045184|GO:0005829|GO:0048814|GO:0046328|GO:0006184|GO:0
001934|GO:0034613|GO:0055037|GO:0055038|GO:0070062|GO:0031954 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_143384_PI430048170 0.3045834987128180.8024300585421770.307682931988166
0.3030362082371050.300617974104824A A A 1.00710051487248 0.401875991440701
0.360420185160854A A A LNCV6_143384_PI430048170 mRNA
CCTTCCCATAAAGCCTAGTTGTACATGAGTGACATTTTGTTTCACCTCTTAATAAAAATG NM_020643RefSeq chr11
- 8920075 8933006 C11orf16 56673 chromosome 11 open reading frame 16 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129678_PI430048170 0.0449901506154391 0.6012279786529489.3946271767633
9.31672600193246 9.90800649931102 P P P 9.99186322933643 10.2409222617251
10.5978447681466 P P P LNCV6_129678_PI430048170 mRNA
GAATCTGCTTTGTGTTGGGACGCTTTAATGTCAGGGTTTCACTAAATAAATGAATTTTCA NM_198887RefSeq chr6
- 149724315 149746572 NUP43 348995 "nucleoporin 43kDa, transcript variant 1"
GO:0007077|GO:0005515|GO:0010467|GO:0019221|GO:0019058|GO:0005635|GO:0044281|GO:0015031|GO:0008
645|GO:0005829|GO:0007059|GO:0015758|GO:0016032|GO:0005975|GO:0019083|GO:0055085|GO:0010827|GO:0

007067|GO:0031080|GO:0009405|GO:0000777|GO:0000776|GO:0051028|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145279_PI430048170 0.00350254164813289 0.1885970974977283.48151321562579 4.36812646539721 3.78809020634342 P P P 6.46516647594511 6.451435330437 6.0466984407038 P P P LNCV6_145279_PI430048170 mRNA AAAGAGCAAGATGGAGCAATGGAGAGAAGACCTCTTCCTGAATCACTGGACTCCAGAAAT NM_005518RefSeq chr1 - 119747995 119768932 HMGCS2 3158 "3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial), transcript variant 1"
GO:0005739|GO:0006695|GO:0004421|GO:0046951|GO:0005759|GO:0046950|GO:0005743|GO:0044281|GO:0008299|GO:0044255 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75907_PI430048170 0.0935770607601349 0.6999152114549373.83798275572456 4.07282168104772 4.45938964871654 P P P 4.70186654059306 4.67818029102014 4.60162699449296 P P P LNCV6_75907_PI430048170 mRNA CCTTTTGTTGTACACTGGCTAAACAATAAAGAACTGCATTTTACTTTGTCCATGGAAGTT NM_001290322 RefSeq chr5 + 119071086 119249129 DMXL1 1657 "Dmx-like 1, transcript variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135053_PI430048170 0.22413497983261 1.04940292221537 0.3570847866634 0.3594891226759610.478963179027837A A A 0.3229425682889860.306113276059514 0.360630033857848A A A LNCV6_135053_PI430048170 mRNA AGCCAGGTGGTTTGCTCTAAATCATTTGACTTTATTGTTTAGTGTGTAGTGGTGAAATCT NM_001001394 RefSeq chr2 - 233742749 233744015 DNAJB3414061 "DnaJ (Hsp40) homolog, subfamily B, member 3" GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138024_PI430048170 0.00410629884535454 0.7037694093229299.12447819250611 8.98025284617946 8.94128940505195 P P P 9.59070689528387 9.39484643332156 9.57921513399316 P P P LNCV6_138024_PI430048170 mRNA CATCATCCATATGTAACTTGTTTTGAAGAGAAGTGTTTCCGTTGTGTGTCTTGATGTAAA NM_015048RefSeq chr12 + 121804731 121832656 SETD1B 23067 SET domain containing 1B
GO:0005515|GO:0006355|GO:0005694|GO:0003723|GO:0006325|GO:0042800|GO:0006351|GO:0005737|GO:0035097|GO:0000166|GO:0016607|GO:0048188|GO:0005654|GO:0051568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143517_PI430048170 0.0130941882427485 0.7096395404766049.06864600248806 9.07117088905157 8.80519925273618 P P P 9.35422399587332 9.60139453077593 9.47919218870998 P P P LNCV6_143517_PI430048170 mRNA GTATATAATGATATCTATATTTTTGCCCAGGTCTGGGTATTGCTCCTGCCCAGACCCTGA NM_001978RefSeq chr8 + 22059144 22082527 DMTN 2039 "dematin actin binding protein, transcript variant 1"
GO:0035585|GO:0005515|GO:0048471|GO:0035584|GO:0030036|GO:0005886|GO:0090303|GO:0008360|GO:0005884|GO:0050732|GO:0010812|GO:0043621|GO:0015629|GO:0051895|GO:0005829|GO:0010591|GO:0051489|GO:0010763|GO:1900026|GO:0033137|GO:0048821|GO:0032956|GO:1900025|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145627_PI430048170 0.1519285980406050.7091214603629566.11605827066938 6.15134779202758 6.13650210165744 P P P 6.20654141626362 6.69500758345976 6.90444726736174 P P P LNCV6_145627_PI430048170 mRNA AGATGTTGCATTCAGACTATGAAAATAGCAAATAAAGCTTTGGTGCAAGTTGCATTGGAG NM_001145206 RefSeq chr22 + 25027973 25197448 KIAA1671 85379 KIAA1671 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94745_PI430048170 0.1060931360667690.8699117998423135.17526736274434 4.90780209087219 5.0539701795962 P P P 5.29708837197616 5.20783748741706 5.24628747756163 P P P LNCV6_94745_PI430048170 mRNA ATTTCGCTTCACCGAGTGACCTTGAGCCCAGGGCGACGGTCAGCTTGTTAATTCCTGGCT NM_138381RefSeq chr3

+ 16265159 16306087 OXNAD1 92106 oxidoreductase NAD-binding domain containing 1
GO:0005739|GO:0008150|GO:0003674|GO:0016491|GO:0005575|GO:0055114 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141466_PI430048170 0.1847314218164591.62662329588798 2.11729397975808
1.51464502927574 1.83857082904224 A A A 1.75218717249659 0.315150209694809
1.00710051487248 A A A LNCV6_141466_PI430048170 mRNA
CTCATAGGAAGTGAAGAGATCCTTCTGTAAAGGTTTTTGGAATTATGTCTGCTGAATAAT NM_001257118 RefSeq
chr11 - 105025509 105035157 CASP1 834 "caspase 1, apoptosis-related cysteine peptidase, transcript
variant 6"
GO:0097300|GO:0005515|GO:0035872|GO:0005829|GO:0005737|GO:0050717|GO:0050718|GO:0006508|GO:0032
496|GO:0033198|GO:0043123|GO:0072559|GO:0001666|GO:0006919|GO:0072557|GO:0071310|GO:0072558|GO:0
050727|GO:0097194|GO:0006915|GO:0005576|GO:0008656|GO:0070269|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128787_PI430048170 0.0194761780326112.28797594981645 4.25517376075651
4.11634701125619 4.873453709943 P P P 3.36586155084295 3.50169383956161
2.82820995554925 P P P LNCV6_128787_PI430048170 mRNA
TGCTTCGACAACAGGTGGAAGATCTTAAAAACAAGAATCTGCTGCTTCGAGCTCAGTTGC NM_007122RefSeq chr1
- 161039250 161045979 USF1 7391 "upstream transcription factor 1, transcript variant 1"
GO:0005515|GO:0006366|GO:0042826|GO:0003705|GO:0005634|GO:0045990|GO:0042803|GO:0003690|GO:0045
944|GO:0006006|GO:0000432|GO:0009411|GO:0005667|GO:0001666|GO:0032869|GO:0019086|GO:0006357|GO:0
019901|GO:0046982|GO:0055088|GO:0051918|GO:0043425|GO:0042593|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133335_PI430048170 0.5177219751260640.9575910534980940.537182237565255
0.5729706510457380.465395268309071A A A 0.5607323971226360.470543806324014
0.722518047990632A A A LNCV6_133335_PI430048170 mRNA
ACTAACCAATTCATCTTTGATGGAGCTTGAATCAAACTAAGGGTATTGGACTTTTGAAAG NM_032530RefSeq chr17
- 5179535 5191883 ZNF594 84622 zinc finger protein 594
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132936_PI430048170 0.13977369394276 0.9649224520573530.439816015871221
0.3793409344981010.398878787413246A A A 0.477972139066872 0.479454261636998
0.414879154808794A A A LNCV6_132936_PI430048170 mRNA
ACTGCATTAGAAATTAGCTGTGTGAAATACCAGTGTGGTTTGTGTTTGAGTTTTATTGAG NM_000450RefSeq chr1
- 169722639 169734079 SELE 6401 selectin E
GO:0005515|GO:0048471|GO:0019722|GO:0005886|GO:0007202|GO:0050900|GO:0050901|GO:0005615|GO:0006
954|GO:0070492|GO:0043274|GO:0007159|GO:0032496|GO:0033691|GO:0070555|GO:0007157|GO:0030029|GO:0
002523|GO:0050727|GO:0005905|GO:0007596|GO:0005901|GO:0002687|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144660_PI430048170 0.6730067084123850.9839086732829850.408415865356667
0.3804646900406010.245947526969301A A A 0.3449234996924020.393736245198132
0.371140815428231A A A LNCV6_144660_PI430048170 mRNA
GAGAGCCCTTCATGCATTTGCACTATTGGAAGGAGTTAGATGTTGGTACTAGATACTGAA NM_001781RefSeq chr12
- 9752485 9760901 CD69 969 CD69 molecule
GO:0007165|GO:0005887|GO:0005509|GO:0030246|GO:0035690|GO:0009897|GO:0004888 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141404_PI430048170 0.0664414294472132 0.57899044112614 3.33097479981364
3.30653781113587 3.38772105600544 P P P 4.42167752794663 4.17371803914662
3.70779606215007 P P P LNCV6_141404_PI430048170 mRNA
GTAATAGGGGGAAAATGTCAATTAGTAGCTTACCACAGATACTGTTTCCTACCATTTATA NM_017922RefSeq chr14

+ 45084098 45115601 PRPF39 55015 pre-mRNA processing factor 39
GO:0008380|GO:0006397|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140031_PI430048170 0.0509423962728127 1.24933476509428 11.5301180619276
11.519008458754 11.459474738317 P P P 11.019341570923 11.2993265206129
11.2133677375912 P P P LNCV6_140031_PI430048170 mRNA
TCCTCCCTCAGATCCCACCAGACCCACCAGGTGCCATAATAAAGCGGATTCTAGACGGAG NM_030573 RefSeq chr22
- 20999771 21002115 THAP7 80764 "THAP domain containing 7, transcript variant 1"
GO:0047485|GO:0016607|GO:0005694|GO:0070742|GO:0045892|GO:0003677|GO:0046872|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134898_PI430048170 0.756301828063091 1.14159871135614 1.29160404914399
1.53838883737918 0.319926323542498 A A A 1.11359060392911 0.319467896133031
1.24519605901837 A A A LNCV6_134898_PI430048170 mRNA
ATCAAGAGGAAGAGGCACTTGGATTTTCTGGACATCCTCCTCTTGGCCAAAATGGAGAAT NM_001010969 RefSeq
chr1 + 47137424 47148854 CYP4A22 NA "cytochrome P450, family 4, subfamily A, polypeptide 22"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145457_PI430048170 0.0599533359617036 0.590251672931058 6.27465682604563
6.40212934420852 6.9896528797332 P P P 7.33132125396052 7.25045223400515
7.46307732739339 P P P LNCV6_145457_PI430048170 mRNA
GTGGTACTTATTCTGTAAGTTCAGAGTATGCTGAGTGTTAATAGATTATCATATTGCCTG NM_019054 RefSeq chr10
+ 87095195 87191465 FAM35A 54537 "family with sequence similarity 35, member A" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_145360_PI430048170 0.911375477847187 1.00945621994913 14.1789301194394
14.2542474396853 14.4412944318373 P P P 14.2726849395025 14.1921001339976
14.3758490000394 P P P LNCV6_145360_PI430048170 mRNA
AAGGATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGCGGGACATG NM_033183 RefSeq chr19
- 49047637 49049111 CGB8 NA "chorionic gonadotropin, beta polypeptide 8" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126966_PI430048170 0.585911841734426 1.64414723562656 0.483638150958337
2.43071422584391 0.437332865001937 A A A 0.393704307978371 1.15087092719824
0.504941859374768 A A A LNCV6_126966_PI430048170 mRNA
AAGATCACTGTGCAAAAGGGAGAAGAGAAGACAGTGTACAACTTCTGTAGCGAAGACACA NM_006229 RefSeq
chr10 + 116590958 116609175 PNLIPRP1 5407 "pancreatic lipase-related protein 1, transcript variant
1" GO:0006629|GO:0004806|GO:0005509|GO:0005576|GO:0005615|GO:0016298 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_71067_PI430048170 0.0511917579064416 1.22242448760904 10.9077680934091
10.8679187228679 10.8473425412686 P P P 10.4604552137 10.7153670346512 10.567221393772 P
P P LNCV6_71067_PI430048170 mRNA
GGTTTGACTGGTTCTTCCTTGATCCTATTACAAGTAGTGGAATTAAATTTGCAAATGATG NM_001042472 RefSeq
chr20 - 25300197 25390982 ABHD12 26090 "abhydrolase domain containing 12, transcript variant
1" GO:0006660|GO:0010996|GO:0032281|GO:0047372|GO:0007628 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_53807_PI430048170 0.0332181660850124 1.35768126915324 4.83200911072967 4.8521393698122
4.65342465863671 P P P 4.54750196116945 4.23946614685641 4.21062537160612 P P P
LNCV6_53807_PI430048170 mRNA
AGAACCTGCAGGCTCAGGAAGAAGAGCGGGAGTTTTATAATGCCAGGCGACGGGAGCATC NM_024700 RefSeq
chr1 - 37534448 37554344 SNIP1 79753 Smad nuclear interacting protein 1
GO:0005515|GO:0006355|GO:0005737|GO:0035196|GO:0007249|GO:0005654 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_88310_PI430048170 0.00595150379286992 0.463032210141691 8.52217184315876

8.51309788300502 8.51931223249137 P P P 9.45424702111348 9.73260228899296
9.68510904464297 P P P LNCV6_88310_PI430048170 mRNA
GGGTTGTAGAGAACTCTTTGTAAGCAATAAAGTTTGGGGTGATGACAAATGTTTCCAGGC NM_003954 RefSeq chr17
- 45263118 45317064 MAP3K14 9020 mitogen-activated protein kinase kinase kinase 14
GO:0023014|GO:0005515|GO:0031295|GO:0007249|GO:0005524|GO:0038061|GO:0005829|GO:0000187|GO:0000
186|GO:0004704|GO:0006955|GO:0004672|GO:0004702|GO:0000165|GO:0006468|GO:0071260|GO:0043123|GO:0
004709|GO:0004708. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69274_PI430048170 0.0567745532642590.7473212012149223.34529230474338 3.66297469393298
3.7494573933947 P P P 3.81965677403588 4.13883972021234 4.07121334656249 P P P
LNCV6_69274_PI430048170 mRNA
ATTACTATACAGAAACTTCATCCCCGGAAGGGCAAATCAGTGCTGCAGATACGACTTACC NM_017950 RefSeq chr17
+ 80036631 80100613 CCDC40 55036 "coiled-coil domain containing 40, transcript variant 1"
GO:0060287|GO:0001947|GO:0005929|GO:0003674|GO:0003356|GO:0035469|GO:0005737|GO:0003351|GO:0071
910|GO:0030324|GO:0070286|GO:0071907 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137108_PI430048170 0.5817725231084611.40628233001258 0.410042185737355
0.3534012115304841.84911115844659 A A A 0.4785601145650620.760102544789926
0.409556581964324 A A A LNCV6_137108_PI430048170 mRNA
CCAGCGTGGCTGCTTTCAAGTTCTTTGCAATTAAAGGTTCTGTATAAAACCAAGAAAAAA NM_006001 RefSeq chr13
- 19173769 19181852 TUBA3C 7278 "tubulin, alpha 3c"
GO:0005515|GO:0051258|GO:0005874|GO:0003924|GO:0005634|GO:0005525|GO:0006184|GO:0005737|GO:0006
457|GO:0005200|GO:0051084|GO:0007017|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135009_PI430048170 0.0178043587625734 0.5461610670148597.23585835008858
7.23855966944678 7.27366585182283 P P P 7.87497130969809 8.20772792374727
8.25462167716571 P P P LNCV6_135009_PI430048170 mRNA
CGGTATTTGTTGGTTGGCTGTTAGCTTTGCTTTATGATTTCATGTTTCTTTTAAAGGTTG NM_015264 RefSeq chr22 -
45192241 45212466 KIAA0930 23313 "KIAA0930, transcript variant 1" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145256_PI430048170 0.1101496415201810.8731622939615291 0.5862992232478
10.7872561394402 10.8222008821425 P P P 10.9316911816506 10.9113838729731
10.9505042584787 P P P LNCV6_145256_PI430048170 mRNA
TCTCTGAGACCTCTTAAGTTCTAAGATTAAATGCCCCTCGCTGTTCTTCCTCTGAAAAAA NM_004899 RefSeq chr2
+ 27890614 28338900 BRE 9577 "brain and reproductive organ-expressed (TNFRSF1A modulator),
transcript variant 1"
GO:0005515|GO:0005164|GO:0000268|GO:0031572|GO:0006915|GO:0005634|GO:0045739|GO:0000152|GO:0006
974|GO:0006302|GO:0070531|GO:0007165|GO:0005737|GO:0070552|GO:0010212|GO:0031593|GO:0016568 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107231_PI430048170 0.4046175632451851.08135098238711 0.473392962696838
0.7523027283228860.430819069521003 A A A 0.4473169927627260.438812163807539
0.453411694288146 A A A LNCV6_107231_PI430048170 mRNA
GAAGGAACCTGGATGACTCCTATTCCTTTCATTATTGCTTTGAAAGAAGCTGGACTGAAT NM_001082972 RefSeq
chr12 - 25108288 25195160 CASC1 55259 "cancer susceptibility candidate 1, transcript variant 3"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130013_PI430048170 0.0581851491154427 0.4497750638751152.157922375898
1.97470336760699 3.1439025009414 A A P 3.16684632049547 3.81370663936041
3.93268342620568 P P P LNCV6_130013_PI430048170 mRNA
TTCTTGCACGATGGAAATTACTAGAGAAGTGGGATAATTCTTTGTTGTGGGGAAAATAAA NM_001039547 RefSeq
chr3 - 142157526 142225607 GK5 256356 "glycerol kinase 5 (putative), transcript variant 1"
GO:0016310|GO:0019563|GO:0004370|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132786_PI430048170 0.9937601962304661.00779870261229 5.37375207746298

4.80485586594001 5.15463680742062 P P P 5.2946412711592 5.01141430902552
5.03199104954396 P P P LNCV6_132786_PI430048170 mRNA
TCGTTGGCTCCAAAACCAGGGAGCAGACCATGCCCTCCCAACCCTGGAGTTGTCAGGGAG NM_020982 RefSeq chr16
+ 3012455 3014505 CLDN9 9080 claudin 9
GO:0016338|GO:0070830|GO:0005886|GO:0005198|GO:0034329|GO:0016032|GO:0016021|GO:0005923|GO:0045
216|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142730_PI430048170 0.112619639389071 0.483890250010813 0.331131740637926
1.22020002391752 1.90638460182475 A A A 2.17253999946822 2.15271501400045
2.63381293346221 A A P LNCV6_142730_PI430048170 mRNA
TGGAAAAACCTTCAGATCTACCTCACACCTTCGAAAACATGGTAGGACTCACACTGGATA NM_001012753 RefSeq
chr19 + 11965053 11980383 ZNF763 NA zinc finger protein 763 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136226_PI430048170 0.0534607628506651 0.626745613143415 10.0211154079491
10.165373695377 10.6225883058255 P P P 10.6573985474539 10.9327110698445
11.2502702862632 P P P LNCV6_136226_PI430048170 mRNA
GTACTGGCAAATGGTGGTATTCAGTGTGGGATAGTGTCATAACTAATTTGACAATTTATT NM_013438 RefSeq chr9
- 83659962 83708253 UBQLN1 29979 "ubiquilin 1, transcript variant 1"
GO:0005515|GO:0043234|GO:0048471|GO:0034976|GO:0005737|GO:0000502|GO:0005783|GO:0019904|GO:0071
456|GO:0031396|GO:0005654|GO:0019900 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127486_PI430048170 0.421909512991121 1.87063039153772 0.961901469374771
2.17820460227894 3.3014514425437 A A P 2.13356949860019 1.49258438940004
0.612827892439281 A A A LNCV6_127486_PI430048170 mRNA
AAGAAAGTAGCAGGTATTGGTCTTTCCTGTGGTCCCTGATGATCTATCCACTTGACCTCT NM_152554 RefSeq - -
0 0 --- NA chromosome 6 open reading frame 195 NA . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_99282_PI430048170 0.297373706428578 1.10690836456976 7.7997548860321 8.03096447181018
8.07824155720489 P P P 7.90185140807706 7.64880802803994 7.91831168850584 P P P
LNCV6_99282_PI430048170 mRNA
TAAAACAAGAACCACAGAAGGTTAAGGTGAGCTCATCGATTCAGCACCCAGAAACACCTC NM_014062 RefSeq chr16
- 69741853 69754968 NOB1 28987 "NIN1/RPN12 binding protein 1 homolog (S. cerevisiae), transcript
variant 1" GO:0005634|GO:0007601|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127186_PI430048170 0.533869297306355 0.882214533917311 0.564912870703822
0.615353358475804 0.552352476697696 A A A 0.588398432128653 0.469395967026861
1.12923267287963 A A A LNCV6_127186_PI430048170 mRNA
CCACAGCTCCTATAGGCATTTTAGAGATCTTGGATTTTTATGTACAGTCTTAGTCATTTT NM_001278182 RefSeq
chr3 - 27715948 27722715 EOMES 8320 "eomesodermin, transcript variant 1"
GO:0001191|GO:0003700|GO:0045597|GO:0005634|GO:0035914|GO:0001714|GO:0021796|GO:0021772|GO:0045
944|GO:0002302|GO:0032609|GO:0021895|GO:0001102|GO:0001706|GO:0001707|GO:0000977|GO:0060706|GO:0
000122|GO:0060809|GO:0001829|GO:0003677|GO:0006351|GO:0043565|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137427_PI430048170 0.439171175046904 1.04192407789905 0.285614212871048
0.295687128116986 0.468144837903236 A A A 0.310774628272502 0.27650452674362
0.291604167011186 A A A LNCV6_137427_PI430048170 mRNA
GCACCGTATTGCATAAAATAGAAGGCTTCCGTGATGAAAATACCAGTGAAAAGATTTTTT NM_001098486 RefSeq
chr6 - 25845099 25874243 SLC17A3 10786 "solute carrier family 17 (organic anion transporter),
member 3, transcript variant 1"
GO:0019534|GO:0048471|GO:0015562|GO:0005886|GO:0035435|GO:0015760|GO:0031526|GO:0046415|GO:0005
737|GO:0016324|GO:0044070|GO:0034220|GO:0006855|GO:0015711|GO:0006817|GO:0008514|GO:0035725|GO:0
006814|GO:0015893|GO:0008308|GO:0055085|GO:0015143|GO:0005436|GO . NA - . NA NA NA

NA NA NA NA NA NA
LNCV6_137639_PI430048170 0.232840137808721 1.01287192806302 0.320792901412065
0.3351321913195 0.354710208955705 A A A 0.330031686741633 0.323751105456285
0.301543223787991 A A A LNCV6_137639_PI430048170 mRNA
CTGTCTCGATGCAATGAACACTTAATAAAAAACAGTCGATTGGTCAATTGATTGAGCAAT NM_017460 RefSeq
chr7 - 99756959 99784188 CYP3A4 1576 "cytochrome P450, family 3, subfamily A, polypeptide 4,
transcript variant 1"
GO:0006629|GO:0006706|GO:0034875|GO:0006805|GO:0017144|GO:0030343|GO:0070989|GO:0044281|GO:0050
649|GO:0047638|GO:0043231|GO:0004497|GO:0005737|GO:0009822|GO:0070576|GO:0016712|GO:0005496|GO:0
008202|GO:0046483|GO:0005506|GO:0042359|GO:0008395|GO:0008209|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_91340_PI430048170 0.303464974082174 0.899055478103087 10.2347341195584
10.2285320666483 10.3948236804841 P P P 10.2990409537888 10.3593928682567
10.642646674404 P P P LNCV6_91340_PI430048170 mRNA
GACCAGATACAGAATGCACAGTATTTGCTGCAGAACAGTGTGAAGCAGTATGCAGATGTT NM_002140 RefSeq
chr9 - 83968082 83980654 HNRNPK 3190 "heterogeneous nuclear ribonucleoprotein K, transcript
variant 1"
GO:0005515|GO:0008380|GO:0010467|GO:0000790|GO:0003723|GO:0002102|GO:0005634|GO:0042995|GO:0071
013|GO:0005737|GO:0003697|GO:0045944|GO:0016032|GO:0010988|GO:0072369|GO:0070062|GO:0006396|GO:0
045716|GO:0000978|GO:0006351|GO:0007165|GO:0001077|GO:0016020|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138612_PI430048170 0.529407988026402 0.972031594613945 0.42344406895688
0.422456206379628 0.256820560294875 A A A 0.378444295914172 0.446952437978037
0.405565476559425 A A A LNCV6_138612_PI430048170 mRNA
GGGCCAAGTCAAAGACATTCTGACATCTTAGTATTTGCATATTCTTATGTATGTGAAAGT NM_000579 RefSeq
chr3 + 46370141 46376206 CCR5 1234 "chemokine (C-C motif) receptor 5 (gene/pseudogene),
transcript variant A"
GO:0071791|GO:0005515|GO:0019722|GO:0005886|GO:0030260|GO:0007267|GO:0007204|GO:0019957|GO:0005
737|GO:0006955|GO:0006954|GO:0006935|GO:0000165|GO:0004950|GO:0016032|GO:0006816|GO:0070098|GO:0
009986|GO:0023052|GO:0002407|GO:0003779|GO:0014808|GO:0015026|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_54861_PI430048170 0.163570513609715 1.12860087129637 10.9968642981084
11.0010134518727 11.2217271751032 P P P 10.9218489933387 11.0074389393909
10.7682746282629 P P P LNCV6_54861_PI430048170 mRNA
GAGTGACAGTTCATTCAATTTCTTCGTTTTCTTCTTCATTTTCTTCGTCCAGGATGTGCT NM_005698 RefSeq
chr1_GL383519v1_alt - 61001 67408 SCAMP3 10067 "secretory carrier membrane protein 3, transcript
variant 1" GO:0000139|GO:0006892|GO:0032526|GO:0016021|GO:0015031|GO:0031625|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_101947_PI430048170 0.153408664198548 0.792698395084495 4.50386240768466
4.94285211121045 5.03040759330485 P P P 5.09519902326881 5.13646976850197
5.29618842184757 P P P LNCV6_101947_PI430048170 mRNA
AAAGTAGACGGACTGCCAAAGACCTTTGGGAAGTTGTTGTTCAAATCTGTAGTGTGTCCA NM_017864 RefSeq
chr8 + 94823289 94880493 INTS8 55656 "integrator complex subunit 8, transcript variant 1"
GO:0005515|GO:0032039|GO:0016180 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_138870_PI430048170 0.0302106648947891 0.657594816137839 5.96006960388686
5.73987154450352 5.98842679618497 P P P 6.50853035915841 6.24449941591744
6.7226775177157 P P P LNCV6_138870_PI430048170 mRNA
CAACCTGCACAGATCCTGAACAACAAATGAATAACGATGAATGTCTTTTTGGTTGTAATT NM_181789 RefSeq

chr15 + 51341515 51408012 GLDN 342035 gliomedin
GO:0005581|GO:0045162|GO:0005886|GO:0032528|GO:0034113|GO:0016021|GO:0005615|GO:0086080 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_138295_PI430048170 0.000290102028577434 0.433249825611545 8.93242329025261
8.77157156102468 8.95773345739439 P P P 10.1243349424276 10.0313246815308
10.1310923139382 P P P LNCV6_138295_PI430048170 mRNA
GTGAGTCCGCTTGATGAATTCTAATGCTTTGCTTAGAGCTATGAGAAATGTTTGTTTTAA NM_001199729 RefSeq
chr8 + 10095551 10428891 MSRA 4482 "methionine sulfoxide reductase A, transcript variant 4"
GO:0005739|GO:0005737|GO:0008113|GO:0016020|GO:0030091|GO:0006555|GO:0005654|GO:0015629|GO:0006
979|GO:0006464|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_105578_PI430048170 0.759352034428394 1.03628532367413 2.78804710888718
2.83602614367512 3.07003098549843 A A P 2.98119769153729 3.04222705106103
2.46608147673742 P P P LNCV6_105578_PI430048170 mRNA
ATAACTCAGTTTTAGCCTGTGGAGCCCAGGCCTCTTGGAGCATCTTTGGGGCTGACGCAG NM_130385 RefSeq
chr11 - 10573090 10693988 MRVI1 10335 "murine retrovirus integration site 1 homolog, transcript
variant 2"
GO:0005515|GO:0048471|GO:0016529|GO:0007596|GO:0005789|GO:0019934|GO:0016021|GO:0031095|GO:0060
087 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143542_PI430048170 0.207295507626666 0.605353044734436 5.02550407593956
6.52168109753458 6.32617013825533 P P P 6.94948647274592 6.88615887663781
6.588618977358 P P P LNCV6_143542_PI430048170 mRNA
AGCCCTCTTCCTTGTGCCTTATCAAACAGGACAAATACGTTCTGTTTTATGTCTTGAATT NM_001206627 RefSeq
chr11 - 89911471 89917710 TRIM49D1 NA tripartite motif containing 49D1 NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_129032_PI430048170 0.321006238975561 0.923290402929793 0.524320990296252
0.567939003739941 0.490583821437379 A A A 0.568938309432293 0.806476396843041
0.538734151570846 A A A LNCV6_129032_PI430048170 mRNA
GTCACCATCATCTTTTGCAATGTGTTGCTCACTGTTGTCAATAAACTAATTTTTCCTGGC NM_033184 RefSeq
chr17_JH159146v1_alt - 214613 215377 KRTAP2-4 85294 keratin associated protein 2-4 GO:0045095
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139929_PI430048170 0.186566375304568 0.331298777997548 0.379741274035034
0.361781457758248 0.259323714985919 A A A 2.20024004648867 2.47752195536155
0.326366415850548 A P A LNCV6_139929_PI430048170 mRNA
TGGGAGGCACTCATGGCTCTCTGGGTCTAATGAATAAAGTCCTCCACAGCCTAGAAAAAA NM_001145304 RefSeq
chr19 - 18257095 18274509 KIAA1683 80726 "KIAA1683, transcript variant 1"
GO:0005739|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143472_PI430048170 0.180474541588185 0.432026945159377 0.317514204863116
0.354099107529692 0.363942364585894 A A A 1.99484235407424 0.360970071889381
1.82859252170738 A A A LNCV6_143472_PI430048170 mRNA
CAGCGACTAACTGGCAAGGCACTCAAAACATGTCATTCATTAAATGTTGTTTTTATTTAC NM_001244072 RefSeq
chr7 - 150625375 150632648 GIMAP6 474344 "GTPase, IMAP family member 6, transcript variant 2"
GO:0005525|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132906_PI430048170 0.161470830753067 1.26681516827202 0.775548145050701
0.486009626935023 1.03089480112218 A A A 0.533097324815237 0.474155308024798
0.302959963368175 A A A LNCV6_132906_PI430048170 mRNA
GGAAACAGTCTTAAAATTGGAGAAAATTTCCACATTTTAGGAAAAACAGCTTTCCCCCTG NM_014695 RefSeq
chr17 + 16690324 16774999 CCDC144A 9720 "coiled-coil domain containing 144A, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_140003_PI430048170 0.00700224749589509 1.57158548673191 10.750584035123 10.992243131359 1 11.0667821097988 P P P 10.3006770444124 10.165373695377 10.39621319545 P P P LNCV6_140003_PI430048170 mRNA GTGTATGGATCTGTGGTCATTGTCCCTCTGCAGAATAAAGATTGCTCAGGCCTGCCTGGC NM_032514 RefSeq chr20 + 34558696 34560345 MAP1LC3A 84557 "microtubule-associated protein 1 light chain 3 alpha, transcript variant 1" GO:0005515|GO:0006995|GO:0008017|GO:0005776|GO:0000422|GO:0005770|GO:0008429|GO:0000421|GO:0005874|GO:0050811|GO:0031410|GO:0000407|GO:0005829|GO:0005543|GO:0031090|GO:0061025|GO:0000045|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58895_PI430048170 0.000837656032350705 0.305953883270221 9.64082072419571 9.31589385673727 9.74743394900234 P P P 11.1275051743286 11.1483923695474 11.5481760182213 P P P LNCV6_58895_PI430048170 mRNA CACAGAGAATCATGTGTACCTAACTAAGGATGATCTAGGATAAGTAACTCCTGTTTTATA NM_001278387 RefSeq chr12 - 46183055 46269425 SLC38A1 81539 "solute carrier family 38, member 1, transcript variant 3" GO:0005886|GO:0005283|GO:0006865|GO:0007268|GO:0003333|GO:0055085|GO:0015804|GO:0005887|GO:0001504|GO:0015175|GO:0016021|GO:0006814|GO:0070062|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133603_PI430048170 0.00593447191213726 1.56253628207567 12.3095686272869 12.374153951825 12.601796860042 P P P 11.9385146749093 11.6675085391272 11.7509202068794 P P P LNCV6_133603_PI430048170 mRNA CAGTGATACTTGTGTAGGGGTACATGTACTTTATTTGTCAATAAACGTATCTGTACACTG NM_001040011 RefSeq chr9 + 128276145 128288989 SWI5 375757 SWI5 recombination repair homolog (yeast) GO:0005515|GO:0032798|GO:0000724|GO:0005634|GO:0071479 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140895_PI430048170 0.106644721860027 0.460748812392535 0.254179576508094 0.293864737918197 0.976624409386311 A A A 2.32699161817334 0.9714286549051 1.34588750455982 A A A LNCV6_140895_PI430048170 mRNA GCTTTCAATTTGCTTAGAAGGCAATATTAGAAGGTTAGAGTTCAGCAGAAAGAGAGAATT NM_001164465 RefSeq chr15_KI270850v1_alt - 128985 138553 GOLGA6L10 647042 golgin A6 family-like 10 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119419_PI430048170 0.494413268581001 0.867395248890404 0.304986400620445 0.283964726653974 0.351882040971388 A A A 0.906446305371023 0.277782894689758 0.278006699894398 A A A LNCV6_119419_PI430048170 mRNA AGAAAAGCTTCGTGGACTCGACCAGAGAAGCAAGAGCTCTGGATGGGCACATGGTGGTGC NM_001242607 RefSeq chr11 + 112961246 113278436 NCAM1 4684 "neural cell adhesion molecule 1, transcript variant 5" GO:0005886|GO:0009986|GO:0019221|GO:0031225|GO:0042802|GO:0000139|GO:0016020|GO:0007411|GO:0030198|GO:0016021|GO:0007155|GO:0009897|GO:0070062|GO:0060333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145421_PI430048170 0.00176877076158935 0.712482403168659 11.4509708143972 11.3788524240361 11.3128445812031 P P P 11.8447187739741 11.9099250141671 11.8577264670721 P P P LNCV6_145421_PI430048170 mRNA GGGCTGTGTACAGAGTGCAAATGTTTATTTAAAATAAAGTTCTATTTATCCCTTGTGACC NM_014966RefSeq chr3 + 47802908 47850196 DHX30 22907 "DEAH (Asp-Glu-Ala-His) box helicase 30, transcript variant 2" GO:0042645|GO:0005739|GO:0005515|GO:0004004|GO:0003725|GO:0006396|GO:0005737|GO:0003682|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131895_PI430048170 0.0534050136018651 0.568840825245573 4.87873335098167 4.38459865889876 5.19532600760988 P P P 5.53054523492493 5.59998328959608 5.86108326564202 P P P LNCV6_131895_PI430048170 mRNA

CTCTAGGTTATCTATACTGTATAAAAAAGCAATTACCCTTAAAACTGTACTCTGGCCTAC NM_005254 RefSeq chr15 - 50277191 50355408 GABPB12553 "GA binding protein transcription factor, beta subunit 1, transcript variant beta-1" GO:0005515|GO:0006996|GO:0003700|GO:0046982|GO:0044212|GO:0006357|GO:0045944|GO:0005654|GO:0005634|GO:0007005|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_134509_PI430048170 0.2502353583611480.9620342571886030.415563626348416 0.3986044797554170.380679030860408 A A A 0.49982157095745 0.474977282255778 0.385278982468994 A A A LNCV6_134509_PI430048170 mRNA
GAGTGTTGCAAATGTGTTCTTTGTCCTGTTATATGTATATCAGGAATACAAGGATGTGAA NM_002438 RefSeq chr10 + 17809342 17911162 MRC1 4360 "mannose receptor, C type 1" GO:0005515|GO:0005886|GO:0009986|GO:0005537|GO:0006898|GO:0007165|GO:0071222|GO:0071346|GO:0005887|GO:0004872|GO:0071353|GO:0010008|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_142142_PI430048170 0.1287325097486470.8065561217714697.13820284273643 6.91981895450844 7.33718791329981 P P P 7.41092630618583 7.27223070467256 7.64741837102409 P P P LNCV6_142142_PI430048170 mRNA
GGTGGGCATGCACTGCAAGAATTAAGTATCTCAGACTGAAATAAAACCGTTCATAATTAA NM_181581 RefSeq chr7 + 107563956 107578523 DUS4L 11062 "dihydrouridine synthase 4-like (S. cerevisiae), transcript variant 1" GO:0050660|GO:0017150|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_138188_PI430048170 0.2497974125807341.69777981298183 0.276939222747079 1.67677537679718 1.16755232946614 A A A 0.4482536189328650.371200304856452 0.335755693507167 A A A LNCV6_138188_PI430048170 mRNA
TGAACTGAAGTATGTGCAGTCTGCCATCTCACATTAAAATGTAGGCATTTTGTCAAAAAA NM_001085429 RefSeq chr7 + 138797993 138806026 TMEM213 155006 transmembrane protein 213 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_116065_PI430048170 0.2240167187982531.55154485997979 4.07170733175562 3.00710467215949 3.25459298489515 P P P 2.88129688423699 2.91875694290115 2.85611712310059 P P P LNCV6_116065_PI430048170 mRNA
ACTTGAAACTACAGGAGAAAGAAGGATCTAGCGAAATATGGCTACAGAGAGCCCTGCTAC NM_001289030 RefSeq chr15 + 49170015 49329805 GALK2 2585 "galactokinase 2, transcript variant 3" GO:0004335|GO:0005737|GO:0033858|GO:0005975|GO:0046835|GO:0006012|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135649_PI430048170 0.3874976694600391.08943530268553 7.6169379207746 7.30956517898095 7.47216686610108 P P P 7.2690237928523 7.52557809815415 7.2315799294789 P P P LNCV6_135649_PI430048170 mRNA
TTACTCTAAGATATCAAAAGATTGAAGCAAGCCATGAAACCTCTGCGCGGAGAGAGCCGA NM_006233 RefSeq chr19 - 36113708 36115304 POLR2I 5438 "polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa" GO:0008380|GO:0010467|GO:0006368|GO:0006367|GO:0006366|GO:0003899|GO:0006370|GO:0005634|GO:0003677|GO:0001193|GO:0050434|GO:0006281|GO:0000398|GO:0006283|GO:0034587|GO:0005665|GO:0016032|GO:0008270|GO:0005654|GO:0006289|GO:0035019 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_128347_PI430048170 0.2479541716677071.85956349060063 0.421782357267633 2.08212008069042 1.23678546467995 A A A 0.8477707330211420.314500035094276 0.288613430570118 A A A LNCV6_128347_PI430048170 mRNA
AGGACTTCTGGATCTGGGTGTCCATGACCGTGTGCGTCTTCTGGCTGATGTGCATGTGTC NM_173821 RefSeq chr2_KI270776v1_alt + 81831 85428 RTP5 285093 receptor (chemosensory) transporter protein 5 (putative) GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_129211_PI430048170 0.3574078190031320.8941712028556971 1.2649097388373 11.1050457319613 10.9079060107078 P P P 11.432892788237 11.282384201608 11.0421490919885 P P P LNCV6_129211_PI430048170 mRNA
ATTCAGGCAGACCCTGACCTCTCCCTCAGGCAGCCCAACCATCCAGAATGAATATTCTTG NM_145652 RefSeq chr20

- 45109451 45115172 WFDC5 149708 WAP four-disulfide core domain 5
GO:0010951|GO:0004867|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131255_PI430048170 0.9828274392778551.00010987898509 13.0406881596988
12.9818434093305 12.9367973811168 P P P 12.9891730460733 12.893163948689
13.0728090927414 P P P LNCV6_131255_PI430048170 mRNA
GGCCCTTCCTTGTGTTGCCAATTTATTAACAGCAAATAAACCAATTAAATGGAGACTATT NM_015638RefSeq chr20
- 35002403 35092815 TRPC4AP 26133 "transient receptor potential cation channel, subfamily C, member 4 associated protein, transcript variant 1"
GO:0005515|GO:0006511|GO:0034220|GO:0016567|GO:0005886|GO:0019902|GO:0070588|GO:0031464|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136447_PI430048170 0.00302188926211237 0.8481270368747988.56159109250918
8.60119539052077 8.65235030964713 P P P 8.79196602573466 8.85774949240405
8.87839583045702 P P P LNCV6_136447_PI430048170 mRNA
GCTGGGGAATTTGAATATTGTGAGTTTCAGATGTTGGAAATTTGGGATTTTGCAGTTTTG NM_020899RefSeq chr17
- 7459365 7484249 ZBTB4 57659 "zinc finger and BTB domain containing 4, transcript variant 1"
GO:0005515|GO:0008327|GO:0000977|GO:0019901|GO:0010428|GO:0005634|GO:0000122|GO:0001227|GO:0046872|GO:0006351|GO:0006974|GO:0042803|GO:0043565|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130275_PI430048170 0.0260575457478650.6900162099393470.0318498405669
9.94106326113571 9.91205243517188 P P P 10.2893950230305 10.5475412453133
10.6347186481907 P P P LNCV6_130275_PI430048170 mRNA
GCTTCTAGCGTGTGGCATCTGACCAATTTTGAATTGGTCCTTTCTATAAAATCAATATTT NM_001080469 RefSeq chr19 - 45710628 45730893 FBXO46 23403 F-box protein 46 GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55801_PI430048170 0.4484987759458680.9154658326448726.19053887837675 6.06518884012959
6.48108179322967 P P P 6.46663780481934 6.18578301322833 6.48001207343141 P P P LNCV6_55801_PI430048170 mRNA
AGTCTTAAATAAAGTTGAAGTTCAATATAAGACTCTCCCAGGATGGAACACAGACATATC NM_001126RefSeq chr1
- 244408491 244452134 ADSS 159 adenylosuccinate synthase
GO:0046040|GO:0005515|GO:0000287|GO:0006531|GO:0009168|GO:0005886|GO:0004019|GO:0055086|GO:0044281|GO:0044208|GO:0005525|GO:0014074|GO:0005829|GO:0006184|GO:0071257|GO:0005737|GO:0006167|GO:0006144|GO:0042301|GO:0060359|GO:0070062|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75688_PI430048170 0.0931612365293303 0.6614026160782038.00890001218721
7.91807579977278 8.26945072303478 P P P 8.24370422325681 8.72042047239695
8.95642165672807 P P P LNCV6_75688_PI430048170 mRNA
TAAGCAACTAGTTTTTATTCCCCACTACTCTTGTCTCTATCAGATACCATTTATGAGACANM_000791RefSeq chr5 - 80626225 80654981 DHFR 1719 "dihydrofolate reductase, transcript variant 1"
GO:0050661|GO:0050999|GO:0031427|GO:0006767|GO:0044281|GO:0005575|GO:0003729|GO:0009165|GO:0005829|GO:0000082|GO:0000083|GO:0006766|GO:0008144|GO:0046653|GO:0046654|GO:0046655|GO:0046209|GO:0005654|GO:0006545|GO:0000278|GO:0006730|GO:0055114|GO:0004146 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137533_PI430048170 0.0708967496819203 0.6698341582968162.58392767725904
3.11209485221026 3.02177898452323 A A P 3.30805637379055 3.31530076024847
3.82024909526588 P P P LNCV6_137533_PI430048170 mRNA
GTTGGGATATCATACCCAGCTGAAAAAGAACAAACTGCTTAACATAAGTATATGTATCGT NM_005426RefSeq chr1
- 223779892 223845972 TP53BP2 7159 "tumor protein p53 binding protein 2, transcript variant 2"
GO:0005515|GO:0048471|GO:0017124|GO:0051059|GO:0005634|GO:0009967|GO:0045786|GO:0007417|GO:0009792|GO:0042802|GO:0007507|GO:0007165|GO:0005737|GO:0007049|GO:0072332|GO:0005070|GO:0010212 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128144_PI430048170 0.1639223357056510.86102884070656 8.6015594128394
8.35220420687242 8.37098623020801 P P P 8.68400879390928 8.80564107982628
8.47741330035915 P P P LNCV6_128144_PI430048170 mRNA
ACATTACATAGGTTACGTCAGCCTACTGTGGCTGTTGAGCAAAGCATTTCTCCTTTCTGG NM_017882RefSeq chr15
- 68206991 68229742 CLN6 54982 "ceroid-lipofuscinosis, neuronal 6, late infantile, variant"
GO:0044265|GO:0005515|GO:0031965|GO:0005783|GO:0031987|GO:0045862|GO:0042803|GO:0043231|GO:0030
163|GO:0016020|GO:0001573|GO:0005789|GO:0005788|GO:0005654|GO:0007042|GO:0016021|GO:0007601|GO:0
030203|GO:0008203. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128434_PI430048170 0.3167108574843891.03580441323153 0.306627777278206
0.2579816154858950.387492686353086A A A 0.27817396095422 0.24663456296258
0.27778896376914 A A A LNCV6_128434_PI430048170 mRNA
TTCTCAGGCTCCCATGAGAAAACAATCTATACTTATCTTCCGTGAATAAACAAGTGTCAC NM_152781RefSeq
chr17_KI270857v1_alt - 89487 103423 HEATR9 256957 HEAT repeat containing 9 GO:0002244 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100855_PI430048170 0.0286925335395561 0.6767684879471475.11576323110301
5.08957519590596 5.05819042024244 P P P 5.53718697028543 5.84598495680716
5.54904640438757 P P P LNCV6_100855_PI430048170 mRNA
TTGTGTCTCTGTGGTTTGCTGCTGGAGCTGGTGACCGGGAGAGAAACAAGGGAGACAAGG NM_001293294
RefSeq chr11 + 69294137 69297287 MYEOV 26579 "myeloma overexpressed, transcript variant 3"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128797_PI430048170 0.0942186630756860.874745804060501 14.2906719161506
14.5173440849081 14.4303167481185 P P P 14.6053296153706 14.6269288349157
14.5940786513596 P P P LNCV6_128797_PI430048170 mRNA
GAGCGACAGAAATGAGGGACTGGGATCTGCACAGCCATTAAATTATAAATCTGGAAAAAA NM_001031827
RefSeq chr16 - 30192934 30194306 BOLA2 NA bolA family member 2 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_128749_PI430048170 0.1883067971306890.5525479463033990.350710448455828
0.41412678114934 0.343796553730062A A A 1.72635517989799 0.405037324316365
1.25286511915804 A A A LNCV6_128749_PI430048170 mRNA
GGGGAAAAAAGTAGGCTGTTTTCCTGATAGGTCTAGCCATTCATTCAGTAAACCATATTG NM_018718RefSeq chr7
- 130393770 130441210 CEP41 95681 "centrosomal protein 41kDa, transcript variant 1"
GO:0005515|GO:0005813|GO:0006996|GO:0005814|GO:0072372|GO:0015031|GO:0036064|GO:0005829|GO:0018
095|GO:0042384|GO:0016020|GO:0000086|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92673_PI430048170 0.7258048814486961.05786707219259 7.89207970374895 8.4073316465283
8.00446487495906 P P P 8.06668821517655 7.84990368942652 8.17706010683762 P P P
LNCV6_92673_PI430048170 mRNA
ATGTCAACAGAGCTATCAATGTTCTTCTGGAAGGAAACCCAGACACGATTCCTGGGAGAT NM_014847RefSeq chr1
+ 154220848 154270853 UBAP2L 9898 "ubiquitin associated protein 2-like, transcript variant 1"
GO:0005515|GO:0005671|GO:0007339 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107587_PI430048170 0.0260948843512244 0.5456768176590781 0.9308649473615
10.6022826964931 10.9320222813475 P P P 11.3546838333455 11.6724509778688
12.0098025548678 P P P LNCV6_107587_PI430048170 mRNA
TTCCCTCTTCCCCCTAAAAATGGTAAATCTGATCATATCTACATGTATGAACTTAACATG NM_003016RefSeq chr17
- 76734114 76737411 SRSF2 6427 "serine/arginine-rich splicing factor 2, transcript variant 1"
GO:0005515|GO:0006397|GO:0008380|GO:0010467|GO:0006369|GO:0006366|GO:0003714|GO:0031124|GO:0005
634|GO:0005737|GO:0006406|GO:0016607|GO:0000166|GO:0000398|GO:0016605|GO:0005654|GO:0005681|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_32801_PI430048170 0.5872298262189741.12074803942832 3.61441666262075 3.33277363503035

3.17096651838878 P P P 3.01279081117585 3.88515799209091 2.35250218947577 P P A
LNCV6_32801_PI430048170 mRNA
TTGAACCAGTAGCCATAAGCTGGGGTAGACCCTGTCCAGTCCTGTCGGGGGTAGGAGAAANM_001256795 RefSeq
chr19 + 51415905 51417425 LOC100129083 NA uncharacterized LOC100129083 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135461_PI430048170 0.4574798533229110.8378507232901291.8710167525798
2.04478525527854 2.71401635369405 A A A 2.33672836446694 2.2198646158496
2.88980546049272 A A P LNCV6_135461_PI430048170 mRNA
GAGGATCAAACACTGTCAGAATTGCTGAAATCAATACACAAAGAGATAAAGTTTAGCTTC NM_015693 RefSeq chr4
+ 127632931 127716779 INTU 27152 inturned planar cell polarity protein
GO:0010839|GO:0045880|GO:0042384|GO:0021513|GO:0005737|GO:0009986|GO:0030216|GO:0008589|GO:0060
173|GO:0051782|GO:0031069|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59900_PI430048170 0.1917724519459340.2602157849759410.2785867857204390.794222870234771
0.276541191475117 A A A 0.4934136968270032.25054678960271 3.29488826284734 A A P
LNCV6_59900_PI430048170 mRNA
ACTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTGGAAACTGTGTT NM_148957 RefSeq chr13
+ 23570369 23676105 TNFRSF19 55504 "tumor necrosis factor receptor superfamily, member 19,
transcript variant 2" GO:0005031|GO:0007254|GO:0006915|GO:0016021|GO:0043123|GO:0001942|GO:0033209
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130719_PI430048170 0.0921730101823097 2.27237287989088 3.10148905804012
3.17930105332648 3.73721137239716 A P P 2.21421927183827 1.16964915315386
2.75323579329649 A A P LNCV6_130719_PI430048170 mRNA
GAGGCAATGGAGTGGTCTAGGATTGAGCAAAAAGCAATTTTTGTTACATCTTTATGCTAA NM_032788 RefSeq chr2
- 95147654 95159518 ZNF514 84874 zinc finger protein 514
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132337_PI430048170 0.0521176790495855 0.67072635691867 6.61786902533716
6.40706286858531 6.94960457599957 P P P 7.28960272535366 7.14288990058413
7.31704804977477 P P P LNCV6_132337_PI430048170 mRNA
GCCTTGTATGAGGGGAGTTTGAATGTTAATAAACATGTTTTCCACTTTAAGATCCAGTAA NM_007282 RefSeq chr3
+ 149812687 149962138 RNF13 11342 "ring finger protein 13, transcript variant 1"
GO:0005515|GO:0004842|GO:0000139|GO:0016874|GO:0031902|GO:0005789|GO:0005637|GO:0008270|GO:0016
021|GO:0005765|GO:0051865 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139962_PI430048170 0.8111940251187741.0386787538745 0.50750594547706
0.7681288395117040.258326813885418 A A A 0.4051706061329650.530656093885418
0.476134520075378 A A A LNCV6_139962_PI430048170 mRNA
GCTACCCAGAAATTGAGCTTCAGAAGATTGAGGATAGCCTTTGATTGGTATTTAAAATAA NM_001282880 RefSeq
chr3 + 44712642 44723831 ZNF502 91392 "zinc finger protein 502, transcript variant 5"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127771_PI430048170 0.63352746407172 0.9523356208537416.94963507778914
6.86521166215576 6.6060868901222 P P P 6.93455846949964 7.0050526907747
6.69671771557695 P P P LNCV6_127771_PI430048170 mRNA
CCCCAATTAAGTGCCTTCACACAGCACTGGTTTAATGTTTATAAACAAAATAGAGAAACT NM_001142502 RefSeq
chr19 - 45379633 45406349 PPP1R13L 10848 "protein phosphatase 1, regulatory subunit 13 like,
transcript variant 1"
GO:0003229|GO:0005515|GO:0042633|GO:0030054|GO:0003714|GO:0006915|GO:0003215|GO:0005634|GO:0000
122|GO:0009791|GO:0060048|GO:0006351|GO:0045171|GO:0042802|GO:0048871|GO:0005737|GO:0031076|GO:0
035264|GO:0008134. NA - . NA NA NA NA NA NA NA NA NA

LNCV6_143294_PI430048170 0.19904394195816 1.04599496057503 0.367320738199526
0.3733447471787170.474793546766267A A A 0.3334773567109730.317493559198216
0.37186511821025 A A A LNCV6_143294_PI430048170 mRNA
CCACTATGTAGAATAAAAATGCAAAGTTCACTGGAGTCTCAACATCTATGACTCATGAAA NM_005142RefSeq chr11
- 59829272 59845501 GIF 2694 gastric intrinsic factor (vitamin B synthesis)
GO:0015889|GO:0009235|GO:0031419|GO:0006767|GO:0005576|GO:0044281|GO:0005615|GO:0005902|GO:0016
324|GO:0006766|GO:0005768|GO:0006824|GO:0043202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129885_PI430048170 0.8137129424387021.01492447998721 7.46113657036136 7.3863302841411
7.43405784729326 P P P 7.3451421887137 7.60542556260406 7.2432844430229 P P P
LNCV6_129885_PI430048170 mRNA
AGATCCTGTTCAATGATGAAATGGATGACTTCAGCTCTCCCAACATCACCAACGAGTTTG NM_001282879 RefSeq
chr22 + 22644619 22647898 GGTLC291227 "gamma-glutamyltransferase light chain 2, transcript
variant 3" GO:0019370|GO:0003840|GO:0006749|GO:0031362|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143155_PI430048170 0.1200325188281870.87809993439193411.7629817911126
11.5975548396764 11.7271791391047 P P P 11.7388414274547 11.9945110167551
11.9105409887774 P P P LNCV6_143155_PI430048170 mRNA
ATGAGCGGATGGGCAAAAAGTTGACAGAGTTGTCTATGCAGGATGAAGAGCTGATGAAGA NM_012456RefSeq
chr11 - 57528462 57530759 TIMM1026519 translocase of inner mitochondrial membrane 10 homolog
(yeast)
GO:0005515|GO:0005215|GO:0007605|GO:0006626|GO:0051087|GO:0005743|GO:0042719|GO:0042803|GO:0005
739|GO:0005744|GO:0005758|GO:0045039|GO:0008565|GO:0008270|GO:0072321|GO:0044267 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132101_PI430048170 0.00880645968863527 0.4804364331470735.44595348585327
5.18088488409026 5.75815764224718 P P P 6.31296676224127 6.62056407587406
6.65799472891779 P P P LNCV6_132101_PI430048170 mRNA
CCTGAGGGCTGGAATTATGCCTTAACTATATCTATAGTATTTAACAGTGAATCCTTTGTA NM_001002926 RefSeq
chr7 - 19695461 19709037 TWISTNB 221830 TWIST neighbor
GO:0010467|GO:0006363|GO:0005730|GO:0006362|GO:0006361|GO:0005634|GO:0006360|GO:0005736|GO:0045
814|GO:0001054|GO:0015630|GO:0040029|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145534_PI430048170 0.3000666369892011.02916958682122 0.333344631411891
0.2599562402795860.35873167019293 A A A 0.2803512247523810.265512589543606
0.28347722340473 A A A LNCV6_145534_PI430048170 mRNA
TTTTCTACCCTTGGCATGAGGGGAAATGATTGATATTCAAGCAAGTTCTCTAGGAAAAAA NM_017551RefSeq chr10
- 85599554 86366493 GRID1 2894 "glutamate receptor, ionotropic, delta 1"
GO:0035235|GO:0034220|GO:0030054|GO:0008328|GO:0045211|GO:0005234|GO:0035176|GO:0004970|GO:0035
249|GO:0030425|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134693_PI430048170 0.2462181622951210.88376280853209 3.76704754511808
3.82212541474652 3.8805346857152 P P P 4.08770171479945 4.11474444746284
3.78110175407786 P P P LNCV6_134693_PI430048170 mRNA
AAGGGCACCAAGGCCCCATTCAGCCCTCCGTGTATCTAATAAAGTCTGACCCTGTGAAAC NM_178553RefSeq chr2
- 27136846 27139464 PRR30 339779 proline rich 30 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129435_PI430048170 0.1349807042610431.22098678432075 5.4333595438085
5.32548242082449 5.31307820494751 P P P 5.15408675573805 4.80709873506825
5.21685441590245 P P P LNCV6_129435_PI430048170 mRNA
GAACTACTTGAGATGACTTAAGAAGCATCCCATGCAAATATCTTGTTTTGCCCTAATAAA NM_004863RefSeq chr14
- 77505996 77616767 SPTLC2 9517 "serine palmitoyltransferase, long chain base subunit 2"
GO:0006665|GO:0004758|GO:0006686|GO:0030148|GO:0044281|GO:0005739|GO:0030170|GO:0005789|GO:0016

021|GO:0017059|GO:0046513|GO:0046512|GO:0046511 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138733_PI430048170 0.000735792572045302 2.66631826739436 7.00855099850608
7.03580936622747 7.15025366713513 P P P 5.69229932360563 5.76688310665326 5.4796763754693
P P P LNCV6_138733_PI430048170 mRNA
AAAGAGTTTTGTAACCTTCAAGTGCTGTTCAGCTGCGGGGATTTAGCACAGGAGACTCTA NM_019118RefSeq chr1
- 32216196 32222325 TMEM234 56063 transmembrane protein 234 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_51702_PI430048170 0.2917009047444170.88211923400815 4.94180956292812 4.76311549768589
5.21204327659569 P P P 5.2914832915976 5.03837794120899 5.15452549070011 P P P
LNCV6_51702_PI430048170 mRNA
CATTATCGCTGTGCTCTGATCGCCCTTGAACATGGTGCAGATGTCAACAATTCTACCTAT NM_022096RefSeq chr20
+ 10034998 10056762 ANKEF1 63926 "ankyrin repeat and EF-hand domain containing 1, transcript variant
1" GO:0005509 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78003_PI430048170 0.00331146478095451 0.6715123190772566.90748536428396
6.92379903540956 6.99841947741303 P P P 7.41423590461684 7.52133412177406
7.61250350885514 P P P LNCV6_78003_PI430048170 mRNA
TGATTCTGTGGCCCAAAACAATCATTGTTAACATCTTCATGTGTTTCATTCTGATCTTTC NM_001286379 RefSeq
chr6_KI270798v1_alt + 17940 143632 FAM120B 84498 "family with sequence similarity 120B,
transcript variant 1" GO:0006355|GO:0005634|GO:0030154|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142611_PI430048170 0.2722033631267681.04319620254555 0.356346205390472
0.3601786481414750.479069965338111A A A 0.3352946077824950.312620819490406
0.367524833087908A A A LNCV6_142611_PI430048170 mRNA
CACCAGCATTGTCTGGAATATTAAATGTTGTTATGCTTTGAGATTGGCACTTATGCCATT NM_207440RefSeq chr13
+ 112647043 112684497 ATP11AUN NA ATP11A upstream neighbor NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144558_PI430048170 0.8547424973179671.02137008867253 6.66750325837867
6.87572938849798 7.04662492788743 P P P 6.92018543947834 6.63921320314773
6.94430817677659 P P P LNCV6_144558_PI430048170 mRNA
ATGAAAGGTGGTTTGGTTTTGGTTCTAAGGAGCTCTACAGTTTAACAGAGAGAGGGACCT NM_138367RefSeq
chr8_KI270815v1_alt - 95391 130068 ZNF251 90987 zinc finger protein 251
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138329_PI430048170 0.5190894054321 0.7182608827570821.91441788669196
0.9521009270180210.314568257840521A A A 0.5639971394440641.8870223193786
2.16871198660295 A A A LNCV6_138329_PI430048170 mRNA
CTGCAATTTTACCTAGCTACCACTAGGTGGATAGTAAATTTATACTTATGTTTCCCTCAA NM_001301746 RefSeq
chr17 + 32927909 32941649 TMEM98 26022 "transmembrane protein 98, transcript variant 3"
GO:0005783|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_14181_PI430048170 0.7170340016594160.9650710350993371 1.7569089613751 11.1861890554776
11.4091164266836 P P P 11.5041519303676 11.5825625103559 11.4751855621213 P P P
LNCV6_14181_PI430048170 mRNA
GCACCAGTTCCTAATGTATAAAGTTCTCTCTCTCTCTCTCTCAATAAACAATGCAGAAAA NM_001080475 RefSeq
chr2 - 207821287 208025560 PLEKHM3 389072 "pleckstrin homology domain containing, family M,
member 3" GO:0035556|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140041_PI430048170 0.9703628998884641.00308183014762 0.270939934810451
0.2759242284646150.441515969955622A A A 0.3510293431186480.297935496785971
0.332209698981797A A A LNCV6_140041_PI430048170 mRNA
CCGAATATGTACATGTACTGTATGTATTACCGTAGAGATTGGAATCAACTTACTGTATGT NM_001270941 RefSeq

chr5 - 147585440 147782848 JAKMIP2 9832 "janus kinase and microtubule interacting protein 2, transcript variant 1" GO:0008017|GO:0005794|GO:0019900 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122603_PI430048170 0.56750508127039 0.979111549586046 0.253399949632797 0.263678425402879 0.392898780430462 A A A 0.372690272351951 0.312918939339822 0.319212600953939 A A A LNCV6_122603_PI430048170 mRNA TCCTTGAACTTGACCGGAGAATTGTACTGGACCAAGGTGAAAGTCAACTTTGACAACGTG NM_198056 RefSeq chr3 - 38548061 38649672 SCN5A 6331 "sodium channel, voltage gated, type V alpha subunit, transcript variant 1" GO:0005515|GO:0005516|GO:0086010|GO:0086070|GO:0060307|GO:0060048|GO:0019228|GO:0060371|GO:0086067|GO:0086069|GO:0060373|GO:0060372|GO:0010765|GO:0007411|GO:0086002|GO:0001518|GO:0045760|GO:0086006|GO:0031625|GO:0086004|GO:0086005|GO:0050679|GO:0019901|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141960_PI430048170 0.0197643475674399 1.69736649223081 6.35799644457063 5.95639439593631 6.06449969977774 P P P 5.05387861428522 5.44027181664959 5.57592199870482 P P P LNCV6_141960_PI430048170 mRNA AGGGGTGAGAACAACTAGCTGTAGCATGTGTAGGCTATATACTTTACCATTTGACTTCTT NM_001017995 RefSeq chr5 - 172333498 172454523 SH3PXD2B 285590 SH3 and PX domains 2B GO:0005515|GO:0071800|GO:0030054|GO:0001654|GO:0006801|GO:0080025|GO:0070273|GO:0002102|GO:0072657|GO:0042995|GO:0032266|GO:0030154|GO:0007507|GO:0060348|GO:0001501|GO:0005737|GO:0022617|GO:0045600|GO:0060612|GO:0010314|GO:0042169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131763_PI430048170 0.0131197634558874 0.710973433293904 11.3813178054183 11.6110397099987 11.4439998244241 P P P 12.0076818691739 11.9382663694635 11.9758459383947 P P P LNCV6_131763_PI430048170 mRNA CCCACCCCTTTTTGTAAATCTTGTTCATTGTAAATCAAATACAGCGTCTTTTTCACTCTG NM_012401 RefSeq chr22 - 50274978 50307572 PLXNB2 23654 plexin B2 GO:0005515|GO:0009986|GO:0008360|GO:2001222|GO:0001843|GO:0007405|GO:0005622|GO:0017154|GO:0005887|GO:0007420|GO:0071526|GO:0001932|GO:0050772|GO:0032319|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140848_PI430048170 0.0303642774967236 0.620861152344864 7.01182812273583 6.7816354386589 6.99083487656315 P P P 7.41807115239099 7.48544078174229 7.90509602966967 P P P LNCV6_140848_PI430048170 mRNA TATTTTGAAAACTGGTGCATCACCTTGTCCTTAGCAATAAAATGTGTTGAGCAGAGGAAA NM_014663 RefSeq chr1 + 43650125 43705518 KDM4A 9682 lysine (K)-specific demethylase 4A GO:0005515|GO:0016577|GO:0005730|GO:0006325|GO:0005634|GO:0035064|GO:0051864|GO:0006351|GO:0070544|GO:0005737|GO:0014898|GO:0016032|GO:0005654|GO:0008270|GO:0045892|GO:0031625|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130309_PI430048170 0.311854147236346 0.87394195452319 0.304353952777584 0.276974546835325 0.435601571045317 A A A 0.608089765512644 0.254350398874541 0.704803515951327 A A A LNCV6_130309_PI430048170 mRNA GTAAGTCTAGCTACCTATCCAATACTAAATACCCCTTAAAGTATTAAATGCACTATCTGC NM_030787 RefSeq chr1 + 196977536 197009673 CFHR5 81494 complement factor H-related 5 GO:0006957|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126954_PI430048170 0.537988991082243 1.06953108980924 11.0826755378351 10.9631942471301 10.9148926024439 P P P 10.6213988277833 11.1278787116479 10.8814789229834 P P P LNCV6_126954_PI430048170 mRNA TCCCAAGGACCCACCATGCAGAAGTGTCAATAAACCACAAGTTCTGAACTCTGTAAAAAA NM_014634 RefSeq chr22 - 21919418 21952878 PPM1F 9647 "protein phosphatase, Mg2+/Mn2+ dependent, 1F" GO:0005515|GO:0048471|GO:0016576|GO:0010811|GO:0051894|GO:0035690|GO:0097193|GO:0046872|GO:0005

829|GO:0043280|GO:0010628|GO:0043234|GO:0016791|GO:0035970|GO:0050921|GO:0044387|GO:0033137|GO:0051496|GO:0004722|GO:0006469|GO:0010634|GO:0045892|GO:0045927|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138929_PI430048170 0.00487703386194871 0.6266759186783429.507712759647 9.3128329742602 9.47799997686434 P P P 10.188778926079 9.92807296354902 10.1960480137544 P P P LNCV6_138929_PI430048170 mRNA GAGTGTGAACTAAAAGGTAACATTTTCCACTCTCAAGTTTTCTACTTTGTCTTTGAACTG NM_001242767 RefSeq chr6 + 150865678 151101887 MTHFD1L 25902 "methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like, transcript variant 1"
GO:0015942|GO:0004329|GO:0004477|GO:0005524|GO:0042803|GO:0005829|GO:0035999|GO:0005739|GO:0004488|GO:0006760|GO:0016020|GO:0046653|GO:0009396|GO:0006730|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104225_PI430048170 0.22018984072682 0.7442157180781235.69410455896006 5.73763750814285 5.56028901128691 P P P 5.6291852837979 6.39940648119436 6.14484406493923 P P P LNCV6_104225_PI430048170 mRNA AGCTACTGAAACAGGCACTGGAGCGAATCCCTGAGCTGCAGGGGATCGTGGGGGACTGGT NM_015302RefSeq chr19 + 35612743 35625349 HAUS5 23354 "HAUS augmin-like complex, subunit 5"
GO:0051297|GO:0003674|GO:0007067|GO:0005813|GO:0005737|GO:0005874|GO:0005819|GO:0070652|GO:0051225|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143198_PI430048170 0.00899582088121264 0.4041122827075866.22500323554543 6.10372908319117 5.88789499519931 P P P 7.05514141330427 7.32102417372032 7.70683810314742 P P P LNCV6_143198_PI430048170 mRNA TCCCAATTCATATTACTCTTGTATCGAGTCCATGAGGTCTAAGGCAACTTAGATCAAAGT NM_005392RefSeq chr9 + 93576626 93679587 PHF2 5253 PHD finger protein 2
GO:0005515|GO:0032454|GO:0032452|GO:0005506|GO:0003713|GO:0005730|GO:0006325|GO:0051213|GO:0005634|GO:0035064|GO:0006351|GO:0001889|GO:0005737|GO:0006482|GO:0000777|GO:0061188|GO:0005654|GO:0008270|GO:0055114|GO:0033169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_3341_PI430048170 0.0224438804227514 0.80483906082911810.1687447942056 10.0679086376927 9.96814582192111 P P P 10.3574480872465 10.4231535619298 10.3700054887251 P P P LNCV6_3341_PI430048170 mRNA TCATGTTCTTTGGGAAAAGGGAAGGCGTGCTGTGGAAATAAAATGTTTATTTGCTTCTCT NM_033549RefSeq chr5 + 181223262 181235808 TRIM41 90933 "tripartite motif containing 41, transcript variant 1"
GO:0005515|GO:0005737|GO:0016567|GO:0016874|GO:0005730|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142105_PI430048170 0.1854236442478981.14494903950285 9.43382642654979 9.65156787669512 9.77068789634378 P P P 9.47002692539278 9.3533533249401 9.46387110971457 P P P LNCV6_142105_PI430048170 mRNA TTGTGCGTCTGTGAAATGTTTTACAGTGTTTCTCATCATCTGTTTCCCAGCAAGGTCTTT NM_006324RefSeq chr16 - 75293709 75433489 CFDP1 10428 craniofacial development protein 1
GO:0008150|GO:0003674|GO:0042127|GO:0008360|GO:2000270|GO:0000777|GO:0007275|GO:0005575|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142117_PI430048170 0.00125511692607242 2.53919564978956 5.70942450345013 5.49990640992608 5.58158620332414 P P P 4.45604310166973 4.10227725326772 4.18299388670534 P P P LNCV6_142117_PI430048170 mRNA AGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATA NM_138455RefSeq chr8 + 103371514 103383004 CTHRC1115908 "collagen triple helix repeat containing 1, transcript variant 1"
GO:0017147|GO:0005581|GO:0043932|GO:0060122|GO:0005578|GO:0090177|GO:0005615|GO:0032092|GO:0005109|GO:0045669|GO:0005737|GO:0016477|GO:0090103|GO:0033690|GO:0090090|GO:0060071 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_110708_PI430048170 0.1036128205585741.64769913777726 1.21437031208829
1.22289717324271 1.96934232694677 A A A 0.4461709892424 1.19972971127004
0.624871686132398 A A A LNCV6_110708_PI430048170 mRNA
TTCTTTACTGATTCCTTGTCCTTCAGTAAGGAAAAAGACAAAACTCTCCTTAGTTTACAC NM_001039693 RefSeq
chr2 - 199928910 199955736 TYW5 129450 "tRNA-yW synthesizing protein 5, transcript variant 1"
GO:0000049|GO:0005506|GO:0016706|GO:0031591|GO:0042803|GO:0055114 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144618_PI430048170 0.4729100909608970.88691533583508 0.318568612436191
0.3026439875659150.317060433797163 A A A 0.3013980255810650.810085487782713
0.281841132880544 A A A LNCV6_144618_PI430048170 mRNA
GCACTTTTATTTTTTCCTGTGTGTCATGTTGGTTTTTGGTACTTGTATTGTCATTTGGAG NM_002993 RefSeq chr4 +
73836555 73838760 CXCL6 6372 chemokine (C-X-C motif) ligand 6
GO:0008009|GO:0070098|GO:0002446|GO:0007267|GO:0005576|GO:0045236|GO:0005615|GO:0002690|GO:0007
165|GO:0006955|GO:0006954|GO:0006935|GO:0007186|GO:0060326|GO:0042127|GO:0032496|GO:0008201|GO:0
042742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94399_PI430048170 0.10231212775701 1.03133834671223 0.3889209418742080.398368248853547
0.440053001064403 A A A 0.3574810832708770.3449391183090930.391480691858374 A A A
LNCV6_94399_PI430048170 mRNA
TTTGCCTTTTGAGCAAATAGGGAATCTAAGGGAGGAAATTATCAACTGTGCACAAGGAAA NM_006417 RefSeq chr1
+ 78649791 78664078 IFI44 10561 interferon-induced protein 44 GO:0005737|GO:0009615 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145103_PI430048170 0.4067878046469730.9078392329149684.40809736216346
4.37092937572505 4.80201463575075 P P P 4.59504160504513 4.61573683439131
4.81867172937035 P P P LNCV6_145103_PI430048170 mRNA
ATTCATTCACAAAACACAAACCCAGGACTTTCTGCCTAAGGCAGAGCACAAGACTCACAG NM_015274 RefSeq chr4
+ 6575173 6622406 MAN2B2 23324 "mannosidase, alpha, class 2B, member 2, transcript variant 1"
GO:0030246|GO:0008270|GO:0004559|GO:0070062|GO:0006013 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132790_PI430048170 0.5407698883298841.03311226680196 11.0920840785627 11.244157367079
11.2372407387178 P P P 11.0826755378351 11.10625910283 11.2433374479074 P P P
LNCV6_132790_PI430048170 mRNA
CTTTCTCTGTGTATGAGTGTGAATGATCAAGTCCTTTGTGAATATTTTCAACTATGTAGG NM_001130847 RefSeq
chrX - 130129362 130165887 AIFM1 9131 "apoptosis-inducing factor, mitochondrion-associated, 1,
transcript variant 5"
GO:0005515|GO:0048471|GO:0030261|GO:0005743|GO:0005634|GO:0051402|GO:0005829|GO:0005739|GO:0005
758|GO:0071949|GO:0030182|GO:0016651|GO:0046983|GO:0016174|GO:0043065|GO:0006919|GO:0009055|GO:0
006915|GO:0003677|GO:0032981|GO:0006308|GO:0006309|GO:0070059|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134903_PI430048170 0.0340809323862730.5457509177010915.10297230460007
4.49786780029341 5.05953626657077 P P P 6.09895918167872 5.75583843234599
5.42284425581399 P P P LNCV6_134903_PI430048170 mRNA
CAAGTTGATGTAAATTGGTTTGTCAACAAGAATGTTAACTGATGAAAGTGGATAGAACCC NM_004582 RefSeq chr1
+ 75786193 75795090 RABGGTB 5876 "Rab geranylgeranyltransferase, beta subunit, transcript variant
1" GO:0005515|GO:0017137|GO:0018344|GO:0005968|GO:0004663|GO:0008270|GO:0007601|GO:0006464 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133655_PI430048170 0.7930018798059091.20725416573005 2.6940322628508
0.8657367345527362.60538911868684 A A A 1.0433378548847 1.82928407220021
2.65441720915281 A A P LNCV6_133655_PI430048170 mRNA
ACTCCAGGTCAGACTCATTAGGAACTCAAGATTCTCGTAAAGAAAGTTGTTTCCAAAAAA NM_000748 RefSeq chr1

+ 154567780 154579877 CHRNB2 1141 "cholinergic receptor, nicotinic, beta 2 (neuronal)"
GO:0030054|GO:0007605|GO:0060084|GO:0042220|GO:0045759|GO:0006939|GO:0034220|GO:0015464|GO:0045211|GO:0042166|GO:0007613|GO:0007612|GO:0001661|GO:0015276|GO:0008306|GO:0051963|GO:0046982|GO:0005892|GO:0007271|GO:0042113|GO:0032226|GO:0032225|GO:0008542|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137061_PI430048170 0.1074936167085550.6901933414597375.25527203652876 5.3604779410762 5.30059081605978 P P P 5.48940913248858 5.82669050420018 6.13518186864267 P P P LNCV6_137061_PI430048170 mRNA
TGAATTTCTCAGGGAGTACTAAGGCTGTGCAGAGGCTGAGAATCTGAAAAATAAAATACT NM_152617RefSeq chr3 - 196468785 196503768 RNF168 165918 "ring finger protein 168, E3 ubiquitin protein ligase"
GO:0005515|GO:0006511|GO:0035518|GO:0043130|GO:0004842|GO:0016567|GO:0016874|GO:0000151|GO:0005634|GO:0045739|GO:0006302|GO:0042393|GO:0005737|GO:0070534|GO:0070535|GO:0010212|GO:0034244|GO:0070530|GO:0045190|GO:0035861|GO:0031491|GO:0006974|GO:0003682|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63623_PI430048170 0.0327020586293256 1.61807732989899 3.80076929668204 3.87933279316799 3.85685143689582 P P P 3.16814195794596 2.88747721259959 3.36082854734924 P P P LNCV6_63623_PI430048170 mRNA
TCACTCTGTGCAGCTAACCAGGAAGAAGGAAGAGGAAACATTTAAGAGGAAGCATGAGGA NM_198082RefSeq chr17 - 82101469 82212813 CCDC57 284001 coiled-coil domain containing 57 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142195_PI430048170 0.1457995709167170.83581874718038415.9118704894157 15.5671775339455 15.5790618130709 P P P 16.0786959763235 15.9877954489902 15.7788558801574 P P P LNCV6_142195_PI430048170 mRNA
CATTTCTGCCCAGTGCCTTTATATTTATATAACATTTTCACTGTGACCAGACTTGATGAT NM_001160364 RefSeq chr16 + 18984286 19063940 TMC7 79905 "transmembrane channel-like 7, transcript variant 2"
GO:0016021|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137674_PI430048170 0.2995956658627140.65108646787854 3.10096234633264 1.71545837377575 3.44625645048512 P A P 2.96605922459548 3.77117919617976 3.75442505319841 P P P LNCV6_137674_PI430048170 mRNA
TTCAAAAGATGATCCTTTCTTGTCACATTATAGCCAAAAGAAGCAGAGAACTTCATTGTC NM_007358RefSeq chr1 + 93079234 93139081 MTF2 22823 "metal response element binding transcription factor 2, transcript variant 1"
GO:0010467|GO:0061087|GO:0007379|GO:0061086|GO:0005634|GO:0000122|GO:0035064|GO:0003677|GO:0048863|GO:0005737|GO:0035098|GO:0045944|GO:0045814|GO:0019827|GO:0040029|GO:0005654|GO:0008270|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137491_PI430048170 0.5647611917775090.9466258460716860.273805394280138 0.2798845019816460.469455707749732A A A 0.3432717619221830.292970435511214 0.61218938517039 A A A LNCV6_137491_PI430048170 mRNA
GGTAGCAGGTACCCATTTTAGGACCCTACACTCAAATGTGCAAAATAAAATTTCTATCAT NM_001008494 RefSeq - - 0 0 --- NA - NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94022_PI430048170 0.0771816476007675 1.25402364651693 11.1015431695557 11.2356488862134 11.4204500318055 P P P 10.8627691982617 10.785718504385 11.1250049504234 P P P LNCV6_94022_PI430048170 mRNA
GCCCTCCTTAATCAACTTCAAGGAGCACCTTCATTAGTACAGCTTGCATATTTAACATTT NM_033306RefSeq chr11 - 104942866 104956695 CASP4 837 "caspase 4, apoptosis-related cysteine peptidase, transcript variant gamma"
GO:0072559|GO:0005739|GO:0004197|GO:0005737|GO:0072557|GO:0050727|GO:0006508|GO:0005789|GO:0097194|GO:0006915|GO:0042981|GO:0097169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139246_PI430048170 0.0354903898259116 0.8446512519221471 1.7541001224227

11.9418770764884 11.8382682661806 P P P 12.062081900999 12.1223253361306
12.0860601287098 P P P LNCV6_139246_PI430048170 mRNA
AGAGACTCCCTGCCCATCAAGTCTGAAACCCCCATGGATGAGGTCAGCTCCTTGTCTGCT NM_144716RefSeq chr3
- 46921729 46982010 CCDC12 151903 "coiled-coil domain containing 12, transcript variant 1"
GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127407_PI430048170 0.2659864537041110.59858979398444 0.674093754197995
0.4001129823865230.330950235944736A A A 1.83420832177789 1.06310908112202
0.396463490039228A A A LNCV6_127407_PI430048170 mRNA
ATTATAAAATAAAGTATCTTAACAGACTCCTCAGTTTTCCATACCCTTCCATCACCACCA NM_022778RefSeq chr1
+ 26234152 26279038 CEP85 64793 "centrosomal protein 85kDa, transcript variant 1"
GO:0005515|GO:0005813|GO:0005737|GO:0000922|GO:0005794|GO:0005730 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144190_PI430048170 0.0628945702085127 0.5360677427042990.421668552479531
0.3765558162873230.401986454896339A A A 1.66745013048964 1.24622149270236
0.877050542721048A A A LNCV6_144190_PI430048170 mRNA
CTCTTAAGGACTTGAAAAGATTAGGAATCTACGCATACACTGAGAGAGAAAAAAGTGAGANM_022725RefSeq chr11
- 22622532 22625841 FANCF 2188 "Fanconi anemia, complementation group F"
GO:0005515|GO:0008150|GO:0003674|GO:0004842|GO:0001541|GO:0016567|GO:0006281|GO:0005654|GO:0007
283|GO:0043240 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99576_PI430048170 0.00669065306152848 0.46851808434223 8.43156536719835
7.90209559351109 8.05844737641513 P P P 9.00404813802086 9.19415215806725
9.48640784686848 P P P LNCV6_99576_PI430048170 mRNA
GAAGGACCGGGAAAAGTCCAAGCATAGCAACAGGAACATAAAGATTCTGAAAAGAAACAC NM_003286RefSeq
chr20 + 41028821 41124486 TOP1 7150 topoisomerase (DNA) I
GO:0005515|GO:0003917|GO:0003918|GO:0042493|GO:0005730|GO:0005634|GO:0012501|GO:0000228|GO:0003
677|GO:0032922|GO:0006260|GO:0016310|GO:0007059|GO:0040016|GO:0000932|GO:0003682|GO:0043204|GO:0
016032|GO:0007623|GO:0006338|GO:0005654|GO:0031298|GO:0001046|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139080_PI430048170 0.3450678743383030.6541896991037640.333352837643612
0.3200936484159240.265341943506667A A A 0.5203483202981990.285299209225075
1.59387338228689 A A A LNCV6_139080_PI430048170 mRNA
AAGGGTACCTGACATTCTAAGATATCAAGACACTTAATATGTGGGCTATTAGCTGCTTAT NM_032160RefSeq
chr18_GL383571v1_alt - 152308 162457 DSEL 92126 dermatan sulfate epimerase-like
GO:0030208|GO:0000139|GO:0005975|GO:0009405|GO:0008146|GO:0044281|GO:0016021|GO:0030204|GO:0016
853|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137668_PI430048170 0.000683581049016591 0.6192058211972945.17279604473309
5.16636061831247 5.33045992245568 P P P 5.83918211600866 5.90771942623082
5.99884406604868 P P P LNCV6_137668_PI430048170 mRNA
CAGGTTATAGAAATTATGTTGTATTTAGTCAGTATGTCTTTTTGTGTAATGGACTGGGCC NM_031924RefSeq chr6
- 158977233 159000166 RSPH3 83861 radial spoke 3 homolog (Chlamydomonas) NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_105921_PI430048170 0.6767033799675870.9335854729742425.93251706113248
5.92267624864895 6.06680436739877 P P P 5.8119520199479 5.98325905177331
6.37081141804183 P P P LNCV6_105921_PI430048170 mRNA
GGGTATTTTCAAGATGGTGTGGAGGGAGATACAATTTGATGCAAGTCTTATACTTTTGAT NM_001104546 RefSeq
chr10 + 90871951 90908555 RPP30 10556 "ribonuclease P/MRP 30kDa subunit, transcript variant 1"
GO:0004526|GO:0005634|GO:0005655|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144030_PI430048170 0.0631029850864371 1.76874486993197 4.75611353900861
4.7747227627182 4.54622063340355 P P P 3.89222877431738 4.22627782401517

3.37830426718108 P P P LNCV6_144030_PI430048170 mRNA
TGTCCTGAAACATGAACCCAAAAAGAGACCCACAATAAACTCGTGACTTGTCCCCTCAAA NM_001136007 RefSeq
chr19 + 35115827 35124324 FXYD3 5349 "FXYD domain containing ion transport regulator 3,
transcript variant 3"
GO:0006821|GO:0050790|GO:0034220|GO:0005886|GO:0005887|GO:0034707|GO:0005789|GO:0051117|GO:0055
085|GO:0005254|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140338_PI430048170 0.30166224914525 0.8577779615589127.3677158546548 6.8988636534324
6.80591975738822 P P P 7.19637311303733 7.3996319760754 7.19559826318303 P P P
LNCV6_140338_PI430048170 mRNA
CCTGAGTCATGTGACCCATTCTCTAAAGACTAGAATATTTAACTTAAATCAGTGAGAAAC NM_024516RefSeq chr16
+ 29816206 29822495 PAGR1 79447 PAXIP1 associated glutamate-rich protein 1
GO:0005515|GO:0035097|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66437_PI430048170 0.0265002996462516 0.6465936120884218.1333305341186
7.83502958455472 8.23601801994155 P P P 8.46105796870586 8.69131640426504
8.93047745166858 P P P LNCV6_66437_PI430048170 mRNA
CTTCTGCAATAGTTCTTTAAAATCACAACAGTTAGCAAGCTGACTTTTGTAATGTGCTCA NM_005721RefSeq chr2
+ 113889933 113961552 ACTR3 10096 "ARP3 actin-related protein 3 homolog (yeast), transcript variant 1"
GO:0005515|GO:0034314|GO:0030056|GO:0005885|GO:0005884|GO:0002102|GO:0051491|GO:0006928|GO:0015
629|GO:0005829|GO:0016344|GO:0010592|GO:0009743|GO:0051015|GO:0007411|GO:0005911|GO:0046677|GO:0
070062|GO:0008356|GO:0033206|GO:0048013|GO:0060076|GO:0005524|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127475_PI430048170 0.0765458842505775 1.10600322907563 10.6541031233881
10.6577238063129 10.7161032222144 P P P 10.590502531582 10.4344112163611
10.5630281228109 P P P LNCV6_127475_PI430048170 mRNA
GGACTGTCATGGCATTTAGTTCAGAGTGGAGGGGCTTTGGCCTGAAATAAAATGCAAGTA NM_152244RefSeq chr17
+ 48107557 48122743 SNX11 29916 "sorting nexin 11, transcript variant 1"
GO:0016050|GO:0006886|GO:0019898|GO:0006897|GO:0005768 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130522_PI430048170 0.2012069656929988.73136254809232 0.287218781694002
4.43857896659524 3.48114904057023 A P P 0.3764106029147130.406957644261914
0.354106603986329A A A LNCV6_130522_PI430048170 mRNA
CAGTGGCCCAATGTGGCCAACGGAAGTTTTATAAAAGACAAAATGTATATCAATAAACAT NM_001098515 RefSeq
chr11 - 69004393 69013382 MRGPRF 116535 "MAS-related GPR, member F, transcript variant 1"
GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134588_PI430048170 0.1156874718713720.6644569242810544.89148253830339
4.74004633366419 4.95674437141655 P P P 5.02000600167743 5.47327080586122
5.77491902612541 P P P LNCV6_134588_PI430048170 mRNA
GGAATGGACCTGGTGTAACACACTTGAATATGTGTGATGCCAAACTTTTTAAAATACAAT NM_007246RefSeq chr4
+ 165207617 165323156 KLHL2 11275 "kelch-like family member 2, transcript variant 1"
GO:0005515|GO:0005737|GO:0016567|GO:0031463|GO:0003779|GO:0015629|GO:0001726|GO:0030027|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135215_PI430048170 0.6679014291445110.95663970448638 0.283740658769659
0.30134360663239 0.466578398626457A A A 0.31776576881554 0.284157600590793
0.623897600322883A A A LNCV6_135215_PI430048170 mRNA
AGCATGAAATAAGGCACTTTCACCTCATGGTAATCAACAATGACCTCAAATTGACTTAGA NM_001039112 RefSeq
chr8 + 123851986 124120061 FER1L6 NA fer-1-like family member 6 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127456_PI430048170 0.0256344118213639 0.6289703345193843.66118199315994

3.48008009790969 3.94933462261568 P P P 4.28258498155514 4.46951071391675
4.37845763678017 P P P LNCV6_127456_PI430048170 mRNA
TCCAGTGTCGTTTAACCTATGCAGTAAGATTCTGTCTTTGTAAAAGTAGTTCGTAGCAGA NM_024936RefSeq chr4
+ 25312773 25370383 ZCCHC4 29063 "zinc finger, CCHC domain containing 4"
GO:0008168|GO:0008270|GO:0003676|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135825_PI430048170 0.7005230273644190.9162308460583941 2.0601718802097
11.6780054219673 11.6200349702725 P P P 12.1494063018132 12.074944502282
11.4590018029516 P P P LNCV6_135825_PI430048170 mRNA
CACAGAAGGTTTTGAACTCTAAGAAATAAATTGGTTTGGTAATAAATGGCTTCTGGTCAG NM_003757RefSeq chr1
+ 32222369 32231604 EIF3I 8668 "eukaryotic translation initiation factor 3, subunit I"
GO:0005515|GO:0010467|GO:0005852|GO:0016282|GO:0033290|GO:0001731|GO:0003743|GO:0006412|GO:0006
413|GO:0005829|GO:0071541|GO:0006446|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134983_PI430048170 0.0430285493894092 1.36423384874189 6.3544897743518
6.30126580265324 6.63964145735956 P P P 6.03178981303375 6.01077599782616
5.92998776922788 P P P LNCV6_134983_PI430048170 mRNA
CTGTGTTGGAAATTTGACCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA NM_003785RefSeq chrX
- 49687450 49695993 PAGE1 8712 "P antigen family, member 1 (prostate associated)" GO:0006968
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130675_PI430048170 0.0404873292042086 0.6136113887209517.64422366953064
7.69429659097008 7.75005819976308 P P P 8.10958718166731 8.41515781277413
8.63238249704693 P P P LNCV6_130675_PI430048170 mRNA
ACAAATGGCCATTTGCTGTTAATAATTTGTTCTCAACTCTAGGATGTGGCTTGGTTTTTTNM_012342RefSeq chr10 +
28677494 28682939 BAMBI 25805 BMP and activin membrane-bound inhibitor
GO:0008284|GO:0005886|GO:0008360|GO:0090263|GO:0010718|GO:0035413|GO:0005114|GO:0032092|GO:0005
109|GO:0005737|GO:0016477|GO:0007179|GO:0016021|GO:0045893|GO:0030512 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_112663_PI430048170 0.0162914410874531 0.8043528700830896.14734811867679
6.30210107029207 6.32044917582603 P P P 6.56925701882997 6.61671080860169
6.53114281122071 P P P LNCV6_112663_PI430048170 mRNA
TTCTGCAGCCTGGATTATGTGAACCGGCTCTTTCTGAACTGGACAGAGGGTCAGGAGAGC NM_178238RefSeq chr7
+ 100358002 100367831 PILRB 29990 paired immunoglobin-like type 2 receptor beta
GO:0005515|GO:0007171|GO:0005887|GO:0007169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138472_PI430048170 0.1688637974853580.7230943488939153.75916879739761
4.52710819199463 3.92249806140985 P P P 4.82616990495034 4.581119617968
4.26883695751978 P P P LNCV6_138472_PI430048170 mRNA
CTTGTTAGGTGCTTTCCCATAGGAGGCCCTTCTTGAGAAACAATAAACTAGGTAGAACTA NM_004767RefSeq chr1
+ 202122900 202129506 GPR37L1 9283 G protein-coupled receptor 37 like 1
GO:0048712|GO:0043235|GO:0005515|GO:0042277|GO:0045665|GO:0005886|GO:0021940|GO:0008528|GO:0045
879|GO:0016021|GO:0043410|GO:0007193 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91627_PI430048170 0.02635667686997 1.43774259390567 6.13555662165603 6.18810237643528
5.99274105524997 P P P 5.39450465291686 5.78779701901606 5.54207894013394 P P P
LNCV6_91627_PI430048170 mRNA
TAAATGGGGACTTCGATGGCGGAAACTTTTATTTCACTGAACTGGATGCCAAGACCGTGA NM_001243246 RefSeq
chr1 - 42746334 42767084 P3H1 64175 "prolyl 3-hydroxylase 1, transcript variant 3"
GO:0008285|GO:0005783|GO:0005518|GO:0005634|GO:0019511|GO:0032403|GO:0003674|GO:0030278|GO:0006
457|GO:0030198|GO:0030199|GO:0032991|GO:0070062|GO:0031418|GO:0005506|GO:0005578|GO:0050821|GO:0
060348|GO:0061077|GO:0016020|GO:0019797|GO:0018126|GO:0032963|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_140680_PI430048170 0.0938245744087746 1.3376355803549 8.29602745628651
8.74518617301627 8.47976046219656 P P P 8.31764279345034 8.10878387462661
7.83003776837374 P P P LNCV6_140680_PI430048170 mRNA
AAGGGTTCCTGTGATTGCGTTTAGCGCCCTCCCGTTCTGTCCATTTGTCTTGTCTGCCGA NM_006653 RefSeq chr6
- 41770175 41779905 FRS3 10817 fibroblast growth factor receptor substrate 3
GO:0005515|GO:0007165|GO:0005886|GO:0008543|GO:0005158|GO:0005104 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143525_PI430048170 0.50111888154976 1.44482749085409 0.278290645539396
0.297130635213654 1.66614522920746 A A A 0.422357167599361 0.361247884883217
0.335370668397683 A A A LNCV6_143525_PI430048170 mRNA
GCCAACCTTTGTATGGAGATGATTTTATAACCATGCACTTTTGTAACTGTGCAGAATTTT NM_001005210 RefSeq
chr11 + 57181746 57191714 LRRC55 219527 leucine rich repeat containing 55
GO:0005886|GO:0016021|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122645_PI430048170 0.259890668474522 0.835102031049388 0.514007513472435
0.524890630701838 0.336739055165937 A A A 1.01907322970336 0.570639411543959
0.519428678515549 A A A LNCV6_122645_PI430048170 mRNA
ACCTTCACGCCATCTATGAAGTCCACCAAGGATTATCCTGATGAGGTGATCAACTTCATG NM_004186 RefSeq chr3
+ 50155414 50189075 SEMA3F 6405 "sema domain, immunoglobulin domain (Ig), short basic
domain, secreted, (semaphorin) 3F"
GO:0021785|GO:0045499|GO:0016020|GO:0007411|GO:0021637|GO:0050919|GO:0048843|GO:0021675|GO:0004
872|GO:0048846|GO:0021612|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128746_PI430048170 0.315599372132475 1.02519310392236 0.300478383781494
0.278520101000156 0.367528001456753 A A A 0.291842808692353 0.271040926036957
0.277373946526539 A A A LNCV6_128746_PI430048170 mRNA
CCAGAGAGCAAGTGAGGCAATCTGGCAAAAGATTAATAAAGATGTAAACCCCTGGAAAAA NM_052959 RefSeq
chr11 + 124611556 124620355 PANX3 116337 pannexin 3
GO:0005886|GO:0007267|GO:0005921|GO:0055077|GO:0016021|GO:0055085|GO:0034214|GO:0006811 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65190_PI430048170 0.0494605151999609 2.6191612172831 2.9014674879316
2.59004305195841 2.61121515653775 A A A 0.510786085377505 1.73348059802337 1.4512345025383
A A A LNCV6_65190_PI430048170 mRNA
TTCAACCCTCAGGAATCCAAGCGCTTTGTGCAGTGGCAGTCGTCTATCTGAGCCCCTCCT NM_001201461 RefSeq
chr19_GL949746v1_alt + 321948 343243 TTYH1 57348 "tweety family member 1, transcript variant 3"
GO:0006821|GO:0005886|GO:0005509|GO:0031589|GO:0034707|GO:0031527|GO:0055085|GO:0032433|GO:0044
070|GO:0007067|GO:0016337|GO:0034220|GO:0030868|GO:0005381|GO:0006826|GO:0072320|GO:0046847|GO:0
016021|GO:0034755. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105114_PI430048170 0.100810674520227 0.891194653462185 5.64265199879406
5.44934132207797 5.63826560437821 P P P 5.67855145575596 5.79864706318716
5.75736796177309 P P P LNCV6_105114_PI430048170 mRNA
AAAGCTCTGAGGAACATGAATACAGTGATGAAGCTCCTCAGGAAGATGAGGGCTTTATGG NM_024551 RefSeq chr12
+ 1691080 1788679 ADIPOR2 79602 adiponectin receptor 2
GO:0007565|GO:0019395|GO:0030308|GO:0046982|GO:0005886|GO:0007584|GO:0033211|GO:0055100|GO:0042
562|GO:0042802|GO:0007507|GO:0009755|GO:0046326|GO:0004872|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141996_PI430048170 0.659768066352612 0.940342238382973 4.6049830023173
4.10931820852264 4.31572320446534 P P P 4.66729958295944 4.41442760630635
4.22322546597894 P P P LNCV6_141996_PI430048170 mRNA
AGGGGAGACGTGTGACCCTCTCCAGGATTTGAGGGGCTTAAGACACCCCCAACCAAAAAA NM_001144950
RefSeq chr19 + 55488502 55519099 SSC5D 284297 "scavenger receptor cysteine rich family, 5

domains, transcript variant 1"
GO:2000483|GO:0050830|GO:0042494|GO:0050840|GO:0007275|GO:0005615|GO:0006898|GO:0005622|GO:0031012|GO:0050829|GO:0005737|GO:0016020|GO:0045087|GO:0043236|GO:0001968|GO:0005044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142682_PI430048170 0.0870927640572225 0.8421595595074597.88815265790846 7.87509585734818 8.12934810850279 P P P 8.19040884732166 8.10104306565182 8.34818276258463 P P P LNCV6_142682_PI430048170 mRNA
CTGGCATTGCTTTGCCTTATCATCTCATCTGGAGTTTTTAAATGCCATTTGTTTCAGTTG NM_001047RefSeq chr5 + 6633386 6669562 SRD5A16715 "steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)"
GO:0003865|GO:0006702|GO:0005789|GO:0009055|GO:0007548|GO:0044281|GO:0016021|GO:0047751|GO:0030154|GO:0008202|GO:0055114|GO:0007530 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90982_PI430048170 0.0373350588981504 1.87645127143283 3.18322465650013 2.52105421377507 3.1376694787818 P A P 1.63761797396205 2.21335220736848 2.27527251075753 A A A LNCV6_90982_PI430048170 mRNA
CAGATGAAATTGATGTATGAACATAATCTTCAGAGAACAGCCTGCAATATGACCTATGGA NM_198428RefSeq chr7 + 33129539 33606068 BBS9 27241 "Bardet-Biedl syndrome 9, transcript variant 2"
GO:0005515|GO:0034464|GO:0060170|GO:0006996|GO:0015031|GO:0005829|GO:0003674|GO:0005929|GO:0042384|GO:0045444|GO:0000242|GO:0007601|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52239_PI430048170 0.00964056621253781 1.56321014819785 5.30069592893469 5.15642189913748 4.9873010810413 P P P 4.43755789698277 4.5097075582415 4.577228800742 P P P LNCV6_52239_PI430048170 mRNA
TATACAGGATCTCCTATTGCACAGCAGACAAGATGCACGACAAGGTGTTTGCATACATCG NM_015627 RefSeq chr1 + 25543584 25568886 LDLRAP1 26119 low density lipoprotein receptor adaptor protein 1
GO:0005515|GO:0030424|GO:0035615|GO:0035612|GO:0005883|GO:0030159|GO:0005829|GO:0090205|GO:0031623|GO:0009925|GO:0001540|GO:0030276|GO:0006810|GO:0008203|GO:0090118|GO:0042632|GO:0035591|GO:0030121|GO:0030122|GO:0043393|GO:0005546|GO:0009967|GO:0042982|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141799_PI430048170 0.164413773432194 0.579594981362831 6.15720190058541 4.9165861959281 4.78563921355775 P P P 6.45803393211688 6.32319972082265 5.77730959129035 P P P LNCV6_141799_PI430048170 mRNA
CTCCTCCCATTTGTGCATCAATGAGACATATTTATAAAGTGCTAAATTATTCTGTGCCAT NM_000621 RefSeq chr13 - 46831541 46897076 HTR2A 3356 "5-hydroxytryptamine (serotonin) receptor 2A, G protein-coupled, transcript variant 1"
GO:0008219|GO:0030424|GO:0008284|GO:0001659|GO:0005886|GO:0043267|GO:0050731|GO:0048148|GO:0007268|GO:0051378|GO:0007202|GO:0032403|GO:0044380|GO:0014059|GO:0005829|GO:0070852|GO:0001965|GO:0004993|GO:0045907|GO:0043406|GO:0043198|GO:0071886|GO:0008144|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135338_PI430048170 0.00128378680055707 1.4794994961204 10.1585533298665 10.2109682527423 10.078532562038 P P P 9.56625697822566 9.67977699436026 9.50424344967769 P P P LNCV6_135338_PI430048170 mRNA
CATGGTAGGAGCTGGACCAACTGTATATAGTTTTCAATAAACTTTTTCCTTTTCTGTTCA NM_054035 RefSeq chr17 - 28546706 28552628 UNC119 9094 "unc-119 homolog (C. elegans), transcript variant 2"
GO:0005515|GO:0005813|GO:0061098|GO:1900186|GO:0007268|GO:0051233|GO:0007109|GO:0005829|GO:0006897|GO:0008289|GO:0045171|GO:2001287|GO:0000922|GO:0042953|GO:0007602|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129343_PI430048170 0.902616321187181 1.00172758064181 0.78128640526688 0.838961714220984 0.798182021161336 A A A 0.636911178498609 1.1306726108875 0.577906203054423 A A A LNCV6_129343_PI430048170 mRNA

GGATACTGGCAAAAGTGCACATATTTCATAACCAAATTAGTAGCACCAGTCTTAATTTGA NM_005409 RefSeq chr4 - 76033686 76036197 CXCL11 6373 "chemokine (C-X-C motif) ligand 11, transcript variant 1" GO:0005515|GO:0008009|GO:0070098|GO:0048248|GO:0007267|GO:0005576|GO:0005615|GO:0002690|GO:0010818|GO:0007165|GO:0006955|GO:0006954|GO:0006935|GO:0007186|GO:0042127|GO:0032496|GO:0043950|GO:0030816|GO:0051281|GO:0008201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97910_PI430048170 0.153787739856591 0.763131660988879 6.43844462159119 6.07372745605056 6.01658252631273 P P P 6.80973645069102 6.63224036481735 6.23577485533905 P P P LNCV6_97910_PI430048170 mRNA
AGTGTCCCCCAAAGAGCCCAGTACAGTGTCTGCCTCCAGCTTCCTCTGGCTGTGCCCCAA NM_032563 RefSeq chr1 - 152579383 152580504 LCE3D 84648 late cornified envelope 3D GO:0031424 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127580_PI430048170 0.0209945823873446 0.504478033790492 2.73993038580349 3.18963339900461 2.68336925663382 A P A 3.83803235666451 3.94006132494116 3.84910421748328 P P P LNCV6_127580_PI430048170 mRNA
CCCATGTGTTTTGATTCCTGCTCTTTGTTACAGTTCCATTAAATGAGTAATAAAGTTTGG NM_003483 RefSeq chr12 + 65824459 65966291 HMGA2 8091 "high mobility group AT-hook 2, transcript variant 1" GO:0005515|GO:0003906|GO:0030261|GO:0004677|GO:0006325|GO:0046332|GO:0035985|GO:0010564|GO:0035986|GO:0035987|GO:0035988|GO:0071158|GO:0000989|GO:0032993|GO:0002062|GO:0045444|GO:0000975|GO:0008301|GO:0071141|GO:0031492|GO:0007275|GO:0001047|GO:0000122|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128262_PI430048170 0.91857952081552 1.03291739279575 0.42598433016271 1.10993986150717 0.366805433235804 A A A 0.996625560406852 0.394591881130924 0.410079282547601 A A A LNCV6_128262_PI430048170 mRNA
GAGTTTCAGATGGAATGACTTGTCTGAAATTTGTAAAGCTTAATATAGGTTTTGGGGGAA NM_153235 RefSeq chr6 - 139240060 139292071 TXLNB 167838 taxilin beta GO:0019905|GO:0005515|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137363_PI430048170 0.117775683963344 1.05784701395958 7.88895020296263 7.7841479765163 7.83113588389626 P P P 7.71064528358265 7.74700857085609 7.80357599862434 P P P LNCV6_137363_PI430048170 mRNA
CTCTTGGGAAGCTTCTTTTCTGTTCTAACAGTTCCCTGTTAAAATGAAAATCTTAGGCCA NM_174921 RefSeq chr4 - 39550925 39638861 SMIM14 201895 small integral membrane protein 14 GO:0005783|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142498_PI430048170 0.257150855374432 0.779207176615152 3.30019878669835 2.46089359552813 2.69423152122084 P A A 3.19964693224276 2.9938370972668 3.44096295842213 P P P LNCV6_142498_PI430048170 mRNA
TGTGGAAAGTACCAAGACCCTGGCATGACGCAATATGGATTGTAATCATCGTCCCCATTT NM_013435 RefSeq chr18 - 59267034 59273393 RAX 30062 retina and anterior neural fold homeobox GO:0007389|GO:0001077|GO:0045944|GO:0060173|GO:0043010|GO:0005634|GO:0021854|GO:0000978|GO:0007601|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143046_PI430048170 0.209503064551158 0.731328899804974 11.4850035134754 10.669716125888 10.6234486775356 P P P 11.4868456616092 11.4570944835488 11.3566484795605 P P P LNCV6_143046_PI430048170 mRNA
GAGGGAATCCTGGCCCCCTCCCCAGAAGCCATTTGTCAATAAACCATTTCTAAGAAAAAA NM_198998 RefSeq chr2 + 240691844 240698483 AQP12A 375318 aquaporin 12A GO:0005215|GO:0006810|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133785_PI430048170 0.910589806821056 1.01322706887602 0.931519176755973 0.601638363844924 0.283972004079754 A A A 1.04761144065399 0.357945771434639

0.30212386077601 A A A LNCV6_133785_PI430048170 mRNA
ATATTATTGCAGGAACAAGGAATGGAAAAGGAAGAGTACCTAATACATACGAGGTTCTGA NM_001005164 RefSeq
chr11 - 5058649 5059627 OR52E2 NA "olfactory receptor, family 52, subfamily E, member 2" NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_130930_PI430048170 0.0267904525885035 0.743677814864526 7.91940772208536
8.0694625674573 8.11313440476158 P P P 8.37417696052208 8.35074261108225
8.64676191514452 P P P LNCV6_130930_PI430048170 mRNA
TGGAAGGCTATGAAAAGAACTTGAAATTGTCGGAATATGTGCTCTCTTCATGTCATATTC NM_153232 RefSeq
chr19 - 39538805 39540198 EID2 163126 EP300 interacting inhibitor of differentiation 2
GO:0005515|GO:0046332|GO:0006351|GO:0030154|GO:0005622|GO:0007183|GO:0007181|GO:0007517|GO:0042
127|GO:0005654|GO:0017015|GO:0045892|GO:0030512 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_73807_PI430048170 0.922906304490093 1.00952167771104 0.721656139246967
2.11657219573478 0.545547027457257 A A A 1.0411646997649 0.618028266809416
1.91929577427347 A A A LNCV6_73807_PI430048170 mRNA
GAAGAAATTCCTCAGATTCCTTCTGTAGGAATTCAGAGGACAAGATTTATGGTTATAGGA NM_001042601 RefSeq
chr3 + 180602129 180611130 TTC14 151613 "tetratricopeptide repeat domain 14, transcript variant
2" GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137859_PI430048170 0.0345111217402589 0.668572688052885 7.07739932515925
7.26865755162714 7.48739496676453 P P P 7.84349367396689 7.62321551458193
8.09910291284875 P P P LNCV6_137859_PI430048170 mRNA
GTGAGTAGGGTGAACTGGACTGCATATTAGTTTATTTGTTGCCATAATCACATTTTTGAA NM_153256 RefSeq
chr10 + 11823397 11872277 PROSER2 254427 proline and serine rich 2 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127559_PI430048170 0.735151701120441 1.06007690111642 4.14017331659832
3.57847729884189 3.74175801290497 P P P 3.87938311667471 3.72984929093914
3.64818970546124 P P P LNCV6_127559_PI430048170 mRNA
AAGTCGTGAAAAAGTCATCAGGAGTTAATCCACAGAACCTTGGAGAGTACATGGCCCTGT NM_032207 RefSeq
chr19 + 16496310 16521369 C19orf44 84167 "chromosome 19 open reading frame 44, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135624_PI430048170 0.258733247823238 1.13513681272803 11.8689048451933
11.9872977693202 12.2333741640546 P P P 11.7463027579403 11.7934276013529
12.0114245873243 P P P LNCV6_135624_PI430048170 mRNA
GGGATGTTTGTTGGCTCTGTTGTGTTTATTCACCAATTTGTACATTATTTGTTGTCCTTT NM_001286416 RefSeq
chr21 - 44805616 44818129 SUMO3 6612 "small ubiquitin-like modifier 3, transcript variant 2"
GO:0005515|GO:0034504|GO:0016925|GO:0005634|GO:0005737|GO:2000060|GO:0016605|GO:0019789|GO:0000
776|GO:0005654|GO:0044267|GO:0043687|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132036_PI430048170 0.0816616297457996 1.30289195460514 9.10818343166932
9.24229917370366 9.23504289695568 P P P 8.54773180289423 8.89622345336056
8.96645901959402 P P P LNCV6_132036_PI430048170 mRNA
TGAACAGCAGGGGGTTGTGTGTCTGTTCTGTTTCTCTGCTTGCCGAACTTTCTCAATAAA NM_001199803 RefSeq
chr2 + 24793305 24822376 CENPO 79172 "centromere protein O, transcript variant 2"
GO:0034080|GO:0006334|GO:0000777|GO:0005654|GO:0000278|GO:0005829 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_140659_PI430048170 0.987232037999973 0.999938230894666 0.296021777412997
0.335947567463455 0.389394724323995 A A A 0.360564301404601 0.339913494318149
0.32242446970348 A A A LNCV6_140659_PI430048170 mRNA
CCTGGTTGGGACTGATATTGTCATAGCTATGATAAACTTTGGATATTAGCAGAATTTGGG NM_052862 RefSeq

chr1 + 167630236 167706249 RCSD1 92241 RCSD domain containing 1
GO:0071474|GO:0051015|GO:0003009|GO:0005884 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135387_PI430048170 0.0198523964924943 0.326156247039898 2.99458234894085
1.8595784175419 2.64747922605793 P A A 3.78099715805505 4.4968336494054
4.20548843921923 P P P LNCV6_135387_PI430048170 mRNA
CCAGTCAACCACTTCAAATTCCTACACTGTCTCAAGAGTATTAAAAGGATTATATGAAGT NM_145007 RefSeq
chr19 - 55785396 55836762 NLRP11 204801 "NLR family, pyrin domain containing 11, transcript
variant 1" GO:0016715|GO:0005524|GO:0055114 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130925_PI430048170 0.512970853680584 0.987194294372086 0.396598296888092
0.401740311817115 0.355868272367599 A A A 0.441315881377737 0.369412320497981
0.398789971427925 A A A LNCV6_130925_PI430048170 mRNA
GTAGAAGGAACGTTTAGGTAGCACCTATTTTGTACTGATTCTACAAGTAGGGCCCGAGGT NM_031309 RefSeq
chr8 - 144330564 144336281 SCRT1 83482 scratch family zinc finger 1
GO:0006355|GO:0003700|GO:2001222|GO:0005634|GO:0000122|GO:0003677|GO:0046872|GO:0006351 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_144719_PI430048170 5.53626041825251e-05 2.41046191636183 5.62388056356768
5.59957939732797 5.479428640038 P P P 4.35384609103278 4.29290883819309
4.25043574772543 P P P LNCV6_144719_PI430048170 mRNA
ATGGAGGTGTAGGCTGGAGAGACATTGTGGGTGTGTATCTTCTTATCTCATTTCACAAGA NM_001271749 RefSeq
chr19 + 47332146 47342015 C5AR2 27202 "complement component 5a receptor 2, transcript
variant 1"
GO:0005515|GO:0050679|GO:2000482|GO:0004944|GO:0005886|GO:0032720|GO:0045177|GO:0006954|GO:0009
925|GO:1900165|GO:0006935|GO:0007186|GO:0090024|GO:0016021|GO:0070374 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_127636_PI430048170 0.0816120958517138 1.5264825371115 5.90745762361383
5.66239076277266 5.21800666710147 P P P 5.27982845836392 4.95062525749444
4.76075072463154 P P P LNCV6_127636_PI430048170 mRNA
CCACCCTCCGGCCAGCGAGTGGTCAAGGATTTTTATAAAAATCACGATAAGATTAAAAAA NM_001130964 RefSeq
chr3 - 38007495 38024787 PLCD1 5333 "phospholipase C, delta 1, transcript variant 1"
GO:0070300|GO:0043647|GO:0005886|GO:0005509|GO:0044281|GO:0001525|GO:0005829|GO:0016042|GO:0032
794|GO:0035556|GO:0005737|GO:0004435|GO:0042127|GO:0060716|GO:0001786|GO:0004871|GO:0006644|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104614_PI430048170 0.0978341978838664 1.24615649820764 9.82375142985079
9.83732398916839 9.73855796321537 P P P 9.54933398393934 9.62596664850305
9.24663016575735 P P P LNCV6_104614_PI430048170 mRNA
AGATAGAGAGGTTTGAGTTTTATGAACGGGCTAAGAAGGCTTTTGCTGTTGTGGCAACGG NM_001301828 RefSeq
chr10 - 133355153 133358025 FUOM 282969 "fucose mutarotase, transcript variant 4"
GO:0045665|GO:0060180|GO:0016857|GO:0042806|GO:0006004|GO:0036065 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_137816_PI430048170 0.833753900372559 0.986501311838037 0.404078930647529
0.295677833099535 0.296660618497737 A A A 0.262089391627999 0.305292260866255
0.481123072228098 A A A LNCV6_137816_PI430048170 mRNA
GGGTTGTGTGATCTAGCTGTGAATGTAGCAATATAGAACGTTTAATAGAATGATAAGCAA NM_003866 RefSeq
chr4 - 142028028 142846451 INPP4B 8821 "inositol polyphosphate-4-phosphatase, type II, 105kDa,
transcript variant 1"
GO:0046850|GO:0005794|GO:0006661|GO:0043647|GO:0036092|GO:0006874|GO:0045671|GO:0034594|GO:0044
281|GO:0016316|GO:0051896|GO:0005829|GO:0008289|GO:0007165|GO:0016311|GO:0034597|GO:0006644|GO:0

046822 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130739_PI430048170 0.000923271321832023 1.41891238551413 13.6315056271022
13.7135896794668 13.6554956913876 P P P 13.2382685845274 13.114233153271
13.1318246806962 P P P LNCV6_130739_PI430048170 mRNA
TGCACTGAGTGTCACTTTGCTGCAGCTCGTTTCTTTCCAATAAAAGTTTCTGTGACTTAG NM_032272 RefSeq chr8
+ 144104401 144107612 MAF1 84232 MAF1 homolog (S. cerevisiae)
GO:0030424|GO:0005813|GO:0005886|GO:0005730|GO:0060077|GO:0005634|GO:0000994|GO:0030425|GO:0006
351|GO:0043231|GO:0005829|GO:0005622|GO:0005737|GO:0070217|GO:0016480|GO:0001032|GO:0005654|GO:0
001030|GO:0001031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133398_PI430048170 0.366006737125728 1.1865003234248 11.3371709428643
11.1621280905297 11.2519342422845 P P P 11.4542832692987 10.6428366256584
10.7833989473689 P P P LNCV6_133398_PI430048170 mRNA
GGGGTGGTAGAAAAGGTAGAGTAGGCTGTGGCAATGGAATAAAACACGATTAAAAACGTT NM_004911 RefSeq
chr7 - 149003061 149028690 PDIA4 9601 "protein disulfide isomerase family A, member 4"
GO:0005515|GO:0042470|GO:0034976|GO:0009306|GO:0061077|GO:0009986|GO:0006457|GO:0005783|GO:0005
788|GO:0003756|GO:0045454 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137524_PI430048170 0.239448619828186 0.740662923121968 0.361574490095039
0.401182990633835 0.333023654798364 A A A 1.19951666931545 0.38272599215269
0.694176089807529 A A A LNCV6_137524_PI430048170 mRNA
TATTTCTGCTTAAAATGTGGTGTGTTTGGGGATGCCCCACACAACAAGACAGGCTTTTCC NM_153033 RefSeq
chr7 + 66628880 66643229 KCTD7 154881 "potassium channel tetramerization domain containing
7, transcript variant 1" GO:0005886|GO:0051260|GO:0005829 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129969_PI430048170 0.543248367436977 1.21576093285986 1.17354216201729
0.298059023046942 1.27443959509861 A A A 1.23389634092562 0.31261632786318
0.336168310490301 A A A LNCV6_129969_PI430048170 mRNA
CAAAAAGATGAAGGAAATCACCGAGACAGTGACCAACACAGTCACAAATGCCATCACCCA NM_001137549
RefSeq chr10 - 47995339 47999791 FAM25G NA "family with sequence similarity 25, member G"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130162_PI430048170 0.581900765091862 0.941486436610585 0.340352728346649
0.347918781251264 0.273888187276639 A A A 0.272726761924627 0.287459706205325
0.634316938392378 A A A LNCV6_130162_PI430048170 mRNA
GACCTGGTCACATTGGGTCTTTTTAATTGATACTGTACAATCTTGTTGTCACTATGTTTA NM_001220484 RefSeq
chr14 - 73478483 73558947 HEATR4 399671 "HEAT repeat containing 4, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107455_PI430048170 0.0124201703090736 3.62733902755557 1.92762488806663
2.45303080427234 2.74980837156355 A A A 0.4787502728763160.50075498202704
0.681827187668582 A A A LNCV6_107455_PI430048170 mRNA
ACAGACCATTGAGACAGAGGAGGTGAACAAGACTCTGAAGGCGACACTGCAGGCCCTGCT NM_001164741
RefSeq chrX - 153907375 153926260 ARHGAP4 393 "Rho GTPase activating protein 4, transcript variant
1"
GO:0005515|GO:0051056|GO:0048011|GO:0030336|GO:0043065|GO:0005794|GO:0007264|GO:0005874|GO:0009
967|GO:0007266|GO:0097190|GO:0032855|GO:0005100|GO:0030426|GO:0005829|GO:0048365|GO:0005737|GO:0
010764|GO:0030517|GO:0005070|GO:0007010|GO:0005654|GO:0030675|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134704_PI430048170 0.0194459942838113 1.82630183886878 9.48640784686848
9.79095360660682 10.0076218880075 P P P 8.96409770240093 8.79218549344805 8.9621822392592
P P P LNCV6_134704_PI430048170 mRNA
ACTACCCCTATAAGTTTGCCAATAAAACCATCACCTGCTTACACCTTTTTGAACTTTATA NM_001145450 RefSeq

chr2 + 38875961 38882709 MORN2 729967 MORN repeat containing 2 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_95602_PI430048170 0.9886041655724720.9935350185145436.83234381696378 6.76002500257503
6.47613957079649 P P P 6.42195456193443 6.73098917626006 6.92391106207574 P P P
LNCV6_95602_PI430048170 mRNA
CCGCCAAGAAGCAGGAATTAGAAGAGATCTGCCATGACCTAGAGGCCAGGGTGGAGGAGG NM_002473 RefSeq
chr22 - 36281276 36388067 MYH9 4627 "myosin, heavy chain 9, non-muscle"
GO:0005515|GO:0005516|GO:0031594|GO:0042641|GO:0008360|GO:0031032|GO:0038032|GO:0050900|GO:0015
031|GO:0042803|GO:0000910|GO:0051015|GO:0007411|GO:0006509|GO:0070062|GO:0008305|GO:0031532|GO:0
005819|GO:0007520|GO:0001701|GO:0043234|GO:0043534|GO:0043531|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134927_PI430048170 0.1699300156609121.08441264005555 10.9665054519057
10.8617010841003 11.02627571019 P P P 10.9148926024439 10.7402562270112
10.8480219531264 P P P LNCV6_134927_PI430048170 mRNA
CATTCTCTCTGAGGGCAGATGAGGCGCAGGAAAATAGTCTTGGAAATGTTAAATATGATG NM_032286 RefSeq chr5
- 6371925 6378526 MED10 84246 mediator complex subunit 10
GO:0005515|GO:0010467|GO:0006367|GO:0001104|GO:0045944|GO:0019827|GO:0016592|GO:0005654 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141443_PI430048170 0.0384866633685262 0.4896109673827295.90982037730642
5.40117551407618 5.72617618941144 P P P 6.19669880290727 6.78256255077475
7.06376285422781 P P P LNCV6_141443_PI430048170 mRNA
GGTTGGTTTTGGTGTAACATCTTCAACATGTCACACTGGCTATCAAAGAATAAGAAAATT NM_001282936 RefSeq
chr1 - 47250138 47314147 STIL 6491 "SCL/TAL1 interrupting locus, transcript variant 3"
GO:0005515|GO:0043066|GO:0005813|GO:0007368|GO:0033504|GO:0005814|GO:0008283|GO:0045737|GO:0001
843|GO:0001701|GO:0005829|GO:0007224|GO:0001947|GO:0051298|GO:0005737|GO:0000578|GO:0035264|GO:0
060271|GO:0071539|GO:0021915|GO:0071174|GO:0030900|GO:0030903|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136503_PI430048170 0.1887478977602540.60282517190168 0.27551895443482
0.3057773901737320.388488517467096 A A A 1.4689967347737 0.335729953422157
1.13722949496407 A A A LNCV6_136503_PI430048170 mRNA
GGCAACCACAGGTTTAAATGAAGACAAGCTGAAACAACACAAAACTGTTTTTATCTAAGA NM_133179 RefSeq chrX
- 52862528 52868088 XAGE3 170626 "X antigen family, member 3, transcript variant 1" GO:0005515
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144557_PI430048170 0.0614126001438250.6525837229806512.48658219500381
2.20727015168767 2.18660239631861 A A A 2.78407446071973 2.64457170446901
3.24784229067733 P P P LNCV6_144557_PI430048170 mRNA
CCTGAAAGATGCGACATTGCTTTTACCAACACCTCCACATTTCCTATACATAAAAATAAA NM_021047 RefSeq chr19
+ 19865904 19893484 ZNF253 56242 zinc finger protein 253
GO:0006355|GO:0008270|GO:0005634|GO:0045892|GO:0003677|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_29793_PI430048170 0.2473928794477281.41790799951214 1.2632721303671 1.79414043694204
1.66757547700032 A A A 1.4747497720541 0.3145700655979131.23653711035928 A A A
LNCV6_29793_PI430048170 mRNA
TGGTGAAGGGGTGGAGCAAAGGAAACTAGTCCACTCTCATCAGGGCCAACTCACGCACCT NM_001242885
RefSeq chr16 + 89321132 89325110 LOC100287036 NA uncharacterized LOC100287036 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_130032_PI430048170 0.16252351238968 0.7916909185413756.32631119026784
6.37202583341308 6.85746909996622 P P P 6.69777379639231 6.94960457599957
6.96616527896439 P P P LNCV6_130032_PI430048170 mRNA

GTGTACTCATCAGCCAGCTTAAGATACAGATGTTGTCGACATTTTAGAAGTTCCCTAAGG NM_139126RefSeq chr6 - 149504494 149546102 PPIL4 85313 peptidylprolyl isomerase (cyclophilin)-like 4 GO:0000413|GO:0000166|GO:0006457|GO:0003755|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130353_PI430048170 0.000369788058608888 1.62603959093109 8.10326455023177 7.96005426985447 8.09372055355072 P P P 7.41881455320272 7.35133916282071 7.28404782363774 P P P LNCV6_130353_PI430048170 mRNA
ATTATGAACTACTCAGTCAAACATCCCAAATACCCACCTCGGAAAGACTTGGTCCGAGCT NM_006645RefSeq chr11 - 72754728 72793705 STARD10 10809 StAR-related lipid transfer (START) domain containing 10 GO:0005515|GO:0005902|GO:0046581|GO:0035360|GO:0016020|GO:0032782|GO:0008289|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141793_PI430048170 0.0384144627415307 0.969741371136782 0.338764783148097 0.369198812251853 0.338755542922225 A A A 0.40645630660605 0.400664159877312 0.372570206657184 A A A LNCV6_141793_PI430048170 mRNA
CCTTCTTTCTGTTCAGTCCTAAAATTCGAAATAAAGTGAGACTATGGTTCACCTGTATAA NM_005335RefSeq chr3 - 121631397 121660948 HCLS1 3059 "hematopoietic cell-specific Lyn substrate 1, transcript variant 1" GO:0005515|GO:0051897|GO:0008284|GO:0017124|GO:2000251|GO:0050731|GO:0005634|GO:0032403|GO:0042993|GO:0005739|GO:0035556|GO:0005737|GO:0033138|GO:0030833|GO:0045944|GO:0030854|GO:0001085|GO:0030041|GO:0009725|GO:0005667|GO:0006355|GO:0042531|GO:0019901|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133377_PI430048170 0.61891158745186 0.973046412723153 0.475542182849212 0.434285542698932 0.247051080866867 A A A 0.379494170832537 0.470872435409847 0.433437198618452 A A A LNCV6_133377_PI430048170 mRNA
TCCCACACTGTCTTAGAGAACTTGTCACCAGAAACCACATGTATTTGCATGTTTTTTGTT NM_003240RefSeq chr1 - 225936597 225941383 LEFTY2 7044 "left-right determination factor 2, transcript variant 1" GO:0010862|GO:0030168|GO:0042981|GO:0005576|GO:0007275|GO:0060395|GO:0005125|GO:0005160|GO:0005615|GO:0031012|GO:0007596|GO:0043408|GO:0002576|GO:0016049|GO:0031093|GO:0007179|GO:0048468|GO:0008083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136737_PI430048170 0.154902905267716 1.33311553234335 0.533055782445705 1.08375323520994 1.06404287399526 A A A 0.423500185358335 0.515451410563004 0.558817663838018 A A A LNCV6_136737_PI430048170 mRNA
AAATTCTACTCACTGTGCTCCATATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTCA NM_001004489 RefSeq chr11 + 6785016 6786014 OR2AG1 NA "olfactory receptor, family 2, subfamily AG, member 1 (gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71064_PI430048170 0.0204156586564735 1.50834183152226 9.98099470423961 9.57106168433793 9.70047994657655 P P P 9.18576291394081 9.30770287529224 8.99386760058656 P P P LNCV6_71064_PI430048170 mRNA
TGTGTCTGCATAAACCCTCCTGTCCTGGACGTGACTTCATCCTGAGGAGCCACAGCACAG NM_001247RefSeq chr20 + 25195702 25226724 ENTPD6955 "ectonucleoside triphosphate diphosphohydrolase 6 (putative), transcript variant 1" GO:0051592|GO:0017111|GO:0009986|GO:0005886|GO:0000139|GO:0045134|GO:0008152|GO:0032026|GO:0008894|GO:0016021|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136798_PI430048170 0.832006651782633 1.01646339912418 13.1099300673387 13.2556612334852 13.3686871053729 P P P 13.3079917545187 13.0904671488791 13.2676063867369 P P P LNCV6_136798_PI430048170 mRNA
AGTCTTTTAGGAGATTTACAATATCTGTTCTTTTGCTCATCTTAGACCACAGACTGACTTNM_001165258 RefSeq chr6 + 10722914 10731129 TMEM14C 51522 "transmembrane protein 14C, transcript variant 1" GO:0031966|GO:0016021|GO:0006783 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144534_PI430048170 0.882464590126327 1.01854131816539 7.04743678028694

6.77349591774277 6.67551663215768 P P P 6.89543055627429 6.85014782339321
6.68953411523164 P P P LNCV6_144534_PI430048170 mRNA
GCCTTCCCTATCCCCTGTACCTGACAATCTATGAGTTTGCTTCTTTATTTCTGTCTATAC NM_052917 RefSeq chr2 +
153871897 154453977 GALNT13 114805 "polypeptide N-acetylgalactosaminyltransferase 13, transcript
variant 1"
GO:0004653|GO:0006493|GO:0000139|GO:0030246|GO:0016266|GO:0016021|GO:0044267|GO:0046872|GO:0043
687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138836_PI430048170 0.0730258824999599 0.6624556703849343.83594310126938
3.55654437275644 4.00828443874019 P P P 4.31345338755456 4.09193955826288
4.73733496697587 P P P LNCV6_138836_PI430048170 mRNA
CCAATGTATGGGTTCTTGTTAACAGAATGTGTAACAGAAATACTGAAAGACTTTTGCCTA NM_001023567 RefSeq
chr15 - 34525282 34536021 GOLGA8B NA "golgin A8 family, member B, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122240_PI430048170 0.3630754093713810.7876175851099840.417358910635183
0.5881004738803380.834189238152922A A A 1.13436706411304 0.405863509459291
1.23126045860921 A A A LNCV6_122240_PI430048170 mRNA
TTTCCTAAAGGCTGTGCATTCAATCCTGCGTGATAAGCACAGAAGACAGCTCCTCAAAAC NM_003253 RefSeq chr21
- 31118417 31558977 TIAM1 7074 T-cell lymphoma invasion and metastasis 1
GO:0051056|GO:0048011|GO:0043065|GO:0048013|GO:0007264|GO:0044291|GO:0097190|GO:0032855|GO:0005
829|GO:0031234|GO:0005085|GO:0016601|GO:0005543|GO:0046875|GO:0007160|GO:0016477|GO:0032321|GO:0
005911|GO:0007411|GO:0050772|GO:0005057|GO:0005089|GO:0030676 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_135962_PI430048170 0.5967894984986031.09500854966535 5.67000675445858
5.86365359077016 6.23374911408948 P P P 5.76337877350112 6.0618755054366 5.563066280777
P P P LNCV6_135962_PI430048170 mRNA
TACTCATCTTTTACCTAATGGTGTCCTCAGTTGTGGGCTTCTATAGCTCTCCACTCTTCC NM_001300750 RefSeq chr12
- 49097139 49110900 LMBR1L 55716 "limb development membrane protein 1-like, transcript variant 2"
GO:0005886|GO:0016021|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139693_PI430048170 0.0183897450993973 0.8787979389827791 0.0936002721809
9.99441170924639 10.027932643804 P P P 10.1525173070791 10.2734327433637 10.248155783682
P P P LNCV6_139693_PI430048170 mRNA
TTTTTTGTTATTTGTTTGCATCCCTCCCCCACACCCTGGTGTTTTAAAATGAAGAAAAAA NM_002355 RefSeq chr12
- 8940360 8949761 M6PR 4074 "mannose-6-phosphate receptor (cation dependent), transcript
variant 1"
GO:0048471|GO:0005770|GO:0008333|GO:0005765|GO:0005537|GO:0015761|GO:0006898|GO:0007165|GO:0015
578|GO:0016020|GO:0005887|GO:0004888|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144883_PI430048170 0.000595442559253492 0.27494305241898 5.36162935766338
5.40147972292475 4.99216091194971 P P P 7.14656731810917 7.25712505338907 6.9585355093172
P P P LNCV6_144883_PI430048170 mRNA
AGGGAGATGCAAGGGCTAAAGTAAAATTTTGTCAAGTAATGGCTGATTGTGTCATTTTTT NM_001177996 RefSeq
chr12 - 111360650 111369121 FAM109A 144717 "family with sequence similarity 109, member A,
transcript variant 1"
GO:0005802|GO:0005515|GO:0001881|GO:0030136|GO:0042147|GO:0007032|GO:0055037|GO:0042803|GO:0005
769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132476_PI430048170 0.4188282907557950.848832577855751 1.31278200544294
0.460328259081962 1.17596609774453 A A A 1.15438067835212 1.13426333268226
1.47941588835322 A A A LNCV6_132476_PI430048170 mRNA
GCAAAGATTAGGGAAAGAGACTTGACCCCAGGACTGTACTACGACTCTTAAGAGAACACT NM_032726 RefSeq chr2
+ 218607764 218637186 PLCD4 84812 "phospholipase C, delta 4"

GO:0035556|GO:0016042|GO:0031965|GO:0005737|GO:0005886|GO:0005783|GO:0004435|GO:0046488|GO:0005509|GO:0007340|GO:0004871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135796_PI430048170 0.0193217645685671 0.71541790625109 6.82502370010846 6.51464370912465 6.78925596873643 P P P 7.09611493878087 7.3134148699147 7.17998934805833 P P P LNCV6_135796_PI430048170 mRNA GATCCTGTTTTGGGGTTTGCACATGGATCGTATGTTAAGCTTTTTCTTTTCAATAAATGANM_078483RefSeq chr5 + 151447595 151492381 SLC36A1 206358 "solute carrier family 36 (proton/amino acid symporter), member 1" GO:0005280|GO:0005886|GO:0005783|GO:0015078|GO:0006865|GO:0005765|GO:0055085|GO:0015180|GO:0015193|GO:0015816|GO:0035524|GO:0015187|GO:0016021|GO:0015808|GO:0006811|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127350_PI430048170 0.0308184191247947 1.08940607032703 0.680442288404668 0.7451252974713320.645593148830961A A A 0.6088999009907720.547120418125054 0.545377006460857A A A LNCV6_127350_PI430048170 mRNA TTGTGTGTCTTTTTTTTGGATGACATTTCCTTATCAGATAAATATGTATCTTGAAAATAT NM_001131034 RefSeq chr4 - 1071477 1113564 RNF212 285498 "ring finger protein 212, transcript variant 1" GO:0000795|GO:0051026|GO:0016925|GO:0016874|GO:0008270|GO:0006311|GO:0007131 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128903_PI430048170 0.0165705077253805 1.76795285751833 5.62366697755662 5.75890297596264 5.3859088076638 P P P 4.67025004230566 5.06758494175577 4.53430319375764 P P P LNCV6_128903_PI430048170 mRNA ATTGTTCTCTCAGAATTCCAAATTCCACTTCTGAGGCTCTAAGCCCAGCCTAGGATCTGA NM_001256716 RefSeq chr19 - 55158660 55166722 DNAAF3 352909 "dynein, axonemal, assembly factor 3, transcript variant 4" GO:0044458|GO:0005737|GO:0070286 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130442_PI430048170 0.4103935955563161.11652898037222 5.50278672949963 5.36741259612166 5.47645378811204 P P P 5.50437822811097 4.93726983842405 5.37252167378757 P P P LNCV6_130442_PI430048170 mRNA TTACCTGTCAAGTAAATAAATAATAAAACACCCAACTGGGAGTGCTGACTTTGAGGTTAT NM_018357RefSeq chr15 - 70831523 70854265 LARP6 55323 "La ribonucleoprotein domain family, member 6, transcript variant 1" GO:0006396|GO:0005737|GO:0000166|GO:0030529|GO:0003723|GO:0005634|GO:0006417 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142917_PI430048170 0.2374761135416791.01802708221243 0.306786951599137 0.2598799133098790.306363666238378A A A 0.2708610578978450.257518671284865 0.267791155961024A A A LNCV6_142917_PI430048170 mRNA CTGCAGAAGCTAATACAAGGGACACTGGTCTTTTGACAAAATAAACTTGTGTAAATTTTG NM_001080433 RefSeq chr2 + 56184122 56386174 CCDC85A 114800 coiled-coil domain containing 85A NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141802_PI430048170 0.00324512486167845 1.48280267361914 11.8001004949783 11.7644198486825 11.6479295789245 P P P 11.1210865450429 11.2983503522819 11.0831192734824 P P P LNCV6_141802_PI430048170 mRNA GATGGGGACAGCTGTCAATCACAAGCCCTTAAATAAAGCAGCCAGCGCACATCCAAAAAA NM_032377RefSeq chr19 - 11553042 11559236 ELOF1 84337 elongation factor 1 homolog (S. cerevisiae) GO:0006355|GO:0005634|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141158_PI430048170 0.0445979641932521.52094012146771 5.89591286633784 6.02440272279566 5.98720833102392 P P P 5.58459060816466 5.38762682918599 5.07911303084607 P P P LNCV6_141158_PI430048170 mRNA CAGCAGTTCCAGTATGGATAGGGGTTCCTGTTTTACTAGCTTTTACATCTTTTTATTTAA NM_145166RefSeq chr3 + 42653683 42667580 ZBTB47 92999 zinc finger and BTB domain containing 47 GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_135026_PI430048170 0.00370997552666839 0.8558401360775967.62510948271685
7.53644441910739 7.57418503702772 P P P 7.83271188095124 7.78259782323324
7.79509091566844 P P P LNCV6_135026_PI430048170 mRNA
CCACACCCTGTAGCAATACCAAGTGCTATTACATAATCAATGGACGATTTATACTTTTAT NM_053279RefSeq chr8
- 11421463 11466767 FAM167A 83648 "family with sequence similarity 167, member A" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_143068_PI430048170 0.6133786956529010.9646783513693470.542036613140092
0.5205265127402030.28285287362616 A A A 0.4061251903871120.588025294874398
0.51518258275575 A A A LNCV6_143068_PI430048170 mRNA
CATGTTGAATCCTTTGATTTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAA NM_001005243 RefSeq
chr12 + 55129768 55130776 OR9K2 NA "olfactory receptor, family 9, subfamily K, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110516_PI430048170 0.0833754006344259 1.54969305358179 8.47100308707528
8.22620906115712 8.24733164594142 P P P 8.09372055355072 7.47435464734255
7.38614128034995 P P P LNCV6_110516_PI430048170 mRNA
TGCAGACAGACTTTAGCTCCGATCCACTGCAGAAAGTTGTGTGCTTCAACCACGATAATA NM_013388RefSeq chr2
- 27130755 27134674 PREB 10113 prolactin regulatory element binding
GO:0006355|GO:0005634|GO:0048208|GO:0015031|GO:0003677|GO:0006351|GO:0030968|GO:0006888|GO:0000
139|GO:0016020|GO:0005789|GO:0061024|GO:0016021|GO:0006987|GO:0044267|GO:0043687|GO:0018279 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138898_PI430048170 0.0105623212625427 0.4546290826830528.60903723255954
8.41029000656365 8.60619667467444 P P P 9.38183557014115 9.67741116433965
9.93427248361853 P P P LNCV6_138898_PI430048170 mRNA
GTCCCCCTCATTTCCCAAATGTTTAAATGTATTGGATTTGGATTCTCAATGTATAAGTTG NM_001256426 RefSeq
chr4 + 94451856 94668227 PDLIM5 10611 "PDZ and LIM domain 5, transcript variant 6"
GO:0043005|GO:0051963|GO:0030018|GO:0030054|GO:0042805|GO:0014069|GO:0003779|GO:0015629|GO:0005
829|GO:0047485|GO:0016020|GO:0045211|GO:0005080|GO:0008270|GO:0061001 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145734_PI430048170 0.197813914412962 1.13203697666293 6.74710323701678
6.42544878619466 6.63107881083027 P P P 6.48001207343141 6.35817747671068
6.44416504075119 P P P LNCV6_145734_PI430048170 mRNA
GATTCTGTAATTGGTTCTTATAGTAACAAATAAAAAGCTGTTTTCTTCAGCTTCTCCTGG NM_004739RefSeq chr11
- 62593202 62601840 MTA2 9219 "metastasis associated 1 family, member 2"
GO:0001103|GO:0005515|GO:0005667|GO:0016575|GO:0000790|GO:0003700|GO:0043044|GO:0031492|GO:0006
325|GO:0000122|GO:0000978|GO:0000989|GO:0006333|GO:0006306|GO:0043234|GO:0000118|GO:0016581|GO:0
016020|GO:0045944|GO:0001085|GO:0008270|GO:0000980|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136692_PI430048170 0.799205754490072 0.96890465822164 6.28259427853425
6.28992939399409 6.51422830119891 P P P 6.22787152285827 6.34250955980945
6.63434732915666 P P P LNCV6_136692_PI430048170 mRNA
CCCTTACTTAGCATTGTGTTAGACATACTAATAGGTGCACAGTGAAATACTTATTGTTGA NM_017614RefSeq chr5
+ 79069723 79090074 BHMT2 23743 "betaine--homocysteine S-methyltransferase 2, transcript variant 1"
GO:0046500|GO:0033477|GO:0047150|GO:0008270|GO:0071267|GO:0032259|GO:0008898|GO:0033528|GO:0006
577|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135737_PI430048170 0.583899991467358 0.897700661161632 4.70253426637042
4.71950820201219 5.62610431861448 P P P 4.99781740070204 5.17178761360027
5.50372319569584 P P P LNCV6_135737_PI430048170 mRNA
CTAGTATGCTCCTGGTCTAATGCATTTACATTGTTTAGGTAACTGGTTCCTAATAAAAAG NM_007149RefSeq chr6
- 27450741 27473118 ZNF184 7738 zinc finger protein 184

GO:0006355|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67054_PI430048170 0.6745011228008540.9370617824607256.62785033073021 5.85768977349619 5.72411789325492 P P P 6.0883331461408 6.43584797057583 6.1130948393084 P P P LNCV6_67054_PI430048170 mRNA
ATGCCCCTCTTCATCACGATCACTTCCTACAGTCTCATGGAGCAGAAACTGGGGAAGAGT NM_002921 RefSeq chr10 + 84245052 84259188 RGR 5995 "retinal G protein coupled receptor, transcript variant 1"
GO:0005515|GO:0018298|GO:0070098|GO:0009881|GO:0007186|GO:0006935|GO:0005887|GO:0004930|GO:0004950|GO:0007602|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137561_PI430048170 0.0146038309271241 0.3997104193932094.48392388131159 5.08463706091684 5.21427326471448 P P P 5.84314160753343 6.26881721866247 6.63283832126916 P P P LNCV6_137561_PI430048170 mRNA
GCTCTGACATACTTTCATGTGGTAGGTTCTTTCTCAGGAACTCAGTTTAACTATTATTTA NM_014572 RefSeq chr13 - 20973035 21061583 LATS2 26524 large tumor suppressor kinase 2
GO:0005515|GO:0046620|GO:0005815|GO:0045736|GO:0005634|GO:0035329|GO:0005524|GO:0046872|GO:0005829|GO:0035556|GO:0000082|GO:0000922|GO:0005737|GO:0007067|GO:0009755|GO:0004674|GO:0030216|GO:0006468|GO:0034613|GO:0090090|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129505_PI430048170 0.5340730903550740.8273654739750380.296271741742321 0.3048462882980920.518793105711246 A A A 1.1649132537425 0.276604374908747 0.328143800527595 A A A LNCV6_129505_PI430048170 mRNA
CAGCAGTGTGACTGGTGAAAATGCTGACCCCACACAGAGTGCAACCAGTAAGTGAAAACA NM_020063 RefSeq chr1 - 90712021 90717237 BARHL2 343472 BarH-like homeobox 2
GO:0043565|GO:0030516|GO:0005737|GO:0001077|GO:0001709|GO:0045944|GO:0030182|GO:0045727|GO:0005654|GO:0001764|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128927_PI430048170 0.00954627827465437 1.47282228721985 4.79664611646739 4.5136317025562 4.59805726570122 P P P 4.08677626623663 4.22044617589842 3.92505882918578 P P P LNCV6_128927_PI430048170 mRNA
TATGTGGGGTTGGTGACCAATCAGTTGAGCCACATCAAAGCTAAGATCCGAGCTAAAATC NM_005619 RefSeq chr19 - 45485287 45497055 RTN2 6253 "reticulon 2, transcript variant 1"
GO:0005515|GO:0046324|GO:0014802|GO:0005783|GO:0030315|GO:0030176|GO:0065002 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94975_PI430048170 0.6078416472868371.08246052799431 0.2755759850987370.32069764394453 0.774843554169317 A A A 0.4069159332289840.3280639101679550.346580004902125 A A A LNCV6_94975_PI430048170 mRNA
GAACGCATATGCTGCAGTGTCTTTGTGGCAAGAGTCTTAAGAAAAACAAGAACCCAACTG NM_175929 RefSeq chr13 - 101720854 102401774 FGF14 2259 "fibroblast growth factor 14, transcript variant 2"
GO:0008344|GO:0007254|GO:0007267|GO:0007268|GO:0005104|GO:0005576|GO:0005634|GO:0007399|GO:0050905|GO:0007165|GO:0008543|GO:0010765|GO:0008083|GO:0008201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88788_PI430048170 0.3378009548980321.07340014815207 3.41940949259493 3.57693821824057 3.54149906273679 P P P 3.33708424219948 3.56836078932508 3.31675299005434 P P P LNCV6_88788_PI430048170 mRNA
TATGAAACTGCTGCCCAAAATCCTGGCTCACTCTATTGAACACAACCAGCACATTGAGGA NM_015589 RefSeq chr14 + 54567611 54793315 SAMD4A 23034 "sterile alpha motif domain containing 4A, transcript variant 1"
GO:0017148|GO:0005737|GO:0030054|GO:0045202|GO:0045727|GO:0030371|GO:0030425 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141012_PI430048170 0.0391095284973516 0.4307195782125026.83660909913027 6.28343088488828 6.74905666460916 P P P 7.26271063976053 7.82469000625947 8.30222802654852 P P P LNCV6_141012_PI430048170 mRNA

GCAATATCTAGTCAAACTTTGAGTGTACTGGTTCTGTGAACCACCTGAAAAAACAAATTA NM_017754RefSeq chr6 + 34792016 34877514 UHRF1BP1 54887 UHRF1 binding protein 1
GO:0005515|GO:0042826|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138215_PI430048170 0.3496737564165230.9480792002878370.432318245139207
0.4516238229598020.28298010901185 A A A 0.4018687118385 0.563878890998335
0.432588533551264A A A LNCV6_138215_PI430048170 mRNA
ATGTTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGCTGTGTAGCTAAATCATATAAC NM_001252383 RefSeq
chr6 - 87085497 87095147 CGA 1081 "glycoprotein hormones, alpha polypeptide, transcript variant 1"
GO:0005515|GO:0007165|GO:0008284|GO:0030335|GO:0016486|GO:0005179|GO:0045944|GO:0007267|GO:0005576|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129517_PI430048170 0.000353212277243606 0.4512494433316511.2020247218922
11.1773844461028 11.0482903461977 P P P 12.2524007662669 12.4233192181011
12.1904754569838 P P P LNCV6_129517_PI430048170 mRNA
CCACCATTGTAAGGAAACACTTTCAGAAATTCAGCTGGTTCCTCCAAACCCTTCAAAAAA NM_004252RefSeq chr17 + 74748611 74769360 SLC9A3R1 9368 "solute carrier family 9, subfamily A (NHE3, cation proton antiporter 3), member 3 regulator 1"
GO:0005515|GO:0045859|GO:0032416|GO:0008013|GO:0031528|GO:0031698|GO:0031526|GO:0043621|GO:0032403|GO:0032415|GO:0043231|GO:0032782|GO:0070373|GO:0016055|GO:0050780|GO:0070062|GO:0005813|GO:0030336|GO:0019902|GO:2001244|GO:0014067|GO:0030165|GO:0030643|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144069_PI430048170 0.146134251342356 1.06714570571532 0.647449139450468
0.5237230271028230.62013546846059 A A A 0.4324037736466250.528631825782129
0.549232641186794A A A LNCV6_144069_PI430048170 mRNA
AAGACCAAGCAGATTCAAAGAAGCATTATTCGCCTATTTTCTGGGCAGAGTAGGGCTTGA NM_033179RefSeq chr11 - 5301013 5301946 OR51B4 79339 "olfactory receptor, family 51, subfamily B, member 4"
GO:0050911|GO:0007608|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_59498_PI430048170 0.157600391639382 1.07866940575244 0.515129753380166 0.448754560375241
0.557406495578949A A A 0.3059566726015190.3988384835061620.485244074223798A A A
LNCV6_59498_PI430048170 mRNA
GGGGTCTTCTTACTTCTTCCCTTTGAGGACAAAGTTTCTCTCGAATAAAGAGACTGAAGC NM_001142343 RefSeq
chr12 - 108288043 108339317 CMKLR1 1240 "chemokine-like receptor 1, transcript variant 1"
GO:0050848|GO:0005515|GO:0070098|GO:0005886|GO:0004930|GO:0032088|GO:0001501|GO:0006955|GO:0006935|GO:0007186|GO:0032695|GO:0005887|GO:0045600|GO:0004950|GO:0010759|GO:0004872|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143559_PI430048170 0.3377894699352030.64696139642509 1.24734140711353
0.7709296612549540.769389649471421A A A 0.6136215435339341.93541888658278
1.84267357147156 A A A LNCV6_143559_PI430048170 mRNA
GATGCAATGGATTTATTTGATTCAGGGGACCTGTGTTTCCATGTCAAATGTTTTCAAATA NM_000448RefSeq chr11 + 36568012 36579760 RAG1 5896 recombination activating gene 1
GO:0005515|GO:0004842|GO:0002331|GO:0090305|GO:0005634|GO:0048538|GO:0042803|GO:0046872|GO:0042393|GO:0006955|GO:0030183|GO:0045580|GO:0043029|GO:0043154|GO:0033077|GO:0033151|GO:0016881|GO:0070244|GO:0006310|GO:0003677|GO:0051865|GO:0002250|GO:0043565|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_90131_PI430048170 0.481262958162142 0.902479124857955 5.45926231062594 5.32839063828741
4.82704963613702 P P P 5.45986753084449 5.43355278281068 5.22848150929549 P P P
LNCV6_90131_PI430048170 mRNA
AAGGCAAAAGGGAATCACAGACTTAAGCTTCCTGCCCTATATTTCTGAGCTACACCCAAG NM_178831RefSeq chr7

- 100200654 100272232 GATS 352954 "GATS, stromal antigen 3 opposite strand, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140714_PI430048170 0.00069834018253688 1.20176216673085 0.865736734552736
0.8999163847275920.903247715712938A A A 0.6619836463922440.606399586268694
0.604620771940898A A A LNCV6_140714_PI430048170 mRNA
CTCTTAATAAGACCAATGGTGGCTGTTCCACAGAGAAGTCTAGGAAATGATCAGTCCAGG NM_005549RefSeq chr1
- 110517216 110519175 KCNA10 3744 "potassium channel, voltage gated shaker related subfamily A, member 10"
GO:0005251|GO:0005886|GO:0008076|GO:0005221|GO:0007268|GO:0051260|GO:0034765|GO:0016021|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138407_PI430048170 0.0376346824052735 0.2776437113551731.92146216553106
1.4778196042974 0.295234874216025A A A 2.74118215860011 3.21995006225099 3.5959060305307
P P P LNCV6_138407_PI430048170 mRNA
TATTTAGGCATTGGCCTGTGAGCTATGGGTGTGTTTGCAGATGACATGAGGATGTGTTTG NM_001130514 RefSeq
chr19 + 41443157 41444765 ERICH4 100170765 glutamate-rich 4 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143563_PI430048170 0.1852899398118081.06307008895129 0.626848406852446
0.7335267305633390.585186421673088A A A 0.5746444051702420.559760993272984
0.550426910204624A A A LNCV6_143563_PI430048170 mRNA
TCTCACCACAGTCACTGCATAGAAAGTGGTTAAGTTTAACATAAGACATGTTGGATGTTA NM_001145080 RefSeq
chr17 + 44656393 44675797 C17orf104 284071 chromosome 17 open reading frame 104 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141962_PI430048170 0.0278162690096242 1.37410213237972 6.32550008022595
6.1146080093075 6.07140880128552 P P P 5.72277566063122 5.72357303203488
5.70261128111465 P P P LNCV6_141962_PI430048170 mRNA
TTTATTGCTTGTCTGGGTGGATGGGGCAGGAGGGGCTGAGGGCCTGTCCCAGACAATAAA NM_015136RefSeq chr3
+ 52495339 52524495 STAB1 23166 stabilin 1
GO:0005515|GO:0005886|GO:0007267|GO:0015035|GO:0030169|GO:0006898|GO:0030666|GO:0005041|GO:0006954|GO:0005540|GO:0005887|GO:0016525|GO:0007155|GO:0042742|GO:0055114|GO:0005044 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130033_PI430048170 0.0142526300076963 0.5212653241663461.18019306404599
1.7254677855134 1.59753991419248 A A A 2.33310887315988 2.24485220879076
2.74803605478786 A A P LNCV6_130033_PI430048170 mRNA
GAAGAGACTTTGGTGAGATGAACGTGAGGTAAAAATTTCGTTCGGCAAAAAGTGCAAAAANM_015191RefSeq chr11
+ 111602390 111726917 SIK2 23235 salt-inducible kinase 2
GO:0035556|GO:0008286|GO:0005515|GO:0005737|GO:0046777|GO:0000287|GO:0004674|GO:0046626|GO:0006468|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144769_PI430048170 0.4346589701208170.4619523056627120.395907689774635
0.4136794646115840.451547514588167A A A 0.4013872666053342.59861202577305
0.394327002010354A P A LNCV6_144769_PI430048170 mRNA
TTTCTCTAGTTCAAGTTCACCAGACTCTATAAATAAAACCTGACAGACCATGACTTTCAA NM_000062RefSeq chr11
+ 57597553 57614853 SERPING1 710 "serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, transcript variant 1"
GO:0005515|GO:0001869|GO:0004867|GO:0008015|GO:0007568|GO:0030168|GO:0072562|GO:0005576|GO:0005615|GO:0010951|GO:0007596|GO:0045087|GO:0007597|GO:0002576|GO:0006958|GO:0031093|GO:0042730|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133500_PI430048170 0.00721603025978145 0.4730867150217668.29582899764153
8.04371678628953 8.314312843422 P P P 9.01852397209476 9.30191301494694 9.5413029027639
P P P LNCV6_133500_PI430048170 mRNA

CTGAAAAGTCATGTTGCAAATCTTTCTGTGAAACAGATGCTATTTTAAATTCACTGGGAG NM_001570 RefSeq chr3 + 10164878 10243743 IRAK2 3656 interleukin-1 receptor-associated kinase 2
GO:0005515|GO:0034142|GO:0005886|GO:0070423|GO:0007249|GO:0005634|GO:0051403|GO:0042803|GO:0035872|GO:0005829|GO:0035556|GO:0045323|GO:0002756|GO:0000187|GO:0005737|GO:0051092|GO:0006954|GO:0002755|GO:0031663|GO:0034138|GO:0070555|GO:0070498|GO:0038124|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130781_PI430048170 0.3574877733883330.9012074873984338.31222981404485 8.0346519808195 7.93806530447569 P P P 8.10017400001094 8.42290840492575 8.22007782563195 P P P LNCV6_130781_PI430048170 mRNA
AGACCCAGTTCCCCTCCACTGTCAGCACTGTGTACAGGACAAGTGAGAAGCTGGTGAAGG NM_001012759 RefSeq chr16 + 88706482 88715378 CTU2 348180 "cytosolic thiouridylase subunit 2 homolog (S. pombe), transcript variant 1"
GO:0005739|GO:0005515|GO:0002098|GO:0043234|GO:0005737|GO:0000049|GO:0016779|GO:0034227|GO:0032447 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142049_PI430048170 0.6462104809100660.9395440974613029.2440407684699 9.65301853400842 9.65104559021685 P P P 9.73497036548349 9.35668939195085 9.73174600556805 P P P LNCV6_142049_PI430048170 mRNA
ACTGTTGTAACCCATTACGTTCTGAATCTTCTGTTATCTTTGAAGTATCATTTTTGGCAC NM_198498 RefSeq chr11 + 111255981 111286404 C11orf53 NA chromosome 11 open reading frame 53 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133818_PI430048170 0.0883065101075720.56852583097255 8.48459165524211 8.40871433740474 8.32456453898117 P P P 8.67681904138736 9.48948198984479 9.37421714333513 P P P LNCV6_133818_PI430048170 mRNA
CCTCCAAGGTTAGATTTAATCCTTAGGATAACTCTTTTAAAGTGATTTTCCCCAGTGTTT NM_012291 RefSeq chr12 + 53268298 53293643 ESPL1 9700 extra spindle pole bodies homolog 1 (S. cerevisiae)
GO:0005515|GO:0005813|GO:0045842|GO:0006915|GO:0005634|GO:0003824|GO:0045875|GO:0000212|GO:0005829|GO:0000910|GO:0000070|GO:0045143|GO:0040001|GO:0006508|GO:0008234|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136121_PI430048170 0.2995425037282340.9728702710940710.382476356208326 0.4076832232538580.31082537789396 A A A 0.3973265474650540.428895262369418 0.395300120702096 A A A LNCV6_136121_PI430048170 mRNA
CGAAGCCCCAAGCTGGGCACAAAGTAGTTTTTTACGTGGTGGGTGTCTTTTTGTAAAAAA NM_014012 RefSeq chr20 + 31475287 31484905 REM1 28954 RAS (RAD and GEM)-like GTP-binding 1
GO:0006184|GO:0005516|GO:0016020|GO:0007264|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143451_PI430048170 0.0132697748463618 0.4793363802257799.37216490389368 9.13357020410829 9.37780350441894 P P P 10.0649754944914 10.3013043563744 10.652083100574 P P P LNCV6_143451_PI430048170 mRNA
ACTGTTTCAGGGGTTTTCTCTTGCCCAATCCCCACCTAATAAAGTTCTGAGAGCATGAAA NM_018449 RefSeq chr9 - 33921692 34048949 UBAP2 55833 "ubiquitin associated protein 2, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142371_PI430048170 0.0511368970901726 1.31161462945024 5.98790220067583 6.04364467053369 6.30063635777839 P P P 5.59101381993404 5.63810015115752 5.92548188544715 P P P LNCV6_142371_PI430048170 mRNA
CGGACACATAATATGACAACCACATTTTTCCTCATCATCCATGAGGAAATGGATGATTTC NM_001102402 RefSeq chr17 + 55751104 55777387 PCTP 58488 "phosphatidylcholine transfer protein, transcript variant 2"
GO:0015914|GO:0008525|GO:0006869|GO:0031210|GO:0008203|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83825_PI430048170 0.3353557121163780.8890046870104611.5355832774915 11.0740914984227

11.1680416108005 P P P 11.3158977992717 11.554105314338 11.4493267353266 P P P
LNCV6_83825_PI430048170 mRNA
TTTTGGGGAGAGTTTGGAGGGGAGGGAGAATTTATTAATAAAAGAATCTTTAACTTTAAA NM_016639 RefSeq chr16
+ 3020311 3022382 TNFRSF12A 51330 "tumor necrosis factor receptor superfamily, member 12A"
GO:0005515|GO:2001238|GO:0043065|GO:0005886|GO:0009986|GO:0045773|GO:0045765|GO:0001525|GO:0097
191|GO:0001726|GO:0006931|GO:0061041|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_39395_PI430048170 0.3974551067074510.81835629920113 3.20968823285937 2.27078616268936
3.22229668503909 P A P 3.33574039431141 2.99434489758764 3.39798333309281 P P P
LNCV6_39395_PI430048170 mRNA
GAAGAGCACAAAAAGGAGTATGAAGATGCTGAAAATACTTCAACTCAGTCCAAAGTTATG NM_025211 RefSeq chr9
- 83739420 83817837 GKAP1 80318 "G kinase anchoring protein 1, transcript variant 1"
GO:0007165|GO:0005794 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138555_PI430048170 0.0387313525644685 0.80006162275484912.9407839259356
12.8644448881039 12.9642445886345 P P P 13.1956479285761 13.1384606054912
13.3904365251573 P P P LNCV6_138555_PI430048170 mRNA
CAGGCTGCATTCTAACTCATACTGTGAAGACAAAGGTGTTTTTGATTCAGAAATATATGA NM_001098576 RefSeq
chr12 + 49741808 49764934 TMBIM6 7009 "transmembrane BAX inhibitor motif containing 6,
transcript variant 2"
GO:0006986|GO:0016020|GO:0070059|GO:0005887|GO:0005783|GO:0032469|GO:0005789|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133648_PI430048170 0.6900530289614130.9871009354067150.433212123938549
0.4605147196610820.368289512752382A A A 0.5048862813827780.398920366734693
0.413650583248199A A A LNCV6_133648_PI430048170 mRNA
TTCATCACCAGCTATCTCGAAGAAGCCTACATCCCAGTTGTCAATGATGTGCTTCAAGTG NM_174897 RefSeq chr20
+ 33031647 33044047 BPIFB6 128859 "BPI fold containing family B, member 6" GO:0005576|GO:0008289
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136158_PI430048170 0.3549694372943641.06114059845284 9.5888967096939
9.80421732748289 9.64652504987758 P P P 9.68946087800525 9.54547398559925
9.55192203889712 P P P LNCV6_136158_PI430048170 mRNA
GGGCCTGGGAGGAAGATGTTTACATTTTTAAAGGTACACTGGTATTTATATTTCAAACAT NM_005985 RefSeq chr20
+ 49982975 49988883 SNAI1 6615 snail family zinc finger 1
GO:0005515|GO:2000810|GO:0010718|GO:0005634|GO:0001837|GO:0046872|GO:0031069|GO:0005737|GO:0061
314|GO:0060972|GO:0060021|GO:0019900|GO:0001707|GO:0000977|GO:0030335|GO:0060707|GO:0000122|GO:0
060806|GO:0001649|GO:0001078|GO:0016477|GO:0043518|GO:0060536|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_120013_PI430048170 0.7994731901748270.85416822439443 0.30751710491987
2.08385379970105 1.66591314503381 A A A 1.08977891120433 0.985345465848549
2.58945873939451 A A P LNCV6_120013_PI430048170 mRNA
TCGACGAGGCCAAGCGTCTACGCGCCATGCACATGAAGGAGCACCCCGACTACAAGTACC NM_007084 RefSeq
chr13 - 94709624 94712543 SOX21 11166 SRY (sex determining region Y)-box 21
GO:0048863|GO:0006355|GO:0003700|GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0005575|GO:0003
677|GO:0001942 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102931_PI430048170 0.0600130236124325 3.49080452403599 2.14915149540406
2.84539687910827 1.32769521946631 A A A 0.4758587832918010.321430837254611
0.493894251412818A A A LNCV6_102931_PI430048170 mRNA
GTTTTTGTCTTCAGTGCTGGTAAGTCAGGTAAACCATAAATAGTTAAAAGCAACCTTTTG NM_003913 RefSeq chr6
+ 4021334 4064983 PRPF4B 8899 pre-mRNA processing factor 4B
GO:0008380|GO:0005515|GO:0004672|GO:0005694|GO:0004674|GO:0000398|GO:0006468|GO:0005654|GO:0071
013|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_135743_PI430048170 0.0707099305126470.2739986363738822.22283320037977
0.3625570416372790.257611455037435A A A 2.10781132436172 3.79955154701791
2.97408719760297 A P P LNCV6_135743_PI430048170 mRNA
TTGGTGTGCCCTAGTATACCATATAGTATAGCATCATCTGTATATATAGCATGTCTACAT NM_033213RefSeq chr1
- 247034637 247078813 ZNF670 93474 "zinc finger protein 670, transcript variant 1"
GO:0005515|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130203_PI430048170 0.00939595113194819 0.4800038532355267.601701591851
7.6780923337552 7.14565011572972 P P P 8.76212066325625 8.6009099897498 8.2473890915789
P P P LNCV6_130203_PI430048170 mRNA
GGCAGCCAGCCCAGCACCTACTTGTAAAAATTTTGTAATAAAAAGTTTTTCCTAGAGACG NM_203468RefSeq chr9
- 137048098 137054051 ENTPD2954 "ectonucleoside triphosphate diphosphohydrolase 2, transcript variant
1"
GO:0017111|GO:0017110|GO:0007186|GO:0005886|GO:0009181|GO:0005789|GO:0005605|GO:0030168|GO:0016
021|GO:0005524|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140825_PI430048170 0.5183026974519041.03035596026914 0.282622603990831
0.30745788398048 0.451958020143165A A A 0.32713412921871 0.295141441484579
0.295962219806138A A A LNCV6_140825_PI430048170 mRNA
CTACTGGAAAAGGCAGAGGGACAGAGGAAACACCAAAAAATACTTACATATAAACCTAAT NM_176821RefSeq
chr11_KI270829v1_alt - 191109 195013 NLRP10 338322 "NLR family, pyrin domain containing 10"
GO:2000318|GO:0050829|GO:0005737|GO:2000778|GO:0045087|GO:0002827|GO:0050832|GO:0035397|GO:0005
524|GO:2000484|GO:0019897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132711_PI430048170 0.8955892694063141.09028505873728 0.422043499934072
1.70961884459839 0.400668167007347A A A 0.4079701269481781.47545355340272
0.413644626395077A A A LNCV6_132711_PI430048170 mRNA
AATAAGGAATTCAAATCAGCCCTACGAAGAACAATCGGCCAAACTTTCTATCCTCTTAGT NM_001004473 RefSeq
chr1 + 158465561 158466503 OR10K1 NA "olfactory receptor, family 10, subfamily K, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139495_PI430048170 0.37325833122327 0.6883488678669890.81776172230545
1.52261950570541 2.28921742622235 A A A 1.82590852601061 2.83367580738283
1.66055841360456 A P A LNCV6_139495_PI430048170 mRNA
GCTTCCAGTGACCCTGGCTTTGTCTTGCTTTGTATTAGATTACTCAGCTCCCTGGTATTANM_021153RefSeq chr18 -
66501186 66604138 CDH19 28513 "cadherin 19, type 2, transcript variant 1"
GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133681_PI430048170 0.6177607415065480.7691983191766740.417584131772693
1.28125145231685 1.40500972218318 A A A 1.91133838990312 1.69791812631455
0.414833343486195A A A LNCV6_133681_PI430048170 mRNA
TGAGGGTTTTGCTAGTTGGTTTTGTTTTGCGTTTTACAGCCGTGGGGGGAAGCACATAAT NM_001141RefSeq chr17
+ 8039039 8049133 ALOX15B 247 "arachidonate 15-lipoxygenase, type B, transcript variant d"
GO:0006629|GO:0019369|GO:0008285|GO:0005886|GO:0005634|GO:0044281|GO:0008289|GO:0005829|GO:0005
622|GO:0005737|GO:0035360|GO:0045618|GO:0030856|GO:0030850|GO:0005856|GO:0045926|GO:0090197|GO:0
070062|GO:0030336|GO:0005506|GO:0010744|GO:0005509|GO:0019372|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140979_PI430048170 0.4933647245449720.9137601838363449.42064187445889
9.29956383928126 9.59446584923508 P P P 9.41638066536623 9.43548670928496
9.82965332023167 P P P LNCV6_140979_PI430048170 mRNA
GGATTAGCAGTTCTTAGTAAGTTTACTGTGTATAGGAACGGTTTGTATTTCATTACAGCT NM_003580RefSeq chr8
- 58583504 58659845 NSMAF 8439 "neutral sphingomyelinase (N-SMase) activation associated factor,
transcript variant 1"

GO:0005515|GO:0016230|GO:0043065|GO:0006672|GO:0043085|GO:0012505|GO:0035556|GO:0007165|GO:0005
737|GO:0005543|GO:0016197|GO:0005057|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113462_PI430048170 0.6923526773411581.24485996911077 1.71771553407877
0.4195468015957510.531526856054065A A A 0.5808508975724030.773505219009547
0.742094193172936A A A LNCV6_113462_PI430048170 mRNA
ACAGCAAGCTGGGAAAATGTGGTCAGATGTGGGCATGCGCAAAGCGGCTACCTGTGAGAG NM_001166426
RefSeq chrX + 48597835 48605194 WDR13 64743 "WD repeat domain 13, transcript variant 2"
GO:0005737|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141655_PI430048170 0.0713520458273269 1.22403414953463 9.50544812230543
9.68860601347449 9.82256477655739 P P P 9.32852904246772 9.29637281939983
9.52360272729727 P P P LNCV6_141655_PI430048170 mRNA
TGGTTACATTCAGGATACTTGAGCACTTTATATACTACCGTAGCACTGTAGCTATTTTTT NM_033417RefSeq chr19
- 17049760 17075533 HAUS8 93323 "HAUS augmin-like complex, subunit 8, transcript variant 1"
GO:0051297|GO:0003674|GO:0007067|GO:0005813|GO:0005737|GO:0000922|GO:0005874|GO:0070652|GO:0051
225|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114594_PI430048170 0.0281371726746358 0.2701155992001561.53703500803917
0.3188818718047210.749911929024694A A A 2.93768468490434 2.72958539794121
2.86645347574871 P P P LNCV6_114594_PI430048170 mRNA
CAGAAGGCTGTAACAAGAACAAAAAGGCCAGGATTGATGACAAAGTACTCAACATCAAAG NM_016218RefSeq
chr5 + 75511831 75599821 POLK 51426 polymerase (DNA directed) kappa
GO:0006260|GO:0003684|GO:0006281|GO:0071897|GO:0003887|GO:0006297|GO:0005654|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143626_PI430048170 0.0853039929316948 1.29607042259185 10.3347142586832
10.0902102945995 10.0944256240437 P P P 9.73537507632427 10.0462284269838 9.5910328879298
P P P LNCV6_143626_PI430048170 mRNA
CTCTCAGAGACCTTAAAAAGAAGTTTACTGCAATGTGAATAATTTAATCTCTGGTTGCCA NM_031443RefSeq chr7
+ 45000187 45076470 CCM2 83605 "cerebral cavernous malformation 2, transcript variant 2"
GO:0005515|GO:0048839|GO:0048845|GO:0001701|GO:0051403|GO:0060039|GO:0045216|GO:0060837|GO:0043
234|GO:0005737|GO:0001885|GO:0035264|GO:0061154|GO:0007229|GO:0001570 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128879_PI430048170 0.0685413251423544 0.959902470086571 0.293319950733344
0.3369666730481370.353939650458028A A A 0.4096662779123130.393848706169003
0.358023817759622A A A LNCV6_128879_PI430048170 mRNA
ACTGGAGGCATGTCGTTACCTAAAAATCTCAGGGGCCTAGTTTTACATATGTACAAGCCC NM_002242RefSeq chr2
- 232765801 232776565 KCNJ13 3769 "potassium channel, inwardly rectifying subfamily J, member 13,
transcript variant 1" GO:0005242|GO:0005887|GO:0010107|GO:0034765|GO:0006813 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_125344_PI430048170 0.3440233081280430.9785601424391550.358503916150245
0.3814303113101680.338106278408138A A A 0.43611403303261 0.351991303273418
0.382805014552945A A A LNCV6_125344_PI430048170 mRNA
CAGCAATCTGTCTTCTGGATTAAAACTGAAGATCAACCTACTTTCAACTTACTAAGAAAG NM_001160170 RefSeq
chr8 + 18210102 18223689 NAT1 9 "N-acetyltransferase 1 (arylamine N-acetyltransferase),
transcript variant 1" GO:0006805|GO:0004060|GO:0044281|GO:0005829 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_141178_PI430048170 0.0138072305032126 0.5045382102459584.05959452431979
3.84057367680167 4.35986339039917 P P P 5.13500338549431 4.98050497601487
5.14693403585041 P P P LNCV6_141178_PI430048170 mRNA
TAATTTATAACAGTCCCACTCACCTCTATTTATTCATTTTTGGGAAAACCCGACCTCCCA NM_001080424 RefSeq
chr17 + 7839916 7854800 KDM6B 23135 lysine (K)-specific demethylase 6B

GO:0005515|GO:0070301|GO:0008013|GO:0006325|GO:0005634|GO:0051213|GO:0046872|GO:0043565|GO:0006954|GO:0045944|GO:0071557|GO:0005654|GO:0045446|GO:0048333|GO:0055007|GO:0071558|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130324_PI430048170 0.3301729376861670.8057738877698136.51377688225714 6.19528029854635 6.68963384001018 P P P 6.40175619750299 6.72981200266962 7.14729109392448 P P P LNCV6_130324_PI430048170 mRNA GACATTCTACAGTAGCCTGTGCTGAACTGATCTCTTAAATAAACTTGCTTCTGGTTAACT NM_001624RefSeq chr6 + 106511854 106570449 AIM1 202 absent in melanoma 1
GO:0008150|GO:0003674|GO:0030246|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135150_PI430048170 0.1341611802196380.8813460823788791 1.0613339489987 10.9991043776251 10.7976884072806 P P P 11.1897693862681 11.1861890554776 11.0365567918455 P P P LNCV6_135150_PI430048170 mRNA GGTCACACATTGCAAAACACTGCCCAGAACAGTAAAAAGAGCCTGCATGCCATGAAAAAA NM_005533RefSeq chr17 + 43006724 43014459 IFI35 3430 interferon-induced protein 35
GO:0005515|GO:0060337|GO:0019221|GO:0005634|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139647_PI430048170 0.2815005281014561.02029786031441 0.319997709130167 0.2520681447108220.280734687768176A A A 0.2565785498515860.252016941149031 0.258034105764866A A A LNCV6_139647_PI430048170 mRNA GGGTAATGGACCTTGATAGATTAAGAAGACAAAATATCTAGGAATTAGATGCCTACTACA NM_001080460 RefSeq chr3 + 169821921 169837772 LRRIQ4 NA leucine-rich repeats and IQ motif containing 4 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142202_PI430048170 0.00859471807378781 1.96249165657018 9.80085480151731 10.0756171950269 10.3075226183557 P P P 9.12102589466407 8.93401057914433 9.23891401154282 P P P LNCV6_142202_PI430048170 mRNA ATTGGCTATGAGGTTCAAATGTGTGTGGTGCAGTTTCTGTGTTAATAAAGCAGGTTACAG NM_017984RefSeq chr7 - 100400871 100428808 ZCWPW1 55063 "zinc finger, CW type with PWWP domain 1, transcript variant 1"
GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140904_PI430048170 0.00750395127427598 0.7503152030516068.98262434768192 8.7954965621265 8.87061105619829 P P P 9.18435088661217 9.3106801815857 9.39538771644226 P P P LNCV6_140904_PI430048170 mRNA TAGGGCTTTCAGCAATCGTGAGACCGTCTAGTATAAGACAGAGCACGAAAGGCATTTTTA NM_001284401 RefSeq chr3 - 11790441 11846919 TAMM41 132001 "TAM41, mitochondrial translocator assembly and maintenance protein, homolog (S. cerevisiae), transcript variant 1"
GO:0031314|GO:0004605|GO:0016024|GO:0032049 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136865_PI430048170 0.464575879336972 0.8035618678681 2.0083042517285 1.97034880677212 1.85935113674976 A A A 2.08191978191367 2.75123957255947 1.77902475104869 A P A LNCV6_136865_PI430048170 mRNA ATAAAATTTGTGAATTCAGCCTGGGGCTGGACATGCACTTTCTTAGGGGGCTTTGTGTTG NM_203402 RefSeq chr14 + 24131465 24132849 FITM1 161247 fat storage-inducing transmembrane protein 1
GO:0003674|GO:0019915|GO:0010890|GO:0005789|GO:0030176|GO:0008654|GO:0034389 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144277_PI430048170 0.159018520415653 0.677971570910657 6.85059575689975 6.40682473148152 6.07306749100648 P P P 7.33546449748742 7.12079099882881 6.55447977571652 P P P LNCV6_144277_PI430048170 mRNA AGCCAGCCTCCTGTCTCCAGAGAAGTTCTCCATTAAAAAATAATTTAGCAAATCAAAAAA NM_006657 RefSeq chr21_KI270872v1_alt - 4474 14626 FTCD 10841 "formimidoyltransferase cyclodeaminase, transcript variant B"

GO:0030412|GO:0005794|GO:0019557|GO:0005814|GO:0019556|GO:0006548|GO:0044281|GO:0030409|GO:0035999|GO:0005829|GO:0034641|GO:0005542|GO:0005737|GO:0006760|GO:0007010|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145635_PI430048170 0.212276674093658 0.751189163019285 9.10656368196595 9.05988245285033 9.27807084629509 P P P 9.16076790832591 9.52401775738496 9.91018274345477 P P P LNCV6_145635_PI430048170 mRNA GCCTTAAAATAGTAGCCTGCTACAATGACTTCTTTGGGTAGCCATTTTCATAAGAAATAA NM_052865 RefSeq chr20 + 17969118 17991118 MGME1 92667 mitochondrial genome maintenance exonuclease 1 GO:0005739|GO:0008297|GO:0043504|GO:0006264|GO:0000738 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128083_PI430048170 0.00245554787209448 0.351542099449617 6.12128771158705 5.61266718153157 6.09955351677299 P P P 7.24643215730005 7.41646779136792 7.71145165727167 P P P LNCV6_128083_PI430048170 mRNA CTCTGTGTGTGTATGAGAGAGAGAGTGTGTGTTTGTGTGTTTCAAGGTCAGAACAGGTTT NM_001007559 RefSeq chr18 - 26016252 26090647 SS18 6760 "synovial sarcoma translocation, chromosome 18, transcript variant 1"
GO:0005515|GO:0097150|GO:0005881|GO:0048013|GO:0042493|GO:0000226|GO:0005634|GO:0071564|GO:0006351|GO:0035556|GO:0000902|GO:0030374|GO:0045944 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137080_PI430048170 0.0243219927325369 1.61341253060024 9.26732261151674 9.20448172698899 9.20803129356392 P P P 8.30606229719864 8.7067955195859 8.56920612283666 P P P LNCV6_137080_PI430048170 mRNA GACATTGGCTCACGCACTGTGAGATTTTGTTTTTATACTTGGAAGTGGTGAATTATTTTA NM_000757 RefSeq chr1 + 109910610 109930994 CSF1 1435 "colony stimulating factor 1 (macrophage), transcript variant 1"
GO:0048471|GO:0008284|GO:0005886|GO:0008283|GO:0005157|GO:0046579|GO:0005615|GO:0042803|GO:0030154|GO:0048873|GO:0006954|GO:0030278|GO:0045657|GO:0045860|GO:0042476|GO:0030225|GO:0040018|GO:0002158|GO:0070062|GO:0030097|GO:0030335|GO:0010744|GO:0010743|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143808_PI430048170 0.643649642494147 1.12616675367588 4.46428706985916 3.95828048678477 4.79767345640612 P P P 4.20363865003491 4.34138758298957 4.27823075292713 P P P LNCV6_143808_PI430048170 mRNA CGTGTAGGAGATTTTGTTAGTGGAGCACTAAATAAATTTAAACCTAACAGAACACCTTCT NM_001039841 RefSeq chr15_KI270905v1_alt + 4830644 4843373 ARHGAP11B NA Rho GTPase activating protein 11B NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136414_PI430048170 0.767684360676766 0.957921487782716 0.450660705255715 0.514414347408497 0.515271580736742 A A A 0.347487854675238 0.817321863067263 0.459883330051887 A A A LNCV6_136414_PI430048170 mRNA AAGAGAGTTTTGCCAACAATTCCCCTTAAAAGGAAACAGATCAACTACACCGCATCCCAA NM_003285 RefSeq chr1 - 175322798 175743616 TNR 7143 tenascin R
GO:0008306|GO:0072534|GO:0022408|GO:0009986|GO:0051968|GO:0005578|GO:0060291|GO:0005576|GO:0005634|GO:0051971|GO:0022029|GO:0005737|GO:0050808|GO:0007411|GO:0030198|GO:0048692|GO:0050805|GO:0050885|GO:0045121|GO:0005654|GO:0007155|GO:0035641|GO:0007158 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127823_PI430048170 0.104552187936922 1.20374857377703 6.99146426939582 7.23941268129265 7.26976222907763 P P P 6.92571816843415 7.04441051352713 6.72596491318352 P P P LNCV6_127823_PI430048170 mRNA TATTAAAAAAGAAAAAACAGTCTGTTGGCTTCTCAGTCTGCATCTTGGAGGCAGGGAGGT NM_152493 RefSeq chr1 + 33256572 33300719 ZNF362 149076 zinc finger protein 362
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_126646_PI430048170 0.5672888414628850.9347685947701071 0.3230656471484
10.4241396886643 9.91633188000486 P P P 10.4705866866676 10.2550558414558 10.268005407442
P P P LNCV6_126646_PI430048170 mRNA
AGTAGGTTTCCAAACCATTTGACTCGGTTTGCCTCCCTGCCCGTTGTTTAAACCTTACAA NM_183240RefSeq chr2
+ 119431869 119438520 TMEM37 140738 transmembrane protein 37
GO:0005262|GO:0005244|GO:0070588|GO:0034765|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134036_PI430048170 0.2198961977081911.04350449000206 0.45936761401937
0.3790675086192250.429101188406367A A A 0.3031230312675520.356898360284104
0.421887537937417A A A LNCV6_134036_PI430048170 mRNA
GCCAATTAGAATTTGCCTGAAATCATAGACTCACCCTAGTTTTATTGCTGTAGTTGTTTT NM_018974RefSeq chr6
+ 167291314 167316014 UNC93A 54346 "unc-93 homolog A (C. elegans), transcript variant 1"
GO:0008150|GO:0003674|GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145428_PI430048170 0.00994710960004047 2.14018170866886 5.38016924969433
5.8931705344742 5.7613727349839 P P P 4.83733433982366 4.65364869164473
4.23393253031817 P P P LNCV6_145428_PI430048170 mRNA
GAGGAGCTTGAAACCCGTGGCGCTTTCTGCAGTTTGCAGGTTATCATTGTGAACTTTTTT NM_001671RefSeq chr17
- 7173430 7179564 ASGR1 432 "asialoglycoprotein receptor 1, transcript variant 1"
GO:0005515|GO:0005887|GO:0031668|GO:0030246|GO:0004873|GO:0005576|GO:0046872|GO:0042803|GO:0006
898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140499_PI430048170 0.0734122296324577 0.57291227702809 12.4267117706234
11.6215116231099 11.7266942950257 P P P 12.8156288613192 12.8290990178084
12.6748994994753 P P P LNCV6_140499_PI430048170 mRNA
ACCCCTGCTCCCCACTGCCGCTGCTGCCTCAATAAATCTGCTGATTTGCTGCCTAAAAAA NM_001270639 RefSeq
chr19 - 50505996 50511355 JOSD2 126119 "Josephin domain containing 2, transcript variant 1"
GO:0016579|GO:0004843|GO:0006508|GO:0008242|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136137_PI430048170 0.7427588007910220.9693763568632260.281775666474323
0.3039661122326910.464644396127145A A A 0.5855327334520760.290343675171167
0.29593058923234 A A A LNCV6_136137_PI430048170 mRNA
CCCCTAATAGGGTGGGAAAAATCGCTACTCATGATTACTCCTAAATTTGTGAAGTTTATA NM_002487RefSeq chr15
- 23685406 23687303 NDN 4692 "necdin, melanoma antigen (MAGE) family member"
GO:0048011|GO:0005813|GO:0006355|GO:0008285|GO:0043015|GO:0008347|GO:0048675|GO:0005634|GO:0042
995|GO:0009791|GO:0007417|GO:0003677|GO:0019233|GO:0006351|GO:0005829|GO:0007399|GO:0048871|GO:0
003016|GO:0007413|GO:0071514|GO:0043204|GO:0001764|GO:0040008 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140945_PI430048170 0.2019416810236571.07285879771211 9.81701041362962 9.9725263305482
9.82755069034794 P P P 9.84181546750117 9.77800244595129 9.69440304510419 P P P
LNCV6_140945_PI430048170 mRNA
TCAAAATCATGGGCAACCTGAACTTGCCTAAACCTCAGCAGATAGACTTTGCTGTTCCAG NM_014297RefSeq chr19
- 43506718 43527244 ETHE1 23474 ethylmalonic encephalopathy 1
GO:0005506|GO:0050313|GO:0006749|GO:0044281|GO:0005739|GO:0034641|GO:0005737|GO:0000096|GO:0000
098|GO:0005759|GO:0005654|GO:0070813|GO:0070221 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57892_PI430048170 0.3091345034684480.7970874913830514.04758666391454 3.52243422695778
3.1107022157094 P P P 3.68992139826074 4.07156147069271 4.02505035795404 P P P
LNCV6_57892_PI430048170 mRNA
CAACTTTCTCCAACCCATCAAATCAATGGATTTTTTACCATTGTTTCATCAACGTCTAAG NM_001286577 RefSeq
chr11 - 74012713 74171019 C2CD3 26005 "C2 calcium-dependent domain containing 3, transcript

variant 1"
GO:0005515|GO:0021997|GO:0005813|GO:0006996|GO:0005814|GO:0034451|GO:0035058|GO:0001701|GO:0036064|GO:0005829|GO:0001947|GO:0030162|GO:0007420|GO:0008589|GO:0016485|GO:0071539|GO:0021915|GO:0042733 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81321_PI430048170 0.121745400934596 2.15837786422145 2.25660068970808 2.17890188993678 2.56173678678322 A A A 2.00281573554826 0.2584640097985050.882339024368044 A A A
LNCV6_81321_PI430048170 mRNA
TCAGCAGCTGACCTCTGAGAAGGAGGTGCTGCATAATCAGCTACTGCTGCAGACCCAGCT NM_004486 RefSeq chr9 - 128255828 128275989 GOLGA2 2801 golgin A2
GO:0032091|GO:0019905|GO:0005515|GO:0030134|GO:0005801|GO:0005794|GO:0019901|GO:0000139|GO:0032580|GO:0005634|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144762_PI430048170 0.00164577471273675 2.2528125998591 5.43499044038612 5.2721170881281 5.06578497223666 P P P 4.23883436279959 3.86707046582941 4.14982460301673 P P P LNCV6_144762_PI430048170 mRNA
TAAATGGGGGCTCCATTAGTTCTGCTGCCGAGACTAATAAAGATTTGGTTGGCTCTAGCA NM_021200 RefSeq chr11 + 73646177 73662819 PLEKHB1 58473 "pleckstrin homology domain containing, family B (evectins) member 1, transcript variant 1"
GO:0005515|GO:0005737|GO:0045595|GO:0007275|GO:0016021|GO:0004871|GO:0008022|GO:0007602|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143743_PI430048170 0.245788051676762 1.01293939730217 0.320494690681264 0.288170581205573 0.284130330843689 A A A 0.284148260612351 0.280096278576963 0.27316213988256 A A A LNCV6_143743_PI430048170 mRNA
GCAGTTAATGTGTGTCCTTGAAGAGTTATTAAATTTTCTGACTTGCAGACCCTGAAAAAA NM_207365 RefSeq chr3_GL383526v1_alt + 155088 178941 AADACL2 344752 arylacetamide deacetylase-like 2
GO:0052689|GO:0008152|GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134034_PI430048170 0.17310712430612 1.03164562855083 0.401720199935247 0.353029828627926 0.384567002243125 A A A 0.304246581890283 0.322035889033678 0.377595591071027 A A A LNCV6_134034_PI430048170 mRNA
GAATCCGTATTGAATTTGTGTGGTATGTCACTCAGAAAGAATCGTAATGGGTATATTGAT NM_001193471 RefSeq chr11 - 49146634 49208670 FOLH1 2346 "folate hydrolase (prostate-specific membrane antigen) 1, transcript variant 3"
GO:0005737|GO:0006760|GO:0016020|GO:0005887|GO:0006508|GO:0004180|GO:0008233|GO:0016805|GO:0046872|GO:0008237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138809_PI430048170 0.0957269070547443 0.489357165186786 1.39298109302235 1.16805245095909 2.41823416832278 A A A 2.73261277113162 2.88879964073646 2.77151764084496 A P P LNCV6_138809_PI430048170 mRNA
GTTAGGGTAGGAAATGAATCATAGGGTAAAATGGATGAGTAGATAGAAGTCTCTCATTTA NM_024491 RefSeq chr3 - 138494338 138594383 CEP70 80321 "centrosomal protein 70kDa, transcript variant 1"
GO:0005515|GO:0031965|GO:0005813|GO:0005737|GO:0006996|GO:0000086|GO:0005654|GO:0000278|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138030_PI430048170 0.0109618332291026 0.555111317631654 5.43179442833589 5.28659552453236 5.62310121194769 P P P 6.10835682957291 6.18915730636594 6.56835138431962 P P P LNCV6_138030_PI430048170 mRNA
CCTGCAATTGTGCTTTGGCTTAATGTCTAGCTCACTGTACTTGTAAATGATTAATATTCA NM_003747 RefSeq chr8 + 9555934 9782346 TNKS 8658 "tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase"
GO:0005515|GO:0090263|GO:0015031|GO:0005829|GO:0003950|GO:0006471|GO:0032212|GO:0032210|GO:0018105|GO:0005643|GO:0018107|GO:0045944|GO:0007052|GO:0016055|GO:0070198|GO:0000242|GO:0000784|GO:0000209|GO:0000781|GO:0031965|GO:0005794|GO:0051225|GO:0043392|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_122466_PI430048170 0.00747355397655623 0.69635522235032 11.4568867278379
11.25337546966 11.4067486158034 P P P 11.8050899440121 11.8237112191695
12.0492130906327 P P P LNCV6_122466_PI430048170 mRNA
TTCAGGACCACTAAATGCTGAAATGTGGATGCATACCGAAATAAAAGCAATTCATTGTGT NM_199203 RefSeq chr20
- 50081123 50153798 TMEM189-UBE2V1 NA TMEM189-UBE2V1 readthrough NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_133157_PI430048170 0.9694781097620681.0033625388846 0.306514898278688
0.3057375314783330.502102441289749 A A A 0.3060233847967170.343039620388302
0.455531775300808 A A A LNCV6_133157_PI430048170 mRNA
GAGAGTATGGGAAGAAACAATACAGGATTGCCTTTAATTAATTAAGAATTGCCTCCTGAT NM_001270989 RefSeq
chr4 + 74308469 74316803 EPGN 255324 "epithelial mitogen, transcript variant 1"
GO:0050679|GO:0000187|GO:0008284|GO:0005154|GO:0043406|GO:0005887|GO:0000165|GO:0045741|GO:0045
840|GO:0001525|GO:0008083|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129955_PI430048170 0.1658351916431651.17896130105067 0.76724135002442
0.3953731558453880.683889399526467 A A A 0.2803333269262430.425073424445463
0.448664798399339 A A A LNCV6_129955_PI430048170 mRNA
ATTAATGATTTGAATCAGCAAGTGTGGACCCTTCAGGGTCAGAACCTTGTGGCAGTTCCA NM_019618 RefSeq chr2
+ 112978018 112985672 IL36G 56300 "interleukin 36, gamma, transcript variant 1"
GO:0032755|GO:0005149|GO:0006954|GO:0045087|GO:0019221|GO:0007267|GO:0005615|GO:0005125|GO:0045
662 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140718_PI430048170 0.186367256268976 1.06408093947296 11.6834033186228 11.674478159489
11.7206543318911 P P P 11.5140974323961 11.6156533138913 11.6757724220096 P P P
LNCV6_140718_PI430048170 mRNA
TGTGGCCTCTTTCTACACCTGGAAATTTACTCTTGAATAAATAAAAACTCGTTTGTCTTG NM_006432 RefSeq chr14
- 74479939 74493381 NPC2 10577 "Niemann-Pick disease, type C2"
GO:0042632|GO:0005515|GO:0033344|GO:0005783|GO:0019747|GO:0030301|GO:0009615|GO:0005764|GO:0015
914|GO:0015485|GO:0046836|GO:0019899|GO:0032367|GO:0070062|GO:0008203|GO:0032366 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_93414_PI430048170 0.157370177925526 3.3629310120051 0.47718667602477 2.43304779190374
2.5641168825494 A A A 0.2854137011893930.345564121756281 0.366173262137817 A A A
LNCV6_93414_PI430048170 mRNA
TCAGTGATGCTTTTGTATTTGTGGCGATTTTAATAAAAAGGATATGGCCTTCCCAATGCA NM_001290020 RefSeq
chr10 - 27812163 27998906 ARMC4 55130 "armadillo repeat containing 4, transcript variant 1"
GO:0005930|GO:0030030|GO:0021591|GO:0036158|GO:0005654|GO:0005634|GO:0003341|GO:0070986|GO:0005
856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128666_PI430048170 0.603814678428886 1.26063498887225 0.291165339655691
0.288150614047316 1.42265498109491 A A A 0.3024439182469930.51681378886154
0.48725342756731 A A A LNCV6_128666_PI430048170 mRNA
TGTTAATAGAGGAACTTCAAAGTCAAGGAAAGTCAAAATCACCCCGAAGAGATGCAGATGNM_001267585 RefSeq
chr17 + 18744012 18779349 FBXW10 NA "F-box and WD repeat domain containing 10, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108114_PI430048170 0.665673211598728 1.05540078722707 7.5582291065621
7.70414434849528 7.92919300497929 P P P 7.39835051287321 7.65043691948898
7.89175778509564 P P P LNCV6_108114_PI430048170 mRNA
GTGTTTGGAGTGTGGATCCTTTATATCCTCAAGTTAAATTATACTACTGAAGAATGTGAC NM_003896 RefSeq chr2
- 85839147 85889034 ST3GAL5 8869 "ST3 beta-galactoside alpha-2,3-sialyltransferase 5, transcript
variant 1"
GO:0008373|GO:0047291|GO:0005975|GO:0006688|GO:0030173|GO:0000139|GO:0004513|GO:0005887|GO:0001

574|GO:0016021|GO:0006488|GO:0044267|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138907_PI430048170 0.0603845979367291 1.44840898676545 10.1444575430251
10.3152998068558 10.6762638816486 P P P 9.81717836860978 9.74680551796521 10.007834940645
P P P LNCV6_138907_PI430048170 mRNA
TACACAAACCTACGGATTGGCAGAAAAAGATCCTCATATGGTCAGGTCGCTTCAAAAAGG NM_014367RefSeq chr3
+ 122384175 122410114 FAM162A 26355 "family with sequence similarity 162, member A"
GO:0005739|GO:0005515|GO:0005737|GO:0043065|GO:0006919|GO:0090200|GO:0006927|GO:0071456|GO:0005
634|GO:0016021|GO:0051402|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131505_PI430048170 0.0697007875789573 1.1147628801913 14.3675751479578
14.5359435862982 14.4526812888367 P P P 14.2864648709264 14.268948377213
14.3346805340081 P P P LNCV6_131505_PI430048170 mRNA
GAGAGCCCCAGCTGACATGGAAATACAGTTGTTGGCCTCCGGCCTCCCCTCTGTAAAAAA NM_001909RefSeq chr11
- 1752751 1763992 CTSD 1509 cathepsin D
GO:0005515|GO:0042470|GO:0005576|GO:0005615|GO:0005764|GO:0031012|GO:0019886|GO:0022617|GO:0030
198|GO:0030574|GO:0006508|GO:0004190|GO:0070062|GO:0043202 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140177_PI430048170 0.00470993270624228 0.543285476955691 7.40406805060548
7.52767052534232 7.7251902491585 P P P 8.23645307447396 8.41570649259209
8.63590641707467 P P P LNCV6_140177_PI430048170 mRNA
TCCCATAATTTGGGCCTATGCTATCCTGTTGATTTTTATGTCTAGCTTAAAAGGTATTTG NM_030791RefSeq chr14 -
63684215 63728095 SGPP1 81537 sphingosine-1-phosphate phosphatase 1
GO:0042392|GO:0006665|GO:0030148|GO:0016311|GO:0006670|GO:0005789|GO:0044281|GO:0016021|GO:0097
191|GO:0097193|GO:0006668 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119657_PI430048170 0.470043375894177 1.10104473550961 0.79414480484612
0.481916983990709 0.319852044880167 A A A 0.517060385884225 0.414432342143313
0.278799367292032 A A A LNCV6_119657_PI430048170 mRNA
TAGAGAAGGAATACGCGGCTAGCAAGTTCATCACCAAAGAGAAGCGCCGGCGCATCTCCG NM_017410RefSeq
chr12 + 53938791 53946544 HOXC13 3229 homeobox C13
GO:0043565|GO:0005515|GO:0001077|GO:0045944|GO:0003682|GO:0035878|GO:0005634|GO:0009952|GO:0043
587|GO:0009653|GO:0001942|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126881_PI430048170 0.0439501786789909 0.714541913840618 4.1304497540235
4.11711651900147 4.25650762454644 P P P 4.75757046692242 4.40610339301663
4.77049924947353 P P P LNCV6_126881_PI430048170 mRNA
CCCCAAGTTCCAATGGATTTGCCTTCTCAAAATGTACAACTAAGCAACTAAAGAAAATTA NM_152692RefSeq chrX
- 120625673 120630150 C1GALT1C1 29071 "C1GALT1-specific chaperone 1, transcript variant 1"
GO:0005515|GO:0004653|GO:0006493|GO:0000139|GO:0030168|GO:0016266|GO:0051347|GO:0016021|GO:0044
267|GO:0070062|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130237_PI430048170 0.0294808802065799 0.309402901403449 0.361517971159841
1.5323332524259 0.330884207721351 A A A 2.03127143728327 2.27555828616844
3.11051297339193 A A P LNCV6_130237_PI430048170 mRNA
CAGGTTTAACTTGGCTTATCACTTTTCGTATTGCTCAGTATGTCCAAGATAGGAATAAAA NM_001731RefSeq chr12
- 92140277 92145897 BTG1 694 "B-cell translocation gene 1, anti-proliferative"
GO:0003712|GO:0005515|GO:0006355|GO:0030308|GO:0008285|GO:0005634|GO:0045766|GO:2000271|GO:0005
737|GO:0016477|GO:0045663|GO:0019899|GO:0019900|GO:0045603 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139514_PI430048170 0.0232965558468013 1.14276228502156 0.711373906083511
0.775856286610286 0.773209799770693 A A A 0.639966677756567 0.512669363143982
0.527764817817342 A A A LNCV6_139514_PI430048170 mRNA

GCCTAAGTGATATTACAGCCACCTCATTCTTCTAAAAGTGGATATTTTTCTGTAAATAGC NM_005925 RefSeq chr18 + 32190023 32220403 MEP1B 4225 "meprin A, beta" GO:0005515|GO:0006954|GO:0005886|GO:0005887|GO:0007586|GO:0006508|GO:0008270|GO:0004222|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137216_PI430048170 0.1711654886751390.5769913065721561.67048014578739 2.92098030667854 3.0696917994417 A A P 3.41390553155832 3.7189458929271 3.22774767226273 P P P LNCV6_137216_PI430048170 mRNA
CTGGAGGAAGATTTTCCCTTGCTTCTGCATAAAATTTTAACTCCATAACTTATAAGCTCA NM_017654 RefSeq chr7 - 93099512 93118023 SAMD9 54809 "sterile alpha motif domain containing 9, transcript variant 1" GO:0005515|GO:0005737|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133983_PI430048170 0.5084308848889130.8291899195995320.286747524782898 2.12558691066266 1.71926924743 A A A 1.85202374769818 1.60392048138412 2.01975445059269 A A A LNCV6_133983_PI430048170 mRNA
TGAAGGAGCCATCTCATCCACAGCTCTTCCTTGAGCAGCCATGGCCAGCTCCAGGCGAGG NM_001501 RefSeq chr20 + 3043621 3045745 GNRH2 2797 "gonadotropin-releasing hormone 2, transcript variant 1" GO:0007165|GO:0005179|GO:0007275|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132749_PI430048170 0.00902920271492545 0.8013449003257154.86973448180275 4.95425254337184 4.84071893498882 P P P 5.27416125314694 5.23805214361207 5.10820326456548 P P P LNCV6_132749_PI430048170 mRNA
AGAACTGGACTCAGATTTCAGCCCCATCCCCAATGAAGAGCTTGAGTTTGAAGATTATAC NM_052884 RefSeq chr19 - 49948992 49961172 SIGLEC11 114132 "sialic acid binding Ig-like lectin 11, transcript variant 1" GO:0030246|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144886_PI430048170 0.5838677753721040.9730590049720944.56147899333231 4.65284506858426 4.50907717016155 P P P 4.51485972972768 4.64857137866603 4.67672748735638 P P P LNCV6_144886_PI430048170 mRNA
CTTGCAAAGACCTTTGTTTCTGTGATGTACCAACTTTACAGTTGTGTTGCCATTTAAACC NM_001301087 RefSeq - - 0 0 --- NA "Myb/SANT-like DNA-binding domain containing 2, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139989_PI430048170 0.00692749982377984 0.6544912554057096.28954828875743 6.09598635893845 6.05213197040299 P P P 6.58366268832259 6.88568276985056 6.79771635803001 P P P LNCV6_139989_PI430048170 mRNA
CCCATCGGCTTCTGTAATAATCGTATTGCCTATATACTTGAATTAAAAATATATGGTGGC NM_148842 RefSeq chr7 - 75027119 75073881 WBSCR16 81554 "Williams-Beuren syndrome chromosome region 16, transcript variant 2" GO:0005739|GO:0008150|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127767_PI430048170 0.0121811480425932 0.5857872242410366.25241594289062 6.1599056718392 6.35464985700114 P P P 6.7952612415373 7.05605076428326 7.20721382630564 P P P LNCV6_127767_PI430048170 mRNA
TGTCCTTCCTAAAAATGGAATAGTGGGATGTAGTGCTTAATGGAAACTGCTAAATCTTTT NM_001040653 RefSeq chr3 - 126458900 126475919 ZXDC 79364 "ZXD family zinc finger C, transcript variant 2" GO:0005515|GO:0003700|GO:0030275|GO:0070742|GO:0005634|GO:0005575|GO:0045893|GO:0003676|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141297_PI430048170 0.3569910698892750.9533528520100247.48293054531066 7.41194648483085 7.5856215816349 P P P 7.64890052043379 7.51030000492821 7.529407517695 P P P LNCV6_141297_PI430048170 mRNA
GGGGGAGGGGAATATCAAATGGACAAGATCACTTTTAAATGGTAGTTTTTATAAGATGTT NM_001004304 RefSeq chr12 + 53180750 53190870 ZNF740 283337 zinc finger protein 740 GO:0006355|GO:0005634|GO:0003676|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144351_PI430048170 0.000227340170946226 2.50868048290812 12.5877359566132

12.7600127011225 12.6973470528509 P P P 11.4965147791087 11.2911705074231
11.2708986595799 P P P LNCV6_144351_PI430048170 mRNA
GAGAGAAAATTTTGTCCTCTTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTAA NM_001288565 RefSeq
chr1 - 201134770 201154555 TMEM9 252839 "transmembrane protein 9, transcript variant 3"
GO:0008150|GO:0003674|GO:0005770|GO:0031902|GO:0006810|GO:0016021|GO:0005765|GO:0005764 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144297_PI430048170 0.00874611230828288 0.5998048985675863.62432777266234
3.60476679761533 3.96566009212764 P P P 4.65276783603979 4.39779064278203
4.36849749829129 P P P LNCV6_144297_PI430048170 mRNA
AATATTTTCTGCTAAAGGAGTGACTGTGCATATAAGTAAAGGCAACCTCTCAGGAAAAAA NM_182833RefSeq chr11
- 77216557 77287418 GDPD4 220032 glycerophosphodiester phosphodiesterase domain containing 4
GO:0006629|GO:0016021|GO:0008889|GO:0006071|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141418_PI430048170 0.2105361775583717.05764096421297 0.42861820707886
3.36647840157412 4.36874646874793 A P P 0.9491921316075280.393410525603606
0.416884228826811 A A A LNCV6_141418_PI430048170 mRNA
TGTCACACCTTTTCTGTCAAAATAAAATGTCTTGGAGGTTATGACTCCTTGGTGAAAAAA NM_006060RefSeq chr7
+ 50304668 50405100 IKZF1 10320 "IKAROS family zinc finger 1 (Ikaros), transcript variant 1"
GO:0003700|GO:0060041|GO:0005634|GO:0048538|GO:0045660|GO:0046872|GO:0048535|GO:0005737|GO:0048
541|GO:0051138|GO:0045944|GO:0030183|GO:0001779|GO:0040018|GO:0046982|GO:0000122|GO:0003677|GO:0
006351|GO:0043565|GO:0043234|GO:0007049|GO:0005721|GO:0030217|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135891_PI430048170 0.0418639008918551 0.4584878940662933.749107831954
2.97489541566651 2.9343312070083 P A P 4.29402026676988 4.49665940814676
4.38921378092614 P P P LNCV6_135891_PI430048170 mRNA
CCGCATTTTGGGTGCCATTAAATAGGGAAAAAACATGTAAAAAATGTAAAATGGAGACCA NM_000553RefSeq chr8
+ 31033261 31173761 WRN 7486 "Werner syndrome, RecQ helicase-like"
GO:0005515|GO:0008408|GO:0090305|GO:0010259|GO:0071480|GO:0032403|GO:0042803|GO:0006302|GO:0004
527|GO:0004003|GO:0000723|GO:0032508|GO:0016887|GO:0006979|GO:0009267|GO:0032389|GO:0043140|GO:0
005813|GO:0030145|GO:0000287|GO:0051345|GO:0000405|GO:0007569|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134163_PI430048170 0.1184467303280690.6325891455449756.38021829381631
6.11213441033628 5.75542685350616 P P P 7.10064867406942 6.83097576065822
6.23506257665557 P P P LNCV6_134163_PI430048170 mRNA
CTTCAGATATTTATTTTTCTTTTCACTGTTTTAAAATAAAACCAAAGTATTGATAAAAAA NM_022164RefSeq chr1 +
31576484 31587686 TINAGL1 64129 "tubulointerstitial nephritis antigen-like 1, transcript variant 1"
GO:0005576|GO:0005615|GO:0006898|GO:0031012|GO:0005737|GO:0006955|GO:0016197|GO:0043236|GO:0006
508|GO:0030247|GO:0008234|GO:0070062|GO:0005044|GO:0005201 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_2840_PI430048170 0.4644050268565310.9596142498834931 3.733899429009 13.6890949128143
13.9109123518468 P P P 13.7994684905107 13.8299905732438 13.8910127944091 P P P
LNCV6_2840_PI430048170 mRNA
TGTGGCAGAAGATGATGATGAAAGTCTTCTTGGACACTTAATGATTGTTGGCAAGAAATG NM_005340RefSeq chr5
- 131159282 131165348 HINT1 3094 "histidine triad nucleotide binding protein 1, transcript variant 1"
GO:0006355|GO:0005886|GO:0005634|GO:0009154|GO:0006351|GO:0007165|GO:0005737|GO:0000118|GO:0072
332|GO:0000166|GO:0016787|GO:0005080|GO:0005856|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141039_PI430048170 0.0469090469245167 0.5984358429737827.3863302841411
7.29132697322552 7.64110198234124 P P P 7.79278855937927 8.22710455236111

8.46554688306126 P P P LNCV6_141039_PI430048170 mRNA
GTAAACCAAAAACTTTTAAATTTCTTCAGGTTTTCTAACATGCTTACCACTGGGCTACTG NM_018131 RefSeq chr10
+ 93496631 93529092 CEP55 55165 "centrosomal protein 55kDa, transcript variant 1"
GO:0005515|GO:0000920|GO:0006997|GO:0005813|GO:0016020|GO:0005814|GO:0000281|GO:0030496|GO:0007
080|GO:0032154|GO:0045184|GO:0045171 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63049_PI430048170 0.1876185220653121.1906546128821 7.69737165599599 8.13620497507473
7.88234663474152 P P P 7.79292431070465 7.59839312213166 7.59411331668322 P P P
LNCV6_63049_PI430048170 mRNA
AAAGAGCAGGTTGTGAATGGAGATGTTGGGGCTGTTTCAGAGCCTCCCTGCCTCCCCAAG NM_001135704 RefSeq
chr17 + 45132599 45144176 ACBD4 79777 "acyl-CoA binding domain containing 4, transcript variant
1" GO:0000062|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143100_PI430048170 0.0174068201943403 0.3311377583511832.270016108954
2.64282250365076 2.60654144455125 A A A 3.89132715215141 3.68792141878523
4.59049782835004 P P P LNCV6_143100_PI430048170 mRNA
ATCCAACCCACACCTGAGAACTCGTCTCATTACTTTATAGTCATGTCATGTATGTTTTTT NM_152641 RefSeq chr12 +
45729836 45908036 ARID2 196528 "AT rich interactive domain 2 (ARID, RFX-like)"
GO:0005515|GO:0006355|GO:0005886|GO:0005654|GO:0006337|GO:0003677|GO:0046872|GO:0006351|GO:0016
568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142825_PI430048170 0.9998882837001720.9983361254646019.13152908097745
9.07162986277732 9.20604809079592 P P P 9.00926248288486 9.25312875484471
9.14685243513283 P P P LNCV6_142825_PI430048170 mRNA
AGAACTCCTAGTCAGGAAGCAATATCATTTCAGGTCTAAAGAAAGGGACGTGCATCTGGC NM_015897 RefSeq chr19
+ 4007597 4039386 PIAS4 51588 "protein inhibitor of activated STAT, 4"
GO:0005515|GO:0016874|GO:0016925|GO:0032088|GO:0005634|GO:0000122|GO:0003677|GO:0006351|GO:0016
363|GO:0005737|GO:0019789|GO:0016605|GO:0033235|GO:0005654|GO:0008270|GO:0016055|GO:0045892|GO:0
031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133567_PI430048170 0.0565109960719842 1.30925194551886 8.38993321791545
8.63700910673973 8.39295568843777 P P P 8.06915157516239 8.28581015410759
7.88492561176251 P P P LNCV6_133567_PI430048170 mRNA
GTCCACCCCCATACATTTATTTCTGTAAATAATGTGCACTGAATAAATTGTACAGCCGGC NM_002428 RefSeq chr16
+ 58025377 58046900 MMP15 4324 matrix metallopeptidase 15 (membrane-inserted)
GO:0005515|GO:0005886|GO:0005509|GO:0043085|GO:0035987|GO:0031012|GO:0022617|GO:0005887|GO:0030
198|GO:0030574|GO:0006508|GO:0008270|GO:0004222|GO:0008047|GO:0032355|GO:0006464 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_94165_PI430048170 0.1497832409840431.15175105753734 5.0551998487897 4.81706662115023
4.81141939468713 P P P 4.74907045694673 4.7936479576294 4.52952457028862 P P P
LNCV6_94165_PI430048170 mRNA
ATATGGACGAGCAGCTGACAAGTTTCTCTCCCTAATCCCACGCTGTTGTCGGCACCACGC NM_032127 RefSeq chr11
- 6211333 6234711 FAM160A2 84067 "family with sequence similarity 160, member A2, transcript
variant 1" GO:0005515|GO:0008333|GO:0007032|GO:0045022|GO:0015031|GO:0007040|GO:0070695 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133220_PI430048170 0.0018052125679936 0.4314665956113065.87526340613874
5.76107111850526 6.02565359809892 P P P 6.94400832856524 7.01681070146002
7.32284917197427 P P P LNCV6_133220_PI430048170 mRNA
ACTTACATGTTGACGTTGAAGGCTCAAAGCTATACTAAGAAGCTTTCTGAAAGATTGGGC NM_006805 RefSeq chr5
- 137751383 137754350 HNRNPA0 10949 heterogeneous nuclear ribonucleoprotein A0
GO:0006397|GO:0008380|GO:0010467|GO:0019901|GO:0003723|GO:0005634|GO:0006954|GO:0000166|GO:0000
398|GO:0030529|GO:0032496|GO:0017091|GO:0005654|GO:0070935 . NA - . NA NA NA NA NA NA
NA NA NA

LNCV6_141260_PI430048170 0.7489762201286870.9597128028037384.3274121625309
3.25802017657322 4.397814596453 P P P 4.26546302615629 4.19408770893754 3.9369626364306
P P P LNCV6_141260_PI430048170 mRNA
TTTGCCAACCACCTCTGCTTGCCTGTCCACATTTAAAAATAAAATCATTTTAGCCCTTTCNM_003665RefSeq chr1 -
27369109 27374824 FCN3 8547 "ficolin (collagen/fibrinogen domain containing) 3, transcript variant 1"
GO:0005515|GO:0006956|GO:0051607|GO:0005581|GO:0046597|GO:0045087|GO:0030246|GO:0072562|GO:0043
654|GO:0005576|GO:0003823|GO:0001867 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132513_PI430048170 0.000407112693950246 0.4188762758342718.79791551508234
8.55254563390755 8.53549863357793 P P P 9.74817392108268 9.96084945954293 9.9486428456751
P P P LNCV6_132513_PI430048170 mRNA
CTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAAGTCTTTA NM_203380RefSeq chr10
+ 112375264 112428380 ACSL5 51703 "acyl-CoA synthetase long-chain family member 5, transcript
variant 3"
GO:2001236|GO:0001676|GO:0005783|GO:0005730|GO:0005743|GO:0005634|GO:0005741|GO:0044281|GO:0035
338|GO:0005524|GO:0004467|GO:0005739|GO:0016020|GO:0005789|GO:0019432|GO:0016021|GO:0044255 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144717_PI430048170 0.2948050001076861.05159065018821 0.334122117217415
0.3311437343778450.484731417986101A A A 0.3110825878260570.286271677504843
0.339832581197838A A A LNCV6_144717_PI430048170 mRNA
CTGTGTATGTCTATTTGCACAAGATTGTCTTTTCCTATTTTGGAGTGGTCAGACATTTTA NM_003320RefSeq chr11 +
8038632 8106107 TUB7275 "tubby bipartite transcription factor, transcript variant 1"
GO:0006909|GO:0060041|GO:0005886|GO:0007605|GO:0005576|GO:0005634|GO:0032403|GO:0008020|GO:0005
829|GO:0009584|GO:0050766|GO:0005737|GO:0044259|GO:0009725|GO:0007602 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136695_PI430048170 0.0924736872414108 0.5865995940191864.38242182617057
4.606495429985 4.99073095308465 P P P 5.89098748034892 4.96742156432884 5.3454831937615
P P P LNCV6_136695_PI430048170 mRNA
GTACTTTGTATTCTGGAAGCGTGAATTGCTTTTGAAGTCTGTCAGTATTACTGGTATTTTNM_014454RefSeq chr6 -
108986436 109094505 SESN1 27244 "sestrin 1, transcript variant 1"
GO:0008285|GO:0007050|GO:0005634|GO:0051896|GO:0006974 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140849_PI430048170 0.0600155066371588 1.28165820138569 6.4862292104581
6.13272560778506 6.37595594678894 P P P 6.04554373688112 5.88789499519931
6.00514795074027 P P P LNCV6_140849_PI430048170 mRNA
CACATTATGATCTTGACAGGTGCACTTTACTGGGGAGAATAAAAAGGACCATACGGTAAA NM_013375RefSeq chr6
+ 26596942 26600049 ABT1 29777 activator of basal transcription 1
GO:0005515|GO:0005667|GO:0021522|GO:0006366|GO:0006357|GO:0000166|GO:0003713|GO:0005730|GO:0005
634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132274_PI430048170 0.0644625029576803 0.9545892596802010.423647727015609
0.3587156938896990.375578122318112A A A 0.47360769983983 0.468153355016998
0.417451811863473A A A LNCV6_132274_PI430048170 mRNA
GCACTCGATTAATGTGACAACCTTTTCAATAAGCAGAAATAACGTAGGTACACATCACTC NM_001199527 RefSeq
chr21 + 42062958 42142995 UMODL1 89766 "uromodulin-like 1, transcript variant 3"
GO:0010466|GO:0005509|GO:0042981|GO:0030414|GO:0005615|GO:0097211|GO:0007338|GO:0048609|GO:0005
737|GO:0016021|GO:0060612|GO:0009897|GO:2000354 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132508_PI430048170 0.00405022138048766 0.4882423294314523.49237256537029
3.44581146272458 3.49200986067341 P P P 4.59749492265421 4.35687166629791
4.56759695995796 P P P LNCV6_132508_PI430048170 mRNA
TGGGAGGAGGACTTTTGCATACATTTTTACTCTTTAAATAACGACAACGACACTTATACT NM_002040RefSeq chr21

+ 25735017 25772460 GABPA 2551 "GA binding protein transcription factor, alpha subunit 60kDa, transcript variant 1"
GO:0005515|GO:0000790|GO:0006996|GO:0003700|GO:0046982|GO:0044212|GO:0006366|GO:0003713|GO:0005634|GO:0000122|GO:0000978|GO:0001228|GO:0001701|GO:0003677|GO:0030154|GO:0045653|GO:0001077|GO:0045944|GO:0003682|GO:0005654|GO:0007005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90773_PI430048170 0.341885138097861 1.16784954063482 0.8702648865647740.328664923411009
0.433294394230288 A A A 0.2833577174039730.362124778949279 0.372416883188542 A A A
LNCV6_90773_PI430048170 mRNA
TGTAGGAGTTACTGGAAAAGCAAGAATAACTTATGCGGATTAACAATATGGAAACATCCT NM_001258419 RefSeq
chr11 - 40114200 41459636 LRRC4C 57689 "leucine rich repeat containing 4C, transcript variant 2"
GO:0005515|GO:0030054|GO:0016020|GO:0045211|GO:0016021|GO:0050770|GO:0005615 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128103_PI430048170 0.7798470117043391.05149431766266 2.18461651375258
0.3003936273184610.283697223691607 A A A 0.8878497756414 1.037626692117
1.45892308831599 A A A LNCV6_128103_PI430048170 mRNA
GGGGCACACTTACACAACTCTCTCTGCAATATGTGCAATAGCAAAATGCAGTGATGCATG NM_001146040 RefSeq
chr5 - 151822512 151924836 GLRA1 2741 "glycine receptor, alpha 1, transcript variant 1"
GO:0005515|GO:0006821|GO:0022824|GO:0030054|GO:0005886|GO:0051970|GO:0016934|GO:0043231|GO:0001964|GO:0002087|GO:0006936|GO:0034220|GO:0007218|GO:0045211|GO:0050884|GO:0042391|GO:0007628|GO:0006811|GO:0034707|GO:0060077|GO:0055085|GO:2000344|GO:0030977|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130301_PI430048170 0.0528297970404573 1.23931391159951 11.2724269342468
11.2674144603908 11.1456635520382 P P P 10.9072114093019 10.7653605593729
11.0715437018056 P P P LNCV6_130301_PI430048170 mRNA
CCCAGAAATGACTGCTAAGCCTCTTGCCTTGTCTTTAGTAGCTAATGATCAGAGAGATTT NM_001131025 RefSeq
chr12 + 7189685 7211483 PEX5 5830 "peroxisomal biogenesis factor 5, transcript variant 4"
GO:0005515|GO:0051262|GO:0005794|GO:0031267|GO:0016560|GO:0005782|GO:0006625|GO:0016561|GO:0000268|GO:0045046|GO:0008022|GO:0005829|GO:0005622|GO:0043234|GO:0005737|GO:0047485|GO:0016020|GO:0005052|GO:0019899|GO:0016558|GO:0005778|GO:0005777 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_126648_PI430048170 0.9152700877975070.9058253079919930.90237463208008
2.19320580163078 1.65663456977145 A A A 1.41783127645871 0.32220737361397
2.73782421103873 A A P LNCV6_126648_PI430048170 mRNA
AATCTATTGTATCTACCTGCAGTCTCCATTGTTTCCAGAGTGAACTTGTAATTATCTTGT NM_000074 RefSeq chrX + 136648176 136660390 CD40LG 959 CD40 ligand
GO:0005164|GO:0043066|GO:0005886|GO:0045190|GO:0030168|GO:0032735|GO:0005125|GO:0005615|GO:0051023|GO:0006954|GO:0042100|GO:0005887|GO:0050776|GO:0030183|GO:0007159|GO:0016021|GO:2000353|GO:0048305|GO:0009897|GO:0005174 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143052_PI430048170 0.3682813687526280.7912897086025080.301408756934944
0.5153854699553810.375887787835741 A A A 0.4969195694377390.380759919851202
1.19563484873607 A A A LNCV6_143052_PI430048170 mRNA
GAAGTGCTCTTTTTATGCTTTCTGGAGATGTTACTGTTAAATGTCTTTCTACATCAGGCT NM_173485 RefSeq chr20 + 52972406 53495330 TSHZ2 128553 "teashirt zinc finger homeobox 2, transcript variant 1"
GO:0006355|GO:0007275|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142875_PI430048170 0.2469383671183120.6688244302033396.17457483365063
4.99932162358376 4.77125412924827 P P P 6.24647028851042 6.14808194581865
5.63837180887695 P P P LNCV6_142875_PI430048170 mRNA
CCTCCCCTCAGACTAGCTTTCAGTCTTCTGTCAGCAGTAAAACTTATATATTTTTTAAAANM_014219 RefSeq

chr19_GL949752v1_alt + 642865 688658 KIR2DL2 3803 "killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2" GO:0005886|GO:0050776|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133622_PI430048170 0.0133694278982681 2.05601024529716 9.34650254170908 9.6322505816444 9.89550230010842 P P P 8.68382936184465 8.4747901701698 8.63974967055541 P P P LNCV6_133622_PI430048170 mRNA
GCCTTTTTTAAGAAATAAATTTTTTGTTCACATGACCAAAGCCCCTCCTGTGTGTGTTAA NM_203462 RefSeq chr4 - 6707700 6709879 MRFAP1L1 114932 Morf4 family associated protein 1-like 1 GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127934_PI430048170 0.153723373594726 1.05850791477985 0.511086947429781 0.635047920646044 0.536464589975616 A A A 0.437488409148488 0.488484673996195 0.512509412969007 A A A LNCV6_127934_PI430048170 mRNA
TCTCACCATTTCCTAAGAGATACATTGTAAAACGTGACAGTAAGACTGATTCTAGCAGAA NM_002783 RefSeq chr19 - 42924131 42937178 PSG7 5676 "pregnancy specific beta-1-glycoprotein 7 (gene/pseudogene), transcript variant 1" GO:0007565|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128201_PI430048170 0.163308518031818 0.812560516870398 7.90072977562606 8.20910247837369 7.98702311637593 P P P 8.32360530453695 8.56394237754916 8.08592580006511 P P P LNCV6_128201_PI430048170 mRNA
CAAGTAATTAAGAGGCTTGACACCATACTCATTCACCCCAAAGGCTCTTTTAAGAGCCAC NM_175065 RefSeq chr1 - 149887468 149887916 HIST2H2AB 317772 "histone cluster 2, H2ab" GO:0008150|GO:0003674|GO:0046982|GO:0005634|GO:0000786|GO:0003677|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137887_PI430048170 0.160415544044781 0.848027146327796 7.31508841062105 7.15790554517674 7.49542162042928 P P P 7.39253395390923 7.5575386266143 7.73166478379023 P P P LNCV6_137887_PI430048170 mRNA
TTTCAGAACCACCAACTGCTCTTGACAATTGTTAACCCACTAGGCTCCTTTGGTTAGAGA NM_001278141 RefSeq chr1 + 146938544 146996093 NBPF12 NA "neuroblastoma breakpoint family, member 12" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139476_PI430048170 0.0258145453147514 1.45674272242335 10.3912229998129 10.6585367071642 10.7802273821127 P P P 9.96107172728365 9.9646977907737 10.2792878826791 P P P LNCV6_139476_PI430048170 mRNA
TGTTCTTTCACTTGTAAGTTTCAGTCATTTTCTTTTACCTCGTTGTCAGTGTACAGAATG NM_007080 RefSeq chr4 + 146175682 146190061 LSM6 11157 "LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)" GO:0005515|GO:0008380|GO:0010467|GO:0005730|GO:0043928|GO:0005732|GO:0008033|GO:0005829|GO:0030490|GO:0000398|GO:0000932|GO:0030532|GO:0005681|GO:0046540|GO:0005688|GO:0070062|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126929_PI430048170 0.545640439941136 0.896663894142144 5.67642266492463 5.35558255515576 4.90940102386081 P P P 5.43141023899349 5.76061625817548 5.27966121570345 P P P LNCV6_126929_PI430048170 mRNA
AATAATCCCTGCTCACATTTTCCCCTACACTTTGTCATTAAAACAGCACGAAAACTCAAA NM_013268 RefSeq chr19 + 39602528 39607474 LGALS13 29124 "lectin, galactoside-binding, soluble, 13" GO:0005515|GO:0004622|GO:0030246|GO:0006915|GO:0006644 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131869_PI430048170 0.338688620993812 1.08768993049292 9.07342502293706 9.36118619650937 9.09353825712128 P P P 9.10719335747251 9.07342502293706 8.9998976176176 P P P LNCV6_131869_PI430048170 mRNA
ACATCAGATTTTGGGGGGATGCCCTCTCTCCTATGTATGGTCTACACATTCTGATTTTTT NM_005047 RefSeq chr9 - 120816053 120843021 PSMD5 5711 "proteasome (prosome, macropain) 26S subunit, non-ATPase, 5, transcript variant 1"

GO:0005515|GO:0002474|GO:0010467|GO:0090263|GO:0044281|GO:0031145|GO:0005829|GO:0034641|GO:0000082|GO:0016032|GO:0090090|GO:0006977|GO:0000209|GO:0000502|GO:0043066|GO:0006521|GO:0042590|GO:0051437|GO:0006915|GO:0042981|GO:0051436|GO:0051439|GO:0008540|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118962_PI430048170 0.902935036580339 1.0262061757562 0.962953920140844 0.481081728629377 0.435292726131968 A A A 0.528727498198848 0.436183698164624 0.833206933547785 A A A LNCV6_118962_PI430048170 mRNA
ATTTCTTGGAGCCTGAAAAGAAGAGCAGCGACTGGACCCAGAGCCATGTGGCTGTGCCCT NM_005411 RefSeq chr10 + 79610938 79615443 SFTPA1 653509 "surfactant protein A1, transcript variant 1"
GO:0005581|GO:0007585|GO:0006869|GO:0005578|GO:0030246|GO:0005576|GO:0005615|GO:0005319 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134224_PI430048170 0.572073579435378 0.880215699566292 1.61351900177849 0.297327861961729 0.487901844680876 A A A 0.799403310118168 1.41074622900928 1.04726569107044 A A A LNCV6_134224_PI430048170 mRNA
GAGGTGTTGTTTTTGCAATGACTGTGTATTCATTGAGGAAAGGTTTCCAATGAAATTTCA NM_020961 RefSeq chr4 + 118685369 118712270 METTL14 57721 methyltransferase like 14
GO:0061157|GO:0019827|GO:0003723|GO:0080009|GO:0005654|GO:0005634|GO:0016422 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100831_PI430048170 0.155963926822523 0.938449538265651 0.24479582759056 0.294776725505111 0.293540672155236 A A A 0.449413113848229 0.350024625761269 0.305394417150506 A A A LNCV6_100831_PI430048170 mRNA
TAGATTATGCTGTAGAAGGGACAGAATCCAGCTCTATCCTGTTGACCTATCTGGATGAAA NM_001198950 RefSeq chr13 + 108629222 109208007 MYO16 23026 "myosin XVI, transcript variant 1"
GO:0048471|GO:0005737|GO:0003774|GO:0051015|GO:0008285|GO:0005886|GO:0008152|GO:2000134|GO:0021549|GO:0005654|GO:0016459|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134595_PI430048170 0.381297660162448 1.69345646172108 1.89796972204525 0.307075687249793 0.443223826820034 A A A 0.340658920185132 0.305054782793701 0.301480459841857 A A A LNCV6_134595_PI430048170 mRNA
AAGGGAAGACCCATCCTTATATTATAGAGGAAGAATGTTGACTCTCTTTTTTCTGGATTT NM_001135659 RefSeq chr2 - 49918504 51032536 NRXN1 9378 "neurexin 1, transcript variant alpha2"
GO:0005515|GO:0090126|GO:0090129|GO:0030054|GO:2000311|GO:2000310|GO:0051490|GO:0016339|GO:0030198|GO:0007411|GO:0050885|GO:0030534|GO:0007612|GO:0050839|GO:0097091|GO:0051965|GO:2000821|GO:2000463|GO:0009986|GO:0060134|GO:0005509|GO:0051968|GO:0007416|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140574_PI430048170 0.470585958436014 1.04694055105772 0.283281927017408 0.293250833461117 0.50079678525646 A A A 0.314094498992248 0.274388543253622 0.300642552317159 A A A LNCV6_140574_PI430048170 mRNA
ATGCTGAGTGTGGGTTGTTTAAACATGCATATTGAAATAACACATATAGTAACGTGGGAA NM_004962 RefSeq chr10 + 47300223 47313574 GDF10 2662 growth differentiation factor 10
GO:0010862|GO:0042981|GO:0005125|GO:0005160|GO:0005615|GO:0060395|GO:0001501|GO:0043408|GO:0045444|GO:0007179|GO:0048468|GO:0008083|GO:0040007 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69025_PI430048170 0.424074255804604 0.681110421605129 0.503387070822687 2.33285866293562 2.18420686164786 A A A 1.58949593251511 2.36354784845799 2.99906206362474 A A P LNCV6_69025_PI430048170 mRNA
TTCAAGTCCAATGAAGGGAACAGCGCTAGAGGGTTCCAGGTCCCATACGTGACATATGAT NM_020974 RefSeq chr11 - 9019499 9091603 SCUBE2 57758 "signal peptide, CUB domain, EGF-like 2, transcript variant 1"
GO:0005509|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130632_PI430048170 0.257808138680784 1.12318159058334 10.1247224603203 9.93956457181618 9.76613538512029 P P P 9.79965959804457 9.73200168856532

9.81689045285655 P P P LNCV6_130632_PI430048170 mRNA
ACCTGGCCTGATGTGGAGTAGCTCCTGAGTAAAGAAGTTACCCTTTTGAAGGTGAAAAAA NM_001013694 RefSeq
chr22 + 26483883 26491938 SRRD 402055 SRR1 domain containing GO:0048511 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137904_PI430048170 0.0281672802895336 0.8185757618558295.70422455179756
5.50524743653772 5.50953156610759 P P P 5.87513948745224 5.76600699256804
5.94761247158442 P P P LNCV6_137904_PI430048170 mRNA
TGTGAAGCTGGCAGAAATCACTAGTAAATGCTTCAGTTTCCTGAAATGGAATGGAAAAAA NM_001301275 RefSeq
chr9 + 94259265 94301829 ZNF169 169841 "zinc finger protein 169, transcript variant 3"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144594_PI430048170 0.4040766234454451.51752219070208 1.65871396733717
0.3909038969881770.3012286352199 A A A 0.2871947816122740.395515284980786
0.287997523319056A A A LNCV6_144594_PI430048170 mRNA
AGGAACAAGATTCTCACAGCCACAGTGGACAATGCCAATGTCCTTCTGCAGATTGACAAT NM_000526RefSeq chr17
- 41582278 41586895 KRT14 3861 "keratin 14, type I"
GO:0005515|GO:0005882|GO:0042633|GO:0034329|GO:0007568|GO:0005634|GO:0010043|GO:0071944|GO:0005
829|GO:0005737|GO:0008544|GO:0010212|GO:0030855|GO:0045110|GO:0005200|GO:0031581|GO:0045095|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133502_PI430048170 0.0395456574175152 1.09966660607043 11.919524693441
11.8737563678526 11.7994169521671 P P P 11.6896683350025 11.7794184203567 11.713445874158
P P P LNCV6_133502_PI430048170 mRNA
TTGACATGTGCCTGCTCCTGGCATTTCAATAAAACCCGGCTTGGGTCTGTGTCTTGAGTG NM_001135635 RefSeq
chr11 - 65916811 65919060 C11orf68 83638 "chromosome 11 open reading frame 68, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70771_PI430048170 0.0593012404142247 0.88917458891455 13.2956200089287
13.3602626423252 13.1875536105903 P P P 13.4392330561138 13.4961484815745
13.4206116786959 P P P LNCV6_70771_PI430048170 mRNA
CAGCCTGGGACTGCTGTGATGGGGTATCACGGTGATGGTCCCATTAAACTTCCACTCTGC NM_018226RefSeq chr2
+ 240568586 240578732 RNPEPL1 57140 arginyl aminopeptidase (aminopeptidase B)-like 1
GO:0019370|GO:0004177|GO:0006508|GO:0008270|GO:0008237 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136733_PI430048170 0.1331067723405881.22880412631753 5.66711916071507 5.5706658210488
5.81790077055635 P P P 5.3656465250169 5.61551208333638 5.15695293233544 P P P
LNCV6_136733_PI430048170 mRNA
AGCTGATTTCCTACCAGCCTTTGCCTCTTCCTTCAATGTGGTTTCCATGGGAATTTGCTT NM_002185RefSeq chr5 +
35856874 35879603 IL7R 3575 "interleukin 7 receptor, transcript variant 1"
GO:0005515|GO:0033089|GO:0008361|GO:0005886|GO:0004917|GO:0005576|GO:0003823|GO:0048535|GO:0048
872|GO:0010628|GO:0000902|GO:0007165|GO:0006955|GO:0030217|GO:0042100|GO:0001915|GO:0038111|GO:0
016049|GO:0016021|GO:0000018|GO:0009897|GO:0002377|GO:0007166 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129072_PI430048170 0.0938135818348895 0.7047707450929489.68396599884517
9.70935546293949 9.79841199133641 P P P 9.90107421821029 10.2869700470352
10.4644955495269 P P P LNCV6_129072_PI430048170 mRNA
CACCTAGATATAAATGCTAATGATACTTGGGTTTATAGCCTTCTGATCCTTTATTTCTGCNM_001264573 RefSeq chr17
- 44924710 44947711 KIF18B 146909 "kinesin family member 18B, transcript variant 2"
GO:0008017|GO:0000235|GO:0005515|GO:0005871|GO:0005886|GO:0005730|GO:0035371|GO:0005634|GO:0005
524|GO:0000070|GO:0003774|GO:0005737|GO:0008574|GO:0008152|GO:0005654|GO:0019894|GO:0000278|GO:0
016887|GO:0051302|GO:0007019|GO:0051301|GO:0007018 . NA - . NA NA NA NA NA NA NA NA

NA
LNCV6_77518_PI430048170 0.5962732563109050.8970126489504440.44071748637465 0.353770541990487
0.395683079877972 A A A 0.3002057434784370.3416064801042450.930430286771753 A A A
LNCV6_77518_PI430048170 mRNA
TGAGGTCAAGGTGAACTTAACTAGAGATGTGGATGAAACCTAATTACAGACAACGTTTTA NM_001031743 RefSeq
chr6 + 87407971 87464473 C6orf165 154313 chromosome 6 open reading frame 165 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_128663_PI430048170 0.2338793375071830.9428347323169090.350273300802839
0.3861095655312330.312094836204047 A A A 0.5142350616749390.443763465318211
0.340955517165856 A A A LNCV6_128663_PI430048170 mRNA
TTTCATTGTATTTTAAGCTTACCTGTGAATAGCCCAATAAACATGACACACTGTGTTGGC NM_001301109 RefSeq
chr15 + 83447227 83618741 SH3GL3 6457 "SH3-domain GRB2-like 3, transcript variant EEN-B2-L3"
GO:0005515|GO:0007165|GO:0031901|GO:0007417|GO:0070062|GO:0042802|GO:0008289|GO:0006897 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127537_PI430048170 0.000453910221075723 0.1181519220114690.605500971277455
0.5232014463435620.65291948702325 A A A 3.80630360445617 3.44783725411147
3.74922674599041 P P P LNCV6_127537_PI430048170 mRNA
TTACTGAAAGTTTGTGTAGGTGAAAAGCAGTTAAATCATCAGTTGCTCTAAAGAGGTCTT NM_181836RefSeq chr5
- 115613207 115626179 TMED7 51014 transmembrane emp24 protein transport domain containing 7
GO:0030126|GO:0005793|GO:0030127|GO:0005794|GO:0005783|GO:0033116|GO:0005789|GO:0016021|GO:0015
031|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79894_PI430048170 0.1729951643740330.5296521761202641.30100215844792 0.288019077916532
2.06886946131103 A A A 2.2441931913533 1.77576626664259 2.7477717090613 A A P
LNCV6_79894_PI430048170 mRNA
CCTTAGAAATGGAGTCCCCAACTACTCATTCAAAAGAAATCAGACATAAAATAAACAGAC NM_173519RefSeq chr8
+ 61287965 61501645 CLVS1 157807 clavesin 1
GO:0005802|GO:0005215|GO:0031901|GO:0030136|GO:0080025|GO:0006810|GO:0007040|GO:0005768 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137896_PI430048170 0.0103591671167578 3.13768723556856 5.7992191411649
6.00769209001491 6.23764733265553 P P P 3.86023812415629 4.40159030773747 4.7357914841164
P P P LNCV6_137896_PI430048170 mRNA
CCTTAGTCAACACCAGAGAATTCACATGAGGGAAAACCTATTAATGTAAGGAACTTAAAT NM_003447RefSeq chr6
+ 28080703 28089562 ZNF165 7718 zinc finger protein 165
GO:0005515|GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_90886_PI430048170 0.0998838743165791.28585707832382 6.63426464619055 7.0072819289287
6.80632109259196 P P P 6.592701278069 6.18758707559816 6.56891175178074 P P P
LNCV6_90886_PI430048170 mRNA
AGGATAGACTACAGTGCCGCTGTTATCTATGACTTTCTGGCTGTGGATGATATAAACGGG NM_032039RefSeq chr16
+ 234545 266125 ITFG3 83986 "integrin alpha FG-GAP repeat containing 3, transcript variant 1"
GO:0008150|GO:0003674|GO:0009986|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_98023_PI430048170 0.85119017025124 1.00635461389648 0.5010441811987110.532018829745823
0.433833664876739 A A A 0.5547347099814840.4390227096611550.444482787264208 A A A
LNCV6_98023_PI430048170 mRNA
GAATATGCTTCTTCAAACCTTTGAGGCTATAAAGAAACAAATGATAGAGGAGGAAGACAA NM_198515RefSeq chr10
+ 116324427 116380029 CCDC172 374355 coiled-coil domain containing 172 NA . NA - . NA
NA NA NA NA NA NA NA NA NA
LNCV6_140835_PI430048170 0.18615605796909 0.93945538455539 0.246213434436719

0.3217638106586140.285215568907238A A A 0.4608379540955550.356248082500897
0.302908312586287A A A LNCV6_140835_PI430048170 mRNA
GGAAATGGCTACTACTGCCCATCTTGCTATGGAAGATATTGGTCATATGGTTTCTACTGA NM_181615RefSeq chr21
+ 30616454 30616625 KRTAP20-1 NA keratin associated protein 20-1 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_125570_PI430048170 0.2453896941960781.37482793090898 0.481592927880658
1.21427880897412 1.3169448937101 A A A 0.3305817659560960.833206933547785
0.56193543083795 A A A LNCV6_125570_PI430048170 mRNA
CTTCACACTTGCGGGCTGCATCAGCACACGCTCCTATCAACCCAAGTACTGTGGAGTTTG NM_003882RefSeq chr8
+ 133191038 133231689 WISP1 8840 "WNT1 inducible signaling pathway protein 1, transcript variant 1"
GO:0007165|GO:0005737|GO:0005178|GO:0060548|GO:0007267|GO:0005578|GO:0016055|GO:0007155|GO:0008
201|GO:0005615|GO:0001558|GO:0005520 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128859_PI430048170 0.5089421650161950.9145483386290540.387178331773601
0.3876230039272790.404524601135394A A A 0.3778728118479 0.350703188888357
0.793460477296653A A A LNCV6_128859_PI430048170 mRNA
TTGAGAACAAGATAAAGTGTAGCTAACTGAGACCTCAGAGTATGTAGGAGTAAATAGTAT NM_001302809 RefSeq
chr17 + 74584678 74594209 C17orf77 146723 "chromosome 17 open reading frame 77, transcript
variant 1" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143377_PI430048170 0.9261120028963320.9468376424619690.287443708866934
0.9996229264228870.510555882698046A A A 1.26542289311746 0.339206856901343
0.306021323183234A A A LNCV6_143377_PI430048170 mRNA
GTGTTGGTGGTATTTTATTGTTGTTTTTCTGTGTTTATGTGTCTCAGCTTTCTCCAAGGA NM_001282400 RefSeq chrX
- 101882287 101932066 ZMAT1 84460 "zinc finger, matrin-type 1, transcript variant 2"
GO:0008270|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105500_PI430048170 0.0187776621649693 0.5339513228767536.30782029485181
5.93630201693726 6.49482199120101 P P P 7.08444859909857 7.11603095344166
7.29937655196362 P P P LNCV6_105500_PI430048170 mRNA
ATCTTCGGGCAAAAACCATTGTCAAGTTCTCAGATGAATACCTGACAAAGCAGTGGAAGT NM_003925RefSeq chr3
- 129430943 129440179 MBD4 8930 "methyl-CpG binding domain protein 4, transcript variant 1"
GO:0009314|GO:0005515|GO:0007095|GO:0008630|GO:0004520|GO:0005634|GO:0005737|GO:0006281|GO:0003
696|GO:0006284|GO:0045008|GO:0006285|GO:0005654|GO:0008263|GO:0000737|GO:0000785 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134155_PI430048170 0.5870811406892570.7601117288025040.312635843107444
0.9716742604154170.355801787092359A A A 0.3121084127519361.69133978253924
0.512429852642673A A A LNCV6_134155_PI430048170 mRNA
CCTGAGCCAAAGAGCTGGGGTTGATGGGGTTTCCTAAATAAAGCAAGTAATTTTCTCAGA NM_015063RefSeq chr19
- 47428021 47472050 SLC8A2 6543 "solute carrier family 8 (sodium/calcium exchanger), member 2"
GO:0005516|GO:0007154|GO:0005886|GO:0007596|GO:0035725|GO:0006816|GO:0016021|GO:0055085|GO:0005
432|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137653_PI430048170 0.3675611000480820.92399163067474 0.441913851275528
0.4608190861837890.430445325627056A A A 0.53636047656595 0.721881687521454
0.398959574207588A A A LNCV6_137653_PI430048170 mRNA
GTGCTGATCGATCCCACATCCTGAATAAAGAATAAAGATCTCTCAGAAAATTCCAAAAAA NM_007352RefSeq chr1
+ 21976924 21989354 CELA3B 23436 "chymotrypsin-like elastase family, member 3B"
GO:0004252|GO:0006508|GO:0008233|GO:0008203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127888_PI430048170 0.4702540224492550.8585750475630369.19271869601242
9.40880617255012 9.55146503663197 P P P 9.25075681729027 9.51267462990559
9.97665994191385 P P P LNCV6_127888_PI430048170 mRNA
TCTTGAAACTTTGTGAACTGACTTGCTGTATTTGCACTTTGAGCTCTTGAAATAAATGTG NM_006745RefSeq chr4

+ 165327665 165343162 MSMO1 6307 "methylsterol monooxygenase 1, transcript variant 1"
GO:0006695|GO:0005886|GO:0005506|GO:0005783|GO:0006631|GO:0005789|GO:0006633|GO:0044281|GO:0016
021|GO:0008202|GO:0000254|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96959_PI430048170 0.9320738770863770.9643285984742790.3174499514956790.282471100127726
0.998133869808306 A A A 1.1312818390079 0.3018627566543670.264862944542231 A A A
LNCV6_96959_PI430048170 mRNA
AGCCAGCTCATTCTGGATGAATGAATGATTACACTAAGTGTCCTCCACATTCCTCTGTGG NM_012454 RefSeq chr6
+ 155090288 155257723 TIAM2 26230 "T-cell lymphoma invasion and metastasis 2, transcript variant 1"
GO:0051056|GO:0048011|GO:0043065|GO:0007264|GO:0044281|GO:0030175|GO:0097190|GO:0030027|GO:0005
829|GO:0030426|GO:0005085|GO:0016020|GO:0032321|GO:0005057|GO:0005089|GO:0044255|GO:0070062|GO:0
005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141311_PI430048170 0.0110898415677141 0.6752782619836037.1696115485745
6.85827325636684 7.11453031151962 P P P 7.49015011220832 7.59752049748658
7.75996428185286 P P P LNCV6_141311_PI430048170 mRNA
CAAGGTAACGGTGAAAGCTCCTCAAAACAATAGGGATGTTTTTAATAAACTCTATTTTCG NM_020706 RefSeq chr21
- 31670999 31732118 SCAF4 57466 "SR-related CTD-associated factor 4, transcript variant 1"
GO:0000166|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138409_PI430048170 0.0271505808478424 1.8736980714514 6.14520279565869
5.97340735378079 5.92886878397763 P P P 5.37823860669015 5.14789060613283
4.74277946641715 P P P LNCV6_138409_PI430048170 mRNA
TGGCTTCTGCATGTACAGTATTTGGGCAGCAAAACATGATTAAAGTCAGTTTGAAAATGG NM_014747 RefSeq chr1
- 40620679 40665652 RIMS3 9783 regulating synaptic membrane exocytosis 3
GO:0048786|GO:0030054|GO:0017156|GO:2000300|GO:0042391|GO:0006836|GO:0044325 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_60717_PI430048170 0.0110631662315297 1.27812835749516 9.61240263241898
9.66652064959075 9.49198647266405 P P P 9.26184125494095 9.25732156049103
9.19415215806725 P P P LNCV6_60717_PI430048170 mRNA
ATCTTCAAACTCTAAGTCAAGGGTTAGAGACATTTGCGAAGGCCCAAACTGGGCCTTTGA NM_001199823 RefSeq
chr14 - 24213936 24232370 NEDD8-MDP1 NA NEDD8-MDP1 readthrough NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_88894_PI430048170 0.7246827468825130.9160600722836041.25488837681035 2.48068046190966
2.64234999962305 A A A 2.83803262568191 2.11051213819871 2.01610772166906 P A A
LNCV6_88894_PI430048170 mRNA
CCCTACCCTTTGAGAAGAACTGTGGAGCCGACCATATCTGCCAGGACAATCTCGGCATCT NM_000887 RefSeq chr16
+ 31355133 31382997 ITGAX 3687 "integrin, alpha X (complement component 3 receptor 4 subunit),
transcript variant 2"
GO:0005515|GO:0008305|GO:0005886|GO:0009986|GO:0050900|GO:0046872|GO:0016020|GO:0007229|GO:0007
596|GO:0030198|GO:0009887|GO:0004872|GO:0034113|GO:0007155 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134570_PI430048170 0.1170769324492251.09427728469312 0.688334208008099
0.8185131565322080.657762244236417 A A A 0.58303922893044 0.61061959523612
0.585955053998738 A A A LNCV6_134570_PI430048170 mRNA
TGTGAATTCAGTGGGTCACTAGTGTCACCAATTCATTCATCACCCATCATTCACTCATTT NM_138573 RefSeq chr15
- 75941985 76012444 NRG4 145957 neuregulin 4
GO:0048011|GO:0005886|GO:0048015|GO:0005102|GO:0005576|GO:0048513|GO:0005615|GO:0035556|GO:0007
173|GO:0008543|GO:0045087|GO:0016021|GO:0008083|GO:0038095 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130563_PI430048170 0.34994399000384 0.65368557255462 0.407438866087238
1.91162658723639 2.80492058863509 A A A 1.99241580944357 2.99290420566548

2.70824238926042 A P P LNCV6_130563_PI430048170 mRNA
CGATTAATGATGACATGTACAACCATATTTAAAGAGCAATAGTGTCCGTGTGTCATGAAA NM_001039753 RefSeq
chr2 + 54725011 54972020 EML6 400954 echinoderm microtubule associated protein like 6
GO:0005737|GO:0005874 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133076_PI430048170 0.84262049756594 0.9583810557430471.14558692392063
0.4527813162062260.370884053224144A A A 1.12701502232354 0.354519168832155
0.698864767522476A A A LNCV6_133076_PI430048170 mRNA
TGACAGGACCCACTCTTTCATTGAAAGGTGATGAAAATCAAATAAAGAATCTCTTCACAT NM_018659RefSeq chr4
- 5014585 5019470 CYTL1 54360 cytokine-like 1
GO:0007165|GO:0051091|GO:0050650|GO:0048839|GO:0002062|GO:0045944|GO:0005102|GO:0005615 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121372_PI430048170 0.2254567860012781.51478940455429 3.83419847654706
3.15349652846918 3.47114637313071 P P P 3.53734869157031 2.15714155778024
2.70932284231738 P A P LNCV6_121372_PI430048170 mRNA
GGCACTGGTCATGGAAAACGAATTGTTCTGCTCGGGCGTCCTGGTGCATCCGCAGTGGGT NM_001302961 RefSeq
chr19 - 50906351 50910738 KLK4 9622 "kallikrein-related peptidase 4, transcript variant 2"
GO:0030163|GO:0022617|GO:0004252|GO:0097186|GO:0006508|GO:0008236|GO:0005576|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141232_PI430048170 0.5396187114997641.23348434408367 4.21486306486011
3.24741207552331 3.27768988186264 P P P 3.56613158887555 3.4389463083046
2.98668649251078 P P P LNCV6_141232_PI430048170 mRNA
CGCCCCTCGCAGAGAGTGTATCATCTGTTTTATTTTTGTAAAAACAAAGTGCTAAATAAT NM_005806RefSeq chr21
+ 33025907 33029195 OLIG2 10215 oligodendrocyte lineage transcription factor 2
GO:0021522|GO:0006366|GO:0021530|GO:0003705|GO:0042552|GO:0005634|GO:0000122|GO:0048663|GO:0003
677|GO:0042803|GO:0021794|GO:0005737|GO:0045665|GO:0048714|GO:0071837 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128270_PI430048170 0.0110365705270166 0.4770633209975161 0.636063564081
10.5815834919304 10.6850089131159 P P P 11.548025140401 11.5790999100416
11.9457958710045 P P P LNCV6_128270_PI430048170 mRNA
CCCTGCACTTTGTTACATCTGGGATACAGTCTAACTCATCTGATTTAATATGCATTTAAA NM_053024RefSeq chr3
- 149964904 149970954 PFN2 5217 "profilin 2, transcript variant 1"
GO:0005515|GO:0030036|GO:2000300|GO:0005546|GO:0032781|GO:0003785|GO:1900028|GO:0005737|GO:0033
138|GO:0030838|GO:0043195|GO:0032233|GO:0051496|GO:0030837|GO:0005856|GO:0070062|GO:0000774|GO:0
010633 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101872_PI430048170 0.0731884092676175 1.19068832002129 6.34254381215698
6.09354214799545 6.19630405760033 P P P 5.9736292976158 5.94512978435681
5.96898190557635 P P P LNCV6_101872_PI430048170 mRNA
ACAACAGACACGCGAGGTCAGGAAGAAGCCGCTTATAAATTACCGCTTCCTTCGCGCCGC NM_003043RefSeq chr3
+ 14402575 14489349 SLC6A6 6533 "solute carrier family 6 (neurotransmitter transporter), member 6,
transcript variant 1"
GO:0006520|GO:0005886|GO:0005328|GO:0006865|GO:0055085|GO:0030977|GO:0005887|GO:0015734|GO:0006
810|GO:0006836|GO:0016021|GO:0005369|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126818_PI430048170 0.3911327123929041.21085778067665 5.39880581554264 5.0624380009047
5.20187350636498 P P P 4.60272202217502 5.50300397594939 4.53538187028644 P P P
LNCV6_126818_PI430048170 mRNA
TGCATTTCCAAATCAAAGGACAAGCGGACAAAATGCATCCCAAGATCAAGGAAGGGACAG NM_001164761
RefSeq chr7 - 549196 713207 PRKAR1B 5575 "protein kinase, cAMP-dependent, regulatory, type I,
beta, transcript variant 1"
GO:0034236|GO:0005886|GO:0008603|GO:0007202|GO:0044281|GO:0005829|GO:0030552|GO:0007173|GO:0071

377|GO:0007611|GO:0006833|GO:0034199|GO:2000480|GO:0005952|GO:0048011|GO:0055085|GO:0003091|GO:0
007165|GO:0006112|GO:0050796|GO:0007596|GO:0008543|GO:0045087|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129937_PI430048170 0.0235144215182785 0.59404032573001 6.25220517874202
5.76821639901655 6.23564154724744 P P P 6.93498837864213 6.68476297133859
6.92695437377863 P P P LNCV6_129937_PI430048170 mRNA
ATTCTATGTCTGTAAAAACCAACAAAGGCATTGGACTTGTGTGAATGTACAGGGTTTTTT NM_001008539 RefSeq
chr8 + 17497087 17570568 SLC7A2 6542 "solute carrier family 7 (cationic amino acid transporter, y+
system), member 2, transcript variant 2"
GO:0006520|GO:0005292|GO:0005886|GO:0043030|GO:0050727|GO:0006865|GO:0055085|GO:0002537|GO:0005
289|GO:0006809|GO:0016020|GO:0042116|GO:0005887|GO:0006810|GO:0015174|GO:0006811 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138139_PI430048170 0.0439083864764772 0.75163353468155 10.1537816117907
10.4224334545259 10.4983394705934 P P P 10.6848308616283 10.6662948780801
10.9619690868699 P P P LNCV6_138139_PI430048170 mRNA
CTTCTTTTCATGGCTTTTATTCACTGTGACTAATAAGCTTCCTAATAAATCCTTGCCAGA NM_020362 RefSeq chr1 +
23778385 23788232 PITHD1 57095 PITH (C-terminal proteasome-interacting domain of thioredoxin-like)
domain containing 1 GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138516_PI430048170 0.0535525942214873 1.91208820478527 3.80582502616662
4.5585810208188 4.47408727949146 P P P 3.27443402878581 3.51024727078592
3.34923419475472 P P P LNCV6_138516_PI430048170 mRNA
TACCGTTCTTCTTGGGTCAGTTCTTACCATTTCCTGAACAATAGAATTGTGAAAGTGTTA NM_013280 RefSeq chr11
+ 64103889 64119173 FLRT1 23769 fibronectin leucine rich transmembrane protein 1
GO:0035556|GO:0008150|GO:0005887|GO:0005578|GO:0005057|GO:0030674|GO:0007155|GO:0005615 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132483_PI430048170 0.914282775567966 0.994421302110319 4.41341513344112
4.17419346626735 4.18464555104799 P P P 4.34865994176096 4.17892480314034
4.27675421359169 P P P LNCV6_132483_PI430048170 mRNA
AAGTATCAATATTAAAAATATTTTTGCTGGACATGGTGTCTCAGGCCTGTAATCCCAGCT NM_001170747 RefSeq
chrX + 72181675 72263964 PIN4 5303 "protein (peptidylprolyl cis/trans isomerase) NIMA-
interacting, 4 (parvulin), transcript variant 2"
GO:0000413|GO:0006364|GO:0003755|GO:0005730|GO:0005819|GO:0005634|GO:0003677|GO:0005737|GO:0003
690|GO:0005759|GO:0003681|GO:0030684|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135869_PI430048170 0.444074457111839 0.933944229805782 10.1674865154115
9.79618552083117 10.0488796676923 P P P 10.1094228993118 10.0374245507604
10.1823687563076 P P P LNCV6_135869_PI430048170 mRNA
GGCAAACCAAGAAGATGATGGACAAGGTGGAGTTTGTCCATATGCTCAATGCTACCATGT NM_006513 RefSeq chr1
+ 109213892 109238182 SARS 6301 "seryl-tRNA synthetase, transcript variant 1"
GO:0010467|GO:0003723|GO:0004828|GO:0005524|GO:0006412|GO:0097056|GO:0008033|GO:0005829|GO:0006
418|GO:0005739|GO:0005737|GO:0006434|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129490_PI430048170 0.212095170588337 0.900868481663624 8.47754370103015
8.42809045355811 8.53695766923517 P P P 8.5045065850158 8.5924491883877 8.7851049806641
P P P LNCV6_129490_PI430048170 mRNA
CTGGAAACTTTCTGCCTCAATGTTTACTGTGCCTTTGTTTTTGCTAGTTTGTGTTGTTGA NM_017940 RefSeq chr1 -
16562426 16613605 NBPF1 55672 "neuroblastoma breakpoint family, member 1" GO:0005737 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134293_PI430048170 0.0359544244773290 3.05970545544419 0.341082532853187
0.314443246405857 1.24092934100171 A A A 1.47954480129507 2.60062495122856
2.82267026381212 A P P LNCV6_134293_PI430048170 mRNA

TCTTGCCATCAGCGACCACTTTCCAGTGGAGGTGACCCTCAAGTTCCACCGATGACTCGA NM_001374RefSeq chr16 + 2236466 2238711 DNASE1L2 1775 "deoxyribonuclease I-like 2, transcript variant 1" GO:0003335|GO:0005737|GO:0004536|GO:0005509|GO:0004520|GO:0005634|GO:0005576|GO:0006259|GO:0016888|GO:0003677|GO:0001942|GO:0000737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101113_PI430048170 0.284475365508787 1.63767431336274 0.721284279393503 0.778737327470063 1.97124610969604 A A A 0.634515981906995 0.528432376730764 0.539842372832126 A A A LNCV6_101113_PI430048170 mRNA AGCTTGTCAACAAGTTTACTCTCCGTCTTGTGTCATGTGTTCAGCTGGCCAGCAAACTTT NM_173478 RefSeq chr17 + 42798835 42811587 CNTD1 124817 cyclin N-terminal domain containing 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134884_PI430048170 0.0289494052633444 2.33057988708425 3.0325101953662 3.05032546370412 2.68068611059297 P P A 1.32543083854378 2.20032365475681 1.44068852119528 A A A LNCV6_134884_PI430048170 mRNA GGAACGTGCAGGCCCTTCCATTGATGATATTCCCTTCTCAACATTTTTAAACAAGCACAA NM_172362 RefSeq chr1 - 210678314 211134115 KCNH1 3756 "potassium channel, voltage gated eag related subfamily H, member 1, transcript variant 1" GO:0023014|GO:0005251|GO:0005515|GO:0005516|GO:0005886|GO:0005637|GO:0007268|GO:0007520|GO:0000155|GO:0000160|GO:0005737|GO:0008076|GO:0042391|GO:0034765|GO:0005654|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141987_PI430048170 0.0801710168782445 1.0436312100118 0.39757298834716 0.40764225824863 0.437682371930985 A A A 0.325234787464618 0.338056403357306 0.394138191072818 A A A LNCV6_141987_PI430048170 mRNA ATTTCCTTGACCTCTTTACCCTGAAGCTTTTGTCAAATAAACTGCTACATCAACCTGAAA NM_147198 RefSeq chr20 - 45607938 45631268 WFDC9 259240 WAP four-disulfide core domain 9 GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139738_PI430048170 0.0734423543090806 0.747385381644725 6.15970489599464 5.84701553187015 6.31311065326793 P P P 6.438003573758 6.61383021903445 6.56097180977697 P P P LNCV6_139738_PI430048170 mRNA TACAATACATTTATGTTGAATGGAACTCCAAGATCTCACCTCTCCATCCAGGAATGGAGT NM_032303 RefSeq chr9 + 112379908 112472405 HSDL2 84263 "hydroxysteroid dehydrogenase like 2, transcript variant 1" GO:0005739|GO:0008150|GO:0003674|GO:0016020|GO:0016491|GO:0055114|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100449_PI430048170 0.21310351222763 0.842016312364237 10.1275849621135 9.70289774749184 10.1102287657675 P P P 10.0795354061565 10.2193280714515 10.4060813202917 P P P LNCV6_100449_PI430048170 mRNA TCGTAAATGCAAAAATTGCTTGCCTTGACTTCAGCCTGCAAAAAACAAAAATGAAGCTTG NM_030752 RefSeq chr6 - 159778497 159789703 TCP1 6950 "t-complex 1, transcript variant 1" GO:0005515|GO:0005813|GO:0005794|GO:0001669|GO:0005832|GO:0005874|GO:0007339|GO:0005524|GO:0044297|GO:0005829|GO:0005720|GO:0006457|GO:0007021|GO:2000109|GO:0051084|GO:0002199|GO:0051082|GO:0044267|GO:0044053|GO:0000242|GO:0031625|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134190_PI430048170 0.385280293720243 0.59681880209759 0.428260868314811 0.525186895196223 0.435147437697022 A A A 2.01949530904026 0.397338048976025 0.641442293118497 A A A LNCV6_134190_PI430048170 mRNA CTGCAAAGGGTGTTTCCCTGTCCTCAGTGGTTTTGCTGCAATCAAACACTGTTTATTACC NM_001042506 RefSeq chrX + 73003512 73005712 PABPC1L2B 645974 "poly(A) binding protein, cytoplasmic 1-like 2B" GO:0000166|GO:0003723|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139623_PI430048170 0.0213343048507083 5.10965115067638 3.6764804939943
3.96558452489567 3.26810517321179 P P P 0.846343940569983 0.518750645914175
2.07538778393148 A A A LNCV6_139623_PI430048170 mRNA
TTTGGCCATTAGCATTTCATGTCTTTCCCCAAATGAAGATGCCCTGCAAAGGGCAGTAAC NM_012396 RefSeq
chr1 - 201465493 201469171 PHLDA3 23612 "pleckstrin homology-like domain, family A, member 3,
transcript variant 1"
GO:0051898|GO:0043065|GO:0005886|GO:0043325|GO:0005547|GO:0080025|GO:0005546|GO:0032266|GO:0009
653|GO:0042771|GO:0005737|GO:0010314|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_2380_PI430048170 0.103348559014131 2.03755119852173 1.62329074545847
2.14821610242527 1.76816928890439 A A A 0.270969985819521 0.267669544530729
1.56012055579808 A A A LNCV6_2380_PI430048170 mRNA
TAAGAAATTGGTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGAC NM_001288987 RefSeq
chr9 - 133205278 133209250 OBP2B 29989 "odorant binding protein 2B, transcript variant 1"
GO:0007608|GO:0007635|GO:0006810|GO:0005576|GO:0005549|GO:0005575 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_143074_PI430048170 0.010676082186063 0.708644526059623 11.6170608943224
11.3455538333284 11.4055075874299 P P P 11.8229775854584 12.0660743866081
11.973612291899 P P P LNCV6_143074_PI430048170 mRNA
CCACTGCCTTCTACCTTGTTTGAAACCTGAATCCTAATAAAGAATTAATAACTCCCAAAA NM_003334 RefSeq
chrX + 47193801 47215128 UBA1 7317 "ubiquitin-like modifier activating enzyme 1, transcript
variant 1"
GO:0030057|GO:0000792|GO:0005515|GO:0004842|GO:0016567|GO:0004839|GO:0005634|GO:0005765|GO:0005
524|GO:0006974|GO:0005829|GO:0005739|GO:0005737|GO:0030867|GO:0019941|GO:0010008|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134334_PI430048170 0.172950966185194 1.01112231736086 0.327415219018473
0.311182900837301 0.302702305025868 A A A 0.305396966100529 0.302680968692303
0.285377655845272 A A A LNCV6_134334_PI430048170 mRNA
CTGAAACTGCATTCTTAGAACTCGACTCTTGTTTTATTTAAATACGTGCGTAGATATCTG NM_003638 RefSeq
chr10 - 15513948 15720335 ITGA8 8516 "integrin, alpha 8, transcript variant 1"
GO:0001656|GO:0005886|GO:0005783|GO:0046872|GO:0045184|GO:0016337|GO:0030198|GO:0048745|GO:0034
446|GO:0043204|GO:0007613|GO:0048333|GO:0030511|GO:0008305|GO:0042472|GO:0009986|GO:2000721|GO:0
001822|GO:0014069|GO:0045177|GO:0034678|GO:0007160|GO:0032591|GO . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144380_PI430048170 0.00454784277687295 0.3832783156044296.23374911408948
6.52447017596021 6.65912494797619 P P P 7.78731959718152 7.91733378613232
7.89217505076831 P P P LNCV6_144380_PI430048170 mRNA
AAGGGTTTGCACTGGTCTTGAGTGTTGTGCTTTTCTGTGTTGTGTGTTTTGATTTTTGTC NM_001142651 RefSeq chr5
+ 172641265 172691530 NEURL1B 54492 neuralized E3 ubiquitin protein ligase 1B
GO:0005737|GO:0016567|GO:0007219|GO:0016874|GO:0008270 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128677_PI430048170 0.139915862416088 1.07689632444524 0.658705970999361
0.767471183660238 0.617352716120056 A A A 0.584673131197431 0.578940000854075
0.563390993346356 A A A LNCV6_128677_PI430048170 mRNA
TTTGCTTCATCCGGGGATGCAGGATGCAGAATAAACCAAACTAGTTACTCAACTTGGAAA NM_144634 RefSeq chr3
- 42397077 42410602 LYZL4 131375 "lysozyme-like 4, transcript variant 1"
GO:0008152|GO:0003796|GO:0005634|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92694_PI430048170 0.196931309595711 0.53368596667754 0.337556549474402 0.365070239602009
0.339857526252481 A A A 0.360927945976229 1.78351574392741 1.27834790378372 A A A

LNCV6_92694_PI430048170 mRNA
ATTCAGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGANM_019055RefSeq chr11
- 124884217 124897935 ROBO4 54538 "roundabout, axon guidance receptor, homolog 4 (Drosophila),
transcript variant 1"
GO:0030334|GO:0030336|GO:0004872|GO:0016021|GO:0001525|GO:0030154|GO:0009897|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99982_PI430048170 0.7204750894668491.06122811029473 3.34103893475929 2.79630134957753
3.05926490443316 P A P 2.76268522806934 3.32779551435209 2.83222335192254 P P P
LNCV6_99982_PI430048170 mRNA
GGCTGAGCAAGAGGCTTCCCTGCAGAAACTGAGAGAAGAGTTGGAGTCTCAACAGAAGGC NM_014956RefSeq
chr11 + 117327854 117413266 CEP164 22897 "centrosomal protein 164kDa, transcript variant 1"
GO:0005515|GO:0005813|GO:0006996|GO:0005814|GO:0005615|GO:0005829|GO:0042384|GO:0007067|GO:0006
281|GO:0000086|GO:0005654|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128896_PI430048170 0.00513196139739387 0.2986752161928911.74046457192008
1.82275781207889 1.66948286631813 A A A 3.21453669713225 3.44616130449208
3.75490264147644 P P P LNCV6_128896_PI430048170 mRNA
GAGGCTAAGTGATAGGAATCAAGGATAATCGTGGTTACTATGTATTTGAACTTCAGTTGT NM_001244189 RefSeq
chr14 + 58427384 58548831 KIAA0586 9786 "KIAA0586, transcript variant 1"
GO:0042384|GO:0005813|GO:0005737|GO:0070201|GO:0060271|GO:0036064|GO:0007224 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131834_PI430048170 0.5898655963753551.01724843730336 0.471481086375354
0.4426752291270050.3565256230406 A A A 0.3566491346080320.419067983725699
0.422466253412272A A A LNCV6_131834_PI430048170 mRNA
TGTTTATGGTGTGAGAACCAAGGAGATCAAGCAGGGAATCCAAAACCTGCTGAAGAGGTTNM_001005179 RefSeq
chr11 - 6002050 6003148 OR56A4NA "olfactory receptor, family 56, subfamily A, member 4" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141838_PI430048170 0.00126305214145354 1.24968828359032 12.0295370883947
12.0896668029442 11.991382482751 P P P 11.7283389824019 11.6757724220096
11.7426203161412 P P P LNCV6_141838_PI430048170 mRNA
CGTGGGTCCACCAGGCTTCTGGAAAAGTCCTCAATGCAATAAAAACAATTTCTTTCTTGC NM_016539RefSeq chr19
- 4174108 4182599 SIRT6 51548 "sirtuin 6, transcript variant 1"
GO:0005515|GO:0070932|GO:0016575|GO:0017136|GO:0005730|GO:0070403|GO:0005634|GO:0010569|GO:0043
231|GO:0003950|GO:0006471|GO:0003682|GO:0003956|GO:0005724|GO:0005654|GO:0008270|GO:0046969 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89876_PI430048170 0.3940407916932660.92734314107225 10.7675396280637 10.9286185486548
10.8864899423261 P P P 10.802116323944 10.9680091276126 11.1256838159324 P P P
LNCV6_89876_PI430048170 mRNA
AAATGTTTTAGTTCTTTCCCCACTCGTTGGGTTCAACTAGATTAAAAGGCTGATTTTCAG NM_001031711 RefSeq
chr5 + 172834219 172952685 ERGIC1 57222 endoplasmic reticulum-golgi intermediate compartment
(ERGIC) 1
GO:0006888|GO:0005515|GO:0005793|GO:0016020|GO:0000139|GO:0033116|GO:0005789|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56372_PI430048170 0.0576909817388076 0.7885674826534838.96250246309912 8.9489943074396
9.25381798486091 P P P 9.3039197226273 9.33246903088888 9.56369945903716 P P P
LNCV6_56372_PI430048170 mRNA
GCCTGTGGGTTATTTTGGTCTTGTAAGGATCCATTTCTTTAAAATACTGACATATAGAGT NM_018464RefSeq chr10
+ 58269101 58289259 CISD1 55847 CDGSH iron sulfur domain 1
GO:0005739|GO:0051537|GO:0005741|GO:0016021|GO:0043457|GO:0046872|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_129982_PI430048170 0.3273676093457411.42533882000072 0.287289873189206
1.45820296866288 0.789766804770935A A A 0.5272550407148480.429624354793506
0.273499796674916A A A LNCV6_129982_PI430048170 mRNA
AAAGCAAAAGAACACTGCAATAACTTTCAGCCACCTTTTTGGCCGACCCAGTGGGTGTTT NM_198493RefSeq chr1
- 173608335 173669862 ANKRD45 339416 ankyrin repeat domain 45
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128785_PI430048170 0.3823535296223830.9184973939882460.38173447876825
0.3122362313327530.286854185694472A A A 0.25354804258562 0.462683021794678
0.611947433473159A A A LNCV6_128785_PI430048170 mRNA
CCAGAGAGGCATTGGTGCGAGGGATTGAATAAAGAAACAAATGAATGGCTGCCCAAAAAA NM_144585RefSeq
chr11 + 64590809 64602353 SLC22A12 116085 "solute carrier family 22 (organic anion/urate
transporter), member 12, transcript variant 1"
GO:0019725|GO:0005886|GO:0042493|GO:0031526|GO:0030165|GO:0046415|GO:0055085|GO:0015143|GO:0016
324|GO:0015747|GO:0015849|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136911_PI430048170 0.00325228899920783 0.3357562272493212.26079268066297
2.74241976729525 2.406139253032 A A A 3.95563518508694 4.15878927973616
4.05437762904392 P P P LNCV6_136911_PI430048170 mRNA
CCAGAGCCCAGAGATTATAAACAGTAGGTGAAATAGATTTATGACTTACGAAATATGTTG NM_016010RefSeq chr8
+ 78666046 78719762 ZC2HC1A 51101 "zinc finger, C2HC-type containing 1A" GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135566_PI430048170 0.1114576260764721.3947862428565 6.14849088618507
6.57285253976162 6.12207758100546 P P P 6.03030366740074 5.92206342216383 5.4281414416014
P P P LNCV6_135566_PI430048170 mRNA
TTGTATAAATAAAATCTTGTTGGGTCTGTGTTCCAGCTGCAGTCTGCCCTGCCTGGAGAT NM_001039548 RefSeq
chr11 - 75422393 75430629 KLHL35 283212 kelch-like family member 35 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_139843_PI430048170 0.6033087815879990.9203324902056698.06554161608622
8.67148398286033 8.95834714694992 P P P 8.84258757756915 8.61624624428419
8.72489852051081 P P P LNCV6_139843_PI430048170 mRNA
TTTTGAAATAACAGCATAAGGAACTTCACTGTCTCTGCTCAATAAAATACCTGTAACTGG NM_005783RefSeq chr2
- 99319023 99336397 TXNDC9 10190 thioredoxin domain containing 9
GO:0005515|GO:0008150|GO:0005813|GO:0005737|GO:0030496|GO:0045454|GO:0005634|GO:0005575 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96065_PI430048170 0.0260019547118475 1.51521818521066 6.24904681296823
6.06761799576665 6.15414016997377 P P P 5.36209566530211 5.49724446021561
5.78567316863229 P P P LNCV6_96065_PI430048170 mRNA
TAATTACTCCACCATCTGGTGTAACGATCATTTCATCCATGCTAAGGCCATGCGGAAGGT NM_014003RefSeq chr16
+ 72093715 72112912 DHX38 9785 DEAH (Asp-Glu-Ala-His) box polypeptide 38
GO:0005515|GO:0008380|GO:0006369|GO:0010467|GO:0006366|GO:0031124|GO:0005634|GO:0071013|GO:0005
524|GO:0004004|GO:0005737|GO:0006406|GO:0016020|GO:0000398|GO:0005654 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144659_PI430048170 0.0535101002642147 0.4456489571447490.370148560566628
0.3766513824197120.471106108652529A A A 1.92774503547564 0.999815082735225
1.64139851522634 A A A LNCV6_144659_PI430048170 mRNA
TTGGCAAATGAGGTACTGGGTGAAAGGAGAGAAGACTTCATCTCCATAGATTCACGAGAG NM_176884RefSeq
chr12_GL877876v1_alt - 290013 291040 TAS2R43 259289 "taste receptor, type 2, member 43"
GO:0060170|GO:0033038|GO:0007186|GO:0005886|GO:0031514|GO:0008527|GO:0016021|GO:0001580 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59157_PI430048170 0.0234073366869493 2.05500743692862 7.49807131742605

7.97762748335303 7.61634286980965 P P P 7.05187488352711 6.59100025144872
6.26720002278766 P P P LNCV6_59157_PI430048170 mRNA
AAATCCTAGGGGGTGTTGGACTCTTCTTTAGCTTTACAGAGATCCTTGGTGTTTGGCTAG NM_005981 RefSeq chr12
+ 57745000 57748243 TSPAN31 6302 tetraspanin 31 GO:0008284|GO:0016020|GO:0005887 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101968_PI430048170 0.2217254150479371.11323399429578 5.14267694120085
4.89729948771984 5.11062354870513 P P P 4.85103580322754 4.79551475536309
5.04032998257054 P P P LNCV6_101968_PI430048170 mRNA
GGAATCTTGTGAAGAGAAAAATCAACTCATCTTGACAGCCTCTGCTGATAGAACAGTTAT NM_018268 RefSeq chr5
- 77432243 77492507 WDR41 55255 WD repeat domain 41 GO:0005765 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_142967_PI430048170 0.1328505665657511.04894230280284 0.443150521551283
0.5042851228134970.495175801255909 A A A 0.352991423725265 0.432933937249938
0.448814281147429 A A A LNCV6_142967_PI430048170 mRNA
CACTATACCATGACTCCAAAATTGTCTCTATTGCTAATAGATACGTATAGTATACAGGGA NM_001144823 RefSeq
chr15 - 65660618 65792293 DENND4A 10260 "DENN/MADD domain containing 4A, transcript variant
1" GO:0017112|GO:0006355|GO:0032851|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138846_PI430048170 0.0106771339451318 0.5422206299261087.20633618366209
6.7318099390492 7.14619256293835 P P P 7.80657486154442 7.79881889180789
8.14499831512992 P P P LNCV6_138846_PI430048170 mRNA
GAGTGAGTTCAGCCTGTAAAAAGGATGTTAAGCTGTGGGTAAAATATGCAAACGAAAAGA NM_015113 RefSeq chr17
- 4004444 4142959 ZZEF1 23140 "zinc finger, ZZ-type with EF-hand domain 1"
GO:0005509|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126940_PI430048170 0.4312255138395370.7485226684469321.75468700705491
0.7546605002857532.0120416747606 A A A 1.4463070542141 2.54265732589327
1.84770920715114 A A A LNCV6_126940_PI430048170 mRNA
GAGATAAGAAACAACCTGTACCATCAATGAGCTCACAATAACAGGCCACTGCCACTACCA NM_022061 RefSeq chr11
- 6680384 6683401 MRPL1763875 mitochondrial ribosomal protein L17
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0019904|GO:0005743|GO:0005
762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99814_PI430048170 0.7245047620627390.9504692945382220.4150694185535180.416373086985138
0.431192894946842 A A A 0.3207327212941270.35004218891143 0.76724135002442 A A A
LNCV6_99814_PI430048170 mRNA
GGATGGCAGATCATTCAACCTTCTTTTTCTTGAGTTTTCTACTCTGCTGTCATCTTCCAC NM_001304428 RefSeq chr5
+ 58491434 58496358 GAPT 202309 "GRB2-binding adaptor protein, transmembrane, transcript variant
1" GO:0002322|GO:0001782|GO:0005886|GO:0002381|GO:0016021 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139488_PI430048170 0.0478874201941556 0.3097763834426331.61700235826116
0.3544769105520340.332681776351952 A A A 2.48530612522355 2.68560901174785
2.59965850882578 A P P LNCV6_139488_PI430048170 mRNA
ACCCAACACATATATACTCCACAAGGATTTTGCATGGACCCCAGTTTAAGAAGCAACAAT NM_017686 RefSeq chr1
- 117863484 117929679 GDAP2 54834 "ganglioside induced differentiation associated protein 2, transcript
variant 1" GO:0032526|GO:0005765 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106971_PI430048170 0.5065432392865391.16047246652461 1.3009706381814
0.6011694126552531.02775870518057 A A A 0.5972793609462650.448909406475901
1.20755212303432 A A A LNCV6_106971_PI430048170 mRNA
TAATTATGACTTCCAGGCCCGCAACAGCAGTGAGCTGTCGGTCAAGCAGCGGGACGTACT NM_133180 RefSeq
chr19_KI270938v1_alt + 1058334 1066126 EPS8L1 54869 "EPS8-like 1, transcript variant 1"

GO:0005515|GO:0035023|GO:0003779|GO:0032587|GO:0007266|GO:0032855|GO:0043234|GO:0005737|GO:0042608|GO:1900029|GO:0032321|GO:0005089|GO:0030676|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145589_PI430048170 0.00117569492687657 0.68878205038089 11.1894881378521 11.1436957002912 11.0349273186757 P P P 11.5680199878611 11.7033102570053 11.7103486324987 P P P LNCV6_145589_PI430048170 mRNA
GACCCACCATACCCTGTGTATGTATGCATGTTTTTGTAAAAAGGAAGAAAATGGAAAAAA NM_015401 RefSeq chr12 - 47782710 47819980 HDAC7 51564 "histone deacetylase 7, transcript variant 1"
GO:0005515|GO:0005634|GO:0046970|GO:0046872|GO:0071889|GO:0005737|GO:0007219|GO:0005080|GO:0070491|GO:0090050|GO:0033613|GO:0046969|GO:0032041|GO:0032703|GO:0070932|GO:0070933|GO:0019901|GO:0003714|GO:0000122|GO:0006351|GO:0000118|GO:0045668|GO:0003682|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136888_PI430048170 0.267436968362940.8449960529213586.57388410829498 6.54830673519297 6.62461984875071 P P P 6.73686119787766 6.59403439333405 7.09816335872624 P P P LNCV6_136888_PI430048170 mRNA
GATGCTCGCCTCTTTGCAATTTTAACACTCATTCGACAATAAAGTCAGTAAAAAACACAA NM_005105 RefSeq chr1 - 145921556 145927536 RBM8A 9939 RNA binding motif protein 8A
GO:0008380|GO:0005515|GO:0010467|GO:0006369|GO:0006366|GO:0003723|GO:0031124|GO:0005634|GO:0071013|GO:0003729|GO:0006417|GO:0005829|GO:0005737|GO:0006406|GO:0016607|GO:0000166|GO:0000184|GO:0000381|GO:0000398|GO:0005654|GO:0035145 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117898_PI430048170 0.150560571902633 0.7831674763098074.92733771987317 4.81837126976697 4.3878647679093 P P P 5.03549202319554 5.12344389626056 5.08555127744021 P P P LNCV6_117898_PI430048170 mRNA
GCGAAATGTCAGACACAAACGGACCCAGATTCCAGAAACAAGAAAAAGGAAAGACAAAGG NM_033410 RefSeq chr16 - 30553763 30558321 ZNF764 92595 "zinc finger protein 764, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138325_PI430048170 0.611924294444757 1.02050021143447 15.867669593657 15.926278155591 16.0013439021294 P P P 15.9413306735313 15.8301759832359 15.9363632671494 P P P LNCV6_138325_PI430048170 mRNA
CCGCAAAGGCAAATAAATCCTTGTTTTGTCTTCACCCATGTAATAAAGGTGTTTATTGTT NM_001012 RefSeq chr1 + 44775573 44778740 RPS8 6202 ribosomal protein S8
GO:0000462|GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0005634|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0000184|GO:0022627|GO:0030529|GO:0016032|GO:0044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130923_PI430048170 0.637784055029001 0.979021587105797 8.58502661907591 8.68805059134188 8.79343017548626 P P P 8.71468747569465 8.72489852051081 8.7261814811408 P P P LNCV6_130923_PI430048170 mRNA
TTGATGAAATGTATCTCCTTGTACCTGGAAGATGAAGCCCAAACACCCACACCTCTGTCT NM_130807 RefSeq chr19 - 2071035 2096270 MOB3A 126308 MOB kinase activator 3A GO:0005622|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131717_PI430048170 0.191363676916495 0.773558517197215 6.24652159303377 6.417747332115 6.61292450888475 P P P 6.40813009221394 6.97669362364718 6.95800370055825 P P P LNCV6_131717_PI430048170 mRNA
GTGTGATCTTTACTGATGCACTCATGACAAGTACCCAATGTATTTTAGCTATTTTAGTAG NM_001142483 RefSeq chr5 - 111729302 111756251 NREP 9315 "neuronal regeneration related protein, transcript variant 11" GO:0005515|GO:0031103|GO:0005737|GO:0045664|GO:0005634|GO:0017015 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139409_PI430048170 0.672644831551816 0.923660171058687 0.80156525802442

2.60955739743252 0.351902388746644 A A A 0.8529624433337452.13187638157067
1.88255684371996 A A A LNCV6_139409_PI430048170 mRNA
TAATGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACT NM_022367 RefSeq chr1
+ 156153530 156177751 SEMA4A 64218 "sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A, transcript variant 1"
GO:0005515|GO:0010594|GO:0045063|GO:0005886|GO:0007411|GO:0008360|GO:0016525|GO:0071526|GO:0004872|GO:0016021|GO:0001525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142958_PI430048170 0.0235182463762687 0.2110050543174832.90084697632098
1.73122655074314 1.81779623412106 A A A 4.4282851254835 4.57652465729355
4.48850665405322 P P P LNCV6_142958_PI430048170 mRNA
TCTGCCTATCCCTTCTTTTTACTCCAAAGAGGAGATGATAGAATAATACATTCAGTATAC NM_005665 RefSeq chr1
- 92508695 92792404 EVI5 7813 ecotropic viral integration site 5
GO:0005515|GO:0017137|GO:0005794|GO:0005815|GO:0008283|GO:0005819|GO:0032851|GO:0005634|GO:0007275|GO:0043231|GO:0005829|GO:0007049|GO:0033126|GO:0042147|GO:0005097|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144990_PI430048170 0.473524265996364 1.23056774285412 1.53188820197572
2.20660144689734 1.33207047722511 A A A 0.926072563871558 1.86948058222229
1.37443135500311 A A A LNCV6_144990_PI430048170 mRNA
TTCAGAAGAGGCTCTGTGGCTGCATTCAGAGACCAGATCTCTGCTCAGGCTGAGGAGGCT NM_000741 RefSeq chr11
- 46384791 46386608 CHRM4 1132 "cholinergic receptor, muscarinic 4"
GO:0040012|GO:0007165|GO:0030054|GO:0005886|GO:0008283|GO:0005887|GO:0045211|GO:0007197|GO:0007213|GO:0016907|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53272_PI430048170 0.900650701059682 1.09267839877015 3.32054090207419 1.61438994255003
2.59411344610302 P A A 1.55511230152672 2.99064898872414 2.71903153141202 A P P
LNCV6_53272_PI430048170 mRNA
GAGACCCTGGCTGCTGAGCAGAGAACACATGGATGCAGCACCAATAAAATTCTATCTTTT NM_001291366 RefSeq
chr1 - 975198 982117 PERM1 84808 "PPARGC1 and ESRR induced regulator, muscle 1, transcript variant 1" GO:0006355|GO:0005737|GO:0014850|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140842_PI430048170 0.0516304503742916 0.566245174614288 0.389595812211254
0.582282691989618 1.14757382773466 A A A 1.20651768071612 1.52171278367184
1.88400633056136 A A A LNCV6_140842_PI430048170 mRNA
TTCTCCTGCAAATAGCGCCCTCTAAAAAGAAGAGTCAGACAATAAACTGGTTGAAATATC NM_024817 RefSeq chr15
+ 71141448 71783383 THSD4 79875 "thrombospondin, type I, domain containing 4, transcript variant 1"
GO:0006508|GO:0001527|GO:0004222|GO:0070062|GO:0048251 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129337_PI430048170 0.176552340305521 0.856897967171672 6.93706683656845
7.07051205193707 7.32746072781938 P P P 7.35505107276544 7.21814019350233 7.4486188031326
P P P LNCV6_129337_PI430048170 mRNA
GGACCATGTGTTGCAAGACTAATTGGCTATAATTATATCCTATCAAAGAAATCGATACGT NM_015948 RefSeq chr6
- 8413066 8435567 SLC35B3 51000 "solute carrier family 35 (adenosine 3'-phospho 5'-phosphosulfate transporter), member B3, transcript variant 1"
GO:0005794|GO:0006805|GO:0050427|GO:0005975|GO:0050428|GO:0044281|GO:0055085|GO:0043231|GO:0005739|GO:0000139|GO:0009405|GO:0016021|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130241_PI430048170 0.522011214088439 0.685601339320859 5.88005786210821
6.54767656916822 5.99147007062914 P P P 7.5206706650911 6.00983481166136
6.06784039156829 P P P LNCV6_130241_PI430048170 mRNA
TGGGGCAAAGGGGTGGGCGATTTCTTTTGTAAGTGTAAAATAAATGAACACGCATTGAAT NM_003325 RefSeq chr22
- 19330700 19431696 HIRA 7290 histone cell cycle regulator

GO:0005515|GO:0000790|GO:0003700|GO:0007369|GO:0006357|GO:0003714|GO:0005634|GO:0006336|GO:0009653|GO:0001649|GO:0006351|GO:0042692|GO:0043234|GO:0016605|GO:0003682|GO:0005654|GO:0070062|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140407_PI430048170 0.0276192167784346 3.17772045980826 2.67051062456949 2.77102435152534 2.54077298158661 A A A 1.4673698308645 0.368754569168698 0.945854373456338 A A A LNCV6_140407_PI430048170 mRNA ACAGAGCCAAGGAGGCTGGATCTCTCTTCCAATAAAGACCCTTACTGACCATACAAAAAA NM_001143833 RefSeq chr3 - 51778560 51779187 IQCF6 440956 IQ motif containing F6 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130720_PI430048170 0.0324698619714931.33494126629968 7.20663524762259 7.15180978190103 7.4725421964315 P P P 6.72512893080685 6.87886468411873 6.98563681500863 P P P LNCV6_130720_PI430048170 mRNA CTACCAGATTTGAACATCTAGTGAGGTTCACATTCATACTAAGTTTTCAACATTGTGTTC NM_005542RefSeq chr7 + 155297775 155310235 INSIG1 3638 "insulin induced gene 1, transcript variant 1" GO:0005515|GO:0006695|GO:0042472|GO:0045599|GO:0005783|GO:0008283|GO:0045717|GO:0044281|GO:0010894|GO:0060363|GO:0032933|GO:0008152|GO:0032937|GO:0005789|GO:0060021|GO:0006641|GO:0042474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133016_PI430048170 0.1687918003747921.18887540356055 0.596075628363728 0.4177976183108640.814345608433963A A A 0.3546818337912960.353389203786785 0.398324099483876A A A LNCV6_133016_PI430048170 mRNA TGAAACAGCAGTATCCAAATACAGCAATTTGGATGCTGAAACGATGTGAGACAGGGATGG NM_032174RefSeq chr1 + 161225938 161230746 TOMM40L 84134 "translocase of outer mitochondrial membrane 40 homolog (yeast)-like, transcript variant 1" GO:0046930|GO:0043234|GO:0008150|GO:0003674|GO:0015288|GO:0005741|GO:0015031|GO:0055085|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143468_PI430048170 0.00735002533019796 0.2966650139575993.0573908301907 2.88524374954953 3.52338403360644 A A P 4.37079073087282 5.13337734096864 5.16737278176838 P P P LNCV6_143468_PI430048170 mRNA CCAGTGCTTGCCATAATTTGTCTGAGAAGGAATCTGTTAAATAAAAGCTTTTATCCTCTA NM_007043RefSeq chr12 - 75497638 75511638 KRR1 11103 "KRR1, small subunit (SSU) processome component, homolog (yeast)" GO:0005515|GO:0000462|GO:0005737|GO:0016020|GO:0032040|GO:0005730|GO:0005634|GO:0045171 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145747_PI430048170 0.1017731581832320.8467607955359095.90966731382526 5.71637825893299 5.98847599208864 P P P 5.9579328565628 6.15240961693172 6.22451027527066 P P P LNCV6_145747_PI430048170 mRNA GAAACGCAGTGAAAGGGAGGAACTTGTCCTTTACCCAGTTTTTCCTTTGTAGGATGGGAA NM_015033RefSeq chr9 - 129887186 130043194 FNBP1 23048 formin binding protein 1 GO:0005515|GO:0005905|GO:0005886|GO:0016023|GO:0005856|GO:0005938|GO:0005764|GO:0042802|GO:0008289|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137075_PI430048170 8.11973228577686e-05 0.20660573062243 5.75884924628833 5.83055378396273 6.08207582227895 P P P 7.99409891546003 8.16799402164914 8.33476639189541 P P P LNCV6_137075_PI430048170 mRNA TACACAACGATTACTCGAAGATGACTGCAAAGGTAAAAGGAAAATAAAAGTGTATTGCAC NM_013233RefSeq chr2 - 167954019 168247595 STK39 27347 serine threonine kinase 39 GO:0023014|GO:0005515|GO:0071476|GO:0019901|GO:0050727|GO:0006950|GO:0043268|GO:0005634|GO:2000687|GO:0005524|GO:0035556|GO:0016323|GO:0005737|GO:0016324|GO:0004702|GO:0018105|GO:2000681|GO:0004674|GO:0018107|GO:0006468|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_38423_PI430048170 0.4497917346581637.16006083762338 0.4013015179151341.15727605375317 5.27136790338664 A A P 0.5333169809799530.3896264639503691.64745182578022 A A A

LNCV6_38423_PI430048170 mRNA
CTCATAAGTGTATAGTACCAAATATCCAGCATTTTCGGCAACACCAACATTGCTTAGAAG NM_181806 RefSeq chr4
- 56338284 56387508 AASDH 132949 "aminoadipate-semialdehyde dehydrogenase, transcript variant 1"
GO:0006631|GO:0016878|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126709_PI430048170 0.848805430595246 1.08742912476616 0.46330751950084
1.58584812374294 0.490633107929864 A A A 1.4089709432583 0.377676838192036
0.449657683122439 A A A LNCV6_126709_PI430048170 mRNA
GGGGTAAGTTAGCTGAAGTCATTTAAAGATGGAAAGGTGGGAAAATTCTTTGATATTTGA NM_015393 RefSeq chr4
+ 74933074 75050115 PARM1 25849 prostate androgen-regulated mucin-like protein 1
GO:0005794|GO:0005886|GO:0000139|GO:0005770|GO:0016021|GO:0010008|GO:0005769|GO:0051973 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128981_PI430048170 0.712349155700446 1.03724022002081 11.3134412488646
10.9908931872684 11.0969563520575 P P P 10.9309765350966 11.2481448109282
11.0652092191037 P P P LNCV6_128981_PI430048170 mRNA
TATTCCAACACCCTCAACTTTCAGATCAGTGAAGTGGAGCCCAAATACTATGCAGATGGG NM_003491 RefSeq chrX
- 153929826 153935154 NAA10 8260 "N(alpha)-acetyltransferase 10, NatA catalytic subunit, transcript variant 1"
GO:0031415|GO:0005515|GO:0008080|GO:0004596|GO:0005730|GO:0005634|GO:0006323|GO:0018002|GO:0005622|GO:0005737|GO:0022626|GO:0016020|GO:0043022|GO:0016407|GO:0006475|GO:0017198|GO:0006474 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141936_PI430048170 0.0169904671423989 1.95955278015297 6.43110514340219
6.48980788279091 6.24496213412724 P P P 5.54303300638472 5.6031024786473
5.06053079579327 P P P LNCV6_141936_PI430048170 mRNA
CCGCCAGCCCTTGGTCCTTATCTGTGTGAGGTTTACAAATAAAGCTTCTGATGTCAAATG NM_013313 RefSeq chr22
- 21697536 21735834 YPEL1 29799 "yippee-like 1 (Drosophila), transcript variant 1" GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130734_PI430048170 0.39679126058994 0.738173481689537 0.378395925570011
0.402268671542918 0.306821785649558 A A A 0.386047007789809 1.38626787969582
0.385390263800572 A A A LNCV6_130734_PI430048170 mRNA
GGTTTATCATTACTATAGCACACTGTAAAGTGCTAGAAAAGTCATAACCTGATTCTCCAA NM_024686 RefSeq chr1
- 83869373 83999150 TTLL7 79739 tubulin tyrosine ligase-like family member 7
GO:0018095|GO:0005929|GO:0005737|GO:0016874|GO:0043204|GO:0005856|GO:0030425|GO:0030154|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130696_PI430048170 0.548493497241294 0.647142208497723 4.40733110828584
4.19463014117042 4.12801563677782 P P P 3.98472999791869 5.75414904518481
4.19370446861677 P P P LNCV6_130696_PI430048170 mRNA
GAGTTTTCAAGAAACTGCGTTCTACTTCCAGAAGATGGTCACTTTAACCTTGTAAATATT NM_021619 RefSeq chr9
+ 130664593 130682997 PRDM12 59335 PR domain containing 12
GO:0006355|GO:0008168|GO:0005634|GO:0032259|GO:0003677|GO:0046872|GO:0006351|GO:0022008 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136803_PI430048170 0.484795522989966 1.47992290030179 1.73575343765001
0.406027201701375 0.249943771091846 A A A 0.367042787221252 0.428679481786644
0.393567583062994 A A A LNCV6_136803_PI430048170 mRNA
AAGACGCAGTGATCACTGTAATGTACACGGCAGTGACCCCAATGTTAAATCCTTTCATCT NM_014565 RefSeq chr17
+ 3215620 3216550 OR1A1 8383 "olfactory receptor, family 1, subfamily A, member 1"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138526_PI430048170 0.250045007775232 1.4486608088476 9.76909947850732
10.8159353426104 10.2167721457184 P P P 10.0457036540642 9.84050136742951

9.43958331607588 P P P LNCV6_138526_PI430048170 mRNA
AATGGTATCTGGGCGGAGCTCACAGAGTTCTTGGAATAAAAGCAACCTCAGAACACTTTG NM_139314 RefSeq chr19
+ 8364126 8374375 ANGPTL4 51129 "angiopoietin-like 4, transcript variant 1"
GO:0004857|GO:0005515|GO:0001666|GO:0043066|GO:0005578|GO:0070328|GO:0072562|GO:0005576|GO:0001
525|GO:0044281|GO:0005615|GO:0030154|GO:0045766|GO:0051005|GO:0051260|GO:2000352|GO:0044255 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134315_PI430048170 0.3891850536057120.8048614754579030.484396306246976
0.4567163612259970.248852910471765 A A A 0.3931320635344861.1642890997467
0.449145078880283 A A A LNCV6_134315_PI430048170 mRNA
CCTATGGACTGGCTGTGGCAATGTAATGCCTGTATAATGTTTTCAAATAAAAATAAATGC NM_001029858 RefSeq
chr6 + 117907525 118317676 SLC35F1 222553 "solute carrier family 35, member F1"
GO:0006810|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127184_PI430048170 0.41775308324939 0.8662015018439130.410723438694251
0.3843451329068770.256075541409758 A A A 0.3330236547983640.375040265676346
0.898203966038254 A A A LNCV6_127184_PI430048170 mRNA
TGTATGTCCGTGTTGCAAAAATAATACATGCCTCAAAAACCTGCCTAGGGGAGCCCTAGT NM_015715 RefSeq chr22
- 31134806 31140607 PLA2G3 50487 "phospholipase A2, group III"
GO:0001675|GO:0043303|GO:0005886|GO:0005814|GO:0007288|GO:0005509|GO:0019372|GO:0036148|GO:0005
576|GO:0044281|GO:0005615|GO:0042629|GO:0016042|GO:0060271|GO:0047498|GO:0006644|GO:0036151|GO:0
046474|GO:0036152. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128509_PI430048170 0.0115555571996216 1.29110017006432 13.202781311662
13.3636730209095 13.3142242251336 P P P 12.8751800438304 13.0498254400584
12.8460146313391 P P P LNCV6_128509_PI430048170 mRNA
AATGGGAATGAAATCAGGGGGCTGTCTACTAGAGCCTGGAATAAATATGCTGCTTTGTGG NM_134323 RefSeq chr12
+ 53500920 53506431 TARBP2 6895 "TAR (HIV-1) RNA binding protein 2, transcript variant 1"
GO:0030423|GO:0003725|GO:0005515|GO:0010467|GO:0048471|GO:0006355|GO:0050689|GO:0030422|GO:0006
357|GO:0005634|GO:0046782|GO:0042803|GO:0006417|GO:0035068|GO:0005829|GO:0016442|GO:0005737|GO:0
035198|GO:0035197|GO:0031054|GO:0035280|GO:0005654|GO:0006469|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142774_PI430048170 0.3529021160711291.03008472090759 0.436286412554333
0.3285143680500590.373533700555816 A A A 0.2950590753568530.332829301073048
0.382845953277607 A A A LNCV6_142774_PI430048170 mRNA
GAGGCAGAGAAACAATTTTTGAAAAAGAGCAAACCCATGGAAAATGTCTCAGATCTAATA NM_057168 RefSeq chr7
+ 121329035 121341104 WNT16 51384 "wingless-type MMTV integration site family, member 16, transcript
variant 1"
GO:0003408|GO:0046330|GO:0005578|GO:0090403|GO:0005576|GO:0014068|GO:0005615|GO:0043616|GO:0005
109|GO:0010628|GO:0060317|GO:0005737|GO:0045165|GO:0046849|GO:0030216|GO:0030182|GO:0060548|GO:0
090399|GO:0016055. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145244_PI430048170 0.0568175422845447 0.7006267078848496.87960313885955
6.71257759991728 6.91842803812407 P P P 7.11217257699038 7.29544095277975
7.60711241335157 P P P LNCV6_145244_PI430048170 mRNA
GACATGAATGAAAACTGCTGTTTTAAAGTGGTTTATTATGTTCCATGGAAGAAACTGGTC NM_024635 RefSeq chr9
+ 85941141 86022302 NAA35 60560 "N(alpha)-acetyltransferase 35, NatC auxiliary subunit"
GO:0005515|GO:0043066|GO:0031417|GO:0005737|GO:0048659|GO:0005844 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137693_PI430048170 0.0125207432906878 2.09402371011646 5.61447629508648
5.18139718357286 5.215534035153 P P P 3.96308164521183 4.61378209906748 4.2007811907883
P P P LNCV6_137693_PI430048170 mRNA
TGGAGCATATGACCCGTCACCTGGAGGAGAGTGAGAAGGCCATGCAGGAGCGGGTGCAGA NM_144999 RefSeq

chr17 + 82023301 82031151 LRRC45 201255 leucine rich repeat containing 45
GO:0005813|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136437_PI430048170 0.2534455689495311.15609077311745 8.90879014533171
8.62112554873894 8.85072114544664 P P P 8.48601508313106 8.83696676983543
8.40865122388483 P P P LNCV6_136437_PI430048170 mRNA
TTTTGTGTTTCTGGAACAGCTACGCAAAAACTTTGGCATCAAAGTGCCATCCTGACCAGC NM_001270888 RefSeq
chr17 + 81712235 81721016 SLC25A10 1468 "solute carrier family 25 (mitochondrial carrier;
dicarboxylate transporter), member 10, transcript variant 1"
GO:0005515|GO:0005310|GO:0005975|GO:0005743|GO:0006094|GO:0005634|GO:0044281|GO:0055085|GO:0034
641|GO:0000096|GO:0000098|GO:0009405|GO:0006006|GO:0006835|GO:0016021|GO:0070221|GO:0006839|GO:0
006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115851_PI430048170 0.2531007516361161.07956858991789 11.6252835049184
11.6642870502766 11.5332306774746 P P P 11.3542355133434 11.5771774989921
11.5529404977994 P P P LNCV6_115851_PI430048170 mRNA
CTTCTTCAGCTGACACCCCGTGAGCCTTGTCAGTGTGTAAATAAAGCTCTTTTGCCACCC NM_005035 RefSeq chr19
- 617222 633568 POLRMT 5442 polymerase (RNA) mitochondrial (DNA directed)
GO:0042645|GO:0005739|GO:0005515|GO:0010467|GO:0006996|GO:0003899|GO:0005759|GO:0006391|GO:0007
005|GO:0006390|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136563_PI430048170 0.1434020306668991.18077047821227 6.02885351572469
6.12432182733378 5.96489338590446 P P P 5.96296500633573 5.83071226412914
5.58446648904396 P P P LNCV6_136563_PI430048170 mRNA
AGAATCTGCTCTTCCGCCTGATGGAAGGCCTACTCTCCTGCCCAAGGGAAGATCTGCTCT NM_178543 RefSeq chr17
+ 79731102 79742222 ENPP7 339221 ectonucleotide pyrophosphatase/phosphodiesterase 7
GO:0006665|GO:0006685|GO:0005794|GO:0006684|GO:0008285|GO:0005886|GO:0006687|GO:0004767|GO:0044
281|GO:0005902|GO:0016020|GO:0008156|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59095_PI430048170 0.4289972892713781.66646604615993 0.3421241767088841.92838150445445
0.303836497219205 A A A 0.2491600101932460.49108122971138 0.252702919960241 A A A
LNCV6_59095_PI430048170 mRNA
TCTCAGAAGAGAAGCTTTGTTTATGTCTGGAAGACCTGGGGCCAATACTGGCAAGTTCTA NM_006928 RefSeq chr12
- 55954104 55966712 PMEL 6490 "premelanosome protein, transcript variant 3"
GO:0005515|GO:0042470|GO:0005794|GO:0042438|GO:0005886|GO:0032438|GO:0032585|GO:0005789|GO:0005
576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139248_PI430048170 0.0461551020718061.5322671542115 6.77489379751853
6.98724371470297 6.63987976884563 P P P 5.88538665376122 6.48009306998109
6.14914702322849 P P P LNCV6_139248_PI430048170 mRNA
ATGGAAAAAGACATCTGAGGCCATCCAGGGCAAGGAACTGTCTTTCTGGTTCAATAGACT NM_001200016 RefSeq
chr3 - 50296401 50299421 NAT6 24142 "N-acetyltransferase 6 (GCN5-related), transcript variant 2"
GO:0005737|GO:0008080|GO:0008152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132162_PI430048170 0.7178108515688410.987315247766819 0.260092498279242
0.2762219567044790.402647966720078 A A A 0.3696499904197470.317099150974591
0.311006650734422 A A A LNCV6_132162_PI430048170 mRNA
GATACTCATAAGCAATTTTCTGTGTGTAGGATAAAATAAACCATCTTGTATGGGATCTGC NM_001288743 RefSeq
chr10 - 49154723 49188400 C10orf128 170371 "chromosome 10 open reading frame 128, transcript
variant 5" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127064_PI430048170 0.0197841688212502 1.43682650479134 4.06661162420671
3.8659292042939 4.18737411351898 P P P 3.58428830406818 3.45484809475571
3.52730060854004 P P P LNCV6_127064_PI430048170 mRNA
GTGGGTTTCCTGCAGCTTCTTTGGCTATGAAGAAAAGCACCCCCAGGGCTGTGTCCTTGG NM_022719 RefSeq chr22
- 19130278 19144677 DGCR14 8220 DiGeorge syndrome critical region gene 14

GO:0005515|GO:0003674|GO:0000398|GO:0005634|GO:0071013|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141658_PI430048170 0.00523336370683615 0.2918229339813344.87132512786943 4.35172007280895 5.17790112007118 P P P 6.22934828677896 6.59231582564586 6.94006969621439 P P P LNCV6_141658_PI430048170 mRNA CAGAAGTCTGAACAATTGGATAAATTTGACTTCCAAGACAGCTAAACTTTTCAACTGCAA NM_014899RefSeq chr5 + 95731145 95796367 RHOBTB3 22836 Rho-related BTB domain containing 3
GO:0005515|GO:0017137|GO:0005794|GO:0007264|GO:0008152|GO:0042147|GO:0005525|GO:0016887|GO:0005524|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139800_PI430048170 0.1018583672091561.18376655680897 6.55942099214915 6.69267291778066 6.73682366206016 P P P 6.60378756672926 6.3266194669133 6.3153302841615 P P P LNCV6_139800_PI430048170 mRNA TCTGTAAGTGAAGATTGTCGTATTCCAAGTCTAAAATACACCTGGATCTGTCTAGTCAAT NM_001202554 RefSeq chr1 + 26788187 26798403 PIGV 55650 "phosphatidylinositol glycan anchor biosynthesis, class V, transcript variant 1"
GO:0006501|GO:0000030|GO:0016254|GO:0005789|GO:0016021|GO:0044267|GO:0006506|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145362_PI430048170 0.1582166326138030.8014704475653419.11497552490105 9.20259945920608 9.04979319971114 P P P 9.14771016139385 9.62275014306388 9.5169630885437 P P P LNCV6_145362_PI430048170 mRNA CTGAGGAGAGTGGAACAGAAGGGGTGGAGTTTTGTATAAATAAAGTTTCTTTGTCTCTTT NM_001257407 RefSeq chr16 + 27313908 27364778 IL4R 3566 "interleukin 4 receptor, transcript variant 4"
GO:0005515|GO:0043627|GO:0004913|GO:0043032|GO:0002532|GO:0042832|GO:0005615|GO:0043235|GO:0035556|GO:0007165|GO:0006955|GO:0005887|GO:0042127|GO:0045626|GO:0005057|GO:0035771|GO:0045630|GO:0030728|GO:0090197. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113089_PI430048170 0.2024952460745840.7623187049872736.78142069888966 6.60251819674234 6.47662187370437 P P P 7.1405487863264 7.24127358067147 6.58794959205511 P P P LNCV6_113089_PI430048170 mRNA TCTTTTCTAACCGTGCAGCCTCTTCCTCGGCTTCTCCTGAAAGGGAAGGTGGAAGCCGTG NM_001304718 RefSeq chr10 + 87863437 87971930 PTEN 5728 "phosphatase and tensin homolog, transcript variant 2"
GO:0005515|GO:0010997|GO:0042995|GO:0010043|GO:0035335|GO:0035749|GO:0007507|GO:0007173|GO:0007611|GO:0033198|GO:0002902|GO:0007613|GO:0032355|GO:0033032|GO:0021542|GO:0030336|GO:0000287|GO:0019901|GO:0007568|GO:0033555|GO:0014067|GO:0030165|GO:0005161|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128764_PI430048170 0.7607736770857231.02851183381354 11.9762045384777 12.058352520572 12.2516551429894 P P P 11.8789665520295 12.0342999270515 12.2421612914791 P P P LNCV6_128764_PI430048170 mRNA AGAGACAGCACCAATGGCCAGGATGACTCTTAAGCACATAGTGGGGTTGAGAAATCTTAT NM_001136561 RefSeq chr1_KI270766v1_alt - 61030 62397 HNRNPCL2 NA heterogeneous nuclear ribonucleoprotein C-like 2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128260_PI430048170 0.4012579566386421.03629599256555 0.290545370483424 0.2887863161812410.431182730173971 A A A 0.3026763290457940.272545889606635 0.285502281706569 A A A LNCV6_128260_PI430048170 mRNA CTAGCCTATTCTTACTTACTCTACAGTGTCTTAAGCAATATTAAAGGTTCCTTTTCCCAA NM_003814RefSeq chr14 - 70522360 70535015 ADAM20 8748 ADAM metallopeptidase domain 20
GO:0007338|GO:0005886|GO:0006508|GO:0008270|GO:0016021|GO:0007339|GO:0004222|GO:0008237|GO:0032504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143038_PI430048170 0.0300402829205206 0.7025459229314927.2234397661475 7.26880708407315 7.55313096773833 P P P 7.65509143778092 7.86606094550098

8.04813735161112 P P P LNCV6_143038_PI430048170 mRNA
GGTATCAGTATTTCAGAATCCTGCGACGATTTTATTTCTAAATTCATGTACTGTATGTCC NM_014016RefSeq chr3
+ 45689261 45745408 SACM1L 22908 SAC1 suppressor of actin mutations 1-like (yeast)
GO:0005515|GO:0005794|GO:0006661|GO:0043812|GO:0030176|GO:0044281|GO:0034593|GO:0008150|GO:0016
791|GO:0000139|GO:0004438|GO:0046856|GO:0032281|GO:0005789|GO:0006644 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129007_PI430048170 0.2340230710530450.7392753146979281.19154012157427
1.49749169957934 2.06519389629662 A A A 1.64985799537159 2.22329197034175
2.25156014757804 A A A LNCV6_129007_PI430048170 mRNA
GGTTAAAAAACACACACACACATACACAAACCGTTTCTATGAGAGATTGATGAACTTTGT NM_015267RefSeq chr12
+ 111034023 111350556 CUX2 23316 cut-like homeobox 2
GO:0051965|GO:0000977|GO:2000463|GO:0007614|GO:0071310|GO:0005634|GO:0000122|GO:0006351|GO:0010
628|GO:0043565|GO:0050890|GO:0050775|GO:0061003|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140751_PI430048170 0.0399389720710428 0.7877775122576589.12336292199157
9.02674266571342 9.16076790832591 P P P 9.58284643708199 9.28867239482915
9.46003278707426 P P P LNCV6_140751_PI430048170 mRNA
CAGCAGTGTTTAAATCTAAATACGTTGTGAGTCTGTTATCTGTCCTATCGCGTTTTTTAANM_194071RefSeq chr7 -
137874978 138002101 CREB3L2 64764 "cAMP responsive element binding protein 3-like 2, transcript
variant 1"
GO:0034976|GO:0044212|GO:0051216|GO:0005783|GO:0035497|GO:0005634|GO:0000978|GO:0006351|GO:0030
968|GO:0006888|GO:0001077|GO:0002062|GO:0045944|GO:0005789|GO:0016021|GO:0045893 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143424_PI430048170 0.00491114192742575 0.4039050812213935.45953347805489
5.60979804660176 5.76016118784204 P P P 6.59617800080359 7.00980645202863
7.11280054805692 P P P LNCV6_143424_PI430048170 mRNA
CCCTGGATTGAAAAAGTCTTCCTCGTGGTAGTTATATGTAGTTTCAAACATGAATAAACT NM_006195RefSeq chr9
+ 125747337 125967376 PBX3 5090 "pre-B-cell leukemia homeobox 3, transcript variant 1"
GO:0007388|GO:0005667|GO:0008344|GO:0006355|GO:0003700|GO:0007387|GO:0007585|GO:0005634|GO:0006
351|GO:0021516|GO:0043565|GO:0002087|GO:0048666 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135558_PI430048170 0.0340868941132345 0.2879762283695251.54431952694687
0.2876879149274261.63126969570392 A A A 3.40701463227816 2.83376356724965
2.88508127796874 P P P LNCV6_135558_PI430048170 mRNA
TGATGTGGTTTACAATAGTGTGACAACGATGAAAATGCTTGGTTATGTAAAGTGATTGGA NM_014912RefSeq chr10
- 92048639 92291118 CPEB3 22849 "cytoplasmic polyadenylation element binding protein 3, transcript
variant 1"
GO:0017148|GO:0005515|GO:0035613|GO:0043005|GO:1900365|GO:0003723|GO:0045202|GO:0005634|GO:0006
412|GO:0035925|GO:0030014|GO:0030425|GO:1900248|GO:0005737|GO:0000166|GO:0071230|GO:0048167|GO:0
003730|GO:0060998|GO:0060999|GO:0007616|GO:0060213|GO:0045727|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140637_PI430048170 0.0827966051435911 2.00845297664233 4.21962262358774
3.74640396222361 3.69924863326771 P P P 2.86247248523431 3.42300801676124
2.14644114782701 P P A LNCV6_140637_PI430048170 mRNA
AGAGGATCGACCAGTCAGAGTTCGAAGGCTTTGAGTATATCAACCCATTATTGCTGTCCA NM_002744RefSeq chr1
+ 2050469 2185395 PRKCZ 5590 "protein kinase C, zeta, transcript variant 1"
GO:2000553|GO:0005515|GO:0032753|GO:0030054|GO:0050732|GO:0015459|GO:0060291|GO:0030010|GO:0043
560|GO:0018105|GO:0047496|GO:0043274|GO:0046326|GO:0007179|GO:0070374|GO:0070062|GO:0035748|GO:2
000664|GO:0031584|GO:2000667|GO:2000463|GO:0007616|GO:0005815|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_142084_PI430048170 0.1190541878264761.20007878434109 8.78435456691619
9.11497552490105 8.83533161711193 P P P 8.70805459884036 8.74875080743744
8.49859574053596 P P P LNCV6_142084_PI430048170 mRNA
AAAGGATAAATTTGGAGTGGGGGGTCTCTAAACAGATTGCCTGGATTCCGTTCTTTCCTG NM_001301860 RefSeq
chr20 + 41340852 41360585 LPIN3 64900 "lipin 3, transcript variant 1"
GO:0006646|GO:0003713|GO:0005634|GO:0008195|GO:0044281|GO:0009062|GO:0016311|GO:0045944|GO:0005
789|GO:0019432|GO:0006644|GO:0006656|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134119_PI430048170 0.0268387829762866 1.14665725415543 13.4167395688686
13.5598657935896 13.4574673680657 P P P 13.3020407705365 13.3343569791207 13.2061024052 P
P P LNCV6_134119_PI430048170 mRNA
CTTTGATAAAGCACTGACATCTCCTTCCTAATAAATAGACCCTGAGTTCTGTACAAAAAA NM_015853 RefSeq chr11
- 62676497 62679117 UBXN1 51035 "UBX domain protein 1, transcript variant 1"
GO:0005515|GO:0043130|GO:0000502|GO:0005634|GO:0071796|GO:0032435|GO:0030425|GO:0005737|GO:0043
025|GO:0051117|GO:0043161|GO:0031397|GO:0034098|GO:0031625|GO:0031593 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143050_PI430048170 0.41181209319536 0.5239242549741390.495717160997755
0.3919971547335410.48020203508553 A A A 0.4495013325999720.498472829724602
2.34484085073082 A A A LNCV6_143050_PI430048170 mRNA
AGACACAAGTGGAAGGAGAAAGGCAGTAACTGTAGGGTGCATTTAAGGTTTTAAATGTTA NM_001134657 RefSeq
chr3 - 139042101 139044892 PRR23C NA proline rich 23C NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_137618_PI430048170 0.9623437219137231.00328545139013 5.24893135580032
4.99173157431394 4.40990670641716 P P P 5.34737280058437 4.88342857446392
4.36282356401394 P P P LNCV6_137618_PI430048170 mRNA
CACCACCGCCCAAGTTCTTTTTCCATCATTATAATTCATCCTCATTATCTTGGTAAAATA NM_198565 RefSeq chr3 +
196639695 196662003 NRROS 375387 negative regulator of reactive oxygen species
GO:0006955|GO:0006954|GO:0005886|GO:0005783|GO:0045087|GO:0006801|GO:0005789|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135431_PI430048170 0.0504007271630709 0.4024897994674650.354831939411623
1.03956833018487 1.1496501237888 A A A 1.85770602773297 1.65690170214345
2.81127619188961 A A P LNCV6_135431_PI430048170 mRNA
AGTCAATTCAGCATTGACTTGAGTTTCAGTTGACTTGACATTGAGTTCAAGCATTAATTG NM_001137674 RefSeq
chr3 + 31981773 31991736 ZNF860 NA zinc finger protein 860 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129596_PI430048170 0.5147535308800050.9489646609661510.4087261885706
10.1527120517356 10.4619432179501 P P P 10.3460975963597 10.521733743821 10.395089226971
P P P LNCV6_129596_PI430048170 mRNA
TGTGTGGTTTTACGGTTCAAGGAACTACTTGATGATTTTGAGGAAACACTTGCCAGAAAC NM_016510 RefSeq chr2
+ 238060923 238099413 SCLY 51540 selenocysteine lyase
GO:0006520|GO:0030170|GO:0009000|GO:0016740|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131828_PI430048170 0.0134861724147316 4.46416524965739 4.28586047919005
4.0885732889643 4.67490473998308 P P P 1.40546182218746 2.57625324513738
2.40316026619275 A P P LNCV6_131828_PI430048170 mRNA
CAGTCTGACAAAAGTCTATGGTTCCTAAATATGACATCAGTGTTGCCAATAAAATGTTTC NM_004411 RefSeq chr7
+ 95772505 96098424 DYNC1I1 1780 "dynein, cytoplasmic 1, intermediate chain 1, transcript variant
1"
GO:0005515|GO:0008017|GO:0048471|GO:0005874|GO:0030507|GO:0003777|GO:0031982|GO:0005829|GO:0019
886|GO:0000922|GO:0003774|GO:0047496|GO:0008152|GO:0000777|GO:0000776|GO:0005868|GO:0055037 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62154_PI430048170 0.28295618618305 1.27174207958491 0.31124747267923 1.02835556094411
0.487531454301518 A A A 0.3020899174745950.26911044729698 0.314964218620808 A A A
LNCV6_62154_PI430048170 mRNA
TACCAGAGACCCATAGGAGTCCTGTTGAAGAAGTCGGCAGCCTGGAAGAAAGACCGGGTG NM_001099773
RefSeq chr15 - 74337761 74366212 CYP11A1 1583 "cytochrome P450, family 11, subfamily A,
polypeptide 1, transcript variant 2"
GO:0042542|GO:0006805|GO:0009651|GO:0018963|GO:0006701|GO:0006703|GO:0071560|GO:0033591|GO:0033
595|GO:0014037|GO:0005759|GO:0060992|GO:0071356|GO:0033197|GO:0018958|GO:0010332|GO:0030061|GO:0
051412|GO:0005506|GO:0007617|GO:0042359|GO:0060135|GO:0021549|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130399_PI430048170 0.07580125289542 0.6460017480019993.83953991578185
3.47582640885513 3.93563370936569 P P P 3.96106345769384 4.61304605638972
4.52509082059621 P P P LNCV6_130399_PI430048170 mRNA
CTGTGTTGTCAGATAAGAGAACACATCCAAAATGCATGATTCTTACAAACTAAAGGAAGT NM_005230RefSeq chr12
+ 96194381 96269835 ELK3 2004 "ELK3, ETS-domain protein (SRF accessory protein 2), transcript
variant 1"
GO:0005515|GO:0003700|GO:0006357|GO:0006366|GO:0000981|GO:0003714|GO:0005634|GO:0032422|GO:0001
525|GO:0000978|GO:0030154|GO:0043231|GO:0005739|GO:0007165|GO:0001077|GO:0045944|GO:0042060|GO:0
005654|GO:0045892. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136637_PI430048170 0.2041527302330760.83899246186315 5.68095872558651 5.4093203837963
5.59039372954985 P P P 5.82308321666908 5.56708971678079 6.02692669526753 P P P
LNCV6_136637_PI430048170 mRNA
CCTCCTTACTACCCTTGTCAAGAAAGAATATGAACATAACAAGAGACTGCAAGACTTCAA NM_138363RefSeq chr17
+ 64507039 64537944 CEP95 90799 centrosomal protein 95kDa GO:0005813|GO:0005737|GO:0000922
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140406_PI430048170 0.3410126610906731.03562640023412 0.299295208882126
0.2599250151854830.394525665909879 A A A 0.2810862494835410.246940372394879
0.277305003460018 A A A LNCV6_140406_PI430048170 mRNA
TTGTAAGGTGCAACAATGCATACCCCTTCCATTAAAAGAATGACCAGGTCTGCTAAAAAA NM_001145059 RefSeq
chr3 - 51873720 51875584 IQCF5 389124 IQ motif containing F5 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_80402_PI430048170 0.0065307765303019 1.5999220626955 7.74568317452115
8.02151174499468 7.87138523998182 P P P 7.21070169890624 7.14524726552981
7.25959467178614 P P P LNCV6_80402_PI430048170 mRNA
GTCTGATTATGCATGGTTCTAAATGGTTTCAGTGGCAAATACATAACATTGTACTACTGA NM_178564RefSeq chr8
- 143833584 143840974 NRBP2 340371 nuclear receptor binding protein 2
GO:0043524|GO:0005737|GO:0004672|GO:0030182|GO:0016242|GO:0006468|GO:0005524 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133850_PI430048170 0.00797016099814135 0.8063050577960689.51312170787034
9.41796630191527 9.46513757973601 P P P 9.68353011259819 9.82041380681786
9.82134599867318 P P P LNCV6_133850_PI430048170 mRNA
GGAGTTTTCTAACGTGAGGATGAAGTCTACACTTCAGATTAAAAAGGGTTATGTTGTAAA NM_005049RefSeq chr21
+ 44107326 44131181 PWP2 5822 PWP2 periodic tryptophan protein homolog (yeast)
GO:0000462|GO:0005737|GO:0030515|GO:0032040|GO:0005730|GO:0034388|GO:0000028 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143001_PI430048170 0.2399267943249811.19035226277707 11.9223688990676
11.8129079629158 11.9556516025367 P P P 11.3084566899409 11.8512506218151
11.7266942950257 P P P LNCV6_143001_PI430048170 mRNA

CAGCTGCAGTGATATATATTTTTTATCAGTGCTTGGTTGGTTTTAAATAAAGTGCACGCT NM_024092RefSeq chr11
+ 60913898 60923443 TMEM109 79073 transmembrane protein 109
GO:0005640|GO:0042771|GO:0003674|GO:0060548|GO:0033017|GO:0071480|GO:0016021|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139207_PI430048170 0.0118031992747675 0.5272297162965577.02516466846128
6.62830751601315 6.81288947977361 P P P 7.42283091557927 7.9257909878519
7.86529663361531 P P P LNCV6_139207_PI430048170 mRNA
CGAGAGGCAAAGGGCAAGTTTTGGATTTTGCTTCTTCCAAGTTTGTTTTTAAACGACAAA NM_003482RefSeq chr12
- 49018974 49055324 KMT2D 8085 lysine (K)-specific methyltransferase 2D
GO:0005515|GO:0043627|GO:0006342|GO:0006355|GO:0008284|GO:0048477|GO:0044212|GO:0006325|GO:0001
555|GO:0005634|GO:0042800|GO:0003677|GO:0006351|GO:0035097|GO:0045944|GO:0005654|GO:0008270|GO:0
033148|GO:0051568. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101537_PI430048170 0.8420131804517991.0703669893901 3.03730475487287
3.78738892946447 3.07471481517886 A P P 3.28545326716823 3.25719162282384
3.19053732446043 P P P LNCV6_101537_PI430048170 mRNA
AGGAAGAGAATAGATGTTTTACAAGACCACAGGCTGAGATCTCTTTCTGCCCCCATGATG NM_005490RefSeq chr19
- 6752161 6767512 SH2D3A 10045 SH2 domain containing 3A
GO:0043547|GO:0005515|GO:0005085|GO:0007264|GO:0005070|GO:0007254|GO:0009967 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_101562_PI430048170 0.01720718388989 2.76070808420568 2.10581215112923
2.45360247470054 1.62510493237352 A A A 1.14429321690234 0.326524232670873
0.258635099446179A A A LNCV6_101562_PI430048170 mRNA
TTTCCTCTCTACCATGTCAATGAAAAGCCATCCAGTCTCTTGTCCAAGCAGGTGTACTTG NM_152864RefSeq chr20
- 63240783 63254540 NKAIN4 128414 Na+/K+ transporting ATPase interacting 4
GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144454_PI430048170 0.6431595321464751.01112930235914 0.475676456895685
0.5108071798268760.414621041319687A A A 0.466525847255791 0.43820429968255
0.449968749138267A A A LNCV6_144454_PI430048170 mRNA
TTTTCAGTGGTTTTAACTCATGTGAAATAATGATTTTCCACCAGCTCTGATGCAAAGAGA NM_021110RefSeq chr8
+ 120125107 120372034 COL14A1 7373 "collagen, type XIV, alpha 1"
GO:0003229|GO:0005581|GO:0005518|GO:0005578|GO:0005596|GO:0005576|GO:0005614|GO:0005615|GO:0061
050|GO:0031012|GO:0016337|GO:0048873|GO:0022617|GO:0030198|GO:0030199|GO:0030574|GO:0005788|GO:0
030674|GO:0070062|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109155_PI430048170 0.42755670105985 1.33873815196415 1.70599912738445
0.5204252659246831.21400727066754 A A A 0.3235972119928081.3983760934349
0.437027942715353A A A LNCV6_109155_PI430048170 mRNA
AAAGACTGTGGAACCTCTTACTGTGAAACAGAAGCCCAGTGGGTCAGAGATGGAGAAAAA NM_152751RefSeq
chr10 - 13438483 13502976 BEND7 222389 "BEN domain containing 7, transcript variant 1"
GO:0005515|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128875_PI430048170 0.00855202697232808 0.4825354730664154.68874769960648
4.91154027469084 5.00903620021981 P P P 5.66923048076197 5.85383434099559
6.20616944934662 P P P LNCV6_128875_PI430048170 mRNA
TATGACAAAAGACAGTCATTTTTGGTCAGAGTGATATTTGGTGACGGAAACTTGTTCATA NM_153371RefSeq chr13
- 27545912 27620583 LNX2 222484 ligand of numb-protein X 2
GO:0005515|GO:0051260|GO:0008270|GO:0030165 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57597_PI430048170 0.0011697779896051 0.7891332019308291 1.3650546543647
11.2627400760425 11.2991022932102 P P P 11.5960054466041 11.6654097231254
11.6906725123362 P P P LNCV6_57597_PI430048170 mRNA
TTTTAAGACTCCCTGTGAAATGCTTTCCGCACCTTAACCCCAGTGAGCGTGAAAAAGAAA NM_015533RefSeq chr11

+ 61333181 61348759 TKFC NA dihydroxyacetone kinase 2 homolog (S. cerevisiae) NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131859_PI430048170 0.0654070171051767 1.12720939415738 0.600559500558766
0.7293128995177840.740737202655855A A A 0.6196028531742970.458925799786988
0.472402333659046A A A LNCV6_131859_PI430048170 mRNA
CTTGGGATTTCTCCTTGTTTTTGTGAGTACCTGGGAAGTGTTGTTTGTTTTCTTATTTTC NM_012188RefSeq chr5 +
170105912 170109725 FOXI1 2299 "forkhead box I1, transcript variant 1"
GO:0043565|GO:0001077|GO:0042472|GO:0003700|GO:0044212|GO:0008301|GO:0045944|GO:0005634|GO:0009
790|GO:0000978|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143365_PI430048170 0.8807717300835780.98757563074709414.5006318446102
14.3268379026403 14.0990566720422 P P P 14.3958647821232 14.428936533581
14.1702443126617 P P P LNCV6_143365_PI430048170 mRNA
GCTTTCTGCATGCTTAGAGCATGTTCTTGGAACATGGAATTTTATAAGCTGAATAAAGTT NM_001256530 RefSeq
chr22 + 43151934 43163242 TSPO 706 "translocator protein (18kDa), transcript variant 3"
GO:0071294|GO:0006820|GO:0006821|GO:0006694|GO:0008347|GO:0030325|GO:0051928|GO:0008283|GO:0006
626|GO:0007268|GO:0060242|GO:0050810|GO:0005741|GO:0010042|GO:0043231|GO:0005739|GO:0005737|GO:0
051901|GO:0045019|GO:0015485|GO:0014012|GO:0005497|GO:0008202|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134279_PI430048170 0.1591766783450481.87988275914032 0.391828930565951
1.21493640391086 1.66716514616133 A A A 0.2608682971298990.297633501343763
0.256825530894715A A A LNCV6_134279_PI430048170 mRNA
GACCTGAACTTTTTAGCAAATTATTATTCTCAGTTTCCATTACCTGTTTGGCCAAACAGA NM_173508RefSeq chr1
+ 233904711 234324518 SLC35F3 148641 "solute carrier family 35, member F3, transcript variant 1"
GO:0015888|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113707_PI430048170 0.2259293419929860.7901575986958710.331161299531742
0.3220475450915780.307787463866721A A A 0.6514612340243540.312715759925157
0.947063770543447A A A LNCV6_113707_PI430048170 mRNA
ATAGCTGATACAGTACTCAATGATGATGATATTGGTGACAGCTGTCATGAAGGCTTTCTT NM_001256054 RefSeq
chr9 - 27546545 27573866 C9orf72 203228 "chromosome 9 open reading frame 72, transcript variant
3"
GO:0005515|GO:0017137|GO:0005776|GO:0006914|GO:0005634|GO:0031410|GO:0015629|GO:0005615|GO:0005
764|GO:0045171|GO:0006897|GO:0005737|GO:0005654|GO:0005768 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141024_PI430048170 0.00847043670642908 2.57480950019828 3.15733823031852
3.45043139517554 2.88423998663714 A P A 2.06084692946847 1.93928645365926
1.36211869903937 A A A LNCV6_141024_PI430048170 mRNA
ACCAATGCACTTACCAGGAGGCACAAGACTCTTGAAGAAGATGTACAATGAACCTTTTTT NM_033387RefSeq chr9
- 131258077 131276519 FAM78A 286336 "family with sequence similarity 78, member A" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_57864_PI430048170 0.9997608479673931.01767944456614 2.64777142494351 1.44780591943841
2.14668275296133 A A A 2.61850191167177 1.93987843329807 1.68345190519207 A A A
LNCV6_57864_PI430048170 mRNA
TATCATCTCCCAGAAGCGGCTGGGCTGCAATGGGCTGGGCTTCTCAGACCTGCCAGGGAA NM_002599RefSeq chr11
- 72576139 72674453 PDE2A 5138 "phosphodiesterase 2A, cGMP-stimulated, transcript variant 1"
GO:0005515|GO:0030424|GO:0048471|GO:0005886|GO:0005783|GO:0004118|GO:0030818|GO:0006626|GO:0071
560|GO:0046069|GO:0005634|GO:0019934|GO:0046872|GO:0042803|GO:0030425|GO:0005829|GO:0005737|GO:0
030552|GO:0030553|GO:0061028|GO:0005759|GO:0008144|GO:0033159|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135221_PI430048170 0.1180948704293071.84735825177111 1.94847183389123

2.41084760537342 1.59760689237344 A A A 1.73575343765001 0.966783960574818
0.401783173761094 A A A LNCV6_135221_PI430048170 mRNA
ATCTTCATGTACTTGAAGCCCAAGAGTAAGGAAGCCCACATCTCTGATGAGGTCTTCACA NM_001004487 RefSeq
chr9 - 35869462 35870401 OR13J1 NA "olfactory receptor, family 13, subfamily J, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132152_PI430048170 0.1459134485565560.7472332719990366.0466984407038 5.5313775093461
5.82811836971361 P P P 5.99772216345739 6.55831452904705 6.09274174504447 P P P
LNCV6_132152_PI430048170 mRNA
CGGGCCAGGTAAATGCTATTGGATGTAATCCAGTAGTGTGTAATATAAATTCAAACCATA NM_001123385 RefSeq
chrX - 40051245 40097466 BCOR 54880 "BCL6 corepressor, transcript variant 5"
GO:0005515|GO:0031519|GO:0035518|GO:0000415|GO:0004842|GO:0044212|GO:0042826|GO:0003714|GO:0070
171|GO:0005634|GO:0000122|GO:0030502|GO:0065001|GO:0006351|GO:0007507|GO:0031072|GO:0051572|GO:0
042476|GO:0060021|GO:0045892|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102108_PI430048170 0.0599910343092082 0.4994767988869955.28697075913093
4.25517376075651 4.7970536287424 P P P 5.38001953790082 5.78231577232764
6.23606851723777 P P P LNCV6_102108_PI430048170 mRNA
TCAGCTTAGTCCATACTGCAAAGATGAACCCTGTAAGAATGGCGGAACATGCTTTGACAG NM_005245 RefSeq chr4
- 186587782 186723833 FAT1 2195 FAT atypical cadherin 1
GO:0005515|GO:0048471|GO:0005886|GO:0005509|GO:0007267|GO:0005634|GO:0030175|GO:0009653|GO:0030
027|GO:0016337|GO:0007163|GO:0016477|GO:0005887|GO:0005911|GO:0007015|GO:0007155|GO:0005925|GO:0
007156|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132087_PI430048170 0.2974287379337861.41056679964898 2.03127143728327
2.71042515373869 2.12613302147583 A A A 1.30675909541677 2.53573995072059
1.23890320784296 A A A LNCV6_132087_PI430048170 mRNA
TTGTTCAACCTCTGTCTCTTTATGTTAACTGGATTTCTGCATTAAATGACTGCCCCCTTG NM_152390 RefSeq chr2 +
39665894 39717963 TMEM178A 130733 "transmembrane protein 178A, transcript variant 1" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68647_PI430048170 0.4984177333720571.02933014167894 0.2851274641068970.309800366389889
0.441883228491169 A A A 0.3256878561515520.2961702200691550.294595636590218 A A A
LNCV6_68647_PI430048170 mRNA
CGAGATGGAATGTGTAGACAGTCTTTCACGGGACATGTCTCAGATATCAATGCTGTCAGT NM_021629 RefSeq chr3
- 179396087 179451583 GNB4 59345 "guanine nucleotide binding protein (G protein), beta polypeptide
4"
GO:0007165|GO:0006112|GO:0005886|GO:0071377|GO:0021762|GO:0044281|GO:0004871|GO:0005765|GO:0032
403|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143836_PI430048170 0.1054660125453770.7838129498781675.13279472471202
5.35656676500364 5.59679389642354 P P P 5.52167602056981 5.78396701654423
5.85147446605088 P P P LNCV6_143836_PI430048170 mRNA
GTACCTTGCCAGGGAAGCAAAAATTGGAATTATTGTAGCTTTTCATGTATACACACTTTT NM_003350 RefSeq chr8
+ 48008434 48061894 UBE2V2 7336 ubiquitin-conjugating enzyme E2 variant 2
GO:0051965|GO:0000209|GO:0005515|GO:0016567|GO:0031372|GO:0008283|GO:0032436|GO:0005634|GO:0045
739|GO:0006301|GO:0070534|GO:0043524|GO:0005737|GO:0006282|GO:0019787|GO:0010976|GO:0000729|GO:0
031625|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141904_PI430048170 0.00252136670763635 0.4597033122662336.53000161039066
6.73938260727846 6.85733889442235 P P P 7.68318985497714 7.72263177915168
8.07103029382807 P P P LNCV6_141904_PI430048170 mRNA
GGTTGGTTGTATTGTAGCTATTACTTATACAGCAACATTTCTTCAATTAGCAGTCTAGAC NM_138423 RefSeq chr15
+ 44288710 44415761 CASC4 113201 "cancer susceptibility candidate 4, transcript variant 1"
GO:0005794|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_127080_PI430048170 0.0196406194426716 5.44151083734756 3.69062065277985 3.50218155457179 4.29808285774329 P P P 2.18234381597984 0.503896024280002 1.07955993356978 A A A LNCV6_127080_PI430048170 mRNA CTGTAAGTTTTTCTGTCAGAAGAGGACTTTCATCAACTTTCATGGAAAGATGTTTATTGC NM_001159560 RefSeq chrX - 102153706 102155790 BEX5 340542 "brain expressed, X-linked 5, transcript variant 2" GO:0005737|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135033_PI430048170 0.00322071130096288 0.76826476134783810.2423116599753 10.2132249050889 10.1100503928561 P P P 10.652083100574 10.5520444668236 10.5016715142012 P P P LNCV6_135033_PI430048170 mRNA GCCTCCTGACCCAGGACTGCTGAATACAAAGATGTTAATTTTTAAAATGTTACTAGTATA NM_001193379 RefSeq chr20 - 63939828 63951174 UCKL1 54963 "uridine-cytidine kinase 1-like 1, transcript variant 2" GO:0005515|GO:0016310|GO:0005737|GO:0044211|GO:0044206|GO:0004849|GO:0016032|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142013_PI430048170 0.0556971355921406 1.43924528832855 5.61477657948514 5.39282010296561 5.85751096480401 P P P 4.8624726340147 5.35885136964148 5.06167799883379 P P P LNCV6_142013_PI430048170 mRNA AATTGGAAGGCAGAAGTTGGCTAAGAAAATGTTCTTCTAGTGCTCCCTCCTTCTTGCTGC NM_001010886 RefSeq chr6 + 35781053 35788064 CLPSL1 NA colipase-like 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135533_PI430048170 0.37815719388078 1.9781254320447 0.420090515771356 2.65970673000948 2.26241772229546 A A A 1.65439207907903 0.821557434995219 0.465870186306641 A A A LNCV6_135533_PI430048170 mRNA GACTTTGGGTTATGATTTTTCACCTTCTACTCCCCTGAAATCATTATCCTAAAGTAACTT NM_001142447 RefSeq chrX + 120362084 120383249 ATP1B4 23439 "ATPase, Na+/K+ transporting, beta 4 polypeptide, transcript variant 1" GO:0006355|GO:0005887|GO:0015077|GO:0006810|GO:0005637|GO:0005890|GO:0015672|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101538_PI430048170 0.396725012452241 0.818426707117217 0.54033185015574 0.6024676491212 0.543544549847591 A A A 0.582996050209726 0.57386859074409 1.27891401949994 A A A LNCV6_101538_PI430048170 mRNA ATGTCATCGGAGGCTTCGAATGTGCCTGTGCTGACGGCTTTGAGCCTGGCCTCATGATGA NM_032447 RefSeq chr19 - 8065402 8147501 FBN3 84467 fibrillin 3 GO:0005509|GO:0005578|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135005_PI430048170 0.015161258903156 1.44150094537405 10.5413447891899 10.5035017907583 10.5106204515897 P P P 10.004385353052 9.8581340142557 10.1002717204631 P P P LNCV6_135005_PI430048170 mRNA ATATCCGATGCTTTGAATCATGCACTGTGTTGAATAAACGTATCTGCTAAATCAGGCAAA NM_182760 RefSeq chr3 - 4361144 4467282 SUMF1 285362 "sulfatase modifying factor 1, transcript variant 1" GO:0006665|GO:0006687|GO:0016491|GO:0005788|GO:0044281|GO:0044267|GO:0046872|GO:0042803|GO:0055114|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139867_PI430048170 0.0289700728662124 0.617200186287071 4.60296079631007 4.35683728303997 4.90775451122111 P P P 5.48968443235694 5.06315610445652 5.42098176366485 P P P LNCV6_139867_PI430048170 mRNA CAGATTTTGGGTACATAATTTAGCTCTTTTAGTCAATCCAAGAGATTTAAGTGACCCCCC NM_001288984 RefSeq chr4 - 75949905 75990962 SDAD1 55153 "SDA1 domain containing 1, transcript variant 3" GO:0003674|GO:0030036|GO:0005730|GO:0042273|GO:0005634|GO:0015031|GO:0000055 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122328_PI430048170 0.726277504018834 1.07264884834114 3.10765570678684 3.34818337942963 3.79266589511976 P P P 3.18863370577908 2.79324525757151

3.84801443920065 P P P LNCV6_122328_PI430048170 mRNA
CTTGGCATTTACACTGTGGCTTTAGCTTTCAAACCAGAGGTTCCTCTTACCCAGCAAAAA NM_033171 RefSeq
chr21 + 39657319 39662889 B3GALT5 10317 "UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase,
polypeptide 5, transcript variant 3"
GO:0005794|GO:0000139|GO:0008499|GO:0005783|GO:0006486|GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_129201_PI430048170 0.333796608567221 0.750349288553251 0.283235622980181
0.424337369285895 0.312154002678323 A A A 0.470554738695797 0.360945358169469
1.2600144115304 A A A LNCV6_129201_PI430048170 mRNA
TGCAGAGAAGTTAGATCCTGCTAAATTTCAATTAAGAGGGGACCTTAAAATAAGGATCAA NM_019119 RefSeq
chr5 + 141187126 141191538 PCDHB9 56127 protocadherin beta 9
GO:0016339|GO:0005886|GO:0005509|GO:0007268|GO:0016021|GO:0007416|GO:0007156 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140303_PI430048170 0.745036969088886 0.791177592460255 0.538791089022016
1.29104642952999 0.626134288924136 A A A 0.606073729236955 0.438822718438232
2.00083093334267 A A A LNCV6_140303_PI430048170 mRNA
CAGCACTTAGAAGAGACATTCAAATACATTTCATTTCCTGTTACCCAGATTGTTCGGAAA NM_001193434 RefSeq
chr10 + 113751453 113782433 PLEKHS1 79949 "pleckstrin homology domain containing, family S
member 1, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57300_PI430048170 0.437918925300603 0.907285692492605 7.33899764082949
7.505089695095 7.84152702848789 P P P 7.62131978948374 7.63492283202289
7.88150678533056 P P P LNCV6_57300_PI430048170 mRNA
TCATGATTGTGGTATTTGGAGATGAACCTCCAGTCTTCTCTCGTCCTATTTCGGCATCCT NM_006292 RefSeq
chr11 - 18480310 18526956 TSG101 7251 tumor susceptibility 101
GO:0005515|GO:0043130|GO:0000813|GO:0008285|GO:0005886|GO:0019058|GO:0046755|GO:0015031|GO:0001
558|GO:0042803|GO:0005737|GO:0016197|GO:0061024|GO:0016032|GO:0007050|GO:0031625|GO:0070062|GO:0
005770|GO:0005771|GO:0003714|GO:0019082|GO:0005730|GO:0019068|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130657_PI430048170 0.00467480628913098 0.601675383112886 5.35375701085734
5.29932538334315 5.57538857849431 P P P 5.98378746575293 6.12853911589441
6.31129384557133 P P P LNCV6_130657_PI430048170 mRNA
CTCTACCTGAGCATGTATTCAGGGGCTATAGGTACATTTAACTCTAACTAACTGAAAAAA NM_182969 RefSeq
chr11 - 74840909 74949187 XRRA1 143570 "X-ray radiation resistance associated 1, transcript
variant 1" GO:0003674|GO:0005737|GO:0010165|GO:0005634 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_128590_PI430048170 0.171922066180265 0.709976687123408 0.393514134191872
0.399221780982653 0.271831872425195 A A A 0.368211460962091 1.03740002860421
1.04611697965238 A A A LNCV6_128590_PI430048170 mRNA
TCTTTAAAATCTGCCATTGCAAATAGCTGTTTTAATAAACCAATTTTGCCTTGGCCCCTG NM_001145122 RefSeq
chr2 - 31173055 31217545 CAPN14 440854 calpain 14
GO:0005737|GO:0004198|GO:0005509|GO:0006508|GO:0005654 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_141487_PI430048170 0.00495510370255295 1.58438106768319 7.87550895899965
7.92952640442262 7.64672394012441 P P P 7.26678373024728 7.13114032126028
7.07035533542028 P P P LNCV6_141487_PI430048170 mRNA
CTCTGTACAAAGCCCTTGTCCCCATGAAATTGTATATAAATCATCCTTTTCTACCAAAAA NM_001204502 RefSeq
chr19 + 49474208 49486231 FLT3LG 2323 "fms-related tyrosine kinase 3 ligand, transcript variant 1"
GO:0030971|GO:0008284|GO:0030885|GO:0005102|GO:0032825|GO:0005125|GO:0005615|GO:0042803|GO:0031
233|GO:0007165|GO:0016020|GO:0045663|GO:0001934|GO:0030098|GO:0016021|GO:0035162 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_133181_PI430048170 0.0179659573778715 0.570762051020765 7.56364715917013
7.51063614241714 7.71579649683771 P P P 8.30059356141509 8.20811898690445
8.67332786375199 P P P LNCV6_133181_PI430048170 mRNA
CCTCCCTTTAGTTTGTTGGGGGATATAAATTATTCTCAGGAAGAATATAATGAACTGTAC NM_001199649 RefSeq
chr8 - 140658381 141001313 PTK2 5747 "protein tyrosine kinase 2, transcript variant 3"
GO:0005515|GO:0008360|GO:0030010|GO:0009790|GO:0046777|GO:0007172|GO:0043552|GO:0007173|GO:0007
411|GO:0030198|GO:0042127|GO:0045860|GO:0007179|GO:0032319|GO:0005856|GO:0042169|GO:0038083|GO:0
005938|GO:0022408|GO:0051964|GO:0030335|GO:0005815|GO:0019901|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_109789_PI430048170 0.256305651623232 1.13747288325529 5.20112915633124
5.10929981893693 5.45318221735133 P P P 4.92850258374293 5.24797035072614
5.03337557169947 P P P LNCV6_109789_PI430048170 mRNA
GGCACAGATCCTTCCGTTTAGAGAAGACTCACTAGATAGTGTTTTATTTTTAAAGAAGAT NM_001278513 RefSeq
chr13 + 113208192 113265078 CUL4A 8451 "cullin 4A, transcript variant 3"
GO:0005515|GO:0030097|GO:0051246|GO:0008284|GO:0008285|GO:0016567|GO:1900087|GO:2000001|GO:0080
008|GO:0097193|GO:0000082|GO:0006281|GO:2000819|GO:0016032|GO:0030853|GO:0043161|GO:0007050|GO:0
031464|GO:0035019|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127226_PI430048170 0.183043418911437 0.967958314751689 0.295644942556916
0.341806342969051 0.328988172789312 A A A 0.414245783514642 0.333262232532755
0.359083778997334 A A A LNCV6_127226_PI430048170 mRNA
TCCAGAAGCAGGCTTAGTTCTAGATTGAGTTCTAGAGTGCTAGGCTGATAAAATGTCCCA NM_001011718 RefSeq
chr20 + 31968001 31998453 XKR7 NA "XK, Kell blood group complex subunit-related family,
member 7" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137705_PI430048170 0.000152499429062276 0.114431637406198 1.38020034484256
1.46378382252627 1.74307651343481 A A A 4.48990435620574 4.4996073843002
4.95485956492956 P P P LNCV6_137705_PI430048170 mRNA
TACATCCATTTGAAATGGATGTCTATGGCTGTTTGAGATGAGTTCTCTACTCTTGTGCTT NM_003266RefSeq chr9
+ 117704174 117717491 TLR4 7099 "toll-like receptor 4, transcript variant 3"
GO:0005515|GO:0032755|GO:0032715|GO:0007249|GO:0032757|GO:0045348|GO:0002756|GO:0002755|GO:0010
572|GO:0032496|GO:0032497|GO:0032609|GO:0031663|GO:0032689|GO:0042742|GO:0032729|GO:0032728|GO:0
002322|GO:0038124|GO:0032760|GO:0038123|GO:0032727|GO:0034134|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131974_PI430048170 0.614596132903341 1.08362586365154 6.47404619359373 6.2290822307777
6.7155777007272 P P P 6.45162613610418 6.00998529496366 6.58912153061623 P P P
LNCV6_131974_PI430048170 mRNA
CGACTGGATGCTGCTAGTAACACATTGTTTGTATTGCTTTACCATTTTTAACTGTTAGATNM_020808RefSeq chr1 -
232397965 232515497 SIPA1L257568 signal-induced proliferation-associated 1 like 2
GO:0043547|GO:0051056|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134427_PI430048170 0.915226201921352 1.00326736027395 0.486055979801905
0.511567386653583 0.404769633988949 A A A 0.495327109072662 0.44354565388845
0.451000402513997 A A A LNCV6_134427_PI430048170 mRNA
CATATTGTACAATATCTTGTCCATTTGTTTGCAGCAGAGTAAAACCGGTTTCTAAGTTGT NM_001172173 RefSeq
chr2 + 165469646 165689407 CSRNP3 80034 "cysteine-serine-rich nuclear protein 3, transcript variant 1"
GO:0043565|GO:0043065|GO:0003700|GO:0045944|GO:0010923|GO:0006915|GO:0005634|GO:0001228|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98567_PI430048170 0.436541875450768 1.26595946934602 1.28826198551631 0.481843638661946
0.361354952159043 A A A 0.533789410864947 0.461399860166228 0.28985857873359 A A A
LNCV6_98567_PI430048170 mRNA

TTTGACATCACAGCCACCAGCAACCACTGGGTGGTCAATCCGCGGCACAACCTGGGCCTG NM_001719 RefSeq chr20 - 57168752 57266651 BMP7 655 bone morphogenetic protein 7
GO:0001656|GO:0005515|GO:0001657|GO:0034504|GO:0051216|GO:0005615|GO:0048596|GO:0009880|GO:0030198|GO:0007411|GO:0060548|GO:0072040|GO:0034116|GO:0032355|GO:0010664|GO:0010800|GO:0045746|GO:0030501|GO:0001707|GO:0030509|GO:0045786|GO:0005125|GO:0005160|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128699_PI430048170 0.0519852526461937 1.46126965021772 6.7789390931456 7.14619256293835 6.63293227924672 P P P 6.25928880986565 6.48145308947995 6.21043669500955 P P P LNCV6_128699_PI430048170 mRNA
GGAAGCAGGTCGCCTGTTTCTATAGTGACGGTAATAAACCAAGTCAATTTTCTATAGTGA NM_022834 RefSeq chr1 + 1435522 1442882 VWA1 64856 "von Willebrand factor A domain containing 1, transcript variant 1"
GO:0030198|GO:0005614|GO:0048266|GO:0005615|GO:0070062|GO:0042802|GO:0005604 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140223_PI430048170 0.0533081554585068 0.727338236084664 11.4695215028515 11.9301194529073 11.7674277593684 P P P 12.1252649849396 12.0745004189693 12.3653607803602 P P P LNCV6_140223_PI430048170 mRNA
CCCCCTTTTTTAAACAAGTGTTACTTGTGCCGGGAAAATTTTGCTGTCTTTGTAATTTTA NM_005318 RefSeq chr22 + 37805106 37807436 H1F0 3005 "H1 histone family, member 0"
GO:0005515|GO:0000790|GO:0005794|GO:0005719|GO:0006334|GO:0006915|GO:0005634|GO:0015629|GO:0006921|GO:0031490|GO:0006309|GO:0005654|GO:0000786 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142331_PI430048170 0.232819528328519 0.98030557789281 0.355273535054546 0.385128568748392 0.325669188180244 A A A 0.382814419497881 0.400469800709298 0.369320182628383 A A A LNCV6_142331_PI430048170 mRNA
AATATTTCTGTTCTAGGGCATCGTTTCAATCGCATCGTATCTCTACTTGGGCACAAAAAA NM_173683 RefSeq chr8 - 10896145 11201366 XKR6 286046 "XK, Kell blood group complex subunit-related family, member 6"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113165_PI430048170 0.401666895820438 0.838846117656971 3.42640628844494 2.69534853775554 3.07828171291334 P A P 3.62508903041857 2.99889723941001 3.36096461899326 P P P LNCV6_113165_PI430048170 mRNA
TGTGAACTCTTCCAGAAAACAGGATCTTTTAAGTTCGTGGTGCTCTCAATGCCGTCAGAA NM_021947 RefSeq chr17 + 2303942 2325264 SRR 63826 "serine racemase, transcript variant 1"
GO:0070178|GO:0005886|GO:0009069|GO:0042803|GO:0070179|GO:0008721|GO:0003941|GO:0005737|GO:0051289|GO:0030378|GO:0032496|GO:0043025|GO:0042866|GO:0000287|GO:0042493|GO:0007568|GO:0005509|GO:0045177|GO:0043278|GO:0030165|GO:0005524|GO:0018114|GO:0007420|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133879_PI430048170 0.0114411538705234 1.07288201628183 0.419887073830693 0.471143576119269 0.460813146234571 A A A 0.319172957546198 0.351331543595035 0.376795275293121 A A A LNCV6_133879_PI430048170 mRNA
GGAACTTCAAGGGCAGAAACATTACCTTTGAATAAAATGAACCTGAATGTTCACTCTAAT NM_001136002 RefSeq chr7 - 124030915 124033469 TMEM229A 730130 transmembrane protein 229A
GO:0006355|GO:0003700|GO:0042025|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131238_PI430048170 0.0924730680335333 0.884037030025647 0.38455917430843 0.347709701760114 0.328772445131113 A A A 0.489928048190808 0.449468229189729 0.647956690202503 A A A LNCV6_131238_PI430048170 mRNA
CATAGCTCCTAAGACCTGAAAACTCTTCTCAAGAAAATCTATGTGCAGATTATGAATTGT NM_001122965 RefSeq chr1 - 152153594 152159228 RPTN 126638 repetin GO:0005509|GO:0005578|GO:0001533 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141730_PI430048170 0.654650352218025 1.08482448911989 3.12795826217465 3.42722225219558 2.96317013953473 P P P 2.45188256444728 3.25999538615505

3.33798609600945 A P P LNCV6_141730_PI430048170 mRNA
TGCTGCACTTGTGAAGAATCCTGAGCTTTGATTCCTCTTCAGTCTACGCATTTCTCTCTT NM_018039 RefSeq chr11 +
94973680 94999512 KDM4D 55693 lysine (K)-specific demethylase 4D
GO:0032454|GO:0006355|GO:0006325|GO:0072562|GO:0051213|GO:0005654|GO:0046872|GO:0006351|GO:0055
114|GO:0033169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144788_PI430048170 0.0166201039062403 0.6231212669081349.31304437989624
8.94716901494601 9.31566988799881 P P P 10.0522924815082 9.64322845082613
9.92792572954049 P P P LNCV6_144788_PI430048170 mRNA
GAGGCATATGGGATTTATACAGATTCACTTGTAAATGTTGGATTGGGGATTTTTGTGTAA NM_006827 RefSeq chr14
- 75131467 75176646 TMED10 10972 transmembrane emp24-like trafficking protein 10 (yeast)
GO:0005515|GO:0005801|GO:0035459|GO:0005886|GO:0030137|GO:0005783|GO:0048208|GO:0051259|GO:0006
886|GO:0032403|GO:0048205|GO:0035964|GO:0045055|GO:0033116|GO:0007030|GO:0030140|GO:0070062|GO:0
030658|GO:0019905|GO:0042470|GO:0005793|GO:0005794|GO:0070765|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141361_PI430048170 0.3239130011812631.25743902049437 1.01301565498409
0.2716347740274860.420751683643045 A A A 0.2890167062674250.253326724536869
0.281882250593846 A A A LNCV6_141361_PI430048170 mRNA
GGCTGCAAAAACCTCATTGAGTGCAGAAATGCAAAATAGAACCGAAGCATGTATAAAAAA NM_031274 RefSeq
chrX - 105218928 105220693 TEX13A 56157 "testis expressed 13A, transcript variant 1" GO:0008270
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136018_PI430048170 0.8874940393428441.01035858475646 11.8634455156019
12.1022331626893 11.9925290543879 P P P 11.8142014485141 12.0912709634957
12.0042583945111 P P P LNCV6_136018_PI430048170 mRNA
TCCGCCTTTTCAAATTTTTGTATAACCCCGTGTTGTGTAAATACAGTTTTTGCTCCGGTG NM_001256270 RefSeq chr16
+ 29790967 29805385 KIF22 3835 "kinesin family member 22, transcript variant 3"
GO:0008017|GO:0005871|GO:0005874|GO:0005819|GO:0005634|GO:0003777|GO:0003677|GO:0005524|GO:0005
829|GO:0019886|GO:0007067|GO:0005737|GO:0006281|GO:0007596|GO:0007062|GO:0000776|GO:0005654|GO:0
007080|GO:0016887|GO:0000785|GO:0005925|GO:0007018 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_141920_PI430048170 0.0299415346831983 1.08690964900219 0.365548652403194
0.4512563100729460.395722192659218 A A A 0.2724509359986320.301834844241573
0.278692594804074 A A A LNCV6_141920_PI430048170 mRNA
CCAGCTCAAGTACATGCCAATGTTGTTTAAGAAACAGTTATGATCCTAAACTTTTTGGAT NM_022138 RefSeq chr6
+ 168441150 168667994 SMOC2 64094 "SPARC related modular calcium binding 2, transcript variant 1"
GO:0007165|GO:0030198|GO:0010811|GO:0005509|GO:0005614|GO:0008201|GO:0005604 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127125_PI430048170 0.1164509275097641.33720668914427 3.41243975352674
3.87840214551512 3.47050523868414 P P P 3.25459298489515 3.37361366882572
2.87603513285047 P P P LNCV6_127125_PI430048170 mRNA
GTACAGATGTTGAGATTTTGCACTGCTTATAAAATGCCTACCATGTTTTTTGCATAATGG NM_001191058 RefSeq
chr7 - 31751178 32299404 PDE1C 5137 "phosphodiesterase 1C, calmodulin-dependent 70kDa,
transcript variant 3"
GO:0007165|GO:0005516|GO:0048011|GO:0007173|GO:0008543|GO:0045087|GO:0004117|GO:0008152|GO:0007
202|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139503_PI430048170 0.1076563954404061.25060294621657 6.44319155173846
6.37654597108807 6.64975064551673 P P P 6.41186817852761 6.07361885733364
5.99566216897443 P P P LNCV6_139503_PI430048170 mRNA
GGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCCTCCCTTTTATTTTTT NM_014441 RefSeq chr19
+ 51124879 51130310 SIGLEC9 27180 "sialic acid binding Ig-like lectin 9, transcript variant 2"

GO:0005887|GO:0030246|GO:0007155|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144977_PI430048170 0.0894246848868522 0.947335733962571 0.400456866789558
0.360048263158076 0.349721358879088 A A A 0.489215791772305 0.459336485064102
0.394720095888599 A A A LNCV6_144977_PI430048170 mRNA
GATGAGAATAACATGTCCTCGGGAATTAGAGAACTTAGTTTGAGACTATGGATTTCTCAA NM_001080508 RefSeq
chr6 - 84732495 84764236 TBX18 9096 T-box 18
GO:0050679|GO:0000976|GO:0003700|GO:0022409|GO:0046982|GO:0001106|GO:0001756|GO:0007605|GO:0005
634|GO:0000122|GO:2000729|GO:0003163|GO:0060829|GO:0006351|GO:0042803|GO:0009948|GO:0016331|GO:0
072189|GO:0090103|GO:0051145 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75694_PI430048170 0.0966569681962627 1.22132392241054 6.97815056382892
6.95494013427613 7.03102293875546 P P P 6.52344619604451 6.67565686941499
6.87862178606316 P P P LNCV6_75694_PI430048170 mRNA
TCTGGGTGTGGCCAAAAACAATTTTCTTTATTCTGTCTATCAAATAGTACTTCTACCACT NM_032280 RefSeq chr5
+ 81301582 81313146 ZCCHC9 84240 "zinc finger, CCHC domain containing 9, transcript variant 1"
GO:0010923|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139008_PI430048170 0.0165198315436012 0.687348142938245 12.6661279309116
12.567220878714 12.346692950853 P P P 13.2393296147899 13.0611327209578
12.9005948308093 P P P LNCV6_139008_PI430048170 mRNA
TGCCCCTCCCCTGAATGGCCCCCAATGCTGCTGTTTTTCAATAAAACCAGAGTTGAAGGC NM_178557 RefSeq chr4
+ 2059511 2069089 NAT8L 339983 "N-acetyltransferase 8-like (GCN5-related, putative)"
GO:0005739|GO:0005737|GO:0031966|GO:0017188|GO:0051586|GO:0030867|GO:0008152|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141817_PI430048170 0.0216635775241648 0.762384347798278 8.82461485988106
8.92557199441078 8.92018108160025 P P P 9.13037274172543 9.3718785911854
9.33309398786775 P P P LNCV6_141817_PI430048170 mRNA
GCACTTTAGAAAAAGCCTGATGTGGGTCTTACATAAATGAATGTCTGTATAAGAAAATGG NM_015697 RefSeq chr4
- 83263823 83284914 COQ2 27235 coenzyme Q2 4-hydroxybenzoate polyprenyltransferase
GO:0006744|GO:0047293|GO:0005743|GO:0044281|GO:0016021|GO:0008299|GO:0006071|GO:0002083 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127565_PI430048170 0.458815457556936 1.19970926501109 8.45003291081278
9.06120740338282 8.25462167716571 P P P 8.39471141123035 8.27542157957086
8.43016419292765 P P P LNCV6_127565_PI430048170 mRNA
CCCACAGGAGCATGTACATATGGAAAAACAGAACAACAGTGGACTTTTTATGATATAATA NM_004193 RefSeq chr10
+ 102245497 102382899 GBF1 8729 "golgi brefeldin A resistant guanine nucleotide exchange factor 1,
transcript variant 1"
GO:0005515|GO:0005802|GO:0005801|GO:0005794|GO:0006996|GO:0005795|GO:0006890|GO:0006892|GO:0048
205|GO:0043547|GO:0005739|GO:0005086|GO:0016020|GO:0000139|GO:0061024|GO:0032012|GO:0016032|GO:0
005788|GO:0016192|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130553_PI430048170 1.67999151123133e-05 0.426412807107332 9.00153106455267
8.93095796237254 8.88079427829836 P P P 10.1210308176094 10.2386102211536
10.1424930223468 P P P LNCV6_130553_PI430048170 mRNA
TTGATTAGCAGCGGAACAAGGAGTCAGACATTTTAAGATGGTGGCAGTAGAGGCTATGGA NM_001291549 RefSeq
chr6 + 36676536 36687339 CDKN1A 1026 "cyclin-dependent kinase inhibitor 1A (p21, Cip1),
transcript variant 3"
GO:0005515|GO:0030308|GO:0046685|GO:0019912|GO:0032403|GO:0060574|GO:0043231|GO:0034605|GO:0043
068|GO:0007173|GO:0031668|GO:0045860|GO:0033158|GO:0031625|GO:0006977|GO:0051412|GO:0030332|GO:0
010243|GO:0009636|GO:2000134|GO:0071479|GO:0042771|GO:0008543|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136741_PI430048170 0.0743708496159776 1.06768563258541 0.566054769034885

0.5035916235149910.580553305775731A A A 0.3953973781990940.474576563428956
0.49598418427379 A A A LNCV6_136741_PI430048170 mRNA
ATGAAGCTCTGTTAGAAACACCGTGTGCTTTGGGAAGAGACAATAAAGATGTCTTTATTT NM_052955RefSeq chr15
- 43276280 43302255 TGM7 116179 transglutaminase 7 GO:0018149|GO:0003810|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116_PI430053867 0.0863484299948325 1.20479198700159 6.53878826496085 6.3029221196061
6.53552000481227 P P P 6.05916002204038 6.14695235911126 6.36036650075514 P P P
LNCV6_116_PI430053867 mRNA
GGTTGTTGGGAAGAGGGTGTAAGATAGTGTTTAATTTGACTTTGATAAGTTAAATGTGCA NM_030895RefSeq chr8
+ 143291388 143299950 ZNF696 79943 zinc finger protein 696
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128237_PI430048170 0.0862204217512270.9308578124167310.349826379374868
0.3318289608379140.303392880136266A A A 0.4923317779293560.430613210160502
0.369990886267939A A A LNCV6_128237_PI430048170 mRNA
CGGCATAAAAAGTAACCCTCAAGTGAAGTGTCTCTATACTGTTTTATAGAGTACTTTAAC NM_153618RefSeq chr15
+ 47718488 47774223 SEMA6D 80031 "sema domain, transmembrane domain (TM), and cytoplasmic
domain, (semaphorin) 6D, transcript variant 4"
GO:0005737|GO:0005886|GO:0007411|GO:0021591|GO:0030215|GO:0004872|GO:0016021|GO:0014912|GO:0014
911 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142908_PI430048170 0.16402530638098 2.23928363729712 1.35563295314619
2.97429609464609 1.73735463655873 A P A 1.19417721773871 1.19417721773871
0.64615205584548 A A A LNCV6_142908_PI430048170 mRNA
ACTGAGGAACTCACAATTCCAAACATACAAGAGGCTCCCTCTTAACACGGCACTTAGACA NM_015868RefSeq
chr19_KI270882v1_alt - 134873 192519 KIR2DL3 NA "killer cell immunoglobulin-like receptor, two
domains, long cytoplasmic tail, 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139732_PI430048170 0.0778607522407012 1.12257253729478 12.0781345144863
11.9474722665253 11.9175711138992 P P P 11.8083681560422 11.8212845649708
11.8181697868239 P P P LNCV6_139732_PI430048170 mRNA
TCTGGTTCGACAAGTTCAAATATGACGACGCAGAAAGGAGATTCTACGAGCAGATGAACG NM_032378RefSeq chr8
- 143579696 143597675 EEF1D 1936 "eukaryotic translation elongation factor 1 delta (guanine
nucleotide exchange protein), transcript variant 1"
GO:0005515|GO:0010467|GO:0005853|GO:0006355|GO:0005730|GO:0005634|GO:0003746|GO:0003677|GO:0006
412|GO:0006351|GO:0005829|GO:0006414|GO:0007165|GO:0005737|GO:0004871|GO:0043123|GO:0044267|GO:0
008135 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145482_PI430048170 0.0559111859438659 2.36025401194857 5.24426145128228
5.25685511013745 4.60669736202117 P P P 4.4914547506431 3.30748686329704
3.34873686348037 P P P LNCV6_145482_PI430048170 mRNA
AAATTGAGGGCTTCTTTGATGGTGAGTGGAGAAAAGATAGAGGAGAAGGTTGCCCCTGAA NM_015513RefSeq
chr3 + 9933839 9945413 CRELD1 78987 "cysteine-rich with EGF-like domains 1, transcript variant 2"
GO:0003279|GO:0003197|GO:0005509|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77222_PI430048170 0.1403620002177891.15902914693625 9.92128965780522 9.94810042514997
9.98522704811448 P P P 9.6168678248367 9.91864790990086 9.66237603921318 P P P
LNCV6_77222_PI430048170 mRNA
TCAAATCCTGGATTCACTGCTGGAAGTACCTGAGTGTGCAGGGCCAGCTCTTCCGAGGCT NM_001271641 RefSeq
chr6 - 36968134 36986551 MTCH1 23787 "mitochondrial carrier 1, transcript variant 2"
GO:0005739|GO:0005622|GO:0005515|GO:0043065|GO:0006919|GO:0045161|GO:0006810|GO:0005743|GO:0016
021|GO:0009966 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144580_PI430048170 0.42384269100973 1.06223582881262 4.98411209450207

4.95656093429692 4.73494585066377 P P P 4.88167571191257 4.8262567834219
4.71405140487509 P P P LNCV6_144580_PI430048170 mRNA
GTCATTGAATTATGTCACAATTGGAGGTGAAACCTGTGGCTGCCTTGCCCATGAAATCTT NM_000197 RefSeq chr9
- 96235306 96302152 HSD17B3 3293 hydroxysteroid (17-beta) dehydrogenase 3
GO:0061370|GO:0030539|GO:0006702|GO:0005789|GO:0047045|GO:0044281|GO:0008202|GO:0055114|GO:0043
231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135757_PI430048170 0.2195580263624912.79282151347592 1.11459512821282
2.99488440178466 3.35380067553028 A P P 1.49299167069496 1.2199934931995
1.10170889866788 A A A LNCV6_135757_PI430048170 mRNA
GTGTTTGGTCATGTGGAAAACTCAATGTATAATTTAGACGTCTGTCAAAAATCCGACAAA NM_004311 RefSeq chr10
- 102673726 102714433 ARL3 403 ADP-ribosylation factor-like 3
GO:0005515|GO:0008017|GO:0005881|GO:0042461|GO:0007264|GO:0003924|GO:0005634|GO:0015031|GO:0046
872|GO:0007224|GO:0000910|GO:0042073|GO:0005876|GO:0070062|GO:0005813|GO:0005794|GO:0006996|GO:0
001822|GO:0006892|GO:0030496|GO:0072372|GO:0005525|GO:0006184|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126939_PI430048170 0.0441345275262396 1.38142949532667 11.3206774990806
11.6013097764771 11.6982262209032 P P P 10.999633057017 10.9226189645456
11.2978054800105 P P P LNCV6_126939_PI430048170 mRNA
ACTGAAAGAAGGATTCTGCATTTCTATTCCCCTCAGCCTACCCACTGAAGTCTTTGGGTA NM_017840 RefSeq chr11
- 59806134 59810872 MRPL1654948 mitochondrial ribosomal protein L16
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0019843|GO:0005
762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63228_PI430048170 0.2784800808899530.7012124952004283.97231860750529 3.18322465650013
3.56794678942224 P P P 4.22228666276118 4.49436984538794 3.46541821248814 P P P
LNCV6_63228_PI430048170 mRNA
AAAGCCCAAAGCTGGCCCTTTTGGGAAATAGCAGTAAATCATTGATATGTGAAGGTTCCC NM_001085430 RefSeq
chr17 - 56791912 56833895 C17orf67 339210 chromosome 17 open reading frame 67 GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130020_PI430048170 0.6149207313717571.04846820840481 9.87272099447909
10.0887220198353 10.1708713969644 P P P 9.96814582192111 9.82649459706988
10.1327092747008 P P P LNCV6_130020_PI430048170 mRNA
GATTGCTTTTGACCTTTTAGAAGATTGGTCTCCAGTAAAGGTGGACATTTTTGAGATTTT NM_001287742 RefSeq
chr8 + 11795572 11839309 FDFT1 2222 "farnesyl-diphosphate farnesyltransferase 1, transcript
variant 1"
GO:0006695|GO:0006694|GO:0051996|GO:0005783|GO:0044281|GO:0008299|GO:0045338|GO:0005789|GO:0016
491|GO:0016021|GO:0044255|GO:0004310|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141975_PI430048170 0.10552817315519 0.8959387894422711.7021837263568
11.5821736647636 11.5610204186673 P P P 11.7533265213345 11.8834276070807
11.6809188513604 P P P LNCV6_141975_PI430048170 mRNA
TCCAGCATTGAGTGTGTACATGTGTGTGTGACACATAAATATACTCATAAGGACACCTCC NM_032790 RefSeq chr12
+ 121626549 121642040 ORAI1 84876 ORAI calcium release-activated calcium modulator 1
GO:0005515|GO:0005516|GO:0051928|GO:0042802|GO:0043234|GO:0002115|GO:0016020|GO:0005887|GO:0007
596|GO:0051924|GO:0070588|GO:0015279|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145272_PI430048170 0.6116604064108490.9578963897000430.421851461472726
0.2808641288077140.32668069014317 A A A 0.2846981697521580.581533470823217
0.33514758273849 A A A LNCV6_145272_PI430048170 mRNA
TTCAACTTTCATGGAAATGAGACCTCCATGAATGCTCTGAAAGACCTGCTGCGTCACACA NM_001291381 RefSeq
chr1_KI270766v1_alt + 247006 252375 LOC645382 NA PRAME family member 10-like NA . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_143387_PI430048170 0.0354624567182673 0.6874884454822961 0.027932643804
9.5743960774626 9.81617685335313 P P P 10.1367737305051 10.3980376673025
10.5153800251472 P P P LNCV6_143387_PI430048170 mRNA
ACACACAGACCCCTCCCCAATCTGGACATTGAATAAATATTCATTTTCCTTTGCATTGTT NM_000202 RefSeq chrX
- 149478763 149505354 IDS 3423 "iduronate 2-sulfatase, transcript variant 1"
GO:0030207|GO:0005975|GO:0004423|GO:0009405|GO:0006027|GO:0044281|GO:0030204|GO:0030203|GO:0046
872|GO:0043202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139877_PI430048170 0.398350317831635 0.839805258759984 6.00333016917183
5.70670620511473 5.29730967944524 P P P 6.13131149649228 6.08563618106136
5.56634878986389 P P P LNCV6_139877_PI430048170 mRNA
TGCCTTTGCCCTCCCTTTACACTGTCTGCCGGCGTCAACAAGCGACACAGACCGAAAAAA NM_001013653 RefSeq
chr9 - 137168758 137170039 LRRC26 NA leucine rich repeat containing 26 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_138224_PI430048170 0.193376098126624 1.26059787090013 3.65365239816697
4.23132551827669 3.86357707083203 P P P 3.67197681097303 3.39831860352253
3.71596253919965 P P P LNCV6_138224_PI430048170 mRNA
CCATACAAATGCACAACATAAAGTGAACATATTCCTAGGCCCTTTCTGCCTGTGTCAGGG NM_139320 RefSeq chr15
- 30361239 30393661 CHRFAM7A NA "CHRNA7 (cholinergic receptor, nicotinic, alpha 7, exons 5-10) and
FAM7A (family with sequence similarity 7A, exons A-E) fusion, transcript variant 1" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_131681_PI430048170 0.334921448120026 1.21520527793751 4.06119108194858
4.75958587892955 4.45476636464713 P P P 4.21104880569207 4.2029256969287
4.09899566391744 P P P LNCV6_131681_PI430048170 mRNA
AGAAAGAAGCAGTTCTCACAATGTTGCTAGTTTTTTGCTTCTCTTTCCCCCACCCTACTC NM_003155 RefSeq chr8
- 23841920 23854807 STC1 6781 stanniocalcin 1
GO:0030336|GO:0007566|GO:0006874|GO:0071456|GO:0005634|GO:0033280|GO:0090280|GO:0035988|GO:0005
615|GO:0071385|GO:0060348|GO:0046697|GO:0010596|GO:0044070|GO:0005737|GO:0016324|GO:0001503|GO:0
005179|GO:0001886|GO:0003421|GO:0051926|GO:0071320|GO:0086004 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140055_PI430048170 0.0629824912837345 1.07005260660468 13.6418730001389
13.6755674997293 13.6798687610939 P P P 13.5694436616707 13.515839457111
13.6174892754458 P P P LNCV6_140055_PI430048170 mRNA
GTACTTGTCACATTGGTGTTGGACACATTTGCGCCAAAAGTATGGTAATTCTATTATTAA NM_012203 RefSeq chr9
+ 37422709 37436989 GRHPR 9380 glyoxylate reductase/hydroxypyruvate reductase
GO:0031406|GO:0007588|GO:0005782|GO:0043648|GO:0008465|GO:0044281|GO:0070402|GO:0051259|GO:0016
618|GO:0042803|GO:0005829|GO:0034641|GO:0005737|GO:0051287|GO:0008152|GO:0046487|GO:0030267|GO:0
070062|GO:0055114. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143315_PI430048170 0.0303942084136265 1.16259232024152 8.44518601344696
8.52962699978442 8.4142988447817 P P P 8.14707438948565 8.2651525911511
8.32186031668449 P P P LNCV6_143315_PI430048170 mRNA
CGGATCGTTTATGGTTATTTACAATGCAGTTACTCTTGAAGATTATTGTTAGAGGTAGAC NM_001301726 RefSeq
chr20 - 62851493 62861763 TCFL5 10732 "transcription factor-like 5 (basic helix-loop-helix), transcript
variant 2"
GO:0006355|GO:0003700|GO:0006366|GO:0042127|GO:0046983|GO:0045595|GO:0007275|GO:0005634|GO:0007
283|GO:0001673|GO:0003677|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127054_PI430048170 0.505412021677391 0.957866454316506 0.387051099806522
0.378838966911959 0.270360035013927 A A A 0.544679661362549 0.335281962387933
0.335222926845005 A A A LNCV6_127054_PI430048170 mRNA
AGATCCTCTGGTGATGAGTATGTTGCACTTTCTTTTCTCAATAAATTGCACTGAACTTCA NM_015848 RefSeq chr12

- 52768154 52777345 KRT76 51350 "keratin 76, type II"
GO:0005882|GO:0005198|GO:0007010|GO:0005634|GO:0045095|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134921_PI430048170 0.8174115050347041.3915531067689 2.29277419223403
0.4135269283743960.244688091467595A A A 0.8844052883183871.07008026035037
0.469137525170033A A A LNCV6_134921_PI430048170 mRNA
CCCTATCCCTTGTCGATGACAGTCATCCTAATGATAATAAAACCTGCATCCAGATAATCA NM_007117RefSeq chr3
+ 129974392 129977938 TRH7200 thyrotropin-releasing hormone
GO:0051412|GO:0001666|GO:0005886|GO:0045471|GO:0014050|GO:0009409|GO:2000252|GO:0007267|GO:0005
576|GO:0005634|GO:0014054|GO:0009749|GO:0007165|GO:0001692|GO:0009755|GO:0007628|GO:0042755|GO:0
032024|GO:0008437|GO:0030141|GO:0005184 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145192_PI430048170 0.5570070452631891.08707477378458 5.21891746322686
5.16570161430031 5.63138875672922 P P P 5.19329943968511 5.12218103933733
5.37375207746298 P P P LNCV6_145192_PI430048170 mRNA
GGTAGCGCTATTGACCTTAGCTGATGAGGATGACCGGGAAATTTATGATATTATTTCCAT NM_006568RefSeq chr14
+ 54509868 54538616 CGRRF1 10668 cell growth regulator with ring finger domain 1
GO:0008285|GO:0006950|GO:0008270|GO:0007050|GO:0005654|GO:0043231 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145230_PI430048170 0.45180467237281 1.04193862878613 0.315797251693785
0.3222269903353350.501550734737699A A A 0.3285464985682770.292338646225631
0.348134687411873A A A LNCV6_145230_PI430048170 mRNA
TCAGTAGTTGCCATCTTGGCCATGCAAGAAAAGAAAAGAAGGCATTTACTCTATGTCGGG NM_052999RefSeq chr16
+ 66566446 66579135 CMTM1 113540 "CKLF-like MARVEL transmembrane domain containing 1, transcript
variant 17" GO:0006935|GO:0016021|GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133993_PI430048170 0.8909590434918421.09329159713423 2.11990465105583
2.94710252610106 3.47235547502749 A A P 3.14818637681105 2.29446072645256
2.88956105558813 P A P LNCV6_133993_PI430048170 mRNA
TGGTAGTGTAGAAGTGAAAAAGGTAATGGCATGCCCCAGGTGTATTTTGACAACGGTGGA NM_017898RefSeq chr1
+ 220748333 220784254 MARCH2 NA mitochondrial amidoxime reducing component 2 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_69795_PI430048170 0.3082623604806660.8269241428859980.4731451093738320.553540890381213
0.485053739215504A A A 1.08495966004283 0.4434421288921420.735489683799067A A A
LNCV6_69795_PI430048170 mRNA
AAGACGAGGAGGAAGATGAAGGCAACTGAATCCCAAGAGGCACCTGCAGCCAGGAAGGAA NM_004258RefSeq
chr1 + 117001749 117036551 CD101 9398 "CD101 molecule, transcript variant 1"
GO:0005886|GO:0016812|GO:0008152|GO:0002763|GO:0016021|GO:0007166|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139309_PI430048170 0.2404433135039462.00593089962486 0.450889231273823
2.19382650695591 1.23653711035928 A A A 0.3915716085972940.480559491438804
0.515828744816198A A A LNCV6_139309_PI430048170 mRNA
AAACCTGAGCTTGAAGTCCTTTTCCCCAAAAAGAGGGAAGAGTCACAAAAAGTCCAGACC NM_080869RefSeq chr20
- 45123425 45124465 WFDC12 128488 WAP four-disulfide core domain 12
GO:0010951|GO:0004867|GO:0005576|GO:0042742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132521_PI430048170 0.00366327939507759 0.1590986309130932.15734283887794
2.40506215670531 2.45209714359566 A A A 4.48641694471172 5.15015738259997
5.24027266359749 P P P LNCV6_132521_PI430048170 mRNA
ATCAAGCATTGGGTATTAAAAGAGAATCCTTTCAACCCTTCATCTTCGTATGCTTATACA NM_199072RefSeq chr7
+ 114922153 115019916 MDFIC 29969 "MyoD family inhibitor domain containing, transcript variant 1"

GO:0005515|GO:0005794|GO:0030111|GO:0030332|GO:0005730|GO:0005634|GO:0007257|GO:0030957|GO:0006351|GO:0050434|GO:0005737|GO:0042308|GO:0016032|GO:0005654|GO:0045893|GO:0045892|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131532_PI430048170 0.5175068605324151.12661167126677 0.349045146475614 0.9084130215283740.338872600421923 A A A 0.4286367862739220.347520850447254 0.37952060199226 A A A LNCV6_131532_PI430048170 mRNA
GGGAGCTTCTACCTGGAAAAGAAAAGAAATGAATAGACTATCTAGAACTTGAGAAGATTT NM_004963 RefSeq chr12 - 14612633 14696585 GUCY2C 2984 guanylate cyclase 2C
GO:0005515|GO:0005886|GO:0009636|GO:0004383|GO:0005525|GO:0005524|GO:0035556|GO:0004672|GO:0042127|GO:0006182|GO:0015643|GO:0005789|GO:0006468|GO:0016021|GO:0007168 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135319_PI430048170 0.0531714373679455 0.6004837648653888.89802313549068 8.5947865158863 8.34829830574289 P P P 8.94638298945011 9.64434304724952 9.42511940563301 P P P LNCV6_135319_PI430048170 mRNA
TGGATTAGTTTGCAGCAACTCAATCCCAAAGGAACCAAAGGCTCTTTTCAGAGCCACCTA NM_003509 RefSeq chr6 + 27808198 27808667 HIST1H2AI NA "histone cluster 1, H2ai" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89571_PI430048170 0.0529919150471491.09671208685158 7.68203773505959 7.56504519474136 7.57785741852223 P P P 7.42111850222614 7.47693922531035 7.52821745159981 P P P LNCV6_89571_PI430048170 mRNA
TTGCACTGCCATTTTGAGGGGAGAAGAATCAATTAGTGGCAAACATTTAAAAATGCAATT NM_001199469 RefSeq chr3 - 129127415 129161230 ISY1 57461 "ISY1 splicing factor homolog (S. cerevisiae), transcript variant 1" GO:0005515|GO:0000398|GO:0071013 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135542_PI430048170 0.000494738020433972 2.79616781933716 7.07486575114874 6.91244911738304 7.17420382161507 P P P 5.77244505122286 5.47850511798975 5.44962591478984 P P P LNCV6_135542_PI430048170 mRNA
AAGTAGCAAGAAGCTACATCCCTCAAACTTCGGCAATGAAAATAAAGTTTGAGAAGCTGA NM_032461 RefSeq chrX + 141002590 141003706 SPANXB1 728695 "SPANX family, member B1"
GO:0003674|GO:0005737|GO:0007286|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129306_PI430048170 0.1709005380854370.9618186073225940.256742980494871 0.28281422449576 0.340998590993242 A A A 0.3947303379455230.322280877250093 0.332254562617808 A A A LNCV6_129306_PI430048170 mRNA
GGCCAAGGTAACACTCATCGTATTCACGGAGTGAAATACTATATGATGATAGTTATTATA NM_005986 RefSeq chr13 + 112067598 112071706 SOX1 6656 SRY (sex determining region Y)-box 1
GO:0005515|GO:0006355|GO:0003700|GO:0021521|GO:0002089|GO:0006325|GO:0005634|GO:0001046|GO:0021884|GO:0001764|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93426_PI430048170 0.1058502158540290.91581329312146 9.64463407354964 9.65863684842713 9.55115443340385 P P P 9.6863235352301 9.83937324756164 9.70687038525306 P P P LNCV6_93426_PI430048170 mRNA
ACACCCCAGAAGTGCTCTGAACCCCAATCCTCAAAATGAAGATACTGACACCACCTTTGC NM_001012631 RefSeq chr16 + 3065311 3069667 IL32 9235 "interleukin 32, transcript variant 1"
GO:0005515|GO:0006955|GO:0016020|GO:0006952|GO:0007155|GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130663_PI430048170 0.0173771523401477 0.5981738185466195.33323473736045 5.65984860756418 5.21186331681024 P P P 6.06712737780947 6.26861214308671 6.12367481739717 P P P LNCV6_130663_PI430048170 mRNA
TTCAGTGTCCCATGTTCCGACTGCACCTTCTTTACAATAAAGACTGTAACTGAGCTGACT NM_004209 RefSeq chr16 + 1989944 1994275 SYNGR39143 synaptogyrin 3
GO:0047485|GO:0031594|GO:0030054|GO:0021762|GO:0032411|GO:0030672|GO:0016021|GO:0042169|GO:0008

021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127724_PI430048170 0.0107500702573671 0.7758432207862196.53015269701468
6.41429719554477 6.48434031781276 P P P 6.73354370450833 6.85284432432478
6.93609220264319 P P P LNCV6_127724_PI430048170 mRNA
TTCCAGCAGTTTACACAGGACTGTTTTATAAACTCTATCATAAGGAACTGCCAGAGAATT NM_007083RefSeq chr4
- 122892643 122922606 NUDT6 11162 "nudix (nucleoside diphosphate linked moiety X)-type motif 6,
transcript variant 1" GO:0005739|GO:0008150|GO:0016787|GO:0008152|GO:0005634|GO:0005575|GO:0008083
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117813_PI430048170 0.00207153914430911 0.2962272589113784.99319791297191
4.41112305356315 4.92032482507195 P P P 6.31227565551192 6.44575100515084
6.84453291307257 P P P LNCV6_117813_PI430048170 mRNA
GCATGTCACTGTACATCATACCTTGCAATAAATATTCTGTTAAATTGTGCTGGTGCAATT NM_002486RefSeq chr9
+ 97633422 97673747 NCBP1 4686 "nuclear cap binding protein subunit 1, 80kDa"
GO:0005515|GO:0000339|GO:0008380|GO:0006369|GO:0010467|GO:0006368|GO:0006366|GO:0003723|GO:0031
124|GO:0005634|GO:0031047|GO:0005829|GO:0005739|GO:0005737|GO:0006406|GO:0000184|GO:0016032|GO:0
006379|GO:0008334|GO:0045292|GO:0006370|GO:0034660|GO:0000387|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_101076_PI430048170 0.0408341470574208 0.9608960352384410.418281356223074
0.3953502127881670.366106102744811A A A 0.4335756270354470.468663942335833
0.450401524557636A A A LNCV6_101076_PI430048170 mRNA
CCTGGATGTGATGTTGAAATTTTGTGTTGCTTTAACCGCCTTTACTTTCTGAGCTAGGGG NM_001291813 RefSeq
chr14 - 100291110 100306547 SLC25A29 123096 "solute carrier family 25 (mitochondrial
carnitine/acylcarnitine carrier), member 29, transcript variant 2" GO:0005743|GO:0016021|GO:0015227 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133449_PI430048170 0.4541678407422650.7002763242337490.383518970569229
0.26071647821278 0.281231488097349A A A 1.52980337593664 0.291320452428961
0.260457476196048A A A LNCV6_133449_PI430048170 mRNA
GCTTGGATGAGCAGGGGATGAGAGCTGCAGGGAAATAAATGAGATATTCGTCCTTATTTC NM_005185RefSeq chr10
+ 5524888 5526268 CALML3 810 calmodulin-like 3 GO:0005515|GO:0005509|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118924_PI430048170 0.0454597677857422 1.41867086660693 5.04056729095206
5.42931584572449 5.44874763463162 P P P 4.59937344113421 4.84987094194358
4.96724055600272 P P P LNCV6_118924_PI430048170 mRNA
CATTTCCTAATCAAGAAGTTGGCGTGCAGCTGGGAGAGCTAGACTAAGTTGGTCATGATG NM_002727RefSeq chr10
+ 69088071 69104811 SRGN 5552 "serglycin, transcript variant 1"
GO:0005515|GO:0005794|GO:0005518|GO:0030168|GO:0005576|GO:0050710|GO:0030502|GO:0031214|GO:0005
615|GO:0042629|GO:0042588|GO:0000139|GO:0007596|GO:0016485|GO:0002576|GO:0033373|GO:0031093|GO:0
033382|GO:0033364|GO:0008626|GO:0033371 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134707_PI430048170 0.3699867122046320.9324583893246318.6569876488826
8.85446953564811 8.63461643956439 P P P 8.95544673425337 8.72000438780274
8.77287729944797 P P P LNCV6_134707_PI430048170 mRNA
AGCGGTGTGATTCTACTGTGCTCAGCCTAGTCAATTTCGCATTAAACTGATTATCAGCTG NM_021075RefSeq chr21
+ 42893267 42909663 NDUFV3 4731 "NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa,
transcript variant 1"
GO:0022904|GO:0005739|GO:0005747|GO:0006120|GO:0005743|GO:0005654|GO:0044281|GO:0008137|GO:0044
237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132461_PI430048170 0.1838487931084814.62946769275398 0.387486988136948
3.08476077542546 3.07205039032025 A P P 0.4164402888332770.359181428033242
0.39442231287521 A A A LNCV6_132461_PI430048170 mRNA

CATCAGCTGCCATGCACATAACAAAGAGACAATGCATTCCTTCTTATTTTTCCTTTTTAA NM_020777 RefSeq chr4
+ 7192646 7742837 SORCS2 57537 sortilin-related VPS10 domain containing receptor 2
GO:0016020|GO:0007218|GO:0016021|GO:0008188 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133088_PI430048170 0.0464554970110340 .47486219005724 3.35900581342902
2.65789757910911 3.64494676269964 P A P 3.85512478419796 4.44090946563759
4.64674244182306 P P P LNCV6_133088_PI430048170 mRNA
CATCCTTTGAGTGTGTGAGTATAGTATCAGAGGCTTAATTTTGTATTTATGGAGCTATTC NM_022840 RefSeq chr18
- 2537524 2571503 METTL4 64863 methyltransferase like 4
GO:0006139|GO:0008168|GO:0003676|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137453_PI430048170 0.0742057919601176 1.77452660403328 4.37182704886301
4.33132400117833 3.9679904205628 P P P 3.90701257833211 3.17011419581929
2.96858788147363 P P P LNCV6_137453_PI430048170 mRNA
TCAAACCTACTAATCCAGCGACAATTTGAATCGGTTTTGTAGGTAGAGGAATAAAATGAA NM_021822 RefSeq chr22
+ 39077004 39087743 APOBEC3G 60489 "apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G"
GO:0030895|GO:0005515|GO:0009972|GO:0047844|GO:0003723|GO:0016553|GO:0045869|GO:0048525|GO:0010529|GO:0042803|GO:0005829|GO:0051607|GO:0005737|GO:0000932|GO:0045087|GO:0002230|GO:0030529|GO:0004126|GO:0016032|GO:0008270|GO:0070383|GO:0045071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140779_PI430048170 0.602062249761613 1.04752071501565 5.94050435800924
5.75376340974264 5.9205363096957 P P P 5.88001842250305 5.93680151368105
5.57927625820604 P P P LNCV6_140779_PI430048170 mRNA
AGATAGCTTGCTCTCTGAGTGTGTCTCATTGATTCATTCAGCCTGTGTGTCCTAAAGCCT NM_133444 RefSeq chr19
+ 42220339 42228201 ZNF526 116115 zinc finger protein 526
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133734_PI430048170 0.0639535361968844 0.6185059751297 1.816560933798
1.78059587975419 1.72132912639953 A A A 2.62666216283669 2.62833076643209
2.07792868588851 A P A LNCV6_133734_PI430048170 mRNA
TAAGATGACTAAGTCGTTTATGTTGCTCCCACCTCACACAAAGTTAAAACTATTTGTTAC NM_014265 RefSeq chr8
+ 24294039 24359018 ADAM28 10863 "ADAM metallopeptidase domain 28, transcript variant 1"
GO:0005886|GO:0006508|GO:0008270|GO:0005576|GO:0016021|GO:0007283|GO:0004222|GO:0008237 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107014_PI430048170 0.8407103700762750 .98452726687131911.0983125431691
11.2505621377223 11.461488314888 P P P 11.3647334644341 11.1622441353014
11.3647334644341 P P P LNCV6_107014_PI430048170 mRNA
CTATGGCTATCCGAATTCTCTGAAAAAATAATAAAAGTCCCCTCTATTATATGAGCCTGT NM_001551 RefSeq chrX
+ 70133467 70166323 IGBP1 3476 immunoglobulin (CD79A) binding protein 1
GO:0005515|GO:0035306|GO:2001234|GO:0008601|GO:0005874|GO:0019904|GO:0035308|GO:0031434|GO:0000122|GO:0032873|GO:0007165|GO:0042113|GO:0060632|GO:0005737|GO:0045944|GO:0034612|GO:0043154|GO:0070555 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144404_PI430048170 0.866246774922286 1.06299295686677 3.40980107846503
3.20655727230343 4.21528085593541 P P P 2.96138563750925 3.68612715234943
3.95385607347192 P P P LNCV6_144404_PI430048170 mRNA
GAGGGTGTGCTTTACTTTTTGATAAAGAGAAAGATGTTTACTCATAAACCCTTCAAAAGG NM_017791 RefSeq chr14
+ 75578596 75648169 FLVCR2 55640 "feline leukemia virus subgroup C cellular receptor family, member 2, transcript variant 1" GO:0015886|GO:0015232|GO:0005886|GO:0016021|GO:0055085|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140114_PI430048170 0.0100379152394988 0.3378858962636543 .70067589388124

3.60750916725408 3.60689445043484 P P P 4.89827777630391 5.16674242161201
5.48774465473072 P P P LNCV6_140114_PI430048170 mRNA
CTAGTGAGTTGATGGAGCATTTGCTTCATCATCCTCATCAAGAGAATCATATAAATTAAG NM_018122RefSeq chr1
+ 173824658 173858544 DARS2 55157 "aspartyl-tRNA synthetase 2, mitochondrial"
GO:0005515|GO:0010467|GO:0000049|GO:0050560|GO:0005634|GO:0070145|GO:0004815|GO:0005524|GO:0042
803|GO:0006418|GO:0005739|GO:0005759|GO:0005654|GO:0043039 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144535_PI430048170 0.3451836727487660.80088619674792 2.5342429242426 2.2771040875503
3.29829028853541 A A P 2.84180969142525 3.19994232927293 3.2031765107185 P P P
LNCV6_144535_PI430048170 mRNA
GAGATGCGTTGAGGATGGGATTTGGATTATTTCCTAATCAATTTTAGGAATTGTGTTAGT NM_006594RefSeq chr1
- 113894194 113905124 AP4B1 10717 "adaptor-related protein complex 4, beta 1 subunit, transcript
variant 1" GO:0005802|GO:0005215|GO:0030131|GO:0005905|GO:0008565|GO:0016192|GO:0006886 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141087_PI430048170 0.0153806865782423 0.1674678935958920.317422551291469
0.2756330532347080.409661752666862A A A 2.33460784150225 3.44711960316181
2.73350503833016 A P P LNCV6_141087_PI430048170 mRNA
GGTCATGTTAAGCTTCTTGCACATTAATATGATTATGGAAGGAAAGGCAGTGAAGCATAA NM_001247989 RefSeq
chr14 + 39267123 39351193 CTAGE54253 "CTAGE family, member 5, transcript variant 6"
GO:0016020|GO:0043085|GO:0008047 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143393_PI430048170 0.3851135350329840.7352088159956950.572220943522089
0.4775293379704940.634871248920146A A A 0.29978187031309 1.44650680469753
1.05084493154726 A A A LNCV6_143393_PI430048170 mRNA
TTTCTACTCATATAGTGGCCAGTTGGCTCAGGCAGGCATTTCAAGAGGAATCTGCTTGTT NM_004969RefSeq chr10
- 92451683 92574095 IDE 3416 "insulin-degrading enzyme, transcript variant 1"
GO:0031597|GO:0005515|GO:0008286|GO:0043130|GO:0010992|GO:0005782|GO:0005886|GO:0006200|GO:0005
634|GO:0010815|GO:0051291|GO:0005615|GO:0008340|GO:0042803|GO:0005829|GO:0005739|GO:0005737|GO:0
001948|GO:0001540|GO:0051289|GO:0051603|GO:0006508|GO:0016032|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126868_PI430048170 0.1065245896563770.3245037923459530.276359943087097
2.26569877584034 2.51590488086998 A A A 2.77771735957172 3.87400229776435 3.8735578010181
P P P LNCV6_126868_PI430048170 mRNA
GGGAAAGAAAATGAGTATTTTGTCCTTTTGTGTTCCTACAGACACTTTCTTAAACCAGTT NM_001146RefSeq chr8
- 107249481 107498026 ANGPT1 284 "angiopoietin 1, transcript variant 1"
GO:0051897|GO:0005886|GO:0072012|GO:0050731|GO:0002040|GO:0050900|GO:0005615|GO:0030154|GO:0002
740|GO:0043524|GO:0007171|GO:0033138|GO:0031398|GO:0070374|GO:0043122|GO:0070062|GO:0030097|GO:0
030971|GO:0043066|GO:0048014|GO:0032680|GO:2000446|GO:0031589|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145460_PI430048170 0.92852911131662 1.00575975571894 0.269335043201344
0.2756907348484220.447953640377138A A A 0.34928972474925 0.296907702675381
0.32865413441997 A A A LNCV6_145460_PI430048170 mRNA
AATAAGGAATTTAAGAATGCCTTGAAAAAAGCCTTCGGCTTGACGAGCTGCGCCGTAGAG NM_173351RefSeq chr2
- 240045076 240046072 OR6B3 NA "olfactory receptor, family 6, subfamily B, member 3" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_95268_PI430048170 0.2333057514499971.02853944024682 0.3532718124762120.313498954348158
0.396070870964626A A A 0.3274970806524790.2866587348683890.327690879902707A A A
LNCV6_95268_PI430048170 mRNA
TAGAAACCACTTTAATCATATCCAGGAGTTTGCAAGAAACAGGTGCTTAACACTAATTCA NM_001001548 RefSeq
chr7 + 80638515 80679277 CD36 948 "CD36 molecule (thrombospondin receptor), transcript variant

1"
GO:0032755|GO:0002474|GO:0035634|GO:0050830|GO:0019915|GO:0050731|GO:0030301|GO:0042992|GO:0005615|GO:0060100|GO:0005041|GO:0015911|GO:0042953|GO:0002755|GO:0044130|GO:0043123|GO:0044255|GO:0005794|GO:0038124|GO:0009986|GO:0032760|GO:0038123|GO:0010744|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107928_PI430048170 0.000906673655933918 2.07541193479779 6.14370190681652 6.37359958132263 6.12589971151724 P P P 5.32745042804276 5.03351374530292 5.11947944002093 P P P LNCV6_107928_PI430048170 mRNA
AAGAGAGGGACTTCCTGCGGTGCCAGCTGGACAAATTCATCTCTTCTGCTCGGATGGAGG NM_013301 RefSeq chr19 + 55647587 55653160 CCDC106 29903 coiled-coil domain containing 106
GO:0005515|GO:0005737|GO:0005730|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133581_PI430048170 0.0132588585936887 0.4882390369393464.19650160768567 3.64521226266559 3.68075661294373 P P P 4.76924217792581 4.82822036651004 5.07752195283064 P P P LNCV6_133581_PI430048170 mRNA
CTCTGTAAGCAAGCTTGCAAGTGTATTTTGTGTACATTTTATCTGAGGTGGAAATGAAAA NM_020340 RefSeq chr6 + 138161915 138344663 ARFGEF3 NA ARFGEF family member 3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128091_PI430048170 0.8737935494873870.9947900377283020.417805177963251 0.3902184470297580.258582017998785 A A A 0.3362002900460430.382197620345094 0.375356997884343 A A A LNCV6_128091_PI430048170 mRNA
GAGAGGCTCTTTGTAGTTAACCTATATGAAGTAATGTATAAGGTAGGTCAGAGTAATACT NM_052852 RefSeq chr19 + 20167213 20200490 ZNF486 90649 zinc finger protein 486
GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130905_PI430048170 0.0288712530648492 0.5224923045521941 1.5815180591825 12.2078917334807 11.7952821574104 P P P 13.1718569280814 12.7439948940109 12.4599039863532 P P P LNCV6_130905_PI430048170 mRNA
AGACCCTGCTGCGTCTCCCTTCCAAACTCTGGTGCTGAATAAACCCTTCTGATCTGGTCT NM_000407 RefSeq chr22 + 19723542 19724774 GP1BB 2812 "glycoprotein Ib (platelet), beta polypeptide"
GO:0005515|GO:0005886|GO:0007596|GO:0005887|GO:0007597|GO:0030168|GO:0007155|GO:0007166|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137943_PI430048170 0.1444387158254981.80884279716445 1.19383460043423 1.13034829428782 2.23067696680538 A A A 0.467676666946689 1.16146797707715 0.536004975436533 A A A LNCV6_137943_PI430048170 mRNA
GCTGTGAGGCCATAGGTACTAGACAACCAATACATGCAGGGTTGGGTTTTCTAATTTTTT NM_003015 RefSeq chr10 - 97766750 97771999 SFRP5 6425 secreted frizzled-related protein 5
GO:0051898|GO:0042813|GO:0017147|GO:0008285|GO:0004930|GO:0090179|GO:0006915|GO:2000057|GO:0048546|GO:0005615|GO:0009653|GO:0035414|GO:0043433|GO:0030154|GO:0060028|GO:2000041|GO:0007165|GO:0007163|GO:0016021|GO:0043508|GO:0090090|GO:0007601|GO:0035567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128076_PI430048170 0.0391107461864035 0.5020658775874874.44010849730007 3.67385921495758 4.14610721105904 P P P 5.01755740334579 5.1604321637315 5.16049327666085 P P P LNCV6_128076_PI430048170 mRNA
GAGACGGTCGAGAGAGAGACCTATTTTGCAATCAGTGACATTGATTTTTAGATTATTTAT NM_145647 RefSeq chr8 + 123072679 123152152 TBC1D31 93594 "TBC1 domain family, member 31, transcript variant 1"
GO:0005813|GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133202_PI430048170 0.3289514356081510.7705532965612030.405760420999731 0.3920936273909490.252357665046735 A A A 0.4340595324924960.409297152254223

1.19477796783886 A A A LNCV6_133202_PI430048170 mRNA
TCCTATTCTCTAGATCAAGATAAAATGACCTCATTGTTTTACACCCTTGTGGTTCCCATG NM_001001960 RefSeq
chr11 - 55913649 55914582 OR5W2 NA "olfactory receptor, family 5, subfamily W, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110714_PI430048170 0.3368272830725110.8492195637223645.47386011581734 4.8093554455148
4.97213844240226 P P P 5.54369765277742 5.27976043713385 5.20229520614798 P P P
LNCV6_110714_PI430048170 mRNA
ATTATCATATTAGGCAGCTAGGATGACACATCAAAGAAGCAAGAAGTGGAGCAGCGCTAG NM_138468RefSeq
chr2 - 202773149 202871985 ICA1L 130026 "islet cell autoantigen 1,69kDa-like, transcript variant 1"
GO:0019904 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127156_PI430048170 0.5091116947264080.61370703812647 0.418305646818806
0.4377227590698970.686114412193603A A A 0.3840896047301122.12772962124649
0.412393051672061A A A LNCV6_127156_PI430048170 mRNA
GGTCCAAGAGTGTTTCAATGATGGAAAACATTTCAGGGGAAAAAATCATGAATAGAATTG NM_001004125 RefSeq
chr9 - 25676388 25678858 TUSC1 286319 tumor suppressor candidate 1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_143274_PI430048170 0.7875904183841971.00269357787914 0.395840438404095
0.3962809875286410.383647343770976A A A 0.4026479667200780.362927850106375
0.398258420235661A A A LNCV6_143274_PI430048170 mRNA
AGAAAATCCTCACTGTCCAGGTTCCTCAAGTAGAATAGGTCATTAAACATCAGCATTTGC NM_001008693 RefSeq
chr20 - 23602409 23605973 CST9 128822 cystatin 9 (testatin) GO:0010951|GO:0004869|GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138320_PI430048170 0.0416574948388821 0.6852173942973889.2823067394128
9.15801313313797 9.51267462990559 P P P 9.67245899267661 9.76267890821449
10.1340973550945 P P P LNCV6_138320_PI430048170 mRNA
GCAGTCTTTAATCATGCTGTTTAAACTGTTGTGGCACAAGTTCTCTTGTCCAAATAAAAT NM_001042388 RefSeq
chr18 - 9546790 9614607 PPP4R1 9989 "protein phosphatase 4, regulatory subunit 1, transcript
variant 1"
GO:0005515|GO:0030289|GO:0007165|GO:0050790|GO:0030362|GO:0016311|GO:0006468|GO:0004721 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137093_PI430048170 0.0652171986625039 0.676565595825127 12.4548807189648
11.8961402588532 12.1894491169949 P P P 12.7109325348847 12.7651526056108 12.807655519296
P P P LNCV6_137093_PI430048170 mRNA
TCTTAGAGGGTAAAATCCAGTACAAGGAATATATCATTGAAGGATTTGAAAACATGCCAG NM_001146108 RefSeq
chr9 - 111562966 111599855 PTGR1 22949 "prostaglandin reductase 1, transcript variant 1"
GO:0019369|GO:0019371|GO:0047522|GO:0009636|GO:0044281|GO:0006691|GO:0032440|GO:0036132|GO:0005
737|GO:0008270|GO:2001300|GO:0055114|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139686_PI430048170 0.00307804310681398 1.3436693874495 12.6665830782026
12.7074060491068 12.5459789437222 P P P 12.1775306739677 12.1601911996055
12.3042258623987 P P P LNCV6_139686_PI430048170 mRNA
CTGCCTACCATCCAGGAAAACTTGTGCTGGAATTGCTGATGGAAACAATTAAATATTTAC NM_003634RefSeq chr22
- 29554808 29581337 NIPSNAP1 8508 "nipsnap homolog 1 (C. elegans), transcript variant 1"
GO:0005739|GO:0097060|GO:0005743|GO:0042165|GO:0019233 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144586_PI430048170 0.0565434658024667 1.77510925341167 8.55089624084782
8.88645818762295 8.41996137131775 P P P 8.23026106501801 7.68777142978238
7.36057585395973 P P P LNCV6_144586_PI430048170 mRNA
AGGAATGCTGAATATGGGAAGCAGGGGTGCTTGTGACCCTAATAAATTCCAAGTCCTCTT NM_014234RefSeq chr6
+ 33204636 33206831 HSD17B8 7923 hydroxysteroid (17-beta) dehydrogenase 8

GO:0005515|GO:0004303|GO:0005886|GO:0008209|GO:0006703|GO:0005759|GO:0047035|GO:0006633|GO:0003857|GO:0005740|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139353_PI430048170 0.4377641757139680.8814028266185987.40455405178007 7.01384804353633 6.77727478116804 P P P 7.41842961807474 7.35426804464808 7.00680462509291 P P P LNCV6_139353_PI430048170 mRNA CGCCCCCGTGGGTCTCTGACTCTGTCGCTTTTCTCTAAGTAAAGATTTCACGTCCACCGG NM_015722RefSeq chr10 - 133325423 133336971 CALY 50632 calcyon neuron-specific vesicular protein GO:0045807|GO:0032051|GO:0005887|GO:0031410|GO:0007212|GO:0032403|GO:0030659|GO:0048268|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136225_PI430048170 0.7078219509087570.9772237420402940.282865166816998 0.2900501059083730.488739844833928A A A 0.33638725816809 0.493028830350224 0.33580387634007 A A A LNCV6_136225_PI430048170 mRNA GGCTCTGAAGAGAGAGCTTGTTAGAAAAATACTTTCTCATGATGCTTGTTATTTTAGTAG NM_153444RefSeq chr11_KI270829v1_alt - 16841 17810 OR5P2 120065 "olfactory receptor, family 5, subfamily P, member 2" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126644_PI430048170 0.0475739743439361 0.5566826830853863.34591453498951 3.24213400489996 3.38010288881322 P P P 3.77706300880069 4.20139352265719 4.45011391672999 P P P LNCV6_126644_PI430048170 mRNA TCAGAGCTCCTCAGACCTGGGACTTTGTTTTTGCTGGTTCAGTGCATTTTGTGTATTTAA NM_015474RefSeq chr20 - 36891823 36951843 SAMHD1 25939 SAM domain and HD domain 1 GO:0005515|GO:0032567|GO:0046061|GO:0006203|GO:0005886|GO:0003723|GO:0019221|GO:0005634|GO:0008832|GO:0003676|GO:0005622|GO:0051607|GO:0006955|GO:0060337|GO:0051289|GO:0045088|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130031_PI430048170 0.1656041993927280.9676898510140440.451655646226325 0.3742905652050260.409177831512976A A A 0.4669669061565910.482030438081275 0.428797557775994A A A LNCV6_130031_PI430048170 mRNA TTAGAGACAGTGGAGTGTAAATCTGTGGCTAATTCTGTTGGTCGTTTGTATTATAAATGT NM_001002919 RefSeq chr2 - 279560 288308 FAM150B 285016 "family with sequence similarity 150, member B" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137956_PI430048170 0.0216877826581503 0.4543707797603646.55042917798101 5.91939582330014 6.13604749112062 P P P 7.32507124645619 7.42909494341262 7.33611137312704 P P P LNCV6_137956_PI430048170 mRNA CACTTTTTTGTTGCTAATGTAATCGGTTTTTGTAATGGCGTCAGCAAATAAAAGGATGCT NM_001271014 RefSeq chr14 + 55580206 55684584 KTN1 3895 "kinectin 1 (kinesin receptor), transcript variant 5" GO:0016020|GO:0005887|GO:0005783|GO:0005789|GO:0019894|GO:0016021|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140264_PI430048170 0.1455849029003051.55320521159859 4.29113434555863 4.53588167368536 4.52491630351712 P P P 4.04119361803663 4.09061197331229 3.14749524637518 P P P LNCV6_140264_PI430048170 mRNA CCAAGAGCCTAGAATGACATGGCCCTTCTCAGCAGTAATAACAGATGGTCTCAGCGCCTC NM_016642RefSeq chr15 - 41848145 41894077 SPTBN5 51332 "spectrin, beta, non-erythrocytic 5" GO:0008091|GO:0030036|GO:0034452|GO:0030507|GO:0003779|GO:0043621|GO:0051693|GO:0005829|GO:0045505|GO:0043234|GO:0005737|GO:0016020|GO:0007411|GO:0007030|GO:0032391|GO:0051260|GO:0007041|GO:0019894|GO:0032029|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143403_PI430048170 0.0300643577771508 0.9548737813034190.409146686994379 0.3738791539657460.360152796883055A A A 0.4434002217003090.460046338051089 0.439949845503089A A A LNCV6_143403_PI430048170 mRNA ACTTGGTTTCTGATTTGCTCTATTTCAGCAGATCTTTTCTACCTACTTTGTGTGATCAAA NM_032411RefSeq chr2 +

106065656 106078153 C2orf40 84417 chromosome 2 open reading frame 40
GO:0030133|GO:0008054|GO:0005615|GO:0070314|GO:0090398 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_110572_PI430048170 0.00546614461968328 1.3623178356138 10.8037358665843
10.7655911005374 10.6337177264521 P P P 10.3971048573229 10.279670817826
10.1857512084954 P P P LNCV6_110572_PI430048170 mRNA
ATCTTTCCCATGGGGCTGTCTTCCAGTGAAGGGGACATCCCATAAGTAGTTTTGAGAGGG NM_012477 RefSeq chr2
+ 74458399 74460891 WBP1 23559 WW domain binding protein 1
GO:0005515|GO:0008150|GO:0050699|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142921_PI430048170 0.6224154015189480.8568635374319132.90230233368536
2.24188928926205 0.337160241833305 A A A 2.79153241432011 2.55366789325135
1.54832473956274 A A A LNCV6_142921_PI430048170 mRNA
AAGGGCTCCCTCATCAGAGACGTGCGACATGTAAACCAAATTAAACTATGGTGTCCAAAG NM_004942 RefSeq chr8
+ 7894564 7896716 DEFB4A 1673 "defensin, beta 4A"
GO:0006955|GO:0007186|GO:0006935|GO:0005796|GO:0045087|GO:0005576|GO:0042742 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_62725_PI430048170 0.2838448351510660.8582088595238510.2737467621117310.28280281040214
0.385794725371125 A A A 0.7957068342366480.3113126423491730.45619618163354 A A A
LNCV6_62725_PI430048170 mRNA
AACACCAGTGTCTTTCATCTGAGGAACTGAAGCAACGTTTCCCAAATATTCGGTTGCCCA NM_016518 RefSeq chr17
+ 29042899 29057218 PIPOX 51268 pipecolic acid oxidase
GO:0008115|GO:0050031|GO:0033514|GO:0046653|GO:0005102|GO:0055114|GO:0005777 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128768_PI430048170 0.11970338882917 0.7382183402071975.64750510042227
5.18568996290055 5.80563825333688 P P P 5.94050435800924 5.92374578157158
6.14675031533029 P P P LNCV6_128768_PI430048170 mRNA
AGCCTTCCCTACTGTCACCAACAACCAAGCTAAATAAAGTCAACAGCCTGATGTGTAAAA NM_003821 RefSeq chr8
+ 89757746 89791064 RIPK2 8767 receptor-interacting serine-threonine kinase 2
GO:0005515|GO:0032755|GO:0050830|GO:0046330|GO:0007249|GO:0050731|GO:0042803|GO:0002756|GO:0002
755|GO:0031398|GO:0046641|GO:0043123|GO:0005856|GO:0031663|GO:0050700|GO:0032729|GO:0010800|GO:0
032728|GO:0038124|GO:0032760|GO:0038123|GO:0032727|GO:0034134|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_80205_PI430048170 0.8414225279229690.9934215999246550.2759578000569930.280328179280266
0.415987021089965 A A A 0.3592143823882140.3037178087765090.341788517999609 A A A
LNCV6_80205_PI430048170 mRNA
TGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTGCTCGGCTC NM_006438 RefSeq chr8
+ 119067184 119106963 COLEC10 10584 collectin sub-family member 10 (C-type lectin)
GO:0005737|GO:0005581|GO:0005576|GO:0005537 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139496_PI430048170 0.9724009347731120.9994257986956970.3357988276015
0.3381790906036860.393897567683175 A A A 0.3728408742771570.325443426661313
0.372318064032202 A A A LNCV6_139496_PI430048170 mRNA
CTAAGACTGAGGAAATAAAAAAGGTTTGGTGTTTTCCTAGGGAGAGAGCATGCCAGGCAG NM_023068 RefSeq
chr20 - 3686969 3707128 SIGLEC1 6614 "sialic acid binding Ig-like lectin 1, sialoadhesin"
GO:2001238|GO:0016337|GO:0006954|GO:0007160|GO:0005886|GO:0030246|GO:0070234|GO:0005576|GO:0016
021|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135866_PI430048170 0.4913782644102850.9531656519459321 1.8605813570693
11.9189917153708 12.0943362608545 P P P 12.0420681880299 11.9175711138992
12.1247499300546 P P P LNCV6_135866_PI430048170 mRNA
TAGGAGTCAACATCTTCATCATTGGGCTTTCTTTAAAACGTGCACTTTGTAATTTGAAAG NM_017841 RefSeq chr11

+ 61430124 61446767 SDHAF2 54949 succinate dehydrogenase complex assembly factor 2
GO:0005739|GO:0005515|GO:0006470|GO:0005759|GO:0006121|GO:0018293|GO:0010719|GO:0090090 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133415_PI430048170 0.1429128711464781.11987619444534 0.609747241306763
0.3729589678718570.562197478608791A A A 0.2802906801049490.398150772779308
0.384307921092556A A A LNCV6_133415_PI430048170 mRNA
GTCACCTATGGAATCTGAGTGGTTTTATTTTTTAGATTTCTCAGTCCCAAAGATCTAAGA NM_002302RefSeq chr5
- 135946910 135955034 LECT2 3950 leukocyte cell-derived chemotaxin 2
GO:0005737|GO:0001501|GO:0006935|GO:0030178|GO:0005615|GO:0042802 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_67585_PI430048170 0.4583096573225980.8823478214239492.57625324513738 2.97667432249219
2.84160324257906 A P P 2.65489356658003 3.01905718279517 3.23266185671693 P P P
LNCV6_67585_PI430048170 mRNA
TCTAGTAACGGAAGAAGTTCTTTCAGTAGAAACACGTGTGCAAACTGAACCTGTAACATC NM_001297548 RefSeq
chr5 + 43121507 43176324 ZNF131 7690 "zinc finger protein 131, transcript variant 1"
GO:0006355|GO:0003700|GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0003677|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129966_PI430048170 0.50688544793695 1.16286916842822 1.01158914381952
0.37722409093505 0.297110439426182A A A 0.4573125365314070.351949036822336
0.331145167885905A A A LNCV6_129966_PI430048170 mRNA
TACAACTGAATGAAGAAGCATTAACGAAAACCAGTATTTAAGTACAGTGGACAGCTTAGG NM_207355 RefSeq
chr15_KI270727v1_random - 136159 167571 POTEB3 102724631 "POTE ankyrin domain family, member
B3, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128030_PI430048170 0.0157547271089219 0.512125218947272 7.54227211029921
6.98373812870572 7.51635888636454 P P P 8.14488711869481 8.31101084998265
8.52348230506958 P P P LNCV6_128030_PI430048170 mRNA
CACTGGTGTTGGACTTAAATCAGTTGAAATGTATTTCTGTACCACAATTTACGCTTCAAT NM_001634 RefSeq chr6
+ 110874783 110895712 AMD1 262 "adenosylmethionine decarboxylase 1, transcript variant 1"
GO:0008295|GO:0034641|GO:0004014|GO:0006597|GO:0006595|GO:0006557|GO:0044281|GO:0005829 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_138957_PI430048170 0.464513400287186 0.719999565414661 0.348966726170948
0.400366508284639 0.319573273157597 A A A 0.264923519748405 0.367815641718189
1.50760903320542 A A A LNCV6_138957_PI430048170 mRNA
GCACCAAAATCCACTATACAAATGCAGACAGCATAAAGTAACCTAGTTTCGCTTTAAATT NM_012311 RefSeq
chr10 - 7750961 7788027 KIN 22944 "Kin17 DNA and RNA binding protein, transcript variant 1"
GO:0006397|GO:0003723|GO:0005634|GO:0006310|GO:0003677|GO:0046872|GO:0006974|GO:0016363|GO:0043
231|GO:0006260|GO:0005737|GO:0003690|GO:0006281|GO:0016032 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130359_PI430048170 0.816487757676766 1.39314822422146 3.03356475312728
0.90119823965709 0.915416877637728 A A A 1.91217271951466 1.71831098706473
0.601898844035498 A A A LNCV6_130359_PI430048170 mRNA
GTTGGGGAGTGGGGAACGAGGAACAGAACAATAACGCATTAAAGTAAATAACTCTGGAAA NM_016531 RefSeq
chr4 + 38664168 38701508 KLF3 51274 Kruppel-like factor 3 (basic)
GO:0006355|GO:0003700|GO:0007275|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142601_PI430048170 0.529806610310224 1.00605686362569 0.403655479742889
0.406129908192936 0.389543133749047 A A A 0.401808107724384 0.368681198180667
0.402500808392388 A A A LNCV6_142601_PI430048170 mRNA
TTTGGTCATATGAGCTTCCTTCTGTGAAAGTACATTTGGAGACACAACTATTTTTCCAAA NM_003381 RefSeq chr6

+ 152750796 152759766 VIP 7432 "vasoactive intestinal peptide, transcript variant 1"
GO:0005515|GO:0007589|GO:0045732|GO:0043066|GO:0008284|GO:0070459|GO:0060406|GO:0043267|GO:0010579|GO:0048662|GO:0005576|GO:0009966|GO:0032880|GO:0001938|GO:0005179|GO:0007186|GO:0045909|GO:0007611|GO:0043025|GO:0048255|GO:0005184|GO:0051930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127257_PI430048170 0.0304503513884272 2.79236826877553 2.53058152303002 2.46902739541952 1.6284766283766 A A A 1.39105260965463 0.315328389190092 0.369926044107595 A A A LNCV6_127257_PI430048170 mRNA
CTCAGGTCTTAATTAGGAATAAATGAGGTGGGAAATAAACATTCTTATGACAGTTCTACC NM_181707 RefSeq
chr17 + 60422503 60431426 C17orf64 124773 chromosome 17 open reading frame 64 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132134_PI430048170 0.0500495270386256 1.20814566397816 11.5988190191022 11.4947397709893 11.6735877812084 P P P 11.2326701493055 11.4692952608897 11.2395846073936 P P P LNCV6_132134_PI430048170 mRNA
AGTCCTTACGATAAACTCCATAATTTATGGCCTGCAGTATCTCTTCTTGGAGCCCAACCC NM_003969 RefSeq
chr19 - 58555711 58558976 UBE2M 9040 ubiquitin-conjugating enzyme E2M
GO:0005515|GO:0004842|GO:0016567|GO:0045116|GO:0005524|GO:0005829|GO:0005737|GO:0043525|GO:0019788|GO:0018169|GO:0007179|GO:0006464|GO:0031625|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135419_PI430048170 0.00498760343500909 0.619167885408003 9.6912287149115 9.70803013408388 9.90563147021603 P P P 10.4054671676154 10.3299416840124 10.6363472919537 P P P LNCV6_135419_PI430048170 mRNA
GGAAAAGGTGATATCCATTCTTTCTGATAACTAGATGGTGCTGAGAAGCTTTTGAATAAA NM_000386 RefSeq
chr17 - 30248194 30292166 BLMH 642 bleomycin hydrolase
GO:0000209|GO:0005515|GO:0002474|GO:0042493|GO:0009636|GO:0005634|GO:0005829|GO:0004197|GO:0005737|GO:0004177|GO:0004180|GO:0006508|GO:0005654|GO:0008234|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128187_PI430048170 0.326283124831234 1.38208453624527 1.29727683097668 0.36776188241182 0.375764559670494 A A A 0.261467168773603 0.33351769667555 0.253241088821551 A A A LNCV6_128187_PI430048170 mRNA
GCTGTACTATTTTCACTCAGAAGCATGTTCATTTATGTAGATGCCACTTTAAGCTTTATC NM_006071 RefSeq
chr22 - 46255662 46263322 PKDREJ 10343 polycystin (PKD) family receptor for egg jelly
GO:0005262|GO:0060046|GO:0050982|GO:0016020|GO:0005886|GO:0005509|GO:0070588|GO:0016021|GO:0007340 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137770_PI430048170 0.268488394712886 0.846744450469551 7.7839728859904 7.84289442076764 8.06031890855491 P P P 8.03327587952277 7.92529391532453 8.41624271683276 P P P LNCV6_137770_PI430048170 mRNA
CCCATTGCTCTGCAACTTCCAAACCAGTTTGAGTCATACAAATGTTTTCTAAACTTTTAT NM_014924 RefSeq
chr14 - 55366390 55411858 ATG14 22863 autophagy related 14
GO:0005515|GO:0005776|GO:0005930|GO:0008333|GO:0016236|GO:0005634|GO:0090207|GO:0045335|GO:0005737|GO:0010608|GO:0034045|GO:0005654|GO:0044233|GO:0000045|GO:0010508 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127363_PI430048170 0.281352686068771 0.876329144980089 0.299578492763247 0.336303975880425 0.339007888199284 A A A 0.403172812246907 0.74997741268177 0.361071543483419 A A A LNCV6_127363_PI430048170 mRNA
GCTACCTTGATTAGACAGGAAGGAGAACAACTACTACAACAAAGAGAATAAAATACATTC NM_004529 RefSeq
chr9 - 20341664 20622543 MLLT3 4300 "myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3, transcript variant 1"
GO:0005515|GO:0006355|GO:0007379|GO:2000096|GO:0005634|GO:0009952|GO:0090090|GO:0008023|GO:0006

351|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100958_PI430048170 0.0244940499676868 0.595172645542599 2.69378912516216
2.5086149569178 3.00349184170139 A A P 3.56073050207878 3.52915057256056
3.40077653743975 P P P LNCV6_100958_PI430048170 mRNA
TTCAGCCTTCTAGATGTCTCTCTCGTGGACATCTGTTCTTTAGCTGTTGGCTTTCTCTGA NM_014640 RefSeq chr2
+ 218710844 218755415 TTLL4 9654 tubulin tyrosine ligase-like family member 4
GO:0018095|GO:0005929|GO:0005737|GO:0015631|GO:0016874|GO:0005856 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_134064_PI430048170 0.135673800579103 0.669944046108216 2.51135531641546
2.82049061897077 3.16828634513991 A A P 2.93311615323418 3.63136444470738
3.63733045495659 P P P LNCV6_134064_PI430048170 mRNA
AAACTCACTACACAGTTCTTGTTCAAGCATTATTGGGAAACCACCAGAGGGCACTCTCAC NM_172177 RefSeq
chr12 + 93467489 93503772 MRPL42 28977 "mitochondrial ribosomal protein L42, transcript variant
2"
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005886|GO:0005
743|GO:0006412|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138372_PI430048170 0.650083559309808 0.959370494730409 6.64885166314388
6.3588172386149 6.38654898021044 P P P 6.57110095174692 6.64280150686446
6.36358000474306 P P P LNCV6_138372_PI430048170 mRNA
TGTGTAGAGCCTGCATCTGTCTGTCCTTCCTTCCATTGCTCCCAGTGCCAAACTTGGGCC NM_003055 RefSeq
chr10 + 49610300 49612720 SLC18A3 6572 "solute carrier family 18 (vesicular acetylcholine
transporter), member 3"
GO:0060201|GO:0015870|GO:0016020|GO:0005886|GO:0005887|GO:0072488|GO:0005277|GO:0007268|GO:0007
269 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70436_PI430048170 0.346501872637255 1.03995535315136 0.503091639440927
0.531423051125197 0.560644366651304 A A A 0.503509195321817 0.536661522820314
0.381406222493797 A A A LNCV6_70436_PI430048170 mRNA
GGCTGTATTTCTGCAGTTTCGGTTTTCATTTGCTTCAGCTTACTAAGAAGCTTCAAATCT NM_001261435 RefSeq
chr2 + 201806578 201895550 CDK15 65061 "cyclin-dependent kinase 15, transcript variant 1"
GO:0005515|GO:0051726|GO:0006468|GO:0005524|GO:0046872|GO:0004693 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_122116_PI430048170 0.290773941034115 0.806022934700036 3.05892072490531
3.13683218649637 3.36647840157412 A P P 3.39066383396593 3.17621283743051
3.85998445201843 P P P LNCV6_122116_PI430048170 mRNA
TATCACCGCAAGAGCTACCATTCATCTAGCACAACCTGACCATCCTCACACTGGTCAGTT NM_005417 RefSeq
chr20 + 37344684 37405432 SRC 6714 "SRC proto-oncogene, non-receptor tyrosine kinase,
transcript variant 1"
GO:0005515|GO:0042542|GO:0005158|GO:0005764|GO:0010907|GO:0016337|GO:0007172|GO:0007173|GO:0018
105|GO:0007411|GO:0016301|GO:0042127|GO:0005080|GO:0034446|GO:0031667|GO:0007179|GO:0042169|GO:0
038083|GO:0032463|GO:0022407|GO:0032869|GO:0030331|GO:0030168|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132408_PI430048170 0.339299321140567 0.822030920994461 4.1068859632832
3.3891237482544 3.42836198183017 P P P 4.21062537160612 3.93778645582683
3.6962667045322 P P P LNCV6_132408_PI430048170 mRNA
GGAATGCCCAGCTAGTTAAAGAATGCAAAGGAAAATATTTTCACAAAGGGTTATCTGATA NM_019046 RefSeq
chr10 - 5861725 5889897 ANKRD16 54522 "ankyrin repeat domain 16, transcript variant 1" NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_135415_PI430048170 0.531592815265072 1.03790368891366 0.278408827391095
0.296480588198459 0.488409947867092 A A A 0.324950028407421 0.28525538695982

0.301324103895674 A A A LNCV6_135415_PI430048170 mRNA
TCACCTGGCAAGTTTCTGCCTAACTAAAGAGAAGAAAAGTTTTTATCGTATTCATACTAC NM_018932 RefSeq
chr5 + 141208718 141212126 PCDHB12 56124 protocadherin beta 12
GO:0005887|GO:0005509|GO:0007155|GO:0007156|GO:0007399 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140207_PI430048170 0.719417662245974 1.07943452882746 1.72108999918913
2.39008386836803 2.24733325381738 A A A 2.19589721922526 1.83675294795765
2.0549243423574 A A A LNCV6_140207_PI430048170 mRNA
TGGGAGGAGTCTAATACAAAAACTGAAAACCTTTGGTCCTGGGAATTTATTTTCATGGCT NM_018010 RefSeq
chr3 - 108160811 108222570 IFT57 55081 intraflagellar transport 57
GO:0005515|GO:0005813|GO:0006355|GO:0005794|GO:0006996|GO:0006919|GO:0050680|GO:0044292|GO:0001
843|GO:0006915|GO:0042981|GO:0072372|GO:0003677|GO:0036064|GO:0006351|GO:0007224|GO:0001947|GO:0
042384|GO:0005929|GO:0042073|GO:0060972|GO:0032391|GO:0030992 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_142807_PI430048170 0.00843981684364235 4.18067520194817 2.3782908092785
2.05575530163551 2.7384722071244 A A A 0.402969516365214 0.32549065031236
0.33239179963035 A A A LNCV6_142807_PI430048170 mRNA
GCAGAGCTTTCAAGGATAGGCTTTATTCTGCAAGCAATCAAATAATAAATCTATTCTGCT NM_000184 RefSeq
chr11 - 5253190 5254781 HBG2 NA "hemoglobin, gamma G" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135106_PI430048170 0.01504963968558 0.6620948517407398.62806696909464
8.67681904138736 8.68420574007328 P P P 9.13286769310483 9.21960130439785
9.40807284953079 P P P LNCV6_135106_PI430048170 mRNA
GGACAAACTTGGAGAGTATGGACAACTTTGATATTGCTTGGCACAGATGGTATTAAAAAA NM_001130004 RefSeq
chr14 - 68874122 68979366 ACTN1 87 "actinin, alpha 1, transcript variant 1"
GO:0005515|GO:0003725|GO:0030018|GO:0005886|GO:0005634|GO:0042995|GO:0005615|GO:0005829|GO:0031
143|GO:0005916|GO:0005737|GO:0051015|GO:0030374|GO:0043197|GO:0030198|GO:0048041|GO:0031093|GO:0
051764|GO:0051017|GO:0070062|GO:0001725|GO:0034329|GO:0005509|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141670_PI430048170 0.0627139528462515 1.04612239602729 0.347433615998984
0.3353680765710020.282786464867528A A A 0.2458192745579740.277035012522816
0.248184806549379A A A LNCV6_141670_PI430048170 mRNA
CCTTTAGCTTTCTAAGCTTTCTTACAATGTGGACTGATTACTGTAACATTTCACGTGTAANM_004171RefSeq chr11 -
35251204 35419558 SLC1A2 6506 "solute carrier family 1 (glial high affinity glutamate transporter),
member 2, transcript variant 1"
GO:0005515|GO:0015501|GO:0005886|GO:0051938|GO:0042493|GO:0007632|GO:0070779|GO:0005313|GO:0009
611|GO:0007268|GO:0010259|GO:0055085|GO:0021537|GO:0035264|GO:0016020|GO:0046326|GO:0031668|GO:0
030534|GO:0030673|GO:0016021|GO:0017153|GO:0043200|GO:0006811 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_133499_PI430048170 0.150411609248566 1.05174411861847 14.8025649993876
14.8887644909552 14.8973873736108 P P P 14.7358479180107 14.8116892702957
14.8231697549927 P P P LNCV6_133499_PI430048170 mRNA
TGTCTTCAGAAGCAAGTCAGGTTTCATGTAACCGAGTGTCCTCTTGCGTGTCCAAAAGTA NM_001569RefSeq chrX
- 154010505 154019891 IRAK1 3654 "interleukin-1 receptor-associated kinase 1, transcript variant 1"
GO:0005515|GO:0004842|GO:0051403|GO:0051259|GO:0042803|GO:0034605|GO:0002756|GO:0004704|GO:0046
777|GO:0016301|GO:0002755|GO:0031072|GO:0032496|GO:0007178|GO:0043123|GO:0031663|GO:0005811|GO:0
038124|GO:0046982|GO:0038123|GO:0034134|GO:0007568|GO:0002224|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_94095_PI430048170 0.604933873816285 0.734429530724058 0.454948282929338 1.27179526705883

1.41900342195674 A A A 2.24656410473308 0.5069617163906871.39424138150772 A A A
LNCV6_94095_PI430048170 mRNA
GCAATGAAGAGAGAGGACATCTACACTTTAGATGAAGAGTTACCCAAGAGAGTGAAAGCT NM_015061 RefSeq
chr9 + 6757640 7175648 KDM4C 23081 "lysine (K)-specific demethylase 4C, transcript variant 1"
GO:0032454|GO:0000790|GO:0008284|GO:0006357|GO:0006325|GO:0051213|GO:0050681|GO:0006351|GO:0005
654|GO:0008270|GO:0019899|GO:0033169|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77242_PI430048170 0.17724489468364 0.4415482844134290.5379916072926651.07993511172758
0.961334513440486 A A A 1.51187432514108 1.22144972440073 2.86829183341889 A A P
LNCV6_77242_PI430048170 mRNA
TACAATTCATGTCAGACAATTTTGATGGCACACTGTGGCCTGTCAGAGATTTCTTTAGCA NM_001304793 RefSeq
chr6 - 39104062 39115186 SAYSD1 55776 "SAYSVFN motif domain containing 1, transcript variant 2"
GO:0016021|GO:0030659|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69304_PI430048170 0.00177567317282689 1.31331854611612 8.98050382405473
8.90776211085401 8.93491578617036 P P P 8.50411378457042 8.61823021145787
8.51944656725196 P P P LNCV6_69304_PI430048170 mRNA
ACCGACCTCTTCGACCGCAGTGGCTTCGTGTTCGACTATGAGTACGACTGGGCCGGGAAG NM_001319 RefSeq chr19
+ 1941161 1981337 CSNK1G2 1455 "casein kinase 1, gamma 2"
GO:0051219|GO:0005515|GO:0006665|GO:0042277|GO:0000287|GO:0030148|GO:0008360|GO:0090263|GO:0005
634|GO:0044281|GO:0005524|GO:0005829|GO:0006897|GO:0007165|GO:0046777|GO:0001948|GO:0018105|GO:0
016020|GO:0004674|GO:0006468|GO:0016055 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110769_PI430048170 0.1104287728262841.28928583087631 5.53622379558662
5.87934737572841 5.79359494297855 P P P 5.38962262104723 5.10004006777102
5.59853805751608 P P P LNCV6_110769_PI430048170 mRNA
CGTGGTATATCATGATCTTACCTGTTGTTTGACTATGAAAAAGAAATTTGATGCTGATCC NM_019593 RefSeq chr20
- 5544433 5611026 GPCPD1 56261 glycerophosphocholine phosphodiesterase GDE1 homolog (S.
cerevisiae) GO:0007519|GO:0044281|GO:0047389|GO:0006644|GO:2001070|GO:0046474|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90908_PI430048170 0.111824982060391 1.59222468642787 5.75721397483038 5.39432692197219
5.91031753159298 P P P 5.54090641235705 4.66535117319 4.71290451642874 P P P
LNCV6_90908_PI430048170 mRNA
TCCGATCAGTAGAGATTGGAAAGATTGTTGGGAGTGGCACACCACTAGGGAAAAGAAGAA NM_016607 RefSeq
chrX + 101623129 101627841 ARMCX3 51566 "armadillo repeat containing, X-linked 3, transcript
variant 1" GO:0045944|GO:0034613|GO:0031307 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101644_PI430048170 0.2138612125007090.5955880917413014.00039293060401 2.8038979334112
2.99118782020159 P A P 3.32447323922477 4.24985980985118 4.51750667392413 P P P
LNCV6_101644_PI430048170 mRNA
CCTCAGATTTGTAATTGTTGATGTTTGAGTCTTCAGGAAGTATTTGCATCTCTGAAATCT NM_006465 RefSeq chr15
+ 74541176 74598131 ARID3B 10620 AT rich interactive domain 3B (BRIGHT-like)
GO:0008150|GO:0001077|GO:0045944|GO:0001205|GO:0005654|GO:0005634|GO:0000980|GO:0000978|GO:0003
677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128421_PI430048170 0.60748588514346 1.01661409013403 0.328128611931432
0.3302377878184820.438696678686066 A A A 0.3520651229415050.311628023503367
0.364322717058429 A A A LNCV6_128421_PI430048170 mRNA
TTGCCAAAGCCCAAATTAACGAGTATTATAAAAGGATAATAAAGCATCCCTGAAGCCAAA NM_147223 RefSeq chr2
+ 24584476 24770701 NCOA1 8648 "nuclear receptor coactivator 1, transcript variant 2"
GO:0005515|GO:0043005|GO:0000790|GO:0021987|GO:0060713|GO:0035257|GO:0042698|GO:0033142|GO:0050
681|GO:0044281|GO:0032403|GO:0032870|GO:0046965|GO:0005737|GO:0030374|GO:0045944|GO:0046983|GO:2
001038|GO:0032526|GO:0004871|GO:0045925|GO:0032355|GO:0044255|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_137121_PI430048170 0.3013654940704450.85645024829561 6.27052489336046
6.13087439335866 6.50602165217076 P P P 6.78470391442864 6.4877448154873
6.28697051278435 P P P LNCV6_137121_PI430048170 mRNA
TGTTCATTGTATAAAACCCAAAAAGCAGCTAAAAAATAAAGCGGGAAAGGAACTACTGGT NM_005918RefSeq chr7
+ 76048018 76067508 MDH2 4191 "malate dehydrogenase 2, NAD (mitochondrial), transcript variant
1"
GO:0044262|GO:0006099|GO:0046554|GO:0005886|GO:0005975|GO:0005743|GO:0006094|GO:0006107|GO:0006
108|GO:0005634|GO:0044281|GO:0043621|GO:0006734|GO:0005739|GO:0005759|GO:0009405|GO:0030060|GO:0
006006|GO:0005654|GO:0006475|GO:0044237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_135062_PI430048170 0.2438779231592171.07146521422083 0.604174776380276
0.7802067756986940.596181564695049A A A 0.5364814994061530.58013969433133
0.572411115410089A A A LNCV6_135062_PI430048170 mRNA
TCTCATCACTTGTATGTTTCTAACACAGCATGGGACTTTAATAAAACCATCCTGGAAACT NM_001301056 RefSeq
chr1 + 212950519 212991585 VASH2 79805 "vasohibin 2, transcript variant 4"
GO:0005737|GO:0001938|GO:0045766 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137053_PI430048170 0.0971489495230544 0.8402209282537195.96914335097049
5.66085238618603 5.7170939730202 P P P 5.95990234984108 6.10805362229189
6.04779621314597 P P P LNCV6_137053_PI430048170 mRNA
ATTGTGCAAACATTTCTCAAATATGGAAAAGAAAACCCTGTAGGCAGGGAGCCCTCTGCC NM_002509RefSeq chr20
- 21511021 21514026 NKX2-2 4821 NK2 homeobox 2
GO:0021554|GO:0003700|GO:0021530|GO:0048708|GO:0007224|GO:0003326|GO:0003327|GO:0051091|GO:0045
944|GO:0003329|GO:0021522|GO:0003713|GO:0048665|GO:0003323|GO:0048565|GO:0060580|GO:0006351|GO:0
009749|GO:0043565|GO:0045665|GO:0007420|GO:0045666|GO:0048714|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_95209_PI430048170 0.0749973614846042 0.7275437021177735.45364910144226
5.53699697613618 5.61701464573979 P P P 5.88925850945725 5.79747179087497
6.25969192511368 P P P LNCV6_95209_PI430048170 mRNA
TGTGCTGCTTTTTAATAATTGAGTTATTTTGAGCTTGCCAAGTAGGATCTATTGCCTGGA NM_001271872 RefSeq
chr1 + 121185061 121389200 SRGAP2C 653464 SLIT-ROBO Rho GTPase activating protein 2C
GO:0046982|GO:2001224|GO:0051490|GO:0061000|GO:0042803|GO:0021816 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134159_PI430048170 0.6769267236744 0.9614470766951156.16008651433371
6.54320843966759 6.5875177390896 P P P 6.41172174873779 6.57680936849135
6.50476828224988 P P P LNCV6_134159_PI430048170 mRNA
GGACAGATATCTTGTACTCCCAGTGACCTCAATAAAGTACTTTTCATGGTCCTCTTGAAA NM_199285RefSeq chr19
+ 42302131 42310821 PRR19 NA proline rich 19 NA . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_64365_PI430048170 0.000322422965407461 2.86253429139254 5.10422579730263
5.30473474197878 5.33222934251222 P P P 3.6847413280443 3.8065368194539
3.70563294025043 P P P LNCV6_64365_PI430048170 mRNA
TCAAGAAACTCTTGAACAAGACCAACAAGAAGGCAGCGGAGTCCTGAAGGCCCCGTGCTC NM_020428RefSeq
chr19 + 10625494 10644559 SLC44A2 57153 "solute carrier family 44 (choline transporter), member
2, transcript variant 1"
GO:0015220|GO:0005886|GO:0015871|GO:0044281|GO:0005765|GO:0055085|GO:0007165|GO:0004871|GO:0016
021|GO:0006644|GO:0043123|GO:0070062|GO:0006656|GO:0046474 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132630_PI430048170 0.2793764643614542.20267711718588 0.318545494596744
0.88997369394375 2.33159038479091 A A A 0.3100218199947290.302324393712264

0.286690470818894 A A A LNCV6_132630_PI430048170 mRNA
CCAAGTGAGGTGTAGGTTATGCCTATATGCAAATTAAACTTCACCTTTCTTGAATATTCA NM_006909 RefSeq chr5
+ 80960688 81230162 RASGRF2 5924 Ras protein-specific guanine nucleotide-releasing factor 2
GO:0005516|GO:0051056|GO:0048011|GO:0043065|GO:0005886|GO:0007264|GO:0007268|GO:2000310|GO:0097
190|GO:0005829|GO:0032321|GO:0005789|GO:0005089 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_30901_PI430048170 0.00494812166567185 0.6820623878680943.44050807363357
3.64230024119146 3.40643251866629 P P P 3.99804397309454 3.99668355281112
4.15612717833416 P P P LNCV6_30901_PI430048170 mRNA
CCGCTGTCAAGCCGCATAACAGACCAATTTTTATTCCACGAGGAGGAGTACCTGGAAATT NM_014960 RefSeq chr17
+ 68259181 68420859 ARSG 22901 "arylsulfatase G, transcript variant 1"
GO:0006665|GO:0006790|GO:0006687|GO:0005783|GO:0005788|GO:0004065|GO:0044281|GO:0044267|GO:0005
764|GO:0005615|GO:0046872|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137109_PI430048170 0.1567592115064781.03179569024362 0.3413111841581
0.29215727063894 0.270284057130147 A A A 0.2489283054812950.26989944118736
0.250276999845798 A A A LNCV6_137109_PI430048170 mRNA
CTCTTCACAGAATAAATGTATCTGGAAGAATTAGCACTACTTTGGTGTTGTTTGGTCATT NM_001282201 RefSeq
chrX - 48058177 48071658 ZNF630 57232 "zinc finger protein 630, transcript variant 3"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143357_PI430048170 0.0301097624462716 0.5403829112985194.7319080282241
4.73796755852878 5.26610506547411 P P P 5.81320510960812 5.8990607598563
5.75131316477601 P P P LNCV6_143357_PI430048170 mRNA
GATGTCTTAGGCCCTAATTCACCATTTCTTTTTTAAGATCTGATATGCTATCATTGCCTT NM_001304430 RefSeq chr13
- 94574053 94596275 TGDS 23483 "TDP-glucose 4,6-dehydratase, transcript variant 2"
GO:0050662|GO:0008460|GO:0009225 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126595_PI430048170 0.0674215422659820.88221464586082 15.1725630674789
15.2606325387306 15.2984855358288 P P P 15.4435119567437 15.316202028101
15.5105331661868 P P P LNCV6_126595_PI430048170 mRNA
ATTGCTCAAGAAAAACTGGCAGAATGTCCGGGCCTTATATATCAAGAGCACCATGGGCAA NM_007104 RefSeq chr6
+ 35468400 35470781 RPL10A 4736 ribosomal protein L10a
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0005730|GO:0005634|GO:0006
415|GO:0009653|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005739|GO:0005737|GO:0016020|GO:0
000184|GO:0016032|GO:0022625|GO:0044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140494_PI430048170 0.0861478748773622 0.79777903168744210.6951726013482
10.4730124739566 10.5682954838268 P P P 10.7129392015433 11.1029966169371
10.8803306946298 P P P LNCV6_140494_PI430048170 mRNA
GTGTTTTCCATCCCTCTCCCTTAACAGGATTGAAATAAAACATGCTTCTGTTTTTGTAAA NM_001271634 RefSeq
chr2 + 218568579 218596435 RQCD1 9125 "RCD1 required for cell differentiation1 homolog (S.
pombe), transcript variant 1"
GO:0005515|GO:2000327|GO:0010467|GO:0006355|GO:0019904|GO:0019221|GO:0005634|GO:0031047|GO:0042
803|GO:0030014|GO:0006351|GO:0006417|GO:0005829|GO:0016020|GO:0000932|GO:0007548|GO:0033147|GO:0
000289|GO:0000288. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134841_PI430048170 0.6596717867092060.9117452947467511.93244233626412
1.21396156014829 0.519328361186881 A A A 1.74391366292025 1.5065468512497
1.07866265968403 A A A LNCV6_134841_PI430048170 mRNA
AGAGAAATATGCTGAAATGCTGTTTGAAGCCTTCAACACCCCTGCAATGCACATCGCCTA NM_006687 RefSeq chr9
+ 108862227 108863755 ACTL7A 10881 actin-like 7A
GO:0043234|GO:0005737|GO:0005794|GO:0031514|GO:0005200|GO:0005634|GO:0005856|GO:0001673 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131858_PI430048170 0.3391046982613281.27492098806834 1.10189879517804
0.2871229957335750.47363419341743 A A A 0.3391944073120710.294547586776444
0.30828146439689 A A A LNCV6_131858_PI430048170 mRNA
CACTCCCCATAAGCAATACAATTAAAGAAGACCAGGAAAGGAAAATAAATTCCTTAGCTT NM_207426RefSeq chr10
+ 127737273 127741186 FOXI2 NA forkhead box I2 NA . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_139889_PI430048170 0.0979989214039458 0.9091046664604027.29299580671814
7.30969158621798 7.44981872031134 P P P 7.4218561281309 7.48806988224324
7.55705365116265 P P P LNCV6_139889_PI430048170 mRNA
GCATTTTATCACATTTTCTGAAAACAATTGTTCTTGGTTTGCTTATGTAGAGTCCTGCCT NM_001326RefSeq chr11 -
33084583 33161491 CSTF3 1479 "cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa, transcript
variant 1"
GO:0008380|GO:0006379|GO:0010467|GO:0006378|GO:0006369|GO:0006366|GO:0000398|GO:0003723|GO:0031
124|GO:0005654|GO:0005634|GO:0003729 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144914_PI430048170 0.9539964942582781.05413407431423 2.69691601936371
2.00246220119116 3.13896452344024 A A P 2.53136885832513 2.33113584050127
2.90603453497757 P A P LNCV6_144914_PI430048170 mRNA
GGTGCTCTTAAAGTGAGCTTAAAATTTATCCAAGACGTATATCCAAATTTGTCCTGTAGT NM_003692RefSeq chr9
+ 100473237 100577636 TMEFF1 8577 transmembrane protein with EGF-like and two follistatin-like
domains 1 GO:0005886|GO:0007275|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141999_PI430048170 0.0855659626969909 0.7733900443592335.33708985748691
5.40363272482499 5.70414614723811 P P P 5.65019878959986 5.84842864858749
6.05685650049756 P P P LNCV6_141999_PI430048170 mRNA
GGGGGATTGTTTTTTGTAAAAATGTCATTATCAGGTCACATAAATCTGCCTTTATGTTGC NM_006322RefSeq
chr13_KI270838v1_alt - 285974 305687 TUBGCP3 10426 "tubulin, gamma complex associated protein 3,
transcript variant 1"
GO:0005515|GO:0005827|GO:0005813|GO:0043015|GO:0005814|GO:0005819|GO:0005829|GO:0007338|GO:0005
737|GO:0016020|GO:0005198|GO:0000086|GO:0007020|GO:0005200|GO:0000278 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141079_PI430048170 0.2428310313430961.43382569133563 6.3369853108128
7.32526032565354 6.71062234921828 P P P 6.31944265623933 6.47040630406882
6.18468657382649 P P P LNCV6_141079_PI430048170 mRNA
CTTCCAAAACCTGCTTCCTTCAGTTTGTAAAGTCGGTGATTATATTTTTGGGGGCTTTCC NM_002608RefSeq chr22
- 39223679 39244952 PDGFB 5155 "platelet-derived growth factor beta polypeptide, transcript variant
1"
GO:0005515|GO:0005518|GO:0005615|GO:0042803|GO:0042802|GO:0007507|GO:0043552|GO:0007173|GO:0018
105|GO:0030198|GO:0007179|GO:0032355|GO:0035793|GO:0032868|GO:0030336|GO:0030335|GO:0045743|GO:0
009986|GO:0045740|GO:0010512|GO:0001892|GO:0030168|GO:0045840|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129579_PI430048170 0.0615448226527339 0.5862781734353381 0.3055115143182
10.0708415081033 10.051386105497 P P P 10.4914449429192 11.2410505369305
10.9240654830205 P P P LNCV6_129579_PI430048170 mRNA
GTAAATTGTCTTGTGAATGTGTGCTAACCAAAACCCAAAGGCTCTTTTCAGAGCCAACCA NM_003530RefSeq chr6
- 26196783 26199293 HIST1H3D 8351 "histone cluster 1, H3d"
GO:0005515|GO:0010467|GO:0046982|GO:0006325|GO:0006335|GO:0005576|GO:0005634|GO:0000228|GO:0003
677|GO:0032776|GO:0043234|GO:0060968|GO:0016020|GO:0000183|GO:0007596|GO:0045814|GO:0040029|GO:0
005654|GO:0000786|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139042_PI430048170 0.00141290570380706 0.6867937004677826.80058723898738

6.63711505348867 6.7440636789643 P P P 7.22118607524787 7.26236659783034
7.32713448260369 P P P LNCV6_139042_PI430048170 mRNA
CAGGGCACCCTGTTCAACCATATTTAAAAATTGGAATTTGTATAAAGTTGCTTCCAAGTT NM_022769 RefSeq chr15
+ 90529885 90645345 CRTC3 64784 "CREB regulated transcription coactivator 3, transcript variant 1"
GO:0097009|GO:0032793|GO:0008140|GO:0005737|GO:0050995|GO:0051289|GO:0045944|GO:0016032|GO:0005
654|GO:0043951|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142991_PI430048170 0.135000364119361 0.92145932359384 10.1518802055342
9.99218387417331 10.0381541948121 P P P 10.2518386811359 10.1775485608176
10.1079823642132 P P P LNCV6_142991_PI430048170 mRNA
GGGTCTATAGGTTTGTGATTAAAATAATAAAAGCTAGGCGTGTTTGATGCGCTTTTAACT NM_006521 RefSeq chrX
- 49028725 49043517 TFE3 7030 "transcription factor binding to IGHM enhancer 3, transcript variant
1"
GO:0005737|GO:0003700|GO:0044212|GO:0045944|GO:0006959|GO:0046983|GO:0005654|GO:0005634|GO:0045
670|GO:0006351|GO:0045785 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128178_PI430048170 0.0316114938413709 0.368171449311495 0.311744048283875
0.696110470770013 0.36247344229706 A A A 2.31324004616203 1.95517056064004
1.27267131035921 A A A LNCV6_128178_PI430048170 mRNA
GCGGAGCTTCCCTGTGGCATGAACCCCACGGGGTATTAAATTATGAATCAGCTGAAAAAA NM_001011880 RefSeq
chr16 - 74408630 74421470 CLEC18B 497190 "C-type lectin domain family 18, member B"
GO:0030246|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131923_PI430048170 0.482523362819053 0.8761053288615 0.354845984572536
0.352067308179719 0.266464200369881 A A A 0.290391747234278 0.303721432103397
0.873615445704549 A A A LNCV6_131923_PI430048170 mRNA
AAGTGGACAGCTGGTCGCTATTGTGATATTCTGTGAAAAATACAATCATATAACATCCAA NM_001146197 RefSeq
chr13 - 102729366 102759072 CCDC168 643677 coiled-coil domain containing 168 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136017_PI430048170 0.0722644714011548 0.509212047947201 6.62122985945318
6.60915997005369 6.87611696787342 P P P 7.11575341852726 7.66457895520301
8.09876474034097 P P P LNCV6_136017_PI430048170 mRNA
GCCCTGGTCTGAATTTCTTAAGGTTTTATAAACAAATGCTGCTATTTATTAGCTGCAAGA NM_138555 RefSeq chr15
+ 69414245 69448427 KIF23 9493 "kinesin family member 23, transcript variant 1"
GO:0005515|GO:0008017|GO:0051256|GO:0072686|GO:0005634|GO:0005829|GO:0000910|GO:0019886|GO:0016
887|GO:0007018|GO:0005871|GO:0005813|GO:0000281|GO:0032467|GO:0000022|GO:0005874|GO:0005819|GO:0
030496|GO:0003777|GO:0005524|GO:0045171|GO:0007596|GO:0008152|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136891_PI430048170 0.404591572120142 1.97921981456734 2.29792402567423
0.315991035373814 0.421654101860174 A A A 0.348160811584997 0.358873798999182
0.304432752550015 A A A LNCV6_136891_PI430048170 mRNA
GGGTAAAGACCATTTAATTTGCCCTCTCAGGGAATTTGAAATAAATTATTTGTCCTGGAT NM_001003760 RefSeq
chr6 - 53647900 53665708 KLHL31 NA kelch-like family member 31 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138364_PI430048170 0.379809264810268 0.819255752835104 3.81309674259557
2.85704602483489 3.05198344979274 P A P 3.68582972816642 3.75018395983119
3.29259710679732 P P P LNCV6_138364_PI430048170 mRNA
ATCATCAACCCCCAACCCTCTGGGTCTCTTGGATTTCAGAGTGAAAACTTGATTGGCATT NM_002981 RefSeq chr17
- 34360327 34363233 CCL1 6346 chemokine (C-C motif) ligand 1
GO:0008009|GO:0007165|GO:0006955|GO:0006935|GO:0060326|GO:0006874|GO:0016032|GO:0005615 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92260_PI430048170 0.284057785994116 0.767091388433662 1.71111505708416 2.65145009752772

2.57331538249339 A A A 2.8326451570708 2.5479942125943 2.85713994071566 P P P
LNCV6_92260_PI430048170 mRNA
GATGAAAAGGAACTTAATTTGATATTAACAACTGGAGGAACAGGATTTGCACCACGAGAT NM_020806 RefSeq chr14
+ 66507406 67181808 GPHN 10243 "gephyrin, transcript variant 1"
GO:0030054|GO:0005886|GO:0006767|GO:0060077|GO:0072579|GO:0044281|GO:0018315|GO:0005524|GO:0046
872|GO:0032324|GO:0005737|GO:0007529|GO:0006766|GO:0045211|GO:0006777|GO:0005856|GO:0016740 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56928_PI430048170 0.996529975589062 0.988923725007634 0.777711609255109 0.495142961781632
0.549585390955935 A A A 0.391328906793665 0.472189670340086 0.956132751329323 A A A
LNCV6_56928_PI430048170 mRNA
GGAAAGGTGGGCACAAAAATCTTCATGAGCAATACTTCTTAGTAGATTGTTTTGTTATTC NM_152644 RefSeq chr10
- 122849093 122879641 FAM24B 196792 "family with sequence similarity 24, member B, transcript
variant 1" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143444_PI430048170 0.281425054610759 0.809960511503602 0.256395802550893
0.322133019972103 0.304875816469149 A A A 0.430969075041924 0.336846148179546
0.950301303183577 A A A LNCV6_143444_PI430048170 mRNA
ATTTTATTTCCTTCTTGTGCTGCTCTGGAAGAGAGGCAGTAGCAAAGAGATGAGCTCCTG NM_177550 RefSeq chr17
- 6684712 6713421 SLC13A5 284111 "solute carrier family 13 (sodium-dependent citrate
transporter), member 5, transcript variant 1"
GO:0071422|GO:0016323|GO:0015746|GO:0015141|GO:0005886|GO:0035674|GO:0015137|GO:0017153|GO:0016
021|GO:0006814|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131553_PI430048170 0.125513823304082 0.849536886380327 8.18362578828427
8.00971162978754 8.17537348078317 P P P 8.22200947667701 8.2965575910483
8.54264782404188 P P P LNCV6_131553_PI430048170 mRNA
CTATTTGAGTATCTAGAGAAAAATTAAAATGCAATGAGTTAGCAGTATACCCTGGCACAC NM_022149 RefSeq chr3
- 184710366 184712048 MAGEF1 64110 melanoma antigen family F1 GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133352_PI430048170 0.227836747737446 2.02057426845375 0.453269624192343
2.15977814037672 1.22443856610926 A A A 0.442269771332312 0.416696726102507
0.434986660857642 A A A LNCV6_133352_PI430048170 mRNA
GGTGTTACATGTTGGCTGATACATATTCATGCATTTACATGATTGCAGTACTTTATAGCT NM_002619 RefSeq chr4
- 73980824 73982124 PF4 5196 platelet factor 4
GO:0048248|GO:0019221|GO:0005615|GO:0045653|GO:0006955|GO:0006954|GO:0045944|GO:0042127|GO:0045
347|GO:2001240|GO:0032496|GO:0030816|GO:0043950|GO:0031093|GO:0008201|GO:0008009|GO:0070098|GO:0
032760|GO:0010744|GO:0030595|GO:0030168|GO:0005576|GO:0045651|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140563_PI430048170 0.0275896696361847 0.531082222838779 4.6052384931608
4.53374190908895 5.2036307549187 P P P 5.79574816256841 5.44448298604441
5.90051766170564 P P P LNCV6_140563_PI430048170 mRNA
GAAGACTACGCTGCATATTCAAGAGTTGTACCTTAACATTGGTGAAACATTTTTTCTAAG NM_032783 RefSeq chr4
- 168987590 169010317 CBR4 84869 carbonyl reductase 4
GO:0044598|GO:0005515|GO:0048038|GO:0044597|GO:0051289|GO:0005759|GO:0003955|GO:0006633|GO:0070
402|GO:0008753|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141739_PI430048170 0.610128400896057 1.07912828524383 5.62456480113404
5.27019376962728 5.32562279060612 P P P 5.57627572197841 5.35505480325176
4.90692033084987 P P P LNCV6_141739_PI430048170 mRNA
TAGTCTCTAGTGTTCTCTGAGGCCCCAGCAATAAAGTGTCTTGATGTAGAACTCAAAAAA NM_001145018 RefSeq
chr11 - 119190253 119195874 CCDC153 283152 coiled-coil domain containing 153 NA . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_138345_PI430048170 0.0235191722448849 0.1285235371355363.27291693007542
1.8667757992047 3.53038421625582 P A P 5.8591539515964 5.97916469116362
6.17707444592639 P P P LNCV6_138345_PI430048170 mRNA
CGTATTTTAGGTGACTGAAATTGCAACAGTGATCATAATGAGGTTTGTTAAAACGATAGC NM_005845RefSeq chr13
- 95019828 95301446 ABCC4 10257 "ATP-binding cassette, sub-family C (CFTR/MRP), member 4,
transcript variant 1"
GO:0014070|GO:0031088|GO:0005886|GO:0042493|GO:0042626|GO:0010243|GO:0030168|GO:0055085|GO:0048
661|GO:0005524|GO:0008150|GO:0016323|GO:0016020|GO:0007596|GO:0002576|GO:0016021|GO:0055114|GO:0
016404 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138994_PI430048170 0.417742881561796 0.697302379070239 0.459793208876797
0.468480617444377 1.34554616338121 A A A 0.402192072740949 1.48928037002515
1.79580406733855 A A A LNCV6_138994_PI430048170 mRNA
GAGATGTAAAGTCTCCTATTCAGTGAGCCAATGTTCTTTGAATGCCTATATGAAATTTTC NM_001131065 RefSeq
chr5 + 95646878 95657145 RFESD 317671 "Rieske (Fe-S) domain containing, transcript variant 1"
GO:0051537|GO:0016491|GO:0046872|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139854_PI430048170 0.0162903303040788 1.34246694346152 13.482080628905
13.7484657755228 13.6286705164912 P P P 13.2321481224908 13.1164234318329
13.2448385103377 P P P LNCV6_139854_PI430048170 mRNA
CTTGGTGTAGACAAATACCAGTTCCCATTGGTGTTGTTGCCTATAATAAACACTTTTTTC NM_080592RefSeq chr2
+ 27212030 27217178 ATRAID 51374 "all-trans retinoic acid-induced differentiation factor, transcript
variant 2"
GO:0045669|GO:0010468|GO:0005515|GO:2000599|GO:0003674|GO:0048471|GO:0033689|GO:0030501|GO:0005
886|GO:0016021|GO:0005635|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102836_PI430048170 0.00543307283135075 1.94523494122959 11.8981545538253
12.2232540977639 12.1797583350167 P P P 11.1585301673986 11.0722051949851
11.2084114830999 P P P LNCV6_102836_PI430048170 mRNA
GTGAGATTTTAGTATTGTTAATCCTGCCAGTCTTTCTCTTCAAGCCAGGGTGCATCCTCA NM_177433RefSeq chrX
+ 54807598 54816015 MAGED2 10916 "melanoma antigen family D2, transcript variant 2"
GO:0016020 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143573_PI430048170 0.484760959672444 0.629137096849152 2.65694257216009
2.48216578798587 2.42682602163627 A A A 2.42579178635208 2.45918170472432
4.05139240488593 A A P LNCV6_143573_PI430048170 mRNA
TCCTACACACAAGCCCTGGTCAGTGTGTCTTGACGACAGGTTCAATTTAGCTCATCAAAT NM_001123364 RefSeq
chr6 - 110245945 110358272 METTL24 NA methyltransferase like 24 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_134022_PI430048170 0.498212121215448 1.14907692145114 0.938580386544948
0.727052907212465 1.32146501164551 A A A 0.620010781511156 1.23714261588397
0.47431039416413 A A A LNCV6_134022_PI430048170 mRNA
TGTTCCAAAAACCCAAGTAGTCAGTCCCTTGTGTACTGTGGTAAACCTGTTTATGTTCAC NM_139214RefSeq chrY
+ 3579084 3580041 TGIF2LY 90655 "TGFB-induced factor homeobox 2-like, Y-linked"
GO:0006355|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142122_PI430048170 0.000934279029004603 0.533093011325819 7.62929869252487
7.43013916705597 7.57992431856645 P P P 8.3544487811692 8.40054653939172
8.60216046767938 P P P LNCV6_142122_PI430048170 mRNA
CTCAAGTGGGATTAGAAGACTATCAAAATACATGTATGTTTCAGGATATTTGACCTGTCA NM_002835RefSeq chr7
+ 77537455 77640071 PTPN12 5782 "protein tyrosine phosphatase, non-receptor type 12, transcript
variant 1"
GO:0005515|GO:0017124|GO:0005737|GO:0030054|GO:0006470|GO:0005886|GO:0002102|GO:0042995|GO:0035
335|GO:0005829|GO:0004726 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_144207_PI430048170 0.1510027411242471.10269934285227 9.53784236549407
9.67652238923713 9.75145116796088 P P P 9.51835075136086 9.54197468148395
9.48998279295174 P P P LNCV6_144207_PI430048170 mRNA
TATTTGATTCAGTTTTTTCAGCGTCTTTCTGGGGCGGAATGTTGGTACCCATTGGTGATA NM_015380RefSeq chr22
+ 43955380 43996532 SAMM50 25813 SAMM50 sorting and assembly machinery component
GO:0005739|GO:0005515|GO:0001401|GO:0006626|GO:0005743|GO:0005741|GO:0016021|GO:0045040|GO:0044
267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129512_PI430048170 0.00232046042065657 0.5570432125325767.05654234507758
7.07154995848094 7.03494583768439 P P P 7.99433910413105 7.8508680623322
7.84548712373408 P P P LNCV6_129512_PI430048170 mRNA
ACCTGATGTGGCAACGTTTTACAGTCTTGCTATTGTTTCTTGAGTCCTTTAATCTATAAGNM_004756RefSeq chr19 -
40665905 40690658 NUMBL 9253 "numb homolog (Drosophila)-like, transcript variant 1"
GO:0005515|GO:0005737|GO:0021849|GO:0021670|GO:0050769|GO:0050775|GO:0019221|GO:0007409|GO:0019
538|GO:0034332|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133235_PI430048170 0.6694757235916671.03613662282499 14.786288774274
14.8640868140548 15.0293452528596 P P P 14.7276947499819 14.7718454396068
15.0198140328779 P P P LNCV6_133235_PI430048170 mRNA
GAAGGAGCCTGAGCTGCTGGAACCTATTCCCTATGAATTCATGGCATAATAGGTGTTAAA NM_000982RefSeq chr13
+ 27251554 27256565 RPL21 6144 ribosomal protein L21
GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0005730|GO:0006415|GO:0006
412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0000184|GO:0016020|GO:0016032|GO:0022625|GO:0
044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131764_PI430048170 0.1996752653480960.8873193977710611.3067260004662
11.2198249667811 10.9926717881471 P P P 11.2389762900239 11.4400712265793
11.3683865957074 P P P LNCV6_131764_PI430048170 mRNA
TGAAACTCTGCCTGCAGCAGGACTGGCCGCCCCTGCTGTGGGGGGTTCAGAAAATAAAAT NM_003683RefSeq chr21
+ 43789536 43804102 RRP1 8568 ribosomal RNA processing 1
GO:0006364|GO:0005730|GO:0005634|GO:0030688 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117593_PI430048170 0.0723540223682091 0.3939925338305560.333375099197618
0.2678918685887330.37115345713698 A A A 0.9442106489827811.60557793157025
2.19200295079673 A A A LNCV6_117593_PI430048170 mRNA
GATGGACAGTTCCCATTGTGCATTGCCTTTGATAAATTTGGCCTTAATTTATATAACGAT NM_001164746 RefSeq
chr12 + 26052557 26072874 RASSF8 11228 "Ras association (RalGDS/AF-6) domain family (N-terminal)
member 8, transcript variant 1" GO:0007165 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127059_PI430048170 0.1881122011757831.01564446814205 0.314043767533619
0.2755948359091680.286761834733984A A A 0.2728456193344420.268315132245087
0.268320183184353A A A LNCV6_127059_PI430048170 mRNA
CCACTAGGATCCCAGAAGGAAACTAAATTCATCCAAGGTAGTTCAATTAAATTGACTTTT NM_173352RefSeq chr12
- 52837803 52848994 KRT78 196374 "keratin 78, type II, transcript variant 1"
GO:0005198|GO:0045095|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134189_PI430048170 0.4144368175636820.8881098805743730.319181900053205
0.3275668375857920.386249942589351A A A 0.3746244317121150.322314819972965
0.801258420077467A A A LNCV6_134189_PI430048170 mRNA
CAAGCAAAAGAATCAGTCAAGAATCACATGTTTGCTTATGGCTTACAAATAAAAACGCTG NM_145314RefSeq chr10
- 13221765 13234328 UCMA 221044 "upper zone of growth plate and cartilage matrix associated,
transcript variant 1" GO:0048471|GO:0045668|GO:0016235|GO:0005578|GO:0005615 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_129986_PI430048170 0.1637715924222390.83121561429262 5.43882527947668 5.1585107283103
5.5005218027187 P P P 5.46136053430075 5.58299965182993 5.84856836108563 P P P

LNCV6_129986_PI430048170 mRNA
GTCTGGTTCTGTCCTAGAGGAAATAAATTCACTATTAATTCATGTCTTAAGTTACTTGGG NM_052855 RefSeq chr17
- 50693189 50707909 ANKRD40 91369 ankyrin repeat domain 40
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68315_PI430048170 0.28708228072408 1.12330846695661 9.62581418030608 9.79328455360897
9.92161043449502 P P P 9.59314679329283 9.4302657558674 9.80467330158458 P P P
LNCV6_68315_PI430048170 mRNA
GAAGAAGTTCTTCAGTACTGTCAGGAGATGTATCCAGAGCTACAGATCACAAATGTGATG NM_001642 RefSeq chr11
+ 130069820 130144811 APLP2 334 "amyloid beta (A4) precursor-like protein 2, transcript variant 1"
GO:0005515|GO:0005886|GO:0004867|GO:0007617|GO:0046914|GO:0043393|GO:0005634|GO:0003677|GO:0042
802|GO:0010951|GO:0001967|GO:0006878|GO:0016020|GO:0007186|GO:0030198|GO:0007176|GO:0050885|GO:0
030901|GO:0007626|GO:0030900|GO:0016021|GO:0008201|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138860_PI430048170 0.2030693705654521.0482201915015 0.467527647881437
0.3880782878051210.446924920670461 A A A 0.3038042206953420.36289456912447
0.430396794258004 A A A LNCV6_138860_PI430048170 mRNA
CAAAACTGCTCAACTCTGTTAACTTCTGTTACTATAAATAAAGGCATGTGCCTAGTTTTG NM_152570 RefSeq chr9
- 27948085 28719305 LINGO2 158038 "leucine rich repeat and Ig domain containing 2, transcript variant
1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135086_PI430048170 0.4449212729355091.12945617203532 2.85486323151065
2.41927599144622 2.96360041591671 A A P 2.69448145626186 2.58538494813763
2.47837817241031 P P P LNCV6_135086_PI430048170 mRNA
AACAGAGTTTATTTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCTTGGCCCTTATAGGAC NM_014693 RefSeq chr3
+ 184249656 184293031 ECE2 9718 "endothelin converting enzyme 2, transcript variant 1"
GO:0008168|GO:0007267|GO:0032259|GO:0046872|GO:0007507|GO:0000139|GO:0016486|GO:0007420|GO:0006
508|GO:0010002|GO:0016021|GO:0004222|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131851_PI430048170 0.0687242558014953 1.25608335850857 6.7729297066933
6.91448688964699 6.92449303695275 P P P 6.33380749490221 6.69112807063071
6.58223179674604 P P P LNCV6_131851_PI430048170 mRNA
TTGTTTGAGAATAGCAAATACGCATGTTGATTGCGAGTGTGTGGAGACAAAGGCAGTTCC NM_001042476 RefSeq
chr16 - 8852941 8868401 CARHSP1 23589 "calcium regulated heat stable protein 1, 24kDa,
transcript variant 2"
GO:0035556|GO:0043488|GO:0006355|GO:0019902|GO:0000932|GO:0000177|GO:0043186|GO:0003730|GO:0003
677|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132734_PI430048170 0.00452332031103478 0.5027756808133844.57077104952392
4.97413531667504 4.94245640539346 P P P 5.80712836679855 6.00080599337973
5.67000675445858 P P P LNCV6_132734_PI430048170 mRNA
TCTGCTTCCCGAGCAACATCTGCGTGTCGGTCTGCTTTTATTACCTCCCAGACTGAGCCC NM_182563 RefSeq chr16
- 2209252 2211068 BRICD5 283870 BRICHOS domain containing 5 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127338_PI430048170 0.0357872188047142 1.48665887695488 5.28613423168195
5.15514407068391 4.86384588443126 P P P 4.74049659377143 4.56555381718027
4.27725342296389 P P P LNCV6_127338_PI430048170 mRNA
GGAGTAGGGAAGGTTTAATAGTAAAATAAACGTGGCTATATTTTAACATAAGATGTAAAA NM_001017981 RefSeq
chr22 - 30378813 30387313 RNF215 200312 ring finger protein 215 GO:0008270|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63607_PI430048170 0.0909568034072544 1.23397399496002 12.8544791588397 12.916689360588
12.8404366787835 P P P 12.3589071475956 12.6105760761248 12.7109325348847 P P P
LNCV6_63607_PI430048170 mRNA

TCCCCAGGCTATAAATTTGTTCTCACAAAGCAACATCAATAAATCAAAACTGTCTCTCCC NM_144998RefSeq chr17 - 82018702 82022909 STRA13 201254 "stimulated by retinoic acid 13, transcript variant 2" GO:0005515|GO:0071821|GO:0006334|GO:0003677|GO:0043240|GO:0034080|GO:0007067|GO:0051382|GO:0003690|GO:0006281|GO:0000712|GO:0000777|GO:0031398|GO:0005654|GO:0031297|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139927_PI430048170 0.980119546949082 1.00011142310951 0.264745128788435 0.281999743093568 0.425414723403282 A A A 0.35791074302138 0.30952430190645 0.309146824823016 A A A LNCV6_139927_PI430048170 mRNA
GAGTTCTTTCTTTTGGTGTGGATTAGTATATCAGTTGATTTGTGTGAATTGTGGTGAAAC NM_001369RefSeq chr5 - 13690328 13944480 DNAH5 1767 "dynein, axonemal, heavy chain 5" GO:0008150|GO:0021670|GO:0005930|GO:0008152|GO:0005874|GO:0005858|GO:0003341|GO:0070986|GO:0005575|GO:0003777|GO:0016887|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145040_PI430048170 0.0142086155799129 0.60726621689633 6.19285472311759 6.14409934090275 6.56257145856577 P P P 7.04799381217755 6.86988316544299 7.16273823883629 P P P LNCV6_145040_PI430048170 mRNA
AAGTGAGGAAGAGTTTATGGCAAAGATTTTTGGCACTTTGTTTTCAAGATGGTGTTATCT NM_033338RefSeq chr10 + 113679668 113730909 CASP7 840 "caspase 7, apoptosis-related cysteine peptidase, transcript variant d" GO:0005515|GO:0008635|GO:0006915|GO:0097194|GO:0005634|GO:0006921|GO:0097193|GO:0005829|GO:0004197|GO:0005737|GO:0006508|GO:0005654|GO:0008234 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129797_PI430048170 0.0780958181635569 0.951628809337394 0.289331804426978 0.312043337124121 0.335730953693104 A A A 0.429183872030775 0.374435992114523 0.347235712580827 A A A LNCV6_129797_PI430048170 mRNA
GCAGTCTGGACTGTTGTAACCTTAGGTTGTAATCTGATTTGGAAATAAGTACATCTTTAA NM_021951RefSeq chr9 + 841689 969091 DMRT1 1761 doublesex and mab-3 related transcription factor 1 GO:0000987|GO:0003700|GO:0046661|GO:0005634|GO:0007283|GO:0048599|GO:0042803|GO:0046872|GO:0035556|GO:1900107|GO:0005737|GO:0060008|GO:0060009|GO:0030238|GO:0045944|GO:0008354|GO:0002176|GO:0046982|GO:0045840|GO:0000122|GO:0006351|GO:0000902|GO:0003682|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141276_PI430048170 0.81881838425238 0.983163826030178 0.281281655340852 0.51644234343404 0.347971462009714 A A A 0.521954107246096 0.420637797519575 0.276378763803932 A A A LNCV6_141276_PI430048170 mRNA
CCCAGTTAATGGGTTTTGATAGTCATGTTATCTCAGTAAGTGTCTTGTCTTAGAAATATG NM_001199295 RefSeq chr19 + 57527324 57540876 ZNF549 256051 "zinc finger protein 549, transcript variant 1" GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65716_PI430048170 0.00508728486543716 0.54915274517764 3.06667967019352 2.9650745965625 2.96499348647415 P A P 3.92796643822309 3.6832764959553 3.96607417952984 P P P LNCV6_65716_PI430048170 mRNA
CAACAATGTGCCTGAGGTGCATGGGAAATATAGTTAGCTATACTCTGAAAATACATTATG NM_177968RefSeq chr2 + 44168802 44234603 PPM1B 5495 "protein phosphatase, Mg2+/Mn2+ dependent, 1B, transcript variant 2" GO:0005515|GO:0050687|GO:0042347|GO:0000287|GO:0030145|GO:0019221|GO:0005829|GO:0006470|GO:0035970|GO:0016020|GO:0004722|GO:0006499|GO:0032688|GO:0043124 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127167_PI430048170 0.618870991071853 0.981656544073245 0.254352626376691 0.264674198544596 0.398124498282349 A A A 0.370151072053195 0.311395422769921 0.319532078959916 A A A LNCV6_127167_PI430048170 mRNA
CAACCCTACATATTTCTGATCATGTGCTGCCTTTTACTGCTGAATTAAAACAGATATTTC NM_032330RefSeq chr16 + 55566671 55567680 CAPNS284290 "calpain, small subunit 2"

GO:0005737|GO:0004198|GO:0005886|GO:0005509|GO:0006508 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134920_PI430048170 0.0938929506424218 0.7222573715699321 1.3192956879824 11.1786204533232 11.6061884991231 P P P 11.7649765416009 11.5832989047735 12.1404860941092 P P P LNCV6_134920_PI430048170 mRNA
CCTCTTGATGAAATGGACATATTATATATTTCTGCCACCTGGATTTTCCTGGATAATTTG NM_013417 RefSeq chr9 - 92210208 92293756 IARS 3376 "isoleucyl-tRNA synthetase, transcript variant 2"
GO:0005515|GO:0010467|GO:0002161|GO:0006428|GO:0004822|GO:0005524|GO:0001649|GO:0005829|GO:0006418|GO:0005737|GO:0016020|GO:0005654|GO:0006450|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80665_PI430048170 0.2975019829277842 .46772285318929 2.43329158963849 3.86638495995911 1.39588091752581 A P A 1.86175578083369 1.06066111927035 1.78447320231514 A A A LNCV6_80665_PI430048170 mRNA
AGCAGAAGCTGAGCAACATGGAGAACAGACTGAAGCCCTTCTTCACATGCGGCTCAGCAG NM_001782 RefSeq chr9 - 35609978 35618427 CD72 971 CD72 molecule
GO:0005515|GO:0007165|GO:0005886|GO:0007411|GO:0005887|GO:0005102|GO:0030246|GO:0007155|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136509_PI430048170 0.5573554958263171.00815521178195 0.367131714989631 0.3638793987318580.400404310162243 A A A 0.3747841038777580.337570078801796 0.38377708770461 A A A LNCV6_136509_PI430048170 mRNA
AGCACACACCCATACACATTAGATAAGGGTGGTTCATTATGGATGATTTTGAATTTTGGT NM_001024613 RefSeq chr7 - 122301308 122304511 FEZF1 NA "FEZ family zinc finger 1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93322_PI430048170 0.0158840448226091.09863248184289 13.1584225285719 13.0930758054696 13.1150133768812 P P P 12.9407839259356 13.0301906130374 12.9877934361167 P P P LNCV6_93322_PI430048170 mRNA
TGTTTCTGAAAACAGCTTGGATATTTTAATGCACGTTGCATTAAACCTCACTGAAACCTG NM_006830 RefSeq chr19 - 1597154 1605484 UQCR11 10975 "ubiquinol-cytochrome c reductase, complex III subunit XI"
GO:0022904|GO:0008121|GO:0070469|GO:0005743|GO:0009055|GO:0044281|GO:0016021|GO:0006091|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145575_PI430048170 0.1869063996971954.06955465683943 0.461225914501091 2.69266621393119 3.16856202623097 A A P 0.5629900096116840.408092265722002 0.413742099081814 A A A LNCV6_145575_PI430048170 mRNA
CATGATTTCAGGAAAATGTGAATTGGCTGTCTTGGTTTATGTTCGGCCACTGATGCACTC NM_173856 RefSeq chr19 + 53258291 53259602 VN1R2 317701 vomeronasal 1 receptor 2
GO:0016503|GO:0007186|GO:0005886|GO:0016021|GO:0019236 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139790_PI430048170 0.1709263660930810.8537397233059370.391083780526706 0.3863597693743390.262703309406603 A A A 0.59224652298588 0.74415836808467 0.367065532371349 A A A LNCV6_139790_PI430048170 mRNA
GTGTTATTACAGGTGCTTTTAAACTAGTAACTGCTTAAATAAAGTGTACTCGAAGCCAGT NM_021209 RefSeq chr2 - 32224448 32265743 NLRC4 58484 "NLR family, CARD domain containing 4, transcript variant 1"
GO:0005515|GO:0004842|GO:0004869|GO:0016567|GO:0005634|GO:0002218|GO:0035872|GO:0042803|GO:0005829|GO:0042802|GO:0005622|GO:0043523|GO:0005737|GO:0051092|GO:0006954|GO:0051260|GO:0005876|GO:0090307|GO:0042742|GO:0043066|GO:0000287|GO:0043065|GO:0006919|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131267_PI430048170 0.0827503295628799 0.7960178827526326.69363995404893 6.67807451154175 6.92117581539204 P P P 6.93764190162931 7.30578968652435 7.02371665702873 P P P LNCV6_131267_PI430048170 mRNA

AATCCTATTTTCTATGGAAGACTGGTACCTGGTTTCTGGAAGAGGGGTCTGTGACTTGGA NM_005729RefSeq chr10 + 79347463 79355333 PPIF 10105 peptidylprolyl isomerase F GO:0000413|GO:0005515|GO:0046902|GO:0043066|GO:0016018|GO:0070301|GO:0070266|GO:0010849|GO:0003755|GO:0090324|GO:0032780|GO:2001243|GO:0005753|GO:0008637|GO:0090201|GO:0016020|GO:0006457|GO:0002931|GO:0005759|GO:0090200|GO:0010939|GO:0071277|GO:2000276|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138094_PI430048170 0.0182014206302391 0.3752083128247271.12429625858989 0.66151293099166 0.28679665305105 A A A 1.66372746536931 2.03286449337283 2.58891027924351 A A P LNCV6_138094_PI430048170 mRNA
ACACCTTAAGGGTCTAACTTGTAATGAAGACAGAAATATGTATGAGGATGATCACTGAAA NM_015394RefSeq chr12 + 133130627 133159463 ZNF10 7556 zinc finger protein 10 GO:0005515|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130941_PI430048170 0.3119754536106850.6354135991507530.537509286879997 0.48844542612198 0.603850156753643A A A 0.3067429024271251.28286755824549 1.68429354285701 A A A LNCV6_130941_PI430048170 mRNA
GTTTCCATGTCTTCTTCTCTTTCCTCCTATGGCAAATAAAACACTGTTTTGCAACACAAANM_004001RefSeq chr1 + 161663114 161678654 FCGR2B 2213 "Fc fragment of IgG, low affinity IIb, receptor (CD32), transcript variant 1" GO:0005515|GO:0007165|GO:0006955|GO:0005886|GO:0019864|GO:0050776|GO:0016032|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143372_PI430048170 0.0932454083553586 0.7577265427025354.88301818280484 4.50520000209247 5.00414067338298 P P P 5.0544485409918 5.29475521037976 5.27727747987249 P P P LNCV6_143372_PI430048170 mRNA
GCCATTTTTCAGAGATACAGTATCAGAAATAGTATTATTACAGAAGCTTTACCCAGGACA NM_014487RefSeq chr4 + 141220886 141234696 ZNF330 27309 "zinc finger protein 330, transcript variant 1" GO:0008150|GO:0005730|GO:0030496|GO:0008270|GO:0046872|GO:0000775 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142078_PI430048170 0.1355924465642370.7873002003965891 2.1961630632515 11.8319972813761 11.6988733474842 P P P 12.2592457069978 12.2629200274865 12.286679473039 P P P LNCV6_142078_PI430048170 mRNA
TGCACTGATGACTTGACCAGCCCCTCCCCCAATAAACTCGCCTCTTGGAAATGGAAAAAA NM_001166111 RefSeq chr19 + 7534704 7561767 PNPLA6 10908 "patatin-like phospholipase domain containing 6, transcript variant 1" GO:0016042|GO:0032502|GO:0016020|GO:0005783|GO:0004622|GO:0005789|GO:0009887|GO:0046470|GO:0016021|GO:0001525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134092_PI430048170 0.53740400319017 0.8540890552588551.56575646463775 0.3413346612635292.62372970100216 A A A 2.08459111520993 1.68568857968606 2.23490082166869 A A A LNCV6_134092_PI430048170 mRNA
CCTAACTGTGATAGTCTTACCTGTGTTCTGCCTTTGTCACTTGTGTTTAAGCCTTTTTTC NM_001143821 RefSeq chr12 + 19129691 19373668 PLEKHA5 54477 "pleckstrin homology domain containing, family A member 5, transcript variant 2" GO:0005515|GO:0008150|GO:0005545|GO:0016020|GO:0080025|GO:0070273|GO:0032266|GO:0010314|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57490_PI430048170 0.0801545261315754 1.25694922732935 11.8481595710602 11.8177005274504 11.7800808042672 P P P 11.2724269342468 11.6177112610742 11.544376065354 P P P LNCV6_57490_PI430048170 mRNA
TTTCCTCTATCTGGCTATGTTGAGTTACGTTATGATGATGAAGTGAAGCGGGTGGTGGCA NM_004551RefSeq chr11 + 47579009 47584563 NDUFS3 4722 "NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)"

GO:0005515|GO:0030308|GO:0031966|GO:0072593|GO:0005743|GO:0009055|GO:0005634|GO:2001243|GO:0044281|GO:0003954|GO:0005739|GO:0022904|GO:0005747|GO:0021762|GO:0006120|GO:0008137|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101195_PI430048170 0.8849518938312320.9925945866052547.97429708520561 8.12438767734389 8.38273453890604 P P P 8.24386183740005 8.13553392922375 8.16186039651084 P P P LNCV6_101195_PI430048170 mRNA
TACATCTTACCCATGCTCTTTCAAAGACTGTGCTGAGAGAGAACTTGTGGCAGTTATATG NM_024699RefSeq chr8 - 81701330 81721304 ZFAND1 79752 "zinc finger, AN1-type domain 1, transcript variant 1"
GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134854_PI430048170 0.57888838963532 1.39378759106272 1.59331384829506 2.33043922218805 0.378682701944819A A A 0.5041250880169931.96523825015071 0.468075830045816A A A LNCV6_134854_PI430048170 mRNA
CAAACCCATATAGGAGAGAAATCTGACGTAGCTGAGGCAGGCTATGTGTTCCCTCAAAAT NM_001128223 RefSeq chr3 - 75736877 75785104 ZNF717 100131827 "zinc finger protein 717, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140467_PI430048170 0.4862108181842031.17226552201429 0.298103807505063 1.02464426088571 0.40122577810276 A A A 0.2830108588441710.248364892521947 0.591018229664287A A A LNCV6_140467_PI430048170 mRNA
TTTTGTAAGAGAAATTAAGGATGGCAAAATGGTTATGACCCTTACTTTTGGTGATGTGGT NM_001446RefSeq chr6 + 122779500 122784073 FABP7 2173 "fatty acid binding protein 7, brain"
GO:0005215|GO:0021846|GO:0008285|GO:0060134|GO:0005634|GO:0042995|GO:0050673|GO:0007399|GO:0008289|GO:0005737|GO:0006810|GO:0043025|GO:0022008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138925_PI430048170 0.0621476725720425 0.8499689520634749.81335320836259 9.84050136742951 9.83070388319935 P P P 10.0566508776699 9.95470094723359 10.1689268130053 P P P LNCV6_138925_PI430048170 mRNA
ATGTTGCCCACACCTAAGTGTTAGAAGCCTATGTCCGTTCATCCCTGAGAGGTCTGAAAG NM_003869RefSeq chr16 + 66934443 66945091 CES2 8824 "carboxylesterase 2, transcript variant 1"
GO:0052689|GO:0005783|GO:0005788|GO:0047374|GO:0009056|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60254_PI430048170 0.2705306121982631.41976707214126 1.71518890575109 1.81115368492543 2.17967919565607 A A A 1.87207409340977 0.54754574238954 1.51256941743133 A A A LNCV6_60254_PI430048170 mRNA
AAGAGATGTAATAGATTTCACATTATGGCAGTTACTAAAGAAGCACGTGACAGACACATC NM_001011724 RefSeq chr13 + 52617469 52643784 HNRNPA1L2 144983 "heterogeneous nuclear ribonucleoprotein A1-like 2, transcript variant 1" GO:0005737|GO:0000166|GO:0003723|GO:0000380|GO:0005681|GO:0051028 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143702_PI430048170 0.00563481320276706 0.2174454501322128.9093740001027 8.8130737231794 8.8172261313179 P P P 10.6653236281665 11.2171426457909 11.1981469560034 P P P LNCV6_143702_PI430048170 mRNA
GACAGTTTATTTGTTGAGAGTGTGACCAAAAGTTACATGTTTGCACCTTTCTAGTTGAAA NM_001901RefSeq chr6 - 131948176 131951378 CTGF 1490 connective tissue growth factor
GO:0060401|GO:0005515|GO:0005801|GO:0010467|GO:0070278|GO:0006367|GO:0045597|GO:0046330|GO:0001558|GO:0005615|GO:0035988|GO:0030154|GO:0043231|GO:0001894|GO:0060548|GO:0070374|GO:0005938|GO:0032355|GO:0044255|GO:0005520|GO:0005794|GO:0034059|GO:0051385|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57602_PI430048170 0.9057826324934270.9838250717564686.81092199465208 6.56843993386826 6.77313278739948 P P P 6.50415559919835 6.80623764606603 6.89577578664918 P P P LNCV6_57602_PI430048170 mRNA

TATTCCATAAGTTCAAAGGGACCATCATCCTGACAGCTGTGTACTTTGCCCTCAGCATCT NM_016464RefSeq chr11 + 61362000 61369503 TMEM138 51524 "transmembrane protein 138, transcript variant 1" GO:0042384|GO:0005929|GO:0005774|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_128640_PI430048170 0.0201334426753021 0.6022339098845117.21063936470568 7.35833808854203 7.68341726767531 P P P 7.92104867504213 8.13256167743077 8.39552242534367 P P P LNCV6_128640_PI430048170 mRNA
GTGACTTTACTTTCTCAAGTTTGATACTGAGTTGACTGTTCCCTTATCCCTCACCCTTCC NM_001142930 RefSeq chr11 + 43311954 43344530 API5 8539 "apoptosis inhibitor 5, transcript variant 1" GO:0005515|GO:0043066|GO:0005737|GO:0016020|GO:0017134|GO:2000270|GO:0006915|GO:0005681|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_141538_PI430048170 0.0475848213591878 0.43543697244793 2.01624289297346 2.98066830513226 2.98633496041495 A P P 3.80390860738158 4.14217868809927 3.80667635233239 P P P LNCV6_141538_PI430048170 mRNA
CTTGTGATGTAAGAAATTTGTATGGTGTGGCAGTGGTCTATTCCTAAGGAACTAAATATC NM_002519RefSeq chr11 - 108157390 108222638 NPAT 4863 "nuclear protein, ataxia-telangiectasia locus" GO:0005515|GO:0010468|GO:0015030|GO:0003714|GO:0003713|GO:0005634|GO:0008022|GO:0006351|GO:0005737|GO:0000083|GO:0047485|GO:0005654|GO:0045893 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_53640_PI430048170 0.7830450825527181.28005006961416 1.97355219513666 0.259558667249038 2.17742809612718 A A A 1.47165926202516 1.6818467481897 0.637238184008827A A A LNCV6_53640_PI430048170 mRNA
ACGGACCTCCTTTGGCTCTCTGACAGACAGCAGTGAAGAGGCACTGGAAGGAATGGTACG NM_001297647 RefSeq chr1 + 26177489 26189884 CNKSR1 10256 "connector enhancer of kinase suppressor of Ras 1, transcript variant 3" GO:0005886|GO:0005911|GO:0007265|GO:0007266|GO:0030674|GO:0007169|GO:0005938 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_145328_PI430048170 0.00832278577188315 0.3351635768984260.276457637407603 0.2929139313321921.02688950956373 A A A 1.76841316129746 2.14915149540406 2.46103482952762 A A P LNCV6_145328_PI430048170 mRNA
CAGCCATACTTGCATGGAAACTGACTACACATACATAATACTGCATTTTATTGTAAGGTT NM_001080416 RefSeq chr8 - 66562174 66613249 MYBL1 4603 "v-myb avian myeloblastosis viral oncogene homolog-like 1, transcript variant 1" GO:0010467|GO:0001077|GO:0045944|GO:0003682|GO:0034587|GO:0005634|GO:0045893|GO:0000978|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_139546_PI430048170 0.00440390384036241 0.3402263302334245.22474692236824 5.24562023642986 5.45172374082357 P P P 6.57151977132913 6.83888648629689 7.13416017576989 P P P LNCV6_139546_PI430048170 mRNA
AGTGTTCTCCACATAATGGAAAATGTACAAATGCCTAGTTGTGTTGCCCATCAATTTTGT NM_024953RefSeq chr12 - 112026688 112108831 NAA25 80018 "N(alpha)-acetyltransferase 25, NatB auxiliary subunit" GO:0005737|GO:0005794|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_138265_PI430048170 0.0908062021732266 0.5292385079512965.19438981500485 3.98083144824121 4.69684264949046 P P P 5.29240329884143 5.75212963202165 5.77970495547599 P P P LNCV6_138265_PI430048170 mRNA
GGCTATGGTGTAGAGACCTCTTTCTAATAAAGAAATGAAAATATGTCTACACCGCTAAAA NM_001037131 RefSeq chr2 + 235494088 236131800 AGAP1 116987 "ArfGAP with GTPase domain, ankyrin repeat and PH domain 1, transcript variant 1" GO:0043547|GO:0008060|GO:0005737|GO:0005543|GO:0032312|GO:0007264|GO:0008270|GO:0015031|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_131004_PI430048170 0.00731488274145134 0.5959119100936491 0.1645611034013 9.96107172728365 10.3021862448066 P P P 10.7872561394402 10.7710856839812 11.1050457319613 P P P LNCV6_131004_PI430048170 mRNA

CCTGAACTGAACACCATTGAAGGCTTAAACCCATATTGTAAAACAGGTAGAATTATCTAA NM_002532RefSeq chr17 - 5386025 5419739 NUP88 4927 nucleoporin 88kDa
GO:0007077|GO:0005215|GO:0010467|GO:0005975|GO:0019083|GO:0019221|GO:0019058|GO:0044281|GO:0015031|GO:0055085|GO:0010827|GO:0005829|GO:0008645|GO:0015758|GO:0005643|GO:0009405|GO:0016032|GO:0005654|GO:0051028|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58097_PI430048170 0.71479626527082 1.76886994956449 2.95915759063028 0.388843080153889 0.489753741417348 A A A 1.5223471555132 0.49911979764262 0.71769067860492 A A A
LNCV6_58097_PI430048170 mRNA
GGGAGGTAGTTTTGTGCATGGGTAAACAAATTAAGTATTAACTGGTGTTTTACTATCCAA NM_001165 RefSeq chr11 + 102317449 102339403 BIRC3 330 "baculoviral IAP repeat containing 3, transcript variant 1"
GO:0005515|GO:0004842|GO:0016567|GO:0034142|GO:0016874|GO:0034121|GO:0070424|GO:0005634|GO:0007283|GO:0051291|GO:0005829|GO:0002756|GO:0005737|GO:0031398|GO:0005876|GO:0090307|GO:0060544|GO:0043123|GO:0034138|GO:0060546|GO:0043027|GO:0043066|GO:0070266|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128139_PI430048170 0.0722526557720051 0.86922803269352 14.8330189499314 14.7344525149597 14.9549169325293 P P P 15.0037840447678 15.0764719976829 15.0562130566324 P P P LNCV6_128139_PI430048170 mRNA
TGTGTTGATACTGTTGCACGTGTGTTTTTCTATTAAAAGACTCATCCGTCTCCCAAAAAA NM_001436 RefSeq chr19 - 39834452 39846414 FBL 2091 fibrillarin
GO:0005515|GO:0016074|GO:0015030|GO:0001652|GO:0031428|GO:0003723|GO:0006364|GO:0005730|GO:0005634|GO:0001649|GO:0008033|GO:0016020|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143146_PI430048170 0.482931299140833 0.896591244919067 3.11461117404161 3.60721161822268 3.84524481376247 P P P 3.59695431857817 3.8115487805179 3.71608842495551 P P P LNCV6_143146_PI430048170 mRNA
TTCTGATTATCAAAGTGATAACCAGTTTTAACTGCCGGTATGTACCAGATTTGTGAACTA NM_001037954 RefSeq chr11 + 111937202 112022650 DIXDC1 85458 "DIX domain containing 1, transcript variant 1"
GO:0005515|GO:0043015|GO:0021695|GO:0021869|GO:0090263|GO:0019904|GO:0046330|GO:0003779|GO:0031435|GO:0005829|GO:0070507|GO:0043234|GO:0007049|GO:0045665|GO:0032956|GO:0021799|GO:0043025|GO:0043679|GO:0050772|GO:0016055|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136001_PI430048170 0.649220992189786 1.23827877788615 1.59556890334325 0.29583054196022 0.493896300343386 A A A 0.301713552586976 0.264858882090191 1.09430116421903 A A A LNCV6_136001_PI430048170 mRNA
GATGGGTTCTGTGTGGAGAAGCCAAACAATAAAACAACCTAGTGGGCAACCTTCTTAATT NM_007374 RefSeq chr14 + 60509219 60511807 SIX6 4990 SIX homeobox 6
GO:0045944|GO:0009887|GO:0001205|GO:0005634|GO:0007601|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139227_PI430048170 0.165667823943378 0.835780851076895 7.99813127034606 8.06681448274568 7.79767730355595 P P P 8.09153182724155 8.44751183725079 8.08253468447717 P P P LNCV6_139227_PI430048170 mRNA
AAATCCAGTGTAAATGCTCAGCCTGAGATTAAGGGGACAGAAGAATGGACTCATAGGTGG NM_207644 RefSeq chr22 - 24585622 24593068 LRRC75B 388886 leucine rich repeat containing 75B NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131600_PI430048170 0.493222429406936 0.922696894307003 9.73996356452563 9.50416110242704 9.59280735907744 P P P 9.776556541813 9.90154742541903 9.48605193337398 P P P LNCV6_131600_PI430048170 mRNA
TTGTCATTTGAGGATGCCAACCGCGCCATGCAGACTGGTGTCACCGGGATCATGATTGCC NM_020175 RefSeq chr19 - 5785141 5791238 DUS3L 56931 "dihydrouridine synthase 3-like (S. cerevisiae), transcript variant 1"

GO:0050660|GO:0017150|GO:0046872|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138570_PI430048170 0.00166714810087238 6.32213109748109 5.19271305019536 5.23236975836476 4.86687781867868 P P P 2.42515544384212 2.47278013669631 2.43950208792725 A P P LNCV6_138570_PI430048170 mRNA GTGATGAACGCTCTGAACCCCCTATAAAAAATGTGCATGTAAATATATACTCTCAACATT NM_144613 RefSeq chr19 - 55349701 55354814 COX6B2 125965 cytochrome c oxidase subunit VIb polypeptide 2 (testis) GO:0005758|GO:0004129|GO:0030061 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141240_PI430048170 0.761426370614964 0.991364702154352 0.380732033976215 0.357579028506236 0.255917277009464 A A A 0.332524860850245 0.36066093269422 0.341467422135212 A A A LNCV6_141240_PI430048170 mRNA CAACTCTTGATTAGAAGTCTTCAGTTGAAATTCCACTACAAAAGACATCATTCCAGACTA NM_001010868 RefSeq chr6 + 87344852 87365463 C6orf163 NA chromosome 6 open reading frame 163 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65635_PI430048170 0.132961796525381 0.83506716569274 7.28986934586677 7.18688594719376 7.51150809952549 P P P 7.40076959378008 7.62890941246241 7.73777879697429 P P P LNCV6_65635_PI430048170 mRNA TATGGCTTTCTTATCTAAACTGCACTGATGAACTAGATTAAAGCCTTGGGAGATTTATAC NM_001042548 RefSeq chr2 - 36552260 36598189 FEZ2 9637 "fasciculation and elongation protein zeta 2 (zygin II), transcript variant 2" GO:0005515|GO:0007165|GO:0007411|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138104_PI430048170 0.182419562577161 1.13824874764619 12.0415051555703 12.1429356773868 12.3204019385046 P P P 11.8910777489238 11.9065100220761 12.1462785059733 P P P LNCV6_138104_PI430048170 mRNA TCTGTTTTTATGGAAACTCAAATGCTGCCTTAGAAATCACTCCTAGATGAAATGTTTCTC NM_138408 RefSeq chr6 + 110958559 110967888 GTF3C6 112495 "general transcription factor IIIC, polypeptide 6, alpha 35kDa" GO:0005515|GO:0042797|GO:0000127|GO:0005654|GO:0042791|GO:0006383|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55798_PI430048170 0.367365398550761 1.82509973715362 3.62207107479062 5.59408658626891 4.88988396755252 P P P 4.2030292288297 3.84266529221244 4.06119108194858 P P P LNCV6_55798_PI430048170 mRNA ATAAAGAGAAACCTCAAGATGTGGATTTACCTTATCCCCTCAACAACTTTTCAGTGGCAA NM_005465 RefSeq chr1_KI270763v1_alt - 511826 855380 AKT3 10000 "v-akt murine thymoma viral oncogene homolog 3, transcript variant 1" GO:0005515|GO:0007165|GO:0005737|GO:0005794|GO:0004672|GO:0005886|GO:0004674|GO:0006468|GO:0005654|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137137_PI430048170 0.0340847320923627 0.78285221291685 4.45362556330136 4.3931021041481 4.52202717879435 P P P 4.64369209792721 4.90460419706382 4.86927608120421 P P P LNCV6_137137_PI430048170 mRNA CATGTACAGGACACCATTCAAAATGGCTTGAAAATATTCAGCATGTTTGTTATTTGCTGT NM_001190826 RefSeq chr20 + 59933763 59948647 FAM217B 63939 "family with sequence similarity 217, member B, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120517_PI430048170 0.075320400916054 1.09221490611078 14.8035780367698 14.9150954036127 14.9361064913935 P P P 14.7398912508191 14.7430209227922 14.7929662323232 P P P LNCV6_120517_PI430048170 mRNA AAGGTGCTCGGTCCTTCCGAGGAAGCTAAGGCTGCGTTGGGGTGAGGCCCTCACTTCATC NM_001003 RefSeq chr15 + 69452819 69455545 RPLP1 6176 "ribosomal protein, large, P1, transcript variant 1" GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0006415|GO:0006

412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0000184|GO:0016032|GO:0022625|GO:0044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133402_PI430048170 0.00187594582478804 0.345103236503062 4.11137649933021 3.72405120703328 4.24768008268258 P P P 5.43639995853338 5.44185465180227 5.82404602812167 P P P LNCV6_133402_PI430048170 mRNA CAGCTTCCAGTGTTTTGACTATGTGAACCATATCCAACTACTTTTTTGAAAATCTAGTTC NM_001126111 RefSeq chr8 + 89902533 89927867 OSGIN2 734 "oxidative stress induced growth inhibitor family member 2, transcript variant 1" GO:0003674|GO:0051321|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99330_PI430048170 0.96802333974613 1.00238199743776 4.40042976894091 4.08146703375223 3.91557778522024 P P P 4.05270613718978 4.07958248910659 4.28610477589338 P P P LNCV6_99330_PI430048170 mRNA TTCAAGATCTTGATCTATATCCATAGATTGGAATATTGGTGGGCCAGCAATCCTCAGACG NM_001005743 RefSeq chr14 - 73275209 73458580 NUMB 8650 "numb homolog (Drosophila), transcript variant 1" GO:0005515|GO:0045746|GO:0045296|GO:0030335|GO:0005886|GO:0008013|GO:0021849|GO:0045294|GO:0030136|GO:0045177|GO:0005634|GO:0016323|GO:0007219|GO:0021670|GO:0050769|GO:0005887|GO:0007411|GO:0060487|GO:0030862|GO:0005925|GO:0005769|GO:0019897|GO:0034332 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124828_PI430048170 0.35839172350195 0.931766490598896 0.439042574237945 0.442244996051482 0.258668925036952 A A A 0.388928837993233 0.629058140776874 0.423533531451157 A A A LNCV6_124828_PI430048170 mRNA TTCATCATGCGCAAATTCCCCTATTACCGCGCCAACCAGCGCGCCTGGCAGAACTCCATC NM_001195127 RefSeq chr7 + 290169 291488 WI2-2373I1.2 NA forkhead box L1-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136108_PI430048170 0.362512183047608 0.451558095830606 0.296801459511778 0.300097311534771 0.291402747386811 A A A 0.478390987204586 2.45712513614518 0.3480658896038 A A A LNCV6_136108_PI430048170 mRNA GCAATGCCGACAGCTGCCTTGTTCTTCATTATTAAAGCACTGGTTCATTCACTGCCCAAA NM_001085474 RefSeq chr1 - 248739415 248755787 LYPD8 646627 "LY6/PLAUR domain containing 8, transcript variant 1" GO:0005886|GO:0031225 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137235_PI430048170 0.512010041856261 0.34227339252641 0.517247805035897 1.06670633094716 0.578785622350868 A A A 0.58281754304786 3.56194121301454 0.440690735679066 A P A LNCV6_137235_PI430048170 mRNA AAGCCATAAACAAATATGCTCCCCTAAACATATTCGGCTTGAAAAAGTTGTTTTGGGGCA NM_001010980 RefSeq chr1 + 24556075 24609327 NCMAP NA noncompact myelin associated protein NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137208_PI430048170 0.299146205841062 0.792555861035712 0.456018101667009 0.60362674058375 0.545883880038211 A A A 1.14489867876618 0.961799132528977 0.412552482142348 A A A LNCV6_137208_PI430048170 mRNA GTAGTCCTGAGTAGGTGCATTTCTGTCTGTCTCAATAAATTTTACTTTGTCTGCAAAAAA NM_004598 RefSeq chr5 - 136975297 137499329 SPOCK1 6695 "sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1" GO:0031594|GO:0004869|GO:0004867|GO:0005509|GO:0005578|GO:0010812|GO:0021953|GO:0014069|GO:0001558|GO:0005615|GO:0007399|GO:0010951|GO:0007165|GO:0016528|GO:0005737|GO:0033268|GO:0008191|GO:0010977|GO:0001764|GO:0007155|GO:0022008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126987_PI430048170 0.0937542846480653 1.27974864430641 10.7814041139672 10.8786704282024 10.94366863945 P P P 10.2510099167092 10.565501501987 10.689611629073 P P P LNCV6_126987_PI430048170 mRNA

CTGAACTCATATTTTTCCTTCCTTCACTGTTGTAGTAAAGAGACATATTTCATGAATGGC NM_024619 RefSeq chr17 + 82716705 82728017 FN3KRP 79672 "fructosamine 3 kinase related protein, transcript variant 1" GO:0016310|GO:0016301 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_140282_PI430048170 0.388731230327327 1.45820848533473 0.625321695956033 1.7212383371125 0.467068495884954 A A A 0.428108615113774 0.554888410013914 0.538426253168087 A A A LNCV6_140282_PI430048170 mRNA
TGAAGATGAAGACTTCAAGAGGCAGGATGCAGAGATGAAGGAAAGCATCCCTTTTGCAGT NM_052838 RefSeq chr16 - 30378132 30382850 SEPT1 NA septin 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135170_PI430048170 0.520698139837387 1.04872744425631 7.61213744488083 7.45677357435037 7.4597783156139 P P P 7.30059752691908 7.59639999405589 7.41579725007792 P P P LNCV6_135170_PI430048170 mRNA
TGAGGCCCCCTTCTAGCCTGTGCAAACCCTGTATGTGCATTAAAAATCTCCAGGTCTGTG NM_001142459 RefSeq chr7 - 151175697 151187391 ASB10 136371 "ankyrin repeat and SOCS box containing 10, transcript variant 1" GO:0035556|GO:0005737|GO:0016567|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140183_PI430048170 0.239007892463669 0.846802441126396 10.1429649716517 9.98171261433525 10.0275663566837 P P P 10.039826399496 10.5233177291944 10.2731183563841 P P P LNCV6_140183_PI430048170 mRNA
GCTGAAGCCCCGTATATTTAATTTATTTTGTTAAACATGAAAGTGCATCCTTTCCCTCCA NM_001004356 RefSeq chr4 + 1011821 1026898 FGFRL1 53834 "fibroblast growth factor receptor-like 1, transcript variant 1" GO:0030133|GO:0005007|GO:0005794|GO:0008285|GO:0005886|GO:0017134|GO:0060412|GO:0044291|GO:0003179|GO:0051291|GO:0001501|GO:0008543|GO:0060539|GO:0034446|GO:0051260|GO:0016021|GO:0008201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60958_PI430048170 0.275819603711442 1.13052428502131 5.3242418242206 5.00606181973616 4.98953778293231 P P P 4.86317280641625 4.84298327213208 5.09421600881213 P P P LNCV6_60958_PI430048170 mRNA
TTTTAAAAAAGAAGGAACTCTCCCTGGGCTCTTTGTTGAAGTTGAGCCTGTACTTCTCTG NM_017799 RefSeq chr14 + 56579792 56649514 TMEM260 54916 transmembrane protein 260 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130922_PI430048170 0.0314118143546579 1.6269984680653 5.87504054968603 5.97709430769784 5.98670881116368 P P P 5.30754668047785 5.43141023899349 4.95455740433949 P P P LNCV6_130922_PI430048170 mRNA
AGCCTTAAAAGCAATAAACAGATACAACTTCCAGCAACTTCCCACTCAGCTGCAAGGCTG NM_152914 RefSeq chr17 - 21238870 21253266 NATD1 256302 N-acetyltransferase domain containing 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131849_PI430048170 0.319930842812266 1.40122527798409 3.82033658632425 4.27250525142178 3.26606598755206 P P P 3.75098642166672 2.65090897454501 3.45884001424684 P P P LNCV6_131849_PI430048170 mRNA
GGGGCGGGTGGAGAAAGTGTTTTTATTTTAATTTAAATTGTGTTTCGTTTTGTTTGTGGA NM_201589 RefSeq chr8 - 143428059 143430432 MAFA 389692 v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog A
GO:0043565|GO:0006355|GO:0003700|GO:0046982|GO:0007263|GO:0045944|GO:0005634|GO:0030073|GO:0003677|GO:0042803|GO:0006351|GO:0009749 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131449_PI430048170 0.383947899669828 1.02601689640477 0.350801897021454 0.351547957293171 0.447490860179317 A A A 0.350086539158512 0.318464261085496 0.371787724193291 A A A LNCV6_131449_PI430048170 mRNA
TGCTTTTTCCCTTCTTTGATGTGATAAACAAGGGGACGAGACGAGTTGTCTTTTCCCCAG NM_207328 RefSeq

chr2 - 96021945 96034979 GPAT2 150763 "glycerol-3-phosphate acyltransferase 2, mitochondrial"
GO:0005739|GO:0019432|GO:0016024|GO:0005741|GO:0004366|GO:0044281|GO:0016021|GO:0006644|GO:0006
072|GO:0006654|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142396_PI430048170 0.540049520860634 1.08196062537695 6.22292760056346
5.87917368254593 5.94568861530521 P P P 5.75815764224718 6.18450964856324
5.74276437896315 P P P LNCV6_142396_PI430048170 mRNA
TACTGAATGAAATATTTTACTAAGCGTTCAGTCTGTGCCTCCTGCATGGGTGGGAGTGAG NM_032854 RefSeq
chr17 - 29614755 29621423 CORO6 84940 coronin 6 GO:0051015|GO:0030036|GO:0015629 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129064_PI430048170 0.934242303524109 1.01028130881785 0.575663924585435
0.411430403864074 0.249084819497017 A A A 0.363300619429266 0.435115603882634
0.411034423080768 A A A LNCV6_129064_PI430048170 mRNA
GCTGAAAAATTCCCTCTTTCCATTCTCTTTCAATTCTGTGATATTGTCCAAGAATGTATC NM_181874 RefSeq chr3
+ 6861114 7741531 GRM7 2917 "glutamate receptor, metabotropic 7, transcript variant 2"
GO:0007608|GO:0030424|GO:0005886|GO:0030818|GO:0007605|GO:0014050|GO:0007268|GO:0007196|GO:0007
194|GO:0019226|GO:0010855|GO:0030425|GO:0032279|GO:0043198|GO:0045211|GO:0001662|GO:0030534|GO:0
001661|GO:0070905|GO:0005938|GO:0051966|GO:0048786|GO:0031279|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140830_PI430048170 0.204748014891728 1.03444976364449 0.354005403238188
0.370106887855104 0.283871568411608 A A A 0.283074154797098 0.299298569772867
0.280397255199084 A A A LNCV6_140830_PI430048170 mRNA
GCAATCAGACCACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAA NM_152635 RefSeq chr10
+ 72893555 72933036 OIT3 170392 "oncoprotein induced transcript 3, transcript variant 1"
GO:0005509|GO:0005635 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121876_PI430048170 0.643192012220248 1.24817233224473 1.86925400059935
0.350409739789902 0.897053863684154 A A A 1.54318734961035 0.347269092140135
0.326447761742995 A A A LNCV6_121876_PI430048170 mRNA
AGGAAAAGTAGGACCAACTGGTGCAACAGGAGATAAAGGTCCACCTGGACCTGTGGGGCC NM_000393 RefSeq
chr2 - 189031914 189179879 COL5A2 1290 "collagen, type V, alpha 2"
GO:0048592|GO:0046332|GO:0005576|GO:0005588|GO:0046872|GO:0031012|GO:0003674|GO:0001501|GO:0071
230|GO:0001503|GO:0022617|GO:0007411|GO:0030198|GO:0030199|GO:0030574|GO:0005788|GO:0043588|GO:0
005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131421_PI430048170 0.218538682633439 0.865419987070718 8.88870276764669 9.1106345532272
9.17445914399772 P P P 9.06259373606252 9.28840555299855 9.43907111384623 P P P
LNCV6_131421_PI430048170 mRNA
CAGAAAAATCCAGGATGAGATCAGAAGGATACTGGTGTTTTCTGACTTTTACAAAATTAC NM_016520 RefSeq chr9
- 129827284 129835293 C9orf78 51759 chromosome 9 open reading frame 78 GO:0005737|GO:0005654
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78229_PI430048170 0.0112459199392454 0.643967085487991 7.6736802000681
7.77161975735713 7.9602370509553 P P P 8.27957057656456 8.38045312826021
8.64073274259336 P P P LNCV6_78229_PI430048170 mRNA
CTGGGAAAAATTCCATTAAAGCCTCCACCTCTGGAACTTCTAAATGTTTAAAAGGGCAAT NM_007342 RefSeq chr7
+ 23181826 23201011 NUPL2 11097 nucleoporin like 2
GO:0007077|GO:0010467|GO:0031965|GO:0005975|GO:0019083|GO:0019221|GO:0019058|GO:0005634|GO:0044
281|GO:0055085|GO:0046872|GO:0010827|GO:0005829|GO:0008645|GO:0005737|GO:0015758|GO:0005643|GO:0
006611|GO:0005049|GO:0009405|GO:0016032|GO:0005654|GO:0051028|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131247_PI430048170 0.451431593507514 1.11934238158063 3.95582005705449
4.35789398836984 3.99447473129579 P P P 4.23837403793838 3.73143344634881

3.83433131406771 P P P LNCV6_131247_PI430048170 mRNA
AATTCAAAAGATAAGTATAGGCTCTACAGTACAAACCCTTCTGCCTCCTAGTTCCTCTCC NM_001253384 RefSeq
chr3 + 23916803 23923696 RPL15 6138 "ribosomal protein L15, transcript variant 6"
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0005634|GO:0006
415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0000184|GO:0016032|GO:0005840|GO:0022625|GO:0
044267|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68329_PI430048170 0.936922059251499 1.0389687795558 0.731614392315253 0.352642927811631
1.33262898300734 A A A 0.83004582877244 1.12462568774192 0.370917708222441 A A A
LNCV6_68329_PI430048170 mRNA
TGTGGAGCTAGGGATCCGCGAGTGCTTCCATCACAGCCGTATCATCAGCTGTGCCAATTG NM_003560 RefSeq chr22
- 38111494 38181754 PLA2G6 8398 "phospholipase A2, group VI (cytosolic, calcium-independent),
transcript variant 1"
GO:0005516|GO:0034976|GO:0043008|GO:0035965|GO:0044281|GO:0007204|GO:0005829|GO:0005739|GO:0045
921|GO:0005737|GO:0090037|GO:0006935|GO:0047499|GO:0045909|GO:0090200|GO:0004623|GO:0014832|GO:0
007613|GO:0032049|GO:2000304|GO:0005815|GO:0035774|GO:0051967|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138950_PI430048170 0.157521882275211 0.570717577505837 2.15844081948121
1.91556232943817 1.92624509872593 A A A 2.97920699246428 3.17381620123912
2.06425147689987 A P A LNCV6_138950_PI430048170 mRNA
TGGGACCTTAGACACCCAGCTCATCTCAGCGGGGTCTGGACTCACCTTCCCTAAAACAGT NM_198532 RefSeq chr19
- 2274631 2282182 C19orf35 NA chromosome 19 open reading frame 35 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_139836_PI430048170 0.98337055618928 1.00475094070591 1.01901319377485
0.329076625395859 0.430481009415733 A A A 0.434953044851081 0.313148798011638
1.01024000992206 A A A LNCV6_139836_PI430048170 mRNA
CTATGCATAGAAAACGACTGGAAAGAAACATTAACAGTGACTATCTTTGCACAGTGAAAA NM_001277348 RefSeq
chr5 + 135033279 135344680 C5orf66 100996485 chromosome 5 open reading frame 66 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_132722_PI430048170 0.880937471000271 0.95414814598046 3.71174763146883
2.99633047099729 2.82664861236035 P A A 3.797358214619 2.86531330970797
3.06004101204108 P P P LNCV6_132722_PI430048170 mRNA
CCCCACTCTGCACCCCAAATGGGAAGCATACGGTCTGAATAAATCCAAGTTTTATTCTCT NM_194293 RefSeq chr3
- 39183215 39192586 XIRP1 165904 "xin actin-binding repeat containing 1, transcript variant 1"
GO:0005916|GO:0005515|GO:0008285|GO:0042391|GO:0045214|GO:0055013|GO:0003779 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_100379_PI430048170 0.0842326719839641 1.20789918169152 5.57604720791008
5.87952946150837 5.67942281281866 P P P 5.36680099296445 5.35993370994524
5.59482793518449 P P P LNCV6_100379_PI430048170 mRNA
TAAAAGAGCTGGAGAAACACAAAATCCAGCTGGAGCAGGTGCAGGAATGGAAGAGCAAAA NM_004082 RefSeq
chr2 - 74361153 74380355 DCTN1 1639 "dynactin 1, transcript variant 1"
GO:0005515|GO:0032402|GO:0005829|GO:0030968|GO:0019886|GO:0005737|GO:0003774|GO:0000086|GO:0042
147|GO:0031252|GO:0005813|GO:0006996|GO:0005874|GO:0007399|GO:0010970|GO:0000922|GO:0007067|GO:0
045502|GO:0016020|GO:0030286|GO:0000776|GO:0006987|GO:0005869|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134442_PI430048170 0.719488599558543 0.974373772108774 0.618211399210175
0.519966548953524 0.324861303229589 A A A 0.421303562686148 0.616757919554 2
0.545868892182111 A A A LNCV6_134442_PI430048170 mRNA
TAGAAGGCAATTAGGGTGTTTCCTTAAACAACTCCTTTCCAAGGATCAGCCCTGAGAGCA NM_032414 RefSeq chr1
+ 110451165 110457354 PROK1 84432 prokineticin 1

GO:0000187|GO:0008284|GO:0045765|GO:0051781|GO:0005576|GO:0001525|GO:0008083 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_54887_PI430048170 0.426393386623496 1.20068528104745 5.64329578628262 4.90931653042795
5.1618680701881 P P P 4.80307071877972 5.37652360064718 4.7554593906665 P P P
LNCV6_54887_PI430048170 mRNA
TCCTCGAGTACAACAATGAAAACGACTTCCTGGCGGGGAGCCCCGACGCAGCAATCGATA NM_001093725
RefSeq chr1 - 156072012 156081998 MEX3A 92312 mex-3 RNA binding family member A
GO:0000932|GO:0008270|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129661_PI430048170 0.413323983931079 1.02106984082611 0.346798824675836
0.251308495934129 0.274139878241149 A A A 0.257742243243128 0.269018120797935
0.256942707322293 A A A LNCV6_129661_PI430048170 mRNA
ATTTATGGAGTTAGAACCAAACAGATCGGGGACAGGGTTATCCAAGGATGTTGTGGAAAC NM_001005177 RefSeq
chr11 - 4803432 4804380 OR52R1 NA "olfactory receptor, family 52, subfamily R, member 1
(gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62014_PI430048170 0.00864444329884773 1.40640364368982 7.95773365083016
7.81186765719962 7.73351523372038 P P P 7.24864456979044 7.49348642428785
7.28155885701891 P P P LNCV6_62014_PI430048170 mRNA
GCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAAGAAATAAAA NM_031301 RefSeq chr15
+ 63277549 63309126 APH1B 83464 "APH1B gamma secretase subunit, transcript variant 1"
GO:0005515|GO:0030133|GO:0048011|GO:0007220|GO:0043065|GO:0048013|GO:0005886|GO:0031293|GO:0043
085|GO:0097190|GO:0007219|GO:0007411|GO:0016485|GO:0008233|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137323_PI430048170 0.570853502823796 0.976794415922013 0.433299914363293
0.426072919426461 0.278246471075035 A A A 0.378765182368009 0.453424162071304
0.41132210758916 A A A LNCV6_137323_PI430048170 mRNA
AGCCTCCTAACCTGGGTTGGACCTTTGAAAAATATATTTGTAGCACATATTATAGATGGA NM_001136103 RefSeq
chr12 + 128267402 128707915 TMEM132C 92293 transmembrane protein 132C
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68282_PI430048170 0.471579505255334 0.968128796750765 0.447597621317484 0.470052631779416
0.302329443970453 A A A 0.410747133379433 0.498104292479822 0.455672395517517 A A A
LNCV6_68282_PI430048170 mRNA
GACTTGAATGTCCAACGCAAAGCAATACATGAACTCATCCAAGTGATGGCTGAACTGTCG NM_000619 RefSeq chr12
- 68154769 68159741 IFNG 3458 "interferon, gamma"
GO:0051712|GO:0019221|GO:0005615|GO:0030968|GO:0060334|GO:0045348|GO:0051607|GO:0044130|GO:0042
742|GO:0060333|GO:0000060|GO:0045410|GO:0032760|GO:0030593|GO:0042832|GO:0000122|GO:0005125|GO:0
032224|GO:0045084|GO:0002026|GO:0048304|GO:0009897|GO:0045080|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144044_PI430048170 0.583353326768031 0.856214337929132 0.913732086878897
2.23169444147952 0.747852396020721 A A A 2.18102694116032 1.40384386713419
1.30238612654365 A A A LNCV6_144044_PI430048170 mRNA
ATAGAGGAATAAATGTCTTCAGTTGTCTCTCCATTACCCCTAAGTTATTAGTTTGTCTAG NM_172193 RefSeq chr14
+ 49693104 49753152 KLHDC1 122773 kelch domain containing 1 GO:0005737 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140239_PI430048170 0.0661017242361805 0.344680704365472 2.19790260075034
0.623014505676405 1.48554344030633 A A A 3.0623366664368 3.10449629804971
3.16177446532934 P P P LNCV6_140239_PI430048170 mRNA
CAACGTTGTCTTAGCCTTTGAACAACTGAGTACAACTTTTTGGGAAAAGTTAAACAAAGT NM_017631 RefSeq chr4
- 168216290 168318807 DDX60 55601 DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
GO:0003725|GO:0005515|GO:0003727|GO:0004386|GO:1900246|GO:1900245|GO:0009615|GO:0005524|GO:0005

737|GO:0051607|GO:0003690|GO:0045087|GO:0008152|GO:0045111 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_50678_PI430048170 0.8844261387823791.00718063626948 0.5626668957780450.477481156051915 0.389443278005446 A A A 0.4035873161602570.5046522542153220.493468864565892 A A A
LNCV6_50678_PI430048170 mRNA
TATTTTTCTACATCGGGTTTTCTTAGGGCTCTCGGGAAGCACAAGGGGCTGTATTGCAAA NM_001080423 RefSeq chr3 - 14489110 14540343 GRIP2 80852 glutamate receptor interacting protein 2
GO:0005886|GO:0030159|GO:0007268|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121597_PI430048170 0.7124015964899550.9309843984336246.62696598436465 6.760639586698 6.36145829168546 P P P 7.01432776604547 6.62505528203089 6.37447417816023 P P P
LNCV6_121597_PI430048170 mRNA
ACCCCGGGCATCTCATCCCTCAACTGTAAAATAATCGCTAAGGATTCCTTCCTGACTTTG NM_016170RefSeq chr2 + 74514468 74517148 TLX2 3196 T-cell leukemia homeobox 2
GO:0043565|GO:0008150|GO:0003674|GO:0006355|GO:0005737|GO:0001707|GO:0050774|GO:0005634|GO:0005575|GO:0006351|GO:0048484 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137442_PI430048170 0.5782282181869311.03727461581726 0.28020635289745 0.2901281766423440.507324107492431 A A A 0.3269303733926410.281667511836931 0.321848734859461 A A A LNCV6_137442_PI430048170 mRNA
AACCATCAAGTTGTGCCAAATTATTCTCCTATGTTTGGCTGCTAGAACATGGTTACCATG NM_001164617 RefSeq chrX - 133535745 133985646 GPC3 2719 "glypican 3, transcript variant 1"
GO:0005515|GO:0045732|GO:0001658|GO:0007603|GO:0005886|GO:0060422|GO:0030324|GO:0010466|GO:2000096|GO:0050680|GO:0045879|GO:0044281|GO:0030282|GO:0005615|GO:0009653|GO:0072180|GO:0045807|GO:0060976|GO:0045880|GO:0030513|GO:0072138|GO:0009948|GO:0046326|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136955_PI430048170 0.00111556534708151 1.66597454715503 11.9951252607984 12.1274931369952 11.9160584600398 P P P 11.2052396621857 11.3484948775467 11.2802424197043 P P P LNCV6_136955_PI430048170 mRNA
AGCTTCTCATTGTGTAGAATTTCTAGATCCCCCGATTACATTTCTAAGCGTGGCAAAAAA NM_001145722 RefSeq chr19 - 18929200 18940304 HOMER3 9454 "homer scaffolding protein 3, transcript variant 1"
GO:0005515|GO:0030054|GO:0005886|GO:0019904|GO:0007216|GO:0045178|GO:2001256|GO:0005575|GO:0006605|GO:0008022|GO:0005829|GO:0005737|GO:0035256|GO:0045211 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145134_PI430048170 0.9756860172248010.9984059938638160.441451785271284 0.4871109631287110.443057049720414 A A A 0.5348398632719780.406643058919289 0.434331630197884 A A A LNCV6_145134_PI430048170 mRNA
CCTTGACTTTTTGTAAATGAAGAGGTCCTTTTCCTCAAGTTCTTAGTCCCACTCATCCTA NM_032571 RefSeq chr19 - 14619116 14674918 ADGRE3 NA "adhesion G protein-coupled receptor E3, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140428_PI430048170 0.00770977605995635 2.39549661482427 2.21689601351657 1.80275929041997 1.59238519474803 A A A 0.89596060392164 0.295388354912342 0.648802569365694 A A A LNCV6_140428_PI430048170 mRNA
CCAATAACCCAAGGACACGGGTCTCCAAAGAAATCTATTATTTCTTTGAATAAAAAGCAT NM_020919RefSeq chr2 - 201700262 201781172 ALS2 57679 "amyotrophic lateral sclerosis 2 (juvenile), transcript variant 1"
GO:0005515|GO:0071902|GO:0035022|GO:0032851|GO:0032855|GO:0042803|GO:0030425|GO:0032853|GO:0005829|GO:0030426|GO:0005085|GO:0016050|GO:0008104|GO:0051036|GO:0043197|GO:0001881|GO:0007528|GO:0045860|GO:0016197|GO:0007626|GO:0007032|GO:0001662|GO:0006979|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138984_PI430048170 0.4328488296515130.2620528488500050.501474813999299 0.3696205862401790.258200964110179 A A A 0.3431588518236963.62652733114775

0.352953300200467 A P A LNCV6_138984_PI430048170 mRNA
TTGGGAAGTGGCAAGCATCGCTGGGTTTAAGATAAAGGAGTCACAAAAACTAATCAAAAT NM_022454 RefSeq chr8
+ 54457934 54460896 SOX17 64321 SRY (sex determining region Y)-box 17
GO:0005515|GO:0030308|GO:0008013|GO:0044212|GO:0003705|GO:0045597|GO:0007283|GO:0060913|GO:0001
947|GO:0003143|GO:0003308|GO:0003142|GO:0042074|GO:0060914|GO:0061009|GO:0060956|GO:0042789|GO:0
001706|GO:0046982|GO:0023019|GO:0003713|GO:0000122|GO:0048643|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_55477_PI430048170 0.3589686352809770.6755845820322222.83107350510455 3.3479386040647
3.5548645744869 A P P 2.92958925243666 4.18077829233291 4.10812671993282 A P P
LNCV6_55477_PI430048170 mRNA
AATAGAGTAAAGAGGAGGCTAGACTCAAGCTGTCTGGAGAGTGTGAAACAAAAGTGTGTG NM_016448 RefSeq
chr1 + 212035552 212105006 DTL 51514 "denticleless E3 ubiquitin protein ligase homolog (Drosophila),
transcript variant 1"
GO:0000209|GO:0005515|GO:0006511|GO:0031965|GO:0004842|GO:0005813|GO:0006513|GO:0005694|GO:0031
572|GO:0005730|GO:0005634|GO:0019985|GO:0006974|GO:0043231|GO:0006260|GO:0005737|GO:0051726|GO:0
031465|GO:0005654|GO:0031464|GO:0009411 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127165_PI430048170 0.4776367859999841.43405428500672 2.53071260204464
0.9344705811962441.37913268074845 A A A 0.3546430779433990.789071769523674
2.05985431947355 A A A LNCV6_127165_PI430048170 mRNA
AAGGAGGTGAAAGGGGCATTAAAGAAAGTTCTAGCAAAGGCTCTGGGAGTAAATATTTTA NM_001001915 RefSeq
chr1 + 247588359 247589313 OR2G2 NA "olfactory receptor, family 2, subfamily G, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111831_PI430048170 0.5737777801803180.8664631024480141.02835556094411
3.40484768519619 3.48400288025992 A P P 3.47872883386664 2.97322240256695
3.08582343288679 P P P LNCV6_111831_PI430048170 mRNA
CTTATATTAAAGCTTATTACCTAACTGAGAATGACATGGAACGGTGGATCAAAGAGCACA NM_001257998 RefSeq
chr7 + 93232339 93361123 CCDC132 55610 "coiled-coil domain containing 132, transcript variant 3"
GO:0016020|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133970_PI430048170 0.2858495084799780.4887017569047050.592591463272616
0.5367062765362251.14166101429527 A A A 2.62765945974393 0.625831869877834
1.50863561836264 A A A LNCV6_133970_PI430048170 mRNA
GCACTGTTTTGAATGCATCTGCTATTTATACATCTGCAAGTGGGTATGTCATAAGGAGTC NM_018078 RefSeq chr4
+ 128061265 128211143 LARP1B 55132 "La ribonucleoprotein domain family, member 1B, transcript variant
1" GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145588_PI430048170 0.00153798154074019 1.37934459208803 6.08068967314161
6.13695745734511 6.16180510117019 P P P 5.6658596933279 5.67201152146136
5.65074235185672 P P P LNCV6_145588_PI430048170 mRNA
GGTGTGTTTTCCCCCTCTTTGGAGACAAGAAAATTTTATTATGACTCTAGATAATTGTGA NM_001135032 RefSeq
chr2 - 75492317 75560966 EVA1A 84141 "eva-1 homolog A (C. elegans), transcript variant 1"
GO:0005886|GO:0006914|GO:0005789|GO:0006915|GO:0016021|GO:0005765|GO:0043231 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_76050_PI430048170 0.3511390124761681.50856894288259 1.75014160917461 2.80333430447082
2.28500437476362 A A A 0.3007822243575441.60620791922121 2.53889779931163 A A P
LNCV6_76050_PI430048170 mRNA
AAGACCAGATCTATGAAGCCCACCAACAAGGCCGAGGGGCTCTGGAGGCATTGCTATGTG NM_016459 RefSeq
chr5 - 139387567 139389916 MZB1 51237 marginal zone B and B1 cell-specific protein
GO:2001274|GO:0005515|GO:0008284|GO:0005737|GO:0034663|GO:0042127|GO:0006915|GO:0005788|GO:0030
888|GO:0005576|GO:0033622|GO:0002642 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139903_PI430048170 0.2786730491767280.8965709185117650.46789764588009

0.3710816953787430.424956655163785A A A 0.7769713100522290.485442971524416
0.453154061188223A A A LNCV6_139903_PI430048170 mRNA
AAAGTGTGGTTTGCAGATGATCTGGGCTTGTTTCTGGCAGAGATTCTGGTACAGAGAAAG NM_004676RefSeq chrY
+ 22490396 22514637 PRYNA "PTPN13-like, Y-linked" NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145704_PI430048170 0.0642249589611777 3.10199655917307 6.24403673959251
6.15190132349997 6.01318724311652 P P P 5.31065373695632 3.8521200557028
3.81234812932299 P P P LNCV6_145704_PI430048170 mRNA
ATTTGTGAATAAAGCTGATTGCCTTCTCAGAGCCAGGCCTAGAAAATGGCCTCCTGAGAT NM_147196RefSeq chr3
+ 46701332 46710923 TMIE 259236 transmembrane inner ear GO:0042472|GO:0007605|GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128107_PI430048170 0.3974401475257471.0536537868334 0.303269692828449
0.3048880791443850.506937519905484A A A 0.3074956550966280.270819844091777
0.31978005488204 A A A LNCV6_128107_PI430048170 mRNA
GTTCTTTACAATGTCTGTAATTAGTGTTTCACTTGAGAAAGCCTTTTGTGGGTCGTAAAT NM_002063RefSeq chrX
+ 14529297 14731811 GLRA2 2742 "glycine receptor, alpha 2, transcript variant 1"
GO:0034220|GO:0030054|GO:0022824|GO:0005886|GO:0007218|GO:0005887|GO:0045211|GO:0034707|GO:0016
594|GO:0055085|GO:0016934|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59357_PI430048170 0.1643582456109080.7935478442423833.33213329485122 3.49539329059234
3.79812968277607 P P P 3.60958968329071 3.92762390839119 4.08821539229381 P P P
LNCV6_59357_PI430048170 mRNA
GAGTCTAATCTTGCTTTGAAGCGAGATGATGTAACACTGCTCAGACAAGAGGTCCAAGAC NM_003566RefSeq chr12
- 92772508 92929331 EEA1 8411 early endosome antigen 1
GO:0005515|GO:0005516|GO:0005969|GO:0031410|GO:0045022|GO:0006906|GO:0042803|GO:0044308|GO:0005
829|GO:0006897|GO:0005545|GO:0030742|GO:0005737|GO:0016020|GO:0031901|GO:0016189|GO:0008270|GO:0
055037|GO:0005769|GO:0019897|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127646_PI430048170 0.9594738892705061.02700394286922 1.86705800798927
0.2824664938764150.368755872680435A A A 0.2945558598490450.274904604566184
1.83070964476375 A A A LNCV6_127646_PI430048170 mRNA
AGGGGGAAGCAAAAGGCTGCCTCGGGTGTTTTAATAAAGTTGTTGTTTATTTCCAAAAAA NM_001282448 RefSeq
chr11 - 65088371 65089109 TMEM262 NA "transmembrane protein 262, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82623_PI430048170 0.0633230733071085 0.7976479334952334.98155472426541
4.80747960674091 5.0370256776366 P P P 5.06695784760757 5.34524372088744
5.38209771612392 P P P LNCV6_82623_PI430048170 mRNA
GGTCAAATTTGAGATTCTCTGTGGCTTCAGTATACAGTAACTGAATAAATGTCCTGAAGG NM_020314RefSeq chr16
+ 19555414 19701163 C16orf62 57020 "chromosome 16 open reading frame 62, transcript variant 1"
GO:0005515|GO:0016021|GO:0006893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126631_PI430048170 0.0235275831536036 0.5079230873849285.26286677046015
5.02121526830616 4.69837426161215 P P P 5.54731599442151 6.17560919493624
6.16180510117019 P P P LNCV6_126631_PI430048170 mRNA
GTCTCTACCTAATGGACCTCCGTGGCCAAAAAGTACCATTAAAACCAGAAAGGTGATTGG NM_030952RefSeq chr1
- 205302062 205321791 NUAK2 81788 "NUAK family, SNF1-like kinase, 2"
GO:0005515|GO:0043066|GO:0030036|GO:0000287|GO:0004674|GO:0006915|GO:0006468|GO:0042149|GO:0005
524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137908_PI430048170 0.0121793391491669 0.6726210469056075.7500299636689
5.99405294782395 5.82454083395459 P P P 6.42396610361818 6.46299782292383
6.40845797462738 P P P LNCV6_137908_PI430048170 mRNA
ACTTTCTGGTGTGAGAGGAGATGCCAAGGCATACAGTGAATAAAAGCCTTGTCTCTGAAA NM_001161586 RefSeq

chr11 - 86441107 86672636 ME3 10873 "malic enzyme 3, NADP(+)-dependent, mitochondrial, transcript variant 3"
GO:0048037|GO:0072592|GO:0004470|GO:0004473|GO:0006108|GO:0004471|GO:0046872|GO:0005739|GO:0009060|GO:0051287|GO:0006090|GO:0005759|GO:0008948|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134203_PI430048170 0.2954065050173890.74432356250512 0.754443867574341 1.31779848684837 0.618260898930583A A A 1.46800021311223 1.66917511048585 0.791784348907285A A A LNCV6_134203_PI430048170 mRNA
GGGGTTTTTCCAACTGCTCTCCAAGGAAACTGCCAAATAGTATGCTTACTATACAAGACT NM_001013650 RefSeq
chr3 - 139019030 139020926 PRR23B NA proline rich 23B NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137837_PI430048170 0.2310841431293160.8418645237581949.55618832661619 9.55949821828569 9.56939931551221 P P P 9.98996772653643 9.87272099447909 9.52862038065899 P P P LNCV6_137837_PI430048170 mRNA
GCGAAAGGATACTGTGAAATCACTAATTAACTAATAAACCTGTCTCAAGTTGAGGATTTG NM_213649RefSeq chr10 - 119140912 119165692 SFXN4 119559 "sideroflexin 4, transcript variant 1"
GO:0034220|GO:0015075|GO:0005743|GO:0016021|GO:0055072|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138746_PI430048170 0.3974771701216691.23422006012749 0.326936028340495 1.05906610966121 0.327694539314816A A A 0.3202260576495020.316870519293513 0.295340037587817A A A LNCV6_138746_PI430048170 mRNA
CTGGCTGTTTGATAGCAGAAGAAAAAGTTGCAGTCTCAGAAAGCCTTCCATTAAAACAAT NM_000458RefSeq
chr17_KI270857v1_alt - 1925498 1984134 HNF1B 6928 "HNF1 homeobox B, transcript variant 1"
GO:0005515|GO:0003700|GO:0006366|GO:0030111|GO:0044212|GO:0003705|GO:0048793|GO:0042663|GO:0005634|GO:0060261|GO:0009952|GO:0001714|GO:0072181|GO:0061296|GO:0060677|GO:0042803|GO:0048806|GO:0005667|GO:0046982|GO:0001822|GO:0001826|GO:0039020|GO:0000122|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130667_PI430048170 0.0789026462818797 0.7979845384948044.33224748651757 4.45193145509057 4.35756736982491 P P P 4.55981339597587 4.90289979624635 4.63559014914692 P P P LNCV6_130667_PI430048170 mRNA
CTTTGGGGGAATGTTTGGCAACCTTTGTGTTACAGATTAAAAATTCAGCAATTCAGTAAA NM_003102RefSeq chr4 + 24795462 24800845 SOD3 6649 "superoxide dismutase 3, extracellular"
GO:0005515|GO:0005802|GO:0001666|GO:0005507|GO:0005796|GO:0005576|GO:0005634|GO:0005615|GO:0031012|GO:0005737|GO:0019430|GO:0008270|GO:0046688|GO:0000302|GO:0008201|GO:0070062|GO:0055114|GO:0004784 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136238_PI430048170 0.8774959809094031.22916370138013 1.38544640745115 2.17629542926737 3.37346145386895 A A P 1.70709241823224 2.39797518984179 2.51058208613858 A A P LNCV6_136238_PI430048170 mRNA
GTGTTCTATGCATTTATTGGCTCTTGAATTTCCTCATCTATGAATTGTCATTCATACACC NM_004155RefSeq chr6 - 2887265 2903312 SERPINB9 5272 "serpin peptidase inhibitor, clade B (ovalbumin), member 9"
GO:0005515|GO:0002448|GO:0043066|GO:0004867|GO:0071391|GO:0005634|GO:0002020|GO:0005615|GO:0005829|GO:0010951|GO:0005737|GO:0006955|GO:0016020|GO:0043154|GO:0043027|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128883_PI430048170 0.0260216559130537 1.25016860037102 11.3775020229632 11.3067260004662 11.2652268768784 P P P 10.9295211524991 11.1291842576542 10.9166299027404 P P P LNCV6_128883_PI430048170 mRNA
AGTGCTGTTGATGACGAGTTGTCTTGAATAAATCATGTGTTCTTTGCAATGGGCAAAAAA NM_018201RefSeq chr9 + 128787206 128810432 TBC1D13 54662 "TBC1 domain family, member 13, transcript variant 1"
GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_106837_PI430048170 0.9124437282731731.00257912219668 12.3212660972853
12.2620842228818 12.2470851022226 P P P 12.316096704072 12.259695163248
12.2435566774042 P P P LNCV6_106837_PI430048170 mRNA
TGTCCCCACCGCCCACTTGTTTGATGTCACTGACTGTCTACATAGTAAGACCAACTTGAA NM_006319RefSeq chr16
- 29858355 29863288 CDIPT 10423 "CDP-diacylglycerol--inositol 3-phosphatidyltransferase, transcript
variant 1"
GO:0005794|GO:0030145|GO:0005886|GO:0006661|GO:0043178|GO:0046341|GO:0044281|GO:0019992|GO:0000
139|GO:0016020|GO:0005789|GO:0030246|GO:0016021|GO:0006644|GO:0046474|GO:0003881 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132480_PI430048170 0.1661515915205620.8931145736026771 0.4745682004171
10.3598932005087 10.2139754682907 P P P 10.4352842753628 10.6311585594951
10.4755164362859 P P P LNCV6_132480_PI430048170 mRNA
CATCTTTTCTTTCTGCCGCTCGGCTCCGGCCATTTTGTTTTATACAAAAATGGGAAAAAA NM_001288962 RefSeq
chr19 + 6739681 6751526 TRIP10 9322 "thyroid hormone receptor interactor 10, transcript variant
1"
GO:0005515|GO:0051056|GO:0048471|GO:0030036|GO:0005794|GO:0007264|GO:0001891|GO:0042995|GO:0005
764|GO:0043231|GO:0042802|GO:0008289|GO:0005829|GO:0006897|GO:0007165|GO:0005737|GO:0007154|GO:0
005654|GO:0005856|GO:0005938|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135874_PI430048170 0.6414866608070761.18763613423854 0.368726264051952
1.33348126863015 0.366116083574612A A A 0.5359492546321410.666050293638486
0.330887266420337A A A LNCV6_135874_PI430048170 mRNA
TTTGAGTTTCTTTACCCAGGATGTTCCATCAGATCTCTCTGCTTCCGGGAAGTCCTATTC NM_001039614 RefSeq
chr15 - 73735430 73751475 C15orf59 388135 "chromosome 15 open reading frame 59, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128535_PI430048170 0.2996012751714021.26286403848931 2.63367621132783
2.75803601428864 2.24601039183313 A A A 2.62657238027231 1.74617694745909
2.16895726977247 A A A LNCV6_128535_PI430048170 mRNA
GACCTCTGCCAGATACAGGATTTTCCATCCCAGAGGCCTCCAGTGTCAACACCAAGCCAG NM_001013641 RefSeq
chr1 + 15742491 15747797 TMEM82 NA transmembrane protein 82 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_127478_PI430048170 0.4861726036151121.03991786712151 11.4338007514036
11.3324506994541 11.4499570538811 P P P 11.2502702862632 11.3210492485205
11.4695215028515 P P P LNCV6_127478_PI430048170 mRNA
GTTCATTCTTCTGTCAGACAATGTCATATTCAACTCTGTTCATATTAAACCACTGTGAAG NM_001256185 RefSeq
chrX - 71059246 71073426 SNX12 29934 "sorting nexin 12, transcript variant 1"
GO:0005515|GO:2000642|GO:0042177|GO:0051224|GO:0015031|GO:0006897|GO:0016050|GO:0030100|GO:0010
629|GO:0010955|GO:0019899|GO:0035091|GO:0005769|GO:0070062|GO:0005768|GO:0019898 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145709_PI430048170 0.91215341174259 0.9954218781852911.32471989219792
0.3579069059673600.297467835696659A A A 0.3411619333333461.15176044780251
0.632114630110632A A A LNCV6_145709_PI430048170 mRNA
CCACCTTCGCTGTGTTCTTGCTGCAAAGTCTGGTCAATAAATCACTGCACTGTTAAAAAA NM_004826RefSeq chr2
- 232479826 232487859 ECEL1 9427 "endothelin converting enzyme-like 1, transcript variant 1"
GO:0003016|GO:0007218|GO:0005887|GO:0006508|GO:0004222|GO:0046872|GO:0008237 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131847_PI430048170 0.0374650959842779 0.3487279904127290.25066524506215
1.32578675591624 0.297837446643328A A A 2.5420223284025 1.44567087110143
2.47948073429625 A A P LNCV6_131847_PI430048170 mRNA
CTGTTTTTACTGGAAACATAGCAAACCTTGATTTAGCTCCAAGAAATTGAGTAGGGAAAT NM_020208RefSeq chr3

- 45755448 45796543 SLC6A20 54716 "solute carrier family 6 (proline IMINO transporter), member 20, transcript variant 1"
GO:0016324|GO:0015816|GO:0015171|GO:0005886|GO:0005887|GO:0005328|GO:0015824|GO:0006865|GO:0006836|GO:0055085|GO:0003333|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145253_PI430048170 0.0192128886476126 0.6161121389110296.35642174410513
6.27288827286505 6.19176325232116 P P P 6.71944002458339 7.07462459992499
7.09767136410857 P P P LNCV6_145253_PI430048170 mRNA
CTGTTAAAGTATTGTACGTTTGTGTACAGTTTAAGAAAATAAAAGATTGAGTGCCACGGG NM_002193RefSeq chr2
+ 120346142 120351807 INHBB 3625 "inhibin, beta B"
GO:0005515|GO:0048471|GO:2001235|GO:0060395|GO:0048599|GO:0005615|GO:0030154|GO:0042803|GO:0001541|GO:0043408|GO:0044320|GO:0045444|GO:0048468|GO:0046676|GO:0009267|GO:0032869|GO:0010862|GO:0046882|GO:0006952|GO:0005576|GO:0042981|GO:0046881|GO:0032924|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128236_PI430048170 0.0443515624922992 0.8445778875353329.29054405210419
9.47002692539278 9.29067651370838 P P P 9.58782788634787 9.56978454752253
9.63156351158291 P P P LNCV6_128236_PI430048170 mRNA
TAATAAGGATTCATGGCTCAGAGGGATTTTCTGATGGTTTTGCTGATTTGTTTCTAGTTT NM_144997RefSeq chr17
- 17212212 17237188 FLCN 201163 "folliculin, transcript variant 1"
GO:0051898|GO:0005515|GO:0032006|GO:0030308|GO:0032007|GO:0032008|GO:0005886|GO:0035024|GO:0005634|GO:0035065|GO:1900181|GO:0032403|GO:0005737|GO:0045944|GO:0070373|GO:0030511|GO:2001170|GO:0030097|GO:0031929|GO:0030336|GO:0032465|GO:0043065|GO:0044291|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_60986_PI430048170 0.000106366200440541 1.63169376900525 9.05918666165008
9.03791954486887 9.14685243513283 P P P 8.32915268018015 8.36032623028651
8.43560873241364 P P P LNCV6_60986_PI430048170 mRNA
ACGGGTACAGCAAGCTTTATAATAGAAGATGACGACCCATTGAGGGATGGATTTCTTCTC NM_144581RefSeq chr14
- 59472687 59484355 L3HYPDH 112849 L-3-hydroxyproline dehydratase (trans-)
GO:0050346|GO:0018112|GO:0016836|GO:0008152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129954_PI430048170 0.3322850929854690.8308484295622681 0.831159957866
10.3665039969407 10.3472908284264 P P P 11.1029966169371 10.7422601663227
10.4889171319493 P P P LNCV6_129954_PI430048170 mRNA
GGCTGCCCGGCAGGCTTGGTGGACTCTGCTGGCAGCAAATAAAGAGATGACGGCAAAAAA NM_174983RefSeq
chr19 - 3544198 3557584 MFSD12 126321 "major facilitator superfamily domain containing 12, transcript variant 3" GO:0006810|GO:0016021|GO:0005765 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_109970_PI430048170 0.0382331794613318 0.6767177946267079.10616115445435
8.63735623421143 8.74491852468782 P P P 9.18155468903859 9.42962471602301
9.58216334430389 P P P LNCV6_109970_PI430048170 mRNA
TCTGACAGTGACGATGAGTGGACATTTGGGAGCAATAAAAATAAGAAGAAAGGAAAAGCC NM_015138RefSeq
chr15 + 41417103 41483563 RTF1 23168 "Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)"
GO:0005515|GO:0006352|GO:0080182|GO:0005730|GO:0000122|GO:0001711|GO:0003697|GO:0051571|GO:0019827|GO:0045944|GO:0032968|GO:0016593|GO:0016055 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128457_PI430048170 0.00577917826556056 0.79358107276496 8.85036746280286
8.82171164982173 8.7636032858633 P P P 9.19377761500902 9.18276242957893
9.05719355360526 P P P LNCV6_128457_PI430048170 mRNA
AAATGCGGTTTACTTTGTAGGCCACGTTGGTTCAATAAATGATGCAGCGGACACAAAAAA NM_198075RefSeq
chr11_KI270832v1_alt + 67162 84556 LRRC56 115399 leucine rich repeat containing 56 NA . NA -
. NA NA NA NA NA NA NA NA NA

LNCV6_143538_PI430048170 0.0471404852193487 0.5692910019221397.37901093127725
7.22416266161875 7.66041502747859 P P P 7.83439951919067 8.2133358587322
8.59008017760649 P P P LNCV6_143538_PI430048170 mRNA
CAGGGACTTGACCCATTAGGGTATGAAATTCAGTTATAGTTTAATCTTTGTAATCTCACT NM_020401RefSeq chr12
+ 68686950 68742693 NUP10757122 nucleoporin 107kDa
GO:0007077|GO:0005515|GO:0010467|GO:0019221|GO:0019058|GO:0044281|GO:0005635|GO:0051292|GO:0015
031|GO:0005829|GO:0008645|GO:0006406|GO:0015758|GO:0005643|GO:0016032|GO:0017056|GO:0031965|GO:0
005813|GO:0005975|GO:0019083|GO:0055085|GO:0010827|GO:0005487|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143733_PI430048170 0.6024626645213220.9423265844761130.371874780557091
0.4970606426955720.388056790244578A A A 0.7164659431627240.474464252218244
0.295268695059656A A A LNCV6_143733_PI430048170 mRNA
CCCTGGTAATGCTTTAGTCAAAGGGATATCTCTCTTGTATCAGAGGCTGTGTCTTTTAGT NM_001850RefSeq chr3
+ 99638595 99796733 COL8A11295 "collagen, type VIII, alpha 1, transcript variant 1"
GO:0005591|GO:0010811|GO:0005576|GO:0001525|GO:0048593|GO:0035987|GO:0050673|GO:0043231|GO:0031
012|GO:0022617|GO:0030198|GO:0030574|GO:0005788|GO:0007155|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129385_PI430048170 0.4699987390898381.17450640915656 0.3695906231369151.0465415821568
0.388501099918724A A A 0.4843792908053180.342311639983661 0.38566939582127 A A A
LNCV6_129385_PI430048170 mRNA
GCAACAGAAGTGCCCGGTCATATGGTGTAAAAATGTAAATACAGGAAAATTTCATTTTTC NM_001134407 RefSeq
chr16 - 9753404 10182406 GRIN2A 2903 "glutamate receptor, ionotropic, N-methyl D-aspartate 2A,
transcript variant 1"
GO:0005515|GO:0030054|GO:0005886|GO:0005783|GO:0045471|GO:0005234|GO:0017146|GO:0007268|GO:0030
425|GO:0001964|GO:0042417|GO:0034220|GO:0008104|GO:0048167|GO:0004972|GO:0045211|GO:0007611|GO:0
006810|GO:0007613|GO:0022008|GO:0005262|GO:0043065|GO:0009986|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_112524_PI430048170 0.00270770744633148 0.3968403279207471 0.656760469833
10.4407157217409 10.2092448868193 P P P 11.8516746147521 11.8363513455034
11.6442769144756 P P P LNCV6_112524_PI430048170 mRNA
CGCACTCCTTTCCTTTTGGAAGCAAGAAGAAAATACGTGAAAACGGAAATTAAAGATTTA NM_031213RefSeq chr19
- 1876975 1885519 ABHD17A 81926 "abhydrolase domain containing 17A, transcript variant 1"
GO:0005515|GO:0008150|GO:0016787|GO:0016020|GO:0008152|GO:0005576 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139580_PI430048170 0.0146904823352915 0.55485815491897 6.22254566734219
6.4315123410532 6.72296828453868 P P P 7.57658701037453 7.07041992043063
7.27832245210059 P P P LNCV6_139580_PI430048170 mRNA
CTGTAATTGGACAGCTCTCTCGAAGAGATCTTACAGACTGTATCAGTCTAATTTTTAAAT NM_001162407 RefSeq
chr2 - 200853008 200864561 CLK1 1195 "CDC-like kinase 1, transcript variant 2"
GO:0005737|GO:0046777|GO:0018105|GO:0008283|GO:0004674|GO:0018107|GO:0043484|GO:0018108|GO:0005
634|GO:0004712|GO:0005524|GO:0004715 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144638_PI430048170 0.00632121216948748 0.2187211449868465.18565263538134
4.93910211561667 5.48882480250905 P P P 6.81593112768356 7.47651332910387
7.78921474967193 P P P LNCV6_144638_PI430048170 mRNA
CGATGGATAATACCTAATAAACTGCCCTCAGTAAATCCATGGTTAATAAATGTGGTTTCT NM_004523RefSeq chr10
+ 92593067 92655395 KIF11 3832 kinesin family member 11
GO:0008017|GO:0007100|GO:0032403|GO:0005829|GO:0019886|GO:0005737|GO:0007059|GO:0008574|GO:0005
876|GO:0090307|GO:0007051|GO:0007052|GO:0016887|GO:0007018|GO:0005871|GO:0019901|GO:0005874|GO:0
005819|GO:0046602|GO:0003777|GO:0005524|GO:0000922|GO:0007067|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_126979_PI430048170 0.0149940075506108 0.4704909882540282.60735525119606
1.91210544656971 2.39085942690656 A A A 3.58761298034127 3.5041467886908
3.12603492076385 P P P LNCV6_126979_PI430048170 mRNA
GGCTCCCTCTTATTTTTACAAGTTTCATTTTTAAAAGTAGGCAACTACTTTGGGTTACAG NM_001242784 RefSeq
chr21 - 36750887 36966656 HLCS 3141 "holocarboxylase synthetase (biotin-(proprionyl-CoA-carboxylase (ATP-hydrolysing)) ligase), transcript variant 3"
GO:0005515|GO:0009305|GO:0008283|GO:0006768|GO:0006767|GO:0044281|GO:0071110|GO:0016363|GO:0042803|GO:0005829|GO:0005739|GO:0005737|GO:0018271|GO:0000785|GO:0004080|GO:0016570|GO:0005524|GO:0070781|GO:0006766|GO:0005652|GO:0009374|GO:0004078|GO:0004077|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128361_PI430048170 0.0983017661784394 1.55951409863696 6.7334838926081
6.61556446135666 6.25267978049351 P P P 6.19630405760033 6.0260617800201
5.37533512455598 P P P LNCV6_128361_PI430048170 mRNA
GAGAGAGAGAGAGAAATCTGAGAGAACTCTTTAAAACATACACCATCATCACCATCCCGT NM_001136483 RefSeq
chr17 + 43780434 43784686 C17orf105 284067 chromosome 17 open reading frame 105 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141702_PI430048170 0.00165689405227202 2.14014076725397 8.31764279345034
8.65062306573968 8.57403381077189 P P P 7.54744481634993 7.34426128281933
7.36953322507416 P P P LNCV6_141702_PI430048170 mRNA
AAGAGTTTCAATCAGACATGACTGTGACGTGCATCCTCAATTAGAATTAAAGTGATGTAT NM_001128592 RefSeq
chr6 + 3258927 3268066 PSMG4 NA "proteasome (prosome, macropain) assembly chaperone 4, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143016_PI430048170 0.0594286802921639 0.6953312537890776.5313706727563
6.32728957431564 6.88210786919007 P P P 6.98866914269068 7.04914862723209
7.31030876128764 P P P LNCV6_143016_PI430048170 mRNA
AAATATTGATCTGGTGATCTCCTTCTTTAGCTCAAGGTTGCTGCAAGCTGGAGCTGAGCT NM_017653RefSeq chr18
- 49043801 49460709 DYM 54808 dymeclin
GO:0005515|GO:0060348|GO:0005737|GO:0005794|GO:0007030|GO:0019899 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_100811_PI430048170 0.8310027637866550.9693974055177713.66714542342049
3.71217149309107 3.61092854555177 P P P 3.9193109994002 3.71523976437143
3.45473362306054 P P P LNCV6_100811_PI430048170 mRNA
CCTCTTTTCAAGTGACATCTCAAAATGTTGGACAACTTACTGTTTATCTACATGGAAATC NM_004937RefSeq chr17
+ 3636467 3663103 CTNS 1497 "cystinosin, lysosomal cystine transporter, transcript variant 2"
GO:0042470|GO:0006520|GO:0046034|GO:0005886|GO:0007616|GO:0005770|GO:0006749|GO:0005765|GO:0005764|GO:0043231|GO:0050890|GO:0042438|GO:0015184|GO:0002088|GO:0007420|GO:0008542|GO:0015811|GO:0007628|GO:0045111|GO:0016021|GO:0007625|GO:0005769|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_143201_PI430048170 0.000728707150816744 0.21531934148848 5.25755599015851
4.84225244218024 5.28537169999051 P P P 7.01639491583767 7.37901093127725 7.6153656551021
P P P LNCV6_143201_PI430048170 mRNA
GCGCTGAAGTTAGACCAAGGTATACAGTTTTGTTCTAACAGACATTTAGGTTAATTGTAA NM_032458RefSeq chrX
+ 134373311 134428792 PHF6 84295 "PHD finger protein 6, transcript variant 2"
GO:0051219|GO:0005515|GO:0006355|GO:0042826|GO:0005730|GO:0005634|GO:0003677|GO:0006351|GO:0042393|GO:0015631|GO:0097110|GO:0043021|GO:0000777|GO:0005654|GO:0008270|GO:0019899 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_88613_PI430048170 0.3577480608350461.11647471360265 6.9905327460799 7.41683763122683
7.13179129634552 P P P 7.00072298848578 7.10989767384918 6.98147557057926 P P P

LNCV6_88613_PI430048170 mRNA
TAACAACTTTGAGGTAAAGTCACTGATCTTTGACCAGAGTGGTACCTACCTGGCTCTTGG NM_014502 RefSeq chr11
- 60890547 60906589 PRPF19 27339 pre-mRNA processing factor 19
GO:0048026|GO:0005515|GO:0008380|GO:0010467|GO:0016874|GO:0001833|GO:0034450|GO:0005634|GO:0071
013|GO:0006303|GO:0042802|GO:0070534|GO:0005737|GO:0072422|GO:0005662|GO:0005811|GO:0000974|GO:0
000244|GO:0000209|GO:0000245|GO:0071006|GO:0008610|GO:0000349|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137793_PI430048170 0.1472668297912310.5925296601792090.384787548358019
0.4726250159221360.371813089076393 A A A 0.4994908819768031.39469851417348
1.42556394917705 A A A LNCV6_137793_PI430048170 mRNA
GGGCACTGGAGTGAGGGAGTAGATAAAACAGCTGCAATATAAACAGTCCTCTGGAATAAA NM_153356 RefSeq
chr15 + 73873585 73889214 TBC1D21 161514 "TBC1 domain family, member 21, transcript variant 1"
GO:0017137|GO:0001669|GO:0032851|GO:0003779|GO:0005097|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_107426_PI430048170 0.0470706748833228 0.8158195558148841 0.4159591419053
10.2492878024047 10.4849279296448 P P P 10.5394309066895 10.8008474691871
10.6891260069359 P P P LNCV6_107426_PI430048170 mRNA
ATCTCTAGATCAACAAGCAAAGGAGGTGCCAAGCCTGTTTGTCTTCATTGTGACACTGGA NM_001280794 RefSeq
chr7 + 142855013 142871093 EPHB6 2051 "EPH receptor B6, transcript variant 2"
GO:0005003|GO:0048013|GO:0005886|GO:0007411|GO:0005887|GO:0006468|GO:0005576|GO:0004872|GO:0005
524|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139336_PI430048170 0.2888426626733611.03605341665472 0.407498146442617
0.3030449005199660.300568074555731 A A A 0.2950283068840930.307511198478621
0.257408843653491 A A A LNCV6_139336_PI430048170 mRNA
AGGATTGTTATTTGGCGTGCTGTTTTCTACCTCTGGTCTTATCTGTGATACATAATTTCA NM_000865 RefSeq chr6 +
86937305 87016679 HTR1E 3354 "5-hydroxytryptamine (serotonin) receptor 1E, G protein-coupled"
GO:0004993|GO:0007186|GO:0005886|GO:0007187|GO:0005887|GO:0004930|GO:0007268|GO:0030815|GO:0051
378|GO:0007193|GO:0007210 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130813_PI430048170 0.0340329499191545 1.44107690344452 9.12102589466407
9.06675516168101 8.80625321208826 P P P 8.72118157723257 8.37635355369916
8.29834206519482 P P P LNCV6_130813_PI430048170 mRNA
TCTGGACCCCCATCTCAGGGCCTGCCCTTGGCTAAAGTCAATAAAGTCTATTCTAAGAGC NM_001193308 RefSeq
chr1 + 27341991 27353932 SYTL1 84958 "synaptotagmin-like 1, transcript variant 1"
GO:0005515|GO:0042470|GO:0017137|GO:0005886|GO:0006887|GO:0042043|GO:0006886|GO:0019897|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113160_PI430048170 0.4943731211512190.8183348519431181.80912868960209
0.5469859665405172.30477682561285 A A A 1.74730367865802 1.92911215288462
2.30446932765595 A A A LNCV6_113160_PI430048170 mRNA
TACAATCGCAAGAAGGTGAAATATCGGAAGGATGGTTACCTCTGGAAGAAGCGGAAGGAT NM_001171167
RefSeq chr17 - 4967991 4987370 CAMTA2 23125 "calmodulin binding transcription activator 2,
transcript variant 4"
GO:0005515|GO:0042826|GO:0006357|GO:0045944|GO:0003682|GO:0014898|GO:0005634|GO:0003677|GO:0006
351|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132458_PI430048170 0.0987387693146444 0.8962346225018111 6.6005405537255
16.4208096445976 16.4208096445976 P P P 16.6664187766053 16.6738594784235
16.5817996676127 P P P LNCV6_132458_PI430048170 mRNA
GGGTGTGTCCAAGAAGAAATAAGTCTGTAGGCCTTGTCTGTTAATAAATAGTTTATATAC NM_022551 RefSeq
chr6_GL000256v2_alt + 4720755 4721408 RPS18 6222 ribosomal protein S18
GO:0005515|GO:0010467|GO:0003735|GO:0042254|GO:0019083|GO:0006614|GO:0019058|GO:0015935|GO:0005

634|GO:0019843|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0
000184|GO:0022627|GO:0016032|GO:0005840|GO:0044267|GO:0005925|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143289_PI430048170 0.4539804665478890.7594914683064350.42053396290356
0.5681101168626710.493400545073204A A A 0.5427107249276531.48207364814289
0.397999687886672A A A LNCV6_143289_PI430048170 mRNA
GAGGTGTGTTAGGATAATTGTCCAGTTAATTTGAAAAGGCCCCAGATGAATCAATAAATA NM_001281469 RefSeq
chr14 + 52267712 52276724 PTGDR 5729 "prostaglandin D2 receptor (DP), transcript variant 2"
GO:0005515|GO:0006954|GO:0007186|GO:0005886|GO:0030238|GO:0071799|GO:0046085|GO:0030431|GO:0016
021|GO:0001785|GO:0004956 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130294_PI430048170 0.4696255550090550.8232916932568040.290655849577314
0.3190340717552140.419027340720596A A A 0.33069945027681 1.09726558716938
0.296170220069155A A A LNCV6_130294_PI430048170 mRNA
CTGTCACTAAACTTGGATAAATGGGTCAGAAAGTACAGATTTAATAAAGTCGTACCTCTA NM_153234RefSeq chr5
- 97091869 97142816 LIX1 167410 Lix1 homolog (chicken) NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_69787_PI430048170 0.000192344376243423 0.3216507423279538.37434833659415
8.44451226441269 8.41837571333736 P P P 10.1116541515716 9.94886488526656 10.08173560474
P P P LNCV6_69787_PI430048170 mRNA
TTCAAGGAACAGATCATCCACCATGTGGCCACCATCATTCTCATCAGCTTTTCCTGGTTT NM_181746RefSeq chr1
- 150965172 150975003 CERS2 29956 "ceramide synthase 2, transcript variant 1"
GO:0006665|GO:0005515|GO:0031965|GO:0016020|GO:0005783|GO:0030148|GO:0005789|GO:0050291|GO:0044
281|GO:0016021|GO:0046513|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143076_PI430048170 0.6250403952242960.9403133652226727.44809289713968 7.7347616601647
8.0748549608497 P P P 7.7257160527012 7.87236050521316 7.98289587108942 P P P
LNCV6_143076_PI430048170 mRNA
GCTTCTTTTAGAGGAGGAAGCATACAACCTCTTTTGTGTGAATTTTGTTATTATGGTCAA NM_003968RefSeq chr3
- 69054729 69080373 UBA3 9039 "ubiquitin-like modifier activating enzyme 3, transcript variant 1"
GO:0005515|GO:0046982|GO:0016881|GO:0045116|GO:0007113|GO:0051726|GO:0006508|GO:0005634|GO:0005
524|GO:0019781|GO:0006464|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138362_PI430048170 0.0414065386763384 0.4346880989331713.6553669615645
3.87203284201046 3.80971506013295 P P P 4.41919087239611 5.11853159367996
5.27780247779168 P P P LNCV6_138362_PI430048170 mRNA
GTTCTGAGCACCAGAAGGGTCATGTAAATCTGAAGTTGTTATTAAAGGTTTTTCTATAGT NM_003101RefSeq chr1
+ 179293713 179358679 SOAT1 6646 "sterol O-acyltransferase 1, transcript variant 1"
GO:0042632|GO:0005515|GO:0033344|GO:0010878|GO:0005783|GO:0010742|GO:0034379|GO:0042986|GO:0034
736|GO:0016020|GO:0015485|GO:0004772|GO:0005789|GO:0034435|GO:0016021|GO:0000062|GO:0008203 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103366_PI430048170 0.8685935479765461.00395328233435 13.2949930285512
13.2811083790576 13.2525104871574 P P P 13.3283499992198 13.26419157291
13.2171551698955 P P P LNCV6_103366_PI430048170 mRNA
GATGCTTGGATGGAAAGGGAAAAATGGACCCTGTGATGCTAATAAAACTGTTCTCCCTTA NM_032593RefSeq chr9
- 35812959 35815045 HINT2 84681 histidine triad nucleotide binding protein 2
GO:0005739|GO:0006694|GO:0016787|GO:0000166|GO:0005730|GO:0006915 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143272_PI430048170 0.5978815011001341.31159440202617 1.63165408620705
0.2812826149417970.420121245231283A A A 0.3604901381181020.83686980037181
0.309435922949255A A A LNCV6_143272_PI430048170 mRNA
GGCAGCATGGTAGCACCTCCTAACAGATTAAATAGATCACATTTGCTTCTAAAATTAAAA NM_003650RefSeq chr20

+ 24949229 24959928 CST7 8530 cystatin F (leukocystatin)
GO:0010951|GO:0005515|GO:0006955|GO:0005737|GO:0004869|GO:0004866|GO:0005576 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140816_PI430048170 0.0476979926680205 2.11004181257523 3.9832690860312
3.56427938386588 3.1549522278978 P P P 2.49595281245363 2.57969784980968
2.51187959480588 A P P LNCV6_140816_PI430048170 mRNA
ACAGCAGCAGATGGCTCCGAAGAAGTGGAGCGTTTTCATCAGGTTCAACTTTGAAACCTC NM_001282670 RefSeq
chr1 - 2189548 2212720 C1orf86 199990 "chromosome 1 open reading frame 86, transcript variant
6"
GO:0005515|GO:0043130|GO:0030054|GO:0005694|GO:0005654|GO:0019985|GO:0070530|GO:0046872|GO:0006
974|GO:0043240|GO:0031593 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128315_PI430048170 0.0446555508156441 0.866353823263173 14.4327359908841
14.4904481224677 14.3088355348141 P P P 14.5264628656463 14.6828657789336 14.644955262437
P P P LNCV6_128315_PI430048170 mRNA
CCCCAAGGACCCCATTCTGCCTCCTTCTGGGGAAATAAATGAGTGTCTGTTTCAGCAGCT NM_003801 RefSeq chr8
+ 144082620 144086216 GPAA1 8733 glycosylphosphatidylinositol anchor attachment 1
GO:0005515|GO:0006501|GO:0034235|GO:0016255|GO:0003923|GO:0006461|GO:0015631|GO:0016020|GO:0005
789|GO:0042765|GO:0006621|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51819_PI430048170 0.944709698886527 1.00194402415119 11.8496060477252 11.7994169521671
11.7509202068794 P P P 11.6875443816962 11.7603041252864 11.9341363267533 P P P
LNCV6_51819_PI430048170 mRNA
TGGAGTGTTTGTGGCCTTCACAGATTTCACAGGAACCAATAAATCCCTCAGAGAAGTAAA NM_033428 RefSeq
chr9 - 7796490 7799799 TMEM261 90871 transmembrane protein 261 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145069_PI430048170 0.763301242469267 0.914370699182937 5.13607610719723
5.19212010819406 5.09201245470165 P P P 5.63686964040126 5.27448438574018
4.76962092178601 P P P LNCV6_145069_PI430048170 mRNA
GGCAGGAAAGAGTGGTTATTTATGTACTTAAAGTTTCATTAAAGTTAAAATCGGAAAAAA NM_207336 RefSeq
chr7 - 149764363 149773206 ZNF467 168544 zinc finger protein 467
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_73548_PI430048170 0.378992911152828 1.02715274441674 0.296826543233931
0.309723740996976 0.403990615952875 A A A 0.314713364249887 0.293839612453703
0.288290634318293 A A A LNCV6_73548_PI430048170 mRNA
ACACTCACCAGCTACACGTACTAATTCAGATTTTGCACATGTTGGTGGAAAACATGTCAA NM_001040061 RefSeq
chr3 + 138947233 138953988 FOXL2NB NA FOXL2 neighbor NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_141454_PI430048170 0.0240654317289291 0.383952830496659 4.28455102434835
3.51924319921773 4.46781365266303 P P P 5.251185966891 5.59485579614553
5.69588151563588 P P P LNCV6_141454_PI430048170 mRNA
AGTGACAATCAGAACAAGTTTCAGTATCAGATGTTCAAGAGGAAGTTGCTATTGCATTGA NM_001297598 RefSeq
chr5 - 56919601 56952130 MIER3 166968 "mesoderm induction early response 1, family member 3,
transcript variant 1" GO:0006355|GO:0003682|GO:0005634|GO:0003677|GO:0006351 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_139432_PI430048170 0.0382616658830432 0.360755772995656 5.66792149529649
5.36055630702911 5.35288049794248 P P P 6.3179116968981 7.43356819407849
6.85110940893255 P P P LNCV6_139432_PI430048170 mRNA
AAATGGCATTTTGAAGCCCAGTCATTCTCTAAAAAGGCCCTTTTTAGGGCCCCTAAGCTT NM_003495 RefSeq
chr6 + 27139308 27139678 HIST1H4I 8294 "histone cluster 1, H4i"

GO:0005515|GO:0010467|GO:0006325|GO:0005634|GO:0045653|GO:0000723|GO:0000183|GO:0000786|GO:0070062|GO:0035574|GO:0035575|GO:0046982|GO:0006334|GO:0006335|GO:0005576|GO:0006336|GO:0000228|GO:0003677|GO:0032776|GO:0034080|GO:0043234|GO:0016020|GO:0045814|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135108_PI430048170 0.466457148499643 1.05017583933322 0.288019077916532 0.296615936039775 0.516205476031919 A A A 0.313911137827699 0.272594239891588 0.313835156035073 A A A LNCV6_135108_PI430048170 mRNA GGGGGTCAGTAGTCTCTATCTGCTAATAAATGAAGAAAGGAAGTAAACTCTGAAAAATAA NM_001278344 RefSeq chr1 + 236686453 236764627 ACTN2 88 "actinin, alpha 2, transcript variant 3"
GO:0008092|GO:0005515|GO:0030018|GO:0030035|GO:0005884|GO:0043267|GO:0043268|GO:0007268|GO:0030175|GO:0051373|GO:2000273|GO:2000009|GO:0042802|GO:0005829|GO:0031143|GO:0030375|GO:0051015|GO:0043197|GO:0051289|GO:0048041|GO:0042391|GO:0030274|GO:0046983|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131330_PI430048170 0.404056508712247 0.345700158454072 0.244895500183749 0.313674300519353 0.292573338348595 A A A 3.00992154389947 0.347630415186187 0.308494715081851 P A A LNCV6_131330_PI430048170 mRNA GGAAAGACTAAACAGTGGACAATCAATCTTGGGACTATGAATTTTATGCTGGAATAAAGT NM_173353 RefSeq chr12 + 71938845 72032441 TPH2 121278 tryptophan hydroxylase 2
GO:0071285|GO:0014823|GO:0043005|GO:0043627|GO:0005506|GO:0009072|GO:0051384|GO:0044281|GO:0005829|GO:0051592|GO:0034641|GO:0004510|GO:0042427|GO:0046219|GO:0007623|GO:0031667|GO:0016597|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80062_PI430048170 0.2012720858671491.44033149485929 2.66393971743996 3.33968686819273 2.49182321620296 A P A 2.25894413296455 2.43398794037995 2.36287746090523 A P P LNCV6_80062_PI430048170 mRNA TTTACAGCTTTGTCCAGACACAGAGACAAGGCTAAATGCTGCTTATTCATTTGGAACAAC NM_153704RefSeq chr8 + 93754843 93818119 TMEM67 91147 "transmembrane protein 67, transcript variant 1"
GO:0005515|GO:0005813|GO:0060170|GO:0006996|GO:0010826|GO:0036038|GO:0030433|GO:0042384|GO:0031005|GO:0060271|GO:0005789|GO:0016021|GO:0051082|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133560_PI430048170 0.00121262418523185 1.97342468292934 10.5703323149643 10.4755164362859 10.4331373328668 P P P 9.38446100494761 9.6427265682719 9.50151687104707 P P P LNCV6_133560_PI430048170 mRNA GGGAGCATGAAGTACGAGGAAAACTTGAATTCCAGATTTTTAGTGCAAAGTATTTATCAT NM_178507RefSeq chr11 + 120211038 120229941 OAF 220323 OAF homolog (Drosophila) GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142411_PI430048170 0.0956912557763599 1.20234456737269 7.60536333229362 7.57740553826813 7.31924128007365 P P P 7.08499683805239 7.35795235558381 7.2651777572862 P P P LNCV6_142411_PI430048170 mRNA CCCTGCTCTGGGCTTCTCTCCTGTTTTCCCCAATAAATATGTGCCTCATGTAATAAAAAA NM_173080RefSeq chr1 + 152970652 152972573 SPRR4 163778 small proline-rich protein 4 GO:0018149|GO:0031424|GO:0005938 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142364_PI430048170 0.50323998823739 1.30254829303855 1.56810735975048 0.4465521505577690.516668247432801A A A 0.37115345713698 0.913507180238679 0.314994052639298A A A LNCV6_142364_PI430048170 mRNA AGAATCCCACAGTTGATCTTTTTTGCTGCCCTGAATGTGACCCAAGGCTTAGTAGTCAGT NM_001145108 RefSeq chr12 - 44508274 44876464 NELL2 4753 "NEL-like 2 (chicken), transcript variant 3"
GO:0005515|GO:0005509|GO:0005576|GO:0070050 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136992_PI430048170 0.0150427381083323 0.6869428066825291 0.9385396685009 10.7738348301968 10.8617010841003 P P P 11.2425554680071 11.3764644026777

11.5665056027322 P P P LNCV6_136992_PI430048170 mRNA
CTACCCTGTTGCTTTTCACAAATCATGGTAATAAAACAAGTTATTCTTGAGGACTAGTCA NM_032830RefSeq
chr16_GL383557v1_alt - 60801 86649 CIRH1A 84916 "cirrhosis, autosomal recessive 1A (cirhin)"
GO:0030490|GO:0005515|GO:0006355|GO:0005730|GO:0034455|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133561_PI430048170 0.00578510355721332 0.3647342704558768.54668813460051
8.32051739642498 8.67361271927938 P P P 9.79370411830653 9.73831714935118
10.3214766184993 P P P LNCV6_133561_PI430048170 mRNA
CTGTAAACAATTTCTTAGGACACCATTTGGGCTAGTTTCTGTGTAAGTGTAAATACTACA NM_006164RefSeq chr2
- 177230302 177265131 NFE2L2 4780 "nuclear factor, erythroid 2-like 2, transcript variant 1"
GO:0005515|GO:0070301|GO:0003700|GO:0016567|GO:0044212|GO:0005886|GO:0006366|GO:0005634|GO:2000
121|GO:0005829|GO:0030968|GO:0001221|GO:0005737|GO:0045944|GO:0071356|GO:0000785|GO:0036003|GO:0
071499|GO:0001102|GO:0005813|GO:0000976|GO:0036091|GO:0019904|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_55000_PI430048170 0.2291856351030551.02601373864504 0.3360735961821730.274402678115851
0.26799275390448 A A A 0.2507671805171860.2654794841301750.252010298282485A A A
LNCV6_55000_PI430048170 mRNA
AAGAGTAACGTTATGCCATGTGGTCATACTCTCAGCTTGCTGAGTGGATGACAAAAAGAG NM_001136219 RefSeq
chr1 + 161505414 161519570 FCGR2A2212 "Fc fragment of IgG, low affinity IIa, receptor (CD32),
transcript variant 1" GO:0005886|GO:0019864|GO:0045087|GO:0016021|GO:0038096|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131562_PI430048170 0.3764188562775950.92102499486437 0.474817163796519
0.3937200478999630.431700864033456A A A 0.4119198956157110.739534620828929
0.485143241024939A A A LNCV6_131562_PI430048170 mRNA
AGTTTTTCAGATTTACAGAAAAGATGATAAACCTTAGAAACATTATATGCTAAGTGAAAG NM_014855RefSeq chr7
+ 4775630 4794395 AP5Z1 9907 "adaptor-related protein complex 5, zeta 1 subunit"
GO:0005515|GO:0044599|GO:0005737|GO:0000724|GO:0016197|GO:0005654|GO:0005634|GO:0030119|GO:0015
031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143057_PI430048170 0.4760871697756131.1304154455092 3.54574167442499
3.93833347312399 3.58328210521891 P P P 3.60035030411249 3.789162180612
3.09468564537521 P P P LNCV6_143057_PI430048170 mRNA
TTAAAGGTCAAGGAAGGAAAATACTACCTGTCCCCTATGCCACTAAGCCAACGTGTGTGT NM_003593RefSeq chr17
+ 28523940 28538157 FOXN1 8456 forkhead box N1
GO:0006357|GO:0006366|GO:0000981|GO:0033081|GO:0048538|GO:0005634|GO:0006952|GO:0050673|GO:0043
565|GO:0008544|GO:0030216|GO:0035878|GO:0009887|GO:0001942|GO:0002260 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135178_PI430048170 0.9171798291241711.04015188782276 0.268506037466488
0.3395155248433650.987424197762461A A A 0.4323488934372950.737087352489528
0.338476673200691A A A LNCV6_135178_PI430048170 mRNA
AGATCAATAAGGATGAGATGGAATGGCAGGTGAAATCTCCAGCCACGTTTGGACTATCAG NM_212556RefSeq chr2
- 236194871 236264345 ASB18 NA ankyrin repeat and SOCS box containing 18 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_135876_PI430048170 0.0127446119703277 1.45449154303072 7.10004185548551
7.27742317680364 7.00989257403127 P P P 6.57925086082227 6.64701266916491
6.55080500496838 P P P LNCV6_135876_PI430048170 mRNA
CCCAGAGTCCCTGCAGGCCTGTCCATGCATTAAAAATTCCTATTGTCTCTCTTTAAAAAA NM_014010RefSeq chr9
- 116425224 117415039 ASTN2 23245 "astrotactin 2, transcript variant 1"
GO:0016021|GO:0060187|GO:2000009|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133565_PI430048170 0.7663685627732751.03409778135342 5.91127289192288 6.2380035952309

6.16789424862536 P P P 5.84655833690355 5.96296500633573 6.33620675753455 P P P
LNCV6_133565_PI430048170 mRNA
GGGATCAGTGTGTGTGTATGTGATTTGTTTATTGAGTTGGCTTTGCTTTTTTAGTTTTTC NM_012300 RefSeq chr5 -
171861551 172006873 FBXW11 23291 "F-box and WD repeat domain containing 11, transcript variant 3"
GO:0000209|GO:0005515|GO:0042347|GO:0004842|GO:0005813|GO:0016567|GO:0000151|GO:0005634|GO:0031
146|GO:0045862|GO:0005829|GO:0031648|GO:0006470|GO:0000086|GO:0046983|GO:0042753|GO:0043161|GO:0
048511|GO:0045893|GO:0000278|GO:0016055|GO:0045892|GO:0019005 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140187_PI430048170 0.5758449752170320.9560575643832560.393558430999539
0.2567155901060010.294221282092251 A A A 0.5494194597958970.298435306156678
0.278522509553665 A A A LNCV6_140187_PI430048170 mRNA
CTGTGTCCAGAATTTTAATAGGCTCTCTATTGGAAGGAGAAAGAATTTCAAGTTAACAGT NM_001130690 RefSeq
chr6 - 165327286 165662100 PDE10A 10846 "phosphodiesterase 10A, transcript variant 1"
GO:0004114|GO:0004118|GO:0047555|GO:0010738|GO:0046069|GO:0046872|GO:0005829|GO:0007165|GO:0030
552|GO:0030553|GO:0007596|GO:0043949|GO:0006198 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136343_PI430048170 0.0294630005224038 1.08382653410226 0.37919914404378
0.4594585486933810.412666376068631 A A A 0.2881125299634870.312415700492393
0.303417781322536 A A A LNCV6_136343_PI430048170 mRNA
CGGATTGTCCACAAGAAACCAATCAGTTATGCAAAATCTTTTCCAAAGGAAATGGGAAAT NM_001024607 RefSeq
chr7 - 108883974 108884587 C7orf66 NA chromosome 7 open reading frame 66 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139037_PI430048170 0.7322320320300541.02331477613056 14.8182477932248
14.8358070737755 14.981479652642 P P P 14.7301670672174 14.7942764099206
15.0026985653099 P P P LNCV6_139037_PI430048170 mRNA
ATTAGGTATCCCTCCTGATGATGAAGACTGAAGGTGTAGACTCAGCCTCACTCTGTACAA NM_004546 RefSeq chr7
+ 140696680 140706646 NDUFB2 4708 "NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2,
8kDa" GO:0022904|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0008137|GO:0044237 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_143493_PI430048170 0.5978755909855311.04899147598525 10.0536405715738 10.340752518121
10.3357963812193 P P P 10.1463302220956 10.0909866837971 10.2962645342047 P P P
LNCV6_143493_PI430048170 mRNA
TGACTATATCTCTGCTTGACTGTGAATAAAGTCAGCTGTGCAGTATTTATAGTCCATGTA NM_002495 RefSeq chr5
+ 53560634 53683341 NDUFS4 4724 "NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa
(NADH-coenzyme Q reductase)"
GO:0072593|GO:0005743|GO:0048146|GO:0044281|GO:0051591|GO:0005739|GO:0022904|GO:0032981|GO:0045
333|GO:0005747|GO:0007420|GO:0019933|GO:0006120|GO:0001932|GO:0008137|GO:0044237 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136515_PI430048170 0.0209764988838078 0.4169874994247612.58857021395567
3.21660073113137 3.16801871720793 A P P 4.23515262421793 4.3495042274992
4.25205643932494 P P P LNCV6_136515_PI430048170 mRNA
TGTCACTTCCAATCCTCTTGGCCTTCATACTAAAGTCACTGCTGTGGCAACCAGTTTCAA NM_015412 RefSeq chr3
- 113002444 113019708 C3orf17 25871 "chromosome 3 open reading frame 17, transcript variant 1"
GO:0045747|GO:0045665|GO:0005634|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133740_PI430048170 0.8082475049189071.18407444107184 0.546743033252903
1.76444474634496 0.271878673363385 A A A 0.4105988995425861.24459219975405
0.509841581814521 A A A LNCV6_133740_PI430048170 mRNA
AACTAAGTTCATGGACCAGAAAAACAGCCTGTACTTAATGCCAATCCTGCCTGTACCCTC NM_194302 RefSeq chr2
- 219002845 219041551 CCDC108 255101 "coiled-coil domain containing 108, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_141282_PI430048170 0.0696586195687294.10526961773228 3.35071526143464
4.13595316003392 3.97672945705534 P P P 2.84245873110556 0.412825505418339
1.06964683591169 P A A LNCV6_141282_PI430048170 mRNA
CTTGCGATGAATTCTGCATTGTTCGGTGTTTTTTGTACATGTCAACTCGTAAATCTGATT NM_001277075 RefSeq chr19
- 47520684 47555856 ZNF541 84215 zinc finger protein 541
GO:0006355|GO:0003682|GO:0007275|GO:0005634|GO:0007283|GO:0003677|GO:0046872|GO:0030154|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145750_PI430048170 0.6785514124847690.8938824477504730.918887210454164
0.3192609829368980.278332280914791 A A A 0.4883107069554831.14930988279137
0.318239085570079 A A A LNCV6_145750_PI430048170 mRNA
AGTAGGAGAGAAATCTCTTAATTATGATTAATATGGTATTGCCTTTACATGCCTCAGCCT NM_021217 RefSeq chr19
- 2933217 2944971 ZNF77 58492 zinc finger protein 77
GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144634_PI430048170 0.0191423860722720.7473582376018771 3.8942079871997
13.7492047926153 13.6790605353333 P P P 14.2109009950493 14.1748312989528
14.2052742357868 P P P LNCV6_144634_PI430048170 mRNA
AGCCCCACCTCCTTGAGCTTTATTTACCTAAATTTAAAGGTATTTCTTAACCCGAAAAAA NM_016292 RefSeq chr16
- 3658036 3717597 TRAP1 10131 "TNF receptor-associated protein 1, transcript variant 1"
GO:0005515|GO:0005811|GO:0005164|GO:0019901|GO:0005743|GO:0006950|GO:0005524|GO:0005739|GO:0005
758|GO:0061077|GO:0016020|GO:0005759|GO:0005654|GO:0051082|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_126893_PI430048170 0.0123602071090223 1.40364098113802 5.87662977932216
5.71930242779113 6.00451187907667 P P P 5.49126751048108 5.23277528534787
5.41097081192617 P P P LNCV6_126893_PI430048170 mRNA
GGATTACCACTGTACACAAATCTAATCAATAAAAACGTTAGAACCTTCTGCTTAGAGTAC NM_001302617 RefSeq
chr14 - 75053224 75069483 ACYP1 97 "acylphosphatase 1, erythrocyte (common) type, transcript
variant 4" GO:0003998|GO:0006796|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132512_PI430048170 0.0251218635051521 0.6379215400029723.87526942770125
4.11650865302207 4.14937508650886 P P P 4.47186008425489 4.63801348221006
4.95062525749444 P P P LNCV6_132512_PI430048170 mRNA
TGCTAATTCTTTGCAAAAATCCAAATATTGTTAAGGGACCAGGGAGATGCCACTACCCCT NM_022977 RefSeq chrX
- 109641334 109733392 ACSL4 2182 "acyl-CoA synthetase long-chain family member 4, transcript
variant 2"
GO:0006629|GO:0047676|GO:0001676|GO:0030307|GO:0005741|GO:0035338|GO:0044281|GO:0005737|GO:0019
432|GO:0043025|GO:0070672|GO:0060996|GO:0044233|GO:0031957|GO:0005778|GO:0044255|GO:0070062|GO:0
005811|GO:0008610|GO:0007584|GO:0060136|GO:0005524|GO:0004467|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_72017_PI430048170 0.1513000627959171.35319963473271 9.07185748531974 8.96851195673621
9.59070689528387 P P P 8.56028098543249 8.88270076619747 8.93127455274174 P P P
LNCV6_72017_PI430048170 mRNA
TAATGGAGATCGTAAAATAAAGGTTTCCAACACCCTGGAAAGCCGGCTGGATCTCATAGC NM_001696 RefSeq chr22
- 17592135 17628822 ATP6V1E1 529 "ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1,
transcript variant 1"
GO:0005515|GO:0008286|GO:0051701|GO:0016469|GO:0005765|GO:0055085|GO:0005829|GO:0005739|GO:0006
879|GO:0033572|GO:0005902|GO:0016324|GO:0008553|GO:0046961|GO:0008152|GO:0015991|GO:0051117|GO:0
090382|GO:0070062|GO:0033178|GO:0005768|GO:0015992 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_133186_PI430048170 0.8311615651471661.01377719527425 3.2367042236466

3.28856589471417 3.24462112014844 P P P 3.61161220511519 3.05115692862271
2.95862803326232 P P P LNCV6_133186_PI430048170 mRNA
TACCTCAATGTCCCCAACAAGATTGCTTAATAAATTGTGTTTCCTCCAAGCTATTCAATT NM_003212RefSeq chr3
+ 46577585 46582462 TDGF1 6997 "teratocarcinoma-derived growth factor 1, transcript variant 1"
GO:0005515|GO:0048471|GO:0008284|GO:0007369|GO:0005886|GO:0002042|GO:0050731|GO:0030879|GO:0005
634|GO:0048146|GO:0031225|GO:0009790|GO:0005615|GO:0030154|GO:0007507|GO:0000187|GO:0016324|GO:0
007173|GO:0018105|GO:0045944|GO:0035729|GO:0071356|GO:0071354|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130704_PI430048170 0.0139207689186671.33635897812776 9.1801058303543 9.0897943740333
9.01922565345421 P P P 8.8130737231794 8.55323325832962 8.66054201586322 P P P
LNCV6_130704_PI430048170 mRNA
TAGGATCCTAGATAAGCAGGTGAAATTTAGGCTTCAGAATATATCCGAGAGGTGGGGAGGNM_023935RefSeq chr20
- 3190365 3204649 DDRGK1 65992 DDRGK domain containing 1
GO:0005515|GO:0034976|GO:0051092|GO:0005783|GO:0044389|GO:0033146|GO:0005789 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128456_PI430048170 0.522296472270312 1.03897988534408 0.299122014711472
0.3086470343435640.505467880360635A A A 0.3284001246673240.287193343171048
0.341135160124021A A A LNCV6_128456_PI430048170 mRNA
CTCTCTTATTCCACTTCGGTAGAGGATTTCTAGTTTCTTGTGGGCTAATTAAATAAATCA NM_000477RefSeq chr4
+ 73404254 73421412 ALB213 albumin
GO:0005515|GO:0051087|GO:0072562|GO:0043252|GO:0005634|GO:0044281|GO:0005615|GO:0043069|GO:0001
895|GO:0008144|GO:0019836|GO:0006810|GO:0031093|GO:0008206|GO:0046010|GO:0070062|GO:0009267|GO:0
043066|GO:0005504|GO:0010033|GO:0016209|GO:0007584|GO:0005507|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142915_PI430048170 0.7019066233183071.01363470820376 6.89206302243378
6.87192303643378 6.82479332746473 P P P 6.75818962919489 6.90835510921419
6.86039252854325 P P P LNCV6_142915_PI430048170 mRNA
CACTTCTTGTTTTATGTACAGGATGTCATATGTCCCCCTACCCCTGTACCTGCCAAGGAT NM_178435RefSeq chr1
- 152565698 152566753 LCE3E 353145 late cornified envelope 3E GO:0031424 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_132556_PI430048170 0.000369202703179771 0.3118204477610145.05719145922928
4.86435942276811 5.24900729553625 P P P 6.81784267201281 6.5515946357007
6.85201607142049 P P P LNCV6_132556_PI430048170 mRNA
GGACTATGTACATACGTTACTGAGATTGTGTAAAAAGTAGATCCTGAACAGTTATCACAT NM_018372RefSeq chr1
- 110947189 110963944 LRIF1 55791 "ligand dependent nuclear receptor interacting factor 1, transcript variant 1"
GO:0005515|GO:0006355|GO:0005815|GO:0005634|GO:0042974|GO:0015629|GO:0016363|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133418_PI430048170 0.5730229798230670.8656563609042621.96727234747425
0.2739099735942892.31761168892981 A A A 2.23434501502305 1.82859252170738
1.77195493041677 A A A LNCV6_133418_PI430048170 mRNA
TAAAAATACCATGTCTGTGATAGGGAAGAAGGCCTGCTCACCAATGATGAGGCCTGTGAA NM_176792RefSeq chr10
- 100977821 100987515 MRPL4384545 "mitochondrial ribosomal protein L43, transcript variant 2"
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005761|GO:0005743|GO:0006
412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129548_PI430048170 0.71494257703693 0.9682035299003551 0.3191248918259
9.92025935264461 10.0313246815308 P P P 10.2431801534014 10.1607938495474
10.0283681883657 P P P LNCV6_129548_PI430048170 mRNA
TTAAATAAGTCAATTCCTAGAAGTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCAGAA NM_002117RefSeq

chr6_GL000253v2_alt - 2577800 2581178 HLA-C 3107 "major histocompatibility complex, class I, C, transcript variant 1"
GO:0002474|GO:0005886|GO:0005783|GO:0019221|GO:0006955|GO:0060337|GO:0042605|GO:0030670|GO:0071556|GO:0016032|GO:0070062|GO:0060333|GO:0012507|GO:0002480|GO:0005794|GO:0002486|GO:0009986|GO:0042612|GO:0005102|GO:0042590|GO:0005576|GO:0000139|GO:0005887|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132020_PI430048170 0.0278405758352299 0.8260069431343465.91993524220916 6.04414268233608 5.98679973544026 P P P 6.36002896667821 6.14618611249538 6.2667218990144 P P P LNCV6_132020_PI430048170 mRNA
AACACTGGACCAGCTGTAAAAGTAAACAGTGTGTTTATGCATTGAGATACTAAAGCATTT NM_001008211 RefSeq chr10 + 13100081 13138276 OPTN 10133 "optineurin, transcript variant 1"
GO:0005802|GO:0005515|GO:0008219|GO:0048471|GO:0043001|GO:0090161|GO:0005634|GO:0005829|GO:0005737|GO:0000086|GO:0007030|GO:0001920|GO:0043122|GO:0070530|GO:0000042|GO:0043124|GO:0017137|GO:0005794|GO:0005776|GO:0016236|GO:0008022|GO:0050829|GO:0007165|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144721_PI430048170 0.4494193774399850.6085277434133590.277917737268735 0.3007780080410570.473225826591969A A A 0.3300026881158661.92973224109417 0.299906508160005A A A LNCV6_144721_PI430048170 mRNA
CGACCACTGATGAGATCAACAACAGGTGAACTATAAACCTATTATTTATTGCAGAACTAA NM_003251RefSeq chr11 + 78063860 78068357 THRSP 7069 thyroid hormone responsive
GO:0006629|GO:0006355|GO:0005654|GO:0010866|GO:0046890|GO:0042803|GO:0006351|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134380_PI430048170 0.0190594305784634 0.5779383612262318.90798872973121 8.53670873950424 8.73400333958783 P P P 9.33908232795805 9.36156646037712 9.82178152753816 P P P LNCV6_134380_PI430048170 mRNA
GATGTTGCACTGGTGGCAATTCATCATGGAGCATAATAAAATTAATTTGACCCAAATAGA NM_003941RefSeq chr7 - 123681926 123749071 WASL 8976 Wiskott-Aldrich syndrome-like
GO:0005515|GO:2000370|GO:0005886|GO:0050999|GO:0051491|GO:0006928|GO:0005634|GO:0044281|GO:0006900|GO:0015629|GO:0005829|GO:0032880|GO:0009617|GO:0016050|GO:0005083|GO:0007411|GO:0034629|GO:0046209|GO:0070062|GO:0006355|GO:0048013|GO:0030478|GO:0003779|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140711_PI430048170 0.0435540446344486 0.7182701358444665.62985637633797 5.18135610028524 5.38652455135726 P P P 5.98393867699682 5.73704854674619 5.93239733412046 P P P LNCV6_140711_PI430048170 mRNA
CTCCTTGTTCTCCTACTAATATTCCCAAGCTCCATATGCCAATTAAAGAAGAAACAAAAA NM_021645RefSeq chr13 + 52024690 52033600 UTP14C 9724 "UTP14, U3 small nucleolar ribonucleoprotein, homolog C (yeast)"
GO:0030490|GO:0051321|GO:0032040|GO:0005730|GO:0007275|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142515_PI430048170 0.0179710798867773 0.4270340092506820.422133049318054 0.4009331593102510.419612058117195A A A 1.35318249683171 1.92203022211067 1.59338205884102 A A A LNCV6_142515_PI430048170 mRNA
GAGAAAGTTCACCAGAGACACTGACAAGACACCCCAATCCATTTACAGAAAAGAATACAT NM_152290RefSeq chr1 + 12746185 12761169 C1orf158 93190 chromosome 1 open reading frame 158 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145193_PI430048170 0.2330473054308031.30347645667724 1.55692522983683 1.48937945861999 1.48344433622597 A A A 0.5891426590471461.3897487891062 1.28196841796953 A A A LNCV6_145193_PI430048170 mRNA
CACAAGAGGATTTAAGGGAGGAATGTTTATAGGACACACACACAAAAGCTCTTTCTATTT NM_007068RefSeq chr22 - 38518948 38570196 DMC1 11144 "DNA meiotic recombinase 1, transcript variant 1"

GO:0005515|GO:0000781|GO:0000794|GO:0005694|GO:0007286|GO:0005634|GO:0007292|GO:0007283|GO:0001556|GO:0003677|GO:0005524|GO:0007129|GO:0001541|GO:0007126|GO:0007141|GO:0008094|GO:0007131 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136653_PI430048170 0.11799944486553 0.8697701687487299.53847844455503 9.40236888292601 9.61155282790352 P P P 9.73388799274082 9.57471287979353 9.84290646482576 P P P LNCV6_136653_PI430048170 mRNA
TTGGGAAATCCATTCCATTTTGTGAATTGTGACAAATAACAGCAGTGGAAAAAGTATGTG NM_001166386 RefSeq chrX + 152733861 152737669 MAGEA12 4111 "melanoma antigen family A12, transcript variant 1" GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137211_PI430048170 0.160495864886602 1.12637174631131 7.4466288504095 7.38556649920777 7.45160415833561 P P P 7.09816335872624 7.38191104019945 7.27549149731919 P P P LNCV6_137211_PI430048170 mRNA
ATCAAGGTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGCTGA NM_138352 RefSeq chr19 - 14088416 14090420 SAMD1 90378 sterile alpha motif domain containing 1 GO:0005737|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109625_PI430048170 0.00964716563673311 0.4332623283773441 0.404956326673 10.1352310442768 9.96580467460791 P P P 11.3877789697655 11.4185064833088 11.3533486563279 P P P LNCV6_109625_PI430048170 mRNA
CCACTGCTTTTCTATGGGAGACACTCTTAATTTAACAGATGAGAATATTTTGAAACTCTG NM_052897 RefSeq chr12 + 57522875 57530148 MBD6 114785 methyl-CpG binding domain protein 6
GO:0010369|GO:0003682|GO:0005730|GO:0005654|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132155_PI430048170 0.0300129771251011 0.2744921045274391.61663756648951 0.7628761835772062.1897446616656 A A A 3.26584542176094 3.4099154160231 3.77892781680438 P P P LNCV6_132155_PI430048170 mRNA
GAGTTCACAGTGGTAAGACTCATATGCCTGTATGTGTTGCTAATAAATTAGATTTTGGAT NM_144715 RefSeq chr3 - 19879473 19934214 EFHB 151651 "EF-hand domain family, member B" GO:0005509 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131731_PI430048170 0.2986766719481141.36920809251065 1.14970680475886 1.30947172144486 0.370104748375375 A A A 0.90830899708346 0.29950102945739 0.341379308463652 A A A LNCV6_131731_PI430048170 mRNA
GTGGCCCGTTGAAATGTTGGTGGCACTTAATAAATATTAGTAAATCCTTCAAAGACAAAA NM_031310 RefSeq chr19 - 17351447 17377349 PLVAP 83483 plasmalemma vesicle associated protein
GO:0005515|GO:0048471|GO:0009986|GO:0000165|GO:0005901|GO:0016021|GO:0002693|GO:0070528|GO:0042803|GO:0033209|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130084_PI430048170 0.496649549403720.9081082438294711.0652092191037 11.0134087532901 11.0535959330612 P P P 10.8702665842113 11.3537597671333 11.2804341213415 P P P LNCV6_130084_PI430048170 mRNA
ACCCCTGTGACTCAATATTACCATAGTGCGATGTCGTTTTGTGCTATTTTGAACAATTAA NM_005334 RefSeq chrX - 153947556 153971368 HCFC1 3054 host cell factor C1
GO:0005515|GO:0003700|GO:0006366|GO:0006325|GO:0005634|GO:0070461|GO:0042802|GO:0005739|GO:0005737|GO:0071339|GO:0048188|GO:0045944|GO:0043996|GO:0043995|GO:0000123|GO:0043025|GO:0006355|GO:0006996|GO:0003713|GO:0050821|GO:0001205|GO:0000122|GO:0045787|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83127_PI430048170 0.73856435906957 1.10745560873815 3.51174763660549 4.42726646481252 4.15643625942279 P P P 3.64875310967258 3.99087032264475 4.11997667361422 P P P LNCV6_83127_PI430048170 mRNA
AGAAATAAAGGCGATGATTTCCGACCATGCTCGCGTTCTCCGCGGAGTCTGTGCTACACC NM_001129979 RefSeq chr16 + 77199451 77213079 SYCE1L 100130958 synaptonemal complex central element protein 1-like

GO:0000795|GO:0007130 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135728_PI430048170 0.2159554199547610.8167218419277254.92944195709251 5.3638940544199
5.48744738516574 P P P 5.77270891715713 5.4384140692479 5.47988489940425 P P P
LNCV6_135728_PI430048170 mRNA
GGTTTTGCATGCAATTAAAAATCCTTATTTCTTGTTCTAGGGCTTCCCTTAGTTAATGGT NM_197977 RefSeq chr9 +
101398853 101410660 ZNF189 7743 "zinc finger protein 189, transcript variant 2"
GO:0006355|GO:0003700|GO:0005634|GO:0000122|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142655_PI430048170 0.23569990996716 0.8134384625645897.68633768954864
7.60578123633236 7.88423148249969 P P P 7.71145165727167 8.01114356177173
8.30172717536435 P P P LNCV6_142655_PI430048170 mRNA
GCTCATGTTTTGGTTTAGTTATAGTCGCTATGGATTTGGCCAAATAAAAAGGCAAACAAC NM_012341 RefSeq chr10
+ 988408 1017768 GTPBP4 23560 GTP binding protein 4
GO:0005515|GO:0048471|GO:0031965|GO:0030336|GO:0022408|GO:0033342|GO:0005794|GO:0008285|GO:0042
254|GO:0050821|GO:0003924|GO:0005730|GO:0005634|GO:0000079|GO:0005525|GO:0001649|GO:0005737|GO:0
016020|GO:0008152|GO:0031397|GO:0008156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130944_PI430048170 0.1946828389390920.7808176674149218.20293524423875 8.1763623371583
8.70935853619997 P P P 8.5232024789645 8.62386521617533 9.02665982124236 P P P
LNCV6_130944_PI430048170 mRNA
GGCTACCCTTGACAAGAAAAGACATACTGTCATGTATTTATATTCTAGCATAGACTAAAC NM_006571 RefSeq chr8
+ 30156296 30183639 DCTN6 10671 dynactin 6
GO:0019886|GO:0005813|GO:0045502|GO:0000777|GO:0007052|GO:0005869|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143280_PI430048170 0.1774057922779930.88269503515699 7.06829407449278 7.15707016066
7.14763402261087 P P P 7.15115137022829 7.29084965532139 7.45645038621967 P P P
LNCV6_143280_PI430048170 mRNA
CTGGGCACCTGGCACCACAAGACCATGTTTTCTAAGAACCATTTTGTTCACTGATACAAA NM_002606 RefSeq chr21
+ 42653751 42775508 PDE9A 5152 "phosphodiesterase 9A, transcript variant 1"
GO:0005515|GO:0048471|GO:0005794|GO:0004114|GO:0005783|GO:0047555|GO:0032587|GO:0019934|GO:0046
872|GO:0005829|GO:0007165|GO:0007596|GO:0008152|GO:0043204 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138729_PI430048170 0.0856355997187365 0.8459742650106591 1.7923347379149
11.7252766370208 11.9576121801508 P P P 12.0274603252123 11.9508098104132
12.2176717954567 P P P LNCV6_138729_PI430048170 mRNA
GCCTAGAGGACTAGATCACCTTAGTTTGATTCTATTTTTTAGCTTGCAAAAAGTGACTTA NM_001009924 RefSeq
chr20 - 5099837 5113087 TMEM230 29058 "transmembrane protein 230, transcript variant 2"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52934_PI430048170 0.0461959049467707 0.6562730736253625.94661417831816 5.6880921694317
6.19094204993739 P P P 6.40357137677792 6.38259411330695 6.85504924371181 P P P
LNCV6_52934_PI430048170 mRNA
TTTGGCCTTCTGAGAAAAGAGCTTCTAGTAATTGAACCATGGGAAACCCAGCTTCTGGAG NM_001145369 RefSeq
chr9 - 109375693 109451384 PTPN3 5774 "protein tyrosine phosphatase, non-receptor type 3,
transcript variant 3"
GO:0005515|GO:0008092|GO:0051045|GO:2000649|GO:0035335|GO:0005737|GO:0006470|GO:0045930|GO:0009
898|GO:0051117|GO:0001784|GO:0005856|GO:0004725|GO:0017080 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134849_PI430048170 0.0370003041128771.87855170107418 4.08770171479945 3.6912382257558
3.78414431128754 P P P 2.52023658257757 3.32231396420308 2.91100589116594 P P P
LNCV6_134849_PI430048170 mRNA

CCTCCTGAAATGGTTCCCACCCAGAACTAATTTATTTTTTATTAAAGATGGTCATGACAA NM_001288608 RefSeq chr1 + 150549368 150560936 ADAMTSL4 54507 "ADAMTS-like 4, transcript variant 4" GO:0005515|GO:0043065|GO:0006915|GO:0005575|GO:0002020|GO:0005614|GO:0036066|GO:0006493|GO:0030198|GO:0006508|GO:0005788|GO:0004222|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140734_PI430048170 0.0320439067047145 1.21775629798758 9.81409013532338 9.86479683884062 9.69519035281611 P P P 9.41721131523538 9.64017927824346 9.45937208574574 P P P LNCV6_140734_PI430048170 mRNA
AAGGTTGGTAACATTAGAGGCTGTGAGCTTGTGTTACATGGTAATAAAGCCAATGAAGAG NM_017638 RefSeq chr1 + 28329001 28335967 MED18 54797 "mediator complex subunit 18, transcript variant 1" GO:0005515|GO:0001104|GO:0006366|GO:0006357|GO:0016592 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142636_PI430048170 0.165604366660868 0.69149483413096 6.40779992635773 6.23870229235691 5.75164853632967 P P P 6.95325811788311 6.81870231718173 6.19191136644605 P P P LNCV6_142636_PI430048170 mRNA
GCTTGCTTTTTCTCCATGTCTCCCAGTTTGTATAGTTAAATTGTCCAGTTGTATAGTTAA NM_182595 RefSeq chr7 + 53035655 53036925 POM121L12285877 POM121 transmembrane nucleoporin-like 12 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137045_PI430048170 0.231021898597837 0.763423413386976 10.4643544673982 10.0395560617769 9.76400889417832 P P P 10.7744985466433 10.5509179750377 10.1245536031107 P P P LNCV6_137045_PI430048170 mRNA
GGCTCCCTCCCATCTCACTCAAGGTTCTCTGAGGACATTAAAGTGGTGGATTCACCCTGG NM_182623 RefSeq chr1 - 16057768 16073632 FAM131C 348487 "family with sequence similarity 131, member C" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111946_PI430048170 0.0941876342379538 1.1737941714901 6.0123738354359 6.01565162568295 5.95911367698399 P P P 5.8987351963906 5.76377729238309 5.61816326850223 P P P LNCV6_111946_PI430048170 mRNA
ATAATTACTGCCGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCG NM_000930 RefSeq chr8 - 42174717 42207676 PLAT 5327 "plasminogen activator, tissue, transcript variant 1" GO:0005515|GO:0004252|GO:0043434|GO:0045202|GO:0005615|GO:0051591|GO:0005737|GO:0048167|GO:0006508|GO:0030141|GO:0070062|GO:0001666|GO:0009986|GO:0035249|GO:0014909|GO:0045177|GO:0005576|GO:0055085|GO:0045861|GO:0031012|GO:0007596|GO:0031639|GO:0048008|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129011_PI430048170 0.130095442685321 1.06589851899649 0.459765410908888 0.484013324302028 0.521549645495584 A A A 0.326218727391099 0.396269294889181 0.464013678599632 A A A LNCV6_129011_PI430048170 mRNA
GGTCTAAGTTGTTCTAAACCCAGGGTTCTCAAATGTGTTGTACAAAAAGTTTCATGTAAT NM_181654 RefSeq chr18 - 59295403 59318649 CPLX4 339302 complexin 4 GO:0019905|GO:0030054|GO:0016020|GO:0006836|GO:0046928|GO:0045202|GO:0006887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132100_PI430048170 0.514629222643961 0.969979279229703 0.429211372661282 0.436136958919358 0.261766240654818 A A A 0.38716380730425 0.461019807149539 0.416559640967247 A A A LNCV6_132100_PI430048170 mRNA
CTTCTGCTATGATACACAAGAACTTATGTTGGAATGAAGTGAAAAGTAAAATGGCCATTC NM_001284322 RefSeq chr10 - 96343215 96359365 OPALIN 93377 "oligodendrocytic myelin paranodal and inner loop protein, transcript variant 6" GO:0005794|GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76673_PI430048170 0.00242544412427397 0.709410276888054 5.64601037584777 5.48289780227423 5.48580269472364 P P P 5.97941677303569 6.12728690467824

5.99543333772239 P P P LNCV6_76673_PI430048170 mRNA
CCTTCAATCTTATCCTAACCAAATGAGAATAATGACATATTGAAAACAGCCTCTAGCTTC NM_001302777 RefSeq
chr6 + 3118375 3153198 BPHL 670 "biphenyl hydrolase-like (serine hydrolase), transcript variant 3"
GO:0005739|GO:0006520|GO:0016787|GO:0009636|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139822_PI430048170 0.0028219819678996 0.2357645883996754.2298670526124
3.61182571469858 4.2856082505954 P P P 5.9114160375541 6.21384050708467
6.31738900583468 P P P LNCV6_139822_PI430048170 mRNA
GCAGATTCCATGAGTAACTCTGACAGGTATTTTAGATCATGATCTCAACAATATTCTTCC NM_024312RefSeq chr12
- 101745496 101830867 GNPTAB 79158 "N-acetylglucosamine-1-phosphate transferase, alpha and beta
subunits"
GO:0009306|GO:0005794|GO:0003976|GO:0000139|GO:0005509|GO:0046835|GO:0005634|GO:0016021|GO:0007
040|GO:0030154|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129925_PI430048170 0.5349411072160340.918302144223282 3.99744266172494
4.01724448380633 3.84383079237548 P P P 4.35156626041142 3.91419471374454
3.92316931022313 P P P LNCV6_129925_PI430048170 mRNA
ATATATTCCTACAGTGATGTCAATTTTTATTAATCCCTGTCCCCAGGGAGGGTGGGAGCC NM_004463RefSeq chrX
- 54445453 54496166 FGD1 2245 "FYVE, RhoGEF and PH domain containing 1"
GO:0030036|GO:0031267|GO:0007264|GO:0008360|GO:0046872|GO:0005829|GO:0005085|GO:0005737|GO:0007
010|GO:0009887|GO:0046847|GO:0005856|GO:0005089|GO:0051056|GO:0048011|GO:0005794|GO:0043065|GO:0
007275|GO:0001726|GO:0097190|GO:0030027|GO:0043088|GO:0043547|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142092_PI430048170 0.1430829222968750.521043660693895 0.408754425791924
0.41681164420771 0.266298015161835 A A A 0.64112425658274 1.89022915327825
1.10551884974356 A A A LNCV6_142092_PI430048170 mRNA
AAACCTGTTTGAGAATCACTGAATTATAAATATAATCCATAGGCCTTGAGGCCCAAGATT NM_018655RefSeq chr1
+ 154993585 154994315 LENEP 55891 lens epithelial protein GO:0007275|GO:0003677 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141280_PI430048170 0.0308689476693301 1.21954397693874 7.21296743869981
7.12079099882881 7.13025530614603 P P P 6.95510856529989 6.90284154565001
6.74023077287752 P P P LNCV6_141280_PI430048170 mRNA
GCTTCATGTTTTAGAATTTGTGTATTGTCAATACTTAATTGGGGGTGGGAGAGACTGAGC NM_001198953 RefSeq
chr14 + 103715743 103733668 ZFYVE21 79038 "zinc finger, FYVE domain containing 21, transcript
variant 1" GO:0016023|GO:0005925|GO:0046872|GO:0005768 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135158_PI430048170 0.000470373280485459 0.4751863709121011 11.2217271751032
11.4119767169016 11.342740473338 P P P 12.4513460146862 12.3947724227773
12.3554019844841 P P P LNCV6_135158_PI430048170 mRNA
GTCCTTCCCCGTGCCTCCCAAAGTTACTTTAAGATCCTTAGAATATTTCTTTAAATATTT NM_016101RefSeq chr16 +
69339511 69343110 NIP7 51388 "NIP7, nucleolar pre-rRNA processing protein, transcript variant 1"
GO:0005515|GO:0042255|GO:0005730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131139_PI430048170 0.784354205258244 1.02574426118315 7.47754444305922
7.40968920371897 7.55223039517687 P P P 7.06582036477022 7.54029377589296
7.66091471600028 P P P LNCV6_131139_PI430048170 mRNA
GGGATGTAAGTTTGTGTAAATTAATGGTTTATTCTTTGCAAATAAAACGCTTTCCCCGTC NM_001399RefSeq chrX
+ 69616066 70039471 EDA 1896 "ectodysplasin A, transcript variant 1"
GO:0005515|GO:0010467|GO:0042346|GO:0005581|GO:0005886|GO:0090263|GO:0030154|GO:0043231|GO:0006
955|GO:0051092|GO:0042475|GO:0060662|GO:0005856|GO:0005164|GO:0005102|GO:0045177|GO:0005576|GO:0
060789|GO:0007398|GO:0007165|GO:0061153|GO:0007160|GO:0016020|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_133861_PI430048170 0.1183936206632341.98798135198831 2.94618062248519
3.68781301591823 3.66281769844471 P P P 1.60207540194585 3.14311530790257
2.28096180556099 A P A LNCV6_133861_PI430048170 mRNA
TTGTGTTTAATTCCTGGCACAGTTGTCCTGGAAATGCCTTTTTCTCTTGCCTGGGAACCA NM_005724RefSeq chr15
- 77044017 77071228 TSPAN3 10099 "tetraspanin 3, transcript variant 1"
GO:0008150|GO:0003674|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144222_PI430048170 0.2690078211433191.16651101710029 7.81831491597126
7.83340836319949 7.69387441196078 P P P 7.86120976253538 7.3836582176452
7.38370688413946 P P P LNCV6_144222_PI430048170 mRNA
GTGTGTTCTGAGCTGGACCCAGCCTCTTGTTCGAGAATAAAAACTCTTCTTCTCTTGCAT NM_001267868 RefSeq
chr19 + 5680764 5688523 HSD11B1L 374875 "hydroxysteroid (11-beta) dehydrogenase 1-like,
transcript variant g" GO:0016491|GO:0005576|GO:0055114 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_127441_PI430048170 0.6860155959342921.04304401216612 8.96207516075808
8.91552224521117 9.14228570210532 P P P 8.6622408140067 8.99119184026529
9.15184292286252 P P P LNCV6_127441_PI430048170 mRNA
TCAGACAAGCTAGCAGTTGTAGATGAATGGAGAAAAGAAATGGGCCTGTGCTGGAAAGAA NM_018686RefSeq
chr12 + 22046175 22065672 CMAS 55907 cytidine monophosphate N-acetylneuraminic acid
synthetase
GO:0016020|GO:0006054|GO:0008781|GO:0005654|GO:0005634|GO:0006488|GO:0044267|GO:0043687|GO:0018
279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57692_PI430048170 0.68442992965267 0.9147067884184956.88480593848255 6.71905168493273
6.86796260658554 P P P 6.54261161120062 7.26852749725316 6.96184115138551 P P P
LNCV6_57692_PI430048170 mRNA
ATCAGTAGTTCTTCCGGAACTTCAGACAGATTCAGCCGAATACTCAAGCACATCTTGACC NM_002689RefSeq chr11
+ 65261851 65298685 POLA2 23649 "polymerase (DNA directed), alpha 2, accessory subunit"
GO:0046982|GO:0005658|GO:0003887|GO:0003677|GO:0006260|GO:0003674|GO:0006271|GO:0000082|GO:0005
737|GO:0071897|GO:0000723|GO:0006270|GO:0000722|GO:0005654|GO:0000278|GO:0032201|GO:0000060 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137635_PI430048170 0.0159783859246098 0.5705011457349564.9455533951029
4.5718389877661 4.88247660002729 P P P 5.30276703581556 5.80177508504987
5.70453568365076 P P P LNCV6_137635_PI430048170 mRNA
TGTAGAGGAAGGCTCAAAGGAGTCAACATTTATATCTGGAAGGGACAAGTCATGCCTTGG NM_007192RefSeq chr14
- 21351471 21384266 SUPT16H 11198 suppressor of Ty 16 homolog (S. cerevisiae)
GO:0005515|GO:0010467|GO:0006368|GO:0006366|GO:0005694|GO:0005634|GO:0006337|GO:0050434|GO:0006
260|GO:0006281|GO:0032786|GO:0016032|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129170_PI430048170 0.9215403377858090.9732980268479653.48444060560951
3.40391890171554 3.32532433406822 P P P 3.61638494921411 3.58420807455519
3.07299247376179 P P P LNCV6_129170_PI430048170 mRNA
GCCCTCTAGTGGTTTTCCCCTACCTGCATATTGGTTTTCATGTTTTATATTCACTGTTAC NM_174932RefSeq chr22 -
32413846 32457386 BPIFC 254240 BPI fold containing family C GO:0001530|GO:0005543|GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141970_PI430048170 0.0758576717191488 1.0413630064221 0.382881727608385
0.3758666637549290.424164093623976A A A 0.3154068430309180.31826764664429
0.373544743725462A A A LNCV6_141970_PI430048170 mRNA
CATCCACCGGATTATGTGATTCAAAATCAGATTGGCATGTTCTTAAACTACATTTGTTAG NM_182495RefSeq chr11
+ 114678477 114706930 NXPE2 120406 "neurexophilin and PC-esterase domain family, member 2"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_60332_PI430048170 0.0190690875871129 0.3526960685061271.57225053824347
1.39533147416397 1.40816773651648 A A A 2.59097077946086 2.81827358561443
3.36963305517432 A P P LNCV6_60332_PI430048170 mRNA
CCGAGATGTGACTAATAACCAAGAGAAGCATTTCTATACTTTCACTAATGAGCACCATAG NM_014953RefSeq chr13
- 72755401 72782128 DIS3 22894 "DIS3 exosome endoribonuclease and 3'-5' exoribonuclease,
transcript variant 1"
GO:0005515|GO:0016075|GO:0010467|GO:0090305|GO:0003723|GO:0006364|GO:0005730|GO:0043928|GO:0071
034|GO:0000178|GO:0005829|GO:0043547|GO:0005085|GO:0004519|GO:0016020|GO:0000175|GO:0000176|GO:0
005654|GO:0000288. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128695_PI430048170 0.4685295587467191.78836542192721 1.34687361003304
2.71004101697736 3.67334479058288 A A P 2.55258684426292 1.49390253248931
1.82039908641499 A A A LNCV6_128695_PI430048170 mRNA
AAGAAAGCTTCATGGGCTAACTAAAGCCTCATGCCATTCTGTGTTCAGTGCCAGTCATGA NM_033318RefSeq
chr22_KI270928v1_alt + 2035 6629 SMDT1 91689 single-pass membrane protein with aspartate-rich
tail 1 GO:0006851|GO:0051560|GO:0031305 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140272_PI430048170 0.2942731470228620.8415192747230061 2.135146311477
11.6863617661632 11.5972886779614 P P P 11.8129079629158 12.2516551429894 12.125798202436
P P P LNCV6_140272_PI430048170 mRNA
CCCTGGTCCCCTGTCCCTGGGGCTGTTTGTTAAAAAAGAGTAATAAAAGGATTTAAAAAA NM_004638RefSeq
chr6_GL000253v2_alt + 2925713 2942818 PRRC2A 7916 "proline-rich coiled-coil 2A, transcript
variant 2" GO:0005515|GO:0005737|GO:0016020|GO:0005634|GO:0070062|GO:0043231 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_143521_PI430048170 0.0524136129249110.7995787484008112.1309991142788
12.2809038904906 12.3599843176974 P P P 12.4076537061361 12.6043726106387
12.7201005089855 P P P LNCV6_143521_PI430048170 mRNA
CTGGAAGGTTCCTGAGAACTGCTTCAATGTGGTATCTTTGTATGGCAATGTATATAGATT NM_024844RefSeq chr17
+ 75205449 75235759 NUP85 79902 "nucleoporin 85kDa, transcript variant 1"
GO:0007077|GO:0005515|GO:0010467|GO:0019221|GO:0030032|GO:0019058|GO:0005635|GO:0044281|GO:0015
031|GO:0008645|GO:0005829|GO:0015758|GO:0016032|GO:0031965|GO:0005975|GO:0019083|GO:0005819|GO:0
055085|GO:0010827|GO:0016020|GO:0031080|GO:0009405|GO:0000777|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129216_PI430048170 0.3084698774756871.07762705446373 9.21253140340964
9.05244016783589 9.21368102028317 P P P 8.93047745166858 9.02820578987696
9.19027142045116 P P P LNCV6_129216_PI430048170 mRNA
CTTTCCCATAGATTCCCCCACCTTTCAAACTGGTTTGTATTTATTTCAAAGGAAGAAAAT NM_001003694 RefSeq
chr3 + 9731749 9748015 BRPF1 7862 "bromodomain and PHD finger containing, 1, transcript
variant 1"
GO:0005515|GO:0070776|GO:0005737|GO:0043966|GO:0006325|GO:0008270|GO:0005654|GO:0005634|GO:0045
893|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127153_PI430048170 0.5659373689897540.9672626600901770.476411241125207
0.4605253788160240.252247120801274A A A 0.3955607999046340.498295126519801
0.448221896770522A A A LNCV6_127153_PI430048170 mRNA
TTACAGGAATTCTTTCTGAAGAGCTGCACACAGTCATTCCTCAAAGGAGGGCATCCTAGT NM_001013579 RefSeq
chrX + 70234654 70240661 AWAT1 158833 acyl-CoA wax alcohol acyltransferase 1
GO:0006629|GO:0005789|GO:0016021|GO:0047196 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143622_PI430048170 0.9093296751334271.0280975759615 10.4098715776108
10.6484504628126 11.0552139600984 P P P 10.4714078169054 10.6172334254421
10.9394109880282 P P P LNCV6_143622_PI430048170 mRNA
GAAGGATACATTATTCGTGTTTGCAACGGTCTTTGAAGAGCTTGGAAATAAAATTTCTGC NM_004125RefSeq chr9

+ 111631351 111670246 DNAJC25-GNG10 NA DNAJC25-GNG10 readthrough NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_142812_PI430048170 0.2333829907014340.6940356277269620.40655299634864
0.36046073394153 0.389162029465205A A A 0.8358635902532441.35413212174562
0.384383817438859A A A LNCV6_142812_PI430048170 mRNA
AAGGAGCTGAAGAATGCCATAAATAAAAACTTTTACAGAAAATTCTGTCCTCCAAGTTCC NM_001004465 RefSeq
chr19 + 15949007 15949958 OR10H4 126541 "olfactory receptor, family 10, subfamily H, member 4"
GO:0050911|GO:0008150|GO:0003674|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139803_PI430048170 0.2547477406668361.11704566192046 8.26025333369926
8.38864490059216 8.46115171706326 P P P 8.00025291908851 8.32336038560489
8.29296736466212 P P P LNCV6_139803_PI430048170 mRNA
TATGCCATCACACTGACCTTCAACGTTGGGCAGATCCTGCTCATCTCTGATTACTTCTAT NM_080476RefSeq chr20
- 34560541 34677285 PIGU 128869 "phosphatidylinositol glycan anchor biosynthesis, class U"
GO:0006501|GO:0034235|GO:0005886|GO:0016255|GO:0046425|GO:0030176|GO:0003923|GO:0016020|GO:0005
789|GO:0042765|GO:0044267|GO:0006506|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130860_PI430048170 0.4321444902726981.03295433204609 0.288684512429274
0.3048188228581820.435083235820428A A A 0.3153463605204850.287226998379008
0.290028011320316A A A LNCV6_130860_PI430048170 mRNA
GGCATCTCCTTATAGTAAAAGTGCAATCATATGGATGGCTAACTTTGTAATCTCTACAAA NM_182502RefSeq chr4
- 68226652 68245694 TMPRSS11B 132724 "transmembrane protease, serine 11B"
GO:0008150|GO:0003674|GO:0005886|GO:0004252|GO:0005887|GO:0006508|GO:0008236|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128424_PI430048170 0.0632759340033923 0.5926547769190761 0.1458981472226
10.0822798850213 10.5989150669636 P P P 10.7145782437763 10.8669505948225
11.4562865572154 P P P LNCV6_128424_PI430048170 mRNA
GTTGCAGCTCTGTAGTTTCTTGAGGCCAAACACACTGTATTTTACAAGTCAAAATATAAT NM_001145260 RefSeq
chr10 - 46005087 46030714 NCOA4 8031 "nuclear receptor coactivator 4, transcript variant 1"
GO:0003713|GO:0005634|GO:0050681|GO:0009725|GO:0045893|GO:0030521|GO:0008584|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136966_PI430048170 0.1422111246545520.4667071136211751 0.0631531062073
8.29846235695089 8.35986110685936 P P P 10.3527057507658 10.3458391358538
10.0522924815082 P P P LNCV6_136966_PI430048170 mRNA
TTCTGGTTCCCCACGCCACTCCCCACCCAAGAGATTGGTGGAATAAAAGGGAAGAGGGCANM_138435RefSeq chr22
+ 39994948 40030039 FAM83F 113828 "family with sequence similarity 83, member F" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_139597_PI430048170 0.1584476578478481.09059220901726 0.535584031083538
0.4823898513150530.597231440725041A A A 0.3063932800344540.413644626395077
0.51461683773887 A A A LNCV6_139597_PI430048170 mRNA
CTCTTGGAACTGTAGGACATGATCCAGCTAAAATAAATAACAAATAACACAGCTAAGCAA NM_030569RefSeq chr10
- 7559269 7666998 ITIH5 80760 "inter-alpha-trypsin inhibitor heavy chain family, member 5,
transcript variant 1" GO:0010951|GO:0004867|GO:0030212|GO:0005576 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132701_PI430048170 0.1400042844741370.5698172715568123.5879698478474
2.24257766057065 2.70254403657406 P A A 3.90492960270191 3.77918406358679 3.5997212435297
P P P LNCV6_132701_PI430048170 mRNA
CCCCGCCAAATGGAACACCAGTCCTCAATGTTAATAAAGTATTGCTTCTTTAAATATTTT NM_001013742 RefSeq
chrX - 50365406 50470738 DGKK NA "diacylglycerol kinase, kappa" NA . NA - . NA NA
NA NA NA NA NA NA NA

LNCV6_131250_PI430048170 1.51912085094332e-05 0.4589748164719379.23891401154282
9.14139017045213 9.23069405664331 P P P 10.3265985781502 10.2855364634048
10.3701739092301 P P P LNCV6_131250_PI430048170 mRNA
AGGGCCGCAAGCCCCAAATGGAAAACTGTTTTTAGAAAATATGATGATTTTTGATTGCTT NM_001008530 RefSeq
chr14 - 92703806 92748702 LGMN 5641 "legumain, transcript variant 2"
GO:0005770|GO:0042359|GO:0010447|GO:0045177|GO:0044281|GO:0002224|GO:0005764|GO:0003014|GO:0004197|GO:0019886|GO:0043524|GO:0040015|GO:0051603|GO:0045087|GO:0032801|GO:0006508|GO:0008233|GO:0008202|GO:0070062|GO:0043202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58054_PI430048170 0.9196700970458020.9764420056027955.03555998402201 5.7991573921964
5.75325941086271 P P P 5.86151367376157 5.09411527708953 5.7430058041912 P P P
LNCV6_58054_PI430048170 mRNA
CTAAAGAAGAAAGAAAATGGCTTGTGCTGAGTTTTCTTTTCATGTACCAAGTCTTGAAGA NM_001286067 RefSeq
chr11 + 93741593 93763102 C11orf54 28970 "chromosome 11 open reading frame 54, transcript variant 1" GO:0005515|GO:0008152|GO:0016788|GO:0008270|GO:0005634|GO:0070062 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_143415_PI430048170 0.6517878289361160.9410536766129254.25719119530043
3.94287822194417 4.47342759988184 P P P 4.46301237772068 4.40666183258387
4.08778712830402 P P P LNCV6_143415_PI430048170 mRNA
TACTACCATCGCCTGAGGAACCTGCCCACCATCAACAAACTGGAAGTGGGTGGCGACATC NM_001042685 RefSeq
chr17 - 20449862 20467535 LGALS9B NA "lectin, galactoside-binding, soluble, 9B" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_124042_PI430048170 0.0500766142692823 1.17845473197793 9.07727731915382
8.98845075052006 8.98169299495497 P P P 8.84459593026609 8.84039446502585
8.64483959221505 P P P LNCV6_124042_PI430048170 mRNA
TCTTCTACTGTCACATGGTGCGCGCTGTTTTCTAATCACGTGGCTGCCACCCAGCGTAGG NM_015921 RefSeq
chr6_GL000256v2_alt - 4865266 4867013 CUTA 51596 "cutA divalent cation tolerance homolog (E. coli), transcript variant 2" GO:0005515|GO:0008104|GO:0016020|GO:0010038|GO:0019899|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134488_PI430048170 0.00590219069631881 3.00759225275353 2.01090119186734
2.24009630560977 2.68904955643066 A A A 1.1566262601817 0.49889334082588
0.498311467958239 A A A LNCV6_134488_PI430048170 mRNA
TATATGGCTTTTTATGTGGGTCCTCTGACTGATGCTTTCAGATTAAAATTGTTTCCAAGA NM_001261453 RefSeq
chr2 - 206175315 206218047 GPR1 2825 "G protein-coupled receptor 1, transcript variant 4"
GO:0043005|GO:0042923|GO:0007186|GO:0007218|GO:0007187|GO:0005887|GO:0004930|GO:0007268 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142015_PI430048170 0.00732122176204757 2.01366412973182 12.1186180951701
12.0940967696864 11.7382157168234 P P P 10.8927716110015 11.0667821097988 10.987145322426
P P P LNCV6_142015_PI430048170 mRNA
TTTTGCACATGTCATGCAGCTCAGCTGGGAGCTGCTTAGGTGGAAAACTCCAAATAAAGT NM_001458 RefSeq chr7
+ 128830428 128859274 FLNC 2318 "filamin C, gamma, transcript variant 1"
GO:0005515|GO:0008092|GO:0030018|GO:0005886|GO:0034329|GO:0030506|GO:0005829|GO:0048747|GO:0042383|GO:0005737|GO:0016528|GO:0051015|GO:0043034|GO:0005856|GO:0005925 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131285_PI430048170 0.0751338210303487 0.8348106421058830.636654469764414
0.5238665207379490.35608922910894 A A A 0.8496830725088960.623236188585511
0.828197191439512 A A A LNCV6_131285_PI430048170 mRNA
GCAGAGCACTGAAGTACATTTTGCTAGGTAAAATTTTCAGCTCATGTTTCCATAATACTA NM_001033080 RefSeq
chr6 - 132617149 132624275 TAAR2 9287 "trace amine associated receptor 2, transcript variant 1"
GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0001594 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_139869_PI430048170 0.2414387439538370.8155218874223076.65095491013113
6.63479270937856 7.04566702746892 P P P 7.05210102383044 6.79556834885874
7.35125125302819 P P P LNCV6_139869_PI430048170 mRNA
GTCCAGTTTTCCAAGATAAGCTCAGTCCTTTTTCAAATGTCCCCTTTTTACCAATACTTT NM_014735RefSeq chrX +
46912432 47061242 JADE3 9767 "jade family PHD finger 3, transcript variant 1"
GO:0043981|GO:0043983|GO:0043982|GO:0043966|GO:0043984|GO:0000123|GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143210_PI430048170 0.00305862201492871 1.69974930137853 11.2137595834237
11.2798193872467 11.1712342498879 P P P 10.3977491364022 10.5940455563594
10.3685561146807 P P P LNCV6_143210_PI430048170 mRNA
CCGCCCAGGCTGCTGCCAGTGCACACTTTTACAAATTTAATATAAAGCAAGTCCAGTCTT NM_032799RefSeq chr9
- 128720869 128724129 ZDHHC12 84885 "zinc finger, DHHC-type containing 12"
GO:0018345|GO:0005794|GO:0005783|GO:0016409|GO:0008270|GO:0016021|GO:0019706 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136991_PI430048170 0.00595553182056787 0.2995469343780763.84524481376247
3.01696386012558 3.24833376472198 P P P 4.89182355142364 5.03122593671474
5.47050047730952 P P P LNCV6_136991_PI430048170 mRNA
GTCGGTTTTATGTTTCTATCCTTCAATAGCTGCACTGTTTTCTAATGTGCTGTAGAGTTT NM_001164665 RefSeq chr7
- 138831380 138981318 KIAA1549 57670 "KIAA1549, transcript variant 2" GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137079_PI430048170 0.0676153435123441 0.6356964484945456.1529644983467
6.1313815729974 6.70013419974279 P P P 6.83554447075126 6.75994165235861
7.35040987534545 P P P LNCV6_137079_PI430048170 mRNA
GAGCATGTAATAATACAAGAACTGTTTCCCCCTCAAAACCTGAACCTGAATTATTTGTAA NM_015251RefSeq chr16
+ 81035852 81047346 ATMIN 23300 "ATM interactor, transcript variant 1"
GO:0005515|GO:0045502|GO:0044212|GO:0005634|GO:0045893|GO:0046872|GO:0006974|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138744_PI430048170 0.68036965980182 0.9189732779890971.94235460364243
2.08045596752876 0.60946595302705 A A A 2.10201720176538 1.75934683085468
1.46789955821723 A A A LNCV6_138744_PI430048170 mRNA
CCAATATACCCCCTTCACCAGCAAAGGTCACAGAACGGGTTCCAACTCAGATGCCTTTCA NM_031273RefSeq chrX
- 107980863 107982370 TEX13B 56156 testis expressed 13BNA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142205_PI430048170 0.3988132846252140.8710699274189860.374000409561426
0.3472413073966250.254811700634707A A A 0.3323689213357440.340559259254745
0.842082440350742A A A LNCV6_142205_PI430048170 mRNA
GGCCCTTTGTTCAAAAATGGATAACTTAAAATGGCTGGCCAAGCTATTATAATTCTCAGA NM_001040432 RefSeq
chr3 + 28349148 28525141 ZCWPW2 NA "zinc finger, CW type with PWWP domain 2" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_114100_PI430048170 0.0320272164740578 0.5476172352004425.35610213020104
4.76565761773016 5.35697316840539 P P P 5.95754846289471 5.98500195104814
6.20605728362585 P P P LNCV6_114100_PI430048170 mRNA
ATGGTAGAAGAATTCGGGTGGATTATTCTATAACCAAGAGAGCGCACACACCAACACCAG NM_001282759 RefSeq
chr7 - 23504781 23532041 TRA2A 29896 "transformer 2 alpha homolog (Drosophila), transcript
variant 4" GO:0000166|GO:0000398|GO:0005730|GO:0005634|GO:0043231 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143854_PI430048170 0.0828474850788842 0.3036769690694232.30742556207818
0.3801041821116872.11883528504756 A A A 3.28623910912577 3.65702701540198

3.64596444582115 P P P LNCV6_143854_PI430048170 mRNA
CTCGATGTTTTCTTTCAACTGAGAAGCCTAAAACAAACAAAAACCTTGTGTGTTATCCTG NM_203406RefSeq chr5
- 90458202 90474768 MBLAC2 153364 metallo-beta-lactamase domain containing 2
GO:0008150|GO:0003674|GO:0016787|GO:0008152|GO:0046872|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144147_PI430048170 0.4458044191656121.04580670301655 9.88224806262308
9.73996356452563 9.67717839737131 P P P 9.75929445390268 9.72998431692895
9.62028630649178 P P P LNCV6_144147_PI430048170 mRNA
TGAGGTCTTCGTGTTCAAGGAGAAGCTATTATATTTTGTTAAGAAAGTGGGGAGAAAAAA NM_003223RefSeq chr16
- 4257185 4273000 TFAP4 7023 transcription factor AP-4 (activating enhancer binding protein 4)
GO:0005515|GO:0071157|GO:0008285|GO:0006366|GO:0042826|GO:0044212|GO:0003705|GO:0045736|GO:0005
634|GO:0042803|GO:0017053|GO:0045944|GO:0006978|GO:0043065|GO:0046982|GO:0006357|GO:0003713|GO:0
070888|GO:2001269|GO:0000978|GO:0003677|GO:0043923|GO:0043392|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131868_PI430048170 0.5379147825596140.91997917239978 11.2740236971381 11.591989845506
11.7103486324987 P P P 11.488830541898 11.559790368077 11.8905946351082 P P P
LNCV6_131868_PI430048170 mRNA
CACAATGTGCCCAGGTCAGCTGTATAAAATAAATACTGCATTGTTGTTTCTTTCCAAAAA NM_001271779 RefSeq
chr3 - 64010548 64023606 PSMD6 9861 "proteasome (prosome, macropain) 26S subunit, non-
ATPase, 6, transcript variant 1"
GO:0002474|GO:0010467|GO:0090263|GO:0044281|GO:0031145|GO:0005829|GO:0034641|GO:0000082|GO:0006
508|GO:0016032|GO:0090090|GO:0016887|GO:0070062|GO:0006977|GO:0000209|GO:0000502|GO:0043066|GO:0
005838|GO:0006521|GO:0051437|GO:0042590|GO:0006915|GO:0042981|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_91831_PI430048170 0.5168507065369280.9273300327309445.94649838381963 5.94972004365983
6.29411158067472 P P P 6.00929935486982 6.14496054837901 6.36802411477718 P P P
LNCV6_91831_PI430048170 mRNA
ACATAGTAGTGGTATCTGTGGCAGGAGCTTTTCGTAAAGGGAAGTCATTTCTACTGGACT NM_022374RefSeq chr2
- 38293956 38377290 ATL2 64225 "atlastin GTPase 2, transcript variant 1"
GO:0005515|GO:0005783|GO:0003924|GO:0005525|GO:0042802|GO:0006888|GO:0016020|GO:0008152|GO:0005
789|GO:0007030|GO:0051260|GO:0016021|GO:0007029 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139129_PI430048170 0.0265949416483931 0.5225043162845144.1554448618526
3.6756051935012 4.20848500533691 P P P 4.91694647885964 5.02769475433721
4.95947273095991 P P P LNCV6_139129_PI430048170 mRNA
CATACCAGAAAAGTACAGTTGAGATAGTTAAGATATAACCACAAGTCAGAGTACATTGGT NM_018323RefSeq chr4
+ 25234030 25279209 PI4K2B 55300 phosphatidylinositol 4-kinase type 2 beta
GO:0004430|GO:0046854|GO:0005737|GO:0016020|GO:0006661|GO:0044281|GO:0006644|GO:0005524|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127611_PI430048170 0.4145452795000370.8612077251823110.288745965592153
0.2993435893218720.405535887717146A A A 0.3631832280467140.309267357335205
0.895352390868267A A A LNCV6_127611_PI430048170 mRNA
TCCAACAAGGATTCTTTTCTAGTCTATACATTCTGATTAATTTGCAGTCAGAGGCAATGC NM_017418RefSeq chr9
+ 115141817 115402644 DEC1 NA deleted in esophageal cancer 1 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128997_PI430048170 0.3485115565901640.8760051616628745.95526769526822
5.42795512824976 5.4745033198599 P P P 5.69968117906301 5.82395345597453
5.95668970665213 P P P LNCV6_128997_PI430048170 mRNA
GGCTATTGAGAGTTTTACAGGGTTATACATTGTTAAGGGACCAAGAATCAAGTACAAAAA NM_014704RefSeq chr1
- 3812080 3857233 CEP104 9731 centrosomal protein 104kDa

GO:0005814|GO:0016594|GO:0016596|GO:0016595 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133489_PI430048170 0.11743643012895 0.6315609504802422.72705708355177
3.07779885932471 2.89345829014808 A P P 3.02779974544561 3.85068676025604
3.70434450252723 P P P LNCV6_133489_PI430048170 mRNA
CCATTGTTCCAAGGGTCTGAGGTTTTCCCCTTATTTCATTTATCCTAATAACAAACATTANM_001126049 RefSeq chr10
- 87859160 87863437 KLLN NA "killin, p53-regulated DNA replication inhibitor" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_92196_PI430048170 0.0415181076180988 0.6049143574726863.07457014268512 3.7366813552447
3.3183118033435 P P P 3.92362492827 4.17016209156137 4.26872082804072 P P P
LNCV6_92196_PI430048170 mRNA
CATTATCAGGAAGATCAAGGCAGCTGGTGGAATCATTCTAACAGCCAGCCACTGCCCTGG NM_021965 RefSeq chr9
+ 68356898 68531061 PGM5 5239 phosphoglucomutase 5
GO:0030018|GO:0001725|GO:0000287|GO:0005978|GO:0019388|GO:0005829|GO:0042383|GO:0005914|GO:0005
913|GO:0016010|GO:0014704|GO:0005198|GO:0004614|GO:0043034|GO:0006006|GO:0009898|GO:0007155|GO:0
005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131376_PI430048170 0.2131302995953020.5043134893215782.2157792245717
0.4230488616224820.346816947080736A A A 1.84658150303907 1.55550525513324
2.97373536705704 A A P LNCV6_131376_PI430048170 mRNA
GACAAACGTGTTTCATAAAATTCGTTGTTGATGGTATTGATTGAAACTATCTGAGCCATG NM_052957 RefSeq chrX
+ 71578023 71613583 ACRC 93953 acidic repeat containing GO:0005634 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_135806_PI430048170 0.1299116115615640.5380380208981713.37970082464082
3.10470243169723 2.75049213510114 P P A 3.98676663481359 3.25830011695914
4.48661420027205 P P P LNCV6_135806_PI430048170 mRNA
TGGTCTCCCTTTTCTATGGAAACATCATCTACATGTACATGCAGCCAGGAGCCAGTTCTT NM_001001957 RefSeq
chr1 + 247895586 247896531 OR2W3 343171 "olfactory receptor, family 2, subfamily W, member 3"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143405_PI430048170 0.7703790927335060.9891238124011981 0.1991487821809
10.2910671662143 10.3701739092301 P P P 10.3167619540592 10.2655295292073
10.3297031074402 P P P LNCV6_143405_PI430048170 mRNA
TCCTGCTTCTCTGTGGGTACGTGCCCCTCTGTTTAAAAATAAACTGAATATGGATGTTTA NM_006510 RefSeq
chr6_GL000256v2_alt - 212403 233384 TRIM27 5987 tripartite motif containing 27
GO:0034314|GO:0005515|GO:0004842|GO:0008283|GO:0016874|GO:0005634|GO:0007283|GO:0090281|GO:0046
872|GO:0070534|GO:0070206|GO:0051091|GO:0005737|GO:1900041|GO:0042147|GO:0002820|GO:0031965|GO:0
032897|GO:0032720|GO:0018108|GO:0000122|GO:0003676|GO:0003677|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144033_PI430048170 0.4442735459032541.02195935519737 0.297346782884356
0.3221660430015390.403795795699606A A A 0.3279213951613980.308251394145671
0.295095271567232A A A LNCV6_144033_PI430048170 mRNA
CTTCGTTGTAGAGAGAGTTCGTTCCAAGTTACTTTCTGAGGTATTTTATGTATCGATTTANM_015078 RefSeq chr3 -
183178003 183428269 MCF2L223101 MCF.2 cell line derived transforming sequence-like 2
GO:0032321|GO:0005089 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131437_PI430048170 0.0881445845264061.03775569064211 0.392155831884922
0.4013799845366840.440294909145025A A A 0.3251283452876530.359539349245119
0.388518733534885A A A LNCV6_131437_PI430048170 mRNA
CAAAGAAATACAAGTTAAATACGCAGACTTCCAGGAATTTTACCAGTTAGTGAGTACTTG NM_207430 RefSeq chr11
+ 111514784 111537031 C11orf88 399949 "chromosome 11 open reading frame 88, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_134505_PI430048170 0.9293751147321421.00456793161094 15.4603579278637
15.6026262355556 15.6142012151984 P P P 15.5158998394538 15.5105331661868
15.6327221960151 P P P LNCV6_134505_PI430048170 mRNA
CCTCTGTCCTATGAAGACCGCTGCCATTGGTGTTGAGAATAATAAAGCTCTGTGTTTTTT NM_177542RefSeq chr19
- 45687453 45692185 SNRPD2 6633 "small nuclear ribonucleoprotein D2 polypeptide 16.5kDa,
transcript variant 2"
GO:0005515|GO:0008380|GO:0000245|GO:0010467|GO:0034660|GO:0071013|GO:0000387|GO:0034709|GO:0005
829|GO:0000398|GO:0030532|GO:0034715|GO:0005654|GO:0005681|GO:0005687|GO:0034719|GO:0005685|GO:0
005689|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90787_PI430048170 0.2027653235724690.7241453874558493.43286774424873 2.50853932251989
3.20520741990128 P A P 3.56941833966689 3.48281720500066 3.63880421218112 P P P
LNCV6_90787_PI430048170 mRNA
ATTGTCCAGGCAGCTGTGTGCAAGCCAAAGAAGCATGAGGACACTGGAAGACTCCTCGGG NM_016201RefSeq
chr3 - 134355344 134374585 AMOTL2 51421 "angiomotin like 2, transcript variant 2"
GO:0005515|GO:0016324|GO:0035329|GO:0031410|GO:0005923|GO:0055037|GO:0016055|GO:0042802|GO:0005
829. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136209_PI430048170 0.00146676206709378 1.60684768762167 13.001280750702
13.0999711010499 12.9953626167376 P P P 12.3947724227773 12.4137891743248 12.230845404938
P P P LNCV6_136209_PI430048170 mRNA
AACCAGAAGCCCCTATAGAGGCCCCAGTCCCAACTCCAGTAAAGACACTCTTGTCCTTGG NM_017767RefSeq chr8
- 144412413 144416533 SLC39A4 55630 "solute carrier family 39 (zinc transporter), member 4, transcript
variant 1"
GO:0071577|GO:0016324|GO:0005886|GO:0005385|GO:0016023|GO:0006882|GO:0016021|GO:0034224|GO:0055
085|GO:0055038|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131775_PI430048170 0.0103674920659911.92844491520156 9.75356773998319 9.5140295237836
9.55192203889712 P P P 8.88469742639886 8.68000676299144 8.38011476228887 P P P
LNCV6_131775_PI430048170 mRNA
TATTGTTGCTTCCTCAGGGGGAGACAGTCAAGAATAAAAAGTATTCTACCACCTAAAAAA NM_018956RefSeq chr9
+ 132878902 132890031 C9orf9 11092 chromosome 9 open reading frame 9 GO:0005881|GO:0001669
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129747_PI430048170 0.1210488457575990.59336338610212 8.92699843945839
8.00269811413824 8.09112874247242 P P P 9.303648038479 9.43407175151849 8.6015594128394
P P P LNCV6_129747_PI430048170 mRNA
CCCCTTCCCCCAATGCCAAGACCAAAGCACAATAATGAATATTTTTATTGAAGTTCGATA NM_002803RefSeq chr7
+ 103347523 103369395 PSMC2 5701 "proteasome (prosome, macropain) 26S subunit, ATPase, 2,
transcript variant 1"
GO:0005515|GO:0002474|GO:0006511|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005
829|GO:0034641|GO:0005737|GO:0000082|GO:0000932|GO:0016032|GO:0090090|GO:0016887|GO:0006977|GO:0
000209|GO:0043066|GO:0000502|GO:0006521|GO:0051437|GO:0042590|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132367_PI430048170 0.0130599838263226 0.4680387431203956.54992191795592
6.55494779252197 7.01163663195166 P P P 7.72762269785711 7.86511131926709
7.85591621563105 P P P LNCV6_132367_PI430048170 mRNA
CATGTGGCCCTTTCAATATTTGAACTGCTAAGCAATGACATCTGTAGTTTTATCTCCTTTNM_018569RefSeq chr4 +
112231738 112270056 AP1AR 55435 "adaptor-related protein complex 1 associated regulatory protein,
transcript variant 1"
GO:0030133|GO:0035650|GO:0005794|GO:0005770|GO:0034315|GO:2000146|GO:0015031|GO:0048203|GO:1900
025|GO:0001920|GO:0019894|GO:0034613|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139625_PI430048170 0.0370412004918422 0.2936005313102358.10111679957175

7.96187486743095 8.26630001749966 P P P 9.09793857679374 9.98013926815009
10.3164599057173 P P P LNCV6_139625_PI430048170 mRNA
GCATGGTCAGAACTTGTGTAAATATGTCTCTTAGATGATTTTGGGGAGATGTGATTTATT NM_007350RefSeq chr12
- 76025446 76031776 PHLDA1 22822 "pleckstrin homology-like domain, family A, member 1"
GO:0005515|GO:0043065|GO:0005886|GO:0045210|GO:0021879|GO:0005730|GO:0006915|GO:0005654|GO:0030
659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55199_PI430048170 0.129177394076317 0.666219199278588 0.247133944570135
0.319383824063885 0.294930196148709 A A A 0.544818036557338 1.2719319847526
0.697960889335614 A A A LNCV6_55199_PI430048170 mRNA
TCTGTGGCATTGTTTTAAAATGTGGGATACAAATCTGGTAAGCAGATTTCAGGTCATTAT NM_004736 RefSeq
chr1 + 180632009 180890279 XPR1 9213 "xenotropic and polytropic retrovirus receptor 1,
transcript variant 1"
GO:0005794|GO:0007186|GO:0005886|GO:0005887|GO:0004930|GO:0001618|GO:0004872|GO:0009615|GO:0004
888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130006_PI430048170 0.331801226209191 0.820531207897532 0.269189799067095
0.283747176881351 0.367418222738969 A A A 0.967142656007349 0.381663610527619
0.341110322569228 A A A LNCV6_130006_PI430048170 mRNA
CAGTGATCTCCTTTAGCAGAGCCCTTTTAGGATTAGCCTGGCTAAGAAAGGAAGAAAAAA NM_001291702 RefSeq
chr6 - 132722786 132734765 VNN3 55350 "vanin 3, transcript variant 4"
GO:0017159|GO:0008150|GO:0006807|GO:0005886|GO:0031225|GO:0005575 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_128096_PI430048170 0.560758754688751 0.889837047238462 0.465940344254077
0.339496607373827 0.331126159453244 A A A 0.922034029131184 0.329958385659753
0.305854750638306 A A A LNCV6_128096_PI430048170 mRNA
TGCAATTGGAGTGTAAACATTCTGTGTGGCAACAGTTAAAAGCTGTTATAACAATTTGCT NM_133464 RefSeq
chr9 + 111525158 111544432 ZNF483 158399 "zinc finger protein 483, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_141364_PI430048170 4.95948062060328e-05 0.318895300416965 7.36564675828894
7.3518205837666 7.542147108651 P P P 9.12424678809168 8.97877613431338
9.10671154237581 P P P LNCV6_141364_PI430048170 mRNA
CCCCTTATAAATTGTAATTCCTGAAATACTGCTGCTTTAAAAAGTCCCACTGTCAGATTA NM_016072 RefSeq
chr12 + 21501764 21518403 GOLT1B 51026 golgi transport 1B
GO:0006629|GO:0007165|GO:0016020|GO:0000139|GO:0005783|GO:0016021|GO:0004871|GO:0043123|GO:0016
192|GO:0015031|GO:0016298 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130139_PI430048170 0.188181900310923 2.25242689216794 1.58774413865957
2.09438173977746 0.366057969923272 A A A 0.387285881838086 0.322768844889732
0.314901861886899 A A A LNCV6_130139_PI430048170 mRNA
GATTGTTCCATTATCTGTACTCCCAACAACCCTGCCGGATATATTTGTTGGCTTTCACTC NM_138450 RefSeq
chr13 + 49628298 49633872 ARL11 115761 ADP-ribosylation factor-like 11
GO:0005622|GO:0005515|GO:0007264|GO:0002244|GO:0005525 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_131128_PI430048170 0.541408745694345 0.966537274760709 0.466774840274704
0.469696555862826 0.263314702264516 A A A 0.401246352050916 0.50213435875822
0.45149546785358 A A A LNCV6_131128_PI430048170 mRNA
AAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATTGTCTGTAGGATGGTCAGTTTAA NM_001005469 RefSeq
chr11 - 58402464 58403409 OR5B3 NA "olfactory receptor, family 5, subfamily B, member 3" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130132_PI430048170 0.514240222605559 1.06647155604644 12.4271697811338

12.618753050522 12.7201005089855 P P P 12.4029867619839 12.3826021428325
12.6953840747159 P P P LNCV6_130132_PI430048170 mRNA
CAGCAGGTCCAGGTCACTTTGTATATAGAATTTTGCTGTATTCAATAAATCTGTTTGGAG NM_006402 RefSeq chr1
- 110401254 110407924 LAMTOR5 10542 "late endosomal/lysosomal adaptor, MAPK and MTOR
activator 5"
GO:0005515|GO:0008361|GO:0043066|GO:0032008|GO:0009615|GO:0005764|GO:0019079|GO:0005829|GO:0005
085|GO:0043547|GO:0071986|GO:0032947|GO:0071230|GO:0043154 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_56831_PI430048170 0.216753233073428 0.822950129425187 6.45813474163051
6.24345627333855 6.42774591592254 P P P 6.66529533637462 6.36856926066328
6.89947612036188 P P P LNCV6_56831_PI430048170 mRNA
GCAAGTTCAGACAGTTTTGCTTCTACTCAACCTACTCATTCATGGAAAGTAGGAGACAAG NM_005871 RefSeq
chr10 - 110293039 110304949 SMNDC1 10285 survival motor neuron domain containing 1
GO:0005515|GO:0006397|GO:0008380|GO:0000245|GO:0015030|GO:0006915|GO:0005634|GO:0005737|GO:0016
607|GO:0000375|GO:0005654|GO:0005681|GO:0045111 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145417_PI430048170 0.41899379226217 1.0512597407018 9.86229076952781
9.70954102443612 9.65863684842713 P P P 9.58598977333928 9.75754374418234
9.67334523819298 P P P LNCV6_145417_PI430048170 mRNA
GAGCACTGGTGTTCACGTGGGACCACAGGCTGCACCATAAGACCCACTCACAATAAAAAA NM_014681 RefSeq
chr19 + 47349280 47382704 DHX34 9704 DEAH (Asp-Glu-Ala-His) box polypeptide 34
GO:0004004|GO:0006396|GO:0005737|GO:0016020|GO:2000623|GO:0000956|GO:0005634|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_38385_PI430048170 0.0284679189274370.5631763658723956.61591654138699 6.55447977571652
6.86462421162024 P P P 7.23610287225275 7.39115378074579 7.84145595152975 P P P
LNCV6_38385_PI430048170 mRNA
AGAGCAAATAACCATTCCTTTCATGTTTTGATCACTGAGTGTGTCTGTAATCATACCTAC NM_014691RefSeq chr15
- 34856350 34969794 AQR 9716 aquarius intron-binding spliceosomal factor
GO:0005515|GO:0016020|GO:0000398|GO:0005654|GO:0005634|GO:0071013 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130244_PI430048170 0.6882704543410671.26653121259423 2.97936322742613
1.40788277507369 2.90639540975712 P A P 2.06837874569514 1.60687710315621
2.80764604228238 A A P LNCV6_130244_PI430048170 mRNA
GGATGGAGCAAAGTCAGCAGTATTAATGGTTGAATATTAATGGTTGATTTTGGCTACTTG NM_001272093 RefSeq
chr18 + 76495520 76498088 C18orf65 NA chromosome 18 open reading frame 65 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145434_PI430048170 0.000582425548518339 0.0884217375978664 0.317859435709849
0.3181827138770740.313561584573212A A A 3.64510815575422 3.92171020612459
3.86655657302091 P P P LNCV6_145434_PI430048170 mRNA
CCCACAGAAGACTTACTTCAAGTGACTTGAAAACTTAGTATTTTGTCTGTACTTTGCTAA NM_016006RefSeq chr3
+ 43690882 43722725 ABHD5 51099 abhydrolase domain containing 5
GO:0005811|GO:0004806|GO:0042171|GO:0010898|GO:0005634|GO:0044281|GO:0003841|GO:0030154|GO:0043
231|GO:0005829|GO:0005737|GO:0010891|GO:0006631|GO:0019433|GO:0006654|GO:0051006 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145488_PI430048170 0.0359946381606324 0.6515781363590076.95209900062747
6.50459457301567 6.49303634225044 P P P 7.24693120371536 7.5063936740485
7.06504770558982 P P P LNCV6_145488_PI430048170 mRNA
ATCCAGGCGCTGCCCGTGCGTTCAGTGACTAATAAAATGACCCTTAGGGCCAGGAAAAAA NM_213613RefSeq chr4
- 987656 993440 SLC26A1 10861 "solute carrier family 26 (anion exchanger), member 1, transcript variant

3"
GO:0006821|GO:0006805|GO:0050427|GO:0019531|GO:0005886|GO:0050428|GO:0005975|GO:0019532|GO:0044281|GO:0055085|GO:0015116|GO:0005887|GO:0015108|GO:0015301|GO:0008272|GO:0009405|GO:0008271|GO:0016021|GO:0030203|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124441_PI430048170 0.00544284117711108 1.6589037904987 7.24396034741023
6.92309516953654 7.10177507119634 P P P 6.49387729960219 6.40988201948862
6.17338848514839 P P P LNCV6_124441_PI430048170 mRNA
TGACAGGGAACGGAAAGGACCTCAGGATGACCCTGGCTCATATCAAGGACCAGAAAGAAG NM_001289152 RefSeq chr6_GL000256v2_alt + 2702060 2717592 MICA 100507436 "MHC class I polypeptide-related sequence A, transcript variant 3"
GO:0005515|GO:0030881|GO:0009408|GO:0009986|GO:0046703|GO:0042267|GO:0002418|GO:0046629|GO:0003823|GO:0005615|GO:0006974|GO:0051607|GO:0005737|GO:0001913|GO:0005887|GO:0019882|GO:0019835|GO:0016032|GO:0042742. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127612_PI430048170 0.00477198287025731 1.59922717976524 5.47659727637746
5.69401617384953 5.4151783242378 P P P 4.75549223865582 4.92642575736246
4.88145474119082 P P P LNCV6_127612_PI430048170 mRNA
CCTGACCCAATTCAGAGATTCTTTATGCAAAAGTGAGTTCAGTCCATCTCTATAATAAAA NM_001007271 RefSeq chr10 - 75094431 75109212 DUSP1351207 "dual specificity phosphatase 13, transcript variant 1"
GO:0005737|GO:0007126|GO:0006470|GO:0008138|GO:0007283|GO:0035335|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132784_PI430048170 0.0263829754497450.6049454327771222.36867472682943
2.05994053263439 2.23023247987597 A A A 3.20551009993887 2.65995263589657 2.933843464356
P P P LNCV6_132784_PI430048170 mRNA
TGGCCCAAGTGTGACCAGGAAGGTCTCTTTCCTTCCTGTTGTCTCCATCTGTTTAAAAAA NM_001004325 RefSeq chr11_KI270903v1_alt - 73719 74837 KRTAP5-2 NA keratin associated protein 5-2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141843_PI430048170 0.0821821171747547 0.4451813652248141.08852065601779
0.3300719892726420.331428420243274A A A 2.34101000942333 1.01380667888174
1.74035216599756 A A A LNCV6_141843_PI430048170 mRNA
TAGCTAACCCTATTCTCTTAGTCTTTCAAAATGTAGAATGGGTCCAATAATGGCTATAAG NM_001135091 RefSeq chr11 - 26559031 26572268 MUC15 143662 "mucin 15, cell surface associated, transcript variant 1"
GO:0006493|GO:0005886|GO:0005796|GO:0016266|GO:0005576|GO:0016021|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136570_PI430048170 0.0185645395266190.4648481489249527.70165486178866
7.52572098464112 7.82547295030902 P P P 8.4604851799572 8.70702407499786
9.13458932014966 P P P LNCV6_136570_PI430048170 mRNA
GGACGGCTCCAAATCATGTCCTTAGAAAATCTTTCTATTGAAAAGGAGACTAAATTGTAA NM_019048 RefSeq chr2 + 189661398 189670831 ASNSD1 54529 asparagine synthetase domain containing 1
GO:0008150|GO:0003674|GO:0004066|GO:0005575|GO:0006529|GO:0006541 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128489_PI430048170 0.5937562043612310.9738124024186340.445165281242643
0.41462428831704 0.242355801513441A A A 0.3694601554147650.444643569413176
0.410087063708725A A A LNCV6_128489_PI430048170 mRNA
TCCCAGACATTAACGGTATTAGAGAGTTTGCCTCATTCATCCATTTTTCTTAAAAGCTGG NM_000451 RefSeq chrY + 624343 646823 SHOX 6473 "short stature homeobox, transcript variant 1"
GO:0043565|GO:0005515|GO:0006355|GO:0001501|GO:0003700|GO:0006366|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131245_PI430048170 0.00703472343298908 0.6316723422761448.97496503212711
8.79622454539529 8.65871604019013 P P P 9.30933628397706 9.62982718008406

9.47872847124484 P P P LNCV6_131245_PI430048170 mRNA
GAGACAAGGACTTTGGTTTTTGTAAGACAAACGATGATATGAAGGCCTTTTGTAAGAAAA NM_138440RefSeq
chr16_KI270855v1_alt + 74170 85851 VASN 114990 vasorin
GO:0005739|GO:0050431|GO:0009986|GO:0005886|GO:0071461|GO:0071456|GO:0016021|GO:0010719|GO:0005
765|GO:0005615|GO:0030512|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137511_PI430048170 0.000744822014925678 1.56637780504828 11.6184758208289
11.7192290117954 11.5457432681907 P P P 11.0388453898543 11.0171157791961
10.8857609322438 P P P LNCV6_137511_PI430048170 mRNA
GCACAACCGGAGAAGACAGAATTACCTCTGCTCTTTTAATATATAATGATGGCTTTAAAT NM_001177701 RefSeq
chr22 - 36758201 36776133 IFT27 11020 "intraflagellar transport 27, transcript variant 1"
GO:0005515|GO:0005813|GO:0006996|GO:0031514|GO:0097225|GO:0003924|GO:0097228|GO:0072372|GO:0005
525|GO:0006886|GO:0007224|GO:0012505|GO:0006184|GO:0005929|GO:0042073|GO:0030992|GO:0032482|GO:0
019003 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134675_PI430048170 0.0706663225861431 0.7929678704026195.83879372723549
5.52803500086994 5.80816526577378 P P P 6.17441247768705 5.87230726808494
6.13389189355406 P P P LNCV6_134675_PI430048170 mRNA
AAGAGGCTTGTATGCCGGTCATACTGTAAAGACCAACAAAGAGACCACAGTGGAGAAAAC NM_001129996
RefSeq chr19 + 44025341 44033109 ZNF222 7673 "zinc finger protein 222, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134626_PI430048170 0.9671508954920071.01451047187026 1.49056114566263
0.47235034063276 0.478957485836214A A A 0.3459599629435660.923619667693153
1.22851252453551 A A A LNCV6_134626_PI430048170 mRNA
CTTTCTTTGGCCTTAATATTATTGGATTAAAGAATTACTGCCTCTCACTAGGAGCATCAT NM_176823RefSeq chr1
+ 153416523 153423225 S100A7A 338324 S100 calcium binding protein A7A GO:0005737|GO:0005509
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145265_PI430048170 0.106101550894217 1.25848036896159 9.30770287529224
9.15473972892925 9.13698107553452 P P P 8.61813187644862 9.06929745626333
8.88783087688968 P P P LNCV6_145265_PI430048170 mRNA
CATTTGTCCTGGGAAACACGGTATTTAAGAGAGAACTATATTGGTATTAAAGCTGGTTTG NM_004579RefSeq chr11
- 64789100 64803254 MAP4K2 5871 mitogen-activated protein kinase kinase kinase kinase 2
GO:0005515|GO:0046330|GO:0007254|GO:0031435|GO:0007257|GO:0005524|GO:0006903|GO:0035556|GO:0016
323|GO:0005083|GO:0005737|GO:0006955|GO:0000139|GO:0004702|GO:0004674|GO:0045087|GO:0006468 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133122_PI430048170 0.0841745254603518 1.05242039734015 0.354458122427861
0.3974225731404560.31320511515528 A A A 0.2735021638928970.296146368440082
0.275423858585914A A A LNCV6_133122_PI430048170 mRNA
GGCCCTGTGAAGTCAAGTATTTTTACCAAGTAAAAAGATTGGCAATAAAACATTTCCACA NM_144713RefSeq chr2
+ 37950443 38067142 RMDN2 151393 "regulator of microtubule dynamics 2, transcript variant 1"
GO:0005739|GO:0005737|GO:0000922|GO:0005874|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_71160_PI430048170 0.3214059975419291.14307375442879 9.50122780776611 9.69660046140007
9.60536058496111 P P P 9.09851886652653 9.43616569212744 9.64463407354964 P P P
LNCV6_71160_PI430048170 mRNA
CTTGGGGACCAGCTAAGTCTCTGCAGTAGTGTGAAATTCCAAATGGTTGTTTTATCATTG NM_001199514 RefSeq
chr20 + 36573472 36593952 TGIF2 60436 "TGFB-induced factor homeobox 2, transcript variant 1"
GO:0010467|GO:0005813|GO:0006355|GO:0003700|GO:0006367|GO:0060041|GO:0005634|GO:0000122|GO:0003
677|GO:0006351|GO:0045666|GO:0010470|GO:0038092|GO:0005654|GO:0007179 . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_137513_PI430048170 0.8537991650795341.02711970349704 2.06565841349415
0.4442910620496610.259303987418836A A A 1.57189932457685 1.16979098487854
0.425444265423696A A A LNCV6_137513_PI430048170 mRNA
GATGTCTCCTTCCGCAGATTCATTTCTTTGTACTTAATAAACTTTAGTAAGTGGAAATGC NM_001080529 RefSeq
chr7 + 29806553 29917066 WIPF3 644150 "WAS/WASL interacting protein family, member 3"
GO:0017124|GO:0045087|GO:0007275|GO:0003779|GO:0007283|GO:0038096|GO:0030154|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143109_PI430048170 0.43794992523755 0.9499049302191267.68085610258711
7.78483089918075 7.9184188346604 P P P 7.77308622448895 7.87982949755843 7.9575591612256
P P P LNCV6_143109_PI430048170 mRNA
TTTTAACATTATGAGAGACTGCTCAGATTCTAAGTTGTTGGCCTTGTGTGTGTGTTTTTT NM_000113RefSeq chr9 -
129812941 129824162 TOR1A 1861 "torsin family 1, member A (torsin A)"
GO:0044319|GO:0008092|GO:0005515|GO:0030133|GO:0000338|GO:0034504|GO:0030054|GO:0006200|GO:0045
104|GO:1900244|GO:0005635|GO:2000008|GO:0031175|GO:0043231|GO:0030426|GO:0051787|GO:0051584|GO:0
051260|GO:0006998|GO:0072321|GO:0007155|GO:0005856|GO:0030141|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141886_PI430048170 0.2836674742205130.0979154628047191 0.487986883863095
0.2817722348451070.395586024424731A A A 5.13765229400519 1.8987445625549
0.312007176272926P A A LNCV6_141886_PI430048170 mRNA
TGTCAAGATAACCTGTCAATGTAGTAGGAAAACAGGAGGGGACAGTAACAGAAAAGCACG NM_001164835
RefSeq chr1 + 62194801 62212328 L1TD1 54596 "LINE-1 type transposase domain containing 1,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55078_PI430048170 0.00350448960628842 0.4564784514870265.65113423107132 5.2810598368442
5.60152359662213 P P P 6.74125389224722 6.54652584407767 6.6607035964332 P P P
LNCV6_55078_PI430048170 mRNA
TTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCATTGAC NM_199344RefSeq chr1
+ 168226016 168242850 SFT2D2 375035 SFT2 domain containing 2
GO:0008150|GO:0003674|GO:0016021|GO:0016192|GO:0015031|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_80911_PI430048170 0.0101968024519358 0.3292418989315043.23764055191723
2.58724500140916 3.19413812564333 P A P 4.57642770864599 4.77268793808458
4.55497137094499 P P P LNCV6_80911_PI430048170 mRNA
GTGCCATTGTGCCAGAAACATTGTGTTATCTTTTATGTTGTTGTTGTTGCTGTTAAACTA NM_001282748 RefSeq chr9
+ 79571772 79726881 TLE4 7091 "transducin-like enhancer of split 4, transcript variant 1"
GO:0005515|GO:0006366|GO:0003705|GO:0003714|GO:0005634|GO:0000122|GO:0003674|GO:0008150|GO:0007
219|GO:0003682|GO:0070491|GO:0005654|GO:0016055 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133123_PI430048170 0.8016390834847930.9913056588744380.458504935995779
0.4835496735497120.385542214766663A A A 0.5248765929725410.413991166032549
0.425719603767312A A A LNCV6_133123_PI430048170 mRNA
CCAGGAATGATTGCAGCTGTGTCCTGAATTCCTGAAGCACGTCTCTGAATCTGTCCTCCT NM_001012708 RefSeq
chr11_KI270903v1_alt - 84117 85016 KRTAP5-3 NA keratin associated protein 5-3 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129923_PI430048170 0.4645508488749731.44828021040806 2.61341994973739
1.08932175793212 2.35650443890879 A A A 0.86245866512205 1.69346948707679
2.06286946702957 A A A LNCV6_129923_PI430048170 mRNA
TGCTAGTGGCACACAGTGCTTATCTGCATAAATAAACACTGGCCACCAGCAGTGAAAAAA NM_001083536 RefSeq
chr9 + 92947318 93036236 FGD3 89846 "FYVE, RhoGEF and PH domain containing 3, transcript
variant 1"
GO:0051056|GO:0048011|GO:0043065|GO:0005794|GO:0030036|GO:0031267|GO:0007264|GO:0008360|GO:0097

190|GO:0001726|GO:0046872|GO:0030027|GO:0043088|GO:0005829|GO:0043547|GO:0005085|GO:0005737|GO:0
032321|GO:0007010|GO:0046847|GO:0005089|GO:0005856 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131081_PI430048170 0.1317758727597651.12792588884623 14.987602215123
15.2327509948507 15.0753014897308 P P P 14.9035109591796 14.9692710141697
14.9117337072935 P P P LNCV6_131081_PI430048170 mRNA
ATGTGCTGTAAAGTTTCTTCTTTCCAGTAAAGACTAGCCATTGCATTGGCTCCTTCTCCC NM_001862RefSeq chr2
+ 97646057 97648194 COX5B 1329 cytochrome c oxidase subunit Vb
GO:0022904|GO:0005739|GO:0007585|GO:0004129|GO:0005743|GO:0044281|GO:0055085|GO:0046872|GO:0044
237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64135_PI430048170 0.179516563622223 1.6272121691385 1.71873329030478 1.02821880821852
0.608022562345141 A A A 0.3207743625070060.433132164116139 0.690331268828424 A A A
LNCV6_64135_PI430048170 mRNA
AAACTGGCAAGTCCTGAAAGACAGGTGTCCCAGGTATCCAGGGCAGCCCAAATGGCAGTC NM_016585RefSeq
chr19 - 362056 376013 THEG 51298 "theg spermatid protein, transcript variant 1"
GO:0005515|GO:0007275|GO:0005634|GO:0007283|GO:0051131|GO:0030154 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_120776_PI430048170 0.18362914052949 1.09556389165722 11.352871790137 11.432892788237
11.5793034435983 P P P 11.3458576120514 11.2502702862632 11.3800070624197 P P P
LNCV6_120776_PI430048170 mRNA
GAGAATGAGGAGGACAACAGCTACAACCGGGGATGAACTCTTTGCCAGCAGAGAGGATCC NM_021079RefSeq
chr17 + 45061298 45109014 NMT1 4836 N-myristoyltransferase 1
GO:0030054|GO:0005886|GO:0007603|GO:0006915|GO:0004379|GO:0022400|GO:0015629|GO:0001701|GO:0018
008|GO:0097193|GO:0005829|GO:0005737|GO:1900740|GO:0016032|GO:0016056|GO:0019898 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142433_PI430048170 0.0024237033272202 0.71341328666147 7.40968920371897
7.50754888549774 7.58469084272063 P P P 7.90868673444283 7.9731568223562
8.08165217538892 P P P LNCV6_142433_PI430048170 mRNA
GAGACACTTTGAACAAAGACCATGGAAATGATAAGGAATCAAATGTTCTGCATCAGTAAT NM_001166263 RefSeq
chr13 - 27435638 27450602 MTIF3 219402 "mitochondrial translational initiation factor 3, transcript
variant 1"
GO:0070124|GO:0005739|GO:0032543|GO:0006996|GO:0003743|GO:0043024|GO:0032790|GO:0008135 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140311_PI430048170 0.1693917243857380.6922865180597023.93848999453794
3.79344369096569 3.7261860006711 P P P 4.77416426064747 4.18770362232292
3.97324634660041 P P P LNCV6_140311_PI430048170 mRNA
TGCCACCTCCCATCAGCAATTCTGGAAATGCACTATTTCTACTGGTATTCTTGCTTTTTT NM_002522RefSeq chr17 -
80466832 80476604 NPTX1 4884 neuronal pentraxin I
GO:0030133|GO:0043005|GO:0005886|GO:0007268|GO:0007417|GO:0043653|GO:0046872|GO:0005739|GO:0035
865|GO:0060385|GO:0006810|GO:0071333|GO:0006839 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107150_PI430048170 0.5996182642115 1.10169753679604 3.33505273944207 3.4721502366544
3.88989402393333 P P P 3.06195342797713 3.48944111792316 3.7122120378284 P P P
LNCV6_107150_PI430048170 mRNA
TGCATCAGTTGTATTGGATGCAAGTCAACTCTGGAGTCCTCATCCCTTGAATGGACTTGT NM_001109662 RefSeq
chr12 - 112160187 112382092 HECTD4 283450 HECT domain containing E3 ubiquitin protein ligase 4
GO:0005737|GO:0004842|GO:0042787|GO:0016874|GO:0006006|GO:0005634|GO:0042593|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129324_PI430048170 0.4421034041606521.2055641001441 0.491228691052242
0.86931053417042 1.31249779806023 A A A 0.4476500733176360.49598418427379

0.976266841763831 A A A LNCV6_129324_PI430048170 mRNA
CCCCACCAAAAACAAAAGAGAAGAAAAAGAATAGAAAGAATTATCCAGTGTCAGCTTCCA NM_006729 RefSeq
chrX + 96684662 97600598 DIAPH2 1730 "diaphanous-related formin 2, transcript variant 156"
GO:0005794|GO:0048477|GO:0005102|GO:0005730|GO:0003779|GO:0007275|GO:0007292|GO:0005829|GO:0043
231|GO:0005739|GO:0000910|GO:0030041|GO:0017048|GO:0005769 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143101_PI430048170 0.0107699750641918 0.5079726420604924.11456803312104
3.64690516975945 3.69327358083096 P P P 4.6803229501594 4.82417254651583
4.91922573344229 P P P LNCV6_143101_PI430048170 mRNA
TGTGTAGGAGCCATTAAAATTCATAACAGTATGTGCCCCTTCAGCGTTTTAATCTTATGA NM_016094 RefSeq chr3
- 149738469 149752499 COMMD2 51122 COMM domain containing 2 GO:0005515 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130590_PI430048170 0.89370246025039 1.01381591756045 5.98821541270926 5.7851641074064
5.60901523575434 P P P 6.01610685971817 5.77524329191389 5.51298544012603 P P P
LNCV6_130590_PI430048170 mRNA
TGGCCCCACGTACACCCACATACTTCTCAGATGGCTCCCACATTTTAAGATTTTAAAAAT NM_005146 RefSeq chr11
+ 65961688 65980136 SART1 9092 squamous cell carcinoma antigen recognized by T cells
GO:0005515|GO:0005794|GO:0015030|GO:0045292|GO:0000481|GO:0071013|GO:0000387|GO:0097193|GO:0005
829|GO:0005737|GO:0000398|GO:0005654|GO:0007050|GO:0046540|GO:0045585 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_121808_PI430048170 0.4003037700352590.6562437517395050.560022294603181
0.4752642572597840.365722208152476 A A A 0.4039304643724271.80756210566798
0.589588691415781 A A A LNCV6_121808_PI430048170 mRNA
AATTTCATATGCAGAATAAATGGTAATTAAAATGTGCAGGATGACAAGATGGAGCAAACA NM_001202435 RefSeq
chr2 - 165989159 166149132 SCN1A 6323 "sodium channel, voltage gated, type I alpha subunit,
transcript variant 4"
GO:0030018|GO:0086010|GO:0005886|GO:0005248|GO:0030315|GO:0019227|GO:0019228|GO:0043194|GO:0033
268|GO:0014704|GO:0050884|GO:0043025|GO:0007628|GO:0001518|GO:0034765|GO:0035725|GO:0006814 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132663_PI430048170 0.1618400004441040.9411568218702820.243873042181975
0.3049062588552310.29356618537428 A A A 0.4472422198037620.347692412518843
0.306986643100507 A A A LNCV6_132663_PI430048170 mRNA
AACAATGCGATTAAAAAACTGTTCTGTCTTCAAAAAGTGTTGAACAAGCCTGGAGGTTAA NM_001005327 RefSeq
chr1 - 158717167 158718115 OR6K3 NA "olfactory receptor, family 6, subfamily K, member 3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54387_PI430048170 0.0766841190985834 0.7141347854920825.60612302516875
5.52258111279802 5.922015319115 P P P 5.97018655270206 6.04525354198443
6.47167556659924 P P P LNCV6_54387_PI430048170 mRNA
TGAATCTTCCTGATTCATGGAAAACCTATGCAATGACCGGATTCGTAGCCTGGCATGTTG NM_001013660 RefSeq
chr1 - 99708702 99765793 FRRS1 391059 ferric-chelate reductase 1
GO:0000293|GO:0016021|GO:0046872|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137191_PI430048170 0.0159382403726842 0.5744347618223919.51149963293715
9.22285055722674 9.50482805616229 P P P 9.99738852952459 10.119640649097
10.4926810725123 P P P LNCV6_137191_PI430048170 mRNA
GCTCTGTACATCAGACAATTGCATTGCTACCAAGTTTCATACCAAATATTTGAAAGGATG NM_005476 RefSeq chr9
- 36214440 36258499 GNE 10020 "glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine
kinase, transcript variant 2"
GO:0008761|GO:0006054|GO:0006045|GO:0006047|GO:0005524|GO:0046872|GO:0004553|GO:0005829|GO:0005
737|GO:0046835|GO:0009384|GO:0006488|GO:0007155|GO:0044267|GO:0018279|GO:0043687 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_142641_PI430048170 0.39078152653241 1.01609057368633 0.334614114732747
0.316783631684124 0.264901587294874 A A A 0.283846702813829 0.289158885786813
0.275077531168028 A A A LNCV6_142641_PI430048170 mRNA
CCTCATTTGGTTTTGATATCAACAAGGAAAAAGCACATTCAGGAGGCATAAAGATATTGT NM_022122 RefSeq chr11
- 102691683 102705737 MMP27 64066 matrix metallopeptidase 27
GO:0031012|GO:0030574|GO:0005509|GO:0006508|GO:0008270|GO:0042406|GO:0004222 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128283_PI430048170 0.86293266193441 1.01534676393419 0.703800166215123
0.440181137649675 0.457497636192855 A A A 0.341062772217158 0.764149377057254
0.409019657474032 A A A LNCV6_128283_PI430048170 mRNA
CCTAACACCATCCAGGATGTGGAAAATGACAGAAAAGATTCAAGAAACATAAAGCAGGAA NM_001136506
RefSeq chr11 - 63079939 63144221 SLC22A24 283238 "solute carrier family 22, member 24, transcript
variant 3" GO:0016021|GO:0055085|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110526_PI430048170 0.22520758659053 1.10259904382583 4.20877643989995
4.20222623766329 4.43255559653087 P P P 4.15730556572101 4.03210245987816
4.23624015655069 P P P LNCV6_110526_PI430048170 mRNA
AACTTGATCAGCTTCTCCAGGATAAAATTAAAAACCCAAGCATTGATCTGTGTACGTGTC NM_198963 RefSeq chr2
- 38797730 38875879 DHX57 90957 DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57
GO:0005739|GO:0004004|GO:0006396|GO:0005634|GO:0005524|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128515_PI430048170 0.00892354719497693 1.53156066800996 6.36251211577632
6.6318136173822 6.33451267906583 P P P 5.81092516416633 5.94322805237468 5.7413976364961
P P P LNCV6_128515_PI430048170 mRNA
GGGAGCGGGCCTAAGGCATATTTTTAAGTGGTCGATCTAAAGGCTCTTTTCAGAGCCACT NM_001123375 RefSeq
chr1 - 149813224 149813681 HIST2H3D 653604 "histone cluster 2, H3d"
GO:0005515|GO:0010467|GO:0046982|GO:0005576|GO:0005634|GO:0003677|GO:0032776|GO:0000183|GO:0007
596|GO:0045814|GO:0040029|GO:0005654|GO:0000786|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128630_PI430048170 0.230018676423256 0.802935826267583 11.7126589691885
11.9130286353796 12.3156175506691 P P P 12.1412994114645 12.1846920507419
12.5884272780105 P P P LNCV6_128630_PI430048170 mRNA
CAGTATTTTTAAGTACACCTGTCAGCTGTTTCTTACCACTTCGATGGTTGTGATTAATTT NM_021821 RefSeq chr12 +
27710772 27756304 MRPS35 60488 "mitochondrial ribosomal protein S35, transcript variant 1"
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0005737|GO:0032543|GO:0006996|GO:0003735|GO:0042
769|GO:0005743|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133446_PI430048170 0.0398544383254516 1.49897838404059 3.10689042885145
2.82969402041285 2.61226421994479 P A A 2.40783039765819 2.22639657274056
2.19626920072798 A A A LNCV6_133446_PI430048170 mRNA
ATATACAGGGTGGGGGGAGTGGGCGGTTCTCATTAAACGTCACCATTTCATGAGAAAAAA NM_147164 RefSeq chr9
- 34551431 34589737 CNTFR 1271 "ciliary neurotrophic factor receptor, transcript variant 1"
GO:0008284|GO:0003360|GO:0097059|GO:0005102|GO:0031225|GO:0070120|GO:0070110|GO:0007399|GO:0007
165|GO:0043524|GO:0001967|GO:0019955|GO:0060538|GO:0007548|GO:0004897|GO:0019898 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134766_PI430048170 0.402593594748971 1.17036315191454 0.356682428527558
0.875705895367963 0.262366644188353 A A A 0.295047414770829 0.307855664843362
0.289186916621165 A A A LNCV6_134766_PI430048170 mRNA
GAGGTAAAAACTGCATTGAAAAGAGTTCTTGGAATGCCTGTGGCAACCAAGATGAGCTAA NM_001004475 RefSeq
chr1 - 158398521 158399466 OR10T2 128360 "olfactory receptor, family 10, subfamily T, member 2"

GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99997_PI430048170 0.4232892438123340.8189577812843161.4124419214678 1.00217874711296 0.365604640410033 A A A 0.9093906384764261.55692522983683 1.29211599307002 A A A
LNCV6_99997_PI430048170 mRNA
CTACTTCGCAAAAGACTAGAAGAACTGGAAACAACACAAAGAAAACAACTAGAGGAACTT NM_016122 RefSeq chr12 - 94308279 94459988 CEP83 51134 "centrosomal protein 83kDa, transcript variant 1"
GO:0005515|GO:0042384|GO:0003674|GO:0006996|GO:0005794|GO:0005814|GO:0071539|GO:0048278|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132132_PI430048170 0.3387093625751011.07998583356568 9.83968284815302 9.90165532108086 9.86588570190499 P P P 9.56502278350328 9.85479300073464 9.83715991426749 P P P LNCV6_132132_PI430048170 mRNA
GAGATGTGAATGCCTACTGCTTACGATATCTGTATAAAGTGCTGTGTGATTAAACTTTTT NM_022066 RefSeq chr17 - 76389531 76453206 UBE2O 63893 ubiquitin-conjugating enzyme E2O
GO:0005515|GO:0004842|GO:0006513|GO:0016874|GO:0005634|GO:0005524|GO:0030513|GO:0005737|GO:0070534|GO:0019787|GO:0042147|GO:0005654|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138282_PI430048170 0.0810346523425797 0.7659795305599017.48194093663103 7.4002297927137 7.63595809615227 P P P 8.00355445336143 7.62429711160101 8.02046414224653 P P P LNCV6_138282_PI430048170 mRNA
ATCAATTGGAATCAGTACCTTAACAGAAAAAGGCAGCTCTTCAATGGAATTAACGTGATA NM_022373 RefSeq chr7 - 35632659 35695162 HERPUD2 64224 HERPUD family member 2
GO:0006986|GO:0016021|GO:0007283 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136707_PI430048170 0.2418289784069391.04391905106892 0.541817124510909 0.6438206413309590.524611855929579 A A A 0.5041293264554960.50762755269766 0.515340554601625 A A A LNCV6_136707_PI430048170 mRNA
GGGAGCAGTTTAAATAACCGTTTCCTTTCATTTACTGTGGCTTCTTAATCTTTTCACAAA NM_006144 RefSeq chr5 + 55102645 55110252 GZMA 3001 "granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)"
GO:0001772|GO:0005515|GO:0043065|GO:0004252|GO:0051354|GO:0006915|GO:0005576|GO:0005634|GO:0042803|GO:0043392|GO:0006955|GO:0032078|GO:0051603|GO:0019835 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134943_PI430048170 0.0081417211193861 1.65540855635143 9.59171955439678 9.42915040236424 9.21960130439785 P P P 8.62308288024084 8.82128067129083 8.62959085684885 P P P LNCV6_134943_PI430048170 mRNA
GGCTCAGGGTCTGCGCAAGATGTTTGGCTGATTAAAAGTTAAACCTTAAAAGAGAAAAAA NM_022110 RefSeq chr6_GL000254v2_alt - 3470726 3472310 FKBPL 63943 FK506 binding protein like
GO:0009314|GO:0005515|GO:0000413|GO:0061077|GO:0005789|GO:0003755|GO:0005528 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130970_PI430048170 0.0426752762083587 0.6670003637314275.66871596281883 5.78160805428634 5.80461549601463 P P P 6.4513826312065 6.051158647408 6.47112924406085 P P P LNCV6_130970_PI430048170 mRNA
TTTTAACTTTGTCATATATTAGCAAGAATTGGTCTACTGTGATGTTTGGGGAGGAGGAGG NM_006912 RefSeq chr1 - 155897807 155911402 RIT1 6016 "Ras-like without CAAX 1, transcript variant 2"
GO:0006184|GO:0005515|GO:0007165|GO:0005516|GO:0048011|GO:0005886|GO:0007264|GO:0007265|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131001_PI430048170 0.0925768993328788 0.7472298205710872.67832311505645 2.95046300170062 2.42166370570408 A P A 3.18954002345588 3.25406281054995 2.8910189876253 P P P LNCV6_131001_PI430048170 mRNA
TACTGGTGTAGAATCTACCGCCCTTCTGACAACTCTGTCTCTAAGTCCGTCAGATTCTAT NM_001199509 RefSeq

chr6 + 41335789 41350887 NCR2 9436 "natural cytotoxicity triggering receptor 2, transcript variant 2" GO:0007165|GO:0006968|GO:0005886|GO:0005887|GO:0045087|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135466_PI430048170 0.1150516532726 0.9254057558789250.309228759306032 0.3213533453637260.287125104236048A A A 0.4926477916950450.411800068637287 0.345209946631801A A A LNCV6_135466_PI430048170 mRNA
GGGCCTGAGACCTTTGTGGGATTTGTGCAATAAAGTGTTTTTATTTAAAACCAAAAACAA NM_001104577 RefSeq
chr17 - 5032601 5035432 SLC52A1 55065 "solute carrier family 52 (riboflavin transporter), member 1, transcript variant 1" GO:0032217|GO:0005887|GO:0001618|GO:0032218|GO:0009615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94009_PI430048170 0.0655431451910771 0.5359663999572856.3068526377203 6.48415150733363 6.73454876995306 P P P 6.8637063223319 7.48361977772519 7.76809045830748 P P P LNCV6_94009_PI430048170 mRNA
CTCGGATGGACTACCTGAGAGAATGTATATTTGGAGAAGTCAAGTCATGTTTGTAGTTTT NM_024622 RefSeq chr2 - 169529750 169573921 FASTKD1 79675 "FAST kinase domains 1, transcript variant 1" GO:0005739|GO:0045333|GO:0004672|GO:0006468 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137610_PI430048170 0.5288569917922820.9722616185285320.466048969183844 0.4856519730773020.326593336813217A A A 0.4072272860593190.516104093641251 0.479747934366225A A A LNCV6_137610_PI430048170 mRNA
GCCAAGTGATATCCTGTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCCATAT NM_013371 RefSeq chr1 + 206828876 206842981 IL19 29949 "interleukin 19, transcript variant 2" GO:2001237|GO:0007165|GO:0006955|GO:0006954|GO:0072593|GO:0006915|GO:2001244|GO:0042226|GO:0005576|GO:0005615|GO:0005125|GO:0046427 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100199_PI430048170 0.2398141900501891.06926419680508 0.61116765763025 0.7746403320306860.594624344782182A A A 0.5461989183834940.580943490601547 0.570163836305049A A A LNCV6_100199_PI430048170 mRNA
TTTGGTCTTCTGTGGGATCTCATTGTGGATGGAATCTTCCTTCAGCCTGATGAAGACAAG NM_001122646 RefSeq
chr2 - 96875881 96986564 FAM178B 51252 "family with sequence similarity 178, member B, transcript variant A" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130142_PI430048170 0.31044901660614 0.90003665540086 7.32232523219988 7.3106801815857 6.97815056382892 P P P 7.44945146259492 7.40481458546166 7.22920287711652 P P P LNCV6_130142_PI430048170 mRNA
TGCAGGCTCCCCTTCCTGCACCACCATTGTCTCAGCAGTAAAGGCGACATTTGGAACCAC NM_001001794 RefSeq
chr22 - 50311962 50327060 DENND6B 414918 DENN/MADD domain containing 6B GO:0017112|GO:0032851|GO:0055037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92515_PI430048170 0.5266868429630031.07366622065495 7.15954812343478 7.4795236273805 7.4454195164694 P P P 7.04186682637377 7.32672503704604 7.40445995860897 P P P LNCV6_92515_PI430048170 mRNA
TGATAACGATGACGATGAAGATGTTCAAGTTGAGGTGGCTGAGAAAGTGCAGAAATCGTC NM_183372 RefSeq chr1 - 148102045 148152190 NBPF11 200030 "neuroblastoma breakpoint family, member 11, transcript variant 3" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78090_PI430048170 0.00871687339706274 1.664523904695 10.0201062352539 10.1275849621135 10.3367555417606 P P P 9.47670314180272 9.36207020499458 9.4559324292766 P P P LNCV6_78090_PI430048170 mRNA
TTTGCCAAAATTAACTGTTTGGTGAAGCCCGCAAAACCTCCTCGCTTTGCATGCATGAAC NM_001278299 RefSeq
chr7 + 5190203 5233855 WIPI2 26100 "WD repeat domain, phosphoinositide interacting 2, transcript variant 6" GO:0000046|GO:0005515|GO:0006995|GO:0005776|GO:0000422|GO:0080025|GO:0000407|GO:0032266|GO:0034497|GO:0005829|GO:0043234|GO:0034045|GO:0005737|GO:0006497|GO:0005654|GO:0000045|GO:0019898 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131500_PI430048170 0.1661188956970680.6335673805016463.26104582372061 2.3946767035105
3.24198569118624 P A P 3.64719105577894 3.15580831850681 4.0809078963676 P P P
LNCV6_131500_PI430048170 mRNA
GCTGGCCATAAACCTAAGAAGACATTGAATCCCATTCACTCCTTAACATTCCTTAATATA NM_138467RefSeq chr1
+ 74733155 74766676 TYW3 127253 "tRNA-yW synthesizing protein 3 homolog (S. cerevisiae), transcript
variant 1" GO:0008168|GO:0032259|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69127_PI430048170 0.4778478969565490.97021685778498 0.4203153109108150.43707234426161
0.276507047845949A A A 0.3929698313988830.4597282587003950.416600533691487A A A
LNCV6_69127_PI430048170 mRNA
TTTATCTCTGATGGGACTAAGACAAAGCACTCCTGTTAGTACAACCCAGCTTGCGTTCCT NM_001243476 RefSeq
chr13 - 33103134 33676835 STARD13 90627 "StAR-related lipid transfer (START) domain containing
13, transcript variant 4"
GO:0043547|GO:0005811|GO:0005515|GO:0051056|GO:0031966|GO:0007264|GO:0008289|GO:0005829|GO:0005
096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138129_PI430048170 0.1434426442177880.4500325440381520.813502935837317
2.43315696282023 2.64588815024611 A A A 3.44792360824299 3.29774224087397
3.18063955216025 P P P LNCV6_138129_PI430048170 mRNA
CCCCTGCCATTTTGAAATAGCTGAACAAGTTAAAGTAATATGTTCCAAAAACTGGAAGTG NM_001278472 RefSeq
chr12 + 62466816 62597583 MON2 23041 "MON2 homolog (S. cerevisiae), transcript variant 5"
GO:0043547|GO:0005802|GO:0005515|GO:0005086|GO:0030036|GO:0016192|GO:0015031|GO:0006895|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140525_PI430048170 0.20038896584368 1.03180060823838 0.454323314343772
0.4469920372848030.385854809759691A A A 0.3447969542649830.397866836889215
0.409173033128052A A A LNCV6_140525_PI430048170 mRNA
CAGCAGATACTTTGTCAGCAATACTAAGGGAAGAAACAAAGTTGAACCGTTTCTTTAATA NM_005191RefSeq chr3
- 119524292 119559634 CD80 941 CD80 molecule
GO:0005515|GO:0048011|GO:0045425|GO:0005886|GO:0009986|GO:0048015|GO:0031295|GO:0007267|GO:0050
731|GO:0009967|GO:0015026|GO:0035556|GO:0045086|GO:0042110|GO:0007173|GO:0008543|GO:0045087|GO:0
045627|GO:0046641|GO:0016032|GO:0016021|GO:0045893|GO:0038095|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128573_PI430048170 0.5396063910925680.82932831827567 4.05364804663619
4.26797156198359 4.09605195085309 P P P 4.88597744273413 4.28401348075612
3.89002783200612 P P P LNCV6_128573_PI430048170 mRNA
GCATTTTCCACAATGCTGATTAAACATAATAAACAATCCAGAAAAGCAGTTTTGCCCAGA NM_014020RefSeq chr7
- 150791287 150801360 TMEM176B 28959 "transmembrane protein 176B, transcript variant 1"
GO:0031965|GO:0009887|GO:0016021|GO:2001199|GO:0030154 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141671_PI430048170 0.7360847827606241.01245450035962 0.311038679308577
0.3163801756740180.439025192748212A A A 0.3512072554788820.306697879906512
0.358097460726635A A A LNCV6_141671_PI430048170 mRNA
CATGCACTCAGTGTGGACTGGGAAGCATTACTTTGTAGATGTATTTTCAATAAAGAAAAA NM_004172RefSeq chr5
+ 36606354 36688334 SLC1A3 6507 "solute carrier family 1 (glial high affinity glutamate transporter),
member 3, transcript variant GLAST"
GO:0005886|GO:0007605|GO:0005314|GO:0070779|GO:0005313|GO:0007268|GO:0042995|GO:0031223|GO:0048
667|GO:0050885|GO:0043025|GO:0009416|GO:0043205|GO:0017153|GO:0046677|GO:0006811|GO:0009986|GO:0
006537|GO:0051938|GO:0021545|GO:0042493|GO:0009611|GO:0055085|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138122_PI430048170 0.1862878328750141.05759381772166 0.485877083853742

0.3900971708398580.479238236930695A A A 0.301672645076828 0.370452232707294
0.439412324686466A A A LNCV6_138122_PI430048170 mRNA
GTCTCTTAGAATTTATTTCCCACTGACACAAACAAGCCATTTTGTCTGCTTGTATAACCC NM_052889RefSeq chr11
- 105041325 105045324 CARD16 114769 "caspase recruitment domain family, member 16, transcript
variant 2" GO:0010951|GO:0004869|GO:0042981 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116195_PI430048170 0.00108277666766908 0.3597252416165983.80614134569813
3.7269637848816 3.76888847045274 P P P 5.12971129639662 5.21173692932505
5.37576013530567 P P P LNCV6_116195_PI430048170 mRNA
GTGCCACAGTAATTGCCAAAATAAACCAACATTAAGGTTCCCAGATGACCAAGTAAATAA NM_018353RefSeq chr14
- 45203189 45253402 MIS18BP1 55320 MIS18 binding protein 1
GO:0034080|GO:0005515|GO:0007067|GO:0003682|GO:0006334|GO:0005654|GO:0003677|GO:0000775|GO:0051
301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135222_PI430048170 0.602651674965105 1.08990654750844 1.03779792537863
1.11347225439982 1.19308171264478 A A A 0.27979470438987 0.39806884585794 1.7802866489334
A A A LNCV6_135222_PI430048170 mRNA
GAAAGATATTTGGCATTACATTGGCATATAGTACCAGCTCTCATGTTTTCATGATTCTAC NM_001283027 RefSeq
chr8 + 123416724 123442240 WDYHV1 55093 "WDYHV motif containing 1, transcript variant 3"
GO:0005515|GO:0070773|GO:0005634|GO:0006464|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139924_PI430048170 0.591449470866168 1.12064728249243 0.308949965096821
0.9728223988322430.384607522637858A A A 0.535912769606221 0.44932894003018
0.270836166334698A A A LNCV6_139924_PI430048170 mRNA
ATGGGGGAAAACCTGTGCAAATTAATTCACATACATGGTTCAGAAAATTCACAGCAGGAG NM_024967RefSeq chr19
+ 2867334 2878505 ZNF556 80032 "zinc finger protein 556, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127213_PI430048170 0.000395513401284857 0.671819267403181 13.9587783454404
13.9939545484401 13.9549089074048 P P P 14.5921739678073 14.5021869338668
14.5337180573731 P P P LNCV6_127213_PI430048170 mRNA
GGCGTGGCTGAGACCAACTGGTTTGCCTATAATTTATTAACTATTTATTTTTTCTAAGTG NM_014330RefSeq chr19
+ 48872391 48876062 PPP1R15A 23645 "protein phosphatase 1, regulatory subunit 15A"
GO:0005515|GO:0005783|GO:0005741|GO:0005829|GO:0030968|GO:0005739|GO:0008599|GO:0005737|GO:0033
138|GO:0045943|GO:0000164|GO:0071862|GO:0007179|GO:0007050|GO:0030512|GO:0005794|GO:0019901|GO:0
035308|GO:0006915|GO:0070972|GO:0006974|GO:0010628|GO:0032058|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142414_PI430048170 0.459980091897072 1.02779159655761 0.590813731702942
0.492759977877698 0.477153683608846A A A 0.415813460495986 0.513850153380887
0.512889118235951A A A LNCV6_142414_PI430048170 mRNA
GCAGGTTGTTAAGTTGAGAACATGGTTGAAGAATGAATTTTATAAACTGGGCAATGAAAC NM_001271706 RefSeq
chr9 - 24543214 24545676 IZUMO3 NA IZUMO family member 3 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_127653_PI430048170 0.0402057498777626 1.25118091002439 8.98025284617946
9.03807195732414 9.02850699430442 P P P 8.60041490936536 8.63167727305623
8.83419797079709 P P P LNCV6_127653_PI430048170 mRNA
TACCCATTTATCTAGGATGAAAGTGTGAATTAGAGGGACTCCTTCCAATAAAGTTCAAAC NM_006831RefSeq chr11
+ 57657743 57661865 CLP1 10978 "cleavage and polyadenylation factor I subunit 1, transcript variant
1"
GO:0030423|GO:0006379|GO:0006388|GO:0008380|GO:0010467|GO:0006369|GO:0006378|GO:0006366|GO:0021
695|GO:0031124|GO:0005634|GO:0000214|GO:0005524|GO:0035087|GO:0046404|GO:0016310|GO:0005737|GO:0

000398|GO:0005654|GO:0005849|GO:0051736|GO:0051733 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138301_PI430048170 0.24100237968608 0.9349013050138 9.81617685335313 9.85071833299591 9.68494943847581 P P P 9.85020103527901 9.81530712932561 9.97780933932152 P P P LNCV6_138301_PI430048170 mRNA AGTATCATTGTGGAGAACCAAGAGGGCCTCTTAACTGTAACAATGTTCATGGTTGTGATG NM_013986RefSeq chr22 + 29268008 29300525 EWSR1 2130 "EWS RNA-binding protein 1, transcript variant 1" GO:0005515|GO:0005516|GO:0006355|GO:0005886|GO:0003723|GO:0005730|GO:0005634|GO:0006351|GO:0042802|GO:0005737|GO:0000166|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102625_PI430048170 0.0678144656118148 1.31204292433659 10.5494322120669 10.6395565691273 10.8901569703698 P P P 10.2358161566512 10.1292471638102 10.5301548108663 P P P LNCV6_102625_PI430048170 mRNA GCCACAGATCCCTGCTTCATAGATTTGCATCATTCAAGCATATCTTGTAAAACAAACACA NM_016410RefSeq chr9 + 33264878 33282069 CHMP5 51510 "charged multivesicular body protein 5, transcript variant 1" GO:0005515|GO:0006997|GO:0008333|GO:0019058|GO:0005634|GO:0010824|GO:0015031|GO:0005829|GO:0000920|GO:0001919|GO:0016197|GO:0061024|GO:0016032|GO:0007080|GO:0007040|GO:0010008|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129692_PI430048170 0.000766369624352274 0.48656916634141 7.19606141924559 7.03644032618117 6.93256085881497 P P P 8.20547975594232 8.14133928821366 7.93470834493991 P P P LNCV6_129692_PI430048170 mRNA GCAACCCCAAAAGAGTTGATGTGTGTTTTAAAAGAAAAAACCCAATGAGGAACAATTGGA NM_016433RefSeq chr12 - 109850942 109880488 GLTP 51228 glycolipid transfer protein GO:0005737|GO:0051861|GO:0016020|GO:0017089|GO:0046836|GO:0070062|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133236_PI430048170 0.0242173743473747 0.446100369816947 2.20975949642987 1.7985719065695 2.62429710185176 A A A 3.34382531431113 3.60298111947774 3.27587987721738 P P P LNCV6_133236_PI430048170 mRNA CCTGTTTATGTTGCATTCACTACCCTATGAAGTAAAAATTTAGAAGGGAAAAAACACTCG NM_144974RefSeq chr13 - 43836352 43879690 CCDC122 160857 coiled-coil domain containing 122 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95281_PI430048170 0.0139824386729161 0.670969034903572 4.40561258147037 4.68111572769456 4.68068770443418 P P P 5.218090647412 4.96709035181097 5.30541104604962 P P P LNCV6_95281_PI430048170 mRNA CTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAATCAGGTCAGGTGACACTGGAAGA NM_001161344 RefSeq chr12 - 132840351 132887618 CHFR 55743 "checkpoint with forkhead and ring finger domains, E3 ubiquitin protein ligase, transcript variant 1" GO:0000209|GO:0005515|GO:0006511|GO:0004842|GO:0007093|GO:0016874|GO:0005634|GO:0007067|GO:0000166|GO:0016605|GO:0019941|GO:0008270|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126727_PI430048170 0.0955623682178953 1.61346505430536 6.02819701205523 6.00766196915681 5.81998624974686 P P P 4.73859816156335 5.60979804660176 5.31503299443136 P P P LNCV6_126727_PI430048170 mRNA CAAAAACAGTCAAAAAACCCCCACAGATTTTGAATAAAGGATCTACTTTGGTACGGAAAA NM_172229RefSeq chr16 + 2964215 2968383 KREMEN2 79412 "kringle containing transmembrane protein 2, transcript variant 4" GO:0007154|GO:0016020|GO:0005886|GO:0031901|GO:0016021|GO:0016055|GO:0090090 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135564_PI430048170 0.301109052832089 0.703030400635163 3.56427938386588 2.10558120222876 2.42591748193537 P A A 3.32018207505746 2.93703532221706 3.69432603207039 P P P LNCV6_135564_PI430048170 mRNA TTGGTTCCCACCCCACACCAAACCAAACCTGCTGGGTGAAGAGGGAGCAACAGTGTATGG NM_001109997 RefSeq

chr14 - 20428810 20435642 KLHL33 123103 kelch-like family member 33 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_54797_PI430048170 0.0363012355698497 1.0592855994277 0.34803751569172
0.3727569402482980.30253185897324 A A A 0.2450120466973140.28105773430016
0.248585060401145 A A A LNCV6_54797_PI430048170 mRNA
AGTGTCCTCAGTATATCAGGAAAAAGGGTGCAGACGTCTGGTTCAAAGAGTTGGATATCA NM_002964RefSeq chr1
- 153390031 153391188 S100A8 6279 S100 calcium binding protein A8
GO:0005515|GO:0008017|GO:0035662|GO:0050544|GO:0005886|GO:0030307|GO:0045471|GO:0050832|GO:0005
634|GO:0001816|GO:0005615|GO:0010043|GO:0005829|GO:0051092|GO:0006954|GO:0050786|GO:0032602|GO:0
032496|GO:0005856|GO:0042742|GO:0070062|GO:0002526|GO:0002523|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131223_PI430048170 0.479685113628128 1.04788340360797 0.293396422266755
0.3026826841880740.518985837340365 A A A 0.3182308314878830.277352242215754
0.328025601065866 A A A LNCV6_131223_PI430048170 mRNA
GAATAAGGCTTCTCTCATTTGTTTTTGATACCTTGGGAATTTCTATGCAGGGCTTTAAAA NM_178456RefSeq chr20
+ 58150926 58161127 C20orf85 128602 chromosome 20 open reading frame 85 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_105828_PI430048170 0.12415742590112 1.29561331106945 7.50897381238945
7.58029726500584 7.62463561454704 P P P 7.09022359554879 7.4855881015857
6.96747265375831 P P P LNCV6_105828_PI430048170 mRNA
TTTTTCGGGAAGTCCACCCTCCCGTTCATGGCCACGGTGTTGGAGTCCGCAGAGCACTCG NM_024299RefSeq chr20
+ 63520779 63522171 PPDPF 79144 pancreatic progenitor cell differentiation and proliferation factor
GO:0007275|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106845_PI430048170 0.293459619827276 1.12002002033617 5.00899647459336 4.8713634914746
5.12387598110464 P P P 4.7102380582937 5.06226759487984 4.72395758638584 P P P
LNCV6_106845_PI430048170 mRNA
TCCACGGCCTGCAGAGTAAGATAGAAGACCACCTGGACGAGGCCATCCACGTGCTCCGCA NM_003200RefSeq
chr19 - 1609289 1652329 TCF3 6929 "transcription factor 3, transcript variant 1"
GO:0005515|GO:0000790|GO:0003700|GO:0044212|GO:0042803|GO:2000045|GO:0042692|GO:0048541|GO:0032
496|GO:0000788|GO:0002326|GO:0033077|GO:0033152|GO:0046982|GO:0003713|GO:0031435|GO:0070888|GO:0
000122|GO:0000978|GO:0045787|GO:0035326|GO:0043234|GO:0051149|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143250_PI430048170 0.246251845199522 1.03625196189345 0.334459545067164
0.2822913663408810.391731065652945 A A A 0.2887050627212460.270742714511824
0.296863986948822 A A A LNCV6_143250_PI430048170 mRNA
TTCTGAAGCCCAGAGTTAAAAATCATCTGTCCACCTGGCTCCAAAGACAAAAAATAAAAA NM_002125RefSeq chr6
- 32517376 32530229 HLA-DRB5 3127 "major histocompatibility complex, class II, DR beta 5"
GO:0002437|GO:0050852|GO:0005886|GO:0019221|GO:0031295|GO:0042088|GO:0005765|GO:0005615|GO:0042
130|GO:0019886|GO:0006955|GO:0002381|GO:0042605|GO:2001179|GO:0071556|GO:0032689|GO:0070062|GO:0
060333|GO:0030658|GO:0012507|GO:0051262|GO:0035774|GO:0042613|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139993_PI430048170 0.161978833511571 0.5709716408380580.403153174896493
0.4232333888650110.442973211743992 A A A 1.20259136740978 0.5487964726285
1.71414218952111 A A A LNCV6_139993_PI430048170 mRNA
CCCAAAAGCCAACAAGAAATTAATGCTGATATAAAACGTCAATTAGTGAAGGAACTCCGA NM_152582RefSeq chrX
- 135863775 135871812 CT45A2 NA "cancer/testis antigen family 45, member A2" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126986_PI430048170 0.0973811467775111 1.25956190191534 6.89130566169078
7.27821619204917 6.94277649295409 P P P 6.58682087708884 6.79883405217428

6.75075836300468 P P P LNCV6_126986_PI430048170 mRNA
CCAATAACCTCTTTCCTTCTTATTACTCATCTGTTTTTGAGGGGAAGTAGAGTTTTGATT NM_001080401 RefSeq chr19
+ 45498472 45502506 PPM1N 147699 "protein phosphatase, Mg2+/Mn2+ dependent, 1N (putative)"
GO:0030145|GO:0000287|GO:0016311|GO:0004721 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76257_PI430048170 0.216201168999995 1.20292654287574 8.50625937474045 8.86978331143029
8.87812261130616 P P P 8.37165868331724 8.32042751304262 8.75297131969224 P P P
LNCV6_76257_PI430048170 mRNA
AATTGTTGGACTTCTCTACTAGAATCTGAATATGCAGCGGATCCTTGGGTGCAAGACCAA NM_145266 RefSeq chr5
- 163453579 163460137 NUDCD2 134492 NudC domain containing 2
GO:0005622|GO:0005515|GO:0005737|GO:0000922|GO:0005815|GO:0015630|GO:0000777|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143614_PI430048170 0.369599964856981 1.02398055049179 0.356965067273984
0.356761688624819 0.269036418954799 A A A 0.29063501253081 0.304808019512099
0.286461019944327 A A A LNCV6_143614_PI430048170 mRNA
ATGACATAGAACTGTTTCCTCTGTCATCAGTCATTCAATAAACACTGTTTGAGCACCTAC NM_080831 RefSeq chr20
+ 227257 229886 DEFB129 140881 "defensin, beta 129" GO:0009986|GO:0045087|GO:0005576|GO:0042742
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137948_PI430048170 0.82410998008603 0.985799490192106 0.276696584407286
0.50524707655004 0.346268901300883 A A A 0.502022644529133 0.394085312262902
0.296257966387864 A A A LNCV6_137948_PI430048170 mRNA
CATTCTTGTAACCTTCTATGGTGTTTTGTGGCTCTTATCTTGTGGACCATAAATAACACG NM_144642 RefSeq chr3
+ 63443076 63616921 SYNPR 132204 "synaptoporin, transcript variant 2"
GO:0043005|GO:0005215|GO:0030054|GO:0030285|GO:0006810|GO:0030672 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128847_PI430048170 0.510916743389758 0.721743278405291 0.526108718999285
0.721056887265608 0.617200512934664 A A A 1.81025580526085 0.504409883390917
0.564428412014493 A A A LNCV6_128847_PI430048170 mRNA
GATAGTGGAAATGATATAGTTGGACTGGTGCTTGATGTCACTAATAAATGAAACTGTCAG NM_000379 RefSeq chr2
- 31334321 31414745 XDH 7498 xanthine dehydrogenase
GO:0051898|GO:2001213|GO:0008762|GO:0050660|GO:0044281|GO:0005615|GO:0042803|GO:0005829|GO:0006
195|GO:1900745|GO:0005777|GO:0016903|GO:0005506|GO:0006919|GO:0004854|GO:0051537|GO:0004855|GO:0
009055|GO:0055086|GO:1900747|GO:0043546|GO:0007595|GO:0006144|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129553_PI430048170 0.596601376073867 0.852706282880277 0.54856337899957
0.668507816138948 0.64572778576922 A A A 0.598619449185845 0.441709480561822
1.34571391125324 A A A LNCV6_129553_PI430048170 mRNA
AGCCAGGATGCTCTAATATCAGTATCCTACACTATTATAACTCCATTGTTCAACCCAATG NM_001004476 RefSeq
chr1 - 158419927 158420866 OR10K2 NA "olfactory receptor, family 10, subfamily K, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136689_PI430048170 0.443813545178635 0.88305686269943 1.94130316527632
1.24276111999222 1.76725498285036 A A A 1.90704114099602 1.97109426746531 1.6838497348506
A A A LNCV6_136689_PI430048170 mRNA
ATCTGGCATACTGAATAAATAACATTAACTTGGGAGCCAAGAGCTGGGTAAGCCTTACCT NM_016255 RefSeq chr6
+ 17600286 17611719 FAM8A1 51439 "family with sequence similarity 8, member A1" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135927_PI430048170 0.0464481549737563 0.774614038738717 11.7204065915423
11.6082174679232 11.407335665635 P P P 11.9543202866649 11.9957533149751
11.9071247014726 P P P LNCV6_135927_PI430048170 mRNA
TGACTCTCCTCTTGGGGCTGCTGCCATTAAAACGCTACTACTAAGACTCAGGTCAAAAAA NM_001173498 RefSeq

chr19 - 12646507 12666777 MAN2B1 4125 "mannosidase, alpha, class 2B, member 1, transcript variant 2"
GO:0006517|GO:0030246|GO:0008270|GO:0005764|GO:0006464|GO:0004559|GO:0070062|GO:0006013 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129062_PI430048170 0.2327079887922842.02926207015663 2.88423998663714
2.34962401092031 4.04746684550825 A A P 1.12471169970883 2.70449995785379
2.48530612522355 A P P LNCV6_129062_PI430048170 mRNA
TTTCCCACCAGCTGGAAGAAAGAACTTTCATTTGTCTTGAAATGAGAAAAATGTTCTTAG NM_001146106 RefSeq
chr3 - 122531772 122564347 PARP9 83666 "poly (ADP-ribose) polymerase family, member 9, transcript variant 6"
GO:0005515|GO:0005737|GO:0016477|GO:0016020|GO:0005634|GO:0060330|GO:0006302|GO:0005829|GO:0003950 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135954_PI430048170 0.0618325799449221 1.2201223116408 6.08371088457134
6.35861809068007 6.12353035806981 P P P 5.78914561378673 6.01663637949521
5.90560365877849 P P P LNCV6_135954_PI430048170 mRNA
TTTTCTTTTTAATTTTATTTTGAGACTGGGGTGCATCTCCAGAGCCACTCACACCCTCAANM_023072RefSeq chr19 + 13795459 13832230 ZSWIM4 NA "zinc finger, SWIM-type containing 4" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_127061_PI430048170 0.32563468167684 1.90051617970102 0.395940857434843
1.13807316652054 2.3363007191463 A A A 0.3336180455543570.95083765700897
0.39442231287521 A A A LNCV6_127061_PI430048170 mRNA
ATAAAGAGGAGAGAGCGCTTCATAGACTTTAAGTTTTCCCGAGCCTCATGTCTACCGATG NM_000513RefSeq chrX + 154219733 154234001 OPN1MW 2652 "opsin 1 (cone pigments), medium-wave-sensitive"
GO:0018298|GO:0009881|GO:0007603|GO:0007186|GO:0005886|GO:0042622|GO:0032467|GO:0005887|GO:0004930|GO:0007601|GO:0001523 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143677_PI430048170 0.0178861167165209 0.5812296828842827.77883836930552
7.59711695819762 7.63128754287136 P P P 8.1869258006673 8.64887146743849
8.48897405266498 P P P LNCV6_143677_PI430048170 mRNA
GGGTTCAGGCATTGTCTTTTTTCCTCCTTGTATATAAGAATGTATATTTGATGCCTCATA NM_001111125 RefSeq chrX - 53232875 53321324 IQSEC2 23096 "IQ motif and Sec7 domain 2, transcript variant 1"
GO:0043547|GO:0005802|GO:0005086|GO:0030054|GO:0030036|GO:0032012|GO:0005634|GO:0016192 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104716_PI430048170 0.2524067155501530.8109971320820444.01486095109673
4.60953956997118 4.65775279470584 P P P 4.59522047635957 4.88361470729983
4.77969108088845 P P P LNCV6_104716_PI430048170 mRNA
CCCAATAAATCTTCAGCTTCAATATTTATAATGATGCCTTGCCACTCTACTCCTTATTAC NM_004855RefSeq chr15 + 55318934 55355648 PIGB 9488 "phosphatidylinositol glycan anchor biosynthesis, class B"
GO:0006501|GO:0000030|GO:0016254|GO:0005789|GO:0016021|GO:0044267|GO:0006506|GO:0043687 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139280_PI430048170 0.4282319412463960.9555617623728229.68374802832897
9.58753842223166 9.65972420981147 P P P 9.72478730261088 9.59126064930995
9.80537455405881 P P P LNCV6_139280_PI430048170 mRNA
GAAGCAGAGGCACTTAAAACATGTACCAGGAACCATTTAACAAAGAATATAAAATGTCAC NM_014049RefSeq chr3 + 128879489 128913114 ACAD9 28976 "acyl-CoA dehydrogenase family, member 9, transcript variant 1"
GO:0005739|GO:0005515|GO:0032981|GO:0050660|GO:0005634|GO:0003995|GO:0030425|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140881_PI430048170 0.2855790956833170.8689143284953813.13180536212227
3.39052982419799 3.01796076524781 A P A 3.55538485645629 3.14996918262483
3.43910691053216 P P P LNCV6_140881_PI430048170 mRNA

TGTGACTGTCTATGGGTGCATTGCCTTCTGGGTTGTCTCGATCTGTGTTTCAATAAATGC NM_002283 RefSeq chr12 - 52360005 52367525 KRT85 3891 "keratin 85, type II, transcript variant 1" GO:0008544|GO:0005198|GO:0045095|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_129642_PI430048170 0.1509767186592950.3716471891882130.778225681135853 0.8715014605828361.48148253933386 A A A 1.14563485295035 2.96484009156662 2.81375810791172 A P P LNCV6_129642_PI430048170 mRNA
GTGGACCTGTGGACCATTTCTAAAGGTGCACAACAAATAATAAATGTGTCCTTCTTTGTT NM_177403 RefSeq chr1 - 205976739 205994439 RAB7B 338382 "RAB7B, member RAS oncogene family, transcript variant 1" GO:0005802|GO:0032755|GO:0034144|GO:0005794|GO:0005770|GO:0007264|GO:0005525|GO:0015031|GO:0005764|GO:0045335|GO:0045654|GO:0051092|GO:0034499|GO:0030670|GO:0034164 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128990_PI430048170 0.00267563173538273 0.2193579176301632.89008579543264 2.71389629740349 2.21247491990451 A A A 4.81181376689552 4.64756299706867 4.98558444845023 P P P LNCV6_128990_PI430048170 mRNA
CCTTTGTTTTTGAACATTCAATCCGTTCATTTTGTATGTATGCTTAATACGTGTCGGTCA NM_015358 RefSeq chr21 + 36320188 36376646 MORC3 23515 MORC family CW-type zinc finger 3 GO:0018105|GO:0051457|GO:0016605|GO:0007569|GO:0050821|GO:0048147|GO:0008270|GO:0006468|GO:0005654|GO:0045111|GO:0009791 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81699_PI430048170 0.3644537387066011.87059549504216 0.9554288691349462.50789115485388 3.04964723317187 A A P 2.10084351681095 0.6961104707700131.37520461916272 A A A LNCV6_81699_PI430048170 mRNA
AAACCAGAATAACCTTTTAAGTCATGTGAAAGTATTGATTAAGGAGAGGGGCTATGAACA NM_007130 RefSeq chrX - 47446161 47482946 ZNF41 7592 "zinc finger protein 41, transcript variant 1" GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130543_PI430048170 0.0118719088411243 0.9495143980836780.381621530862575 0.3646376088908130.337095201507103 A A A 0.4487633689041440.441541554502771 0.417427326848993 A A A LNCV6_130543_PI430048170 mRNA
CACCCATAACATCTTTTCAATTTCTTGCGCCACTACAAGCAGATATATTTCCACAAAAAA NM_001004316 RefSeq chr3 + 156826306 157046129 LEKR1 NA "leucine, glutamate and lysine rich 1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138695_PI430048170 0.4614856687079910.8357819511973080.282043427058309 0.2896260510062960.493644089273908 A A A 0.3346306271178881.05721006295912 0.333427416791164 A A A LNCV6_138695_PI430048170 mRNA
CGTCTTAAGAGCAGATAAGTGACTAAGACTGAACACATACATTTTGTGGAGTATATAGTT NM_197978 RefSeq chr9 - 97926790 97938393 HEMGN 55363 "hemogen, transcript variant 1" GO:0005515|GO:0045667|GO:0007275|GO:0005654|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_5462_PI430048170 0.3985597767648791.51483940801045 1.58331945791432 0.248980610224787 0.326280769508785 A A A 0.2669805857411970.2427397421500110.267567717780352 A A A LNCV6_5462_PI430048170 mRNA
GTGGCTGTGACTTTTTCCTCTTGTTTTATCAACGTTTTGGAGACTACACAATGAAAACAC NM_032372 RefSeq chr10 + 80356767 80368073 DYDC2 84332 "DPY30 domain containing 2, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144640_PI430048170 0.0300120761704388 1.22116853780727 11.7745259317739 11.8142014485141 11.8398878953968 P P P 11.6024600196863 11.5508757405265 11.403966933555 P P P LNCV6_144640_PI430048170 mRNA
GTATGGACCTGTGTATGCAATACTGTTCTGTCATCTGGAGCTATTTTTAAGATGTGTGTG NM_024747 RefSeq chr10 + 102065366 102068038 HPS6 79803 Hermansky-Pudlak syndrome 6

GO:0030742|GO:0017137|GO:0031084|GO:0006996|GO:0016020|GO:0007596|GO:0005783|GO:0031901|GO:0030318|GO:0072657 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_13737_PI430048170 0.155824683083101 0.959520079228111 0.272649754132305 0.329410001443557 0.316012822820072 A A A 0.420123221957761 0.332495224855526 0.343316207069387 A A A
LNCV6_13737_PI430048170 mRNA
TGTGTACCTGGGAAATAATCTCGTTTGTATGCTTGTTTCTAGGATGTCTTTTACTCTTCA NM_001256368 RefSeq chr2 - 154435852 154457438 LOC100144595 100144595 uncharacterized LOC100144595 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135908_PI430048170 0.491258057562192 1.24778157244631 0.276956845209327 0.399296896812153 1.24039157633343 A A A 0.462765547746081 0.355353004158307 0.337976127915489 A A A LNCV6_135908_PI430048170 mRNA
AATGGAGTTCTAAAGCTTTAGGGCAAGAAACTTTTGCTTCCGCAAAAACATCTAAACATC NM_001010906 RefSeq chr8 - 28021963 28083871 NUGGC NA "nuclear GTPase, germinal center associated" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145568_PI430048170 0.661522393275737 1.06157918735324 6.29672664861077 6.10394003890968 5.89079346204802 P P P 6.23582877493135 6.07437716398597 5.70007557665272 P P P LNCV6_145568_PI430048170 mRNA
ATAGGAAGTCTCTGCCTCTTTCGCCTAGTATCTCTGCCTTTGTTTCAATTTGTTTTGATT NM_201550 RefSeq chr12 - 69608564 69611162 LRRC10 NA leucine rich repeat containing 10 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129284_PI430048170 0.345055524353942 0.959213042528003 0.412194935893685 0.424848473959954 0.271773797320422 A A A 0.384476656083694 0.446046913627052 0.462307844325858 A A A LNCV6_129284_PI430048170 mRNA
CTGTTCAAACCTTGCAGCGATAATATTTGGAAAAGAGCACTTGGAAATTATATTCCTGTT NM_032028 RefSeq chr5 - 113432553 113435031 TSSK1B 83942 testis-specific serine kinase 1B
GO:0000287|GO:0001669|GO:0031514|GO:0004674|GO:0007286|GO:0007275|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128255_PI430048170 0.00432393577691843 0.515510285497796 7.32042645998236 7.34117972689787 7.46673668283828 P P P 8.20639520364317 8.24650824453245 8.52614238473396 P P P LNCV6_128255_PI430048170 mRNA
GGTAATCAACTCTGCTACTGGCATGATGAAATAGTACATAACTGGTCATTAATTATGAAC NM_001252668 RefSeq chr2 + 188291668 188595925 GULP1 51454 "GULP, engulfment adaptor PTB domain containing 1, transcript variant 2" GO:0007165|GO:0005737|GO:0006869|GO:0006915|GO:0004871|GO:0006911 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135211_PI430048170 0.0124485861160796 0.363113167613277 3.24498957610966 2.38720356539322 2.8935585049041 P A P 4.14634906221613 4.25479809799661 4.5958822466635 P P P LNCV6_135211_PI430048170 mRNA
TGTGTCAGATTCTGAGCAATCATAGAGTCATCTAAGTTGTAAATAAAACCTTGCATAGCA NM_144710 RefSeq chr2 - 109542796 109614206 SEPT10 NA "septin 10, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140500_PI430048170 0.0020308276594976 0.582820578314155 10.683758290287 10.9103747765084 10.9394109880282 P P P 11.7474501318228 11.5046414944447 11.6211832863412 P P P LNCV6_140500_PI430048170 mRNA
AATAACGGGCAACCCTAGGCTTTTTGTTTTTCTTGCTTTTATTCCTTTTTGTTGTTGGCC NM_014876 RefSeq chr22 - 38685542 38700454 JOSD1 9929 Josephin domain containing 1
GO:0005737|GO:0016020|GO:0005886|GO:0006508|GO:0008242 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110475_PI430048170 0.0493644195396053 0.825162508341578 4.89551097941122 4.88380301507866 5.12472081061202 P P P 5.32831792645324 5.17638075589983

5.24005019272991 P P P LNCV6_110475_PI430048170 mRNA
AACATCAGCTTTCCAAACCAGATGTGGTATCTCAGTTAGAGGAGGCAGAAGATTTCTGGC NM_001278734 RefSeq
chr19 + 58182988 58213562 ZNF274 10782 "zinc finger protein 274, transcript variant ZNF274d"
GO:0043565|GO:0005515|GO:0006355|GO:0005813|GO:0005737|GO:0003700|GO:0003714|GO:0005730|GO:0005
654|GO:0005634|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128343_PI430048170 0.81142294288416 0.9322937756567060.439136927242659
0.4496453588090521.28031903226402 A A A 0.4787649392185270.613466745896654
1.37905733965269 A A A LNCV6_128343_PI430048170 mRNA
ATGGAGGAAGGGGGTCACTTATATAAAGATGGGACACTTTAATAAAGACAGGATATCTTC NM_153708RefSeq chr3
+ 187197485 187201465 RTP1 132112 receptor (chemosensory) transporter protein 1
GO:0009986|GO:0005886|GO:0051205|GO:0016021|GO:0031849 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137945_PI430048170 0.6390673761812850.6257508524550092.32291235034035
1.68005507365392 0.467191298574501A A A 0.3584046082571762.76557873374707
2.85673489725286 A P P LNCV6_137945_PI430048170 mRNA
TATCTGTGTATTGTACTAAATGGACTGATGCTGCGCACATGAGCTGAAAATGAAGAGCCC NM_020163RefSeq chr3
- 52433251 52445027 SEMA3G 56920 "sema domain, immunoglobulin domain (Ig), short basic
domain, secreted, (semaphorin) 3G" GO:0016020|GO:0007275|GO:0004872|GO:0070062 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_101795_PI430048170 0.00594901263810609 3.64741815132172 2.81649577550495
3.70059951551085 3.33205070737213 A P P 1.46666470400891 1.72730658880862
1.12563842898673 A A A LNCV6_101795_PI430048170 mRNA
TGCCAGGTCAGCCAATGTGTCAGCAGTTCACCCTTCTACTGCCAACCATGCCTAGACTGC NM_148965RefSeq chr1
- 6461153 6466195 TNFRSF25 8718 "tumor necrosis factor receptor superfamily, member 25,
transcript variant 1"
GO:0007165|GO:0005031|GO:0005886|GO:0005887|GO:0006915|GO:0042981|GO:0005576|GO:0004872|GO:0097
190|GO:0033209|GO:0007166|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130123_PI430048170 0.611654683142618 1.03329236124484 0.280281364556771
0.2891903503363310.502698570181453A A A 0.3302221144217880.284107898572631
0.326805287946238A A A LNCV6_130123_PI430048170 mRNA
GTGATGTATACATTTGGATGGGTGATATATAAAGTACTTTTCATAGATCTGGGCAAGAGA NM_001201450 RefSeq
chr7 - 96481625 96503523 C7orf76 NA "chromosome 7 open reading frame 76, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142538_PI430048170 0.136696229458631 0.674328039617733 3.62672427928964
2.98502725682519 2.74091000760203 P P A 3.75736129408772 3.58837798245245
3.85011564417724 P P P LNCV6_142538_PI430048170 mRNA
CCCTATTCCCCAACCCTGGGAACACAATTTAACATATTAGTTCATTTGTATTTAAGATCT NM_004120 RefSeq chr1
- 89106132 89126159 GBP2 2634 "guanylate binding protein 2, interferon-inducible"
GO:0005515|GO:0035458|GO:0050830|GO:0019221|GO:0020005|GO:0003924|GO:0042832|GO:0005634|GO:0031
410|GO:0005525|GO:0005829|GO:0044406|GO:0006955|GO:0071222|GO:0060337|GO:0000139|GO:0008152|GO:0
060333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83448_PI430048170 0.03111362140994 1.92917716967219 4.01634937455294
3.2597498409217 3.55763504057791 P P P 2.9608814182175 2.54820487062274
2.54141840050745 P P P LNCV6_83448_PI430048170 mRNA
TGAAGCCATTTTATGATCTGTCATGTGCCACCTGAGCCTCCAGTAAAAACAAAAACAGGC NM_015982 RefSeq
chr17 - 7288251 7294557 YBX2 51087 Y box binding protein 2
GO:0017148|GO:0006355|GO:0006366|GO:0005730|GO:0007286|GO:0005634|GO:0007283|GO:0048599|GO:0045
182|GO:0003677|GO:0008289|GO:0051100|GO:0005737|GO:0003682|GO:0043021|GO:0009386|GO:0048255|GO:0
003730|GO:0005844 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_128558_PI430048170 0.0101016354511607 0.413425277941669 7.45844229565768 7.2372418343613 7.35806154957999 P P P 8.27478774205548 8.72633500097587 8.82637634930954 P P P LNCV6_128558_PI430048170 mRNA CTACTGCTGAAGTCTCTTGTAACATTCCAAATCTATGTGACACACTGTATAATGATGAAT NM_003028 RefSeq chr9 - 37915897 38069213 SHB 6461 Src homology 2 domain containing adaptor protein B GO:0005515|GO:0048010|GO:0007165|GO:0005886|GO:0005070|GO:0006915|GO:0009967|GO:0001525|GO:0030154|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127440_PI430048170 0.533613299764354 1.39852292398507 0.345825543133711 1.67965747206195 0.299842540072553 A A A 0.329164249573069 0.660319571442739 0.313683248155299 A A A LNCV6_127440_PI430048170 mRNA CCTCTAAGTGTGAAAATGTGTAATTATGTACGGTATTTAGAAAAAGCCCTTATGTGTCCA NM_001010908 RefSeq chr10 - 16513742 16522005 C1QL3 389941 "complement component 1, q subcomponent-like 3" GO:0005581|GO:0050807|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137969_PI430048170 0.0670927324583628 0.62132999129502 1.81053866337393 2.57983379163434 2.1171411830298 A A A 2.64315259860457 3.15076528929024 2.83229766204259 A P P LNCV6_137969_PI430048170 mRNA TCAAGTAGCACGTATAACGTGATGCTTTCATGTTTCTGCCTTAAATAAAATAACCCTCAA NM_181783 RefSeq chr12 + 88142295 88199887 TMTC3 160418 transmembrane and tetratricopeptide repeat containing 3 GO:0048747|GO:0010468|GO:0048286|GO:0016021|GO:0009791|GO:0060447 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144600_PI430048170 0.112042603004505 0.876369292616065 9.19114453135635 9.3685774304637 9.10890969029318 P P P 9.50336158981142 9.34665973124388 9.39764978572556 P P P LNCV6_144600_PI430048170 mRNA CCCACATCACTACATTCCCTCGGCCCGTGTTAGTGAATAAAGTATTATATCCTCAAAAAA NM_016643 RefSeq chr16 + 30407413 30418595 ZNF771 51333 "zinc finger protein 771, transcript variant 1" GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141849_PI430048170 0.18463251581964 0.842075409705438 12.4029867619839 12.4373020050545 12.7334280313753 P P P 12.5472668589107 12.860793554036 12.9070993767948 P P P LNCV6_141849_PI430048170 mRNA CCCAGGTGTTTATACTGTGTGTGTCTGAGGTCTTTAAAGTTATTGCTTTATTTGGTTTTT NM_016084 RefSeq chr17 - 17494438 17496395 RASD1 51655 "RAS, dexamethasone-induced 1, transcript variant 1" GO:0006184|GO:0007165|GO:0048471|GO:0007263|GO:0007186|GO:0005886|GO:0007264|GO:0003924|GO:0005634|GO:0005525|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138486_PI430048170 0.318385066765797 0.893605506461078 5.10910803781134 5.27093422295552 4.86412232617459 P P P 5.39726533004293 5.23716489027388 5.11105503706872 P P P LNCV6_138486_PI430048170 mRNA TTTATTGACTTTTATGAAGTTTCCCCTTCCATCCGATCCCTACTGCCCATGTTGTCCTGA NM_005876 RefSeq chr2 + 219434977 219493632 SPEG 10290 "SPEG complex locus, transcript variant 1" GO:0060541|GO:0008285|GO:0007517|GO:0004674|GO:0055013|GO:0006468|GO:0005634|GO:0005524|GO:0001701 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137638_PI430048170 0.566720151434664 0.964402030262584 0.304603538765622 0.33419282292174 0.388844365640935 A A A 0.339274729032221 0.531636308930813 0.30434805284382 A A A LNCV6_137638_PI430048170 mRNA CCTCCTGAGATTCAGAAAAGTTGTCTTAATATGTTGATTCAGTCCTTAGTAAGTATAACC NM_183242 RefSeq chr1 + 92080304 92147841 BTBD8 284697 BTB (POZ) domain containing 8 GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140939_PI430048170 0.160330387281576 1.0845824065888 0.525736318978282

0.705444650861943 0.583404029509162 A A A 0.411736988295592 0.506727856443496
0.547242845387855 A A A LNCV6_140939_PI430048170 mRNA
AGTGGAGAGGACCTAACATATGTCTCTACCTAGAACGGATGGTTTCATTAAAGAATGTGG NM_012465 RefSeq
chr10 - 96364605 96513926 TLL2 7093 tolloid-like 2
GO:0022617|GO:0030198|GO:0005509|GO:0006508|GO:0008270|GO:0007275|GO:0005576|GO:0004222|GO:0030
154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129799_PI430048170 0.0327849895070405 0.894656136362808 13.3558563641853
13.4326832573945 13.3354337167802 P P P 13.6075659269923 13.5199155964523
13.4770257728362 P P P LNCV6_129799_PI430048170 mRNA
TCAACACACAGGCTGTGGCTCTGGACATCCGGATATTAAAAGGAGCGTTGCTGGAAAAAA NM_012088 RefSeq
chr19 + 17511622 17521288 PGLS 25796 6-phosphogluconolactonase
GO:0005975|GO:0009405|GO:0017057|GO:0044281|GO:0048029|GO:0006098|GO:0009051|GO:0070062|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139228_PI430048170 0.000227770766456845 2.05854224174717 9.94477966825284
9.86925668665223 10.0649754944914 P P P 8.97924825962211 8.84223676730753
8.93606054917623 P P P LNCV6_139228_PI430048170 mRNA
CAAGAAGAAATAGGCGAACGCCTACTTCTAAAACCCAAAAGGCTCTTTTCAGAGCCACCA NM_005319 RefSeq
chr6 - 26055739 26056471 HIST1H1C 3006 "histone cluster 1, H1c"
GO:0005515|GO:0005719|GO:0006334|GO:0016584|GO:0005634|GO:0000786|GO:0031490 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140243_PI430048170 0.00223162120605996 0.3367822822676483.86693022652434
3.72110611727337 3.63450229370415 P P P 5.12155389278141 5.21120699350022
5.56979678567082 P P P LNCV6_140243_PI430048170 mRNA
GTTCTGTATACATTTCTCAAATGTACACTTGTATTATAATAACCTCCCAGTTCTAGGGGA NM_133372RefSeq chr5
- 131641713 131797063 FNIP1 96459 "folliculin interacting protein 1, transcript variant 1"
GO:0005515|GO:0031929|GO:0032007|GO:0000122|GO:0043547|GO:0005085|GO:2000973|GO:0005737|GO:0033
138|GO:0002904|GO:0001934|GO:0001932|GO:0002327|GO:0043154|GO:0009267 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_90442_PI430048170 0.4140270989716170.8557729999773890.4900008124694440.514714453846149
0.404732582025096A A A 0.5044409023488970.445959189434281 1.05436518291392 A A A
LNCV6_90442_PI430048170 mRNA
ACACTTGCCGAGGCCATATTCCAGATTTTCCAAGAAAACAAGTCAGAGGACCAGCATCTA NM_022475RefSeq chr4
+ 144645995 144738729 HHIP 64399 hedgehog interacting protein
GO:0005515|GO:0060170|GO:0048038|GO:0009986|GO:0016901|GO:0005975|GO:0048705|GO:0045879|GO:0005
576|GO:0009953|GO:0007224|GO:0007405|GO:0005737|GO:0060441|GO:0040036|GO:0005887|GO:0008270|GO:0
009968|GO:0097108|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130280_PI430048170 0.00870809548928129 0.3621775879795332.80287410482585
3.0728743183344 3.3112899456937 A P P 4.17024382853088 4.41726282988909
4.93254776886041 P P P LNCV6_130280_PI430048170 mRNA
TTGGCTCATATTTTATGACATTGTAGTTCATCCCCATGGTCAATTTAAGGTAGAGTTCTTNM_030755RefSeq chr14 +
51240167 51257654 TMX1 81542 thioredoxin-related transmembrane protein 1
GO:0034976|GO:0006457|GO:0005783|GO:0005789|GO:0005730|GO:0015036|GO:0003756|GO:0045454|GO:0016
021|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141654_PI430048170 0.1855407195573580.8398970506610765.18684043202518
5.12868279966816 5.56547587998772 P P P 5.59085952077228 5.45192601677507
5.62752474068763 P P P LNCV6_141654_PI430048170 mRNA
CCAAAAATGTTTTGTCTGTTTGGATCTATGTTGCCTCTCTTATACGCAACAGGTAATTTTNM_001080522 RefSeq chr4
+ 15469864 15601557 CC2D2A 57545 "coiled-coil and C2 domain containing 2A, transcript variant 1"
GO:0042384|GO:0006996|GO:0060271|GO:0035869|GO:0036038|GO:0005856|GO:0007224|GO:0005829 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58815_PI430048170 0.1067575440581860.85856030233887 6.26411977575704 6.15754433441885
5.9775900695942 P P P 6.46747168024759 6.34949260953513 6.24837496425326 P P P
LNCV6_58815_PI430048170 mRNA
CTGGAGCCAATGTATCTAACATACAGCTTCAGCAAAAAATTTCAAGTCTGGAGATTAAAC NM_018318 RefSeq chr12
+ 28257199 28550166 CCDC91 55297 coiled-coil domain containing 91
GO:0005794|GO:0016020|GO:0005654|GO:0015031|GO:0042802 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139833_PI430048170 0.2505816062634271.04079173776395 0.549147192775237
0.4816178975973870.572826301599739 A A A 0.4695480926013930.53707867306182
0.423186945455167 A A A LNCV6_139833_PI430048170 mRNA
GGTAGTCCTACTCACTTGCTATTGTCAAATCATTTGTTTTATCATGGATTTGAGATCCTT NM_001164479 RefSeq chr5
- 127042557 127073492 C5orf63 NA "chromosome 5 open reading frame 63, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133046_PI430048170 0.2324624224447140.5572053361309390.35304389134392
0.34950623733852 0.465427050471148 A A A 0.3142348860553771.78325890323054
1.24576904517072 A A A LNCV6_133046_PI430048170 mRNA
CCAAATGAGCTGCAAAAGATAATTATTGCTGCCCAGTAAACAAAATGTATGTCAAATCAG NM_001256006 RefSeq
chr1 + 209938173 210164288 SYT14 255928 "synaptotagmin XIV, transcript variant 5"
GO:0005543|GO:0046982|GO:0016021|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138798_PI430048170 0.8670230716221560.9878339157258380.2931687125396
0.3098374457991920.57061496461357 A A A 0.3746932357063920.317030613527962
0.542380890329365 A A A LNCV6_138798_PI430048170 mRNA
CACGACCAAAAAGTCCTGAAGAGTATCTGCACAATTGCCTGATTATTGTAAATACTCTTT NM_173695 RefSeq - -
0 0 --- NA - NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53920_PI430048170 0.1955290539235860.5148753858570281.84892320672665 0.380534416636891
1.32829630968524 A A A 1.27834790378372 2.72870075060037 2.4189262677527 A P P
LNCV6_53920_PI430048170 mRNA
AAAGTTACCAAGAGCCTCTTTGGCAGAAAGAAGAAGAGTAAGAATCATGCCCAGGAGAGG NM_004073 RefSeq
chr1 + 44800363 44805995 PLK3 1263 polo-like kinase 3
GO:0005515|GO:0007093|GO:0005634|GO:0031122|GO:0090166|GO:0030425|GO:0002039|GO:0005737|GO:0000
082|GO:0000086|GO:0007113|GO:0043025|GO:2000777|GO:0009314|GO:0005813|GO:0043066|GO:0032465|GO:0
005795|GO:0005730|GO:0006915|GO:0006970|GO:0090316|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133397_PI430048170 0.00472291257610867 0.6327184710379394.62111647416848
4.49870924403308 4.76390336678258 P P P 5.23272534408526 5.17410302862461
5.45479465383222 P P P LNCV6_133397_PI430048170 mRNA
TGCTAAACCCTTCTAATAATATAATAAATGGCACTGCCACAGCCAACATGCCTGAAAAAA NM_001199479 RefSeq
chr6 + 28225250 28233486 ZSCAN9 7746 "zinc finger and SCAN domain containing 9, transcript
variant 1" GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_140969_PI430048170 0.1146974149656211.06081334256298 0.447206066393644
0.4894538776443040.504920509545743 A A A 0.3346177375586040.395304142758627
0.45428224853489 A A A LNCV6_140969_PI430048170 mRNA
TGCTTCTGTGAGACCAATTTTGTGCTAATGAGCATTGAGACTGATGCTTTGTAAGTCACA NM_020125 RefSeq chr1
+ 159826688 159837492 SLAMF856833 SLAM family member 8
GO:0004872|GO:0033860|GO:0016021|GO:0090383|GO:0035690|GO:0043549|GO:0042742 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132094_PI430048170 0.1359747681913510.5230070785311953.30975853815927 2.2342130184391

3.39862509111903 P A P 4.25899547304139 4.28649172031702 3.2416702069955 P P P
LNCV6_132094_PI430048170 mRNA
CCCTGAGGGCACAATCGTCCTTGCAGTTTAAGATGACACTTTAAAAATAAATTCTTTCCT NM_152375 RefSeq chr1
+ 18480929 18485986 KLHDC7A 127707 kelch domain containing 7A GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129660_PI430048170 0.7729687568822360.9767530306678430.389529550837115
0.4051956631920872.00261479801445 A A A 1.66704525347668 0.717606313009084
0.985116753564275 A A A LNCV6_129660_PI430048170 mRNA
TTAAAGTTGGTGACAATCCACCTCAGTCTCTCAATGTGTGCTATTAATGAGGCCTCTGAG NM_018055 RefSeq chr10
- 70431935 70441709 NODAL 4838 nodal growth differentiation factor
GO:0033505|GO:0035987|GO:1900224|GO:0005615|GO:0048701|GO:0009880|GO:0001947|GO:0016015|GO:0042
074|GO:0090010|GO:1900164|GO:0010470|GO:0070374|GO:0048018|GO:0001944|GO:0050679|GO:0022409|GO:0
001893|GO:0060136|GO:0001892|GO:0060137|GO:0060766|GO:0032927|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_103065_PI430048170 0.2244458852988911.25821727620546 3.93063390129247
4.01692265897604 4.42751510760472 P P P 3.61433907292113 4.1414220273552 3.6080597137789
P P P LNCV6_103065_PI430048170 mRNA
TACTAAGCACAAGTACTTGCCACTGCCATCACTGCCAAGTAACTAGATGTCTCTGTTTCC NM_020897 RefSeq
chr1_GL383519v1_alt + 82449 94871 HCN3 57657 "hyperpolarization activated cyclic nucleotide
gated potassium channel 3, transcript variant 1"
GO:0030552|GO:0005886|GO:0005887|GO:0005249|GO:0042391|GO:0005248|GO:0007268|GO:0035725|GO:0034
765|GO:0071320|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134517_PI430048170 0.0165045542668873 1.61318054165442 7.95043254462877
7.66912718546072 8.08767339571254 P P P 7.14697760411169 7.4494020751192
7.04034196582606 P P P LNCV6_134517_PI430048170 mRNA
TTACAGGGAGGCGGTCTTTAAGATGCTCAGCAATAAGGAGTCTCTGGATCAGATCATTGT NM_001286741 RefSeq
chr15 - 74445976 74461188 UBL7 84993 "ubiquitin-like 7, transcript variant 5"NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138363_PI430048170 0.0370923067280798 0.5788485625395125.54009473380712
5.21811752007893 5.48003618162603 P P P 6.53992427056654 5.88893182177352
6.11869876956237 P P P LNCV6_138363_PI430048170 mRNA
TTAGAGCTGGAAATGTAGTGGCTTTCATTAAATACTTGCTGTAAAGTCTTTCTAAGACCA NM_001286706 RefSeq
chr13 + 38349770 38363007 UFM1 51569 "ubiquitin-fold modifier 1, transcript variant 5"
GO:0034976|GO:0005737|GO:0071569|GO:0033146|GO:0005634|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127288_PI430048170 0.2160250326289121.47102828147113 5.05438747009396
5.38179660096091 5.21494502721954 P P P 4.99579669214667 4.89102613501354
3.86817344802492 P P P LNCV6_127288_PI430048170 mRNA
ACTCGCTGCGCATCATCTTCGCCATCGAGAGCACGTTTGTGGGCTCCTGGCTGCCCTTCA NM_005298 RefSeq chr1
+ 200872954 200874178 GPR25 2848 G protein-coupled receptor 25
GO:0007186|GO:0005887|GO:0004930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140400_PI430048170 0.0205664581743781 1.44046380875674 9.05169945541707
8.7594425484949 8.73621874985004 P P P 8.12934810850279 8.45067721589036
8.38984920578751 P P P LNCV6_140400_PI430048170 mRNA
GCAGAGGCCTCTCTGCTCTTGTTTAACCCCATAAAGAAATAAATGGTAAGACTTGATGAT NM_015686 RefSeq chrX
+ 69505234 69532508 FAM155B 27112 "family with sequence similarity 155, member B" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131104_PI430048170 0.2994651093514740.6964909417925013.16309199113479
2.77197594655304 3.26226198154256 P A P 4.17956386319614 3.19804155102046

3.19314052479346 P P P LNCV6_131104_PI430048170 mRNA
GGCCTTGTCAAGTTGTGTTTGAAGAGAATAAATAATCCTTTGCCCAGGTGGGGCCCTAAA NM_001303477 RefSeq
chr20 + 5750386 5864407 C20orf196 149840 "chromosome 20 open reading frame 196, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143098_PI430048170 0.0516845845240508 0.72160240297059 7.25900344766923
7.37752738229191 7.71358447451595 P P P 7.81447885943288 7.85174008960087
8.11626389593967 P P P LNCV6_143098_PI430048170 mRNA
CAATAGTGACAAGAATGGTTCAGTTCTAGGAATGTTCTGGAAGATGCTGTTAATTTTACT NM_173510RefSeq chr22
+ 28772673 28789301 CCDC117 150275 "coiled-coil domain containing 117, transcript variant 1"
GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134306_PI430048170 0.3325732145184271.57451856984725 0.617659895060903
0.7158091925821141.91115690278262 A A A 0.57263214255777 0.54846391644665
0.542601778896224A A A LNCV6_134306_PI430048170 mRNA
GGACGTCCATGTTGCCTTTTCAGAACATTCTCTTCATTTTTCTCCTCTCAGTTTGACCAT NM_001271682 RefSeq chrX
- 37042881 37043794 FTH1P18 NA "ferritin, heavy polypeptide 1 pseudogene 18" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139801_PI430048170 0.0999344343822887 0.7326104973775348.1456481628909
7.6847999231241 7.57461358302435 P P P 8.42277528322865 8.29834206519482 8.0748549608497
P P P LNCV6_139801_PI430048170 mRNA
TATGTACCCCATCCCCCATACTCACCTCTTTCCATTTTGAGTAATAAATGTCTGAGTCTG NM_025261RefSeq
chr6_GL000256v2_alt - 3017943 3021030 LY6G6C 80740 "lymphocyte antigen 6 complex, locus
G6C" GO:0005886|GO:0031225 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_21725_PI430048170 0.3607612172709640.7781857087981720.4774478249659220.375342539280713
0.43741010648593 A A A 1.27099800363679 0.4885588821242090.464519982392819A A A
LNCV6_21725_PI430048170 mRNA
ATTTCTGAAGTGTATACAAGGATGGCTGAAGTGTGGACATGAGACTGGAAACAGAGGCAG NM_001004352
RefSeq chr9 + 26066674 26118408 LOC100506422 NA putative deoxyuridine 5'-triphosphate
nucleotidohydrolase-like protein FLJ16323 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132313_PI430048170 0.0970495781520865 1.23323816532596 12.5096158092857
12.7377705103529 12.5537317571411 P P P 12.074944502282 12.4628693326538 12.3394668289 P
P P LNCV6_132313_PI430048170 mRNA
TCCACACCATTCTTGGTGCTGGGGTGTGTTAAGCTTTACCATTAAACACAACGTTTCTCT NM_005175RefSeq chr17
+ 48892785 48895870 ATP5G1 516 "ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C1
(subunit 9), transcript variant 1"
GO:0005215|GO:0015078|GO:0005743|GO:0044281|GO:0005753|GO:0008289|GO:0005739|GO:0022904|GO:0042
776|GO:0015991|GO:0016021|GO:0044237|GO:0045263 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126934_PI430048170 0.9405139659092851.00086552796811 0.678811998141611
0.7634424536210230.636109198782038A A A 0.919844603742134 0.569405214698005
0.55823824098808 A A A LNCV6_126934_PI430048170 mRNA
GACCAATTTTGCTCTGTTTTCAAATTGCATATGATGGGGTATTATGCTGAAACTGCTAAT NM_001174123 RefSeq
chr18 + 74315874 74359187 C18orf63 NA chromosome 18 open reading frame 63 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134759_PI430048170 0.0723282571819482 0.77021537819074710.1204512845029
9.96372187324363 9.85269507042204 P P P 10.1208924073484 10.5336772222553
10.3948236804841 P P P LNCV6_134759_PI430048170 mRNA
TTTCGGCGGTTGAGCTGTCCCCACAGCTTCTCTACAGACTCCAAAAGGCCCTTTTCAGGG NM_175054RefSeq chr12
- 14770719 14771131 HIST4H4 121504 "histone cluster 4, H4"
GO:0005515|GO:0010467|GO:0006325|GO:0005634|GO:0045653|GO:0000723|GO:0000183|GO:0000786|GO:0070
062|GO:0035574|GO:0035575|GO:0046982|GO:0006334|GO:0006335|GO:0005576|GO:0006336|GO:0000228|GO:0

003677|GO:0032776|GO:0034080|GO:0043234|GO:0016020|GO:0045814|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133293_PI430048170 0.0711917522349697 0.6037059515521054.08220923224558 4.70444134128431 3.99390347214835 P P P 5.11030101368313 4.97851606584998 4.9802854586332 P P P LNCV6_133293_PI430048170 mRNA
GCCTGTGGCTTATTCCCCGCCAGTGATCTGTTTCCCCCAATAAAGTCTCAAATCTTTGGG NM_145807RefSeq chr19 - 48661406 48673081 NTN5 126147 netrin 5 GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127692_PI430048170 0.0259492952361989 2.57600542501831 3.18261711546878 4.06847548622555 3.88266913174828 P P P 2.83182442245692 2.35216744882091 1.8229786303406 P A A LNCV6_127692_PI430048170 mRNA
ATTTCTGGCTTTGCAGGACTCTTACCATGGCCAGGCATTCCTGCCCAGCCTTTACCTCCT NM_001005922 RefSeq chr11_KI270903v1_alt - 60878 61820 KRTAP5-1 NA keratin associated protein 5-1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142030_PI430048170 0.00162100803611591 0.3611973919845895.98317907928398 5.82559616379814 6.2188734639975 P P P 7.24221472476242 7.44205687806456 7.73519032559156 P P P LNCV6_142030_PI430048170 mRNA
CTTTAAGTTCTACTTTTCATTAACCATGGCCTGATATTAGTTCTTAGAGCTTCTTGTGGC NM_001184742 RefSeq chrX + 120250754 120258396 ZBTB33 10009 "zinc finger and BTB domain containing 33, transcript variant 1"
GO:0005515|GO:0008327|GO:0005886|GO:0005730|GO:0005634|GO:0006351|GO:0046872|GO:0035556|GO:0043565|GO:0005737|GO:0005654|GO:0016055|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141618_PI430048170 0.00861717839824459 1.8209264201015 12.1105224053868 12.235224989768 12.3736981409363 P P P 11.3197421091496 11.1675284346065 11.6139910011222 P P P LNCV6_141618_PI430048170 mRNA
GGGGATTTGTTCCTTATATTGGAATTGTGACGATCCTCATGAATGACTATCCTAAATTTA NM_001271918 RefSeq chr15 - 84669536 84716460 SEC11A 23478 "SEC11 homolog A (S. cerevisiae), transcript variant 5"
GO:0010467|GO:0050796|GO:0006614|GO:0006508|GO:0005789|GO:0008236|GO:0016021|GO:0044267|GO:0006412|GO:0070062|GO:0006465 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133414_PI430048170 0.6620936473892390.91842135764200715.5951327925953 15.0356363662545 14.9886198989383 P P P 15.5492315107711 15.4892398641739 14.9621497543572 P P P LNCV6_133414_PI430048170 mRNA
CGAGTGATGCTGTACCCCTCAAGGATTTAAACTAACGAAAAATCAATAAATAAATGTGGA NM_000996RefSeq chr3 + 197950180 197955850 RPL35A 6165 ribosomal protein L35a
GO:0010467|GO:0000049|GO:0003735|GO:0019083|GO:0006364|GO:0006614|GO:0019058|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005739|GO:0000184|GO:0016020|GO:0016032|GO:0042273|GO:0022625|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59618_PI430048170 0.0662362858434487 0.7736200088533078.86027075098779 8.84634396773511 8.77537894818854 P P P 8.99093520089666 9.23572430787933 9.34522647896255 P P P LNCV6_59618_PI430048170 mRNA
GTTTCTCCAATTATGCCCATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGCAAA NM_001109903 RefSeq chr12 + 116738290 116853631 RNFT2 84900 "ring finger protein, transmembrane 2, transcript variant 1"
GO:0008270|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144106_PI430048170 0.00949455073701104 0.5882668299397686.62929796386157 6.620892144366 6.7555595346397 P P P 7.33701972430985 7.3106801815857 7.63536551921204 P P P LNCV6_144106_PI430048170 mRNA
TCCCCACAACCACTTTAAACATAAGAAATGTGGTGGCAATATAAAGTTTGTAGCCTTTCC NM_005880RefSeq chr16 - 46955361 46973714 DNAJA2 10294 "DnaJ (Hsp40) homolog, subfamily A, member 2"
GO:0005515|GO:0042026|GO:0008284|GO:0016020|GO:0009408|GO:0031072|GO:0051087|GO:0051082|GO:0005524|GO:0046872|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_126896_PI430048170 0.0493075885437396 1.22393567144438 7.02572575148445
6.88135085123175 6.78455783433826 P P P 6.45155239936795 6.66586921304832
6.69768276341985 P P P LNCV6_126896_PI430048170 mRNA
CCTGTATCATCTCATTTGGACAAATGCTGGCACGTTGAAATTAAAATGTTAAAAAACAGC NM_003918RefSeq chrX
+ 2828821 2882820 GYG2 8908 "glycogenin 2, transcript variant 2"
GO:0005975|GO:0005978|GO:0009405|GO:0006006|GO:0008466|GO:0044281|GO:0005980|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141350_PI430048170 0.0149544036337911 0.6890759351000458.30033730574013
8.46858990110704 8.64472431072272 P P P 8.86978331143029 9.0073931986115
9.15473972892925 P P P LNCV6_141350_PI430048170 mRNA
CACCTTGATGGCTCTTGATGGCTCTAAAAAGTTGTAGGATTTTTTGTTTTTGTAGCTAAC NM_130466RefSeq chr12
+ 109477622 109536705 UBE3B 89910 "ubiquitin protein ligase E3B, transcript variant 1"
GO:0005737|GO:0004842|GO:0042787|GO:0016874|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127068_PI430048170 0.00957089189322472 0.4655007909431657.75176474219357
7.67908723417416 7.87761952177191 P P P 8.74320369156126 8.68477526533307
9.15095212160695 P P P LNCV6_127068_PI430048170 mRNA
CAGTGCAATAGATTTGTTTGACTGCTTGTGTCTTTTTATGACCTGTTTGCCTTTTAGAAA NM_022817RefSeq chr2 -
238244037 238288566 PER2 8864 period circadian clock 2
GO:0005515|GO:0043130|GO:0048471|GO:0042826|GO:0006094|GO:0019249|GO:0035257|GO:0070345|GO:0005
634|GO:2000678|GO:0000989|GO:0019229|GO:0001222|GO:0005737|GO:0050767|GO:0051726|GO:0006631|GO:0
004871|GO:0031397|GO:0070063|GO:0051946|GO:0036002|GO:0019900|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_120535_PI430048170 0.00389492714413023 3.97099660427291 5.26037254626857
5.49837183179731 6.08477455625326 P P P 3.22841814275393 3.75252114566312
3.93336411851006 P P P LNCV6_120535_PI430048170 mRNA
TGCACACCCTCCAGAGACAACAGGTAAAACAGGGCCACATAGATGCTGATGGAGCCTTCCNM_000499RefSeq chr15
- 74719541 74725536 CYP1A1 1543 "cytochrome P450, family 1, subfamily A, polypeptide 1"
GO:0019369|GO:0046685|GO:0006805|GO:0017144|GO:0017143|GO:0033189|GO:0009792|GO:0010041|GO:0016
711|GO:0032496|GO:0070576|GO:0044255|GO:0046677|GO:0005506|GO:0070330|GO:0042359|GO:0007568|GO:0
060137|GO:0009635|GO:0006778|GO:0097267|GO:0055093|GO:0016491|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129178_PI430048170 0.0978743152915258 0.6866686787874140.437806192655529
0.2866509880365780.339883116808544A A A 1.23266321243932 0.627246352781849
0.763498402692637A A A LNCV6_129178_PI430048170 mRNA
GCATCTAAAACCTTGAGCGTACGTAAAATATTACCATTCATATGTTAGAACAATCCTGTC NM_001012303 RefSeq
chr3 - 167441788 167474132 SERPINI2 5276 "serpin peptidase inhibitor, clade I (pancpin), member
2, transcript variant 1"
GO:0010951|GO:0005515|GO:0004867|GO:0006928|GO:0030155|GO:0005615|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140757_PI430048170 0.0266003005984415 0.6375803823426998.57793846507947
8.68237407969297 8.87188830090508 P P P 9.23681407172161 9.1805952848203
9.63461063169493 P P P LNCV6_140757_PI430048170 mRNA
TATATGTCCTTCCAAAAATGTTGTTGTGTACAAACCATGCTTTCAATGTTGGCTTCCAAG NM_001102426 RefSeq
chr2 - 101007227 101151384 TBC1D811138 "TBC1 domain family, member 8 (with GRAM domain)"
GO:0008284|GO:0016020|GO:0008015|GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133746_PI430048170 0.00574439895421576 0.6180148259869625.45015423235773
5.37520089986406 5.69581583078165 P P P 6.09058667512776 6.35896872733595

6.16068876686382 P P P LNCV6_133746_PI430048170 mRNA
CTCTGGGAATGGGGAGGGAAATTATATGTAATAGAGCTTAAAAATAAAGTGTCAATTTCC NM_002863 RefSeq chr14
- 50905216 50944530 PYGL 5836 "phosphorylase, glycogen, liver, transcript variant 1"
GO:0032052|GO:0070266|GO:0016208|GO:0005886|GO:0005975|GO:0005977|GO:0008184|GO:0019842|GO:0044
281|GO:0042593|GO:0005524|GO:0042803|GO:0005536|GO:0005829|GO:0005737|GO:0008144|GO:0030170|GO:0
009405|GO:0006006|GO:0006015|GO:0002060|GO:0005980|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129500_PI430048170 0.1315818205023511.45494567385566 6.37986322752293
6.27808650081001 5.66485659749282 P P P 5.63921696624114 5.77905625240005
5.34676764878546 P P P LNCV6_129500_PI430048170 mRNA
GGGGGCGGGTGCTGGGGTCTTCTCCAATAAATGGGGTGTCAACCTTACCCAAGGAAAAAA NM_020404 RefSeq
chr11 - 66314486 66317044 CD248 57124 "CD248 molecule, endosialin"
GO:0008284|GO:0060033|GO:0005509|GO:0005578|GO:0050840|GO:0048535|GO:0003674|GO:0008150|GO:0005
737|GO:0016477|GO:0030246|GO:0016021|GO:2000353|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142252_PI430048170 0.00924307479036194 0.3261633106411162.45030095413121
2.05173780495392 1.67797264127339 A A A 3.64145150326294 3.5845391679225
3.88777983196751 P P P LNCV6_142252_PI430048170 mRNA
CGGTGTTTATGTTTTGCTTTGGGGGTTTGTGTGTATGTGTGTAGTTTTTATTTATATTGG NM_001297563 RefSeq chrX
+ 13653105 13665408 TCEANC 170082 "transcription elongation factor A (SII) N-terminal and central
domain containing, transcript variant 2" GO:0006357|GO:0032784|GO:0005634|GO:0003677|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131840_PI430048170 0.5551180874077460.9367441676026686.23941105819991
6.36946921734701 6.76844367773718 P P P 6.55261722871755 6.60752147667313
6.55327960036548 P P P LNCV6_131840_PI430048170 mRNA
GTTGTGGGAATCTTGGTCATTGAATGTAAAGGGACTTAGTAAAGGGTATAGATATTTTTC NM_001303031 RefSeq
chr1 - 37681569 37690595 C1orf109 54955 "chromosome 1 open reading frame 109, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49628_PI430048170 0.00315560313427193 4.35612908222447 7.37912128739354
7.31157955559706 7.39349614394555 P P P 5.47810166657882 5.18913703983306
5.01009442564981 P P P LNCV6_49628_PI430048170 mRNA
CCAGTGGCCACACTGGGATAGGGTGGGGAGGCTGGCAGCCCTCTTTTATAAATATTATAC NM_006841 RefSeq chr3
+ 50205245 50220979 SLC38A3 10991 "solute carrier family 38, member 3"
GO:0005290|GO:0005886|GO:0006865|GO:0055085|GO:0015180|GO:0015297|GO:0005887|GO:0006867|GO:0006
868|GO:0015182|GO:0015186|GO:0006814|GO:0015817|GO:0015808|GO:0006811|GO:0015293 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137160_PI430048170 0.00104234813207603 0.4494876372223687.08875838649965
6.96358735028424 6.75398272887162 P P P 8.07177982779749 8.22192113375986
7.98301875986222 P P P LNCV6_137160_PI430048170 mRNA
GAGCATGGGGCCAGGAAAGTCTGGTAATAAATGTGACTCAGCATCACCCACCTTAAAAAA NM_002386 RefSeq chr16
+ 89917878 89920977 MC1R 4157 melanocortin 1 receptor (alpha melanocyte stimulating hormone
receptor)
GO:0005515|GO:0051897|GO:0009650|GO:0005886|GO:0042562|GO:0030819|GO:0032720|GO:0008528|GO:0007
275|GO:0010739|GO:0019233|GO:0004977|GO:2000253|GO:0035556|GO:0090037|GO:0042438|GO:0005887|GO:0
007187|GO:0045944|GO:0004980|GO:0070914|GO:0043473|GO:0031625 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142799_PI430048170 0.2741233005419931.18111611852215 5.34975042377394
5.21434463895201 5.15984752706935 P P P 5.24494507773373 5.05175781300326
4.65165448256181 P P P LNCV6_142799_PI430048170 mRNA

AACAAGGAAGTGACCAGAGCATTAATGAAAATCTTAGGAAAGGGCAAGTCTGGAGATTGA NM_001004691 RefSeq chr1 - 248323629 248324568 OR2M7 NA "olfactory receptor, family 2, subfamily M, member 7" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141042_PI430048170 0.365309377025061 1.26861776398279 0.422852652251403 0.448307016330884 1.19999725158797 A A A 0.381634819310447 0.385169441592577 0.416151911346162 A A A LNCV6_141042_PI430048170 mRNA
TAGATTCGAAAATGGGAATCTGAATGTCTAGAGTGGAATTCAGGCTTGAGAATACATGAG NM_001098376 RefSeq chr1 + 13315580 13322595 PRAMEF15 NA PRAME family member 15 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132089_PI430048170 0.000390616205213279 1.89775318501117 5.54398840051587 5.74043102017288 5.70590171136938 P P P 4.80359291716248 4.79118485990587 4.62325663789836 P P P LNCV6_132089_PI430048170 mRNA
GTCTTCAAGAAAATATTGCCTATGGCCTGACCCAGAAGCCAACTATGGAGGAAATCACAG NM_000593 RefSeq chr6_GL000256v2_alt - 4244460 4253223 TAP1 6890 "transporter 1, ATP-binding cassette, sub-family B (MDR/TAP), transcript variant 1"
GO:0005515|GO:0002474|GO:0042288|GO:0042825|GO:0042626|GO:0030176|GO:0042803|GO:0005739|GO:0015833|GO:0046967|GO:0019885|GO:0042605|GO:0015197|GO:0015440|GO:0019060|GO:0042590|GO:0006952|GO:0055085|GO:0005524|GO:0016020|GO:0043531|GO:0008152|GO:0005789|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134937_PI430048170 0.419183233753908 0.910094468214691 6.98769631044602 7.47075159397581 7.17772050410878 P P P 7.48288928036045 7.34213676108735 7.2507797097549 P P P LNCV6_134937_PI430048170 mRNA
ATGTGAAATTTTCTCTGCACCTCTGTACAGAGAATACACCTGCCCCTGTATATCCTTTTT NM_004040 RefSeq chr2 + 20447070 20449443 RHOB 388 ras homolog family member B
GO:0005515|GO:0070301|GO:0005886|GO:0007264|GO:0006927|GO:0003924|GO:0005634|GO:0007266|GO:0006886|GO:0032154|GO:0005829|GO:0000910|GO:0007411|GO:0007155|GO:0070062|GO:0051056|GO:0043065|GO:0008333|GO:0006915|GO:0030168|GO:0001525|GO:0045786|GO:0005525|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141207_PI430048170 0.227440141743352 0.567478952285931 0.268678555088636 0.290872399440885 0.420563425387923 A A A 1.05523314438648 1.73176679217842 0.30791002323879 A A A LNCV6_141207_PI430048170 mRNA
CTTTTCTATCTCCATCTCCTCATTAAAAAATACGTACATTTCGAGGTAATGGTATAGGGA NM_001185085 RefSeq chr13 + 24680410 24711785 ATP12A 479 "ATPase, H+/K+ transporting, nongastric, alpha polypeptide, transcript variant 1"
GO:0005886|GO:0055075|GO:0008900|GO:0055085|GO:0005524|GO:0006885|GO:0046872|GO:0016323|GO:0034220|GO:0005889|GO:0008152|GO:0035725|GO:0006813|GO:0005391 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138402_PI430048170 0.249428058831051 0.793665258877872 6.48210588269461 6.33242977932869 6.38308339686927 P P P 6.33327037362748 6.80849439424943 6.98426841831067 P P P LNCV6_138402_PI430048170 mRNA
TTCCCTGTTTCATATCACATGACAGAGAAACCTGTTCTCATGGCATGTAACATCCCTGTG NM_001286050 RefSeq chr11 - 73400477 73598189 FAM168A 23201 "family with sequence similarity 168, member A, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96992_PI430048170 0.00964291623858683 0.765508223961492 5.94522367933939 6.13263551436536 5.94229835857418 P P P 6.43634784554798 6.29890082140597 6.4451870206608 P P P LNCV6_96992_PI430048170 mRNA
AGGGCTTGTCTCATTATAGAGGCACATTGTGGCTGTGTAGGTGAAACCAGAATCTTTTTT NM_032870 RefSeq chr6 - 99399964 99425331 PNISR 25957 "PNN-interacting serine/arginine-rich protein, transcript variant 1"
GO:0005737|GO:0016607|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_135559_PI430048170 0.000957770374815318 0.2456202976364375.03894056555869
4.63574839454416 4.99359405885013 P P P 6.60012105118862 6.935228552331
7.18358890353264 P P P LNCV6_135559_PI430048170 mRNA
AAATCTCCAGTCTGTCTGTTGTACTGGTAATTTAACTCTGTAATGGAATAGTTTGCTGCC NM_001177382 RefSeq
chr4 + 15002673 15070153 CPEB2 132864 "cytoplasmic polyadenylation element binding protein 2,
transcript variant D"
GO:0032869|GO:0071456|GO:0005634|GO:0008187|GO:0035925|GO:1900248|GO:0005737|GO:0000166|GO:0043
022|GO:0043023|GO:0043024|GO:0034599|GO:0005095|GO:0071243|GO:0005844|GO:0034260|GO:2000766|GO:0
000900 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143417_PI430048170 0.186122357706924 1.44063319201711 3.42722225219558
4.05084295850376 4.08920645808746 P P P 3.42963631576549 3.69599010246974
2.81784363536797 P P P LNCV6_143417_PI430048170 mRNA
CAATTCCCTTACAAGTAATGGAGCCGGGGATGGAAATAAATGACGTCCAAGGTCAAAAAANM_015950RefSeq chr6
- 43054028 43059545 MRPL2 51069 "mitochondrial ribosomal protein L2, transcript variant 1"
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0005840 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140065_PI430048170 0.0936636191330759 0.6641878765333556.57911760524138
7.21350460209587 6.82556601859334 P P P 7.10467213128256 7.5031421174949
7.77565099057574 P P P LNCV6_140065_PI430048170 mRNA
TTAGGGTAGTACAGCTGGCATTTGTTTTATAGACTCTTGTCTTTGGAATTGGGGGGAGGG NM_014470RefSeq chr12
- 48857132 48865870 RND1 27289 Rho family GTPase 1
GO:0005515|GO:0005886|GO:0007264|GO:0003924|GO:0005102|GO:0005525|GO:0005829|GO:0016322|GO:0007
162|GO:0005912|GO:0007411|GO:0008152|GO:0007015|GO:0005856 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_92518_PI430048170 0.00226693952843102 1.53171186488683 12.6123178234836 12.822820220643
12.6965910510394 P P P 12.0513415104754 12.221222877356 12.0129218109532 P P P
LNCV6_92518_PI430048170 mRNA
TGAGGAAATCAAGAAAGCTCAAAGGACCGGCGCCTGAGGCTTGCTGTCTGTTCTCGGCAC NM_000858RefSeq chr1
+ 228140227 228148954 GUK1 2987 "guanylate kinase 1, transcript variant 2"
GO:0046054|GO:0046060|GO:0015949|GO:0046034|GO:0017144|GO:0046711|GO:0004385|GO:0019673|GO:0055
086|GO:0044281|GO:0005524|GO:0005829|GO:0006185|GO:0046939|GO:0046037|GO:0034436|GO:0006163 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140175_PI430048170 0.531201673328676 0.83329776015166 0.42468349991787
0.7034125999493140.903936010539037 A A A 1.45014379330327 0.566233251128578
0.675721404081241 A A A LNCV6_140175_PI430048170 mRNA
CTTTATTCACGGCTACTATGCCTGAACTCTATCTGAGCCATTAGAATAATGAATAATTCT NM_014227RefSeq chr22
- 32218475 32255331 SLC5A4 6527 "solute carrier family 5 (glucose activated ion channel), member 4"
GO:0008643|GO:0016021|GO:0006814|GO:0055085|GO:0015293 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_95119_PI430048170 0.147230718639326 1.06999144174279 11.6954797405509 11.6839498480556
11.5757402111599 P P P 11.4810685669314 11.5677556871881 11.6134277479748 P P P
LNCV6_95119_PI430048170 mRNA
GCCTTATCTAAATCACCAGAGACCAAACAAGGACTAATCCAATACCTCTTGGATTTTATT NM_000270RefSeq chr14
+ 20469378 20478006 PNP 4860 purine nucleoside phosphorylase
GO:0046638|GO:0004731|GO:0034356|GO:0044281|GO:0005829|GO:0005622|GO:0006955|GO:0006195|GO:0005
737|GO:0001882|GO:0008144|GO:0042102|GO:0043101|GO:0002060|GO:0005856|GO:0070062|GO:0070970|GO:0
042493|GO:0055086|GO:0006738|GO:0034418|GO:0006148|GO:0006139|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136110_PI430048170 0.0170620606054679 1.0792075277953 0.354761420107941

0.4125324300999790.344156483865215A A A 0.2447714765618410.288497617314896
0.248801026056309A A A LNCV6_136110_PI430048170 mRNA
GTGAGCTACAGATAATTAGAACAGTTATTTGGAATAGAATTAGGGAAGTTTGGACTTGCC NM_023920RefSeq
chr12_KI270904v1_alt - 106631 108268 TAS2R13 50838 "taste receptor, type 2, member 13"
GO:0033038|GO:0007186|GO:0005886|GO:0032467|GO:0008527|GO:0016021|GO:0001580 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_111298_PI430048170 0.55615619331688 1.08944495969947 4.55829171959532
4.28516544947906 4.61800269065286 P P P 4.0239015810617 4.67519350769097
4.33954932103113 P P P LNCV6_111298_PI430048170 mRNA
AACGAGAGAGAGAGCATCTTTCAACAGAATGGTCATGCATAGTGCTGCTTCTCCAACACA NM_014264RefSeq chr4
+ 127880860 127899222 PLK4 10733 "polo-like kinase 4, transcript variant 1"
GO:0005515|GO:0005813|GO:0006996|GO:0007099|GO:0005814|GO:0060707|GO:0005730|GO:0005524|GO:0032
154|GO:0046601|GO:0042802|GO:0005829|GO:0004674|GO:0000086|GO:0006468|GO:0000278 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138152_PI430048170 0.3751074875922021.10745390134315 11.4570944835488
11.0365567918455 11.2559882763326 P P P 11.041269110433 11.1317756299194 11.162660392727
P P P LNCV6_138152_PI430048170 mRNA
GCAGACACACCGAGGATGCGATTTAAAATAAATGCAGATGTTTACTTGGAATGGAAAAAA NM_020385RefSeq chr9
- 133406057 133418096 REXO4 57109 "REX4, RNA exonuclease 4 homolog (S. cerevisiae), transcript variant
1" GO:0006355|GO:0004527|GO:0003700|GO:0090305|GO:0005730|GO:0005634 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137132_PI430048170 0.4546382559135821.30296727679338 2.40460375547529
2.53971294777424 1.49562319660844 A A A 2.53582188471164 1.19355477097515
1.38093230168941 A A A LNCV6_137132_PI430048170 mRNA
TGGAGTCCTCCTGATGGAAGTTGTCACTTATGGGCGGGTGCCATACCCAGGGATGAGCAA NM_001715RefSeq chr8
+ 11494011 11564599 BLK 640 "BLK proto-oncogene, Src family tyrosine kinase"
GO:0050853|GO:0005515|GO:0005102|GO:0005524|GO:0031234|GO:0035556|GO:0030217|GO:0042127|GO:0045
087|GO:0071375|GO:0032024|GO:0004713|GO:0004715|GO:0007169|GO:0038083 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129475_PI430048170 0.17517787095937 0.5471020020781432.46506983092715
2.36882784332221 0.91330675147589 A A A 2.6130696965338 3.05148101035402
3.09881282250083 A P P LNCV6_129475_PI430048170 mRNA
CTGTCCTCTCGACTTCCTTCCTTAGCTTCATGTGAAATAAAAGCTATTCTGGCCAAAAAA NM_001012973 RefSeq
chr10 + 80132501 80145028 PLAC9 219348 placenta-specific 9 GO:0005576 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_144601_PI430048170 0.0140558014795255 1.75784376993507 11.1852154227229
11.4109543343657 11.2545101926391 P P P 10.6792849412758 10.4961014495918
10.2039662674156 P P P LNCV6_144601_PI430048170 mRNA
AGTGATGCTAGTTGGGGCATGCTTTTGTGCACACTCTCTGGGGCTCCAGTGTGAAGGGTG NM_020857RefSeq chr15
+ 40894429 40903975 VPS18 57617 vacuolar protein sorting 18 homolog (S. cerevisiae)
GO:0005515|GO:0019905|GO:0030897|GO:0005770|GO:0005884|GO:0035542|GO:0003779|GO:0046718|GO:0005
765|GO:0005764|GO:0006886|GO:0046872|GO:0006904|GO:0031902|GO:0007032|GO:0030674|GO:0007040|GO:0
005769|GO:0005768. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133721_PI430048170 0.0443875882604324 1.68090810945424 9.73101696695493
10.3415234561699 9.82671152274377 P P P 9.28152037473878 9.35915691622049
9.07326232868354 P P P LNCV6_133721_PI430048170 mRNA
ATGAGGCTGGTGACGTTCAGCCTTTGTCAATAAACCTGTCATGTGCGGATCCTTAAAAAA NM_001039966 RefSeq
chr7 + 1086806 1093815 GPER1 2852 "G protein-coupled estrogen receptor 1, transcript variant
3"

GO:0005802|GO:0005515|GO:0030054|GO:0045599|GO:0019228|GO:0005622|GO:0032024|GO:0005496|GO:0048786|GO:0045745|GO:0005794|GO:0030335|GO:0031966|GO:0045742|GO:0004930|GO:0014069|GO:0014068|GO:0044327|GO:0043280|GO:0042734|GO:0007049|GO:0007186|GO:0005887|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129365_PI430048170 0.0268452947728858 0.816891746164101 8.57515636817432 8.61507869015701 8.76838532848883 P P P 8.93754900271183 8.84134660359013 9.05445558677176 P P P LNCV6_129365_PI430048170 mRNA AACTCAACAACATTCTATAACTGATAACTCCCTGAGCCTCAAGACACCTACTGAGTGTCT NM_001282524 RefSeq chr16 - 28342517 28362860 NPIPB6 NA "nuclear pore complex interacting protein family, member B6" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134574_PI430048170 0.266847179341477 1.08830142044895 6.04447525045738 5.83191354450759 5.81304212835251 P P P 5.70378238658444 5.74239877429269 5.88246021489688 P P P LNCV6_134574_PI430048170 mRNA GGCTTGATTGCTATAAATCAGAATAGAGCATGATGTGGCCACAGAATACAATTCATTTAA NM_004814 RefSeq chr1 - 31259567 31296797 SNRNP40 9410 small nuclear ribonucleoprotein 40kDa (U5) GO:0008380|GO:0005515|GO:0010467|GO:0006396|GO:0005737|GO:0000398|GO:0000375|GO:0005732|GO:0005654|GO:0005682|GO:0071013 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128150_PI430048170 0.0599602038796968 0.574601135863104 10.0903914240231 9.75121486837406 10.0758414045286 P P P 10.3314150520651 10.772474727003 11.1278787116479 P P P LNCV6_128150_PI430048170 mRNA CAGTCTCTCATGGACCTATCTCTATTGTAGAATTATGACTTATGTCTTACTTGCCAAATT NM_001166108 RefSeq chr4 + 168497065 168928457 PALLD 23022 "palladin, cytoskeletal associated protein, transcript variant 1" GO:0005515|GO:0030018|GO:0005886|GO:0005884|GO:0003779|GO:0005634|GO:0015629|GO:0001726|GO:0030027|GO:0005739|GO:0051371|GO:0005737|GO:0007010|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70743_PI430048170 0.0189800360140812 1.29876403352902 8.56360375456016 8.58763995846943 8.74286024447657 P P P 8.25262120489157 8.27573164402089 8.2407525418234 P P P LNCV6_70743_PI430048170 mRNA TGGGCTCCCACAAGAACATTAAAGGATGTCGTTTGGGGATTAAACTCTTTGTTTACTGAT NM_080678 RefSeq chr2 + 237966944 238042782 UBE2F 140739 "ubiquitin-conjugating enzyme E2F (putative), transcript variant 1" GO:0005515|GO:0005737|GO:0016567|GO:0045116|GO:0019788|GO:0016874|GO:0005524|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143873_PI430048170 0.16040130094556 1.018262787056 0.313999446158418 0.313018795715589 0.350676262173618 A A A 0.311479167229342 0.301094685481449 0.287006570085323 A A A LNCV6_143873_PI430048170 mRNA AATACTTTGTTTTGGTACATTTGGTTGTGCTTGTGGGGAAAATAAAAACGCAGAGATCCT NM_005604 RefSeq chr6 + 98834703 98838790 POU3F2 5454 POU class 3 homeobox 2 GO:0005515|GO:0005667|GO:0021985|GO:0001105|GO:0008284|GO:0003700|GO:0071310|GO:0022011|GO:0021869|GO:0021979|GO:0005634|GO:0006351|GO:0042802|GO:0043565|GO:0008544|GO:0014002|GO:0045944|GO:0030182|GO:0021799|GO:0040018|GO:0050770 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136923_PI430048170 0.456805302059453 1.26954166442249 0.298279040225212 1.2507447488682 0.376476728673652 A A A 0.552116021167933 0.250595721112262 0.274559702945378 A A A LNCV6_136923_PI430048170 mRNA AATGGTTCCTGCCTTCAGGAAAGTGAAAGACGCTTAGGCTGTCAACACTTAAAGGAAGTC NM_004822 RefSeq chr17 + 9021541 9244000 NTN1 9423 netrin 1 GO:0005515|GO:0030334|GO:0008284|GO:0042472|GO:0045773|GO:0006915|GO:0005576|GO:0005604|GO:0033564|GO:0005737|GO:0016337|GO:0040023|GO:0007411|GO:0030517|GO:0001764|GO:0060603 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129847_PI430048170 0.00764209514433862 2.3795716421664 7.39747356136276

8.0200223603912 7.69079210838605 P P P 6.25298524958483 6.5854695089096
6.56173930156473 P P P LNCV6_129847_PI430048170 mRNA
AAAGTGATCAACCACTGTTCCTTCTATGGGGCTCTTGCTCTAGTGTCTATGGTGAGAACA NM_001304771 RefSeq
chr16 - 19858970 19885634 GPRC5B 51704 "G protein-coupled receptor, class C, group 5, member B,
transcript variant 2"
GO:0001664|GO:0005886|GO:0009986|GO:0019901|GO:0004930|GO:0061098|GO:0090263|GO:0005730|GO:0005
634|GO:0042593|GO:0030295|GO:0005615|GO:0043231|GO:0007186|GO:0045666|GO:0050729|GO:0010976|GO:0
060907|GO:0045121|GO:0007626|GO:0016021|GO:0043123|GO:0030659|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_58328_PI430048170 0.3310438834033141.05026336807372 0.3340446841061450.336696710775189
0.49785562560034 A A A 0.3200664717232490.2931062013547690.348808249020234 A A A
LNCV6_58328_PI430048170 mRNA
ACATTAGAATGTCAGATGCTTGCATCCATGTGGACCACGATGGGCCTCTAAAAATTGGTG NM_003105 RefSeq chr11
+ 121452202 121633762 SORL1 6653 "sortilin-related receptor, L(DLR class) A repeats containing"
GO:0032091|GO:0005802|GO:0005515|GO:0045732|GO:0030306|GO:2001137|GO:0005783|GO:0008283|GO:0014
910|GO:0006605|GO:0005615|GO:0051604|GO:0001540|GO:0050768|GO:0043407|GO:0045053|GO:0034362|GO:0
005641|GO:0043025|GO:0070062|GO:0032460|GO:0000042|GO:0008203|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129938_PI430048170 0.200982265105867 1.00989733456144 0.33099500495495
0.32598270323368 0.313670605371344 A A A 0.3174099315857650.316169284875762
0.294382154574391 A A A LNCV6_129938_PI430048170 mRNA
TTCTTGTCTATTTTAACCCGTCTGCTTCTAAATGATGTCTAGCTGCTTACCAACTTTAAA NM_032803 RefSeq chrX -
70925579 70931125 SLC7A3 84889 "solute carrier family 7 (cationic amino acid transporter, y+ system),
member 3, transcript variant 1"
GO:0005886|GO:0015181|GO:0006865|GO:0016021|GO:0015809|GO:0055085|GO:0015189|GO:0006811 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132996_PI430048170 0.0254675819113472 2.89337841303371 3.61665403232247
2.80801782550645 2.76318980592015 P A A 1.67178279414719 1.41633768314399
1.65588697684076 A A A LNCV6_132996_PI430048170 mRNA
TAGTACAAACAATAAAAATTCTCATTCCGCATCATCATGCGGTCCATGATGATGAGGCCG NM_002800 RefSeq
chr6_GL000256v2_alt + 4253412 4259100 PSMB9 5698 "proteasome (prosome, macropain)
subunit, beta type, 9"
GO:0005515|GO:0002474|GO:0010467|GO:0090263|GO:0044281|GO:0031145|GO:0005829|GO:0004298|GO:0034
641|GO:0005737|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0005839|GO:0
000502|GO:0043066|GO:0006521|GO:0042590|GO:0051437|GO:0006915|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129208_PI430048170 0.10337867215577 1.05740770147256 0.48164510548636
0.581728684915337 0.513557615016928 A A A 0.4013015179151340.454036531240541
0.480688733024367 A A A LNCV6_129208_PI430048170 mRNA
ATAGACTAATATGGGTAATTACCCTTTGGTTTATCTAAAGTGTGTTCATGATGACTGAGG NM_018937 RefSeq chr5
+ 141100241 141103823 PCDHB3 NA protocadherin beta 3 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140982_PI430048170 0.00754373494976291 1.61080031762951 10.4799762471019
10.4669208886242 10.2583196947639 P P P 9.91394370958346 9.64123275969517 9.5743960774626
P P P LNCV6_140982_PI430048170 mRNA
AGCTGGGGGCACACAGAATAGTTTTGTATAATAAAGTCTCATTTTCAGAGAGCCTAAAAA NM_001243473 RefSeq
chr17 - 19343169 19362733 B9D1 27077 "B9 protein domain 1, transcript variant 1"
GO:0005813|GO:0006996|GO:0060563|GO:0036038|GO:0001701|GO:0036064|GO:0005829|GO:0007224|GO:0032
880|GO:0042384|GO:0016020|GO:0060271|GO:0035869|GO:0008158|GO:0043010|GO:0042733|GO:0001944 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137690_PI430048170 0.4175514807702070.93658158400190412.2042231641811
12.3089784111789 12.038595649491 P P P 12.1673002686497 12.4084803011571
12.2620842228818 P P P LNCV6_137690_PI430048170 mRNA
TCGCAAAGGACCAGGGACACAGCTAACTAACTTATTCAGCTTTGGGCCGATGGGGGTGGGNM_152892RefSeq chr7
+ 102464942 102473165 LRWD1 222229 leucine-rich repeats and WD repeat domain containing 1
GO:0005515|GO:0008327|GO:0005815|GO:0006325|GO:0005634|GO:0035064|GO:0005737|GO:0071169|GO:0005
721|GO:0006270|GO:0003682|GO:0031933|GO:0005664|GO:0016568 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_115574_PI430048170 0.1446954633821730.7033979743611663.74386301546755
4.21991981722937 4.11939408394876 P P P 4.08999424618852 4.66255919767176
4.80178275749529 P P P LNCV6_115574_PI430048170 mRNA
TATCATATGATGAGGTTGTAAATCAGTCTAGTCCAAGCAACTGTACTGTATACTGTGGAG NM_022173RefSeq chr2
- 70209443 70248647 TIA1 7072 "TIA1 cytotoxic granule-associated RNA binding protein, transcript
variant 2"
GO:0042036|GO:0017148|GO:0005515|GO:0048024|GO:0005737|GO:0000166|GO:0010494|GO:0008143|GO:0097
165|GO:0017091|GO:0006915|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74005_PI430048170 0.1034675524461771.36285689266652 4.19283342376172 3.74629950761726
4.18417514367173 P P P 3.57333782435374 3.86863228135494 3.33532944160253 P P P
LNCV6_74005_PI430048170 mRNA
AGTATATCAGAAAATTCTACACAGATGCTGCCTTCCTGCTAAGTGACGCTCATGTCACGG NM_001145642 RefSeq
chr3 - 197671393 197749699 KIAA0226 9711 "KIAA0226, transcript variant 1"
GO:0005515|GO:0005794|GO:0005770|GO:0045806|GO:0010507|GO:0006914|GO:0005764|GO:0005769|GO:0006
897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_22307_PI430048170 0.0524783630598702 1.52024813681368 6.93598429917082
7.47310379093333 7.2499504550742 P P P 6.61466666076022 6.72194664274812
6.55428639118959 P P P LNCV6_22307_PI430048170 mRNA
ACTTCTAGAAGGTCAGCCTGTCCGATTCTTGTAACCTGGAGGTCCCTCCCCATCTGCAGC NM_001265582 RefSeq
chr9 + 128371318 128392016 URM1 81605 "ubiquitin related modifier 1, transcript variant 3"
GO:0016783|GO:0005515|GO:0002098|GO:0034227|GO:0032447|GO:0070062|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140432_PI430048170 0.9263369135471761.00205238114232 10.9558098348965
10.9049114189659 10.9626948138946 P P P 10.8575142720537 10.7749006920641
11.1546214124384 P P P LNCV6_140432_PI430048170 mRNA
GGGATTTTGTACCTGTTTGTACAACTTTGGTCTTGATGGGAAAAATGGAGAATTAAAAAG NM_021807RefSeq chr7
+ 133253066 134065760 EXOC4 60412 "exocyst complex component 4, transcript variant 1"
GO:0005515|GO:0006996|GO:0005886|GO:0032584|GO:0015031|GO:0030165|GO:0005829|GO:0006904|GO:0005
737|GO:0047485|GO:0000145|GO:0016020|GO:0061024|GO:0044267|GO:0017160|GO:0035748 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138608_PI430048170 0.96695214996173 0.9880034717094581.65637463444818
0.5176289527418961.00263963922562 A A A 0.9822676271382951.77190036447955
0.352623692091231 A A A LNCV6_138608_PI430048170 mRNA
GGTTTTAATTAGCAGCAAGTTGTGATCACTTTCCCAGGTGAATAAATCATTTCAAAGCAT NM_001295RefSeq chr3
- 46201708 46208341 CCR1 1230 chemokine (C-C motif) receptor 1
GO:0071791|GO:0005515|GO:0005886|GO:0051928|GO:0019221|GO:0007267|GO:0006887|GO:0007204|GO:0019
957|GO:0006955|GO:0006954|GO:0006935|GO:0004950|GO:0006816|GO:0070374|GO:0007155|GO:0070098|GO:0
006874|GO:0002407|GO:0009611|GO:0045672|GO:0030502|GO:0005887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130347_PI430048170 0.4131116908057821.05274028843571 0.304173283136882

0.3084332042561320.513359355818745A A A 0.3115589931465240.27475344075604
0.326770664678713A A A LNCV6_130347_PI430048170 mRNA
CAACATCTGAGACACTAGGATGAATTATCTTGGATGAGAAAGATGGGCAATCCTGGGCTG NM_144699RefSeq chr1
+ 160151561 160186977 ATP1A4 480 "ATPase, Na+/K+ transporting, alpha 4 polypeptide, transcript variant 1"
GO:0005886|GO:0007283|GO:0030317|GO:0005890|GO:0055085|GO:0005524|GO:0046872|GO:0009566|GO:0034
220|GO:0005887|GO:0042391|GO:0008152|GO:0030641|GO:0015991|GO:0035725|GO:0006814|GO:0006813|GO:0
005391 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137672_PI430048170 0.0363210215433518 1.14487861538074 12.7644833305418
12.9309273932172 12.8223154223769 P P P 12.6135463862479 12.7096101479619
12.6117735468047 P P P LNCV6_137672_PI430048170 mRNA
AATTCTTTCATTCCCTGACCAGTGAGAGGGTTCCTGGGGGAAGTATGGTGAATAAACTGA NM_022077RefSeq chr20
+ 37289647 37317260 MANBAL 63905 "mannosidase, beta A, lysosomal-like, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133570_PI430048170 0.1646830425601190.7991033230027987.86948537358202
7.78022850326645 8.13688160318511 P P P 7.96966683026274 8.29165857704163
8.47555524442376 P P P LNCV6_133570_PI430048170 mRNA
ATGGTGGGGTGGAAGTTTCAGGTGAACAATGGATAACAAAAAGCAAGTTATGGAAGATTG NM_032810RefSeq
chr10 - 87753117 87818160 ATAD1 84896 "ATPase family, AAA domain containing 1"
GO:0030054|GO:0051967|GO:0005634|GO:0031122|GO:0005524|GO:0005739|GO:0008568|GO:0016020|GO:0045
211|GO:0008152|GO:0007613|GO:0007612|GO:0016887|GO:0002092|GO:0005778 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133590_PI430048170 0.000462569652982348 4.10341047773836 7.96359530680999
8.05563755149235 8.33075198925897 P P P 5.98955121735742 6.19214450930682
6.07637424297545 P P P LNCV6_133590_PI430048170 mRNA
TTTTAAGTGATTTCTCAGTGCTGAAAAGCCTGTCCAGGTTTCCTTCCCTTTCCCAAGCCT NM_015993RefSeq chr16
- 57256096 57284672 PLLP 51090 plasmolipin
GO:0043218|GO:0042552|GO:0009611|GO:0045121|GO:0016021|GO:0070062|GO:0006811 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133512_PI430048170 0.0896301313057037 0.393841518906608 0.289157931410454
0.2999822602863020.514589823838932A A A 0.8078953505656371.86123317441307 2.1609254574065
A A A LNCV6_133512_PI430048170 mRNA
GACAGATGCTCATTGTTGAATCTCTTAAATTTTTCCAGCTAACCTCAGTTTGGAAGAAAA NM_004760RefSeq chr7
+ 43583092 43627379 STK17A 9263 serine/threonine kinase 17a
GO:0035556|GO:0043065|GO:0004674|GO:0006915|GO:0006468|GO:0005634|GO:2000377|GO:0005524|GO:2000
271 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130658_PI430048170 0.0199950897980828 2.38366621150223 2.7491249275676
2.22274079012498 3.08214606013595 A A P 1.11252455247244 1.39205349994668
1.82569880540466 A A A LNCV6_130658_PI430048170 mRNA
GGACTCACTTCTTGAAGATATGCTTGTTGCTTTACAACATATGTAAGCTATTCTTTAGCA NM_017933RefSeq chr2
- 229023972 229271341 PID1 55022 "phosphotyrosine interaction domain containing 1, transcript
variant 1"
GO:0070346|GO:2000045|GO:0071398|GO:0005737|GO:0045944|GO:0044320|GO:0071356|GO:0045444|GO:0071
354|GO:2001170|GO:0090298|GO:2001171|GO:0046627|GO:0051881|GO:0010628|GO:2001274|GO:0006112|GO:0
070584|GO:0071345|GO:0090005|GO:0001933|GO:0005654|GO:2000377|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134987_PI430048170 0.9738851474263571.00334353994984 0.441006929068525
0.4800903333577941.77938713704611 A A A 0.3938468761175951.80817805386316
0.431552895713446A A A LNCV6_134987_PI430048170 mRNA
AACGCCATGAGGAAAGTGTGGTGTTGTCAAATACTCCTGAAAAGAAATCAACTTTTCTGA NM_001004124 RefSeq

chr11 + 55638357 55639296 OR4P4 NA "olfactory receptor, family 4, subfamily P, member 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91687_PI430048170 0.6426858275570290.985320077790587 0.4179626617129420.449779864190827 0.360510645771857 A A A 0.4952044605498860.389651792440982 0.406576034036797 A A A
LNCV6_91687_PI430048170 mRNA
ACTCCAGAGCAGATGCCAGCTCAGGAGACTGGGACACTGAAAATTGCCAGACCCTGGAGA NM_001294335
RefSeq chr1 - 31727104 31764063 ADGRB2 NA "adhesion G protein-coupled receptor B2, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64277_PI430048170 0.0941984282254966 0.5523383358085267.38835645824708 6.40732592415083 6.35781981667995 P P P 7.7571028308546 7.89022789247241 7.24707176684834 P P P LNCV6_64277_PI430048170 mRNA
CGCTCATCGCCCGCCACGCTTGAAATGGCGATTGAAAACCTCCAAAAAAGCGAAGGAATC NM_000635 RefSeq chr19 - 5993163 6110653 RFX2 5990 "regulatory factor X, 2 (influences HLA class II expression), transcript variant 1" GO:0003700|GO:0006357|GO:0005634|GO:0000978|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141806_PI430048170 0.00664770317929772 0.5950525656130058.0664402214858 7.97209954538841 7.93818520910033 P P P 8.91198507375548 8.61583945154367 8.68169223579822 P P P LNCV6_141806_PI430048170 mRNA
TTCCCAGCTCTAACAAGGTAACTGGTTAGCATGACATTAAAGCTTGGGCAAGGCTTCAAA NM_144611 RefSeq chr17 + 4143167 4157697 CYB5D2 124936 "cytochrome b5 domain containing 2, transcript variant 1" GO:0016020|GO:0045666|GO:0005576|GO:0020037|GO:0012505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51942_PI430048170 0.00197187715972023 1.70523335812218 6.56038865555783 6.69260387872699 6.53992427056654 P P P 5.90342480948523 5.67529142898704 5.89758697771521 P P P LNCV6_51942_PI430048170 mRNA
AGTCCTATGAGCTCATCCGGAAGATTGAGGCCTACATGGAAGACGACAGGATCTGCTCGC NM_014216 RefSeq chr14_KI270847v1_alt - 54284 230480 ITPK1 3705 "inositol-tetrakisphosphate 1-kinase, transcript variant 1" GO:0052835|GO:0052825|GO:0000287|GO:0043647|GO:0052725|GO:0044281|GO:0003824|GO:0005524|GO:0052831|GO:0052830|GO:0052726|GO:0005829|GO:0007165|GO:0016310|GO:0007596|GO:0032957|GO:0016311|GO:0016853|GO:0047325. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144371_PI430048170 0.4107212259432591.42813531389678 0.417433448141571 1.57833567335035 0.401732758518791 A A A 0.4000033776284120.380861855681873 0.410994457338157 A A A LNCV6_144371_PI430048170 mRNA
TCCCCAATATGTTGATACACAGGTGAGAAAGGGAAGAATTCCTAATAAACTGCTATTACT NM_033656 RefSeq chr21 - 39185477 39313786 BRWD1 54014 "bromodomain and WD repeat domain containing 1, transcript variant 2" GO:0003674|GO:0005737|GO:0006357|GO:0008360|GO:0007010|GO:0005730|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143849_PI430048170 0.4350412500571551.05066169686763 0.303500869847234 0.3102450237081090.51670152494335 A A A 0.3160614570849150.278315468298317 0.331988664567109 A A A LNCV6_143849_PI430048170 mRNA
ATGACGTGCTTACTACTGCAGTGCATTTGTCATTAGTCTTCATGTTAATACAGTACATTT NM_014600 RefSeq chr2 + 31234013 31268394 EHD3 30845 EH-domain containing 3 GO:0005515|GO:0048471|GO:0005886|GO:0072661|GO:0005509|GO:0032456|GO:0005634|GO:0030139|GO:0003676|GO:0005525|GO:0005524|GO:0005737|GO:0007596|GO:0051260|GO:0086036|GO:0055038|GO:0005925|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139624_PI430048170 0.1610165882932641.08861721628474 0.519400831929744 0.5144308439434870.596453845817355 A A A 0.3143001529749570.421298714684344

0.521255481180193 A A A LNCV6_139624_PI430048170 mRNA
GTGGTCCTCTTTATGGTGGCACATGTAAATCTAAAAATACCTGTATGTAATGCTACAAAT NM_032149 RefSeq chr4
+ 99511003 99542303 C4orf17 84103 chromosome 4 open reading frame 17 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_143562_PI430048170 0.00430995705360097 0.652022832885684 10.7330800239492
10.9883150908272 10.8814789229834 P P P 11.4043889766489 11.5487204603809
11.5082927100728 P P P LNCV6_143562_PI430048170 mRNA
GGGGAGGTCCAAGCAGAGTGTTTTATTATTATCGCTTTATGTTTTTGGTTATTGGTTTTT NM_002230 RefSeq chr17 -
41754606 41786712 JUP 3728 "junction plakoglobin, transcript variant 1"
GO:0005515|GO:0030057|GO:0030056|GO:0030018|GO:0090263|GO:0016342|GO:0042803|GO:0086069|GO:0016
337|GO:0032993|GO:0050982|GO:0042127|GO:0002159|GO:0005856|GO:0086005|GO:0070062|GO:0071665|GO:0
045296|GO:0019901|GO:0045294|GO:0019903|GO:0034329|GO:0003713|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144795_PI430048170 0.751191283671935 1.17297622702494 5.33327213305217
4.28879681699095 4.14755079103234 P P P 4.71857424700385 4.3645647285639 4.2641372952176
P P P LNCV6_144795_PI430048170 mRNA
ATGTTCTGCTCTTGTGCCCTTCTGAGCCCACAATAAAGGCTGAGCTCTTATCTTGCAAAA NM_000552 RefSeq chr12
- 5948873 6124670 VWF 7450 von Willebrand factor
GO:0005515|GO:0005783|GO:0005518|GO:0051087|GO:0002020|GO:0042803|GO:0042802|GO:0001948|GO:0019
865|GO:0030198|GO:0031091|GO:0051260|GO:0031093|GO:0007155|GO:0070062|GO:0033093|GO:0031589|GO:0
005578|GO:0009611|GO:0030168|GO:0005576|GO:0001890|GO:0001889|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130904_PI430048170 0.00187277889188116 0.303076065880521 7.08900901996164
7.31207185407101 7.00692756934295 P P P 8.82387167048029 8.88948261816089
8.87807237668212 P P P LNCV6_130904_PI430048170 mRNA
TGCCGCCTGATGGGGCAAAGAAACAAAAAACATTTCTTACTCTTCTGTGTTTTAACAAAA NM_001258355 RefSeq
chr20 + 44401255 44432845 HNF4A 3172 "hepatocyte nuclear factor 4, alpha, transcript variant 7"
GO:0005515|GO:0006629|GO:2000189|GO:0010467|GO:0030308|GO:0003700|GO:0006367|GO:0006805|GO:0008
285|GO:0044212|GO:0003705|GO:0060398|GO:0003707|GO:0070328|GO:0005634|GO:0060395|GO:0042803|GO:0
005737|GO:0045944|GO:0043401|GO:0010470|GO:0007548|GO:0004879|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134636_PI430048170 0.110934208168401 1.24673345233075 10.7490467505865
10.8719618203732 10.8237980468359 P P P 10.7340524686144 10.3988149343787
10.3265985781502 P P P LNCV6_134636_PI430048170 mRNA
ACAGAGAGGCTTTCGACGTGTACCTTGACATCTGTGATGATGATGACTTTTAAGGACCCT NM_007075 RefSeq chrX
- 49074432 49101121 WDR45 11152 "WD repeat domain 45, transcript variant 1"
GO:0006995|GO:0034045|GO:0000422|GO:0080025|GO:0006914|GO:0006497|GO:0032266|GO:0000045|GO:0034
497|GO:0019898|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140744_PI430048170 0.17702831277638 0.805401265679381 12.3916925937409 12.520657145364
12.9285795349044 P P P 13.0161104449846 12.742136177349 13.0554296014199 P P P
LNCV6_140744_PI430048170 mRNA
CCCCAAACCATAAAACCCTATACAAGTTGTTCTAGTAACAATACATGAGAAAGATGTCTA NM_000700 RefSeq chr9
+ 73151730 73170394 ANXA1 301 annexin A1
GO:0005515|GO:0070301|GO:0046632|GO:0005615|GO:0042803|GO:0003697|GO:0042127|GO:0032508|GO:0030
674|GO:0032355|GO:0070062|GO:0033031|GO:2000483|GO:0031966|GO:0009986|GO:0005509|GO:0031394|GO:0
071385|GO:0042063|GO:0043234|GO:0005929|GO:0000733|GO:0005925|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128050_PI430048170 0.00333518986068685 0.557989405550129 10.1448520547871
10.2334182765344 10.4639188807539 P P P 11.0258871377944 11.0283373126465

11.3128445812031 P P P LNCV6_128050_PI430048170 mRNA
CTCACTCAATTCAATGTCACACTTCTGCCTCTTGCAAAATTGCTGGAAAAAGTAATAATA NM_007051 RefSeq chr1
- 50441262 50960264 FAF1 11124 Fas (TNFRSF6) associated factor 1
GO:0045859|GO:0005515|GO:0043130|GO:0008219|GO:0048471|GO:0043065|GO:0051059|GO:0042176|GO:0019
901|GO:0031265|GO:0007253|GO:0019904|GO:0006915|GO:0005634|GO:0005635|GO:0030155|GO:0005829|GO:0
019887|GO:0031334|GO:0031072|GO:0043161|GO:0034098|GO:0031625 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_62893_PI430048170 0.3282533453335940.9127119995045951 5.5462891415546 15.2726288130715
15.1843325388638 P P P 15.5313653661723 15.4636449014733 15.4267084842471 P P P
LNCV6_62893_PI430048170 mRNA
ACATACTGGCCTCTGTGATTACATAGATCAGCCATTAAAATAAAACAAGCCTTAATCTGC NM_000981 RefSeq chr17
+ 39200282 39204727 RPL19 6143 ribosomal protein L19
GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0005730|GO:0006415|GO:0006
412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0000184|GO:0016032|GO:0022625|GO:0
044267|GO:0005925. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116001_PI430048170 0.22727215851052 0.81152611470264 7.07875391769314
7.35597150542354 7.73990974347972 P P P 7.70309066085316 7.61272059657865
7.83129288540454 P P P LNCV6_116001_PI430048170 mRNA
TGGGTACGATCTGTATCTTTTAGCCATGATGGACTGCATGTTGCAAGCCTTGCTGATGAT NM_015626 RefSeq chr17
+ 27294079 27313619 WSB1 26118 "WD repeat and SOCS box containing 1, transcript variant 1"
GO:0035556|GO:0005622|GO:0005515|GO:0008150|GO:0016567 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144677_PI430048170 0.0432216645107767 0.7314990383923169.73235977217935
9.5992094498687 9.32831099170726 P P P 10.1141295019722 9.99972777834049
9.92161043449502 P P P LNCV6_144677_PI430048170 mRNA
AGCCTTTACCCTGTGCTGCCTGGTGCTCCCACCTTCTTGAATTGGGGTTGCCAACAAAGC NM_015201 RefSeq chr8
- 144262045 144291438 BOP1 23246 block of proliferation 1
GO:0070545|GO:0005515|GO:0000463|GO:0008283|GO:0042254|GO:0030529|GO:0051726|GO:0043021|GO:0005
654|GO:0030687|GO:0000448 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97210_PI430048170 0.2152817367302550.8453777445997236.20348419805731 6.3548126247418
6.42589228999926 P P P 6.51001610621482 6.36145829168546 6.81157780724764 P P P
LNCV6_97210_PI430048170 mRNA
CAGAAGAACATTAGGCGAAGAGTTTATGATGCTTTAAATGTGCTAATGGCAATGAACATA NM_001178138 RefSeq
chr3 - 141944427 142149544 TFDP2 7029 "transcription factor Dp-2 (E2F dimerization partner 2),
transcript variant 1"
GO:0003712|GO:0005667|GO:0010467|GO:0003700|GO:0006367|GO:0019904|GO:0003677|GO:0006351|GO:0007
219|GO:0045944|GO:0005654|GO:0007179|GO:0000278|GO:0008134 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133659_PI430048170 0.0166408255552188 0.7643613558249731 1.2210253596936
11.2874657537982 11.2758426256218 P P P 11.5304460862627 11.7393612392154
11.6706223203085 P P P LNCV6_133659_PI430048170 mRNA
TGGCCAGGCCTCCCAGGCAGGTGTTTTATGTTCAGCAATAAAGGTTCTATCCGTAACTGG NM_015117 RefSeq
chr8_KI270816v1_alt - 26296 31490 ZC3H3 23144 zinc finger CCCH-type containing 3
GO:0006378|GO:0003674|GO:0016973|GO:0005634|GO:0010793|GO:0046872 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_134501_PI430048170 0.256395459414757 1.0375858678586 0.449117251109151
0.361204175940329 0.40661993160533 A A A 0.300811523512804 0.347535552787616
0.408227621096325 A A A LNCV6_134501_PI430048170 mRNA
GCAGTAGTTGGGTATTGTTAGCTTTTGAAACAAAAGCCCTACTGGTCTTCTAATTTTGGA NM_006499 RefSeq

chr1 + 236523438 236552979 LGALS8 3964 "lectin, galactoside-binding, soluble, 8, transcript variant 1" GO:0005515|GO:0005737|GO:0016020|GO:0031295|GO:0002317|GO:0030246|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134842_PI430048170 0.0569441494909638 0.566353976918976 3.75273895913806 4.18972284200013 4.59323134986499 P P P 4.65720391083022 5.07537774278061 5.31084008099354 P P P LNCV6_134842_PI430048170 mRNA GTTGTCTTTTTGCTTCTACTGGCCATTGAGAAACTTTGATGATAAAAAAGAACGGTATAG NM_016316 RefSeq
chr2 - 99400474 99490018 REV1 51455 "REV1, polymerase (DNA directed), transcript variant 1" GO:0006260|GO:0005515|GO:0003684|GO:0042276|GO:0006281|GO:0000287|GO:0017125|GO:0003887|GO:0005654|GO:0009411 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118679_PI430048170 0.167557360378243 1.12632516547681 0.648410525998622 0.412427468465854 0.648802569365694 A A A 0.287552928545089 0.414766968595633 0.497392485289701 A A A LNCV6_118679_PI430048170 mRNA GACAACTTTTCACCCGGGCAGGAAGTGTTCTACAGCTGTGAGCCCGGCTATGACCTCAGA NM_000651 RefSeq
chr1 + 207496127 207641765 CR1 1378 "complement component (3b/4b) receptor 1 (Knops blood group), transcript variant S" GO:0030449|GO:0005886|GO:0009986|GO:0001861|GO:0001855|GO:0001851|GO:0005887|GO:0045087|GO:0006958|GO:1900005|GO:0045959|GO:1900004|GO:0045957|GO:0004877|GO:0002430|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_50760_PI430048170 0.135924292617856 1.10871237556847 12.5364587064031 12.5358552383864 12.6283964393678 P P P 12.3361217526254 12.5472668589107 12.363377032094 P P P LNCV6_50760_PI430048170 mRNA TGACGCATTCATCTCTGAGAATGGCTGGGTGGAGGACTACTGAGGTTCCCTGCCCTACCT NM_001293197 RefSeq
chr16 + 680110 682768 STUB1 10273 "STIP1 homology and U-box containing protein 1, E3 ubiquitin protein ligase, transcript variant 2" GO:0032091|GO:0005515|GO:0006511|GO:0004842|GO:0005886|GO:0005783|GO:0016874|GO:0034450|GO:0051879|GO:0032436|GO:0000151|GO:0046332|GO:0042803|GO:0005829|GO:0030968|GO:0051787|GO:0051604|GO:0070534|GO:0005737|GO:0090035|GO:0031398|GO:0051443|GO:0007179|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95151_PI430048170 0.198119486108888 1.05409573000436 0.529666218036267 0.654324936096454 0.535810606624672 A A A 0.471474669907408 0.503784615964266 0.51956236819275 A A A LNCV6_95151_PI430048170 mRNA AACACCCGTGGTGGCTATAAGTGCATTGATCTTTGTCCAAATGGAATGACCAAGGCAGAA NM_031935 RefSeq
chr1 + 185734550 186190953 HMCN1 83872 hemicentin 1 GO:0031012|GO:0030054|GO:0005509|GO:0007601|GO:0005938|GO:0050896|GO:0070062|GO:0005604 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90377_PI430048170 0.932259880631518 1.1291580119807 0.75882691014067 0.397229237361373 2.03977892295949 A A A 1.28560738756752 1.35054778767218 0.398851796685978 A A A LNCV6_90377_PI430048170 mRNA ACTGAGCTTGATTCTAAAGGGGACAGATCTTGAGCAAGGCAAGAAGTGGGATTCAGGAAT NM_003179 RefSeq
chrX - 49187811 49200202 SYP 6855 synaptophysin GO:0005215|GO:0043005|GO:0030054|GO:0048499|GO:0043621|GO:0032403|GO:0042802|GO:0048168|GO:0015485|GO:0048169|GO:0030672|GO:0017075|GO:0042169|GO:0044306|GO:0048786|GO:0071310|GO:0060076|GO:0008021|GO:0006897|GO:0042734|GO:0043234|GO:0030285|GO:0016188|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129468_PI430048170 0.656998737545108 1.62387201845986 3.07747397118868 1.17438180876776 0.483919454147856 P A A 2.10114584024424 0.455144385142855 0.838319840389818 A A A LNCV6_129468_PI430048170 mRNA AGGAGTCAGCAGAGCAAAACCTGCAGGCCAAGAACCTGCCTCTGGATGTGGCCATTGAGT NM_014466 RefSeq

chr1 + 36084074 36088275 TEKT2 27285 tektin 2 (testicular)
GO:0036159|GO:0005737|GO:0031514|GO:0030030|GO:0005874|GO:0005634|GO:0030317 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134585_PI430048170 0.0133246939823035 1.70803980126241 6.73121540219599
6.39435599268364 6.76836736337078 P P P 5.58859526792722 6.03658553248583
5.9427314015569 P P P LNCV6_134585_PI430048170 mRNA
ATGACATTCACTTAGTGACATTATGTGTGACAGAATTAAATGACCGGGAAGAAAACGAAA NM_173474 RefSeq
chr16_KI270853v1_alt + 613599 631834 NTAN1 123803 "N-terminal asparagine amidase, transcript
variant 1" GO:0008344|GO:0005737|GO:0008418|GO:0008152|GO:0007613|GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143243_PI430048170 0.000307698880799332 0.12859282896576 2.74392303124782
2.87884691765933 2.30753014174901 A A A 5.37984988809908 5.7434360668245
5.71642371601024 P P P LNCV6_143243_PI430048170 mRNA
AATCGAAGTTATTTCAGCTAAATGTGCTTCAGCAAAGGTGCATTGGTTGAAACTTAAATG NM_176814 RefSeq
chr7 - 127370042 127392724 ZNF800 168850 zinc finger protein 800
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_130620_PI430048170 0.499395183063455 1.50968427075162 0.373379458544561
1.84438592083788 0.320196707181911 A A A 0.477529337970494 0.438334729941758
0.396478469200055 A A A LNCV6_130620_PI430048170 mRNA
CTCATCGTTTTGAAGATTTGAGGACACTTTAGAGAAACCCTGTGTATGTAAGTCATGTGC NM_198535 RefSeq
chr19 - 9295309 9305119 ZNF699 NA zinc finger protein 699 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_123220_PI430048170 0.365150964007781 0.709127440646681 2.28211020618977
1.02770704939442 0.26838416687224 A A A 1.48531389751364 2.35113863231552
1.81986911144777 A A A LNCV6_123220_PI430048170 mRNA
AAGTAAGAAAAGACCAGTGCCCTCAGTCTGAGCAACGTTGCTGGAGTATTCTACATCCTT NM_000826 RefSeq
chr4 + 157220583 157366074 GRIA2 2891 "glutamate receptor, ionotropic, AMPA 2, transcript
variant 1"
GO:0005515|GO:0030054|GO:0005886|GO:0005234|GO:0035249|GO:0007268|GO:0030425|GO:0008021|GO:0030
666|GO:0007165|GO:0035235|GO:0034220|GO:0005887|GO:0045211|GO:0004971|GO:0032281|GO:0004970|GO:0
005789 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106421_PI430048170 0.0798215909961164 1.46641141766728 6.54787467083414
6.50408818128745 6.14914702322849 P P P 5.94322805237468 6.09937039535206
5.45959047028871 P P P LNCV6_106421_PI430048170 mRNA
TCCTGGGAAATGGGGCGGACAGTGTTTCCTTGACTGACTATTGTGAGCGCCCTCTCTCTC NM_003273 RefSeq
chr11 + 65111853 65116235 TM7SF2 7108 "transmembrane 7 superfamily member 2, transcript
variant 1"
GO:0043235|GO:0006695|GO:0050613|GO:0005887|GO:0005783|GO:0005789|GO:0044281|GO:0055114 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_66468_PI430048170 0.00820964569907135 1.43391089871246 8.35650655170186
8.44494922969508 8.55147666853263 P P P 7.82092171657204 8.08635812020751
7.87870429589419 P P P LNCV6_66468_PI430048170 mRNA
GGAAGAGCCCAGTATTCACATTTTTTCCCCATTTTTCAGAAGCGACATTTCATATATAGG NM_002881 RefSeq chr2
+ 120252837 120294710 RALB 5899 v-ral simian leukemia viral oncogene homolog B
GO:0005515|GO:0032091|GO:0005886|GO:0071902|GO:0003924|GO:0007265|GO:0032092|GO:0001928|GO:0000
910|GO:0000145|GO:0051117|GO:0031625|GO:0009267|GO:0070062|GO:0048011|GO:0005776|GO:0006915|GO:0
030496|GO:0005525|GO:0006184|GO:0007165|GO:0071360|GO:0001934|GO . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_140450_PI430048170 0.0299914428029283 0.185443536826553 0.503328888432546
0.299436603779608 1.99803798379406 A A A 3.57836411631077 3.25665523281406
3.83973423274537 P P P LNCV6_140450_PI430048170 mRNA
AAAGCTTCAAAAGACAGGTTACTGACCATTGAGTGTTTACTATGTACCCAATGTGTATAT NM_014296 RefSeq
chr3 + 15206225 15252916 CAPN7 23473 calpain 7
GO:0005515|GO:0005737|GO:0004198|GO:0004175|GO:0097264|GO:0005654|GO:0010634|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_145523_PI430048170 0.226053105799473 1.63731297016899 2.10257913646913
2.25366283341262 2.68576765742225 A A A 2.49919358834415 0.812684822361094
1.03933998270588 P A A LNCV6_145523_PI430048170 mRNA
ACAAGTGTGGGATGAAGAACCATCATCCTGAACAGCAAAGCTCCCTGCTAAAACTCTCTT NM_001256863 RefSeq
chr4 + 9267618 9269211 USP17L22 NA ubiquitin specific peptidase 17-like family member 22 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129480_PI430048170 0.265059997942744 1.44346601100126 0.394359016918699
0.738942606646766 1.42773130818857 A A A 0.332902704609046 0.441664247790365
0.392631209173267 A A A LNCV6_129480_PI430048170 mRNA
AGTTCTGGGGAGTTCCAACATAATCTAAGGCATATTAGATTATTCCTCCATGATCAGATC NM_001197287 RefSeq
chr14 - 19712903 19714332 OR11H2 NA "olfactory receptor, family 11, subfamily H, member 2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136577_PI430048170 0.0854875254322531 0.560691246003195 2.23506227659403
3.06864011652871 3.07717237238134 A P P 3.73379322918219 3.65413233144954 3.6459943521248
P P P LNCV6_136577_PI430048170 mRNA
AATCTGCCTTGTATTTAGTCAGAGGGCTAGAGGTGCAGATTTCATATTTTCTTAATGAAA NM_170725 RefSeq chr1
+ 248906242 248919146 PGBD2 267002 "piggyBac transposable element derived 2, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138939_PI430048170 0.0358884054789229 0.277009751214686 0.501605422369045
0.860101226221731 2.10004390960178 A A A 3.63934126824293 2.90119321853306
2.84981909475861 P P P LNCV6_138939_PI430048170 mRNA
AAAGATAGTGTCACTGCTGTGGAAAACCTGAACAGACAGTATGATCCAGAATGTCAGGTG NM_006991 RefSeq chr3
+ 44625018 44645260 ZNF197 10168 "zinc finger protein 197, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138784_PI430048170 0.372446242313902 1.03597513450109 0.422740546253889
0.279631226338931 0.310352026675322 A A A 0.270921879990728 0.314788932509826
0.277622253140949 A A A LNCV6_138784_PI430048170 mRNA
TGCAGCTACCCGTAGGAAGACTTCGCGCATATCACTAATAAACCTGAAGTCGTGATGAAA NM_005503 RefSeq
chr15_KI270905v1_alt + 1196591 1393360 APBA2 321 "amyloid beta (A4) precursor protein-binding,
family A, member 2, transcript variant 1"
GO:0010468|GO:0005515|GO:0001540|GO:0035264|GO:0005886|GO:0007268|GO:0007626|GO:0015031|GO:0001
701|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143256_PI430048170 0.128330817441168 1.08752019679491 0.534198758206032
0.709823790225772 0.618052236700744 A A A 0.441381134551754 0.515129753380166
0.545801856678353 A A A LNCV6_143256_PI430048170 mRNA
GCCTAGATGCAGAGAGCTGCTATACATGTGAAAAGTAAAGTGGTGACATGAAACTAGAAA NM_203412 RefSeq
chr1 + 110112439 110113947 UBL4B 164153 ubiquitin-like 4B GO:0005737 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_90066_PI430048170 0.778059170090314 0.981050256977251 12.8903224245166 12.5415720292838
12.8517654030568 P P P 12.80908117805 12.7680655429589 12.8135690794165 P P P
LNCV6_90066_PI430048170 mRNA

AGGGATGATAAAGACACGATCGAGAAACTGAAGGAGAAGAAGCTGACTCCCATCACCTAT NM_018890RefSeq chr7 + 6374494 6403967 RAC1 5879 "ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1), transcript variant Rac1b" GO:0005515|GO:0005802|GO:0045453|GO:0009653|GO:0031529|GO:0043552|GO:0030838|GO:0007411|GO:0021799|GO:0034446|GO:0030334|GO:0042470|GO:0017137|GO:0021831|GO:0019901|GO:0045740|GO:0030168|GO:0001891|GO:0045216|GO:0030027|GO:0030742|GO:0007186|GO:0045087|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143073_PI430048170 0.4420416684258961.82940315675358 3.05032546370412 1.66661935893209 0.705910242673415A A A 2.00318513798776 0.402760007989589 0.867411663362871A A A LNCV6_143073_PI430048170 mRNA
TAAAATTAGTGACTTCGGTTGCTCTGAGAAGTTGGAAGATCTGCTGTGCTTCCAGACACC NM_005372RefSeq chr8 - 56112941 56113982 MOS 4342 v-mos Moloney murine sarcoma viral oncogene homolog GO:0040020|GO:0000187|GO:0005737|GO:0000186|GO:0051296|GO:0046777|GO:0004674|GO:0000165|GO:0006325|GO:0005524|GO:0004709|GO:0000212 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127488_PI430048170 0.0917481572607297 1.2073024610664 8.47381930750235 8.24370422325681 8.56499370551401 P P P 8.05542244967281 8.29189244197404 8.12828343267421 P P P LNCV6_127488_PI430048170 mRNA
CCCATAAAGCCCAATTATGATATGACTCTGACAAATGCTTGTATTGCCTTAAGTCAAAGA NM_000895RefSeq chr12 - 96000752 96035661 LTA4H 4048 "leukotriene A4 hydrolase, transcript variant 1" GO:0019369|GO:0019370|GO:0044281|GO:0004463|GO:0006691|GO:0005829|GO:0005737|GO:0006954|GO:0004177|GO:0006508|GO:0005654|GO:0008233|GO:0008270|GO:0043171|GO:0008237|GO:0070062|GO:0004301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141410_PI430048170 0.938156100345412 1.03800766762925 3.15701990763755 1.74601910904046 2.06135957004031 P A A 2.00187020319665 2.8007430020772 2.28466968639222 A P A LNCV6_141410_PI430048170 mRNA
TAAAACCTAGGTCTTAGGTACATCCTAAAGGGAGCACAGAACCCATCGTTTCACACATGG NM_001146344 RefSeq chr1 - 12824759 12831410 PRAMEF11 NA PRAME family member 11 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129333_PI430048170 0.00293676705592322 2.1848868284128 8.12108250752124 8.28414987549006 7.85245543511252 P P P 6.8255194640016 7.1190023081199 6.94784233388475 P P P LNCV6_129333_PI430048170 mRNA
CAGCAGAGACTTGGGACATTGCCTTTTCTAGCCCGAATACAAACACCTGGACTTAAAAAA NM_001099786 RefSeq chr17 - 64002594 64020634 ICAM2 3384 "intercellular adhesion molecule 2, transcript variant 1" GO:0016337|GO:0005178|GO:0016020|GO:0005886|GO:0030198|GO:0005887|GO:0050776|GO:0001931|GO:0007155|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127465_PI430048170 0.892759098698006 1.01006576672262 7.68972896930068 7.69894550092992 7.45705290058888 P P P 7.31501427022402 7.78232654164311 7.67732852843636 P P P LNCV6_127465_PI430048170 mRNA
ATCATCTCAAGTGGTATTTGTAGCCAAGTGGGAGCTATTTTCTTTTTTGTGCATATAGAT NM_005253RefSeq chr2 + 28392911 28414649 FOSL2 2355 FOS-like antigen 2 GO:0051412|GO:0008219|GO:0007565|GO:0000977|GO:0003700|GO:0006357|GO:0006366|GO:0042493|GO:0043278|GO:0005634|GO:0048146|GO:0051591|GO:0032870|GO:0009612|GO:0003690|GO:0032570|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106580_PI430048170 0.0177761544306679 1.25471159730789 14.1129898881203 14.1414849205329 14.1079624280539 P P P 13.7135896794668 13.7804037480256 13.8816243149226 P P P LNCV6_106580_PI430048170 mRNA
CAACCCTTGACCCAATGACACCAAACACAGTGTTTTTGAGCTCGGTATTATATATTTTTT NM_001286084 RefSeq chr11 - 64316491 64318084 TRMT112 51504 "tRNA methyltransferase 11-2 homolog (S. cerevisiae), transcript variant 3" GO:0005515|GO:0043234|GO:0018364|GO:0008276|GO:0070062 . NA - . NA NA

NA NA NA NA NA NA NA
LNCV6_131643_PI430048170 0.2452828854632620.69112783610602 10.4001130677985
10.4209640986678 10.7480067690721 P P P 10.4511671433135 11.0798904014465
11.4831254121628 P P P LNCV6_131643_PI430048170 mRNA
CCAAAGTCAGATCTGGTCTAGTTAACCTAGAAGTATTTTTGTCTCTTAGAAATACTTGTG NM_002592RefSeq chr20
- 5114952 5126622 PCNA 5111 "proliferating cell nuclear antigen, transcript variant 1"
GO:0005515|GO:0043626|GO:0032405|GO:0008283|GO:0033993|GO:0005634|GO:0032077|GO:0019985|GO:0042
802|GO:0007507|GO:0006271|GO:0005737|GO:0000082|GO:0000083|GO:0006272|GO:0000723|GO:0030855|GO:0
000722|GO:0070557|GO:0005663|GO:0006297|GO:0006298|GO:0043596|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129124_PI430048170 0.7505334870832731.06291899080246 7.27239402055748
7.16828433911819 6.67908796158417 P P P 7.16415069598696 7.07384861144085
6.62978188526676 P P P LNCV6_129124_PI430048170 mRNA
AATGTGAATGACAGCGTCCCCCGTGTGTGGAATGTGGGGATTAAAAGCATTTATCAACCT NM_001001414 RefSeq
chr19 + 39196963 39201882 NCCRP1 NA non-specific cytotoxic cell receptor protein 1 homolog
(zebrafish) NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118535_PI430048170 0.0769673711838157 0.7983463619729176.65723037847512
6.61842774238053 6.41644504621812 P P P 7.01511244963579 6.96680788868067
6.67315138647209 P P P LNCV6_118535_PI430048170 mRNA
GCCATCCCGTCGACTCTCCATTTAAATTGTTTCTCTTTCTGCATAATAAACATTTGTTAA NM_001765RefSeq chr1 +
158289772 158294774 CD1C 911 CD1c molecule
GO:0071723|GO:0030881|GO:0051861|GO:0005886|GO:0005887|GO:0030884|GO:0030883|GO:0048007|GO:0010
008|GO:0002286 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128167_PI430048170 0.0370238193324530.7461274095677544.38728176842539
4.31998082616046 4.08283782146128 P P P 4.7226978024982 4.64694467319487
4.70430456617531 P P P LNCV6_128167_PI430048170 mRNA
ACAGAGGCCAGTACAAAACTCTCAAACAAAAGGAAGTTGACTCTGCTTTGAGGGGAAGGT NM_006582RefSeq
chr1 + 28668727 28715603 GMEB1 10691 "glucocorticoid modulatory element binding protein 1,
transcript variant 1"
GO:0006355|GO:0005737|GO:0003700|GO:0003713|GO:0005654|GO:0005634|GO:0003677|GO:0046872|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140253_PI430048170 0.0942169107064341.29516641810974 5.34376389187096
5.56634878986389 5.52513640461442 P P P 5.32886948732486 5.1124572308394
4.84344139189028 P P P LNCV6_140253_PI430048170 mRNA
AATGAGAAAATGACCATCTAAAGCCTGCCCTTCATTGGTCTGGTTCACGTCTCCAAACCA NM_020406RefSeq chr19
+ 43353658 43363172 CD177 57126 CD177 molecule
GO:0005886|GO:0007596|GO:0031225|GO:0050900|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131307_PI430048170 0.000310281548361078 0.1013151018123721.26077060504464
1.08331618320532 1.69722966733754 A A A 4.24256135080832 4.75769428508397
4.93499315381745 P P P LNCV6_131307_PI430048170 mRNA
GCTGCAAATATGCTTTCCAAGTGCTTTGCTTTCAAATTTTGTTTATGGTGCTTTTTGACA NM_015351RefSeq chr14 +
70641786 70675360 TTC9 23508 tetratricopeptide repeat domain 9 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_99765_PI430048170 0.30879884084016 1.07283099337973 13.7366834379809 13.7994684905107
13.8339903349191 P P P 13.5718197844502 13.6490278375369 13.8339903349191 P P P
LNCV6_99765_PI430048170 mRNA
AGAAAAGCCATCTATGTACTGAACCCGGGACTAGAAGGAAAATAAATGATCTATATGTTG NM_002818RefSeq chr14
- 24143364 24146646 PSME2 5721 "proteasome (prosome, macropain) activator subunit 2 (PA28 beta)"

GO:0010467|GO:0002474|GO:0090263|GO:0044281|GO:0031145|GO:0005829|GO:0034641|GO:0000082|GO:0008537|GO:0016032|GO:0090090|GO:0006977|GO:0070062|GO:0000209|GO:0000502|GO:0043066|GO:0006521|GO:0042590|GO:0051437|GO:0006915|GO:0042981|GO:0051436|GO:0051439|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126937_PI430048170 0.000447301414071908 4.61362856118335 7.86731179465633 8.29602745628651 7.91005893917534 P P P 6.11546150721773 5.71372664955457 5.61642136639171 P P P LNCV6_126937_PI430048170 mRNA CTTCAGCTTGGGTACACACACAGAGGAGACCTCAGCCTCACACCAGAAATATTATTTTTT NM_206539 RefSeq chr6 - 43450351 43456632 DLK2 65989 "delta-like 2 homolog (Drosophila), transcript variant 2"
GO:0045746|GO:0046982|GO:0045598|GO:0005509|GO:0016021|GO:0042803|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130131_PI430048170 0.00904137441976498 1.74751384112758 14.0528535842413 14.4312998643549 14.2881014940573 P P P 13.5569047524379 13.4144467046014 13.4049236061206 P P P LNCV6_130131_PI430048170 mRNA GGAGACCTCCCTTTGTGCTCCCTCACTCCCTAATAAACATGAGTCTGATGTTCTCCAGCC NM_001008395 RefSeq chr7 + 100148906 100154210 LAMTOR4 NA "late endosomal/lysosomal adaptor, MAPK and MTOR activator 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134243_PI430048170 0.53264313402827 1.17670433308605 4.28329798785834 3.58026208549778 3.96373828561169 P P P 2.9462334094829 4.10864279473526 3.90817818722796 P P P LNCV6_134243_PI430048170 mRNA GCACCCGTGGAGAATAAAGAGACCTCAATAAACAAGAATAATCATGTGAACGTGGAAAAA NM_001256012 RefSeq chr17 - 8474204 8630761 MYH10 4628 "myosin, heavy chain 10, non-muscle, transcript variant 1"
GO:0005515|GO:0005516|GO:0031594|GO:0060041|GO:0042641|GO:0008360|GO:0031032|GO:0006887|GO:0007512|GO:0051015|GO:0007411|GO:0043025|GO:0050885|GO:0055003|GO:0005938|GO:0070062|GO:0000281|GO:0005819|GO:0030496|GO:0001701|GO:0030027|GO:0043531|GO:0021592|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135256_PI430048170 0.0623760713348537 0.305814173894179 0.342486505980928 2.21452610273574 1.71489228628568 A A A 3.3538570507483 2.82004427054483 3.67487753561311 P P P LNCV6_135256_PI430048170 mRNA CTAGAGGTGTTATTGTTTTCTGTTTGTGCCAATCATTTGCTTAGTAATTTCTGCTGGGTT NM_001170464 RefSeq chr12 - 96278260 96400588 CDK17 5128 "cyclin-dependent kinase 17, transcript variant 2"
GO:0005515|GO:0004672|GO:0051726|GO:0006468|GO:0005524|GO:0004693 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132846_PI430048170 0.0187730925493350.576106776708933 6.2990673144098 6.09149730671777 6.32194687985674 P P P 6.7335794051786 7.10790263971208 7.22450451937537 P P P LNCV6_132846_PI430048170 mRNA GAAGTGATATATGTCAAATTACATTTCCTACTGCAGTATTTGAGCAGGGACAGTCATTTT NM_001137552 RefSeq chr2 + 237692163 237765915 LRRFIP1 9208 "leucine rich repeat (in FLII) interacting protein 1, transcript variant 3"
GO:0003725|GO:0005515|GO:0005886|GO:0006357|GO:0005634|GO:0005575|GO:0003677|GO:0042803|GO:0006351|GO:0005829|GO:0008150|GO:0005737|GO:0045087|GO:0032481|GO:0005856|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139888_PI430048170 0.139141305079131 0.875017052250589 0.426702015151668 0.340521812232976 0.321845243341181 A A A 0.705887099321081 0.420801977491913 0.527937760811394 A A A LNCV6_139888_PI430048170 mRNA ATCCACTTGCAATGGTAAGAAATTGAAGTATCCTTAAAGGCCATGAAGCCATATGTCCCT NM_001744 RefSeq chr5 + 111224248 111485050 CAMK4 814 calcium/calmodulin-dependent protein kinase IV
GO:0005516|GO:0007268|GO:0033081|GO:0007202|GO:0005829|GO:0046827|GO:0006954|GO:0007173|GO:0043

011|GO:0004683|GO:0070062|GO:0048011|GO:0006996|GO:0007616|GO:0005730|GO:0045670|GO:0005524|GO:0
006913|GO:0007270|GO:0007165|GO:0008543|GO:0045087|GO:0006468|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129614_PI430048170 0.5085623739208 2.09317669646344 0.690503215113702
1.15340802692113 3.44955393552581 A A P 2.08474796516003 0.478822222797311
0.503232364948389 A A A LNCV6_129614_PI430048170 mRNA
GACCCTGCCAAGTGGCACCTGATTTACTCTAGAAAATAAAAGTAGAAAATACTGAGTCCA NM_000336 RefSeq chr16
+ 23302269 23381299 SCNN1B 6338 "sodium channel, non voltage gated 1 beta subunit"
GO:0005515|GO:0007588|GO:0005886|GO:0050699|GO:0034706|GO:0055078|GO:0055085|GO:0015280|GO:0016
324|GO:0034220|GO:0050909|GO:0005887|GO:0050891|GO:0035725|GO:0006814|GO:0050896|GO:0009897|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140154_PI430048170 0.13478279361869 0.700145203855715 0.446732637656575
0.4649458022873050.341510727377617 A A A 1.143216853539 0.499578217083098
1.07401178032057 A A A LNCV6_140154_PI430048170 mRNA
CGAGTAACTATGTTTTTCTATTGGAGACAAAATGAACATCGTAACGTCAAAGTACCAAGA NM_033647 RefSeq chr12
+ 66302554 66343643 HELB 92797 helicase (DNA) B
GO:0006260|GO:0004004|GO:0006396|GO:0005737|GO:0043141|GO:0017116|GO:0005658|GO:0006269|GO:0032
508|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136490_PI430048170 0.00494419698641064 0.4036953842585143.67416928843823
3.327597695881 3.86966745402267 P P P 4.90404945768611 4.6503639144026
5.23444058108664 P P P LNCV6_136490_PI430048170 mRNA
TTAGGCTCTTAATTGTAGTTTAAATTCCAGTACTGCCTACTCAGACCCAAAAGTTTTGTT NM_003111 RefSeq chr2
- 173906458 173965702 SP3 6670 "Sp3 transcription factor, transcript variant 1"
GO:0005515|GO:0000987|GO:0005886|GO:0006366|GO:0030324|GO:0000981|GO:0048706|GO:0005634|GO:0043
353|GO:0048596|GO:0046872|GO:0005737|GO:0003690|GO:0017053|GO:0030183|GO:0030224|GO:0001779|GO:0
030851|GO:0006355|GO:0005794|GO:0006357|GO:0060136|GO:0001892|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130714_PI430048170 0.0126201430903777 0.6490891005117485.52492413687264
5.82207573139445 5.88314867833841 P P P 6.25643814883568 6.34138076267706
6.51550893791715 P P P LNCV6_130714_PI430048170 mRNA
CGTGTTTTGTCATCAGCATCTTTTCTATTAAGAGGTAAAATGTAGTCCTTGTTTGACTCT NM_080632 RefSeq chrX -
119834025 119853028 UPF3B 65109 "UPF3 regulator of nonsense transcripts homolog B (yeast), transcript
variant 1"
GO:0008380|GO:0005515|GO:0010467|GO:0006369|GO:0006366|GO:0031124|GO:0045727|GO:0005634|GO:0003
729|GO:0005829|GO:0005737|GO:0006406|GO:0000166|GO:0000184|GO:0005487|GO:0000398|GO:0005654|GO:0
035145 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131538_PI430048170 0.690144148380566 1.20842429212074 2.60478897293425
2.72278354637854 1.49146687257708 A A A 2.25735052701284 1.94437621778938
2.06820892529565 A A A LNCV6_131538_PI430048170 mRNA
GCAACAGTCCTCTGGTCCCACAGCTGAGTTTATTATACTTGTTTTCTTTTACAAAATTAA NM_144965 RefSeq chr9
+ 127716078 127731600 TTC16 158248 tetratricopeptide repeat domain 16 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_98214_PI430048170 0.0209188135321558 0.471205812763929 0.430493320118054
0.621270609540187 1.08765224618916 A A A 2.21083540317513 1.67231060072083 1.4947585564044
A A A LNCV6_98214_PI430048170 mRNA
AGCGAAAGACCTAATTCAGCGTCTTTTGATGAAAGATCCCAAGAAGAGATTGGGATGTGG NM_004755 RefSeq chr14
- 90870825 91060649 RPS6KA5 9252 "ribosomal protein S6 kinase, 90kDa, polypeptide 5, transcript
variant 1"
GO:0005515|GO:0034142|GO:0005634|GO:0001818|GO:0051403|GO:0035066|GO:0035556|GO:0002756|GO:0005

737|GO:0051092|GO:0006954|GO:0007173|GO:0007411|GO:0045944|GO:0002755|GO:0034138|GO:0070498|GO:0
048011|GO:0006355|GO:0038124|GO:0000287|GO:0038123|GO:0034134|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_59126_PI430048170 0.2316007979705060.8558563468570831 1.8224384516986 11.5832989047735
11.9989127554576 P P P 11.877257864116 11.9749322633411 12.2323459722447 P P P
LNCV6_59126_PI430048170 mRNA
TTCACATTATTCTATGTAAGTGATGACTTGTCAGTGTTCCAGGTGTATCTTAGCTAAAAC NM_001282604 RefSeq
chr12 - 56663340 56688408 PTGES3 10728 "prostaglandin E synthase 3 (cytosolic), transcript variant 5"
GO:0019371|GO:0005515|GO:0019369|GO:0000781|GO:0005697|GO:0003720|GO:0005634|GO:0044281|GO:0005
829|GO:0034605|GO:0007165|GO:0050220|GO:0005737|GO:0000723|GO:0001516|GO:0070389|GO:0005654|GO:0
051082|GO:0006278|GO:1900034|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141927_PI430048170 0.8697612625920920.9450307934920822.97108123502676
2.81906700343831 2.5652661953458 A A A 2.33203513961608 3.11506984825976
3.05804219003769 A P P LNCV6_141927_PI430048170 mRNA
ATACAGTGTGACGTGTACTGTCATCAAGGGGTATGCTCCATGCTTTGAGTCACCAATGAA NM_176798 RefSeq chr11
+ 73269893 73298625 P2RY6 5031 "pyrimidinergic receptor P2Y, G-protein coupled, 6, transcript
variant 2"
GO:0030321|GO:0016323|GO:0045029|GO:0016324|GO:0005886|GO:0045028|GO:0005887|GO:0004930|GO:0007
200|GO:0035589|GO:0014911 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142666_PI430048170 0.1478639358378460.7495804817363010.353404175809198
0.3838472993711020.330587674301156 A A A 0.9505515269166530.40782505106764
0.897980109323942 A A A LNCV6_142666_PI430048170 mRNA
TGTCCAGAAATTTATGGTTGGACCTTGAAGCAAGAGTAGGAAAAAACTAATACCAGAAAA NM_024899 RefSeq chr18
- 12672626 12702777 CEP76 79959 "centrosomal protein 76kDa, transcript variant 1"
GO:0005515|GO:0043234|GO:0005813|GO:0006996|GO:0005814|GO:0000086|GO:0046599|GO:0000278|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143998_PI430048170 0.8427895321796891.04860757370556 5.85448332237606
5.36154730700937 6.04425607306949 P P P 5.49508047941904 5.70560898153225 5.9076733658729
P P P LNCV6_143998_PI430048170 mRNA
ATGGATTGGCTAAAGTCTATTACGACCCCAACAAGAGTCAGAGGGGAGCAAAATTATGTG NM_018034 RefSeq chr5
+ 37379309 37752672 WDR70 55100 WD repeat domain 70 GO:0019899 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_130297_PI430048170 0.7160205145721140.9672343092773510.373341405933662
0.3816574278467350.470215275933155 A A A 0.3318909340969780.644307317299141
0.374952102199233 A A A LNCV6_130297_PI430048170 mRNA
TACAATTGGGTCATTCCCCAGTTTCAACTAACTGGAGCTCCTAAAAGCAGCAGACAGGAA NM_001043229 RefSeq
chr11 + 62665306 62667451 METTL12 751071 methyltransferase like 12
GO:0005739|GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141246_PI430048170 0.4026368291334610.6420330655284794.07499858114399
0.8152077406901783.39454610698264 P A P 4.54226878222229 3.56785491974896
3.35220323856039 P P P LNCV6_141246_PI430048170 mRNA
CCACCTGTTTCCATAACTCCCATAAGTTATTAAATGCATGTGATTCTGCCCTTGAAAAAA NM_139285 RefSeq chr17
- 35744510 35752878 GAS2L2 246176 growth arrest-specific 2 like 2
GO:0008017|GO:0005737|GO:0001725|GO:0051015|GO:0001578|GO:0005874|GO:0007026|GO:0007050|GO:0005
856|GO:0008093 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132225_PI430048170 0.3767651741050641.32759569924791 2.06465778647694
2.12438350342828 2.23689095641275 A A A 2.31093288055406 0.62035743775244
1.80184754923857 A A A LNCV6_132225_PI430048170 mRNA
TACAGCCCCCGTGGGCATGGACCACCTTTATTTTATACAAAATTAAAAACAAGTTTTTAC NM_002403 RefSeq chr1

- 16974503 16980678 MFAP2 4237 "microfibrillar-associated protein 2, transcript variant 2"
GO:0030198|GO:0001527|GO:0005576|GO:0001968|GO:0070051|GO:0030220 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128674_PI430048170 0.1367188373700520.8025313821696277.04058361908052
7.32980605330611 7.00054596051277 P P P 7.67563318387089 7.40731054160781
7.22740463749071 P P P LNCV6_128674_PI430048170 mRNA
TCTCTTTCTCTCTTTAATTTTGGTTTCTCTCAAGCTTCCAAATGGTGCTCAGTGCTCCAA NM_198988RefSeq
chr19_GL949746v1_alt - 368310 370225 LENG9 94059 "leukocyte receptor cluster (LRC) member 9,
transcript variant 1" GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132632_PI430048170 0.5783821803016491.30444343165444 0.393939290812356
0.3789351215565251.61085743989565 A A A 0.815714090330085 0.349761983056923
0.390842096957193 A A A LNCV6_132632_PI430048170 mRNA
AGGGGGGACAAAACGTTGAATGAATAACAACTCATCTTTTCTACAAATGCTTCCTTTGAT NM_004617RefSeq chr3
+ 149474580 149503394 TM4SF4 7104 transmembrane 4 L six family member 4 GO:0016021|GO:0042246
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_9022_PI430048170 0.0245108906228473 1.34166151860708 9.72442420769971
9.98426725036057 9.73174600556805 P P P 9.36875751079731 9.54613211820538
9.25381798486091 P P P LNCV6_9022_PI430048170 mRNA
AGATGGTGCTGTGCTGAGGAAAGGGGATGCAGAGCCCTGCCCAGCACCACCACCTCCTATNM_001286520 RefSeq
chr6 - 44254100 44257571 SLC35B2 347734 "solute carrier family 35 (adenosine 3'-phospho 5'-
phosphosulfate transporter), member B2, transcript variant 9"
GO:0005794|GO:0006805|GO:0050427|GO:0050428|GO:0005975|GO:0044281|GO:0055085|GO:0007165|GO:0000
139|GO:0016020|GO:0046964|GO:0046963|GO:0009405|GO:0004871|GO:0016021|GO:0043123|GO:0030203 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_9470_PI430048170 0.000786849652391327 6.63545946850423 4.16824314818906
4.01052191456923 3.44618903491352 P P P 0.784271820868519 1.35159949752665
1.32591413572998 A A A LNCV6_9470_PI430048170 mRNA
TTCTGCACAAACTAGATTCTGGACACCAGTGTGCGGAAATGCTTCTGCTACATTTTTAGG NM_032413RefSeq chr15
+ 45430528 45433449 C15orf48 84419 "chromosome 15 open reading frame 48, transcript variant 2"
GO:0005739|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129257_PI430048170 0.0812005924628833 1.15344897856866 9.6187169842368
9.6903656138592 9.66144695235316 P P P 9.58216334430389 9.40137621974967
9.36023963472835 P P P LNCV6_129257_PI430048170 mRNA
GAGGAAATACAAATAAAGTTATAGCCCTTTACTGCACGACCATGCTGCCCCCTGAAAAAA NM_001039619 RefSeq
chr14 - 22920510 22929585 PRMT5 10419 "protein arginine methyltransferase 5, transcript variant 2"
GO:0005515|GO:0019918|GO:0010467|GO:0008283|GO:0008168|GO:0006325|GO:0005634|GO:0008469|GO:0005
829|GO:0005737|GO:0001046|GO:0006355|GO:0007088|GO:0003714|GO:0018216|GO:0000122|GO:0034660|GO:0
035246|GO:0000387|GO:0006351|GO:0032922|GO:0034709|GO:0035243|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133728_PI430048170 0.4126019597557680.7433690024415570.263363863730358
0.2806149939527730.388608092244888 A A A 1.32953390452879 0.32636361602814
0.313498954348158 A A A LNCV6_133728_PI430048170 mRNA
CTACAGACAGCTCAACTTTCCTTGATATGTAACACTTTAGGAAAATAACTGCCTTGTAAA NM_001025266 RefSeq
chr3 - 185078049 185153014 C3orf70 285382 chromosome 3 open reading frame 70 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143540_PI430048170 0.999536460939805 0.953643747108245 2.21092676139009
0.3662375270186320.478364235652979 A A A 0.333306882144751 2.35504122071032
0.368843019079388 A A A LNCV6_143540_PI430048170 mRNA
TGAGATAGAGAAGATCGTGGGCTCAGAAATAGACAGTACGGGAAAATTCGCTTTTCCTGG NM_178469RefSeq chr9

- 136754387 136758279 LCN8 138307 lipocalin 8 GO:0006810|GO:0005576|GO:0009725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138959_PI430048170 0.6244050477593470.948094613308511 0.319499515829089 0.2818098438690950.417926306990632 A A A 0.2896947717045720.640660411131342 0.294213448304149 A A A LNCV6_138959_PI430048170 mRNA
AGTGAATTTTTACAAGAAAACTCCCTGTGGGTGCAATGAGTCTGGAAAAGACCATTGAGT NM_018555 RefSeq chr19 + 53520922 53580269 ZNF331 55422 "zinc finger protein 331, transcript variant 1"
GO:0006355|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132287_PI430048170 0.2130890021452861.06472766991567 0.548974637284755 0.7047175081611460.558465368517426 A A A 0.4813194381438310.523553759853209 0.540530900860928 A A A LNCV6_132287_PI430048170 mRNA
GATTGTTTTCCTTGTTAATCTGCTCCAACCACCTGAACATCTAAGTAAACATTTATCTGG NM_021165 RefSeq chr1 + 177171387 177282422 BRINP2 57795 bone morphogenetic protein/retinoic acid inducible neural-specific 2 GO:0071300|GO:0045930|GO:0045666|GO:0007050|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140324_PI430048170 0.00858998000923978 0.6759506854814575.98536035123512 6.10537535476129 6.27963676520757 P P P 6.7434442129699 6.5921063873714 6.73999578870501 P P P LNCV6_140324_PI430048170 mRNA
ATTGATGAGTTAATGTCTTCTGACGTGTTTCCTCTCTTAAGGCTTTCTCCTACCCCGGCA NM_001951 RefSeq chr8 + 85177383 85214521 E2F5 1875 "E2F transcription factor 5, p130-binding, transcript variant 1"
GO:0005515|GO:0010467|GO:0005667|GO:0003700|GO:0006367|GO:0005730|GO:0005634|GO:0003677|GO:0006351|GO:0005737|GO:0045944|GO:0030030|GO:0051726|GO:0009887|GO:0005654|GO:0007179|GO:0000278|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136056_PI430048170 0.4131695263191831.44777464264227 1.67731248700795 0.49570471234687 0.43402242428349 A A A 0.5263449678277470.495674187118156 0.340207006140183 A A A LNCV6_136056_PI430048170 mRNA
TGACCAGGCTTTCTTAATGTAAAACAAAACAGTGTACCAATAGATGATGTGTGTTTACTC NM_198721 RefSeq chr4 - 108810720 109302643 COL25A1 84570 "collagen, type XXV, alpha 1, transcript variant 1"
GO:0005581|GO:0001540|GO:0022617|GO:0005886|GO:0030198|GO:0005887|GO:0030574|GO:0005788|GO:0005576|GO:0016021|GO:0008201|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105635_PI430048170 0.4710382448583730.9200002906674763.36928067322412 3.06695655641895 2.95752094479814 P P P 3.29859634481243 3.07319930104304 3.39621007660941 P P P LNCV6_105635_PI430048170 mRNA
ATCTCTTAATGAGGGACAACCTGTTTGAAATAATAACAAGCTCCAGGACCTTCTACGTAC NM_021623 RefSeq chr8 + 38901234 38973911 PLEKHA2 59339 "pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2"
GO:0005515|GO:0043234|GO:0005737|GO:0016020|GO:0005886|GO:0043236|GO:0005634|GO:0001968|GO:0001954|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138474_PI430048170 0.0674143356913368 0.7857498527909691 1.0720318643963 11.1024499276648 11.3111160278361 P P P 11.669971396508 11.30035637395 11.5465874366317 P P P LNCV6_138474_PI430048170 mRNA
GTGTCCCTAGTCCTAAGCTTTGGTTCTTTAGGGTGACTGTGGTAAGAAGGATATTTAATC NM_002079 RefSeq chr10 - 99396869 99430773 GOT1 2805 "glutamic-oxaloacetic transaminase 1, soluble"
GO:0031406|GO:0006531|GO:0006532|GO:0006533|GO:0006094|GO:0005634|GO:0047801|GO:0044281|GO:0005764|GO:0019551|GO:0005829|GO:0019550|GO:0034641|GO:0005737|GO:0019509|GO:0006103|GO:0006595|GO:0006006|GO:0043679|GO:0004609|GO:0004069|GO:0080130|GO:0070062|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60705_PI430048170 0.4654567444019481.03095513109746 13.3079917545187 13.3132720259485

13.2963681873768 P P P 13.2331531069601 13.1880700199082 13.3590299089919 P P P
LNCV6_60705_PI430048170 mRNA
TTCTGTTGAGATTTTTCCCTCACCTTGCCTCTCAGGCACAATAAATATAGTTATACCACTNM_176783 RefSeq chr14 +
24136157 24138967 PSME1 5720 "proteasome (prosome, macropain) activator subunit 1 (PA28 alpha),
transcript variant 2"
GO:0002474|GO:0010467|GO:0090263|GO:0044281|GO:0031145|GO:0005829|GO:0034641|GO:0005737|GO:0000
082|GO:0008537|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0000502|GO:0043066|GO:0
006521|GO:0042590|GO:0051437|GO:0006915|GO:0042981|GO:0051436|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131541_PI430048170 0.00521580148066562 0.4679303565662845.08030668139132
4.85332278134732 5.04008145371811 P P P 5.84251620713883 6.09053431318033
6.30126580265324 P P P LNCV6_131541_PI430048170 mRNA
TGAAGCTACTGATTGGCAGTGGCTCTACTCTAAAACTGCTTTTTAGCAATTGTATTTTTTNM_001281293 RefSeq chr1
- 200404946 200410058 ZNF281 23528 "zinc finger protein 281, transcript variant 2"
GO:0005515|GO:0010172|GO:0003700|GO:0044212|GO:0003714|GO:0001047|GO:0005634|GO:0000122|GO:0000
978|GO:0046872|GO:0006351|GO:0048863|GO:0043565|GO:0001078|GO:0010629|GO:0005654|GO:0045893|GO:0
045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139193_PI430048170 0.774026625584735 1.32622572923778 2.49941995551736
0.5253202194322240.997224351537647 A A A 1.50201721139771 1.37720150538082
0.509953198812779 A A A LNCV6_139193_PI430048170 mRNA
TTATTGGTTTCCTTTCCCCCAATTAAGGCCAAATAAAGTCGTGAGAACATTACCCATTTA NM_007085 RefSeq chr3
- 120394213 120451071 FSTL1 11167 follistatin-like 1
GO:0005515|GO:0042594|GO:0005509|GO:0005576|GO:0030509|GO:0008201|GO:0005615|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128377_PI430048170 0.359287018555796 1.38871082213869 0.384488076297982
1.46753329941034 1.36167386073474 A A A 0.9304302867717530.741636684098699
0.267849341676992 A A A LNCV6_128377_PI430048170 mRNA
TATAAATCTGCTTAGGAGGCCTGATTCACAGACGCTACAGGATGGAGCGGGGCGCAGGAG NM_001144939
RefSeq chr17 - 4785284 4786434 VMO1 284013 "vitelline membrane outer layer 1 homolog
(chicken), transcript variant 2" GO:0008150|GO:0003674|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_138082_PI430048170 0.562808452918889 1.03673095589722 0.455496355080269
0.648346095534637 0.42743203774159 A A A 0.483805116863749 0.491301389762407
0.408778877321609 A A A LNCV6_138082_PI430048170 mRNA
TGTGAAGTCTTCAGGCTCTTAGAAGGCTCCAGCCTGAGAGAGCCCTTTATTATTGACATT NM_001258205 RefSeq
chr17 - 3510501 3557995 TRPV3 162514 "transient receptor potential cation channel, subfamily V,
member 3, transcript variant 1"
GO:0043235|GO:0005262|GO:0034220|GO:0009408|GO:0005886|GO:0070588|GO:0016021|GO:0042636|GO:0090
280|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135069_PI430048170 0.114213188304997 0.709422382245427 10.0419080429687
9.98355205947439 10.4816443924697 P P P 10.4596541194283 10.4907367465933
11.0233672960127 P P P LNCV6_135069_PI430048170 mRNA
TGGCTAACATTGTTTCTTTCATTCCTTGTTCTAGAGCTAACCACTCTAAAATTGTTTGGT NM_030918 RefSeq chr1 +
151612185 151699083 SNX27 81609 sorting nexin family member 27
GO:0001772|GO:0005515|GO:0001770|GO:0008333|GO:0032266|GO:0006886|GO:0005829|GO:0007165|GO:0005
737|GO:0031901|GO:0016197|GO:0071203|GO:0005654|GO:0005769|GO:0030904 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133813_PI430048170 0.736699369085436 1.13234474947485 2.40194523682011
2.51440096487674 3.35351408508216 A A P 2.69071897572817 2.48040658369167

2.74482275325451 A A P LNCV6_133813_PI430048170 mRNA
ATATAAATATATTTGTGTCATGAACCTCTTATCCCGTTGCTGGAGTTGTAATCTCCATCA NM_020202RefSeq chr3
+ 100334717 100355634 NIT2 56954 "nitrilase family, member 2"
GO:0005739|GO:0005813|GO:0005737|GO:0006107|GO:0006528|GO:0050152|GO:0070062|GO:0006541 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141902_PI430048170 0.0158446580370860.7469345881750421 0.0460190592888 9.8481837017622
9.78424748500981 P P P 10.3131911963407 10.2369602265988 10.3996206195753 P P P
LNCV6_141902_PI430048170 mRNA
CATTTGTGATCAGCATTGTGACTTGGAGATAATAAAATTTAGACTATAAACTTGGCTCCC NM_007359RefSeq chr17
+ 40140253 40172178 CASC3 22794 cancer susceptibility candidate 3
GO:0005515|GO:0006397|GO:0008380|GO:0010467|GO:0048471|GO:0008298|GO:0006417|GO:0042802|GO:0005
829|GO:0008150|GO:0000184|GO:0016607|GO:0030529|GO:0051028|GO:0019899|GO:0035145|GO:0031625 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103578_PI430048170 0.0151692894032270.6584377337731027.50764124660996
7.27316493295783 7.5158814119709 P P P 7.86574656894412 7.98156652083718
8.24445588873447 P P P LNCV6_103578_PI430048170 mRNA
GGTGGCCATGACAACATTTCTGCACGAAAATTTTTAGATGCTGCAAAGCAGACTGAAGAC NM_013326RefSeq chr18
+ 23503469 23531807 C18orf8 29919 "chromosome 18 open reading frame 8, transcript variant 1"
GO:0005765 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138136_PI430048170 0.1550304636717431.03205852459403 0.360424773879135
0.3074047132412250.378023058793631 A A A 0.29423876334587 0.289075055682384
0.326609922081801 A A A LNCV6_138136_PI430048170 mRNA
AGAAACCAGCAGGTGAAACAAGCATTTAAGGATGTTCTGAGAAAGATTTCCCACAAAAAA NM_001005183 RefSeq
chr12 + 55426253 55427192 OR6C76 NA "olfactory receptor, family 6, subfamily C, member 76" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139696_PI430048170 0.5223288925233560.8560102649755580.383823250877961
0.3893500241215550.44378432540169 A A A 0.3230905348308581.0645166143445
0.379494170832537 A A A LNCV6_139696_PI430048170 mRNA
TGTAATACCTGCACATCATAAAATGTGAAAAGGGGGTTATTTTTGTCCAAATACACCCAT NM_178822RefSeq chr3
- 151435989 151458709 IGSF10 285313 "immunoglobulin superfamily, member 10, transcript variant 1"
GO:0001503|GO:0007275|GO:0005576|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140866_PI430048170 0.00044980133353701 2.31019624194779 7.47666480327026
7.54029377589296 7.41640867575325 P P P 6.36418272944696 6.29764441968114
6.14116088388998 P P P LNCV6_140866_PI430048170 mRNA
GGATACAGAACACAAGTCTTGGCACATATGTGATGGAAATAAAGTGTTTTGCAATCTTTA NM_138456RefSeq chr11
- 64987944 64997045 BATF2 116071 "basic leucine zipper transcription factor, ATF-like 2, transcript
variant 1"
GO:0043565|GO:0005515|GO:0003700|GO:0006357|GO:0042832|GO:0005634|GO:0043011|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142164_PI430048170 0.0459207087951787 0.95679702408403 0.324587721976993
0.3474174006956550.335448058959372 A A A 0.4282678372669090.39854848102411
0.371310167945783 A A A LNCV6_142164_PI430048170 mRNA
GGCAAAAGAACCATGAAACTGTATTTTGAGTTTCTATGTTATAGCAGTCAGCAAATCCTA NM_198274RefSeq chr2
+ 88067779 88113383 SMYD1 150572 SET and MYND domain containing 1
GO:0005515|GO:0003714|GO:0010831|GO:0034968|GO:0005634|GO:0035914|GO:0003677|GO:0046872|GO:0006
351|GO:0018024|GO:0007507|GO:0005737|GO:0045663|GO:0006338|GO:0045892 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_53910_PI430048170 0.7264209551751781.04486273623137 6.23129242552242 6.03037816372015
6.41348698084658 P P P 6.46297056635498 5.98257880202799 6.0132877933327 P P P

LNCV6_53910_PI430048170 mRNA
CAATGTGGTCATCTGCATCGCCTTCTACTACTTCTTCTCGTCCATGACGCACGTGCTGCC NM_201649 RefSeq chr1
- 43996482 44017340 SLC6A9 6536 "solute carrier family 6 (neurotransmitter transporter, glycine),
member 9, transcript variant 2"
GO:0015375|GO:0015816|GO:0016020|GO:0005886|GO:0005887|GO:0005328|GO:0006836|GO:0006810|GO:0055
085|GO:0003333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139303_PI430048170 0.3211780401755371.91702933257205 2.85370102528619
2.08076270681948 0.78852424221982 A A A 0.63425776218425 0.582104257152766
1.93706285708559 A A A LNCV6_139303_PI430048170 mRNA
AAGTACAATGTCAACGAAGATGCCAAGGCAGCAATGACTGAACTCAAGTCCTGCAGAGAT NM_001097610
RefSeq chr17_GL383563v3_alt + 77570 78992 SCGB1C2 NA "secretoglobin, family 1C, member 2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128602_PI430048170 0.4491633014124250.9766013667988590.358587708314647
0.4141420291576270.333678339298994A A A 0.4659621047108050.361163648049948
0.380772108210061A A A LNCV6_128602_PI430048170 mRNA
AGTGAAGCTGCTATGGAGCAACAGGAAACTGGTGATAAAGCTCAGCTGAACGACAAAAAA NM_013356 RefSeq
chr22 - 38078136 38083163 SLC16A8 23539 "solute carrier family 16 (monocarboxylate transporter),
member 8"
GO:0005886|GO:0015129|GO:0044281|GO:0050900|GO:0055085|GO:0015727|GO:0016020|GO:0035879|GO:0005
887|GO:0006090|GO:0007596|GO:0015355|GO:0044237|GO:0015293 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128372_PI430048170 0.0586687328209484 0.8140588050298341 0.4214149514208
10.3280559090369 10.488691233953 P P P 10.5472547671953 10.7203819363069
10.8495540544533 P P P LNCV6_128372_PI430048170 mRNA
GTGACCCATGCCGCCTCGTTGGATTGTCGGAATGTAGACAGAAATGTACTGTTCTTTTTT NM_001006634 RefSeq
chr16 - 24919383 25015378 ARHGAP17 55114 "Rho GTPase activating protein 17, transcript variant 1"
GO:0043547|GO:0005515|GO:0051056|GO:0017124|GO:0005886|GO:0007264|GO:0005923|GO:0005829|GO:0005
096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140202_PI430048170 0.0552738207060091 0.7404208577825247.80452181918712
7.45836382051017 7.81594884096394 P P P 8.10753923715105 8.09960336091005
8.19815966656797 P P P LNCV6_140202_PI430048170 mRNA
CTGGTTTTTACACCATCCTAAAGAAAAACTTTACAAGGGTGTTTTGGAGTAGAAAAAAGG NM_030939 RefSeq chr6
- 24704860 24719175 C6orf62 81688 chromosome 6 open reading frame 62
GO:0005622|GO:0008150|GO:0003674 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111214_PI430048170 0.0182714524651223 0.2158110967399771.26389896226019
0.6639718143377272.04367072520399 A A A 3.4977765088767 3.4556088375784
3.93606954260161 P P P LNCV6_111214_PI430048170 mRNA
TTCCAGATGTCTGTATGGTAATTGCATCAGAAATTGCCGTGGATATTGTAAAACATGCCT NM_153365 RefSeq chr4
- 16160504 16226538 TAPT1 202018 transmembrane anterior posterior transformation 1
GO:0007186|GO:0048706|GO:0016520|GO:0016021|GO:0009791|GO:0001701 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_75375_PI430048170 0.3759201073261021.21604137461785 4.38903958569016 4.87229951015901
5.14986591682477 P P P 4.46054992952085 4.51140773596049 4.68297090129134 P P P
LNCV6_75375_PI430048170 mRNA
TTGAAAGCGAAGTTCAGGAAGAGTGACACCAATGAGTGGAACAAGAATGATGACCGGCTA NM_001145525
RefSeq chr5 + 34684506 34832612 RAI14 26064 "retinoic acid induced 14, transcript variant 6"
GO:0005739|GO:0005737|GO:0005654|GO:0005634|GO:0015629|GO:0005938 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142738_PI430048170 0.0164534777923024 0.5801544976202411 0.0261979579654

10.1346090200747 9.69326966568763 P P P 10.6428366256584 10.7950668006029 10.802816558779
P P P LNCV6_142738_PI430048170 mRNA
TCAGGCTTTGGAGCCCCTGAGTTTGAGTTCAATAAAAACTTTATGTGGTAAACGAAAAAA NM_024671 RefSeq chr16
- 30524000 30526589 ZNF768 79724 zinc finger protein 768
GO:0006355|GO:0006366|GO:0005665|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142302_PI430048170 0.344195221725197 1.16470587381533 9.75331565593519
10.1866273885791 10.2386102211536 P P P 9.59618394683098 9.9167309796234
10.0201062352539 P P P LNCV6_142302_PI430048170 mRNA
CCCTGGTTTTGGAAAAATTCCGTGTTCCTGACCCATGTTTAGTTTTTTCCTACCATTTCT NM_002601 RefSeq chr2 -
231732424 231781327 PDE6D 5147 "phosphodiesterase 6D, cGMP-specific, rod, delta, transcript variant 1"
GO:0005515|GO:0017137|GO:0006996|GO:0004114|GO:0072372|GO:0031410|GO:0043086|GO:0005829|GO:0033
124|GO:0008152|GO:0005095|GO:0005856|GO:0007601|GO:0050896|GO:0030659 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141929_PI430048170 0.169967590102935 0.929596540707359 0.270172206257591
0.315583831593421 0.277671385687499 A A A 0.482503956617763 0.384400672517641
0.307564209866301 A A A LNCV6_141929_PI430048170 mRNA
TTCAAAAAATCCGCTAGACATGTCATAAGTTTTAACTGTAATGCCCAGGAAAGGATATCT NM_001278074 RefSeq
chr9 + 134641804 134844842 COL5A1 1289 "collagen, type V, alpha 1, transcript variant 2"
GO:0035313|GO:0048592|GO:0005588|GO:0035989|GO:0046872|GO:0022617|GO:0007411|GO:0030198|GO:0030
199|GO:0030574|GO:0045112|GO:0043206|GO:0007155|GO:0008201|GO:0070062|GO:0001568|GO:0048407|GO:0
043394|GO:0005576|GO:0005604|GO:0031012|GO:0003007|GO:0005178|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137892_PI430048170 0.428928168649086 0.77405565018376 0.349286232953289
0.434749019796959 0.338565801002498 A A A 1.288041735006 0.363692540257154
0.375106361573938 A A A LNCV6_137892_PI430048170 mRNA
AAAGGGGCTGTCAAGAGGACAATCACTCAAAAAGTCTTACAGAAGTTAGATGTGTTTTGA NM_001005280 RefSeq
chr12 + 55221024 55221975 OR10A7 NA "olfactory receptor, family 10, subfamily A, member 7" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137423_PI430048170 0.113953000319629 0.754829173542379 11.193713025959
10.8340704213151 10.642646674404 P P P 11.5352619282553 11.2372407387178
11.1404437012937 P P P LNCV6_137423_PI430048170 mRNA
GACTGTAAATCCTGCCCTGCCCCACTCCCAATAAAAGCTTTGGTGTATAGGCTCAAAAAA NM_020309 RefSeq chr19
- 49429397 49441551 SLC17A7 57030 "solute carrier family 17 (vesicular glutamate transporter),
member 7"
GO:0030054|GO:0005886|GO:0005313|GO:0035435|GO:0007268|GO:0015319|GO:0060203|GO:0007269|GO:0044
341|GO:0015321|GO:0006817|GO:0030672|GO:0035725|GO:0006811|GO:0048786|GO:0007616|GO:0051938|GO:0
044300|GO:0035249|GO:0060079|GO:0014047|GO:0055085|GO:0060076|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140009_PI430048170 0.281463031475887 0.947294843191246 0.253107995384313
0.370992081124733 0.283905992435725 A A A 0.472547904164994 0.365465226242183
0.30175559033148 A A A LNCV6_140009_PI430048170 mRNA
GGAGATTTGACTTTATACATGCATAGATTTGCATTTTACTTTCCCTTTTGAGGCAGCATT NM_213606 RefSeq chr10 -
89430293 89535556 SLC16A12 387700 "solute carrier family 16, member 12"
GO:0035879|GO:0005887|GO:0015129|GO:0005308|GO:0015293 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_60947_PI430048170 0.17495307608491 1.15187855108633 12.0337163632934 11.9538932932173
12.2571339637835 P P P 11.996750337685 11.7184571004821 11.9207956581066 P P P
LNCV6_60947_PI430048170 mRNA

CCTTCCACTTTAACCCACGCTTCAATGAGAACAACAGGAGAGTCATTGTTTGCAATACAA NM_002306RefSeq chr14
+ 55129216 55145430 LGALS3 3958 "lectin, galactoside-binding, soluble, 3, transcript variant 1"
GO:0008380|GO:0005515|GO:2001237|GO:0071677|GO:0070232|GO:0005886|GO:0005743|GO:0005634|GO:0071
674|GO:0090280|GO:0005615|GO:0005737|GO:0019863|GO:0030198|GO:0045806|GO:0030855|GO:0042129|GO:0
005681|GO:0070062|GO:0006397|GO:0001772|GO:0030593|GO:0005578|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133616_PI430048170 0.000621987309849586 0.6346722407361557.23716645214578
7.30660797159934 7.14252950507357 P P P 7.92081224118408 7.81867664987681
7.91694681712988 P P P LNCV6_133616_PI430048170 mRNA
CTGCACAGTGAATGTTTTGATAGGATTCATTACTTGCTCCATAAATGTCAATTTTGGATC NM_145262RefSeq chr3
+ 52287819 52295256 GLYCTK 132158 "glycerate kinase, transcript variant 1"
GO:0005739|GO:0005515|GO:0005737|GO:0006468|GO:0005524|GO:0008887 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134936_PI430048170 0.993547564519293 1.08058229230413 2.17812294319099
3.14474880521306 1.47765703817461 A P A 1.77918021058876 2.75857608209771
2.24810918033858 A P A LNCV6_134936_PI430048170 mRNA
ACAGTGCTTTTTATTACTGTGGGGAGAGGGCAGTGCTAAATAAATTAATCACTACTGATA NM_020400RefSeq chr12
- 6618834 6636131 LPAR5 57121 "lysophosphatidic acid receptor 5, transcript variant 1"
GO:0008150|GO:0003674|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0005575 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127191_PI430048170 0.4696882054821040.9538480058620860.278240503056703
0.4336164853605310.296272945978143A A A 0.5138866954565770.411758678122498
0.282785891683389A A A LNCV6_127191_PI430048170 mRNA
ATGTTCCTGGGATGTTTAATCAAGAGAGACAAAATTGCTGAGGAGCTCAGGGCTGGATTG NM_007232RefSeq chr20
- 62214960 62220267 HRH3 11255 histamine receptor H3
GO:0050679|GO:0043005|GO:0014070|GO:0014061|GO:0005886|GO:0014050|GO:0014053|GO:0045776|GO:0004
969|GO:0007194|GO:0007204|GO:0007269|GO:0014063|GO:0042756|GO:0005887|GO:0007187|GO:0007420|GO:0
043209|GO:0008144|GO:0042755|GO:0007613|GO:0007612 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_142355_PI430048170 0.0468639636683181 0.3771850531451682.19438432511983
3.39774054410443 3.26002932042228 A P P 4.8136970636134 3.75236217993818
4.57749519551666 P P P LNCV6_142355_PI430048170 mRNA
CACAAGATGATGGAGAGGTCATAAAAACTGTGGTAGTATGCTTAGAAACTGTTGATTTAA NM_005622RefSeq chr16
+ 20763989 20797157 ACSM3 6296 "acyl-CoA synthetase medium-chain family member 3, transcript
variant 1"
GO:0042632|GO:0015645|GO:0003674|GO:0005759|GO:0008217|GO:0006633|GO:0005575|GO:0005524|GO:0047
760|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128716_PI430048170 0.000636948781847506 3.25417004007998 6.51290724358752
6.82742896163851 6.92951798161022 P P P 5.261817558114 4.83566634292911
5.06605358918566 P P P LNCV6_128716_PI430048170 mRNA
TGCAGCTGAGTGAATCAGGAAGTGACAGTGATGACTGAAGAAATATTTAGCTATAAATAA NM_018456RefSeq chr3
+ 121835186 121886526 EAF2 55840 ELL associated factor 2
GO:0060770|GO:0005515|GO:0030308|GO:0000977|GO:0016607|GO:0045944|GO:0032783|GO:0006915|GO:0001
228|GO:0008023|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132625_PI430048170 0.3312880559583720.5986700823678560.506257652771546
1.37868020526655 0.603674686204458A A A 2.01159397395051 1.93201353439995
0.491707921844659A A A LNCV6_132625_PI430048170 mRNA
TTGGGATTACGACATTGGAAAATCCAACGATTTCATTGGTGGTGTGGTTCTGGGCATCCA NM_003585RefSeq
chr17_GL383563v3_alt - 86804 120562 DOC2B 8447 "double C2-like domains, beta"

GO:0005544|GO:0005215|GO:0005737|GO:0008104|GO:0005886|GO:0048791|GO:0045956|GO:0031340|GO:0031
201|GO:0032024|GO:0008021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139587_PI430048170 0.2035370522629870.91487136663852 10.8430349896105
10.9342114112348 11.0443778388538 P P P 10.9787179656765 11.0421490919885
11.1850848944298 P P P LNCV6_139587_PI430048170 mRNA
CCTCCTGTATAAGAAGTACCGTATTTTCTGCCCATCATACTTTGTAATAAAACTTGAACA NM_005828RefSeq chr17
+ 63550434 63594281 DCAF7 10238 "DDB1 and CUL4 associated factor 7, transcript variant 1"
GO:0005515|GO:0043234|GO:0005737|GO:0016567|GO:0007275|GO:0005654|GO:0080008|GO:0016363 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145345_PI430048170 0.1632637907193440.6029803299564631.82061624977661
1.90368605160558 2.98468728868499 A A P 2.70207188832199 3.50318940228741
2.87669616522355 P P P LNCV6_145345_PI430048170 mRNA
TCATTTCCAATGTCCTTCTAACTTCTGGCCAATTCCCAGTAGGCTATAGAATAAACAGTT NM_001918RefSeq chr1
- 100186921 100249853 DBT 1629 dihydrolipoamide branched chain transacylase E2
GO:0042645|GO:0005739|GO:0034641|GO:0005759|GO:0043754|GO:0005947|GO:0009083|GO:0044281 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142005_PI430048170 0.2216411288649810.7334099627336514.78464670984891
4.97172517265108 5.1588132415321 P P P 4.91362594029169 5.54308679375346
5.70897689632541 P P P LNCV6_142005_PI430048170 mRNA
GTCAGTAGTACAAAGTGTATATAGGCTGTTTACTCTTACATTTCCTACTGTAAGATACAG NM_052903RefSeq chr15
- 22999176 23039673 TUBGCP5 114791 "tubulin, gamma complex associated protein 5, transcript variant 1"
GO:0008017|GO:0005813|GO:0005737|GO:0000922|GO:0007020|GO:0000086|GO:0005874|GO:0005654|GO:0000
278|GO:0008274|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129006_PI430048170 0.4971792884267231.30118984965051 1.43918693892708
0.4453138908675560.33296696065967 A A A 0.4192909603717530.481167687532559
0.449249516297092A A A LNCV6_129006_PI430048170 mRNA
CAAGCAAGACAAATGAAGACTGAAACCAAGAACGTTATTCTTAATCTGGAAATTTGACTG NM_207339RefSeq chrX
+ 55089051 55092836 PAGE2 203569 "P antigen family, member 2 (prostate associated)" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_139115_PI430048170 0.2756536266334663.19916615837136 0.353773740710177
3.28892711121446 1.71811645218948 A P A 0.2990403054931631.02022043246491
0.292111515698488A A A LNCV6_139115_PI430048170 mRNA
TAGCACCAGAGCCACTGGCCAGATGTAGAAAATAAATAGAAAAATATCTTTCTTTTAGAG NM_005943RefSeq chr6
- 39904257 39927716 MOCS1 4337 "molybdenum cofactor synthesis 1, transcript variant 1"
GO:0032324|GO:0051539|GO:0006766|GO:0006777|GO:0006767|GO:0005634|GO:0044281|GO:0019008|GO:0005
525|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129973_PI430048170 0.0131921227711396 0.3875680257648166.52425075688955
5.93773777582722 6.41789714493689 P P P 7.16276727010136 7.83960860990318
7.93020509778443 P P P LNCV6_129973_PI430048170 mRNA
GCTATTCCAATCTACAACTGGAAGATACATAAAAGTGCTTTGCATTGAATTTGGGATAAC NM_006904RefSeq chr8
- 47773107 47960183 PRKDC 5591 "protein kinase, DNA-activated, catalytic polypeptide, transcript variant 1"
GO:0005515|GO:0004677|GO:0001756|GO:0006303|GO:0035234|GO:0005829|GO:0006302|GO:0031648|GO:0007
507|GO:0018105|GO:0000723|GO:0000724|GO:0045944|GO:0032481|GO:0002360|GO:0002328|GO:0005958|GO:0
002326|GO:0010332|GO:0005667|GO:0033077|GO:0032869|GO:0043065|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143282_PI430048170 0.2577376391693620.7794607822707995.60079336106145
4.95330264863363 4.72986532958246 P P P 5.45593118987302 5.57815950774704

5.47193880388358 P P P LNCV6_143282_PI430048170 mRNA
TCCTGGAGGTTCCCCAGCCCCACTTACCGCGTAATGCGCCAATAAACCAATGAACGAAGC NM_005332 RefSeq chr16
+ 152854 154505 HBZ 3050 "hemoglobin, zeta"
GO:0005515|GO:0043249|GO:0019825|GO:0005833|GO:0005506|GO:0005344|GO:0000122|GO:0070062|GO:0020
037|GO:0015671 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139217_PI430048170 0.3070301619488730.8977688337209250.423518113461027
0.4206947417050790.360529467608475 A A A 0.4257493185482970.766075090038378
0.455342740495935 A A A LNCV6_139217_PI430048170 mRNA
GCAAGTCTTCTTTTCCTCCTTTACCTCATGTTATAATAAAGCTCTGATCTCTGACTCACT NM_178429 RefSeq chr1 +
152675314 152676573 LCE2C 353140 late cornified envelope 2C GO:0031424 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_104339_PI430048170 0.635415972905636 1.06383650786862 14.4825577822017
14.7143491897566 14.9192392006137 P P P 14.3990866252062 14.6749436600491
14.7808123658327 P P P LNCV6_104339_PI430048170 mRNA
CTTGTCTGAAGCTATGGGTCTCTTTTGTTTGATGGTTGCTTTCTTGATTTTGTTTGCCAT NM_001190329 RefSeq chr2
- 175176257 175181762 ATP5G3 518 "ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C3
(subunit 9), transcript variant 4"
GO:0022904|GO:0005215|GO:0042776|GO:0015078|GO:0015991|GO:0005741|GO:0044281|GO:0016021|GO:0045
263|GO:0044237|GO:0008289|GO:0005753 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128043_PI430048170 0.120484209982486 0.701023630898921 4.42533139821818
3.88448705289326 4.592129789944 P P P 4.87358158752242 4.74665834832231
4.90504300384824 P P P LNCV6_128043_PI430048170 mRNA
CAGAGTTCCAGTCATTATTGTTACATCATGTTTGCAGAAACCTTGTCTTATTTAGTGTCT NM_017935 RefSeq chr4 +
101790606 102074812 BANK1 55024 "B-cell scaffold protein with ankyrin repeats 1, transcript variant 1"
GO:0051898|GO:0042113|GO:1900165|GO:0050869|GO:0045947|GO:0043410 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139793_PI430048170 0.0103119333827392 0.4239160549644527.09484093736333
7.15009725228894 7.32551399172446 P P P 8.15462151791297 8.34321259219521
8.73529104010154 P P P LNCV6_139793_PI430048170 mRNA
CTCCCTACCCAAAATGTTTTTCTTCCTGTCTGAAAATGGAACTAATTTGTCTTATTCGTG NM_015137 RefSeq chr8 +
131904108 132013639 EFR3A 23167 EFR3 homolog A (S. cerevisiae) GO:0005622|GO:0005886|GO:0070062
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140194_PI430048170 0.0236097696339523 0.45821271604414 3.10553108579324
2.64457170446901 2.76896343440156 P A A 3.49639148713393 4.29402026676988
4.03598820287721 P P P LNCV6_140194_PI430048170 mRNA
TGTGGATAAAATGAGGTTGGCAGTGAAGAAAATTAAAAACAGCCTCATTCATGTAACTGG NM_018638 RefSeq chr12
+ 22625141 22690674 ETNK1 55500 "ethanolamine kinase 1, transcript variant 1"
GO:0004305|GO:0016310|GO:0006646|GO:0005737|GO:0016020|GO:0005886|GO:0005654|GO:0044281|GO:0006
644|GO:0005524|GO:0046474|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72914_PI430048170 0.4492495437707361.17080496478072 2.71051453215854 3.02311915049069
3.24242573383711 A P P 2.24290142962039 2.92382129885241 3.05225975025114 A P P
LNCV6_72914_PI430048170 mRNA
ATGGCAGTTCTGATCAACAATAAAGCTTGTGGCAAAATTCCTGTGCCCCAACAAGTTGCC NM_015340 RefSeq chr3
+ 45388582 45548836 LARS2 23395 "leucyl-tRNA synthetase 2, mitochondrial"
GO:0005739|GO:0010467|GO:0002161|GO:0005759|GO:0006450|GO:0004823|GO:0006429|GO:0005524|GO:0006
418|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140217_PI430048170 0.1340594548815220.93004625199344 0.489127056195515
0.5005777296753860.365540627277509 A A A 0.62422101670815 0.536832408242966
0.509409554461223 A A A LNCV6_140217_PI430048170 mRNA

GCTATTCTCACTCTGAGAACTCTCCAATAACAATTTCTTTTCCACAGTTAACAACAAAGT NM_020721 RefSeq chrX
- 119078634 119150579 KIAA1210 57481 KIAA1210 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140896_PI430048170 0.2637984151251171.62860901734364 3.45769227605391
3.86764084058249 4.17142275639738 P P P 4.11067852698149 2.4581454293233 2.0007903202586
P A A LNCV6_140896_PI430048170 mRNA
CTTTATGCCAGAGTGGTTTACCCCATTCACAAAATTTCTTATGCATACATTGCTATTGAA NM_001130675 RefSeq
chr4 - 140388452 140427661 CLGN 1047 "calmegin, transcript variant 2"
GO:0007338|GO:0006461|GO:0044183|GO:0006457|GO:0005783|GO:0005509|GO:0005789|GO:0051082|GO:0016
021|GO:0005635|GO:0007339 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134184_PI430048170 0.0290540988613257 1.11731957089746 9.60515300731574
9.64414593198793 9.62608331687518 P P P 9.43407175151849 9.53018658330927
9.42899225152405 P P P LNCV6_134184_PI430048170 mRNA
TCAATTAGTCTCAGTTCTCTTAATTTTCAGGAAGAAAGGGAAATTGCAGCCCCTCAGCCC NM_004649 RefSeq chr21
+ 44133611 44145723 C21orf33 8209 "chromosome 21 open reading frame 33, transcript variant 1"
GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137854_PI430048170 0.4663223336553641.95113577627349 0.3647373289846072.404675912475
0.331309342919153 A A A 0.4357171264101970.4274102246844020.401923307959693 A A A
LNCV6_137854_PI430048170 mRNA
GTGGCAGGCGTTTTAGGGAATCTTTTACTTGATAAATGTCTCAGTGAGAAAGCAGTAAAG NM_001001968 RefSeq
chr14 - 20640695 20641691 OR6S1 NA "olfactory receptor, family 6, subfamily S, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144419_PI430048170 0.0379478891027347 0.8230336269673831 0.8308081792681
10.7029873268906 10.5810877296289 P P P 10.9968642981084 11.0599505268285
10.9077680934091 P P P LNCV6_144419_PI430048170 mRNA
GAGACCTTCCCTTCAAATCTAAAATTGGCAAAAAGTCACTTAAAATAGTGGACTTCTGTA NM_033271 RefSeq chr14
+ 105248541 105251093 BTBD6 90135 BTB (POZ) domain containing 6 GO:0000932 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145623_PI430048170 0.3400202508261940.8517226332669897.57418503702772
7.32069481505004 7.10681869898934 P P P 7.74364791897113 7.69689034867625
7.24281493151617 P P P LNCV6_145623_PI430048170 mRNA
GTCTAGTTTGTGTTCAAAATGTCAGAATAAACACAGAATAAATGTTCCCACGGCCAAAAA NM_006676 RefSeq chr9
+ 129835416 129881838 USP20 10868 "ubiquitin specific peptidase 20, transcript variant 1"
GO:0071108|GO:0005515|GO:0005813|GO:0016579|GO:0048471|GO:0001664|GO:0004843|GO:0006897|GO:0004
197|GO:0008277|GO:0070536|GO:0061136|GO:0008270|GO:0043161 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_137547_PI430048170 0.2019948977025130.9580267998176280.245707051949453
0.2629817064274370.345832590788824 A A A 0.3988284529470680.32625907904393
0.315588024181469 A A A LNCV6_137547_PI430048170 mRNA
GCCAAGCTACCTTGCAAGATTCTTCAAAGGATTTAAACATTTTAAGTGGGAGAATAAGTA NM_005893 RefSeq chr9
+ 36169391 36171334 CCIN 881 calicin
GO:0033150|GO:0007275|GO:0005634|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129718_PI430048170 0.1402180297247181.08575120511222 0.503867537127532
0.6477772951748290.58434970610119 A A A 0.3670153807033880.476546903199163
0.534941763106899 A A A LNCV6_129718_PI430048170 mRNA
CCTGTGTTTGTAGAGAACTCCCTTATACAGAGTTTTGGTTCTAGTTTTATTTCGTAGATT NM_005546 RefSeq chr5 +
157180895 157255099 ITK 3702 IL2-inducible T-cell kinase
GO:0005515|GO:0050853|GO:0050852|GO:0007202|GO:0001816|GO:0046872|GO:0005829|GO:0035556|GO:0005

911|GO:0042127|GO:0032609|GO:0038083|GO:0005102|GO:0005524|GO:0001865|GO:0031234|GO:0002250|GO:0
007165|GO:0006968|GO:0042110|GO:0045087|GO:0032633|GO:0007169|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_123709_PI430048170 0.102095460051031 1.12575502273498 12.5702548252712
12.4882218805368 12.6985925396036 P P P 12.4480551160795 12.3931688964629
12.4104494522899 P P P LNCV6_123709_PI430048170 mRNA
AGGTTGTGGTGCTAGTTTCTCTAAGCCATCCAGTGCCATCCTCGTCGCTGCAGCGACACA NM_006098 RefSeq
chr5 - 181236927 181243906 GNB2L1 10399 "guanine nucleotide binding protein (G protein), beta
polypeptide 2-like 1"
GO:0017148|GO:0005515|GO:0030308|GO:0042803|GO:0005080|GO:0043025|GO:0005856|GO:0042169|GO:0070
062|GO:0032464|GO:0030335|GO:0019903|GO:0051343|GO:0030496|GO:2001244|GO:0001891|GO:0008656|GO:0
001649|GO:0043547|GO:0007049|GO:0048511|GO:0019899|GO:0051302|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135493_PI430048170 0.513245025795471 0.827350388326175 2.14759184440452
1.04739064513163 2.30872821099937 A A A 1.87618739328802 2.61278874089015
2.019361509735 A P A LNCV6_135493_PI430048170 mRNA
GAACATTGGTTTGTGAAGGAAAAACAGATTATCTAAAGCCATCTCTATGTTTCTGTTCAG NM_020921 RefSeq
chr14 - 50719762 50831121 NIN 51199 "ninein (GSK3B interacting protein), transcript variant 2"
GO:0005515|GO:0051642|GO:0005813|GO:0000922|GO:0090222|GO:0005814|GO:0005874|GO:0005509|GO:0005
730|GO:0034454|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135208_PI430048170 0.125668270775707 1.94200010264562 2.40554069821441
2.06525043223016 3.27248464823096 A A P 2.04502218159635 1.02514753723097
1.88643321828201 A A A LNCV6_135208_PI430048170 mRNA
GGGCCAGAAAAATCTTGTACAGAATAATGATTTCTCCTAATGTAAATCTTGGAAAGGGTT NM_052864 RefSeq
chr4 - 112275625 112285903 TIFA 92610 TRAF-interacting protein with forkhead-associated
domain GO:0005515|GO:0007249 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53346_PI430048170 0.000400564110726976 0.47445937897411 10.8468158324077
11.0038230968492 10.7567207359137 P P P 11.8283316871483 12.0532153296949
11.9548802285759 P P P LNCV6_53346_PI430048170 mRNA
ACCCGGCAGGGAGATTTCGGTTTTGAGGTTTCTAAATACATTAAAGTTATTTCTTAAGAA NM_014448 RefSeq
chr1 + 3454582 3481113 ARHGEF16 27237 Rho guanine nucleotide exchange factor (GEF) 16
GO:0005515|GO:0030971|GO:0051056|GO:0048011|GO:0043065|GO:0007264|GO:0030165|GO:0032863|GO:0097
190|GO:0032864|GO:0005829|GO:0060326|GO:0017048|GO:0005089|GO:0090004 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_145205_PI430048170 0.817371050958927 0.913697996261907 0.729812174841244
0.800830752413021 0.819391606379577 A A A 0.64941189633479 0.510415110175721
1.41146448206201 A A A LNCV6_145205_PI430048170 mRNA
TGCTCTGTACCTGTCAAAAATTTTGAATGTACACCACATGCTATTGTCTGAACTTGAGTA NM_030774 RefSeq
chr11 - 4680170 4697846 OR51E2 81285 "olfactory receptor, family 51, subfamily E, member 2"
GO:0071398|GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0043401|GO:0003707|GO:0038
023|GO:0016021|GO:0045777|GO:1900135 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_134688_PI430048170 0.0386416669043568 0.371135768718884 6.7184248768136
6.51533328411266 6.82011563565011 P P P 7.47522826418528 8.16266985363437
8.53207690583133 P P P LNCV6_134688_PI430048170 mRNA
GCTAAGGCAACGTTAGTTTCTCTTACTCTGCTTTTTTCTAGTAAAGTACTACATGGTTTA NM_000875 RefSeq chr15
+ 98648538 98964530 IGF1R 3480 "insulin-like growth factor 1 receptor, transcript variant 1"
GO:0005515|GO:0005158|GO:0030879|GO:0030010|GO:0043560|GO:0007409|GO:0042802|GO:0043231|GO:0046
328|GO:0046777|GO:0033197|GO:0038083|GO:0043559|GO:0005520|GO:0030335|GO:0032467|GO:0045740|GO:0

045840|GO:0014065|GO:0051389|GO:0043235|GO:0008544|GO:0007420|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128857_PI430048170 0.0508368493394929 0.664243551409203 5.77478811362456 5.26773303780123 5.74048764391544 P P P 5.9558850200567 6.18517310558741 6.42750245300098 P P P LNCV6_128857_PI430048170 mRNA CAAGGCATAAACTTTTGTACTAGCTGTCTCCATATTATGTTCAATAAATTCTGTGCTCTG NM_004738 RefSeq chr20 + 58389118 58451100 VAPB 9217 "VAMP (vesicle-associated membrane protein)-associated protein B and C, transcript variant 1"
GO:0008017|GO:0005515|GO:0005783|GO:0044281|GO:0042803|GO:0030968|GO:0045070|GO:0006665|GO:0046725|GO:0005794|GO:0046982|GO:0090114|GO:0030148|GO:0006874|GO:0048487|GO:0070971|GO:0006888|GO:0000139|GO:0019048|GO:0005789|GO:0016021|GO:0006987|GO:0019899|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130760_PI430048170 0.740133133618952 0.959955077858112 4.12631571007604 4.23264272298955 4.61490886341738 P P P 4.40199173218088 4.1938687081654 4.57649754860855 P P P LNCV6_130760_PI430048170 mRNA GGAAACCCTTTTGGAATTAGAATTCTTGTTCTGATGCTGAACTATTTGGTAATAAAGTGC NM_001268 RefSeq chr13 - 48488962 48533256 RCBTB2 1102 "regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2, transcript variant 2" GO:0005087|GO:0032853 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132612_PI430048170 0.862895402071261 0.949009083310653 1.61446391725804 0.549446897255134 0.328853205597548 A A A 1.63839185168538 0.609406851878799 0.539376222829644 A A A LNCV6_132612_PI430048170 mRNA ATGGATGGCAGGGGAGAGTGTTCCTTTTGTTCTTAACTAGTTTAGGGTGTTCTCAAATAA NM_016186 RefSeq chr14_KI270847v1_alt - 1397874 1407586 SERPINA10 51156 "serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10, transcript variant 1"
GO:0010951|GO:0060046|GO:0007596|GO:0004867|GO:0008201|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133378_PI430048170 0.0103803327439467 0.386781652295975 4.8093554455148 4.16126977032073 4.7669659464181 P P P 5.7887247700265 6.13896092034879 5.98625857952147 P P P LNCV6_133378_PI430048170 mRNA CTGGTACAGTGTAGTTTTTCCCCTTTCATTTGAATAAAAGCATGGCACCAAATGAAAAAA NM_001297707 RefSeq chr1 + 200739557 200860707 CAMSAP2 23271 "calmodulin regulated spectrin-associated protein family, member 2, transcript variant 1"
GO:0005515|GO:0005813|GO:0005737|GO:0051011|GO:0000226|GO:0033043 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130085_PI430048170 0.000658488342058836 0.322561481399175 4.44225260564729 4.27838527506173 4.55665349708476 P P P 5.81953905548995 6.13912485872379 6.20088003905587 P P P LNCV6_130085_PI430048170 mRNA CTCTTCAAGAACAATGAATGTCTTCATTAAATCATCTTTTGTGGGAGAGCTTTTGGTTTC NM_139281 RefSeq chr5 + 111092171 111130502 WDR36 134430 WD repeat domain 36
GO:0008150|GO:0030516|GO:0001895|GO:0006364|GO:0032040|GO:0005730|GO:0005575|GO:0034388|GO:0007601|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144042_PI430048170 0.523226494785275 0.960420533687358 10.2061362304428 10.4697233777355 10.3556473140783 P P P 10.344312554301 10.4001130677985 10.4711173321906 P P P LNCV6_144042_PI430048170 mRNA TGACACTTGTGAAAAAGCTTGTAAGAAAGCCCCTCCCTTTTTTCTTTAAACCTTTAAATG NM_032569 RefSeq chr16 - 4803202 4847302 GLYR1 84656 glyoxylate reductase 1 homolog (Arabidopsis)
GO:0004616|GO:0005737|GO:0051287|GO:0005794|GO:0005654|GO:0035064|GO:0006098|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_127830_PI430048170 0.0437881249210608 0.6365238727402 6.36526834143955 6.8494547694635 6.936648715011 P P P 7.3235288984958 7.24723146667134 7.57765704786414 P P P LNCV6_127830_PI430048170 mRNA TGCAGTCTTAAAATTACACTTCTTGACTTCTGAATGTCTCTTATTTGCGTGCACTGACAA NM_153687 RefSeq chr12 - 98624251 98645051 IKBIP 121457 "IKBKB interacting protein, transcript variant 1" GO:0005515|GO:0016020|GO:0010165|GO:0005783|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79940_PI430048170 0.190398788346482 0.975462613184922 0.361148672097988 0.390057354799708 0.324209499259589 A A A 0.393370983968643 0.410241773432225 0.379921630803594 A A A LNCV6_79940_PI430048170 mRNA CACAGCTTATCTGTTCAGTGTGAGAGTCACTACTATATAGTGCAAGAGAAATTATTAGAA NM_001193502 RefSeq chr8 - 66946500 66962590 TCF24 NA transcription factor 24 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139428_PI430048170 0.0758449050094759 0.859277212271546 4.12445069821061 4.11479024781651 3.93952546239425 P P P 4.14234399731331 4.36288024217326 4.32777010601587 P P P LNCV6_139428_PI430048170 mRNA GAACCATGCTGCTTGGGAATGTGTGTGATGCCTTCTGTCAATAAAAACACATTACACAAA NM_080879 RefSeq chrX - 103499752 103519489 RAB40A NA "RAB40A, member RAS oncogene family" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135284_PI430048170 0.473536469130649 1.29339747522638 0.407051580345951 1.37303787722895 0.35022978623623 A A A 0.474286855376862 0.380829724512584 0.402781651322957 A A A LNCV6_135284_PI430048170 mRNA CACACCACAGATCCTCTTTTTAAAGCAGGTAATAAAGTAGCTTTTTCCTTTTGAAACATC NM_019018 RefSeq chr5 + 14581781 14616178 FAM105A 54491 "family with sequence similarity 105, member A" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71278_PI430048170 0.00478998690792229 0.751456742873706 13.995391032046 13.8371548408435 13.9515550431602 P P P 14.2359186121814 14.4167767497983 14.3667193788746 P P P LNCV6_71278_PI430048170 mRNA GTGGTGGACGGACTGTAATTGATAGATTGATTATGGAATTAAATTGGGTACAGCTTCAAA NM_001127695 RefSeq chr20 + 45890951 45898819 CTSA 5476 "cathepsin A, transcript variant 2" GO:0006665|GO:0006687|GO:0005783|GO:0044281|GO:0043085|GO:0005764|GO:0006886|GO:0043231|GO:0004185|GO:0016020|GO:0004180|GO:0006508|GO:0005654|GO:0006488|GO:0008047|GO:0044267|GO:0070062|GO:0043687|GO:0043202|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137554_PI430048170 0.00674777466857542 1.24849724593374 10.3616603593731 10.5082719915483 10.3788087222354 P P P 10.1422583621179 10.1127276260435 10.0355825590278 P P P LNCV6_137554_PI430048170 mRNA AGTGTTCTGGAAATACATACTTTCTGAATGACCAACCGTCCCTGGACTGTGGAATGTTCC NM_172231 RefSeq chr19 - 19276512 19320512 SUGP1 57794 SURP and G patch domain containing 1 GO:0008380|GO:0005515|GO:0010467|GO:0000398|GO:0005681|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138712_PI430048170 0.0612448697930611 1.12191953084418 7.21780780807424 7.08649523932146 7.11669623042078 P P P 6.87824168541852 6.9992905568883 7.04381455688612 P P P LNCV6_138712_PI430048170 mRNA ATTTTGACTTTGGCTGGGGAGTACTTCTTGCAAGCAGAGCTGACAAGCAACGTCTTAAAA NM_032807 RefSeq chr10 + 5894385 5937595 FBXO18 84893 "F-box protein, helicase, 18, transcript variant 1" GO:0005515|GO:0004003|GO:0001934|GO:0005634|GO:0032508|GO:0072429|GO:0005524|GO:0003677|GO:0000737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131658_PI430048170 0.62429298055571 0.978346643247268 6.42038507496181 6.45133633232739 6.51814406757915 P P P 6.40005706495622 6.56342075450032

6.51798279746452 P P P LNCV6_131658_PI430048170 mRNA
CCAGGGACCAACCGGCTGCTTACTTTTGCAAATAAAATTTTACTAGAACACGGCAAAAAA NM_024610 RefSeq
chr3 - 122739996 122793819 HSPBAP1 79663 HSPB (heat shock 27kDa) associated protein 1
GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137419_PI430048170 0.0260971078980903 0.739877896188184 9.4796164192594
9.44327217591765 9.49126090211105 P P P 9.79169989126333 9.8675121676236
10.0472299967525 P P P LNCV6_137419_PI430048170 mRNA
GGACAAGCGTCTGGTCCTCATTAATCTGCCAATGAATGGTTTCGTCATTAAATAAAAATC NM_021242 RefSeq
chrX + 38801431 38806530 MID1IP1 58526 "MID1 interacting protein 1, transcript variant 1"
GO:0006629|GO:0051351|GO:0051258|GO:0045723|GO:0015630|GO:0005874|GO:0007026|GO:0005634|GO:0008022|GO:0046890|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132900_PI430048170 0.00557200456302841 1.46915749492258 8.83475740100714
8.59983444619002 8.64103332174317 P P P 8.21595696925699 8.1348068813841
8.06709953060447 P P P LNCV6_132900_PI430048170 mRNA
AAGGCAGTAGCTCAAAGGGCTTTGCAAAATTTTAATATATTAAAACAAGAGGCATCTGCT NM_018310 RefSeq
chr8 - 37843879 37849913 BRF2 55290 "BRF2, RNA polymerase III transcription initiation factor 50 kDa subunit" GO:0010467|GO:0006352|GO:0006355|GO:0008270|GO:0005654|GO:0006383 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141609_PI430048170 0.4475688176821470.8912613351172144.88468965342182
4.85137918109938 5.4530579528746 P P P 5.09694020614419 5.39450465291686
5.26297986542003 P P P LNCV6_141609_PI430048170 mRNA
GAATATGAAGTTCTATCTAGTACTTGAGCAGCTGTATTTCTTTTCTACACATTGATGGAC NM_003157RefSeq chr3
- 52710779 52770949 NEK4 6787 "NIMA-related kinase 4, transcript variant 1"
GO:0023014|GO:0030145|GO:1900062|GO:0005524|GO:0006974|GO:0035556|GO:0005929|GO:0005737|GO:0007067|GO:0004702|GO:0004674|GO:0006468|GO:2000772|GO:0000278|GO:0051301 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140286_PI430048170 0.4706668839249380.7860998251773760.524596143997163
0.5714648593867320.440562821523326A A A 1.41438083344347 0.475590775415223
0.47593381657618 A A A LNCV6_140286_PI430048170 mRNA
CACATTTTGCAATGTAATTGCAGTGAATGGCAAAACCATAGCACTTCTAAAAACACATCT NM_001102562 RefSeq
chr5 - 16067364 16179788 MARCH11 NA membrane-associated ring finger (C3HC4) 11 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139583_PI430048170 0.8395641040641890.9363331761333652.37747505374074
1.86312769755829 2.36537666232034 A A A 2.74444336246275 2.20494418184495
1.85848986165158 A A A LNCV6_139583_PI430048170 mRNA
ACAGGCCCATCCCACATTAACAAAACAAAACAAGAAACCACACCACAAATAAAATTACGANM_001204856 RefSeq
chr1 + 151166021 151170297 SCNM1 79005 "sodium channel modifier 1, transcript variant 2"
GO:0008380|GO:0006397|GO:0016607|GO:0005730|GO:0005634|GO:0019899|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_106916_PI430048170 0.3956740930789640.7571571677001241.37845816856257
0.3845099033915240.278723713645998A A A 1.44583394816914 1.37377087811472
0.530474986549828A A A LNCV6_106916_PI430048170 mRNA
CACCTCATTCTTGCTGCTTCAGCCCCTATCACATAGCTCACTGGAAAATGATGTTAAAGT NM_001288763 RefSeq
chr19 - 43795926 43800029 LYPD5 284348 "LY6/PLAUR domain containing 5, transcript variant C"
GO:0005886|GO:0031225 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141700_PI430048170 0.2998282062036240.8271572012637573.92818869152063 3.1631982200275
3.47539687093631 P P P 3.76696400353565 3.9238299490638 3.79597763706612 P P P
LNCV6_141700_PI430048170 mRNA
CACCCTCCTGCCCCGTGGGGCAATTTAACCTTTTTCATGAAAGTTATTTACAATGAAAAG NM_001454RefSeq chr17

- 76136333 76141299 FOXJ1 2302 forkhead box J1
GO:0007389|GO:0060429|GO:0060428|GO:0003700|GO:0030036|GO:0006366|GO:0033085|GO:0000981|GO:0035
089|GO:0045409|GO:0005634|GO:0072016|GO:0007283|GO:0050900|GO:0042130|GO:0060972|GO:0006959|GO:0
045944|GO:0002635|GO:0002924|GO:0000976|GO:0050869|GO:0035502|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128086_PI430048170 0.8614416873159041.15550654501798 2.35875374982784
0.36258920832547 2.46456598535984 A A A 0.485401923290901 1.67699564399249
2.51875597443554 A A P LNCV6_128086_PI430048170 mRNA
GTGATCACCAAATAGGGGAACAACTGAAAAATGTGAATGAAAGAAGTATGTACCTATACT NM_001289773 RefSeq
chrX + 40735395 40738701 MED14OS 100873985 MED14 opposite strand NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_144647_PI430048170 0.9482087052475590.9958995723325151 2.8203836887639
13.3111983316819 12.9359889790009 P P P 13.2556612334852 12.9096435211845
12.9407839259356 P P P LNCV6_144647_PI430048170 mRNA
GCTTAATGGTGTTGCCACTGCCCTTTTGTACACACATGGAAATCCCTCATTTTTTCTGTG NM_001005190 RefSeq
chr19 - 14840947 14841877 OR7A10390892 "olfactory receptor, family 7, subfamily A, member 10"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137232_PI430048170 0.1443663170123140.5734628993349344.64934729978585
4.25742442822065 4.44969507356471 P P P 4.55174814263257 5.36680099296445
5.65820667376031 P P P LNCV6_137232_PI430048170 mRNA
ATGAACTTTCTGGAATATTCTGCTAGTCTGAAATTACAGTAGGTTGTCTGGGGTAGGGGG NM_014503 RefSeq chr12
+ 101280126 101386619 UTP20 27340 "UTP20, small subunit (SSU) processome component, homolog
(yeast)"
GO:0000462|GO:0005515|GO:0000472|GO:0008285|GO:0006364|GO:0032040|GO:0005730|GO:0000480|GO:0005
737|GO:0005654|GO:0000447|GO:0030688|GO:0030686 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134783_PI430048170 0.0262921543608235 1.58350927150652 3.05883488360524
3.31650144733679 3.24928667636097 P P P 2.74657809614291 2.6038990837576
2.25344979301978 A P A LNCV6_134783_PI430048170 mRNA
AACAAAGGAAAACTACGAACCGGCTGTCCAAGGCTGAGCGGTGACTGTCCCCACAGACTG NM_018942 RefSeq
chr4 - 8867046 8871817 HMX1 3166 H6 family homeobox 1
GO:0043565|GO:0007275|GO:0005634|GO:0045892|GO:0003677|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143899_PI430048170 0.0324710297554279 1.5890431972927 4.76443896057548
5.2366321614446 5.03330802187006 P P P 4.63850870459651 4.11268970861459
4.26546302615629 P P P LNCV6_143899_PI430048170 mRNA
AAGGGCAGATTACAGTCATTTCCTACCCTTTAAAGGTAACTTCTCCCTTCTCCTGACCTA NM_003393 RefSeq chr10
+ 100463054 100483642 WNT8B 7479 "wingless-type MMTV integration site family, member 8B"
GO:0007369|GO:0071300|GO:0090263|GO:0005578|GO:0005576|GO:0005615|GO:0007399|GO:0005109|GO:0010
628|GO:0007165|GO:0045165|GO:0030182|GO:0010629|GO:0048263|GO:0032526|GO:0016055|GO:0032355 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94794_PI430048170 0.0263379972796531.71635717235299 5.07139979078284 5.11263800379279
5.43495759150624 P P P 4.07342637976124 4.50510798752745 4.66729958295944 P P P
LNCV6_94794_PI430048170 mRNA
CCTGGAGATAGCCTTTGCGATATTTAAATGTCCGTGGATACAGAAATCTCTGCAGGCAAG NM_004616 RefSeq chr12
- 71125096 71157999 TSPAN8 7103 tetraspanin 8 GO:0030195|GO:0016021|GO:0070062 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_109842_PI430048170 0.1930864909317260.7608177448870937.32397211727194
7.20024064165226 7.24693120371536 P P P 7.44160838535206 7.42346346006486

8.01139052794829 P P P LNCV6_109842_PI430048170 mRNA
CAAAAGGCGTTAATGGAAGAAGCCAGGCTTTCTTAGCCATTCTTTGCAGCAGAAGATTTC NM_002687 RefSeq chr14
+ 39175182 39183218 PNN 5411 "pinin, desmosome associated protein"
GO:0030057|GO:0005882|GO:0006355|GO:0005886|GO:0071013|GO:0003677|GO:0006351|GO:0005737|GO:0016
020|GO:0016607|GO:0000398|GO:0005198|GO:0005911|GO:0005654|GO:0007155|GO:0035145 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_6629_PI430048170 0.2040152224259460.8423791302582076.76610556760799 6.50193620013232
6.31320539334877 P P P 6.93116722422356 6.81401937653525 6.59455469512355 P P P
LNCV6_6629_PI430048170 mRNA
CCCCCCACAAAATAATTCACTACTTGTTGAGAATCTTGATTCTCCCTAATAAATGTTCTA NM_001145197 RefSeq
chr9 + 81928427 81934998 SPATA31D4 NA "SPATA31 subfamily D, member 4" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144599_PI430048170 0.2033994337333211.21593936566921 5.63264571009221
5.71217507061373 5.33346905577417 P P P 5.14455567019543 5.56634878986389
5.10098535440851 P P P LNCV6_144599_PI430048170 mRNA
GGTCTGTTGTACTAGGAAATAATAACGCCTCCCATTTATCAAGGGTTTACTCTGTAAAAA NM_001286526 RefSeq
chr16 - 30834040 30894302 BCL7C 9274 "B-cell CLL/lymphoma 7C, transcript variant 1"
GO:0006915 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130338_PI430048170 0.0227906755673083 1.29774356928771 12.5272304268431
12.2788180708186 12.3253836036397 P P P 11.8928854887507 11.9777783877477
12.1345202827299 P P P LNCV6_130338_PI430048170 mRNA
GTGCTTCTGAACCGCAAGGAGCAAACACTGAAATAAAATAGTTTATTTTTCACACTCAAA NM_004613 RefSeq chr20
- 38128460 38165298 TGM2 7052 "transglutaminase 2, transcript variant 1"
GO:0005515|GO:0043065|GO:0005886|GO:0019904|GO:0043277|GO:0005525|GO:0048661|GO:0046872|GO:0045
785|GO:0005829|GO:0005739|GO:0051561|GO:0001974|GO:0051482|GO:0003810|GO:0050729|GO:0051260|GO:0
018153|GO:0060662|GO:0043123|GO:0005925|GO:0032471|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130533_PI430048170 0.4205079443729020.6269658475316070.337434037636808
0.3639328358052280.339373442976598 A A A 0.35905016550404 1.82263416899707
0.34032494302578 A A A LNCV6_130533_PI430048170 mRNA
GTTTCCTTGCTCTTAGGAAAAGTACTGACAGCTCATAATTGGTTGTATTTCTTAGGATAT NM_001291410 RefSeq
chr2 + 14635090 14650819 LOC653602 NA uncharacterized LOC653602 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_129734_PI430048170 0.0315589740910768 0.4938859308776954.8450769210267
4.96413813491819 5.01417591209878 P P P 5.56958435616476 5.97670505912559
6.25479853882486 P P P LNCV6_129734_PI430048170 mRNA
CTGGCTCTTTAGCCAAAATAAGCACTGTAACATGGATGTATTACTATTACTGCCAAATAA NM_001270384 RefSeq
chr1 + 77779623 77879540 FAM73A 374986 "family with sequence similarity 73, member A,
transcript variant 2" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132241_PI430048170 0.6007615192813250.9762983795829431 3.350298309377
13.4392330561138 13.2321481224908 P P P 13.3622045260685 13.3875072276162
13.3831114616756 P P P LNCV6_132241_PI430048170 mRNA
TGAAGGCTGAGGCACTTCTTTTTCAGATGCCAATAAAGAGCACTTTATGAGTCCAAAAAA NM_145729 RefSeq chr1
- 156737301 156741131 MRPL2479590 "mitochondrial ribosomal protein L24, transcript variant 1"
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0005840 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141315_PI430048170 0.4636570589493220.9242090061449880.409495575823114
0.3906914368271360.266769053376301 A A A 0.3277612980075040.365936044912453
0.690344530579755 A A A LNCV6_141315_PI430048170 mRNA

AGAACACAGAGCAAGACGTCGACTTCAACGCAGAAGCATTCTGGACGACAACTCCCCGGG NM_001136273 RefSeq chrX + 153418322 153421628 ZFP92 NA ZFP92 zinc finger protein NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133843_PI430048170 0.5008358978103230.96708716628334 12.3726792712436 12.3547693123939 12.3385123946731 P P P 12.5021700442356 12.395196985258 12.3070107810502 P P P LNCV6_133843_PI430048170 mRNA
GCTGTACAGAGACTCTATTTTAATGTATATTTGCTGCAAAGAGAAACCGCTTTTGGTTTT NM_001282450 RefSeq chr11 + 64306226 64316740 ESRRA 2101 "estrogen-related receptor alpha, transcript variant 2"
GO:0005515|GO:0010467|GO:0006367|GO:0051216|GO:0003707|GO:0005634|GO:0045944|GO:0042127|GO:0015630|GO:0043401|GO:0004879|GO:0005496|GO:0006355|GO:0006996|GO:0019904|GO:0005730|GO:0045670|GO:0000122|GO:0000978|GO:0003677|GO:0045171|GO:0043565|GO:0001078|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139799_PI430048170 0.2201376878941690.9275314284230987.24723146667134 7.09083120566442 7.21801664809435 P P P 7.27494851755589 7.3986113141423 7.20623604768818 P P P LNCV6_139799_PI430048170 mRNA
ATGTTCCCTGGAGAGGTCGCTTTGTGAAGAAACCATCAGCAGGCTGTGAGCATCGCCAGG NM_004204RefSeq chr16 + 569967 584136 PIGQ 9091 "phosphatidylinositol glycan anchor biosynthesis, class Q, transcript variant 2"
GO:0017176|GO:0006501|GO:0005975|GO:0016254|GO:0005789|GO:0016021|GO:0044267|GO:0000506|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69797_PI430048170 0.00120860755274845 0.30227609492479 3.75381113521129 4.01680709936582 4.25911565291655 P P P 5.47546642662739 5.7293976891693 5.99953935358884 P P P LNCV6_69797_PI430048170 mRNA
ATCCTGAAAATGAGCCAATCCCCACTTGAATGGTTACTGGAGTAAACCCACCTTTACCAC NM_015906RefSeq chr1 - 114392776 114511160 TRIM33 51592 "tripartite motif containing 33, transcript variant a"
GO:0005515|GO:0010467|GO:0004842|GO:0006367|GO:0016567|GO:0016874|GO:0070410|GO:0070412|GO:0005634|GO:0000122|GO:0003677|GO:0006351|GO:0043231|GO:0030514|GO:0005654|GO:0007179|GO:0008270|GO:0017015|GO:0045892. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140076_PI430048170 0.62058717584608 1.39350357617133 0.313911137827699 1.83764707227309 0.318387342443682A A A 0.4550186231933820.351647059896427 0.769773290533604A A A LNCV6_140076_PI430048170 mRNA
ATAAATGTGCAGGTGGGACAGATGCCACTAGAAATACACTCTATATTTCTCAGCAAAAAA NM_001141917 RefSeq chr9 - 34723052 34729538 FAM205A 259308 "family with sequence similarity 205, member A"
GO:0005634|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140196_PI430048170 0.0139898284200903 1.24039174334215 0.812582559774411 0.8910556804173210.965444953662694A A A 0.6892967746816550.502952936313787 0.541722151059373A A A LNCV6_140196_PI430048170 mRNA
GTTGAGTGGTTTAAAACTTAAAGATGGCACAGGAAGCTGTATCATTTACAGGTGAAAAAA NM_014586RefSeq chr21 + 31873314 32004064 HUNK 30811 hormonally up-regulated Neu-associated kinase
GO:0007165|GO:0004674|GO:0007275|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135220_PI430048170 0.8313018375428580.97102314704464 0.333607493889972 1.13225712225542 0.266265807441509A A A 0.8806673731115650.290849560732618 0.790093617122513A A A LNCV6_135220_PI430048170 mRNA
ATCCTGTTCCTCTACAATGACCTATTGAAGAAAAGAGCAGCCTTCACCAAACTCAGGAGG NM_152494RefSeq chr1 + 155033805 155050930 DCST1 149095 "DC-STAMP domain containing 1, transcript variant 1"
GO:0008270|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118633_PI430048170 0.0123795407762588 0.6703130770048163.97885900091078 3.79752250170976 4.15017905056625 P P P 4.50574169959375 4.6961334190117

4.46689157901686 P P P LNCV6_118633_PI430048170 mRNA
CTGGCGGCGCTGCGGATCCAGGGGGTCGGCTGCCAGGTACAGTTTCCTAAAGACAAAAAA NM_001173524
RefSeq chr1 + 193059421 193085985 TROVE2 6738 "TROVE domain family, member 2, transcript
variant 5"
GO:0005737|GO:0030529|GO:0003723|GO:0060271|GO:0030620|GO:0005654|GO:0002520|GO:0009411|GO:0006
383|GO:0046872|GO:0007224 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134708_PI430048170 0.2551879236768971.10893510590547 8.28281020795569
8.37718753386327 8.08434654519963 P P P 8.0172700804266 8.23627431611089
8.04871690579662 P P P LNCV6_134708_PI430048170 mRNA
CCGTAGGCTTGAACATGTGTTGAGTGCATGAAAAATAAATGCTGTTCATGTGTGTAGCTC NM_020201 RefSeq chr17
+ 17303365 17347663 NT5M 56953 "5',3'-nucleotidase, mitochondrial"
GO:0009223|GO:0046079|GO:0055086|GO:0044281|GO:0046872|GO:0005739|GO:0006260|GO:0046135|GO:0000
166|GO:0005759|GO:0016311|GO:0008253|GO:0008252|GO:0006206 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144898_PI430048170 0.30452933973148 1.03404513018658 0.556174167263041
0.5973172668594040.51862267157554 A A A 0.5758892933189570.475093964633585
0.474938703203994A A A LNCV6_144898_PI430048170 mRNA
CTTACTATGTGTGGAATTTCTTTTTCACACCATCATGGGCTGTATTTTCAAGTTGATTCA NM_001007540 RefSeq chr3
- 49790733 49799835 CDHR4 389118 cadherin-related family member 4
GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68938_PI430048170 0.0940613920257412 0.8082984280560741 1.3594991164443
11.2941548991343 11.2143622309933 P P P 11.7698343319104 11.3963850067413
11.6024600196863 P P P LNCV6_68938_PI430048170 mRNA
TGTCGACCAGCCCCCAAATGTCGAAGAATTTTCTTCTTGCCAATTTTGTTGTTTAAAAAA NM_001162383 RefSeq
chr1 - 155946838 155978545 ARHGEF2 9181 "Rho/Rac guanine nucleotide exchange factor (GEF) 2,
transcript variant 1"
GO:0008017|GO:0005515|GO:0032755|GO:0000132|GO:0050731|GO:0006886|GO:0032855|GO:0042127|GO:0071
356|GO:0043025|GO:0005089|GO:0005856|GO:0030676|GO:0060546|GO:0071474|GO:0005794|GO:0032760|GO:0
005819|GO:0043234|GO:0032321|GO:0045087|GO:0008270|GO:0005923|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128936_PI430048170 0.0233162840154621 1.29160329376875 9.38004147167876
9.44154697124208 9.36763661726133 P P P 9.15424319443864 8.9206162088308
8.99807211344486 P P P LNCV6_128936_PI430048170 mRNA
AGCGAGCACATGAGGAAGCTGAGTCTTTCACCAATAAACAGTTGTGGTTTGTCTAAAAAA NM_021147 RefSeq chr5
- 55231152 55233717 CCNO 10309 "cyclin O, transcript variant 1"
GO:0004844|GO:0042384|GO:0007049|GO:0005737|GO:0042493|GO:0006284|GO:0005654|GO:0051301 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138011_PI430048170 0.00580868545147917 0.5520675714609655.91446566169323
5.63752229200463 5.89092491756504 P P P 6.54245674204264 6.55244449858332
6.90495831498137 P P P LNCV6_138011_PI430048170 mRNA
GAATGAGGTTGACTAATGCATATTATGAATTGAGTCCACAAAGGAACACAAAACTCTTTG NM_001300813 RefSeq
chr4 + 109433771 109540459 SEC24B 10427 "SEC24 family member B, transcript variant 3"
GO:0005515|GO:0005215|GO:0002474|GO:0048471|GO:0060088|GO:0044281|GO:0048208|GO:0006886|GO:0005
829|GO:0019886|GO:0061024|GO:0016192|GO:0021747|GO:0018279|GO:0012507|GO:0030127|GO:0035909|GO:0
001843|GO:0090178|GO:0003151|GO:0006888|GO:0061156|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_55591_PI430048170 0.1549679301340051.19650247064211 11.251157106772 11.3128445812031
11.4129869120256 P P P 10.833157858116 11.0727438164202 11.2667873213738 P P P
LNCV6_55591_PI430048170 mRNA

CATCTTCCTTCTCAACTTACCTGTTGCCACTTGGAATATATATCGATACATTATGGTGCC NM_001277199 RefSeq chr1 + 224356810 224376884 CNIH4 29097 "cornichon family AMPA receptor auxiliary protein 4, transcript variant 4" GO:0035556|GO:0005783|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137004_PI430048170 0.2944838478065541.07638191109482 8.14641618875355 8.00788328300511 8.16336756612673 P P P 7.93143072880943 8.14322698797825 7.91819717843858 P P P LNCV6_137004_PI430048170 mRNA
ACTCTCTCAAGTATGCCTATAACATAAGTCTAAAGGAGGTGATGCAGGTACTGAGCCACG NM_003907 RefSeq chr3 + 184135021 184145311 EIF2B5 8893 "eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa" GO:0005515|GO:0010467|GO:0034976|GO:0009408|GO:0048708|GO:0003743|GO:0043434|GO:0005634|GO:0006412|GO:0006413|GO:0005829|GO:0005085|GO:0005737|GO:0001541|GO:0045948|GO:0005851|GO:0042552|GO:0035690|GO:0009749|GO:0043547|GO:0032057|GO:0014002|GO:0014003|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143884_PI430048170 0.2185668389003470.706956813221665 1.8099493016134 2.69423152122084 2.83127872957393 A A A 2.99442325783752 3.21947435230245 2.78620235477332 P P P LNCV6_143884_PI430048170 mRNA
GCTAAGACAATATAGTCTGGAGTATAAGTGGGAAAGCTTGATTTAAATACTGTGAACTCT NM_006277 RefSeq chr2 - 24202865 24360528 ITSN2 50618 "intersectin 2, transcript variant 1" GO:0005515|GO:0005737|GO:0032321|GO:0005070|GO:0005509|GO:0009967|GO:0005089|GO:0070062|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141520_PI430048170 0.3827292992003260.866639999900565 0.401608441927607 0.3972801753637440.259260674217306 A A A 0.363555183845111 0.877285262521743 0.38014815356977 A A A LNCV6_141520_PI430048170 mRNA
GGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAGATCTTATTGATGACAGAGTG NM_024850 RefSeq chr5 + 180899076 180950906 BTNL8 79908 "butyrophilin-like 8, transcript variant 1" GO:0005515|GO:0016021|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128184_PI430048170 0.0731912949035593 0.4482908078332611.33745535140982 2.2347970233233 2.62052506528535 A A A 3.34652231396223 3.46328118441495 3.11332505404429 P P P LNCV6_128184_PI430048170 mRNA
TAGTGTACCTGTCACCCAAGTTATTTTGTTCCTTTTTGGGTCCTCCAGTATAATCCCCCC NM_138959 RefSeq chr1 + 115641952 115698224 VANGL1 81839 "VANGL planar cell polarity protein 1, transcript variant 1" GO:0005515|GO:0007275|GO:0016021|GO:0016328 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144089_PI430048170 0.886746008238345 1.00135689429094 0.367586149108105 0.3643878115452190.392206216475095 A A A 0.3797516229839640.353953139899323 0.384579987311717 A A A LNCV6_144089_PI430048170 mRNA
GGCTCGTGTACAGCATAAATCTATCAAACTTGGAATTGTGTATACATTTATATGCCAGAT NM_014979 RefSeq chr5 + 76083413 76333956 SV2C 22987 "synaptic vesicle glycoprotein 2C, transcript variant 1" GO:0030054|GO:0005886|GO:0022857|GO:0009405|GO:0006836|GO:0030672|GO:0016021|GO:0055085|GO:0008021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141698_PI430048170 0.00760181747217739 0.2592362848434070.348993590419261 1.14835604325583 0.269893039691678 A A A 2.40629588348449 2.14875024542738 3.06681345686621 P A P LNCV6_141698_PI430048170 mRNA
GTGGACCCTGTGTGAATGAGAAAATTCAGTTATAAATTGTAATAAAACCTGCTTACTGGA NM_001270470 RefSeq chr12 + 93571680 93576745 SOCS2 8835 "suppressor of cytokine signaling 2, transcript variant 5" GO:0005515|GO:0043066|GO:0016567|GO:0005159|GO:0046627|GO:0019221|GO:0005131|GO:0007568|GO:0060396|GO:0009967|GO:0060397|GO:0009966|GO:0001558|GO:0007259|GO:0046426|GO:0032870|GO:0005829|GO:0005737|GO:0008269|GO:0005070|GO:0004860|GO:0006469|GO:0032355 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137662_PI430048170 0.6980101461135190.7277733571241341.15466702144136
0.4971287039054261.37720150538082 A A A 0.7586767027773770.670013026057996
2.40182489695689 A A A LNCV6_137662_PI430048170 mRNA
GCATTGCCCTTCATCACAGAAGTATTCAACTCTGACAAATAAATATGTCATCCTGAATTA NM_017734RefSeq chr1
+ 99645874 99694541 PALMD 54873 palmdelphin GO:0005737|GO:0043197|GO:0016020|GO:0008360
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135286_PI430048170 0.4398803170399620.9209644233351812.3190317217629
12.3492627042509 12.4271697811338 P P P 12.3070107810502 12.4254117904995
12.6939184237367 P P P LNCV6_135286_PI430048170 mRNA
TGTCTCTGAGATTTTGTATTCCACATTCTAGGGTATTCTGTAATTTGGCTCCTTACCAAT NM_001012732 RefSeq chr4
- 182890090 182917477 DCTD 1635 "dCMP deaminase, transcript variant 1"
GO:0046134|GO:0055086|GO:0008270|GO:0044281|GO:0006220|GO:0006206|GO:0009165|GO:0004132|GO:0070
062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142992_PI430048170 0.0286055712817971.38111687061282 8.75837597238427
8.72912616614194 8.42509453693901 P P P 8.04857850969058 8.31529669303904
8.16176023196905 P P P LNCV6_142992_PI430048170 mRNA
CCCCCAGGTGGCCACCAAGTTGTGGAAGCACATTTCTAAATAAAAACTGCTCTTAGAATG NM_022047RefSeq chr6
+ 35297817 35321771 DEF6 50619 differentially expressed in FDCP 6 homolog (mouse)
GO:0005737|GO:0016020|GO:0005886|GO:0005911|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130042_PI430048170 0.00820371991495107 0.4061269785819361.42288520620095
1.17401953859286 1.63423057439529 A A A 2.57144265131149 2.43217853767187
3.08068281649694 A P P LNCV6_130042_PI430048170 mRNA
GGATACTTGGGGATAACAATTATTATGGCACTTTAACAGTGCACTTTAATATATACCACC NM_007156RefSeq chrX
- 57905429 57910633 ZXDA 7789 "zinc finger, X-linked, duplicated A"
GO:0005515|GO:0003700|GO:0070742|GO:0005634|GO:0045893|GO:0003676|GO:0046872|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140919_PI430048170 0.5297837932549911.06608069287623 7.02620821910102 7.3634759877252
7.24822108466848 P P P 7.01596879231611 7.05265951821161 7.29607894090447 P P P
LNCV6_140919_PI430048170 mRNA
ATGGGGTAAGAAAACTACCCATGCATGATGTAGAGAGCTGTTGATTTGTTTCTGTTTTTT NM_001007237 RefSeq
chr1 - 116574397 116667755 IGSF3 3321 "immunoglobulin superfamily, member 3, transcript variant
2" GO:0032808|GO:0003674|GO:0009986|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132573_PI430048170 0.0141909589219379 0.3275480626271954.34898209341287
3.90914696854418 3.71297887094031 P P P 4.99672565232989 5.86771784531345
5.85292549266013 P P P LNCV6_132573_PI430048170 mRNA
AAGGGAATGAGAATGTCATGGTGCTAAACCTGACAAATAAGAGATCATTGAAATGCTGAA NM_000232RefSeq chr4
- 52020694 52038319 SGCB 6443 "sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)"
GO:0048747|GO:0042383|GO:0005737|GO:0007517|GO:0016010|GO:0005887|GO:0016012|GO:0055013|GO:0097
084|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128722_PI430048170 0.00865314525015648 0.4469851634103264.82818921804575
4.43978557011235 4.38867988286173 P P P 5.79977113723958 5.64860181574808 5.7305857972333
P P P LNCV6_128722_PI430048170 mRNA
GTGTGTGTGTTTAAGGGAAGTAGGTGGTGGTTAAAATTCTTGGAAAATTTTCAGAATACT NM_014106RefSeq chr15
- 34978340 34988296 ZNF770 54989 zinc finger protein 770
GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0003677|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128858_PI430048170 0.0776403810862486 1.33153913066118 9.44586868793332
9.68828455451811 9.9167309796234 P P P 9.2592813155132 9.16775134899649

9.41221154539614 P P P LNCV6_128858_PI430048170 mRNA
GTGAACCCATCTGTCTGCATTTTCTACTCTGAGCCCATTTGTTAATAAACACTTATTTTT NM_018250 RefSeq chr8 -
28767657 28890181 INTS9 55756 "integrator complex subunit 9, transcript variant 1"
GO:0005515|GO:0005737|GO:0032039|GO:0005654|GO:0016180 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145055_PI430048170 0.438098356644527 1.12080048995376 12.6915759291567
12.9853308327035 13.1802592793506 P P P 12.7003855654855 12.641454057478
13.0317119703667 P P P LNCV6_145055_PI430048170 mRNA
TGGGGTCCATTTTACAATCCATTATTTTTGACCACTGCTATGTGTTCAAGTAGTATGAGA NM_001297738 RefSeq
chr5 - 77691168 77776361 TBCA 6902 "tubulin folding cofactor A, transcript variant 1"
GO:0005737|GO:0007021|GO:0006457|GO:0015630|GO:0005874|GO:0051087|GO:0005730|GO:0051084|GO:0051
082|GO:0007023|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69800_PI430048170 0.517138037905886 0.942943429286123 10.6755741153222 10.7221991661033
10.9222090004525 P P P 10.7485435552014 10.7875765289639 11.0333752780114 P P P
LNCV6_69800_PI430048170 mRNA
TATTTATATACTGTGAACATCCTGTCAGCTGCCCGAATGTTGTTGCACAGGTGCTACAAG NM_006468 RefSeq chr1
+ 145824068 145844401 POLR3C 10623 "polymerase (RNA) III (DNA directed) polypeptide C (62kD),
transcript variant 1"
GO:0032728|GO:0010467|GO:0006386|GO:0006385|GO:0003899|GO:0006359|GO:0005634|GO:0003677|GO:0006
383|GO:0005829|GO:0051607|GO:0045089|GO:0001056|GO:0045087|GO:0005666|GO:0005654|GO:0032481 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144043_PI430048170 0.0837799435177878 0.864627769120333 9.83927316494033
10.0059006183079 9.76138085805099 P P P 10.1179302699743 10.0986730579038
10.0288982681354 P P P LNCV6_144043_PI430048170 mRNA
TTTTTATCGATACGTTGATTAAAACGCGTGGTTCCCCGTGTGCCTGAAGCAGACAAAAAA NM_015395 RefSeq chr7
- 98215442 98252251 TECPR1 25851 tectonin beta-propeller repeat containing 1
GO:0005515|GO:0000046|GO:0000421|GO:0006914|GO:0032266|GO:0031410|GO:0016021|GO:0005765 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130678_PI430048170 0.0699939700212912 1.09945702614461 7.55890471939863
7.59661579153575 7.66326550334582 P P P 7.55190534919928 7.45271636252293
7.40166658583953 P P P LNCV6_130678_PI430048170 mRNA
ATTGCCGCCATGACCAACAGTCTCTTCATCGACCGCCAGAAGTGCATGGCCCATCGTACT NM_001286559 RefSeq
chr2 + 94871432 94876829 TEKT4 150483 "tektin 4, transcript variant 2"
GO:0005737|GO:0031514|GO:0030030|GO:0005874|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142619_PI430048170 0.105496043760489 1.22768292419517 12.2479132762512
12.1453664594259 12.1517591601491 P P P 11.7393612392154 12.1022331626893
11.7905977494611 P P P LNCV6_142619_PI430048170 mRNA
AAGCTGATCAAGGAAATCAAGAACTACATCCAAGGCATCAACCTCGTCCAGGCAAAGAAG NM_002949 RefSeq
chr17 + 81703369 81707526 MRPL126182 mitochondrial ribosomal protein L12
GO:0005515|GO:0070124|GO:0070125|GO:0070126|GO:0003735|GO:0006996|GO:0032543|GO:0003723|GO:0005
743|GO:0006390|GO:0005762|GO:0005739|GO:0045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137288_PI430048170 0.673519937427074 0.968495787808987 7.16148195130556
7.36031423087426 7.4327437104703 P P P 7.30881044587515 7.29103221851497
7.49752002549729 P P P LNCV6_137288_PI430048170 mRNA
CAGCTATCCCAATGTGAAATGTATTTTGGATGTATCTGGTGTCATTTTTCTATTAAGACC NM_181656 RefSeq chr17
- 67991098 67993649 C17orf58 284018 "chromosome 17 open reading frame 58, transcript variant 2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144413_PI430048170 0.0636531088804081 1.03858264038513 0.434236606484222

0.4801389453577750.451295527632409A A A 0.3732760644750340.398373721821779
0.429986710385371A A A LNCV6_144413_PI430048170 mRNA
CCCTGGACTAGGAGAAAGGCTAAAGAATGTCAGTAAATAAAAGAGCTTTCATCCAAAAAANM_173650RefSeq chr2
+ 27275420 27281431 DNAJC5G 285126 "DnaJ (Hsp40) homolog, subfamily C, member 5 gamma,
transcript variant 1" GO:0016020 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133118_PI430048170 0.0153769010211938 0.6547847657465824.18068362588587
4.03057459482843 4.23906727146534 P P P 4.61697956637696 4.67593464571542
4.97239106552659 P P P LNCV6_133118_PI430048170 mRNA
GTAGAGAAGCCGTGCATGAAAGAATTTGTTTAATGTCTTGTTTTGCGTATGTGTTTTTTG NM_032256RefSeq chr12
+ 43835860 44389762 TMEM117 84216 "transmembrane protein 117, transcript variant 1"
GO:0008150|GO:0003674|GO:0005783|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141378_PI430048170 0.1006972964629240.85923151574498414.8173576938098
14.5569289940189 14.60823248668 P P P 14.8545164140114 14.8803808570599
14.9169687361261 P P P LNCV6_141378_PI430048170 mRNA
ATTGGGTTCCCCCCTCCCCCCACCTTTTTTGCTGTGAAACTGAAATAGTGAACTTTTCTA NM_001193582 RefSeq
chr7 - 108147625 108456397 NRCAM 4897 "neuronal cell adhesion molecule, transcript variant 4"
GO:0031290|GO:0005515|GO:0043005|GO:0005886|GO:0030506|GO:0045202|GO:0001525|GO:0007409|GO:0007
417|GO:0019227|GO:0007416|GO:0086080|GO:0043194|GO:0030516|GO:0016337|GO:0007413|GO:0008104|GO:0
045162|GO:0045666|GO:0005887|GO:0007411|GO:0034113|GO:0001764|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137289_PI430048170 0.6007037866897011.03790288388979 6.79986706527255
6.78361325650134 6.57637648548535 P P P 6.60051173376885 6.62010208310006
6.78185834079125 P P P LNCV6_137289_PI430048170 mRNA
AATGCTGTAAGATAAGCAACCAACGCAGACAGGCCTCAGCTAAGAGTATAGTGTGTGTGT NM_001145073 RefSeq
chrX + 49879866 49882564 USP27X 389856 "ubiquitin specific peptidase 27, X-linked"
GO:0006511|GO:0008234 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145647_PI430048170 0.1821984007582561.1220061246378 0.644307317299141
0.3763975441081460.6015293411427 A A A 0.2844301117760810.40632931210889
0.442615165219055A A A LNCV6_145647_PI430048170 mRNA
CCTATGGACTTTTGCATTATTTCATTGTGCATGCATCCAGTGATTATACATAAGCAACAT NM_003558RefSeq chr9
+ 68705413 69009176 PIP5K1B 8395 "phosphatidylinositol-4-phosphate 5-kinase, type I, beta,
transcript variant 2"
GO:0005515|GO:0046854|GO:0016020|GO:0006661|GO:0044281|GO:0001931|GO:0006644|GO:0005524|GO:0016
308|GO:0012505|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134684_PI430048170 0.000832464511323461 4.71362104560893 3.25448925841144
2.80024376226207 2.95700564967071 P A P 0.6582392127028470.80058132458481
0.871683602969305A A A LNCV6_134684_PI430048170 mRNA
TGGATATGTCTGTGAGGCTCCTGAAAGGAGACAAATAAAGTCAATATATTTGCACAGTGC NM_001145033 RefSeq
chr11 + 43942555 43943883 C11orf96 387763 chromosome 11 open reading frame 96 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_93794_PI430048170 0.5213692729167310.9393661729109774.15094101430433 3.85515884570238
3.78813493860961 P P P 3.88253985629722 4.1286579885199 4.06886037762411 P P P
LNCV6_93794_PI430048170 mRNA
GTCGACTTATCAAAGGATCTCCCTCACTGGAACAAGCTTAAAGCAGATGAGAAGTACTTC NM_015713RefSeq chr8
- 102204500 102239118 RRM2B 50484 "ribonucleotide reductase M2 B (TP53 inducible), transcript variant
1"
GO:0009186|GO:0015949|GO:0001822|GO:0009200|GO:0055086|GO:0044281|GO:0046872|GO:0003014|GO:0005
737|GO:0006281|GO:0009263|GO:0005654|GO:0004748|GO:0006264|GO:0006979|GO:0070062|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_143014_PI430048170 0.0343809649577725 2.01697744717908 3.37265313012634
2.92352516418386 2.56556549470311 P P A 2.10069849790318 2.06711212198292
1.74513928434763 A A A LNCV6_143014_PI430048170 mRNA
CCCCTAGGACCTGAACAACCAAGACTTTAAATAAATTTTAAAATGCAAAAACTCGGAGAA NM_004877RefSeq chr19
- 39328356 39336086 GMFG 9535 "glia maturation factor, gamma, transcript variant 1"
GO:0005622|GO:2000249|GO:0034316|GO:0071933|GO:0004860|GO:0006468|GO:0003779|GO:0006469|GO:0043
085|GO:0008047|GO:0008083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131240_PI430048170 0.426853356458764 1.04973680869756 6.92253035080809 6.8460861580904
7.00420890972741 P P P 6.74731889328684 6.8376130909428 6.97314920545822 P P P
LNCV6_131240_PI430048170 mRNA
CACTGAACGCTGCAGGGCAGGGAAGAAATAAATGGTCTCATAGTTTAATCCATTGATAAA NM_032816RefSeq chr19
- 32878997 32972029 CEP89 84902 centrosomal protein 89kDa
GO:0042384|GO:0005758|GO:0005813|GO:0005737|GO:0000922|GO:0006996|GO:0005886|GO:0005814|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129162_PI430048170 0.144879607654728 1.95166982589673 6.81972307962078
7.00491251297401 6.74822248604365 P P P 6.70695362486869 5.20340190827085
5.22711812975308 P P P LNCV6_129162_PI430048170 mRNA
GGGTCTGAGTTTCACATTTGAACCAAATAAAATGCTGTCAAGAGAAAACTCTCCAGTGCA NM_006262RefSeq chr12
+ 49295125 49298698 PRPH 5630 peripherin
GO:0005882|GO:0016020|GO:0042622|GO:0005198|GO:0045104|GO:0044299|GO:0005883|GO:0045098|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140396_PI430048170 0.00454120975683673 0.843886172558952 15.337554831559
15.2418438447664 15.2870018576427 P P P 15.5118392169901 15.5313653661723
15.5590347603982 P P P LNCV6_140396_PI430048170 mRNA
GCTACAGCAAAGCCCATTGGCCAGAAAGGAAAGACAATAATTTTGTTTTTTCATTTTGAA NM_001353RefSeq chr10
+ 4963261 4977966 AKR1C1 1645 "aldo-keto reductase family 1, member C1"
GO:0031406|GO:0044598|GO:0046683|GO:0032052|GO:0006805|GO:0044597|GO:0007603|GO:0047086|GO:0005
829|GO:0030299|GO:0016655|GO:0071395|GO:0042574|GO:0030855|GO:0047115|GO:0051260|GO:0008206|GO:0
047042|GO:0070062|GO:0042632|GO:0047718|GO:0007586|GO:0047006|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_82195_PI430048170 0.894891753060892 0.997342467338262 0.322226990335335 0.327792985512286
0.395696604978343 A A A 0.370103632123822 0.320616204218607 0.367147933928669 A A A
LNCV6_82195_PI430048170 mRNA
ATTCATCGACGAGGCCAAGCGACTTCGCGCCGTGCACATGAAGGAGTATCCGGACTACAA NM_005634RefSeq chrX
- 140502986 140505060 SOX3 6658 SRY (sex determining region Y)-box 3
GO:0003700|GO:0001106|GO:0021983|GO:0048515|GO:0005634|GO:0000122|GO:0007417|GO:0021854|GO:0000
979|GO:0003677|GO:0006351|GO:0007530|GO:0007423|GO:0060009|GO:0045665|GO:0048666|GO:0060324|GO:0
009887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72581_PI430048170 0.011291805717421 1.3468185155917 8.00540962588944 8.1333305341186
8.19422341821187 P P P 7.76630202378945 7.73990974347972 7.53338801003774 P P P
LNCV6_72581_PI430048170 mRNA
ATAGAATTTGGTTACTTGGACTATGCCCAGTCTCGGTTCCAGTTCTACTTCCAGCAGAAG NM_005198RefSeq chr22
- 50578957 50582999 CHKB 1120 choline kinase beta
GO:0004305|GO:0016310|GO:0006646|GO:0004103|GO:0044281|GO:0006657|GO:0006644|GO:0005524|GO:0046
474|GO:0006656|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132191_PI430048170 0.0173943109285702 0.945677531319145 0.354782695658914
0.349555718133342 0.325518761178888 A A A 0.450710319061139 0.423172779020999
0.397388983136739 A A A LNCV6_132191_PI430048170 mRNA
CCTGAGTTTTACCACAGTCTTAAGCAGATTTGAAATAAATTCTTTTGACACTGCCAACAA NM_001004342 RefSeq

chr1 + 231162927 231221568 TRIM67 NA "tripartite motif containing 67, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132865_PI430048170 0.4329762336717521.85096691540935 0.335233809769161 0.3175822562852872.18470441721413 A A A 0.2843953448829880.467562947837716 0.275478370112912A A A LNCV6_132865_PI430048170 mRNA GCCAGATTTTGACTCCCAGATTCCTTTACAAAACGCACTCATTCATTCATTTATATATGTNM_024785RefSeq chr2 - 224378697 224401994 FAM124B 79843 "family with sequence similarity 124B, transcript variant 2" GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138349_PI430048170 0.2987136066972742.48946916824268 1.41619200476225 2.80150845515695 0.326355926076994A A A 0.8697846971396040.337036782630282 0.36246184648028 A A A LNCV6_138349_PI430048170 mRNA GATTGATTCACTGATTAGTTTTACTGCCATGTGCCTATAACTATAGGTTATTCTCTTTCC NM_020297RefSeq chr12 - 21797389 21936694 ABCC9 10060 "ATP-binding cassette, sub-family C (CFTR/MRP), member 9, transcript variant SUR2B"
GO:0005215|GO:0005886|GO:0008282|GO:0008281|GO:0042626|GO:0005267|GO:0007268|GO:0010107|GO:0015459|GO:0055085|GO:0030017|GO:0005524|GO:0044325|GO:0042383|GO:0007165|GO:0051607|GO:0008076|GO:0008152|GO:0006813. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132742_PI430048170 0.00607467125141583 1.25975543550923 10.9363217627672 11.0515354706506 11.029072992708 P P P 10.7613092393931 10.6536445062723 10.6004299011569 P P P LNCV6_132742_PI430048170 mRNA CCCCTCTGCTTTATTTATTGTAAGCATTCCCACGTTAAATAAACTTTGGCTGTTGTCTAC NM_145214RefSeq chr1 - 228393675 228406816 TRIM11 81559 tripartite motif containing 11
GO:0005515|GO:0004842|GO:0016567|GO:0016874|GO:0019904|GO:0032897|GO:0005634|GO:0046598|GO:0051607|GO:0005737|GO:0050768|GO:0046597|GO:0045087|GO:0008270|GO:0045892|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135894_PI430048170 0.0610861338333961 0.8333572929149448.59997245747727 8.35870027879268 8.52865459595509 P P P 8.76571203358474 8.73861726678516 8.78217220290133 P P P LNCV6_135894_PI430048170 mRNA GGAGCAACTTTGCTATTTGGTCCAGTAAGTGGACACCTTGTGATATAAATGTGGAAATAA NM_004831RefSeq chr19 - 16574906 16628204 MED26 9441 mediator complex subunit 26
GO:0005515|GO:0010467|GO:0006367|GO:0001104|GO:0006357|GO:0016592|GO:0003713|GO:0005654|GO:0003677. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131195_PI430048170 0.89584419143407 0.9959765267113910.266398772101764 0.2863107566175860.413877647371169A A A 0.36298468776092 0.315871314438761 0.309061722144725A A A LNCV6_131195_PI430048170 mRNA TCCTTCTCACGATCTTACTGCTGTCTGAATGCACAATTCTCTTGGGATATCAAAACCATA NM_018013RefSeq chr6 + 107490112 107661309 SOBP 55084 sine oculis binding protein homolog (Drosophila)
GO:0042472|GO:0032184|GO:0007605|GO:0007626|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121829_PI430048170 0.0689363066851586 0.5429380225379581 0.1054879012238 9.43792871450689 10.2198614608682 P P P 10.3580115705349 10.7833989473689 11.245660646863 P P P LNCV6_121829_PI430048170 mRNA AAACAGTGGATCACAAAGTGGAACGAAAATGAAAGCTACTCATAGCGGGGGCCTAAAAAA NM_000210RefSeq chr2 + 172427585 172506453 ITGA6 3655 "integrin, alpha 6, transcript variant 2"
GO:0005515|GO:2001237|GO:0030056|GO:0033627|GO:0005886|GO:0097186|GO:0010811|GO:0030175|GO:0050900|GO:0046872|GO:0016337|GO:0009925|GO:0005913|GO:0030198|GO:0045944|GO:0031668|GO:0031581|GO:0046847|GO:0010668|GO:0043065|GO:0022409|GO:0009986|GO:0034329|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137368_PI430048170 0.9190009494622951.09014663524387 0.42411875539844

2.53646757400717 1.20774784621637 A A A 0.9941663458419022.39438261602485
0.507954944833512 A A A LNCV6_137368_PI430048170 mRNA
TTAGACTTTATACCCTTAGCTTTCCCATAAGAGCTCCCTTTGTGGGGAACTTGCCCTCTT NM_007163 RefSeq chr18
+ 45614800 45683095 SLC14A2 8170 "solute carrier family 14 (urea transporter), member 2, transcript
variant 1"
GO:0005515|GO:0016324|GO:0016020|GO:0005886|GO:0015204|GO:0016021|GO:0071918|GO:0055085|GO:0050
839|GO:0015840 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55474_PI430048170 0.00655628833014523 0.4376914253104553.63757489130169
3.43316580031641 3.83473093290667 P P P 4.84452391636954 4.78262593137993 4.8805466032661
P P P LNCV6_55474_PI430048170 mRNA
CAGGACAAAGGACTGACAGCAAATCAAAAGGCCTCCAGTGGATAATAGATACAACGATAG NM_014873 RefSeq
chr1 - 211743456 211830772 LPGAT1 9926 lysophosphatidylglycerol acyltransferase 1
GO:0008150|GO:0003674|GO:0005737|GO:0016746|GO:0016020|GO:0036148|GO:0005789|GO:0044281|GO:0016
021|GO:0006644|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83410_PI430048170 0.0999400967459872 1.63093855700279 11.5434451337864
11.2685227993263 11.3818229373507 P P P 11.1501660455935 10.214221723454
10.5682954838268 P P P LNCV6_83410_PI430048170 mRNA
CTTCTTGATAGATGAGGCCATGGTGTAAATGGAAGTTTCAGAGAGGACAAAATAAAACGG NM_016041 RefSeq chr17
- 5471250 5486230 DERL2 51009 "derlin 2, transcript variant 1"
GO:0005515|GO:0008284|GO:0005770|GO:0005783|GO:0030307|GO:0030970|GO:0030176|GO:0030433|GO:0030
968|GO:0001967|GO:0016020|GO:0005789|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126829_PI430048170 0.0301374876209826 1.90269585696575 7.89960928435926
8.09328127774199 7.93913624971394 P P P 7.38484906734308 6.96962838454114
6.72186940045903 P P P LNCV6_126829_PI430048170 mRNA
CTGTCGTGCCTTGAGAAAGCTGGAACGGGAATCAATTAAACATTGTGGTGCTGGCGCCTG NM_080662 RefSeq chr19
- 7476869 7489038 PEX11G 92960 "peroxisomal biogenesis factor 11 gamma, transcript variant 1"
GO:0005515|GO:0043234|GO:0031231|GO:0005779|GO:0044375|GO:0016559|GO:0005777 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_65038_PI430048170 0.5496970395947021.48580775823051 0.581452806753672 0.869730090139239
2.43533580303009 A A A 1.73330321262046 0.37970061673124 0.323512227330702 A A A
LNCV6_65038_PI430048170 mRNA
CGTCTGGGGTGAAGAATTTCATGACGTGGAGGATGCAGAGACCTACAAAAAGATGCTGGC NM_020650 RefSeq
chr19 + 49527617 49543633 RCN3 57333 "reticulocalbin 3, EF-hand calcium binding domain"
GO:0005515|GO:0005509|GO:0005788 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136069_PI430048170 0.0174682474788922 0.7243361479644568.32774940603324
8.04046891645991 8.2824484542313 P P P 8.5585772837434 8.66631763437212
8.82525260470326 P P P LNCV6_136069_PI430048170 mRNA
CTGGTGGGAAGGTTTTGCTGCTAATGTATTTATGGAATGAATGTATTTCATTCAAATCTG NM_012406 RefSeq chr12
- 107732865 107761137 PRDM4 11108 PR domain containing 4
GO:0007165|GO:0048011|GO:0006355|GO:0006366|GO:0008283|GO:0008168|GO:0008270|GO:0005634|GO:0045
786|GO:0032259|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117074_PI430048170 0.0262910044036874 1.22901935262757 6.90262970181729
6.96162332828694 6.74081250161041 P P P 6.64169167844601 6.47293762288219
6.60153439234017 P P P LNCV6_117074_PI430048170 mRNA
GCAGCCGAGCCAGCCAAGCTCTACTCCAGGAAGTGAAAATGTGCTGCCTCGAGAGCCGCT NM_004565 RefSeq
chr1 + 10474945 10630761 PEX14 5195 peroxisomal biogenesis factor 14
GO:0008017|GO:0005515|GO:0032091|GO:0034453|GO:0036250|GO:0016561|GO:0005634|GO:0043433|GO:0043
231|GO:0005622|GO:0007031|GO:0051260|GO:0016558|GO:0005778|GO:0005777|GO:0003714|GO:0005730|GO:0
005102|GO:0048487|GO:0043234|GO:0006461|GO:0047485|GO:0016020|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_132904_PI430048170 0.3636175177784831.03453667950208 0.294213448304149
0.2751752527561540.406661741890429A A A 0.2913612222737970.261103890862759
0.279998850153703A A A LNCV6_132904_PI430048170 mRNA
TTCATGACCGAGCTCTTGGAGAGCTGTGAGAAGAAGGAAAGCGGCTGAGCCTGGTGTGGA NM_152898RefSeq
chr7 - 19144781 19145421 FERD3L 222894 Fer3-like bHLH transcription factor
GO:0050767|GO:0033504|GO:0046983|GO:0005634|GO:0048468|GO:0045892|GO:0003677|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136697_PI430048170 0.1812230997583482.53108709424719 0.346371109543045
2.19634385833123 1.85909863417877 A A A 0.3364865888153850.289192318077729
0.335384580328967A A A LNCV6_136697_PI430048170 mRNA
TTAAGCTTCTTGATTTGTAGATGAATATGTCAACTCTAACAAGGGGCTGGCTAATGCTTG NM_001005270 RefSeq
chr11 - 49981472 49982535 OR4C12NA "olfactory receptor, family 4, subfamily C, member 12" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145386_PI430048170 0.5340762061287530.91909513036771 8.36005402395034
7.87914710793217 8.10163300659515 P P P 8.11415017750535 8.47805459888847
8.12338564284201 P P P LNCV6_145386_PI430048170 mRNA
TGATGAGAACTATAACTCCGTCAACACAAGAATGAGAAAAACCCAGCATGGGGTCCTGTC NM_001272095 RefSeq
chr16 + 31033490 31040167 STX4 6810 "syntaxin 4, transcript variant 1"
GO:0005802|GO:0005515|GO:0035493|GO:0048471|GO:0008284|GO:0005886|GO:0043311|GO:0042581|GO:0045
202|GO:0031201|GO:0060291|GO:0006886|GO:0005615|GO:0005829|GO:0035749|GO:0005622|GO:0016323|GO:0
050921|GO:0043197|GO:0000149|GO:0017157|GO:2000010|GO:0061024|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134222_PI430048170 0.0192839230881695 0.8527481616161241 1.0506718529076
10.9672620495278 10.9693402296365 P P P 11.1695085384724 11.3151706061239
11.1892284594142 P P P LNCV6_134222_PI430048170 mRNA
GCTCTTTATTGGAACAGATCTGGTGGTTCAAATAAACACAGTCATGCAAGCCTGAAAAAA NM_019108RefSeq chr19
- 43731148 43754990 SMG9 56006 SMG9 nonsense mediated mRNA decay factor
GO:0005622|GO:0005515|GO:0010467|GO:0000184|GO:0042802|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_105617_PI430048170 0.3229686435446810.8717133065668950.448123729882519
0.3662023635705730.402951149226111A A A 0.4613832698679980.873077163997546
0.435150816664017A A A LNCV6_105617_PI430048170 mRNA
TCAGACAACTACGGCTTTGATTTTCCAAGTGGTTCAGAATGTAAATATGATCTGACCTTT NM_001291956 RefSeq
chr5 - 19473045 20575873 CDH18 1016 "cadherin 18, type 2, transcript variant 3"
GO:0005886|GO:0034329|GO:0005509|GO:0016021|GO:0007156|GO:0045216|GO:0034332 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134931_PI430048170 0.0974628614435942 0.5664456174335 1.0169223619195
0.3586157817271521.4762770354521 A A A 1.54559809574262 1.90772468102342
2.02731786147603 A A A LNCV6_134931_PI430048170 mRNA
GCACCCTGGCATAGAAGCTTTCACTCTCTTACACTAAATTTAACCTAATCTAAACTTAAT NM_024753RefSeq chr2
- 165873361 165953838 TTC21B 79809 tetratricopeptide repeat domain 21B
GO:0000790|GO:0006996|GO:0006357|GO:0072372|GO:0007224|GO:0005929|GO:0005737|GO:0021798|GO:0008
589|GO:0060271|GO:0021591|GO:0030991|GO:0035735|GO:0005856|GO:0035721 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_120208_PI430048170 0.00459452913367938 0.6039037315684985.38594106742804
5.35336369876291 5.49089482864243 P P P 5.97916469116362 6.16250875381518
6.26093138558326 P P P LNCV6_120208_PI430048170 mRNA
AGCTACTAGTTTTTATCCCTAGACCTTCTCTGCTCCAGTGTCTTGTTCATGTGTCCTGAC NM_033141RefSeq chr14 -

70722525 70809171 MAP3K9 4293 "mitogen-activated protein kinase kinase kinase 9, transcript variant 1"
GO:0005515|GO:0006355|GO:0043065|GO:0006915|GO:0018108|GO:0007256|GO:0005575|GO:0007257|GO:0005524|GO:0042803|GO:0006351|GO:0004706|GO:0046777|GO:0004674|GO:0006468|GO:0004713|GO:0004708 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134097_PI430048170 0.9755432286816481.00565309304639 8.13935804218723 8.4617193990162 8.62857920120541 P P P 8.56010542462159 8.13359220825321 8.51663669453879 P P P
LNCV6_134097_PI430048170 mRNA
CTGAATCTTCTTTGTTTCAAATGGTGCTGCATGTTTTCAACTACAATAAGTGCACTGTAA NM_004688RefSeq chr2 - 151270467 151289916 NMI 9111 N-myc (and STAT) interactor
GO:0005515|GO:0003712|GO:0005737|GO:0006954|GO:0006366|GO:0005654|GO:0007259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114643_PI430048170 0.1236504471093081.65617501794347 3.14354076656381 3.0735918170526 3.09408182499959 P P P 2.89054721411889 1.83169148900173 2.20156454741677 P A A
LNCV6_114643_PI430048170 mRNA
TGGGAAGATAAATTCACACTTCACCCCTTGTTGAGATCTCCAGCCTTGCTCCTCTGATAA NM_001242400 RefSeq chr5 + 42424451 42721878 GHR 2690 "growth hormone receptor, transcript variant 3"
GO:0005515|GO:0042977|GO:0006549|GO:0005886|GO:0019530|GO:0000255|GO:0019221|GO:0050731|GO:0042523|GO:0060396|GO:0060397|GO:0005615|GO:0042803|GO:0032870|GO:0031623|GO:0006101|GO:0000187|GO:0019838|GO:0006105|GO:0040014|GO:0006103|GO:0006631|GO:0044236|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122621_PI430048170 0.3934579068526980.228323715323795 0.262790229073209 1.48169840046545 1.14945871422845 A A A 0.375335495293119 4.46504326670146 1.93326442755217 A P A LNCV6_122621_PI430048170 mRNA
CATCAGAGACTTCACACTCAAGAGAAAGCATTTAAATGTAGGGTGTGTGGGAAAGCCTTC NM_181489RefSeq chr3 - 44439769 44477670 ZNF445 353274 zinc finger protein 445
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141748_PI430048170 0.2389527282166410.469903456435666 4.80646404048553 3.65758497902272 3.79406940464571 P P P 6.03375966451553 5.08204554689788 4.04770196519367 P P P LNCV6_141748_PI430048170 mRNA
CTCTCCCCAGATCTAGCTATTCTTTTGATATGGACAAAATAGTTTCTACATTTTACACTGNM_001005213 RefSeq chr11_JH159137v1_alt + 7153 8071 OR9G1 NA "olfactory receptor, family 9, subfamily G, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135101_PI430048170 0.4429809742374481.0500040466214 0.4061128514374020.3726102296657 0.57508654899833 A A A 0.477149019698607 0.370105864626064 0.297982446225373 A A A
LNCV6_135101_PI430048170 mRNA
AAAGAGATTCAGGACTACTCCCATCTTTGGTTACAAGAGAAGGAAACAGGTTATAATCCC NM_206996RefSeq chr1 - 117953664 118185225 SPAG17 200162 sperm associated antigen 17
GO:0005737|GO:0005874|GO:0036126|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135008_PI430048170 0.5269211183346651.23296123487073 0.277337302952886 1.29653611103023 0.484974024675874 A A A 0.327898675742398 0.287874018818062 0.708694904698491 A A A LNCV6_135008_PI430048170 mRNA
ATTTCTATACATAAGAACAAAAGCAAACACCTAGGACAGCAAACGCCAGGCGGTACAGGC NM_001256627 RefSeq chr11 + 1389898 1462689 BRSK2 9024 "BR serine/threonine kinase 2, transcript variant 1"
GO:0048471|GO:0005813|GO:0000287|GO:0031532|GO:0019901|GO:0005783|GO:0050321|GO:0030010|GO:0007409|GO:0006887|GO:0005524|GO:0005737|GO:0007067|GO:0018105|GO:0070059|GO:0004674|GO:0030182|GO:0000086|GO:0006468|GO:0061178|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130853_PI430048170 0.0383765519317687 1.89957023069311 1.58762734073844

1.51256941743133 2.11410672773562 A A A 1.15811379722408 0.888171999025859
0.357049793658968 A A A LNCV6_130853_PI430048170 mRNA
TGCCCTCTCTTAATAGTCACAGATACTGACACAAAACTTAAAAATGACCAGAAAACAATG NM_138966 RefSeq chr18
- 72743755 72867575 NETO1 81832 "neuropilin (NRP) and tolloid (TLL)-like 1, transcript variant 3"
GO:0032983|GO:0030054|GO:2000463|GO:0035255|GO:0045211|GO:0008542|GO:0048169|GO:0097120|GO:0014
069|GO:0007613|GO:0005576|GO:0060076 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136978_PI430048170 0.7010183057311731.16259709698091 1.87687830766781
2.59010714457907 1.09760708876057 A A A 2.3436404825298 0.364499035069481
1.93201353439995 A A A LNCV6_136978_PI430048170 mRNA
ATGCACACCTCTCTGATATTTTCTAGAACTACCTGAAACATTTTTGTCTGTAGGTCTAGT NM_001012977 RefSeq
chrX - 73077337 73079512 PABPC1L2A NA "poly(A) binding protein, cytoplasmic 1-like 2A" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141480_PI430048170 0.0179461638996032 0.5930967092975465.25512118896917
4.89369493398528 4.90107798537151 P P P 5.79844596574742 5.82386401910243
5.71674475585222 P P P LNCV6_141480_PI430048170 mRNA
GAATTGTCACACTTTTCCCTTCCCCACCAGTTCTTTAATAAAAGTATTTGAAAGGCAACA NM_001164425 RefSeq
chr19 - 7056204 7058634 MBD3L3 NA methyl-CpG binding domain protein 3-like 3 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_139828_PI430048170 0.0465948802969978 0.7889244032494 10.0166598560681
10.201409831558 10.1554042008532 P P P 10.6482607998438 10.3728786601149
10.3665039969407 P P P LNCV6_139828_PI430048170 mRNA
AACCAAACTGCTCCATGCCGGGTTATTTAAAAGAAAGGCAGAGTTTGTGGTGGCTTTTTT NM_013368 RefSeq chr19
- 40440840 40442598 SERTAD3 29946 "SERTA domain containing 3, transcript variant 1"
GO:0005515|GO:0030308|GO:0006355|GO:0005634|GO:0045893|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143547_PI430048170 0.0856529440361896 0.3360824759404062.941586378008
0.9906987214844041.79609738904259 A A A 3.73177591393987 3.60154162245479
3.77408350287925 P P P LNCV6_143547_PI430048170 mRNA
AGTGATAGAAGCATGTCAGAATTGAGAAGACATTTTGAAGCAAGAACAATGTGATGTACC NM_015473 RefSeq chr14
- 31291787 31420582 HEATR5A 25938 HEAT repeat containing 5A NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_78979_PI430048170 0.0210499900142456 0.667185642548776 4.11959314804514
4.36966829794085 4.15478098659684 P P P 4.61378209906748 4.7438028895
5.02054220409441 P P P LNCV6_78979_PI430048170 mRNA
AAGCAGGTTTTGTGAAGACATTTATTCTTTCTTGGACCTCAGATTTACCAGACATCTCAT NM_182931 RefSeq chr7
+ 105014189 105114085 KMT2E 55904 "lysine (K)-specific methyltransferase 2E, transcript variant 1"
GO:0005515|GO:0002446|GO:0005886|GO:0071300|GO:0003713|GO:0006325|GO:0042800|GO:0006351|GO:0045
171|GO:0043231|GO:0048384|GO:0006306|GO:0005737|GO:0016607|GO:0070688|GO:0030854|GO:0030218|GO:0
005654|GO:0007050|GO:0008270|GO:0042119|GO:0045893|GO:0019899|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138258_PI430048170 0.026499206175291 0.507988182541426 6.82985913466133
6.75818962919489 6.78751498160374 P P P 7.43924025177903 7.81766695550262
7.99627461897061 P P P LNCV6_138258_PI430048170 mRNA
CCTTGCCCTGGCATATATTGTGCCTTATTTATGCTGCAAATATAACATTAAACTATCAAG NM_006856 RefSeq
chr12 - 53512058 53626415 ATF7 11016 "activating transcription factor 7, transcript variant 2"
GO:0005515|GO:0006355|GO:0003700|GO:0005634|GO:0000122|GO:0000978|GO:0046872|GO:0006351|GO:0043
565|GO:0001078|GO:0005737|GO:0034399|GO:0016032|GO:0005654|GO:0019899|GO:0051019|GO:0008134 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126869_PI430048170 0.637215017812266 0.985047940859688 0.413812852906921

0.448066536219302 0.358871764668474 A A A 0.493383635499292 0.3871750224137
0.404529869143743 A A A LNCV6_126869_PI430048170 mRNA
GATGTGTTCTCAGACAACAAAGTCCCTTCAGAATCTTCATGTTGCATAAATGTTATGAAT NM_001147 RefSeq
chr8 - 6499650 6563263 ANGPT2 285 "angiopoietin 2, transcript variant 1"
GO:0005515|GO:0014070|GO:0005886|GO:0072012|GO:0031100|GO:0010812|GO:0005634|GO:0042995|GO:0050
928|GO:0050900|GO:0007281|GO:0005615|GO:0046872|GO:0009314|GO:0001666|GO:0014823|GO:0030971|GO:0
048014|GO:0060135|GO:0005102|GO:0005576|GO:0001525|GO:0045766|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137852_PI430048170 0.0585968494718337 1.42042142420096 5.74147691894029
5.91596348879042 5.48233347299425 P P P 5.46974436906714 5.17297421230411
4.96593062422482 P P P LNCV6_137852_PI430048170 mRNA
GTACCCCATCTTCCACATCTTTAAAGCTCATGTGAAAAATGCTGCATTTTTAATAAACTG NM_024608 RefSeq
chr15 + 75346989 75355251 NEIL1 79661 "nei endonuclease VIII-like 1 (E. coli), transcript variant 2"
GO:0003906|GO:0005815|GO:0005694|GO:0005634|GO:0008022|GO:0032074|GO:0003684|GO:0019104|GO:0005
737|GO:0016798|GO:0006284|GO:0005654|GO:0008270|GO:0006289|GO:0000737|GO:0006979 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135237_PI430048170 0.426002367410735 0.172739458608187 1.27385173348722
0.282417208043784 0.298214628394903 A A A 4.64530786835816 0.348369164684222
0.894709650075802 P A A LNCV6_135237_PI430048170 mRNA
ACTAAGCCAATACTGGAAGGGGCTAAGCAGATGTTTTCAAATCTTGCCAAAGGATCTAAA NM_001005162 RefSeq
chr11 + 5580876 5581884 OR52B6 NA "olfactory receptor, family 52, subfamily B, member 6" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139250_PI430048170 0.943668428888836 0.996067357557107 13.3123099789241
13.1903965415857 13.487070948259 P P P 13.2994282940421 13.2533960798542
13.4611543139903 P P P LNCV6_139250_PI430048170 mRNA
TTCACCTGCTATTTGGATGCAGGCCTTGCCAGAACTACCACTGGCAATAAAGTTTTTGGT NM_000969 RefSeq
chr1 + 92832036 92841924 RPL5 6125 ribosomal protein L5
GO:0005515|GO:0010467|GO:0006364|GO:0003723|GO:0019058|GO:0005634|GO:0006412|GO:0006413|GO:0006
414|GO:0005829|GO:0005737|GO:0000184|GO:0016032|GO:0008097|GO:0042273|GO:0070062|GO:0003735|GO:0
006614|GO:0019083|GO:0005730|GO:0006415|GO:0016020|GO:0030529|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138641_PI430048170 0.139436443645566 0.830328725098003 5.34395121799468
5.26778702435644 5.62238513870616 P P P 5.5289700155994 5.64776583285453
5.86624494253912 P P P LNCV6_138641_PI430048170 mRNA
GATAGAGTGCCATAGTGAAACTAAACACTGTGCATAAAGGTACATGAATTATTCCAGTTT NM_001302350 RefSeq
chr7 + 7640635 7879220 UMAD1 729852 "UBAP1-MVB12-associated (UMA) domain containing 1,
transcript variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138694_PI430048170 0.0448973065777493 1.44764652904669 7.94526707345941
8.31500430401457 8.39002826328128 P P P 7.72183083471318 7.78528919869963
7.57191516661543 P P P LNCV6_138694_PI430048170 mRNA
TTTTCTGTTTTGAGTGTCTTTCTTTGCAGGTTTCTGTAGCCGGAAGATCTCCGTTCCGCT NM_004643 RefSeq chr14
+ 23320187 23326185 PABPN1 8106 "poly(A) binding protein, nuclear 1"
GO:0005515|GO:0008380|GO:0006369|GO:0006396|GO:0010467|GO:0019054|GO:0006366|GO:0003723|GO:0031
124|GO:0019058|GO:0005634|GO:0005737|GO:0006936|GO:0046778|GO:0000166|GO:0016973|GO:0000398|GO:0
030529|GO:0019048|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51874_PI430048170 0.237197438457985 0.639053305558304 0.597575985864925
0.754531807274825 0.581921463032739 A A A 0.538762951608972 1.44458341071802
1.66699225069279 A A A LNCV6_51874_PI430048170 mRNA
TCTCCGAGACGCAGTGAAGGTGTGGTTCCAGAACCGGAGGACAAAGTACAAACGGCAGAA NM_004097 RefSeq

chr2 + 72917474 72934891 EMX1 2016 empty spiracles homeobox 1
GO:0043565|GO:0005515|GO:0021796|GO:0006355|GO:0005737|GO:0042493|GO:0005634|GO:0009791|GO:0001
701|GO:0021895|GO:0048854 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136820_PI430048170 0.531007199419507 0.977953008084587 0.254952918668681
0.268915391394693 0.387248653876926 A A A 0.377467696241685 0.320239904546001
0.312720541629263 A A A LNCV6_136820_PI430048170 mRNA
TTCTCAGACTCTATTCCGACATCCTCCAACATGGAGGAAACGCAGCAGAAATCCAACTTA NM_022579 RefSeq
chr17 - 63909604 63911258 CSHL1 1444 "chorionic somatomammotropin hormone-like 1,
transcript variant 1" GO:0008150|GO:0005179|GO:0005576|GO:0005575|GO:0046872 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_140795_PI430048170 0.537728685450158 1.08278332444764 10.4426088664911
10.2025722591962 10.5269647388359 P P P 10.0015534887524 10.2605713400576
10.5356790932689 P P P LNCV6_140795_PI430048170 mRNA
GGCTGGAGGTGTGCTTTGTGTGAAAGGTGAGCAATAAAGTATCTGTTAAGTTCTAAAAAA NM_015475 RefSeq
chr2 - 33583660 33599362 FAM98A 25940 "family with sequence similarity 98, member A,
transcript variant 1" GO:0072669 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127796_PI430048170 0.539473009838358 1.20014445741131 0.316521334877906
0.35337672541432 1.17641969380825 A A A 0.386581972875564 0.376039723865253
0.464988133485146 A A A LNCV6_127796_PI430048170 mRNA
ATCATGGAAATGATTCTCATTGACTAATGCATCATCTCACACTTTCATGAGTTCTTCCAT NM_021057 RefSeq chr9
- 21201468 21202205 IFNA7 NA "interferon, alpha 7" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145705_PI430048170 0.412602482825956 0.945362791171335 0.396588798715034
0.368128933832156 0.24827570257138 A A A 0.33515229066915 0.558810971355064
0.355709217426026 A A A LNCV6_145705_PI430048170 mRNA
TGGGACGGTCATTGTTTACTCTCAATAGTATGTGTTTGCCTTTGTCTTTTTGAGACATTT NM_031939 RefSeq chr18
- 50795119 50820064 MRO 83876 "maestro, transcript variant 1" GO:0005730 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134138_PI430048170 0.349101666544483 1.13956316030445 0.717887317558118
0.30329054304902 0.273556509375346 A A A 0.248592700650535 0.275422130234862
0.249160010193246 A A A LNCV6_134138_PI430048170 mRNA
TGGTGACCTGTAGCTGCAACTCCTTTTATTGTCAGAGAATGCCAAAAGCTATTTTTAAAA NM_001146684 RefSeq
chr17 - 8390704 8397826 RNF222 NA ring finger protein 222 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136840_PI430048170 0.999262183872677 0.992992544796446 2.04224532336349
0.440046266046633 2.2585995746876 A A A 0.413584153918149 2.3113990656194
2.01348101918668 A A A LNCV6_136840_PI430048170 mRNA
GAGGAAAATCGGTAATAAAATAACATGGATTGAATGTTTACTGTGCGTCAAGCACAGTTA NM_003828 RefSeq
chrX + 150693363 150765103 MTMR1 8776 myotubularin related protein 1
GO:0005737|GO:0006661|GO:0005886|GO:0004438|GO:0046856|GO:0044281|GO:0006644|GO:0035335|GO:0004
725|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56793_PI430048170 0.713519820569234 0.941107232521369 0.433790053580941
0.421369098889646 0.441040581427301 A A A 0.316896984130847 0.36078639389746
0.82462381401345 A A A LNCV6_56793_PI430048170 mRNA
AGGACTCTGGACCTTTGGAGGAAATGAAAGGGACCCAGTTGGAAATATAGTCTTTCTTCG NM_024326 RefSeq
chr10 + 102419813 102423136 FBXL15 79176 F-box and leucine-rich repeat protein 15
GO:0005515|GO:0030513|GO:0005737|GO:0004842|GO:0016567|GO:0000086|GO:0030282|GO:0009953|GO:0031
146|GO:0019005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138590_PI430048170 0.209921315579466 0.606525619272519 0.299510602701519

0.309233242086404 0.650739288759518 A A A 1.2900613251491 1.55278068722879
0.357573642535585 A A A LNCV6_138590_PI430048170 mRNA
CTTCCATTTACACATTTAGCTAGCCTCCCTAAAGTGTACTCTACCAATAATTGAAATCTT NM_001163941 RefSeq
chr7 + 20615621 20757014 ABCB5 340273 "ATP-binding cassette, sub-family B (MDR/TAP), member
5, transcript variant 1"
GO:0002481|GO:0005886|GO:0015562|GO:0002485|GO:0042626|GO:0055085|GO:0002591|GO:0005524|GO:0030
154|GO:0005887|GO:0008152|GO:0042391|GO:0002489|GO:0048058 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127568_PI430048170 0.602379849998914 0.963933304028246 0.54523942635671
0.501210588874214 0.266170539553415 A A A 0.411498559455003 0.567292645595585
0.503881611207686 A A A LNCV6_127568_PI430048170 mRNA
GCTACAGTTCGAGTGAAGAACAAAATGATACCCGGAAGCAACTTTCCAAGGAACAGAATG NM_001005365 RefSeq
chr8 + 43292441 43363185 POTEA NA "POTE ankyrin domain family, member A, transcript variant
2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136703_PI430048170 0.224653616563082 1.11427195926855 13.1040029401077
13.1679053390379 13.2364795385168 P P P 12.8965764278284 12.9309273932172
13.1965703668026 P P P LNCV6_136703_PI430048170 mRNA
ATGCTTGTGTGAGGCAATCATGGTGGCATCACCCATAAAGGGAACACATTTGACTTTTTT NM_018648 RefSeq
chr15 - 34341715 34343161 NOP10 55505 NOP10 ribonucleoprotein
GO:0005515|GO:0030515|GO:0015030|GO:0006364|GO:0005730|GO:0005732|GO:0072588|GO:0001522 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_34881_PI430048170 0.0132382190648032 0.649952415319213 5.72678372572299
6.00539253918888 5.69426979626035 P P P 6.38433827665616 6.51955694829857
6.40429809832047 P P P LNCV6_34881_PI430048170 mRNA
GGGGGGAATGGGTCTTTTCTAAATTGTTAAAAGCAGTTCATGCCATTATTCTTAATAAAC NM_006743 RefSeq
chrX + 48574352 48581165 RBM3 5935 "RNA binding motif (RNP1, RRM) protein 3"
GO:0005515|GO:0006396|GO:0003723|GO:0009409|GO:0015934|GO:0045727|GO:0005634|GO:0006412|GO:0006
417|GO:0030425|GO:0005737|GO:0000166|GO:0035196|GO:0043023 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139050_PI430048170 0.747481230153389 0.79117589724707 0.680965212220921
0.974148214455631 1.76681937508511 A A A 1.23953888230154 2.33079295036586
0.504402594686537 A A A LNCV6_139050_PI430048170 mRNA
GAGGCTTCCCACGGGGAGGCAGGAAGAAATAAAGGTCTTTGGCTTTCTCCAGGCAAAAAA NM_176782 RefSeq
chr1 - 54609176 54623527 FAM151A 338094 "family with sequence similarity 151, member A"
GO:0008150|GO:0003674|GO:0016020|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_110279_PI430048170 0.0294889502225956 0.79072869245188 13.2114476741016
13.281747167773 13.2354227920278 P P P 13.4787376884158 13.5499972308517
13.7074306754408 P P P LNCV6_110279_PI430048170 mRNA
AAATACAGGAAGCTCCAGGGCTGGAGCACCTCTGAGATGGAATTGATAACATGGTCTTAA NM_001303471 RefSeq
chr18 - 79972866 79988592 TXNL4A 10907 "thioredoxin-like 4A, transcript variant 2"
GO:0008380|GO:0005515|GO:0010467|GO:0000245|GO:0007067|GO:0000398|GO:0000375|GO:0005681|GO:0005
654|GO:0005682|GO:0046540|GO:0051301 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_139957_PI430048170 0.351925971141106 0.959688314068807 11.2766238325861
11.2460387713968 11.1419457558313 P P P 11.2336418442458 11.3584677849331
11.2508150542175 P P P LNCV6_139957_PI430048170 mRNA
CACCTGTGAATAAATCTCAGCTGACCCCAGCCCACCTGTGAATAAATGTTTTTGCAGGAG NM_024078 RefSeq
chr12 + 132144426 132152473 NOC4L 79050 nucleolar complex associated 4 homolog (S.

cerevisiae)
GO:0005515|GO:0000462|GO:0031965|GO:0006364|GO:0032040|GO:0005730|GO:0005634|GO:0016021|GO:0030692 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76946_PI430048170 0.8656573826171 1.12771640088476 3.42264215485279 2.02263922132129 2.81185494457698 P A A 2.70794224037685 2.92604991199902 2.37967437368124 A P A LNCV6_76946_PI430048170 mRNA
ATTTGTACTGATCCTCTGGTGTCCAAAATTTCCTTTACTGGTTCAACAACTACAGGAAAG NM_170740 RefSeq chr6 + 24494968 24537207 ALDH5A1 7915 "aldehyde dehydrogenase 5 family, member A1, transcript variant 1"
GO:0006678|GO:0009013|GO:0004777|GO:0006536|GO:0046459|GO:0004029|GO:0007268|GO:0006749|GO:0006083|GO:0009791|GO:0007417|GO:0042803|GO:0007269|GO:0006681|GO:0022904|GO:0005739|GO:0051289|GO:0006105|GO:0005759|GO:0009450|GO:0006006|GO:0006650|GO:0042135|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72994_PI430048170 0.177009277103143 1.14644165561419 5.38943258532176 5.19110048316481 5.1585107283103 P P P 4.92658468283109 4.97585820675949 5.23651047656483 P P P LNCV6_72994_PI430048170 mRNA
TCGAGTGACCATTCCAACAGATTTGATTGCCTCCAGTGGAGATATCATCAAGGTATCAGC NM_001165928 RefSeq chr3 + 49470131 49535618 DAG1 1605 "dystroglycan 1 (dystrophin-associated glycoprotein 1), transcript variant 1"
GO:0005515|GO:0002162|GO:0034453|GO:0071679|GO:0016340|GO:0006607|GO:0005615|GO:0032403|GO:0016010|GO:0016011|GO:0001618|GO:0030198|GO:0045211|GO:0006509|GO:0008307|GO:0005856|GO:0042169|GO:0070062|GO:0030336|GO:0005509|GO:0030027|GO:0005604|GO:0060441|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133494_PI430048170 0.206342582314845 0.528519358325255 0.270884514165995 2.37684957862231 0.301758360292974 A A A 2.08948187975065 2.30455119723656 2.3913646088838 A A P LNCV6_133494_PI430048170 mRNA
GCTTAGTAATGAGTCATAGCTACCCACAATAACCTAATAAAAACTCAAGTTCATCCCAAA NM_001286533 RefSeq chr12 + 110502199 110532086 RAD9B 144715 "RAD9 homolog B (S. pombe), transcript variant 4"
GO:0006260|GO:0005515|GO:0030896|GO:0006281|GO:0005654|GO:0000077 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108039_PI430048170 0.0168971277926371 0.633914781880028 4.10290275855945 4.32409459754589 4.27686858189888 P P P 4.90860454076287 5.08320414745475 4.66378844265942 P P P LNCV6_108039_PI430048170 mRNA
TGTATGGTCACTAGAGATTGGGACTTACCCTTTAGGTTTTAGGAGGCTTGAGAATGGAAG NM_015726 RefSeq chr1 - 160215714 160262560 DCAF8 50717 "DDB1 and CUL4 associated factor 8, transcript variant 1" GO:0005515|GO:0005737|GO:0016567|GO:0005634|GO:0080008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134256_PI430048170 0.394657856276826 1.75832623045587 3.45328791057475 1.80940051801113 3.77360835531352 P A P 3.03722983185392 1.97621764789549 1.94748606579925 P A A LNCV6_134256_PI430048170 mRNA
TCACCCTCTTCGGAAACGTCGTAAAAGAAAGAAGAAAGAAGAAGAAATGGAAACTCTGGG NM_001729 RefSeq chr4 - 74746237 74794672 BTC 685 betacellulin
GO:0005515|GO:0048011|GO:0005154|GO:0008284|GO:0043066|GO:0005886|GO:0048015|GO:0045597|GO:0045840|GO:0005576|GO:0048146|GO:0005615|GO:0007173|GO:0008543|GO:0045087|GO:0016021|GO:0035810|GO:0008083|GO:0038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135914_PI430048170 0.205482953784992 1.0853154794789 14.0278534549353 13.8893348975831 13.8203977173397 P P P 13.7905723306433 13.8773712154242 13.7187108830953 P P P LNCV6_135914_PI430048170 mRNA
CCTCACACGCTTTTCTACAATGGCATTCAATAAAGTGCACGTGTTTCTGGTGCTAAAAAA NM_021034 RefSeq

chr11 - 319672 320914 IFITM3 10410 "interferon induced transmembrane protein 3, transcript variant 1"
GO:0005515|GO:0005886|GO:0035456|GO:0019221|GO:0035455|GO:0032897|GO:0005765|GO:0009615|GO:0051607|GO:0006955|GO:0060337|GO:0046597|GO:0031902|GO:0016021|GO:0034341|GO:0070062|GO:0045071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143317_PI430048170 0.551463182401361 0.96975737215562 0.28267366179444 0.447032164649472 0.313862972644469 A A A 0.481363875142422 0.371678733741557 0.324241053615403 A A A LNCV6_143317_PI430048170 mRNA
CCTTCTTTCTTCTTTTCATAACTTTGGGTTATGTTTCTGCTACCAGCAGAGATTCTTAGC NM_033191 RefSeq
chr17_JH159148v1_alt - 56456 57423 KRTAP9-4 85280 keratin associated protein 9-4 GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136210_PI430048170 0.121511160536305 0.532565964611509 3.8506050908415 3.58888316249759 2.58181130152528 P P A 4.30903111500544 4.33384612772416 4.3878647679093 P PP LNCV6_136210_PI430048170 mRNA
ATGGAGGCGGGACACAGGGCCAGTAGGAGCAATAGGATTTTAATAAACAGAACCCATCCC NM_173596RefSeq
chr12 + 56230035 56237845 SLC39A5 283375 "solute carrier family 39 (zinc transporter), member 5, transcript variant 1"
GO:0048026|GO:0001654|GO:0070315|GO:0030509|GO:0034224|GO:0055085|GO:0061351|GO:0003674|GO:0016323|GO:0046873|GO:0006829|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67274_PI430048170 0.0644408824392938 1.86427165380713 5.10964465430956 4.84953446071312 5.27678727217388 P P P 3.56603818239598 4.39470676738868 4.45298072128057 P P P LNCV6_67274_PI430048170 mRNA
TTGAAGAGAGCGAGGAGAACCATTCTGGAAACTCTAGGCTATGCATGTTTAAAGATCTGG NM_053064RefSeq chr14 + 51860303 51969800 GNG2 54331 "guanine nucleotide binding protein (G protein), gamma 2, transcript variant 1"
GO:0031681|GO:0005886|GO:0008283|GO:0005834|GO:0007268|GO:0030168|GO:0044281|GO:0071380|GO:0007191|GO:0006112|GO:0016020|GO:0071377|GO:0007596|GO:0071870|GO:0004871|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128158_PI430048170 0.35599589797498 0.848140599479201 0.492808933774684 0.46185226517874 0.430674043410401 A A A 0.38491277039361 1.0072361738254 0.638225708086416 A A A LNCV6_128158_PI430048170 mRNA
TTGGATTATTGCTATAGTGTTTCAGTAAACACCTTTGTGGACTGAATCCATCTATGTGGA NM_003257RefSeq
chr15_KI270905v1_alt - 1983495 2106621 TJP1 7082 "tight junction protein 1, transcript variant 1"
GO:0005515|GO:0005516|GO:0030054|GO:0005886|GO:0045471|GO:0007605|GO:0005634|GO:0006921|GO:0005829|GO:0043296|GO:0016323|GO:0046581|GO:0005737|GO:0016324|GO:0005913|GO:0014704|GO:0032496|GO:0061024|GO:0071333|GO:0042493|GO:0019904|GO:0001825|GO:0045177|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142473_PI430048170 0.571381942048783 0.785105908856003 0.456512675036611 0.400989976064928 0.318902333763185 A A A 0.269566505794768 1.3816127641112 0.271916511309856 A A A LNCV6_142473_PI430048170 mRNA
GAAAATCTGTGTTTAATCAACTGAGGCCTCTCAACCAAATAACATCTCAGAGATTAAGTT NM_000329RefSeq chr1 - 68428823 68449959 RPE65 6121 retinal pigment epithelium-specific protein 65kDa
GO:0008286|GO:0052885|GO:0005886|GO:0007603|GO:0005783|GO:0060042|GO:0052884|GO:0001523|GO:0046872|GO:0044297|GO:0071257|GO:0050908|GO:0001895|GO:0042574|GO:0006776|GO:0031090|GO:0042572|GO:0007468|GO:0007601|GO:0004744 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143368_PI430048170 0.127048473256383 1.01303621380277 0.317952402118819 0.290686691785248 0.302682684188074 A A A 0.292647582164886 0.28546418683221 0.277241066981298 A A A LNCV6_143368_PI430048170 mRNA
GGGATTTTAGAAAATAGAAGTTACCTTTGTGTGTGTTTTAGGGAAGGTAGAGAAGAATCT NM_000888RefSeq chr2

- 160099665 160200313 ITGB6 3694 "integrin, beta 6, transcript variant 1"
GO:0008305|GO:0005886|GO:0007275|GO:0009615|GO:0043235|GO:0005178|GO:0006954|GO:0007160|GO:0001618|GO:0007229|GO:0030198|GO:0016032|GO:0007155|GO:0009897|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134867_PI430048170 0.000443883829712188 1.88746642666105 4.97569254398654 4.86984213094712 4.75736387226305 P P P 4.04735981482802 3.95797138313107 3.8496929127047 P P P LNCV6_134867_PI430048170 mRNA
ATACTCAGAAAGTTTAACGCTGCTTTCTTTCTCTTTGCGCGCGTCACACTTGCTTGGAGA NM_213604RefSeq chr19
- 1505017 1513189 ADAMTSL5 339366 ADAMTS-like 5
GO:0006508|GO:0005578|GO:0001527|GO:0008270|GO:0005576|GO:0004222|GO:0008201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131024_PI430048170 0.6141351893592520.9346807675472078.47940041209749 8.82263806486745 9.0508622989287 P P P 8.79177099365866 8.78622164593963 9.10072965444376 P P P LNCV6_131024_PI430048170 mRNA
CCGTCTTGCAAAGTATAGTGACCCCTGTTTCCATTAAATTTGAATAAAGACTATTTTTGC NM_005626RefSeq chr1
- 29147737 29182125 SRSF4 6429 serine/arginine-rich splicing factor 4
GO:0006397|GO:0008380|GO:0006369|GO:0010467|GO:0048025|GO:0006366|GO:0031124|GO:0005634|GO:0006406|GO:0000166|GO:0016607|GO:0000398|GO:0002244|GO:0000375|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143598_PI430048170 0.0911473003827719 0.8489866703709040.444109385525858 0.4673577438908790.315458086930882A A A 0.6395540127564590.496895800302703 0.788854537115543A A A LNCV6_143598_PI430048170 mRNA
CGTACGTCCTTCCAATCCACCGTTCATGTGTTTATTTACATATATGTGTATCTGTGAAAA NM_018969RefSeq chrX
+ 53049323 53080614 GPR173 54328 G protein-coupled receptor 173
GO:0007165|GO:2001223|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0097211|GO:0004968 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130534_PI430048170 0.2989449896108070.694233970103105 1.39939880742521 0.3940827506104331.10833966846643 A A A 1.38845416773387 2.06593259571559 0.995055234396826A A A LNCV6_130534_PI430048170 mRNA
TCACCCTAAATCCTGGAGAATACAAGAAAAATTTGAAAAGGGGCCAGACGCTGTGGCTCA NM_138441RefSeq chr6
- 73425132 73452320 MB21D1 115004 Mab-21 domain containing 1
GO:0071360|GO:0051607|GO:0045087|GO:0002230|GO:0032481|GO:0002218|GO:0009190|GO:0005525|GO:0005524|GO:0003677|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130019_PI430048170 0.4502804548161541.16715948335325 4.03680265531345 3.82504628576097 3.51369784968181 P P P 3.42683793875542 4.02345349483847 3.16590545550051 P P P LNCV6_130019_PI430048170 mRNA
TATCCCCGCCAAGGGTTTCCTCTCAGTCATTTGTTTACCAGAAACATGAAAACTGCCTGT NM_031475RefSeq chr1
+ 6424787 6460944 ESPN 83715 espin
GO:0005903|GO:0017124|GO:0005737|GO:0051015|GO:0031941|GO:0051494|GO:0030046|GO:0007605|GO:0051491|GO:0032420|GO:0007626|GO:0032426 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134822_PI430048170 0.6082985565056371.46680979487678 2.03130296624727 0.2713533403152460.419126428517972A A A 0.3609496643783950.306963776243604 0.999902855263337A A A LNCV6_134822_PI430048170 mRNA
TCCTGAGTTCTACAGTATGTGAACAATATCGTGTGAAGTGTGTTTTTGCATTTGTGCATT NM_020923RefSeq chr2
+ 206274640 206314426 ZDBF2 57683 "zinc finger, DBF-type containing 2, transcript variant 1"
GO:0008270|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129758_PI430048170 0.8294485074456621.21786085388443 3.06695655641895 2.31655830952909 1.0890587670261 P A A 1.88868383542341 1.47399414617027 2.64089312351808 A A P LNCV6_129758_PI430048170 mRNA

GGAGGGGTGGACAATGAGAGTTGAGAATCCTGATTTGGTATAACAAATAAATTTACTTCC NM_001010979 RefSeq chr1 - 154199085 154206365 C1orf189 388701 chromosome 1 open reading frame 189 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135965_PI430048170 0.4404324486525456.41265754835087 1.21271811396902 4.94515679052232 0.313594717319834A P A 0.9874241977624610.331960182816937 1.08261131111911 A A A LNCV6_135965_PI430048170 mRNA
AAACTGGGGCAATAGGTGAGCAGGGAGAAGAGTCATGGCCAAATAAAATTGAGACATACC NM_178344RefSeq chr3 + 37386268 37418374 C3orf35 339883 "chromosome 3 open reading frame 35, transcript variant G" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78483_PI430048170 0.7728661868836421.02820914801559 7.12665182254646 7.06248405313221 7.12134321754439 P P P 6.63670661259014 7.30660797159934 7.16496305831758 P P P LNCV6_78483_PI430048170 mRNA
TGGTATTTCGAAGGACTCTATCCAACCTATTATATATGCCGCTCCTACGAGGACTGCTGT NM_030796RefSeq chr7 - 55470612 55572507 VOPP1 81552 "vesicular, overexpressed in cancer, prosurvival protein 1, transcript variant 1" GO:0007165|GO:0006355|GO:0031301|GO:0004871|GO:0030659|GO:0006351|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117400_PI430048170 0.00828615772309382 1.68385272119665 9.79428651080993 9.86326693356818 9.80182786461471 P P P 9.19758104843372 9.08092853403634 8.91242008472116 P P P LNCV6_117400_PI430048170 mRNA
ATGAGAAGATAGCATACGGGGATGTGATGTTGGAGAACTACAGCCATCTAGTTTCTGTGG NM_001242713 RefSeq chr7 + 102363860 102380633 LOC100289561 NA uncharacterized LOC100289561 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_38415_PI430048170 0.2479238042088910.43519155911606 0.3963549778155090.44416929889228 0.387467871376464A A A 2.400644624959 0.3309301257578211.38858798012994 A A A LNCV6_38415_PI430048170 mRNA
GTACCTTGCCTTTCTGTCCAGGTTTGGTGGAATTGACCTATATATAAATGGTATAAAGAG NM_022785RefSeq chr22 - 43528743 43812337 EFCAB6 64800 "EF-hand calcium binding domain 6, transcript variant 1" GO:0006355|GO:0005509|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57623_PI430048170 0.00182551808356239 1.20011455785915 13.389540417392 13.3264561956472 13.3646235204574 P P P 13.1230439785529 13.1225950476043 13.0447642520295 P P P LNCV6_57623_PI430048170 mRNA
TAAAAAGTTTGCAGAGACCCAACCTAAAAAGGACACACCACGGAAAGAGAAGGGTTCACG NM_001404RefSeq chr11 - 62559600 62573988 EEF1G 1937 eukaryotic translation elongation factor 1 gamma GO:0005515|GO:0010467|GO:0016020|GO:0005634|GO:0009615|GO:0003746|GO:0044267|GO:0006412|GO:0070062|GO:0006414|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131261_PI430048170 0.11112738680899 1.05812535095488 0.610309495880081 0.6586905874438780.581791179976859A A A 0.5986740716262390.501818718287587 0.504696486734282A A A LNCV6_131261_PI430048170 mRNA
ATCTTTGCTGGCTTACCTGTAAAATCTGTGGTCTCCATAAATACTGGGAAAATAAATAGG NM_001244898 RefSeq chr9 - 112217714 112333026 PTBP3 9991 "polypyrimidine tract binding protein 3, transcript variant 6" GO:0008380|GO:0006397|GO:0048025|GO:0043249|GO:0000166|GO:0033119|GO:0003723|GO:0045595|GO:0005634|GO:0009653 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140695_PI430048170 0.3926364076127571.05265346431214 0.311646234722431 0.3147979988885310.510219626267773A A A 0.3128251350218180.278151653990431 0.332176303411256A A A LNCV6_140695_PI430048170 mRNA
CTTTTATGATTCTTTTTGTAAGCCCTAGGGGCTCTAAAATGGTTTCACTTATTTATCCCA NM_000586RefSeq chr4 - 122451470 122456495 IL2 3558 interleukin 2 GO:0008284|GO:0005134|GO:0031851|GO:0030307|GO:0030890|GO:0007267|GO:0042523|GO:0007204|GO:0005

615|GO:0007205|GO:0042104|GO:0006955|GO:0030101|GO:0043208|GO:0045944|GO:0002903|GO:0046013|GO:0
007155|GO:0060999|GO:0045822|GO:0032729|GO:0043066|GO:0032740|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140356_PI430048170 0.232466023181416 1.06492824669736 0.51382472493877
0.329644642875379 0.430362535838071 A A A 0.281852782029404 0.361600315891303 0.362514775014 8
A A A LNCV6_140356_PI430048170 mRNA
GGTGTCATAACTAGAGCACGGGCGTTATGTAAGTTTCTAAGAATTTAGAGGATAAATAAT NM_003042 RefSeq chr3
+ 10992733 11039249 SLC6A1 6529 "solute carrier family 6 (neurotransmitter transporter), member 1"
GO:0030424|GO:0010288|GO:0005886|GO:0009986|GO:0005328|GO:0051939|GO:0007268|GO:0009636|GO:0014
054|GO:0042220|GO:0055085|GO:0014074|GO:0007269|GO:0051592|GO:0016020|GO:0005887|GO:0009744|GO:0
006810|GO:0032229|GO:0051260|GO:0016021|GO:0007612|GO:0032355|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132972_PI430048170 0.358742458174296 0.696684554708512 0.455769524172476
0.467614939796436 0.360921580175703 A A A 1.5756898994413 0.505894824323989
0.481375931456374 A A A LNCV6_132972_PI430048170 mRNA
TCTTATCTGTGTGTCTGCATTTTCTAATCCTTTTTGCCCCAGGCAAGGTCCCTGTATCTC NM_001010909 RefSeq
chr6_GL000255v2_alt + 2238873 2244003 MUC21 NA "mucin 21, cell surface associated, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67755_PI430048170 0.0081351054671915 1.5756793589969 5.80906702023767
5.97984975251961 6.15169899087476 P P P 5.35496785397641 5.15930295767929
5.46253837189963 P P P LNCV6_67755_PI430048170 mRNA
AGATTGAAAGAACTCTGTGAGCAGTATGGCATATGGCTTCATGTGGAGGGTGTGAATCTG NM_015027 RefSeq chr16
+ 14974962 15038330 PDXDC1 23042 "pyridoxal-dependent decarboxylase domain containing 1,
transcript variant 1" GO:0005794|GO:0030170|GO:0016831|GO:0019752|GO:0043231 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_132946_PI430048170 0.176538493124048 1.42186877229902 11.5155275389363
11.5930569453369 11.6606623236292 P P P 11.5513334422212 10.6141645900633
10.9218489933387 P P P LNCV6_132946_PI430048170 mRNA
GGACTCCTCATCTTTATATTCACGAAAAAGCAATCTGAAGAAAACAAATAAAAGCCTGTG NM_021237 RefSeq chr3
- 53885198 53891962 SELK 58515 selenoprotein K
GO:0005886|GO:0070059|GO:0005783|GO:0005789|GO:0006816|GO:0016021|GO:0006979|GO:0042802 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130171_PI430048170 0.00379037429084382 0.677261143972828 11.9453645176725
11.8870636929015 11.7194365249271 P P P 12.3375202556777 12.4914147526828
12.4148962959885 P P P LNCV6_130171_PI430048170 mRNA
GATGGTTAACATAGAGCTGCTTCTGTGTAAATGCTGCTTATTTTAAACACTAAAAAGCGT NM_004421 RefSeq chr1
- 1335277 1349112 DVL1 1855 dishevelled segment polarity protein 1
GO:0005515|GO:0034504|GO:0006366|GO:0090263|GO:0035372|GO:0045202|GO:0031122|GO:0042802|GO:0005
109|GO:0007507|GO:0007411|GO:0043025|GO:0016055|GO:0019901|GO:0060134|GO:0050808|GO:0001505|GO:0
010976|GO:0035176|GO:0019899|GO:0045893|GO:0071340|GO:0032091|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139848_PI430048170 0.790967171894165 0.993417591610006 0.371375784379021
0.352335709381299 0.262412309865843 A A A 0.330683026672607 0.352891396746105
0.33336205528544 A A A LNCV6_139848_PI430048170 mRNA
TACAGCAAACTTTGGCATTTATGTGGAGCATTTCTCATTGTTGGAATCTGAATAAACCAA NM_019604 RefSeq chr11
+ 122838497 122872639 CRTAM 56253 "cytotoxic and regulatory T cell molecule, transcript variant 1"
GO:0008037|GO:0051606|GO:0005886|GO:0001913|GO:0050776|GO:0045954|GO:0005102|GO:0002860|GO:0050
798|GO:0002355|GO:0050715|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101697_PI430048170 0.672459265414472 0.887282326981995 2.20601341807358

2.15391815366201 2.76363529171507 A A A 2.88818102803975 2.0003457244838
2.69271370738338 P A P LNCV6_101697_PI430048170 mRNA
AGTGTACCTCTGCACTCAATGCTGGAATCAAATCCAAAGCTTTTAATTCTCTCAACAAGA NM_139168 RefSeq chr5
+ 66144834 66183616 SREK1 140890 "splicing regulatory glutamine/lysine-rich protein 1, transcript
variant 2" GO:0008380|GO:0006397|GO:0000166|GO:0005681|GO:0005654 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134112_PI430048170 0.3525062648201141.36145777728153 2.02586628337187
2.91350437187512 2.91860014201891 A A P 2.42851847380062 1.55733255941306
2.52418694669501 A A P LNCV6_134112_PI430048170 mRNA
GACACATTGCTCTGTACTTAGTAATTACCCACCCTTCTTTTCCTTTCAATAAAATGTCCA NM_001167940 RefSeq chr7
- 122318423 122886759 CADPS2 93664 "Ca++-dependent secretion activator 2, transcript variant 3"
GO:0045921|GO:0042734|GO:0030054|GO:0016082|GO:0045211|GO:0015031|GO:0046872|GO:0030659|GO:0009
267|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128226_PI430048170 0.605980942793435 1.57097856677142 0.323092524145122
2.14973687836551 0.268869402250918 A A A 0.2553298757109340.692534771277346
0.658279130707483 A A A LNCV6_128226_PI430048170 mRNA
CAGGGTTCACTTTTGTCATAGAATTGTTTCTTGGCCCATTTAAGAGAGATACTTTGTTTA NM_080743 RefSeq chr6
- 89095958 89118081 SRSF12 135295 serine/arginine-rich splicing factor 12
GO:0000395|GO:0000244|GO:0048025|GO:0000166|GO:0000381|GO:0003723|GO:0016482|GO:0005654|GO:0051
082|GO:0050733 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102643_PI430048170 0.00938739346370813 0.7323810694724081 1.0523120697242
11.0568193387601 11.1223329943347 P P P 11.4845788168666 11.6404605861392
11.4481830857388 P P P LNCV6_102643_PI430048170 mRNA
GACTTTGCTCGAGGCACCTTTTTTCCTGTTTCTCCTTTTCTGTTGTCGAGTAAAATTTCA NM_004629 RefSeq chr9 -
35073837 35080016 FANCG 2189 "Fanconi anemia, complementation group G"
GO:0005515|GO:0009314|GO:0005886|GO:0005730|GO:0007286|GO:0043240|GO:0003684|GO:0005739|GO:0001
541|GO:0005737|GO:0006281|GO:0000075|GO:0005654|GO:0007005 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_136267_PI430048170 0.2900137822351170.7067945112105997.30609162181115 7.1442835012847
7.5942270522946 P P P 7.2309791909329 7.83913165154147 8.31395384197809 P P P
LNCV6_136267_PI430048170 mRNA
CCATTCAGATAAGCTATAATCTGGTCTTTAAGGAACACAACTTTAAAACTGCAGCTTTCT NM_015261 RefSeq chr11
- 134152441 134224532 NCAPD3 23310 "non-SMC condensin II complex, subunit D3"
GO:0005515|GO:0007076|GO:0016020|GO:0042585|GO:0000799|GO:0005654|GO:0035064|GO:0031618|GO:0000
278|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128003_PI430048170 0.000922016308832343 2.58620569869966 9.40286238326406
9.22859208942979 9.27124042016126 P P P 8.09112874247242 7.92677365089213
7.75896025580835 P P P LNCV6_128003_PI430048170 mRNA
TTCCAGAGCCCCAGTTTGTAAATGAACCTGTGTCACATTTGATAAACACTATCCTGGGCG NM_001042576 RefSeq
chr20 - 17613677 17682283 RRBP1 6238 "ribosome binding protein 1, transcript variant 1"
GO:0016020|GO:0005783|GO:0005840|GO:0030176|GO:0004872|GO:0015031|GO:0006412|GO:0001649 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140468_PI430048170 0.0210497287453832 0.5259028186168249.05129029701222
9.1060526835936 9.09061956797358 P P P 9.73567239379757 10.0464300562403
10.2085302247933 P P P LNCV6_140468_PI430048170 mRNA
CTGTCCTAGGAATTTGATTCTTCCAGAATGACCTTCTTATTTATGTAACTGGCTTTCATT NM_001178010 RefSeq chr22
+ 19479825 19520612 CDC45 8318 "cell division cycle 45, transcript variant 1"
GO:0005515|GO:0005813|GO:1900087|GO:0005656|GO:0005634|GO:0003688|GO:0006260|GO:0006271|GO:0000
082|GO:0005737|GO:0000083|GO:0003697|GO:0006270|GO:0003682|GO:0000076|GO:0000727|GO:0043138|GO:0

005654|GO:0032508|GO:0031298|GO:0000278|GO:0031938|GO:0031261|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138732_PI430048170 0.2700136059266281.60276626009364 0.362452307915966
0.702033792004351 1.63761797396205 A A A 0.3142975036789750.303941230247628
0.356746864069172 A A A LNCV6_138732_PI430048170 mRNA
TAGGTAACACATGCCTGTCTGTCATAAACAGTACAAACGTGAGCAAACACTGTCAAAAAA NM_001204210 RefSeq
chr17 + 78231309 78240987 TMEM235 NA "transmembrane protein 235, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129345_PI430048170 0.9871935931297741.03608639802555 0.34290408455082
0.507225482515665 1.39110193266544 A A A 0.4660937049582131.05117241937314
0.743131031262594 A A A LNCV6_129345_PI430048170 mRNA
TGTAGCTTCCTAGCTAGTGTCATTTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAA NM_198477 RefSeq chr19
- 42428542 42442984 CXCL17 284340 chemokine (C-X-C motif) ligand 17
GO:0006935|GO:0005576|GO:0001525|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138981_PI430048170 0.0723621797127866 0.5583107790222218.32994773665577
8.48965813021672 8.35335850818478 P P P 8.7181508466512 9.44619749512293
9.42468170996473 P P P LNCV6_138981_PI430048170 mRNA
AAGATAATGATGAGTAACTTAACCAGCACATTTCTCCTGTTTACACTCGGGGGATTTTTT NM_005686 RefSeq chr1
+ 204073117 204127743 SOX13 9580 SRY (sex determining region Y)-box 13
GO:0043565|GO:0005515|GO:0006355|GO:0003700|GO:0045586|GO:0005654|GO:0005634|GO:0009653|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134965_PI430048170 0.7495043647725211.01754012864472 10.2459823015899
10.3418262318626 10.3696026168859 P P P 10.1829100888353 10.2720909577018
10.4200444203542 P P P LNCV6_134965_PI430048170 mRNA
ACAGCAGTGGTATGGGGTTTATGATGCTATAAAACAATGTCTGAAAAGTTGCCTAGAATA NM_018145 RefSeq chr15
- 40735883 40755336 RMDN3 55177 "regulator of microtubule dynamics 3, transcript variant 1"
GO:0005739|GO:0005515|GO:0000922|GO:0005874|GO:0006874|GO:0006915|GO:0005741|GO:0005634|GO:0016
021|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141174_PI430048170 0.0393960171290660.6043707016321461 0.3974789093741
10.3857268945195 10.8631270830849 P P P 11.0017835981341 11.201462334919
11.6082174679232 P P P LNCV6_141174_PI430048170 mRNA
GTTGGGTTTCTCATAAGTATCCTAGTTCATGTACATCCGAATGCTAAATAATACTGTGTT NM_145808 RefSeq chr7
- 135926754 135977456 MTPN 136319 myotrophin
GO:0051247|GO:0030424|GO:0048471|GO:0030307|GO:0005634|GO:2000812|GO:0010557|GO:0006417|GO:0005
829|GO:0021707|GO:0051092|GO:0006584|GO:0030182|GO:0016049|GO:0016202|GO:0043403|GO:0008290|GO:0
051146|GO:0010613|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137424_PI430048170 0.5475016033532551.02208966588076 0.420677676648751
0.279809301335175 0.325039746242844 A A A 0.2844052558033060.316536124852093
0.333198838970216 A A A LNCV6_137424_PI430048170 mRNA
CTCCTGAGTTTTGGTTTGCTATTATATTAATGGGGATGCCTCTAACACAGACAGCAACAC NM_001286121 RefSeq
chr6 + 25754698 25781175 SLC17A4 10050 "solute carrier family 17, member 4, transcript variant 2"
GO:0016324|GO:0005436|GO:0016020|GO:0005887|GO:0035435|GO:0035725|GO:0006796|GO:0006814 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64332_PI430048170 0.0487382263179144 1.41265480697529 2.49413954748198
2.42839166457163 2.0755795222726 A A A 2.07264132233878 1.68198463859164
1.75158176281205 A A A LNCV6_64332_PI430048170 mRNA
GTCTCTGTTGACCTGCCAGATAGGAAATAGCGCCAGAGTTGCTGCAATCCACGTCTCCCT NM_144693 RefSeq chr19
- 8809575 8832304 ZNF558 148156 "zinc finger protein 558, transcript variant 1"
GO:0008150|GO:0006355|GO:0005634|GO:0005575|GO:0003677|GO:0046872|GO:0006351 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_73064_PI430048170 0.16835986782653 1.17146572025836 12.0540105904416 12.1800144899619
12.3556608938509 P P P 11.9223688990676 11.8102762643751 12.1650006003704 P P P
LNCV6_73064_PI430048170 mRNA
GCCCAGTTGGGTTTTGATTTATATAAGTAGTTTAGACCTTCTCTTCATAATCTTGCTCTG NM_014041 RefSeq chr3 +
52705840 52708181 SPCS1 28972 signal peptidase complex subunit 1 homolog (S. cerevisiae)
GO:0005515|GO:0005787|GO:0010467|GO:0006614|GO:0030176|GO:0006412|GO:0045047|GO:0003674|GO:0050
796|GO:0005789|GO:0006508|GO:0008233|GO:0044267|GO:0006465 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_106924_PI430048170 0.1347740241196180.9568547115940020.252737661889169
0.2840286916987760.329956711857215 A A A 0.4030989889692 0.325538428865629
0.328673941299025 A A A LNCV6_106924_PI430048170 mRNA
GAAGACAACAATAAATTAATCAAGAGCTTTCCTCATATCTCAGAACCTATCCTCTGTAAG NM_001278309 RefSeq
chr12 - 4615507 4649047 AKAP3 10566 "A kinase (PRKA) anchor protein 3, transcript variant 1"
GO:0005515|GO:0001669|GO:0006928|GO:0005634|GO:0010738|GO:0097228|GO:0007338|GO:0005737|GO:0008
104|GO:0035686|GO:0007178|GO:0007340|GO:0051018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131197_PI430048170 0.0764559856575470.8454145652625111.1051734458294
11.0330234977445 11.0705491041389 P P P 11.1970141199172 11.4505128674138
11.2771816063653 P P P LNCV6_131197_PI430048170 mRNA
CTCCAGGCCTCAATTTTCCCTTCTTGTAAAATGGAATCTATATCTATAAAGGTTTCTTCA NM_016533 RefSeq chr12 -
564295 663741 NINJ2 4815 "ninjurin 2, transcript variant 1"
GO:0005887|GO:0042246|GO:0007399|GO:0007158 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127870_PI430048170 0.6888673200019320.9707255088902961 0.590502531582 10.312588564045
10.2782984823134 P P P 10.4429143030891 10.520628992499 10.3628659925002 P P P
LNCV6_127870_PI430048170 mRNA
TGTCACTGGTGGTCATGTTGCTTAGTTGAAGAGAATAAAGGGAATAAGATTTCCTGGGTG NM_001080417 RefSeq
chr16 - 30778448 30787202 ZNF629 23361 zinc finger protein 629
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140491_PI430048170 0.4883574151844941.02065786068473 0.380753086938313
0.3810099452696410.278966298674863 A A A 0.3049301412749670.325753412776419
0.323836786837135 A A A LNCV6_140491_PI430048170 mRNA
AACTACAACATCAACACCTATGCCCGATTCTGCAAGTGCTGCCGTGAGGTGGGCCTGCAG NM_001277269 RefSeq
chr11 + 17547372 17645944 OTOG NA "otogelin, transcript variant 1" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_136720_PI430048170 0.0162155909411531 0.2365586858262766.27816522781898
6.07080254072701 6.44967496449349 P P P 7.72145822239121 8.29903366311791
8.83197749521999 P P P LNCV6_136720_PI430048170 mRNA
TCAGATCAAACCATTTTACCTGGAGTTTGGTACTGGTTTTTACTTCTCTGAATCTGTATA NM_015472 RefSeq chr3 -
149517234 149658101 WWTR1 25937 "WW domain containing transcription regulator 1, transcript variant 1"
GO:0005515|GO:0010467|GO:0008284|GO:0006367|GO:0016567|GO:0045599|GO:0017145|GO:0010718|GO:0005
634|GO:0031146|GO:0035414|GO:0042803|GO:0032835|GO:0005829|GO:0005737|GO:0035264|GO:0045944|GO:0
072307|GO:0060993|GO:0007179|GO:0090090|GO:0005667|GO:0006355|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_65232_PI430048170 0.0325887451386401 1.44851803629236 14.2044543535623
14.2955708180533 13.9995507021885 P P P 13.8866733438148 13.4972369891592
13.4910525040957 P P P LNCV6_65232_PI430048170 mRNA
GAGGGGAAGAAGAGTCTCAGACTGTGGGACACGGACTCGCAGAATAAACATATATGTGGC NM_024710 RefSeq
chr19 - 55452978 55461682 ISOC2 79763 "isochorismatase domain containing 2, transcript variant 2"

GO:0031648|GO:0005739|GO:0005515|GO:0005737|GO:0008152|GO:0005634|GO:0003824 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128783_PI430048170 0.419074447187121 0.425680374522627 0.364342329766756 0.34239956397816 0.262916059911686 A A A 0.322279319519566 0.338734609599029 2.65680794835613 A A P LNCV6_128783_PI430048170 mRNA
ATAAAGATATTGTTCAAATTGAAGGGCAAAGGCCAGGTTCAGCAATTTTCAAACTGTATG NM_001039752 RefSeq chr11 + 63289957 63311774 SLC22A10 387775 "solute carrier family 22, member 10"
GO:0022857|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65639_PI430048170 0.366861180983533 0.627774128460915 1.80170954863423 1.39216664181799 1.7751760824556 A A A 1.29116964311058 2.45159274624723 2.86181614827115 A P P LNCV6_65639_PI430048170 mRNA
AACTACAGAATGAAGCTGTATTTATGTGGACTGCTGAACTAGAAAATATAGCCACTCTCT NM_019024 RefSeq chr2 - 36981000 37084345 HEATR5B 54497 HEAT repeat containing 5B GO:0016020|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133853_PI430048170 0.000211179225405913 1.85626179916353 11.0359434499859 11.1844841468256 11.0911376041423 P P P 10.1146826493782 10.2875935350551 10.2306659203387 P P P LNCV6_133853_PI430048170 mRNA
ATTGCCGTATCTGTGCGTTCCTTCATCCTGGTCCTGGCTTTATGGAACACCATGTTTTTA NM_006675 RefSeq chr12 + 3077354 3286564 TSPAN9 10867 "tetraspanin 9, transcript variant 1"
GO:0008150|GO:0003674|GO:0005886|GO:0097197|GO:0016021|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137054_PI430048170 0.072015108600225 1.0480422662606 0.439176652977573 0.496082387300654 0.475115500971871 A A A 0.364397804269516 0.403095352256905 0.43938927347153 A A A LNCV6_137054_PI430048170 mRNA
TGTTATCTATCTATCTATCTATATAACTATAACCACACGCCGTGTAGACACCCGCTGCCA NM_145285 RefSeq chr10 + 99532932 99536523 NKX2-3 159296 NK2 homeobox 3
GO:0048621|GO:0043367|GO:0005634|GO:0005575|GO:0050900|GO:0048536|GO:0006351|GO:0048535|GO:0043565|GO:0003674|GO:0008150|GO:0048541|GO:0045944|GO:0042127|GO:0002317|GO:0006641|GO:0030225|GO:0042475|GO:0022612|GO:0001776 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67040_PI430048170 0.060501398912278 1.03173737106784 0.431044517821653 0.467316873517734 0.435873911352434 A A A 0.37997650948539 0.394709487967275 0.424238817945611 A A A LNCV6_67040_PI430048170 mRNA
CTGTTGGAGTCCTGTACATAGAATGGCTGGATGCCTTTGGTGAAGGAAAAGGAAAAACAG NM_194298 RefSeq chr10 - 59650763 59709891 SLC16A9 220963 "solute carrier family 16, member 9"
GO:0015718|GO:0034220|GO:0005886|GO:0008028|GO:0016021|GO:0046415|GO:0015293 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124228_PI430048170 0.0259738064756817 0.349785721793842 0.530553058584402 0.50266955024758 0.265849481435962 A A A 2.06179255379703 2.28504413944328 1.36105563051341 A A A LNCV6_124228_PI430048170 mRNA
AAGAAGCTGGTGGAACAGAATGGAACAGATGACTGGAAAGTTATTGCCAATTATCTCCCG NM_001130173 RefSeq chr6 + 135181314 135219173 MYB 4602 "v-myb avian myeloblastosis viral oncogene homolog, transcript variant 1"
GO:0005515|GO:0048538|GO:0016363|GO:0005829|GO:0048872|GO:0000082|GO:0071987|GO:0045944|GO:0030183|GO:0071354|GO:0006816|GO:0006338|GO:0006355|GO:0000122|GO:0048566|GO:0000978|GO:0001701|GO:0006351|GO:0051574|GO:0001077|GO:0051571|GO:0007596|GO:0003682|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141862_PI430048170 0.22076293898723 1.04809504061122 0.535889053844572 0.647562267978704 0.529062135070589 A A A 0.489190268005328 0.505951210094362 0.517021991775877 A A A LNCV6_141862_PI430048170 mRNA

GTTGTAGTTTGAACTTTAAAGGATTCCAGTCCTCCGAAAAACAGGATTAGACTCAAATCA NM_001172655 RefSeq chr19 + 52570663 52587174 ZNF701 55762 "zinc finger protein 701, transcript variant 1" GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131891_PI430048170 0.839600341342379 0.903159713855571 1.86582322541781 1.26878479396282 0.252417445444561 A A A 0.360954438638484 1.98164980949979 1.4796034334709 A A A LNCV6_131891_PI430048170 mRNA
GTGCTTGTTATTATATATTTGAATAAACAGTGCTGCAAGTACTTGCCATGAAGGATCTGA NM_001040709 RefSeq chr1 + 109466477 109482142 SYPL2 NA synaptophysin-like 2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135585_PI430048170 0.0391787732570409 0.75412960763329 7.53184356880286 7.29116394446893 7.25534210350702 P P P 7.75616154270433 7.76268333698744 7.79647792246511 P P P LNCV6_135585_PI430048170 mRNA
CCAGCAAGTATCCAACCAACTTGGTTCTGCTTCAATAAATCTTTGGAAAAACTCAAAAAA NM_003380 RefSeq chr10 + 17228258 17237593 VIM 7431 vimentin GO:0005882|GO:0005515|GO:0003725|GO:0043005|GO:0005212|GO:0045109|GO:0005886|GO:0070307|GO:0006928|GO:0060395|GO:0006921|GO:0005829|GO:0042802|GO:0005737|GO:0001948|GO:0097110|GO:0060020|GO:0016032|GO:0045111|GO:0005856|GO:0031252|GO:0070062|GO:0005777|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140526_PI430048170 0.915478015030826 1.00317836395985 0.441459753180442 0.490516734339131 0.469141259706626 A A A 0.517450737988169 0.50466123640745 0.360485081391553 A A A LNCV6_140526_PI430048170 mRNA
TCCTAGCACCTGGCTAGTTTCTAACATGTTTTGTGCAGCACAGTTTTTAATAAATGCTTG NM_006889 RefSeq chr3 + 122077848 122121141 CD86 942 "CD86 molecule, transcript variant 2" GO:0005515|GO:0008284|GO:0005886|GO:0045404|GO:0031295|GO:0007267|GO:0001878|GO:0043231|GO:0042104|GO:0051607|GO:0006955|GO:0002309|GO:0007173|GO:0016032|GO:0004872|GO:0043011|GO:0034341|GO:0045630|GO:0070062|GO:0048011|GO:0043017|GO:0009986|GO:0048015|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141659_PI430048170 0.0510826124779061 0.785178304835505 10.9538856563624 11.1047863397699 10.9029137004908 P P P 11.5277784320189 11.2217271751032 11.2460387713968 P P P LNCV6_141659_PI430048170 mRNA
TAGCTGTGTGTCAGTGTCAGCCCTGTATTGTATTTGATTATCTCCTGAATAAAGTTATGA NM_001166269 RefSeq chr14 - 22946227 22957142 HAUS4 54930 "HAUS augmin-like complex, subunit 4, transcript variant 1" GO:0051297|GO:0003674|GO:0007067|GO:0005813|GO:0005737|GO:0005874|GO:0005819|GO:0070652|GO:0051225|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67823_PI430048170 0.609705952089417 0.966251143890559 9.44873875718906 9.24310244211834 9.17204311381366 P P P 9.26253624095641 9.41076490837712 9.34983917681011 P P P LNCV6_67823_PI430048170 mRNA
AATCTGCATGAACGGACTCTGAGCGTGCTGGCCTGCCGGTACGTGTCAGAAGTGGTGATT NM_001282203 RefSeq chr17 - 81902900 81911239 PCYT2 5833 "phosphate cytidylyltransferase 2, ethanolamine, transcript variant 5" GO:0006646|GO:0004306|GO:0005789|GO:0044281|GO:0008654|GO:0005575|GO:0006644|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143267_PI430048170 0.38499637368317 1.93009310512165 2.37377811531448 2.10044278738706 0.295733798189795 A A A 0.891548673608718 1.12278899105235 0.594887367934279 A A A LNCV6_143267_PI430048170 mRNA
ATGAACAGCCAGAACTGCAGAAGAAACAGTTGTGCTCTTTCCAGATCTACGAAGTTCCCT NM_001322 RefSeq chr20 - 23823766 23826675 CST2 1470 cystatin SA GO:0010951|GO:0004869|GO:0005615|GO:0001580 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_143392_PI430048170 0.0105056932898875 0.3232506619147273.88215554800276
3.14354076656381 3.59672695004858 P P P 4.64785249341095 5.24940912155222
5.56287986807273 P P P LNCV6_143392_PI430048170 mRNA
AACCAAGTGTGTATTCCTGTGTATGAATTTGTAGAACTGATTTCTGCTTCAAGAGAAGCT NM_033224RefSeq chr7
- 44876292 44885385 PURB 5814 purine-rich element binding protein B
GO:0003700|GO:0003690|GO:0003697|GO:0046332|GO:0045637|GO:0005654|GO:0005634|GO:0000122|GO:0003
729|GO:0005662|GO:0006351|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139685_PI430048170 0.2466691855534660.8926811792648760.412278413437015
0.3541284347253610.362031706753136A A A 0.7266838889893860.462498062770866
0.411040752395466A A A LNCV6_139685_PI430048170 mRNA
AAAGTTGCCAAAAAAGAAAAGCCGAAAGCCGTGATTCCGATCTACGAAGGCGATTACCAC NM_001098519
RefSeq chr12 + 122183119 122203471 LRRC43 254050 "leucine rich repeat containing 43, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145365_PI430048170 0.0524754128706811.37980543597416 3.5913303484541
3.79395777044634 4.04532952764671 P P P 3.31969326526772 3.50102447263768
3.23995093815371 P P P LNCV6_145365_PI430048170 mRNA
ATAGAGTTCTGTCAAAAAGATGGGGAAAGAGCATCAGGCCATGGTCTAAAAACCTTCCCC NM_015545RefSeq chr7
- 99416738 99438839 PTCD1 26024 pentatricopeptide repeat domain 1
GO:0005739|GO:0000049|GO:0005759|GO:0042780 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130863_PI430048170 0.45316167586097 1.13222214978474 8.82757119886992
9.14771016139385 9.40110901851916 P P P 8.87409779133514 8.81165576552937
9.18196512296149 P P P LNCV6_130863_PI430048170 mRNA
CAGTGCTACTGTGCCTTCTATTTAATTCTTTCAGTCCTTCAATAAAAAGCTGCTTATTGA NM_024528RefSeq chrX -
119925049 119943772 NKAP 79576 NFKB activating protein
GO:0005515|GO:0046638|GO:0033077|GO:0000122|GO:0006351|GO:0031490|GO:0071425|GO:0005737|GO:0007
219|GO:0003682|GO:0019827|GO:0005654|GO:0030851|GO:0045892 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127238_PI430048170 0.0658162191154964 1.04160590090797 0.436590247952357
0.4867830098774570.459340857148925A A A 0.3713945579368980.401147485174942
0.433512334404184A A A LNCV6_127238_PI430048170 mRNA
CTTAACACTACCAATTTCCCATTTTGGAACCTAATAAATATTTAGTCTGCATTGCTGGCA NM_020989RefSeq chr2
- 208128136 208129830 CRYGC 1420 "crystallin, gamma C"
GO:0005515|GO:0005737|GO:0005212|GO:0043010|GO:0005634|GO:0007601 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_62552_PI430048170 0.1501427315556761.20597909639268 9.52642193469392 9.74785976107631
9.50726687664546 P P P 9.52332089869068 9.34077213497314 9.08639947847415 P P P
LNCV6_62552_PI430048170 mRNA
ATCCTGCCACAGTCGCTGGACCTGTTGCTCTGCATCAACATGGCCCATGTCAGCCCCCTG NM_032366RefSeq chr16
- 634426 636366 C16orf13 84326 "chromosome 16 open reading frame 13, transcript variant 1"NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143981_PI430048170 0.2344929973850081.09595819408684 7.55863831292666
7.69093989859041 7.67246140889668 P P P 7.56942235511385 7.60219654033249
7.34391469012551 P P P LNCV6_143981_PI430048170 mRNA
GGGGATGGTGGGATATTTGTGTCTGTGTTCTTATAATATATTATTATTCTTCCTTGGTTC NM_002999RefSeq chr20 -
45325288 45348424 SDC4 6385 syndecan 4
GO:0005515|GO:0001657|GO:0007603|GO:0005886|GO:0044281|GO:0051894|GO:0030198|GO:0005080|GO:0045
860|GO:0001968|GO:0030204|GO:0030203|GO:0070062|GO:0043202|GO:0009986|GO:0005975|GO:0005796|GO:0
006027|GO:0001523|GO:0006024|GO:0008150|GO:0005887|GO:0051496|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_139058_PI430048170 0.6510403676833420.9450821247794035.48200092409064
5.79095896455993 5.93015706827054 P P P 5.84847213284028 5.61233185497192
5.99674549666808 P P P LNCV6_139058_PI430048170 mRNA
CTAGCACATCCACATTTTTAATAACTTAGTGATTTTCAAGGTCCCCTGTCCACATTAAAA NM_001160305 RefSeq
chr16 + 58515478 58520527 SETD6 79918 "SET domain containing 6, transcript variant 1"
GO:0005515|GO:0005737|GO:0051059|GO:0050727|GO:0032088|GO:0005654|GO:0005634|GO:0018026|GO:0016
279. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97113_PI430048170 0.0917369441987974 0.6348467653638242.77921392397263
3.39373860156958 3.28545326716823 A P P 3.80256082464616 3.41541550348064
4.17828267084572 P P P LNCV6_97113_PI430048170 mRNA
TTAAGAGTTCTAGAAGATGGAAAACAGCAGGTTCAAGTGGTGGGATTACAGGAACGGGAG NM_001243952
RefSeq chr5 + 62306161 62387184 KIF2A 3796 "kinesin heavy chain member 2A, transcript variant
3"
GO:0008017|GO:0005515|GO:0005813|GO:0005871|GO:0097228|GO:0003777|GO:0005524|GO:0030154|GO:0007
399|GO:0005829|GO:0019886|GO:0000922|GO:0003774|GO:0016020|GO:0007596|GO:0008152|GO:0005876|GO:0
090307|GO:0000278|GO:0007052|GO:0016887|GO:0007019|GO:0051301|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128002_PI430048170 0.2733989810994051.03256065174158 0.332247801648278
0.2684166667040020.373937602847252A A A 0.2835401630715090.266534642887379
0.287713236394634A A A LNCV6_128002_PI430048170 mRNA
GAAAACTATCTTCTTTGTTTGAAAGGAACTATTGCTAAATGCAGAACAAGCTCATTGCAG NM_001033953 RefSeq
chr11 - 14966668 14972286 CALCA 796 "calcitonin-related polypeptide alpha, transcript variant 3"
GO:0005515|GO:0009408|GO:0010523|GO:0005615|GO:0032403|GO:0032757|GO:0042802|GO:0031623|GO:0001
984|GO:0007218|GO:0051482|GO:0071356|GO:0043025|GO:0001944|GO:0007566|GO:0007568|GO:0045651|GO:0
002031|GO:0002027|GO:0005179|GO:0043542|GO:0007189|GO:0045892|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142276_PI430048170 0.2175095642460231.64742337183618 1.32617010828743
1.45382886749913 0.309684941777617A A A 0.4851093993429050.376081410831985
0.309918827057367A A A LNCV6_142276_PI430048170 mRNA
TAATCATTCACAGTGCAAGGGAGCTGGGCCATGAGCCCTCCATGCAGGAGCTGAAGGAGT NM_183374RefSeq
chr10 + 93061263 93068697 CYP26C1 NA "cytochrome P450, family 26, subfamily C, polypeptide 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137141_PI430048170 0.3221996420891930.9437815921769439.48072807671078
9.54920622281409 9.35370688246559 P P P 9.47848691656295 9.63651517576989
9.52117165677021 P P P LNCV6_137141_PI430048170 mRNA
CCTGGATCCTTACTCCTGCATTGTTCTTTGCCAGAGACCTATTTAAAAATTTTAAAATTCNM_001381RefSeq chr2 +
74554384 74557551 DOK1 1796 "docking protein 1, 62kDa (downstream of tyrosine kinase 1), transcript
variant 1"
GO:0008286|GO:0005515|GO:0007165|GO:0048471|GO:0005737|GO:0005158|GO:0007265|GO:0005634|GO:0005
057|GO:0007169|GO:0007166|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144695_PI430048170 0.159283664905851 1.12211499753011 0.630763615522084
0.4289620620671660.652686871247931A A A 0.2896481320799220.415989904578746
0.510040156147492A A A LNCV6_144695_PI430048170 mRNA
CAGCATGTATTATGCACTTCATTTCTCTACTGTGTGGAGAAAGCAATAAACATTATGAGA NM_012259RefSeq chr6
+ 125749585 125761269 HEY2 23493 hes-related family bHLH transcription factor with YRPW motif 2
GO:0005515|GO:0060045|GO:0000988|GO:0003700|GO:0006366|GO:0000983|GO:0003184|GO:0003186|GO:0007
219|GO:0016580|GO:0017053|GO:0014031|GO:0060716|GO:0046983|GO:0010667|GO:0001102|GO:0045746|GO:0
000122|GO:0065004|GO:0060347|GO:0060633|GO:0045607|GO:0061156|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_135202_PI430048170 0.00196723000908102 0.4478654977822844.39184572179507
4.18224111996247 4.57679309647545 P P P 5.56866821208628 5.33426237844675
5.72491002257804 P P P LNCV6_135202_PI430048170 mRNA
GGATCATTCCAGTCATAAAGACTTATTACATGTACTATTTCTTGCTACCTGTGAAAAGGT NM_012287RefSeq chr3
- 195274735 195443088 ACAP2 23527 "ArfGAP with coiled-coil, ankyrin repeat and PH domains 2"
GO:0043547|GO:0008060|GO:0017137|GO:0016020|GO:0032312|GO:0036010|GO:0008270|GO:0010008 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135557_PI430048170 5.79531561398733e-05 0.2057583655747834.21726109523188
3.98754325669276 4.28410604730229 P P P 6.28419576947253 6.44802440511476
6.59896513644944 P P P LNCV6_135557_PI430048170 mRNA
ATTGTACTACTTGGCTGAATTTCCATATAGTTTTTACTGTGTATGGGGAGGTTGTAGTAT NM_030627RefSeq chr5
+ 173888327 173960991 CPEB4 80315 cytoplasmic polyadenylation element binding protein 4
GO:0005515|GO:0043524|GO:0035235|GO:0005737|GO:0071230|GO:0000166|GO:0005783|GO:0002931|GO:0014
069|GO:0005634|GO:0042149|GO:0030425 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103116_PI430048170 0.0734240436834955 0.6962244182905145.67236819880095
5.39319307897056 5.85379509264014 P P P 6.36914020597113 5.83471842016168
6.26571570738051 P P P LNCV6_103116_PI430048170 mRNA
GTATTCCTTTCCAATTCCGTCCAGAAAATGAGGAAGACATCCTGGTTGTTACCACTCAGG NM_001261390 RefSeq
chr17 + 48830987 48865245 CALCOCO2 10241 "calcium binding and coiled-coil domain 2, transcript
variant 1"
GO:0005515|GO:0048471|GO:0005737|GO:0005794|GO:0016020|GO:0016032|GO:0005634|GO:0034341|GO:0005
856|GO:0042803|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55767_PI430048170 0.3499664884554890.9208566627773095.63222923893763 5.32037016527065
5.63034052311428 P P P 5.71532145845613 5.61783690464655 5.62637605391557 P P P
LNCV6_55767_PI430048170 mRNA
TTATAATCAGTGCTTTCCCAACTCTTGGGTTGCTCTCCATAACTATGTATTTGTGAAAGA NM_020066RefSeq chr1
+ 240091884 240475189 FMN2 56776 formin 2
GO:0048471|GO:0005886|GO:0048477|GO:0015629|GO:0015031|GO:0005829|GO:0035556|GO:0003674|GO:0016
192|GO:0005938|GO:0030659|GO:0043066|GO:0042177|GO:0070649|GO:0005819|GO:0005730|GO:0071456|GO:0
007275|GO:0003779|GO:0046907|GO:0006974|GO:0005902|GO:0051295|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132083_PI430048170 0.4547700237562370.7790818698777980.433498981173686
0.4849668089182570.584034228636335A A A 0.3475010833113460.625309147783826
1.40003499348799 A A A LNCV6_132083_PI430048170 mRNA
TATTTGTCTAAAGAATGGGGAAAGAGAAGCGGTTGTCTGTTCACCTCATCCTTGCCACTC NM_000428RefSeq chr14
- 74498182 74612331 LTBP2 4053 latent transforming growth factor beta binding protein 2
GO:0031012|GO:0005515|GO:0009306|GO:0019838|GO:0005509|GO:0005578|GO:0007179|GO:0006605|GO:0008
201|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137391_PI430048170 0.4808237030294270.6465941509952520.53844744398094
1.56733077967867 0.373908564254489A A A 0.2794504747254231.61505440098239
2.18800458798424 A A A LNCV6_137391_PI430048170 mRNA
TTCTGAAACCAACTTGTCCCAGGCCACAGGAGTGTATATGTTTCATAATCTTTATCAAGA NM_033284RefSeq chrY
+ 6910685 7091683 TBL1Y 90665 "transducin (beta)-like 1, Y-linked, transcript variant 1"
GO:0016575|GO:0000118|GO:0006357|GO:0003714|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131040_PI430048170 0.0871230630018666 1.55727785027784 6.30944925047401
6.43723317742255 6.2399243100432 P P P 6.00494626696666 5.72976270636991
5.24111159875631 P P P LNCV6_131040_PI430048170 mRNA
AGTTACCGCATGTCACAGAAGGTGCACCGGAAAATGCTCCCGTCCAACCTGAGTCCTACC NM_033194RefSeq chr17

+ 42122737 42123353 HSPB9 94086 "heat shock protein, alpha-crystallin-related, B9"
GO:0005515|GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137797_PI430048170 0.481490350324069 0.755762054032742 0.444119989842727
0.506043149732313 0.484203452822703 A A A 1.50631783317522 0.408426010644253
0.445760951944677 A A A LNCV6_137797_PI430048170 mRNA
CCTGTAGTGCCTCTATAGAAGTACCCACAGAAAGTAAAGTATCACATTTATAAATACCAA NM_007361 RefSeq chr14
- 52004801 52069228 NID2 22795 nidogen 2 (osteonidogen)
GO:0031012|GO:0005515|GO:0009986|GO:0007160|GO:0030198|GO:0005518|GO:0005509|GO:0071711|GO:0005
576|GO:0007155|GO:0070062|GO:0005604 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144565_PI430048170 0.791156162007736 0.986067341734016 11.428393238449
11.3465544538219 11.1523171694695 P P P 11.3204379495804 11.3331123856906
11.3480658450339 P P P LNCV6_144565_PI430048170 mRNA
TGTCTGCTTCTCAGATTCCAAGGACTGGAATTAAAACCTTTCCTGGGACTCTGGAAAAAA NM_015399 RefSeq chr11
- 66337332 66345111 BRMS1 25855 "breast cancer metastasis suppressor 1, transcript variant 1"
GO:0005515|GO:0016575|GO:0051059|GO:0042826|GO:0006325|GO:0006915|GO:0005634|GO:0032088|GO:0000
122|GO:0006351|GO:0090312|GO:0005737|GO:2000210|GO:0005654|GO:0004407|GO:0070822|GO:0045892 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136495_PI430048170 0.508977950580058 1.022901242699 0.422866463107589
0.291813395571505 0.337421991409751 A A A 0.288041636540495 0.319790611841882
0.348711783532383 A A A LNCV6_136495_PI430048170 mRNA
ATTGATATAACAAGGGTTCTGGAAGGGTACACAGAAAACCCACAGCTCGAAGAGTGGTGA NM_001302753
RefSeq chr20 + 46118253 46129745 CD40 958 "CD40 molecule, TNF receptor superfamily member 5,
transcript variant 3"
GO:0005515|GO:0035631|GO:0005886|GO:0030890|GO:0032735|GO:0005615|GO:0003823|GO:0032855|GO:0043
231|GO:0051607|GO:0005737|GO:0051092|GO:0006954|GO:0090037|GO:0043406|GO:0042100|GO:0045944|GO:0
043089|GO:0004872|GO:0004871|GO:0043123|GO:0031625|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131691_PI430048170 0.429078084198236 1.04984532449782 0.307884500202238
0.314291644269853 0.514854470937057 A A A 0.318144025768373 0.281229529254189
0.336326610931735 A A A LNCV6_131691_PI430048170 mRNA
GGGATTTTTCTAGTTAACTCTGAGTTAAGCACGAACTCCTTTCTTTTGTTAATTGTTGGA NM_001102608 RefSeq chr3
+ 130560333 130677044 COL6A6 131873 "collagen, type VI, alpha 6"
GO:0005581|GO:0022617|GO:0030198|GO:0030574|GO:0005578|GO:0005576|GO:0007155 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140781_PI430048170 0.295599410114781 0.641323705596966 0.325969611494543 1.1080487768715
2.35332884359888 A A A 1.7454137583192 2.62257619139787 1.91539373912385 A P A
LNCV6_140781_PI430048170 mRNA
GGAAAGAGACATAGCAGGTGAAAGTTTAAATAAAACCCCTCACTACTTCCTGTTGACTAC NM_001160243 RefSeq
chr17 + 5419640 5429665 RPAIN 84268 "RPA interacting protein, transcript variant 1"
GO:0006261|GO:0005737|GO:0006281|GO:0016605|GO:0005730|GO:0006310|GO:0005634|GO:0006606|GO:0032
403|GO:0009411|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110389_PI430048170 0.105860227619835 1.28348018107395 6.75516327991121
6.71702248158365 6.78054422923938 P P P 6.46941631323216 6.55170641620014
6.11605827066938 P P P LNCV6_110389_PI430048170 mRNA
TTATTCTGCTCTGGCATCTCTGCTGGCCCAAGGAGAAAGCCGACCCCTATCCCTATCCTG NM_024660 RefSeq
chr19 - 35739249 35742450 IGFLR1 79713 IGF-like family receptor 1
GO:0005515|GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_58006_PI430048170 0.24902416311173 0.509458574104139 3.2088242914435

0.266664404832234 2.30150614519993 P A A 3.241544853286 3.5873478873373
3.12241808524895 P P P LNCV6_58006_PI430048170 mRNA
AACACTATTCAGAATGGGTGTAGCAAGAGGAACCATCACAACATTAAGAAATGGAGAAGT NM_022918 RefSeq
chr11 + 87037843 87328834 TMEM135 65084 "transmembrane protein 135, transcript variant 1"
GO:0007031|GO:0016021|GO:0005777 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_130270_PI430048170 0.233264137139734 0.491922054308414 0.660319571442739
3.2881451446912 2.93992039044593 A P P 3.74589487619708 3.69692414043949
3.61890001333785 P P P LNCV6_130270_PI430048170 mRNA
GCTAAAGCATGTAAGAGTGAATTTATTATAGCAGTAATCTTGTGTTTCTCCTGATGTGCA NM_022129 RefSeq
chr10 - 68282659 68332927 PBLD 64081 "phenazine biosynthesis-like protein domain containing,
transcript variant 1"
GO:0005515|GO:0009058|GO:0050680|GO:0010719|GO:0060394|GO:0060392|GO:0003674|GO:0005737|GO:0030
277|GO:0016853|GO:0030512|GO:0010633|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_137321_PI430048170 0.808397276456169 1.01812264461215 4.39974577822175
4.50927525846208 4.41678007866513 P P P 4.43177771689084 4.61819596936151
4.16494740870027 P P P LNCV6_137321_PI430048170 mRNA
ATTTTATATGGGCACCCTGCCACTCTTCTAAAAGACTACATTTTGCAGGCAATTTTGCAA NM_001101337 RefSeq
chr3 + 153484494 153502697 C3orf79 NA chromosome 3 open reading frame 79 NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_134838_PI430048170 0.355040383186989 0.813464481568231 4.76640611141848
4.05505332167585 4.82448096553257 P P P 4.52847838664772 5.03305056928421
5.04015263336573 P P P LNCV6_134838_PI430048170 mRNA
GCTTCAAGAACATTCAAGCTGTTGGTGTGTTAAAAAATGCATTGTATTGATTTGTACTGG NM_001130518 RefSeq
chr8 - 19404160 19602545 CSGALNACT1 55790 "chondroitin sulfate N-
acetylgalactosaminyltransferase 1, transcript variant 1"
GO:0008037|GO:0051216|GO:0008283|GO:0044281|GO:0015014|GO:0009653|GO:0046872|GO:0005622|GO:0030
206|GO:0030198|GO:0032580|GO:0030204|GO:0047238|GO:0030203|GO:0047237|GO:0050653|GO:0008955|GO:0
050650|GO:0050651|GO:0005975|GO:0019276|GO:0015020|GO:0008376|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_142272_PI430048170 0.0430760133804425 1.48951208281358 7.43969003517128
7.82262829330788 7.9310773753958 P P P 7.04588395255494 7.13540284650821
7.3188420879824 P P P LNCV6_142272_PI430048170 mRNA
CTATGGCTGTTGAGGTTCTCATTTTGGTTTGTTTTAATTTTTTGAACTTTGGGTACCTGT NM_199186 RefSeq chr7
+ 134646778 134679815 BPGM 669 "2,3-bisphosphoglycerate mutase, transcript variant 2"
GO:0007585|GO:0004082|GO:0005975|GO:0004083|GO:0048821|GO:0016311|GO:0004619|GO:0006096|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130859_PI430048170 0.509360472910595 0.795938114678335 0.98677958699346
0.287016128062783 0.296057636134494 A A A 0.573510742228362 0.413582529249476
1.45690933283604 A A A LNCV6_130859_PI430048170 mRNA
GGAAGTATGGGAACTAAGTTAAGGAAATCCAGAAAGAAGCCAAGATATATCCTTATTTTC NM_014058 RefSeq
chr4_GL000257v2_alt + 141139 191291 TMPRSS11E 28983 "transmembrane protease, serine 11E"
GO:0050890|GO:0004252|GO:0005887|GO:0006508|GO:0008236|GO:0005576 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_142029_PI430048170 0.345730317995521 0.739849954665448 2.25680637286105
0.638473796456489 1.32220295019877 A A A 1.91942602496674 2.24188928926205
1.77851397761286 A A A LNCV6_142029_PI430048170 mRNA
ACATTAATGAATGATGAGATTGGAGTACACTGTCACCAAGGGCAGGCACAGATGCCTTCT NM_000085 RefSeq

chr1 + 16043735 16057326 CLCNKB 1188 "chloride channel, voltage-sensitive Kb, transcript variant 1"
GO:0007588|GO:0044070|GO:0034220|GO:0005886|GO:0005887|GO:0005247|GO:0034707|GO:0006810|GO:0034765|GO:0055085|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91400_PI430048170 0.578129911658295 1.06876659664953 5.44254164102645
5.33607827728173 5.6170806377043 P P P 5.06916688464208 5.58124713916512
5.4249070880446 P P P LNCV6_91400_PI430048170 mRNA
AAAGGCATCAAGTTTGAGATCTTCCACAAAGGGTCCTTCTTCAGAAGCGACAAGCTGGTT NM_032449 RefSeq
chr1 - 52350592 52366205 CC2D1B 200014 coiled-coil and C2 domain containing 1B
GO:0001078|GO:0005654|GO:0000122|GO:0000978|GO:0006351|GO:0043231 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_139396_PI430048170 0.513374345190897 0.916695115563694 5.90317809674638
5.24998536570962 5.63313662520051 P P P 5.7010308245548 5.78206580550626
5.75190516743519 P P P LNCV6_139396_PI430048170 mRNA
TGGTGGAGTAGAGGAGAAAGCTAAAAATAATGCCGTTTTACTGAGGGAATTTGTGGGCTG NM_001166010 RefSeq
chr6 - 4115692 4135468 ECI2 10455 "enoyl-CoA delta isomerase 2, transcript variant 3"
GO:0005739|GO:0016020|GO:0005782|GO:0004165|GO:0008152|GO:0005102|GO:0005654|GO:0000062|GO:0043231|GO:0009062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137889_PI430048170 0.127875591289501 1.27920617271628 5.68605438997519
5.7614342608144 5.64655107816059 P P P 5.50394295055021 5.45309335616786
5.02797623181418 P P P LNCV6_137889_PI430048170 mRNA
TTTGAACAACCAAATGTGCATTGAATACTCTGAAACCGAAGGGACTGGATCTGCAGGTGG NM_000260RefSeq chr11
+ 77128263 77215241 MYO7A 4647 "myosin VIIA, transcript variant 1"
GO:0005515|GO:0005516|GO:0006200|GO:0007605|GO:0060088|GO:0045202|GO:0005765|GO:0006886|GO:0030898|GO:0042803|GO:0005829|GO:0005737|GO:0000146|GO:0016324|GO:0051015|GO:0051904|GO:0005938|GO:0031477|GO:0030048|GO:0042470|GO:0019904|GO:0048563|GO:0030507|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144636_PI430048170 0.153917989049991 1.01246216026731 0.321341183358064
0.295989717277084 0.296789049612055 A A A 0.293843378359163 0.288646304642869
0.278126114571945 A A A LNCV6_144636_PI430048170 mRNA
ACCCCTTGCTGTTCAGAGAGCTACTCTTTGTAGTGTTCTTGCATGCATATATAATAAATG NM_024534RefSeq chr4
- 52743516 52751640 ERVMER34-1 100288413 "endogenous retrovirus group MER34, member 1, transcript variant 1" GO:0019031|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137949_PI430048170 0.923709342915745 0.939201947497055 1.45332410946454
0.524673866247787 1.87882544070886 A A A 0.545511278581884 1.40606367604534
2.08866566051389 A A A LNCV6_137949_PI430048170 mRNA
CCAGCACTGCAGATAGAAGTATAATGTAAGTCACACACGTACTTCTTTAAAAAGATATGT NM_138809RefSeq chr5
- 10277594 10308056 CMBL 134147 carboxymethylenebutenolidase homolog (Pseudomonas)
GO:0016787|GO:0008152|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74864_PI430048170 0.553256360266678 1.01607730418577 0.461602246444486 0.536058372521366
0.487824173467269 A A A 0.525975634603988 0.430209433582804 0.459585323048092 A A A
LNCV6_74864_PI430048170 mRNA
AACCTTCTCTTTTCCAGCATGTGGGTATACATTCATCATTCCCTAGAAAAGAACAATATG NM_001277353 RefSeq
chr4 - 140443374 140498377 MGAT4D 152586 "MGAT4 family, member D"
GO:0016758|GO:0016020|GO:0005975|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140682_PI430048170 0.199654066154062 1.01173486640853 0.32466584671589
0.301812510021303 0.294729191375 1 A A A 0.29704513386431 0.293604263088069
0.280179285571055 A A A LNCV6_140682_PI430048170 mRNA
GGACTTGGTATGTCAACCTGTGTCTTTACCACATGATCTTTTACTTAAAAGTCATTTTAG NM_001004329 RefSeq

chr12 - 45014755 45051099 DBX2 440097 developing brain homeobox 2
GO:0043565|GO:0006355|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123016_PI430048170 0.4546953099381630.9094596157363615.5557738740088
15.0612041653303 15.0249893458366 P P P 15.399826308784 15.3330418780697
15.3821157405139 P P P LNCV6_123016_PI430048170 mRNA
GAAGATGCCAGATGACACTTAAGACCTACTTGTGATATTTAAATGATGCAATAAAAGACC NM_001024921 RefSeq
chr4 - 39454124 39458587 RPL9 6133 "ribosomal protein L9, transcript variant 2"
GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0003723|GO:0019058|GO:0005730|GO:0005634|GO:0019
843|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0000184|GO:0
016032|GO:0005840|GO:0022625|GO:0044267|GO:0005925 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_129738_PI430048170 0.6393992002660611.21457212205533 1.56350179752388
2.65990405159453 1.64293649599671 A A A 1.76227432231892 1.56376486234134
1.94847183389123 A A A LNCV6_129738_PI430048170 mRNA
CAACCTTCAGGTTCTAGAAGATTGGTTGCACTCCCAAACCTTTATTCTATTATATTACTA NM_005630RefSeq chr3
- 133932695 134030076 SLCO2A1 6578 "solute carrier organic anion transporter family, member 2A1"
GO:0015132|GO:0016020|GO:0015732|GO:0005886|GO:0005887|GO:0006869|GO:0043252|GO:0055085|GO:0005
319 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130369_PI430048170 0.3899015929492820.6003776961647640.303546976117546
0.3305666412473250.34000175454752 A A A 1.87757281749603 0.382845953277607
0.356128068232565A A A LNCV6_130369_PI430048170 mRNA
GAGGACTTCTCCAGACATGATTCTTCATAGAGTGGTAATACAATTTATAGTACAATCACA NM_176891RefSeq chr9
- 21480839 21482313 IFNE 338376 "interferon, epsilon"
GO:0005132|GO:0019221|GO:0033141|GO:0045343|GO:0005125|GO:0005615|GO:0002250|GO:0051607|GO:0042
100|GO:0045087|GO:0006959|GO:0030183|GO:0043330|GO:0002286|GO:0042742|GO:0002323 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_114106_PI430048170 0.3217416039958051.1555495462151 10.779321834342 11.12275456429
11.2624029124554 P P P 10.9380574853284 10.6514798903338 10.97017577021 P P P
LNCV6_114106_PI430048170 mRNA
GAGAAAGATGCTGCATTTTATAATCAAAGCCCAAACTCCTTTCTTATCTTGACCATACTA NM_005402RefSeq chr7
+ 39623552 39708124 RALA 5898 v-ral simian leukemia viral oncogene homolog A (ras related)
GO:0005515|GO:0005886|GO:0003924|GO:0051491|GO:0007265|GO:0030139|GO:0006887|GO:0032154|GO:0000
910|GO:0006935|GO:0051665|GO:0017157|GO:0061024|GO:0016032|GO:0051117|GO:0030659|GO:0031625|GO:0
070062|GO:0048011|GO:0009986|GO:0031532|GO:0030496|GO:0005525|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138427_PI430048170 0.2980681337049911.0795282825223 7.64890052043379
7.55636950628902 7.78708512706797 P P P 7.67840882335063 7.47345533609057
7.51030000492821 P P P LNCV6_138427_PI430048170 mRNA
GAAGCCAATTAATGAAGGAGCCTTGAATGGTTTTAGAAATACAGGGCTGTCTGTTTCTTT NM_001008222 RefSeq
chrX - 129803287 129843585 ZDHHC9 51114 "zinc finger, DHHC-type containing 9, transcript variant
2"
GO:0018345|GO:0005794|GO:0005783|GO:0018230|GO:0002178|GO:0031228|GO:0005737|GO:0005789|GO:0016
409|GO:0043849|GO:0008270|GO:0016021|GO:0019706 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131147_PI430048170 0.2047385387663940.8122135383973180.282904358074983
0.30541978970424 0.340875175061574A A A 0.423141038530595 0.899401879923593
0.456954002566414A A A LNCV6_131147_PI430048170 mRNA
CACTGCTGTGAGCCCACCTGCTAAAAGCCAGGTTGCTGATCGCTTAAGAATGAAAGGGGA NM_001257305 RefSeq
chr17_JH159146v1_alt - 179071 179520 KRTAP1-4 NA keratin associated protein 1-4 NA . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_137655_PI430048170 0.4795400694020980.9479659144914585.10750410367492
5.05688788699509 4.97936673367631 P P P 4.97538034633338 5.12888340377894
5.25966499987288 P P P LNCV6_137655_PI430048170 mRNA
ATGGCTGAGTTCTCTAAGACTCAGGGTGGGAATTATAATCCCTGGTCTAAGCTGATATGA NM_001142524 RefSeq
chrX + 102720713 102752441 BHLHB980823 "basic helix-loop-helix domain containing, class B, 9,
transcript variant 1"
GO:0051965|GO:0043524|GO:0005737|GO:0050769|GO:0007611|GO:0005634|GO:0061003|GO:0042803|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107389_PI430048170 0.2856434665720061.02933861568224 0.307249804524945
0.25066524506215 0.349867934511778 A A A 0.2702243844727790.242922378373785
0.271019943240432 A A A LNCV6_107389_PI430048170 mRNA
CTGATCAGTCACTTTCCCGTCTATCCTTCATTTATTGAAGCCAACTATGAACGACTAAAG NM_001102658 RefSeq
chr15 - 71110243 71115500 CT62 NA cancer/testis antigen 62 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133252_PI430048170 0.9053258092219311.00287605188162 0.328012614049378
0.3306896229039790.406142791353327 A A A 0.3655637693791690.319530017292362
0.368175879866474 A A A LNCV6_133252_PI430048170 mRNA
GCTCAGAGTAGGTGTTGATTTTTTATTACTGTATACATGGATAATTCTGGATCCAGTATG NM_001013628 RefSeq
chrX - 126163498 126166097 DCAF12L2 NA DDB1 and CUL4 associated factor 12-like 2 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_132446_PI430048170 0.4840700393463240.9146573164872690.331618988485451
0.3072769225239460.270533726439243 A A A 0.2893691086891690.690234558663756
0.277174468843318 A A A LNCV6_132446_PI430048170 mRNA
CAGCTCTGAATGTATGAACCTGCTCAATCACCTCATCTTAAAAATAAAATCACTGTCCCT NM_176811 RefSeq chr19
+ 55947831 55988629 NLRP8 126205 "NLR family, pyrin domain containing 8"
GO:0003674|GO:0005737|GO:0070997|GO:0005575|GO:0005524 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_63972_PI430048170 0.2240031699056540.7677580514256541.22508496457321 1.49709318299875
1.87145237282423 A A A 1.836674659623 1.63185411811204 2.26792176348847 A A A
LNCV6_63972_PI430048170 mRNA
TTAATGAATTCCCACTCTGTTCACTTCCTGAAGGTGTTGACCAAGAAGTCTTCAAGCAGC NM_007195 RefSeq chr18
+ 54269478 54298234 POLI 11201 polymerase (DNA directed) iota
GO:0006260|GO:0005622|GO:0005515|GO:0003684|GO:0006281|GO:0071897|GO:0003887|GO:0005654|GO:0005
634|GO:0046872|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90017_PI430048170 0.0663584237133076 0.6604668822071085.68351128720453
5.19982380350799 5.82373085103706 P P P 5.93887679463906 6.16460790091135
6.42858141085747 P P P LNCV6_90017_PI430048170 mRNA
GGGGGAATTGGCATTGCGAAAGACTTGAAAACTAATGAGTAAAGTCTGCTGAATGAATAA NM_004830 RefSeq chr6
- 131586737 131628239 MED23 9439 "mediator complex subunit 23, transcript variant 1"
GO:0005515|GO:0010467|GO:0005667|GO:0006355|GO:0006367|GO:0006357|GO:0016592|GO:0003713|GO:0005
654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103443_PI430048170 0.0893076807010255 0.7112048717642856.65274133419228
6.21940456091748 6.81899061165173 P P P 7.04759164401518 6.96827075120753
7.20447349412762 P P P LNCV6_103443_PI430048170 mRNA
TGGATTTTAACCTCTTAGAGGAAGAAAAAAGGTTAGGGAAGTGTCAACTCTGGATGAAGG NM_007271 RefSeq chr6
- 36493882 36547516 STK38 11329 serine/threonine kinase 38
GO:0035556|GO:0005515|GO:0005737|GO:0000287|GO:0070688|GO:0004674|GO:0043407|GO:0031435|GO:0006
468|GO:0005634|GO:0005524|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131160_PI430048170 0.1000857066383930.2931837795524823.47980468322085 2.3624234112921

2.54751440265646 P A A 4.02182762607441 3.58089962619853 5.56446282126382 P P P
LNCV6_131160_PI430048170 mRNA
GGGTTAAAATATCCCCCTATTCGCCCCCAAAATGCAATAAAAGAAGATAAAAGAGAGAGGNM_000326RefSeq chr15
- 89209866 89221691 RLBP1 6017 retinaldehyde binding protein 1
GO:0005502|GO:0005215|GO:0007603|GO:0006776|GO:0006810|GO:0005575|GO:0019841|GO:0007601|GO:0001
523|GO:0044297|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119133_PI430048170 0.3161452299478370.7999487608670673.8778119666984
3.39702167835823 4.26006556294456 P P P 4.4702410725273 4.18293736008243
3.92309275227204 P P P LNCV6_119133_PI430048170 mRNA
GTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGATGCTACCACCCTGGATGACAATGGA NM_000613RefSeq chr11
- 6431037 6441024 HPX 3263 hemopexin
GO:0005515|GO:0015886|GO:0020027|GO:0015232|GO:0042511|GO:0072562|GO:0005576|GO:0005615|GO:0046
872|GO:0006898|GO:0006879|GO:0060335|GO:0002925|GO:0002639|GO:0071682|GO:0016032|GO:0042168|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132909_PI430048170 0.4109748836167750.773308634779841 1.39178082364337
2.86231314915838 1.26711456350981 A A A 1.9776728326411 2.67026443429204
2.48672539804434 A P P LNCV6_132909_PI430048170 mRNA
CAGGATTATTCTAGTAGGAATAGGCGATTGCTGTCATAATCAATTCTCATGTTGATTTCA NM_001278631 RefSeq
chr15 - 26543545 26773076 GABRB3 2562 "gamma-aminobutyric acid (GABA) A receptor, beta 3,
transcript variant 5"
GO:0005230|GO:0030054|GO:0005886|GO:0004890|GO:0007605|GO:0034707|GO:0060119|GO:0007268|GO:0055
085|GO:0005254|GO:0022851|GO:0060384|GO:0007165|GO:0043524|GO:0034220|GO:0005887|GO:0045211|GO:0
090102|GO:0006810|GO:0060021|GO:0071420 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127085_PI430048170 0.0374168989540141 0.1939171842399091.26063041698484
0.3512618990860612.35759967141311 A A A 3.72032607995158 4.25876425245939 3.7049007295615
P P P LNCV6_127085_PI430048170 mRNA
GGCTCCTTAAACCCTCGCTTTGTTGTAAAAGCTAAAATAAACAGCATGCTATATTGTAAT NM_033305RefSeq chr9
+ 77177444 77417483 VPS13A 23230 "vacuolar protein sorting 13 homolog A (S. cerevisiae), transcript
variant A"
GO:0005622|GO:0005515|GO:0008104|GO:0045053|GO:0035176|GO:0031045|GO:0006623|GO:0007626|GO:0006
895|GO:0019898|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144587_PI430048170 0.5197466789308181.14646718568872 7.28444472852675
7.74716951530173 8.02021242652494 P P P 7.48790875108676 7.4877717151701
7.57610323097395 P P P LNCV6_144587_PI430048170 mRNA
CTTCACTGGACAGTTTTCCTTAGAAGGTAGTTTTGTGTGACTGTGACTAAACTATTTTAT NM_022496RefSeq chr12
+ 100200086 100224424 ACTR6 64431 "ARP6 actin-related protein 6 homolog (yeast), transcript variant 1"
GO:0005515|GO:0005737|GO:0006338|GO:0005634|GO:0005856 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131778_PI430048170 0.3486398349587691.14978209612034 9.29956383928126
9.28720738638478 9.30884957191822 P P P 9.42915040236424 8.80189337841595
8.98690961990457 P P P LNCV6_131778_PI430048170 mRNA
TTCTTTTCACCATGCAAATAACATGCCCAGCAAAAACTTGCTTTATGGGTCTGCCTGGAG NM_002237RefSeq chr20
- 51003655 51023138 KCNG1 3755 "potassium channel, voltage gated modifier subfamily G, member
1"
GO:0005251|GO:0005886|GO:0008076|GO:0007268|GO:0005267|GO:0051260|GO:0034765|GO:0016021|GO:0006
813|GO:0071805|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129414_PI430048170 0.0030077965471768 1.82538953583485 10.3045833473904
10.477949972297 10.3700054887251 P P P 9.68338167831635 9.47799997686434
9.37458098417089 P P P LNCV6_129414_PI430048170 mRNA

TCAGCAGCAAGCACCAGCCTTCCACAACAACACTATATTTTTATGCTACTTTCCTGTTTG NM_001002880 RefSeq chr22 + 38656652 38673851 CBY1 25776 "chibby homolog 1 (Drosophila), transcript variant 2" GO:0005515|GO:0005802|GO:0008013|GO:0030178|GO:0005634|GO:0005829|GO:0042802|GO:0008104|GO:0016607|GO:0045444|GO:0005654|GO:0045892|GO:0055007 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_141478_PI430048170 0.00429579757393201 0.6317576191917444.71188251003883 4.66583624897245 4.8988255507407 P P P 5.25440136094475 5.47386011581734 5.53203902361047 P P P LNCV6_141478_PI430048170 mRNA
GGAGCCCTGTGTTAGGAGTCCCCATAAACATGTACTGTAATTCTTTGTATATAGAAAAAA NM_022455RefSeq chr5 + 177133831 177300213 NSD1 64324 "nuclear receptor binding SET domain protein 1, transcript variant 2" GO:0003712|GO:0034770|GO:0005694|GO:0016571|GO:0003714|GO:0030331|GO:0010452|GO:0005730|GO:0006325|GO:0005634|GO:0050681|GO:0000122|GO:0042974|GO:0001702|GO:0006351|GO:0046966|GO:0046965|GO:0042799|GO:0003682|GO:0046975|GO:0005654|GO:0008270|GO:0045893 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_144513_PI430048170 0.0596083674568948 1.24904372317967 6.90134983879623 7.20847694160707 7.16428061753386 P P P 6.68208548133925 6.76447191438037 6.8771133827746 P P P LNCV6_144513_PI430048170 mRNA
TTTAATGTGTACCTGAAAGCTCCTGGCAATGCTGGAAAATTTTTATCCCAGAGGGGTGGG NM_012133RefSeq chr7 - 130506238 130668758 COPG2 26958 "coatomer protein complex, subunit gamma 2, transcript variant 1" GO:0030126|GO:0005198|GO:0006890|GO:0006891|GO:0006886|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_145226_PI430048170 0.0414769270469231 0.4474258950519833.90124503826749 3.62985907620287 4.40024610498022 P P P 4.54387651003277 5.26381177392289 5.53943698139713 P P P LNCV6_145226_PI430048170 mRNA
GTGCTGTCTGCATTTCTGGGTTTATTGAAGACCTCTTGTTGTATATATCCTCAAAAATTANM_194318RefSeq chr13 + 31199974 31332274 B3GALTL 145173 "beta 1,3-galactosyltransferase-like" GO:0006493|GO:0016757|GO:0005789|GO:0016021|GO:0006004|GO:0036066|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_137958_PI430048170 0.00152073517395719 0.3959438996187725.27698256905339 5.1218842110584 5.1761721515652 P P P 6.33961544197565 6.55682603053173 6.67318385397486 P P P LNCV6_137958_PI430048170 mRNA
TGATAACACATTCGGCGGTTACGATGTTGGAATTTAGCAGAACTATCAAATCCAAAATTA NM_003184RefSeq chr8 - 119730773 119832834 TAF2 6873 "TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 150kDa" GO:0005515|GO:0010467|GO:0014070|GO:0006368|GO:0005669|GO:0006367|GO:0044212|GO:0006366|GO:0033276|GO:0045944|GO:0000086|GO:0006508|GO:0016032|GO:0005654|GO:0008270|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_139067_PI430048170 0.0599467728574625 0.5962681144504386.2404953545759 5.58265926400946 5.59303101105051 P P P 6.59596022386885 6.68834158949529 6.46373418227326 P P P LNCV6_139067_PI430048170 mRNA
CAGGAGAGGAAGGAAGTTAATACCTATGTAATACATAGAAACTTCCACAATAAAATGCCA NM_016059RefSeq chr6 - 36854829 36875024 PPIL1 51645 peptidylprolyl isomerase (cyclophilin)-like 1 GO:0005515|GO:0000413|GO:0006457|GO:0000398|GO:0003755|GO:0071013|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_127673_PI430048170 0.4278815460626791.05296170812119 0.386013335882492 0.6104422687717340.523778051407589A A A 0.5340916582547230.3904253819498240.3758197820145 A A A LNCV6_127673_PI430048170 mRNA
GATTTTCCCAGGACTGAACAAGTTCCAGAAAAGACTGAAGAATAATCACAATTCTAATGT NM_002440RefSeq chr1 + 75796870 75913238 MSH4 4438 mutS homolog 4

GO:0005515|GO:0030983|GO:0000795|GO:0005634|GO:0007283|GO:0007292|GO:0003677|GO:0005524|GO:0003684|GO:0032300|GO:0001541|GO:0000710|GO:0051026|GO:0045143|GO:0007131|GO:0008094 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72684_PI430048170 0.0700624053819149 0.825510295634956 5.39276023929105 5.09779933746921 5.24035325867466 P P P 5.48508103270217 5.57355150953152 5.51588982003954 P P P LNCV6_72684_PI430048170 mRNA
TATCGGCTGGATGAAGCTCCCAAGGACATTAAGGGTTATTACTACAATGGTGACTCTGCT NM_006395 RefSeq chr3 + 11272323 11557665 ATG7 10533 "autophagy related 7, transcript variant 1"
GO:0005515|GO:0045732|GO:0021987|GO:0016567|GO:0009791|GO:0015031|GO:0021860|GO:0042803|GO:0070257|GO:0031401|GO:0005829|GO:0030163|GO:0005737|GO:2000619|GO:0021680|GO:0006497|GO:0007628|GO:0034727|GO:0061025|GO:0031396|GO:0009267|GO:0016239|GO:0006995|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132064_PI430048170 0.268073716978083 1.05074428817711 0.342951128749142 0.341521164467758 0.481916983990709 A A A 0.314824540432971 0.293705916440711 0.347666374341546 A A A LNCV6_132064_PI430048170 mRNA
CCATCAAATGCACTTGCTTGTGAATTAATGGACTTGTAAATGAAACAATGCAATCAGTCT NM_198996 RefSeq chr21 - 14108813 14206949 LIPI 149998 "lipase, member I, transcript variant 2"
GO:0052689|GO:0016042|GO:0016020|GO:0005886|GO:0005576|GO:0004620|GO:0008201|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132389_PI430048170 0.24649082070689 0.565257600478893 0.541735530306539 1.53258419269445 1.24377853805142 A A A 0.963196655940395 2.42216584381913 2.1933279347313 A A A LNCV6_132389_PI430048170 mRNA
GCTTAGGAGAGCAAATCAGATACTGTCATTAAACTTACAACTAAAATTACTAGCTGTCAC NM_004800 RefSeq chr13 + 99501373 99564048 TM9SF2 9375 transmembrane 9 superfamily member 2
GO:0005887|GO:0006810|GO:0010008|GO:0070062|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126739_PI430048170 0.476268859037949 0.759086925270267 0.415810035933612 0.450323831659608 0.452194601118636 A A A 1.44997464589372 0.373628539140837 0.413710691935207 A A A LNCV6_126739_PI430048170 mRNA
TGCTCAATGTGATAGACAGCCAGTCTATAATGCAAGCCAATTCTCCGTAGTTTAACCCTG NM_173556 RefSeq chr11 + 85855100 85920020 CCDC83 220047 "coiled-coil domain containing 83, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139862_PI430048170 0.00831922435558248 0.312783081251769 3.36721546427506 4.08893335761887 3.4162984271059 P P P 5.11576323110301 5.4422621728874 5.43882527947668 P P P LNCV6_139862_PI430048170 mRNA
GTATCTTGTCATAGTTATCCACAAATGGCAAAACTGGACTTGATTCTACTGGTATGCAAA NM_138638 RefSeq chr14 - 34710381 34714823 CFL2 1073 "cofilin 2 (muscle), transcript variant 2"
GO:0005515|GO:0030836|GO:0045214|GO:0030042|GO:0003779|GO:0061001|GO:0015629|GO:0005615|GO:0046716|GO:0016363|GO:0070062|GO:0031674 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141244_PI430048170 0.253757074528429 0.978446060100085 0.304510954196891 0.330279911021347 0.353126777633206 A A A 0.391515244560122 0.327464121938961 0.362942433665512 A A A LNCV6_141244_PI430048170 mRNA
CCATTCTGAAGTCTGTAAAAGAAGCAATTTCCTTCTTCTTAAGATTTCGTGGCATGTTTA NM_001123387 RefSeq chr17_JH159146v1_alt - 195935 196709 KRTAP2-1 81872 keratin associated protein 2-1 GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144019_PI430048170 0.140507843286109 1.18262370540649 8.60673344477323 8.47487870521434 8.539453525152 P P P 8.10048722531871 8.48132894893925 8.29119418754154 P P P LNCV6_144019_PI430048170 mRNA
TGGTCAGCTGTATTTGTGTAACAACTTTTGTAATAAATAGAAAAACCCTCTGCTCTGATC NM_007176 RefSeq chr14

- 75650889 75661195 C14orf1 11161 chromosome 14 open reading frame 1
GO:0030133|GO:0008150|GO:0003674|GO:0016126|GO:0005789|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141865_PI430048170 0.3649195528650950.8244090021647940.47465218253917
0.4285722940033180.471127444412596A A A 0.4833473330962870.501886640303934
1.12796689876607 A A A LNCV6_141865_PI430048170 mRNA
AGGCCAGCAAGAGAAGTCTTAGAGTTTTTATCCAAGCTATCCAGTATCATCCCTAGTGCC NM_138702RefSeq chrX
+ 141838315 141897832 MAGEC3 139081 "melanoma antigen family C3, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135236_PI430048170 0.3055115433874371.55473607776137 2.43315696282023
1.66003618033019 1.04896362839856 A A A 1.11049242749827 1.54898310120205
0.808911505670675A A A LNCV6_135236_PI430048170 mRNA
TTCATGCTTATAAATTTCAAGTGGAGTCTCATCTGGGTTGCCTCAAGGTATCAAAAGTAG NM_001290693 RefSeq
chr1 + 241957766 241959062 BECN2 NA beclin 2 NA . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_99370_PI430048170 0.3093132539872130.99002869336645 0.3355472256276880.367074854050578
0.343904876581203A A A 0.3684286542767290.3739785156554050.347543792079944A A A
LNCV6_99370_PI430048170 mRNA
CTGGCACTTTATTTTACTTCTAACCTTGTTTCCTGACGGTGTACAGAATCAACAAAATAA NM_138983RefSeq chr21
+ 33070143 33072422 OLIG1 116448 oligodendrocyte transcription factor 1
GO:0005515|GO:0006355|GO:0046983|GO:0005634|GO:0048663|GO:0003677|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_66849_PI430048170 0.2600814988355710.7954664733158254.59451709972958 4.66321670308537
5.21456333819876 P P P 4.86042603134762 5.19348521252808 5.43499044038612 P P P
LNCV6_66849_PI430048170 mRNA
GTTATTTCGAGACTATGGAAGATATGATAAGACTCAGCTTCGTTTTAAAAAGGGACATTG NM_024770RefSeq chr2
- 171317402 171434802 METTL8 79828 methyltransferase like 8
GO:0005737|GO:0008168|GO:0005634|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143309_PI430048170 0.1769557609631741.13680482656429 10.0208600101836
10.2776621111673 10.3001103556246 P P P 10.0619852931246 10.0022447852836
9.99483790773622 P P P LNCV6_143309_PI430048170 mRNA
CTCACTTGAGGCATTTTGTTGTCGGGTTTTTGTGTTTGTTTTTGTGGGTATTTGCCTCAT NM_013446RefSeq chr7 -
140453039 140479569 MKRN1 23608 "makorin ring finger protein 1, transcript variant 1"
GO:0005515|GO:0000209|GO:0004842|GO:0016874|GO:0003682|GO:0008270|GO:0005575 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_93538_PI430048170 0.11984288038516 0.3499149106270721.73321230590001 0.245056925956639
2.74697737823793 A A A 3.05926490443316 3.08408717532969 3.93145850480654 P P P
LNCV6_93538_PI430048170 mRNA
AGATGGAAGAATGTGTGAAGCTCACAAGTCTGTATTTGTTTGCAAAGAATGTGCGGTCTT NM_014647RefSeq
chr16_KI270853v1_alt - 1252359 1301177 KIAA0430 9665 "KIAA0430, transcript variant 1"
GO:0010468|GO:0003674|GO:0048477|GO:0016020|GO:0000166|GO:0010923|GO:0003723|GO:0007143|GO:0006
302|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129109_PI430048170 0.00404206707278908 0.5316115873331383.3183118033435
3.04222705106103 3.0297824681743 P P P 4.05189757163804 3.97074201290471
4.11743157718098 P P P LNCV6_129109_PI430048170 mRNA
GGAAGGGTAGCCCCTGTGTCTGTCTGATAATAGAAGTACAATAAATTTAATTGAGAAGAT NM_001287510 RefSeq
chr1 + 42456493 42461230 PPCS 79717 "phosphopantothenoylcysteine synthetase, transcript
variant 7"
GO:0015939|GO:0006766|GO:0004632|GO:0006767|GO:0015937|GO:0009108|GO:0044281|GO:0070062|GO:0005

829. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127019_PI430048170 0.1454925240753080.5131703408949242.12865111555017 0.4357880550422
1.32509949745256 A A A 2.23566043703197 2.44943103096739 2.55291263308057 A A P
LNCV6_127019_PI430048170 mRNA
TCCCCTCGACAAGCCAAGAATGAGAATTGGGAATAAGTGAACAGAGTTTGAGGGTTTCTG NM_015086RefSeq chr12
- 48995149 48999305 DDN 23109 dendrin
GO:0005515|GO:0005737|GO:0032591|GO:0006366|GO:0045944|GO:0000982|GO:0005789|GO:0043204|GO:0005
634|GO:0042995|GO:0000978 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132163_PI430048170 0.4723168590365480.8433418314167590.306595679790993
0.2602945926201250.307950967928037A A A 0.9666662211319830.258180798980389
0.268266159177892A A A LNCV6_132163_PI430048170 mRNA
AGGCTGAAACAACGGGAAGAGGTTTTGAGGAAAATCTACACTGACCAATTAAATGAAGAA NM_153236RefSeq
chr7 + 150514856 150521073 GIMAP7168537 "GTPase, IMAP family member 7"
GO:0006184|GO:0005811|GO:0005515|GO:0005737|GO:0003924|GO:0005525|GO:0042803 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_93231_PI430048170 0.0339992212433612 6.67387547745991 4.49940201074051
4.75963869355308 5.04689946330598 P P P 2.83664113503013 0.697764035523582
1.86224142730217 P A A LNCV6_93231_PI430048170 mRNA
AATGATGCTAGCTGCCCTTAAAATTCTTTCAGATTTGGAACTGTATCTGTATGGAAACAA NM_001139488 RefSeq
chr2 + 33476253 33564731 RASGRP3 25780 "RAS guanyl releasing protein 3 (calcium and DAG-
regulated), transcript variant 1"
GO:0048471|GO:0005886|GO:0007264|GO:0005509|GO:0007265|GO:0032854|GO:0019992|GO:0043547|GO:0005
085|GO:0046582|GO:0000165|GO:0005887|GO:0004871|GO:0019900|GO:0017016|GO:0005088|GO:0032045 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129732_PI430048170 0.2724445868323890.681376478092151 2.90324970845015
1.95581165852319 2.33880765626129 A A A 2.30977151110256 3.14137196886808
3.36674881583861 A P P LNCV6_129732_PI430048170 mRNA
CTGTCCTCCAGCAGAGTAACATTATTGTTCTCATTAACAATGAATTTATACCACATTACC NM_005246RefSeq chr5
+ 108747821 109196840 FER 2241 fer (fps/fes related) tyrosine kinase
GO:0005515|GO:0000790|GO:0005154|GO:0042503|GO:0030054|GO:0019221|GO:0030154|GO:0050904|GO:0010
762|GO:0046777|GO:0006935|GO:0030838|GO:0042127|GO:0032496|GO:0034446|GO:0070102|GO:0005938|GO:0
038083|GO:0043304|GO:0017137|GO:0032869|GO:0045296|GO:0030335|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_89475_PI430048170 0.1078291024360941.30495260128341 7.02952227277297 7.24000005729746
6.91858464702962 P P P 6.87264434867329 6.76598620302299 6.3688289256476 P P P
LNCV6_89475_PI430048170 mRNA
TGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGCCGTGCAT NM_153461RefSeq chr3
+ 9917097 9933621 IL17RC 84818 "interleukin 17 receptor C, transcript variant 2"
GO:1900017|GO:0030368|GO:0005887|GO:0019221 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138615_PI430048170 0.5269101173544490.9840632416760050.281686342561571
0.3168705192935130.381778861922167A A A 0.3793947261871430.344851273223613
0.32691973436287 A A A LNCV6_138615_PI430048170 mRNA
CACCTTTGCATCTTTTGTGTCTTTCTTATCATGATTTGGCAAAATGCATCACCTTTGAAA NM_001256369 RefSeq chr3
+ 45886503 45903175 CCR9 10803 "chemokine (C-C motif) receptor 9, transcript variant C"
GO:0006968|GO:0006955|GO:0070098|GO:0009986|GO:0007186|GO:0006935|GO:0005886|GO:0005887|GO:0004
950|GO:0016493|GO:0007204 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77745_PI430048170 0.8493829681459390.991324943594581 0.3292140501956840.488318420224372
0.366822588171555A A A 0.4915288702940810.37237248970568 0.359282688107946A A A
LNCV6_77745_PI430048170 mRNA

ATCCACCTGTCTATTTGCACATGGAGGACTTTTCAAGATGTCAGGATACCCTTCCATCAC NM_198392 RefSeq chr6 + 133889120 133895537 TCF21 6943 "transcription factor 21, transcript variant 1" GO:0060426|GO:0001657|GO:0001658|GO:0042826|GO:0060425|GO:0005634|GO:0050681|GO:0048536|GO:0032835|GO:0007530|GO:0048608|GO:0072277|GO:0060008|GO:0060541|GO:0045944|GO:0030855|GO:0046983|GO:0060021|GO:0014707|GO:0060435|GO:0001944|GO:0048286|GO:0001822|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142329_PI430048170 0.0486280581928611 0.5559982259084213.85533146701042 4.07164384110544 4.06858597747329 P P P 4.39773554782943 4.99667383736309 5.06378046758782 P P P LNCV6_142329_PI430048170 mRNA
ACACAAACAACTGGGTTTGTGAACTGTATTACTCCTGGTATCTTTAAAATATTGTGGGTG NM_001287491 RefSeq chr2 + 73986403 74108175 TET3 200424 tet methylcytosine dioxygenase 3 GO:0005515|GO:0010467|GO:0080182|GO:0035511|GO:0003677|GO:0046872|GO:0005737|GO:0001939|GO:0006493|GO:0045944|GO:0080111|GO:0040029|GO:0001940|GO:0070579 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140172_PI430048170 0.8845764139015450.9768111927950281.09905490349517 1.53653811140018 0.472929004033421 A A A 1.95366604579081 0.424451142915372 0.452145917119452 A A A LNCV6_140172_PI430048170 mRNA
GGGTGGGGAGTTGTGCATATAAACTATTTAATGAGTACCAAACACAAAAGTCAAGCTTGT NM_000343 RefSeq chr22 + 32043031 32113024 SLC5A1 6523 "solute carrier family 5 (sodium/glucose cotransporter), member 1, transcript variant 1" GO:0001656|GO:0005515|GO:0005886|GO:0005975|GO:0044281|GO:0005412|GO:0031526|GO:0055085|GO:0008645|GO:0050892|GO:0016324|GO:0015758|GO:0005887|GO:0005911|GO:0009405|GO:0006814|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127329_PI430048170 0.1397683041995360.9449506816203130.244301502370611 0.2952716342612280.304117147872603 A A A 0.433027087678126 0.338659819445971 0.315071278034884 A A A LNCV6_127329_PI430048170 mRNA
GAGTGCATTTAATAGTCAATAAATTCATCTACCATTCCAGATTATTAAAGGCCCACTGGT NM_001201539 RefSeq chrX + 3041470 3112729 ARSF 416 "arylsulfatase F, transcript variant 3" GO:0006665|GO:0006687|GO:0005788|GO:0004065|GO:0044281|GO:0044267|GO:0046872|GO:0070062|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137215_PI430048170 0.00379923284897323 0.3005022077017584.56043209331222 4.07743243993057 4.43164769523642 P P P 5.67881541527083 6.15807269873364 6.39020074817578 P P P LNCV6_137215_PI430048170 mRNA
CTGTGGTAGCCATACCTTGAAGCACAGTGTTTGTACATAAGTAAATATCTTGATTCTAAA NM_144660 RefSeq chr10 + 75111634 75182123 SAMD8 142891 "sterile alpha motif domain containing 8, transcript variant 2" GO:0003674|GO:2000303|GO:0006686|GO:0030176|GO:0016021|GO:0046513|GO:0016740 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144579_PI430048170 0.0632477740790682 0.9100565681371187.89683753627106 7.85426822610218 7.91548823498747 P P P 7.96722568233436 8.10326455023177 8.00120155751524 P P P LNCV6_144579_PI430048170 mRNA
AATTAAAGTTGCTTCCATCCAACCTGGAGGCTTCCTAACAAATATCGCAGGCACCAGTGA NM_002153 RefSeq chr16 + 82035252 82098534 HSD17B2 3294 hydroxysteroid (17-beta) dehydrogenase 2 GO:0006694|GO:0004303|GO:0047035|GO:0047006|GO:0005789|GO:0032526|GO:0016021|GO:0001890|GO:0001701|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131399_PI430048170 0.0193679071730081 3.13172051386034 3.33806361271039 4.3417406532147 3.95236680637637 P P P 2.18669815403262 2.79041298728168 1.66712104407454 A P A LNCV6_131399_PI430048170 mRNA
TATATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTNM_014400 RefSeq chr19 - 43460793 43465679 LYPD3 27076 LY6/PLAUR domain containing 3

GO:0007160|GO:0043236|GO:0006928|GO:0016021|GO:0046658|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137926_PI430048170 0.0141349152468946 0.4080150995230117.6239220823827 7.03884182407186 7.23017642893378 P P P 8.15865479013659 8.59695780851814 8.96792058388868 P P P LNCV6_137926_PI430048170 mRNA GTGTCATGCCTGTGTGCATACCCAATTAAACACTGGAAATAAAAATTGTTTTGGTGAATT NM_020824RefSeq chr10 - 24583608 24723668 ARHGAP21 57584 Rho GTPase activating protein 21
GO:0005515|GO:0005794|GO:0030054|GO:0072384|GO:0051684|GO:0051683|GO:0005100|GO:0007165|GO:0000139|GO:0032321|GO:0007030|GO:0005856|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71751_PI430048170 0.00488817220633488 0.5191483407059055.77868361313022 5.98012331270833 5.62214057542612 P P P 6.49942648808361 6.78391787808789 6.92531405473892 P P P LNCV6_71751_PI430048170 mRNA TTCTTGAATAGGTATTGATAAATGGAAGCGCTTACCAGCCCAGCTTTGCCAGCCCTAATA NM_138927RefSeq chr21 + 33543037 33577514 SON 6651 "SON DNA binding protein, transcript variant f"
GO:0005515|GO:0006397|GO:0008380|GO:0043066|GO:0003723|GO:0000226|GO:0050733|GO:0003676|GO:0003677|GO:0000910|GO:0016607|GO:0051726|GO:0005654|GO:0043484 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140676_PI430048170 0.0875138981945049 0.7870221828142777.91548823498747 8.15333820820499 8.24092224185506 P P P 8.40518160836899 8.26958786254666 8.66288154517956 P P P LNCV6_140676_PI430048170 mRNA GAACTTCCCCTAATAAAAGGGCCTTGGAAACCTCAAACCTGGGTTTCTGACTTGAAAAAA NM_001243974 RefSeq chr8 + 22440969 22541144 PPP3CC 5533 "protein phosphatase 3, catalytic subunit, gamma isozyme, transcript variant 1"
GO:0005516|GO:1900740|GO:0016311|GO:0006915|GO:0004721|GO:0097193|GO:0046872|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136902_PI430048170 0.0761340643440166 0.5480546797831142.57346436890414 2.49630621748146 2.15286765788162 A A A 2.70849899518675 3.37106366142231 3.63083667779032 P P P LNCV6_136902_PI430048170 mRNA GCCATGTGGTTCGTTGTCCACATCCACATGTACGTTTGTATGTAGTCCACATTGGTTGTT NM_032237RefSeq chr8 + 43093505 43123180 POMK 84197 "protein-O-mannose kinase, transcript variant 1"
GO:0019200|GO:0005524|GO:0019233|GO:0050905|GO:0004672|GO:0006493|GO:0007420|GO:0005789|GO:0007611|GO:0016773|GO:0046835|GO:0006468|GO:0016021|GO:0001764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141819_PI430048170 0.00992451196831002 0.7343476919801159.53213127209532 9.62844572241071 9.46106533779298 P P P 9.88383184041135 9.94398916611476 10.1241523802857 P P P LNCV6_141819_PI430048170 mRNA GAAAGATTACGTTGATGAAAAAGAACATCCTGCCCAGGACCCATCATACATATTTTCAAG NM_182480RefSeq chr14 + 73949933 73963110 COQ6 51004 "coenzyme Q6 monooxygenase, transcript variant 2"
GO:0005739|GO:0006744|GO:0004497|GO:0005794|GO:0050660|GO:0016709|GO:0044550|GO:0044281|GO:0042995|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91438_PI430048170 0.1318680923550070.75172062577434 6.22809915128457 5.64066194377855 5.70497877045956 P P P 6.33096926820066 6.40501750236093 6.1341244693128 P P P LNCV6_91438_PI430048170 mRNA CTGGCCACCACTTTCCCCCATTGGACCATGGACTGAAGAAAACGAGCTGAGGGTCTAACG NM_001170738 RefSeq chr12_GL877875v1_alt + 60897 165178 IQSEC3 440073 "IQ motif and Sec7 domain 3, transcript variant 1"
GO:0043547|GO:0005802|GO:0005086|GO:0030054|GO:0030036|GO:0045211|GO:0032012|GO:0060077|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144661_PI430048170 0.0250171970008689 1.5348276222093 8.56183010311216 8.77525410317702 8.7623421155664 P P P 8.25462167716571 8.15127519418178 7.8130498266482

P P P LNCV6_144661_PI430048170 mRNA
GTGATATGGTGAAGGGAAGTGGGGAGTATTTGAACACAGTTGAATTTTTTCTAAAAAGAA NM_001265RefSeq chr13
- 27962067 27969368 CDX2 1045 caudal type homeobox 2
GO:0060711|GO:0000794|GO:0008284|GO:0001568|GO:0003700|GO:0006366|GO:0003714|GO:0045597|GO:0008
333|GO:0000122|GO:0009952|GO:0001829|GO:0001227|GO:0045197|GO:0003690|GO:0017053|GO:0009887|GO:0
000980|GO:0005654|GO:0045893|GO:0035019 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58300_PI430048170 0.513895173564316 1.18385078774535 3.12043458548875 2.25818853936763
2.58969159009181 A A A 2.54065124377943 2.64719748492394 2.1338098171679 A A A
LNCV6_58300_PI430048170 mRNA
GTCTGGACTGCCGCCATGAGAATACCAGCAGTTCACCCATCCAGTACGAGTTCAGCCTGA NM_006288RefSeq chr11
- 119417944 119423536 THY1 7070 Thy-1 cell surface antigen
GO:0005515|GO:0050852|GO:0034235|GO:0005886|GO:0005783|GO:0031362|GO:0030425|GO:0005829|GO:0030
426|GO:0016324|GO:0016337|GO:0048041|GO:0007010|GO:0051281|GO:0070062|GO:0030336|GO:0019901|GO:0
046549|GO:0001525|GO:0050860|GO:0005100|GO:0043547|GO:0005178|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134498_PI430048170 0.454349086250711 1.34711981522057 0.407182137717649
1.46800021311223 0.357875676232508 A A A 0.450978415210974 0.377539326146361
0.403998066578307 A A A LNCV6_134498_PI430048170 mRNA
TTTCTGGCAAAGAGGAAAATACCGACTGGTCTTATGAGAAGCAGTGGCCAAGACTACCTT NM_153289RefSeq chr20
- 31377162 31390649 DEFB119 245932 "defensin, beta 119, transcript variant 1"
GO:0009986|GO:0045087|GO:0005576|GO:0042742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129359_PI430048170 0.000718974872167457 2.50429114269481 6.86388954642788
7.07540534151455 7.15372039963623 P P P 5.90888950685749 5.63590188373393
5.56730707784186 P P P LNCV6_129359_PI430048170 mRNA
CAGCCCCTGAGCAGGGAGAGAGAAGTTTTGTTGGCATAGGTTTGCTTAGGTAGCCGGCTT NM_012168RefSeq chr1
- 11648360 11654831 FBXO2 26232 F-box protein 2
GO:0004842|GO:0008285|GO:0016567|GO:0005783|GO:0031146|GO:0030433|GO:0005829|GO:0001540|GO:0001
948|GO:0043197|GO:0031090|GO:0006508|GO:0006516|GO:0030246|GO:0031396|GO:0006464|GO:0019005|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145147_PI430048170 0.0170607432733732.55571677253242 3.32672105284249
3.37275577962186 3.66728529384832 P P P 2.41714418868462 2.19309065161491
1.60218541297426 A A A LNCV6_145147_PI430048170 mRNA
AATCAGGTAACTCACCAGACCAGCCTTGGAATCTATCAAATCTAACTGCTGAGCTACCCA NM_002562RefSeq chr12
+ 121132827 121186551 P2RX7 5027 "purinergic receptor P2X, ligand gated ion channel, 7, transcript
variant 1"
GO:0005515|GO:0032755|GO:0006649|GO:0043132|GO:0031594|GO:0010524|GO:0034405|GO:0048705|GO:0006
900|GO:0010043|GO:0042803|GO:0019228|GO:0006884|GO:0016485|GO:0031668|GO:0043025|GO:0032496|GO:0
033198|GO:0001614|GO:0006509|GO:0043029|GO:0000287|GO:0030501|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131038_PI430048170 0.215972149731509 0.859670047620875 11.3240597543018
11.4713145802265 11.5940504564896 P P P 11.4760943128687 11.6691476377852
11.8825656144991 P P P LNCV6_131038_PI430048170 mRNA
GGCCCTTCATGTACATCCATGGTGTGCTGGCTTAAAATGTAATTAATCTTGTAAATATAC NM_005534RefSeq
chr21_GL383581v2_alt + 9450 32093 IFNGR2 3460 interferon gamma receptor 2 (interferon gamma
transducer 1)
GO:0060334|GO:0004896|GO:0005886|GO:0005887|GO:0005783|GO:0004906|GO:0019221|GO:0016021|GO:0009
615|GO:0007166|GO:0060333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133842_PI430048170 0.184616630994022 0.434834378458218 0.297262820620499
0.33804554170456 0.379119276792151 A A A 0.371730024391572 2.11636398033354

1.62941887321338 A A A LNCV6_133842_PI430048170 mRNA
CTTGAAGGTCACATGTACCTATTGTGAAAATGTGAAGCTGTATTTCTGAAGCTGAAATAA NM_015569 RefSeq chr1
+ 171841477 172412717 DNM3 26052 "dynamin 3, transcript variant 1"
GO:0005515|GO:0048471|GO:0005874|GO:0003924|GO:0014069|GO:0005525|GO:0007416|GO:0006897|GO:0005
739|GO:0043197|GO:0008152|GO:0046847|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130828_PI430048170 0.2418649957071341.63547218888474 2.41308109616178
2.79275039057184 1.98007698521889 A A A 1.44808169408277 0.641657001361021
2.48987180316894 A A A LNCV6_130828_PI430048170 mRNA
GTACTTCATCTTTCCACAGTCATCCATCTGCTAATCAGGTGAAATATCAGCTCAGCAGAA NM_001085377 RefSeq
chr5 - 113022098 113488830 MCC 4163 "mutated in colorectal cancers, transcript variant 1"
GO:0005515|GO:0007165|GO:0005737|GO:0005886|GO:0050680|GO:0005654|GO:0005634|GO:0004872|GO:0016
055|GO:0090090|GO:0030027|GO:0010633 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140522_PI430048170 0.5663246581441 1.02299277091422 0.593802805166309
0.4930430105640580.46174297460996 A A A 0.41748979882082 0.518715905150707
0.515051683500073 A A A LNCV6_140522_PI430048170 mRNA
CTAGGGAACTGTCATGTCTACCATGTATTGTACATATGACTTTATGTATACTTGCAATCA NM_003853 RefSeq chr2
+ 102418789 102452564 IL18RAP 8807 interleukin 18 receptor accessory protein
GO:0006955|GO:0006954|GO:0004872|GO:0016021|GO:0007166 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141103_PI430048170 0.3948302459577150.768607099079191 0.861208223790892
0.3053830538375950.476942497002473 A A A 1.3864633337081 0.922408844562942
0.347514094501537 A A A LNCV6_141103_PI430048170 mRNA
TCTGAAGCCAGCTTTTCCTGTTCACTCATCCCTTGATTAAATATGGACATTCTAGCTTCA NM_001007240 RefSeq
chr16 - 20309573 20327620 GP22813 "glycoprotein 2 (zymogen granule membrane), transcript
variant 1" GO:0002412|GO:0016324|GO:0031225|GO:0003823|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_124807_PI430048170 0.7295564343171011.05043308000095 3.94687072554488
4.04203009831211 3.67220543208543 P P P 3.9793258777105 4.05739062800287
3.33306719037589 P P P LNCV6_124807_PI430048170 mRNA
AAGGTGAACATCTGTTTGCAGAATCTGATTCATGAGAAGTTCTCCCCAAGTCCACTGAAC NM_001039651 RefSeq
chr6_GL000256v2_alt + 3062287 3064139 SAPCD1 401251 suppressor APC domain containing 1
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145748_PI430048170 0.5422663511090310.95636800442274 12.7694195446549
13.0375943967095 12.7575633904446 P P P 12.9070993767948 12.9998755433996
12.8651052087476 P P P LNCV6_145748_PI430048170 mRNA
TGACGTGCTGTCCACCAGGCCTTGGAGACAGGCTAGCCTGGCCACAGAATTAAACGTGTT NM_001287343 RefSeq
chr9 + 136848815 136851043 PHPT1 29085 "phosphohistidine phosphatase 1, transcript variant 5"
GO:0051350|GO:0008969|GO:0035774|GO:0050860|GO:2000147|GO:0005829|GO:0044325|GO:2000249|GO:0035
971|GO:2000984|GO:0006470|GO:0019855|GO:0004721|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_131100_PI430048170 0.6749381639144010.9126781076673021.30411302892852
0.9354836353685540.848360339774961 A A A 0.9075053732881861.5587291899704
0.965000230425237 A A A LNCV6_131100_PI430048170 mRNA
AGAAATGAGGAGATGAAAGCAGCTATGAAGAAACTGCAAAACCGACGGGTGACTTTTCAA NM_001004712
RefSeq chr14 - 20014260 20015193 OR4K14 NA "olfactory receptor, family 4, subfamily K, member 14"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130646_PI430048170 0.2193114289732841.0747142636956 0.570586793464826
0.7540365955363010.585062363821543 A A A 0.49037296576571 0.550695652800083
0.563018329490728 A A A LNCV6_130646_PI430048170 mRNA

TAGGATAGAATTTGATCCCCTAACTCACTGTCTGCGGTGCTCATTGCTGCTAACAGCATT NM_005545 RefSeq chr15 + 74173745 74176871 ISLR 3671 "immunoglobulin superfamily containing leucine-rich repeat, transcript variant 1" GO:0007155|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132637_PI430048170 0.76359983981877 0.989753525861228 0.446402344996992 0.474432235864917 0.378765182368009 A A A 0.517405718903027 0.406479527248054 0.419390389652589 A A A LNCV6_132637_PI430048170 mRNA
CACATCTGTGGCAAGGTAAATTTTGTAGAGTGCTTTGTTTATCCAGTTTAATATTCGTGG NM_205849 RefSeq chrX - 9024231 9034127 FAM9B 171483 "family with sequence similarity 9, member B" GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88439_PI430048170 0.0301215937780624 1.64505834287336 4.87007582283228 5.41594678680933 4.99063929305628 P P P 4.34283631659666 4.58408529591777 4.23101773276326 P P P LNCV6_88439_PI430048170 mRNA
TTTTTTGTTTGTTTGTTTTTAATCTCAGCCTTGGCGTGAGCTGGGGCCTTCCTCTCTTCT NM_024522 RefSeq chr1 - 31179744 31239887 NKAIN1 79570 Na+/K+ transporting ATPase interacting 1 GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135416_PI430048170 0.21183845658313 0.52720505450451 3.34887549632056 1.09388261694736 2.51914498723842 P A A 3.53001722713759 3.45681138304179 3.55039099471878 P P P LNCV6_135416_PI430048170 mRNA
TCTCCTGGACTAAAAGAATGTGAAAAGATGGGGAAATAAATCTGTAATCTGAACATGGAA NM_015453 RefSeq chr3 + 9363032 9386791 THUMPD3 25917 "THUMP domain containing 3, transcript variant 1" GO:0005737|GO:0003723|GO:0008168|GO:0005730|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139590_PI430048170 0.103042546154143 1.0685541448458 0.469367658785628 0.566723841308509 0.53165327504677 A A A 0.362206527864871 0.435534544692515 0.482176417472393 A A A LNCV6_139590_PI430048170 mRNA
AAGGCTGTACAAGATTTAGTGTCATTGGGTCTCATATTTGTGTTAGACCATGAAATATTC NM_001167674 RefSeq chr3 + 84958981 86074429 CADM2 253559 "cell adhesion molecule 2, transcript variant 1" GO:0030424|GO:0005737|GO:0030054|GO:0005886|GO:0007420|GO:0034329|GO:0045202|GO:0016021|GO:0007155|GO:0045216|GO:0034332|GO:0032809 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144014_PI430048170 0.0768006912516428 0.515426971054167 0.302492417425975 0.300976961807115 0.378882792035161 A A A 1.29104642952999 1.67161637619896 0.742431121534771 A A A LNCV6_144014_PI430048170 mRNA
GTGGTGAAAGGGGCGTGGAGTTTCAATATCAATAAACCACCTGATATCAATAAGCCAAAA NM_003227 RefSeq chr7 - 100620415 100641550 TFR2 7036 "transferrin receptor 2, transcript variant 1" GO:0006879|GO:0005737|GO:0005887|GO:0004998|GO:0006826|GO:0006898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145208_PI430048170 0.468615931185797 1.4443923371724 1.70696279900063 0.432338558618838 0.353089335381805 A A A 0.522995472053693 0.464031981832159 0.336293919975924 A A A LNCV6_145208_PI430048170 mRNA
ATTGGAGAAGGAATTTCATTGCAAGAAATACCTGAGCTTGACAGAGCGCTCTCAGATCGC NM_001098834 RefSeq chr7 - 151148588 151167548 GBX1 2636 gastrulation brain homeobox 1 GO:0043565|GO:0006355|GO:0021522|GO:0019230|GO:0007628|GO:0005634|GO:0048663|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128580_PI430048170 0.0299974628624257 0.663672047224245 6.1923088607674 6.12196351624103 6.53114281122071 P P P 6.87625856846639 6.80819142115757 6.9650081368209 P P P LNCV6_128580_PI430048170 mRNA
TAAGGGGGTTGGAAGAACCATCGAAGCCTAAGGCATAGAAGAAAATTTGGGGTTAAGAAA NM_012459 RefSeq chr11 - 112084810 112086798 TIMM8B 26521 "translocase of inner mitochondrial membrane 8 homolog B (yeast), transcript variant 1"

GO:0007605|GO:0006626|GO:0005743|GO:0042719|GO:0008270|GO:0072321|GO:0044267|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141329_PI430048170 0.8780022982003470.9173336715131081.2665717817403 0.3602314731856640.354456514423885A A A 1.5159078656914 0.365957314898863 0.341646346735872A A A LNCV6_141329_PI430048170 mRNA
TTTACCTGCTCCTCAAGCCTTATTAAACACAAGAGAAGTCATACTGGAGACAGACCTACA NM_001159522 RefSeq chr7 + 64045442 64078549 ZNF727 442319 zinc finger protein 727
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138591_PI430048170 0.0269652795233993 0.4256052903116857.14964687242279 6.9905327460799 7.42497973665123 P P P 7.90297528343057 8.46875802305325 8.78965878179093 P P P LNCV6_138591_PI430048170 mRNA
GTGTATAACTGGCAGGCTTATTTATCTGTTGCACTTGGTTAGCTTTAATTGTTCTGTATT NM_001031684 RefSeq chr2 - 38743598 38751494 SRSF7 6432 "serine/arginine-rich splicing factor 7, transcript variant 1"
GO:0005515|GO:0006397|GO:0008380|GO:0006369|GO:0010467|GO:0048025|GO:0006366|GO:0031124|GO:0005634|GO:0005737|GO:0006406|GO:0000166|GO:0000398|GO:0005654|GO:0008270|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135452_PI430048170 0.6976461980987350.97395244456545 0.34125624775679 0.4770284437486410.352025241762683A A A 0.5329587348092470.456630597514121 0.288179304443399A A A LNCV6_135452_PI430048170 mRNA
GATGGCAGTCATCTAGACATGTAAAATGCCAAGAATGTCTTAGAATTGCACAATTTAGAA NM_014648RefSeq chr3 + 108589489 108694846 DZIP3 9666 DAZ interacting zinc finger protein 3
GO:0005515|GO:0000209|GO:0005737|GO:0004842|GO:0019902|GO:0016874|GO:0003723|GO:0008270|GO:0031593 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95225_PI430048170 0.5414326332014391.01795905056691 0.3711352381685670.364106399216945 0.265791824980362A A A 0.3015010432833150.319125256814875 0.305695201077279A A A LNCV6_95225_PI430048170 mRNA
AATTGATGCGCATAGTTTTCATCTATGCAATTTTACTTGCTTCTGTCACTTTACGATCTG NM_000217RefSeq chr12 + 4909906 4918256 KCNA1 3736 "potassium channel, voltage gated shaker related subfamily A, member 1"
GO:0005515|GO:0005251|GO:0023041|GO:0015079|GO:0030054|GO:0005886|GO:0005783|GO:0045202|GO:0007268|GO:0019228|GO:0030425|GO:0005829|GO:0050905|GO:0006937|GO:0016324|GO:0010960|GO:0008076|GO:0005249|GO:0042391|GO:0043025|GO:0051260|GO:0050966|GO:0043679|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132932_PI430048170 0.98113831497851 1.00212760083426 0.576462477881128 0.48301207170496 0.382544971204739A A A 0.4128228865188870.519532679083616 0.504677844841819A A A LNCV6_132932_PI430048170 mRNA
GGAGGCAAAGCCAGAATGCTGCCATTTTAATTCCAATCTGTTATTTTCACTAAATCATGT NM_001010904 RefSeq chr6 + 49499957 49528064 GLYATL3 NA glycine-N-acyltransferase-like 3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130145_PI430048170 0.2958424105992170.65742085275854 0.405473985170189 0.3794200501023870.255162241717754A A A 0.3300290470491540.684223886529099 1.55822035991229 A A A LNCV6_130145_PI430048170 mRNA
CTATCTCTAATTTAGAGTGCGGTACATAATTATATCCGCAAATAAAGAAGAGACAAAGGC NM_080552RefSeq chr20 + 38724461 38729372 SLC32A1 140679 "solute carrier family 32 (GABA vesicular transporter), member 1"
GO:0044306|GO:0043005|GO:0005886|GO:0007568|GO:0044292|GO:0007268|GO:0015495|GO:0060077|GO:0055085|GO:0003333|GO:0007269|GO:0030425|GO:0044316|GO:0051286|GO:0015816|GO:0015171|GO:0015812|GO:0015187|GO:0030672|GO:0061202|GO:0016021|GO:0006811 . NA - . NA NA NA NA NA NA NA NA

NA
LNCV6_142499_PI430048170 0.2591593696552710.8450629716276873.90461045864432
3.57200923461414 3.40732913661701 P P P 3.85524225145415 4.08939899604563
3.68426518692746 P P P LNCV6_142499_PI430048170 mRNA
AGTCTGTCCTTACAGAGCTGCAATAAGAAATAACCAAAGATGAAGCTGGTCAAATATTTT NM_007170RefSeq chr1
- 45343882 45491168 TESK2 10420 testis-specific kinase 2
GO:0005515|GO:0030036|GO:0005634|GO:0018108|GO:0007283|GO:0005524|GO:0046872|GO:0005737|GO:0004
672|GO:0004674|GO:0048041|GO:0004712|GO:0005654|GO:0006468|GO:0004713 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_104779_PI430048170 0.3202893716946221.1023880428252 7.9794823589356
7.97581339257726 7.79998978774377 P P P 7.98581537827029 7.62862124112685 7.7009416840551
P P P LNCV6_104779_PI430048170 mRNA
TTGAGTTGACAGCTGGCCTATGGTTTCTGCATTTTGTTAAGAAGCACCTCATGCAAGCGA NM_005779RefSeq chr5
- 78485214 78648825 LHFPL2 10184 lipoma HMGIC fusion partner-like 2
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51826_PI430048170 0.2631800676553490.7639236244455340.3730133693730610.33352792460463
0.323729252047517 A A A 0.5360655030383941.14429321690234 0.403495517446592 A A A
LNCV6_51826_PI430048170 mRNA
GAGCCAGGTAGACTGAAATTACCATGTGTCCAAATTAAAATTGCATACTTCAAGGATTAT NM_001098816 RefSeq
chr11 - 78653282 79440651 TENM4 26011 teneurin transmembrane protein 4
GO:0043005|GO:2000543|GO:0005634|GO:0032289|GO:0060912|GO:0001702|GO:0042803|GO:0060038|GO:0007
165|GO:0005737|GO:0097264|GO:0005887|GO:0048666|GO:0048714|GO:0031643 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131766_PI430048170 0.9158987070339011.08915812862998 1.85271248157249
1.78695601508209 0.50045501682492 A A A 1.6028315287212 1.62551302257816
0.731573556553071 A A A LNCV6_131766_PI430048170 mRNA
TTCCTACTGGAGATACCAGAGACTCTGAAACTATAGAATAAAGCCTCTGTGCTGCACAAC NM_000614RefSeq chr11
+ 58622672 58625732 CNTF 1270 ciliary neurotrophic factor
GO:0005138|GO:0046533|GO:0008284|GO:0042517|GO:0070120|GO:0005615|GO:0097058|GO:0005127|GO:0007
165|GO:0048644|GO:0005737|GO:0043524|GO:0048666|GO:0008083|GO:0040007|GO:0046668 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136626_PI430048170 0.00176576516808693 0.4744658164533084.41416846467175
4.05264658634005 4.30797234785839 P P P 5.31522795335155 5.20944062826515 5.4868351288017
P P P LNCV6_136626_PI430048170 mRNA
CACTGAAATGAGAACTCTAGATGTAACTCTATTCAAATAAACCTTCGTGAGACATTCATG NM_020909RefSeq chr2
+ 120013027 120179121 EPB41L5 57669 "erythrocyte membrane protein band 4.1 like 5, transcript
variant 1"
GO:0008092|GO:0032091|GO:0005886|GO:0010718|GO:0071560|GO:0001839|GO:0031032|GO:0005634|GO:0070
986|GO:0001837|GO:0051894|GO:0032092|GO:0006931|GO:0005737|GO:0032525|GO:0007509|GO:0070201|GO:0
005856|GO:0048319|GO:0003383|GO:0048339|GO:0022408|GO:0019904|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129358_PI430048170 0.00662170420612811 0.3154886029071135.60796796732664
5.31350992257322 5.80812183691942 P P P 6.75782013673264 7.44466679079351
7.45786880918506 P P P LNCV6_129358_PI430048170 mRNA
GGTTTTCCATCTGTTAGCATTTCAGACATTTTATGTTCCTCTTACTCAATTGATACCAAC NM_001142522 RefSeq chr6
- 152970522 152983605 FBXO5 26271 "F-box protein 5, transcript variant 2"
GO:0005515|GO:0019901|GO:0060565|GO:0051437|GO:0005819|GO:0005634|GO:0051436|GO:0001556|GO:0031
145|GO:0051439|GO:0046872|GO:0005829|GO:0016050|GO:0007057|GO:0007346|GO:0046785|GO:0000082|GO:0
005737|GO:0000083|GO:0005654|GO:0000278|GO:0045835|GO:0007091|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_128835_PI430048170 0.88371179220849 1.31584810381317 0.429639796925278
2.76414113019813 2.23984546632078 A A A 1.58738043401204 1.9428338803222
1.54913511456267 A A A LNCV6_128835_PI430048170 mRNA
GAACCTTGTGCCGGCCAGGCCCAGTTTCCTTGTGTGATACACTAATGTATTTGCTTTTTT NM_000299 RefSeq chr1
+ 201283451 201332993 PKP1 5317 "plakophilin 1, transcript variant 1b"
GO:0030057|GO:0005515|GO:0005882|GO:0005886|GO:0006915|GO:0005634|GO:0007275|GO:0030280|GO:0019
215|GO:0006921|GO:0043231|GO:0007165|GO:0016337|GO:0045110|GO:0005654|GO:0004871|GO:0007155|GO:0
005521|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82774_PI430048170 0.0314737470633211 0.803769351853931 6.83021454155871
6.67686699594208 6.65308620250824 P P P 7.18114712064669 6.97591186351221
6.94333049196124 P P P LNCV6_82774_PI430048170 mRNA
CAGCCCCTGCACCTGTCATTTATTCTTCCACTGCCCAATAAATATTCATGGCAGACTTTA NM_152901 RefSeq chr16
- 31215961 31217093 PYDC1 260434 PYD (pyrin domain) containing 1
GO:0005515|GO:0050718|GO:0045087|GO:0008385|GO:0032088|GO:0005634|GO:0006469|GO:0033209|GO:0005
829. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103748_PI430048170 0.00801356926530789 0.632508710624947 5.54243904607388
5.43869833075615 5.76242443023202 P P P 6.2362652899005 6.08041175752964
6.40974251485114 P P P LNCV6_103748_PI430048170 mRNA
AGATTACCTTTGACTCTTGTCCCAGGTGAAAGATTTAGAGAACTAATGGATAAGTTCCTG NM_024561 RefSeq chr13
+ 41311204 41377030 NAA16 79612 "N(alpha)-acetyltransferase 16, NatA auxiliary subunit, transcript
variant 1"
GO:0005515|GO:0031415|GO:0005667|GO:0043066|GO:0004596|GO:0050821|GO:0005634|GO:0005737|GO:0043
022|GO:0016407|GO:0045893|GO:0006474|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138108_PI430048170 0.2247712176479280 .865188742603513 9.38524637421618
9.45763187522951 9.66692345893054 P P P 9.78962360004308 9.48533424053325
9.85071833299591 P P P LNCV6_138108_PI430048170 mRNA
ATAAGACATATTTTATGTCCTTTTGCCAAGGTGGATGTGTTAGTCTCAGGCCCTCCTGGC NM_001190810 RefSeq
chr10 - 47501853 47523638 AGAP9 642517 "ArfGAP with GTPase domain, ankyrin repeat and PH
domain 9" GO:0043547|GO:0008060|GO:0032312|GO:0008270 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132693_PI430048170 0.0204494144080357 0.685115273918396 7.23766441181754
6.99355196219342 7.27494851755589 P P P 7.53127487910798 7.68835557831245
7.91341663169532 P P P LNCV6_132693_PI430048170 mRNA
TTGGGGCAGCTGTCACCAGCTAAAGCAATGTTGTTAAAATTAGCTCAATAAAAATGTCTT NM_015017 RefSeq chr1
- 77695988 77759879 USP33 23032 "ubiquitin specific peptidase 33, transcript variant 1"
GO:0005515|GO:0032091|GO:0006511|GO:0043130|GO:0048471|GO:0016579|GO:0004843|GO:0030891|GO:0032
092|GO:0005737|GO:0070536|GO:0007411|GO:0045111|GO:0009267|GO:0071108|GO:0005813|GO:0005794|GO:0
005776|GO:0001664|GO:0044297|GO:0006897|GO:0004197|GO:0051298|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135722_PI430048170 0.187837557361658 1.17296163450525 7.26761273101389
7.51866679253548 7.20926733045674 P P P 6.89947612036188 7.28101552817232
7.11844417419297 P P P LNCV6_135722_PI430048170 mRNA
GGTTTGTTGATATTTTGCACTCTTAACACCTGCCAATAAAGACGGTCTACACTGAAAAAA NM_052943 RefSeq chr1
- 27005019 27012842 FAM46B 115572 "family with sequence similarity 46, member B" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_39400_PI430048170 0.0104509608208931 .53928089098726 6.83767437196272 7.18995927000416
7.03475623579974 P P P 6.53598737117016 6.32875725357933 6.34292622172451 P P P
LNCV6_39400_PI430048170 mRNA

TGCAAGTTTTTAGTCTTGCTCATCCCACTCTTCCTTTTACTAGCAGGTCTCTCCTTACGG NM_001130965 RefSeq chr7 + 832504 874920 SUN1 23353 "Sad1 and UNC84 domain containing 1, transcript variant 1" GO:0005515|GO:0031965|GO:0090292|GO:0034993|GO:0006998|GO:0090286|GO:0005635|GO:0002080|GO:0005521|GO:0043231|GO:0005639 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_137236_PI430048170 0.0857657752339102 0.3892368289371973.10312101273139 1.3088183803585 2.39594848680253 P A A 3.35131583853352 3.83684028526082 4.12661734072264 P P P LNCV6_137236_PI430048170 mRNA
AATACTGGCAAGTGCACAAGCCACATAAACCTGAATAAAACTTTTGACCTAGGGTTGAAA NM_001357RefSeq chr1 + 182839303 182887982 DHX9 1660 "DEAH (Asp-Glu-Ala-His) box helicase 9, transcript variant 1" GO:0005515|GO:0008380|GO:0003724|GO:0010467|GO:0005634|GO:0005829|GO:0004004|GO:0034605|GO:0005737|GO:0004003|GO:0001085|GO:0032481|GO:0032508|GO:0006396|GO:0005813|GO:0070934|GO:0005730|GO:0005524|GO:0003677|GO:0001649|GO:0016020|GO:0000398|GO:0030529|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_142335_PI430048170 0.25083246874862 0.6154182235028082.00490756681513 1.01325630746182 0.366542489675176A A A 1.34735894471529 1.94592452197554 2.45923242553491 A A P LNCV6_142335_PI430048170 mRNA
AAGACAGACAATGCAAAGGTAACTGGCAAGAGGTGAGCAAATGTTTTAGAACATTTATAT NM_014880RefSeq chr2 - 159768627 159798255 CD302 9936 "CD302 molecule, transcript variant 1" GO:0006909|GO:0005902|GO:0016020|GO:0030246|GO:0030175|GO:0016021|GO:0005938 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_137438_PI430048170 0.1006452997253070.7385853166534046.84917078928918 6.79453539279856 6.49809536513567 P P P 6.84582818739638 7.39484736200118 7.18449569725524 P P P LNCV6_137438_PI430048170 mRNA
TCTCACTGGATCTGTCTGCCAACCCTGAGATCAGCTGTGCCAGCTTGGAAGAGCTCCTGT NM_013432RefSeq chr8 - 144428779 144444429 TONSL 4796 "tonsoku-like, DNA repair protein" GO:0005515|GO:0042555|GO:0042393|GO:0035101|GO:0005737|GO:0000724|GO:0003714|GO:0042994|GO:0031297|GO:0005654|GO:0043596|GO:0005662 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_127953_PI430048170 0.0727323057881281 0.68216184317574412.5045148775676 12.0486107828698 12.1035642984654 P P P 12.4241346135793 12.9129183320137 12.9606652177078 P P P LNCV6_127953_PI430048170 mRNA
CTGGATAAACCACCCTCTGGGGACAGGATAATAAAACATGTAATATTTTTAAGAAGGAAA NM_004924RefSeq chr19 + 38647626 38730531 ACTN4 81 "actinin, alpha 4" GO:0005515|GO:0043005|GO:0048471|GO:0030018|GO:0032417|GO:0035257|GO:0035357|GO:0005634|GO:0042974|GO:0015031|GO:0005615|GO:0042803|GO:0031143|GO:0005737|GO:0051015|GO:0030374|GO:0070830|GO:0005911|GO:0001882|GO:0031093|GO:0051017|GO:0070062|GO:0001666|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_92396_PI430048170 0.5730892069403831.17037209562667 2.12517585527412 2.65556871273045 2.90886307781991 A A A 2.80307938344135 1.4255752277623 2.55156466034226 P A P LNCV6_92396_PI430048170 mRNA
TTGTCAAATTTCATCAGCTATGAAACCCACGTAGTCGAACACCGTGATGCTTCTCCTGCA NM_001042481 RefSeq chr14 + 51489120 51730726 FRMD6 122786 "FERM domain containing 6, transcript variant 1" GO:0043296|GO:0003383|GO:0005737|GO:0032970|GO:0005886|GO:0034613|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_143448_PI430048170 0.6150506930839771.50928857578704 0.41105323010597 2.22737424668243 0.427441871389025A A A 1.17286723441546 0.371305706663501 0.407703524064334A A A LNCV6_143448_PI430048170 mRNA
TACCTGATGATCCACAAGGACATGACCCTGGTGGACGCCATCCAGCAAGTGGCCAAGAAC NM_001003892 RefSeq chr10 - 75037835 75058514 DUPD1 NA dual specificity phosphatase and pro isomerase domain containing 1 NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_127922_PI430048170 0.0153960057170411.49830467530569 11.3261360119049
11.4509708143972 11.5557035359584 P P P 10.698986899293 10.8030756443362
11.0648724128907 P P P LNCV6_127922_PI430048170 mRNA
AGATGACTGAGGAAGGGATGGACTAAGCTAATCCCCTTTTGGTGGTGTTTCTTTAAAAAA NM_001141969 RefSeq
chr6_GL000255v2_alt - 4512986 4517446 DAXX 1616 "death-domain associated protein,
transcript variant 1"
GO:0005515|GO:0000792|GO:0008625|GO:2001235|GO:0005634|GO:0050681|GO:0042803|GO:0005829|GO:0042
393|GO:0002039|GO:0005737|GO:0031072|GO:0045860|GO:0016032|GO:0031396|GO:0006338|GO:0031625|GO:0
070603|GO:0006355|GO:0019901|GO:0000281|GO:0003714|GO:0006334|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_51809_PI430048170 0.00631130210152092 0.18487518159903 4.1343570418135
3.32527616459716 4.28710495017632 P P P 6.19729153763025 6.34409092708056
6.64662430043807 P P P LNCV6_51809_PI430048170 mRNA
CCATAGATAGACTGAGTCTTCTCTCGTAGGTTACCATTACATAGTAATTTTGATTCTGAA NM_024524 RefSeq chr3
- 194402673 194468239 ATP13A3 79572 ATPase type 13A3
GO:0016020|GO:0008152|GO:0016021|GO:0016887|GO:0005524|GO:0046872|GO:0006812 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_62873_PI430048170 0.0325230119713956 0.630199475609729 7.94560906865987
7.96076411874016 8.0400674768091 P P P 8.38636053682167 8.69778650117355
8.82757119886992 P P P LNCV6_62873_PI430048170 mRNA
ATACACACACACATAAAGTTTGTTTCCTGTGGCATTTAAATTAATCTGGTTGGTCCATAG NM_001136498 RefSeq
chr17_KI270857v1_alt + 2765575 2770924 CISD3 284106 CDGSH iron sulfur domain 3
GO:0005739|GO:0051537|GO:0046872 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_143132_PI430048170 0.0062818868880287 1.94336987115524 6.24320159915332
5.9099623074763 5.78600038659135 P P P 4.83811616997064 5.19587742107635
5.0468006103864 P P P LNCV6_143132_PI430048170 mRNA
GAATCCTCAAGGACTAATGAAATAAATGCTAGACTGCTGAAGATGAGTACAAGTGGCAAA NM_001191033 RefSeq
chr2 + 26180715 26189663 GAREML 150946 "GRB2 associated, regulator of MAPK1-like, transcript
variant 2" GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135025_PI430048170 0.275138348333562 0.848327582410885 0.283465251518877
0.350835590114105 0.607046501555254 A A A 0.912044048485062 0.404749836734494
0.611571682916499 A A A LNCV6_135025_PI430048170 mRNA
GGAAAGCTGCCAATTACCTATATGTATGTTCTTCCTATTTTCTTACCTCTTTCCCCATGT NM_015087 RefSeq chr13
- 36301637 36346509 SPG20 23111 "spastic paraplegia 20 (Troyer syndrome), transcript variant 1"
GO:0005515|GO:0005811|GO:0005886|GO:0051881|GO:0030496|GO:0045202|GO:0005741|GO:0034389|GO:0009
838|GO:0030514|GO:0048698|GO:0050905|GO:0005737|GO:0060612|GO:0031625|GO:0051301 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_66507_PI430048170 0.475174330378 0.962626488021871 6.04632389002252 6.00559172797616
5.96140705443621 P P P 5.94892850793303 6.07107290747451 6.15220593563264 P
P P LNCV6_66507_PI430048170 mRNA
GAAAGACCAGTTTTACCTAGATACTAAAGGAAGAATTAAACCGCTGTTAGTTTGAAATGC NM_004805 RefSeq
chr2 - 127846265 127858155 POLR2D 5433 polymerase (RNA) II (DNA directed) polypeptide D
GO:0008380|GO:0010467|GO:0003727|GO:0006368|GO:0034402|GO:0006367|GO:0006366|GO:0005634|GO:0031
990|GO:0003697|GO:0000166|GO:0000932|GO:0034587|GO:0005665|GO:0016032|GO:0045948|GO:0035019|GO:0
000288|GO:0003899|GO:0006370|GO:0050434|GO:0006281|GO:0006283|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132964_PI430048170 0.0243288516095238 0.490683347350186 7.24024149302326
6.5719002546822 7.16911810225375 P P P 7.99615417267488 7.91433051302949

8.22280995349938 P P P LNCV6_132964_PI430048170 mRNA
GTGCCTTTGAATACAAATTTCAGTTCTGCAAAAGTGAAACATTAAACATTGCCAACGCAA NM_005857 RefSeq
chr1 + 40258049 40294184 ZMPSTE24 10269 zinc metallopeptidase STE24
GO:0016020|GO:0008235|GO:0006508|GO:0005789|GO:0071586|GO:0005637|GO:0030327|GO:0006998|GO:0016
021|GO:0004222|GO:0046872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_143670_PI430048170 0.000266898627087652 2.03680982913983 3.83083198939947
3.63560999848253 3.7152600853491 P P P 2.82317576822684 2.65231443204071
2.62593198211973 P P P LNCV6_143670_PI430048170 mRNA
AACCCATCATTCTATGTTTTTCTTAACATAGCTGGCACAGGGTTTAACACATAATTGCCA NM_021955 RefSeq chr7
+ 93906507 93911173 GNGT1 2792 "guanine nucleotide binding protein (G protein), gamma
transducing activity polypeptide 1"
GO:0005886|GO:0007603|GO:0005834|GO:0003924|GO:0071456|GO:0007268|GO:0022400|GO:0001917|GO:0007
165|GO:0008104|GO:0008152|GO:0010659|GO:0004871|GO:0042462|GO:0016056 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_145742_PI430048170 0.789375398208978 0.977620890938808 7.30545591904205
7.07462459992499 7.04722899684805 P P P 7.29456500036284 7.21063936470568
7.02077978984778 P P P LNCV6_145742_PI430048170 mRNA
GGAGAGTTAATAACCTCCCCTTCTCTCTCTACATGTTCAATAAAAGTTGTTGAAAGATTA NM_001062 RefSeq
chr11 - 59852807 59866568 TCN1 6947 "transcobalamin I (vitamin B12 binding protein, R binder
family)"
GO:0015889|GO:0009235|GO:0031419|GO:0006766|GO:0006767|GO:0005576|GO:0044281|GO:0005615|GO:0006
824 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144699_PI430048170 0.0666581427948631 0.705411032062615 10.0607869752996
9.94130789416146 10.3185155070715 P P P 10.4999509967395 10.39923074193
10.9065660779627 P P P LNCV6_144699_PI430048170 mRNA
GTTTCAACGCCAATATGTATTCTACAAAAGAGAATGGTTTTAGGCTCCAGTGTTATACTT NM_007235 RefSeq
chr12 + 64404372 64448683 XPOT 11260 "exportin, tRNA"
GO:0005737|GO:0000049|GO:0006409|GO:0005643|GO:0008536|GO:0005654|GO:0006886 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139674_PI430048170 0.658313151170873 1.06926365724431 9.68415847895321
9.54578562104874 9.40740285565117 P P P 10.0677097417738 9.09383884465591
8.9184001989575 P P P LNCV6_139674_PI430048170 mRNA
TGGACCTCGCTGCTCCAGAGTTTAATAAAGGTAGCACATGCTTATTGCTAGAGCCTTTGC NM_198722 RefSeq
chr3 - 49716833 49719805 AMIGO3 386724 adhesion molecule with Ig-like domain 3
GO:0007420|GO:0016021|GO:0007157 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_144258_PI430048170 0.360280687920272 1.34942886968958 2.51887604975332
3.52022941530914 3.20382582340839 A P P 3.1484589290758 2.10105191041832
2.68267913604533 P A P LNCV6_144258_PI430048170 mRNA
TTATGATCGATGAACTACTTACTCAATTTGGGAACTTGGGGACAGCCCCCACCATCTTCT NM_182554 RefSeq
chr10 + 49679637 49708910 C10orf53 282966 "chromosome 10 open reading frame 53,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127961_PI430048170 0.775562539570591 1.00999479266844 0.400865231214926
0.389870002828947 0.275356828833877 A A A 0.320168511682217 0.35187195175973
0.354077003572576 A A A LNCV6_127961_PI430048170 mRNA
GTGGTTTCAGATTGTAAATAGCGCGTCAGCGAACTTGTCTAAATCATATATTTTTGTCTA NM_024337 RefSeq chr5
+ 3596053 3601403 IRX1 79192 iroquois homeobox 1
GO:0043565|GO:0006355|GO:0072272|GO:0005634|GO:0072086 . NA - . NA NA NA NA NA

NA NA NA NA
LNCV6_127617_PI430048170 0.99943349498134 1.00141552425024 1.23836417768636
0.403821967114047 0.360906227247107 A A A 1.23003696473981 0.37138972516317
0.400757049575755 A A A LNCV6_127617_PI430048170 mRNA
GTTGAAAAGCCTCCCAACTTACAGCAAGGATGATGAAAATATAAGTAAGAGTTCGGCACC NM_001303482 RefSeq
chr18 - 75416016 75427703 SMIM21 NA "small integral membrane protein 21, transcript variant 2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128850_PI430048170 0.129176671480868 0.927928523814988 0.268993277236409
0.284638142832892 0.288854811182729 A A A 0.467902687490718 0.374125643739552
0.320397545656012 A A A LNCV6_128850_PI430048170 mRNA
CCATCAGAAGTCCGAGGACTTTGTTCTTGATAACTACTACCAATAAAAATTGAGTATTTG NM_178844 RefSeq
chr16 - 3539035 3577404 NLRC3 197358 "NLR family, CARD domain containing 3, transcript variant 1"
GO:0003674|GO:0042110|GO:0005737|GO:0032496|GO:0007249|GO:0032088|GO:0031396|GO:0005524|GO:0043
124 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131254_PI430048170 0.0731299519224616 0.339864280536618 0.534347107562447
0.406312076279877 0.242323258096311 A A A 2.35565780501443 0.986559839181734
2.18320440572426 A A A LNCV6_131254_PI430048170 mRNA
AGCAGTCCCTGCATAAGGATTGGAGTGGTTTGAAGTTTCTCTTCCAAGCACTAACATGTC NM_001127211 RefSeq
chr10 - 116883376 117005577 KIAA1598 57698 "KIAA1598, transcript variant 1"
GO:0007411|GO:2001222|GO:2000114|GO:0044295|GO:0019900 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_136556_PI430048170 0.0888623786751559 1.43477822889953 5.5474211403027
5.95295071149378 6.16243580907014 P P P 5.14054050420801 5.45339460578707
5.54231981189137 P P P LNCV6_136556_PI430048170 mRNA
TACATCCTGATTCTGTAGCAAGTAGATTGTTTGCTCTTTGTCTTTAAGAAATACTAGGAG NM_173647RefSeq chr2
- 101275600 101308716 RNF149 284996 ring finger protein 149
GO:0043409|GO:0004842|GO:0031647|GO:0016567|GO:0016020|GO:0016874|GO:0008270|GO:0016021|GO:0035
690|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141189_PI430048170 0.0658382827514651 1.10825106394608 0.720190747875825
0.8262256264371080.691368148662603A A A 0.5984830428405110.610923802659712
0.586945964408527A A A LNCV6_141189_PI430048170 mRNA
AACAAGATGCTGATCCAACCTGAGTGGAGTCAGGTGAGGCATCTTTACATCTAAGAATTT NM_004464RefSeq chr4
+ 80266587 80291017 FGF5 2250 "fibroblast growth factor 5, transcript variant 1"
GO:0008286|GO:0048011|GO:0008284|GO:0008283|GO:0023019|GO:0048015|GO:0007267|GO:0005104|GO:0005
576|GO:0005615|GO:0007399|GO:0007173|GO:0008543|GO:0045087|GO:0010001|GO:0051781|GO:0008083|GO:0
038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136148_PI430048170 0.0882329620369375 0.7441746060617392.85391729121004
2.90863773100243 3.2362612073557 A A P 3.1494806365714 3.63433986464787 3.4824939103782
P P P LNCV6_136148_PI430048170 mRNA
CATAGAAAGCTTGAAAATCAGTCCAGGGGGACAGCATTAATCACCATGTTCTTTCCTTAT NM_020165RefSeq chr3
- 8877195 8963475 RAD18 56852 RAD18 E3 ubiquitin protein ligase
GO:0001741|GO:0005515|GO:0016567|GO:0005657|GO:0016874|GO:0000403|GO:0005634|GO:0007283|GO:0003
684|GO:0006281|GO:0008270|GO:0000785|GO:0009411|GO:0045910|GO:0031625|GO:0031593 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129647_PI430048170 0.0110243128005925 0.5036623875743645.69908007742602
5.37399886725795 5.92384183113775 P P P 6.52964723496355 6.47791149828422
6.95995104092374 P P P LNCV6_129647_PI430048170 mRNA
CAAGTTCAACTTTTTGTGCTAACAATGCATGCAGGACTAAGAGGGATGATCTAAAAAATA NM_020940RefSeq chr10
+ 114821743 114864715 FAM160B1 57700 "family with sequence similarity 160, member B1, transcript

variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133333_PI430048170 0.0153596063737123 0.4684980914367192.54690445842397
2.85544615987329 2.86235828349168 A A P 3.45404212616239 3.94754943371338
4.09216895105444 P P P LNCV6_133333_PI430048170 mRNA
TAGATTCTAGAATGTGTCCTCCTGACTAAGGGGTTCAGGATACTGTTCACCTTCTCCAAC NM_014630RefSeq chr15
+ 84748586 84806432 ZNF592 9640 zinc finger protein 592
GO:0006355|GO:0005654|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143862_PI430048170 0.7616254768475991.03760719348916 4.96094804516921
4.66143893551853 4.77579374018069 P P P 4.27746148955322 4.87839241745295
5.00004373103063 P P P LNCV6_143862_PI430048170 mRNA
GTTTTCAGATACCAGAAAGAGCCTTCAGTAGATTCACAAGATTAAAATTGATGCGCTTAA NM_058169RefSeq chr12
+ 12357078 12466904 LOH12CR1 118426 "loss of heterozygosity, 12, chromosomal region 1, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104135_PI430048170 0.6864542752456191.03147358492934 8.20035558210517 8.1613233896149
8.2879534241349 P P P 8.06746098246971 8.38064100292614 8.04540629203936 P P P
LNCV6_104135_PI430048170 mRNA
TCAAGAAGGAGGATGTCATCTCCACTCTGCAGTACCTCAATCTCATCAACTACTACAAGG NM_182710RefSeq chr11
+ 65712001 65719606 KAT5 10524 "K(lysine) acetyltransferase 5, transcript variant 1"
GO:0005515|GO:0048471|GO:0006325|GO:0005634|GO:0050681|GO:0000812|GO:0032403|GO:0046872|GO:0006
302|GO:0005829|GO:0071392|GO:0045944|GO:0010212|GO:0070491|GO:0035267|GO:0016032|GO:0006978|GO:0
004402|GO:0032703|GO:0005667|GO:0016573|GO:0003713|GO:0005730|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129332_PI430048170 0.00306548882636281 2.47966302888285 9.8581340142557
9.92485037632725 9.9462545514285 P P P 8.54885741360074 8.7757048113592
8.45677898073642 P P P LNCV6_129332_PI430048170 mRNA
TCAACGTAACACATAATGGTACTTATCAGTGCCAAGCGTCCAGCTCACGAGGCAAATACA NM_002162RefSeq chr19
- 10333775 10339669 ICAM3 3385 intercellular adhesion molecule 3
GO:0005515|GO:0016337|GO:0005178|GO:0005886|GO:0030198|GO:0005887|GO:0050776|GO:0005102|GO:0007
155|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127578_PI430048170 0.6573844608702951.17266930283938 0.272580147015786
0.2860576305905591.21525209217287 A A A 0.6005233448271730.353311696854792
0.328893990930238A A A LNCV6_127578_PI430048170 mRNA
CCTGCGGAGTTGCACTCTGGGTGGGAAGCACTCAAATAAAGATGCGTGGTGTTAACAGTG NM_004997RefSeq chr1
- 203167810 203175814 MYBPH 4608 myosin binding protein H
GO:0005515|GO:0032982|GO:0006942|GO:0008307|GO:0007155 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129541_PI430048170 0.000965159211016876 2.1393742094343 5.65388295761017
5.64099079871671 5.57027155074571 P P P 4.53490906964435 4.62392361828776
4.40802147995136 P P P LNCV6_129541_PI430048170 mRNA
TTCAATCTTCTCCTGCTGGTGCTGGTGCTAGGGACCATCTTGCTACCCGCTGTCACCATG NM_203411RefSeq chr17
+ 7855065 7856099 TMEM88 92162 transmembrane protein 88
GO:0005886|GO:0007275|GO:0016021|GO:0016055 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130721_PI430048170 0.40381425617575 1.20585051447068 2.72598532896887
2.32306660518345 3.10324824479972 A A P 2.30775253656997 2.64442161541457
2.47491954304487 A P A LNCV6_130721_PI430048170 mRNA
ATGGTTTACTGATGAGACAGCAAAAATGAGACAGGACCATCAGATGCAATAAAGATTCTA NM_014643RefSeq chr18
- 76357681 76495190 ZNF516 9658 zinc finger protein 516
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_133845_PI430048170 0.5448661881951981.14759194429048 2.17258789474746
2.77426293892169 2.67936437899301 A A A 1.80459846040573 2.25245941034905
2.85070686022341 A A P LNCV6_133845_PI430048170 mRNA
ATCATTGGAGAGGGAAAACAAGTCCAACCTGGAAGAAGACTTCCTTCTAAACCAGGCAGA NM_001143769
RefSeq chr10 - 30844635 30999517 ZNF438 220929 "zinc finger protein 438, transcript variant 5"
GO:0006355|GO:0005737|GO:0003700|GO:0005654|GO:0005634|GO:0045892|GO:0003677|GO:0046872|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138348_PI430048170 0.8589134943193920.9390421798907463.75238822939386
3.79272679480398 3.97890093756343 P P P 4.37571450101288 3.72443181384954
3.57572720722813 P P P LNCV6_138348_PI430048170 mRNA
CCCATACCCCTGCCTGGGTTTTCTAACTGTAAATCACTTGTAAATAAATAGATTTGATTA NM_001287174 RefSeq
chr11 - 17392884 17476845 ABCC8 6833 "ATP-binding cassette, sub-family C (CFTR/MRP), member 8,
transcript variant 1"
GO:0015079|GO:0005886|GO:0005975|GO:0008281|GO:0007268|GO:0042626|GO:0044281|GO:0055085|GO:0005
524|GO:0044325|GO:0007165|GO:0006112|GO:0050796|GO:0008076|GO:0006813|GO:0071805 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_74049_PI430048170 0.0964328276245848 1.18936714178204 14.7718454396068
14.9836863035165 15.03479939236 P P P 14.5973525069301 14.5950873734477
14.8458919142572 P P P LNCV6_74049_PI430048170 mRNA
ACCCTGCGACCCACTCTTTGGACCAGCAGCGGATGAATAAAGCTTCCTGTGTTGTGTGAT NM_007100RefSeq chr4
- 672435 674338 ATP5I 521 "ATP synthase, H+ transporting, mitochondrial Fo complex, subunit E, transcript
variant 1"
GO:0022904|GO:0005739|GO:0042776|GO:0015078|GO:0022857|GO:0005743|GO:0000276|GO:0044281|GO:0016
887|GO:0044237|GO:0005753 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_87311_PI430048170 0.0207190181955790.5591114107390833.77650848270953 3.52532241216207
4.13157041617661 P P P 4.43719821521711 4.7269991039863 4.82304592595482 P P P
LNCV6_87311_PI430048170 mRNA
GAATATGAACAGATAACCCTTGGCCTAACAGCTCCATCAAACCTCCTTGAGAGCAACTAC NM_145206RefSeq chr10
+ 112446997 112818744 VTI1A 143187 vesicle transport through interaction with t-SNAREs 1A
GO:0044306|GO:0012507|GO:0048471|GO:0005794|GO:0005795|GO:0090161|GO:0030136|GO:0031201|GO:0006
891|GO:0048280|GO:0006896|GO:0008021|GO:0006888|GO:0005484|GO:0000139|GO:0050882|GO:0031902|GO:0
000149|GO:0043025|GO:0005789|GO:0042147|GO:0006623|GO:0016021|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143283_PI430048170 0.0168092213980011 1.49183493850148 11.8004735922597
11.987981805235 12.0778513273471 P P P 11.3726031897361 11.1800967732603
11.5697776975312 P P P LNCV6_143283_PI430048170 mRNA
GCCCTTCCTTTCCGTGTTCCCCAACAACCTCATGCTTACGTGATTTTTATTCAAATTAAA NM_001031628 RefSeq chr12
- 51245348 51270418 SMAGP 57228 "small cell adhesion glycoprotein, transcript variant 1"
GO:0030054|GO:0005886|GO:0005654|GO:0016021|GO:0030659 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144333_PI430048170 0.5662832744451891.42661364876267 0.300759815274922
2.22171233950459 1.82174844152555 A A A 0.3100583215648821.8969001417979
0.719953110669095 A A A LNCV6_144333_PI430048170 mRNA
AGTCTTCAGAAGACAAATGCTCAGGTAGTCACTGTTTCCTTTTCACTGTTTTTAAAAACC NM_002120RefSeq
chr6_GL000256v2_alt - 4212174 4216460 HLA-DOB 3112 "major histocompatibility complex,
class II, DO beta"
GO:0019886|GO:0007165|GO:0006955|GO:0002587|GO:0023026|GO:0042613|GO:0016021|GO:0005765|GO:0032
395|GO:0005764|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_127248_PI430048170 0.000741878810594816 3.58849056874914 3.88105798567346
3.91199334997004 4.1252083185258 P P P 2.18358041494421 2.30766302908384
1.87579532856195 A A A LNCV6_127248_PI430048170 mRNA
GCGTGTGTAACATCCCATGTGCCTCACCTAATAAAATGGCTCTTCTTCTGCATCAAAAAA NM_130852 RefSeq chr20
+ 33235995 33243309 BPIFA1 51297 "BPI fold containing family A, member 1, transcript variant 2"
GO:0003674|GO:0050828|GO:0050891|GO:0045087|GO:1900229|GO:0019731|GO:0005576|GO:0005615|GO:0008
289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144490_PI430048170 0.377462284831663 1.58720002976301 0.381503959679265 1.6978623916705
0.286443286472643 A A A 0.268522924864473 0.289948794475109 0.270199242664283 A A A
LNCV6_144490_PI430048170 mRNA
GGTGCTTTTAGCACTGAGAGTCTGCTGTGATGGGAATAAAATGAAGTCCCAGCTCAGAAA NM_021571 RefSeq chr11
- 105137720 105139734 CARD18 59082 "caspase recruitment domain family, member 18"
GO:0010951|GO:0006954|GO:0004869|GO:0042981|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143550_PI430048170 0.109287134765742 0.474494560014275 1.83659623239711
1.20898778091072 0.293302909635391 A A A 1.75674898033155 2.26280365636197
2.76625029413798 A A P LNCV6_143550_PI430048170 mRNA
GACCATATTGAAATGTACGGAATTTGATCCATGCGATACTATGTGTGCATTATTTGAAAG NM_002312 RefSeq chr13
- 108207443 108214782 LIG4 3981 "ligase IV, DNA, ATP-dependent, transcript variant 1"
GO:0005515|GO:0000793|GO:0000012|GO:0051276|GO:0010165|GO:0005886|GO:0008283|GO:0016874|GO:0003
909|GO:0005634|GO:0048146|GO:0051402|GO:0006303|GO:0046872|GO:0006302|GO:0006273|GO:0043524|GO:0
005737|GO:0050769|GO:0016032|GO:0002328|GO:0006297|GO:0005958|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143696_PI430048170 0.976279611014761 0.999395181596498 6.69118233483174 6.7150064874223
6.69962922304432 P P P 6.82633897411584 6.59610933079933 6.67655907669368 P P P
LNCV6_143696_PI430048170 mRNA
CGATGAGGTTTCCATGTATTTACTTACAGACCCCATAATGTAAAGGCTCTAATAATAGAA NM_182498 RefSeq chr19
- 43607223 43619862 ZNF428 126299 zinc finger protein 428 GO:0046872 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_49834_PI430048170 0.0908422686240504 0.926356009831592 0.290491936455639
0.291832781782632 0.297143100883224 A A A 0.468967289517464 0.391748476563012
0.347204619374711 A A A LNCV6_49834_PI430048170 mRNA
GTATTGCATAGACATGTCTGTGAAAATAAAAGCACCCATTTTGCTAAGGCTTTCTGAGAA NM_001303107 RefSeq
chr9 - 101473157 101487221 TMEM246 84302 "transmembrane protein 246, transcript variant 2"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136550_PI430048170 0.665246752959107 1.03202317003438 9.83994300614014
9.75356773998319 9.81110622716808 P P P 9.62028630649178 9.67349727034926
9.95313729098035 P P P LNCV6_136550_PI430048170 mRNA
TCTTTGGTATGTATTGGCTAATAAAATCAGTTCTGTGGAACTGGGATTTTGAAGTCTCAA NM_032360 RefSeq chr1
- 180288216 180502887 ACBD6 84320 acyl-CoA binding domain containing 6
GO:0005737|GO:0000062|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128428_PI430048170 0.0422987314065604 0.304452149412728 1.5958975391783
1.94518554450819 3.09559995992938 A A P 3.73116368683822 4.19024202364199
4.25694144968319 P P P LNCV6_128428_PI430048170 mRNA
TAAAAACGTAATTTTACCAATCTTTCATAATGATTTGCTTTTTCTGGTTTTTGTATAGGA NM_001008393 RefSeq chr4
- 158666674 158672050 C4orf46 201725 "chromosome 4 open reading frame 46, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138031_PI430048170 0.207898785280875 1.19885511856733 5.07084110122048
4.93254776886041 5.10297230460007 P P P 4.45727744459652 4.9581204511439

4.86412232617459 P P P LNCV6_138031_PI430048170 mRNA
CCCATCTGCAGAATTGACTTCTCAAATAAAGATGCTAAAAATCTCCTTGTCTGGAAAAAA NM_002482 RefSeq chr1
+ 45583987 45618906 NASP 4678 "nuclear autoantigenic sperm protein (histone-binding), transcript variant 2"
GO:0000790|GO:0043486|GO:0008283|GO:0001824|GO:0051879|GO:0006335|GO:0005634|GO:0006336|GO:0015031|GO:0006260|GO:0042393|GO:0043234|GO:0005737|GO:0007049|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100836_PI430048170 0.1162573164298491.68053059867986 3.49121152079268 3.7981851669351
3.21675046188037 P P P 3.34781834997919 2.40487274786446 2.32895615738981 P A A
LNCV6_100836_PI430048170 mRNA
TGTCACTCGGCCAGAGCACTTCGACTTTGTAAAGCCTGAGGACCTGGACGGCATTGGCAT NM_001251902 RefSeq
chr17 + 7380973 7389773 TNK1 8711 "tyrosine kinase, non-receptor, 1, transcript variant 1"
GO:0005515|GO:0030308|GO:0051427|GO:0005524|GO:0030154|GO:0031234|GO:0005829|GO:0046580|GO:0005737|GO:0046777|GO:0016020|GO:0016477|GO:0045087|GO:0042127|GO:0006468|GO:0004713|GO:0004871|GO:0038083|GO:0004715|GO:0007169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127045_PI430048170 0.0803750508179733 0.8389494548799535.37204084202968
5.46066825412726 5.59527563548056 P P P 5.89436010988806 5.65019878959986
5.63746201056216 P P P LNCV6_127045_PI430048170 mRNA
ATCTCAAAAAATTGTACCATTCCTCAAAGGGACTTGGATAACATGGCCTTCCCCCAAGCA NM_020212 RefSeq chr15
+ 89690796 89743638 WDR93 56964 "WD repeat domain 93, transcript variant 1"
GO:0016651|GO:0022900 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83258_PI430048170 0.70029326944026 1.01136688281017 15.9508637156938 16.0013439021294
16.0093614106096 P P P 15.9002497547656 15.9945805344257 16.0159070108514 P P P
LNCV6_83258_PI430048170 mRNA
TTCTGCTGAAGAACTGAAACTGGCCACCCAGCTGACCGGACCGGTCATGCCCGTCCGGAA NM_033251 RefSeq chr16
+ 89560710 89566829 RPL13 6137 "ribosomal protein L13, transcript variant 2"
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0005730|GO:0005634|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0022626|GO:0016020|GO:0000184|GO:0016032|GO:0022625|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141193_PI430048170 0.000629129614514971 0.60666520669878212.4414593150157
12.4023727559852 12.2686680673521 P P P 12.9899079206258 13.1657830538451
13.1198116544137 P P P LNCV6_141193_PI430048170 mRNA
CTCCTCTAACCTGTGCCACAGGTGACCACCAATAAAATCCTCTGCTGAGAAGTGAAAAAA NM_003365 RefSeq chr3
- 48598998 48609665 UQCRC1 7384 ubiquinol-cytochrome c reductase core protein I
GO:0014823|GO:0005743|GO:0005750|GO:0044281|GO:0043279|GO:0032403|GO:0046872|GO:0006119|GO:0005739|GO:0009060|GO:0022904|GO:0005746|GO:0008121|GO:0006122|GO:0044237|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140516_PI430048170 0.0645211290557777 1.62855915702026 5.7082396666016
5.8730238138179 6.03650175858358 P P P 4.70463601363088 5.42255685295706
5.30125534464534 P P P LNCV6_140516_PI430048170 mRNA
GCAGTGTTGTGCTTGTTGTCAATGACAAAAATAAAACCATTTTGGTGGTATTGGCCTGTA NM_001071775 RefSeq
chr13 - 72708356 72727800 MZT1 440145 mitotic spindle organizing protein 1
GO:0005515|GO:0005813|GO:0005819|GO:0033566|GO:0008274 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142894_PI430048170 0.1436859073115121.09537390583932 0.511381505340153
0.6638183801615970.609590766696245 A A A 0.35754840139475 0.479679134432317
0.550826804648997 A A A LNCV6_142894_PI430048170 mRNA
CTCCTTGCTAATTTTATCTGTCTAATTAAAAAGAGCAGAAGCATGTCTGGGTTTACGTAA NM_004441 RefSeq chr3
+ 134795256 135260465 EPHB1 2047 EPH receptor B1

GO:0005515|GO:0031290|GO:0030424|GO:0005886|GO:0030010|GO:0048593|GO:0030425|GO:0005829|GO:0061
351|GO:0046328|GO:0005005|GO:0046777|GO:0007411|GO:0060996|GO:0060997|GO:0070372|GO:0050965|GO:0
070062|GO:0022008|GO:0051965|GO:0048013|GO:0031589|GO:0021952|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_98605_PI430048170 0.1001536256952820.4023489227075582.77724859849237 1.87816639730079
0.917476566399828 A A A 3.08427305483436 3.38010288881322 3.5821733008824 P P P
LNCV6_98605_PI430048170 mRNA
ATGACCATGCTGACTGTCATAGAGCAGCCAGTACCTCCAACACCAGCTACCCCTGAGGAC NM_133455 RefSeq chr22
+ 29205911 29259597 EMID1 129080 "EMI domain containing 1, transcript variant 1"
GO:0005581|GO:0005794|GO:0005783|GO:0005578 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140445_PI430048170 0.1209942900086661.81071024249492 3.33426203276349
3.41075043432568 3.79861583120223 P P P 3.32744473918112 2.29567082017002
2.06365911076872 P A A LNCV6_140445_PI430048170 mRNA
ATGTCTCCTCATTCCTACACCTATTTTCTGCTGCAGGATGAGGCTAGGGTTAGCATTCTA NM_003854 RefSeq chr2
+ 102186972 102239351 IL1RL2 8808 interleukin 1 receptor-like 2
GO:0032755|GO:0004909|GO:0007165|GO:0006968|GO:0006954|GO:0005887|GO:0045087|GO:0019221|GO:0004
908|GO:0050727|GO:0070498|GO:0045582 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127538_PI430048170 0.2272477240919531.28182748369931 6.10370317483512
6.69521810500023 6.45551411461576 P P P 6.41628216019878 5.78600038659135
5.96283771812371 P P P LNCV6_127538_PI430048170 mRNA
TTCTGGGGCTTAGTCGAATCAGCTTTGTAATGTTATGGGACAAAAATCAATTATCTCATT NM_144676 RefSeq chr16
- 69343245 69351809 TMED6 146456 transmembrane emp24 protein transport domain containing 6
GO:0006810|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131806_PI430048170 0.1629114328876951.37899757335449 2.28383709418964
3.02023433253837 2.66062013342172 A P A 2.32714107711086 1.98648466100122
2.32741297695612 A A P LNCV6_131806_PI430048170 mRNA
TTTGTGTGTGCCATGGCCACATCTCCTGGGTACAGTTCAAGGAGACATCTTTTCTAAAAG NM_001063 RefSeq chr3
+ 133746132 133779006 TF 7018 transferrin
GO:0005515|GO:0048471|GO:0072562|GO:0030139|GO:0005615|GO:0006879|GO:0033572|GO:0016324|GO:0009
925|GO:0001895|GO:0031625|GO:0070062|GO:0009986|GO:0005770|GO:0045178|GO:0030168|GO:0005576|GO:0
055085|GO:0031982|GO:0008199|GO:0005905|GO:0007596|GO:0002576|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145060_PI430048170 0.0282054895070543 1.60255167974603 4.10547764310529
4.22845470071372 4.38147419622338 P P P 3.6764804939943 3.23982546041684
3.72375604027472 P P P LNCV6_145060_PI430048170 mRNA
CTTATGCTACTTATCTCAGAAACAGGTTTTAAAATGAAGTGCTTTCCAGAGAACCATCAT NM_007341 RefSeq chr21
+ 39451853 39515506 SH3BGR6450 "SH3 domain binding glutamate-rich protein, transcript variant 1"
GO:0017124|GO:0006461|GO:0005070|GO:0009967|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144336_PI430048170 0.5626091936019931.07856793388965 8.21041451715152 8.1703035757265
8.31019460455956 P P P 7.96076411874016 7.84524278527976 8.47940041209749 P P P
LNCV6_144336_PI430048170 mRNA
TTTCCATCAAATGACCAACAGCTTCTCAATAAAACCAGACCATTTCTCACCTGCAAAAAA NM_015254 RefSeq chr8
- 29067277 29263093 KIF13B 23303 kinesin family member 13B
GO:0005515|GO:0008017|GO:0030424|GO:0005871|GO:0019901|GO:0005874|GO:0006605|GO:0003777|GO:0005
524|GO:0071889|GO:0007165|GO:0042110|GO:0005737|GO:0008152|GO:0050770|GO:0007018 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_72403_PI430048170 0.2879373673867581.1179940974786 10.7908646030465 11.153536304262
10.9661080131505 P P P 10.9420422044327 10.7848657346204 10.7141519112012 P P P

LNCV6_72403_PI430048170 mRNA
ACTAGTATGGAGAGCCTGGCCCCCTCCACTGACTCTCTGCATGGCTCCCCAGTGCTGATC NM_001039141 RefSeq
chr22 + 37696987 37776556 TRIOBP 11078 "TRIO and F-actin binding protein, transcript variant 6"
GO:0030047|GO:0005815|GO:0030496|GO:0005634|GO:0015629|GO:0045159|GO:0005737|GO:0007067|GO:0051
016|GO:0051015|GO:1900026|GO:0017049|GO:0005925|GO:0031625|GO:0051301 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_91594_PI430048170 0.6415308477453080.9414904371995755.09550406485931 5.12909586664994
5.46233954187009 P P P 5.46450735963664 5.06663372300224 5.41434049796094 P P P
LNCV6_91594_PI430048170 mRNA
TACAAGGACCTGTGGAATATGAGTGATGACAAACCCTTTCTATGTACTGCGCCTGGATGT NM_001256090 RefSeq
chr2 - 175072249 175168206 ATF2 1386 "activating transcription factor 2, transcript variant 2"
GO:0005515|GO:0003700|GO:0006366|GO:0003705|GO:0006325|GO:0032915|GO:0051403|GO:0002756|GO:0002
755|GO:0045444|GO:0001102|GO:0000977|GO:0038124|GO:0019901|GO:0038123|GO:0046982|GO:0034134|GO:0
003713|GO:0035861|GO:0002224|GO:0045087|GO:0005654|GO:0000980|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_94460_PI430048170 0.00847685418566462 0.3517107297886642.99679462058611
3.48865966967254 3.79068655773333 A P P 4.7107156225425 4.96074159197961
5.19505809839778 P P P LNCV6_94460_PI430048170 mRNA
GCTTTGTCTAGAGGATATGTGAAGGAGATTAACATGACAACAGTAACTTGTTTATTAGAC NM_001080449 RefSeq
chr10 - 68414063 68471973 DNA2 1763 "DNA replication helicase/nuclease 2, transcript variant 1"
GO:0042645|GO:0005515|GO:0016890|GO:0005760|GO:0005634|GO:0033567|GO:0046872|GO:0006271|GO:0000
723|GO:0000722|GO:0043504|GO:0032508|GO:0016887|GO:0000729|GO:0043142|GO:0051539|GO:0045740|GO:0
004386|GO:0005524|GO:0003677|GO:0003678|GO:0006260|GO:0004518|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132353_PI430048170 0.6649248324708061.01420940861158 0.404220113898584
0.3979363662035850.28763565537179 A A A 0.3205300617844860.352976306220906
0.357888134515149A A A LNCV6_132353_PI430048170 mRNA
GCAGGTGAAAGAAGTCTTCTGGGATGTATTACAAAAGAATTTGTGTTTTTCTAAAAGACC NM_001005493 RefSeq
chr12 - 55294287 55295232 OR6C6 NA "olfactory receptor, family 6, subfamily C, member 6" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58062_PI430048170 0.2912110925098610.6065623043786222.82906716081815 2.64560075707509
2.82858873073441 A A P 3.00402634826416 2.88384951810285 4.19691452294923 P P P
LNCV6_58062_PI430048170 mRNA
GGCTTCTTTCTTACTGCAGCATGATGCAGATATCAATGCCCAAACAAAAGGCCTCTTGAC NM_017704RefSeq chr11
+ 94493986 94499578 ANKRD49 54851 ankyrin repeat domain 49
GO:0005515|GO:0005634|GO:0045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141081_PI430048170 0.5544443753952970.9679109240906426.87428044861202
6.99088531371215 7.06717582672017 P P P 7.06605473762751 6.92951798161022
7.07971108163979 P P P LNCV6_141081_PI430048170 mRNA
GGTGAAGTTTGTATGTTTACCTAATATTACCTGTTTTGTATACCTGAGAGCCTGCTATGT NM_002607RefSeq chr7
- 497259 519844 PDGFA 5154 "platelet-derived growth factor alpha polypeptide, transcript variant 1"
GO:0005515|GO:0050730|GO:0005518|GO:0005615|GO:0042803|GO:0010035|GO:0007173|GO:0030198|GO:0032
956|GO:0009887|GO:0051781|GO:0007179|GO:0070374|GO:0001942|GO:0032355|GO:0035793|GO:0048839|GO:0
060683|GO:0030335|GO:0048286|GO:0046982|GO:0009986|GO:0048407|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_90672_PI430048170 0.1945187568976961.12839473822773 0.8716282793224820.558533287562134
0.725345478847079A A A 0.4478169373335220.5946603301998250.601987561343604A A A
LNCV6_90672_PI430048170 mRNA
TTGGTGGGTTCTAAGGTTAGAAGCTCATCCAGGATATTTTCAATATTAAGTCAGTGCATA NM_007257RefSeq chr8

- 26504679 26513967 PNMA2 10687 paraneoplastic Ma antigen 2GO:0005515|GO:0043065|GO:0005730
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115488_PI430048170 0.22373474163592 0.7642189735403010.379031732028535
0.3567457843774070.25629555243276 A A A 1.05433785894027 0.334141353250542
0.68062096785867 A A A LNCV6_115488_PI430048170 mRNA
GAAACTTGCAAGTAGCATTACCTTTACATATACTGCTAAGGCCACTGATGCTCAACTCTG NM_013310RefSeq
chr2_KI270768v1_alt + 25454 71290 C2orf27A 29798 chromosome 2 open reading frame 27A NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65769_PI430048170 0.00276309865933972 0.4087608335252484.3895209237861
4.43628301403342 4.64865823049965 P P P 5.76862174359688 5.77161042632074
5.81910803424353 P P P LNCV6_65769_PI430048170 mRNA
CATCCAGGTCTAGCGTGTCTTCCCTGTCTTCTGTGGATGAGGTATATGAATTTATCCCAA NM_002158RefSeq chr2
+ 48314655 48379295 FOXN2 3344 forkhead box N2
GO:0043565|GO:0006355|GO:0003700|GO:0005654|GO:0005634|GO:0035914|GO:0006351|GO:0043231 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142895_PI430048170 0.1560983728913120.7709876663035757.33927414578455
7.29874276964292 7.16978690353685 P P P 7.3197901205982 7.89284776655631
7.66938848085719 P P P LNCV6_142895_PI430048170 mRNA
GACACCCAAGCAGAGCAATCAGTTAGTGAATTGAATGGAAATAAACGCTTTAGTTATAAT NM_004442RefSeq chr1
+ 22710837 22921500 EPHB2 2048 "EPH receptor B2, transcript variant 2"
GO:0005515|GO:0031290|GO:0030424|GO:0005886|GO:0071679|GO:0001655|GO:0048593|GO:0030425|GO:0005
829|GO:0005005|GO:0007413|GO:0007411|GO:0043025|GO:0060021|GO:0060996|GO:0060997|GO:0007612|GO:0
051965|GO:0042472|GO:0048013|GO:0005102|GO:0005576|GO:0018108|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135525_PI430048170 0.0490232380030609 0.5501739518300655.90894577300205
5.99962034091628 6.15318878317753 P P P 6.51174163917689 6.79896945180015
7.25045223400515 P P P LNCV6_135525_PI430048170 mRNA
CACTGTAGAGTCACTTTTACCTTTTGCTATGGTGGAATGGGATCTGTAGGGTCAGGAACA NM_018196RefSeq chrX
- 155489010 155612961 TMLHE 55217 "trimethyllysine hydroxylase, epsilon, transcript variant 1"
GO:0050353|GO:0005739|GO:0034641|GO:0031418|GO:0051354|GO:0005506|GO:0005759|GO:0045329|GO:0044
281|GO:0016702|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136499_PI430048170 0.12274980598335 0.7032277367327245.04061755323514 5.3170069740125
5.77751685634171 P P P 5.82278163543534 5.98439232959609 5.94439121176185 P P P
LNCV6_136499_PI430048170 mRNA
GCACTACTAACATTTCAATATATTTTCTCCCAGATTTTCAGTAAAGACTTTCAGGCAGTG NM_033017RefSeq chr7
- 99890406 99919600 TRIM4 89122 "tripartite motif containing 4, transcript variant alpha"
GO:0070206|GO:0005737|GO:0005886|GO:0045087|GO:0016874|GO:0008152|GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144444_PI430048170 0.0543009962920379 2.37844195168849 3.82424019386566
3.06128375427438 3.37265313012634 P P P 1.38908326270326 2.68930862935599
2.24814992443956 A P A LNCV6_144444_PI430048170 mRNA
CTTGCCCTTTCTTACCTAGAACACCTGCTATAGTAAAGCAGACAGGAAACTGTTAAAAAA NM_213602RefSeq chr18
+ 45825579 45842556 SIGLEC15 284266 sialic acid binding Ig-like lectin 15
GO:0043234|GO:0005886|GO:0045087|GO:0032956|GO:2001204|GO:0071402|GO:0045124|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111197_PI430048170 0.7536664327178940.9485153128410644.21326613595676
3.97285820218496 3.97040136112016 P P P 3.78749637159406 4.28863134900115
4.26929302765139 P P P LNCV6_111197_PI430048170 mRNA
GGGCCTGATGCTCACCTGCATGTACACAGGAAAGGAGAAAGTCAGTCCGGGTAGAACTTC NM_002111RefSeq

chr4 + 3074509 3243960 HTT3064 huntingtin
GO:0005515|GO:0034452|GO:0000132|GO:0007283|GO:0051402|GO:0006606|GO:0042802|GO:0043524|GO:0048167|GO:0047496|GO:0007030|GO:0005794|GO:0031587|GO:0051938|GO:0007569|GO:0006890|GO:0048487|GO:0007212|GO:0044325|GO:0045505|GO:0006888|GO:0051592|GO:0043234|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135201_PI430048170 0.4110369570963311.15718623294002 3.08170556717923 2.66062013342172 3.11836374081736 P A P 3.09113875218746 2.65869595647569 2.44584118580392 P P P LNCV6_135201_PI430048170 mRNA
AAGCAAAGAATGAAAGCTGGATTAAATCCCACTTTAGCCGCCTTTCCGAAGAGAAGCTGG NM_001009997 RefSeq
chr10 + 97589692 97590934 C10orf62 414157 chromosome 10 open reading frame 62 GO:0005515
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73320_PI430048170 0.5396857902639190.8889005356943910.3892103155869690.387752942171282 0.426727595436151 A A A 0.3183369352733450.93143168226387 0.38224614012097 A A A LNCV6_73320_PI430048170 mRNA
CCTGAGATTTCTATGGTTTGACTCCAGGATCAAAACACAAGGGACTTTGTATTATTTCAC NM_018189RefSeq chr3 - 109326140 109337572 DPPA4 55211 developmental pluripotency associated 4
GO:0005515|GO:0006355|GO:0005634|GO:0060484|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136988_PI430048170 0.2691228984076194.05238558777469 0.388196702385867 3.68379805687752 3.42300801676124 A P P 1.70204960708666 0.740790154247674 0.282394590956903 A A A LNCV6_136988_PI430048170 mRNA
AATAAAAATGCACGTAGCTATGGAGTGGGGTTTAGCTGGAAAGGTGGCCTTCCAACTTCA NM_001286233 RefSeq
chr12 - 7812511 7873039 SLC2A14 144195 "solute carrier family 2 (facilitated glucose transporter), member 14, transcript variant 1"
GO:0015758|GO:0007275|GO:0005634|GO:0016021|GO:0007283|GO:0055085|GO:0030154|GO:0005355 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144162_PI430048170 0.00131950211226172 0.4747881146581389.28772065097731 9.12214124655767 9.38172192511223 P P P 10.1718467507709 10.3225850477949 10.512667717277 P P P LNCV6_144162_PI430048170 mRNA
GACCGGAGTCTGCTGAGTTTATAAGGTTCCAAAAATATGGTAAAATCTTGGTTTTTGTTA NM_004397RefSeq chr11 - 118747763 118791263 DDX6 1656 "DEAD (Asp-Glu-Ala-Asp) box helicase 6, transcript variant 1"
GO:0005515|GO:0003724|GO:0010467|GO:0033962|GO:0010494|GO:0019904|GO:0004386|GO:0043928|GO:0005524|GO:0043231|GO:0005829|GO:0016442|GO:0005737|GO:0016020|GO:0000932|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139914_PI430048170 0.0244590404346212 0.7041493539716776.60147910057379 6.8690870811894 6.60721960423629 P P P 7.18307208704096 7.24095967650484 7.18768627121346 P P P LNCV6_139914_PI430048170 mRNA
TAAAGTGCTAAGCTGTTGTCTGCACTCTTTCATCATAAAGTCACTTTTTTCCACTGCCTGNM_003549RefSeq chr3 - 50292827 50299468 HYAL3 8372 "hyaluronoglucosaminidase 3, transcript variant 1"
GO:0033906|GO:0005975|GO:0051216|GO:0005576|GO:0071493|GO:0031410|GO:0009615|GO:0005764|GO:0006954|GO:0001618|GO:0071356|GO:0071347|GO:0004415|GO:0030214|GO:0046677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143159_PI430048170 0.1306394286612750.6461408293354757.0175984898741 6.73906544075378 7.23542822229354 P P P 7.12178577265871 7.66423416832043 8.0053314895431 P P P LNCV6_143159_PI430048170 mRNA
TTCGGAAAATGCTCCTTGTCACATTAGTGTGCATCCTACAAAAAGTGATCTCTTAATGTA NM_021127RefSeq chr18 + 59899959 59904306 PMAIP1 5366 phorbol-12-myristate-13-acetate-induced protein 1
GO:0005515|GO:0043331|GO:0010165|GO:0048147|GO:0005741|GO:0005634|GO:0001836|GO:0010907|GO:0005829|GO:0005739|GO:0051607|GO:1900740|GO:0043525|GO:0090200|GO:0042149|GO:0032461|GO:0043029|GO:0

009411|GO:0046902|GO:0043065|GO:0006919|GO:0072593|GO:0071456|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140967_PI430048170 0.5261764221163761.31522386653231 0.377222424799686
1.48148253933386 0.277977965129817A A A 0.2596918196731610.71433887304468
0.256506572843099A A A LNCV6_140967_PI430048170 mRNA
CCTTCCTGTATTGCTGGGTTGGGATTGTTTTATTCTGCTTCAATAAAATAATCTTTACTG NM_001024822 RefSeq chr14
- 20590080 20590823 RNASE12 NA "ribonuclease, RNase A family, 12 (non-active)" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143247_PI430048170 0.0640064655553474 1.01337674151299 0.32073699520489
0.3048327210979440.312878870969594A A A 0.3022414421540290.296108534012709
0.282560335931099A A A LNCV6_143247_PI430048170 mRNA
CCGTGCATCTGTATTCACCCTGTATGACAAACACATTACATTATTAAATGTTTCTCAAAG NM_002124RefSeq
chr6_GL000255v2_alt - 3715352 3792416 HLA-DRB1 3123 "major histocompatibility complex,
class II, DR beta 1, transcript variant 1"
GO:0002437|GO:0050852|GO:0005886|GO:0019221|GO:0031295|GO:0042088|GO:0005765|GO:0042130|GO:0019
886|GO:0006955|GO:0002381|GO:0042605|GO:2001179|GO:0071556|GO:0032689|GO:0070062|GO:0060333|GO:0
030658|GO:0012507|GO:0051262|GO:0009986|GO:0002506|GO:0035774|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128577_PI430048170 0.5950455214250811.05050372315108 11.5741444087524
11.4893517605852 11.2529898052765 P P P 11.3670289070561 11.4861213729025
11.2600971277392 P P P LNCV6_128577_PI430048170 mRNA
ATTGCAGAGGGTCCTCCAGGGTCCTGAAGAGCACTGGACTAAGAGTCTAGTGGTTCCAGG NM_006455RefSeq chr17
- 41801952 41812199 P3H4 10609 prolyl 3-hydroxylase family member 4 (non-enzymatic)
GO:0000794|GO:0000795|GO:0005730|GO:0007130 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142809_PI430048170 0.106072137950686 1.1213493235931 10.7334967048105
10.8737351599536 10.9366131578035 P P P 10.6101940553359 10.6596197143065
10.7803996467376 P P P LNCV6_142809_PI430048170 mRNA
ATTACATATGAAAAACCCTCTAAACCATGGCACTTGATGTGATGTGGCAGGAGGGCAGTG NM_003379RefSeq chr6
- 158765740 158818308 EZR 7430 "ezrin, transcript variant 1"
GO:0005515|GO:0005886|GO:0005884|GO:0008360|GO:0030033|GO:0031528|GO:0030175|GO:0015629|GO:0005
615|GO:0036064|GO:0071944|GO:0005829|GO:0031623|GO:0016323|GO:0051286|GO:0016324|GO:0051015|GO:0
061028|GO:0007411|GO:0007159|GO:0022614|GO:0046847|GO:0051017|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142923_PI430048170 0.0972071828698967 0.6428207459354591.03994212437462
0.4397321666107740.245497782340813A A A 1.18301713213992 1.37715050145551
1.19206104395386 A A A LNCV6_142923_PI430048170 mRNA
ATTTAAGTCAACTAAGGGGATTTAACAGTGGACTAGAGGTAATAAGCCACCTCAGTCAGG NM_032539RefSeq chrX
+ 145817828 145825842 SLITRK2 84631 "SLIT and NTRK-like family, member 2, transcript variant 1"
GO:0016021|GO:0007409 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142983_PI430048170 0.4399371306250480.2307059382028350.404754922293678
0.4311661453907980.454934775802841A A A 3.89947809414668 0.353569911645668
0.404060395912945P A A LNCV6_142983_PI430048170 mRNA
CTTGTATCGACTACATATGTATTTGACCCTGTGGGAGGATGGTACTTTTCTTTTTAACTT NM_004650RefSeq chrX -
7898762 7927434 PNPLA4 8228 "patatin-like phospholipase domain containing 4, transcript variant 1"
GO:0016042|GO:0008150|GO:0003674|GO:0004806|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137606_PI430048170 0.8489063053007491.10802389191701 1.72379189297361
0.6518747925825410.413385028117044A A A 0.3147159354529681.44175400380312
0.71433887304468 A A A LNCV6_137606_PI430048170 mRNA

ATTTAATGGAAGGTTCCACAAGTCACCCTGTGATCAACAGTACCCGTATGGGACAAAGCT NM_000641 RefSeq chr19 - 55364381 55370463 IL11 3589 "interleukin 11, transcript variant 1" GO:0008284|GO:0005142|GO:0007267|GO:0050731|GO:0005576|GO:0005125|GO:0005615|GO:0046888|GO:0005737|GO:0033138|GO:0045944|GO:0030219|GO:0030183|GO:0045444|GO:2000352|GO:0043410|GO:0008083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143667_PI430048170 0.12898697542919 0.62133810100034 8.33075198925897 7.53816487076434 7.30394966144191 P P P 8.51944656725196 8.58772826949713 8.3217294852279 P P P LNCV6_143667_PI430048170 mRNA
TCCCCTTTCCTCCCCAACTACTATTTAAAAATGATGAGACGAATTAGTCAATGAAGAGAT NM_004248 RefSeq chr10 - 118593403 118595648 PRLHR 2834 prolactin releasing hormone receptor GO:0005515|GO:0007631|GO:0007565|GO:0004983|GO:0007186|GO:0005886|GO:0007218|GO:0005887|GO:0004930|GO:0042445|GO:0008188 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129809_PI430048170 0.0350772200942608 1.16370563105753 11.5513334422212 11.5390199967418 11.693172713126 P P P 11.3199876054357 11.3333937294473 11.4740086465785 P P P LNCV6_129809_PI430048170 mRNA
GCAGTGTTCTGAGGACTCTTCTATCCTAGGACTATGACAGTGTGTATTAATAAAATATTT NM_001282190 RefSeq chr7 - 130018285 130051451 ZC3HC151530 "zinc finger, C3HC-type containing 1, transcript variant 2" GO:0005515|GO:0031965|GO:0007067|GO:0016567|GO:0019901|GO:2001240|GO:0008270|GO:0005634|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130074_PI430048170 0.3830489117824630.8264313274475920.465753713098723 0.4518180921851240.250944156017362 A A A 0.39118792302706 1.06964683591169 0.438959566868461 A A A LNCV6_130074_PI430048170 mRNA
GCAAGTAAAACAAGCCTTCAAAAATGTGGTCCACAAAGTTGTGTTTTATGCAAATCAATG NM_054104 RefSeq chr12 + 55331700 55332636 OR6C3 NA "olfactory receptor, family 6, subfamily C, member 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75093_PI430048170 0.00398232892983539 3.25640471436782 7.17254101952623 7.79351856030971 7.62500034847144 P P P 6.0058274104124 5.8508139219978 5.67468883235997 P P P LNCV6_75093_PI430048170 mRNA
AGCAAAAGTTGGAAGCCTGGAGTGCCTAAGCCTGCTTGTAGCCAGTGATGCCCAAATTGA NM_181726 RefSeq chr4 + 185396685 185400236 ANKRD37 353322 ankyrin repeat domain 37 GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127342_PI430048170 0.3824060626238211.15999237360314 5.55793355881493 5.67605708925033 5.81150678063173 P P P 5.01896132772141 5.5742870316685 5.72884584166459 P P P LNCV6_127342_PI430048170 mRNA
TTAAAGGGTGGTATACTCTGAAACACAGCCCAACCAAACCATTGTTTGGCCGCTTTCTCT NM_015042 RefSeq chr15 + 64499419 64686067 ZNF609 23060 zinc finger protein 609 GO:0005634|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2879_PI430048170 0.0228276362767764 0.4818844946195822.45618259855221 1.73017698754779 1.85738123998961 A A A 2.70772727376611 3.27515610338324 3.2597498409217 P P P LNCV6_2879_PI430048170 mRNA
TGCTGTTCCTGCTTTATTGTTTGCTTTCTGTGTGCTGTCATATTTTGGTATCAGAGTTAC NM_001039705 RefSeq chrX + 54920562 54931431 TRO 7216 "trophinin, transcript variant 6" GO:0005515|GO:0030308|GO:0005737|GO:0005886|GO:0007566|GO:0005887|GO:0005634|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142460_PI430048170 0.0625830554693511.09628541040564 5.49424369072984 5.50826151165857 5.59904552677236 P P P 5.37178227718907 5.47890818703283 5.35199126559494 P P P LNCV6_142460_PI430048170 mRNA
TTCAGTATCTAATGCCCAGGTCAAAGCAGATGGACACAAAGTCTATGGAGCCATTCTGGT NM_006473 RefSeq chr11 + 62771302 62787341 TAF6L 10629 "TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-

associated factor, 65kDa"
GO:0005515|GO:0006352|GO:0006357|GO:0046982|GO:0030914|GO:0003713|GO:0006325|GO:0003677|GO:0051090|GO:0000118|GO:0043966|GO:0006338|GO:0004402|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106316_PI430048170 0.0220521373371856 0.6215626295015644.80887470467998 4.78257071921029 4.67562052946849 P P P 5.24294205438102 5.39386542815623 5.66044687961638 P P P LNCV6_106316_PI430048170 mRNA
GGCCTTCAGAACTAGACTTGAGACTCACAGAAGAAGGTGAGCGAATGCTGAGTACTTTTA NM_015465RefSeq chr5 - 154887415 154938216 GEMIN525929 "gem (nuclear organelle) associated protein 5, transcript variant 1"
GO:0005515|GO:0010467|GO:0005634|GO:0034660|GO:0000387|GO:0005829|GO:0016604|GO:0005737|GO:0006461|GO:0016020|GO:0000398|GO:0032797|GO:0017069|GO:0005654|GO:0034719 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139890_PI430048170 0.6327268972136411.06189704476474 10.7280270648802 10.7377292877522 10.9472595964626 P P P 10.3450024704765 10.8090843944969 10.9439092425258 P P P LNCV6_139890_PI430048170 mRNA
GGACTCCCATCACCTTCTCTCAGAACAAAATCACTTCATTTTATTGTCTTAGTTTGTATA NM_001325RefSeq chrX + 100820358 100840934 CSTF2 1478 "cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa"
GO:0005515|GO:0006379|GO:0008380|GO:0006369|GO:0006378|GO:0010467|GO:0006366|GO:0003723|GO:0031124|GO:0005634|GO:0071920|GO:0000166|GO:0000398|GO:0005847|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135312_PI430048170 0.3996357618178030.9333003971952529.68061076442864 9.82178152753816 9.69992832621995 P P P 9.79652753805769 9.99418207128545 9.69859693804638 P P P LNCV6_135312_PI430048170 mRNA
AAGGCAGCTGGGCCGTTTCTGTCTGTGTCCCATCCTGCTGTCCTTCTGTCCTGGATGTTT NM_003021RefSeq chr19 - 2754713 2783356 SGTA 6449 "small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha" GO:0005515|GO:0008150|GO:0005737|GO:0016032 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128419_PI430048170 0.00811169713158612 0.5385359813099911 11.9605445908946 11.6623029829733 12.096739034517 P P P 12.5877359566132 12.7734519628415 13.0353272408692 P P P LNCV6_128419_PI430048170 mRNA
GTGAGTCATTATGTAGCTGTCGTACATTGAGCAAATAAACTTACAGATCTGACGCCAGTG NM_012479RefSeq chr7 - 76326790 76359025 YWHAG 7532 "tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma"
GO:0005515|GO:0005159|GO:0071901|GO:0006605|GO:0005829|GO:1900740|GO:0048167|GO:0000086|GO:0005080|GO:0061024|GO:0030659|GO:0070062|GO:0030971|GO:0032869|GO:0006996|GO:0019904|GO:0006915|GO:0009966|GO:0097193|GO:0016020|GO:0045664|GO:0008426|GO:0006469|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80118_PI430048170 0.00405954050913725 0.52593309994947 12.5510404641556 12.3571923398271 12.5176011143707 P P P 13.2135551686051 13.3951355408085 13.5821153171205 P P P LNCV6_80118_PI430048170 mRNA
TTCACAGGTTCCACGAGTCATGTCAACACAGCGTGTTGCTAACACATCAACACAGACAAT NM_002568RefSeq chr8 - 100702915 100722087 PABPC1 26986 "poly(A) binding protein, cytoplasmic 1"
GO:0005515|GO:0010467|GO:0010494|GO:0005634|GO:0031047|GO:0071013|GO:0006412|GO:0006413|GO:0005829|GO:0008266|GO:0005737|GO:0000184|GO:0000166|GO:0008143|GO:0048255|GO:0000289|GO:0070062|GO:0000288|GO:0006378|GO:0060213|GO:0008494|GO:0045727|GO:0008022|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65560_PI430048170 0.0488534657405744 1.40946672025348 13.0436210195807 12.8641484772319 12.929662245069 P P P 12.7074060491068 12.3190317217629 12.2928851114504 P P P LNCV6_65560_PI430048170 mRNA

AGGACTCAGTATATGGTTCTTGGGTATGCCCTACCAGGTGGAATAAAGGACACAGATTTG NM_017727 RefSeq chr2 + 27032905 27041697 TMEM214 54867 "transmembrane protein 214, transcript variant 1" GO:0005881|GO:0005737|GO:0005794|GO:0005783|GO:0005789|GO:0006915|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144740_PI430048170 0.0177621565083667 1.22120629713844 7.45588610498791 7.51909301061936 7.35199883070708 P P P 7.05693850486176 7.15536875911172 7.24831755785891 P P P LNCV6_144740_PI430048170 mRNA
TTCCTCGGAATACTAAGTGAATGTCTAGCATCCATTCACATTCTGTGGGAACAGGGACTG NM_003321 RefSeq chr16 - 28842410 28846408 TUFM 7284 "Tu translation elongation factor, mitochondrial" GO:0042645|GO:0005739|GO:0070125|GO:0032543|GO:0006996|GO:0016020|GO:0003924|GO:0005525|GO:0003746|GO:0070062|GO:0006414 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135685_PI430048170 0.130764609790289 1.06718073533235 0.499914242108435 0.626584605980465 0.543094776597602 A A A 0.401958430372213 0.47677724027873 0.510211185087962 A A A LNCV6_135685_PI430048170 mRNA
TGAGTTTCTTTCCTTGCTGGGGGATATAACCATAGACCACCACAAGATAATGCATGGAGT NM_001045479 RefSeq chr1 - 153436994 153440027 S100A7L2 NA S100 calcium binding protein A7-like 2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58411_PI430048170 0.118546540731798 1.06657787578445 0.488158661437201 0.606300083686851 0.53365038902015 A A A 0.389771454368964 0.462406446925855 0.497352967998825 A A A LNCV6_58411_PI430048170 mRNA
TCTTCCTCTGAGGCGAGCTTCAGATCTGCTCAAGCTTCCTGCAGTGGGGCCAGGAGGCAG NM_001251964 RefSeq chr11 - 128935370 128943399 TP53AIP1 63970 "tumor protein p53 regulated apoptosis inducing protein 1, transcript variant 4" GO:0005739|GO:0003674|GO:0006915 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142248_PI430048170 0.0111956409287321 1.91609688106168 7.08054237245502 7.39172762926429 7.23695988787935 P P P 6.52051973453811 6.34922062218742 5.99262093666061 P P P LNCV6_142248_PI430048170 mRNA
AGATGAACAAAAATAAAAATACAAAAGGCCGGAGGAAAGTCCCAGGCATCCCCCAAAAAA NM_025129 RefSeq chr19 - 49806865 49813310 FUZ 80199 "fuzzy planar cell polarity protein, transcript variant 1" GO:0090301|GO:0001736|GO:0021513|GO:0010172|GO:0030336|GO:0008285|GO:0045724|GO:0001843|GO:0048704|GO:0015031|GO:0035058|GO:2000314|GO:0042384|GO:0005737|GO:0008589|GO:0005856|GO:0090090|GO:0001942|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135598_PI430048170 0.468518919498914 1.04584331980586 11.9498695606453 12.011083200071 11.8605813570693 P P P 11.9600946927354 11.9242582756108 11.7373718584916 P P P LNCV6_135598_PI430048170 mRNA
CTCCGGGTCACTGCTGTATATAACTCCCCTCCCCCAGAAAAATAAATGTCACTGCCAACG NM_006270 RefSeq chr19 - 49635294 49640143 RRAS 6237 related RAS viral (r-ras) oncogene homolog GO:0005515|GO:0030336|GO:0005886|GO:0002521|GO:0003924|GO:0007268|GO:0007265|GO:0005525|GO:0032403|GO:0051896|GO:0045766|GO:0006184|GO:0060325|GO:0007411|GO:0019003|GO:0070372|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140320_PI430048170 0.120574920727098 2.94854656782003 6.19882178736621 6.45890685218345 6.43603876602909 P P P 5.90429574044377 3.68910511059496 3.50104953304596 P P P LNCV6_140320_PI430048170 mRNA
GTTTCCTTATGACTCAGTAAGTTGGCAAGGTCCTGACTTTAGTCTTAATAAAACATTGAA NM_014398 RefSeq chr3 - 183122214 183162879 LAMP3 27074 lysosomal-associated membrane protein 3 GO:0097233|GO:0008283|GO:0016021|GO:0005765|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126952_PI430048170 0.828286778303668 1.02493812481237 7.04197156485593 7.13589428118043 7.39826399624632 P P P 6.80390335648667 7.23664297100437

7.39089506611842 P P P LNCV6_126952_PI430048170 mRNA
CAGAATGGTTGGAGAAATGCCTATGGTGAATTAAAGCTTCATATCTGCTTTCTGAAAAAA NM_001161779 RefSeq
chr8 + 93916946 93926068 PDP1 54704 "pyruvate dehyrogenase phosphatase catalytic subunit 1,
transcript variant 2"
GO:0010510|GO:0035970|GO:0004741|GO:0006090|GO:0005759|GO:0044281|GO:0004722|GO:0046872|GO:0044
237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142948_PI430048170 0.2724028900377180.5682825626494080.278732216703237
2.23622701558943 2.68583992978515 A A A 2.49238587605614 2.85815865125382
3.14902610660907 A P P LNCV6_142948_PI430048170 mRNA
GGGACAGGGCTGTTTTATACCAATAAACAGCAAAATATTGTCCTTACTCATTCAAGAATT NM_001143830 RefSeq
chr11 + 22666613 22813001 GAS2 2620 "growth arrest-specific 2, transcript variant 3"
GO:0016020|GO:0008360|GO:0005884|GO:0006915|GO:0007050|GO:0006921|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137268_PI430048170 0.00101480811985045 1.87079462227681 6.80930146128625
6.64799645256856 6.8991037115005 P P P 6.02970170640054 5.8320871968034
5.78278360640139 P P P LNCV6_137268_PI430048170 mRNA
ACACTTGGGATCCCAGGTCAGAAAGGGCCAGATGAGCAACTAGGAAAGACTTGGGGGCCA NM_001243646
RefSeq chr16 - 30350765 30354934 CD2BP210421 "CD2 (cytoplasmic tail) binding protein 2, transcript
variant 2"
GO:0000244|GO:0005515|GO:0008380|GO:0010467|GO:0005634|GO:0005737|GO:0016607|GO:0000398|GO:0010
923|GO:0043021|GO:0005654|GO:0005682|GO:0046540 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71718_PI430048170 0.172278436409897 1.11614304830706 14.1272252534719 14.1987427584315
14.3375280605846 P P P 13.9324096269221 14.0675993379999 14.1848686293204 P P P
LNCV6_71718_PI430048170 mRNA
TGACTGCTGACAAAGATGGTGTGGCCGATGTGTCTATTGAAGATTCTGTGATCTCACTCT NM_000454 RefSeq chr21
+ 31659621 31668930 SOD1 6647 "superoxide dismutase 1, soluble"
GO:0045859|GO:0005515|GO:0042542|GO:0030346|GO:0060047|GO:0008090|GO:0009408|GO:0007605|GO:0006
801|GO:0033081|GO:0006749|GO:0048538|GO:0001819|GO:0007283|GO:0019226|GO:0048678|GO:0005615|GO:0
042803|GO:0060087|GO:0042802|GO:0006879|GO:0005758|GO:0043524|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_92764_PI430048170 0.673054432418659 1.09423269669365 1.76429377793795 2.38689811241119
2.37752252953055 A A A 1.79883522698805 1.83341347406255 2.48289189877086 A A P
LNCV6_92764_PI430048170 mRNA
TTGGAGTCACTGCCAAAATGGGTTTGTATTTCAGATCTGGGCACGAAAGCTTCTCTCTGT NM_001284325 RefSeq
chr19 - 48795061 48811063 BCAT2 587 "branched chain amino-acid transaminase 2, mitochondrial,
transcript variant c"
GO:0052656|GO:0004084|GO:0052654|GO:0052655|GO:0009083|GO:0044281|GO:0010817|GO:0005739|GO:0034
641|GO:0009082|GO:0005759|GO:0006573|GO:0006551|GO:0006550 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_100756_PI430048170 0.00260669396317188 0.462030654848641 3.39221727794728
3.38538766365234 3.73081908169452 P P P 4.49807232828917 4.64495875680238
4.72575015287355 P P P LNCV6_100756_PI430048170 mRNA
TTTCTTCAAACAAAACAGGTTTCTCCAGCAGCCTTGGCATTTCACACGCTCCTGTTGACA NM_015348 RefSeq chr2
- 97756337 97995891 TMEM131 23505 transmembrane protein 131
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136177_PI430048170 0.0310845575859755 0.598144110292459 4.4676840131711
4.62281226836874 4.08755972487002 P P P 5.11618035987532 5.25363718198984 5.0777146324004
P P P LNCV6_136177_PI430048170 mRNA
CAAAATCCTGCCTAATGATGAGTGCAAAAAAGCCCACGTCCAGAAGGTGACAGACTTCAT NM_002257 RefSeq chr19

- 50819145 50823787 KLK1 3816 kallikrein 1 GO:0004252|GO:0006508|GO:0005634|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130957_PI430048170 0.93695589763313 0.9935599553477047.48343490386084
7.51355667284483 7.43459903986955 P P P 7.56983409429712 7.34627082581052
7.53468028802602 P P P LNCV6_130957_PI430048170 mRNA
GTTCCACCCTCTTCCTAAGTGTTGAAGCTAAATCCTTGTTGAATACTGTATTTTAAATCT NM_002766RefSeq chr17 -
76310786 76354149 PRPSAP1 5635 phosphoribosyl pyrophosphate synthetase-associated protein 1
GO:0033673|GO:0004857|GO:0006139|GO:0000287|GO:0004749|GO:0002189|GO:0019900|GO:0009165 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125003_PI430048170 0.0198411680557176 1.39831266260031 7.63928679878956
7.63590575218559 7.88041860688543 P P P 7.28908655555218 7.21403735486188
7.21398520593502 P P P LNCV6_125003_PI430048170 mRNA
CCATTTTTGGAAAGGATGGTGTATTAAACCAGCCAAACAGTGTCTTTGGACTTATATTTT NM_173517RefSeq chr7
+ 65873269 65959563 VKORC1L1 154807 "vitamin K epoxide reductase complex, subunit 1-like 1,
transcript variant 1"
GO:0017187|GO:0048038|GO:0005789|GO:0034599|GO:0016021|GO:0047057|GO:0042373|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135607_PI430048170 0.4278211308803020.7948080861900862.8462328016614
2.97893543145274 1.97199901348695 A A A 2.46407220454872 3.24368385511197
3.15595273135419 A P P LNCV6_135607_PI430048170 mRNA
GCAGAGAGATAATCACCGCACCGTTTCCAGATGTAATACTGCAAAGAAAACCGATGATGA NM_000150RefSeq chr19
- 5830625 5839731 FUT6 2528 "fucosyltransferase 6 (alpha (1,3) fucosyltransferase), transcript
variant 1"
GO:0017060|GO:0046920|GO:0042355|GO:0005794|GO:0032580|GO:0008417|GO:0006486|GO:0016021|GO:0036
065|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139994_PI430048170 0.0100273888583848 0.4454390274495117.50533706008826
7.28234821271058 7.37380826992273 P P P 8.22856555545971 8.75644101350321 8.6340897038161
P P P LNCV6_139994_PI430048170 mRNA
TAGCCACACCACAGGATTTCCTGAAAGTTTACAATGCAGTAGCATTTTGGGGTGTAGGGT NM_013246RefSeq chr11
- 67364167 67373735 CLCF1 23529 "cardiotrophin-like cytokine factor 1, transcript variant 1"
GO:0005515|GO:0008284|GO:0048295|GO:0046982|GO:0030890|GO:0042517|GO:0019221|GO:0097059|GO:0005
102|GO:0005576|GO:0005125|GO:0007259|GO:0097058|GO:0005127|GO:0043524|GO:0048711|GO:0002639|GO:0
030183|GO:0008083|GO:0007166|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142749_PI430048170 0.8120092219322240.9876361410470590.569856742238184
0.6149642071016870.518465981960271 A A A 0.5694394041821780.495005710277799
0.687724832294245 A A A LNCV6_142749_PI430048170 mRNA
GATGGGATTGGATTGACTTGCGGAAGGAAAGTAAAAATAAAGCCAAATAACTTCCCAAAA NM_001004440 RefSeq
chr1 + 112720566 112727234 FAM19A3 284467 "family with sequence similarity 19 (chemokine (C-C
motif)-like), member A3, transcript variant 2" GO:0005576 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131832_PI430048170 0.0224948233712972 2.07363423119878 5.09021194895311
4.92229253404677 5.07870083990273 P P P 4.32650511052515 3.82574747388269
3.71194838492019 P P P LNCV6_131832_PI430048170 mRNA
AGTTATCAGCCAGCAGAAACAGATCTTCAGGAATCACATGTCTGACTTCCGGATCCAGAA NM_194296RefSeq chr5
- 139396766 139404087 SPATA24 202051 spermatogenesis associated 24
GO:0006355|GO:0005737|GO:0005730|GO:0007275|GO:0005654|GO:0005634|GO:0007283|GO:0003677|GO:0042
803|GO:0030154|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131155_PI430048170 0.6157986162896131.10833788477296 12.4799774256138
11.9597160685866 11.9886439802355 P P P 12.5820578690508 11.729684607026

11.4953966186441 P P P LNCV6_131155_PI430048170 mRNA
CGCCAAAATGGCATAACTGAGATAAGGTGAATAAGTGACAAATAAAGCCAGTTTTTTACA NM_013336 RefSeq chr3
+ 128052368 128071683 SEC61A1 29927 Sec61 alpha 1 subunit (S. cerevisiae)
GO:0005515|GO:0005791|GO:0002474|GO:0006614|GO:0042590|GO:0030176|GO:0045047|GO:0016020|GO:0002
479|GO:0016049|GO:0043022|GO:0006620|GO:0034341|GO:0007029 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_137261_PI430048170 0.00208411087378035 0.7337786626601958.26868904984379
8.28962800647359 8.37829984192671 P P P 8.77671847248301 8.73257798261911
8.76904764293327 P P P LNCV6_137261_PI430048170 mRNA
GACAGTACTTTGAAACTCATGTTGAGATTTTACCCTCTCCTCCAACCATTTTGGGAAAAT NM_001290557 RefSeq
chr1 - 202940824 202958396 ADIPOR1 51094 "adiponectin receptor 1, transcript variant 3"
GO:0019395|GO:0030308|GO:0046982|GO:0005886|GO:0019901|GO:0033211|GO:0055100|GO:0042562|GO:0046
628|GO:0042802|GO:0046427|GO:0009755|GO:0016020|GO:0033210|GO:0004872|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137376_PI430048170 0.4000453648822881.05278419525826 0.407730168444576
0.6152379897294480.538787778766612A A A 0.5436417128094930.393875058651886
0.404295151624992A A A LNCV6_137376_PI430048170 mRNA
TTCATGATTTTGTCGTGAGAGATCCACTCAATAAAAACCAGGCAAATGTAGTGAATCTGG NM_001277945 RefSeq
chr19 - 52612364 52690581 ZNF83 55769 "zinc finger protein 83, transcript variant 10"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142681_PI430048170 0.651285167337305 1.01160728941681 0.405080905556742
0.30347960377112 0.340927705483442A A A 0.3379248215790080.31290109259932
0.350298330043488A A A LNCV6_142681_PI430048170 mRNA
GGCAACGAACGTGCTGGCATCAAAGAATATCAGTTTACATATATAACAAGTGTAATAAGA NM_001113226 RefSeq
chr1 + 107140006 107481853 NTNG1 22854 "netrin G1, transcript variant 1"
GO:0005515|GO:0007409|GO:0046658 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139773_PI430048170 0.427196439278845 1.04611992229804 0.315698601707837
0.3218852173535840.507288075478107A A A 0.3239721184724870.288763739673637
0.344767531430684A A A LNCV6_139773_PI430048170 mRNA
TCGTCAACGAATTCATCAACAGGCAGAAACGCAAGGAATTGTCCAATAGGCTGAACCTCA NM_021193 RefSeq chr2
+ 176099801 176100760 HOXD12 3238 homeobox D12
GO:0043565|GO:0007389|GO:0005667|GO:0006355|GO:0001501|GO:0005634|GO:0042733|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142530_PI430048170 0.0110265760698683 1.85463027346504 6.47717157258769
6.93170076368501 6.51684205828702 P P P 5.6029585205724 5.9062903496949
5.77237730655821 P P P LNCV6_142530_PI430048170 mRNA
TATTTTGTAACCCGTTACACTGTGTGTCCTTGTGTAAATAAACTTGTTTCTGGCAGTGCC NM_001015053 RefSeq
chr17 - 44076752 44123646 HDAC5 10014 "histone deacetylase 5, transcript variant 3"
GO:0005515|GO:0006342|GO:0044212|GO:0006325|GO:0010830|GO:0046970|GO:0005634|GO:0010832|GO:0042
220|GO:0046872|GO:0005829|GO:0007507|GO:0051091|GO:0005737|GO:0006954|GO:0007219|GO:0045944|GO:0
070491|GO:0030183|GO:0005080|GO:0090051|GO:0006338|GO:0004407|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140910_PI430048170 0.611046934433795 1.03000653097372 0.436495905915385
0.6297855759188690.568705691760435A A A 0.5555753586521980.552029759364617
0.400786372336592A A A LNCV6_140910_PI430048170 mRNA
GTGCTGATTAATTTCTGCAACAAAGCAGCATATTAAATGTACTACATCTAGTGTTGTAGC NM_144966 RefSeq chr9
- 14734665 14910995 FREM1 158326 "FRAS1 related extracellular matrix 1, transcript variant 1"
GO:0007154|GO:0007160|GO:0030246|GO:0016021|GO:0097094|GO:0046872|GO:0005604 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_142070_PI430048170 0.0741702230692392 1.24780331859781 6.08840293867741
6.07665596559061 5.77312034438922 P P P 5.75152285923823 5.72302801048177
5.51576400919366 P P P LNCV6_142070_PI430048170 mRNA
AGAGGAAGCTGATGTCATGGCTGGACAAAGTCACGGAGTAAAGCCAGCAAAGCCACCCTC NM_005446 RefSeq
chr22 + 21015174 21028013 P2RX6 9127 "purinergic receptor P2X, ligand gated ion channel, 6,
transcript variant 1"
GO:0035590|GO:0030054|GO:0004931|GO:0014069|GO:0055085|GO:0051291|GO:0005524|GO:0042802|GO:0005
639|GO:0007165|GO:0005737|GO:0006936|GO:0043197|GO:0005887|GO:0043025|GO:0006810|GO:0001614|GO:0
051260|GO:0006812|GO:0004888|GO:0015267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139079_PI430048170 0.0126129586958248 1.17799358999531 9.37764229802518
9.51349150225536 9.42281767331253 P P P 9.2395916478916 9.20584097196624
9.16180397609874 P P P LNCV6_139079_PI430048170 mRNA
AACCTTTAAAAACGGCTGTCAGGTTTGATCTCAGTGTAACAACATGGCCAGTGCCTGTTC NM_002904 RefSeq
chr6_GL000256v2_alt - 3253275 3260276 NELFE 7936 negative elongation factor complex member E
GO:0005515|GO:0010467|GO:0006368|GO:0006366|GO:0003723|GO:0032021|GO:0005634|GO:0050434|GO:0005
739|GO:0008150|GO:0000166|GO:0016032|GO:0005654|GO:0034244 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143062_PI430048170 0.956968452335727 0.98913286680413 12.0076818691739
12.1797583350167 12.3769753953257 P P P 11.9991853188895 12.1305252499726
12.4649595426425 P P P LNCV6_143062_PI430048170 mRNA
TATTAGCAAAACATCCTGTGTCTTTTGGAGTACGATGTGTAAGTGCCCATTGGGTGGCCT NM_002802 RefSeq
chr14 + 90256549 90272622 PSMC1 5700 "proteasome (prosome, macropain) 26S subunit, ATPase,
1"
GO:0005515|GO:0002474|GO:0010467|GO:0030054|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005
829|GO:0034641|GO:0005737|GO:0000082|GO:0016032|GO:0090090|GO:0016887|GO:0006977|GO:0000209|GO:0
043066|GO:0000502|GO:0005838|GO:0006521|GO:0051437|GO:0042590|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139410_PI430048170 0.266720474009606 1.04287041649793 0.566445322161713
0.466541160435599 0.578159084972029 A A A 0.455705181552735 0.53645315113081
0.437973400338024 A A A LNCV6_139410_PI430048170 mRNA
GTGTATAAGCTTTTAAGGTCTGACTGACAAATTCTGTATTAAGGTGTCATAGCTATGACA NM_005577 RefSeq
chr6 - 160531482 160666375 LPA 4018 "lipoprotein, Lp(a)"
GO:0005515|GO:0006629|GO:0004252|GO:0004866|GO:0008015|GO:0034358|GO:0005576|GO:0044281|GO:0006
898|GO:0010951|GO:0006869|GO:0042157|GO:0006508|GO:0034185|GO:0001968|GO:0008201 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131919_PI430048170 0.0724392445482665 0.418175730825634 0.416129386466273
1.71013203595641 1.27778206167687 A A A 2.21671254569933 1.89312102946932
3.07905050548607 A A P LNCV6_131919_PI430048170 mRNA
TATTTTGACTGGACCCCTGTAACTAGCACTGACATAACTGTGCAGGTCAGTGATTCCAGT NM_213601 RefSeq
chr14 - 77341770 77377053 TMED8 283578 transmembrane emp24 protein transport domain
containing 8 GO:0006810|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_51332_PI430048170 0.878045331507932 1.00647510706358 0.559295851155619
0.495550033163854 0.585520234981957 A A A 0.640022842923273 0.544608861535461
0.420946023742395 A A A LNCV6_51332_PI430048170 mRNA
TATAACAGCAACCAGCTGGAGAAAATGGCCTTTTTTCAGTGCAGGGAAGAGGTGGAGAAA NM_001012418 RefSeq
chr6 - 2663628 2750920 MYLK4 NA "myosin light chain kinase family, member 4" NA . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_136303_PI430048170 0.01814797559001 0.89911481121106 11.5790999100416
11.5487204603809 11.5390199967418 P P P 11.6541417701061 11.7426203161412
11.7290850853633 P P P LNCV6_136303_PI430048170 mRNA
TTCAAGCCAGAGACATTCAGAAAGTTTTTAGCTCTATATTTGCATGGTGCTGCGTGAGCG NM_016491 RefSeq
chr1 + 54200166 54218383 MRPL37 51253 mitochondrial ribosomal protein L37
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005761|GO:0005
743|GO:0006412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144012_PI430048170 0.0111626878446017 1.35719275982846 9.013111872393
9.01994755898163 8.95511287707751 P P P 8.52481338233067 8.46625942575029
8.66852485634611 P P P LNCV6_144012_PI430048170 mRNA
CTTGTAAAAGCCACATATCCACATCTCTTTCATTTTTCTCAGTGTGTTATGCAGCAATTT NM_001291832 RefSeq
chr2 + 238159007 238168891 FAM132B 151176 "family with sequence similarity 132, member B"
GO:0006879|GO:0005179|GO:2000193|GO:0005576|GO:0019217|GO:0005615|GO:0042803 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132013_PI430048170 0.0226350767556337 1.54742343618178 7.55963788021291
7.49291735919169 7.55072113724342 P P P 6.78820107716217 7.10728909954775
6.79556834885874 P P P LNCV6_132013_PI430048170 mRNA
AAGCTTCCCTGGATGAGGCAAGTGGCTTTAACATCCCTGCAGAGCAGGCTTCTCGACCCT NM_001077268 RefSeq
chr15 + 40807075 40814569 ZFYVE19 84936 "zinc finger, FYVE domain containing 19, transcript
variant 1"
GO:0005515|GO:0032466|GO:0005813|GO:0005737|GO:0030496|GO:0008270|GO:0032266|GO:0032154|GO:0051
301|GO:0009838 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137592_PI430048170 0.023625260462324 0.936287522905484 11.3987643526081
11.3385828211457 11.4016898353539 P P P 11.4529254401049 11.4713145802265
11.5002074288465 P P P LNCV6_137592_PI430048170 mRNA
CTGGATGACCGACCGCCTGTATGTTTGTGTAATTAATTGCCATAATAAACTTTGATGAGT NM_017966 RefSeq
chr11 - 61130255 61161444 VPS37C 55048 vacuolar protein sorting 37 homolog C (S. cerevisiae)
GO:0005515|GO:0000813|GO:0019082|GO:0019058|GO:0019068|GO:0015031|GO:0016197|GO:0031902|GO:0016
032|GO:0061024|GO:0010008|GO:0048306|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132596_PI430048170 0.0227039927276232 0.616083766288811 6.77961179184472
6.79432206646113 6.67355755462845 P P P 7.24639193474837 7.66875205169485
7.39969989960762 P P P LNCV6_132596_PI430048170 mRNA
CTAGAGATTGTATGAGAATAAACTTGTTATTATGGAAGCCTGGCTCCCACCCCATCTAAA NM_005804 RefSeq
chr19 - 14408797 14419383 DDX39A 10212 "DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A,
transcript variant 1"
GO:0005515|GO:0005737|GO:0006406|GO:0016020|GO:0000398|GO:0004386|GO:0005634|GO:0005524 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_131983_PI430048170 0.0758894192278034 1.21090908676081 3.88695262813042
4.09034916105451 4.17482690359708 P P P 3.62107727332236 3.85261598008609
3.85295964772929 P P P LNCV6_131983_PI430048170 mRNA
AACACAGCCTGGGACCAGGGCATATTAAAGGCTTTTGGCAGCAAAGTGTCAGTGTTGGCA NM_001242823 RefSeq
chr6_GL000251v2_alt + 3459483 3473740 C4B_2 NA "complement component 4B (Chido blood group),
copy 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138757_PI430048170 0.551822678429784 0.919547821693493 0.394585753606858
0.257310776202733 0.292557829506886 A A A 0.270839414817666 0.717666699977267
0.275412435537706 A A A LNCV6_138757_PI430048170 mRNA
CTTGGATTTCTCTCTCTGAAACATCTTTCAGGCTTAACTTTATTTAGCCCTGAAACTTAA NM_001270616 RefSeq
chr1 + 213987934 214041504 PROX1 5629 "prospero homeobox 1, transcript variant 1"

GO:0010468|GO:0005515|GO:0003700|GO:0055010|GO:0006366|GO:0044212|GO:0003705|GO:0060042|GO:0048845|GO:0001946|GO:0031667|GO:0070309|GO:0055005|GO:0045071|GO:0055009|GO:0016922|GO:0021542|GO:0030910|GO:0001709|GO:0003714|GO:0061114|GO:0000122|GO:0045787|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129318_PI430048170 0.290336613848877 1.19379413885579 4.65088324729797 5.10293928114365 4.69044158724271 P P P 4.70453208713406 4.71809534920548 4.25297304845727 P P P LNCV6_129318_PI430048170 mRNA CACTTGGAGGGTGAGACTGCAGTGGGGGTTGTTTTTATTAAAAGCATCATGGACACAGCA NM_001033113 RefSeq chr9 - 137434363 137441449 ENTPD8 377841 "ectonucleoside triphosphate diphosphohydrolase 8, transcript variant 1"
GO:0017111|GO:0017110|GO:0005886|GO:0009124|GO:0016021|GO:0009133|GO:0005524|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128212_PI430048170 0.447702405618114 0.706017042963263 0.311892441401937 0.265314725892879 0.28543186162505 A A A 0.265320167456144 0.25863368249236 1.47954480129507 A A A LNCV6_128212_PI430048170 mRNA CCTAGGATTTGTACAGCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAGTT NM_016352 RefSeq chr7 + 130293133 130324180 CPA4 51200 "carboxypeptidase A4, transcript variant 1"
GO:0016573|GO:0006508|GO:0008270|GO:0005576|GO:0005575|GO:0004181 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139062_PI430048170 0.00313874800922311 2.09136445695862 5.21256894977442 5.29920905651667 5.28448106616861 P P P 4.32441351968001 4.2247610042191 4.04105617805093 P P P LNCV6_139062_PI430048170 mRNA AACAAGTTACTTGAAAGAGTGTCACCAATAATCATTAAAGTACGGCAGGCTGAACCTTCA NM_001291774 RefSeq chr19 - 55132697 55149354 TNNT1 7138 "troponin T type 1 (skeletal, slow), transcript variant 4"
GO:0031014|GO:0045932|GO:0030049|GO:0005861|GO:0003009|GO:0031444|GO:0005523|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129779_PI430048170 0.306847367232311 0.630238950123765 2.17820460227894 0.315933185016916 2.48924234286279 A A A 2.54763268396419 2.40731531219671 2.78948728671168 A P P LNCV6_129779_PI430048170 mRNA GTCTATTTTGAGACTGCTAAAGCTATTAATTGATACTGTGTTTTTATGCCCAAATCCCAG NM_001144978 RefSeq chr4 + 74158111 74303097 MTHFD2L 441024 methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like
GO:0005743|GO:0009086|GO:0004329|GO:0004477|GO:0005829|GO:0035999|GO:0005739|GO:0004488|GO:0004487|GO:0009396|GO:0006730|GO:0000105|GO:0055114|GO:0006164 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142716_PI430048170 0.719922081198112 1.119056457612 0.303129014166102 1.91006148634176 2.42972178027284 A A A 2.74788071056105 0.366575313616817 0.343753383362716 P A A LNCV6_142716_PI430048170 mRNA CATAGGAATGTTTTTCCAAGTCCTTCCAGTCTTTTTAGAACGTGGTGGAGGAGGGTTGTG NM_001125 RefSeq chr3 + 119579432 119589945 ADPRH 141 "ADP-ribosylarginine hydrolase, transcript variant 1"
GO:0003875|GO:0000287|GO:0051725|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128447_PI430048170 0.0446495195665193 1.19703267677542 12.7845243628379 12.8679742720601 12.7077202999144 P P P 12.4998722067285 12.6586293068361 12.4172740817698 P P P LNCV6_128447_PI430048170 mRNA CCTGGGGGCCGTGCTCACTACCAAATGTTAATAAAGCCCGCGTCTGTGCCGCCGAAAAAA NM_004322 RefSeq chr11 - 64269827 64284704 BAD 572 "BCL2-associated agonist of cell death, transcript variant 1"
GO:0019050|GO:0005515|GO:0030346|GO:0042542|GO:0019221|GO:0071396|GO:0007173|GO:0032024|GO:0032355|GO:0050679|GO:0046034|GO:0019901|GO:0046031|GO:0046982|GO:0051384|GO:0060139|GO:0071316|GO:0

008656|GO:0043280|GO:0046931|GO:0071247|GO:0051592|GO:0008543|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137392_PI430048170 0.22667831497637 0.890626133880551 0.398831462122119 0.367757223798752 0.350246384925362 A A A 0.447634910918587 0.720890440931777 0.431339295397887 A A A LNCV6_137392_PI430048170 mRNA TGTCTGGTTCTGTAATCGAAGACAAAAAGAGAAAAGAATGACTCCGCCAGGGGATCAGCA NM_000307 RefSeq chrX + 83508260 83509767 POU3F4 5456 POU class 3 homeobox 4 GO:0006355|GO:0003700|GO:0003690|GO:0006366|GO:0003680|GO:0007605|GO:0021879|GO:0090103|GO:0005634|GO:2001054 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145469_PI430048170 0.349975857464553 1.15223848747234 0.796463472785872 0.313518980063352 0.352675523439521 A A A 0.312000532804281 0.301460207790092 0.287229638742671 A A A LNCV6_145469_PI430048170 mRNA ACACATTTAATTATCATGAGAGTCACGCCTTGAAGGGATTGCCATGGGTGGGCTTGGTAT NM_001145169 RefSeq chr2 - 26308172 26319102 ADGRF3 NA "adhesion G protein-coupled receptor F3, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134767_PI430048170 0.922987145324101 0.997964123324201 0.316860828910716 0.323241839817559 0.400222761016623 A A A 0.367480382003163 0.317824240202569 0.36480361849135 A A A LNCV6_134767_PI430048170 mRNA GAAATGTTAGATCTTGCAACATCAGATCCTTGGAATAAAGAAGCCTCTCTGTGCAAAAAA NM_181844RefSeq chr17 + 7023049 7029642 BCL6B 255877 "B-cell CLL/lymphoma 6, member B" GO:0005634|GO:0000122|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132975_PI430048170 0.0385271624022137 0.3707924573896432.84476147746245 3.0127151106419 1.90355450055292 A P A 4.24948010592602 4.1375245628992 3.8689018828197 P P P LNCV6_132975_PI430048170 mRNA CTGGACATATTCTTTATGCCACACCTACCACGGGATAATAAAAGGGAAAATAATTTGAAA NM_006477RefSeq chr22 - 29312932 29315756 RASL10A 10633 "RAS-like, family 10, member A" GO:0006184|GO:0005886|GO:0007264|GO:0005730|GO:0003924|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69831_PI430048170 0.2328005905548681.08898491068898 7.81355771647782 7.92211130551027 8.06092771687705 P P P 7.8485143430278 7.85114352371574 7.73568971027834 P P P LNCV6_69831_PI430048170 mRNA TTAACCAATAGGATTTTGGTGAGCTTAGCTTCTGTATTCCTACTGCCGCCCAGAAAAGGG NM_001114600 RefSeq chr1 + 16367029 16398148 SZRD1 26099 "SUZ RNA binding domain containing 1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62970_PI430048170 0.0469922987042050.8759743648668691 2.5759953348632 12.4731766052289 12.4063349254026 P P P 12.6793255219922 12.7074060491068 12.6463280675119 P P P LNCV6_62970_PI430048170 mRNA TGACTAGGGCCAGCGCAAATACTGGAACCTGTAACAGAATTAAAGGTGAATGTTCTGAGA NM_025233RefSeq chr17 + 42562073 42566281 COASY 80347 "CoA synthase, transcript variant 1" GO:0005515|GO:0004595|GO:0015939|GO:0006767|GO:0005741|GO:0015937|GO:0044281|GO:0005524|GO:0016310|GO:0005737|GO:0004140|GO:0006766|GO:0005759|GO:0005654|GO:0009108|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133260_PI430048170 0.00688855135371476 1.41354912116977 12.7722026624187 12.9634177073882 12.9748083432933 P P P 12.2966949499151 12.3745560529706 12.539321969592 P P P LNCV6_133260_PI430048170 mRNA GAGAATGTGACCTAATTTATGACAAATACGTAGAGCTCAGGTATCACTTCTAGTTTTACT NM_005001RefSeq chr19 - 8311299 8321396 NDUFA7 4701 "NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa" GO:0022904|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0008137|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_124829_PI430048170 0.0430875234328094 1.59446414663545 10.0459667694797
9.57695376829416 9.51312170787034 P P P 8.94980127981349 9.19716008198952
9.01907466642684 P P P LNCV6_124829_PI430048170 mRNA
TGTCCCCAGAGGAGCAGAGGGTCCTGGAAAGGAAGCTGAAAAAGGAACGGAAGAAAGAGG NM_032350RefSeq
chr7 - 996986 1138257 C7orf50 84310 "chromosome 7 open reading frame 50, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98099_PI430048170 0.2542260969718620.8934675992084871 1.3769050552844 11.4961200960834
11.5761808796778 P P P 11.5553391009949 11.5304460862627 11.8373346342038 P P P
LNCV6_98099_PI430048170 mRNA
CTGGGTCCTCCTTATCCGTCTTGCTTTTAACCTATGTAAATTTCTGTGGTTGCTATCTTA NM_017822RefSeq chr12 -
48653210 48682252 KANSL2 54934 KAT8 regulatory NSL complex subunit 2
GO:0043981|GO:0005515|GO:0043982|GO:0043984|GO:0043996|GO:0043995|GO:0000123|GO:0006325|GO:0046
972|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135151_PI430048170 0.81716216889832 1.02649197092957 4.62085674382747 4.4507085817271
4.24943269911807 P P P 4.69579017762186 4.27178371566229 4.21478226328443 P P P
LNCV6_135151_PI430048170 mRNA
CCCCTACCTCTTCTGGGCGCAGGGAGTAAGTTACTGCTAAATTAAATTAAATGTGTGCCA NM_024533RefSeq chr16
- 75528529 75535170 CHST5 23563 carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5
GO:0006790|GO:0005794|GO:0005975|GO:0031228|GO:0006044|GO:0044281|GO:0042339|GO:0000139|GO:0018
146|GO:0008146|GO:0009405|GO:0006477|GO:0001517|GO:0016021|GO:0030203 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136066_PI430048170 0.2679688044430311.0644126356182 0.415514231214244
0.2890575215868290.488310706955483A A A 0.3325217865260010.288555357772873
0.30829739739512 A A A LNCV6_136066_PI430048170 mRNA
TTATTATGATCTTGAATGCGGACAATTGGGGCCAAACGAGGAAGGACACAGACCCAAAAG NM_021570RefSeq
chr9 - 93951626 93955326 BARX1 56033 BARX homeobox 1
GO:0055123|GO:0043565|GO:0006355|GO:0003700|GO:0030855|GO:0030178|GO:0007267|GO:0005634|GO:0048
536|GO:0009952|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127620_PI430048170 0.4820845948442750.6544822597663490.361211570051566
0.3651596623990150.472531441570599A A A 0.3392194204237430.317208194269927
1.82362811177419 A A A LNCV6_127620_PI430048170 mRNA
CTTAAGTATCTCCTAAATGTGATACAGAAGAACATCTCATCCCATATGCATGAGATACTA NM_002377RefSeq chr6
+ 159906941 159908075 MAS1 4142 "MAS1 proto-oncogene, G protein-coupled receptor"
GO:0008284|GO:0004945|GO:0005886|GO:0008283|GO:0060732|GO:0007283|GO:0009653|GO:0071375|GO:0014
823|GO:0042277|GO:0007250|GO:0009986|GO:0004930|GO:0042493|GO:0045740|GO:0050727|GO:0038166|GO:0
034698|GO:0070528|GO:0021766|GO:0007186|GO:0005887|GO:0001933|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128724_PI430048170 0.3023525141446491.02461413023728 0.343001839596251
0.2655030380596950.269027539289341A A A 0.2526337666021370.268506037466488
0.252426528860734A A A LNCV6_128724_PI430048170 mRNA
GAAGGTGCTACTTTTAAGTAATGTATGTGCGCTCTGTAAAGTGATTACATTTGTTTCCTG NM_002187RefSeq chr5
- 159314782 159330473 IL12B 3593 interleukin 12B
GO:0005515|GO:0032693|GO:0019221|GO:0032819|GO:0005615|GO:0042803|GO:0032816|GO:0042802|GO:0030
101|GO:0045078|GO:0044130|GO:0045519|GO:0002323|GO:0032729|GO:0004896|GO:0046982|GO:0032725|GO:0
032760|GO:0042164|GO:0042832|GO:0005125|GO:0045785|GO:0019953|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130281_PI430048170 0.8644851173177060.9931011539473510.495317215698054
0.4413839677299040.301120250858622A A A 0.3741380737982490.457037732687849
0.442160049001296A A A LNCV6_130281_PI430048170 mRNA

CCCCACTATATGCAAATTCTGTATGTTGAATCAAGCAGTAGATAATTAATTGTCTCCTAC NM_001024680 RefSeq chr2 - 68462370 68467258 FBXO48 NA F-box protein 48 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54206_PI430048170 0.1557016359623180.8050960686922216.81658669423388 6.41314032006661 6.80607761461083 P P P 6.83709496783584 6.9103997876506 7.2309791909329 P P P LNCV6_54206_PI430048170 mRNA
ATCCAAATTCAGCAGCTTGGGCTGCTTATTACGCTCACTATTATCAACAGCAAGCACAGC NM_001303433 RefSeq chr1 - 77948401 77979205 FUBP1 8880 "far upstream element (FUSE) binding protein 1, transcript variant 1"
GO:0010628|GO:0005515|GO:0003700|GO:0006366|GO:0003697|GO:0045944|GO:0001205|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143653_PI430048170 0.6060556998430850.9175751719020418.77221690618304 8.45646058534195 8.69382337287705 P P P 8.54566700417447 8.62360279804737 9.08351850782642 P P P LNCV6_143653_PI430048170 mRNA
TTTGCAACTTAGAAACCAGCTACAGTATGGCCCACTTAATAAAACACCTGAAACAAAAAA NM_015213 RefSeq chr11 - 9138825 9265326 DENND5A 23258 "DENN/MADD domain containing 5A, transcript variant 1"
GO:0005802|GO:0017112|GO:0017137|GO:0005262|GO:0050982|GO:0016020|GO:0042147|GO:0032851|GO:0030904 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81495_PI430048170 0.1197377260945121.23546863567694 9.86557901948654 9.92684632812589 9.78472764177789 P P P 9.74680551796521 9.5743960774626 9.31136275024968 P P P LNCV6_81495_PI430048170 mRNA
AATGCCTTCACCGTGCTGGCCATGATGGACTACCCCTACCCCACTGACTTCCTGGGTCCC NM_013379 RefSeq chr9 - 137110539 137114743 DPP7 29952 dipeptidyl-peptidase 7
GO:0005794|GO:0006508|GO:0016023|GO:0008236|GO:0008239|GO:0005764|GO:0070062|GO:0043231|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145519_PI430048170 0.0901991695376341 0.7776143044818621 0.102741338829 10.2020920017256 10.340752518121 P P P 10.3760953554325 10.5225673101935 10.8110734650197 P P P LNCV6_145519_PI430048170 mRNA
AGAGTTGCTCCTGTGTTCCCGGGTCATGTTGAGTAGGAATAAATAAATCTGATGCTGCCT NM_018032 RefSeq chr16 - 188970 229450 LUC7L 55692 "LUC7-like (S. cerevisiae), transcript variant 1"
GO:0005515|GO:0006376|GO:0050733|GO:0003729|GO:0005685|GO:0045843|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66855_PI430048170 0.0958239544890915 1.24398789960387 4.06271868079764 3.72888138675002 3.73383949630898 P P P 3.4134057453415 3.47179539333379 3.70458446628649 P P P LNCV6_66855_PI430048170 mRNA
AGCTCTTGGCAGGAGTAGCTGATCAAACCAAGGATGGGTTGATCTCCTATCAAGAGTTTT NM_003705 RefSeq chr2 - 171783404 171894306 SLC25A12 8604 "solute carrier family 25 (aspartate/glutamate carrier), member 12, transcript variant 1"
GO:0005975|GO:0005313|GO:0005509|GO:0005743|GO:0006094|GO:0044281|GO:0005739|GO:0051592|GO:0015813|GO:0015810|GO:0015183|GO:0009405|GO:0006006|GO:0043490|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145586_PI430048170 0.1979926246917111.18739123656996 12.4686714277656 12.2637080169563 12.0723399808623 P P P 12.2002839702099 12.0486107828698 11.8136509420353 P P P LNCV6_145586_PI430048170 mRNA
TGGGGTCGATGAAGAGGTGAAGTGACCAAATGAAAGAAAGCTGCATTCTCAGTGAAAAAA NM_018166 RefSeq chr1 - 36322029 36324154 EVA1B 55194 "eva-1 homolog B (C. elegans), transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98787_PI430048170 0.3527242806682021.23377075115732 4.74835728508539 4.39964712742972 5.17729149208398 P P P 4.39536390097079 4.55357451589906 4.56640846366142 P P P

LNCV6_98787_PI430048170 mRNA
AGTTCCGTAACTTAGGACAAAATGAGCCTCACATGCCACTCAACGCCACTTTTCCAGATT NM_005900 RefSeq chr4
+ 145481798 145559173 SMAD1 4086 "SMAD family member 1, transcript variant 1"
GO:0071773|GO:0005515|GO:0001657|GO:0003700|GO:0051216|GO:0001710|GO:0042802|GO:0005622|GO:0009
880|GO:0000165|GO:0007179|GO:0019901|GO:0007276|GO:0010243|GO:0030509|GO:0000978|GO:0000979|GO:0
060038|GO:0007183|GO:0043234|GO:0060348|GO:0050775|GO:0042060|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_99601_PI430048170 0.26288668284124 0.6669896067404712.42698681619295 1.16170906728638
2.20196015561351 A A A 2.97667432249219 2.65611892466906 2.04963558831592 P P A
LNCV6_99601_PI430048170 mRNA
GTAGAATATGTAACATGCCTCCAGAAACGTGCCCTAAACACAAATATATAATTTGGCAAA NM_001205281 RefSeq
chr19 - 46480787 46601200 PPP5D1 100506012 PPP5 tetratricopeptide repeat domain containing 1
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140252_PI430048170 0.0402323920154586 0.7967594988582161 1.6863617661632
11.5223743312457 11.3882735921616 P P P 11.8577264670721 11.9636631666781
11.7677867843637 P P P LNCV6_140252_PI430048170 mRNA
CGCCCCGCGCTCAACTGCTCCCGTGGAAGATTAAAGGGCTGAATCATGGTGCTGAAAAAA NM_003952 RefSeq chr11
+ 67428463 67435408 RPS6KB2 6199 "ribosomal protein S6 kinase, 70kDa, polypeptide 2"
GO:0042277|GO:0048011|GO:0048015|GO:0005524|GO:0006412|GO:0007165|GO:0005737|GO:0004672|GO:0007
173|GO:0004674|GO:0008543|GO:0045087|GO:0043491|GO:0004711|GO:0045948|GO:0005654|GO:0006468|GO:0
038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132384_PI430048170 0.326817406646915 1.03235584291894 0.538748551661775
0.464069284844313 0.557941337431592 A A A 0.4672182581056 0.528707330847806
0.426881067618991 A A A LNCV6_132384_PI430048170 mRNA
TCCTCTATTTAATTTACAGTGGAGTCCAGGAAAGACTCTTCTCATTTATTCCTCATTGAA NM_001012455 RefSeq
chr6 - 28432654 28443502 ZSCAN23 NA zinc finger and SCAN domain containing 23 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134182_PI430048170 0.0132587969129393 0.467772176948593 10.2998895117252
9.9128041039586 10.1687447942056 P P P 10.8960408329795 11.1758903806023
11.5493824730799 P P P LNCV6_134182_PI430048170 mRNA
GATTGTGGTGTGGTGTATCTGAAGGCTATTGAATGCAACTTACAATGCTTAATAAAAATC NM_014612 RefSeq chr9
+ 93451695 93566115 FAM120A 23196 "family with sequence similarity 120A, transcript variant 1"
GO:0005737|GO:0016020|GO:0005886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70671_PI430048170 0.0219669253432694 0.824130103291166 8.35859472261672
8.40602064336681 8.54668813460051 P P P 8.68000676299144 8.69995336239793 8.7735157422041
P P P LNCV6_70671_PI430048170 mRNA
GCTATGACAAGAGTGATTTAGTGTTGCACTTTCAGAGCAATTATCTACTGCAGTAATAAA NM_001282958 RefSeq
chr2 + 232550586 232583645 EIF4E2 9470 "eukaryotic translation initiation factor 4E family member 2,
transcript variant 2"
GO:0017148|GO:0005515|GO:0000339|GO:0019221|GO:0003743|GO:0001701|GO:0031625|GO:0008135|GO:0006
413|GO:0005845|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129316_PI430048170 0.956027176287987 0.986586711755891 4.76715589470031
5.02531721604973 5.17904712906316 P P P 4.89671892778872 4.7977807404913
5.31204576782906 P P P LNCV6_129316_PI430048170 mRNA
CCAGAGTTCTACTCTTTCCTCTGGAGCATTAAAATATATTGCCATTCCTATTAAAACGTA NM_007344 RefSeq chr9
- 132375548 132406851 TTF1 7270 "transcription termination factor, RNA polymerase I, transcript
variant 1"
GO:0006353|GO:0010467|GO:0006355|GO:0005886|GO:0006363|GO:0005730|GO:0006361|GO:0005634|GO:0006
360|GO:0003677|GO:0005737|GO:0045814|GO:0003682|GO:0040029|GO:0005654|GO:0006338|GO:0008156 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134831_PI430048170 0.0010400624877667 0.3384787162444433.58014652985419
3.48365289666558 3.22705806728226 P P P 5.09662183523233 4.98072948596008
4.91909675215096 P P P LNCV6_134831_PI430048170 mRNA
TGGGGCATGATGTTTTAACCTTTGCTTTAGAAGCACAAGCTGTAAATCTAAAAGGCACTT NM_182961RefSeq chr6
- 152121683 152637399 SYNE1 23345 "spectrin repeat containing, nuclear envelope 1, transcript variant
1"
GO:0005515|GO:0031965|GO:0006997|GO:0005794|GO:0090292|GO:0034993|GO:0003779|GO:0005634|GO:0090
286|GO:0005635|GO:0030017|GO:0042803|GO:0042692|GO:0005640|GO:0005737|GO:0051015|GO:0040023|GO:0
045211|GO:0007030|GO:0005654|GO:0016021|GO:0005856|GO:0005521 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_114822_PI430048170 0.1523601923395420.8527309452204056.39683131360819
6.39103975720374 6.7191009834117 P P P 6.77151376731773 6.61020295274505
6.83084227584611 P P P LNCV6_114822_PI430048170 mRNA
TCATAGAGCCCAGTTCTTAGAGTCAACTAAAGAGTTGATAGGAATTTACTAGGTCCAGGG NM_001037442 RefSeq
chr4 + 70721841 70808622 RUFY3 22902 "RUN and FYVE domain containing 3, transcript variant 1"
GO:0050771|GO:0030175|GO:0030426 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144710_PI430048170 0.4544867429828420.7673490778777530.334830534014802
0.2520465711919140.332466667172544A A A 0.29734410227235 0.263806812314978
1.26722655178442 A A A LNCV6_144710_PI430048170 mRNA
GTGATCACAATTTGCAGTAAACTTTTAATTAAATGCTCATCTGGTAACTCAACACCCCAG NM_002995RefSeq chr1
+ 168576472 168582077 XCL1 6375 chemokine (C motif) ligand 1
GO:2000553|GO:2000538|GO:0032733|GO:2000556|GO:2000518|GO:0007267|GO:0071560|GO:2000558|GO:2000
412|GO:2000513|GO:0005615|GO:0042803|GO:0043433|GO:0071636|GO:0006955|GO:0002826|GO:0071353|GO:0
032689|GO:0051281|GO:2000562|GO:0032703|GO:0008009|GO:2000563|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142192_PI430048170 0.2552240808847490.8995577407408560.262910428920654
0.2849488306505860.349824002064097A A A 0.3885383874155780.319809625733449
0.630172925343039A A A LNCV6_142192_PI430048170 mRNA
TGTTACAAACCCCTGCACAGTGCCTGTCAAACAGATGCAAACCTTCCTGAATAAAGCCTT NM_002221RefSeq chr1
- 226631689 226739175 ITPKB 3707 inositol-trisphosphate 3-kinase B
GO:0005515|GO:0046638|GO:0005516|GO:0008440|GO:0043647|GO:0046579|GO:0044281|GO:0005524|GO:0045
059|GO:0005829|GO:0007165|GO:0000165|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128539_PI430048170 0.4794260253849230.7170595145282510.376850643373034
0.3836864156151630.459148385428289A A A 0.3258714532350541.58379793622232
0.374649283129035A A A LNCV6_128539_PI430048170 mRNA
GCTTTAAGGGGAAAGAACTTAAGTTGAGCCTAAAAGGATGGATCTGATATTAACCATATA NM_032603RefSeq chr2
- 74532258 74553964 LOXL3 84695 "lysyl oxidase-like 3, transcript variant 1"
GO:0005515|GO:0005507|GO:0004720|GO:0005576|GO:0005634|GO:0001837|GO:0005615|GO:0006898|GO:0005
737|GO:0016020|GO:0045892|GO:0005044|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139663_PI430048170 0.6407882500816480.96959452508173 0.551317492412948
0.4859656761746290.272429416293438A A A 0.41178154246197 0.545669588305325
0.497240201501952A A A LNCV6_139663_PI430048170 mRNA
CGAATAGCACATAACTCATATTGTGAATCCTATGGGTCTTGAGGCCTGTAGAACCAATCT NM_001134453 RefSeq
chr18 + 31376776 31413917 DSG4 147409 "desmoglein 4, transcript variant 1"
GO:0030057|GO:0016337|GO:0005886|GO:0030216|GO:0005509|GO:0030509|GO:0016021|GO:0007156|GO:0001
942 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128821_PI430048170 0.0141048503845081 0.6132061010215016.4916342442665
6.55120942517371 6.82390958718119 P P P 7.37033824107481 7.27410912019017

7.35924207574252 P P P LNCV6_128821_PI430048170 mRNA
CAGCAAGTCTTCCAAACTGTATATGATGCATCCTGTCTCCATGTGTAATATATTTTAATG NM_005540RefSeq chr1
- 37860696 37947057 INPP5B 3633 "inositol polyphosphate-5-phosphatase, 75kDa, transcript variant 1"
GO:0005515|GO:0051056|GO:0005793|GO:0005794|GO:0052658|GO:0043647|GO:0005886|GO:0007264|GO:0070
613|GO:0044281|GO:0007283|GO:0030317|GO:0001701|GO:0046872|GO:0005829|GO:0004439|GO:0005737|GO:0
016020|GO:0031901|GO:0046856|GO:0030670|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_129834_PI430048170 0.0530540679845251.34717268133928 8.59780296990549
8.89826464369061 8.64307692403195 P P P 8.50304569020505 8.25719719947781
8.07554288159615 P P P LNCV6_129834_PI430048170 mRNA
TGGGGAATCCCGCCAAAGATGGAGGGAATGTCACCGTCTCCCTCTTCTACCGCAATGACT NM_033068RefSeq chr19
+ 50790414 50795224 ACPT 93650 "acid phosphatase, testicular"
GO:0016311|GO:0003993|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138468_PI430048170 0.4660134268729790.8237881000342720.378882792035161
0.37712226801736 0.405092163829864A A A 0.3748755226092310.344275963961719
1.13502071817844 A A A LNCV6_138468_PI430048170 mRNA
GGGATTCTTATTCTGACTGTGGGAGCTCCTGTTGCGGGATCTTGGGAAAAAATAAAGAAG NM_001172501 RefSeq
chr16 + 55655629 55703788 SLC6A2 6530 "solute carrier family 6 (neurotransmitter transporter),
member 2, transcript variant 2"
GO:0005515|GO:0043005|GO:0005886|GO:0009986|GO:0015874|GO:0043014|GO:0042493|GO:0048487|GO:0007
268|GO:0055085|GO:0016020|GO:0005887|GO:0006810|GO:0006836|GO:0008504|GO:0048265|GO:0045121|GO:0
005334|GO:0015844. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108643_PI430048170 0.9948943511203790.9802608296116342.71094852470314 2.6473473622445
2.33003883110249 A A A 2.43851735685301 3.00246838218621 2.25264681446887 A P A
LNCV6_108643_PI430048170 mRNA
TGTAGTCCAGGTTGCCCGCCACATCGATGGAGGCGAACTGGAACATCTGGTCCACCTGCG NM_001294341 RefSeq
chr4 - 681823 689441 MFSD7 84179 "major facilitator superfamily domain containing 7, transcript
variant 1" GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141102_PI430048170 0.0641041515350357 0.3621473031444662.78708327640947
1.18974782390858 2.3476759072411 A A A 3.38453237482215 3.63181332642457
4.05084295850376 P P P LNCV6_141102_PI430048170 mRNA
TAACCTCTCCTGATGATACAGTTCAGAGTACACACACTTTGGTGATGGATCAAGAGCAAT NM_001040697 RefSeq
chr11 - 18531402 18588746 UEVLD 55293 "UEV and lactate/malate dehyrogenase domains, transcript
variant 1"
GO:0008150|GO:0003674|GO:0044262|GO:0015031|GO:0006464|GO:0070062|GO:0055114|GO:0016616 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136346_PI430048170 0.0199332437971371.59018829525173 9.89606301513242
10.0017968252004 10.3055115143182 P P P 9.21714547382405 9.326218235934
9.64871235447389 P P P LNCV6_136346_PI430048170 mRNA
CTGCAGAAGGAACAGTAGTCTCAAATCTTTCCTCATAATGATAACAAAATGCTCTTGCAT NM_016126RefSeq chr1
- 53921560 53945615 HSPB11 51668 "heat shock protein family B (small), member 11"
GO:0005813|GO:0006996|GO:0030324|GO:0070986|GO:0072372|GO:0015031|GO:0046872|GO:0007224|GO:0007
507|GO:0042384|GO:0001501|GO:0030992|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53290_PI430048170 0.00463112234765841 1.42210079473128 2.62704813306964
2.80737147860569 2.83456135702298 A A A 2.36348285623344 2.1643280971681
2.21836751524811 A A A LNCV6_53290_PI430048170 mRNA
AGCTTCCCAACAACAAGCTCCTCACCACCAAGATCGGGCTGCTCAGCACCCTTCGGGGAC NM_001130045 RefSeq
chr1 + 1173905 1197933 TTLL10 254173 "tubulin tyrosine ligase-like family member 10, transcript
variant 1" GO:0018094|GO:0005515|GO:0070735 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_74680_PI430048170 0.3302215848994770.8619987959295041 1.1301356081291 11.1669157286724
11.4743239029667 P P P 11.2685227993263 11.3673833523568 11.7562430096398 P P P
LNCV6_74680_PI430048170 mRNA
CATCTGAAATTCTGCTGTCAAGATTCCCATCTCTAAGGACTCCAAGTGCTAGAGACAAGG NM_176869RefSeq chr4
- 105369076 105474070 PPA2 27068 "pyrophosphatase (inorganic) 2, transcript variant 1"
GO:0010467|GO:0000287|GO:0016311|GO:0005759|GO:0004427|GO:0071344|GO:0004722|GO:0070062|GO:0006
418 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128471_PI430048170 0.5897562174716070.8295487176654662.53559970674512
1.64530923273525 1.57466151877017 A A A 2.74180194040422 2.21403530780911
1.59569046993615 A A A LNCV6_128471_PI430048170 mRNA
GAGGTAGAAAAGGAACTGAAAAAGCTGGCGGGTTTGAGAAATTAATGCTCTATATACATA NM_001042367 RefSeq
chr15 + 73443157 73560012 REC114 283677 REC114 meiotic recombination protein
GO:0051321|GO:0006310 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132617_PI430048170 0.3976678527746241.48572363909999 0.369412320497981
0.2838625327098031.57084330871061 A A A 0.28888718771678 0.290381326841237
0.314774743222822A A A LNCV6_132617_PI430048170 mRNA
TGCCATCAGCTACAAAACCTTCATGAAGACTATTGGAGAAATTAAAACCATCATCCAAGT NM_199136RefSeq chr7
+ 23680113 23702650 FAM221A 340277 "family with sequence similarity 221, member A, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134206_PI430048170 0.0183003098565187 0.5478682048637775.36504082361084
5.68577582281116 5.95683871359178 P P P 6.73175265695397 6.39365833407002
6.52656658289531 P P P LNCV6_134206_PI430048170 mRNA
GACATGTTGCAATAGCAAAACCCCCAGTTAGATTAGTGTTTACACATTTTCTCAGTTATT NM_001286495 RefSeq
chr15 - 52581320 52652050 FAM214A 56204 "family with sequence similarity 214, member A,
transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132470_PI430048170 0.0132049068417949 0.6422676648745667.69079210838605
7.92645760315929 8.02779709938614 P P P 8.33418239228394 8.50509942373303
8.71686866470679 P P P LNCV6_132470_PI430048170 mRNA
AAATATACTAGCCTGGCCATGCCAATAAGTTTCCTGCTGTGTCTGTTAGGCAGCATTGCT NM_001282640 RefSeq
chr9 - 112040780 112175297 SUSD1 64420 "sushi domain containing 1, transcript variant 1"
GO:0005509|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102779_PI430048170 0.00913005983686 0.7257669591976747.41466747945129 7.667894253516
7.5779330537276 P P P 7.91334372358116 8.06357187924914 8.07653210634062 P P P
LNCV6_102779_PI430048170 mRNA
GTTTTGGATGTCAGCAGTACAAGTAGTGAAGATAGCGATGAAGAGAATGAAGAACTGAATNM_173829RefSeq chr5
- 64718150 64768669 SREK1IP1 285672 SREK1-interacting protein 1
GO:0008380|GO:0006397|GO:0008270|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134611_PI430048170 0.5276290814367980.9395743480810194.91172209702612 5.1834388076018
4.82854831563559 P P P 5.08448406822497 5.19964224748302 4.92005036891951 P P P
LNCV6_134611_PI430048170 mRNA
ATGTTCCATGTCTCCACGCCACTGCCAGTGATGACCGGTGGTTTCCTGAGCTGCATCTTG NM_032019RefSeq chr22
- 50245183 50251405 HDAC10 83933 "histone deacetylase 10, transcript variant 1"
GO:0032041|GO:0005515|GO:0070932|GO:0070933|GO:0016575|GO:0006355|GO:0042826|GO:0006325|GO:0046
970|GO:0005634|GO:0000122|GO:0033558|GO:0006351|GO:0005737|GO:0000118|GO:0007219|GO:0014003|GO:0
005654|GO:0004407|GO:0019899|GO:0046969|GO:0045892|GO:0006476|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134245_PI430048170 0.3164001811613590.5839791169230950.400105238350315
0.41950419450554 0.327979264847598A A A 0.4241657064199850.6519877276422681.9207886611566
A A A LNCV6_134245_PI430048170 mRNA

GACTGATAGCATTTCAGAATGTGTCTTTTGAAGGGCTATGATACCAGTTATTAAATAGTG NM_014373 RefSeq chr3 + 170037946 170085395 GPR160 26996 G protein-coupled receptor 160 GO:0043235|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95597_PI430048170 0.00273341456696204 0.7242298361583375.91250756018596 5.87481868319634 5.74555220370308 P P P 6.39628218647557 6.3071710819533 6.22610489893687 P P P LNCV6_95597_PI430048170 mRNA
TAACTTCCTCTTTGACATTCCAAAGATCCTGGACCTCTGCGTGCTCTTTGGAAAAGGCAA NM_032204 RefSeq chr22 - 29788607 29838304 ASCC2 84164 "activating signal cointegrator 1 complex subunit 2, transcript variant 1" GO:0006355|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134726_PI430048170 0.6151902320959931.08696057191834 0.891684110289035 0.4806833051106920.322998581311115 A A A 0.4093994451845360.510802960961677 0.473576876634001 A A A LNCV6_134726_PI430048170 mRNA
AGACCTACGGGTTGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA NM_139209 RefSeq chr3 + 141778200 141817050 GRK7 131890 G protein-coupled receptor kinase 7 GO:0007165|GO:0046777|GO:0004703|GO:0016020|GO:0038032|GO:0050254|GO:0007601|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131899_PI430048170 0.16244088517706 1.29897281497453 2.85678326018989 2.28570591735821 2.41335564435385 A A A 2.14057854021134 2.34780018819049 1.97512333824503 A A A LNCV6_131899_PI430048170 mRNA
GACCCAAGGAGTGGGGATACAGTGAGAATTACCACTGTTGGGGCAAAATATTGGGATAAA NM_199180 RefSeq chr19 + 35856907 35867146 KIRREL2 84063 "kin of IRRE like 2 (Drosophila), transcript variant 3" GO:0016337|GO:0005886|GO:0036057|GO:0001933|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142089_PI430048170 0.9168968980585341.00761600565197 2.47525227948696 3.47461549824845 2.53229821373523 A P A 3.16537725236664 2.92185105870976 2.52163444112617 P P P LNCV6_142089_PI430048170 mRNA
TGCTGGGGCCTGGATTTTTGTAAATAAATTTCCCAAGCGTTTCTTTCCACCTGGAGGGAA NM_014212 RefSeq chr12 + 53973125 53976419 HOXC11 3227 homeobox C11 GO:0001656|GO:0009954|GO:0001759|GO:0000978|GO:0009952|GO:0006351|GO:0001077|GO:0005737|GO:0007492|GO:0045944|GO:0060272|GO:0005654|GO:0042733 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132575_PI430048170 0.737882760560733 0.962373861589863 9.19948635277284 9.30798233241527 9.4112747211748 P P P 9.2390569495942 9.23696825621958 9.58753842223166 P P P LNCV6_132575_PI430048170 mRNA
CTTGGTTGCTTAAAAGTAGTTCCCAAGAGTCTGAGAAGCTATTTCTATTTTTAAGAGTCA NM_018142 RefSeq chr8 + 19817406 19852075 INTS10 55174 integrator complex subunit 10 GO:0005515|GO:0032039|GO:0016180 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127603_PI430048170 0.1181813317126360.967345049350652 0.433186836456044 0.4157909303311840.375953381694229 A A A 0.4232828790385160.481218847013639 0.464104669520509 A A A LNCV6_127603_PI430048170 mRNA
GCTCTTGTTATACAGTCATATGGCTACACGTTTATGTAAAGTTTGCAAAAGTTTGGTGTT NM_152423 RefSeq chrX + 106168304 106208956 MUM1L1 139221 "melanoma associated antigen (mutated) 1-like 1, transcript variant 2" GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140227_PI430048170 0.0170242938321922 2.62207789556147 7.29630306500872 7.33728679510923 7.55250874646475 P P P 5.51461564905376 6.16197788157949 6.2459306571057 P P P LNCV6_140227_PI430048170 mRNA
GTTCTTTTGTTAAGAAATAGCCTAATGGTCCAACTTTGCTGTCTGTTCTTCCAAATGTTT NM_001004298 RefSeq chr10 - 126425004 126521441 C10orf90 118611 chromosome 10 open reading frame 90 GO:0007095|GO:0030308|GO:0005813|GO:0005737|GO:0042826|GO:0010212|GO:0050821|GO:0015629|GO:0009

411 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142359_PI430048170 0.3881589734735910.7667980148902260.591326917190421
0.4897008288096480.401360322767727A A A 1.4041026438578 0.529509307397912
0.51448369891784 A A A LNCV6_142359_PI430048170 mRNA
TCACTGGGCAATGCTGGAAAGAGCAAAAGAATATCATTGGCCCTGATCACATAGATGCTG NM_017888RefSeq chr16
+ 20409533 20440959 ACSM5 54988 acyl-CoA synthetase medium-chain family member 5
GO:0005759|GO:0006631|GO:0005525|GO:0005524|GO:0047760|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139334_PI430048170 0.55643977367395 0.9913845826979240.353980306536378
0.3709746038373220.31286638567031 A A A 0.3564415419896140.37342140806466
0.345891439729993A A A LNCV6_139334_PI430048170 mRNA
GTCTCCTTAATGAAGAGAGGTTGTGAAGGCTTTTCCTTTGCGTTTATAAATATGTACTAA NM_001004467 RefSeq
chr1 - 159313669 159314659 OR10J3 441911 "olfactory receptor, family 10, subfamily J, member 3"
GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138014_PI430048170 0.86164718373859 1.14865308525228 0.884185663510223
3.75368404204544 2.83167777616486 A P A 2.23523045449135 3.09881282250083
2.64895944889394 A P A LNCV6_138014_PI430048170 mRNA
AGACAATGAAGGCTGCTGGCTAATGTGGAAGGAGGCACTTTCTCCTCTAAAACACAAAAC NM_001040272 RefSeq
chr9 + 18474080 18910949 ADAMTSL1 92949 "ADAMTS-like 1, transcript variant 4"
GO:0006493|GO:0006508|GO:0005578|GO:0005788|GO:0008270|GO:0036066|GO:0044267|GO:0008237|GO:0043
687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136811_PI430048170 0.1023219213690460.8578600706507639.50211803536387
9.61043674542481 9.62091054668376 P P P 9.94037370206899 9.65448521784533
9.79095360660682 P P P LNCV6_136811_PI430048170 mRNA
GTGCTAGTCTCCTTTGCATGGACTTCAAGCTGCATGAAATGCAATAAATCTCATTTTAGA NM_001142590 RefSeq
chr1 + 40692007 40771606 NFYC 4802 "nuclear transcription factor Y, gamma, transcript variant 5"
GO:0005515|GO:0006355|GO:0003700|GO:0046982|GO:0044212|GO:0006357|GO:0003713|GO:0005634|GO:0044
281|GO:0003677|GO:0006351|GO:0043565|GO:0016602|GO:0032993|GO:0006457|GO:0005654|GO:0045893|GO:0
044255|GO:0008134. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140011_PI430048170 0.1080440312436491.03339757638304 0.372727227917385
0.33060341064908 0.386989134511005A A A 0.3004459734667740.300860419178989
0.346924731454364A A A LNCV6_140011_PI430048170 mRNA
GTGTAAGCAATGTGGAAAAGCCTTCATTTCTTCTAATTCTATTCGCTATCATAAAAGGAC NM_001080404 RefSeq
chr19 - 12043804 12052967 ZNF878 NA zinc finger protein 878 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138669_PI430048170 0.0237385234875511 4.17484771434595 5.04378762279586
5.25824471875837 5.25458724070394 P P P 3.75609298457452 2.66569728006174
2.66817136733847 P P P LNCV6_138669_PI430048170 mRNA
CCATCTCACTGTAAATAAGTCTCTGTTCTGTAAATAGATGTACAGAAGCCATGTTATTTC NM_170600RefSeq chr9
- 127738316 127778769 SH2D3C 10044 "SH2 domain containing 3C, transcript variant 1"
GO:0043547|GO:0005515|GO:0005085|GO:0005737|GO:0016020|GO:0007264|GO:0005070|GO:0007254|GO:0009
967 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143229_PI430048170 0.00356823525091252 0.4535435714966567.88172324188894
7.82242615587775 7.89652253041304 P P P 8.8464568030824 9.02130829169625
9.14093416751373 P P P LNCV6_143229_PI430048170 mRNA
TATTCTTGATTATAAGCAACTGGACAGAACCATGCCAAAGCTTCCCCGTTTCCCACCAAA NM_024076RefSeq chr19
+ 33796845 33815761 KCTD15 79047 "potassium channel tetramerization domain containing 15,
transcript variant 1" GO:0051260|GO:0007275 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_95150_PI430048170 0.78996995348208 0.971564787643146 12.567220878714 12.1570234402154
11.9845560636979 P P P 12.4233192181011 12.3418259076265 12.1144835051715 P P P
LNCV6_95150_PI430048170 mRNA
CAGGTTTTTCAATTAAACGGATTATTTTTTCAGACCGAAAAGAGATGGTCTGAGTTTGTC NM_001257389 RefSeq
chr12 - 55725442 55729673 CD63 967 "CD63 molecule, transcript variant 3"
GO:0005515|GO:0031088|GO:0005886|GO:0031226|GO:0015031|GO:0005765|GO:2000680|GO:1900746|GO:0070
062|GO:0042470|GO:2001046|GO:0009986|GO:0030168|GO:0031904|GO:0016477|GO:0007160|GO:0007596|GO:0
005887|GO:0002576|GO:0031902|GO:0035646|GO:0048757|GO:0034613|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_39361_PI430048170 0.0598534793553204 0.513068094223173 2.09289315299458
2.67013059461051 3.01151904546853 A A P 3.64621687243447 3.50678006363303 3.6496425117367
P P P LNCV6_39361_PI430048170 mRNA
TCTTGAGTAGACTGCCTTTACCTCCACCTGTTAGTCCCATTTGTACATTTGTTTCTCCGG NM_000059 RefSeq chr13 +
32315479 32399672 BRCA2 675 "breast cancer 2, early onset"
GO:0005515|GO:0010165|GO:0048478|GO:0001833|GO:0005634|GO:0001556|GO:0007283|GO:0002020|GO:0033
593|GO:0006302|GO:0000910|GO:0005737|GO:0003697|GO:0000724|GO:0010485|GO:0030141|GO:0006978|GO:0
010332|GO:0004402|GO:0030097|GO:0005813|GO:0032465|GO:0043015|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139971_PI430048170 0.379913364520635 0.970582686369475 0.401549101095385 0.425825571752
0.298916697092169 A A A 0.399621016876343 0.448396888676833 0.410167406267444 A A A
LNCV6_139971_PI430048170 mRNA
GGATTGTCTACATGGATGATCTCACTTTTCAGGAAACTTAAAATTTACCCATTATTGGGA NM_001001290 RefSeq
chr4 - 9826223 10040248 SLC2A9 56606 "solute carrier family 2 (facilitated glucose transporter),
member 9, transcript variant 2"
GO:0016323|GO:0016324|GO:0015758|GO:0005886|GO:0005887|GO:0005351|GO:0016021|GO:0005635|GO:0046
415|GO:0055085|GO:0005355|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131508_PI430048170 0.247186798430956 1.35227797070099 3.13174514783895 3.2130021602467
2.42913641435273 P P A 2.77724859849237 2.22162856975707 2.53650864525884 P A P
LNCV6_131508_PI430048170 mRNA
AACTCCTGGCTTTCTGCGAGACGCATGCCAAAGATGACCCGCTGGTGACGCCAGTACCCG NM_033258 RefSeq chr19
- 46634075 46634682 GNG8 94235 "guanine nucleotide binding protein (G protein), gamma 8"
GO:0005515|GO:0006112|GO:0007186|GO:0005886|GO:0071377|GO:0005834|GO:0003924|GO:0007268|GO:0044
281|GO:0004871|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139910_PI430048170 0.119977004991216 0.937075958232686 0.258501095684363
0.271526195087271 0.307087736892558 A A A 0.444126175658238 0.35543510009232
0.316290419776384 A A A LNCV6_139910_PI430048170 mRNA
GGGTATATTGCAGTGAAACTGTGAAGGATACTTCACTACCAATGTATAAGCTTTGTTGAA NM_001201 RefSeq chr4
+ 81030964 81057531 BMP3 651 bone morphogenetic protein 3
GO:0051216|GO:0005102|GO:0007267|GO:0010862|GO:0042981|GO:0060395|GO:0005125|GO:0005160|GO:0005
615|GO:0001501|GO:0001503|GO:0070700|GO:0045944|GO:0043408|GO:0048468|GO:0008083|GO:0040007|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128766_PI430048170 0.0446395457216443 1.25383202878051 13.2906526235252
13.5040474160954 13.53561476457 P P P 13.0124270800368 13.0565740736994 13.279893584023
P P P LNCV6_128766_PI430048170 mRNA
TTTAAAAATGTCCTGCCTTTTAACGTAGATATATGCCTTCCCCCACTACCGTAAATGTCC NM_001195132 RefSeq
chr9 - 21967751 21975133 CDKN2A 1029 "cyclin-dependent kinase inhibitor 2A, transcript
variant 5"
GO:0005515|GO:0033088|GO:0030308|GO:0006364|GO:0035985|GO:0035986|GO:0071158|GO:0070534|GO:0008
637|GO:0051444|GO:0055105|GO:0000209|GO:0019901|GO:0010389|GO:0030889|GO:0043234|GO:0005654|GO:0

090399|GO:0000278|GO:0045893|GO:0045892|GO:0090398|GO:0008134|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126885_PI430048170 0.2407370209086841.07349459354191 16.0013439021294
15.8461962383639 15.8150012886616 P P P 15.8611827673751 15.7069315505974
15.7903407747963 P P P LNCV6_126885_PI430048170 mRNA
CAGGCATCGCCCATGCTCCTCACCTGTATTTTGTAATCAGAAATAAATTGCTTTTAAAGA NM_012423RefSeq chr19
+ 49487553 49492307 RPL13A 23521 "ribosomal protein L13a, transcript variant 1"
GO:0017148|GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0015934|GO:0005634|GO:0006
415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0071346|GO:0000184|GO:0016020|GO:0030529|GO:0
016032|GO:0022625|GO:0044267|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60229_PI430048170 0.3023271467038040.7712284882348423.72601065976865 3.49887022100499
2.7912638671606 P P A 3.86136751650027 3.97813276977196 3.39207846521157 P P P
LNCV6_60229_PI430048170 mRNA
ATCCTGTCTCCTGTTTTCAACACATTCCATGGAATAAATTCCTTATTGAAGGTAACTTTCNM_012141RefSeq chr13 -
51361564 51453139 INTS6 26512 "integrator complex subunit 6, transcript variant 1"
GO:0005515|GO:0007165|GO:0032039|GO:0005654|GO:0015629|GO:0016180|GO:0004888 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132204_PI430048170 0.4888344717141581.05042826950688 8.13416479734643
8.21436874800893 8.06797288431088 P P P 8.21302156920137 8.05969749706822
7.91965044382947 P P P LNCV6_132204_PI430048170 mRNA
AATAGCTAAAGCCCCCAGTATCTCTTCAGTCTCTATACCAATAAAGTGACCCTGTTCTCA NM_002769RefSeq chr7
+ 142749467 142753076 PRSS1 5644 "protease, serine, 1 (trypsin 1)"
GO:0009235|GO:0004252|GO:0007586|GO:0006767|GO:0005576|GO:0072562|GO:0044281|GO:0046872|GO:0022
617|GO:0006766|GO:0030198|GO:0006508|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129240_PI430048170 0.5778588146511391.32939219013939 0.404937808882321
0.4298324972579571.71183986408276 A A A 0.9010195283830380.359795515026969
0.403554232940632A A A LNCV6_129240_PI430048170 mRNA
GGTCTGTGTTTTTAAATTCCTTTCCTTCAGTTTTCCTCATGAAGATGTTTCAGATACTGA NM_015566RefSeq chr5 -
74777573 74866838 FAM169A 26049 "family with sequence similarity 169, member A, transcript variant
1" GO:0005637 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109402_PI430048170 0.00126462422569816 0.7047022063684431 2.103992862598
12.1742880184879 12.103992862598 P P P 12.559282278095 12.6361677778597 12.699311882908
P P P LNCV6_109402_PI430048170 mRNA
CTACTGCCTCCTCATTTTTCAGTATGTGTTCTAAGTATAAAAAGTCCTTGGTTCTCATGGNM_002696RefSeq chr11 +
62761538 62766715 POLR2G5436 polymerase (RNA) II (DNA directed) polypeptide G
GO:0008380|GO:0010467|GO:0003727|GO:0006368|GO:0006367|GO:0006366|GO:0000291|GO:0005634|GO:0003
697|GO:0000932|GO:0034587|GO:0005665|GO:0016032|GO:0045948|GO:0035019|GO:0003899|GO:0005730|GO:0
060213|GO:0006370|GO:0006915|GO:0050434|GO:0006281|GO:0006283|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_9916_PI430048170 0.1061106587090550.8987350191610917.27385200072886 7.39661334314482
7.326190216609 P P P 7.38623082667753 7.47754444305922 7.59035100993948 P P P
LNCV6_9916_PI430048170 mRNA
ATAAAAGGGTGTGACTGTAATCTGGAAGGTGTTCTCCCTGAAATATGTGATGCCCACGGA NM_198129RefSeq chr18
+ 23689442 23955065 LAMA3 3909 "laminin, alpha 3, transcript variant 1"
GO:0030334|GO:0034329|GO:0005102|GO:0005606|GO:0005576|GO:0035987|GO:0030155|GO:0005604|GO:0045
995|GO:0005610|GO:0008544|GO:0022617|GO:0005198|GO:0030198|GO:0031581|GO:0007155|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135474_PI430048170 0.5292290481975821.1677931705257 1.13106799619418
0.4924910752940110.344387934423339A A A 0.4016870738715610.524735372501861

0.493345203912391 A A A LNCV6_135474_PI430048170 mRNA
CCAGGCCCCAAAGTCTTGGGCCTTCATTAATTCTGTCAATAAAATGTTTCAAGGAAGCCA NM_001017991 RefSeq
chrX - 155459414 155460008 H2AFB2 474381 "H2A histone family, member B2"
GO:0006397|GO:0046982|GO:0006334|GO:0035327|GO:0005634|GO:0000788|GO:0003677 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138105_PI430048170 0.374335032023109 1.07693496349579 10.2683283385173
10.3679536135078 10.4490936058881 P P P 10.0876450009389 10.2512266912695
10.4130522521958 P P P LNCV6_138105_PI430048170 mRNA
CCAGAAATGAAGAGTCCCTGTAGGTTTTGGTTTTGTTTGTTTTATTTTGTTCTTTCACCT NM_001520 RefSeq chr16 -
27460612 27549930 GTF3C1 2975 "general transcription factor IIIC, polypeptide 1, alpha 220kDa,
transcript variant 1"
GO:0005515|GO:0009304|GO:0010467|GO:0009303|GO:0005730|GO:0005634|GO:0042791|GO:0003677|GO:0006
383|GO:0006351|GO:0042797|GO:0000127|GO:0016020|GO:0030529|GO:0005654 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_52223_PI430048170 0.0262873243738249 1.42156747946027 6.35574897575907 6.3687382053408
6.63479270937856 P P P 5.9864509463499 5.91389200997332 5.9531081002599 P P P
LNCV6_52223_PI430048170 mRNA
TGGATGACGAGAATTGGGTACCACATATCTCTATACAGCCTTTCTACTTCCTTTCCCAGA NM_005671 RefSeq chr8
+ 30744164 30767004 UBXN8 7993 "UBX domain protein 8, transcript variant 1"
GO:0007338|GO:0005515|GO:0030176|GO:0030433 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129572_PI430048170 0.923076757351302 0.996946753738721 0.466280118095312
0.425867276611493 0.293439958706809 A A A 0.359083778997334 0.426034978832017
0.418387692029588 A A A LNCV6_129572_PI430048170 mRNA
CTCTATCTTGGGTTTCTTAATTGCTTCCAAGCTTCCAAAGGCTCTTTTCAGAGCCACTTA NM_003535 RefSeq chr6 -
27890314 27890792 HIST1H3J 8356 "histone cluster 1, H3j"
GO:0005515|GO:0010467|GO:0046982|GO:0006325|GO:0006335|GO:0005576|GO:0005634|GO:0000228|GO:0003
677|GO:0032776|GO:0043234|GO:0060968|GO:0016020|GO:0000183|GO:0007596|GO:0045814|GO:0040029|GO:0
005654|GO:0000786|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139318_PI430048170 0.661963235236933 0.999028551468086 2.93060807260321
1.15290464036597 0.392139525222476 A A A 2.18789007750131 1.81279111574695
1.63297496293057 A A A LNCV6_139318_PI430048170 mRNA
CCTGGGGATGCCCAAGGCCAGAATGACGGGAACACAGGAAATCAGGGGAAACATGAGTGA NM_152228 RefSeq
chr1 + 1331345 1334464 TAS1R3 NA "taste receptor, type 1, member 3" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_127902_PI430048170 0.0377920974455090 0.208780554119795 2.85666917151388
1.27367313041657 1.31127824599757 A A A 4.09821867349314 4.45929411887592
4.25061373905056 P P P LNCV6_127902_PI430048170 mRNA
GTACAGCGTTGACAACTCTAACTAAAAGGATTACAGCCCTTAAAATTTTAGCTTAAGGAC NM_015565 RefSeq chr21
- 28928143 28992956 LTN1 26046 listerin E3 ubiquitin protein ligase 1
GO:0005515|GO:0004842|GO:0016874|GO:0008270|GO:0051865 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_73112_PI430048170 0.0381716601304111 0.733974625919737 8.94739542154459
8.99434744919054 9.11974989687791 P P P 9.33404712243271 9.37042503183551
9.67614106182441 P P P LNCV6_73112_PI430048170 mRNA
ACTATTATTGTTGCCCATTTCCCCTGCAACTGAGGTGAGAGGTTTTCCTGAGTTTGAAGC NM_001098783 RefSeq
chr3 + 58306244 58320193 RPP14 11102 "ribonuclease P/MRP 14kDa subunit, transcript variant 1"
GO:0004526|GO:0003723|GO:0005634|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132666_PI430048170 0.217043596393414 1.03899023861546 0.441946774468886
0.379791724459898 0.41428024635452 A A A 0.305476545557488 0.349774021028322

0.413831984722811 A A A LNCV6_132666_PI430048170 mRNA
ATTTTAGCCAGGAAATAACTGTTTCTTGTGACCTGGAACTAACGTCAAAGCACACAAGAC NM_001171038 RefSeq
chrY + 1615047 1643081 ASMT 438 "acetylserotonin O-methyltransferase, transcript variant 1"
GO:0034641|GO:0046219|GO:2000019|GO:0030187|GO:0044281|GO:0017096|GO:0032259|GO:0008171|GO:0006
412|GO:0042803|GO:0042802|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80858_PI430048170 0.2636347381155330.5504960408141270.3246472231145050.329198968559086
0.940261235298491 A A A 0.5718964938177471.0322901330318 2.17347654902722 A A A
LNCV6_80858_PI430048170 mRNA
TTTAACTGAACGCTAATGTCTGTATAAGAGTTGCTGCAACAATAAACAAGAACTTCACCT NM_001163 RefSeq
chr9_GL383540v1_alt - 976 70597 APBA1 320 "amyloid beta (A4) precursor protein-binding, family A,
member 1"
GO:0010468|GO:0005515|GO:0048471|GO:0005794|GO:0005886|GO:0014051|GO:0005546|GO:0007268|GO:0005
634|GO:0030165|GO:0032403|GO:0014047|GO:0001701|GO:0006886|GO:0008021|GO:0007399|GO:0043234|GO:0
001540|GO:0006461|GO:0035264|GO:0008088|GO:0007626|GO:0007155 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_128495_PI430048170 0.0502144256196601 0.27159122467928 1.46176488576293
2.31111778344809 3.1817543733302 A A P 4.33595207752328 4.52793327906442
4.21414035155185 P P P LNCV6_128495_PI430048170 mRNA
GTCTTACTCTTGAGTCATTTAGTATCATTGATATGGTACCAAGTTGTATAGCAGAGTAAC NM_138773 RefSeq chr5
+ 110738993 110765161 SLC25A46 91137 "solute carrier family 25, member 46, transcript variant 1"
GO:0008150|GO:0003674|GO:0006810|GO:0005743|GO:0016021|GO:0005575 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144086_PI430048170 0.2419000027457680.7295997739510540.916821576106755
0.2898041161405291.3865400364242 A A A 1.42274673473212 1.17116337080734
1.54289764724529 A A A LNCV6_144086_PI430048170 mRNA
GGTCACTAACCTTACTTGATGCAGATAAAATCACTTGTCAATGCAAAATGTGTTAGAACT NM_017709 RefSeq chr1
+ 117605981 117628389 FAM46C 54855 "family with sequence similarity 46, member C" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_144817_PI430048170 0.1088745847776190.8516416302231 9.94398916611476
10.0609041483473 9.81137118779152 P P P 9.99972777834049 10.2565091302358
10.2512266912695 P P P LNCV6_144817_PI430048170 mRNA
CGCCTGCGGTTTCTATGTATTTATAGCAAGTTCTGATGTACATATGTAAAGGACTTTTTT NM_014963 RefSeq
chr19_KI270865v1_alt - 220 48834 SBNO2 22904 "strawberry notch homolog 2 (Drosophila), transcript
variant 1"
GO:0072675|GO:0002281|GO:0045944|GO:0061430|GO:0050727|GO:0030282|GO:0005575|GO:0045892|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142459_PI430048170 0.7412740814987530.8778098339327170.509435060842114
1.46564793892216 1.37767341443076 A A A 1.7122605432479 0.5734758411893181.5672143458612
A A A LNCV6_142459_PI430048170 mRNA
TCTATGAAATCTGTGCAGTCCCAATGACTAAGGACACCCTGGTTTGACAGCAAGATAACT NM_001029869 RefSeq
chr5 - 146084312 146104383 PLAC8L1 NA PLAC8-like 1 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_122264_PI430048170 0.3215688803310621.21576766101855 3.64608018764818
3.96061580627541 3.99429897173564 P P P 3.7666296121547 3.81538722412321
3.09143784062216 P P P LNCV6_122264_PI430048170 mRNA
AACAGTATTTATGAATACATCCATCCTTCTGACCACGATGAGATGACCGCTGTCCTCACG NM_005069 RefSeq chr21
+ 36699132 36749917 SIM2 6493 "single-minded family bHLH transcription factor 2, transcript variant
SIM2"
GO:0009880|GO:0007165|GO:0003700|GO:0046982|GO:0030324|GO:0005654|GO:0004871|GO:0000122|GO:0003

677|GO:0030154|GO:0006351|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91120_PI430048170 0.0335548293423635 0.7562637891432299.34109008360833
9.32705938635078 9.49517684746876 P P P 9.91976123908638 9.59997614462067
9.83994300614014 P P P LNCV6_91120_PI430048170 mRNA
AACCGCTGGAGAAACAAAATTGCTATTTACCAGGAATAATCACAATAGAAGGTCTTATTG NM_012460RefSeq chr14
- 58408651 58427614 TIMM9 26520 "translocase of inner mitochondrial membrane 9 homolog (yeast),
transcript variant 1"
GO:0005515|GO:0005215|GO:0007605|GO:0006626|GO:0005743|GO:0051087|GO:0042719|GO:0042803|GO:0005
739|GO:0005758|GO:0045039|GO:0008270|GO:0072321|GO:0044267 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143156_PI430048170 0.2388660785939161.04228036739576 0.363236503982178
0.36785486518205 0.47357012314702 A A A 0.3379858487102380.317676600692952
0.371968241840972A A A LNCV6_143156_PI430048170 mRNA
CACACACACAATGCTATGCTATGTTTAATAGCATTTCCCTGATTACCAATATTAGGCATT NM_001077637 RefSeq
chr2 - 131360491 131364158 WTH3DI NA RAB6C-like NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130177_PI430048170 0.0136251744892742.31299667426718 4.31198027778358
4.61436090526254 4.97701983328397 P P P 3.83379145906399 3.29287996201149
3.12660952197491 P P P LNCV6_130177_PI430048170 mRNA
CACCCCTTCTCTACAATTTTGTGAACATTTATGCTCCAGTGGCATTCACTGGTTGTTCATNM_001143962 RefSeq chr1
- 223541608 223665734 CAPN8 388743 calpain 8
GO:0005737|GO:0005794|GO:0004198|GO:0007586|GO:0005509|GO:0006508 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143660_PI430048170 0.0176274422128286 0.4630300787928723.14487377794471
3.54027363007317 3.81856683977763 P P P 4.66788682814981 4.48521040668217 4.7486391436878
P P P LNCV6_143660_PI430048170 mRNA
AAAGCACATTCTATCAGGCAGCCAGGCTTGGAAATTAGGTCCATTTAAAGTATGTGGCTT NM_018981RefSeq chr2
+ 182716040 182780023 DNAJC10 54431 "DnaJ (Hsp40) homolog, subfamily C, member 10, transcript
variant 1"
GO:0005515|GO:0034976|GO:0034975|GO:0005783|GO:0051087|GO:0015035|GO:0015036|GO:0032781|GO:0030
433|GO:0051787|GO:0016020|GO:0070059|GO:0034663|GO:0016671|GO:0051117|GO:0001933|GO:0005788|GO:0
030544|GO:0045454|GO:0001671|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129605_PI430048170 0.9764807660160511.11844150809899 0.457908990747195
0.7481647916939992.34056112968141 A A A 1.15942402525195 1.87250919755778
0.44691504253459 A A A LNCV6_129605_PI430048170 mRNA
TGTATGTGTGCTGTGTTTTGATGCTGCTGATTCCTTTCTCTGTAGTCCTTGCTTCCTATG NM_030904RefSeq
chr1_KI270892v1_alt + 56200 57310 OR2T1 NA "olfactory receptor, family 2, subfamily T, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127271_PI430048170 0.1044990204481161.40063768089405 4.52060129085298
5.01611377017202 4.43898054086947 P P P 4.33891188679781 4.20476583788631
4.02679946928427 P P P LNCV6_127271_PI430048170 mRNA
ATTTATGGACATACCCAAGAGATATGTATTGCCTGCTGTGTGCTAGAGAGTGAGTGCGCT NM_173467RefSeq chr22
- 43132205 43143397 MCAT 27349 "malonyl CoA:ACP acyltransferase (mitochondrial), transcript
variant 1" GO:0005739|GO:0008152|GO:0006633|GO:0004314|GO:0016740 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_79331_PI430048170 0.0685384753801057 2.08489827671209 5.68332651746163
6.31961477324377 5.56952121867798 P P P 5.15430033329761 5.06348208980489
4.06028363302755 P P P LNCV6_79331_PI430048170 mRNA
ATGACATTGAGAGCAAAGGGCTGCAGCCCACTCCCATGACTTTGGTGTTCGGCTGCCGAT NM_000603RefSeq chr7

+ 150991055 151014599 NOS3 4846 "nitric oxide synthase 3 (endothelial cell), transcript variant 1"
GO:0005515|GO:0005516|GO:0009408|GO:0010181|GO:0034405|GO:0043267|GO:0006809|GO:0050880|GO:0051
926|GO:0005856|GO:0031663|GO:0003100|GO:0051701|GO:0005506|GO:0051346|GO:0014806|GO:0001542|GO:0
001701|GO:0004517|GO:0003958|GO:0043542|GO:0002028|GO:0031284|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139530_PI430048170 0.2572063747474181.02229544206913 0.304301504830521
0.2535084490776840.321232894651182A A A 0.2688077052475640.247880647872952
0.267680000440792A A A LNCV6_139530_PI430048170 mRNA
CAACAGATGAAAATAAGTGCTTTGGGCGAACTGTATTCCTTTTAACAGATCCAAACTATT NM_001205315 RefSeq
chr7 - 88276428 88306913 STEAP4 79689 "STEAP family member 4, transcript variant 2"
GO:0052851|GO:0005886|GO:0000139|GO:0015677|GO:0045444|GO:0016021|GO:0008823|GO:0055072|GO:0046
872|GO:0070062|GO:0055114|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133844_PI430048170 0.0143319018215664 0.5662465942974969.98640780637534
9.66547899511553 9.52731907639435 P P P 10.26773764078 10.7437157921434
10.6268785040366 P P P LNCV6_133844_PI430048170 mRNA
TCCTGCTGTCCCTCGGCTGAGAATAAAACCCATTTCTGGATGATGGGGAATGTCAAAAAA NM_001288738 RefSeq
chr9 + 128203354 128255248 DNM1 1759 "dynamin 1, transcript variant 4"
GO:0072583|GO:0050998|GO:0005515|GO:0048013|GO:0005886|GO:0019901|GO:0005874|GO:0003924|GO:0005
525|GO:0008022|GO:0032403|GO:0006898|GO:0030117|GO:0042802|GO:0006897|GO:0031623|GO:0007411|GO:0
007032|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95614_PI430048170 0.37093791182461 0.9109374419333976.48001207343141 6.57458161993006
6.65866602672445 P P P 6.57124908476403 6.60947692587375 6.91641507778519 P P P
LNCV6_95614_PI430048170 mRNA
TTAATTCCCTTTCCTTAGAATGACCATGGTTGACACAGAGATGCCATTCTGGCCCACCAA NM_138711 RefSeq chr3
+ 12288936 12434356 PPARG 5468 "peroxisome proliferator-activated receptor gamma, transcript
variant 3"
GO:0005515|GO:0010467|GO:0043627|GO:0030308|GO:0006367|GO:0003700|GO:0044212|GO:0033189|GO:0009
409|GO:0003707|GO:0007507|GO:0042953|GO:0042594|GO:0004879|GO:0019395|GO:0032869|GO:0010745|GO:0
019903|GO:0030331|GO:0000122|GO:0001890|GO:0002674|GO:0045165|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93247_PI430048170 0.00301211268682188 0.5400720067140476.85519811928031
6.99598411815708 7.10302145357775 P P P 7.69978122267103 7.85971139830177
8.05030605621464 P P P LNCV6_93247_PI430048170 mRNA
TGCCTTAACACTGAAAAACATACCCTGCATTTTGAAAATGTTTATGGATGTCTCAGCAGT NM_020466 RefSeq chr6
- 89632223 89638755 LYRM2 57226 "LYR motif containing 2, transcript variant 1" GO:0005739 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133957_PI430048170 0.0138604410397519 1.77999896960033 7.56129329200616
7.81729334825422 8.00233975727238 P P P 7.07029271561366 6.90980453976894 6.9336056445681
P P P LNCV6_133957_PI430048170 mRNA
AGTCAGAAACAAACTTATAGTGATGCGTTGGAAGGTTAATCGAAACCATCCTTACCCCTA NM_016303 RefSeq chrX
+ 103356451 103358469 WBP5 51186 "WW domain binding protein 5, transcript variant 1" GO:0050699
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135266_PI430048170 0.00367097811840239 0.3207141757218857.95690386299869
8.01708621644501 8.35798980492574 P P P 9.4138065977859 9.71599955816243
10.0799868174536 P P P LNCV6_135266_PI430048170 mRNA
CAGGCAGTTGGGTATTGATATGTTATTTGGTGCTCTCATTCATGGCAAAGGATTTGATAA NM_152407 RefSeq chr5
+ 149345413 149354583 GRPEL2 134266 "GrpE-like 2, mitochondrial (E. coli)"
GO:0005739|GO:0050790|GO:0006457|GO:0005759|GO:0006626|GO:0051087|GO:0005743|GO:0051082|GO:0044
267|GO:0042803|GO:0000774 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_145283_PI430048170 0.886199044700512 1.00305717685266 0.334750669908637 0.336194709388446 0.403172812246907 A A A 0.36778200744741 0.322638053142494 0.371045813161005 A A A LNCV6_145283_PI430048170 mRNA AGAGACACTTTGGATAGCTAAGTATCCCAAAGGATTTTACCCTTTTAAACAAAACCAAAG NM_031303 RefSeq chr18 + 46946823 47102243 KATNAL2 83473 katanin p60 subunit A-like 2 GO:0008568|GO:0008017|GO:0051013|GO:0005737|GO:0008152|GO:0005874|GO:0031122|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140675_PI430048170 0.33858668319291 0.655335074807577 0.248078760700523 0.275575985098737 0.302365984694115 A A A 0.442621357490126 1.5579496672423 0.307617122167688 A A A LNCV6_140675_PI430048170 mRNA CTTTGAATGCCTACTGTAGGCCTCCTAAGTCTAATATTTAAGATCACTGTTTATTGTCTT NM_001142353 RefSeq chr10 - 73436427 73496024 PPP3CB 5532 "protein phosphatase 3, catalytic subunit, beta isozyme, transcript variant 1" GO:0005515|GO:0005516|GO:0030346|GO:0030018|GO:0005886|GO:0048675|GO:0005829|GO:0007507|GO:0006470|GO:0042098|GO:0048167|GO:0045944|GO:0008144|GO:0017156|GO:0046983|GO:0007613|GO:0004722|GO:0007612|GO:0043029|GO:0034097|GO:0005955|GO:0033192|GO:0035774|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137182_PI430048170 0.012381760643012 3.98977429141637 2.69201457383704 3.19057203697197 2.32153832221932 A P A 1.39932542886323 0.246437153686119 0.418750901942259 A A A LNCV6_137182_PI430048170 mRNA AAAGATTACCGCTCATGCTAAAAGTATGTAAAGATCCCATGTACAGTATGATAGTGTACT NM_004763 RefSeq chr2 - 9405685 9423514 ITGB1BP1 9270 "integrin beta 1 binding protein 1, transcript variant 1" GO:0005515|GO:0015031|GO:0032403|GO:0030154|GO:0050880|GO:0010764|GO:0007219|GO:0006933|GO:1900025|GO:0090051|GO:0070373|GO:0051781|GO:0005856|GO:0070062|GO:0045747|GO:0019901|GO:0090314|GO:0090315|GO:0030027|GO:0043088|GO:0010595|GO:0005178|GO:0007229|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135535_PI430048170 0.423952892951822 1.81997050304264 0.285943840537107 0.292973683600125 2.0834766892585 A A A 0.3089024686414 0.273935637474322 0.291574454350531 A A A LNCV6_135535_PI430048170 mRNA AGATGCAAAAAAGGTCCATCTTCTTTGTGAGCCTCTTAATAAATTTGAGCATGCTGGCAT NM_031964 RefSeq chr17_GL383564v2_alt + 124565 125344 KRTAP17-1 83902 keratin associated protein 17-1 GO:0005882 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103661_PI430048170 0.577695608241822 1.09219868484109 0.360700632045961 0.846524472893285 0.349425766090733 A A A 0.48302428628886 0.368200749468038 0.378641275020576 A A A LNCV6_103661_PI430048170 mRNA TTTGTGGCACTGTCTTTGATGCAGTGATGTACTTAATGGTGCAATAAAGCTGCTTCGATT NM_015490 RefSeq chr10 - 100486645 100519838 SEC31B 25956 SEC31 homolog B (S. cerevisiae) GO:0012507|GO:0030120|GO:0005789|GO:0016192|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139316_PI430048170 0.0683721040620883 0.779808366626282 8.509266838151 8.11948613202785 8.33738314259377 P P P 8.75297131969224 8.60644315350529 8.70556494483124 P P P LNCV6_139316_PI430048170 mRNA TCTACTGTGGTGTTGGAGCAGGACAATAAAGTCCACTAGAAATGCACCCCAGAACCAAAA NM_080491 RefSeq chr11 - 78215289 78417822 GAB2 9846 "GRB2-associated binding protein 2, transcript variant 1" GO:0005515|GO:0008284|GO:0005886|GO:0048015|GO:0043325|GO:0005547|GO:0030316|GO:0005829|GO:0043306|GO:0005737|GO:0016477|GO:0007229|GO:0045087|GO:0005068|GO:0007169|GO:0038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118299_PI430048170 0.00522086826560545 0.780181183072569 4.25016802460005 4.21276671674105 4.36587318933715 P P P 4.70152595441629 4.65411613506278

4.54770039523679 P P P LNCV6_118299_PI430048170 mRNA
TCACCACCAACAATCGAGTGAAGAGGAGACCTTCCCCCTATGAGATGGAGATTACTGATG NM_003189 RefSeq
chr1 - 47216289 47232335 TAL1 6886 "T-cell acute lymphocytic leukemia 1, transcript variant 1"
GO:0005515|GO:0000790|GO:0003700|GO:0044212|GO:0042826|GO:0006366|GO:0000981|GO:0045799|GO:0005
634|GO:0043249|GO:0031334|GO:0060375|GO:0045944|GO:0042127|GO:0001085|GO:0051781|GO:0007626|GO:0
035162|GO:0030221|GO:0030220|GO:0033193|GO:0030097|GO:0005667|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_6822_PI430048170 0.0906503249176123 0.307579374687187 2.52582291473536
0.407992598359327 2.18845905747962 A A A 3.43467835138444 3.49690076288743
3.97771220924275 P P P LNCV6_6822_PI430048170 mRNA
GCCTTTTATTATTGGCTGCTAGATCCTGGTGTTTCTATGTTCTTTTTTAAGCACCAAAAA NM_001283043 RefSeq
chr14 - 35538351 35809226 RALGAPA1 253959 "Ral GTPase activating protein, alpha subunit 1
(catalytic), transcript variant 3" GO:0032859|GO:0006355|GO:0005737|GO:0017123|GO:0046982|GO:0005634
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130395_PI430048170 0.90060207873162 0.820558376036787 1.70820835565581
0.480788671912299 0.506060080886823 A A A 0.329322162540461 2.27562224760707
0.395091689699345 A A A LNCV6_130395_PI430048170 mRNA
CCACCTGCCAATTCTACATGTATTGTTGTGGTTTTATTCATTGTATGAAAATTCCTGTGA NM_013261 RefSeq chr4
- 23792020 23890077 PPARGC1A 10891 "peroxisome proliferator-activated receptor gamma,
coactivator 1 alpha"
GO:0005515|GO:0006367|GO:0001659|GO:0009409|GO:0006094|GO:2000310|GO:0050681|GO:0071398|GO:0043
524|GO:0042594|GO:0000166|GO:0071356|GO:0005665|GO:0071250|GO:0045820|GO:0031625|GO:0016922|GO:0
019395|GO:0006996|GO:0001104|GO:0014850|GO:0003713|GO:0046321|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_102122_PI430048170 0.523456436691015 1.0655129663838 5.7010308245548
5.44661046288623 5.56058402599635 P P P 5.4799352208214 5.66792149529649
5.26960004863171 P P P LNCV6_102122_PI430048170 mRNA
TCAGATCTCCAAGCGCAAGTGTGAGGCGGCCAATGTGGCTGAACAAAGGAGAGCCTACCT NM_002127 RefSeq
chr6_GL000256v2_alt + 1133009 1137167 HLA-G 3135 "major histocompatibility complex, class I, G"
GO:0002474|GO:0005886|GO:0019221|GO:0032735|GO:0042803|GO:0042130|GO:0060337|GO:0042605|GO:0030
670|GO:0071556|GO:2001199|GO:0060333|GO:0012507|GO:0002480|GO:0042612|GO:0005102|GO:0042590|GO:0
002666|GO:0006968|GO:0002767|GO:0016020|GO:0000139|GO:0001916|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138782_PI430048170 0.040983460262855 0.95938629184316 0.41079207986184
0.395088032746292 0.358237954439558 A A A 0.435162554066822 0.464460559722617
0.444291062049661 A A A LNCV6_138782_PI430048170 mRNA
ACCCATGAAAACCCTAGACTTGTGACCTGAAATAAAGAAAATACGTTAGAAGAGCACTGT NM_033214 RefSeq
chr4 - 79406352 79408218 GK2 2712 glycerol kinase 2
GO:0016310|GO:0019563|GO:0004370|GO:0005741|GO:0006072|GO:0005524|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142365_PI430048170 0.000675531648514276 1.36223395040597 11.0027358011316
11.0661287787944 11.0370970997471 P P P 10.557026774236 10.6495325328492
10.5602527353437 P P P LNCV6_142365_PI430048170 mRNA
AGGCTCCCACCAGGACGGTTCTCATTATTTATATGTTAATATGTTTGTAAACTCATGTAC NM_138462 RefSeq chr9
- 137582078 137590485 ZMYND19 116225 "zinc finger, MYND-type containing 19"
GO:0005737|GO:0005886|GO:0045202|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130520_PI430048170 0.467293128650107 1.74036728191479 2.12812911405288
0.386913283159968 0.280703810208295 A A A 0.503605869885865 0.401715103667264

0.28963975213097 A A A LNCV6_130520_PI430048170 mRNA
GTTGATCGATGTTAAACGTCACAGCAGTACTTGCTCAATAAAGGTCATATTGGAAACATA NM_005382 RefSeq
chr8 + 24913760 24919093 NEFM 4741 "neurofilament, medium polypeptide, transcript variant 1"
GO:0008017|GO:0005515|GO:0030424|GO:0031594|GO:0005883|GO:0031133|GO:0005200|GO:0033693|GO:0000
226|GO:0008088 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109283_PI430048170 0.128934385834721 0.637927901495833 3.61956057897533
3.50646520531363 3.1783572025957 P P P 4.56367524754826 3.84107207543411
3.73265686944162 P P P LNCV6_109283_PI430048170 mRNA
AGTGAAGGCTGATGGGTACGTGGACAACCTCGCAGAGGCAGTGGACCTGCTGCTGCAGCA NM_022126 RefSeq
chr10 + 124461771 124614141 LHPP 64077 "phospholysine phosphohistidine inorganic
pyrophosphate phosphatase, transcript variant 1"
GO:0008969|GO:0005737|GO:0006470|GO:0000287|GO:0004427|GO:0005654|GO:0005634|GO:0006796|GO:0042
803|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136287_PI430048170 0.500353600306912 1.01658543950434 0.347868979776789
0.347155965195638 0.427810316669543 A A A 0.357895658215063 0.321548327573029
0.373208863638125 A A A LNCV6_136287_PI430048170 mRNA
CAGGATAGAAAGACATCACTACCATCTCTATGGTCAGTGATATTATGGACTAATGAATAA NM_001278515 RefSeq
chr18 - 70630518 70650857 GTSCR1 NA "Gilles de la Tourette syndrome chromosome region,
candidate 1 (non-protein coding)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_6076_PI430048170 0.189473679402701 1.15529525430872 8.72000438780274
9.01251136270463 8.93556017702203 P P P 8.75759113365016 8.48244254869204
8.7988989030544 P P P LNCV6_6076_PI430048170 mRNA
GTTTAGAACATTCTTGCTCATGCCTGTATTTGCACAAATAAATGAAACTTCGCTGTCCTT NM_001256915 RefSeq
chr9 + 83623048 83644130 IDNK 414328 "idnK, gluconokinase homolog (E. coli), transcript variant
3" GO:0016310|GO:0008150|GO:0003674|GO:0046316|GO:0005524|GO:0046177 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_139527_PI430048170 0.337732584641328 0.857316135644214 5.36500021665583
5.26899922376639 5.65080858974269 P P P 5.33730118816696 5.72967113221011
5.86190897688389 P P P LNCV6_139527_PI430048170 mRNA
GCTTATGGACATGCGCAATAGTTGATTCAGCTTCAATCAATAAGAACATAAATATGGCAA NM_174899 RefSeq
chr2 + 229922490 230013109 FBXO36 130888 F-box protein 36 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_128796_PI430048170 0.0048543748644837 0.639947989157087 6.5055891990241
6.3123326300378 6.54604847371753 P P P 7.06763674515638 7.25671269833686
6.96706540594656 P P P LNCV6_128796_PI430048170 mRNA
GGGCAGAAGAAAGAAATAAACCTCATCCTATATTTTACAAAGCATGTGAATTCTGGCATT NM_014762 RefSeq
chr1 - 54849626 54887248 DHCR24 1718 24-dehydrocholesterol reductase
GO:0006695|GO:0008285|GO:0008762|GO:0005783|GO:0050660|GO:0007265|GO:0005634|GO:0044281|GO:0016
628|GO:0005829|GO:0030539|GO:0008104|GO:0050614|GO:0042605|GO:0009888|GO:0061024|GO:0007050|GO:0
009725|GO:0043154|GO:0005856|GO:0006979|GO:0042987|GO:0043066|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134648_PI430048170 0.00990290290010459 0.53025336981883 11.2175910218006
11.5882326418461 11.2203483972068 P P P 12.1758575380363 12.322612038818
12.3014621849323 P P P LNCV6_134648_PI430048170 mRNA
GTCGAGATCGCCTAGTATGTTCTGTGAACACAAATAAAATTGATTTACTGTCTGCAAAAA NM_003897 RefSeq
chr6_GL000256v2_alt - 2043994 2045346 IER3 8870 immediate early response 3
GO:0005515|GO:0007095|GO:0043066|GO:0045732|GO:0008630|GO:2001020|GO:0006915|GO:0005634|GO:0009
653|GO:0006282|GO:0050728|GO:0001562|GO:2000377|GO:0016021|GO:0045820|GO:0046822|GO:0003085 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_140474_PI430048170 0.972024507072333 1.03022876960832 0.415600220922916 1.33356398892521 0.374988258220085 A A A 0.509429655554018 0.389821922298379 1.18019306404599 A A A LNCV6_140474_PI430048170 mRNA GGTCAGGAAGAGTGGGAGAAAGAAATTCCTCTTTACGTAGATACTTTTTAGCTTTATTTT NM_004407 RefSeq chr4 + 87650301 87664360 DMP1 1758 "dentin matrix acidic phosphoprotein 1, transcript variant 1" GO:0005509|GO:0010811|GO:0050840|GO:0005578|GO:0005730|GO:0005576|GO:0005634|GO:0031214|GO:0043231|GO:0005737|GO:0005178|GO:0001503|GO:0030198|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130009_PI430048170 0.277060649671184 0.885952350435861 0.259602523846963 0.273502163892897 0.364829946717924 A A A 0.393386910590852 0.687889029384269 0.315791514280216 A A A LNCV6_130009_PI430048170 mRNA GGGTTCCTTCTGGAGATGTTTTTATATTTCTTGGGTTCTCTATGCAGGATAATAAAAACT NM_001099439 RefSeq chr1 - 37715973 37765152 EPHA10 284656 "EPH receptor A10, transcript variant 3" GO:0005515|GO:0008150|GO:0005005|GO:0005003|GO:0048013|GO:0005886|GO:0007411|GO:0005887|GO:0018108|GO:0016021|GO:0005524|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128856_PI430048170 0.0155821859971736 0.741895314814629 15.8436360375576 15.6176473891854 15.678121251824 P P P 16.1738169686766 16.1649968239564 16.1012331354628 P P P LNCV6_128856_PI430048170 mRNA TTCATTTGTTCAATGATTAAAGTCCTACGTGGTCTGAGTTCAGACCGGAGCAAGCCAGGT NM_001190487 RefSeq chr7 + 142666298 142667693 MTRNR2L6 100463482 MT-RNR2-like 6 GO:0005737|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131672_PI430048170 0.164555134140241 0.637393794141893 4.37141133311238 3.60379141842541 3.4852742626906 P P P 4.98535856742586 4.35720231395533 4.08274047830941 P P P LNCV6_131672_PI430048170 mRNA TGTTGTGACTCCCATGTTGAACCCCATTATCTACAGCTTGAGAAATAGCGAGGTGAAGAA NM_178168 RefSeq chr11 + 6845682 6846636 OR10A5 144124 "olfactory receptor, family 10, subfamily A, member 5" GO:0050911|GO:0007608|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145425_PI430048170 0.666292803245271 0.94315773002894 0.399426152518578 0.338648477471127 0.308433204256132 A A A 0.254430455762932 0.305637500561541 0.699042216760842 A A A LNCV6_145425_PI430048170 mRNA ACACCATGGTACCTCCATGCTCCTTTAGTGCACTGTGGAAGCTCAATAAATACTCCAATC NM_001080399 RefSeq chr8 - 132024219 132059380 OC90 NA otoconin 90 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133277_PI430048170 0.00850990833541997 0.622956354183888 4.99397689146492 4.95174187484634 5.2802431389956 P P P 5.69647866529064 5.63203729794492 5.94869027343799 P P P LNCV6_133277_PI430048170 mRNA GCTGAAGGCCAAGCTAAAATGTATCCCTCTTTTTCTGGTACATGCAGCAAAAGTAATATG NM_013238 RefSeq chr13 + 43023225 43109170 DNAJC15 29103 "DnaJ (Hsp40) homolog, subfamily C, member 15" GO:0031333|GO:0005743|GO:0016021|GO:0015031|GO:0019216|GO:0009267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107015_PI430048170 0.974958124144723 0.996931623274999 3.77303596651668 4.1225562163577 3.85383916381307 P P P 3.90371782899365 4.10789204140345 3.75260106794017 P P P LNCV6_107015_PI430048170 mRNA TTAATTTTAAAGTGAAAGAGGAGCCTAAGGAAGGGGAGTCCCTAAGCACGACTTTGCCTC NM_178835 RefSeq chr4 - 145757626 145938960 ZNF827 152485 zinc finger protein 827 GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA

NA NA NA NA
LNCV6_133422_PI430048170 0.756988094197811 1.06586532678552 0.259715638993495
0.945854373456338 0.674316615918104 A A A 0.364841150072866 0.925055536679012
0.311826997666276 A A A LNCV6_133422_PI430048170 mRNA
TCTTACACAAGAATTCTCATTACTGTTTATAGGATGAGCGAGGCAGAGGGGAGGGGAAAG NM_001001824 RefSeq
chr1 - 248649930 248650884 OR2T27 NA "olfactory receptor, family 2, subfamily T, member 27" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142837_PI430048170 0.0124082644599708 2.52571356631045 8.25440129795195
8.57532922456359 8.89414702699754 P P P 7.38118313379149 7.198673398934
7.19667687180331 P P P LNCV6_142837_PI430048170 mRNA
AACAAGTTTGTGATGATGCATTGGAAGCAAAGACATTCACGCAGCCGTCCTTATCCTGTG NM_153333 RefSeq
chrX - 103252994 103255193 TCEAL8 90843 "transcription elongation factor A (SII)-like 8, transcript
variant 1" GO:0006355|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111412_PI430048170 0.365549081031627 1.03452422162409 0.455705181552735
0.3227174947296820.382946082289749 A A A 0.2919393423676930.339970049115836
0.384160906618083 A A A LNCV6_111412_PI430048170 mRNA
AAGATGCATCCATTAGTCTAGAGCCAGATTTGGACAATAGTGGTTCTAATACAGTGTCCA NM_153610 RefSeq chr5
+ 79689835 79800226 CMYA5 202333 cardiomyopathy associated 5
GO:0005515|GO:0048471|GO:0032513|GO:0043034|GO:0014733|GO:0070885|GO:0031430|GO:0042802 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141444_PI430048170 0.2219623788417290.3978608312297180.870651027090514
0.4040315030576520.337414455330306 A A A 2.22398355756603 0.362755827771355
2.36165528774072 A A A LNCV6_141444_PI430048170 mRNA
GTTTTAAGAGGAAATGAGAAGGCCAGCAGAAGTAGATTAAAACTAGAGAGCTGGTTTATT NM_020116 RefSeq chr4
- 161383891 162164034 FSTL5 56884 "follistatin-like 5, transcript variant 1" GO:0005509|GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132756_PI430048170 0.00619373674653555 0.5327146442439617.47479267085249
7.27908370191899 7.60384662658833 P P P 8.21726634685779 8.23680518438991
8.61240361541463 P P P LNCV6_132756_PI430048170 mRNA
GTGACTATTCCTTAGCCTTATAGATTTCTAGTACTGCCCAGGAAATCTAATTTCAATACA NM_005788 RefSeq chr11
+ 20387529 20509333 PRMT3 10196 "protein arginine methyltransferase 3, transcript variant 1"
GO:0005515|GO:0019919|GO:0006355|GO:0008168|GO:0016274|GO:0034969|GO:0008469|GO:0046872|GO:0005
829|GO:0035242|GO:0072341|GO:0005737|GO:0005840|GO:0031397 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_126808_PI430048170 0.0168722801420972 1.49191423604939 6.26959914480796
6.61100952163193 6.31621231089768 P P P 5.8931705344742 5.88012142864349 5.7090896499665
P P P LNCV6_126808_PI430048170 mRNA
ACAAGAAAGGGAAAGTGTACTGGTACAAGGACCAGGAGCCCCTGGAGTTCTCCTACCCCG NM_006983 RefSeq
chr1 + 1632180 1634654 MMP23B 8510 matrix metallopeptidase 23B
GO:0005622|GO:0006508|GO:0005789|GO:0005578|GO:0008270|GO:0016021|GO:0004222|GO:0008237 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68969_PI430048170 0.6712146074414540.9622466352307485.37126436943874 5.24285792087132
5.60635847318664 P P P 5.50316239622841 5.32465269502233 5.57188109641294 P P P
LNCV6_68969_PI430048170 mRNA
ATCTGGATGGGCCTAATTTTTGGTGGGGAAATTTCAGACTGAATTGGGCAGTTGACCGAA NM_152490 RefSeq chr1
- 235447189 235504481 B3GALNT2 148789 "beta-1,3-N-acetylgalactosaminyltransferase 2, transcript
variant 1"
GO:0008375|GO:0006493|GO:0000139|GO:0005783|GO:0006486|GO:0016021|GO:0008378|GO:0008376 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_105818_PI430048170 0.7901789648296410.9304108237122660.734564539672202
0.4019864548963391.53172804001417 A A A 1.28007588252068 0.422253097787419
1.34910177861397 A A A LNCV6_105818_PI430048170 mRNA
TGTCTTCTCAGTGGAGTTGCAGCTGCCTCCCAAGGCTGCAGCCCTGGCTCACTTGGACAG NM_003734RefSeq chr17
+ 42851183 42858131 AOC3 8639 "amine oxidase, copper containing 3, transcript variant 1"
GO:0005515|GO:0048038|GO:0005261|GO:0046982|GO:0005886|GO:0009986|GO:0005507|GO:0005509|GO:0052
596|GO:0052595|GO:0052594|GO:0052593|GO:0042803|GO:0005902|GO:0005737|GO:0008131|GO:0006954|GO:0
009308|GO:0016021|GO:0007155|GO:0046677|GO:0006812|GO:0055114 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129989_PI430048170 0.0611509211437511 1.19996645996592 12.2771239590614
12.3826021428325 12.518044528636 P P P 12.1314916866492 12.1545680413324 12.112560432226
P P P LNCV6_129989_PI430048170 mRNA
ATCCGGTTTTCATTTTCCGGTCCTTTTGCCATACACAGTTACAGAGATCAGTCAAATCCA NM_021959RefSeq
chr6_GL000256v2_alt + 1366073 1369250 PPP1R11 6992 "protein phosphatase 1, regulatory
(inhibitor) subunit 11" GO:0005515|GO:0005737|GO:0004864|GO:0043086 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127670_PI430048170 0.0446126495553726 1.3170168828632 12.1696054107648
12.1540330609583 12.0532153296949 P P P 11.5972886779614 11.9223688990676
11.6464089278944 P P P LNCV6_127670_PI430048170 mRNA
GAGAGATGGAGGACTGATCCTGGAACGTGAAGCAGCTTTCAATAAACCAGCTCCTGGGGA NM_001144026
RefSeq chr9 + 137205666 137219361 NDOR1 27158 "NADPH dependent diflavin oxidoreductase 1,
transcript variant 1"
GO:0050661|GO:0005515|GO:0036245|GO:0008219|GO:0048471|GO:0005506|GO:0016226|GO:0010181|GO:0050
660|GO:0005634|GO:0044281|GO:0005829|GO:0005737|GO:0003958|GO:0016709|GO:0016491|GO:0045111|GO:0
055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122840_PI430048170 0.1466420480328891.35930255266939 3.72375604027472
3.79158540931506 3.68802570920857 P P P 3.12247984968402 2.99404300338105
3.66822126279021 P P P LNCV6_122840_PI430048170 mRNA
AGAAAAGCATTATTACATTGGAATTATTGAAACGACTTGGGATTATGCCTCTGACCATGG NM_000096RefSeq chr3
- 149172500 149222045 CP 1356 "ceruloplasmin (ferroxidase), transcript variant 1"
GO:0006879|GO:0004322|GO:0005507|GO:0051087|GO:0072562|GO:0005576|GO:0005765|GO:0055085|GO:0005
615|GO:0006825|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141966_PI430048170 0.5743445418514680.9667648629403320.487437641275759
0.4711354235588710.254575560777949A A A 0.39993340115843 0.510321760629338
0.458576065436433A A A LNCV6_141966_PI430048170 mRNA
GTGAAGAATGCATTCATGAAGGTTGTTGAGAAGGCAAAATATTCTCTAGATTCAGTCTTT NM_001005489 RefSeq
chr11 - 58358124 58359069 OR5B17NA "olfactory receptor, family 5, subfamily B, member 17" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141114_PI430048170 0.3110188133420341.36392773270569 0.306670517735742
1.24381437887259 0.475883160892807A A A 0.2976974500808740.263395274906365
0.302599987173262A A A LNCV6_141114_PI430048170 mRNA
CTGGAAGGATGAAAAGGATGAAAGGATGTCACAAAAAGTAGCTTTTCTGCTCGATGAAAA NM_001047980 RefSeq
chr1 - 119834764 119844880 NBPF7 NA "neuroblastoma breakpoint family, member 7" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_127306_PI430048170 0.5381115784044980.6986032812374740.529740836216271
0.4940506447468430.554575754812145A A A 0.3603378666943741.82448485217598
0.442949686710716A A A LNCV6_127306_PI430048170 mRNA
ATGGTCCCCTACAATGTTATACCAAGGCTCTGATGTATTTCTTTTAGTAGTTTCTAAGTG NM_020871RefSeq chrX
- 115110619 115234072 LRCH2 57631 "leucine-rich repeats and calponin homology (CH) domain

containing 2, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144505_PI430048170 0.6297840501503220.9824131243513780.354670081157502
0.4466166380326250.346215363912732A A A 0.4807087213558020.366620818300592
0.376336694067844A A A LNCV6_144505_PI430048170 mRNA
ACGCCTTCAAGGGAACTTCAAGGGAAACATGGAATAAACTAAGTCTCAATTGCCAAAAAA NM_002108RefSeq chr12
- 95972661 95996365 HAL 3034 "histidine ammonia-lyase, transcript variant 1"
GO:0034641|GO:0019557|GO:0009058|GO:0019556|GO:0006548|GO:0004397|GO:0044281|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136792_PI430048170 0.00197731620853581 2.32779153374543 3.58820397856447
3.19110586708764 3.34286191124635 P P P 1.91157341343917 2.24021672147849
2.31093288055406 A A A LNCV6_136792_PI430048170 mRNA
GTCTACATTTGATTGTACGTAGAATGTTTAAAAGTCAGTTATAAGCCATCTCATCCCATC NM_032146RefSeq chr3
+ 97764520 97798535 ARL6 84100 "ADP-ribosylation factor-like 6, transcript variant 1"
GO:0005515|GO:0060170|GO:0051258|GO:0007368|GO:0005886|GO:0007264|GO:0030117|GO:0032402|GO:0046
872|GO:0005829|GO:0005737|GO:0005543|GO:0006612|GO:0005879|GO:0045444|GO:0016055|GO:0070062|GO:0
034464|GO:0006996|GO:0005930|GO:0046909|GO:0010842|GO:0072372|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141059_PI430048170 0.0849563623994618 0.82091296714554910.1466088949978
10.2417823378257 10.0055587048486 P P P 10.3283826566221 10.6067310701241
10.3025420935788 P P P LNCV6_141059_PI430048170 mRNA
GGATCTAGGCTTGAGCTTGGTTGGGTTTGCTTTTTTCTTCTTCTTCTTTATAAACAATTC NM_001080825 RefSeq chr12
+ 121712751 121782068 TMEM120B 144404 transmembrane protein 120B
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98142_PI430048170 0.00145710470840432 0.6288344394832133.29865061823812
3.50037557508411 3.33337764689749 P P P 3.98990209537278 4.13515819532232
4.01912217018794 P P P LNCV6_98142_PI430048170 mRNA
AAAGAACCTGAAATTAACACAACTCTTCAGATGCGTTTCTTTGGAAAAAGAGGACAAAGA NM_152726RefSeq chr13
- 21492688 21604216 MICU2 221154 mitochondrial calcium uptake 2
GO:0005739|GO:0005515|GO:0005758|GO:0051562|GO:0046982|GO:0006851|GO:0051561|GO:0005509|GO:0034
704 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145637_PI430048170 0.0135726520317867 0.6421745220589849.37895863917506
9.27533357616776 8.99213795408257 P P P 10.0045544108653 9.88025813619668
9.68828455451811 P P P LNCV6_145637_PI430048170 mRNA
CTCAGGCTGGCTGTTGAGACATGCTACAATTTTCATTTTTGTAAAAATAAAGCTTGATTG NM_022039RefSeq chr10
- 101610663 101694986 FBXW4 6468 F-box and WD repeat domain containing 4
GO:0006511|GO:0003674|GO:0051216|GO:0000151|GO:0002053|GO:0030326|GO:0016055|GO:0042733 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134019_PI430048170 0.3168497637437021.37508521231143 5.83047379789229
6.88330977494771 6.46777393618554 P P P 6.25675945774685 5.66277279876988
6.01068358875033 P P P LNCV6_134019_PI430048170 mRNA
TTTTTCGGACATGCTTTTCTGCCACTCCATATTAAAACATATGACCATTGAGTCCCTGCT NM_004428RefSeq chr1
+ 155127872 155134910 EFNA1 1942 "ephrin-A1, transcript variant 1"
GO:0005515|GO:0033628|GO:0005886|GO:0003180|GO:0050730|GO:0003183|GO:0007267|GO:0050731|GO:0010
719|GO:0014028|GO:0000187|GO:0007411|GO:0034446|GO:0061002|GO:0046658|GO:0070062|GO:0003199|GO:0
048013|GO:0005102|GO:0045765|GO:0005576|GO:0001525|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_73759_PI430048170 0.5522964023806520.8554160114915550.75269564880762 0.554734709981484
0.514058447652772A A A 0.4319194906455590.6560362212343961.28188505897595 A A A
LNCV6_73759_PI430048170 mRNA

GCTGGTATAATTTTTTCCCACGATTTCCAAAATCTTTTATGTACTCAGGTAAAAGTAGCG NM_001099645 RefSeq
chr3 - 170864875 170870256 RPL22L1 200916 ribosomal protein L22-like 1
GO:0003735|GO:0005840|GO:0006412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127495_PI430048170 0.2043281867563911.20580464270522 9.28907068171052
9.28069074704488 9.49904105460161 P P P 8.83308747480771 9.01776744453043
9.36700183310343 P P P LNCV6_127495_PI430048170 mRNA
CAGGATGCAATACTCAGACACTAGCTTTTTTCTCACTTTTGTATTATAACCACCTATGTA NM_005733 RefSeq chr5
+ 138178727 138187715 KIF20A 10112 kinesin family member 20A
GO:0008017|GO:0005515|GO:0005215|GO:0005871|GO:0005794|GO:0019901|GO:0000281|GO:0001578|GO:0005
874|GO:0005819|GO:0030496|GO:0015031|GO:0003777|GO:0005524|GO:0000920|GO:0000910|GO:0008152|GO:0
005654|GO:0016192|GO:0000278|GO:0016887|GO:0007018 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_123527_PI430048170 0.0312444610531174 0.6891752463368133.66329907184234
3.69421866667259 3.34848134671052 P P P 4.15373927858595 4.05322677641392 4.1329711857331
P P P LNCV6_123527_PI430048170 mRNA
GAGACCATGTATAGAACCCAGAAAGAAATGCAAAATCATGAAGATGTTAATGTTGGTTCT NM_032290 RefSeq chr5
+ 94618685 94695868 ANKRD32 84250 ankyrin repeat domain 32 GO:0005813|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122605_PI430048170 0.00513415908568152 1.25366490625664 12.5500238140483
12.5714242002595 12.5820578690508 P P P 12.2275582364639 12.1961630632515
12.2995574861062 P P P LNCV6_122605_PI430048170 mRNA
GGGTCCATACGGCGTTGTTCTGGTTCCCGTCGTAACTTAAAGGGAAATTTTCACAATGTC NM_001304288 RefSeq
chr3 + 39406688 39412541 RPSA 3921 "ribosomal protein SA, transcript variant 3"
GO:0005515|GO:0010467|GO:0000461|GO:0005886|GO:0019058|GO:0005634|GO:0006412|GO:0006413|GO:0005
829|GO:0006414|GO:0006407|GO:0005737|GO:0000184|GO:0016032|GO:0007155|GO:0070062|GO:0000028|GO:0
003735|GO:0006614|GO:0019083|GO:0006415|GO:0016020|GO:0022627|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135827_PI430048170 0.2026745802678940.7199709438196393.42683793875542
2.91067919934078 3.88661956539532 P A P 4.08016872402649 4.04735981482802
3.64118004908502 P P P LNCV6_135827_PI430048170 mRNA
CCCATGTGTCCTGATGCTTTCAGGATACATCAGTTGTTAGTGTTTAAATTGAGTTATTTT NM_016091 RefSeq chr22 +
37849371 37888782 EIF3L 51386 "eukaryotic translation initiation factor 3, subunit L, transcript variant 1"
GO:0005515|GO:0033290|GO:0016282|GO:0005852|GO:0016020|GO:0001731|GO:0006446|GO:0003743|GO:0006
413 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136661_PI430048170 0.0173231172774016 0.7042756935499411.627336967176
11.5426353953246 11.7781254650344 P P P 11.9754857564201 12.1652822131552
12.3147038414398 P P P LNCV6_136661_PI430048170 mRNA
CAGAGATTTGCAAAGACTCACGTTTTTGTTGTTTTCTCATCATTCCATTGTGATACTAAG NM_001270940 RefSeq
chr16 - 28097975 28211918 XPO6 23214 "exportin 6, transcript variant 1"
GO:0005515|GO:0005737|GO:0005886|GO:0008565|GO:0008536|GO:0006611|GO:0005730|GO:0005654|GO:0005
634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141091_PI430048170 0.0147890382161744 0.5140241787297174.8408098922302
4.70337954126454 4.91396311577597 P P P 6.05854141205337 5.54414027113423
5.69413158895311 P P P LNCV6_141091_PI430048170 mRNA
CACAGCAAGACACCTGACAATATTGTTGCTTTCTTCAAAAGTAATTTTGACTGATCTCAT NM_001145659 RefSeq
chr6 - 131708440 131711017 CTAGE9643854 "CTAGE family, member 9" GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143769_PI430048170 0.4427007452549321.01394695359517 0.303794977828141
0.2596967000549760.323918352320645 A A A 0.300886886560875 0.256948703730474

0.270020336375626 A A A LNCV6_143769_PI430048170 mRNA
TTTAAAACCTAGAGGCACAATCTTGACTTGTCAATTACTACCCTTTCACAAGCTACCATC NM_014139 RefSeq chr3
- 38845768 38950561 SCN11A 11280 "sodium channel, voltage gated, type XI alpha subunit, transcript
variant 1"
GO:0086010|GO:0005886|GO:0042493|GO:0044299|GO:0005248|GO:0035725|GO:0034765|GO:0001518|GO:0006
814|GO:0019228|GO:0070062|GO:0051930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102898_PI430048170 0.7093777476411220.9668839748637896.46738869481927
6.54902167610886 6.91142708350778 P P P 6.62135342021412 6.78199564884487
6.70546038251859 P P P LNCV6_102898_PI430048170 mRNA
AAGAAATACAAAGAGAAAAGGACTCTGAACGCTGAGGGGACTGATGCTTTGGGCCCAAAT NM_152904 RefSeq
chr17 + 20087021 20239430 SPECC1 92521 "sperm antigen with calponin homology and coiled-coil
domains 1, transcript variant 3" GO:0005634|GO:0007155 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_132005_PI430048170 0.7812355023510131.2118949531815 1.97621764789549
0.4637940216950171.96040056296432 A A A 0.8027773470724891.39642037841573
1.68661041060519 A A A LNCV6_132005_PI430048170 mRNA
TAAGGTGATGAACCTAACAGGAGACCCTCCACACAATAGGCTGAGACTCCCAAATACTTT NM_001105251 RefSeq
chr5 + 80408012 80479869 ZFYVE16 9765 "zinc finger, FYVE domain containing 16, transcript
variant 2"
GO:0005515|GO:0005547|GO:0030509|GO:0046872|GO:0043231|GO:0005545|GO:0007165|GO:0016050|GO:0005
737|GO:0030100|GO:0031901|GO:0008565|GO:0016197|GO:0006622|GO:0005769 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130540_PI430048170 0.2396483227346390.6749809591670540.541517813064706
0.59706835700191 0.470665966531211 A A A 0.6189698430366081.62874754792589
0.865657166294492 A A A LNCV6_130540_PI430048170 mRNA
CGGTGAAGTGTTAGTCACAGTATTTTCAAAAGTTTGCACATATTGTTCTGTGTAATTGTG NM_021963 RefSeq chrX
- 73212300 73214874 NAP1L2 4674 nucleosome assembly protein 1-like 2
GO:0005515|GO:2000617|GO:0042393|GO:0071442|GO:0045666|GO:0003682|GO:0006334|GO:0005634|GO:2000
035 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134131_PI430048170 0.0986867123647788 1.80155974241106 3.38005965502585
2.36206767355483 3.10021809923815 P A P 1.76136797415826 2.17287507306466
2.45766677935469 A A A LNCV6_134131_PI430048170 mRNA
TACACTACTGCCAATGCCTTCATACTGAGTTCTGGGCCCTTCTGCAAATAAGTCTGAGAA NM_001171868 RefSeq
chr1 - 29119424 29122501 TMEM200B 399474 "transmembrane protein 200B, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140543_PI430048170 0.2519916098036590.9653676279957650.408421119175217
0.4309221665491590.323661547605462 A A A 0.4206212707105330.464760087787506
0.432011102546777 A A A LNCV6_140543_PI430048170 mRNA
GCGCTGCATTTGGCTATTTTCTTTGGAAATAAATAATGTGATGTTTCTCTTCCTCTTTTG NM_032153 RefSeq chr3 -
147386047 147406809 ZIC4 84107 "Zic family member 4, transcript variant 3"
GO:0005634|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132447_PI430048170 0.5993511345119360.9246577610735910.559275943446429
0.6582791307074830.529648562277273 A A A 0.5278155187793860.988894176630526
0.521233031098238 A A A LNCV6_132447_PI430048170 mRNA
CTTCACATGACGCTATGTACTTTCTCACAGGGATAATAAAGTTAGAGCACTCTCGTTGCA NM_001127255 RefSeq
chr19_GL949752v1_alt - 827858 851863 NLRP7 199713 "NLR family, pyrin domain containing 7, transcript
variant 3" GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132644_PI430048170 0.17054877824081 1.1693561062854 0.750608362688337
0.3948333031564750.680663421603688 A A A 0.2813221064188180.422908253594374

0.462574317618591 A A A LNCV6_132644_PI430048170 mRNA
TGTCTGCTGGTACGACAGACATAAATCTCTACTCTGAGAGTTTTTATACACTTGGAAAAA NM_001825 RefSeq chr5
+ 81233319 81266398 CKMT2 1160 "creatine kinase, mitochondrial 2 (sarcomeric), transcript variant 1"
GO:0005739|GO:0004111|GO:0034641|GO:0016310|GO:0006936|GO:0006600|GO:0005743|GO:0044281|GO:0005
524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105288_PI430048170 0.0850853844065242 1.55094408475442 3.82344027529747
4.36063899927019 4.44399688659818 P P P 3.53889235847774 3.6219807326296
3.64076537924326 P P P LNCV6_105288_PI430048170 mRNA
ATCAGATTGATGAGAAGGAACATCCTTATAAGGAAGAAGAAAGCATCTCCCCGGGCACTC NM_052947 RefSeq chr18
- 58481249 58628957 ALPK2 115701 alpha-kinase 2 GO:0004674|GO:0006468|GO:0005654|GO:0005524
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128729_PI430048170 0.396395614591353 0.531823266580118 0.428935806939922 1.2158879197333
1.2227579951582 A A A 1.9207886611566 2.62082074139508 0.433268217828169 A P A
LNCV6_128729_PI430048170 mRNA
TAAGAAGTAAAGAGCTTTCCGGGAGGCCAATTTGGAAAGAACCCAAAGGCTCTTTTAAGA NM_005323 RefSeq chr6
- 26107411 26108136 HIST1H1T 3010 "histone cluster 1, H1t"
GO:0000794|GO:0006334|GO:0007275|GO:0005634|GO:0030317|GO:0007283|GO:0007339|GO:0000786|GO:0003
677|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126994_PI430048170 0.388213492805543 1.02759481627723 0.429960652380022
0.318703552298736 0.361941435017981 A A A 0.293372014602597 0.327750665103574
0.372754897545136 A A A LNCV6_126994_PI430048170 mRNA
TGTATTTCCCAATACACTTGAGCAGTTGCCTGTGAATGTAAGAGGTGTCAACAAACTGGG NM_003886 RefSeq chrX
- 50190767 50201013 AKAP4 8852 "A kinase (PRKA) anchor protein 4, transcript variant 1"
GO:0048471|GO:0005952|GO:0030018|GO:0031514|GO:0006928|GO:0097228|GO:0005634|GO:0010738|GO:0030
317|GO:0007338|GO:0007165|GO:0005737|GO:0008104|GO:0035686|GO:0030030|GO:0007178|GO:0051018|GO:0
005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136028_PI430048170 0.186581689548736 1.04002219598164 0.427918454748192
0.399288692603555 0.420522914316801 A A A 0.312400422858649 0.34990743200798
0.41390110982997 A A A LNCV6_136028_PI430048170 mRNA
CGATTGGACATGAGGCACCAAGGATGTTAAAAAGTCACATCGGAAATTCAGAAATGTCCC NM_032559 RefSeq chr17
+ 53822877 53825212 KIF2B 84643 kinesin family member 2B
GO:0008017|GO:0005871|GO:0005815|GO:0005874|GO:0051983|GO:0005730|GO:0005819|GO:0005634|GO:0003
777|GO:0005524|GO:0005829|GO:0019886|GO:0007067|GO:0007596|GO:0015630|GO:0008152|GO:0000777|GO:0
000278|GO:0016887|GO:0007019|GO:0051301|GO:0007018 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_138927_PI430048170 0.00926358792090712 0.517423506847633 5.88452234113034
6.00347372406503 6.35769914027983 P P P 6.82896218680352 6.95858598644657
7.30914783520522 P P P LNCV6_138927_PI430048170 mRNA
TAAGACTTGCCCTTTCTAACAATAAATGCTCCGTGTTTAAGTTCTGCAGGTCTCAAAAAA NM_001009921 RefSeq
chr3 + 184812142 185052614 VPS8 23355 "vacuolar protein sorting 8 homolog (S. cerevisiae),
transcript variant 1" GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136263_PI430048170 0.448597180438599 0.898257381592042 8.56898327346608
8.58404931893548 8.46745108378571 P P P 8.38146616402276 8.83308747480771
8.82819695232298 P P P LNCV6_136263_PI430048170 mRNA
GATGTACACACATTTCATTATTTGCCAATGGTGCAATAACCACTGCTGACCAACAAAAAA NM_015549 RefSeq - -
0 0 --- NA "pleckstrin homology domain containing, family G (with RhoGef domain) member 3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131528_PI430048170 0.58762762248742 1.02498607355324 0.420720428725056
0.551709922497168 0.471115128687155 A A A 0.5407190149057 0.394958936364128

0.399271190135946 A A A LNCV6_131528_PI430048170 mRNA
TTTGTGGCCAGATTTCAAATAGGGAGTTAAGTGGTACTTTCACAATCCAAAGATTTTTAG NM_001282356 RefSeq
chr8 + 91209493 91398154 SLC26A7 115111 "solute carrier family 26 (anion exchanger), member 7,
transcript variant 3"
GO:0006820|GO:0006821|GO:0019531|GO:0005886|GO:0019532|GO:0055085|GO:0001696|GO:0005254|GO:0016
323|GO:0005737|GO:0015116|GO:0015301|GO:0015106|GO:0008272|GO:0015701|GO:0008271|GO:0016021|GO:0
055038|GO:0005768|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143746_PI430048170 0.5687347390801820.9085002123228311 1.7233927425798
12.5246666681054 11.7791322004947 P P P 12.3492627042509 12.0046757728895
12.2134726958834 P P P LNCV6_143746_PI430048170 mRNA
CTGTATATGCGCTGCTGTAGATACCGGAATGAATTTTCTGTACATGTTTGGTTAATTTTTNM_014417RefSeq chr19 -
47220821 47231194 BBC3 27113 "BCL2 binding component 3, transcript variant 4"
GO:0005515|GO:0034976|GO:2001056|GO:0005741|GO:0001836|GO:0008340|GO:0005829|GO:0005739|GO:0043
525|GO:1900740|GO:0090200|GO:0045926|GO:0032464|GO:0051209|GO:0006919|GO:0070245|GO:0006915|GO:0
071456|GO:0097194|GO:2001244|GO:0097190|GO:0006974|GO:0097193|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133796_PI430048170 0.0665733713622529 3.09832076968948 3.64562598311263
3.9345875809511 2.7356971963486 P P A 0.9202694139130762.76353158159186
1.28767845004086 A P A LNCV6_133796_PI430048170 mRNA
GCCCTGCATGGCAGCCCTGTGAATTCACCCACTCAACAAAGCTCATGGAGTTCCAAAAAA NM_001190228 RefSeq
chr9 + 137227565 137229638 RNF224 NA ring finger protein 224 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137030_PI430048170 0.4635451803651250.8418182885854 9.57064106215218
8.92677276154912 8.73111992537082 P P P 9.58258858646957 9.51546419856015
8.92948961589907 P P P LNCV6_137030_PI430048170 mRNA
GCCCCAGGTCTCCTACTTGGACTCTCCAAGTCTCCAGCCATTCCAGGTAGAAGAAAGAAG NM_032752RefSeq chr1
- 247300319 247331743 ZNF496 84838 zinc finger protein 496
GO:0005515|GO:0016604|GO:0006366|GO:0000981|GO:0005634|GO:0000122|GO:0045893|GO:0043621|GO:0003
677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52871_PI430048170 0.1970435524574011.05191138322957 0.4553187148181270.462637482197761
0.501794944826373 A A A 0.3217949568459050.42152709174288 0.454536697335785 A A A
LNCV6_52871_PI430048170 mRNA
ATGCTGCCAGTGTTCTTTGGGGAGAGCATCAAGGTGAACCCGGAACCCACGCATGAGATC NM_181709RefSeq chr12
+ 124289163 124316024 FAM101A 144347 "family with sequence similarity 101, member A"
GO:0005737|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52370_PI430048170 0.0011858161112753 0.3414544501111256.45106546098094 6.1386880350886
6.01133215455126 P P P 7.6753191431303 7.92625576284765 7.67126352835378 P P P
LNCV6_52370_PI430048170 mRNA
GGGCCAGTCACCCTCTCGGGTTCCAATGCTTCGACTTAGCTCGAGGCCTGAAGAGGTCAC NM_139053RefSeq chr1
- 109750079 109764022 EPS8L3 79574 "EPS8-like 3, transcript variant 1" GO:0005737 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_104885_PI430048170 0.0348588149487247 2.36822424320487 3.00656837296551
3.37343034074189 3.8057313203815 A P P 2.66863000762835 2.1123640207085
1.58121576969463 A A A LNCV6_104885_PI430048170 mRNA
TTCCCCAGAAGTTAAGAAATATTGCTGAACGAACCAATAAAAATAATTACAGCTCCCTCA NM_001145710 RefSeq
chr2 + 24123479 24169638 FAM228B NA "family with sequence similarity 228, member B, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138340_PI430048170 0.0174199203362568 0.7042959421104121 0.8478427040201
10.8535482951797 10.750584035123 P P P 11.4877350427941 11.2113288275066

11.2569801608844 P P P LNCV6_138340_PI430048170 mRNA
GTGCTGCCTGAATCCATTAAAAATGGGAGTACTGATGAAATAAAACTACATGGTCAACAG NM_003786 RefSeq chr17
+ 50634856 50691702 ABCC3 8714 "ATP-binding cassette, sub-family C (CFTR/MRP), member 3,
transcript variant 1"
GO:0016020|GO:0005886|GO:0005887|GO:0015721|GO:0006810|GO:0042626|GO:0008514|GO:0008206|GO:0044
281|GO:0055085|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128358_PI430048170 0.28349012031216 1.5195136066157 2.46699543550132
2.37867632153622 2.49308200543345 A A A 0.61968751522162 2.05849377627356
2.34030228515339 A A A LNCV6_128358_PI430048170 mRNA
CACACCTGGAAACAGACCAATAGACATTTTGGGGTTTTATAATAGGAATTTGTATAAAGC NM_021101 RefSeq chr3
- 190305700 190322446 CLDN1 9076 claudin 1
GO:0005515|GO:0061436|GO:0016328|GO:0045216|GO:0042802|GO:0016324|GO:0016338|GO:0005198|GO:0005
887|GO:0016032|GO:0005923|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129843_PI430048170 0.6048129895375381.01005979770757 0.341882981188095
0.3188695732859050.26458717213832 A A A 0.2965903983902870.302559095042572
0.283893234115242 A A A LNCV6_129843_PI430048170 mRNA
CAGATGCTGTTTAAGTGACTGATGGCTAATGTACTGCATATGAAAGGACACTAGAAGATT NM_002176 RefSeq chr9
- 21077104 21077944 IFNB1 3456 "interferon, beta 1, fibroblast"
GO:2000552|GO:0035458|GO:0005132|GO:2001235|GO:0019221|GO:0033141|GO:0005615|GO:0051607|GO:0060
337|GO:0060338|GO:0030101|GO:0042100|GO:0045944|GO:0006959|GO:0030183|GO:0045581|GO:0002286|GO:0
042742|GO:0002323|GO:0045071|GO:0005576|GO:0009615|GO:0045343|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126436_PI430048170 0.3459461062205650.4581403912071620.499220339199468
0.5106395970133650.313548708547241 A A A 0.6765916321368722.55897696841341
0.50208444495898 A A A LNCV6_126436_PI430048170 mRNA
AAATTGGGTTCTTACTGCATACGCTGCTTGCTGGTTTCTAAATAAAATTGGGTTCTTACT NM_001242780 RefSeq
chr17_KI270907v1_alt - 69149 71433 LOC100506388 100506388 "uncharacterized LOC100506388,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120597_PI430048170 0.6780105518375341.03843735360081 0.597359383372608
0.54934355224985 0.765508579597977 A A A 0.4090536115772310.800634885496375
0.519601281806059 A A A LNCV6_120597_PI430048170 mRNA
TCTTAACCATGGCATCTATGTTGAGGATGTCAATGTTTATTTCAGCAAAGGACGTCATGG NM_001007156 RefSeq
chr15 - 87977364 88256731 NTRK3 4916 "neurotrophic tyrosine kinase, receptor, type 3, transcript
variant 3"
GO:0005515|GO:0008284|GO:0032856|GO:0070306|GO:0071300|GO:0019056|GO:0045471|GO:2000251|GO:0048
678|GO:0050927|GO:0002039|GO:0000187|GO:0005737|GO:0033138|GO:0046777|GO:0032148|GO:0090102|GO:0
060548|GO:0051412|GO:0030335|GO:0042490|GO:0043121|GO:0048665|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133404_PI430048170 0.00454744117560573 2.23848400725395 3.63399432502238
3.27979097590628 3.25497527490822 P P P 2.32941153235741 2.23519807679053 2.1424995939857
A A A LNCV6_133404_PI430048170 mRNA
CCTGGGGCCTTGATGGTGAAAATGCACCCCAAATGAAAAATAATTATTAAAAATGATCTT NM_144672 RefSeq chr16
+ 21678513 21760729 OTOA 146183 "otoancorin, transcript variant 1"
GO:0016324|GO:0007160|GO:0007605|GO:0005578|GO:0031225|GO:0019226 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139944_PI430048170 0.0463245962899948 0.6474928328995315.35475321958257
5.22837061602122 5.72064014265484 P P P 5.75640856519523 6.11652944610262
6.30555906690982 P P P LNCV6_139944_PI430048170 mRNA
TTTGTGTAACGGAGATATACTACTGTAAGTTTTGTACTGTACTGGCTGAAAGTCTGTTAT NM_022465 RefSeq chr12

+ 56020904 56038435 IKZF4 64375 IKAROS family zinc finger 4 (Eos)
GO:0043565|GO:0003700|GO:0046982|GO:0045944|GO:0043425|GO:0005634|GO:0045892|GO:0046872|GO:0042
803|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138296_PI430048170 0.0315385896883323 1.13228266288137 9.55618832661619
9.68316119188245 9.56721023678271 P P P 9.48826454164351 9.42116146711063
9.36003887547628 P P P LNCV6_138296_PI430048170 mRNA
GGTACTGTCTCTGGAATTTTAATCACAATAAAGTTTGGCAAGGAATGTGTACTTGTACTT NM_018089RefSeq chr2
+ 219229756 219236669 ANKZF155139 "ankyrin repeat and zinc finger domain containing 1, transcript
variant 1" GO:0005515|GO:0016020|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114286_PI430048170 0.0466942051499372 0.7153314310168565.42772667166848
5.74105339948935 5.81320510960812 P P P 6.20613261539824 6.11099596815368 6.1415415462094
P P P LNCV6_114286_PI430048170 mRNA
CAATGGTTTGCTGAGCTTTCTGTGGATATGGAAAAGATTTTGGAAATAATCAGGGTTATT NM_005190RefSeq chr6
- 99542386 99568814 CCNC 892 "cyclin C, transcript variant 1"
GO:0005515|GO:0010467|GO:0006367|GO:0019901|GO:0007219|GO:0045944|GO:0016592|GO:0016591|GO:0007
179|GO:0005654|GO:0000079|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127353_PI430048170 0.3865491292674911.08111990158596 10.7141519112012
10.6784595890513 10.4677420698491 P P P 10.3888275867886 10.6792849412758
10.4502443540619 P P P LNCV6_127353_PI430048170 mRNA
GCCAGGCTGTGCCTTTGACTTTAAAATAAAAGTCCACCCAGTGCTGTGTGTGGCAAAAAA NM_003942RefSeq chr11
+ 64359152 64372215 RPS6KA4 8986 "ribosomal protein S6 kinase, 90kDa, polypeptide 4, transcript
variant 1"
GO:0005515|GO:0006355|GO:0000287|GO:0016572|GO:0001818|GO:0005634|GO:0035066|GO:0005524|GO:0035
556|GO:0032793|GO:0033129|GO:0005737|GO:0051092|GO:0006954|GO:0004674|GO:0007411|GO:0045944|GO:0
043987|GO:0043988|GO:0004711|GO:0005654|GO:0006468|GO:0048273|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_70887_PI430048170 0.9536730001062370.98572357194872 4.56911635413398 4.48157773058288
4.73983604419487 P P P 4.67808514854149 4.32657833321235 4.81698200248842 P P P
LNCV6_70887_PI430048170 mRNA
GTGAATTTACCTTGGTAATCGAGATGTCATGCTAAGGACCAATAAACTATCACTGAACAA NM_001009984 RefSeq
chr20 - 3249301 3407662 C20orf194 25943 chromosome 20 open reading frame 194 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134566_PI430048170 0.9483956980501551.00315179668436 0.357508690274807
0.5114967140940110.396453990978607A A A 0.5044710731545320.377714406498233
0.37014604907569 A A A LNCV6_134566_PI430048170 mRNA
GGTGGTGTTGAGTTGTTATGTTTACACTGTTTTAAATAAAAAGGCACCGTATTTGAAAGC NM_001010848 RefSeq
chr10 + 81875313 82987179 NRG3 10718 "neuregulin 3, transcript variant 1"
GO:0007389|GO:0030971|GO:0060596|GO:0005102|GO:0005576|GO:0048513|GO:0001558|GO:0005615|GO:0035
556|GO:0007171|GO:0030297|GO:0005887|GO:0008083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128382_PI430048170 0.8487000456899161.18896382895943 1.86279368289153
0.4206749821477210.244071888789349A A A 0.3739065231812550.451609493469705 1.3320246336735
A A A LNCV6_128382_PI430048170 mRNA
CTGGAGAGAAAAAATCTATTTGTAATGATCTTTAACTGCCTGCTGTTAAGATATTAGGCC NM_024694RefSeq chr6
+ 146598999 146815461 ADGB 79747 androglobin
GO:0005737|GO:0004198|GO:0019825|GO:0005506|GO:0006508|GO:0020037|GO:0015671 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142326_PI430048170 0.6724586071169841.02545580754969 10.7404559591801
10.7059305423216 10.7285587229215 P P P 10.7653605593729 10.5178196200406
10.7690945458029 P P P LNCV6_142326_PI430048170 mRNA

TGTCTTTCAACGCAGCGTGAGTCTAATGGTTGAATAAAACTTACTGATGATCATGGGAAA NM_180699RefSeq chr12 + 123459703 123466394 SNRNP35 11066 "small nuclear ribonucleoprotein 35kDa (U11/U12), transcript variant 3" GO:0008380|GO:0006397|GO:0000166|GO:0003723|GO:0005634|GO:0005689 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140679_PI430048170 0.6775517131908441.07198694306668 5.1757480671174 5.30098036025655 5.64453688504559 P P P 4.84250556360172 5.261817558114 5.64675276043648 P P P LNCV6_140679_PI430048170 mRNA
CACAGAGAAGTTTAATGATCGTGTACAATTTGAGGGTTGATGGTAGGGCTTTCTAAAAAA NM_144632RefSeq chr2 + 102762030 102817679 TMEM182 130827 transmembrane protein 182 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144662_PI430048170 0.38800350024254 1.25181173268105 0.410291168481342 1.22587130154611 0.527590019261622A A A 0.542853002659157 0.393722427175495 0.390674838492176A A A LNCV6_144662_PI430048170 mRNA
GTCACGAACAACTTTTTCTATTAACAAGCATCTATTTCTTTATTCTTCTGGGCTTCATCG NM_013937RefSeq chr6_GL000251v2_alt - 911952 914181 OR11A126531 "olfactory receptor, family 11, subfamily A, member 1" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143579_PI430048170 0.7533842855939830.9707875646144438.56734833014602 8.50659043864001 8.38864490059216 P P P 8.39615163813962 8.71619635912738 8.46419386544836 P P P LNCV6_143579_PI430048170 mRNA
TGGGGAGGGTGTCGGGGACACCGGGGCAAAACAAGAAAGTCCTATTTTTCCAAGCTTGGG NM_024509RefSeq chr19 + 35937119 35945195 LRFN3 79414 leucine rich repeat and fibronectin type III domain containing 3 GO:0042734|GO:0030424|GO:0030054|GO:0045211|GO:0016021|GO:0007155|GO:0030425 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133563_PI430048170 0.0485865919204333 0.75809097901934 5.89314613821874 5.77203787548923 5.84938299769995 P P P 6.23150060279935 6.05499213171405 6.40779992635773 P P P LNCV6_133563_PI430048170 mRNA
GCTGATAGTTTTGTTTAAGGTTTTGGATAAGGAGCACTTTAAAACAAACTGGTGTGTTGT NM_019091RefSeq chr2 + 178480471 178505055 PLEKHA3 65977 "pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 3" GO:0008150|GO:0005545|GO:0005794|GO:0005543|GO:0016020|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141383_PI430048170 0.0855366199584127 0.7044637850138339.64936289347747 9.5888967096939 9.99168346705128 P P P 10.3045833473904 9.91607627983033 10.4993712207892 P P P LNCV6_141383_PI430048170 mRNA
GAAGGAGGTGAGATTTGTGCTACTTTGGGAGATTATGTTCTTTTTTCATGTCTAAGATTT NM_001902RefSeq chr1 + 70411217 70439851 CTH 1491 "cystathionine gamma-lyase, transcript variant 1" GO:0005515|GO:0019344|GO:0005516|GO:0070814|GO:0019346|GO:2001234|GO:0006534|GO:0005634|GO:0044540|GO:0044281|GO:0005829|GO:0030968|GO:0018272|GO:0034641|GO:0005737|GO:0051092|GO:0051289|GO:0004123|GO:0043123|GO:0070062|GO:0016846|GO:0047982|GO:0080146|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56400_PI430048170 0.0541181971619471 0.7721934787142688.12163167942603 8.05083296630265 8.24370422325681 P P P 8.36116469811575 8.44392147459708 8.71277636967446 P P P LNCV6_56400_PI430048170 mRNA
GGTGATGAGCCTGTGGGACAAAGACCATACCAACCTCTACCAGAAGCAAAAAAGAAAAGT NM_001001330 RefSeq chr10 + 63521362 63625123 REEP3 221035 receptor accessory protein 3 GO:0007067|GO:0007084|GO:0005874|GO:0005789|GO:0006998|GO:0016021|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141939_PI430048170 0.3206293383350660.9373430088613430.27276447812115 5

0.2807208424312270.38943263121328 A A A 0.3699726526120750.310161566356437
0.536197991583242A A A LNCV6_141939_PI430048170 mRNA
GCCTTTCAAGCGACAGATGCCTCATTTTGTGAAAACTTAATGATGATTTTGTGTTTAAGT NM_018460RefSeq chr2
+ 143129329 143768352 ARHGAP15 55843 Rho GTPase activating protein 15
GO:0051056|GO:0016020|GO:0007264|GO:0008360|GO:0032855|GO:0030675|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131414_PI430048170 0.2660412023831720.8498035150533949.59508587726324
9.54964273339537 9.07531307623739 P P P 9.59856324788989 9.70728808853043
9.67159461025525 P P P LNCV6_131414_PI430048170 mRNA
ATTATCACTTCCGAAATAAAGCGCGTGTCCTTGCCCCCTCACGCTCCAGGCTATAAAAAA NM_004455RefSeq chr1
+ 26021779 26036463 EXTL1 2134 exostosin-like glycosyltransferase 1
GO:0050508|GO:0001501|GO:0005789|GO:0006486|GO:0016021|GO:0015012|GO:0006024 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131708_PI430048170 0.0141171381318523 0.41383882833504 5.95245137854764
5.76163885522425 5.89605350637414 P P P 6.86548784234471 7.02522447848942
7.47386387602163 P P P LNCV6_131708_PI430048170 mRNA
AAGGCTCCCTAGTGGACACGCTGCAATCTAGTGACAAAGTCGAAAGTTTAACAGGCTTTT NM_003611RefSeq chrX
+ 13734712 13769361 OFD1 8481 oral-facial-digital syndrome 1
GO:0005515|GO:0005813|GO:0010172|GO:0035082|GO:0006996|GO:0043015|GO:0007099|GO:0043014|GO:0005
814|GO:0034451|GO:0005634|GO:2000314|GO:0036064|GO:0005829|GO:0060287|GO:0005929|GO:0007067|GO:0
016020|GO:0000086|GO:0060271|GO:0015630|GO:0090307|GO:0000278 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_138350_PI430048170 0.0196249696008840.9473180717099810.350420263577184
0.3510522478792710.326044323926696A A A 0.4472060663936440.419949798830757
0.394253090594337A A A LNCV6_138350_PI430048170 mRNA
GCTATCAGAAACTTAAACTTGAGGATTTTCTCTGTTTTTCACTCGCAATAAATTCAGAGC NM_006361RefSeq chr17
- 48724764 48728749 HOXB13 10481 homeobox B13
GO:0043565|GO:0005667|GO:0006355|GO:0008544|GO:0060743|GO:0009611|GO:0005654|GO:0001525|GO:0033
574|GO:0040008|GO:0006351|GO:0060527 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135767_PI430048170 0.9583266995722520.9296629630190083.04986109267669
0.3126534220895750.325926777179348P A A 0.4069864785753480.327367272617991
3.17176774863688 A A P LNCV6_135767_PI430048170 mRNA
AAGAATTGTAGGAAGATGAATGTGGCCTACAGTTTTAGTAATCTCCTAGTGGAGTTTTTT NM_152332RefSeq
chr14_KI270844v1_alt - 247546 304321 TC2N 123036 "tandem C2 domains, nuclear, transcript variant 1"
GO:0010468|GO:0003674|GO:0030193|GO:0005634|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145768_PI430048170 0.00790772823638511 1.09439629647153 0.37541686979032
0.4285285233685110.372495636466372A A A 0.2422944135670170.30018437995446
0.243486904846453A A A LNCV6_145768_PI430048170 mRNA
AGTCCAGGATTCAGCTCTGGTTTCAGAATCGAAGAGCCAGGCACTGGGGACAGTCTGGCA NM_012148RefSeq - -
0 0 --- NA - NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144765_PI430048170 0.0389610601091136 1.20646684555388 11.4481830857388
11.2413147606249 11.2460387713968 P P P 11.0877981714131 10.97017577021
11.0722051949851 P P P LNCV6_144765_PI430048170 mRNA
CTCTTTCATCACTTGTTCTGGATGTTTCAATCAGTTTAGTGGAAGGAAAAATAAATGGGG NM_016565RefSeq chr11
- 73872667 73876845 COA4 51287 cytochrome c oxidase assembly factor 4 homolog (S. cerevisiae)
GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58761_PI430048170 0.8249347069805990.9831408869398520.3114857743479130.514368560118954
0.360546697333185A A A 0.5341291856541480.4471986592416970.274529507954618A A A

LNCV6_58761_PI430048170 mRNA
TATTGGATATGTAGATCTGACACTATCAGAATAACTCCTAAGGACTCTCGTTGGGTTGGA NM_019844 RefSeq chr12
+ 20810703 20916909 SLCO1B3 28234 "solute carrier organic anion transporter family, member 1B3"
GO:0016323|GO:0005886|GO:0005887|GO:0015721|GO:0015711|GO:0043252|GO:0008514|GO:0008206|GO:0044
281|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141121_PI430048170 0.6042526028387351.08538259640284 3.8967239322225
4.44175004279509 4.12993016095486 P P P 3.83532602663567 4.19785674396217 4.1085261294671
P P P LNCV6_141121_PI430048170 mRNA
TAGTTTGCAATGTCATAAAAGTGCAATAAAGGTACAGCAGATGTGTGTCGGCCTCACGGG NM_020223 RefSeq
chr7_KI270899v1_alt + 185289 188053 FAM20C 56975 "family with sequence similarity 20, member C"
GO:0005794|GO:0030501|GO:0005509|GO:0070166|GO:0005615|GO:0045669|GO:0097187|GO:0040036|GO:0004
674|GO:0071895|GO:0006468|GO:0051174|GO:0036179|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134313_PI430048170 0.0405785967677469 0.6235563300498435.31939514507833
5.08845329322096 5.47056132193924 P P P 5.62109234017438 6.06527861318669
6.20023900658687 P P P LNCV6_134313_PI430048170 mRNA
GAGACCTGTTCTGTCCGTGTGCCTACGTTCCTTAATAATAGCTAAATAAAAATTTGTAGC NM_033211 RefSeq chr5
+ 103258740 103278660 C5orf30 90355 chromosome 5 open reading frame 30
GO:0005515|GO:0005737|GO:0060271|GO:0035869|GO:0015031 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129760_PI430048170 0.6040557505557530.77665573104513 0.37190451044918
0.3713361918174741.89698039428426 A A A 2.02917309538207 0.335091048249738
1.47711213972925 A A A LNCV6_129760_PI430048170 mRNA
TTTCATCTTTACTCTTCGGAATGACAAAGTCAAAGAGGCCCTCCGAGATGGGATGAAACG NM_001001658 RefSeq
chr7_KI270803v1_alt - 1049266 1050199 OR9A2 NA "olfactory receptor, family 9, subfamily A,
member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135537_PI430048170 0.00267162918766446 0.3910156920492975.07018364331187
5.31509049434905 4.82507614493536 P P P 6.53061512096491 6.50542519595286
6.26535540833349 P P P LNCV6_135537_PI430048170 mRNA
TCTCACCCCCATGTTAAATTTTTTCTGTTGAACTACACTGGATCTGACTTGATAGAACTA NM_080628 RefSeq chr20
+ 36876120 36894231 TLDC2 140711 "TBC/LysM-associated domain containing 2, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133310_PI430048170 0.0234369814586695 0.2518669923096633.71949743256568
2.50146704336277 3.26885663997872 P A P 5.06469233015971 5.31626457385073
5.31259438741843 P P P LNCV6_133310_PI430048170 mRNA
GTTGTACCTGCTGAAACTACAGTAGTTGAATATTGCGGTAGCATTTCAGTTCTCTTTTTT NM_022841 RefSeq chr15
- 56090532 56243285 RFX7 64864 "regulatory factor X, 7"
GO:0003700|GO:0006357|GO:0005634|GO:0000978 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139918_PI430048170 0.7437563662996311.26174274919824 0.330155115664325
1.88034973882797 0.369984932446465 A A A 0.4280097848941050.247066093934845
1.26684279845917 A A A LNCV6_139918_PI430048170 mRNA
TCAACTTGGTGGAGAATAGAAGGCAAATGCTGGTGGCAGCGATCGTGTTTATCAGTTTTG NM_182614 RefSeq chr13
+ 113759242 113811926 TMEM255B 348013 transmembrane protein 255B GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131461_PI430048170 0.9066159918668810.9706049854892631 0.3859276331353
10.3333238412874 10.3453457338578 P P P 10.0419080429687 10.6203418780888
10.4715106158502 P P P LNCV6_131461_PI430048170 mRNA
GGAGCTGATCGTAATGTTTATCATGTTACTTCCCCACCCCTACATTTTTTGAAATAAAAT NM_004265 RefSeq chr11
+ 61828032 61867354 FADS2 9415 "fatty acid desaturase 2, transcript variant 1"

GO:0006636|GO:0016020|GO:0005506|GO:0005887|GO:0004768|GO:0005789|GO:0044281|GO:0036109|GO:0055114|GO:0043651|GO:0033559|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139698_PI430048170 0.6109464094012051.02293884166884 0.422310337112995 0.5481238835683690.466022684093565A A A 0.5406826503069330.395383850293202 0.400301650707584A A A LNCV6_139698_PI430048170 mRNA
GTGTTTTGTGTTTTTTCTTCTTTCGGTGTTTTCCTTTTAAACCAAGGGACTGAAATAGCA NM_178353RefSeq chr1 + 152786276 152788425 LCE1E 353135 late cornified envelope 1E GO:0031424 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126902_PI430048170 0.2874272918684380.8649922331561868.0532622430142 7.9257909878519 8.36538284517318 P P P 8.3126148824807 8.13914935405501 8.52982296328172 P P P
LNCV6_126902_PI430048170 mRNA
AATTACTAACTGGTTATAGTGGGATAGGAGGCAGAAAATGGATGACTTTGTCTTTTCTCA NM_001300764 RefSeq chr1 + 184051650 184074210 TSEN15 116461 "TSEN15 tRNA splicing endonuclease subunit, transcript variant 4" GO:0006397|GO:0006388|GO:0005730|GO:0000213 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62984_PI430048170 0.1114337427721530.8721174764780587.23974617220394 7.05578656751847 7.25278289300238 P P P 7.2594058893537 7.50857192713589 7.37001006740656 P P P
LNCV6_62984_PI430048170 mRNA
CTTGGTGGCAAATTTTTTCCCAAAGAAGTTATTAGAACTTGATAGTTTTCTGAAGGAACC NM_001267045 RefSeq chr17 + 42833141 42843760 PSME3 10197 "proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki), transcript variant 3"
GO:0005515|GO:2001237|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0002039|GO:0034641|GO:0005737|GO:0000082|GO:0008537|GO:0016032|GO:0090090|GO:0006977|GO:0000209|GO:0000502|GO:0043066|GO:0006521|GO:0051437|GO:0042590|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90462_PI430048170 0.1832319841299181.19668909982511 8.02246269485141 7.74989791238357 7.87570338509805 P P P 7.36282929036208 7.83326234595318 7.64932684328966 P P P
LNCV6_90462_PI430048170 mRNA
TTCCAGTATGGGAATTATTGCAAATACTATGGGTACCGCAATCCTTCCTGTGAGGATGGG NM_019606RefSeq chr7 + 100429630 100434126 MEPCE 56257 "methylphosphate capping enzyme, transcript variant 1"
GO:0040031|GO:0001510|GO:0016073|GO:1900087|GO:0008757|GO:0000122|GO:0035562|GO:0008173 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124870_PI430048170 0.4468261878031881.01247207155681 0.33218389555195 0.3085016077035270.26809500990813 A A A 0.2884046331932230.290645136227785 0.276772513130113A A A LNCV6_124870_PI430048170 mRNA
ACTGTAGTTTGTGGTGAGATGTTTATTTTTCTAACAGAGCTTATAACAGTTAGGACAAGG NM_002214RefSeq chr7 + 20331101 20415759 ITGB8 3696 "integrin, beta 8"
GO:0008305|GO:0060674|GO:0005886|GO:0009986|GO:0051216|GO:0005102|GO:0034686|GO:0010628|GO:0007160|GO:0007229|GO:0030198|GO:0010629|GO:0001573|GO:0004872|GO:0007155|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144799_PI430048170 0.2820858836423550.6441399529084090.261929098541911 0.2730839017319781.74267600642106 A A A 1.18480299811836 2.12632127243506 1.19756663324479 A A A LNCV6_144799_PI430048170 mRNA
TGTGTTGTATGCCCTAATACAACAACAGCAAGAAGCCATAGAAAAAAGCAATAGAAAATG NM_018387RefSeq chr9 - 123121628 123268564 STRBP 55342 "spermatid perinuclear RNA binding protein, transcript variant 1"
GO:0003725|GO:0005737|GO:0003727|GO:0015630|GO:0007286|GO:0006928|GO:0007275|GO:0005634|GO:0007638|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138318_PI430048170 0.4603056133995280.9434025736364550.276749688290422 0.2813383300590330.458183541188103A A A 0.3459987635740560.580466154904418

0.335987266935668 A A A LNCV6_138318_PI430048170 mRNA
TAGGTCAAGAAATGAAATCGAAATTTCAGAAATTACAGAAATTCTCCAAGGAAGGAGCCA NM_001009614 RefSeq
chrX + 145247586 145256208 SPANXN1 NA "SPANX family, member N1" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_134069_PI430048170 0.00324530601876058 1.38713180206844 11.5902793606736
11.7629817911126 11.7517554129353 P P P 11.3144642892491 11.1753419364768 11.201462334919
P P P LNCV6_134069_PI430048170 mRNA
GATTCTGTGACACAAACCCCACCAATTGTTAATGCAAGTTTTTATTTGGCTGTATATACA NM_004927 RefSeq chr11
+ 65122243 65127369 MRPL49 740 "mitochondrial ribosomal protein L49, transcript variant 1"
GO:0070124|GO:0005515|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005761|GO:0005
743|GO:0005762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126899_PI430048170 0.138513432192783 0.632020471140698 0.360852303471522
1.11005972648975 0.577529375088895 A A A 1.85071662677312 0.974844982204527
1.16098642847205 A A A LNCV6_126899_PI430048170 mRNA
TTTAGCCTCCACCTTGTCTAAGCTTTGGTCTATAAAGTGCGCTACAGAAATGGCAAAAAA NM_001261461 RefSeq
chr12 - 54292106 54301037 NFE2 4778 "nuclear factor, erythroid 2, transcript variant 3"
GO:0003700|GO:0006357|GO:0050699|GO:0008015|GO:0003713|GO:0007267|GO:0005634|GO:0007275|GO:0006
337|GO:0030502|GO:0015629|GO:0006351|GO:2000758|GO:0043565|GO:0007599|GO:0005737|GO:0047485|GO:0
007596|GO:0016605|GO:0060716|GO:0005654|GO:0045893|GO:0034242 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133667_PI430048170 0.209992212107682 0.868545506731788 9.03480918564223
9.03313034888382 8.98937311591323 P P P 9.00138436040469 9.29207145960387
9.35061827693133 P P P LNCV6_133667_PI430048170 mRNA
TAGAAGTTTAGTGTTTTTGTCACTGTCATGTGTTTCTGTGGGCAGAGCTGGTTCTGGAGG NM_001082968 RefSeq
chr17 - 17843507 17972470 TOM1L2 146691 "target of myb1-like 2 (chicken), transcript variant 3"
GO:0005622|GO:0005515|GO:0045839|GO:0007165|GO:0019901|GO:0030276|GO:0006886|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_36815_PI430048170 0.621756085836856 0.91351641418397 1.64664086433297
1.97488676044329 1.12187910112787 A A A 1.98626310832561 1.47581512733868
1.75249756060942 A A A LNCV6_36815_PI430048170 mRNA
CGGGCGGAGCGCACTGGAACTCAAGGGGGCGCACAGCGGCGCGCTCGCACCGCTCGGCTC NM_138444 RefSeq
chr13 - 76880168 76886405 KCTD12 115207 potassium channel tetramerization domain containing
12 GO:0043235|GO:0042734|GO:0030054|GO:0008277|GO:0045211|GO:0051260|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140295_PI430048170 0.702189189934554 1.13607081054598 1.26878479396282
0.285769351596569 0.509399757188426 A A A 0.935633237953492 0.369524460167472
0.313059847281836 A A A LNCV6_140295_PI430048170 mRNA
TCTTTAGCTCAGCTAGAGTTCACAGGAGAGCCAAAAAAGAAAAGGAAGCTGAGCATCTCC NM_014293 RefSeq
chr22 - 38818450 38844012 NPTXR 23467 neuronal pentraxin receptor GO:0016021|GO:0046872
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105662_PI430048170 0.0549395286976046 1.17774449335625 9.46087536708087
9.33530009037708 9.55880483867717 P P P 9.09975338259771 9.26004914693913
9.28867239482915 P P P LNCV6_105662_PI430048170 mRNA
AATATGACTTCAAAGCTACTGCAGACGACGAGCTGAGCTTCAAAAGGGGGGACATCCTCA NM_002086 RefSeq
chr17 - 75318075 75405708 GRB2 2885 "growth factor receptor-bound protein 2, transcript variant
1"
GO:0005515|GO:0005154|GO:0060670|GO:0043560|GO:0050900|GO:0042802|GO:0031623|GO:0048646|GO:0007
173|GO:0030838|GO:0007411|GO:0070062|GO:0070436|GO:0005794|GO:0019901|GO:0005168|GO:0019903|GO:0
007568|GO:0042059|GO:0030168|GO:0071479|GO:0042770|GO:0046875|GO . NA - . NA NA NA

NA NA NA NA NA NA
LNCV6_123479_PI430048170 0.110465010903731 1.25536247381253 6.6320196976316
6.80781151001043 6.99655788710214 P P P 6.29764441968114 6.43460396013454
6.71162223814082 P P P LNCV6_123479_PI430048170 mRNA
CATGTTTATACACCAAATGATGTCCGTATGGTGATTGAATATGCCAGATTACGAGGAATT NM_001292004 RefSeq
chr5 + 74640022 74721288 HEXB 3074 "hexosaminidase B (beta polypeptide), transcript variant 2"
GO:0048477|GO:0019915|GO:0007605|GO:0008360|GO:0044281|GO:0042803|GO:0030207|GO:0045944|GO:0050
885|GO:0007626|GO:0030204|GO:0030203|GO:0070062|GO:0043202|GO:0006665|GO:0004563|GO:0009313|GO:0
046982|GO:0006687|GO:0001669|GO:0005975|GO:0042552|GO:0006689|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129219_PI430048170 0.626855320716006 1.0176546159624 0.505977793612072
0.617550039085154 0.52325247523317 A A A 0.588723988712522 0.481267421003556
0.501284400120477 A A A LNCV6_129219_PI430048170 mRNA
CAATGAAATTTTCATAGTTAAATTTGGTATTCGTGGGGGAAGAAATGACCATTTCCCTTG NM_002099 RefSeq
chr4 - 144109302 144140786 GYPA 2993 glycophorin A (MNS blood group)
GO:0047484|GO:0016020|GO:0005886|GO:0005887|GO:0001618|GO:0016032|GO:0009615|GO:0007016|GO:0042
803|GO:0009897|GO:0070062|GO:0042802 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_97094_PI430048170 0.0384537687939227 0.7623401189226 14.4628867099953
14.3153947797548 14.1828460301979 P P P 14.7280795874122 14.7047094404898
14.7163389830249 P P P LNCV6_97094_PI430048170 mRNA
CCTGCCCCCTCCCTGAACTATTTTGTGCTGTGTATATCACTGCTTTATATAAGTTATTTT NM_001256732 RefSeq chr5
- 81417359 81751253 SSBP2 23635 "single-stranded DNA binding protein 2, transcript variant 1"
GO:0006355|GO:0005737|GO:0003697|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138690_PI430048170 0.202122056788583 0.799112707159355 4.44288645022735
4.20767762837368 4.23214459403226 P P P 4.29497050643583 4.63407539667277
4.87753052878259 P P P LNCV6_138690_PI430048170 mRNA
GAGTTACGGTCTTTCGGTTGTGTATTAGGCTACAGCTATTTATTAAATTTGTTCTTGTTC NM_001304433 RefSeq chr13
- 113399609 113414393 LOC101928841 NA collagen alpha-1(II) chain-like NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_134026_PI430048170 0.0796240035801291.29281418569993 7.10445495735586
6.70907420604242 7.03513523132319 P P P 6.51636424474026 6.4656360823724
6.76684711668052 P P P LNCV6_134026_PI430048170 mRNA
CTGGCGAAAATGTAGGCAAAGTAGCTTCCAGTTTTAGAATAAATAACCATTTGGATTGAA NM_001079559 RefSeq
chr11 - 62712624 62727385 HNRNPUL2 221092 heterogeneous nuclear ribonucleoprotein U-like 2
GO:0008150|GO:0016020|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95631_PI430048170 0.249516800966889 1.32094813135281 2.31086780033865 2.38260353115417
1.75532224000538 A A A 1.35520528361441 2.15912166700676 1.693760880928 A A A
LNCV6_95631_PI430048170 mRNA
ATAATGGAGACTGGGGCTATATGGTGGACACTTGTATACAACGTCTCTCACCACATTGAC NM_153331 RefSeq chr3
+ 58498364 58502360 KCTD6 200845 "potassium channel tetramerization domain containing 6, transcript
variant 1" GO:0030506|GO:0051260 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79047_PI430048170 0.175573873976587 1.76898591020758 1.70122884143324 1.28643240378954
0.448959608981776 A A A 0.296818292959092 0.321763810658614 0.595005489847555 A A A
LNCV6_79047_PI430048170 mRNA
TGCAGCAGAACAACTACAAGAGTTTTACAAGAAACAGCAAGAGCAGTTACATCTTCAGCT NM_148898 RefSeq chr7
+ 114414996 114693772 FOXP2 93986 "forkhead box P2, transcript variant 2"
GO:0005515|GO:0003700|GO:0021987|GO:0005634|GO:0009791|GO:0042803|GO:0046872|GO:0060501|GO:0048
745|GO:0043010|GO:0046982|GO:0048286|GO:0021549|GO:0002053|GO:0000122|GO:0000978|GO:0003677|GO:0

006351|GO:0043565|GO:0001078|GO:0007519|GO:0042297|GO:0040007|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129750_PI430048170 0.1747928691899441.16054057050219 0.357424685268087
0.4200827883772720.686315103276035A A A 0.2701768519298950.296802888405051
0.273840138881028A A A LNCV6_129750_PI430048170 mRNA
CACCTGTTCTAGTGCCAAAGATCACTCATTGCTAATTTTGTTCTGTACAGCTTATGTAAT NM_005497RefSeq chr17
- 44798447 44830239 GJC1 10052 "gap junction protein, gamma 1, 45kDa, transcript variant 1"
GO:0005243|GO:0005886|GO:0007268|GO:0016264|GO:0048738|GO:0034220|GO:0006936|GO:0014704|GO:0005
789|GO:0006810|GO:0007043|GO:0086014|GO:0061024|GO:0005921|GO:0005922|GO:0048468|GO:0016021|GO:0
001570|GO:0005216|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128219_PI430048170 0.3523562333098690.8856856287822120.439317635037281
0.4065809317656010.267786682343924A A A 0.8058000958638990.403686743028813
0.396110886825813A A A LNCV6_128219_PI430048170 mRNA
CCTTCAGTTTCTCACAGATTTTCACCATGTGGCTTCATCAATTTATGTGCTAATACAATANM_001870RefSeq chr3 +
148865255 148897085 CPA3 1359 carboxypeptidase A3 (mast cell)
GO:0030133|GO:0002003|GO:0006508|GO:0008270|GO:0005576|GO:0030141|GO:0044267|GO:0004181 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145059_PI430048170 0.2803640490867780.8388146808802848.81337285073756
8.58562809081099 8.66577055538542 P P P 8.61081680300406 9.01251136270463
9.15754555544671 P P P LNCV6_145059_PI430048170 mRNA
GGGTTGAAAGCTGGGGAGGAGGATCTACTGCTGTACAGCTAATAAATCATAACGGATTAA NM_006565RefSeq chr16
+ 67562406 67639185 CTCF 10664 "CCCTC-binding factor (zinc finger protein), transcript variant 1"
GO:0005515|GO:0000793|GO:0003700|GO:0044212|GO:0005634|GO:0035065|GO:0010216|GO:0007059|GO:0016
584|GO:0070602|GO:0003714|GO:0005730|GO:0000122|GO:0000978|GO:0006351|GO:0040030|GO:0043565|GO:0
006306|GO:0010628|GO:0001078|GO:0031060|GO:0006349|GO:0040029|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140178_PI430048170 0.2538268851642030.9698212748876490.425848840706401
0.4451652812426430.354431491394218A A A 0.4226142596248520.480447128012175
0.456003202248139A A A LNCV6_140178_PI430048170 mRNA
GCTCCATGGAGTTAGATGACTACACTTAATGCTATTAAGTTGAACTTTTGAATGTCAACT NM_145913RefSeq chr12
- 101156215 101210238 SLC5A8 160728 "solute carrier family 5 (sodium/monocarboxylate cotransporter),
member 8"
GO:0016324|GO:0005886|GO:0006915|GO:0016021|GO:0006814|GO:0055085|GO:0070062|GO:0015293|GO:0006
811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143420_PI430048170 0.1221760788762531.81434807103489 2.30108115126059
3.41948026117351 2.65284447597404 A P A 1.90720654328384 2.42463862586443
1.56559563242965 A A A LNCV6_143420_PI430048170 mRNA
AATGTTCTGGGTGACCAGTCACCTACTTTCTGATCAATAAAAATGTCGACATGCATTTCT NM_013358RefSeq chr1
+ 17205125 17246006 PADI1 29943 "peptidyl arginine deiminase, type I"
GO:0018101|GO:0005737|GO:0005509|GO:0004668|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132102_PI430048170 0.8726446002687350.9714588012180034.42738872419668
3.71581761059969 3.9832690860312 P P P 4.45350023955429 3.96741457037371
3.84819977128148 P P P LNCV6_132102_PI430048170 mRNA
TAGTGGTAAATAGTGAAAGCCTGTCCTTCCCTAAATGTAAAGCCATCTGTCCGGCGTAAG NM_005883RefSeq chr19
+ 1450148 1473244 APC2 10297 adenomatosis polyposis coli 2
GO:0005515|GO:0008017|GO:0005881|GO:0048471|GO:0005794|GO:0008013|GO:0031258|GO:0005884|GO:0016
342|GO:0035414|GO:0005737|GO:0000139|GO:0015630|GO:0016055|GO:0090090 . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_136630_PI430048170 0.7253789708347371.00302532577491 0.326220990488955
0.3511686041027340.353689931912934A A A 0.3475208504472540.346047097370837
0.324481865710297A A A LNCV6_136630_PI430048170 mRNA
CGGAGTAAAAGTGGTAAACAAAAGCAATCAGTACCAATTCCAAAAACTGTATCCAGAAAANM_001278125 RefSeq
chr4 + 174918357 174978180 ADAM29 11086 "ADAM metallopeptidase domain 29, transcript variant
5" GO:0005887|GO:0006508|GO:0008270|GO:0007283|GO:0004222|GO:0008237 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139362_PI430048170 0.146040559774925 1.0985761798996 12.1111720849981
12.3059947381642 12.1793246905408 P P P 12.1115472665879 11.9686433960051
12.1115472665879 P P P LNCV6_139362_PI430048170 mRNA
CCACTTGTTGATTATTTTCTTGTTTGAGCCCCTCCCCCAATAAAGAATTTTTATCGGGTT NM_153357RefSeq chr17 -
7041629 7043923 SLC16A11 162515 "solute carrier family 16, member 11"
GO:0006629|GO:0015718|GO:0034220|GO:0008028|GO:0005789|GO:0016021|GO:0015293 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142880_PI430048170 0.0969726949671744 0.9240591527225 0.298951106028437
0.3023156775880110.290491936455639A A A 0.4802877016926220.401732758518791
0.348539398428368A A A LNCV6_142880_PI430048170 mRNA
CCAGAAAATGAAATCCGTGAAGTCACATTCCACATCTGTTTCAAACTGAATTTGTTCTTA NM_004093RefSeq chr13
- 106489730 106535040 EFNB2 1948 ephrin-B2
GO:0005515|GO:0010839|GO:0048013|GO:0005886|GO:0002042|GO:0007267|GO:0009653|GO:2000727|GO:0046
875|GO:0050920|GO:0005887|GO:0007411|GO:0009887|GO:0016032|GO:0007155|GO:0005925|GO:0001945 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131453_PI430048170 0.00418536925475713 0.3809319434128453.3484446854885
2.82900726844877 2.92075338366807 P A P 4.39675546430786 4.73357786871225
4.13767223816247 P P P LNCV6_131453_PI430048170 mRNA
GCTGTTCATGTAACAAAACATGCTTATAATAGCAAACAAATAGAAATGCCCCCAAAATGC NM_018374RefSeq chr7
+ 12211221 12237264 TMEM106B 54664 "transmembrane protein 106B, transcript variant 1"
GO:0032418|GO:0005515|GO:0048813|GO:0003674|GO:0031902|GO:0006810|GO:0016021|GO:0005765|GO:0070
062|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60681_PI430048170 0.2280851071966250.6011215222169992.04701447040804 1.24870757274131
0.27534137221327 A A A 1.90335409831845 1.74248296903082 2.52461022624242 A A P
LNCV6_60681_PI430048170 mRNA
GGGTGGAGGGGAGGAATCTGGACCTCTAAGTCATTCCCAAATTAAAATATTCAAATTCTA NM_001288746 RefSeq
chr14 + 23376807 23379772 CMTM5 116173 "CKLF-like MARVEL transmembrane domain containing 5,
transcript variant 6" GO:0006935|GO:0016021|GO:0005615|GO:0005125|GO:0045662 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_135239_PI430048170 0.0521062547528458 0.8307761669813366.16261324669488
5.95701232268663 6.16422828151282 P P P 6.2363727714945 6.37375201947169
6.47585238086154 P P P LNCV6_135239_PI430048170 mRNA
GGTTTCCTGCTTTTGAGTTGACCTGACTTCCTTCTTGAAATGACTGTTAAAACTAAAATA NM_015076RefSeq chr6
- 110609977 110815316 CDK19 23097 "cyclin-dependent kinase 19, transcript variant 1"
GO:0051726|GO:0006468|GO:0005524|GO:0004693 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127261_PI430048170 0.1430883223804191.08326256291124 0.507807661387483
0.6609229900034290.577745430864866A A A 0.3801684760597390.485665882541548
0.534295224379442A A A LNCV6_127261_PI430048170 mRNA
TTCTCTTATTCTCAGATTTTCTCCTCCGTCCTAAGAGTATCTGCCAGAGGCCAGCACAAA NM_012377RefSeq chr19
+ 14941488 14942448 OR7C2 26658 "olfactory receptor, family 7, subfamily C, member 2"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_131446_PI430048170 0.00513594348926476 1.58950234683294 8.74653385925099
8.8649842048171 8.9184001989575 P P P 8.03122645143508 8.32685107299403
8.15610659417566 P P P LNCV6_131446_PI430048170 mRNA
CCATTCACTCCCGTTCTCATTTACATCTGTTTTCCTGTTGTATATATCACCTTTGTTGAC NM_138471 RefSeq chr11 +
63813373 63827718 C11orf84 144097 chromosome 11 open reading frame 84 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_51830_PI430048170 0.5879737823282571.18485011714445 2.56492225751637 1.95493378890074
2.96772725158145 A A P 1.78908429313676 2.57830918244549 2.44371347944172 A A A
LNCV6_51830_PI430048170 mRNA
TCAAAATGCTACGGCCTGTGACAATGCTCCAGAAGCCTGGGACCTGCTGCACAGAGTGCT NM_000710 RefSeq chr14
+ 96256209 96264763 BDKRB1 623 bradykinin receptor B1
GO:0005515|GO:0043005|GO:0042277|GO:0004947|GO:0030308|GO:0005886|GO:0005783|GO:0045776|GO:0007
204|GO:0007205|GO:0019233|GO:0009612|GO:0006954|GO:0016477|GO:0005887|GO:0002687|GO:0032496|GO:0
001933|GO:0051281. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129330_PI430048170 0.1719178883655430.7024453337864964.35172007280895
3.41530462109366 3.83038903232486 P P P 4.33681465889895 4.4504101250714
4.48766213065272 P P P LNCV6_129330_PI430048170 mRNA
GGGAAAACCATGGTGCTGTTTAATTGTAAATAGATTGATATAAGATTGGACCAGTACTTG NM_152277 RefSeq chr5
- 172209645 172283791 UBTD2 92181 ubiquitin domain containing 2 GO:0005737 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135401_PI430048170 0.3777068163262991.21843147018469 0.371960995556356
0.2794071678361740.986654852972489A A A 0.2876156709591810.291165339655691
0.310708755780584A A A LNCV6_135401_PI430048170 mRNA
TCTTGTACATGTGTAGCCTGTGCATGTATGTCTTGGACACTGTACAAGGTACCCCTTTCT NM_005356 RefSeq chr1
+ 32251238 32286167 LCK 3932 "LCK proto-oncogene, Src family tyrosine kinase, transcript variant 2"
GO:0005515|GO:0042542|GO:0006882|GO:0050900|GO:0010043|GO:0032403|GO:0042802|GO:0001948|GO:0042
609|GO:0070474|GO:0007173|GO:0042127|GO:0051117|GO:0000242|GO:0038083|GO:0042169|GO:0070062|GO:0
051209|GO:0019901|GO:0019903|GO:0007568|GO:0045588|GO:0030168|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_51827_PI430048170 0.0212365768729272 1.62897777652499 4.79863423353243 5.0127244952213
4.81309691366278 P P P 4.2884466667747 4.31470933344486 3.87962997053005 P P P
LNCV6_51827_PI430048170 mRNA
AACATTCTGACCAACAATCAGACTCTGCGGCTTCTCATGGGGCAGGGGCTTCCAGTGGTG NM_016174 RefSeq chr9
+ 128420479 128437351 CERCAM 51148 "cerebral endothelial cell adhesion molecule, transcript variant
1" GO:0005886|GO:0007159|GO:0006928|GO:0005788|GO:0007155 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_91501_PI430048170 0.2277348931826970.8308063863950023.12874409031016 2.94916778500243
3.48759740489421 P A P 3.46732861299876 3.28438287222864 3.64633758676954 P P P
LNCV6_91501_PI430048170 mRNA
AGAATATAAACACTTTCAGAGGATATATCCCAGCAAAACAAACCGAGCTGCCCGTGGAGC NM_133264 RefSeq chr17
+ 40219321 40282187 WIPF2 147179 "WAS/WASL interacting protein family, member 2"
GO:0005515|GO:0045087|GO:0003779|GO:0005856|GO:0038096|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139213_PI430048170 0.6479820589963090.9514684150106515.31522795335155
4.93736212752203 4.8567854675193 P P P 5.0588193883457 5.27511497235333
5.02006595184506 P P P LNCV6_139213_PI430048170 mRNA
CCCAGTCATTGAAACACCAAAACTATTATACCGGAGGGTGTAATAGTTTTGCTGCCCAGT NM_138797 RefSeq chr22
- 37830854 37844346 ANKRD54 129138 "ankyrin repeat domain 54, transcript variant 1"
GO:0045859|GO:0019887|GO:0005737|GO:0045648|GO:0030496|GO:0005634|GO:0032403|GO:0006913 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131054_PI430048170 0.0210407609455378 1.11036871344368 8.73839906716968
8.71967984062308 8.82140313777439 P P P 8.59885112879206 8.65471627546198 8.5736453573016
P P P LNCV6_131054_PI430048170 mRNA
GACTTCTTGTCTAAATGTTGGCCATTCAGTCTCAGGCCCTCTGTTCCATGGAATTGGGAA NM_023080RefSeq chr8
+ 145052437 145056030 C8orf33 65265 chromosome 8 open reading frame 33 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_137715_PI430048170 0.0175700855249616 0.392102797522517 2.89247036386317
2.41298321761636 3.34728917904236 A A P 3.90719593374503 4.45182246513925
4.43217651056663 P P P LNCV6_137715_PI430048170 mRNA
GCACATCTGTAAATGCAATCTTAATTGCCATATTTATGCAATCTGTGTACCAATTTGGAC NM_002480RefSeq chr12
- 79773562 79935198 PPP1R12A 4659 "protein phosphatase 1, regulatory subunit 12A, transcript
variant 1"
GO:0005515|GO:0015629|GO:0030155|GO:0071889|GO:0005737|GO:0006470|GO:0043292|GO:0000086|GO:0045
944|GO:0004871|GO:0046822|GO:0004857|GO:0005813|GO:0035507|GO:0019901|GO:0043086|GO:0051297|GO:0
007165|GO:0007067|GO:0019208|GO:0000776|GO:0005654|GO:0000278|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144060_PI430048170 0.295116497616432 1.53128207455428 1.87504490063229
2.09366603075983 2.46060711094845 A A A 2.53464683131418 0.503320915735652
0.646846046950901 A A A LNCV6_144060_PI430048170 mRNA
TGAGAAGGCCTTTCACTAGCCCCACCTTGTTAACAACTTGAACATTCATCAAAGTGTGGT NM_001146327 RefSeq
chr19 - 56774555 56840729 ZIM2 23619 "zinc finger, imprinted 2, transcript variant 3"
GO:0006355|GO:0003700|GO:0008270|GO:0005634|GO:0005575|GO:0003677|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_63527_PI430048170 0.16618683516579 1.08140140179857 9.58924721025667 9.76727879914996
9.72720440186005 P P P 9.60843986817343 9.51871602840218 9.62169201624867 P P P
LNCV6_63527_PI430048170 mRNA
TTGTTTTTGCCTTGTAAACTAGCGCCAAGGAACTGCAGCAAATAAACTCCAACTCTGCCC NM_001292018 RefSeq
chr17 - 78674046 78723750 CYTH1 9267 "cytohesin 1, transcript variant 3"
GO:0090162|GO:0005515|GO:0005802|GO:0005886|GO:0030155|GO:0005829|GO:0008289|GO:0031234|GO:0043
547|GO:0005086|GO:0005737|GO:0032012|GO:0005923|GO:0016192 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_97865_PI430048170 0.534847217462547 1.07905989667422 6.89721980973494 6.55942099214915
6.9162943851911 P P P 6.50343113542456 6.65103286185212 6.88973351897096 P P P
LNCV6_97865_PI430048170 mRNA
TTTTGGGAAGATTCAGGCTGAGTTTGAGAAGAAATGGGAGAATGGGACCTTTCCTGGATG NM_006802RefSeq chr1
- 37956979 37990089 SF3A3 10946 "splicing factor 3a, subunit 3, 60kDa"
GO:0008380|GO:0006397|GO:0005515|GO:0010467|GO:0016607|GO:0000398|GO:0000375|GO:0008270|GO:0005
681|GO:0005654|GO:0071013|GO:0000389 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132169_PI430048170 0.106728375086809 0.814413537543135 10.3415234561699 10.294630569752
10.3655562167431 P P P 10.5650412902589 10.4752575197748 10.8272410688626 P P P
LNCV6_132169_PI430048170 mRNA
GTTTCCATTGTAATCTTGACACATGCAATTGTAAATAAAAGTCACCACTTTTGCCAAGCT NM_004786RefSeq chr18
- 56602821 56638689 TXNL1 9352 "thioredoxin-like 1, transcript variant 1"
GO:0005737|GO:0000502|GO:0006662|GO:0015035|GO:0015036|GO:0045454|GO:0005634|GO:0070062|GO:0055
114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52133_PI430048170 0.785425786436681 0.977027792709236 7.49064954708208 8.00065948773811
7.66221725141666 P P P 7.68330590544203 7.76685009747924 7.84673817390472 P P P
LNCV6_52133_PI430048170 mRNA

ATGGCGAGTGCATATCAAGACGATGCCAGCTGCCACATATCGCCTCCTTACAGGCCAGGA NM_004886RefSeq chr19 - 3750772 3761675 APBA3 9546 "amyloid beta (A4) precursor protein-binding, family A, member 3" GO:0010468|GO:0005515|GO:0004857|GO:0048471|GO:0001540|GO:0007268|GO:0019899|GO:0015031|GO:0043086|GO:0001701 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115824_PI430048170 0.195597212607795 1.08969807442455 9.67474022337545 9.79428651080993 9.65022803731345 P P P 9.53432126867346 9.70935546293949 9.49904105460161 P P P LNCV6_115824_PI430048170 mRNA
TTGGTTTGGAGACATCCAAAGCCTGAAGCCAGGTGCCCTGCCTGAGTTGTGTGCATCCAG NM_018049RefSeq chr19 - 2233155 2236329 PLEKHJ1 55111 "pleckstrin homology domain containing, family J member 1, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129766_PI430048170 0.00396564040368935 0.3962885647110645 12.54789779418 8 4.74578590378817 5.2810598368442 P P P 6.18090185319559 6.28063150390698 6.69509697532685 P P P LNCV6_129766_PI430048170 mRNA
AAACACCTCCCGGTCACACAACAGGGTACGTAAATAAATGTGTTGTTACCAGTGAAAAAA NM_015176RefSeq chr1 + 224114086 224162047 FBXO28 23219 "F-box protein 28, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134137_PI430048170 0.0366694403170491 2.53775467073088 3.47766152776649 3.76961783651846 3.13313963618774 P P P 1.44565326032339 2.64614518031499 2.08314169984797 A P A LNCV6_134137_PI430048170 mRNA
GCTGGCCCCGGCTGGGCCCCGTGGCCACGGGGCGCGAGGAGGCTGTGGGGCTCACAATAA NM_001195135 RefSeq chr19 + 58396089 58397079 RNF225 NA ring finger protein 225 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130902_PI430048170 0.739699652375954 1.06096797729917 0.426235945248361 0.629095298596935 1.01110664554993 A A A 0.340264147712999 0.391194340012712 1.03308793433493 A A A LNCV6_130902_PI430048170 mRNA
GCATCCAAAAATCATATCTTGCTTTCATTTAGTTGAGAAAAGCCAGCATAGAGAAAGCAA NM_022063RefSeq chr10 - 118309059 118342327 FAM204A 63877 "family with sequence similarity 204, member A, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139416_PI430048170 0.805013711248149 1.0140355748797 0.453791474317566 0.516375103270026 0.384577592910694 A A A 0.53788296676441 0.466910367678532 0.280549511473357 A A A LNCV6_139416_PI430048170 mRNA
CTGCTCTACATCTCACTTTTGAGTTCAGTTGTAGTCATGAGTGATCCTTCATATTTTATT NM_014906RefSeq chr17 + 58755868 58985179 PPM1E 22843 "protein phosphatase, Mg2+/Mn2+ dependent, 1E, transcript variant 1" GO:0005739|GO:0005515|GO:0043234|GO:0035970|GO:0051496|GO:0005730|GO:0005634|GO:0006469|GO:0004722|GO:0035690|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145035_PI430048170 0.203443265860301 0.809537690606663 9.56482186040854 9.5527972566741 9.53305976147759 P P P 9.5446827546547 9.90067053679572 10.0711294942341 P P P LNCV6_145035_PI430048170 mRNA
ACTGCCAGGATTTTGTATTGCCATCGGGTGCCAAATAAATGCTCATATTTATTACTGAAA NM_032982RefSeq chr7 + 143288214 143307696 CASP2 835 "caspase 2, apoptosis-related cysteine peptidase, transcript variant 1" GO:0005515|GO:2001235|GO:0001554|GO:0005634|GO:0035234|GO:0005829|GO:0005739|GO:0005737|GO:0043525|GO:0016485|GO:0006508|GO:0006977|GO:0048011|GO:0003407|GO:0043065|GO:0097153|GO:0008630|GO:0007568|GO:0019904|GO:0097194|GO:0006915|GO:0097190|GO:0097192|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130557_PI430048170 0.0361565312398281 1.42617456496805 9.61522306886505 9.97365044746402 9.87608921617178 P P P 9.35790149327701 9.32183209987527 9.27081394149529 P P P LNCV6_130557_PI430048170 mRNA
TTTATTATTTTACTAACATGGTGATGGGCTCCCTCCCCTAACCTTGGTGCCTGATCCATC NM_001988RefSeq chr17 - 76006845 76027426 EVPL 2125 envoplakin

GO:0030057|GO:0005737|GO:0018149|GO:0008544|GO:0030216|GO:0005198|GO:0031424|GO:0030674|GO:0005856|GO:0001533|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139076_PI430048170 0.0133227146942424 0.3467745964710919.77825255365381 9.69440304510419 9.63863951210434 P P P 10.8444261939146 11.2701154164399 11.5076749060745 P P P LNCV6_139076_PI430048170 mRNA
ATTAAGATGAATGTAATTATTATTCCTCTTGCTGGTCACTACCGTCGCTTTCTATTTCTC NM_004926RefSeq chr14 - 68787654 68793914 ZFP36L1 677 "ZFP36 ring finger protein-like 1, transcript variant 1"
GO:0005515|GO:0043488|GO:0010467|GO:0033077|GO:0006355|GO:0060710|GO:0003700|GO:0060712|GO:0008283|GO:0006915|GO:0005634|GO:0003729|GO:0003342|GO:0003677|GO:0046872|GO:0006417|GO:0005829|GO:0007507|GO:0035264|GO:0021915|GO:0001570|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130354_PI430048170 0.00256178316344407 0.4696541472131736.95995104092374 6.64177822303463 6.80396916345243 P P P 7.73195707031075 7.80729727751039 8.12424963186402 P P P LNCV6_130354_PI430048170 mRNA
TGATGCTGTTAACCAAAGGGCAGAATAAATAAGCAAAATGCCAAAAGGGGTCTTAATTGA NM_001730RefSeq chr13 + 73058791 73077542 KLF5 688 "Kruppel-like factor 5 (intestinal), transcript variant 1"
GO:0060576|GO:0005515|GO:0008284|GO:0005794|GO:0005886|GO:0006366|GO:0030033|GO:0032534|GO:0000122|GO:0001525|GO:0035914|GO:0000978|GO:0046872|GO:0043231|GO:0071407|GO:0001077|GO:0005737|GO:0045944|GO:0045600|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133884_PI430048170 0.000145761439317839 0.1011672036380225.96661442257604 6.0667244464903 5.77730959129035 P P P 8.9713539602527 9.2796361926277 9.44995679603297 P P P LNCV6_133884_PI430048170 mRNA
GAATGGCAACCAGAGAATGTAAACAACCAAGGTGCATCTGGTTATGTTTTAAAATAAAGA NM_018304RefSeq chr17 + 59155498 59206709 PRR11 55771 proline rich 11 GO:0005737|GO:0016020|GO:0051726|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139093_PI430048170 0.0708197466871331.38654460595568 4.28597819542971 4.7350033672809 4.59483365667574 P P P 4.32721093750461 4.02320063650616 3.84508620708455 P P P LNCV6_139093_PI430048170 mRNA
ATGGATACCGCAGCTGCCGTCCATCATGCTATGGAGGATATGGATTCTCTGGATTTTATT NM_181611RefSeq chr21 - 30501871 30502090 KRTAP19-5 NA keratin associated protein 19-5 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132802_PI430048170 0.4629954244360850.92007185908141211.5882326418461 12.0551243495876 11.9485819892794 P P P 11.8722167999685 12.0536597908222 12.0592078918498 P P P LNCV6_132802_PI430048170 mRNA
CAAATGTGTATAAACTGCTGTCAATAAATGACACCCAGACCTTCCGGCTCAGCCAAAAAA NM_001281715 RefSeq chr17 - 49404047 49414905 PHB 5245 "prohibitin, transcript variant 4"
GO:0005515|GO:0030308|GO:0008285|GO:0006366|GO:0042826|GO:0044212|GO:0000981|GO:0005743|GO:0005634|GO:0005739|GO:0005737|GO:0010944|GO:0071354|GO:0070062|GO:0050847|GO:0006355|GO:0016575|GO:0060766|GO:0042981|GO:0000122|GO:2000323|GO:0001649|GO:0007165|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143935_PI430048170 0.0264090079187076 1.36638247194581 11.9804226133066 12.1320887118522 12.0800582922124 P P P 11.6927323799571 11.4167792343562 11.7172135127064 P P P LNCV6_143935_PI430048170 mRNA
GAAGACCCCGATGAGGATGCAATTCCCATTACTTAGGTTTCCCATAATTCTTAAATTTAA NM_006978RefSeq chrX - 119870531 119871828 RNF113A 7737 ring finger protein 113A GO:0005515|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138541_PI430048170 0.0210849470557928 1.65541908815747 5.52857725716135 5.75300908422218 5.2385917998391 P P P 4.87442813167938 4.93155353013102 4.54961229136353 P P P LNCV6_138541_PI430048170 mRNA

ATTACTACTGCTCTGTTGGCTACGGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGC NM_013378 RefSeq chr22 - 23752742 23754443 VPREB3 29802 pre-B lymphocyte 3 GO:0005783 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133482_PI430048170 0.00643958534007812 0.3240230785008213.76062158030509 3.14880972703341 3.75106517892656 P P P 4.79580122800325 5.12527500644556 5.58723765927847 P P P LNCV6_133482_PI430048170 mRNA
GTTCAGTGTGTCAGCTATTTTGTGAAGATGCTTAGATGTATAGTTTTGATAACCACAGTT NM_003243 RefSeq chr1 - 91680342 91886279 TGFBR3 7049 "transforming growth factor, beta receptor III, transcript variant 1" GO:0005515|GO:0055010|GO:0050680|GO:0046332|GO:0005615|GO:0005114|GO:0034695|GO:0007179|GO:0032354|GO:0070062|GO:0009986|GO:0017134|GO:0043393|GO:0030509|GO:0030165|GO:0005160|GO:0060038|GO:0060347|GO:0001889|GO:0043235|GO:0007181|GO:0005887|GO:0016049|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62713_PI430048170 0.00229122365425515 1.45768619658787 8.68805059134188 8.54841934873051 8.71746211610506 P P P 8.19422341821187 8.12957264325059 7.99779454207903 P P P LNCV6_62713_PI430048170 mRNA
AGTGCTTTTGGTGAGGAAGGTGAAGGTGATTATCTGGATGACTGGACAGTGCTCTGTAAT NM_006923 RefSeq chr17 - 28648355 28662172 SDF2 6388 "stromal cell-derived factor 2, transcript variant 1" GO:0004169|GO:0016020|GO:0006486|GO:0005615|GO:0035269 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128937_PI430048170 0.0274156789757858 1.6353731356021 9.3043875264463 9.71210447596691 9.25583194218819 P P P 8.8432967949679 8.66852485634611 8.66932717755172 P P P LNCV6_128937_PI430048170 mRNA
ATAAAAGTTGCACTGCGTTTCAAAAACCCACCCCTGAATGAATAAAAGGAGCCCTGGCTG NM_016496 RefSeq chr19 + 8413302 8439015 MARCH2 NA "membrane-associated ring finger (C3HC4) 2, E3 ubiquitin protein ligase, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128472_PI430048170 0.1346042312293680.6941901062249719.5446827546547 10.339424701386 10.1056186531058 P P P 10.6303356931301 10.4619432179501 10.5829429428246 P P P LNCV6_128472_PI430048170 mRNA
GCTACCTCTGACCCTGCCCTCCAGCCTGGGACAATAAAAGCCTTTTTTCTAGACAAAAAA NM_203370 RefSeq chr3 + 49803253 49805030 FAM212A 389119 "family with sequence similarity 212, member A" GO:0021915|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75398_PI430048170 0.1532475001453250.5637562148953161.32748033312122 2.4281869774828 2.55243494825525 A A A 2.39954423179535 3.20989193024404 3.30378985478035 A P P LNCV6_75398_PI430048170 mRNA
AAACGCTTCCATGAAATGAAGAAACGAGGACCTAAGCCTTATAGTCTTCATTTAGACCAC NM_001285439 RefSeq chr5 - 38937920 39074408 RICTOR 253260 "RPTOR independent companion of MTOR, complex 2, transcript variant 2" GO:0005515|GO:0051897|GO:0032008|GO:0031295|GO:0050731|GO:0009790|GO:0051896|GO:0005829|GO:0032314|GO:0030838|GO:0018105|GO:0007173|GO:0032956|GO:0031932|GO:0031929|GO:0048010|GO:0048011|GO:0031532|GO:0019901|GO:0048015|GO:0001938|GO:0008543|GO:0045087|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2594_PI430048170 0.1816994789875381.32375184561616 3.0646297945666 3.56417823433399 3.71750954968537 A P P 3.22511350724728 2.97505071151876 2.99629162943378 P P P LNCV6_2594_PI430048170 mRNA
GGGGCTACATTTGTTCATTTCCAGCAGTAGCATAAACTTACGGTGACATGGTAGACTTGT NM_001282687 RefSeq chr2 - 218135 256340 SH3YL1 26751 "SH3 and SYLF domain containing 1, transcript variant 4" GO:0006661|GO:1900027|GO:0019902|GO:0032587|GO:0035091 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130546_PI430048170 0.0144354414915526 0.2272630685701510.599093991960937

1.30458268804372 0.32073699520489 A A A 2.15994327468718 3.49830478671541
2.86007890539455 A P P LNCV6_130546_PI430048170 mRNA
TGGGGCCATGATTGGTTTCTAGGCAGTTCAAAGCAGGATATGTTAAGTAACACTCACCAT NM_000730RefSeq chr4
- 26481395 26490420 CCKAR 886 cholecystokinin A receptor
GO:0007631|GO:0042277|GO:0005886|GO:0007584|GO:0007586|GO:0046883|GO:0007200|GO:0007409|GO:0007
204|GO:0032870|GO:0005887|GO:0004951|GO:0030900|GO:0001764 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_131657_PI430048170 0.0477840088285896 1.73854373438896 4.0554737697342
3.34908837587536 3.62920841805597 P P P 2.77280874169648 2.61990106529188
3.25715638944067 A A P LNCV6_131657_PI430048170 mRNA
GGTTTAACCTCTACTTACTAAACACCTGCTACAATCCTGTTAATTCTTTTGACATGTAAG NM_007238RefSeq chr20
- 33702743 33720330 PXMP4 11264 "peroxisomal membrane protein 4, 24kDa, transcript variant 1"
GO:0005515|GO:0008150|GO:0016021|GO:0005778|GO:0005777 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133171_PI430048170 0.5421779878556171.09100377846043 6.93940635479382
6.60264779920421 7.09293134595682 P P P 6.64350410518083 6.67551663215768 6.9601190038552
P P P LNCV6_133171_PI430048170 mRNA
TACTAGGACACTTGACACAGCAAAAGAAATGGAGCAGATTACAGAAGTAGAGCCACCAGG NM_001173984
RefSeq chr16 - 50319017 50368934 BRD7 29117 "bromodomain containing 7, transcript variant 1"
GO:0005515|GO:0008285|GO:0044212|GO:0006357|GO:0003714|GO:0003713|GO:2000134|GO:0005634|GO:0035
066|GO:0006351|GO:0042393|GO:0002039|GO:0005737|GO:0007049|GO:0070577|GO:0045893|GO:0016055|GO:0
045892|GO:0008134. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69337_PI430048170 0.4426807979033760.5584809065860930.4655169074809420.506682839975576
0.424696576724697A A A 0.44032521125454 0.4300829959868082.23747056419918 A A A
LNCV6_69337_PI430048170 mRNA
CCTGCAGAATATTGCAACTTTGTGTTGTTTTATGATGAGCCTATAGTTGTGATACCAATA NM_018968RefSeq
chr2_KI270773v1_alt + 4167 64734 SNTG2 54221 "syntrophin, gamma 2"
GO:0042383|GO:0005737|GO:0016013|GO:0003779|GO:0030165|GO:0007417|GO:0005856 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137631_PI430048170 0.0152590653516453 0.5159816294858335.05884744993652
4.46890713767932 4.93822320786504 P P P 5.50462764823041 5.893392023888
5.95639439593631 P P P LNCV6_137631_PI430048170 mRNA
GTGACATCTGCATAAGACTTGTAATAGCTGAAGTTAATTGAGCTTAAAGGAATTGTTACC NM_181892RefSeq chr4
- 102794382 102827183 UBE2D37323 "ubiquitin-conjugating enzyme E2D 3, transcript variant 8"
GO:0005515|GO:0006511|GO:0010467|GO:0004842|GO:0034142|GO:0006367|GO:0006513|GO:0016567|GO:0005
886|GO:0016874|GO:0061418|GO:0005829|GO:0002756|GO:0007179|GO:0032480|GO:0034138|GO:0070062|GO:0
000209|GO:0071456|GO:0006915|GO:0000122|GO:0030509|GO:0002224|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127984_PI430048170 0.00863817682256106 0.6269556386636046.292257849085
5.97410777654404 6.17244127710784 P P P 6.67292251461551 6.76379118810108
7.01798405980132 P P P LNCV6_127984_PI430048170 mRNA
GTATATCAAGCCTCCTTGCCCCACAAAGCTTCCAAAGCCCGTAAATTTGTTAATCTAGAG NM_153332RefSeq chr8
+ 9002803 9033339 ERI1 90459 exoribonuclease 1
GO:0008408|GO:0005730|GO:0005634|GO:0019843|GO:0031047|GO:0046872|GO:0031125|GO:0005737|GO:0000
175|GO:0071044|GO:0043022|GO:0071204|GO:0071207|GO:0000467 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144976_PI430048170 0.0884404120701427 0.8745487208436188.85893247655167
8.74541550633661 8.73024135974976 P P P 8.84663852257373 9.0826640518829
8.97924825962211 P P P LNCV6_144976_PI430048170 mRNA

TTGTGTGCTTCCCTTGCTCTCTGAGCCCATTAAATAAAGAGGTTGTCTTGGCGTAAAAAA NM_001214909 RefSeq
chr16 + 30395111 30400108 ZNF48 197407 "zinc finger protein 48, transcript variant 3"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129861_PI430048170 0.9105800677891841.00958582232722 0.696258282958401
0.3000511925341580.472178057014956A A A 0.3172103364538890.28241414368652
0.796011531449917A A A LNCV6_129861_PI430048170 mRNA
ACGCTCAAAGCTTTTCCCAGGGAAAGGAACTCTCTAAAATAGTAATCTGATTTGATGAAA NM_181643RefSeq chr1
+ 111346559 111353017 PIFO 128344 "primary cilia formation, transcript variant 1"
GO:0005515|GO:0005802|GO:0033674|GO:0017137|GO:0019901|GO:0043015|GO:0048487|GO:0005634|GO:0036
064|GO:0031344|GO:0030030|GO:0016023|GO:0019894 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140495_PI430048170 0.1490768886801541.07651272155764 0.508600379646784
0.3409555171658560.424731328210628A A A 0.2756809029182230.359899692341363
0.323245068509389A A A LNCV6_140495_PI430048170 mRNA
GGTGTATGGAGCAAAAACGTGCTTATAAGCCATTATCTTCAGTTATTCAGTGGTTTATTA NM_007009RefSeq chr7
- 49937427 50093264 ZPBP 11055 "zona pellucida binding protein, transcript variant 1"
GO:0001675|GO:0001669|GO:0005634|GO:0005576|GO:0002199|GO:0007339|GO:0044297 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127660_PI430048170 0.0351709753070582 0.87792120797117 7.50041182795899
7.62801944320747 7.53119506787352 P P P 7.65313384152194 7.80284557867525
7.76606604561397 P P P LNCV6_127660_PI430048170 mRNA
CAGCTTGGATCCTCACGTGGCCTGGAGCCAGCATTAAACTCCTGTATGTCCTTCAAAAAA NM_152307RefSeq chr14
+ 103529171 103537073 TRMT61A 115708 tRNA methyltransferase 61A
GO:0031515|GO:0016429|GO:0030488|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_41176_PI430048170 0.9767262521529420.9718783389481631 1.8345609851796 11.7455571055197
11.500848766111 P P P 11.0969563520575 12.0821546976656 11.871315798664 P P P
LNCV6_41176_PI430048170 mRNA
TTCCCTGACCTCTTGCGGCCCCCGAGCGCTGCTGACATTGAGACCTGGTGTCAGCCTTAC NM_005147RefSeq chr16
+ 4425804 4456774 DNAJA3 9093 "DnaJ (Hsp40) homolog, subfamily A, member 3, transcript
variant 1"
GO:0005515|GO:0042645|GO:0030054|GO:0031594|GO:0009408|GO:0043231|GO:0042026|GO:0043069|GO:0060
336|GO:0005083|GO:0006457|GO:0005759|GO:0045211|GO:0031398|GO:0033256|GO:0043124|GO:0033077|GO:0
019901|GO:0007569|GO:0000122|GO:0030544|GO:0051082|GO:0007005|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139891_PI430048170 0.5939784180542750.8730252494530732.16151887486544
0.7782917147371512.41543770147127 A A A 1.81691244427899 2.07264132233878
2.45153709659988 A A P LNCV6_139891_PI430048170 mRNA
GCTCTCAGGTGTTGCCTGTCTTCACGAATGATTAGTATCGATTGACCTCTTTCTTAGGTG NM_001324RefSeq chr20
+ 56392517 56404526 CSTF1 1477 "cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa,
transcript variant 2"
GO:0005515|GO:0006379|GO:0008380|GO:0006369|GO:0006378|GO:0006396|GO:0010467|GO:0006366|GO:0003
723|GO:0031124|GO:0005634|GO:0043231|GO:0005737|GO:0000398|GO:0005654 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_57252_PI430048170 0.6950158864800050.875297758851 0.2733334550740780.287757112097126
1.45738792767063 A A A 0.3352414525442351.5321236726332 0.814822325858196A A A
LNCV6_57252_PI430048170 mRNA
ATCAAATGCTGAAATATGTTTCAACATCTGAATCAGATGGTACAGATTGCTGCAGTGGAA NM_000922RefSeq chr11
+ 14643722 14872058 PDE3B 5140 "phosphodiesterase 3B, cGMP-inhibited"
GO:0033629|GO:0005515|GO:0008286|GO:0032869|GO:0050995|GO:0005794|GO:0004119|GO:0004114|GO:0005

783|GO:0042593|GO:0001525|GO:0043422|GO:0046872|GO:0005829|GO:0007162|GO:0050796|GO:0016020|GO:0
007596|GO:0031018|GO:0016525|GO:0016021|GO:0043951|GO:0032045|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143561_PI430048170 0.506391505536681 1.00839499231694 0.33627755993606 0.317564544316
0.287116315504458 A A A 0.307326804319566 0.308988531767033 0.288799759565897 A A A
LNCV6_143561_PI430048170 mRNA
TTCATCATGGTTGCATCTGCACAATTCAGCATGAATCATGTGATGCTTGCCAAAACCGCT NM_001145805 RefSeq
chr5 + 150846522 150848669 IRGM NA "immunity-related GTPase family, M" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_135569_PI430048170 0.708695812969906 1.09512162167452 0.367693306108373
1.08335510571938 0.443881550625281 A A A 0.84772316927796 0.327435933976738 0.3793872398351
A A A LNCV6_135569_PI430048170 mRNA
TATGACCCTCAATCCAACAAATTTGTCAAATGTGCGGACATGAAAGACCGGAGGATGCAC NM_001081675 RefSeq
chr8 - 123645674 123652950 KLHL38 NA kelch-like family member 38 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135248_PI430048170 0.00221288267851698 0.607867419514588 5.93802081075616
5.93923899983705 6.0883331461408 P P P 6.656276402856 6.60797223186654 6.8496072465455
P P P LNCV6_135248_PI430048170 mRNA
CTTGGCAACTTCAGCTAGCTAGATATATCCATGGTCCAGAAAGCAAACATAATAAATTTT NM_001818 RefSeq chr10
+ 5196834 5218947 AKR1C4 1109 "aldo-keto reductase family 1, member C4"
GO:0044598|GO:0044597|GO:0001758|GO:0007603|GO:0006699|GO:0008209|GO:0009055|GO:0044281|GO:0015
125|GO:0001523|GO:0005829|GO:0047743|GO:0004033|GO:0005737|GO:0016655|GO:0071395|GO:0047023|GO:0
015721|GO:0008206|GO:0008202|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_132876_PI430048170 0.417807870298971 0.8447861510953 0.386227865844471
0.374004120360026 0.390439139868252 A A A 0.383737649731835 1.0135417026217
0.388687160444689 A A A LNCV6_132876_PI430048170 mRNA
GCAGAGCATGAAGAATCAGTGGAAATATTAAGTGTTAAAATGTGATGTTTTCTTTCCTGC NM_003865 RefSeq chr3
- 57197915 57200252 HESX1 8820 HESX homeobox 1
GO:0005515|GO:0030916|GO:0005634|GO:0008022|GO:0003677|GO:0006351|GO:0048853|GO:0043565|GO:0047
485|GO:0007420|GO:0003682|GO:0045892|GO:0043584 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137912_PI430048170 0.043652538614738 1.45474958341254 5.79481071217203
5.59192805178615 5.31610385621183 P P P 4.92560926866068 5.15699437948297
5.02818021154237 P P P LNCV6_137912_PI430048170 mRNA
GACCTGGTTGATGGGGAGTGGGAAGGGGAAGGAATAAAGAGATCTTCCTCAGGTAAAAAA NM_006076 RefSeq
chr7 + 100539210 100568220 AGFG2 3268 ArfGAP with FG repeats 2
GO:0043547|GO:0008150|GO:0008060|GO:0003674|GO:0016020|GO:0032312|GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130486_PI430048170 0.0857260078367052 0.962319413545292 0.412879598174874
0.411049613389395 0.353221122526616 A A A 0.43008005129537 0.468193680260772
0.44565290722289 A A A LNCV6_130486_PI430048170 mRNA
GGTTTCATTTTCTGAATGTACTCAAAACTCCCAACAACAATTGAACAGGATGTTTGCTAA NM_058241 RefSeq chr2
+ 134918821 134959345 CCNT2 905 "cyclin T2, transcript variant b"
GO:0010467|GO:0006368|GO:0006367|GO:0006366|GO:0019901|GO:0005634|GO:0000079|GO:0006351|GO:0007
049|GO:0045944|GO:0016032|GO:0005654|GO:0007179|GO:0051301 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142811_PI430048170 0.533091849179705 0.919750971047136 0.369693165091061
0.514731451837897 0.397702946139905 A A A 0.537509286879997 0.780938280101843
0.287874018818062 A A A LNCV6_142811_PI430048170 mRNA

CAGAGTCCTAGAAAAGTGACTTCAACAGAATTGTTACTAAAATTTGCACTCACAACATGA NM_000369RefSeq chr14 + 80955524 81146302 TSHR 7253 "thyroid stimulating hormone receptor, transcript variant 1" GO:0043235|GO:0005515|GO:0008284|GO:0007186|GO:0005886|GO:0007187|GO:0005887|GO:0004996|GO:0007267. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141787_PI430048170 0.00173107617895412 0.7571906316157829.8026066990206 9.88086788088518 9.78823270402501 P P P 10.2231688484415 10.2936182100131 10.1572427299394 P P P LNCV6_141787_PI430048170 mRNA
GATGAAGCTCTTGTGCTCATGTATATTATGACCTTCTGTGTTTTTGTTTCTGACTTGAAT NM_021922RefSeq chr6 + 35452360 35467104 FANCE 2178 "Fanconi anemia, complementation group E" GO:0003674|GO:0006281|GO:0005654|GO:0005634|GO:0043240 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140912_PI430048170 0.3537111858342830.9533771277599920.325002470061886 0.3602099312912710.355268817143704A A A 0.3717069809917920.524136745059474 0.344983587844347A A A LNCV6_140912_PI430048170 mRNA
CTGTCATTGGTGTTATATTCTGGTGATATGTGGAAATGTAATTTATATGACTGCATGGAG NM_001168235 RefSeq chr4 - 143577407 143700675 FREM3 166752 FRAS1 related extracellular matrix 3 GO:0031012|GO:0007154|GO:0016021|GO:0007155|GO:0005615|GO:0046872|GO:0005604 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140761_PI430048170 0.1952931148546970.83063510568981 7.2850052689876 6.80843164658498 6.87917390723312 P P P 7.30032647488468 7.24221472476242 7.27975929207205 P P P LNCV6_140761_PI430048170 mRNA
ATCTGGGCAGACCCCCCACCCTGCAGATGCTTCTAATAAAAAGCTCTTCTCATCAAAAAA NM_002344RefSeq chr15 - 41503641 41513887 LTK 4058 "leukocyte receptor tyrosine kinase, transcript variant 1" GO:0043066|GO:0005886|GO:0071300|GO:0008283|GO:0018108|GO:0005524|GO:0014065|GO:0007165|GO:0004672|GO:0016020|GO:0005887|GO:0010976|GO:0010666|GO:0006468|GO:0004713|GO:0004714|GO:0007169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130761_PI430048170 0.4434729949074951.2694593262918 0.277247306988945 0.5013790156886781.26031175708782 A A A 0.4997113780620360.391120634630118 0.300297560068543A A A LNCV6_130761_PI430048170 mRNA
CTTAGATACAGGAGAACTATTGCTTTTACCTGCAGAAACTCAAATGTTTTCGCTAAAACT NM_020390RefSeq chr3 - 170888414 170908637 EIF5A2 56648 eukaryotic translation initiation factor 5A2 GO:0005515|GO:0008284|GO:0008612|GO:0007283|GO:0003746|GO:0015031|GO:0005829|GO:0045905|GO:0006452|GO:0005643|GO:0005789|GO:0043022|GO:0051028|GO:0044267|GO:0045901|GO:0010509|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130948_PI430048170 0.48059484031806 1.062877488724 12.6369459514199 12.9113331539995 12.6386726857083 P P P 12.6564342488098 12.7310597823082 12.5472668589107 P P P LNCV6_130948_PI430048170 mRNA
CTCCAGTGGAATGGGTCTTTTCGGTGGAGATAAAAGTTGATTTGCTCTAACCGCAAAAAA NM_016219RefSeq chr9 + 137086926 137109187 MAN1B1 11253 "mannosidase, alpha, class 1B, member 1, transcript variant 1" GO:0009311|GO:0005783|GO:0004571|GO:0005509|GO:0044322|GO:0030433|GO:0031982|GO:0016020|GO:0006457|GO:0005789|GO:0006487|GO:0016021|GO:0044267|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127428_PI430048170 0.0734848344165813 2.0653048021385 1.47233829531434 1.62290411986279 0.69972411192122 A A A 0.2606207026618540.297050065643136 0.256480909031192A A A LNCV6_127428_PI430048170 mRNA
CTTCTCAAATGGATGATTTCTAAATACGCGTCAGATGAAGTGATTCTAACTTTCTCTGTA NM_020869RefSeq chr11 - 30863602 30992686 DCDC5 100506627 doublecortin domain containing 5 GO:0035556 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134211_PI430048170 0.8968600908811931.01227169935558 7.72492216102385

7.84767470625649 7.5178845626157 P P P 7.88548579973235 7.67682756075206
7.46366945287127 P P P LNCV6_134211_PI430048170 mRNA
TGGTTTCATTCATCTCAGACTTGTTATTTCACTCATCTCTAATAAAGGATTGGGGGGTCA NM_017707 RefSeq chr1
- 23428562 23484257 ASAP3 55616 "ArfGAP with SH3 domain, ankyrin repeat and PH domain 3,
transcript variant 1"
GO:0008060|GO:0005737|GO:0016477|GO:0051492|GO:0032850|GO:0008270|GO:0005925|GO:0001726 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128712_PI430048170 0.495263633345324 1.27526211949423 2.00483321887435
0.912201467679727 1.27801776530328 A A A 1.31900772319166 0.368691626771937
1.45329719636808 A A A LNCV6_128712_PI430048170 mRNA
GGTGCAATATGTTTTTTGAACCAGCTATAAAAGAAATTAAGAGGTACATGTGAGGGTAGA NM_001003818 RefSeq
chr11 + 5596634 5612958 TRIM6 117854 "tripartite motif containing 6, transcript variant 1"
GO:0003674|GO:0070206|GO:0005737|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143624_PI430048170 0.105281019058685 1.33276678655808 7.76017225690544
8.16598335191227 7.79157794290344 P P P 7.71782388340794 7.54188158934051
7.20492729109552 P P P LNCV6_143624_PI430048170 mRNA
TGTGTCTGATATTCTTGAGCCTGTTCGAGTTTCCTTTTCCAAGCCTCCTGTTCTCCCACC NM_152468 RefSeq chr17 +
78130777 78142968 TMC8 147138 transmembrane channel-like 8
GO:0005515|GO:0032091|GO:0031965|GO:0005794|GO:0005783|GO:0005102|GO:0001558|GO:0005615|GO:0005
737|GO:0055069|GO:0005789|GO:0016021|GO:0070062|GO:0006811|GO:0032460 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_126117_PI430048170 0.0570426057512016 1.31592096448596 12.1875160065046
12.4312083746326 12.5862831142201 P P P 12.0486107828698 12.1227815215956
11.8605813570693 P P P LNCV6_126117_PI430048170 mRNA
GCCGCGGGAACCCGAGACCCCAGTGTATGCCCCACCCCTGACCCCGCTCGCGACATGTCC NM_003336 RefSeq chrX
+ 119574466 119584429 UBE2A 7319 "ubiquitin-conjugating enzyme E2A, transcript variant 1"
GO:0005515|GO:0002474|GO:0006511|GO:0004842|GO:0000790|GO:0008284|GO:0033522|GO:0033503|GO:0016
874|GO:0006301|GO:0005829|GO:0005737|GO:0019787|GO:0000785|GO:0009411|GO:0031625|GO:0001741|GO:0
000209|GO:0060135|GO:0005524|GO:0001701|GO:0051865|GO:0006281|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137326_PI430048170 0.00074517136905367 0.433325667945605 7.59094091276822
7.66368807729912 7.5960318090493 P P P 8.71063397714728 8.91496055054904
8.83830513135586 P P P LNCV6_137326_PI430048170 mRNA
TGTTGCACTTGGTTTTGACATTGCCAATGGGGTTTGAACCAGTGCTCTCTCTAAATGAAA NM_001130966 RefSeq
chr7 + 139778247 140020325 TBXAS1 6916 "thromboxane A synthase 1 (platelet), transcript variant 3"
GO:0019369|GO:0019371|GO:0006805|GO:0005506|GO:0044281|GO:0006690|GO:0004497|GO:0045907|GO:0030
644|GO:0005789|GO:0016021|GO:0016705|GO:0004796|GO:0055114|GO:0020037 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_110406_PI430048170 0.00934682924698481 0.450383941466121 11.1189336127254
11.2222507211149 11.1829102336325 P P P 12.5500238140483 12.2834759914632
12.1105224053868 P P P LNCV6_110406_PI430048170 mRNA
AAGTGGATGGGGATCTGCAACTTCAATCAATCAACTTCATCGGAGGCCAGCCCCTCCGGC NM_006149 RefSeq chr19
- 38801670 38813100 LGALS4 3960 "lectin, galactoside-binding, soluble, 4"
GO:0005886|GO:0030246|GO:0007155|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145609_PI430048170 0.131174048297794 1.33053764168908 9.49681191033623
9.15367966045264 9.74117195656131 P P P 8.95964638077618 9.02578581504154
9.21714547382405 P P P LNCV6_145609_PI430048170 mRNA
GAGACAGGGTTTTTTCATTTTTGTGGGGGCTAGAAAAAACATAAAATGAGGCAGTTAAAT NM_001008491 RefSeq
chr2 + 241315186 241354026 SEPT2 NA "septin 2, transcript variant 1" NA . NA - . NA NA

NA NA NA NA NA NA NA
LNCV6_129677_PI430048170 0.1528385619851391.20781853106154 14.1771153107168
14.1469440967067 14.1939627895001 P P P 13.6902670325324 13.8532278328632
14.1240864344274 P P P LNCV6_129677_PI430048170 mRNA
CTAAACTTGACCTGCTTAATACATTCTAGGGCAGAGAACCCAGGATGGGACACTAAAAAA NM_006304RefSeq chr7
- 96688766 96709891 SHFM1 7979 split hand/foot malformation (ectrodactyly) type 1
GO:0005515|GO:0000502|GO:0000724|GO:0032039 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_50389_PI430048170 0.2804652937228580.7637216101350480.2777301362574110.521554419307921
0.357777338331028A A A 0.7992673553401551.12496165666521 0.291227198129487A A A
LNCV6_50389_PI430048170 mRNA
TATGAGGGTCAAGAAGCTCTTAGTTTCTAGACACCTCCCAGTGTTCACCTACACAGATGA NM_003813RefSeq chr14
+ 70452156 70459905 ADAM21 8747 ADAM metallopeptidase domain 21
GO:0007338|GO:0030424|GO:0005886|GO:0043025|GO:0006508|GO:0008270|GO:0016021|GO:0007339|GO:0004
222|GO:0008237|GO:0032504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144402_PI430048170 0.0144614330319615 0.2212016623364161.44278181650391
0.482693165656445 1.42849091529303 A A A 3.18249703851518 3.46720714823083
3.41096800881148 P P P LNCV6_144402_PI430048170 mRNA
CCCTGGACAATTGGATAAACAAATGTGATTGCTACCTTATGGATACAACGGACTTTTACA NM_014053RefSeq chr1
+ 212858254 212899363 FLVCR1 28982 feline leukemia virus subgroup C cellular receptor 1
GO:0005515|GO:0046620|GO:0005215|GO:0015886|GO:0031966|GO:0001568|GO:0005886|GO:0015232|GO:0048
704|GO:0007275|GO:0097037|GO:0048536|GO:0055085|GO:0001701|GO:0005739|GO:0006879|GO:0043249|GO:0
035264|GO:0005887|GO:0060323|GO:0030218|GO:0006810|GO:0006839|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_104270_PI430048170 0.1930267375218481.62225035875381 3.37855633685904
2.82959610212387 2.81757526919742 P A P 2.56071772575043 1.40003499348799
2.72239093679791 A A P LNCV6_104270_PI430048170 mRNA
TTACTTACTACGTATGTGCAATGATCTCCTAAGAAGATTGTCTAAATCCCAGAATACAGT NM_005131RefSeq chr18
- 214519 268059 THOC1 9984 THO complex 1
GO:0005515|GO:0008380|GO:2000002|GO:0003723|GO:0048297|GO:0005634|GO:0016363|GO:0046784|GO:0005
737|GO:0006406|GO:0032786|GO:0032784|GO:0006397|GO:0006396|GO:0000347|GO:0000346|GO:0006915|GO:0
003677|GO:0006351|GO:0045171|GO:0007165|GO:0016607|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136699_PI430048170 0.5799564471556820.7896065316570470.492282207564606
0.6083232169789480.576800894975321A A A 0.3497403220027411.53195630284277
0.521077713873082A A A LNCV6_136699_PI430048170 mRNA
ACTTCCTCACTCGGTCTTTCCGTGTGTTCTTTGGATTCTCTCTGAAAATTTTATGCTGAT NM_207417RefSeq chr9 +
132410195 132573319 C9orf171 NA "chromosome 9 open reading frame 171, transcript variant 1"NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130258_PI430048170 0.000368576370023377 2.75716725645878 10.4360585731506
10.4303635130284 10.3438854212809 P P P 9.06459947597041 8.89584546893754
8.85338275407345 P P P LNCV6_130258_PI430048170 mRNA
AGCCCAGTTAGCAAGGTGCCGGGTCACCCTGCAGGTTCCCATAAAAACGATTTGCAGCCA NM_016246RefSeq chr19
- 48813016 48836677 HSD17B14 51171 hydroxysteroid (17-beta) dehydrogenase 14
GO:0005515|GO:0006706|GO:0004303|GO:0047045|GO:0055114|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132067_PI430048170 0.1449138036439730.8429665491794084.60940383765535
4.79305024875473 4.77972224381318 P P P 4.9005354128518 4.82228231620346
5.18079075495986 P P P LNCV6_132067_PI430048170 mRNA
ATGCACTATAAATGCAACTTTCTCTACTGCTTTCTCAGTGCCTTTAGGAAGCTTTCAAAT NM_020731RefSeq chr5

+ 304175 438290 AHRR 57491 "aryl-hydrocarbon receptor repressor, transcript variant 1"
GO:0001191|GO:0007165|GO:0005737|GO:0045944|GO:0046983|GO:0033235|GO:0034753|GO:0004871|GO:0000
122|GO:0009410|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133609_PI430048170 0.8035942160425440.88611385593827 1.91816599672709
1.54697650344172 0.592345883175513A A A 0.7431310312625941.56584710761841 2.2109842533326
A A A LNCV6_133609_PI430048170 mRNA
TGTGCAATGCTACATGTACGTGGACTTATATCAGACCAGTGTGGATCTTCAAGAATCATT NM_002261RefSeq chr12
- 10412314 10420595 KLRC3 3823 "killer cell lectin-like receptor subfamily C, member 3, transcript
variant 1" GO:0007165|GO:0006968|GO:0030246|GO:0016021|GO:0004888 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137298_PI430048170 0.4942989997323641.0480699008879 0.591510119296659
0.46315892053434 0.336951386689004A A A 0.4818308975439550.368668348562757
0.345418518120435A A A LNCV6_137298_PI430048170 mRNA
GGCCACGGTTCAGACAATGGTATATATTTTTGTTATCAGGTGCATGTCTGTCTGATTTCT NM_003924RefSeq chr4
- 41744081 41748970 PHOX2B 8929 paired-like homeobox 2b
GO:0071773|GO:0010468|GO:0071157|GO:0021533|GO:0000790|GO:0008285|GO:0035914|GO:0002087|GO:0060
541|GO:0045944|GO:0021723|GO:0048894|GO:0048839|GO:0021934|GO:0000977|GO:0003360|GO:0048486|GO:0
000978|GO:0048483|GO:0006351|GO:0048485|GO:0048484|GO:0001077|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_101352_PI430048170 0.6960977037785371.0843113746269 3.23278373874262
3.74927913658317 3.87203284201046 P P P 3.7221129581675 3.68169213039691
3.09530429346801 P P P LNCV6_101352_PI430048170 mRNA
TTCTCTCCTGCAAGATCCAGAGCCCTGCGTCTAACTGCTTTTGCCAGCCTCTCTGTGGAG NM_002209RefSeq chr16
+ 30472661 30523185 ITGAL 3683 "integrin, alpha L (antigen CD11A (p180), lymphocyte function-
associated antigen 1; alpha polypeptide), transcript variant 1"
GO:0005515|GO:0005886|GO:0034687|GO:0006928|GO:0050900|GO:0032403|GO:0046872|GO:0050850|GO:0006
954|GO:0005911|GO:0030198|GO:0042102|GO:0007159|GO:0007155|GO:0050839|GO:0007157|GO:0070062|GO:0
001772|GO:0008305|GO:0046982|GO:0009986|GO:0007165|GO:0030369|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128143_PI430048170 0.00361007001207107 0.3906000485471056.17394448268453
6.20568711395623 6.0854016748736 P P P 7.32102417372032 7.48459172237057
7.70494606570635 P P P LNCV6_128143_PI430048170 mRNA
GATGTGCCGTTCTCACCCTGCAGAATACTGGTTTTGTCATTTCATAAATGATATTTTTAT NM_012262RefSeq chr1 +
86914651 87109998 HS2ST1 9653 "heparan sulfate 2-O-sulfotransferase 1, transcript variant 1"
GO:0016020|GO:0000139|GO:0005975|GO:0009405|GO:0008146|GO:0044281|GO:0016021|GO:0030203|GO:0006
024 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142665_PI430048170 0.1060641344460481.54776450877894 9.11005367812798
9.07705914260007 9.30558409276014 P P P 8.95905464731569 8.10195151643515
8.41951311884005 P P P LNCV6_142665_PI430048170 mRNA
CCATAGGACCTACAGCTCCCTTTCTCTTTATTGTGATTATACTTTAAATATGACATTGTC NM_001102559 RefSeq chr8
- 38263131 38269220 PPAPDC1B 84513 "phosphatidic acid phosphatase type 2 domain containing 1B,
transcript variant 1" GO:0005737|GO:0005886|GO:0046839|GO:0016021|GO:0008195 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_128496_PI430048170 0.4425390522230980.8961919244703320.332289417395865
0.3507031888883570.340087957884605A A A 0.7822040288356580.344666440299415
0.322595177477069A A A LNCV6_128496_PI430048170 mRNA
TAAAGACCCCAAAGACTCTGTTGGGAACTGTTGTCAATAAAATGTTTCTGAGGATGTTCA NM_207117RefSeq chr14
+ 100323341 100330378 SLC25A47 283600 "solute carrier family 25, member 47"
GO:0005743|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_131088_PI430048170 0.6397614932402580.9097390960654041 0.6306043212725
10.4081351035835 10.0026015718826 P P P 10.8468158324077 10.3863010009541
10.2092448868193 P P P LNCV6_131088_PI430048170 mRNA
TTATCACACTCGCCCTTTTCTCCTAGACTGTGACTCATGCTTATGGGCCTGGATTTTCTANM_175769RefSeq chr2 +
27149076 27152951 TCF23 150921 transcription factor 23
GO:0007517|GO:0046983|GO:0005634|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145540_PI430048170 0.4016396814808730.9578057274455610.26391782608909 0.4099366808141
0.295511668436988A A A 0.4767090760845060.3683753834712540.310005004136008A A A
LNCV6_145540_PI430048170 mRNA
CCCTGGGAATGTTATGAGCAAATGATACTCCATGAGTAAAATGATATCTATGCAAGTAAA NM_001244RefSeq chr9
- 114901144 114930595 TNFSF8 944 "tumor necrosis factor (ligand) superfamily, member 8, transcript
variant 1"
GO:0005164|GO:0008283|GO:0050830|GO:0005102|GO:0007267|GO:0006915|GO:0005125|GO:0005615|GO:0007
165|GO:0006955|GO:0043374|GO:0005887|GO:0045944 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137480_PI430048170 0.3993857260290731.34564810913243 1.94035070195318
2.24392240361018 2.74479075553865 A A A 2.2928137924047 2.23355510392729
0.807704973582992A A A LNCV6_137480_PI430048170 mRNA
AGTGGCAGAATCAGGGACATAAACTCAGAGAAAAAGGAACAGATGCTCTCTGGCTGCAAA NM_198510RefSeq
chrX - 54748898 54798240 ITIH6 347365 "inter-alpha-trypsin inhibitor heavy chain family, member
6" GO:0010951|GO:0004867|GO:0030212|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58555_PI430048170 0.31984923638945 1.11840020781328 14.3750055951525 14.3643257428906
14.4354531242016 P P P 14.0219445083675 14.1620045597422 14.4704652647481 P P P
LNCV6_58555_PI430048170 mRNA
TTTTCCCTGTGAGGAAACGGCTTTGTATTTTCTCTGTAATAAAATGGGGCTTCTTTGGAA NM_016497RefSeq chr12
- 6492149 6493305 MRPL5151258 mitochondrial ribosomal protein L51
GO:0070124|GO:0005515|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005761|GO:0005
743|GO:0006412|GO:0005762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140299_PI430048170 0.0521330427220411 0.6310686010674727.2575839604526
7.32507124645619 7.75988796135407 P P P 7.78869093019541 8.1192880389416
8.41298202682518 P P P LNCV6_140299_PI430048170 mRNA
GGTGGAATTCTTAGAACCAAAGTTATTCTTAATAAAAATCACCACATGCTTGGACCATGC NM_001282695 RefSeq
chr10 - 14518556 14774897 FAM107B 83641 "family with sequence similarity 107, member B,
transcript variant 1" GO:0007605 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140133_PI430048170 0.5337364998164550.9663094594846290.270262564890436
0.4427439589846660.307591185959886A A A 0.4839810033999320.374990575882826
0.310354334190856A A A LNCV6_140133_PI430048170 mRNA
CACCATTTTACCCAACAAATCATTGTTCGATCATTATTTGCCAGACTTGAATCTCTATGTNM_001303137 RefSeq chr13
+ 24309577 24322531 C1QTNF9 338872 "C1q and tumor necrosis factor related protein 9, transcript
variant 1" GO:0005581|GO:0005179|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102208_PI430048170 0.0041805977439225 1.59008980800169 4.78825590024292
4.54168725706863 4.74734442968917 P P P 4.04770196519367 4.15293824278082
3.86684831782749 P P P LNCV6_102208_PI430048170 mRNA
ACCTGATTTCGGCAAGGTGACCGTTCTGGATGCTAGAGTGAGTGTGCCCACCTGCGTAAG NM_001037806 RefSeq
chr12 - 49791145 49828425 NCKAP5L 57701 NCK-associated protein 5-like NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_105209_PI430048170 0.5614675260582670.9236187132677693.49040786091323
3.26819764300716 2.84366010553969 P P A 3.2331900827099 3.48026917262625
3.29393917027401 P P P LNCV6_105209_PI430048170 mRNA
CTCTGGTAAGAAGAGTGAAAGCAAAGAAGCCAAGAAGTCTGAAGAACCAAGAATTCGGAA NM_001113525

RefSeq chr16 + 89721543 89740924 ZNF276 92822 "zinc finger protein 276, transcript variant a"
GO:0006355|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_116820_PI430048170 0.8589328026553661.0096650478754 6.7225282302457
6.61292450888475 6.83719748859396 P P P 6.17732637857633 6.91028092963776
6.93226428807766 P P P LNCV6_116820_PI430048170 mRNA
ATGATGGCCCAGAAGCGCAAGGGGAAGATGGTGAAGCTGTACGTGCTGGGCAGCGTGCTG NM_015714RefSeq
chr1 + 209675324 209676390 G0S2 50486 G0/G1 switch 2
GO:0005811|GO:0005739|GO:0005515|GO:0003674|GO:2001238|GO:0044281|GO:0097191|GO:0044255 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139190_PI430048170 0.4370485107956071.21605674791675 0.578749238775818
0.45736174698982 1.25621953484802 A A A 0.4870341928933390.377777696703224
0.696589321380882A A A LNCV6_139190_PI430048170 mRNA
CCTCATGGACTGAGATTATACTCACCTTTTATGAAAGCACTGCATGAATAAAATTATTCC NM_003175RefSeq chr1
- 168540764 168543997 XCL2 6846 chemokine (C motif) ligand 2
GO:0008009|GO:0007165|GO:0006955|GO:0060326|GO:0008015|GO:0005576|GO:0005615 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130468_PI430048170 0.0203149699149346 0.4304609236521738.17650288216578
7.81380491534042 8.30222802654852 P P P 8.83475740100714 9.37055384600106
9.66104712524488 P P P LNCV6_130468_PI430048170 mRNA
AGAGTTAGACCTCTAGACTCACCTGTTCTCACGCCCTGTTTTAATTTAACCCAGCTATGG NM_006890RefSeq
chr19_KI270867v1_alt + 4497 8694 CEACAM7 1087 "carcinoembryonic antigen-related cell
adhesion molecule 7, transcript variant 1" GO:0005886|GO:0031225|GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_113720_PI430048170 0.3798498775212471.35247877115982 0.382628891024601
1.36821518668051 0.424468521719217A A A 0.3646284581998610.342499505583636
0.388992372633896A A A LNCV6_113720_PI430048170 mRNA
CGAGGAACACAGCAGAAGCAGAAAGAGAAGACGTCTTAATTTATCATTACAGATATATGA NM_001286646 RefSeq
chr8 - 141207165 141254629 SLC45A4 57210 "solute carrier family 45, member 4, transcript variant 1"
GO:0006810|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140678_PI430048170 0.0024572650603946 0.2575175729823615.60545670144619
5.46751936617794 5.79507952669558 P P P 7.22047345616816 7.63128754287136 7.8398517003593
P P P LNCV6_140678_PI430048170 mRNA
GGATTCCTTTCTTTTACAAATTGTGCTGAGGCAACTATGGCATAGAAATAAACATTTGAC NM_000944RefSeq chr4
- 101023429 101347471 PPP3CA 5530 "protein phosphatase 3, catalytic subunit, alpha isozyme, transcript
variant 1"
GO:0005515|GO:0005516|GO:0030018|GO:0006606|GO:0014883|GO:0005829|GO:0005739|GO:0005737|GO:0000
082|GO:0006470|GO:0045944|GO:0008144|GO:0046983|GO:0006816|GO:0004722|GO:0071333|GO:0005955|GO:0
046676|GO:0033192|GO:0046982|GO:0005509|GO:0033173|GO:0060079|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132686_PI430048170 0.0042630523375312 1.51045690353504 5.86687431651422
5.67765312464395 5.92447801289595 P P P 5.26668698505672 5.29369590247151
5.12976555208078 P P P LNCV6_132686_PI430048170 mRNA
TATACTTTGGATATGGATTTAAATGGTCTCTAAGAGCCGGGGGTAGGGGGCAGGAAAAGT NM_024958RefSeq chr20
+ 346725 354868 NRSN2 80023 neurensin 2
GO:0030133|GO:0008150|GO:0003674|GO:0005886|GO:0043025|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143034_PI430048170 0.4275235594661550.8398781123218955.21302448635635
5.67501750556879 5.58594014631399 P P P 6.1504738718483 5.45778507804562

5.56070879040411 P P P LNCV6_143034_PI430048170 mRNA
CCTGCCCAAGGATTTATTCATAGCTTACCTAAGAATTTCAAATTTCTACCATAACACTGA NM_214461 RefSeq
chr2_KI270768v1_alt - 98953 105653 C2orf27B NA chromosome 2 open reading frame 27B NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130567_PI430048170 0.5001260868751161.04661411031803 0.285476516976735
0.2957111146661670.516790597330899 A A A 0.3183001411694150.275929451425599
0.318183745674344 A A A LNCV6_130567_PI430048170 mRNA
CTAAGTATGAAACAACCTATGGTCTGGAAATTTGTATCGCAAAGCTATATGTGCATATGT NM_016442 RefSeq chr5
- 96760809 96808189 ERAP1 51752 "endoplasmic reticulum aminopeptidase 1, transcript variant 1"
GO:0005138|GO:0005515|GO:0002474|GO:0005783|GO:0005576|GO:0001525|GO:0005151|GO:0005615|GO:0045
766|GO:0005829|GO:0009617|GO:0016020|GO:0019885|GO:0004177|GO:0045088|GO:0008235|GO:0008217|GO:0
005789|GO:0045444|GO:0005788|GO:0008270|GO:0016021|GO:0006509|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144079_PI430048170 0.0868778560205132 0.8607865087669010.392525247494716
0.3743215438494450.344799652274773 A A A 0.4448778199000320.643344269232836
0.662730213981633 A A A LNCV6_144079_PI430048170 mRNA
GAGTGAGCCATGCAAAAATAGCTTTAAAATTATACATGAGCAGCTCAAAGTAAACGTGTA NM_003590 RefSeq chr2
- 224470149 224585397 CUL3 8452 "cullin 3, transcript variant 1"
GO:0005515|GO:0031208|GO:0005827|GO:0001831|GO:0004842|GO:0008284|GO:0006513|GO:0007369|GO:0016
567|GO:0035024|GO:0043149|GO:0017145|GO:0048208|GO:0042803|GO:0005829|GO:0000082|GO:0008054|GO:0
040016|GO:0007050|GO:0016055|GO:0090090|GO:0031625|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128172_PI430048170 0.3089467272867190.8202308100840670.408552277271869
0.3839195345798560.358507648268282 A A A 1.02704361527187 0.461083738512123
0.441287636551365 A A A LNCV6_128172_PI430048170 mRNA
ATGCAGAACGACTTTTACTGGCCATGGCAAATTGCAGTCTACCTGTGCATATCTGTCCAT NM_176883 RefSeq chr7
+ 143477872 143478796 TAS2R41 259287 "taste receptor, type 2, member 41"
GO:0033038|GO:0007186|GO:0005886|GO:0016021|GO:0001580 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142959_PI430048170 0.2267018347631270.5267709822302912.66451443215782
0.4218966915237752.30422500549205 A A A 2.76979493782483 3.21491615317552
2.97267249901556 P P P LNCV6_142959_PI430048170 mRNA
GCATCGATGTCTGTACTGTAAATTTCTAATTTATCACTGTACAAAGAAAACCCCTTGCTA NM_012193 RefSeq chr11
- 86945674 86955398 FZD4 8322 frizzled class receptor 4
GO:0005515|GO:0017147|GO:0030947|GO:0005886|GO:0071300|GO:0007605|GO:0010812|GO:0042701|GO:0061
299|GO:0007223|GO:0042803|GO:0051091|GO:0005911|GO:0030182|GO:0034446|GO:0043507|GO:0016055|GO:0
060070|GO:0031625|GO:0070062|GO:0042813|GO:0046982|GO:0009986|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_91724_PI430048170 0.1690441268682 0.7163131171364593.30192794203088 4.03035564968256
4.05802117184331 P P P 4.2804813980292 4.31264169956526 4.35949914938823 P P P
LNCV6_91724_PI430048170 mRNA
AAGCAGGTGGAGTTGGTTTGAATCTGTCTGCAGCTTCTCGAGTGTTTTTAATGGATCCAG NM_003071 RefSeq
chr3 - 149030116 149086554 HLTF 6596 "helicase-like transcription factor, transcript variant 1"
GO:0000209|GO:0005515|GO:0006355|GO:0006357|GO:0006200|GO:0016874|GO:0004386|GO:0005730|GO:0005
634|GO:0003677|GO:0005524|GO:0006301|GO:0006351|GO:0005737|GO:0016020|GO:0008270|GO:0005654|GO:0
016887|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136468_PI430048170 0.606637929416286 1.11664826029521 3.04611339904784
3.57319753174699 2.96598654017596 A P P 3.55234735281218 2.71801084282159
2.75320109287157 P P P LNCV6_136468_PI430048170 mRNA

CCTGGAAGACAGTCTGCTTAACTGGTGAAAATATACTGGATTATGTTTAATTATGGTTCT NM_030572 RefSeq chr12 + 21526321 21531276 SPX 80763 spexin hormone GO:0030133|GO:0010459|GO:0003084|GO:0031765|GO:0031766|GO:0045944|GO:0035814|GO:0032099|GO:0005184|GO:0044539|GO:0005615|GO:0051930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132425_PI430048170 0.514802890805241 1.03388502826233 13.332591862276 13.2767405943442 13.143387279935 P P P 13.1568472904284 13.2562968144883 13.2001159114995 P P P LNCV6_132425_PI430048170 mRNA
GCAATGTGAGGGTGAGGTACACCTACAGACATTAAATAATTTGCTGTGTCTGTGAAAAAA NM_001257134 RefSeq chr12 + 50111980 50120457 COX14 84987 "COX14 cytochrome c oxidase assembly factor, transcript variant 3" GO:0033617|GO:0005739|GO:0031966|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133852_PI430048170 0.194408548890397 1.25250525775924 7.9575591612256 7.96794920273656 7.96842065975297 P P P 7.26378592681265 7.73893206684553 7.85190912380219 P P P LNCV6_133852_PI430048170 mRNA
CCCAAGTTTACAGCTTGTACTTTACTTTAATGTGTAATACTCAACTCAAGGTACAAGACA NM_001303253 RefSeq chr6 + 159762478 159779112 ACAT2 39 "acetyl-CoA acetyltransferase 2, transcript variant 2" GO:0006629|GO:0005737|GO:0005730|GO:0003985|GO:0005654|GO:0005634|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144822_PI430048170 0.00151984997010721 2.49845389947208 5.77218184097196 5.90771942623082 6.18400959837982 P P P 4.42434536508802 4.63366389058977 4.84337036730772 P P P LNCV6_144822_PI430048170 mRNA
GCAGTCACCCATCAGAGAAAATAAAAATGGAAACCACGTTCACAGCATTTTAAAAGTTTT NM_033201 RefSeq chr16_KI270853v1_alt + 1092444 1246252 C16orf45 89927 "chromosome 16 open reading frame 45, transcript variant 1" GO:0021822|GO:0015630|GO:0007026 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140155_PI430048170 0.376346120718171 0.878785774012401 0.290971454713712 0.3086804742821 0.378354952862609 A A A 0.375539942313629 0.317164481443041 0.797083692377965 A A A LNCV6_140155_PI430048170 mRNA
GCAGAGCACATGTAGGGTTAATTCAACATTCTTTCCCATTATCATGGGTATCTTTTCTGA NM_001080850 RefSeq chr1 + 42534888 42654664 CCDC30 728621 coiled-coil domain containing 30 GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58312_PI430048170 0.66683075386994 0.985515676706036 0.393314232506034 0.372592586248907 0.252558242060604 A A A 0.343394347605343 0.38336754370322 0.358533172696152 A A A LNCV6_58312_PI430048170 mRNA
ATTGCAAAAGGAGCAGCTGCAGCTCAAGATCATTGAGATTGAGGATGAAGCTGAGAAGTG NM_012101 RefSeq chr11 - 120111285 120138155 TRIM29 23650 tripartite motif containing 29 GO:0005515|GO:0002039|GO:0005737|GO:0003700|GO:0006366|GO:0008270|GO:0005654|GO:0045111|GO:0000122|GO:1900181 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126737_PI430048170 0.316348724637256 1.59113852961094 0.468941231267326 1.76897867365497 1.78974941906136 A A A 0.36466954248005 1.2059841302026 0.66928806019295 A A A LNCV6_126737_PI430048170 mRNA
CTGCTGCTCCATGACTTTGTGTACAAAACTTTTTTCATCTGTAATGAATAGTGGCAATAA NM_001156474 RefSeq chr11 + 86374735 86423109 CCDC81 60494 "coiled-coil domain containing 81, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141851_PI430048170 0.70312181099351 0.888161509725896 1.08923101057859 2.82739692377605 2.64177671083652 A A A 2.72130214544102 2.89539863621543 1.75656212220209 A P A LNCV6_141851_PI430048170 mRNA
TGTATATACAAGTACACACAGATGTACACACAGATGTACACATGCTCCAGCCCCAGCTCT NM_014310 RefSeq

chr22 + 35541304 35553998 RASD2 23551 "RASD family, member 2"
GO:0051897|GO:0031681|GO:0005886|GO:0007264|GO:0003924|GO:0005525|GO:0006184|GO:0043949|GO:0001963|GO:0033235|GO:0007626|GO:0031397|GO:0031624 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131037_PI430048170 0.140620411582843 1.38242229160084 2.72830780700745 2.11820593439495 2.14673754157462 A A A 1.77524218553844 2.12214888071192 1.74889526434168 A A A LNCV6_131037_PI430048170 mRNA
TGGGATGGCGCAGGGCTTAAACTGACATAATAAAGATCTATTTCCTGTCCTCCAGCTACA NM_153614 RefSeq
chr11 + 73950318 73970287 DNAJB13 NA "DnaJ (Hsp40) homolog, subfamily B, member 13" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138748_PI430048170 0.224542294245463 0.719456750777388 8.58772826949713 7.80846346052823 7.52767052534232 P P P 8.64633243318821 8.54522320628077 8.36005402395034 P P P LNCV6_138748_PI430048170 mRNA
CACCCTCCCCTTTCTCTCTTTTAAAAATAAAGACAATACTTGAAGTTTGGGAAAATCATC NM_182581 RefSeq chr1
- 162373724 162376854 C1orf111 284680 chromosome 1 open reading frame 111 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_107642_PI430048170 0.2712668134782320.8634150059606846.21262380850908 6.12438011189754 6.5882760146016 P P P 6.51050654952668 6.38447153883133 6.69236449450895 P P P LNCV6_107642_PI430048170 mRNA
TATATGCAATGCTTGGGGAATATAACCACTCAGTGCTCTGTTATGACCACGCTTTGCAGG NM_018259RefSeq chr11
+ 43358884 43494933 TTC17 55761 tetratricopeptide repeat domain 17
GO:0005515|GO:0005737|GO:0005886|GO:0030041|GO:0015629 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130841_PI430048170 0.2007444465284540.6045247443851080.43938927347153 0.4147450533891790.458289776525156A A A 0.4207963195214431.57840837992999 1.26058144328525 A A A LNCV6_130841_PI430048170 mRNA
CTGCCAAAACTGTGGCATTTTCATTACAGGAGAGTTTACTATGCTAAAAGCAAAAAACAA NM_012419RefSeq chr6
- 153010896 153131254 RGS17 26575 regulator of G-protein signaling 17
GO:0043547|GO:0005737|GO:0005886|GO:0038032|GO:0005634|GO:0005096 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138930_PI430048170 0.00440554585101503 0.4621484912899525.48395574144605 5.5005218027187 5.89039241629763 P P P 6.75356170652657 6.49092760455432 6.96932302697231 P P P LNCV6_138930_PI430048170 mRNA
CAGATTCTTCAATGTGGTTTACCCAACTGGAGTAGTGATAAACACCTTAATCATAAAATG NM_014117RefSeq chr16
+ 9091679 9119698 C16orf72 29035 chromosome 16 open reading frame 72 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_108031_PI430048170 0.8333644022875651.00740530373241 7.74581704600327 7.87267385435377 7.80742276147939 P P P 7.74581704600327 7.82441634218684 7.82510655485136 P P P LNCV6_108031_PI430048170 mRNA
ATCTAGATATTTTCTCTTCACCGCATTTTGTAAATAAAGAGATGTGTATGCCTCCCTGAA NM_001042463 RefSeq
chr11 + 695590 704131 TMEM80 283232 "transmembrane protein 80, transcript variant 2" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67862_PI430048170 0.33497474929686 0.6379962961053241.29130286700771 3.36340216087816 3.33067400699437 A P P 3.9792847156794 3.08465990567742 3.52122588972094 P P P
LNCV6_67862_PI430048170 mRNA
GACCTCCAGCTACTCTTTGCATTTGAATATGTTGGGAAAAAATACCACAATTCAGCAAAC NM_017762RefSeq chr15
- 30938940 30991604 MTMR10 54893 myotubularin related protein 10 GO:0016791|GO:0016311 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131248_PI430048170 0.15429000074753 0.8141603582882517.01663578526417

6.97891748314376 7.26761273101389 P P P 7.60957916436563 7.15050552033968
7.37380826992273 P P P LNCV6_131248_PI430048170 mRNA
GAACTTGGAGTTTCTCCTTTATGTAGAGAAGAAGTAACTTAGGGTGTATTTGCAATGAAA NM_001258217 RefSeq
chr17 + 5486373 5490810 MIS12 79003 "MIS12 kinetochore complex component, transcript variant
1"
GO:0005515|GO:0007067|GO:0051382|GO:0007059|GO:0005634|GO:0000444|GO:0000278|GO:0051301|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131242_PI430048170 0.245796604068522 1.23235218681565 4.51996149739282
5.11196525525107 4.71671494573237 P P P 4.56260379060633 4.49025819735352
4.45353272381238 P P P LNCV6_131242_PI430048170 mRNA
TTGCCAAAAAGGAACTTTTCATGTCATGCAGTTGAGGGGACTTAGTCTCAATCCCAGGCT NM_025092 RefSeq chr11
+ 289137 295688 ATHL1 80162 "ATH1, acid trehalase-like 1 (yeast)" GO:0005975|GO:0016798 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_131418_PI430048170 0.628661168015859 1.02655867082056 6.75226495868093
6.91218817172459 6.77668103842477 P P P 6.67629533877013 6.85726025528226
6.79352384913786 P P P LNCV6_131418_PI430048170 mRNA
TCGGTTCCAAAGAATCTGTTTTGTTGTCATTTGTTTCTCCTGTTTCCCTGTGTGGGGAGG NM_178232 RefSeq chr15
- 88877284 88895626 HAPLN3 145864 hyaluronan and proteoglycan link protein 3
GO:0001501|GO:0005540|GO:0005578|GO:0007417|GO:0007155|GO:0005615|GO:0005201 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134575_PI430048170 0.0709563157824868 1.48059380079637 5.00422720918091
4.39707082054754 4.58918990969012 P P P 3.97708709327646 4.04033180929275
4.31921749125994 P P P LNCV6_134575_PI430048170 mRNA
TGGTTTGGAAGACAGCCAAAGAAATAAAAGCAGATTAAACTGTATCAGGTACATTCCAGC NM_031284 RefSeq chr15
- 72751366 72783785 ADPGK 83440 "ADP-dependent glucokinase, transcript variant 1"
GO:0016310|GO:0043843|GO:0016020|GO:0005576|GO:0046872|GO:0006096 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134207_PI430048170 0.231141324665705 1.46815424063024 1.88814575610354
2.25140123553599 2.37596561072784 A A A 1.80852866083034 2.02010679656457
0.799949348961856 A A A LNCV6_134207_PI430048170 mRNA
TCTGCCAAAACCTCCCACTCTCAAGTTTTAAGAGCCAATAAACCTTGTATCTGTAAAAAA NM_001243552 RefSeq
chr17 + 52985519 52987652 C17orf112 NA chromosome 17 open reading frame 112 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_126751_PI430048170 0.0282195937584053 0.685805220718558 8.71513799498911
8.58418916173224 8.33409149353387 P P P 9.25381798486091 9.14664440410606
8.86329285230894 P P P LNCV6_126751_PI430048170 mRNA
TCTTGAGGGTCCGGATGGGCTCAGGTAATAAAGAAACGGAAGCAGCAGCCAGCCAAAAAA NM_001300862
RefSeq chr19 + 4343526 4360086 MPND 84954 "MPN domain containing, transcript variant 3"
GO:0006508|GO:0008233 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128798_PI430048170 0.000294010671636862 1.60684509007875 11.1564303265523
11.2496781112715 11.1735031905063 P P P 10.4907367465933 10.4490936058881
10.5854059172775 P P P LNCV6_128798_PI430048170 mRNA
CAGAATTGCACCAGACCTGATGAGTTGGAAACAATCCTATACATTAAAAGAAATTACACT NM_016074 RefSeq chr1
+ 149899601 149900795 BOLA1 51027 bolA family member 1 GO:0005739|GO:0005576 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141757_PI430048170 0.417178366472469 0.936588640648579 12.286679473039
12.2817249063323 12.0188453866487 P P P 12.3601374474792 12.3427001540921
12.1768806588687 P P P LNCV6_141757_PI430048170 mRNA
CCCCTTCCAAATAATAAAGTCTATGGACAGGGCTGTCTCTGAAGTACTAACACAAGGACA NM_000666 RefSeq chr3

+ 51983283 51989202 ACY1 95 "aminoacylase 1, transcript variant 1"
GO:0006520|GO:0006805|GO:0006508|GO:0044281|GO:0004046|GO:0046872|GO:0008237|GO:0070062|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74240_PI430048170 0.2151215220371341.17153407947779 7.75715651446397 7.47609838124481
7.77969998777623 P P P 7.6175290532523 7.20553392374833 7.49369549665207 P P P
LNCV6_74240_PI430048170 mRNA
CGGCTGGAGAAGAAAACTCTGTAATACCATAAATAAGAGTGCTTGTAATAAAAGACTGTG NM_001145432 RefSeq
chr4 + 25914191 25929879 SMIM20389203 small integral membrane protein 20 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141861_PI430048170 0.000920711784472267 0.3197825302927836.48385328147467
6.10741346756107 6.50431262170907 P P P 7.75996428185286 8.04452572284659
8.22200947667701 P P P LNCV6_141861_PI430048170 mRNA
CTGGGGGCTCAGTTGTGTGCTGTAATGTCTTATTAAAGAAGATATTAAAGAAAACTAAAC NM_001267708 RefSeq
chr8 - 101197037 101205732 ZNF706 51123 "zinc finger protein 706, transcript variant 4" GO:0046872
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64988_PI430048170 0.000669755090955659 0.5650726333674881 2.4520616217837
12.4367051665769 12.3638977894799 P P P 13.1679053390379 13.3378066402342
13.2135551686051 P P P LNCV6_64988_PI430048170 mRNA
GGGTTTCTGATTGTGGCAACGTTTGCAACCGTTCACGATTCAATAAATATTGGATGAATT NM_003009RefSeq chr19
+ 47778584 47784686 SEPW1 6415 "selenoprotein W, 1"
GO:0008430|GO:0005737|GO:0016209|GO:0045454 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134402_PI430048170 0.113967485434271 0.542313370294146 4.26996259211509
2.95242486582193 3.76896325802037 P A P 4.27701109544151 4.79886048525259
4.79505466984181 P P P LNCV6_134402_PI430048170 mRNA
AACATCAAATCTATACGTTTAAAGCAGGGCAGTTAGCACAAATTTGCAAGTAGAACTTCT NM_016507RefSeq chr17
+ 39461510 39534565 CDK12 51755 "cyclin-dependent kinase 12, transcript variant 1"
GO:0070816|GO:0005515|GO:0006397|GO:0008380|GO:0019908|GO:0030332|GO:0005730|GO:0005634|GO:0005
524|GO:0008353|GO:0046777|GO:0004672|GO:0043405|GO:0016607|GO:0051726|GO:0005654|GO:0004693 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142319_PI430048170 0.0625898636764085 0.5546652825161060.503174685267287
0.6057899857145561.36458849327746 A A A 1.4123501424459 2.02972738106742 1.676472934033
A A A LNCV6_142319_PI430048170 mRNA
AAGCCCTGTGGAAGAAAATGGAAAACTTGAAGAAGCATTAAAGTCATTCTGTTAAGCTGC NM_001100RefSeq chr1
- 229431245 229434096 ACTA1 58 "actin, alpha 1, skeletal muscle"
GO:0030240|GO:0005515|GO:0001725|GO:0030049|GO:0005884|GO:0009991|GO:0048741|GO:0072562|GO:0048
545|GO:0015629|GO:0030017|GO:0005524|GO:0005615|GO:0005829|GO:0009612|GO:0006936|GO:0010226|GO:0
043531|GO:0043503|GO:0005200|GO:0005865|GO:0016049|GO:0017022|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141724_PI430048170 0.236894978568615 0.787139668998856 5.71911091137382
5.76807944983021 6.04384101668 P P P 5.85499135504786 6.12282892641313 6.52987973046992 P
P P LNCV6_141724_PI430048170 mRNA
GGCCATTTGCCCACAAATTTAGCTTTCATGTAACTCCTAGTGTGTTATATCATAATGTAT NM_198243RefSeq chr15
+ 100602549 100651699 ASB7 140460 "ankyrin repeat and SOCS box containing 7, transcript variant 2"
GO:0035556|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136607_PI430048170 0.0274769109559342 1.46429891386716 14.8613752384376
15.107485049073 14.7125956013367 P P P 14.2988551733302 14.3026091767007
14.4518485906545 P P P LNCV6_136607_PI430048170 mRNA
AGGGGGAAGTGTCTGCCTTTATGTCCTTTCTTCTGAAATAAAAGTAAAAGCATTTCTGGA NM_001283RefSeq chr7
+ 101154404 101161276 AP1S1 1174 "adaptor-related protein complex 1, sigma 1 subunit"

GO:0030121|GO:0006892|GO:0005765|GO:0009615|GO:0032588|GO:0006886|GO:0006898|GO:0050690|GO:0005
829|GO:0019886|GO:0005905|GO:0000139|GO:0016020|GO:0008565|GO:0061024|GO:0016032|GO:0030659|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144688_PI430048170 0.3047703022005320.8155975105562753.48335111702856
3.89168796583615 4.29057737982095 P P P 4.04993565293673 4.4301284594752
4.15257068227786 P P P LNCV6_144688_PI430048170 mRNA
TTTATGTGAGCTTGGTGTTTCACTTCCTTTTCATTAAAACCTCTTCTGTGCGGGGTCTCC NM_001143674 RefSeq chr1
- 167916674 167937069 MPC2 25874 "mitochondrial pyruvate carrier 2, transcript variant 1"
GO:0005739|GO:0006850|GO:0006090|GO:0050833|GO:0005743|GO:0005634|GO:0044281|GO:0016021|GO:0044
237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144439_PI430048170 0.2532767825491851.13481837218296 10.1919713166024
10.1725829379532 10.1631762992153 P P P 9.74546015849917 10.0624203486602
10.1427932594419 P P P LNCV6_144439_PI430048170 mRNA
GTTGGTGTTCTAAGACTCTGTGTGGCTGTGCAATTTCTGTACATTTGCAATTAGAAATAT NM_032552RefSeq chr9
+ 121567101 121785530 DAB2IP 153090 "DAB2 interacting protein, transcript variant 1"
GO:0005515|GO:0006986|GO:0032403|GO:0042803|GO:0042802|GO:0032312|GO:0043025|GO:0043122|GO:0034
261|GO:0034260|GO:0043124|GO:0019901|GO:0042059|GO:0031235|GO:0031434|GO:0031435|GO:0014067|GO:0
000122|GO:0005123|GO:0032266|GO:0038026|GO:0010596|GO:0007049|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141386_PI430048170 0.321024871248418 1.02885409571048 0.299259264447622
0.2587120550320810.365058477944858A A A 0.2778989167860050.250714475693453
0.273157364532083A A A LNCV6_141386_PI430048170 mRNA
AAGCAAATGGCACATTTGCATTAAACCTTTTGAAAAAGCTAGGGGAAAACAACTCAAACA NM_001123366 RefSeq
chr18 + 63949353 63960411 HMSD NA histocompatibility (minor) serpin domain containing NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143663_PI430048170 0.0206517925444504 0.3854110158497043.9872368730416
3.09817161395807 3.62100563033996 P P P 4.84393302398601 5.17583028645353
4.92712742757731 P P P LNCV6_143663_PI430048170 mRNA
CAGTACACATTAGTATGTATAACTGGCTTTACCAAATTGAATGAAAAGGAGCTTGTGCAA NM_015268RefSeq chr3
+ 132417708 132539032 DNAJC13 23317 "DnaJ (Hsp40) homolog, subfamily C, member 13"
GO:0005515|GO:2000641|GO:0016020|GO:0031901|GO:0071203|GO:0007032|GO:0005765|GO:0010008|GO:0001
649|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144322_PI430048170 0.8364009146488370.9858230389733814.0805441378607
13.8379813370285 13.8636723252512 P P P 13.834941567572 13.9597918858737
14.0534719990836 P P P LNCV6_144322_PI430048170 mRNA
CTTTTCCCTGCCTCACTCCAGGTTTTAGTGAAGTAAACAGTATTTGGAAAGTTGAAAAAA NM_001242597 RefSeq
chr19 + 35545599 35547527 TMEM147 10430 "transmembrane protein 147, transcript variant 2"
GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79072_PI430048170 0.2440730002094560.7733961000527926.9133500071889 7.2989689233978
7.7945334866915 P P P 7.88021175199514 7.57551781739124 7.78259782323324 P P P
LNCV6_79072_PI430048170 mRNA
TAGAAGCTGCAGAAAATGAATACCAGACTGCCATCAGTGAGAATTATCAGACAATGTCGG NM_006136RefSeq chr7
+ 116862508 116919259 CAPZA2 830 "capping protein (actin filament) muscle Z-line, alpha 2"
GO:0006928|GO:0003779|GO:0005576|GO:0015629|GO:0005829|GO:0051016|GO:0006461|GO:0016020|GO:0007
596|GO:0045087|GO:0008290|GO:0030863|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135510_PI430048170 0.1413731824976841.69600135291099 2.34669295011437
2.52407166007225 1.48826716906443 A A A 1.6660792371475 1.10509862652254
1.44372846212757 A A A LNCV6_135510_PI430048170 mRNA
ATATAAAAAGAAAATCACAGACAGGTGCTTCCACCACTCTGAGTGCTACAGTGGCTGCTG NM_001286550 RefSeq

chr6 + 35776593 35779552 CLPSL2 389383 "colipase-like 2, transcript variant 1"
GO:0016042|GO:0007586|GO:0005576|GO:0043085|GO:0008047 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141771_PI430048170 0.8555796929104820.9922931561425530.508277698334583
0.4483915141154990.307272744578097A A A 0.3802904049882030.470304835216077
0.452579269961992A A A LNCV6_141771_PI430048170 mRNA
AGGACCCAAGGCATACAGATTCACAAAATTAACTAATCTTTTTGCCTCAGAATACCAAAA NM_005014RefSeq chr9
- 92414244 92424554 OMD 4958 osteomodulin
GO:0005796|GO:0005975|GO:0005578|GO:0005576|GO:0044281|GO:0042339|GO:0018146|GO:0009405|GO:0042
340|GO:0007155|GO:0030203|GO:0043202|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130722_PI430048170 0.0814931555540932.61970019645717 3.55551286279774
3.27424433887151 2.07770650135844 P P A 2.20996500272496 1.61332246268711
1.07480556700263 A A A LNCV6_130722_PI430048170 mRNA
TGAAGCAAAGTCTAAAGAAAGGGCCAGCTCCCATCAGGAGCTCGGCTTCTTGCTCCAGCC NM_213605RefSeq chr8
+ 144798875 144809144 ZNF517 340385 zinc finger protein 517
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143179_PI430048170 0.5055008001048161.08971411330537 7.06017747695238 7.0082126778833
6.67955401520659 P P P 6.97241074958242 6.84216281230201 6.56000247336739 P P P
LNCV6_143179_PI430048170 mRNA
CACGCAAGTGGCACTTTAAGCCCTGCATCCTCGGTTGAGAGTAAAAGGCTTTTCTCCCTT NM_004813RefSeq chr11
- 45909668 45918123 PEX16 9409 "peroxisomal biogenesis factor 16, transcript variant 1"
GO:0005515|GO:0006625|GO:0005783|GO:0045046|GO:0070972|GO:0008022|GO:0016020|GO:0022615|GO:0032
581|GO:0005789|GO:0007031|GO:0016558|GO:0005779|GO:0016557|GO:0005778|GO:0005777 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140057_PI430048170 0.5752825152477861.19464650680742 4.1965764893115
4.19247904574862 3.29344746807032 P P P 3.7453029565861 3.63342332453121
3.70479175103747 P P P LNCV6_140057_PI430048170 mRNA
ATTGGAGCTTGAGCTTCACACCACCAGCTTCCAGAGATTAAAGTTTGTACAAAACATTGC NM_138281RefSeq chr17
+ 49969197 49974959 DLX4 1748 "distal-less homeobox 4, transcript variant 1"
GO:0043565|GO:0005515|GO:0001078|GO:0006355|GO:0003700|GO:0007275|GO:0005634|GO:0000122|GO:0000
978 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131748_PI430048170 0.3464842745299880.9068811635625325.21266660465505 5.3313215525714
5.62679183349275 P P P 5.4985552270515 5.50437822811097 5.61968547110641 P P P
LNCV6_131748_PI430048170 mRNA
GCTGTGCGTGGAAAAAGACGATGTTTATGTTCTTATAGAATAAAAGCTGTGGAATGAAGC NM_018951RefSeq chr7
- 27170590 27174336 HOXA10 3206 "homeobox A10, transcript variant 1"
GO:0005515|GO:0005667|GO:0060065|GO:0042826|GO:0009954|GO:0005634|GO:0007275|GO:0030326|GO:0007
283|GO:0000978|GO:0009952|GO:0006351|GO:0007338|GO:0001077|GO:0001501|GO:0005737|GO:0045944|GO:0
008584 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145610_PI430048170 0.0256215981390783 1.16975514061554 7.08151912221821
7.02077978984778 7.19192185851994 P P P 6.93989674857355 6.85189247106577
6.82659003037818 P P P LNCV6_145610_PI430048170 mRNA
CCAGATGTGAAAGAAGCTGCCTGTTTACTGATCCATTGAATAAACCCATTTTAATAGAAA NM_000740RefSeq chr1
+ 239629072 239909417 CHRM3 1131 "cholinergic receptor, muscarinic 3"
GO:0005515|GO:0030054|GO:0005886|GO:0008283|GO:0044281|GO:0030425|GO:0032279|GO:0006939|GO:0016
323|GO:0045987|GO:0008144|GO:0045211|GO:0042166|GO:0004872|GO:0043679|GO:0046541|GO:0007213|GO:0
016907|GO:0007399|GO:0007165|GO:0006112|GO:0050796|GO:0007186|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_96773_PI430048170 0.2293847479598651.37939658114875 2.80236477886047 3.35220323856039
2.64438231203707 A P A 2.3041661945371 2.95755985380921 2.09968486454877 A P A
LNCV6_96773_PI430048170 mRNA
AACCAAAGTCAAGCATGTGATAAAGCAGGTGGAATGCATGGATGACCATTACGCCAGTCANM_153710RefSeq chr9
+ 133376412 133406096 STKLD1 169436 "serine/threonine kinase-like domain containing 1, transcript
variant 1" GO:0004672|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135494_PI430048170 0.2801040303218591.14758899079517 6.35781981667995
6.20175924212446 6.4465373515548 P P P 5.87483322950536 6.14096518266632 6.3638203365518
P P P LNCV6_135494_PI430048170 mRNA
GGAAATTTATTTATAGCATGAAAATAAACCTGGTGGCTGGAGTCTGCTTGTACGGTCAAA NM_002705RefSeq chr16
- 4882506 4937135 PPL 5493 periplakin
GO:0030057|GO:0005739|GO:0005515|GO:0005886|GO:0031424|GO:0005200|GO:0005634|GO:0005856|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135070_PI430048170 0.0730498921663484 0.4089957313849193.47555941091687
2.07122127111093 2.80965758268965 P A A 4.25346656006104 4.19833345234939
4.10298223947507 P P P LNCV6_135070_PI430048170 mRNA
GTTGACCCTTGCCTGTAGTTGTTATTGGTTCAGAAGTAAATTTTATTGATGCTACAAGTA NM_173666RefSeq chr5
- 118836073 118988605 DTWD2 285605 DTW domain containing 2 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136898_PI430048170 0.4861103256840671 6.4380912808892 11.0648724128907
5.01165373802974 5.32928203283045 P P P 5.39129108407137 5.21302448635635
5.79870568073048 P P P LNCV6_136898_PI430048170 mRNA
CAACTGAAACTACCATGCTAACAAATATATTACTTAGAACATGTCCACAAGACCACAAAC NM_001204830 RefSeq
chr2 + 99155073 99163150 LIPT1 51601 "lipoyltransferase 1, transcript variant 6"
GO:0006629|GO:0005739|GO:0016746|GO:0009249|GO:0006464 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_97733_PI430048170 0.1263094552345310.8586708906936054.98275975931873 4.91108729683039
4.75453916503349 P P P 5.12411496878328 4.93720438492431 5.23986325759771 P P P
LNCV6_97733_PI430048170 mRNA
CTTAACCCAGAAGTAGCTGAATGTGTTACTCCATTGCTGAGGAGTGACTATCTGTTATAG NM_020240RefSeq chr5
+ 131264008 131394689 CDC42SE2 56990 "CDC42 small effector 2, transcript variant 1"
GO:0006909|GO:0005515|GO:0005737|GO:0005886|GO:0005198|GO:0008360|GO:0001891|GO:0042995|GO:0009
966|GO:0005856|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128094_PI430048170 0.9648572610039691.05515004246854 1.76563488289641
2.23803734990835 3.36922601443758 A A P 1.9793989602898 2.47829726830354
2.99475885828757 A A P LNCV6_128094_PI430048170 mRNA
GTTATAGCATACTGTGTGCTAATTGAAAAGAATGAGGTGGAGCTGTAAATACTGTACAAA NM_145312RefSeq chr10
+ 43606406 43617904 ZNF485 220992 zinc finger protein 485
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142929_PI430048170 0.000545978807488604 2.05344784044335 11.2592847487947
11.414248133408 11.2902677249284 P P P 10.312588564045 10.2939372404075
10.2470442251511 P P P LNCV6_142929_PI430048170 mRNA
GTGGCTGCAGAAGGGCCACCCTAGCCTTTTAACTGCTTTGTCAAAATTAAACATTTTGTA NM_032140RefSeq chr16
- 67662946 67666725 ENKD1 84080 enkurin domain containing 1 GO:0005881|GO:0015630 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59568_PI430048170 0.4110080729104331.13794495204763 7.03605544412031 7.24230000744853
7.59483092031319 P P P 7.01646047641887 7.17911256884141 7.16870921910887 P P P
LNCV6_59568_PI430048170 mRNA

GATTATTGAAGTGTTTGCTAACAGTGTCCAGTTTCCCCATGAGTCCAGCCCTAGATAGCT NM_139078RefSeq chr12 + 111842227 111893424 MAPKAPK5 8550 "mitogen-activated protein kinase-activated protein kinase 5, transcript variant 2"
GO:0005515|GO:0032007|GO:0007265|GO:0090400|GO:0005524|GO:0006417|GO:0000187|GO:0002039|GO:0007165|GO:0005737|GO:0046777|GO:0000165|GO:0004674|GO:0005654|GO:0004708|GO:0051019 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59099_PI430048170 0.000965058508057702 0.7428290666586669.59413167177867 9.64775739791945 9.71487332551337 P P P 10.1267384966452 10.0732340729145 10.0448211949695 P P P LNCV6_59099_PI430048170 mRNA
GGGTGTTGTGGTTTTTTGTTTTTGTTTTGCTTCTGAGAAAGCATTTGCCTTTCTTCCTCT NM_002868RefSeq chr12 + 55974010 55996683 RAB5B 5869 "RAB5B, member RAS oncogene family, transcript variant 1"
GO:0005515|GO:0042470|GO:0005886|GO:0003924|GO:0048227|GO:0030139|GO:0005525|GO:0006886|GO:0005622|GO:0006184|GO:0030742|GO:0016020|GO:0030100|GO:0019882|GO:0031901|GO:0007032|GO:0032482|GO:0019003|GO:0005769|GO:0070062|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130425_PI430048170 0.3231061561757031.22721055043036 3.69926621895908 3.97563385445577 3.86046774839079 P P P 3.63839747057303 3.01357192428316 3.87884842136078 P P P LNCV6_130425_PI430048170 mRNA
TACTCTTTCAAGTATGAGACAGTGCCCAACCTTCTCACGCAGCACTGTGCTTGTATCTAA NM_002191RefSeq chr2 + 219572231 219575713 INHA 3623 "inhibin, alpha"
GO:0045578|GO:0042541|GO:0005515|GO:0007267|GO:0034673|GO:0060395|GO:0030154|GO:0001541|GO:0045077|GO:0042127|GO:0043408|GO:0051726|GO:0043025|GO:0007050|GO:0048468|GO:0046982|GO:0005102|GO:0010862|GO:0046882|GO:0046881|GO:0042981|GO:0005576|GO:0045786|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143410_PI430048170 0.0574314888884014 0.6532962942356614.98420629724589 5.09316808312828 5.59359748656904 P P P 5.88617983408704 5.62819495302098 6.04458449882394 P P P LNCV6_143410_PI430048170 mRNA
GCACTTTGGAAAGTTGGTTCAGTTACTACTATGAGGCCATAATATATTTGCTGGTATTAA NM_024093RefSeq chr2 + 105337358 105348814 C2orf49 79074 "chromosome 2 open reading frame 49, transcript variant 1"
GO:0008150|GO:0003674|GO:0048598|GO:0072669 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131751_PI430048170 0.0761302433841899 1.59807502701428 1.66804679140372 1.68079025035127 1.06287096330252 A A A 0.7868765102475410.455344143442859 1.14112821889497 A A A LNCV6_131751_PI430048170 mRNA
CAGGGCCCAGGTCTGTGTGATATCTGTATATATTGCATTTTGTTGATTTTAATAGAAAAC NM_002516RefSeq chr19 - 45939512 45973399 NOVA2 4858 neuro-oncological ventral antigen 2
GO:0051252|GO:0003723|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140328_PI430048170 0.3288483094601141.41837181323817 5.75864931880123 4.90069834287488 5.27832034556336 P P P 3.89806788206869 5.45932838574196 4.79118485990587 P P P LNCV6_140328_PI430048170 mRNA
AGGTCAGCTTCCTCGCTGTTTTGGTCCTAACTCAAAAGCAGATCCAGTAAAGGTTTTTGT NM_005225RefSeq chr20 - 33675485 33686404 E2F1 1869 E2F transcription factor 1
GO:0005515|GO:0003700|GO:0005634|GO:0048146|GO:0007283|GO:2000045|GO:0071398|GO:0005737|GO:0000082|GO:1900740|GO:0007219|GO:0045944|GO:0035189|GO:0048255|GO:0006355|GO:0008630|GO:0043276|GO:0071456|GO:0006915|GO:0001047|GO:0000122|GO:0003677|GO:0097193|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135812_PI430048170 0.4783422581064710.8382694560020170.311358083032411 0.2486217028713020.301960826174951A A A 0.9872909080162720.245370717138913 0.263500761771814A A A LNCV6_135812_PI430048170 mRNA
TCTGTCACTTTTATATACACACAGGGGAGGGGACCGTTTCCATAGAGAGGGAATATCACA NM_053049RefSeq chr10 + 5365012 5374206 UCN3 114131 urocortin 3

GO:0051412|GO:0035902|GO:0001664|GO:0051431|GO:0007586|GO:0071456|GO:0005615|GO:0009749|GO:0045
838|GO:0042594|GO:0005179|GO:0031669|GO:0043196|GO:0032024|GO:0043679|GO:0007189 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138852_PI430048170 0.1043178284352651.36754524633313 5.69000276875091
5.92047533289103 5.3400273900357 P P P 5.38920660927129 5.16730874776445
5.07954885477533 P P P LNCV6_138852_PI430048170 mRNA
GGGGTTGTGCAGGTGTGAATAAAGAGAATAAGGAAGTTCTTGGAGATTATACTCAGAAAA NM_001142784 RefSeq
chr9 + 34652184 34661901 IL11RA 3590 "interleukin 11 receptor, alpha, transcript variant 3"
GO:0032502|GO:0007165|GO:0004896|GO:0007566|GO:0005887|GO:0019221|GO:0060322|GO:0004871|GO:0004
888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137380_PI430048170 0.3966245782071251.76437273326094 0.379273276123904
0.2519112977743251.96949066985136 A A A 0.2684463511071460.288549235385833
0.270030137166329 A A A LNCV6_137380_PI430048170 mRNA
TCAAGAACATGTGCAAGCTCAAGCCGCTGCTGAACAAGTGGCTGGAGGAGGCGGACTCAA NM_006236 RefSeq
chr2 + 104854067 104858573 POU3F35455 POU class 3 homeobox 3
GO:0072227|GO:0008284|GO:0043066|GO:0003700|GO:0072236|GO:0072218|GO:0021869|GO:0072233|GO:0005
634|GO:0007417|GO:0006351|GO:0072240|GO:0010628|GO:0043565|GO:0045944|GO:0021799|GO:0071837|GO:0
045893|GO:0045892. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135376_PI430048170 0.1431270647424910.481854906784971 1.84365648793924
0.46106784327403 1.91285683431914 A A A 1.9428338803222 2.3975442847142
3.17096651838878 A A P LNCV6_135376_PI430048170 mRNA
GGACACTAAGCTGTACTGTAACTCTGAAAGTGTTAAAAGTAGTTACTGATGACAAAAAGT NM_004234 RefSeq chr19
- 44286347 44305025 ZNF235 9310 zinc finger protein 235
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130740_PI430048170 0.00306695219203604 0.4032713771275881 0.2073196501787
9.88513390240002 10.0627751285627 P P P 11.37380904915 11.3212777023567 11.407335665635
P P P LNCV6_130740_PI430048170 mRNA
TCTGCTTTGGACTCCTCTGCTAGTGTTACAGATGGAAATAAAACCATTAATTTGAACCAA NM_001185009 RefSeq
chr4 + 2469452 2515859 RNF4 6047 "ring finger protein 4, transcript variant 1"
GO:0005515|GO:0004842|GO:0046685|GO:0003700|GO:0016874|GO:0005634|GO:0050681|GO:0090169|GO:0042
802|GO:0005737|GO:0070534|GO:0045944|GO:0085020|GO:0032184|GO:0003713|GO:0031491|GO:0090234|GO:0
003677|GO:0006351|GO:0051865|GO:0070979|GO:0016605|GO:0008270|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140189_PI430048170 0.0265565419687931 0.6216379897771555.69834318963375
5.34474844366136 5.84966614387939 P P P 6.09274174504447 6.3181094314815
6.54887494113349 P P P LNCV6_140189_PI430048170 mRNA
CCTGACTTTTGGCCAAAAGCTTACTTAAAATTAAGGATTTACTAAGTCATCATCAGCTGT NM_015442 RefSeq chr3
+ 32685144 32773875 CNOT10 25904 "CCR4-NOT transcription complex, subunit 10, transcript variant
1"
GO:0005515|GO:0010467|GO:0006355|GO:0016020|GO:0005634|GO:0031047|GO:0030014|GO:0006417|GO:0006
351|GO:0000289|GO:0005829|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140932_PI430048170 0.0229492146931617 0.4989653715666097.7653752852725
7.54345090161307 7.91069928800296 P P P 8.38226937899366 8.69953277790516
9.08426760793584 P P P LNCV6_140932_PI430048170 mRNA
GGAATCTTCACTTTTGCTACCTTGATATAGCATTGGGCTATCATGTTACAACATTGAAAT NM_016076 RefSeq chr1
+ 244653047 244709034 DESI2 51029 "desumoylating isopeptidase 2, transcript variant 1"
GO:0005737|GO:0006508|GO:0008233 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144616_PI430048170 0.3563966684188820.7011973707586043.04176140871973

3.21642930668454 3.05607054637306 A P P 3.20074102193794 4.23509350819604
3.14322414734872 P P P LNCV6_144616_PI430048170 mRNA
GTTGCCCCCATGTTGAATCCCTTTATTTATACACTGAGAAACAAACAAGTAAAAGATGTT NM_001005490 RefSeq
chr12 + 55247287 55248226 OR6C74 NA "olfactory receptor, family 6, subfamily C, member 74" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144701_PI430048170 0.1976188197013970.9061268758855691 2.9866433301914
12.9238794719118 12.8644448881039 P P P 12.9148994210611 13.1551322933968
13.1225950476043 P P P LNCV6_144701_PI430048170 mRNA
TTTGTACACGTGTGACTTCGTCCAGTTACAAACCCAATAAACTCTGTAGAGTGGAAAAAA NM_004068 RefSeq chr3
+ 184174845 184184091 AP2M1 1173 "adaptor-related protein complex 2, mu 1 subunit, transcript variant
1"
GO:0072583|GO:0005515|GO:0005215|GO:0035615|GO:0005886|GO:0007268|GO:0005765|GO:0006886|GO:0008
289|GO:0005829|GO:0005739|GO:0019886|GO:0007173|GO:0007411|GO:0016032|GO:0061024|GO:0005048|GO:0
070062|GO:0048011|GO:0048013|GO:0030122|GO:0042059|GO:0050690|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129910_PI430048170 0.1279603419116781.36062803647523 0.760102544789926
1.33605177624815 0.882291021429966 A A A 0.6653201493187270.507230219375371
0.533756026912989 A A A LNCV6_129910_PI430048170 mRNA
ACCCTTTAATATACAGTCTGAGGAATAAGGATGTGAAGAAAGCATTAAGGAAGGTCTTAG NM_001002917 RefSeq
chr11 - 124309839 124310766 OR8D1 283159 "olfactory receptor, family 8, subfamily D, member 1"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139950_PI430048170 0.5985450761071341.02519212442004 0.598338841434939
0.4848843405536730.609690357737016 A A A 0.5271073785600020.614215278082831
0.44204253066935 A A A LNCV6_139950_PI430048170 mRNA
GAAAAAATTAAAACCACCCATAACTTTACTCTGAAGCAGTAACAGTGGCATGTTTCCTCC NM_006056 RefSeq chr2
- 231523159 231530471 NMUR1 10316 neuromedin U receptor 1
GO:0006821|GO:0019722|GO:0005886|GO:0004930|GO:0048016|GO:0007200|GO:0007202|GO:0008188|GO:0006
939|GO:0007186|GO:0005887|GO:0007218|GO:0001607|GO:0006816|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143968_PI430048170 0.10697978526811 1.56633690093125 7.51254703719644 7.727429605235
7.71622363012408 P P P 6.45954855963208 7.14080319120411 7.29466531553414 P P P
LNCV6_143968_PI430048170 mRNA
GTAGACCTAGTCCATCAGATCATGTGTTCTGGAGAGTGTTCTTTATTCAATAAAGTTTTA NM_000165 RefSeq chr6
+ 121435576 121449744 GJA1 2697 "gap junction protein, alpha 1, 43kDa"
GO:0005515|GO:0060044|GO:0046850|GO:0015075|GO:0034405|GO:0060307|GO:0010232|GO:0051259|GO:0005
764|GO:0007512|GO:0001947|GO:0007507|GO:0034220|GO:0006936|GO:0051924|GO:0006810|GO:0032024|GO:0
043123|GO:0030500|GO:0005794|GO:0048487|GO:0030165|GO:0001701|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141759_PI430048170 0.00783353445314798 0.5139803003068067.32226198003827
6.887508638224 7.20364964440163 P P P 8.0053314895431 8.09910291284875
8.21609532684496 P P P LNCV6_141759_PI430048170 mRNA
CCCATATCTGTGCAATGGAATATAAATATCACAAAGTTGTTTAACTAGACTGCGTGTTGT NM_021999 RefSeq chr13
+ 48233137 48262096 ITM2B 9445 integral membrane protein 2B
GO:0005515|GO:0005794|GO:0005886|GO:0005576|GO:0005524|GO:0005615|GO:0042985|GO:0097192|GO:0043
231|GO:0007399|GO:0001540|GO:0016020|GO:0031301|GO:0030660|GO:0010008|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130402_PI430048170 0.5082352462877760.7464446552378591.59760689237344
0.3195270114913961.05477127656731 A A A 2.00742438846713 1.56877556205436

0.606092053737555 A A A LNCV6_130402_PI430048170 mRNA
TTAAGCTTCTAGACACTCCTTGAAATGTGTGTGTGATGGAGGGAAGGGGACAGATTTGAG NM_004959 RefSeq chr9
- 124481235 124507420 NR5A1 2516 "nuclear receptor subfamily 5, group A, member 1"
GO:0005515|GO:0010467|GO:0006367|GO:0030325|GO:0003705|GO:0003707|GO:0001553|GO:0007267|GO:0050
810|GO:0005634|GO:0010259|GO:0030154|GO:0005543|GO:0003690|GO:0045944|GO:0043401|GO:0009888|GO:0
004879|GO:2000195|GO:0003713|GO:0003677|GO:0043565|GO:0007538|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106129_PI430048170 0.0135145983844327 0.903607285760813 13.1811506000228
13.1456097158383 13.0904671488791 P P P 13.2676063867369 13.3264561956472
13.2624244707727 P P P LNCV6_106129_PI430048170 mRNA
ATCCATCTCTGCTGAGAAGCCTCCTCCCTCCCGAGACAAGATCATCTGCCTGGCCTCTCA NM_001114598 RefSeq
chr19 - 50511599 50513885 ASPDH 554235 "aspartate dehydrogenase domain containing, transcript
variant 1" GO:0050661|GO:0006742|GO:0033735|GO:0009435|GO:0055114 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138575_PI430048170 0.147585760920125 0.794738177836774 3.85428911165006
3.93611446961636 4.15930100641259 P P P 4.03854877806485 4.33835226634172
4.54097319025269 P P P LNCV6_138575_PI430048170 mRNA
CTATAAGTGTCACCCAGACATCTTTATTGAGCATTTTGGAGACTGAGTTTTTAATATCTG NM_139160 RefSeq chr11
+ 33016181 33033582 DEPDC7 91614 "DEP domain containing 7, transcript variant 2"
GO:0051056|GO:0008150|GO:0003674|GO:0007264|GO:0005575|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132558_PI430048170 0.271317411848087 0.871632686668049 5.62281134123609
5.45178411893424 5.83016669976455 P P P 5.85815207700726 5.6305858359197
6.01051434322346 P P P LNCV6_132558_PI430048170 mRNA
CATGCTGCAACATGGTTTATATTCATGCTGCCCTAGAAACTTTTGTAATTATTTGTTGCA NM_152271 RefSeq chr8
- 12721896 12755483 LONRF191694 LON peptidase N-terminal domain and ring finger 1
GO:0004176|GO:0006508|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142878_PI430048170 0.00894511978404607 0.379120496632016 4.49949141348687
4.44928678523962 4.68108329761446 P P P 5.57349223145256 6.16948026890925
6.03019182372818 P P P LNCV6_142878_PI430048170 mRNA
AAGACATTCAAGAAGACCGCCAGCCTGATAGCCAACAGTTGTAAAGCAGTCTCTGTTCTA NM_014317 RefSeq chr10
+ 26697665 26746797 PDSS1 23590 "prenyl (decaprenyl) diphosphate synthase, subunit 1"
GO:0050347|GO:0006744|GO:0000010|GO:0046982|GO:0005759|GO:0051290|GO:0044281|GO:0008299|GO:0046
872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141691_PI430048170 0.115939187833289 1.30541833469619 9.28097954376769
9.35885131104813 9.3636795176551 P P P 9.22899484883509 8.71686866470679
8.85592872231078 P P P LNCV6_141691_PI430048170 mRNA
GGACTTTGGTCTTGACTGTTCTCTGGGTGCTTAATAAATAATACTAATTATGCAAGTTCT NM_001268284 RefSeq
chr19 + 7888504 7902023 LRRC8E 80131 "leucine rich repeat containing 8 family, member E,
transcript variant 2" GO:0005515|GO:0005886|GO:0016021|GO:0006811 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_98400_PI430048170 0.427805343699998 0.93210777915127 7.03773381044788 6.74415001512751
6.69130274659874 P P P 7.01663578526417 6.90394708178646 6.87774768493311 P P P
LNCV6_98400_PI430048170 mRNA
TCACAGCTCGTCCCTCACCAAACATCAGCGAATCCACACTGGGGAGAAGCCCTACGAATG NM_001289402 RefSeq
chr19 + 58059238 58069742 ZNF135 7694 "zinc finger protein 135, transcript variant 7"
GO:0006355|GO:0003700|GO:0022604|GO:0007010|GO:0005634|GO:0003677|GO:0046872|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141450_PI430048170 0.33918532633227 0.530052134749999 3.32342827051937 2.8941515289176

1.64399375861465 P A A 4.1121767481482 4.06214531903293 2.26575712600277 P P A
LNCV6_141450_PI430048170 mRNA
GGCTCCCGTTTAGCATTTTGTACTTAAGGAAATAAAAAACCAACAAAGGATCTCACATTT NM_000599RefSeq chr2
- 216672104 216695549 IGFBP5 3488 insulin-like growth factor binding protein 5
GO:0017148|GO:0005515|GO:0048630|GO:0051897|GO:0031994|GO:0031995|GO:0005615|GO:0001558|GO:0014
912|GO:0010906|GO:0031069|GO:0035556|GO:0044342|GO:0006006|GO:0001968|GO:0030336|GO:0060056|GO:0
005576|GO:0048662|GO:0042593|GO:0016942|GO:0001649|GO:0007165|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129234_PI430048170 0.0463486476350149 2.46399449601585 3.05670597306775
3.25103784846055 3.06200810441295 A P P 2.38078088007128 1.31657684476787
1.55148550230571 A A A LNCV6_129234_PI430048170 mRNA
GGAACTGTGTTCTCTGTCTCTTTACTGAAGATAAAGGTGTAGTAAAAGCTCCCACACACC NM_001068RefSeq chr3
- 25597904 25664372 TOP2B 7155 topoisomerase (DNA) II beta 180kDa
GO:0000792|GO:0042826|GO:0000819|GO:0005634|GO:0007409|GO:0046872|GO:0005829|GO:0005737|GO:0005
080|GO:0003918|GO:0009330|GO:0046982|GO:0008301|GO:0005730|GO:0006312|GO:0008022|GO:0005524|GO:0
003682|GO:0000712|GO:0006268|GO:0005654|GO:0030900|GO:0001764|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_32872_PI430048170 0.302592068966381 1.27853054113677 1.0539522578631 0.848419500869562
1.28622971853029 A A A 0.375937817319712 1.24539789780216 0.346235422933718 A A A
LNCV6_32872_PI430048170 mRNA
TACAAGAATCCCGAGAGATGGTACAGGGCTAGTTTTCCCATCATCACGGTGACCGCCGCC NM_001083899 RefSeq
chr19_KI270938v1_alt - 996188 1020746 GP651206 "glycoprotein VI (platelet), transcript variant 1"
GO:0005515|GO:0005886|GO:0009986|GO:0005518|GO:0030168|GO:0097197|GO:0050900|GO:0005887|GO:0007
596|GO:0004872|GO:0004888|GO:0007167|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129405_PI430048170 0.0495393058124451 0.845703096697442 11.4049161574359
11.458024868898 11.3800070624197 P P P 11.6769772583451 11.7494601030591
11.5347425310069 P P P LNCV6_129405_PI430048170 mRNA
TTCTAATCATGAATGAACAATAAAGCCCACGCTCTTTGTCAGGCTCCACATGCCAAAAAA NM_004148RefSeq chr9
- 93121488 93134288 NINJ1 4814 ninjurin 1
GO:0016021|GO:0042246|GO:0007155|GO:0001954|GO:0007399 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143629_PI430048170 0.0367534659252001 0.5975177698716849.13869541496454
9.73235977217935 9.38132180751528 P P P 9.82483071620894 10.3128612920122
10.3488795333835 P P P LNCV6_143629_PI430048170 mRNA
CAGCAGCTTTTCAAAATGCACTATGCCTGATTGCTGATCGTGTTTTAACTTTTTCTTTTC NM_003670RefSeq chr3 +
4979411 4985180 BHLHE40 8553 "basic helix-loop-helix family, member e40"
GO:0005515|GO:0001191|GO:0003700|GO:0006366|GO:0003705|GO:0000981|GO:0005634|GO:0042803|GO:0043
433|GO:0043153|GO:0001102|GO:0006355|GO:0005794|GO:0046982|GO:0003714|GO:0019904|GO:0005730|GO:0
043426|GO:0043425|GO:0070888|GO:0000122|GO:0032922|GO:0001078|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127975_PI430048170 0.0907889604192053 1.0506423767881 6.72026316342651
6.70810097437056 6.74425693560694 P P P 6.64358474521301 6.70050429117112
6.61359728874518 P P P LNCV6_127975_PI430048170 mRNA
CTATGCAGAGTTACAGTCACAAAGTTGTGTATTTTATGTTACAATAAAGCCTTCCTCTGA NM_012448RefSeq chr17
- 42199176 42276406 STAT5B 6777 signal transducer and activator of transcription 5B
GO:0005515|GO:0003700|GO:0006549|GO:0006366|GO:0019530|GO:0019915|GO:0001553|GO:0032819|GO:0048
541|GO:0003690|GO:0046983|GO:0032496|GO:0043029|GO:0032355|GO:0046543|GO:0007565|GO:0033077|GO:0
046544|GO:0038161|GO:0019903|GO:0045588|GO:0046449|GO:0006953|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_139141_PI430048170 0.0467010403691045 0.397241896715442 11.5234449120207
11.7074935875241 10.8784040052842 P P P 13.2441797201824 12.7109325348847
12.0226482905315 P P P LNCV6_139141_PI430048170 mRNA
TGACTCCTCAGCCAAGCATATTATCAACTGTCGGAAACTAGGTTTTCCCATAGTGATCCA NM_180989 RefSeq chr13
+ 94601849 94634645 GPR180 160897 G protein-coupled receptor 180
GO:0007186|GO:0016021|GO:0019236|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128151_PI430048170 0.0206626092755090 0.579224920780378 5.86617713410626
5.89871101496237 6.01489229785097 P P P 6.726489730622 6.45688544819583 6.926053577925
P P P LNCV6_128151_PI430048170 mRNA
CTTTCACGAATGCATGTTGACGCTTTCAGTTCACCCCTTTCTTTGCTAACTTTCTTCCTA NM_018941 RefSeq
chr8_KI270926v1_alt + 176361 199228 CLN8 2055 "ceroid-lipofuscinosis, neuronal 8 (epilepsy,
progressive with mental retardation)"
GO:0008361|GO:0060041|GO:0005783|GO:0006672|GO:0045494|GO:0005739|GO:0030163|GO:0050881|GO:0033
116|GO:0050884|GO:0050885|GO:0007628|GO:0046513|GO:0044257|GO:0008203|GO:0008306|GO:0060052|GO:0
005793|GO:0008610|GO:0021523|GO:0043066|GO:0051348|GO:0045861|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130763_PI430048170 0.394401199934704 1.03076977372363 0.502561441613489
0.502198021812472 0.54627746140198 A A A 0.495958438971583 0.528678496046293
0.392186795714201 A A A LNCV6_130763_PI430048170 mRNA
GTAGAACTTAGGTATAGTGTTTTCAAATTCTAAAGTCCACTTCAGTTAAGAACCACTGAC NM_006239 RefSeq chr4
- 75859872 75902528 PPEF2 5470 "protein phosphatase, EF-hand calcium binding domain 2"
GO:0005515|GO:0030145|GO:0005506|GO:0005509|GO:0051879|GO:0031435|GO:0010801|GO:0043409|GO:0001
917|GO:0005737|GO:0050906|GO:0006470|GO:0043405|GO:0030544|GO:0043506|GO:0004722|GO:0007601|GO:0
001750 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139606_PI430048170 0.820433983399162 1.0154908954997 8.35252255204677
8.24178791796542 8.36304905101342 P P P 8.10376242072187 8.27340842021112
8.49059372860681 P P P LNCV6_139606_PI430048170 mRNA
CCTTGGCTCTGGAGACAAAATTCTTGCTCTGGCAAGTTTTGAGGTTGAAAAAACAAAAAA NM_032368 RefSeq chr1
- 9929717 9942768 LZIC 84328 leucine zipper and CTNNBIP1 domain containing
GO:0008013|GO:0010212 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145644_PI430048170 0.356024419182341 1.02687934112644 0.378917000594354
0.387302794964811 0.28855367461118 A A A 0.301536512448841 0.321909166604256
0.318508262335134 A A A LNCV6_145644_PI430048170 mRNA
TCAGACAAACCTATGACCTCACACAAATCTGTAACTTCATGTATCACAGTCTCTATAAAA NM_198460 RefSeq chr1
+ 89363876 89388160 GBP6 163351 "guanylate binding protein family, member 6"
GO:0006955|GO:0071346|GO:0008152|GO:0003924|GO:0005525|GO:0042742|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139965_PI430048170 0.505047520410231 1.03177541712115 12.1494063018132
12.1171744090874 12.0845381339331 P P P 11.9631195720149 12.1607343520863
12.0857485675546 P P P LNCV6_139965_PI430048170 mRNA
GCTCCGCCGCCCTGCTGATAAGCTGGCTTCATTAAACTGACACTTCTCATGTGCAAAAAA NM_024682 RefSeq chr19
+ 49877424 49888750 TBC1D17 79735 "TBC1 domain family, member 17, transcript variant 1"
GO:0005515|GO:0005776|GO:0006914|GO:0042147|GO:0032851|GO:0031410|GO:0015031|GO:0005097|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132478_PI430048170 0.0258274134230387 0.418212350454191 4.66921814808872
4.67165909574405 4.95483584098325 P P P 5.62717139600644 5.87805831271813
6.45450249742116 P P P LNCV6_132478_PI430048170 mRNA
AGCCGACTCATATTTCCAAACCTATAACCAATTGCTGATCTCCTGTGTAAAGCATTTTTT NM_001284214 RefSeq
chr2 - 229763836 229922009 TRIP12 9320 "thyroid hormone receptor interactor 12, transcript variant

1"
GO:2000780|GO:0046966|GO:0005515|GO:0005737|GO:0004842|GO:0006281|GO:0042787|GO:0016874|GO:0005654|GO:0005634|GO:0009790|GO:0006974 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62924_PI430048170 0.00263757064947577 0.365314088092003 5.24040204608774 5.44321266326049 5.38064108949869 P P P 6.54250335414598 6.95494013427613 6.89893086968833 P P P LNCV6_62924_PI430048170 mRNA
ACGACCCTGGACTCCAACAACAACACAGTGGCGTCATCACCTACATTGGCTCCAGTGGCT NM_021724 RefSeq chr17 - 40092783 40100725 NR1D1 9572 "nuclear receptor subfamily 1, group D, member 1"
GO:0005515|GO:2000189|GO:0034144|GO:0010467|GO:2000188|GO:0000790|GO:0006367|GO:0044212|GO:0045598|GO:0003707|GO:0035947|GO:0070859|GO:0005634|GO:0010871|GO:0060086|GO:0030154|GO:0030425|GO:0001222|GO:0005737|GO:0043197|GO:0043401|GO:0004879|GO:0001046|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134516_PI430048170 0.0448663974813302 1.06539333078481 0.347112290340173 0.405080905556742 0.327552380616286 A A A 0.258042791962815 0.287194781612274 0.261303536517218 A A A LNCV6_134516_PI430048170 mRNA
TAGTGTGATGCGATCCTCTGGCATATGCTTTAATAAATGGATGTATATTGAGCACATGCA NM_001080534 RefSeq chr15 + 54012903 54628608 UNC13C 440279 unc-13 homolog C (C. elegans)
GO:0035556|GO:0048786|GO:0042734|GO:0005737|GO:0030054|GO:0005886|GO:0007268|GO:0006887|GO:0046872|GO:0019992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130426_PI430048170 0.00945165279112495 1.64724746956734 3.59695431857817 3.19790797245016 3.41151268280701 P P P 2.6473473622445 2.86516913742353 2.54217032959051 A P P LNCV6_130426_PI430048170 mRNA
GTTTTAGGTACCCAAAAAGGGCCTGTCTAGATTTTTTCAGAAAAACGTGGAGTGCTAGGG NM_004112 RefSeq chr17 + 7439026 7444932 FGF11 2256 "fibroblast growth factor 11, transcript variant 1"
GO:0007165|GO:0007267|GO:0005576|GO:0008083|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94142_PI430048170 0.252325197464772 0.657282652511701 0.42321599517621 0.322593793129417 0.361593017343571 A A A 1.51296014387796 0.806425939618132 0.372607815316145 A A A LNCV6_94142_PI430048170 mRNA
ATAACTCTCAGGTTGCAACCACAGGGACTGCTGTGTGCATCAACTTCTGTATCATTATGT NM_001286615 RefSeq chr12 + 100794595 101128641 ANO4 121601 "anoctamin 4, transcript variant 1"
GO:0005622|GO:0006821|GO:0034220|GO:0005886|GO:0017128|GO:0006869|GO:0005229|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128696_PI430048170 0.00117766801680375 2.67180372081634 7.15216076688815 7.00877663844103 7.2176656568176 P P P 5.55939106168735 5.91799449719635 5.63011051053842 P P P LNCV6_128696_PI430048170 mRNA
CTAAAGTATTTTATCCAAATTCGAATAAATTTTCCCAACAACTTGCAGCGGGTGGAATGT NM_001048265 RefSeq chr9 - 135495179 135499915 C9orf116 138162 "chromosome 9 open reading frame 116, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78213_PI430048170 0.361838630728182 1.12766168138017 4.2551254073749 4.29093941972473 3.86841597122787 P P P 3.8381539137912 4.09895609467773 3.98239721353469 P P P LNCV6_78213_PI430048170 mRNA
AGTGGACCAGCATCTATACTTTCAAGATACTTATGTTTTCTACCAGTTTTCCTCTGATGA NM_012294 RefSeq chr7 - 22118289 22356914 RAPGEF5 9771 Rap guanine nucleotide exchange factor (GEF) 5
GO:0030742|GO:0032320|GO:0007264|GO:0005634|GO:0032854|GO:0017034|GO:0007399|GO:0005088 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137284_PI430048170 0.708087848197166 1.27344285308298 1.22683607893238 0.318394785740411 1.96795074698577 A A A 1.01428720378259 1.15785809616801 0.711990990971384 A A A LNCV6_137284_PI430048170 mRNA

AAAGACCTACCTAGATGCTCCTTTTTACGATAACTTACAGCCCTCACTTTCTTATGTTTANM_003140RefSeq chrY - 2786854 2787741 SRY 6736 sex determining region Y GO:0005516|GO:0006357|GO:0006366|GO:0003705|GO:0005634|GO:0003677|GO:0030154|GO:0005737|GO:0016607|GO:0030238|GO:0007548|GO:0045893|GO:2000020|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134768_PI430048170 0.0241547528178516 0.85160299325884 10.5635031182043 10.7017706780116 10.6870253929378 P P P 10.899469086214 10.8974651987919 10.8541090547869 P P P LNCV6_134768_PI430048170 mRNA
GAAAAACCTTCCAAGAGCGCTGGGGTTTATGCTTTCTGAATAAACACTACTGTTTACATG NM_144679RefSeq chr17 - 81228276 81239091 ENTHD2 146705 ENTH domain containing 2 GO:0016023|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106076_PI430048170 0.150066029517567 1.14968140556503 6.27236611818149 6.306556360125 6.18343199220765 P P P 6.12362040113911 6.16041804486484 5.85907147592233 P P P LNCV6_106076_PI430048170 mRNA
TATCTGCTTCCGCGGCCGTGCTTCTCACCCTTCAGGCCACTGTAGACAGCAGTCAGGCTC NM_020457RefSeq chr16 + 67842309 67844195 THAP11 57215 THAP domain containing 11 GO:0005515|GO:0006355|GO:0005737|GO:0008270|GO:0005654|GO:0003677|GO:0006351|GO:0045171 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129067_PI430048170 0.557251987754488 1.23450324872483 2.81254908671057 1.66182863277245 2.19083817359253 A A A 1.43564557206388 2.1724684736021 2.24467611803573 A A A LNCV6_129067_PI430048170 mRNA
GTGGGGTAGCTTCTGGGTTTCTGCTTCATTCAGTCTTTTTGATTCCCATCTGTTTCATTT NM_003960RefSeq chr2 - 73640722 73642410 NAT8 9027 "N-acetyltransferase 8 (GCN5-related, putative)" GO:0005515|GO:0005793|GO:0043066|GO:0042493|GO:0018003|GO:0006749|GO:0050435|GO:0010628|GO:0004468|GO:0033116|GO:0005789|GO:0016021|GO:0047198|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139220_PI430048170 0.00287929452342467 0.871005868597713 10.672415028551 10.6085791839484 10.6755741153222 P P P 10.8355043742593 10.8248772187977 10.8939461243689 P P P LNCV6_139220_PI430048170 mRNA
GTCGGTGATTTGTTTGTCTTTCTGATAGGTTGAAAATTGTGTAATAAACTTGATGACGCT NM_024811RefSeq chr11 - 61402647 61429911 CPSF7 79869 "cleavage and polyadenylation specific factor 7, 59kDa, transcript variant 1" GO:0005515|GO:0008380|GO:0006369|GO:0010467|GO:0051262|GO:0006366|GO:0031124|GO:0005634|GO:0000166|GO:0016020|GO:0000398|GO:0005654|GO:0005849 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137586_PI430048170 0.152123071539849 0.858963533991187 13.53561476457 13.177216086617 13.3392690787362 P P P 13.5485357447608 13.5429863928572 13.6389319248368 P P P LNCV6_137586_PI430048170 mRNA
CAGCGTACCAAGAAAAATAAAGAAGAGGCTGCAGAATATGCTAAACTTTTGGCCAAGAGA NM_001010RefSeq chr9 - 19376255 19380237 RPS6 6194 ribosomal protein S6 GO:0005515|GO:0008286|GO:0010467|GO:0048471|GO:0007093|GO:0007369|GO:0006364|GO:0019058|GO:0015935|GO:0005634|GO:0006412|GO:0006924|GO:0030425|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0000082|GO:0002309|GO:0000184|GO:0048821|GO:0022605|GO:0016032|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127397_PI430048170 0.412022511784358 1.1250299084521 4.13765803139375 3.882990232492 3.81160306602101 P P P 3.82787778107096 4.01207711404278 3.44696449868379 P P P LNCV6_127397_PI430048170 mRNA
ATTTTGAATAGTCGTGTGTTCATGCCTGTTCTCAGTCTTGTCCCCTTTACCGTTTCTCAT NM_001256410 RefSeq chr10 + 27504173 27542237 RAB18 22931 "RAB18, member RAS oncogene family, transcript variant 2" GO:0005515|GO:0005794|GO:0071782|GO:0005886|GO:0007264|GO:0001654|GO:0071786|GO:0003924|GO:0005

525|GO:0034389|GO:0006886|GO:0005622|GO:0006184|GO:0007420|GO:0032482|GO:0019003|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144654_PI430048170 0.7548401246423440.91457127922224 1.43851074773233 1.76516306307476 2.08072814790593 A A A 2.22633516992506 2.02051446900915 1.36111563085413 A A A LNCV6_144654_PI430048170 mRNA TTAGGGAACCTGGCTGAGGAGCTCAATGGCTACAGCAGGAAGAAAGGCGGCTTCAGCTTC NM_198180RefSeq chr9 - 130893427 130893838 QRFP NA pyroglutamylated RFamide peptide NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127873_PI430048170 0.0239986044545445 0.32674771798808 1.57333404703535 1.45205065342277 0.440649279978818A A A 3.24033534621949 2.3624234112921 2.81603777541728 P A P LNCV6_127873_PI430048170 mRNA CAACCCTGAACGTCTCAGGACAAATAATTCAAAAAAGAGATCTACATTTTCTGGAAAATC NM_001082480 RefSeq chr8_KI270816v1_alt + 111991 129199 ZNF623 9831 "zinc finger protein 623, transcript variant 2" GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134870_PI430048170 0.150636674604393 1.06629319347266 0.469696555862826 0.484929612833261 0.529980654230373 A A A 0.32295623535941 0.408268569483913 0.472368538405102 A A A LNCV6_134870_PI430048170 mRNA CGGAGAAATCTGCATAACAGGATAATTCCAATCTTTGTGATAAGTGAGAAGTTGCTAAAT NM_152327RefSeq chr14 + 96392110 96489427 AK7122481 adenylate kinase 7 GO:0002437|GO:0035082|GO:0003351|GO:0004127|GO:0004550|GO:0005634|GO:0004017|GO:0007283|GO:0009142|GO:0005524|GO:0005829|GO:0006165|GO:0005737|GO:0007420 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131580_PI430048170 0.3539443206708551.22702586856414 0.418211720915231 1.09201468242649 0.460099300760992A A A 0.3948733533581840.381171127755517 0.411667940175267 A A A LNCV6_131580_PI430048170 mRNA ATCAATTATGAAGCCTTTGTCAAGCACATCATGTCAGGGTGAAGCAGAGTCTTCCAGGTG NM_001002841 RefSeq chr17 + 47209061 47223679 MYL4 4635 "myosin, light chain 4, alkali; atrial, embryonic, transcript variant 1" GO:0003785|GO:0051015|GO:0030049|GO:0002026|GO:0005509|GO:0032038|GO:0032781|GO:0016459|GO:0060048|GO:0031672|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74865_PI430048170 0.0193967234454542 1.80703334677997 5.29211115731179 5.57777115682745 5.83115499528232 P P P 4.62892121994215 4.69096270580888 4.86031395220624 P P P LNCV6_74865_PI430048170 mRNA CTTGTTCCTGGTATACCAACAATGGAACACTTTCATCAGTTTTACTTTATCTTGTCTATG NM_153702RefSeq chr4 + 140524157 140553770 ELMOD2 255520 ELMO/CED-12 domain containing 2 GO:0050688|GO:0043547|GO:0006909|GO:0051607|GO:0016020|GO:0005856|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145582_PI430048170 0.6560338571974341.05012394617722 7.50605297511711 7.3996319760754 7.63590575218559 P P P 7.143548861417 7.48343490386084 7.66505955183864 P P P LNCV6_145582_PI430048170 mRNA GTTTTCATCTTGTGTGTGGTTATTGCTTAATGCTTTTTAAACTTGGAACACTCACTATGG NM_033055RefSeq chr1 + 100038232 100083373 HIAT1 64645 hippocampus abundant transcript 1 GO:0005215|GO:0005886|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138752_PI430048170 0.140700597069711 0.60960723383777 4.34219618418944 3.76076988242056 3.17920052956254 P P P 4.9086728256881 4.46473970303273 4.18972284200013 P P P LNCV6_138752_PI430048170 mRNA TCTACCTTCCAGCTGCTCCCACAGAGGAGGAAGACAATAAATATTTGTTGAACTGAAAGC NM_001264RefSeq chr6_GL000251v2_alt - 2597462 2602851 CDSN 1041 corneodesmosin

GO:0030057|GO:0016337|GO:0008544|GO:0030216|GO:0005911|GO:0043589|GO:0007155|GO:0042803|GO:0001533|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53271_PI430048170 0.250598852938998 1.09177952305764 11.0542422987522 11.2151701569664 11.090357149693 P P P 10.9759426402701 11.1346935919411 10.8609198746426 P P P
LNCV6_53271_PI430048170 mRNA
TTTTTGTTTTGCATCCGAAACCGAAAGAAATAAAGCGGTGGGAGGCAGGGCCATTGTGTT NM_015658 RefSeq chr1 - 944202 959299 NOC2L 26155 nucleolar complex associated 2 homolog (S. cerevisiae)
GO:0005515|GO:0003714|GO:0005730|GO:0006915|GO:0031491|GO:0005634|GO:2001243|GO:0000122|GO:0035067|GO:0006351|GO:0032066|GO:0042393|GO:0034644|GO:0031497|GO:0002903|GO:0003682|GO:0070491|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143445_PI430048170 0.11804796134154 0.7859414729710948 .30871945097388 8.29546077459916 8.2542180560186 P P P 8.37098623020801 8.70230234312699 8.79467351387561 P P P LNCV6_143445_PI430048170 mRNA
CATGGTCCGGAGTCTGGGACCTACTTTGTTTTTTGTTATTTATGACCTTGTTTAAAGAAA NM_001271593 RefSeq chr11 + 74171062 74254703 PPME1 51400 "protein phosphatase methylesterase 1, transcript variant 2" GO:0050790|GO:0019903|GO:0008601|GO:0006482|GO:0004864|GO:0051722|GO:0051721|GO:0043086 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144707_PI430048170 0.0650399955354089 0.4659584645242543.55211030197322 3.29886720287883 3.8425171290163 P P P 4.02341298133872 4.67188427703088 5.14278271019294 P P P LNCV6_144707_PI430048170 mRNA
GTTGTTAACCTTCTGTGTGCCAAAAACTCTTAAGTTACATTTTCCTTCAAAGCAATGTAC NM_001286491 RefSeq chr15 - 43870760 44195294 FRMD5 84978 "FERM domain containing 5, transcript variant 4"
GO:0008092|GO:0005515|GO:0008150|GO:0003674|GO:0005737|GO:0016021|GO:0005575|GO:0005856|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143963_PI430048170 0.0744510702937591.05155960319944 0.37581681711013 0.3350640191780030.292818532575339 A A A 0.2488529104717650.291576133991633 0.246423451588048 A A A LNCV6_143963_PI430048170 mRNA
GGCGTTTGTTTTATTCTTGGTGTTTTCAGTGCAATAAATAGCTACAAACTTCTGTGCAAA NM_015981 RefSeq chr5 - 150219490 150289840 CAMK2A 815 "calcium/calmodulin-dependent protein kinase II alpha, transcript variant 1"
GO:0005515|GO:0005516|GO:0030054|GO:0005886|GO:0051928|GO:0019221|GO:0007268|GO:0005634|GO:0042803|GO:0005829|GO:0005739|GO:0034605|GO:0000082|GO:0051092|GO:0046777|GO:0048168|GO:0018105|GO:0016301|GO:0010666|GO:0006816|GO:0004683|GO:0060333|GO:0046928|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137753_PI430048170 0.00513018907584594 1.78510957891159 9.35684276182644 9.73637002141506 9.56369945903716 P P P 8.58177472056247 8.75662987307845 8.82461485988106 P P P LNCV6_137753_PI430048170 mRNA
CGCTGTATCGCATATTGCTGAGTTTTCTATTTTTGCAAAATAAAGTGATGGAAACTCATG NM_000966 RefSeq chr12 - 53210565 53232256 RARG 5916 "retinoic acid receptor, gamma, transcript variant 1"
GO:0005515|GO:0008361|GO:0010467|GO:0000790|GO:0008284|GO:0003700|GO:0003430|GO:0006367|GO:0008285|GO:0071300|GO:0003707|GO:0005634|GO:0003708|GO:0009952|GO:0046965|GO:0043068|GO:0031076|GO:0002068|GO:0035264|GO:0045944|GO:0043401|GO:0031641|GO:0032526|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131761_PI430048170 0.0351505927345479 0.4391633454074364.41223109653724 4.33221286946762 4.55497137094499 P P P 5.11467699338531 5.69531070896922 5.94044633366719 P P P LNCV6_131761_PI430048170 mRNA
ACCGTTTGTCTTCTTACCTCATTTTAAGAAGCATGTGAAAATGGGATACTATAGACTACT NM_001278689 RefSeq chr3 - 68975211 69013894 EOGT 285203 "EGF domain-specific O-linked N-acetylglucosamine (GlcNAc) transferase, transcript variant 1" GO:0006493|GO:0016262|GO:0005788 . NA - . NA NA

NA NA NA NA NA NA NA
LNCV6_135502_PI430048170 0.0665895175613787 0.71821228610673910.4866191876242
10.4442065101475 10.5254699125785 P P P 10.7120777003536 10.9787179656765
11.1638498617435 P P P LNCV6_135502_PI430048170 mRNA
GACACCAGCAAAGCAATGTGCTCCTGATCAAGTAGATTTTTTAAAAATCAGAGTCAATTA NM_004900RefSeq chr22
+ 38982398 38992779 APOBEC3B 9582 "apolipoprotein B mRNA editing enzyme, catalytic polypeptide-
like 3B, transcript variant 1"
GO:0051607|GO:0047844|GO:0045087|GO:0008152|GO:0008270|GO:0005634|GO:0010529 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143463_PI430048170 0.4116978086807880.9102140239180138.07177982779749 8.0018986742388
7.73166478379023 P P P 8.26416592030698 8.04473935941676 7.90229169606019 P P P
LNCV6_143463_PI430048170 mRNA
GCCACAAGCATAATAAAGCCCCTTTGCCTTTCTCTGTATTATATTCAATACAATACATCA NM_033401RefSeq chr16
+ 76277277 76559238 CNTNAP4 85445 "contactin associated protein-like 4, transcript variant 1"
GO:2000821|GO:0042734|GO:0030054|GO:0032225|GO:0032228|GO:0016021|GO:0007155|GO:0030425 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92565_PI430048170 0.1162615326372040.89402056342456 7.93163430855401 7.71917556698224
7.77816049014339 P P P 7.97633126868059 7.99587218165917 7.94967168686619 P P P
LNCV6_92565_PI430048170 mRNA
GACTAGAAGAATATCTCACACAGCAGGAAATAGGCAAAAAGGCTCAACAAGAAACAGGAG NM_015114RefSeq
chr12 - 132725666 132761888 ANKLE2 23141 ankyrin repeat and LEM domain containing 2
GO:0005515|GO:0007084|GO:0008601|GO:0035307|GO:0030176|GO:0042326|GO:0007067|GO:0050790|GO:0016
020|GO:0005789|GO:0000278|GO:0051721|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105891_PI430048170 0.11361530729135 1.28536110914662 6.65291314545257
6.80155644631146 7.13073013844464 P P P 6.56626285221413 6.35976212071763
6.60308202362457 P P P LNCV6_105891_PI430048170 mRNA
GATTGGGGGTATAACGTGTATTCTTTCACTAATCTGTGCCTTGGCTCTTGCCTACTTGGA NM_022736RefSeq chr3
+ 158801925 158829719 MFSD1 64747 "major facilitator superfamily domain containing 1, transcript
variant 1" GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144754_PI430048170 0.5685302849133120.979120433220826 0.399906430154427
0.3940960162615040.258810429203863 A A A 0.3611806830063130.409888902461681
0.37701016193014 A A A LNCV6_144754_PI430048170 mRNA
TATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGACCTGTTTCCTC NM_145894RefSeq chr19
- 51029091 51034892 KLK12 43849 "kallikrein-related peptidase 12, transcript variant 2"
GO:0004252|GO:0006508|GO:0008236|GO:0008233|GO:0005615|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139010_PI430048170 0.3708465413139640.7239579883145080.520744571566279
0.5660794557722151.8385363400205 A A A 1.6259637672774 1.98807015715103
0.936107840613364 A A A LNCV6_139010_PI430048170 mRNA
TGAAAGGTTGGCCTTACTGTTGAACAATAAGTAAATCCACAGGCTCCTGTTGTAATCTCA NM_022897RefSeq chr5
+ 170861881 171300015 RANBP17 64901 RAN binding protein 17
GO:0005737|GO:0005643|GO:0008536|GO:0051028|GO:0006606|GO:0005525 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131253_PI430048170 0.0985493683738845 0.7382414199417694.34725485016328
3.90367364891639 3.83351015536152 P P P 4.48893290667479 4.54519792319555
4.41639378386645 P P P LNCV6_131253_PI430048170 mRNA
TCCTCCCTCTCGCAACCGACCAAAATTTTGACAACGATGATGTTCACCAGAAGGAAAAAA NM_014344RefSeq chr11
+ 35618186 35620873 FJX1 24147 four jointed box 1 (Drosophila) GO:0010842|GO:0005615 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_73002_PI430048170 0.0687504986431187 0.5639677318051741.2426397985676
1.74686823682247 1.53643383751308 A A A 2.51804874539885 1.79764693240629
2.60548018971415 A A P LNCV6_73002_PI430048170 mRNA
TTACCTCCGAACCGCATGCACAACTGGAGGAGAACTTCTGCCGGAACCCAGATGGGGATANM_020998RefSeq chr3
- 49683946 49688763 MST1 4485 macrophage stimulating 1
GO:0008150|GO:0003674|GO:0004252|GO:0007566|GO:0006508|GO:0030317|GO:0007283|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142769_PI430048170 0.0244864533159068 0.596561927711269 10.5682954838268
10.0850149910293 10.0591396250524 P P P 11.1441256303262 11.0619762955544
10.7757245341711 P P P LNCV6_142769_PI430048170 mRNA
CCTTCCTCCCCCTCAGTTTTTGTTGGAAAGATTATCTCTAGAGTTATATTTTCTATTAGA NM_020649RefSeq chr17 -
79794376 79797116 CBX8 57332 chromobox homolog 8
GO:0000792|GO:0005515|GO:0031519|GO:0035102|GO:0000790|GO:0003727|GO:0004842|GO:0016574|GO:0005
634|GO:0000122|GO:0035064|GO:0006351|GO:0005654 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_75809_PI430048170 0.0239878949016308 0.400502859874623 2.17670302587394
1.37144557988722 2.09294309038888 A A A 3.40914517049266 3.18180880003366
3.12156622841725 P P P LNCV6_75809_PI430048170 mRNA
TTTAAAGTTTGGTGCTGAAGAACTTTTTAAGGAACCTGAAGGAGAAGAACAAGAGCCCCA NM_001270 RefSeq
chr5 - 98855203 98926534 CHD1 1105 chromodomain helicase DNA binding protein 1
GO:0005515|GO:0005737|GO:0004003|GO:0006357|GO:0006338|GO:0005634|GO:0035064|GO:0032508|GO:0005
524|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142506_PI430048170 0.255607849604088 1.02804216931404 0.407883318773913
0.335942071553122 0.368866108268776 A A A 0.299176537064014 0.321075672001243
0.372651087276194 A A A LNCV6_142506_PI430048170 mRNA
TGCTGCCTATAATTAGGGGTTTACATGATACTTCCTAATTGCTAATTAGGATGTGAATTC NM_016571 RefSeq chr6
- 63275950 63319977 LGSN 51557 "lengsin, lens protein with glutamine synthetase domain,
transcript variant 1" GO:0005886|GO:0004356|GO:0006542 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_103415_PI430048170 0.510449171817014 0.899309974430754 4.57973660257891
4.98072948596008 4.41291653179672 P P P 5.07945982311998 4.77704546932255
4.5944637528962 P P P LNCV6_103415_PI430048170 mRNA
ATAGGATTGGAGAAGGTTTGTGTTCCCGACGCCTTGGTAGTTGGCATAGGCTAAAGAAAA NM_025230 RefSeq
chr14 + 24114776 24125242 DCAF11 80344 "DDB1 and CUL4 associated factor 11, transcript variant
1" GO:0005515|GO:0016567|GO:0005654|GO:0080008 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144737_PI430048170 0.328672637555153 0.698510564627746 2.18596150639803
0.457929559772749 0.929414055444633 A A A 1.76571365774216 2.31507239903384
1.50106482392869 A A A LNCV6_144737_PI430048170 mRNA
GCTTCATCGTTAATAAGTCAATACCTGTTGTTCCTGGGATGTTCTTTTTTGTGCATTAAA NM_178565 RefSeq chr8
- 107899315 108083685 RSPO2 340419 "R-spondin 2, transcript variant 1"
GO:0001664|GO:0009986|GO:0090263|GO:0005102|GO:0005576|GO:0030282|GO:0005615|GO:0001649|GO:0060
441|GO:0035116|GO:0060437|GO:0035115|GO:0060535|GO:0016055|GO:0008201 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_54138_PI430048170 0.669240139844152 0.961139025040248 0.294988032509352
0.274092365165051 0.431707103327948 A A A 0.290423263549881 0.582376317283732
0.284108244142832 A A A LNCV6_54138_PI430048170 mRNA
GACTCTGGAAATGCGCTGTTGGAAGCCAAATAACATCAATACTCTTGTTCTATAATTGAA NM_001276352 RefSeq
chr1 - 67092175 67134971 C1orf141 NA "chromosome 1 open reading frame 141, transcript

variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_20201_PI430048170 0.73474209481578 0.957139539781752 3.82044330461496
4.06782383136019 4.01979426650205 P P P 4.28263637672965 3.89569410608037
3.89550185074228 P P P LNCV6_20201_PI430048170 mRNA
ACTGGTACTGCCATGCTGGTGCTCTGGCTGTTTGCTGTTGGCAATAAACTATTCTGTTTT NM_001290254 RefSeq
chr7 + 128672283 128687872 FAM71F2 346653 "family with sequence similarity 71, member F2,
transcript variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133694_PI430048170 0.42795648245855 0.902900168873981 0.280497487602659
0.285207932713093 0.422095363881939 A A A 0.356771358772187 0.303137861794704
0.735048999712834 A A A LNCV6_133694_PI430048170 mRNA
AAGATTTAGAGAAGCACTTTTTTGCCTTTATTGATGCCCTTGCACAGTCAGGCCAGGAGG NM_001105577 RefSeq
chr13 - 27978105 27988637 URAD NA ureidoimidazoline (2-oxo-4-hydroxy-4-carboxy-5-)
decarboxylase NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127954_PI430048170 0.0285890983876343 0.714950306888087 5.76520585927319
5.67581437897607 5.99582755157619 P P P 6.08140684739545 6.39495719915274
6.40875352017175 P P P LNCV6_127954_PI430048170 mRNA
CCATGTTGCACTTAATCAAATAGTATGTGGGGATTTAAAATCGCTTGCATTGTTTCACAA NM_018469 RefSeq
chr17 - 64147432 64263323 TEX2 55852 "testis expressed 2, transcript variant 1"
GO:0006665|GO:0007165|GO:0003674|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137565_PI430048170 0.0456582566819113 0.637137081906614 6.49452780320367
6.07510729004174 6.65021758193738 P P P 6.84532749814579 6.99571624352192
7.34318082871275 P P P LNCV6_137565_PI430048170 mRNA
GTGGACATTGTGCTAAGGTAGTTTCAGTGTGTCAACTTTATGAATTGAAATATAAACCAG NM_012197 RefSeq
chr9 + 122941008 123104868 RABGAP1 23637 RAB GTPase activating protein 1
GO:0005515|GO:0005813|GO:0017137|GO:0005875|GO:0032851|GO:0003677|GO:0005829|GO:0043547|GO:0007
049|GO:0015631|GO:0033124|GO:0005097|GO:0005096 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143010_PI430048170 0.518444642346921 1.35068545535003 0.3766028593219
1.55845924585027 0.321793629443365 A A A 0.479093253709708 0.44056707369966
0.396412157832805 A A A LNCV6_143010_PI430048170 mRNA
CCTGGAGATTCTGAAGTGCCTTTGCTGTGGTTTTCAAAATAATAAAGATTTGTATTCAAC NM_001271702 RefSeq
chr10 - 47467993 47484158 ANXA8 NA "annexin A8, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135663_PI430048170 0.925736858472133 1.01023642769124 6.11099596815368
6.29002382491331 6.42329001776628 P P P 6.32921277505707 6.20126490746487
6.26383111201488 P P P LNCV6_135663_PI430048170 mRNA
GAGTTGCATTTGATGTTCTAGAGTTTGATTACATGCAGAGTTGTATATAGCCAAAACTTC NM_001024947 RefSeq
chr5 - 144158158 144170714 YIPF5 81555 "Yip1 domain family, member 5, transcript variant 1"
GO:0030134|GO:0060628|GO:0032580|GO:0005789|GO:0016021|GO:0016192|GO:0015031|GO:0070971 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_133199_PI430048170 0.0214812826097265 1.17024312639268 0.716025995776294
0.802045389145325 0.833015818436477 A A A 0.650696864194528 0.498533591028559
0.519194649822277 A A A LNCV6_133199_PI430048170 mRNA
CCCAGCTGCACACGAAATTACACATGACTCACCTTATTAAGGGCTATTGCACTGAAAAAA NM_020945 RefSeq
chr10 + 48685472 48982956 WDFY4 57705 WDFY family member 4
GO:0005543|GO:0016197|GO:0016021|GO:0019898|GO:0012505 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_61321_PI430048170 0.776464487925502 0.972167650686503 8.00085643984769

8.3430559892301 7.99291171897546 P P P 8.12083030195451 8.02282866198418
8.32685107299403 P P P LNCV6_61321_PI430048170 mRNA
TCCCAAGATATGAGCCTGTTGCCTCTTTCTGGCTGGGAAAGTAGAAGAAACACCAAAAAA NM_001099402 RefSeq
chr14 + 99481401 99511515 CCNK 8812 cyclin K
GO:0005515|GO:0071157|GO:0006355|GO:0006366|GO:0019901|GO:0005634|GO:0000079|GO:0001701|GO:0008
353|GO:0006974|GO:0007067|GO:0006468|GO:0004693|GO:0051301 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140745_PI430048170 0.605547447188443 0.919413941034882 0.323816327507989
0.287253657948403 0.418495459240994 A A A 0.291186188694294 0.266609919029168
0.778774467331411 A A A LNCV6_140745_PI430048170 mRNA
GCACTAGAAGAGGGTGCTTAACACTCCTCTATCTATATGAATAAAAAATTATGTTCTCAC NM_003948 RefSeq
chr4 - 75576493 75630537 CDKL2 8999 cyclin-dependent kinase-like 2 (CDC2-related kinase)
GO:0007165|GO:0005813|GO:0005737|GO:0004672|GO:0051726|GO:0007548|GO:0006468|GO:0005654|GO:0005
634|GO:0005524|GO:0004693 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113496_PI430048170 0.597439800768715 1.06015121359226 11.9655446571611
11.7708985423168 11.8261668429185 P P P 11.8686100566345 11.945168153108
11.4568867278379 P P P LNCV6_113496_PI430048170 mRNA
CCACTGCCCCGGCCGGCCGACCGACACCGACCCCGCCTACTGCGGCGCGGGGACCCTTGG NM_001271836
RefSeq chrX + 49053431 49069858 CCDC120 90060 "coiled-coil domain containing 120, transcript
variant 6" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141792_PI430048170 0.00672216417772759 0.2543142098187086.49652019172468
5.67659003376403 6.35861809068007 P P P 7.64222574475878 8.16812669052266
8.61256438762747 P P P LNCV6_141792_PI430048170 mRNA
TCGGGAGTTAGATGTATAGAGTGTTTGTATGTAAACATTTCTTGTAGGCATCACCATGAA NM_001293298 RefSeq
chr15 + 80779342 80951662 CEMIP 57214 "cell migration inducing protein, hyaluronan binding,
transcript variant 1"
GO:0005515|GO:0010800|GO:0030335|GO:0046923|GO:0032050|GO:0005886|GO:0005783|GO:0007605|GO:0090
314|GO:0005576|GO:0005634|GO:0030665|GO:0005737|GO:0005905|GO:0005540|GO:1900020|GO:0004415|GO:0
030214|GO:0051281. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144456_PI430048170 0.8911187799773270.9891794993939698.96851195673621 9.1018299938405
9.10921667105178 P P P 9.21476538049263 9.04917154889095 8.95492847651704 P P P
LNCV6_144456_PI430048170 mRNA
TGAACAGTCGTGTCACTGGATGCCTATTTAGAAATAAAGTGTATGCTGCTGAATTGGAAA NM_001260491 RefSeq
chr20 + 49812712 49892242 SLC9A8 23315 "solute carrier family 9, subfamily A (NHE8, cation proton
antiporter 8), member 8, transcript variant 1"
GO:0015386|GO:0015385|GO:0000139|GO:0051453|GO:0035725|GO:0016021|GO:0055085|GO:0071805|GO:0006
811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77206_PI430048170 0.0359358494018071 1.36230679515516 10.990650368007
10.9265085035784 11.1581029309523 P P P 10.3496673335426 10.6673590681436
10.7044309371938 P P P LNCV6_77206_PI430048170 mRNA
TTGACAAAACAACGGCTGCATTTCAACAAGGAAAGATACCTCCTACTCCATTCTCTGCTC NM_003093 RefSeq chr6
+ 34757093 34773857 SNRPC 6631 "small nuclear ribonucleoprotein polypeptide C, transcript variant
1"
GO:0071004|GO:0005515|GO:0030619|GO:0003727|GO:0015030|GO:0000387|GO:0003729|GO:0042803|GO:0000
395|GO:0000398|GO:0005654|GO:0008270|GO:0000243|GO:0005685 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145364_PI430048170 0.2720766408053390.6996529021522625.44889594177865
4.14681825460638 4.57981643764423 P P P 5.58137515127454 5.48842112061213 4.8657072103587
P P P LNCV6_145364_PI430048170 mRNA

GGACTACCAGGAAATACTAGACTCTCCCATTAAATGAATACCTGATTATTATTGTCTCAT NM_025246 RefSeq chr3 + 136819018 136855892 SLC35G2 80723 "solute carrier family 35, member G2, transcript variant 1" GO:0005794|GO:0005886|GO:0005887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76976_PI430048170 0.0802385602334983 1.30406987009728 5.32612905167858 5.3924512093654 4.97878030921096 P P P 5.01567121139536 4.72137767262374 4.82899691392265 P P P LNCV6_76976_PI430048170 mRNA
ACACAAGATACCTGATACCTGGGGCTTTCTCTCCTGACATCGATGAGAGAGTCACATTTA NM_001145009 RefSeq chr6 + 26402236 26415216 BTN3A1 11119 "butyrophilin, subfamily 3, member A1, transcript variant 4" GO:0005515|GO:0072643|GO:0050852|GO:0050663|GO:0005886|GO:0050798|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134286_PI430048170 0.2378860409954631.09930034208516 7.10489398882369 7.20893061891325 7.04137113139306 P P P 7.1208670126982 6.98309353346087 6.83202650107515 P P P LNCV6_134286_PI430048170 mRNA
AGGGACTGACCGATGCCTTTGGGTAGAGAGAATTATGAAAGAAATTTTGGTATTTTTCTA NM_005957 RefSeq chr1 - 11785729 11806103 MTHFR 4524 methylenetetrahydrofolate reductase (NAD(P)H) GO:0050661|GO:0001666|GO:0006520|GO:0043005|GO:0008015|GO:0042493|GO:0050660|GO:0006767|GO:0009086|GO:0044281|GO:0033274|GO:0050667|GO:0005829|GO:0035999|GO:0072341|GO:0051593|GO:0004489|GO:0006766|GO:0046500|GO:0046655|GO:0043200|GO:0006730|GO:0070555|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139742_PI430048170 0.0495365001649931.06061059046717 0.372896022960771 0.4243660375026740.351898884428029 A A A 0.2885126580113580.310152170193282 0.296694875742946 A A A LNCV6_139742_PI430048170 mRNA
GTCGCAACTGAGATCTCCATGACTGTGTGTTGTGAAATAAAATGGTGAAAGATCAAAAAA NM_000892 RefSeq chr4 + 186227517 186258471 KLKB1 3818 "kallikrein B, plasma (Fletcher factor) 1" GO:0005515|GO:0004252|GO:0005886|GO:0051919|GO:0005576|GO:0005615|GO:0022617|GO:0007596|GO:0030198|GO:0002542|GO:0007597|GO:0006508|GO:0031639|GO:0042730|GO:0031638|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131944_PI430048170 0.1577638060337652.07044425586665 3.69432603207039 3.20035347630838 3.55334073885136 P P P 1.13922422258243 2.50932526195524 3.08166060729782 A P P LNCV6_131944_PI430048170 mRNA
AATGTATCTTTATGTCCCTGGCACATGAATAAACTTTGCTGTGGTTTACTAATCTATGCT NM_207315 RefSeq chr2 - 6848308 6865819 CMPK2 NA "cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138089_PI430048170 0.68280131904882 0.8239680684409540.279741306436108 1.33934987691901 0.282090431820923 A A A 0.5075142333600040.407243423075638 1.71029318829967 A A A LNCV6_138089_PI430048170 mRNA
TCTTCCTGTTAGCAAGGATGAAAGAGAGAGGTCAGTAGGACTGGAACTTGGTAACTGCAA NM_005959 RefSeq chr11 + 92969622 92982782 MTNR1B 4544 melatonin receptor 1B GO:0005515|GO:0050796|GO:0005886|GO:0007187|GO:0005887|GO:0004930|GO:0007268|GO:0042593|GO:0008502 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130730_PI430048170 0.6635551513986591.42889620424312 0.49587727858811 2.53554674886551 2.84586451761096 A A A 2.52495200238459 1.56478226170238 0.445826798762547 A A A LNCV6_130730_PI430048170 mRNA
CCCACATAGAAATAACAATGCATGTATTACCCAGAATTTAATGTTGCGTACCTTATGTTC NM_024783 RefSeq chr11 - 47659590 47715376 AGBL2 79841 ATP/GTP binding protein-like 2 GO:0035610|GO:0005814|GO:0006508|GO:0008270|GO:0036064|GO:0005829|GO:0004181 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55093_PI430048170 0.0502373033174908 2.68698014643939 2.56173678678322 1.86420027845578 3.15951447279763 A A P 0.5963932549896261.77085737119552

0.965809398878765 A A A LNCV6_55093_PI430048170 mRNA
CTCTTCATTCCAGTGGCAGTCATGGTTACTGCATTCTCTGGGTTGGCATTTATCATTTGG NM_000655 RefSeq chr1
- 169690664 169711702 SELL 6402 "selectin L, transcript variant 1"
GO:0005515|GO:0005886|GO:0050900|GO:0002020|GO:0005887|GO:0007596|GO:0043208|GO:0050776|GO:0030
246|GO:0033198|GO:0007155|GO:0008201|GO:0050839|GO:0009897 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_50888_PI430048170 0.5358658891796730.9364534840788979.52444014494609 9.58258858646957
9.72179415871201 P P P 9.48060206974249 9.75588059941678 9.85781759444259 P P P
LNCV6_50888_PI430048170 mRNA
ATCAAAGACTCCAAGTTTGATGACTGGAAGAATATTCGAGGACCCAGGCCTTGGGAAGAT NM_016468 RefSeq chr14
- 70325080 70359731 COX16 51241 "COX16 cytochrome c oxidase assembly homolog (S. cerevisiae),
transcript variant 1" GO:0008150|GO:0003674|GO:0031966|GO:0016021|GO:0005575 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_136663_PI430048170 0.1777489487813941.89274434814347 1.45815903769369
1.50235674279419 0.27570453916259 A A A 0.2482691436737530.277566989423811
0.248648539019606 A A A LNCV6_136663_PI430048170 mRNA
GCCCTGGAGGTTATATTAAATAAAAGAGAAATGGAATAAAAACTGTAAGCCTTTTGGCTC NM_020931 RefSeq chr6
+ 57046531 57055239 KIAA1586 57691 "KIAA1586, transcript variant 1" GO:0003676 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133031_PI430048170 0.3779024398206281.08235886749743 9.19390271983897
9.18155468903859 8.94916954407399 P P P 9.10921667105178 9.04115370920912
8.83020450421132 P P P LNCV6_133031_PI430048170 mRNA
TCTGTAATAGTTTTGAGATGTCTGTCCCTCCTCCCTGGAGCTCCAGAGACCCACCCCTCT NM_001270440 RefSeq
chr19 - 12825476 12835428 RTBDN 83546 "retbindin, transcript variant 3" GO:0005576 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_130759_PI430048170 0.6179626034680890.9880709711924710.484178012121934
0.3940767124116180.462849115727679 A A A 0.4609754378172730.496082387300654
0.436900769124956 A A A LNCV6_130759_PI430048170 mRNA
ATGAAGACGGCAATAAGACGGCTGAGAAAATGGGATGCACATTCTAGTGTAAAGTTTTAG NM_001004195 RefSeq
chr15 - 101922141 101923059 OR4F4 26682 "olfactory receptor, family 4, subfamily F, member 4"
GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142020_PI430048170 0.1678120947145980.5684701439342290.435929457485223
0.4471087122189960.353965180577204 A A A 1.67227235160925 0.48952906350808
1.28392206854887 A A A LNCV6_142020_PI430048170 mRNA
TCTTGTGGTTTTAGCCAAATGAAGTGTTATCAGTAATAAACAGGTCTCTTCATAGGCATG NM_173582 RefSeq chr11
- 74330311 74398465 PGM2L1 283209 phosphoglucomutase 2-like 1
GO:0047933|GO:0016310|GO:0005978|GO:0004614|GO:0019388|GO:0006006|GO:0046872|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136837_PI430048170 0.2984690393202751.1714230293572 6.28019902180085
6.01058252120059 6.45216459672268 P P P 6.23164222938382 6.07549430283179
5.74260783731683 P P P LNCV6_136837_PI430048170 mRNA
TGCCATAGATGTAACCTAAAAAGTTTTGGCATATTTAGGTCAGCCTAGCGGAACTTTTTT NM_004687 RefSeq chr17
- 58489531 58517890 MTMR4 9110 myotubularin related protein 4
GO:0005515|GO:0006661|GO:0044281|GO:0014894|GO:0005615|GO:0046872|GO:0035335|GO:0005829|GO:0006
470|GO:0031901|GO:0007179|GO:0004722|GO:0006644|GO:0004725|GO:0030512 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137276_PI430048170 0.5420602176534720.7080427908197290.403079714289578
0.4191685073024081.3983760934349 A A A 2.06861245972142 0.360726660744974

1.00015087396705 A A A LNCV6_137276_PI430048170 mRNA
TCTCCTACAAGGAGATATGGCTGGACCAAAATAAAATGACATGAAACTGCAAAAATGAAA NM_015051 RefSeq chr9
- 99979180 100099052 ERP44 23071 endoplasmic reticulum protein 44
GO:0006986|GO:0005515|GO:0034976|GO:0009100|GO:0005793|GO:0009986|GO:0006457|GO:0005789|GO:0005
788|GO:0003756|GO:0045454|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135688_PI430048170 0.3945445872575021.23345456304575 8.39295568843777
9.06259373606252 9.14771016139385 P P P 8.49293584665816 8.30961610696982
8.93168610994172 P P P LNCV6_135688_PI430048170 mRNA
TGCCTCAAAAATTGGTCCTCGGTAAGTGCCTTTTGATAAATGATCTCAAATAAATGACTC NM_182505 RefSeq chr9
+ 71911506 71973455 C9orf85 138241 chromosome 9 open reading frame 85 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_142179_PI430048170 0.6316739998492631.03052820759566 0.274922629485554
0.2865784062838210.493035493359625 A A A 0.3326667309229050.286960572664871
0.314987722505534 A A A LNCV6_142179_PI430048170 mRNA
TCTGCTTATGCTAGTTCAGTATTTGGTCTAGGCTTCATTTTGATATGACTGAATTGCAAT NM_032446 RefSeq chr5 +
127290763 127461218 MEGF10 84466 "multiple EGF-like-domains 10, transcript variant 1"
GO:0016323|GO:0034109|GO:0014719|GO:0043654|GO:0014841|GO:0001891|GO:0055001|GO:0042995|GO:0016
021|GO:0051147|GO:0048641|GO:0014816 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144678_PI430048170 0.1645531640105480.7601380326272820.273106625457062
0.8186978866753970.92898826743109 A A A 1.06953880315471 0.947734721360053
1.25533877965179 A A A LNCV6_144678_PI430048170 mRNA
AATAAAACATACAGGAGTCTGTCTCTGCTATGGAATGCCCCATGGGGCATCTCTTGTGTA NM_019111 RefSeq
chr6_KI270758v1_alt - 9686 14891 HLA-DRA 3122 "major histocompatibility complex, class II, DR
alpha"
GO:0050852|GO:0005886|GO:0019221|GO:0031295|GO:0005765|GO:0005764|GO:0019886|GO:0006955|GO:0042
605|GO:0071556|GO:0070062|GO:0060333|GO:0030658|GO:0012507|GO:0009986|GO:0002506|GO:0002504|GO:0
002503|GO:0042613|GO:0032588|GO:0030666|GO:0000139|GO:0050890|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_108015_PI430048170 0.00711043113619208 4.27810467574526 7.09890305335614
7.23182517780651 7.1653716643629 P P P 4.90017173239552 5.43591779297473
4.78569055994634 P P P LNCV6_108015_PI430048170 mRNA
TGTGATTCCTCTGCTTGCCTGGAGACGTGGAACCTCTGTCTCATCCTCCTGGAACCTTGC NM_001975 RefSeq chr12
+ 6914449 6923696 ENO2 2026 "enolase 2 (gamma, neuronal)"
GO:0000287|GO:0005886|GO:0005975|GO:0006094|GO:0044281|GO:0005615|GO:0004634|GO:0006096|GO:0005
829|GO:0001917|GO:0009405|GO:0006006|GO:0043204|GO:0000015|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140827_PI430048170 0.00560599118672315 3.98589649561457 2.70026843417777
2.9398684060171 2.25047205519089 A P A 0.2983003733213260.355581368884953
1.16369633791372 A A A LNCV6_140827_PI430048170 mRNA
TGTGCACTCAACTAGAGTATTAACTGTAAAAAGATTTGTGAAGTTTGGAAGCTCTATTCG NM_001189 RefSeq chr4
- 13540829 13544490 NKX3-2 579 NK3 homeobox 2
GO:0060576|GO:0007368|GO:0043066|GO:0006366|GO:0048706|GO:0048705|GO:0005634|GO:0000122|GO:0000
978|GO:0048536|GO:0048645|GO:0001078|GO:0001501|GO:0031016|GO:0042474|GO:0032331 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130449_PI430048170 0.4048583795597461.05258017801969 8.5169422151921
8.39386248295024 8.483836396641 P P P 8.24912277823904 8.4477477187658
8.46875802305325 P P P LNCV6_130449_PI430048170 mRNA
TCCCTTTTGCAGCTAAAATTTCACAGGGCTATTTCTAATACGTAAGCAAATGTTACCATT NM_005614 RefSeq chr7
- 151466011 151519924 RHEB 6009 Ras homolog enriched in brain

GO:0005515|GO:0008286|GO:0032008|GO:0019901|GO:0005886|GO:0007264|GO:0003924|GO:0005525|GO:0046
872|GO:0030425|GO:0005829|GO:0006184|GO:0007165|GO:0016020|GO:0000139|GO:0043025|GO:0005789|GO:0
005681|GO:0007050|GO:0019003|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108686_PI430048170 0.485315310652248 1.07510546078556 0.390175148380215
0.634399192388042 0.343662358526046 A A A 0.245893773868261 0.559625593819607
0.24301133099179 A A A LNCV6_108686_PI430048170 mRNA
GCATTCGTCAGCACAGTTGGGATCGATTTCAAAGTAAAAACTGTATTCAAAAATGAAAAG NM_138453 RefSeq chr5
+ 58583111 58851579 RAB3C 115827 "RAB3C, member RAS oncogene family"
GO:0005515|GO:0048471|GO:0009306|GO:0005886|GO:0003924|GO:0005525|GO:0072659|GO:0031982|GO:0006
886|GO:0016079|GO:0005829|GO:0006904|GO:0008021|GO:0006184|GO:0031489|GO:0019882|GO:0017157|GO:0
032482|GO:0019003|GO:0030667|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127809_PI430048170 0.00557429891006195 0.4489590589615544 .19148553435797
4.40416685382208 4.32764712909194 P P P 5.2053158065172 5.4879932165956
5.66697449432475 P P P LNCV6_127809_PI430048170 mRNA
CCCCTGACATGGAATAAGATATGAATAAATGCACAGACTTGTCCAAAATCATCCAATTAA NM_213622 RefSeq chr2
+ 73828997 73867168 STAMBP 10617 "STAM binding protein, transcript variant 3"
GO:0005515|GO:0016579|GO:0008284|GO:0004843|GO:0005886|GO:0000281|GO:0005634|GO:0014067|GO:0032
154|GO:0007259|GO:0046872|GO:0046580|GO:0043524|GO:0005737|GO:0006508|GO:0005654|GO:0005769|GO:0
008237|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144261_PI430048170 0.313186813699432 1.15615926932192 8.28292493095942
8.66464745237596 8.55646466999751 P P P 8.56480265235883 8.06823476944311
8.22380262645265 P P P LNCV6_144261_PI430048170 mRNA
CAATAGAGGTTCTGAAAGGTCTGTGTCTTGTCAAAACAAGTAAACGGTGGAACTACGACT NM_022153 RefSeq chr10
- 71747555 71773580 C10orf54 64115 chromosome 10 open reading frame 54
GO:2000562|GO:0048863|GO:0030513|GO:2000738|GO:0002725|GO:0030509|GO:0016021|GO:0009897 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129382_PI430048170 0.0300533970417782 1.479468729161 5.05544817320053
4.90860454076287 5.02476528066941 P P P 4.65074187324821 4.37886173487683
4.23708539194793 P P P LNCV6_129382_PI430048170 mRNA
AAACCATTGGCTGGGCCTTTGAGGACACAGATCAGAAGAAAGAAAGACAACTTTCCTCTG NM_001142397 RefSeq
chr18 + 48539055 48863215 CTIF 9811 "CBP80/20-dependent translation initiation factor,
transcript variant 2" GO:0005515|GO:0048471|GO:0005737|GO:0000184|GO:0003723|GO:0006446 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_46922_PI430048170 0.722242460481857 1.04731982939118 0.442793138185847 0.767801673075223
0.323924624181143 A A A 0.413785959642405 0.496396557983982 0.460351327676393 A A A
LNCV6_46922_PI430048170 mRNA
CAAGAGCAAAAATCAGCTGCACAAAGAAGTTCAAGTTTGAATGTAACTTCAGATCATATG NM_019002 RefSeq chr2
+ 67397309 67410401 ETAA1 54465 Ewing tumor-associated antigen 1 GO:0005737 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142592_PI430048170 0.675372976008281 0.947316097132227 9.50089773437065
9.16694201972726 9.45700842550853 P P P 9.1968855152173 9.5474709405277
9.60425724701994 P P P LNCV6_142592_PI430048170 mRNA
AAAGAGAGAGAGAGAGAGGTGTGAGGGACAAAATGCAAACCTATTTCCCTTGCCTCATAG NM_005219 RefSeq
chr5 - 141515020 141619055 DIAPH1 1729 "diaphanous-related formin 1, transcript variant 1"
GO:0005515|GO:0072686|GO:0043005|GO:0030335|GO:0007605|GO:0008360|GO:0051279|GO:0005102|GO:0035
372|GO:0032886|GO:0003779|GO:0032587|GO:0031175|GO:0044325|GO:0042802|GO:0005737|GO:0007010|GO:0
030041|GO:0017048|GO:0005522|GO:0071420 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79459_PI430048170 0.0568320957078975 1.67313441811695 2.7865015381658
2.41015989696108 2.38016635144919 A A A 1.33557881880316 2.11060361682266

1.83576868318499 A A A LNCV6_79459_PI430048170 mRNA
AATACACTTTTGAGATTTTCGATGGCAAAGACAACCATCAACGCTCCCTTGACCTGTCCG NM_003970 RefSeq
chr8_KI270821v1_alt + 228367 328590 MYOM2 9172 myomesin 2
GO:0005739|GO:0005515|GO:0032982|GO:0006936|GO:0008307|GO:0031430 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144063_PI430048170 0.8701500657681311.01720353169609 7.52936990371578
7.87672688946058 7.77264129483958 P P P 7.93579101494256 7.60410617453642
7.55636950628902 P P P LNCV6_144063_PI430048170 mRNA
TGTTTTGTGGTAGTCCTTTTGGGAAGAATCCAGTATTATCCACAATTATTGGCAAAGTTT NM_001144 RefSeq chr16
- 56361451 56425538 AMFR 267 "autocrine motility factor receptor, E3 ubiquitin protein ligase"
GO:0005515|GO:0006511|GO:0004842|GO:0048471|GO:0016874|GO:0006928|GO:0005634|GO:0030176|GO:0051
259|GO:0030425|GO:0030426|GO:0030968|GO:0007611|GO:0043025|GO:0004872|GO:0000209|GO:0000836|GO:0
007568|GO:0030433|GO:0007165|GO:0043234|GO:0016020|GO:0005789|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143847_PI430048170 0.1532473724383370.74159369838821111.2262173917222
10.7231334523737 10.5078602007433 P P P 11.1709528059258 11.4855500152129
11.1675284346065 P P P LNCV6_143847_PI430048170 mRNA
AGAGAAGTGAAGACTTTCTCCTTGCATTAAAAAGTCTGAACTGTGCGAAAGCTTAAAAAA NM_001282444 RefSeq
chr11 - 64852726 64879713 EHD1 10938 "EH-domain containing 1, transcript variant 1"
GO:0042632|GO:0005515|GO:0005811|GO:0017137|GO:0005886|GO:2001137|GO:0032456|GO:0005509|GO:0005
525|GO:0010886|GO:0005524|GO:0006886|GO:0031175|GO:0006897|GO:0034383|GO:0016020|GO:0007596|GO:0
031901|GO:0051260|GO:0031095|GO:0055038|GO:0010008|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_131115_PI430048170 0.0416993655732576 0.74738093834362912.9784049502652
12.7590992276868 12.6145281540025 P P P 13.1355535735034 13.281747167773
13.2147105313009 P P P LNCV6_131115_PI430048170 mRNA
TGCCCTGTCCTCAGCACGCGTGTGCAAAAGTGAACAATAAATCATTTCAAAGATGCGAGA NM_022156 RefSeq chr17
- 82057871 82065821 DUS1L 64118 dihydrouridine synthase 1-like (S. cerevisiae)
GO:0050660|GO:0017150|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140149_PI430048170 0.000567632457326353 1.81046108134246 12.6163675383048
12.8272723674972 12.7377705103529 P P P 11.7517554129353 11.9462701132663
11.9145956032677 P P P LNCV6_140149_PI430048170 mRNA
AGAATCAGACAGGGCCACAGCCCCCTCAGGCAGCCAGGTCATCTGAGTATCATTAAGAGT NM_030811 RefSeq chr20
+ 3046028 3048250 MRPS26 64949 mitochondrial ribosomal protein S26
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0042769|GO:0043043|GO:0005
743|GO:0005654|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141177_PI430048170 0.4172748664985782.01815317471827 0.439278445180611
0.4519007146053042.45166368984139 A A A 0.4868372306776680.402750004658569
0.418857383007209 A A A LNCV6_141177_PI430048170 mRNA
TTCTTTAAAGGAGACAGGTACTGGGTGTTCAAGGACAATAACGTAGAGGAAGGATACCCG NM_016155 RefSeq chr12
+ 131828395 131851771 MMP17 4326 matrix metallopeptidase 17 (membrane-inserted)
GO:0005887|GO:0005509|GO:0006508|GO:0005578|GO:0008270|GO:0031225|GO:0043085|GO:0008047|GO:0004
222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131424_PI430048170 0.5444610824194380.9341375699776733.1049493116353
3.48668798987391 3.21887437433998 P P P 3.48199837400187 3.16910186944594
3.46063659628406 P P P LNCV6_131424_PI430048170 mRNA
TGTAGAGAGAAAAGGATGTGTCATACATTTAGACCAGGTGGCCTGTCCTGTAAATTTTTT NM_014753 RefSeq chr10
+ 42782505 42834937 BMS1 9790 BMS1 ribosome biogenesis factor
GO:0042255|GO:0005730|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_67679_PI430048170 0.0727608201397427 2.72356736352573 2.63862276800554
2.82061315253526 2.76780287343297 A A A 2.05564784303933 0.816193087058535
0.548889666664536 A A A LNCV6_67679_PI430048170 mRNA
AAGGCCAAAGCCACAGCCAGAGCCAAGAAGCCAGGATTCAAGAAATGAGGAGCCACGCCT NM_001286680
RefSeq chr8 + 22024109 22036897 NPM2 10361 "nucleophosmin/nucleoplasmin 2, transcript
variant 2"
GO:0000790|GO:0045740|GO:0007096|GO:0009994|GO:0005634|GO:0009790|GO:0003676|GO:0043085|GO:0007
338|GO:0042393|GO:0045836|GO:0003682|GO:0000789|GO:0051260|GO:0006338|GO:0019899 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138286_PI430048170 0.8638758486723540.9737560683131384.4700739505772
4.30025334160013 4.44544443042464 P P P 4.1754146848844 4.48396213487899
4.63934862008673 P P P LNCV6_138286_PI430048170 mRNA
TTACTGAAGTGTCAACACATTAGTTTGTGAGCCTCATGTAAGAACATGATGGTCTTTTTT NM_018939RefSeq chr5
+ 141150021 141153287 PCDHB6 56130 "protocadherin beta 6, transcript variant 1"
GO:0016339|GO:0005887|GO:0005509|GO:0007268|GO:0016021|GO:0007155|GO:0007416|GO:0007156|GO:0007
399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_50764_PI430048170 0.00211459459978096 0.61191336220311614.5591228158255
14.6640504629162 14.6333891097927 P P P 15.4040888924721 15.3685575014893
15.2039225625886 P P P LNCV6_50764_PI430048170 mRNA
CCTGCCTCTCCCCTTCCTCCTCTGCTCTTGATCTGTGTTTCAATAAATTAATGTAGCCAA NM_002281RefSeq chr12 -
52285912 52291515 KRT81 3887 "keratin 81, type II" GO:0005515|GO:0005198|GO:0045095|GO:0005615
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139447_PI430048170 0.1012812927702671.21121987251593 10.9079060107078
11.2076784539021 11.2091027018183 P P P 10.8037358665843 10.8011620250086
10.9081591585146 P P P LNCV6_139447_PI430048170 mRNA
GGTGCCTAGGAGGAGATAAAGATGAGGAGGTTTTTCCTTATTGTATAAATGAATATTTGT NM_024294RefSeq chr6
- 34587279 34696850 C6orf106 64771 "chromosome 6 open reading frame 106, transcript variant 1"
GO:0043130|GO:0008150|GO:0003674|GO:0005776|GO:0016236|GO:0005575|GO:0000407 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132989_PI430048170 0.26874270846128 1.17924710449869 10.7465991336624
10.6541031233881 10.8423854412322 P P P 10.7688553307361 10.1821217013203
10.5253134597994 P P P LNCV6_132989_PI430048170 mRNA
TCAGTTCATCTAATCACAGATCATCAAACAGTAGTGTTCCCACCTAGGAGTGTTAGGAAG NM_001085481 RefSeq
chr12 + 116559380 116576620 MAP1LC3B2NA microtubule-associated protein 1 light chain 3 beta 2NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57877_PI430048170 0.8936706808139321.00965555743996 8.75662987307845 8.68890290086983
8.49990785787344 P P P 8.37339467640761 8.84913076732175 8.65426104615069 P P P
LNCV6_57877_PI430048170 mRNA
TATCCTTGTGTCTCCACCCCCTTCCATGTGTTGAATAATAAAAGGTGGGAAAGTGCTGTC NM_032871RefSeq chr11
+ 73376667 73397474 RELT 84957 "RELT tumor necrosis factor receptor, transcript variant 1"
GO:0005737|GO:0005886|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54891_PI430048170 0.0229441629951297 0.6274631878982243.67065945903758
3.82251738146793 4.07851135191506 P P P 4.58209219072416 4.47650147510685
4.55792161518802 P P P LNCV6_54891_PI430048170 mRNA
TCATTGTGGTGGGCTATGAGAGCCTCAAGAAACTCAGCCTCCGACCTGAGCTGGTGGACT NM_001286184 RefSeq
chr1 + 156193931 156212796 SLC25A44 9673 "solute carrier family 25, member 44, transcript variant
1" GO:0005743|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128557_PI430048170 0.2444665927488780.9598713415823021 2.4727220160771
12.5784705818333 12.5659030754572 P P P 12.5884272780105 12.5564090574718

12.6502347102815 P P P LNCV6_128557_PI430048170 mRNA
GACCAACCCATCACCTCAGTTGTTTTTTATTTTTCTAATAAAGTCATGTCTCCCTTCATG NM_001255 RefSeq chr1 +
43358954 43363202 CDC20 991 cell division cycle 20
GO:0005515|GO:0007094|GO:0090129|GO:0008284|GO:0048471|GO:0016567|GO:0005634|GO:0031145|GO:0005
829|GO:0051488|GO:0005737|GO:0031915|GO:0005680|GO:0005813|GO:0005819|GO:0051437|GO:0051436|GO:0
008022|GO:0051439|GO:0040020|GO:0007067|GO:0007049|GO:0000922|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132604_PI430048170 0.0884251404806087 1.23258487557122 14.2281645705706
14.3449104252198 14.2138236659102 P P P 13.8930059958907 14.1628242716263
13.8051214581342 P P P LNCV6_132604_PI430048170 mRNA
AAGGCTGGAGCGGAGGGACTTGCTGGGGGTTGGATTGGGGGTAATAAACCCGGACGGAAG NM_006848 RefSeq
chr11 + 65890403 65891635 CCDC85B 11007 coiled-coil domain containing 85B
GO:0005515|GO:0030308|GO:0005813|GO:0005737|GO:0045599|GO:0005634|GO:0045892|GO:0030154|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136826_PI430048170 0.3282953129549331.03337555702286 0.299536879953299
0.2581431620121030.381801837280456 A A A 0.2782852725057960.24650255103446
0.275146143621876 A A A LNCV6_136826_PI430048170 mRNA
TGGCCAGAAAACGTCCTGCTTATTTATTGCCAGATATGGTTTATTTCTAAGCGTTGTCAA NM_178161 RefSeq chr10
+ 23192530 23194252 PTF1A 256297 "pancreas specific transcription factor, 1a"
GO:0005667|GO:0006355|GO:0070888|GO:0005634|GO:0010842|GO:0021549|GO:0048663|GO:0009790|GO:0003
677|GO:0035881|GO:0006351|GO:0048384|GO:0043565|GO:0001077|GO:0005737|GO:0031016|GO:0045944|GO:0
031018|GO:0003682|GO:0061074|GO:0031017|GO:0046983|GO:0009888 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_145611_PI430048170 0.159009348899091 0.966623214559053 0.280017366021015
0.3232041616028440.331938634881824 A A A 0.4034598870653770.327777850696584
0.350329771586503 A A A LNCV6_145611_PI430048170 mRNA
AAACCTACAGGACTTTCACTAAAGCTAGCCAGAGACAGCCATGAAAATGGACGTTTCACC NM_001006630 RefSeq
chr7 + 136868651 137017024 CHRM2 1129 "cholinergic receptor, muscarinic 2, transcript variant 1"
GO:0030054|GO:0005886|GO:0008016|GO:0009615|GO:0007213|GO:0016907|GO:0007399|GO:0007186|GO:0005
887|GO:0007187|GO:0051482|GO:0045211|GO:0007207|GO:0007188 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_49926_PI430048170 0.2782158656107641.31172693186067 0.4083328887195821.0956833319825
0.356850294793823 A A A 0.2501189269499 0.3150263793778680.243631388441881 A A A
LNCV6_49926_PI430048170 mRNA
GCAAATCATTTCAGAAGTTTTCACACCTAACTCAACATAAGGTAATTCATGCTGGAGAGA NM_003441 RefSeq chr4
+ 337806 373902 ZNF141 7700 zinc finger protein 141
GO:0006355|GO:0006366|GO:0005634|GO:0035108|GO:0009653|GO:0003677|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133281_PI430048170 0.5126791716368940.88439785610158 4.30420046876257
3.80549419176755 3.26952670616846 P P P 4.09216895105444 4.06247261216917
3.93431315123106 P P P LNCV6_133281_PI430048170 mRNA
TCTGTACAACTACCTCCCAACCCCAGTGCCTCAGTCAATAAATTTGCAAATTCATGAGAA NM_000427 RefSeq chr1
+ 153259702 153262124 LOR 4014 loricrin
GO:0005515|GO:0005737|GO:0018149|GO:0030216|GO:0005198|GO:0031424|GO:0005200|GO:0005654|GO:0030
674|GO:0001533 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_50992_PI430048170 0.7646864133867670.9827665944314460.3880798495812260.347582758003871
0.387326693610194 A A A 0.3042249665451880.5206009346761430.365058477944858 A A A
LNCV6_50992_PI430048170 mRNA
CTGTATCTGTCACAAACTGGTCTTATCTAGAAACATCTGCTGAGTCTCTAACCCTTTCAG NM_006147 RefSeq chr1

- 209785622 209806175 IRF6 3664 "interferon regulatory factor 6, transcript variant 1"
GO:0005515|GO:0000975|GO:0003700|GO:0008285|GO:0019221|GO:0005634|GO:0003677|GO:0043616|GO:0006
351|GO:0005829|GO:0005737|GO:0060644|GO:0060337|GO:0030216|GO:0007050|GO:0048468|GO:0045893|GO:0
070062|GO:0060333. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144571_PI430048170 0.15622893400449 1.51300119004571 1.54623987819552
0.7399720654802650.834438047233439A A A 0.3765924877610540.51128771221103
0.574469382739456A A A LNCV6_144571_PI430048170 mRNA
CAGTGAATTCTACACCAACAGGTTAAAACCATGAAAATAAAATCAACCTGAATCGAAAGG NM_001244892 RefSeq
chrX - 146814103 146814731 CXorf51B NA chromosome X open reading frame 51B NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138916_PI430048170 0.1533896751854180.6942415588331627.61506581218666
7.38301186308383 7.97546998110466 P P P 7.94708585712971 7.93427184464521 8.621973884967
P P P LNCV6_138916_PI430048170 mRNA
ATATACCGTGAAAATTGGTTTCATTTAACAAAAGATCAGATCCCTCCTTCAGCTGTACAC NM_004645RefSeq chr17
- 56938199 56961050 COIL 8161 coilin
GO:0005515|GO:0005737|GO:0015030|GO:0016020|GO:0005730|GO:0005654|GO:0005634|GO:0008022|GO:0042
802. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131654_PI430048170 0.00260347882527449 0.43371591791453 5.88893182177352
5.85448332237606 6.10080115340144 P P P 6.93373823261766 7.13926261396742
7.36673645598165 P P P LNCV6_131654_PI430048170 mRNA
ACCATCTGTGAGGTCAGTCATTTTGCATGATGTATGTAATCAAAAAGTTTGAAATGTCTG NM_001077619 RefSeq
chr8 + 58411263 58451501 UBXN2B 137886 UBX domain protein 2B
GO:0008599|GO:0043130|GO:0050790|GO:0005794|GO:0005783|GO:0007030|GO:0061025|GO:0043161|GO:0005
634|GO:0000045|GO:0031468|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130736_PI430048170 0.0172660331771227 0.9556422267434560.361640082970654
0.3724843066604880.330807690344276A A A 0.4362739734845570.425322870711825
0.399788517209593A A A LNCV6_130736_PI430048170 mRNA
CTCTGTTTTCATTTCAGAACATTGTGCTGTCTGTCAGCATATGTATATCAGCTACAAAAT NM_203447RefSeq chr9
+ 214864 465259 DOCK8 81704 "dedicator of cytokinesis 8, transcript variant 1"
GO:0043547|GO:0005515|GO:0005085|GO:0001771|GO:0016020|GO:0070233|GO:0007596|GO:0007264|GO:0031
252|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140427_PI430048170 0.366578113639306 1.0389784976325 0.448274061734565
0.2909333074466360.342840885748903A A A 0.2778610569258280.328800224101968
0.313895653573691A A A LNCV6_140427_PI430048170 mRNA
CTGCACGTCCAGGCATATTTCGTAGTTTTGCAGTAAATAATATTCACATAATGATACTGT NM_000035RefSeq chr9
- 101420559 101435780 ALDOB 229 "aldolase B, fructose-bisphosphate"
GO:0005515|GO:0008092|GO:0070072|GO:0005815|GO:0005975|GO:0034451|GO:0006094|GO:0044281|GO:0032
781|GO:0006096|GO:0042802|GO:0005829|GO:0004332|GO:0030388|GO:0006116|GO:0009405|GO:0051117|GO:0
006006|GO:0070061|GO:0006001|GO:0070062|GO:0006000 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_132812_PI430048170 0.0199443113108131 0.6805028324088348.03594212157793
7.83755203858359 8.11910375595919 P P P 8.37232414754985 8.51568722450177
8.75825009147406 P P P LNCV6_132812_PI430048170 mRNA
CTGTCTCTGATTTCTAGGCTAGTTACTTGAGATATGAATTTTCCATAGAATATGCACTGA NM_015344RefSeq chr8
+ 30095405 30108071 LEPROTL1 23484 "leptin receptor overlapping transcript-like 1, transcript variant
1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128740_PI430048170 0.1979320877263621.09442570048946 0.576159140982003
0.3527496752788390.534916371801766A A A 0.2849222073987560.386609653944218
0.408439235644168A A A LNCV6_128740_PI430048170 mRNA

ACCCTTATTTTACTGACCAATATGGAAGTTCTTGGTATCTTTAAGGCTGACCTTCCTGGT NM_173496RefSeq chr10 - 28050993 28282138 MPP7 143098 "membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)" GO:0005515|GO:0035591|GO:0030054|GO:0046982|GO:0019904|GO:0097025|GO:0009967|GO:0030010|GO:0005739|GO:0032947|GO:0031334|GO:0005912|GO:0070830|GO:0071896|GO:0005923 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131095_PI430048170 0.4094147764240320.8120610397938760.510833842769568 0.5379818366043470.418793891020857A A A 0.5374922238300041.23953888230154 0.460609426115119A A A LNCV6_131095_PI430048170 mRNA
TTCAAAAAGATCATGTTGCTCCACTGGAAGGCTTCTTACAATGGCGGTAAGTCCAGTGCA NM_138964RefSeq chr2 + 68645821 68655576 PROKR110887 prokineticin receptor 1 GO:0043066|GO:0004983|GO:0005886|GO:0007218|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141303_PI430048170 0.3114496627733831.18202623754625 6.60200194768764 6.37384651317797 6.80925024086353 P P P 6.00080599337973 6.5171426787851 6.5171426787851 P P P LNCV6_141303_PI430048170 mRNA
TTGCTGTGAAGAAAAACATGTGTATATATTGCACCTTGAGTTGTCAGAAGGTAGAAACTG NM_001286565 RefSeq chr16 + 85063211 85094222 KIAA0513 9764 "KIAA0513, transcript variant 1" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128054_PI430048170 0.8759023579543021.00422913624599 0.293208998488546 0.3322635962931820.396494544224029A A A 0.3559507053449370.332975627180681 0.316391964410491A A A LNCV6_128054_PI430048170 mRNA
ACTGGTGAGGACAAGGCCTCTATTGTAGTCAGAGTCCTCTCAAAGGACAAAAGCAGATAT NM_001287812 RefSeq chr5 + 172755502 172762562 LOC101928093 NA uncharacterized LOC101928093 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141071_PI430048170 0.4488003912109642.42348245507011 2.90804387377942 0.5164135986474230.356151343027373A A A 0.3921395252224760.557136712384555 0.517932757300429A A A LNCV6_141071_PI430048170 mRNA
GAAGGGTATGTACATTTGTTTTGTGTGTCACATGGGGTCAGTAAGTTCTCAATAAAAATT NM_032498RefSeq chrX + 120158560 120164027 RHOXF2 84528 "Rhox homeobox family, member 2" GO:0043565|GO:0005515|GO:0006355|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138790_PI430048170 0.49755326831499 0.9419217113834650.304393499235474 0.45863380631485 0.31836412528179 A A A 0.6090269707098450.435406172533374 0.282493538094408A A A LNCV6_138790_PI430048170 mRNA
GTCAGATGCCCTAGTTAATCATGTAATTTAATTCTGGTATTGTGAGTGGTTAGCAATCAA NM_152754RefSeq chr7 - 84995555 85121931 SEMA3D 223117 "sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D" GO:0016020|GO:0005576|GO:0004872|GO:0030154|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127131_PI430048170 0.62902686824428 0.9260967964333857.06168080666222 7.26209218241271 6.69190198013905 P P P 7.39708617000581 7.0465316219617 6.91749928565472 P P P LNCV6_127131_PI430048170 mRNA
GGTCCTTCTCCACACCCACTTTGTCCATTTGCAAATATATTTTGGAAAACAGCTAAAAAA NM_001289936 RefSeq chr17 + 39688083 39728662 ERBB2 2064 "erb-b2 receptor tyrosine kinase 2, transcript variant 3" GO:0005515|GO:0033088|GO:0048709|GO:0030307|GO:0042802|GO:0007507|GO:0046777|GO:0007173|GO:0007411|GO:0046983|GO:0070372|GO:0043125|GO:0050679|GO:0023014|GO:0046982|GO:0019903|GO:0018108|GO:0014065|GO:0045785|GO:0043235|GO:0008045|GO:0008543|GO:0032321|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68433_PI430048170 0.80804088340706 0.98154850433629 4.10613261946735 3.27210458105051 3.61759864080805 P P P 3.78912582900861 3.68749503694508 3.72077168483318 P P P

LNCV6_68433_PI430048170 mRNA
GGATTGACTTCTAAAGACTCTTGGTATGTGAGGAAGAAACCTGGAAGAGGAAGAGGAAAG NM_001040185
RefSeq chr19 + 53395143 53412009 ZNF765 91661 zinc finger protein 765
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132509_PI430048170 0.945257835219832 1.03219501353151 0.425552939044492
0.430873205297826 1.60574471745768 A A A 0.383880837596388 1.54625161018874
0.411833144046579 A A A LNCV6_132509_PI430048170 mRNA
CGTTATTAAGAATGGGCAAGATGTCCTTATATACTAGAAGCTTTTGTAAAGTCATGTGTC NM_003764 RefSeq chr6
+ 144150516 144191939 STX11 8676 syntaxin 11
GO:0005515|GO:0043316|GO:0043320|GO:0005794|GO:0005886|GO:0043312|GO:0031201|GO:0006886|GO:0008
021|GO:0012505|GO:0005484|GO:0000149|GO:0061025|GO:0031629|GO:0016021|GO:0048278 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136240_PI430048170 0.767473494649003 0.851656632527389 0.535712085468946
1.86019653293071 0.502429731608738 A A A 2.09389072773601 1.01673971997933
0.418068661094278 A A A LNCV6_136240_PI430048170 mRNA
AAGTTTCTTGCCCTTGAAAATCCAATTGGTTTCTGTTATAGCAGTCCCCACAACATCAAA NM_003784 RefSeq chr18
+ 63775374 63805376 SERPINB7 8710 "serpin peptidase inhibitor, clade B (ovalbumin), member 7,
transcript variant 1"
GO:0010951|GO:0005737|GO:0032967|GO:0004867|GO:0090362|GO:0005615|GO:0072126|GO:0032914 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138360_PI430048170 0.916039990542034 0.982878278331387 3.87038362657401
3.97168471274281 4.41308391774646 P P P 3.90599231850248 3.99710961252707
4.43023497405957 P P P LNCV6_138360_PI430048170 mRNA
CTTGAAGAAAGGGGAAATCTTGAGTAACCTCATTAAAATTAATGTCTGGTGGACCTCTCA NM_001172109 RefSeq
chr15 + 72116850 72140970 SENP8 123228 "SUMO/sentrin specific peptidase family member 8,
transcript variant 3" GO:0019784|GO:0000338|GO:0005737|GO:0006508|GO:0005634 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_109888_PI430048170 0.162627711682241 0.746073786371015 5.62957762208868
5.32949744033392 5.79022449513777 P P P 5.61224219855403 6.15457021418672
6.21476837505784 P P P LNCV6_109888_PI430048170 mRNA
GACACATCTGAGGCAAAGCTAGACAAGTTGGATGGCTTGAGGACTGGTACTAAAAGGAAA NM_019589 RefSeq
chr14 + 74763365 74837310 YLPM1 56252 YLP motif containing 1
GO:0005515|GO:0008150|GO:0001078|GO:0005737|GO:0016607|GO:0032204|GO:0005654|GO:0005634|GO:0000
122|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140596_PI430048170 0.181129308768358 0.692407158068834 4.05456951741233
4.35090430310689 4.08643731472046 P P P 4.15168891239219 4.91396311577597
4.91085591881356 P P P LNCV6_140596_PI430048170 mRNA
GTTTAGCAAATGTTTCCCACCCATGGGGTCTTTTTTATTGTGGTAAAATATACTGAACAT NM_033544 RefSeq chr15
+ 90954875 90963125 RCCD1 91433 "RCC1 domain containing 1, transcript variant 1"
GO:0005737|GO:0005886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101172_PI430048170 0.0478926197925439 1.71373589337938 6.13007559446965
6.21460290387241 6.04938180294211 P P P 5.71385506697709 5.07358269164666
5.19728662239122 P P P LNCV6_101172_PI430048170 mRNA
CTGGACTTGAACATCAGCTATGTAGGTGATGTGCAGATTGATGTGGAAGTGAAGAAATAT NM_001184796 RefSeq
chr12 + 56128201 56144676 ESYT1 23344 "extended synaptotagmin-like protein 1, transcript variant
1" GO:0005515|GO:0005543|GO:0016020|GO:0005886|GO:0006869|GO:0044232|GO:0030176|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121229_PI430048170 0.0320122714007208 0.738257973461965 4.58157972609736

4.35453925847715 4.41425575256211 P P P 5.08810802011499 4.81390497982726 4.7485443322782
P P P LNCV6_121229_PI430048170 mRNA
AGATCGCTGACTTCGGCCTAGCTAAGCTGCTGCCGCTTGACAAAGACTACTACGTGGTCC NM_000215RefSeq chr19
- 17824783 17848032 JAK3 3718 Janus kinase 3
GO:0005515|GO:0007260|GO:0070232|GO:0032693|GO:0007262|GO:0060397|GO:0051427|GO:0005829|GO:0002
731|GO:0035556|GO:0006954|GO:0045944|GO:0042102|GO:0030183|GO:0070670|GO:0070672|GO:2001241|GO:0
035771|GO:0043029|GO:0005856|GO:0038083|GO:0071104|GO:0050868|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139389_PI430048170 0.80504243611946 0.98616280299855 0.294822454800322
0.296236172274835 0.406644963505092 A A A 0.304823767065261 0.280260822620011
0.46845854737933 A A A LNCV6_139389_PI430048170 mRNA
CACAATGGAAATCACTGTGATTTGTACATATGCCCTAGGAAAATTTTACTGCTGTCTAAT NM_005044RefSeq chrX
- 3604342 3713634 PRKX 5613 "protein kinase, X-linked"
GO:0005515|GO:0030334|GO:0031589|GO:0005634|GO:0060562|GO:0001525|GO:2000696|GO:0005524|GO:0030
155|GO:0005737|GO:0046777|GO:0018105|GO:0043542|GO:0060993|GO:0001935|GO:0030099|GO:0007155|GO:0
004691 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132771_PI430048170 0.787366602308809 0.768914035287384 0.291309724365065
1.50228247712891 0.392814540212583 A A A 2.16026412680836 0.338008143514612
0.321223310507033 A A A LNCV6_132771_PI430048170 mRNA
TTTGATATTGGACTGTGGTTGTGCCAGTTGACACTCAGGAGTGGAGACTAGATCTGCAAT NM_001002915 RefSeq
chr19 + 46147781 46161304 IGFL2 147920 "IGF-like family member 2, transcript variant 1"
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135530_PI430048170 0.977882822040453 0.876658355686617 1.6300418006398
1.64977960657889 2.59303180807754 A A A 0.517777420231562 2.8019469208088
2.48208496689931 A P P LNCV6_135530_PI430048170 mRNA
CCCCTTTCAACAATTTAGTTGAATGACTCCCTTCCATCTATCAGTCTTACTCCAAATATANM_138694RefSeq chr6 -
51615346 52087625 PKHD1 5314 "polycystic kidney and hepatic disease 1 (autosomal recessive),
transcript variant 1"
GO:0005515|GO:0051898|GO:0032006|GO:0072686|GO:0008284|GO:0048471|GO:0031362|GO:0036064|GO:0016
337|GO:0016324|GO:0005737|GO:0004872|GO:0070372|GO:0070062|GO:0005813|GO:0043066|GO:0001822|GO:0
006874|GO:0032088|GO:0042592|GO:0010824|GO:0072372|GO:0042384|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126904_PI430048170 0.0917195897776145 0.815327078821932 4.36937178986713
4.40683629354342 4.07170733175562 P P P 4.45249077797382 4.71891430218119
4.57056837668374 P P P LNCV6_126904_PI430048170 mRNA
GAAAGTGGTTTTCAGTATTGTGACAATACAACGTTTTTACAAGGTTGTTTTCTACCACCA NM_001452RefSeq chr6
+ 1389833 1395597 FOXF2 2295 forkhead box F2
GO:0005667|GO:0000977|GO:0003700|GO:0005634|GO:0048566|GO:0001837|GO:0001228|GO:0003677|GO:0048
596|GO:0006351|GO:0042249|GO:0043565|GO:0030198|GO:0045944|GO:0060021|GO:0048806|GO:0045893|GO:0
045892|GO:0008134. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142781_PI430048170 0.204124356973772 0.912396303078303 6.43072400369741 6.6390233230447
6.49698055592422 P P P 6.75218760522367 6.53967775186771 6.67164796312228 P P P
LNCV6_142781_PI430048170 mRNA
TATGGCAAATAAAATGTAAAGGAACATGCAACAGCCCTCATCTTCCTTGATTTTATGGTT NM_001079839 RefSeq
chr4 + 48831226 48861817 OCIAD1 54940 "OCIA domain containing 1, transcript variant 2"
GO:0005739|GO:0005515|GO:0016020|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128617_PI430048170 0.269834498606684 0.820608493878728 3.6002563709278
3.44029260544985 3.48748804295353 P P P 4.12439058977166 3.56263354256619
3.63443491565006 P P P LNCV6_128617_PI430048170 mRNA

CCCCAGAGAGCAAATCAAAGAAAAATTACAGCAAGAAGAGAAAAGTGGTTTATCATTGTGNM_014455RefSeq chr1 - 145746081 145824123 RNF115 27246 ring finger protein 115
GO:0005515|GO:0070534|GO:0004842|GO:0016874|GO:0042059|GO:0008270|GO:0070936|GO:0043162|GO:0051865|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135037_PI430048170 0.4909828714883070.8839821068652077.55001332517131 7.50357188612288 7.85296253901654 P P P 7.562651002733 7.6805089722974 8.15290818514678 P P P LNCV6_135037_PI430048170 mRNA
GGTAACTCACTCAAGTGAATGAATGGTCTTGCATTTTAAAAGCTTATGGGAAACTCAATT NM_001301073 RefSeq chr5 + 154858518 154876792 CNOT8 9337 "CCR4-NOT transcription complex, subunit 8, transcript variant 2"
GO:0005515|GO:0010467|GO:0008284|GO:0006355|GO:0008285|GO:0003700|GO:0003723|GO:0043928|GO:0005634|GO:0046872|GO:0030014|GO:0006351|GO:0006417|GO:0005829|GO:0005622|GO:0004535|GO:0000175|GO:0035195|GO:0061014|GO:0000289|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127790_PI430048170 0.1575790893154121.54755539854541 13.8013720613204 13.9229621842509 13.8516607243858 P P P 13.7874686520293 12.9256761428179 12.7511186077434 P P P LNCV6_127790_PI430048170 mRNA
GTCCTGAGCCATAGTGACTCTTTTATCTGTGTGTCTTTTGCTAAATATGCCCTTTTTATA NM_005851RefSeq chr11 - 67506489 67508728 CDK2AP2 10263 "cyclin-dependent kinase 2 associated protein 2, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133286_PI430048170 0.1857887809475970.8443503854267537.45569956020323 7.47640693666987 7.73262354260288 P P P 7.85493745231977 7.56670507075912 7.96359530680999 P P P LNCV6_133286_PI430048170 mRNA
CTGATGCCTCATTTCTACATTCTGTCATTAGCTATTATCATCTAACGTTTCAGTGTATCC NM_001159704 RefSeq chrX + 136169295 136211359 FHL1 2273 "four and a half LIM domains 1, transcript variant 4"
GO:0005515|GO:0030308|GO:0005886|GO:0043268|GO:2000134|GO:0005634|GO:0030154|GO:0044325|GO:0005829|GO:0003674|GO:0005737|GO:0007517|GO:0010972|GO:0009887|GO:0008270|GO:0003254|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141664_PI430048170 0.0616690159634977 0.6920964869022896.81794271258479 6.9648317915778 7.30384740280059 P P P 7.3348200126626 7.50594569649293 7.83674438642976 P P P LNCV6_141664_PI430048170 mRNA
CATCAAAAATCTGTTCATACCCCACGTTGGTTTCAAAACATACTATGCTTTTTCTTCGTG NM_018097RefSeq chr15 + 42548812 42569992 HAUS2 55142 "HAUS augmin-like complex, subunit 2, transcript variant 1"
GO:0005813|GO:0005794|GO:0006996|GO:0005874|GO:0005819|GO:0051225|GO:0005829|GO:0051297|GO:0003674|GO:0005737|GO:0007067|GO:0000086|GO:0070652|GO:0005654|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144076_PI430048170 0.00360647815371146 1.57586782654004 9.22570998258997 9.32831099170726 9.05516699720072 P P P 8.57423115251903 8.63700910673973 8.43526895882527 P P P LNCV6_144076_PI430048170 mRNA
GGGGTCAGGGGAAGGTAGAGCTGGAGCTTTTACAGAAATAAAACCCAAGAGTTTGATTAT NM_001168370 RefSeq chr6 - 43037616 43053945 CUL7 9820 "cullin 7, transcript variant 1"
GO:0005515|GO:0006511|GO:0048471|GO:0016567|GO:0005634|GO:0001837|GO:0005829|GO:0030968|GO:0005737|GO:0005680|GO:0006508|GO:0007030|GO:0016032|GO:0031625|GO:0005813|GO:0007088|GO:0005794|GO:0000281|GO:0000226|GO:0001890|GO:0050775|GO:0005654|GO:0006987|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135176_PI430048170 0.4241302629255990.9590847042604181 0.5338595317766 10.7075952476522 10.6309041367561 P P P 10.6300131519374 10.7757245341711 10.6482607998438 P P P LNCV6_135176_PI430048170 mRNA
GTGACACCACTTGAGTGGAATTTTCCATGTTCCTTTTTACCTCTAATTTGGATCTTTTTG NM_014329RefSeq chr16 + 67873022 67884514 EDC4 23644 enhancer of mRNA decapping 4

GO:0005515|GO:0010467|GO:0008150|GO:0005737|GO:0016020|GO:0000932|GO:0043928|GO:0005654|GO:0005634|GO:0043231|GO:0005829|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144785_PI430048170 0.1753232299336030.5867501732982160.270331466523098 1.28591291648984 0.384364659514574A A A 0.773994075292591 1.54628091917245 1.92797746481576 A A A LNCV6_144785_PI430048170 mRNA GCGACTGGCATACTATGTGGATGTGACAGTGGCGTTTGTAATGAGAGCACTTTCTTTTTT NM_001299RefSeq chr19 + 11538716 11550323 CNN1 1264 "calponin 1, basic, smooth muscle"
GO:0005516|GO:0031032|GO:0003779|GO:0006940|GO:0005856|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144231_PI430048170 0.1700343497928841.11789787030487 0.349761983056923 0.6128278924392810.480963203746244A A A 0.3187377720750550.299823905781718 0.354084227371133A A A LNCV6_144231_PI430048170 mRNA GGGAAAGTACAAAACAAATTTGCTTGTGACATTTCAATAAGCTGTGCTGCTATTGTCTTT NM_138317RefSeq chr14 - 88180107 88323249 KCNK1054207 "potassium channel, two pore domain subfamily K, member 10, transcript variant 2"
GO:0007165|GO:0005244|GO:0005886|GO:0006810|GO:0007268|GO:0005267|GO:0034765|GO:0016021|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126855_PI430048170 0.0778880412902492 0.6962968494951951 1.9237538420593 11.5716914240347 11.3440775450456 P P P 12.3502842415709 12.2102084809755 11.8628730740512 P P P LNCV6_126855_PI430048170 mRNA GGCCCCTGCCCAGCTCTCCAAAGTCTTTCAGAAAAGTAAATCCTAAATTCAGTGATGAAA NM_014467RefSeq chrX + 100644165 100671299 SRPX2 27286 "sushi-repeat containing protein, X-linked 2"
GO:0005515|GO:0051965|GO:0030054|GO:0009986|GO:0005102|GO:0001525|GO:0071625|GO:0005615|GO:0060076|GO:0042802|GO:0042325|GO:0005737|GO:0016337|GO:0048870|GO:0097060|GO:0090050 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131831_PI430048170 0.8069171298724230.9888166814575680.506114597854375 0.4465030993307820.295924928951244A A A 0.3805940740692840.471804127319321 0.451291834544476A A A LNCV6_131831_PI430048170 mRNA TTTCTGCAGTTATTGAAAGCATGAAGTATTGGCGTGAACATGCACAGAAAACTGTACTTC NM_001170699 RefSeq chr17 - 3440010 3471773 SPATA22 84690 "spermatogenesis associated 22, transcript variant 1"
GO:0009566|GO:0007129|GO:0007276|GO:0005694|GO:0000711|GO:0051445 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137750_PI430048170 0.3622873041574381.321592045396 0.316171698982675 1.26843648964487 0.499075053546304A A A 0.4165045150199710.293499659764519 0.349325227340808A A A LNCV6_137750_PI430048170 mRNA TTTTGATACTGAAGGGAGGTTTGCGTCAACGACTACCTGCTCTGTAATTACTTTAAAAAA NM_001080457 RefSeq chr19 - 50516892 50568045 LRRC4B 94030 leucine rich repeat containing 4B
GO:0051965|GO:0042734|GO:0030054|GO:0044300|GO:0005102|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62098_PI430048170 0.00845923003099809 0.4420919118478576.04594538447146 5.66188500760611 5.67368578210719 P P P 6.59974895561234 7.17477025577014 7.10810360934801 P P P LNCV6_62098_PI430048170 mRNA AGTTAGAAGACAGCATAGCAACTCAGCTCAGGGAGCTACCAGAGAAAAATAGCAACTGAT NM_005078RefSeq chr15 - 70047790 70097917 TLE3 7090 "transducin-like enhancer of split 3, transcript variant 1"
GO:0005515|GO:0007165|GO:0006355|GO:0007219|GO:0009887|GO:0005654|GO:0005634|GO:0016055|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138444_PI430048170 0.5508672626661310.9531494927971119.63011456447557 9.43067566427592 9.7050309951174 P P P 9.68722621517178 9.76446882361086 9.52532530447205 P P P LNCV6_138444_PI430048170 mRNA

GATCTCCAAGGTCATTGTGGTGGGGGACCTGTCGGTGGGGAAGACTTGCCTCATTAATAG NM_031934RefSeq chr17 - 28714280 28717890 RAB34 83871 "RAB34, member RAS oncogene family, transcript variant 1" GO:0005515|GO:0032418|GO:0048471|GO:0005794|GO:0005795|GO:0043001|GO:0003924|GO:0031985|GO:0032587|GO:0005525|GO:0072659|GO:0031982|GO:0045335|GO:0006184|GO:0044351|GO:0019882|GO:0030670|GO:0032482|GO:0019003|GO:0090382|GO:0017160|GO:0090385|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135476_PI430048170 0.0721031257505153 0.4048297552732354.0707842974628 2.63576286403952 3.8763193349706 P A P 4.50901222591265 4.76220820715699 5.43401638409799 P P P LNCV6_135476_PI430048170 mRNA
GGGTTATAGAAATCTGGAAATAAGAAAGGAAGAGCTCTCTGTATTCTATAATTGGAAGAG NM_020760RefSeq chr2 - 196199250 196592611 HECW2 57520 "HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2, transcript variant 1" GO:0005737|GO:0004842|GO:0042787|GO:0016874|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144375_PI430048170 0.0185557350469016 5.26304782097517 4.627750594672 4.56941220254353 4.53220088650158 P P P 2.65400560132824 1.46162101681327 2.18796142334878 P A A LNCV6_144375_PI430048170 mRNA
GTATTTAGTTGTGATTACTGATTGCCTGATTTTAAAATGTTGCCTTCTGGGACATCTTCT NM_001033081 RefSeq chr1 - 39895423 39902015 MYCL 4610 "v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog, transcript variant 1" GO:0006355|GO:0003700|GO:0046983|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144700_PI430048170 0.5993957989694340.8564245091360072.69302488655939 2.59578044489477 2.74074817444287 A A A 3.02023433253837 3.22724705404302 2.30344176633111 P P A LNCV6_144700_PI430048170 mRNA
GAAGACCTAGACTCATCTGAAGGATCTTTGATGGAGGAAGAAGACCCAGACTCATCTGAA NM_001009616 RefSeq chrX - 52796145 52797348 SPANXN5 NA "SPANX family, member N5" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140875_PI430048170 0.78375467008519 1.19938296210023 0.3873485697154542.0817943183597 2.09987755176464 A A A 0.3070444354492371.81909569190481 1.77757170119702 A A A LNCV6_140875_PI430048170 mRNA
TGGACAGTTGGAAAACCAAAAACAGATACCATTTTCTCAATGGAATCAGTTCCCCCTCCA NM_033033RefSeq chr12 - 52393950 52406392 KRT82 3888 "keratin 82, type II" GO:0008150|GO:0045095|GO:0030280 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130073_PI430048170 0.7126201175768410.9656835980874437.34426128281933 7.13820284273643 6.89056012332039 P P P 7.05566276510982 7.23310513561993 7.26236659783034 P P P LNCV6_130073_PI430048170 mRNA
TGGGCGCAGTTGGTCTTTAACCACTTTTCAATGTCTAAAAACATTTGTTTGTGGTCTATA NM_000494RefSeq chr10 - 104031287 104085880 COL17A1 1308 "collagen, type XVII, alpha 1" GO:0005515|GO:0030056|GO:0005581|GO:0005886|GO:0034329|GO:0005576|GO:0005604|GO:0007160|GO:0008544|GO:0022617|GO:0005887|GO:0005911|GO:0030198|GO:0030574|GO:0031581|GO:0005788 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142063_PI430048170 0.2389296831940160.6086135866523150.376070479699447 1.11642420231068 2.03504483883931 A A A 1.61612420870068 1.75886101370218 2.57986544252254 A A P LNCV6_142063_PI430048170 mRNA
TTAATCCTAGTTCTGTTGACATTGGACCAGGCTCAGTAAATAAACGAATGGATTTCCAAA NM_016622RefSeq chr2 + 86199432 86213354 MRPL3551318 "mitochondrial ribosomal protein L35, transcript variant 1" GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005761|GO:0005743|GO:0006412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127215_PI430048170 0.0510450903290020.6499021038864341 0.1442268779547 10.031528634102 10.0525730092108 P P P 10.3814394858362 10.8640473379176 10.8042016211427 P P P

LNCV6_127215_PI430048170 mRNA
GTCTGAGGCCATCGCTGCTACACTTTGTTTTTATTTGTATTTCATACTGAAGTTTCAAAA NM_006231 RefSeq chr12 -
132623761 132687524 POLE 5426 "polymerase (DNA directed), epsilon, catalytic subunit"
GO:0008622|GO:0005886|GO:0003887|GO:0005634|GO:0005737|GO:0000082|GO:0000723|GO:0000166|GO:0006
270|GO:0000722|GO:0006297|GO:0051539|GO:0003677|GO:0001701|GO:0006260|GO:0006281|GO:0006283|GO:0
003682|GO:0000731|GO:0006287|GO:0005654|GO:0008270|GO:0006289|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_83559_PI430048170 0.52261076444898 0.85651803590707 3.96142839386883 2.71383655871361
3.33639170496043 P A P 3.29402421361118 3.69191693453194 3.89802207703939 P P P
LNCV6_83559_PI430048170 mRNA
CACCTCATTCAGGAGGAGTTTGCAAACCAAAGCTGATCAGCAAGTCAAACAGCAGGAAAT NM_006311 RefSeq chr17
- 16030093 16215560 NCOR1 9611 "nuclear receptor corepressor 1, transcript variant 1"
GO:0005515|GO:0010467|GO:0000790|GO:0003700|GO:0006367|GO:0044212|GO:0042826|GO:0006366|GO:0006
325|GO:0035257|GO:0005634|GO:0044281|GO:0046966|GO:0021794|GO:0046965|GO:0060318|GO:0005737|GO:0
046329|GO:0007219|GO:0072362|GO:0016580|GO:0017053|GO:0040014|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133271_PI430048170 0.0223936220344412 1.25525699648578 6.32832468910761
6.34779195744764 6.13827364354359 P P P 5.91068170144567 6.01652165122601 5.9097505868527
P P P LNCV6_133271_PI430048170 mRNA
TAACCCAGAGCCCACCATATAGTTTTATAGGTGCTCAATTTTCTATATCGCTATTAAACT NM_152755 RefSeq chr7
+ 100119641 100125505 CNPY4 245812 canopy FGF signaling regulator 4 GO:0005102|GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144907_PI430048170 0.00631383544429982 0.4146591547726330.503669468040006
0.5672476947650140.446318171796429 A A A 2.01123602340368 1.6065246654929
1.67898967812976 A A A LNCV6_144907_PI430048170 mRNA
CTATAGCTGCAAAGTGGGTTTTATGACCCTATAGCATATTATTATATGTTTCCTCTTAGC NM_001031709 RefSeq
chr10 - 88284101 88583325 RNLS 55328 "renalase, FAD-dependent amine oxidase, transcript variant
1"
GO:0060047|GO:0055062|GO:0003214|GO:0005615|GO:0003073|GO:0042415|GO:0042417|GO:0071871|GO:0002
931|GO:0016491|GO:0071873|GO:0042414|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82921_PI430048170 0.00512926001690671 2.35164995200664 7.02724696005479
7.24525352001968 6.94869755340803 P P P 5.75368680505941 6.12820058970333
5.60315624899249 P P P LNCV6_82921_PI430048170 mRNA
TGTGCCTGATGCCAGGACAGCTGTGCTCTCAGATGTAAATAGAGCAACCTATATAAACCT NM_005952 RefSeq chr16
+ 56682469 56684196 MT1X 4501 metallothionein 1X
GO:0071294|GO:0048471|GO:0007263|GO:0006882|GO:0005634|GO:0046872|GO:0036018|GO:0010273|GO:0005
737|GO:0010038|GO:0008270|GO:0071276|GO:0045926 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95781_PI430048170 0.90736980543685 0.9871738673332323.02156974498227 3.38866165430667
3.67070873984076 P P P 3.10816087969691 3.55942067602145 3.50125751763544 P P P
LNCV6_95781_PI430048170 mRNA
TCCGAAATCCCAGATGAGACCCCGAAGTGAAGCAAGGTGTTCATTAAACTCCGCAATTAT NM_001145020 RefSeq
chr6 - 10671417 10694606 C6orf52 347744 "chromosome 6 open reading frame 52, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129529_PI430048170 0.6349537445124340.93304164797054 5.06741177225099
5.30807528562702 5.71517806739722 P P P 5.2637830479291 5.50955286364347
5.66466558343621 P P P LNCV6_129529_PI430048170 mRNA
CTAGTTGATTTCCTCCATTTTGTAAAACGAGGCATCACTTTTTGTCCATGTTTTTGTGTT NM_016037 RefSeq chr1 +
38012711 38024825 UTP11L 51118 "UTP11-like, U3 small nucleolar ribonucleoprotein (yeast)"
GO:0005515|GO:0005737|GO:0043065|GO:0006364|GO:0032040|GO:0005730|GO:0042274|GO:0005615|GO:0007

399. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107369_PI430048170 0.0158966694983545 1.15756537906551 5.88152248793507
5.83958060358727 5.94044633366719 P P P 5.60890152687595 5.66985817380597
5.74791980769649 P P P LNCV6_107369_PI430048170 mRNA
GAAAACAGTAAATAGCTTGCGAAAACACGAGCATGTTGGAAGCTTTGCCAGGGACCTAGTNM_003198RefSeq chr1
+ 23743365 23762059 TCEB3 6924 "transcription elongation factor B (SIII), polypeptide 3 (110kDa,
elongin A)"
GO:0010467|GO:0006368|GO:0005737|GO:0006366|GO:0006357|GO:0016032|GO:0005654|GO:0005634|GO:0016
021|GO:0005615|GO:0003677|GO:0050434 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139352_PI430048170 0.636341150755961 1.21127531744618 1.68253112449297
0.358849218092284 1.40196507259761 A A A 0.498311467958239 0.450021379028554
1.63774988004508 A A A LNCV6_139352_PI430048170 mRNA
CCTATTCTTCAACCACACTAGTTACTCTGACATAGGAATTTACTTCTTTTCTTTGAATGG NM_001145224 RefSeq chr15
+ 75282840 75295807 GOLGA6D NA "golgin A6 family, member D" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137378_PI430048170 0.919678271392147 1.0399236445679 1.61317423517024
0.491434803746971 0.466234865952847 A A A 1.55933525781906 0.402577572705588
0.43624731797388 A A A LNCV6_137378_PI430048170 mRNA
GAGCTCAGCCCAAGGGATAGAATCCATGTTAAAGTATGTTGAAAATAAAATTGATGAGTT NM_004825 RefSeq
chrY + 18025786 18027746 CDY2A 9426 "chromodomain protein, Y-linked, 2A"
GO:0016573|GO:0005634|GO:0007283|GO:0004402 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_90251_PI430048170 0.707301960322993 1.01510242192306 9.46128591535414
9.43428603344291 9.32437173043055 P P P 9.38606976865699 9.3322100940992
9.43844742172822 P P P LNCV6_90251_PI430048170 mRNA
AAGAAGTACGCCATGGAGCAGAGCATCAAGAGTGTGCTGGTGAAGCAGACCATCGCGCAC NM_001136033
RefSeq chr8_KI270816v1_alt - 293390 301459 PUF60 22827 "poly-U binding splicing factor 60KDa,
transcript variant 3"
GO:0005515|GO:0006397|GO:0008380|GO:0006355|GO:0019907|GO:0005794|GO:0006915|GO:0003677|GO:0006
351|GO:0042802|GO:0005739|GO:0000166|GO:0030529|GO:0005654 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140289_PI430048170 0.99608265277485 1.03048338245342 1.13536697240324
1.50009353113305 0.471975935519656 A A A 0.8413515060779 1.32122128974562
0.950222904920507 A A A LNCV6_140289_PI430048170 mRNA
GGACCGTAAAATGCTGTGTAATGATAAAAGGCTGAAATATCCACTGAATGATTAAAACCA NM_004727 RefSeq
chr15 + 65621931 65656260 SLC24A1 9187 "solute carrier family 24 (sodium/potassium/calcium
exchanger), member 1, transcript variant 1"
GO:0005515|GO:0005886|GO:0007603|GO:0009642|GO:0055085|GO:0016020|GO:0005887|GO:0019867|GO:0006
810|GO:0035725|GO:0006816|GO:0007601|GO:0006811|GO:0008273|GO:0015293|GO:0016056 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132187_PI430048170 0.00301095090873861 5.06316148411372 5.86084426461961
5.09185996016898 5.47316168405304 P P P 3.37299809816899 3.08068281649694
3.02972935375801 P P P LNCV6_132187_PI430048170 mRNA
TTGGAGACGGAAAAACTGGAATTCTAACAAGGAGGAGAGGAGACTAAATCACATCAATTT NM_080878 RefSeq
chr1 - 160945025 160954799 ITLN2 142683 intelectin 2 GO:0030246|GO:0005576 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142221_PI430048170 0.518613513517629 0.904479154875775 15.264927876499
14.6465501789086 14.6115491471761 P P P 15.0796351956108 15.1320417190734
14.8251814933929 P P P LNCV6_142221_PI430048170 mRNA

CCAAAAAGCAACCAACTTAGCCAGTTTTATTTGCAAAACAAGGAAATAAAGGCTTACTTC NM_053275 RefSeq chr12 - 120196699 120201211 RPLP0 6175 "ribosomal protein, large, P0, transcript variant 2" GO:0005515|GO:0010467|GO:0003735|GO:0042254|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0005634|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0000184|GO:0030529|GO:0016032|GO:0022625|GO:0044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134084_PI430048170 0.936213998058295 0.994663974114464 9.33869597912001 9.15614684343321 9.12509630964126 P P P 9.12368442968826 9.33970030808693 9.18028260846892 P P P LNCV6_134084_PI430048170 mRNA
CCGCCTCATCTGGAAATAGTTCCGTTTGTTTCTCTAAAAAGACTTGTAGGTGGGAAAAAA NM_001080543 RefSeq chr19 - 3610628 3626815 CACTIN 58509 "cactin, spliceosome C complex subunit, transcript variant 1" GO:0005515|GO:0032717|GO:0034122|GO:0032720|GO:0005634|GO:0007275|GO:0032088|GO:0071013|GO:0005737|GO:0071222|GO:0060339|GO:0000398|GO:0045087|GO:0071356|GO:0071347|GO:0001933|GO:0005654|GO:0031665|GO:0032688|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137684_PI430048170 0.146885831870346 1.1608212965039 8.15573650125353 8.42951847020443 8.4327801028703 P P P 8.10404157264027 8.13184470236356 8.15342578509079 P P P LNCV6_137684_PI430048170 mRNA
TTACAAAGTTATTTGTTTACAAACAGCGACCATATAAAAGCCTCCTGCCCCAAAGCTTGT NM_001172567 RefSeq chr3 + 38138477 38143021 MYD88 4615 "myeloid differentiation primary response 88, transcript variant 1" GO:0005515|GO:0032755|GO:0034142|GO:0005886|GO:0050830|GO:0005829|GO:0042802|GO:0006954|GO:0002755|GO:0032481|GO:0043123|GO:0070555|GO:0048011|GO:0032740|GO:0043066|GO:0038124|GO:0038123|GO:0034134|GO:0070976|GO:0050727|GO:0032747|GO:0005123|GO:0002224|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141003_PI430048170 0.314957486491657 1.03369590378912 0.302408003432402 0.255883406977914 0.377595591071027 A A A 0.275726705238215 0.24435840020569 0.2747688639266 A A A LNCV6_141003_PI430048170 mRNA
CTGCTACTTTGAAACCAGAAAATAATGACTGGCCATTCGTTACATCTGTCTTAGTTGAAA NM_001111283 RefSeq chr12 - 102395866 102480600 IGF1 3479 "insulin-like growth factor 1 (somatomedin C), transcript variant 1" GO:0010468|GO:0005515|GO:0033160|GO:0009408|GO:0005159|GO:0005158|GO:0046579|GO:0030879|GO:0005615|GO:0030104|GO:0046326|GO:0045445|GO:0045821|GO:0014834|GO:0045740|GO:0030168|GO:0045840|GO:0014068|GO:0014904|GO:0030166|GO:0001501|GO:0007517|GO:0005178|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138791_PI430048170 0.220344535009058 1.04104162556845 0.367251581692929 0.372353914621293 0.469270051878594 A A A 0.340483823021206 0.321158769838184 0.374941904183366 A A A LNCV6_138791_PI430048170 mRNA
GGTGTGCATCTGAGAGGTCTGACATTTCATTATTTACTTATTTCCTAGCTTTTCTGAATT NM_001287258 RefSeq chr8 + 70669364 70735942 XKR9 NA "XK, Kell blood group complex subunit-related family, member 9, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138021_PI430048170 0.0659157826570209 1.2338153094343 11.7033102570053 11.970304493233 11.7058480555889 P P P 11.5951625887224 11.5461404482953 11.3320746951467 P P P LNCV6_138021_PI430048170 mRNA
GCAGTGTCCTGTCTTGAGCCACTGCAGTCTGGGCCCCATCATTAAACGGGCTGCGTTTAA NM_001169109 RefSeq chr22 - 50523567 50526439 SCO2 9997 "SCO2 cytochrome c oxidase assembly protein, transcript variant 2" GO:0014823|GO:0005507|GO:0001654|GO:0005743|GO:0030016|GO:0001701|GO:0003012|GO:0005739|GO:0022904|GO:0006878|GO:0008535|GO:0005654|GO:0006825|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_135932_PI430048170 0.0343360533525801 0.410139257312689 4.33735584479308 4.22138256788932 4.66853349574171 P P P 5.0752530070335 5.86555578628125 6.01696550874118 P P P LNCV6_135932_PI430048170 mRNA GATGTCTCAATCTTACATGTATACCAATCACAATGGAATAAAGTGTTGAGTTGTACTGTG NM_001134445 RefSeq chr1 - 85318484 85578363 DDAH1 23576 "dimethylarginine dimethylaminohydrolase 1, transcript variant 2" GO:0005739|GO:0003073|GO:0007263|GO:0000052|GO:0006527|GO:0003824|GO:0016597|GO:0046872|GO:0045766|GO:0016403|GO:0070062|GO:0045429 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135529_PI430048170 0.283510203058496 1.27368802791605 1.01593817493436 0.287785682291776 0.864042817443919 A A A 0.277168595599172 0.276190783852416 0.63445665896945 A A A LNCV6_135529_PI430048170 mRNA CACCACCAAAGAAAATAAATATATCCTACTTGAAATTTACTCTATGGACTTACCCACTGC NM_032532 RefSeq chr6 + 159169396 159272108 FNDC1 84624 fibronectin type III domain containing 1 GO:0031966|GO:0005886|GO:0005911|GO:0001934|GO:0071456|GO:0010666|GO:0005654|GO:0005576|GO:0051223 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136598_PI430048170 0.176342847753728 0.598611163732978 1.62245413612844 0.269241154914203 0.370835149810813 A A A 1.5084806291849 1.46745782793661 1.89007801088846 A A A LNCV6_136598_PI430048170 mRNA GCAAGCTTTGAAAGGGGCCTTCCATACTTACTTAATTGAATATTCTGGGATATTGAAAAT NM_001197220 RefSeq chr5 - 58969040 59276119 PDE4D 5144 "phosphodiesterase 4D, cAMP-specific, transcript variant 6" GO:0005515|GO:0010469|GO:0032754|GO:0010738|GO:0031698|GO:0030016|GO:0043623|GO:0006939|GO:0051117|GO:0007613|GO:0045822|GO:0031625|GO:0086004|GO:0006198|GO:0032729|GO:0005813|GO:0005794|GO:0007568|GO:0030593|GO:0005891|GO:0044325|GO:0008277|GO:0002027|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133175_PI430048170 0.384525054851142 0.968516157354979 9.85152775395646 9.8350630181487 9.77417452530385 P P P 9.93956457181618 9.84986288524011 9.80778334637981 P P P LNCV6_133175_PI430048170 mRNA CTTGGCCTAATGAAAATACATACTTCTTCATTCGGAGAGACAAAACAAGAACTAGAGTTT NM_001305000 RefSeq chr17 + 4731407 4733610 MED11 400569 "mediator complex subunit 11, transcript variant 2" GO:0005515|GO:0001104|GO:0006366|GO:0006357|GO:0016592 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126741_PI430048170 0.327591713733511 0.807832480094489 0.492199301596518 0.478222357842741 0.414354131187018 A A A 1.16526195017863 0.525186895196223 0.519494770067458 A A A LNCV6_126741_PI430048170 mRNA TGTGGTCTAAATACAGAACACTAGCAAGCTGATTATGTAGTTAATTCCTAAGAGTGCATC NM_198407 RefSeq chr3 - 172443290 172448456 GHSR 2693 "growth hormone secretagogue receptor, transcript variant 1a" GO:0008343|GO:0043005|GO:0005886|GO:0032691|GO:0032100|GO:0016520|GO:0045409|GO:0032094|GO:0046697|GO:0045923|GO:0001616|GO:0030252|GO:0009725|GO:0040018|GO:0046676|GO:0051963|GO:0032869|GO:0009986|GO:0004930|GO:0042536|GO:0009755|GO:0007186|GO:0008154|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142805_PI430048170 0.00185570965871429 0.325453161235094 7.32705526829764 6.95293530160913 7.42315415734549 P P P 8.82999486617562 8.74653385925099 9.01349231564017 P P P LNCV6_142805_PI430048170 mRNA CACCACTGCTTTTGGTGGAAAAGTGCAGAATAGTATGTACCTTTTATGAAGAAAAATGTA NM_178862 RefSeq chr3 + 31532500 31637622 STT3B 201595 "STT3B, subunit of the oligosaccharyltransferase complex (catalytic)"

GO:0006986|GO:0016020|GO:0005783|GO:0043686|GO:0004579|GO:0006516|GO:0016021|GO:0030433|GO:0008250|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132915_PI430048170 0.00210433068382226 3.09572407529136 9.81989188435461 10.1464667649664 10.2109682527423 P P P 8.50060456375363 8.46840723208686 8.34233954531385 P P P LNCV6_132915_PI430048170 mRNA
GCTTCTGTGTTGTGATTCCCTTCTCTTCAACGGTTTCAGTACATATCTCTCTTCAATAAA NM_032882 RefSeq chrX + 153072413 153075019 PNMA6A 84968 paraneoplastic Ma antigen family member 6A NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_27742_PI430048170 0.664145226358144 0.761513388476096 0.522593478145671 0.498191285971347 1.06378455098098 A A A 1.8933205927158 0.534349182850957 0.403914653722057 A A A LNCV6_27742_PI430048170 mRNA
AACAGAACCAGGATCCTTCAAGGTCGATACTGCAAGCAACTTGAACTCTGGTAAAGAGGA NM_152597 RefSeq chr15 - 39600030 39782838 FSIP1 161835 fibrous sheath interacting protein 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135745_PI430048170 0.1714197109012881.31701267015573 6.61919541116421 7.08238769625412 6.46150277578331 P P P 6.44368167939083 6.47081947635751 6.10257194917466 P P P LNCV6_135745_PI430048170 mRNA
GTGCCCAGCACGGGACCCGGCTGCAGGGGACCTTCAATAAACACTTGTCCAGTGAAAAAA NM_004195 RefSeq chr1 - 1203507 1206709 TNFRSF18 8784 "tumor necrosis factor receptor superfamily, member 18, transcript variant 1"
GO:0007165|GO:0043066|GO:0005031|GO:0005887|GO:0006915|GO:0005576|GO:0033209|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128960_PI430048170 0.6371514171022131.10853497136443 0.495771984942254 1.20999218308037 0.816707418282771 A A A 0.4063245949551 0.534339553487057 1.12050179855698 A A A LNCV6_128960_PI430048170 mRNA
AGAAAAGGATACCATAGAGATAGGTTCGGGTTCAGCTGCAGTAGCAGTAGGACTTGATTT NM_001190844 RefSeq chr19 - 17435508 17448567 TMEM221 NA transmembrane protein 221 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90780_PI430048170 0.1530762379840740.7855671673676752.44530175013255 2.63157594363565 2.39065058257086 A A A 2.88872802239936 3.05786534471737 2.52693521210087 P P P LNCV6_90780_PI430048170 mRNA
AACAATGATGACTGGTCATTTTCTTTAACTTTGCAAACTGGTCTTCCTGCTGGCACATAC NM_000699 RefSeq chr1 + 103617331 103625780 AMY2A NA "amylase, alpha 2A (pancreatic)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145407_PI430048170 0.0833323692224801 0.4301469662021740.317870865143172 0.3236766584210981.48780977039852 A A A 1.73221086813899 1.4331323422053 2.65645171229179 A A P LNCV6_145407_PI430048170 mRNA
GGATGCAGAATTCCTGGGTTTTCATTTTAATGAAGGAGGATGCTTGCTAACTTTGAAAAA NM_024295 RefSeq chr8 - 123013163 123042423 DERL1 79139 "derlin 1, transcript variant 1"
GO:0005515|GO:0006986|GO:0000836|GO:0042288|GO:0019060|GO:0005770|GO:0005783|GO:0030970|GO:0030176|GO:0002020|GO:0030433|GO:0045184|GO:0030968|GO:0031648|GO:0016020|GO:0004872|GO:0016021|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111849_PI430048170 0.00315694232757655 1.3003621727021 13.0848857678527 13.183812141103 13.1263131253014 P P P 12.7135094552707 12.838371327394 12.7041745938849 P P P LNCV6_111849_PI430048170 mRNA
TTTAAACTTCGCTTCCGAAAAAACTTTCAGGCCCTGTTGGAGGAGCAGAACTTGAGTGTG NM_006349 RefSeq chr7 + 101217703 101224190 ZNHIT1 10467 "zinc finger, HIT-type containing 1"
GO:0005515|GO:0043486|GO:0042826|GO:0031063|GO:0042129|GO:0031491|GO:0005634|GO:0070317|GO:0000122|GO:0000812|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_130194_PI430048170 0.3775966854076911.03247309849203 0.293770588726467
0.2857795883904540.409647271786032A A A 0.2991851549247030.272397484520477
0.282536119848715A A A LNCV6_130194_PI430048170 mRNA
GACAAGTTTGTTGTGTTTAACTCACCAACACGTGGTGTATAATGAAGACAGAACTATAAT NM_020873RefSeq chr3
+ 3799436 3847703 LRRN1 57633 leucine rich repeat neuronal 1 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137043_PI430048170 0.6186532310913281.1639023643272 3.06510719206997
2.05862336038553 2.76901197368557 P A A 3.0796538225815 1.51572195418277
2.40951132543004 P A P LNCV6_137043_PI430048170 mRNA
AGAGGGGTATGTTTAAGTACACTATTAGATGTGACTGACTACCTTGAAACCTGATTTTTT NM_203472RefSeq chr15
- 101270908 101277520 VIMP 55829 "VCP-interacting membrane protein, transcript variant 1"
GO:0005515|GO:0005881|GO:0006983|GO:0005886|GO:0005783|GO:0032715|GO:0080164|GO:0002865|GO:0030
176|GO:0030968|GO:0045184|GO:0034361|GO:0008430|GO:0046325|GO:0034362|GO:0004872|GO:0032869|GO:0
016209|GO:0030970|GO:0032720|GO:2000110|GO:0030433|GO:0045719|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_63293_PI430048170 0.2333755400694330.92735741864721 9.21773370540257 9.28995147349842
9.36904858889189 P P P 9.49838764310985 9.28747764358876 9.41348291184587 P P P
LNCV6_63293_PI430048170 mRNA
TGAAGGAAACCGTGGTTACTGAGGCCCTGTTGAAAAGTGCACGTCTTGTCCAATAAATCA NM_001099432 RefSeq
chr17 + 60677810 61392838 BCAS3 54828 "breast carcinoma amplified sequence 3, transcript variant
1"
GO:0005515|GO:0005881|GO:0034259|GO:2000251|GO:0051491|GO:0035257|GO:0005634|GO:0071944|GO:0051
895|GO:0042393|GO:0005737|GO:0042594|GO:0045944|GO:0031023|GO:0043089|GO:0007030|GO:0045111|GO:0
016192|GO:0031252|GO:0035035|GO:0035148|GO:2000114|GO:0048487|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136866_PI430048170 0.00376423195882652 0.4569131864218747.44229441346638
7.25805874416988 7.59671939267396 P P P 8.37396222257009 8.46768658053731
8.82506673978624 P P P LNCV6_136866_PI430048170 mRNA
GTAGAGGGAGATTTTGTAACAAGGGCTTGTTACACAGTGATATGGTAATGATAAAATTGC NM_020870RefSeq chr4
- 169094255 169271098 SH3RF1 57630 SH3 domain containing ring finger 1
GO:0046328|GO:0005515|GO:2001237|GO:0048471|GO:0043066|GO:0016567|GO:0005794|GO:0016874|GO:0008
270|GO:0043154|GO:0030027|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137332_PI430048170 0.1310453955836580.6109862437911620.471240709464697
0.4859389788676730.531154188253176A A A 1.40663698236682 1.45076872745386
0.624422705705007A A A LNCV6_137332_PI430048170 mRNA
CACCTGTGCAATTGTCACTTTTCTTTCACTCCCTGAATAAAATATCTTTGCATACGTAAANM_001024209 RefSeq chr1
- 153093134 153094528 SPRR2E 6704 small proline-rich protein 2E
GO:0005515|GO:0005737|GO:0008544|GO:0005198|GO:0031424|GO:0001533 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_2499_PI430048170 0.4287827160971061.43164535265719 3.05299988541135 1.64068824914887
2.55395323009153 A A A 2.05369217948422 1.98053560829697 1.99236535023477 A A A
LNCV6_2499_PI430048170 mRNA
TGCAGCTGGTGGCCTCCAGGGTGAAATTCAATCAAAAAATCTGTACAAGATTCCACTTAG NM_032293RefSeq chr9
+ 127264476 127393549 GARNL3 84253 "GTPase activating Rap/RanGAP domain-like 3, transcript
variant 1" GO:0043547|GO:0051056|GO:0005083|GO:0005096 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140024_PI430048170 0.5150676260446241.04487290508265 0.28370866033967
0.2941951725680340.515170469184514A A A 0.3199912179261750.277120973817795
0.317618007560851A A A LNCV6_140024_PI430048170 mRNA

CAGCAGATGTCTTAATCTTTCCGAGATCTAGTTTTTCAGCAAAGCAGGATTTAAGAAATG NM_001281834 RefSeq chr1 + 247507057 247577690 GCSAML 148823 "germinal center-associated, signaling and motility-like, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141083_PI430048170 0.28431666939752 1.07909217445064 7.74370591988043 7.51375456811101 7.57131755763835 P P P 7.42797833495654 7.60314759244853 7.47243821858613 P P P LNCV6_141083_PI430048170 mRNA
AAACACTAGAATAGACTGGCCTGAAATCCCCTTGCCCAGTAGAATGGACTGATCTATGTG NM_032836 RefSeq chr19 - 55591370 55599527 FIZ1 84922 FLT3-interacting zinc finger 1 GO:0030971|GO:0006355|GO:0005737|GO:0001934|GO:0005634|GO:0003676|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76822_PI430048170 0.893136010959161 1.00146690090049 0.405809452353180.407927720267183 0.383140511875225 A A A 0.4146798469172130.3719087840708050.403734000198247 A A A LNCV6_76822_PI430048170 mRNA
AATTATGGGGAGATTCCTGAGATGTCAGTCAGTTATGAAAAGGAAGTCACAGCAGAGGGT NM_001170692 RefSeq chr6 - 7326653 7389709 CAGE1 285782 "cancer antigen 1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136067_PI430048170 0.9507373187757680.9958256861432050.41943282031559 0.4956419558683880.436794900993901 A A A 0.5257513504371830.496759908301806 0.341882981188095 A A A LNCV6_136067_PI430048170 mRNA
CTCTGCTGTGAACATCCCTGATGTGAGGCTGTGAAAAGGCATATGGACCTGCAAAGGAGG NM_001135050 RefSeq chr1 - 159927038 159945596 IGSF9 57549 "immunoglobulin superfamily, member 9, transcript variant 1" GO:0030424|GO:0030054|GO:0005886|GO:0050807|GO:0060077|GO:0016021|GO:0007156|GO:0030425|GO:0016358 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112555_PI430048170 0.00472181459587316 0.6440896785723656.43509198371654 6.32044917582603 6.14672255500507 P P P 6.98834890870849 7.01115058924278 6.81325456485486 P P P LNCV6_112555_PI430048170 mRNA
TATGGACCTTGAAACTGGGACTTTCACGAGGGTCCTCCGGGGCCACACAGACTACATCCA NM_024339 RefSeq chr16 + 3024030 3027755 THOC6 79228 "THO complex 6 homolog (Drosophila), transcript variant 1" GO:0006397|GO:0008380|GO:0000347|GO:0043066|GO:0000346|GO:0003723|GO:0006915|GO:0005634|GO:0007417|GO:0046784|GO:0006406|GO:0016607|GO:0000445|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138067_PI430048170 0.0324923711949825 0.554454215771632 10.0059006183079 9.33079037539471 9.6912287149115 P P P 10.4106654608161 10.5501280571517 10.6850089131159 P P P LNCV6_138067_PI430048170 mRNA
TGTGAGGAGATGAGTGAAAAACCCAAAAAGAAGAAAAAGCAAAAGCCCCAGGAGGTTCCT NM_006392 RefSeq chr20 + 2652531 2658393 NOP56 10528 "NOP56 ribonucleoprotein, transcript variant 1" GO:0005515|GO:0005737|GO:0030515|GO:0031428|GO:0016020|GO:0006364|GO:0003723|GO:0070761|GO:0005730|GO:0005732|GO:0005654|GO:0000154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127727_PI430048170 0.276942027354747 1.10837639274885 10.7897645663726 10.9509242390537 11.0585832508011 P P P 10.6225883058255 10.7957008034822 10.9316911816506 P P P LNCV6_127727_PI430048170 mRNA
CTGGTACTCCTTGTAGTAAGCTGTTTTCTGCTCAGCCACTGGGCTCTTTCACTTTTTTAG NM_001006109 RefSeq chr3 + 129278973 129305292 HMCES 56941 "5-hydroxymethylcytosine (hmC) binding, ES cell-specific, transcript variant 1" GO:0006508|GO:0008233|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113547_PI430048170 0.000456204041116864 1.23778196310724 11.1100296367271 11.1301356081291 11.1786204533232 P P P 10.805042772334 10.8373653860872 10.8535482951797 P P P LNCV6_113547_PI430048170 mRNA
TCCTTAAATATGCAGTCTTCACCCAGAGTAAAGTGTTGATCGCAAGAGTCCAGTGTCGTG NM_001039707 RefSeq

chr9 - 136401921 136410602 SDCCAG3 10807 "serologically defined colon cancer antigen 3, transcript variant 1" GO:0005515|GO:0032465|GO:0030496|GO:0055037|GO:0005769|GO:0030904|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91199_PI430048170 0.167852543419336 1.30591589119602 5.74869486484505 5.75744814938867 5.96439678377786 P P P 5.79487767146452 5.32970295049356 5.11587119970222 P P P
LNCV6_91199_PI430048170 mRNA
TTTATCAAGGTGATGTTTGGGGCTGGCTGCTCGGTGCTGGTGAACACCTCTTGCAGGCTG NM_182520 RefSeq
chr22_KI270879v1_alt + 447 2225 C22orf15 150248 chromosome 22 open reading frame 15 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143060_PI430048170 0.0980377304267453 0.54394114553043 5.63326113243238 4.91019043026561 6.06736401253205 P P P 6.30417332695367 6.57614231730231 6.57555497836441 P P P LNCV6_143060_PI430048170 mRNA
CGCTGTAAGTTAAGCTCTACATAGATTAAATTGGAGAAACGTGTTAATTGTGTGGAATGA NM_182691 RefSeq chr7 - 105116373 105269077 SRPK2 6733 "SRSF protein kinase 2, transcript variant 2" GO:0005515|GO:0008380|GO:0000245|GO:0048024|GO:0008284|GO:0000287|GO:0035063|GO:0005730|GO:0005634|GO:0001525|GO:0045787|GO:0005524|GO:0030154|GO:0035556|GO:0010628|GO:0071889|GO:0005737|GO:0043525|GO:0004674|GO:0045087|GO:0005654|GO:0006468|GO:0045070|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131996_PI430048170 0.248689285801966 1.27435603003078 1.0744218590164 0.3854787120696580 0.622616561853547 A A A 0.28120899092032 0.414100525325453 0.420159251815786 A A A LNCV6_131996_PI430048170 mRNA
TAGATTGAATTGGAAGGGAAGAATGTGAAATGAATTAGGATATCCTCTGTTCACCTCTAT NM_012382 RefSeq chr5 - 40711575 40755970 TTC33 23548 tetratricopeptide repeat domain 33 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129953_PI430048170 0.115323602781329 1.10953866864034 0.563018329490728 0.3668358271672970 0.52305169541144 A A A 0.277118394259757 0.383173421260423 0.34807983077559 A A A LNCV6_129953_PI430048170 mRNA
CTTACCCAAGAACTGGGGAAAGCCAACACTACTGACTTTGGGTTAACTATGCTGTTTTAA NM_014440 RefSeq chr2 + 113005871 113008044 IL36A 27179 "interleukin 36, alpha" GO:0032755|GO:0006955|GO:0005149|GO:0006954|GO:0045087|GO:0019221|GO:0005576|GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127569_PI430048170 0.645079336802404 0.930073681663538 0.444133421865533 0.47801469399448 0.495123940133866 A A A 0.331362490344168 0.869226029154186 0.475969084329375 A A A LNCV6_127569_PI430048170 mRNA
TAAGAAATACCTCATGAAGAGGCGCTGGAAGAAAAACTTCATTGCTGTCAGCGCTGCCAA NM_033118 RefSeq chr20 + 31819374 31834697 MYLK2 85366 myosin light chain kinase 2 GO:0005515|GO:0005516|GO:0006941|GO:0005634|GO:0007274|GO:0035914|GO:0060048|GO:0005524|GO:0030017|GO:0014816|GO:0032971|GO:0010628|GO:0005737|GO:0046777|GO:0018107|GO:0004687|GO:0004683|GO:0055008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106190_PI430048170 0.229962700672692 0.78680377416805 5.34109167039488 5.2579059883244 5.44488534937995 P P P 5.40220121568581 5.56648000807313 6.0407608422687 P P P
LNCV6_106190_PI430048170 mRNA
ACAGACAGCTTTGAGTGACATCTTCCAGGCGGTCCTATTTGATGATGAACTACTCATGGT NM_004403 RefSeq chr7 - 24698354 24758020 DFNA5 1687 "deafness, autosomal dominant 5, transcript variant 1" GO:0005737|GO:0060113|GO:0008285|GO:0007605|GO:0006915|GO:2001244 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138801_PI430048170 0.434391041987852 0.673395138880442 0.35018113965979 0.327429782757459 0.261396618806596 A A A 1.62019616535922 0.309952208436191 0.289824060427288 A A A LNCV6_138801_PI430048170 mRNA

CTCTCACCACAGGAAGCATCGCTGTTTCCAATAAATATTGCTGAAGACAGAACCAAAAAA NM_003026 RefSeq chr9 + 17578953 17797128 SH3GL2 6456 SH3-domain GRB2-like 2
GO:0005515|GO:0048011|GO:0005886|GO:0042059|GO:0006892|GO:0048488|GO:0007417|GO:0042802|GO:0005829|GO:0008289|GO:0007165|GO:0019886|GO:0000139|GO:0007173|GO:0007411|GO:0002090|GO:0061024|GO:0030669|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133937_PI430048170 0.4635279407122340.2676739120229421.76594380556218
0.3348064742027390.397815007083895A A A 0.358769847590695 1.16453154254792
4.23384946715682 A A P LNCV6_133937_PI430048170 mRNA
AACAAAGAGATCAAGGATGCCCTGTGGAAGGTGTTGGAAAGGAAGAAAGTGTTTTCTTAG NM_001004728 RefSeq chr11 + 59443168 59444116 OR5A1 219982 "olfactory receptor, family 5, subfamily A, member 1"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126845_PI430048170 0.3974686737970720.7946938922396835.72064014265484
5.46582164606489 5.56737817204256 P P P 5.33618065765413 6.1734146376899 6.1099256992918
P P P LNCV6_126845_PI430048170 mRNA
GATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAAACATTTTATACCA NM_018725 RefSeq chr3 + 53846549 53865800 IL17RB 55540 interleukin 17 receptor B
GO:0030368|GO:0005737|GO:0004896|GO:0016020|GO:0009986|GO:0005887|GO:0019221|GO:0006952|GO:0005576|GO:0001558 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112316_PI430048170 0.2392127916953020.8274168187546641 1.2476833854666
10.8046469264002 10.6660313346624 P P P 11.3729569029707 11.1424888528335
11.0710604033699 P P P LNCV6_112316_PI430048170 mRNA
CATGAAACTGCCCCTCCCTGAATCTTTAAAAGCTTACTTGACATATTTTAGAGACAAATA NM_052937 RefSeq chr8 - 51817574 51899186 PCMTD1 115294 "protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1, transcript variant 1" GO:0004719|GO:0005737|GO:0006479 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133990_PI430048170 0.0315247715264812 0.3300317804532356.88352777362815
6.2246635537095 6.68394432020534 P P P 7.42497973665123 8.40910654160077
8.58540106594531 P P P LNCV6_133990_PI430048170 mRNA
ATAGCTTGTTACTCATAGTTTCTTTTTGATCATTTTTTCGGTCTCCGAGGTGAAATGACT NM_022740 RefSeq chr7 - 139561569 139777894 HIPK2 28996 "homeodomain interacting protein kinase 2, transcript variant 1"
GO:0005515|GO:0001654|GO:0046330|GO:0046332|GO:0048596|GO:0007224|GO:0043524|GO:0030578|GO:0018105|GO:0050882|GO:0018107|GO:0007179|GO:0006978|GO:0001102|GO:0001105|GO:0060235|GO:0003714|GO:0046790|GO:0010842|GO:0000122|GO:0042771|GO:0043388|GO:0045893|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140216_PI430048170 0.4755330798143470.7858902566730112.41927599144622
0.4638247059388770.470608358176858A A A 1.10093661945029 1.81081372157689
2.22377617797741 A A A LNCV6_140216_PI430048170 mRNA
CCTGTATTGTGACAAGGTAATTCTGTGGTATCAGAATAAAAGGACTTGATATAAACAACC NM_003458 RefSeq chr3 + 49554488 49671549 BSN8927 bassoon presynaptic cytomatrix protein
GO:0048786|GO:0044306|GO:0030424|GO:0030054|GO:0014069|GO:0007268|GO:0005634|GO:0048788|GO:0060076|GO:0046872|GO:0030425 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134776_PI430048170 0.3457618302498681.21072006747612 0.502720801431819
0.44782583973131 1.07946379126122 A A A 0.3773629287877530.463959116157192
0.447877402043909A A A LNCV6_134776_PI430048170 mRNA
CCATGCTGAATTCCCTCATCTATAGCCTGAAAAATAAGGAAGTGAAGGGGGAAAGAAGCC NM_001005203 RefSeq chr12 + 48525631 48528103 OR8S1 NA "olfactory receptor, family 8, subfamily S, member 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56366_PI430048170 0.8665530032476241.01005368824753 8.21516287490636 8.18281873964071

8.46319274689401 P P P 7.74284205970482 8.45046800123632 8.52078012765908 P P P
LNCV6_56366_PI430048170 mRNA
GAGAATGTTTTAGGCAGGTGGTTATATGTGGGAAGATAATTTTATTCATGGATCCAAATG NM_032997 RefSeq chr10
- 56357437 56361273 ZWINT 11130 "ZW10 interacting kinetochore protein, transcript variant 2"
GO:0005515|GO:0007093|GO:0005634|GO:0030425|GO:0005829|GO:0000070|GO:0005737|GO:0047485|GO:0000
777|GO:0000776|GO:0051649|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129702_PI430048170 0.1314577679548780.3592104012989950.326861745479043
0.3415725992426910.345483837191493 A A A 2.62202061198957 1.34671412753908
0.893002948562395 P A A LNCV6_129702_PI430048170 mRNA
ATTCTCGGGTGATCAGCTCTTTCCAAGACTTCAATAAATTTGTCAGTTACAGTCAAAAAA NM_014564 RefSeq chr9
- 136196249 136203158 LHX3 8022 "LIM homeobox 3, transcript variant 2"
GO:0005667|GO:0048839|GO:0043066|GO:0006366|GO:0021521|GO:0030324|GO:0021520|GO:0021983|GO:0005
634|GO:0001890|GO:0021527|GO:0021526|GO:0043565|GO:0008045|GO:0001076|GO:0045944|GO:0009887|GO:0
008270|GO:0045893. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143427_PI430048170 0.4371739960128080.7636366468126670.318024329067289
0.3332515351240890.360188014425133 A A A 0.32911151875417 0.321252024258571
1.29720589725724 A A A LNCV6_143427_PI430048170 mRNA
CGTATCTTCTTTTGGTTCCCTCAAAGGTAAAAATAAGACCCAGAATCTGAGTAAATCTAT NM_001047160 RefSeq
chr10 + 5412550 5459056 NET1 10276 "neuroepithelial cell transforming 1, transcript variant 1"
GO:0051056|GO:0048011|GO:0070301|GO:0043065|GO:0005886|GO:0007264|GO:0005634|GO:0097190|GO:0001
558|GO:0071479|GO:0005829|GO:0005085|GO:0007165|GO:1900026|GO:0032321|GO:0017049|GO:0005089|GO:0
051451 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138127_PI430048170 0.6725636345498420.9856035497077980.390805419129153
0.45064117594943 0.357141066550079 A A A 0.4907901973884480.376840643943922
0.392615640529323 A A A LNCV6_138127_PI430048170 mRNA
GGGGTGTAGCAAAAGTGAAATCAGTAGCCTTTGCTAGTTTGAGGGCTGGGCAGCCGTGGG NM_080864 RefSeq
chr19 + 14028204 14030971 RLN3 117579 relaxin 3
GO:0005515|GO:0001664|GO:0005179|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99965_PI430048170 0.6960477518136440.9819581050402264.90595999768378 4.75116607480258
4.9638158758286 P P P 4.88199393511138 4.92639515626972 4.89929431917478 P P P
LNCV6_99965_PI430048170 mRNA
ATGATTTCTACTGCCCCGTCTGTCAGGAGGTGCTCAAAACGCCCGTGCGGACCACGGCCT NM_016271 RefSeq chr18
+ 32091854 32131561 RNF138 51444 "ring finger protein 138, E3 ubiquitin protein ligase, transcript
variant 1" GO:0016567|GO:0019901|GO:0016874|GO:0008270|GO:0005634|GO:0016055 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_49865_PI430048170 0.0690149032396093 1.46901080612525 3.67873392767691
4.24619473300529 3.81205936024004 P P P 3.53373748685977 3.25270128021739
3.33401893731974 P P P LNCV6_49865_PI430048170 mRNA
CAAGTGCTTATGAACAGGTGAAACAAGTTTTGCAAATATCTGAGGAAGCCAATTTTGAAA NM_006642 RefSeq
chr1_KI270763v1_alt + 268112 512199 SDCCAG8 10806 serologically defined colon cancer antigen 8
GO:0005515|GO:0005813|GO:0006996|GO:0005911|GO:0005814|GO:0035148|GO:0000086|GO:0030010|GO:0000
278|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145000_PI430048170 0.0945239602876763 0.3418815300340720.261664999198709
0.26936147685901 0.395590137076409 A A A 1.37377087811472 1.10927318148499
2.61612260073962 A A P LNCV6_145000_PI430048170 mRNA
CAGAAGGTTCTTTTTGCCATTTGGCCTGTGGATGTCTGAGAAGATCATTCACAATACATG NM_001788 RefSeq chr7
+ 35800985 35907105 SEPT7 NA "septin 7, transcript variant 1" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130889_PI430048170 0.3979914450104421.19654806038194 1.78496317125659

2.37468349949142 2.31743258522946 A A A 1.50698557406617 1.963275462288
2.21363288893205 A A A LNCV6_130889_PI430048170 mRNA
AAGATAGATCTAAGCAGCTTGGGTAACTATAAATGGAAGCAGCAGGGGGATTTGAGACCC NM_007167 RefSeq
chr1 - 34986165 35031968 ZMYM6 9204 "zinc finger, MYM-type 6"
GO:0022604|GO:0007010|GO:0008270|GO:0007275|GO:0005634|GO:0003677 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139402_PI430048170 0.18631348182035 1.06182981226603 0.624328806060374
0.72866182744015 0.582044827510555 A A A 0.5741997033016870.55669949439892
0.548330412125843 A A A LNCV6_139402_PI430048170 mRNA
CCAAAAGCAGACCTCGGAATCACTGCCAAATAAGTAACTAGACGTTTACAGGCCAAAAAA NM_006151 RefSeq chr17
+ 58238425 58268518 LPO4025 "lactoperoxidase, transcript variant 1"
GO:0016323|GO:0005737|GO:0018969|GO:0042744|GO:0006979|GO:0005615|GO:0046872|GO:0042742|GO:0001
580|GO:0070062|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133073_PI430048170 0.0443169759119576 0.7603587400431138.28593141824159
8.04195514294848 7.97598845798205 P P P 8.32977152709031 8.67026386532024
8.48821586251571 P P P LNCV6_133073_PI430048170 mRNA
TTTCATTGTAAAAATAAATGTACTTTGCACCACTTCATGATGGAGGGAGAAGTGGTCACA NM_001145297 RefSeq
chr17 - 76080992 76103787 EXOC7 23265 "exocyst complex component 7, transcript variant 4"
GO:0005515|GO:0006996|GO:0005815|GO:0005886|GO:0034451|GO:0032584|GO:0006887|GO:0015031|GO:0005
829|GO:0000145|GO:0016020|GO:0061024|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67138_PI430048170 0.9028769255558611.15886783315574 0.4008224330514011.74259517313636
0.254626673612309 A A A 1.05464406625024 0.6922103906822480.447206066393644 A A A
LNCV6_67138_PI430048170 mRNA
ATGTAGGAGAGGGATTCTTCCAAAGGCCTTCAAATCAAATTAGAATTCACTGAGAATAAT NM_004771 RefSeq chr11
- 102576834 102625332 MMP20 9313 matrix metallopeptidase 20
GO:0005515|GO:0097186|GO:0070173|GO:0005509|GO:0005578|GO:0005576|GO:0005615|GO:0030163|GO:0022
617|GO:0030198|GO:0030574|GO:0006508|GO:0008270|GO:0004222 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141956_PI430048170 0.0315516607331861 0.81554243081318312.7924424888698
12.9885516466897 13.0141163328667 P P P 13.1767343391342 13.2001159114995 13.307405233388
P P P LNCV6_141956_PI430048170 mRNA
AATGTGGCTGCCAGAGAATGTTGTTGCTAACCCACCAGTTTCTTGTTGATTTGGAGAGGT NM_018462 RefSeq chr3
+ 10115648 10127190 BRK1 55845 "BRICK1, SCAR/WAVE actin-nucleating complex subunit"
GO:0031209|GO:0048010|GO:0008284|GO:0030036|GO:0001701|GO:0032403|GO:0030027|GO:0005829|GO:0070
207|GO:0048365|GO:0010592|GO:0016601|GO:0048870|GO:0045087|GO:2000601|GO:0005856|GO:0038096|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138514_PI430048170 0.000238332345334712 0.4213981233549243.67264427554728
3.57608378065787 3.43971293200234 P P P 4.67110981541933 4.83862735093392 4.9175194347208
P P P LNCV6_138514_PI430048170 mRNA
GCCCAGCACATTAGTCCTAAACGTCCCATGTATTTTTCTAGGCATAAAAATAAAAGTTGG NM_198391 RefSeq chr20
- 14323992 14337667 FLRT3 23767 "fibronectin leucine rich transmembrane protein 3, transcript
variant 2"
GO:0035556|GO:0008150|GO:0045499|GO:0007411|GO:0005887|GO:0050919|GO:0005578|GO:0005057|GO:0030
674|GO:0007155|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136235_PI430048170 0.4627504212789150.78971596331523 6.43013587671409
6.18970182576638 6.42755689773712 P P P 6.02206400125485 6.8266952067883
7.04573327315259 P P P LNCV6_136235_PI430048170 mRNA
TTTCAACCTGTGTTCCTCAGCCCCTGAGGAAGCTATTAAGGGGATTCATTACAAGTAAAA NM_012310 RefSeq chrX
+ 70290028 70420924 KIF4A 24137 kinesin family member 4A

GO:0005515|GO:0008017|GO:0051256|GO:0016363|GO:0005829|GO:0019886|GO:0005737|GO:0007411|GO:0008574|GO:0005876|GO:0016887|GO:0007018|GO:0005871|GO:0006996|GO:0005694|GO:0000281|GO:0030496|GO:0003777|GO:0005524|GO:0003677|GO:0016020|GO:0007596|GO:0008152|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128928_PI430048170 0.00558745089485882 1.36346172029486 9.51588985288346 9.5622500257027 9.72003563537354 P P P 9.22133750779138 9.05859835718598 9.17953335998714 P P P LNCV6_128928_PI430048170 mRNA AATACAGTAGCACCTAAGGAGCTTGAATCTTGGTTCCTGTAAAATTTCAAATTGATGTGG NM_001265589 RefSeq chr11 + 63681449 63759891 RTN3 10313 "reticulon 3, transcript variant 5"
GO:0000139|GO:0005783|GO:0071786|GO:0005789|GO:0016032|GO:0006915|GO:0016021|GO:0016192|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133671_PI430048170 0.3378674360700060.8297308535093470.384167723409894 0.41648109486235 0.341157662560486A A A 0.46854421905046 1.00900598793509 0.39173912967952 A A A LNCV6_133671_PI430048170 mRNA CAGCAGATACTCGGTAGATAAAATTCTTTCTGTGTTTTACACAATTTTCACACCTCTCTTNM_001004714 RefSeq chr14 - 20033843 20034758 OR4K13NA "olfactory receptor, family 4, subfamily K, member 13" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131043_PI430048170 0.0174179997862206 0.7042035858772579.32831099170726 9.3654059941805 9.18829928864922 P P P 9.61155282790352 9.8451374361874 9.93053000916254 P P P LNCV6_131043_PI430048170 mRNA GTCCTTTATACATTTCTGTAGTTAACAGAACACTGTAATGTGCCTTGGAGCTTAGTAACT NM_024496RefSeq chr14 - 77024542 77028699 IRF2BPL64207 interferon regulatory factor 2 binding protein-like
GO:0003674|GO:0046543|GO:0045944|GO:0005654|GO:0005634|GO:0000122|GO:0005615|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137577_PI430048170 0.6378162997364141.10815917066187 2.80296627364479 2.12085050420829 2.3631815923509 A A A 2.63986062918267 2.34232537134882 1.8324997756587 A A A LNCV6_137577_PI430048170 mRNA TCCTGGTACTGGGAATACACAACACCAGCTGTTTTATTATTATTTGGGGAGGGGGTTGTG NM_024409RefSeq chr2 - 231922094 231926328 NPPC 4880 natriuretic peptide C
GO:0003419|GO:0003418|GO:0008285|GO:0045471|GO:0009791|GO:0051428|GO:0005615|GO:0042803|GO:0050880|GO:0051447|GO:0045909|GO:0040014|GO:0030814|GO:0030141|GO:0001666|GO:0051053|GO:0042493|GO:0005102|GO:1900194|GO:0048660|GO:0045669|GO:0005179|GO:0001503|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135439_PI430048170 0.5371393232589850.9222656428370180.3923392233391080.3330055778183 0.370279431100066A A A 0.2996238747552880.7448010508452880.360574788834406A A A LNCV6_135439_PI430048170 mRNA GAGCAAGCTGTGATTAATAAAGAATTGGAGTTCTGTGAACTAATAAAGGTTTGGTCTGTT NM_001199214 RefSeq chr8 + 79610813 79666175 STMN2 11075 "stathmin 2, transcript variant 1"
GO:0005515|GO:0043005|GO:0030424|GO:0031115|GO:0048471|GO:0031117|GO:0005794|GO:0031982|GO:0030027|GO:0030426|GO:0005737|GO:0015631|GO:0016020|GO:0010976|GO:0043025|GO:0007026|GO:0010977|GO:0048306|GO:0005768. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134976_PI430048170 0.2933223472978180.8634389484657731 1.4603955694395 11.3197421091496 11.159050970121 P P P 11.2395846073936 11.6720693389805 11.6398595031704 P P P LNCV6_134976_PI430048170 mRNA ACGTTGCTGTGTCCTGGTGAGCAGCCCGACCAATAAACCTGCTTTTCTAAAAGGAAAAAA NM_012232RefSeq chr17 - 42402448 42423320 PTRF 284119 polymerase I and transcript release factor
GO:0005515|GO:0010467|GO:0006355|GO:0005886|GO:0005783|GO:0006363|GO:0006361|GO:0005634|GO:0006360|GO:0043231|GO:0005829|GO:0005739|GO:0043234|GO:0005737|GO:0005901|GO:0005654|GO:0042134 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_141132_PI430048170 0.3563986978749440.6349623370909642.03223270205452
0.2914826408178122.17407463083439 A A A 1.47901079393262 2.59100250622056
2.73641614734757 A P P LNCV6_141132_PI430048170 mRNA
TGAAGAGGACTTCCAAGATGAGTATAAAACAGAAGTCCCTCACCATCACCACCACAGAGT NM_002152RefSeq chr19
- 49151198 49155424 HRC 3270 histidine rich calcium binding protein
GO:0005515|GO:0030018|GO:0051480|GO:0005509|GO:0033018|GO:0010881|GO:0033017|GO:0044325|GO:0006
936|GO:0002027|GO:0010880|GO:0060314|GO:0033135|GO:0051117|GO:0010460|GO:0045823 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_116216_PI430048170 0.5824180835877631.07902120801926 11.1672151088083
11.1317756299194 11.5646347535925 P P P 11.0447129752824 11.1314283959604
11.3784018888575 P P P LNCV6_116216_PI430048170 mRNA
ACGCTATGAGGCAGCTAACTGGAAATACAAGTATGGCTATGAGATTCCTGTGGACATGCT NM_001282232 RefSeq
chr14 + 35292316 35317479 PSMA6 5687 "proteasome (prosome, macropain) subunit, alpha type, 6,
transcript variant 2"
GO:0005515|GO:0002474|GO:0010467|GO:0003723|GO:0090263|GO:0035639|GO:0005634|GO:0044281|GO:0030
016|GO:0031145|GO:0030017|GO:0016363|GO:0004298|GO:0005829|GO:0034641|GO:0000082|GO:0005737|GO:0
051092|GO:0000932|GO:0051603|GO:0016032|GO:0090090|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133109_PI430048170 0.00206294899826085 1.37739937950673 10.8340704213151
10.9305748527678 10.9844156104369 P P P 10.4203909914158 10.4388637430111 10.50653470462
P P P LNCV6_133109_PI430048170 mRNA
GGTGGGCACCCTCTGTTCCTGTTTGTGTGTTTGAATAGTCTGAAATGCTGTGACTTTTTT NM_015353RefSeq chr17
+ 75047183 75065889 KCTD2 23510 "potassium channel tetramerization domain containing 2, transcript
variant 1" GO:0051260|GO:0032403 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135541_PI430048170 0.3381901309080991.02908941172698 0.523211150336961
0.4708248981352410.431304881036795A A A 0.3792997113308420.459535314081408
0.462344668386146A A A LNCV6_135541_PI430048170 mRNA
TTACACTATCCATCCTCAGAGAAGCTGTTCATTCCATTCACGTATGGTAATGGGAAAAAA NM_001139444 RefSeq
chr6 - 116496487 116545610 TRAPPC3L 100128327 trafficking protein particle complex 3-like
GO:0005794|GO:0005783|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127658_PI430048170 0.54800187679682 1.12997977618619 0.347004831902494
0.34807554265173 0.958920853898041A A A 0.31898066096195 0.298644103579952
0.580026782891425A A A LNCV6_127658_PI430048170 mRNA
TAAAGACACGCTTGTGTCCTGGGCGATGGTAATAAAACCAGCTCATGCTGACTGTGCTGT NM_000704RefSeq chr19
- 35550192 35563658 ATP4A 495 "ATPase, H+/K+ exchanging, alpha polypeptide"
GO:0000287|GO:0046982|GO:0005886|GO:0042493|GO:0045851|GO:0008900|GO:0055085|GO:0005524|GO:0005
615|GO:0034220|GO:0005887|GO:0008152|GO:0006810|GO:0015991|GO:0035725|GO:0010155|GO:0006813|GO:0
005391 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145597_PI430048170 0.4602086865307210.6841478318473390.753632203357322
0.8108159832385781.47941588835322 A A A 2.13072784617117 0.54856337899957
1.70582378487729 A A A LNCV6_145597_PI430048170 mRNA
ATAAGAAAGAGAACTGAAAAGTAGCGTGCTATTCGTCCTGTAGGTGCTGTGGTGGATGGA NM_031283RefSeq chr2
+ 85133459 85310388 TCF7L1 83439 "transcription factor 7-like 1 (T-cell specific, HMG-box)"
GO:0048319|GO:0046022|GO:0005667|GO:0006355|GO:0003700|GO:0044212|GO:0030111|GO:0006357|GO:0008
013|GO:0048699|GO:0006325|GO:0005634|GO:0003677|GO:2000036|GO:0006351|GO:0043565|GO:0007420|GO:0
003682|GO:0043588|GO:0005654|GO:0008595|GO:0060070|GO:0045892|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139518_PI430048170 0.0519570373307886 0.6551300972268117.76606604561397
7.51723763033831 7.88594900077394 P P P 8.24728321891642 8.06709953060447

8.64713477314874 P P P LNCV6_139518_PI430048170 mRNA
TTCCCCTCCAGTCAAACCGTAATACAGTTTCCAGAAAATTCGACAGTCTGCAATGCCAAA NM_020839 RefSeq chr3
+ 39051985 39096670 WDR48 57599 "WD repeat domain 48, transcript variant 1"
GO:0050679|GO:0005515|GO:0016579|GO:0048705|GO:0005634|GO:0007283|GO:0005764|GO:0043231|GO:0048
872|GO:0007338|GO:0035264|GO:0000724|GO:0048568|GO:0072520|GO:0016032|GO:0043588 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135077_PI430048170 0.5030734243647810.93225506154733 0.318458418574999
0.2842853824049310.284852360965549A A A 0.6152274726637990.276956845209327
0.271779453571928A A A LNCV6_135077_PI430048170 mRNA
TAGAACAGCACAATATAATAGTGGAATTGGGCCTTTCAGAAGACCTCAACTGATGATTTT NM_207364 RefSeq chr2
+ 130729069 130730336 GPR148 NA G protein-coupled receptor 148 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134312_PI430048170 0.2538939956036890.5526499642267370.605469680292495
0.3171322122283710.390950107744384A A A 0.31900492832677 1.26332862550658
1.89998255332848 A A A LNCV6_134312_PI430048170 mRNA
GGTTTTTGGAGGTTTTAGTGTTAATTGGGAAAATCCTCTGGAGTTTATAAAAGTCTACTC NM_130398 RefSeq chr1
+ 241848190 241889939 EXO1 9156 "exonuclease 1, transcript variant 2"
GO:0005515|GO:0051321|GO:0035312|GO:0008409|GO:0090305|GO:0045190|GO:0051908|GO:0005634|GO:0006
310|GO:0016446|GO:0003677|GO:0046872|GO:0004527|GO:0006281|GO:0045145|GO:0004523|GO:0043566|GO:0
048256|GO:0005654|GO:0006298|GO:0000737|GO:0000738|GO:0002455 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_130098_PI430048170 0.0387607189756306 0.1584140185317152.3962068564173
0.3256353242858581.44191783395983 A A A 4.38284233430427 4.14748716006699 4.3006255291678
P P P LNCV6_130098_PI430048170 mRNA
GGACGTTCCATGCCCAGGTTAACAAAGAACTGTGATATATAGAGTGTCTAATTACAAAAT NM_001167928 RefSeq
chr3 + 190514050 190651519 IL1RAP 3556 "interleukin 1 receptor accessory protein, transcript variant
3"
GO:0042094|GO:0006955|GO:0006954|GO:0006461|GO:0016020|GO:0005886|GO:0005887|GO:0045087|GO:0019
221|GO:0004908|GO:0005576|GO:0004871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129915_PI430048170 0.0335770172091131 1.12358031696364 0.746883138139102
0.8384297079272520.729887275956888A A A 0.6101659992180220.612732291605646
0.590266345516026A A A LNCV6_129915_PI430048170 mRNA
AGCACTCCGTGGTGTGTTTGCAGGGTGATTTCCTAATAAAAGTCCACTCTGACTGTGAAA NM_004535 RefSeq
chr20_KI270870v1_alt + 73064 150844 MYT1 4661 myelin transcription factor 1
GO:0006355|GO:0005737|GO:0003700|GO:0008270|GO:0005654|GO:0005634|GO:0001158|GO:0030154|GO:0006
351|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113350_PI430048170 0.7208973518232720.8911736786958653.1716164510894
3.43380300360333 3.07022589907186 P P P 3.83708056177117 2.86351023541875
3.33517456259441 P P P LNCV6_113350_PI430048170 mRNA
TTCAGGAATACCTGACTCAGCAGACCCATCACGTGAACATGATTTCTGGATCAGTTAGTG NM_001271840 RefSeq
chr10 - 122990805 123008687 IKZF5 64376 "IKAROS family zinc finger 5 (Pegasus), transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135671_PI430048170 0.3038495621871740.6954419537048430.477101775165341
0.4572848658566620.408864726077338A A A 0.3934447575326960.784851109289738
1.51013411483228 A A A LNCV6_135671_PI430048170 mRNA
GCGAAGTTTGAAAGTATGTATCAGGTTTTCCAGAATTGCTACCACTGAATTTTGTCATTT NM_001284209 RefSeq
chr14 - 70583220 70600690 MED6 10001 "mediator complex subunit 6, transcript variant 1"
GO:0005515|GO:0010467|GO:0006367|GO:0001104|GO:0016020|GO:0006357|GO:0045944|GO:0016592|GO:0003

713|GO:0005654|GO:0005634|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127995_PI430048170 0.3032913096448351.55729237136218 2.03217985413035
1.09892424205449 0.698893060140707A A A 1.01737975652402 0.605518038801382
0.583542510807978A A A LNCV6_127995_PI430048170 mRNA
ATGGACTATCCATTAGAGCAACTTTCTGGGGCCTAATAAAACTGATGTGAAACTAAAAAA NM_030657RefSeq chr19
- 51379908 51387956 LIM2 3982 "lens intrinsic membrane protein 2, 19kDa, transcript variant 1"
GO:0005212|GO:0030054|GO:0007043|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132628_PI430048170 0.2405823125217171.02029716695955 0.306388710643992
0.2540345526347770.307853926350963A A A 0.2666699412421740.249437937962954
0.265784745256737A A A LNCV6_132628_PI430048170 mRNA
CCTGTGCTAAATCCCCTCATCTATAGTTTAAAAAATAAGGATGTAAAAAAGGCCCTAAAG NM_001002925 RefSeq
chr11 - 56641488 56642439 OR5AP2 338675 "olfactory receptor, family 5, subfamily AP, member 2"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139763_PI430048170 0.00461247305675995 1.22461334105194 10.6720291062966
10.7877690005577 10.7267096195852 P P P 10.3607622387825 10.4709480957651 10.477196490745
P P P LNCV6_139763_PI430048170 mRNA
CAGTCTTTGGGTACCTATTTTCATTGTAAAACTATCTGAACCATTAAAGTCGAGCTTTTC NM_005663RefSeq chr4
- 1982713 2009235 NELFA 7469 negative elongation factor complex member A
GO:0005515|GO:0010467|GO:0006368|GO:0005737|GO:0006366|GO:0032021|GO:0003682|GO:0016032|GO:0007
275|GO:0005654|GO:0034244|GO:0050434 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145447_PI430048170 0.0077269255298485 1.2956817153143 6.60351072695141
6.51185697199882 6.68756215145863 P P P 6.17100504874446 6.33754061524626
6.17215391238652 P P P LNCV6_145447_PI430048170 mRNA
AGGGTGTGTTGTTGACTCTTTTTACACTTATTTATTATCATTCTCACTTCTCTGGAAGCC NM_007097RefSeq chr5 -
176392454 176416569 CLTB 1212 "clathrin, light chain B, transcript variant 2"
GO:0005515|GO:0005802|GO:0042277|GO:0060170|GO:0030132|GO:0005886|GO:0006886|GO:0030118|GO:0043
231|GO:0005737|GO:0005198|GO:0030130|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127619_PI430048170 0.0198688229801572 0.7036201331470199.20219824276728
9.32763942771743 9.55613709523872 P P P 9.85681431912013 9.77131225803074
9.99307403372859 P P P LNCV6_127619_PI430048170 mRNA
AATCTGCTGCAAAATCTCTCTTGGAATCCATGTGCCCAGGATTATATTAGCATTATTTTT NM_007026RefSeq
chr17_KI270857v1_alt + 1729015 1752653 DUSP1411072 dual specificity phosphatase 14
GO:0000188|GO:0008138|GO:0035335|GO:0017017|GO:0004725 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132859_PI430048170 0.3468094289550131.05292132630954 8.79601661856813
8.74862989761344 8.77478623614486 P P P 8.59491810822262 8.68099190835149 8.8123690636903
P P P LNCV6_132859_PI430048170 mRNA
CTTGTGCAAAGCCCTACTGTGTTTTTATGTTCCTGTTTAAAAGAGAAGTTTACTTAGCAA NM_198526RefSeq chr15
+ 90001490 90082200 ZNF710 374655 zinc finger protein 710
GO:0003712|GO:0006357|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_74149_PI430048170 0.2511471312158920.8092139877535840.2705561315688740.277981534696922
0.299200475438821A A A 0.4584045789017930.9118610526379920.32666237054048 A A A
LNCV6_74149_PI430048170 mRNA
TCTCATTAGTGCAATGTCATATCTGATCCCAGGAAGCCTGGAAAATAAAAGACGATGCAT NM_001130083 RefSeq
chr4 - 7965309 8158832 ABLIM2 84448 "actin binding LIM protein family, member 2, transcript
variant 1"
GO:0030036|GO:0007411|GO:0045944|GO:0008270|GO:0003779|GO:0030016|GO:0015629|GO:0006351 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113346_PI430048170 0.0184554317722841 0.563053371474956 10.0522924815082
10.4001130677985 9.96038182071167 P P P 10.9470178463543 10.9346630645426
11.0523120697242 P P P LNCV6_113346_PI430048170 mRNA
AGATCTACCCCACCATCTGTGGCTGTTCCGGGATGGCCTTCTGCCCGAAAACACCTTCAT NM_000402 RefSeq chrX
- 154531389 154547018 G6PD 2539 "glucose-6-phosphate dehydrogenase, transcript variant 1"
GO:0050661|GO:0006629|GO:0005515|GO:0006695|GO:0014070|GO:0045471|GO:0010734|GO:0006749|GO:0005
634|GO:0044281|GO:0006098|GO:0001816|GO:0032094|GO:0042803|GO:0005536|GO:0043231|GO:0042802|GO:0
005829|GO:0043523|GO:0005737|GO:0043249|GO:0051156|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140337_PI430048170 0.663759559590348 0.983388762493739 0.407992598359327
0.38102360863022 0.246108186313768 A A A 0.345908126245774 0.394975394052475
0.371481173366966 A A A LNCV6_140337_PI430048170 mRNA
GGCCTGGACTTGCTGTGATCTCTGATTTGGCAAAATGAACCAGCAATAGTCTTGCAAAAA NM_001282225 RefSeq
chr22 - 17178789 17219585 CECR1 51816 "cat eye syndrome chromosome region, candidate 1,
transcript variant 3"
GO:0046103|GO:0043394|GO:0007275|GO:0005615|GO:0031685|GO:0042803|GO:0005829|GO:0004000|GO:0006
154|GO:0008270|GO:0043103|GO:0008083|GO:0008201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140601_PI430048170 0.000236519193200708 0.260810913421189 10.6916560011586
10.565501501987 10.3524668632644 P P P 12.2599444738449 12.6480670661894
12.5120396820002 P P P LNCV6_140601_PI430048170 mRNA
CCTTATCCAAATCAATAAAGAGAGAATCCTCCCTCCAGAAGGGTTTCTAAAAACAAAAAA NM_012451 RefSeq chr19
+ 48364393 48376377 SYNGR423546 synaptogyrin 4 GO:0031594|GO:0030672|GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_143255_PI430048170 0.0592048485264113 1.35599753843224 10.0363200272203
10.3412830804028 10.4177215625728 P P P 9.8326532366679 9.88271543701093
9.78787350935719 P P P LNCV6_143255_PI430048170 mRNA
TATGAAAGTGAAAAGTCCAGTGGTATTGGCATTGGCAGCAGGTGAGCAATTTCACCCAGT NM_014235 RefSeq chrX
- 154483716 154486670 UBL4A 8266 ubiquitin-like 4A
GO:0005515|GO:0019787|GO:0006810|GO:0071816|GO:0071818|GO:0006464|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141497_PI430048170 0.133628243945604 1.03544260545334 0.346587436526372
0.302013213008112 0.27250750083446 A A A 0.248393292068282 0.273389905743096
0.249408871236047 A A A LNCV6_141497_PI430048170 mRNA
CACCAACAATCAGCTGTCATTTTATTAATCTATCCCTTTTGTGCATGCACCATTTCTCTC NM_022049 RefSeq chr1 +
100538171 100542027 GPR88 54112 G protein-coupled receptor 88
GO:0007186|GO:0005886|GO:0004930|GO:0050885|GO:0007626|GO:0016021|GO:0005575|GO:0019228 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138126_PI430048170 0.496115716663029 0.994099256827486 0.334430692517056
0.363358003141906 0.344267658634564 A A A 0.361108797867909 0.365720901896861
0.340870390844276 A A A LNCV6_138126_PI430048170 mRNA
GGATACTCATTCTCGAAAAAAGAGACAACTCTACAGTGCATTGGCTAATAAATGTTGCCA NM_005059 RefSeq chr9
- 5299865 5304611 RLN2 6019 "relaxin 2, transcript variant 2"
GO:0007565|GO:0005179|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136986_PI430048170 0.325991391516632 0.752938417107076 2.39490494468496
2.96018052936288 3.65373598344655 A A P 3.57689471548347 3.12846960231518 3.7396907942898
P P P LNCV6_136986_PI430048170 mRNA
CCCCTTTCTGTAGCTACTTTAGACCTGGGTTACTAGAAAATTCCTGAAGAAAATTTCAAC NM_030786 RefSeq chr1
- 32679905 32702760 SYNC 81493 "syncoilin, intermediate filament protein, transcript variant 1"

GO:0042383|GO:0005882|GO:0048471|GO:0030018|GO:0031594|GO:0045103|GO:0005198|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138353_PI430048170 0.4026146345996291.91776757186057 2.3951513881471 0.5133333291176110.544150185714704A A A 0.3287032538322390.669311798163472 0.486827107328547A A A LNCV6_138353_PI430048170 mRNA CCTCTCTCATAAACATTTGGTGACCTTTTACCAAGTGGTGAGTTAGTTAGGTTTTTTAAA NM_001287824 RefSeq chr10 - 114294823 114404778 AFAP1L2 84632 "actin filament associated protein 1-like 2, transcript variant 3"
GO:0035591|GO:0017124|GO:0005886|GO:0045742|GO:0061098|GO:0032757|GO:0007346|GO:0005737|GO:0006954|GO:0030296|GO:0032675|GO:0045893|GO:0042169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77746_PI430048170 0.5855617258993340.94511419963399 7.43913523133733 7.28155885701891 7.69053384648265 P P P 7.52678885758405 7.43208528788289 7.71222169226135 P P P
LNCV6_77746_PI430048170 mRNA TATGCTGAATATGGGCACCAAAGAACCTGTAAAAGTTATCTTTTTCAATTGAATGTGCAC NM_001253676 RefSeq chr6 + 133952169 133987500 TBPL1 9519 "TBP-like 1, transcript variant 1"
GO:0006352|GO:0001675|GO:0006355|GO:0005737|GO:0006366|GO:0007289|GO:0003713|GO:0005672|GO:0006235|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133938_PI430048170 0.4377187489156640.7975249595722511.65712426196905 1.94927930278347 2.49620730518914 A A A 2.81817788929834 1.86796490803791 2.36969860835769 P A P LNCV6_133938_PI430048170 mRNA TGTTACCTGTGGAAATGAGGGAAGATGTAAATGTGTTAGGTTTTAGCATCCCCTCTGGCA NM_175888RefSeq chr3 + 40506038 40518221 ZNF620 253639 "zinc finger protein 620, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128467_PI430048170 0.00491758930524588 0.6534036674441477.79486052047997 7.53755984326382 7.71545630078486 P P P 8.30834608430927 8.22060718974384 8.36884225098508 P P P LNCV6_128467_PI430048170 mRNA TCCCTTTTAAAGAGAAAATGTGACACTTGTGAAAAGGCTTGTAGGAAAGCTCCTCCCTTT NM_002994RefSeq chr4 - 73995641 73998729 CXCL5 6374 chemokine (C-X-C motif) ligand 5
GO:0008009|GO:0008284|GO:0070098|GO:0002446|GO:0007267|GO:0005576|GO:0045236|GO:0005615|GO:0002690|GO:0007165|GO:0006955|GO:0006954|GO:0006935|GO:0007186|GO:0060326|GO:0032496 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130641_PI430048170 0.3109071055839920.60211647479482 0.485756204935381 0.5216973751052981.26173679953768 A A A 0.5675937962625372.16554844651977 1.44568848166449 A A A LNCV6_130641_PI430048170 mRNA TAACAAGTTCTTTGCATGCTTTTTGCTCATTATCCCTTTGAAGTCTTCTCCAGCATAGAC NM_023012RefSeq chr12 - 122504642 122527013 RSRC2 65117 "arginine/serine-rich coiled-coil 2, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139131_PI430048170 0.3649633306418441.04681539487719 0.297863637030477 0.2793120703797630.452899544058414A A A 0.2928097784592140.255329875710934 0.289985217457541A A A LNCV6_139131_PI430048170 mRNA CTTCTATTCATGATGACAGTGATAGCTCCAACAGTGATAATGATACCAAATAGAGAGAAA NM_152401RefSeq chr4 - 55556524 55592212 PDCL2 132954 phosducin-like 2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145116_PI430048170 0.00541102458875157 0.4032007656880974.5157010996562 4.45918349747302 4.39779064278203 P P P 5.53475752079018 5.79375818545442 5.94803348457627 P P P LNCV6_145116_PI430048170 mRNA TGCCCTCGTTTACTCACAGTTTGCTTATTTGCCACCATAAGAAATGGTACAATAAAAATT NM_001012756 RefSeq chr19 - 36510686 36528346 ZNF260 NA "zinc finger protein 260, transcript variant 1" NA . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_142717_PI430048170 0.0443211543080051.42055867680737 13.0722692673068
12.8404366787835 12.9046008806228 P P P 12.6960104456473 12.2768062277969
12.2951176904979 P P P LNCV6_142717_PI430048170 mRNA
GTCACTGTTGAAGAGGATGACACCATCATGGAAGAATTGGTAGATAATCATGGCAAAAAA NM_018946RefSeq chr9
+ 98056676 98083083 NANS 54187 N-acetylneuraminic acid synthase
GO:0050462|GO:0005737|GO:0008781|GO:0006488|GO:0044267|GO:0009103|GO:0070062|GO:0047444|GO:0043
687|GO:0018279|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128843_PI430048170 0.0278185676790029 0.3994238571976519.8048740168027
9.84490117006581 9.94227242308751 P P P 10.7097538694937 11.2573332298369
11.4929569868191 P P P LNCV6_128843_PI430048170 mRNA
GGTACATTACTGCAATGTTCTCTTAACAGTTAAACAAGCTGTTTACAGTTTAAACTGCTG NM_018948RefSeq chr1
- 8011718 8026333 ERRFI1 54206 ERBB receptor feedback inhibitor 1
GO:0005515|GO:0060426|GO:0060428|GO:0019901|GO:0048286|GO:0006950|GO:0005634|GO:0005100|GO:0031
234|GO:0031953|GO:0045616|GO:0005737|GO:0032321|GO:0007175|GO:0043589 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130423_PI430048170 0.41590680637907 1.4223376794873 1.57529498274008
2.69892842513326 2.9251117298749 A A P 3.00154249812333 1.21144701377965
0.745063179756669P A A LNCV6_130423_PI430048170 mRNA
AAGTTTCTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCTCTCATCTACAGTT NM_001005467 RefSeq chr11
- 124396409 124397351 OR8B3 NA "olfactory receptor, family 8, subfamily B, member 3" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128791_PI430048170 0.9129737348051511.01098875401625 13.0658575264447 13.010830966625
12.7791430784347 P P P 12.874568312598 12.9941124076829 12.9530588489798 P P P
LNCV6_128791_PI430048170 mRNA
AGCCCCAAGGGCTCGGTGCTATTTGTAACGGAATAAAATTTGTAGCCAGACCCCAAAAAA NM_032038RefSeq chr16
+ 28974774 28984548 SPNS1 83985 "spinster homolog 1 (Drosophila), transcript variant 1"
GO:0040011|GO:0005515|GO:0046624|GO:0006869|GO:0003376|GO:0005743|GO:0016021|GO:0005765|GO:0055
085|GO:0031982 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129994_PI430048170 0.1518076567894641.26292061173451 5.34137495055922
5.33885800202402 5.78139656735453 P P P 4.94536454937644 5.23512300266958
5.29369590247151 P P P LNCV6_129994_PI430048170 mRNA
ACTGCTCATCAGTTTCTGTAGAGACAAAAACTCTGTACATATTTTGGAATCTGAAGAATC NM_014023RefSeq chr10
+ 1056835 1132297 WDR37 22884 WD repeat domain 37 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_135311_PI430048170 0.3977503681953641.12962196220766 7.39913476958337
7.87477606781301 7.5627882296416 P P P 7.64950960006554 7.41677487208542
7.25671269833686 P P P LNCV6_135311_PI430048170 mRNA
ACATAGGTCAGGAGTCTGGACTGACCCAGGTACGTCTGGCATCTTGCTTGAGGAACAGGG NM_001195833 RefSeq
chr19 - 38867831 38878279 RINL NA "Ras and Rab interactor-like, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_144471_PI430048170 0.0744139350663817 0.61838433514919 3.66541949158059
3.1112380170778 3.83850221995279 P P P 4.24304154782992 4.18783213278918
4.35511660455055 P P P LNCV6_144471_PI430048170 mRNA
ACATTGTGTACACAGCACCTGTGTGAGAGAAAAGAAATAATGCCCCTTGGCATCAAACCC NM_001258353 RefSeq
chr17 - 44850286 44899368 EFTUD2 9343 "elongation factor Tu GTP binding domain containing 2,
transcript variant 3"
GO:0005515|GO:0006397|GO:0008380|GO:0010467|GO:0015030|GO:0003924|GO:0071013|GO:0005525|GO:0005
737|GO:0016020|GO:0016607|GO:0000398|GO:0005654|GO:0005681 . NA - . NA NA NA NA NA NA

NA NA NA
LNCV6_128891_PI430048170 0.1596140899778620.7609968060645363.9723483264574
3.68286970851688 3.88523626428181 P P P 3.93845753107131 4.17526163990058
4.55586512325869 P P P LNCV6_128891_PI430048170 mRNA
GTGATTTAGAGTGCTTTAAAATTTCAGGACTCAGATATGAGGAATTGATGTAATGATGCC NM_198494RefSeq chr1
+ 40477629 40496343 ZFP69 339559 ZFP69 zinc finger protein
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_72970_PI430048170 0.6018622559978171.0544973660389 7.79332194953909 7.77140770346004
7.47285855167626 P P P 7.70762371695574 7.65481918785931 7.45503207472045 P P P
LNCV6_72970_PI430048170 mRNA
AGACAAGCTGCGCATGGAGTACCTCTCCCTGATGCATGCTATAGTCCGCACCACACCCTA NM_016453RefSeq chr3
- 48673838 48685933 NCKIPSD 51517 "NCK interacting protein with SH3 domain, transcript variant 1"
GO:0008092|GO:0005882|GO:0005515|GO:0007165|GO:0017124|GO:0008180|GO:0045087|GO:0007010|GO:0038
096|GO:0006607|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_5491_PI430048170 0.5366637538490440.9536857797183291 1.3858287948723 11.7393612392154
11.5403861471265 P P P 11.6378510393527 11.6215116231099 11.6332620437905 P P P
LNCV6_5491_PI430048170 mRNA
CCAGCCACAGGACCACCTCCTCTGCCAGCAGGAATAAAGACTTGTGCATCCCTCAAAAAA NM_001251888 RefSeq
chr17 + 81977549 82017406 ASPSCR1 79058 "alveolar soft part sarcoma chromosome region,
candidate 1, transcript variant 2"
GO:0005515|GO:0012506|GO:0048471|GO:0005886|GO:0042593|GO:0005575|GO:0006886|GO:0043231|GO:0005
829|GO:0012505|GO:0003674|GO:0008150|GO:0046324|GO:0033116|GO:0061024|GO:0009898|GO:0005654|GO:0
019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141085_PI430048170 0.0123435901399214 0.5724153682001853.68717493451046
3.31463603752582 3.57094621767535 P P P 4.58839503386432 4.11259561001605
4.26977188952039 P P P LNCV6_141085_PI430048170 mRNA
CCAGGACCACAAAAGAAACCTGACAATATTGTTGCTTTCTTCAAAAGTAATTTTGACTGA NM_178561RefSeq chr7
- 143755088 143757750 CTAGE6NA "CTAGE family, member 6" NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_137538_PI430048170 0.0378592987706215 1.56637024206675 6.94829013003239
6.50378554334259 6.79751446072444 P P P 6.14033878756635 6.08469782122943
6.11652944610262 P P P LNCV6_137538_PI430048170 mRNA
TTGAGGGGGGAGTGTTGGGTGGAATCATAGATCCATGCACTCCTAACATGAACTAATTCT NM_018029RefSeq chr3
+ 73061658 73063320 EBLN2 55096 endogenous Bornavirus-like nucleoprotein 2 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145432_PI430048170 0.00481126280746207 0.4037721531330095.76211516943351
5.20793396682322 5.63108050894664 P P P 6.57423767543943 6.82941966331169
7.12593242015123 P P P LNCV6_145432_PI430048170 mRNA
CTATGCCTTACCAAGTACATCCTTAAACAAAGTAGTATGTACATGAAATTGCACTTAACC NM_138340RefSeq chr18
- 21650896 21704805 ABHD3 171586 abhydrolase domain containing 3
GO:0052689|GO:0008150|GO:0003674|GO:0008152|GO:0016021|GO:0005575 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143099_PI430048170 0.0175215632223348 0.7373273216141057.2309791909329
6.99995780806714 7.20213803026516 P P P 7.56079493217336 7.63662727877327
7.56404390447712 P P P LNCV6_143099_PI430048170 mRNA
TGATGCTGTTTCCCCATGTTTAGCCATGGTCAAAAAATGGATTTCTCCTTTTTCTAAAATNM_001282950 RefSeq chr2
+ 231786382 231809253 COPS7B64708 "COP9 signalosome subunit 7B, transcript variant 1"
GO:0005737|GO:0008180|GO:0010388|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_135643_PI430048170 0.5480511358870751.02842712773637 0.623565371687368
0.6850706075771180.62499439457111 A A A 0.61116765763025 0.497483439079139
0.697563299987719A A A LNCV6_135643_PI430048170 mRNA
GCTGAATCCGTTGATTTATAGTTTGAGAAATAAAGATGTAAAGGATGCAGCTGAGAAAGT NM_006637RefSeq chr11
- 55935455 55936400 OR5I1 10798 "olfactory receptor, family 5, subfamily I, member 1"
GO:0050911|GO:0007165|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131365_PI430048170 0.0112772658634232 3.78461829265728 3.37508923533293
2.87901133486048 3.52067189593648 P A P 1.76444474634496 0.669466312221912
1.44882185617195 A A A LNCV6_131365_PI430048170 mRNA
CGGGACCAACTCTTTGTATAACCTACCTGAATGTATTAAAAACTAATTTTGGAGAAGCAA NM_005512RefSeq chr11
- 76657523 76670000 LRRC32 2615 "leucine rich repeat containing 32, transcript variant 1"
GO:0010628|GO:0005887|GO:0046007|GO:0050710 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_133881_PI430048170 0.116208130014191 1.14782346765553 11.147450548095
11.2158094190328 11.352871790137 P P P 11.1186689200007 10.8823239859156
11.1136723950396 P P P LNCV6_133881_PI430048170 mRNA
ACCGTATCGTAGAGGTTTGTAGTTAGTGCTTATTTTTGCATGTTGATGTTGACTAGCTAA NM_001297432 RefSeq
chr4 + 1309442 1340148 MAEA 10296 "macrophage erythroblast attacher, transcript variant 5"
GO:0005826|GO:0005819|GO:0003779|GO:0005634|GO:0016363|GO:0007346|GO:0005737|GO:0007049|GO:0043
249|GO:0048822|GO:0005887|GO:0007010|GO:0005654|GO:0005856|GO:0007155|GO:0033033|GO:0051301 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143930_PI430048170 0.416799357200863 1.2535481578733 0.490618732876819
1.27393048683684 0.444480931980994 A A A 0.465956708148142 0.456591524714886
0.466742652820127 A A A LNCV6_143930_PI430048170 mRNA
GAGCAAATCTGACCTAGCATTTGGTATGCTAGGCTCTGCTTTTCATGATTTTGAAATAAA NM_002649 RefSeq
chr7 + 106865478 106908978 PIK3CG 5294 "phosphatidylinositol-4,5-bisphosphate 3-kinase,
catalytic subunit gamma, transcript variant 1"
GO:0005515|GO:0097284|GO:0010897|GO:0001816|GO:0016303|GO:0035747|GO:0072672|GO:0043303|GO:0036
092|GO:0030593|GO:0030168|GO:0014065|GO:0006897|GO:0042110|GO:0007186|GO:0046875|GO:0046934|GO:0
045087|GO:0055118|GO:0006644|GO:0033628|GO:0051897|GO:0005886|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145144_PI430048170 0.179541064046248 0.661295945919585 10.2826061776535
9.48859976030327 9.17893983724333 P P P 10.4926810725123 10.4892621019635
9.9190153729705 P P P LNCV6_145144_PI430048170 mRNA
GAATCTGCCCAGACTCTTCCCTTAGAAGTCACAACATACTCAGTCCAATAAACCTGTGAG NM_001282165 RefSeq
chr12 + 132618779 132622386 P2RX2 22953 "purinergic receptor P2X, ligand gated ion channel, 2,
transcript variant 8"
GO:0007605|GO:0010524|GO:0046870|GO:0051291|GO:0019228|GO:0050850|GO:0042802|GO:0005639|GO:0009
743|GO:0016324|GO:0050909|GO:0043197|GO:0007528|GO:0043195|GO:0008144|GO:0043025|GO:0001614|GO:0
033198|GO:0051260|GO:0014832|GO:0015276|GO:0016151|GO:0035590|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_100983_PI430048170 0.39822433119862 1.46310033467116 0.346363903758786
1.58744276474578 0.415080238486359 A A A 0.363331834956701 0.323985122703458
0.374143082896105 A A A LNCV6_100983_PI430048170 mRNA
AACAAAGGACGCCGAATAGCTTATTTGTAGCGATGGGTTACCAGCTACCCTGTGTATACA NM_001117 RefSeq
chr18 + 905195 912172 ADCYAP1 116 "adenylate cyclase activating polypeptide 1 (pituitary), transcript
variant 2"
GO:0032755|GO:0034259|GO:0070445|GO:0043267|GO:0032854|GO:0005615|GO:0031175|GO:0042594|GO:0007

218|GO:0045860|GO:0001662|GO:0070374|GO:0005184|GO:0007565|GO:0046034|GO:0002878|GO:0051968|GO:0060078|GO:0045786|GO:0071385|GO:0008277|GO:0010976|GO:0010656|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90221_PI430048170 0.00136746960165048 0.297136075143026 7.97927646407537 7.64110198234124 8.17111506783561 P P P 9.48210065108443 9.56810581774196 9.98996772653643 P P P LNCV6_90221_PI430048170 mRNA GTTTAAATACCGCCTATGTACTCCCAAATGAATAAAACATAATTCTTGTCCTCTGAGAGC NM_030780 RefSeq chr8 - 103398637 103415335 SLC25A32 81034 "solute carrier family 25 (mitochondrial folate carrier), member 32, transcript variant 1"
GO:0006766|GO:0015884|GO:0005743|GO:0006767|GO:0046655|GO:0044281|GO:0016021|GO:0008517|GO:0006839 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100346_PI430048170 0.0249773011891095 0.624133601906265 6.4356602054386 6.5313706727563 6.84118905669382 P P P 7.25343104017699 7.34887477652153 7.27617140844375 P P P LNCV6_100346_PI430048170 mRNA CTCATTTCTATGCACAGTGTTTCTCAGGAGGATGGAGCTAGTTAGCTGTCTGTTGTCTGT NM_025181 RefSeq chr2 - 113712791 113756823 SLC35F5 80255 "solute carrier family 35, member F5, transcript variant 1"
GO:0006810|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131355_PI430048170 0.0663163842671595 1.14526915669292 11.2080245852308 11.1949048707869 11.0247097126574 P P P 11.0010134518727 10.9926717881471 10.8490413186949 P P P LNCV6_131355_PI430048170 mRNA CATACTGTCTAGAGGTTGACTCTTAGTTCTGTAAATAAAGACATCCATTTCAAACAGCAA NM_006545 RefSeq chr3 - 50347487 50351055 NPRL2 10641 nitrogen permease regulator-like 2 (S. cerevisiae)
GO:0043547|GO:0033673|GO:0005515|GO:0004672|GO:0006468|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133101_PI430048170 0.565938776174129 0.944904517600588 7.66041502747859 7.36441134570134 7.81355771647782 P P P 7.75436888476897 7.74903372924696 7.6112414927684 P P P LNCV6_133101_PI430048170 mRNA GCTAAGGTGGGAGTGAACACTGGGGTGAATAAATTTTAAATCAATTCAAGTATCTCAAAA NM_001166305 RefSeq chr3 - 194587672 194633421 TMEM44 93109 "transmembrane protein 44, transcript variant 3"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90187_PI430048170 0.161571132802473 1.47725980861653 4.09343510111446 3.48304000596208 4.34398608733434 P P P 3.71334187863104 3.29041693281685 3.31774379561639 P P P LNCV6_90187_PI430048170 mRNA CAAAAATGGAGGAAGCACCTACGCATCTTAATTCATTTCTTAAGAAAGAAGGATTGACCT NM_032664 RefSeq chr8 - 33370825 33473146 FUT10 84750 "fucosyltransferase 10 (alpha (1,3) fucosyltransferase)"
GO:0097150|GO:0030097|GO:0046920|GO:0042355|GO:0005794|GO:0006605|GO:0009790|GO:0036065|GO:0007399|GO:0009566|GO:0006457|GO:0032580|GO:0021799|GO:0042060|GO:0006486|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58849_PI430048170 0.191003873348933 0.77874110346374 6.09777412989707 6.04458449882394 6.3407414673005 P P P 6.33703447694916 6.30891329353561 6.86622558963663 P P P LNCV6_58849_PI430048170 mRNA CCTCCAGTGTATTGTTCTGCAGTGTTGAAACAGAATGGAAATGACAAGAAATATCTGCAG NM_004572 RefSeq chr12 - 32790745 32896846 PKP2 5318 "plakophilin 2, transcript variant 2b"
GO:0005882|GO:0005515|GO:0030057|GO:2000810|GO:0008285|GO:0030054|GO:0055010|GO:0005886|GO:0034334|GO:0005634|GO:0016264|GO:0086091|GO:0048496|GO:0007507|GO:0003674|GO:0086069|GO:0016337|GO:0005912|GO:0014704|GO:0010765|GO:0005911|GO:0005080|GO:0086002|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135055_PI430048170 0.106842883120062 1.67096583927106 6.9535006628548 6.96211565963987 6.89715106124349 P P P 6.70612849699717 5.90790601571364

5.79878364657972 P P P LNCV6_135055_PI430048170 mRNA
GGTGGGGTCTTTAGGTTTTCTCACTTTGACAACCCCCGAATGTTTTTATAGTAGTTTTTT NM_001135005 RefSeq
chr9 + 34990269 34998433 DNAJB5 25822 "DnaJ (Hsp40) homolog, subfamily B, member 5,
transcript variant 1"
GO:0006986|GO:0005515|GO:0006457|GO:0051087|GO:0005634|GO:0051082|GO:0000122|GO:0005829 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_138879_PI430048170 0.2168444412416 1.36225872092696 1.2447520157359 0.44455735000528
0.934706835452438 A A A 0.488050317085693 0.377743831237136 0.525992834407335 A
A A LNCV6_138879_PI430048170 mRNA
GCAGCCCTCGTGTAATACGGTGAATTAGAGTGGTATTTCACTTTGTATTATTTTGTAAAT NM_006113 RefSeq chr1
- 107571159 107964923 VAV3 10451 "vav 3 guanine nucleotide exchange factor, transcript variant 1"
GO:0050853|GO:0005515|GO:0005154|GO:0005886|GO:0007264|GO:0030890|GO:0030032|GO:0006906|GO:0032
855|GO:0046872|GO:0005829|GO:0005085|GO:0043552|GO:0007411|GO:0030676|GO:0070062|GO:0051056|GO:0
048010|GO:0048011|GO:0043065|GO:0048013|GO:0042493|GO:0030593|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129707_PI430048170 0.323527354716506 1.02028932055477 0.32242446970348
0.246122134690898 0.288921275780783 A A A 0.259402140446244 0.251709964343892
0.26041787112269 A A A LNCV6_129707_PI430048170 mRNA
GCACCTTAAGCACTGATAAATTTCAATCAGTCAACAATAAAGTGAGTGTTCCAACTAGAA NM_001080439 RefSeq
chr17 - 58420166 58488401 HSF5 124535 heat shock transcription factor family member 5
GO:0043565|GO:0006355|GO:0003700|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_89109_PI430048170 0.00128702117854801 3.629688724491 8.72087450507679
8.72748803493043 8.75397695891524 P P P 6.77386561449953 7.01396951465405
6.82390958718119 P P P LNCV6_89109_PI430048170 mRNA
TTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGGCTGGTTCTTTTGTTTTCC NM_021175 RefSeq
chr19 + 35282506 35285142 HAMP 57817 hepcidin antimicrobial peptide
GO:0006879|GO:0006955|GO:0045179|GO:0005179|GO:0050832|GO:0031640|GO:0005576|GO:0042742 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_140503_PI430048170 0.0424011709006469 0.568513541885828 2.69686480732587
3.36827321350301 3.18779463635951 A P P 3.97272879750371 3.99908269540287
3.79772100472882 P P P LNCV6_140503_PI430048170 mRNA
CCACATATTTCAGTGAGGGTAAGTATTTTCCTGTTGTCAAGAATAGCATTGTAAAAGCAT NM_004004 RefSeq
chr13 - 20187464 20192975 GJB2 2706 "gap junction protein, beta 2, 26kDa"
GO:0005243|GO:0005793|GO:0005886|GO:0007605|GO:0007267|GO:0016264|GO:0055085|GO:0016328|GO:0046
697|GO:0030539|GO:0006810|GO:0032570|GO:0061024|GO:0005922|GO:0034599|GO:0016021|GO:0032355 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131042_PI430048170 0.0023459913984258 0.336373169629487 7.67246140889668
7.32370257002748 7.3891049974346 P P P 8.98367883462733 9.03905644104555
9.10007353447045 P P P LNCV6_131042_PI430048170 mRNA
GTGGGAGGGAAGCCGGGAATGTATCCTTTTCAGACAAAATTAAATATTTTGAAATGAGAA NM_003216 RefSeq
chr22 + 41381928 41399328 TEF 7008 "thyrotrophic embryonic factor, transcript variant 1"
GO:0043565|GO:0003700|GO:0003690|GO:0046982|GO:0006357|GO:0045944|GO:0005634|GO:0048511|GO:0042
803|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127298_PI430048170 0.910983726213346 0.993830231636152 0.642195403956338
0.515740706181107 0.396652544870325 A A A 0.428537009615769 0.604364894893755
0.553301680157756 A A A LNCV6_127298_PI430048170 mRNA
GGTGCTGAGAATGAAAATCTAAATGATTGAAGTTTTAAGTCCAAGTAGGAGTTGGTTTGT NM_020724 RefSeq
chr4 - 140865570 141133462 RNF150 57484 ring finger protein 150 GO:0008270|GO:0016021 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130692_PI430048170 0.000480881364404796 0.224571302255063 2.69391577145557
2.86680460931217 3.14745796214738 A A P 4.94448226556054 5.03521868130632
5.21604970507855 P P P LNCV6_130692_PI430048170 mRNA
GAAGCCATGGTACTTTTTTCTTGAGTTACTTTGGATATGTTTTTTCAATGCCATCTGAAG NM_153042 RefSeq chr6
+ 18155387 18223853 KDM1B 221656 lysine (K)-specific demethylase 1B
GO:0006355|GO:0050660|GO:0006325|GO:0005634|GO:0007275|GO:0003677|GO:0006351|GO:0034720|GO:0034
648|GO:0044030|GO:0006349|GO:0016491|GO:0034649|GO:0005654|GO:0008270|GO:0055114|GO:0043046 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131407_PI430048170 0.137152557810277 0.660732299296572 5.9810474946098
5.45758192572085 5.71950254349947 P P P 5.81372809906263 6.40146641121829
6.65921918413876 P P P LNCV6_131407_PI430048170 mRNA
TGAACAGAAACCAATACTGCTGTGCACTGAGAATAAAAACTCATGCCCACTTGTAAAAAA NM_001001396 RefSeq
chr1 + 203626786 203744081 ATP2B4 493 "ATPase, Ca++ transporting, plasma membrane 4,
transcript variant 1"
GO:0005515|GO:0050998|GO:1900082|GO:0005516|GO:0030346|GO:0030018|GO:0005886|GO:0046872|GO:0055
074|GO:0033138|GO:0034220|GO:0045019|GO:0097110|GO:2000481|GO:0006357|GO:0006874|GO:0030315|GO:0
070885|GO:0055085|GO:0005524|GO:0010751|GO:0005388|GO:0043234|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130580_PI430048170 0.411259791083683 1.29323756176523 0.316816468518652
1.03537604985325 1.34168607944585 A A A 0.373602370995547 0.959291773669613
0.34243530290536 A A A LNCV6_130580_PI430048170 mRNA
TCCTCAACAAATGGCATGTGACTTTGTAAGTGTAGAATTGCTGTGAGGTATGGGGCTAGG NM_031417 RefSeq
chr19 + 45251257 45305283 MARK4 57787 "MAP/microtubule affinity-regulating kinase 4,
transcript variant 2"
GO:0005515|GO:0008017|GO:0043130|GO:0043005|GO:0005813|GO:0006996|GO:0043015|GO:0005815|GO:0001
578|GO:0050321|GO:0000226|GO:0005524|GO:0005829|GO:0007399|GO:0043068|GO:0004674|GO:0015630|GO:0
006468 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135837_PI430048170 0.000936361213240742 1.79710940136187 11.2190100614031
11.3654610763879 11.3667747159804 P P P 10.3685561146807 10.4384737593848
10.6020727881909 P P P LNCV6_135837_PI430048170 mRNA
ATCCAGGCACTCACTTGTATTCTACTGCTCAATAAACGTTTATTAAACTTGATCCTGCTA NM_001127393 RefSeq
chr14 - 103912287 103921566 C14orf2 9556 "chromosome 14 open reading frame 2, transcript
variant 2" GO:0008150|GO:0003674|GO:0016021|GO:0005575|GO:0005753 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139126_PI430048170 0.359674767310883 1.02960716854029 0.296033841396942
0.29973053537519 0.402899047108572 A A A 0.306540853842615 0.283638300802005
0.284656688081634 A A A LNCV6_139126_PI430048170 mRNA
CAGCCTATATCCTGAGACTAAGTGGAAGTGGGAAAAGAGTACAAGAGAAGAGACAAAGTG NM_002030 RefSeq
chr19 + 51795157 51826081 FPR3 2359 formyl peptide receptor 3
GO:0004982|GO:0007165|GO:0007186|GO:0006935|GO:0005886|GO:0006928|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142758_PI430048170 0.0177086065390353 0.504194076386924 2.97079719061715
2.97826172117662 3.56515640012277 A P P 3.8952108340516 4.39380732356427
4.22910130280179 P P P LNCV6_142758_PI430048170 mRNA
TCAGCCTTATGTATGCCATTGACTCTGAAATGTATACCAGCCTTTCACTGTGTACCGTGT NM_145061 RefSeq
chr13 - 21153594 21176602 SKA3 221150 "spindle and kinetochore associated complex subunit 3,
transcript variant 1"
GO:0005515|GO:0007067|GO:0005737|GO:0000940|GO:0007059|GO:0031110|GO:0005876|GO:0051301 . NA

- . NA NA NA NA NA NA NA NA NA
LNCV6_133227_PI430048170 0.366317114513181 0.90525423375112 14.1091284479871
13.6844314073805 13.72648764589 P P P 14.0138653850526 14.0079136362751
13.9676540676177 P P P LNCV6_133227_PI430048170 mRNA
AACATGCGCTTTGCCAAGAAGCACAACAAAAAGGGCCTAAAGAAGATGCAGGCCAACAAT NM_000992 RefSeq
chr3 - 51993627 51995942 RPL29 6159 ribosomal protein L29
GO:0010467|GO:0003735|GO:0007566|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0006415|GO:0006
412|GO:0006413|GO:0005829|GO:0006414|GO:0000184|GO:0016020|GO:0016032|GO:0022625|GO:0044267|GO:0
008201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135378_PI430048170 0.0573417797399846 0.376647390565286 3.09603249152651
1.64043660788309 2.14269764639774 A A A 3.81905535071537 4.07482751210539
3.55306587181162 P P P LNCV6_135378_PI430048170 mRNA
TACTGTGAAAGTCTTCTTCAGATCCCCACCTGCATCATTCCGAATGTGTCCTGGAAAAAA NM_153767 RefSeq chr11
- 128838013 128867373 KCNJ1 3758 "potassium channel, inwardly rectifying subfamily J, member 1,
transcript variant 5"
GO:0005242|GO:0007588|GO:0005886|GO:0001822|GO:0005546|GO:0007268|GO:0010107|GO:0009791|GO:0070
294|GO:0005524|GO:0015272|GO:0001894|GO:1900128|GO:0008076|GO:0034765|GO:0072358|GO:0006813 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134527_PI430048170 0.789671121170087 1.02150288615522 12.5840403668432
12.7140147109353 12.7928953345072 P P P 12.8394179058459 12.461897913104
12.6805185320972 P P P LNCV6_134527_PI430048170 mRNA
GTGCTAGTTCATGTGTTCTCCATTCTTGTGAGCATCCTAATAAATCTGTTCCATTTTGAT NM_005008 RefSeq chr22 -
41673932 41688909 NHP2L1 4809 "NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae),
transcript variant 1"
GO:0005515|GO:0008380|GO:0010467|GO:0031428|GO:0003723|GO:0042254|GO:0005730|GO:0005634|GO:0043
234|GO:0030515|GO:0000398|GO:0005654|GO:0005681 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81791_PI430048170 0.205891082493592 0.646141078470032 0.296622308146315 0.276298833623803
0.388274231570853 A A A 0.291399318933275 1.32458136659589 1.05132662159475 A A A
LNCV6_81791_PI430048170 mRNA
TCATGGTGCTGGAGCTGGTGGCACCCGCAACATCTCAGGCACCAGTAAGTTTCATGTGGA NM_000032 RefSeq chrX
- 55009054 55031064 ALAS2 212 "5'-aminolevulinate synthase 2, transcript variant 1"
GO:0042541|GO:0005515|GO:0050662|GO:0001666|GO:0005743|GO:0044281|GO:0006782|GO:0006783|GO:0005
739|GO:0006879|GO:0006778|GO:0005759|GO:0030170|GO:0030218|GO:0016594|GO:0032364|GO:0003870 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137599_PI430048170 0.0775197705402305 1.03333519950406 0.394237905354332
0.407259922534911 0.442197833358924 A A A 0.357383975988544 0.349513106627347
0.394892189370005 A A A LNCV6_137599_PI430048170 mRNA
CCACCTTGCGGGGATAAAGAGAGAAAAACAAATTCATCAAATGGAAGACACATTGAAAGT NM_001172128
RefSeq chr15 + 81196877 81312763 IL16 3603 "interleukin 16, transcript variant 3"
GO:0050930|GO:0006955|GO:0006355|GO:0005737|GO:0005886|GO:0030595|GO:0016032|GO:0005634|GO:0005
615|GO:0005125|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127025_PI430048170 0.430912795305773 0.86482820309315 4.18022041322747
3.53007836031417 3.68736943087052 P P P 4.30142315145746 3.99108294304452
3.76524140391094 P P P LNCV6_127025_PI430048170 mRNA
GTCCAGGTTCCCTACACTCCCCAGGCCAATGCTTTTGAATAAATCTTGACGTCATTGAAT NM_001282479 RefSeq
chr8_KI270813v1_alt + 222729 225553 PRR23D1 NA proline rich 23 domain containing 1 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_135418_PI430048170 0.0026641837288968 0.5623030770502 6.61100952163193
6.78774452884533 6.91226317448011 P P P 7.64064466525582 7.4300615074091

7.73148354545563 P P P LNCV6_135418_PI430048170 mRNA
AATGACGGGATTCCAGGGTAGGAAGTGCTTTTTATTCCCCTTTTGTTTTTTCTTTTAAAA NM_017736 RefSeq chr16 -
20733665 20741964 THUMPD1 55623 "THUMP domain containing 1, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_126743_PI430048170 0.0980118042370514 1.14605685461978 3.42742969106582
3.21754375742158 3.23143711911403 P P P 3.21475253130929 3.0161517399246
3.05746477126841 P P P LNCV6_126743_PI430048170 mRNA
AGTAGTCCCATTATGTCAAGCCTTGCACAATACAAGCCAAATCTCCTATATCAAAAGAAC NM_018219 RefSeq chr11
- 66590168 66593083 CCDC87 55231 coiled-coil domain containing 87
GO:0008017|GO:0000910|GO:0000226 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142258_PI430048170 0.4024202532570731.1364819820875 4.41466888869387
4.12561501179476 4.34491736105646 P P P 3.72562283539213 4.21096766036488
4.34044654970437 P P P LNCV6_142258_PI430048170 mRNA
CCTTGTATCCCCAAAGGACCACACGTGTAATTTTTGATATTATTTCCAAAATCAGGTTTT NM_173543 RefSeq chr3
- 138061984 138115609 DZIP1L 199221 "DAZ interacting zinc finger protein 1-like, transcript variant 1"
GO:0042384|GO:0005814|GO:0046872|GO:0036064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119250_PI430048170 0.3755934434299790.9675879818150440.432238948555843
0.4555533426328920.3205836655487 A A A 0.4158662698233760.487073479177784
0.450739171695257 A A A LNCV6_119250_PI430048170 mRNA
ATCATTTCCTACATCTTCATTGCTTTTGCTAGCCTAAGGATCCACTCAGCATCAGGCAGA NM_001005492 RefSeq
chr11 + 56176617 56177556 OR5J2 NA "olfactory receptor, family 5, subfamily J, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128181_PI430048170 0.0162359453603942 1.23042484713304 12.3120144209691
12.4671579497256 12.428443708052 P P P 12.0752652586618 12.1252649849396
12.1136253004135 P P P LNCV6_128181_PI430048170 mRNA
TCTGCAGTGTGCACGGCCTTGTTCTAACCCGGAATAAAGGTGATTGATTGTATTGCAACT NM_001297576 RefSeq
chr1 + 160205318 160215376 PEA15 8682 "phosphoprotein enriched in astrocytes 15, transcript
variant 1"
GO:0005515|GO:0005737|GO:0005875|GO:0046325|GO:0006810|GO:0008643|GO:0006915|GO:0043278|GO:0000
077 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122033_PI430048170 0.0904527936441084 0.8840585909536597.55278486706508
7.52478877050628 7.41442267312631 P P P 7.79835871400376 7.59563754935093 7.6266669126693
P P P LNCV6_122033_PI430048170 mRNA
GCGAGCTTCTCCTCTCCTCACGACCGAGGCAGCATTATGGCGAACCTTGGCTGCTGGATG NM_000311 RefSeq chr20
+ 4686150 4701588 PRNP 5621 "prion protein, transcript variant 1"
GO:0005515|GO:0008017|GO:0071280|GO:0043008|GO:0005886|GO:0005783|GO:0046007|GO:0051087|GO:0005
741|GO:0005634|GO:0031225|GO:0043433|GO:0042802|GO:0032880|GO:0005737|GO:0006878|GO:0015631|GO:0
007411|GO:0007611|GO:0051260|GO:0007050|GO:0006979|GO:0032689|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137691_PI430048170 0.0111205901916496 1.21753237193825 10.2006915423996
10.148516642361 10.0800989762628 P P P 9.76178817176894 9.91152968399194
9.90182722855492 P P P LNCV6_137691_PI430048170 mRNA
AGATACATGGCAGGTAACTGTTTATGGGAGAAAAGTACAGTGCTGTTACGTGGCACTGTA NM_020710 RefSeq chr1
- 3780219 3796504 LRRC47 57470 leucine rich repeat containing 47
GO:0005515|GO:0008152|GO:0004826 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134961_PI430048170 0.3413423399486620.9667326290089910.418793891020857
0.4439513719707910.314113220635369 A A A 0.4159762079557060.473251634363418
0.436740542861192 A A A LNCV6_134961_PI430048170 mRNA
ATGGTGGAGAAGACTCTTGCTTCCTCCAAGTGTTTGAAAACACAAAATGCGATATGAAAA NM_002563 RefSeq chr3

+ 152834946 152838054 P2RY1 5028 "purinergic receptor P2Y, G-protein coupled, 1"
GO:0005515|GO:0010469|GO:0005886|GO:0060406|GO:0007200|GO:0007204|GO:0007193|GO:0030425|GO:0005
739|GO:0043270|GO:0042312|GO:0016323|GO:0016324|GO:0045944|GO:0045211|GO:0097110|GO:0046887|GO:0
004872|GO:0070374|GO:0046982|GO:0009986|GO:0090075|GO:0023019|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128887_PI430048170 0.00414703696125861 0.4397631400863941 1.3546838333455
11.1483923695474 11.417800135387 P P P 12.2555304840994 12.4583829013694
12.7356116223045 P P P LNCV6_128887_PI430048170 mRNA
CAGTGAGATGGCCGTTTCTGACTTGTAGAGAAATTTTAATAAACCTGGTTTCGTAAATAA NM_025195 RefSeq chr8
+ 125430320 125438405 TRIB1 10221 "tribbles pseudokinase 1, transcript variant 1"
GO:0032436|GO:0007254|GO:0031434|GO:0048662|GO:0005634|GO:0005524|GO:0043433|GO:0014912|GO:0005
737|GO:0004672|GO:0043405|GO:0032496|GO:0004860|GO:0055106|GO:0006468|GO:0006469|GO:0031665|GO:0
031625|GO:0008134. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129914_PI430048170 0.000564712656961456 0.584131586699305 15.6650835456299
15.5403822520248 15.576073402838 P P P 16.3810748251111 16.3390799565262
16.3906433767244 P P P LNCV6_129914_PI430048170 mRNA
GTCCCTGGGTGACATGTCAGATCTTTGTACGTAATTAAAAATATTGTGGCAGGATTAATA NM_001007 RefSeq chrX
- 72272602 72277291 RPS4X 6191 "ribosomal protein S4, X-linked"
GO:0010467|GO:0008284|GO:0015935|GO:0019058|GO:0019843|GO:0006412|GO:0006413|GO:0006414|GO:0005
829|GO:0000184|GO:0016032|GO:0070062|GO:0003735|GO:0006614|GO:0019083|GO:0007275|GO:0045727|GO:0
006415|GO:0016020|GO:0022627|GO:0030529|GO:0005840|GO:0005925|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133326_PI430048170 0.328946357480888 0.596148866673764 0.360429081642198
0.338577951774065 0.309192411399319 A A A 0.493604639953311 0.436681386095401
1.84460660023553 A A A LNCV6_133326_PI430048170 mRNA
CGCAACTATGCTTAACATGGCGAAATGTATTAAACACTCGTCCAACTATTTATGAAATAC NM_001173523 RefSeq
chr4 + 30720414 31146801 PCDH7 5099 "protocadherin 7, transcript variant d"
GO:0005886|GO:0005887|GO:0005509|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130220_PI430048170 0.0224216854754517 1.61824801560525 4.27834475642367
4.76233003319881 4.40283607650584 P P P 3.95440261653892 3.8531558261073
3.57051484525444 P P P LNCV6_130220_PI430048170 mRNA
TGATTATCGACCATTCGGCAGGCGTTCAAAGTCAAAGGCCCCACACTGAGTCCTGGCCCA NM_004558 RefSeq chr19
+ 5823806 5828324 NRTN 4902 neurturin
GO:0030424|GO:0007411|GO:0000165|GO:0001755|GO:0005102|GO:0021675|GO:0005576|GO:0008083|GO:0007
169|GO:0031175|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139534_PI430048170 0.332070990986239 0.815837653380053 4.84706979404696
4.29191390838413 4.20871506277066 P P P 5.02597558468764 4.40222566481839
4.81899291164192 P P P LNCV6_139534_PI430048170 mRNA
ACTGGACTCCTCATCCCCGTAATTATTTAGAGAAGATGCAAGCAGCAGATAGTCTCCATG NM_024735 RefSeq chr16
- 87326986 87383793 FBXO31 79791 "F-box protein 31, transcript variant 1"
GO:0008054|GO:0016567|GO:0030332|GO:0043025|GO:0031571|GO:0031146|GO:0019005|GO:0006974 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127551_PI430048170 0.123294050541495 1.64548823843048 3.64447989550672
4.27003213620041 3.30689975586283 P P P 3.17279769786668 2.78009462369351
3.24064277859153 P P P LNCV6_127551_PI430048170 mRNA
TTCATCTGGGGTTTGGATGCTCCTCACCGTATGTACAATGAAATCATCCATCTGATGCAG NM_001128215 RefSeq
chr10 + 88802729 88820546 LIPM NA "lipase, family member M" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130179_PI430048170 0.0743849147674617 0.614601897182911 0.2565091302358

10.2964742134775 10.6041156595115 P P P 10.6179297699244 11.2771816063653
11.2968040056445 P P P LNCV6_130179_PI430048170 mRNA
CCACTCAGCACATTTCATGGAGGTCATGTCTTTTCACTGATACTTTTTTGATAGTTTTTA NM_001145199 RefSeq chr12
+ 105330635 105371518 C12orf75 387882 chromosome 12 open reading frame 75 NA . NA -
NA NA NA NA NA NA NA NA NA NA
LNCV6_127146_PI430048170 0.774324650084035 1.06707044290817 8.43920935605756
7.80761713810654 7.82124271732775 P P P 8.25399005386544 7.91133276072541
7.65229276018599 P P P LNCV6_127146_PI430048170 mRNA
CTTTGCAAAAGCTTTTAGAAGGAAAAGAAAGAGGATTAAAGAGAATTGCTGGTGATCCTA NM_020664 RefSeq
chr16_KI270854v1_alt + 1003 11633 DECR2 26063 "2,4-dienoyl CoA reductase 2, peroxisomal"
GO:0008670|GO:0006636|GO:0019166|GO:0005102|GO:0005778|GO:0055114 . NA - NA NA NA NA
NA NA NA NA NA
LNCV6_142292_PI430048170 0.28010963006501 0.880647126523643 5.44616363192663
5.64933508341201 5.24412721214425 P P P 5.80071115114631 5.48545269669313
5.61445631971201 P P P LNCV6_142292_PI430048170 mRNA
GTAGACTTTTAAGACAACATTTATGTCACTCCCCACCTCCTCATATTTAATAAAGGAGAT NM_006205 RefSeq chr12
+ 14973021 14981866 PDE6H 5149 "phosphodiesterase 6H, cGMP-specific, cone, gamma"
GO:0004857|GO:0000187|GO:0045745|GO:0030553|GO:0045742|GO:0008152|GO:0047555|GO:0043086|GO:0007
601|GO:0050896 . NA - NA NA NA NA NA NA NA NA NA
LNCV6_136014_PI430048170 0.562160538796543 0.967174760314455 0.474113591162118
0.460553074776685 0.252937641272832 A A A 0.395696604978343 0.497646766789823
0.447386824385001 A A A LNCV6_136014_PI430048170 mRNA
TCTTTCAGTTCCATTTTCACTGGGGCAGTACAAATGAGCATGGTTCAGAACATACAGTGG NM_001128830 RefSeq
chr8 - 85328228 85378154 CA1 759 "carbonic anhydrase I, transcript variant 3"
GO:0015701|GO:0008270|GO:0044281|GO:0004089|GO:0006730|GO:0070062|GO:0005829 . NA - NA
NA NA NA NA NA NA NA NA NA
LNCV6_130445_PI430048170 0.00639562003131548 1.28878598447442 11.0939426054302
11.1478024255306 10.9878358834732 P P P 10.8015050741173 10.7054801908449
10.6236196844602 P P P LNCV6_130445_PI430048170 mRNA
GCCAGAGAGTTCACCGTAGGCATCTTTAATAAACTAACTCCAGCAAAATGTGGGTACGTT NM_153818 RefSeq chr1
- 2404801 2412571 PEX10 5192 "peroxisomal biogenesis factor 10, transcript variant 1"
GO:0005622|GO:0005515|GO:0007031|GO:0008270|GO:0016558|GO:0008022|GO:0005779|GO:0005778|GO:0005
777 . NA - NA NA NA NA NA NA NA NA NA
LNCV6_140957_PI430048170 0.414008537901415 0.527257267431659 0.377487316155792
0.351682127660055 0.255103713305052 A A A 2.20536665352331 0.350266925538772
0.334269675920319 A A A LNCV6_140957_PI430048170 mRNA
GGTGTACCAGTATGACAAAAATGGAAAACCTATAAAAGTATCCCCGTGATTCCATAGGTG NM_001002911 RefSeq
chr16 - 20031720 20073778 GPR139 NA G protein-coupled receptor 139 NA . NA - NA NA
NA NA NA NA NA NA NA
LNCV6_142144_PI430048170 0.2740060155226 1.59092157318847 1.62753952635387
0.438533458141106 1.62317476085308 A A A 0.883583542924171 0.408735045396213
0.639573614699255 A A A LNCV6_142144_PI430048170 mRNA
CTCTCATTTATACACTAAGAAACAAGGACGTGAAGGGGGCTCTGTGGAAAGTACTATGGA NM_001001657 RefSeq
chr5 - 180739122 180740058 OR2Y1 NA "olfactory receptor, family 2, subfamily Y, member 1" NA .
NA - NA NA NA NA NA NA NA NA NA
LNCV6_78908_PI430048170 0.243066122507274 1.40285386489234 0.995154515525894 0.865531933065839
1.51897761509748 A A A 0.278583217650555 0.260085229904517 1.23389634092562 A A A
LNCV6_78908_PI430048170 mRNA
TGGAGACTGGAAGAAATGTGGTCAGCGAAGCGCTTAAGGTGCCGGTGTCTGAAGGCTGCA NM_152742 RefSeq

chr7 - 100169605 100177426 GPC2 221914 glypican 2
GO:0005886|GO:0007603|GO:0005783|GO:0005796|GO:0005975|GO:0005578|GO:0006027|GO:0043395|GO:0044281|GO:0031225|GO:0001523|GO:0005615|GO:0006024|GO:0007224|GO:0030182|GO:0009405|GO:0030204|GO:0030203|GO:0043202. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129273_PI430048170 0.0278293137113418 1.18397546340423 12.8436689370106
12.94666489153 12.9005948308093 P P P 12.5477253453609 12.674506774932
12.7334280313753 P P P LNCV6_129273_PI430048170 mRNA
CCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCCAATATAAAAATATAGACTTTTTT NM_001134693 RefSeq
chr2 - 27070473 27071699 OST4 100128731 oligosaccharyltransferase 4 homolog (S. cerevisiae)
GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139660_PI430048170 0.4794798764793470.7270426457051690.370070144175613
0.3627681691870610.435657749886464A A A 1.52774455361209 0.308475396149828
0.36161285433582 A A A LNCV6_139660_PI430048170 mRNA
CTCCCCAGTTTAGCTGTATTTGAATTACTAAATGCTTTATCGTCAAACTGTACCTAGTCTNM_001942RefSeq chr18 +
31318088 31359246 DSG1 1828 desmoglein 1
GO:0030057|GO:0045295|GO:0005886|GO:0060135|GO:0005509|GO:0050821|GO:0006915|GO:0016328|GO:0006921|GO:0005829|GO:0016339|GO:0016337|GO:0016324|GO:0005911|GO:0015643|GO:0032570|GO:0007043|GO:0009898|GO:0016021|GO:0007156|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129991_PI430048170 0.3424985462917980.8882063091484610.331939456307236
0.4374884091484880.321418425746719A A A 0.5264194241048240.747736841161612
0.297665231539483A A A LNCV6_129991_PI430048170 mRNA
TGTTCTCACAAAGATGGAAAAGATACAAGAGCTTGCCGGAAATAAAGCTACATCTATCCA NM_006658RefSeq chr7
+ 31687016 31708455 PPP1R17 10842 "protein phosphatase 1, regulatory subunit 17, transcript variant 1" GO:0035556|GO:0004865|GO:0010921|GO:0005575|GO:0007417|GO:0043086 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_66763_PI430048170 0.0196560001576266 0.47803862755755 4.73983604419487
4.73997156158808 4.65224497386297 P P P 5.68043398024682 5.52866044275039
6.06500572168445 P P P LNCV6_66763_PI430048170 mRNA
GGTCACCAGTGGGTCATAAATTGGCATATGTTTGGAACAATGACATTTATGTTAAAATTG NM_001935RefSeq chr2
- 161992244 162074542 DPP4 1803 dipeptidyl-peptidase 4
GO:0005515|GO:0008284|GO:0005886|GO:0004252|GO:0031295|GO:0030139|GO:0005765|GO:0002020|GO:0010716|GO:0042803|GO:0042802|GO:0046581|GO:0016324|GO:0071438|GO:0006508|GO:0070062|GO:0001666|GO:0009986|GO:0031258|GO:0005102|GO:0033632|GO:0030027|GO:0042110|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126776_PI430048170 0.1310112010386431.20755070198829 4.13384556565475
3.76883484679143 4.07003233120239 P P P 3.87896854896703 3.65808789134429
3.63214335104555 P P P LNCV6_126776_PI430048170 mRNA
CTAGTAGGGTTAGTTGCAATCATAATATGAGTTGCATCCTCCCTCTCATTTATATCAAAT NM_152695RefSeq chrX
+ 135344770 135363413 ZNF449 203523 zinc finger protein 449
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145195_PI430048170 0.55908584059497 1.1517173512415 1.02697506032409
0.3693713710601820.276763809962095A A A 0.4938221955039240.390187807865568
0.291701168449244A A A LNCV6_145195_PI430048170 mRNA
GGTCTTGGTATTCTTAAGGGAACTTCCACATTATACATTTGATGTATTGACCAGAATATG NM_000439RefSeq chr5
- 96390335 96433281 PCSK1 5122 "proprotein convertase subtilisin/kexin type 1, transcript variant 1"
GO:0030133|GO:0005794|GO:0050796|GO:0016486|GO:0004252|GO:0043043|GO:0008152|GO:0007267|GO:0006508|GO:0044267|GO:0005615|GO:0034774 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145397_PI430048170 0.4559084141135170.8015222886782820.404577643651555

0.3268244013210170.361143243277011A A A 1.19223762436997 0.317218036710514
0.364940669390264A A A LNCV6_145397_PI430048170 mRNA
CCACAGGCACGCGGGGCTTAGGAAAGCCTGAGTGTAATAAACTGCAAGTATTTCATTAAA NM_001099221 RefSeq
chr5 - 135448867 135452399 TIFAB NA "TRAF-interacting protein with forkhead-associated domain,
family member B" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130671_PI430048170 0.1545766349518731.22728618881628 8.81456671179335
8.92608839782545 9.25503160002608 P P P 8.67506150811232 8.66514093881834
8.80207837419051 P P P LNCV6_130671_PI430048170 mRNA
GCAGCAGTTTCATATGTGTGCAATATGTGCATTCTTTCATTTTAGTTTTGCACTTGGTTT NM_001277061 RefSeq chr2
+ 227325150 227357836 MFF 56947 "mitochondrial fission factor, transcript variant 1"
GO:0005515|GO:0030054|GO:0000266|GO:0010821|GO:1900063|GO:0006626|GO:0090314|GO:0001836|GO:0005
741|GO:0090141|GO:0043653|GO:0042803|GO:0008021|GO:0008053|GO:0070584|GO:0032592|GO:0090200|GO:0
051260|GO:0005777|GO:0016559 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68182_PI430048170 0.4295774428210721.09996921181721 7.57105153697506 7.31737899571445
7.39819030336374 P P P 7.17571703408682 7.56661019965145 7.09885569338537 P P P
LNCV6_68182_PI430048170 mRNA
TCTTCTGTGATGTGTATAATCCTCAGAGCAAAACATACTGTAAGCGGCTCCAGGTGCTGT NM_001101654 RefSeq
chr18 - 50282342 50288322 CXXC1 30827 "CXXC finger protein 1, transcript variant 1"
GO:0005515|GO:0006355|GO:0005634|GO:0042800|GO:0006351|GO:0016363|GO:0030968|GO:0045322|GO:0005
737|GO:0035097|GO:0016607|GO:0048188|GO:0005654|GO:0008270|GO:0045893|GO:0006987|GO:0044267|GO:0
051568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123979_PI430048170 0.8242450769648130.9791950232700576.09374206494642
6.26001840858429 6.30450894274555 P P P 6.06518884012959 6.37835040925989
6.29620099724283 P P P LNCV6_123979_PI430048170 mRNA
GCAAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCCTTTCATTCGAGAGGCGGAGC NM_003107 RefSeq
chr6 + 21593740 21598618 SOX4 6659 SRY (sex determining region Y)-box 4
GO:0005515|GO:0003289|GO:0003700|GO:0006366|GO:0090263|GO:0003183|GO:0007507|GO:0060993|GO:0060
548|GO:0002328|GO:0032024|GO:0031397|GO:0006977|GO:0000976|GO:0001105|GO:0046982|GO:0048485|GO:0
001841|GO:0001501|GO:0021782|GO:0060174|GO:2000761|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136093_PI430048170 0.14794125210131 0.68076036136324 9.38446100494761 8.6712170504985
8.49967948931642 P P P 9.54578562104874 9.63863951210434 9.14913193800372 P P P
LNCV6_136093_PI430048170 mRNA
TGGCCCTATGCGGCCCAGCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAA NM_205545 RefSeq
chr8 - 142750209 142752534 LYPD2 137797 LY6/PLAUR domain containing 2
GO:0005886|GO:0031225|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142429_PI430048170 0.0360230356980348 0.2757923155334371.05709069448673
0.3335457278977780.384948309373594A A A 2.83316782854335 2.78631933087692 1.4973938479356
P P A LNCV6_142429_PI430048170 mRNA
CCCCCATGTTAAACCCCATAATCTATAGCTTGAGAAATAAAGATGTAAAAGCTGCTATAA NM_001001919 RefSeq
chr9 - 104526252 104527209 OR13C4138804 "olfactory receptor, family 13, subfamily C, member 4"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141840_PI430048170 0.8929299530702071.00446022324284 0.482412053506451
0.5209677921188180.427218720492314A A A 0.5506198123731340.425136819759497
0.433678616282062A A A LNCV6_141840_PI430048170 mRNA
GGGGCATGGTATTTTATTCATTTCTGACCTCCAATTCCCTAAGTGGAGATTAAATGTTAG NM_004391 RefSeq chr3
- 42872191 42876141 CYP8B1 1582 "cytochrome P450, family 8, subfamily B, polypeptide 1"
GO:0006629|GO:0006805|GO:0005506|GO:0008397|GO:0005783|GO:0006699|GO:0044281|GO:0033778|GO:0019

825|GO:0005789|GO:0008206|GO:0016021|GO:0016125|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134804_PI430048170 0.2633559360705031.0351698088134 0.395166106680338 0.3527752452934760.31324620012435 A A A 0.2513141218890230.304364467451207 0.355200527885614A A A LNCV6_134804_PI430048170 mRNA TATTGCTGTTTGGGGAAAACCACCAATAGAATTGCAGCTAGACTTTTGGGGACTGTGCCT NM_153015RefSeq chr8 - 108783116 108787541 TMEM74 157753 transmembrane protein 74 GO:0000421|GO:0006914|GO:0031410|GO:0016021|GO:0005765 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138048_PI430048170 0.0238636059428608 1.23128258597735 7.51663636626952 7.716438578426 7.70438704321035 P P P 7.43956233144441 7.32625359644443 7.27477042909094 P P P LNCV6_138048_PI430048170 mRNA GTTGGACAAGACTGCTATATGTATATTCTAGGTTTTCCCCTATAGGTATACTTATGTGAA NM_019109RefSeq chr16 + 5071808 5087379 ALG1 56052 "ALG1, chitobiosyldiphosphodolichol beta-mannosyltransferase" GO:0000030|GO:0016020|GO:0005783|GO:0005789|GO:0004578|GO:0006486|GO:0016021|GO:0006488|GO:0044267|GO:0009103|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103611_PI430048170 0.2363882337140051.21700862604488 9.65921637688937 9.53762765623322 9.940065197273 P P P 9.08450024341618 9.57999390778647 9.59618394683098 P P P LNCV6_103611_PI430048170 mRNA AAGTACATGCTGGATTGTAGAACTTCTCTCTCTGCTAAAGTAAATAATGCCAGCCTGATT NM_001135694 RefSeq chr8 + 42391760 42405937 VDAC3 7419 "voltage-dependent anion channel 3, transcript variant 2" GO:0006820|GO:0005739|GO:0046930|GO:0044070|GO:0000166|GO:0015288|GO:0005741|GO:0005634|GO:0015853|GO:0055085|GO:0008308|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67680_PI430048170 0.3076856123813591.18340319253473 4.64803711531167 4.53676816283665 4.67965996773265 P P P 4.75066795561873 4.13309479838464 4.1691175342088 P P P LNCV6_67680_PI430048170 mRNA CACCAGAAGAAATCTCTCTGTTAAAGTCCCTGCTACAACATCTGATTAAACTGCAAAAAA NM_015888RefSeq chr1 + 59814860 59876378 HOOK1 51361 hook microtubule-tethering protein 1 GO:0005515|GO:0030897|GO:0005874|GO:0008333|GO:0007286|GO:0003779|GO:0007275|GO:0015031|GO:0045022|GO:0042802|GO:0007032|GO:0007040|GO:0070695 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140103_PI430048170 0.4685018196895320.9070932713896546.59289618260961 6.60541803090371 6.30156383925608 P P P 6.37329207526242 6.82129765988414 6.71053682998062 P P P LNCV6_140103_PI430048170 mRNA TTATTTTCTCACAGTCTGGTGAGCAGGCAATTAATTAGGAGTAAGGGGGCCTAGTAGAGC NM_001042573 RefSeq chr17 + 79074936 79088603 ENGASE 64772 endo-beta-N-acetylglucosaminidase GO:0033925|GO:0008152|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74351_PI430048170 0.4199610551404361.04356948767166 13.4422303714197 13.5519464083922 13.5621340828519 P P P 13.487070948259 13.3453774543329 13.53561476457 P P P LNCV6_74351_PI430048170 mRNA GCTTCCTAAATTCTGTGTCTGTGACTTTCGAAGTTTTTTAAACCTCTGAATTTGTACACA NM_001014446 RefSeq chr4 - 48885379 48906828 OCIAD2 132299 "OCIA domain containing 2, transcript variant 1" GO:0005743|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137220_PI430048170 0.0480190896317492 1.40969201726768 8.50001625054053 8.41929266290863 8.51309788300502 P P P 8.15030622481097 7.73587312812161 8.03096447181018 P P P LNCV6_137220_PI430048170 mRNA CACTAACGTGATAACATGGTTTTTGTAACAATAAATGTAGGATATTTCCTGGCACATGCA NM_003662RefSeq chrX - 15384800 15493588 PIR 8544 "pirin (iron-binding nuclear protein), transcript variant 1" GO:0005515|GO:0003712|GO:0006355|GO:0005737|GO:0006366|GO:0008127|GO:0030224|GO:0005634|GO:0046872|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139487_PI430048170 0.000235137821146114 0.1258381159208723.5546992903602
3.26179891999237 3.73544473325444 P P P 6.21988981674152 6.46333456260489 6.8160008911402
P P P LNCV6_139487_PI430048170 mRNA
ACAGGACTTTTAGTTGTATCACCTCAAGAGATTTTGAAGTTTGTGATCAAGGTCTGTATA NM_001164579 RefSeq
chr16 + 22008134 22084651 C16orf52 730094 chromosome 16 open reading frame 52 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_136410_PI430048170 0.0830751463320207 0.2457324569612122.70945085274379
0.6674813167503463.05627391683558 A A P 4.20741668891205 4.38079027513716
4.78788724019534 P P P LNCV6_136410_PI430048170 mRNA
GGTAATTTTTCCCAAGCCGTGGATATAATCTATTCAAACATGTTTATGCTATCCATTCTG NM_030624RefSeq chrX
- 23983715 24027186 KLHL15 80311 kelch-like family member 15 GO:0016567 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_136731_PI430048170 0.76658839427689 1.01038238413615 0.524941432770999
0.5661640696073660.437080691599705A A A 0.5398423728321260.472687915269573
0.472905009580219A A A LNCV6_136731_PI430048170 mRNA
CACAGGGAATGCACCTATTATTGCTATATAGATTGTTCCTCCTGTAATTTCACTAACTTT NM_021614RefSeq chr5
+ 114362318 114496500 KCNN2 3781 "potassium channel, calcium activated intermediate/small
conductance subfamily N alpha, member 2, transcript variant 1"
GO:0005516|GO:0030018|GO:0005886|GO:0007268|GO:0030315|GO:0042803|GO:0005790|GO:0016286|GO:0043
197|GO:0051393|GO:0043025|GO:0016021|GO:0006813|GO:0015269|GO:0071805 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127711_PI430048170 0.5041810014543251.0359547319822 0.28120899092032
0.3023859510592450.470445931876383A A A 0.3235189717180580.288551991447523
0.296399864839818A A A LNCV6_127711_PI430048170 mRNA
GGTAGCAATGAATATTCAACTGTTTGACTGCTAAGTGTATCTGTCCATATTTTAGCAAGT NM_003054RefSeq chr10
+ 117241072 117279430 SLC18A2 6571 "solute carrier family 18 (vesicular monoamine transporter),
member 2"
GO:0070083|GO:0005886|GO:0032456|GO:0016265|GO:0007268|GO:0031045|GO:0005275|GO:0042220|GO:0009
791|GO:0010043|GO:0007269|GO:0042594|GO:0043195|GO:0031072|GO:0008144|GO:0015837|GO:0043025|GO:0
007626|GO:0030672|GO:0051589|GO:0006837|GO:0051412|GO:0015222|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_118372_PI430048170 0.1895278969094130.8686692247127936.49140434838804
6.37865198441062 6.6625012113826 P P P 6.71177983831422 6.5453865572872
6.87965128848786 P P P LNCV6_118372_PI430048170 mRNA
TCCCATTTGATGTTCAGCCTGTCCCATTAAGAAGAATTTTGGCACCTGGTGAAGAAGAGA NM_022831RefSeq chr1
- 222668012 222712522 AIDA 64853 "axin interactor, dorsalization associated"
GO:0043496|GO:0005737|GO:0046329|GO:0019904|GO:0009953|GO:0005575|GO:0043508 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136507_PI430048170 0.00872757689406444 0.1963817434463580.317546176118168
0.2647661029780221.3969645681467 A A A 3.51541972328111 2.91171142478395
2.78937512347224 P P P LNCV6_136507_PI430048170 mRNA
GGGCCGTGGTAGACTCATAGTTCCTCTTGTTCTTTATTAAATTCATCCTGCTAATTAGAT NM_015163RefSeq chr14
- 50975262 51095704 TRIM9 114088 "tripartite motif containing 9, transcript variant 1"
GO:0004842|GO:0016567|GO:0030054|GO:0016874|GO:0016079|GO:0030425|GO:0042803|GO:0008021|GO:0035
544|GO:0005737|GO:0045955|GO:0000149|GO:0043161|GO:0008270|GO:0005856 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129651_PI430048170 0.3060306377029011.92437285070795 0.294228704052501
0.9535461134304952.15912166700676 A A A 0.3064034881949080.267423753891285
0.608126836342801A A A LNCV6_129651_PI430048170 mRNA

ATACTTCATGAAAGGCAGTGTATTCTGAAAAAGCCTTCAAATAAAGGTATTGCAACACGA NM_175619 RefSeq chr4 + 48490251 48494389 ZAR1 326340 zygote arrest 1 GO:0005737|GO:0007275 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143750_PI430048170 0.2589018590368250 0.8842034010886574 .74540228410106 4.44437210661145 4.37506805320558 P P P 4.57030930254132 4.82371870950541 4.7197139012609 P P P LNCV6_143750_PI430048170 mRNA
TCCTGTGCTGCAGCCCCCCAAATATATTTTTCTGATATAGACCTTGTATATGGCTTTAAT NM_181900 RefSeq chr15 - 81312665 81324183 STARD5 80765 StAR-related lipid transfer (START) domain containing 5 GO:0032052|GO:0006869|GO:0006700|GO:0044281|GO:0008202|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83615_PI430048170 0.0521910098373552 1.36803856383158 7.61993492468553 7.19692370041528 7.42927477613528 P P P 6.75499020147443 7.11745159504399 7.0241979496213 P P P LNCV6_83615_PI430048170 mRNA
AGTGGAACTTCAAAGGAATGAGTGGGATCCAATCATCGAATGGGCTGAGAAAAGATACGG NM_145691 RefSeq chr17 - 18018019 18039166 ATPAF2 91647 ATP synthase mitochondrial F1 complex assembly factor 2 GO:0005739|GO:0005515|GO:0016607|GO:0043461 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131982_PI430048170 0.2649276660369250 .8605010947335298 .76873587371033 8.7456920810013 9.15224486549294 P P P 9.01388749625912 8.99339212145518 9.3226725062651 P P P LNCV6_131982_PI430048170 mRNA
GAAAGCAGCACACATTGTGTTAACTTATGTCTCTTGTTAAATGAGCTTAATGTCTTTGTG NM_006178 RefSeq chr17_KI270908v1_alt + 1110345 1276874 NSF 4905 "N-ethylmaleimide-sensitive factor, transcript variant 1"
GO:0005515|GO:0006200|GO:0005886|GO:0042623|GO:0043001|GO:0007268|GO:0006887|GO:0005765|GO:0032403|GO:0046872|GO:0005829|GO:0048211|GO:0005737|GO:0043198|GO:0017157|GO:0001921|GO:0017075|GO:0016192|GO:0006813|GO:0016887|GO:0070062|GO:0017137|GO:0005795|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133434_PI430048170 0.5907843341995581 .13861037974303 0.24726998064726 0.3346177375586040 .987854909903007 A A A 0.4616022464444860 .356128068232565 0.304203584560873 A A A LNCV6_133434_PI430048170 mRNA
TTCTATTACCTGTACAGTATGGTTTATACGTTGGTGAGTTTCTAAGGGGGAAGCCGGCCA NM_182553 RefSeq chr11 + 66278200 66284214 CNIH2 254263 "cornichon family AMPA receptor auxiliary protein 2, transcript variant 1"
GO:0005515|GO:0030054|GO:2000311|GO:0035249|GO:0014069|GO:0030425|GO:0035556|GO:0043197|GO:0043198|GO:0045211|GO:0032281|GO:0042391|GO:0005789|GO:0051668 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133188_PI430048170 0.3706164154589011 .07976037468592 12.7542730640536 12.9953626167376 12.8852621777877 P P P 12.6335477988506 12.9285795349044 12.7349857081965 P P P LNCV6_133188_PI430048170 mRNA
GTCACCATTGGACAGTCTCCCTGATGGACCCTCAGTCTTCTCATGAATAAATTCCTTCAA NM_005380 RefSeq chr1 + 19644172 19658456 NBL1 4681 "neuroblastoma 1, DAN family BMP antagonist, transcript variant 2"
GO:0030514|GO:0016015|GO:0038098|GO:0045666|GO:0036122|GO:0035582|GO:0048812|GO:0048263|GO:0090027|GO:0005615|GO:0042803|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145286_PI430048170 0.00107430782925998 0.1910100600078511 .77474482776384 1.22403903903329 1.32458136659589 A A A 3.41497758110618 3.94408146087768 4.10419378119613 P P P LNCV6_145286_PI430048170 mRNA
CTGCTACTTTGCTAATCTCATTAGCTTAGCTGTGTTTGTGCATAGGTTATATTTGGTAAT NM_032116 RefSeq chr13 - 30202629 30307487 KATNAL1 84056 "katanin p60 subunit A-like 1, transcript variant 1"
GO:0008568|GO:0008017|GO:0051013|GO:0005737|GO:0008152|GO:0005874|GO:0031122|GO:0005634|GO:0007283|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_144254_PI430048170 0.0810198261308884 1.04114384833726 0.450147753332821
0.4539970370573660.407723008948573A A A 0.3409827398224460.390195697053879
0.405845269872089A A A LNCV6_144254_PI430048170 mRNA
CCTTCACTGTTGATACAAAGAAATCATACTGTTCAGGCTTTTTTGTACTTTAGTGTCACTNM_138800RefSeq chr2 +
95592017 95599721 TRIM43 129868 tripartite motif containing 43 GO:0005622|GO:0008270 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_127637_PI430048170 0.7177921731547370.9856506162762710.303516125116897
0.3215340121994130.389691803208511A A A 0.3230015414446450.307036690417621
0.444729960331939A A A LNCV6_127637_PI430048170 mRNA
CACCCCAAATTTTGCTGAGGTTTTCTTAATGTTGTAGAGCATTTTGTAGAGTGGTTTAAA NM_152431RefSeq chr11
+ 94567307 94621421 PIWIL4 143689 piwi-like RNA-mediated gene silencing 4
GO:0010467|GO:0051321|GO:0005634|GO:0007275|GO:0007283|GO:0031047|GO:0034584|GO:0006417|GO:0030
154|GO:0005737|GO:0034587|GO:0043186|GO:0071547|GO:0043046 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142689_PI430048170 0.8161394936353190.9812013816315697.57538166996354
7.31332144373745 7.51002446938957 P P P 7.44280322701213 7.39253395390923
7.64561748642533 P P P LNCV6_142689_PI430048170 mRNA
CCTCAGTATTGTTTTAGCCACTCTACTCCAAATGGATAAAATGAGACTCTGATTGAGGAA NM_207343RefSeq chr11
+ 117232624 117285688 RNF214 257160 "ring finger protein 214, transcript variant 2" GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80688_PI430048170 0.2712084521627851.16600743238467 7.25361745466403 7.47907693032569
7.73885349990347 P P P 7.27623904068047 7.16645452197037 7.39592122990158 P P P
LNCV6_80688_PI430048170 mRNA
AATAGAAACTGGGAGAAGCACAGGAAGGCTGACAGACATCGTGAAGTGGATGAGGATTTT NM_001289121
RefSeq chr9 + 37120597 37358148 ZCCHC7 84186 "zinc finger, CCHC domain containing 7,
transcript variant 1" GO:0005737|GO:0005730|GO:0008270|GO:0005634 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_134052_PI430048170 0.0529647011161418 0.3730292775783280.320831903564329
0.3250184210069520.343262967496245A A A 1.14912005436073 2.26637363350424
1.62222038278751 A A A LNCV6_134052_PI430048170 mRNA
GGTGGTTAATTTTTAGCATAGATGTCAGAAAGCCTGTTAATATTCCAGAGGCTTATGATA NM_001254752 RefSeq
chr8 - 96226675 96235634 UQCRB 7381 "ubiquinol-cytochrome c reductase binding protein,
transcript variant 3"
GO:0022904|GO:0009060|GO:0005746|GO:0006122|GO:0005743|GO:0005750|GO:0044281|GO:0044237|GO:0055
114|GO:0006119 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141544_PI430048170 0.0729343810417043 1.03908271519571 0.442177746715894
0.4933154827831840.454299973664158A A A 0.3790096369983690.407453913013616
0.437305341174964A A A LNCV6_141544_PI430048170 mRNA
ATGAGAAGCTGTGCCAGAGGCTCACACAGCGCTATGTGAGCGTCATGAACAGGCTGCAGA NM_198572RefSeq
chr8 + 144012413 144047114 SPATC1 NA "spermatogenesis and centriole associated 1, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134351_PI430048170 0.2698081961211751.19446458476504 12.4406839320128
12.0627590991327 11.9169766641917 P P P 12.0523143908536 11.9359647696453
11.6916488046738 P P P LNCV6_134351_PI430048170 mRNA
GCTGAGGCTTAGAGCTTGGAACAAGGGGGAATAAACCCAGAAAATACAGTTAAACAAAAA NM_002801RefSeq
chr16 - 67934503 67936877 PSMB10 5699 "proteasome (prosome, macropain) subunit, beta type,
10"
GO:0002474|GO:0010467|GO:0090263|GO:0044281|GO:0031145|GO:0005829|GO:0004298|GO:0034641|GO:0000
082|GO:0042098|GO:0006959|GO:0016032|GO:0090090|GO:0006977|GO:0000209|GO:0005839|GO:0000502|GO:0

043066|GO:0006521|GO:0051437|GO:0042590|GO:0006915|GO:0042981|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141126_PI430048170 0.5134029166184170.4744350741538323.13361254081222
2.48327560850312 2.7640400404034 P A A 1.73437124485365 4.33723653723198
4.39654598766372 A P P LNCV6_141126_PI430048170 mRNA
CCCATATACTCTGCTACAGCTCCTATCATGAAAAATAAAATGTTTGTCTTTGCAAAACAG NM_032865RefSeq chr17
- 40475827 40501602 TNS4 84951 tensin 4
GO:0005515|GO:0005737|GO:0008104|GO:0006915|GO:0003779|GO:0005856|GO:0005925 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143865_PI430048170 0.0181395799315404 0.3731119477426053.81060916360286
3.61136500199691 3.82543067539696 P P P 4.69431758058573 5.31585360076875
5.41401428827378 P P P LNCV6_143865_PI430048170 mRNA
CCAAGGTGAGCTAGAGAGAAAGATGTTTGGCATGCCAAATTAACTTGCATGTTTGTTAAA NM_001040100 RefSeq
chr3 - 161344791 161372083 SPTSSB 165679 "serine palmitoyltransferase, small subunit B"
GO:0005515|GO:0004758|GO:0030148|GO:0005789|GO:0016021|GO:0017059 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144327_PI430048170 0.0092325554000247 0.2777664713475422.72971470429177
2.47326657321479 1.84167522631119 A A A 3.62553704377158 4.55386630005999
4.38857542139541 P P P LNCV6_144327_PI430048170 mRNA
ATTTTTTCCTGTCTGCTATAATGGAGACTATATTTCTGCATTCATTACCTCTCATAGGTG NM_001300954 RefSeq chr11
+ 76860872 77026797 ACER3 55331 "alkaline ceramidase 3, transcript variant 3"
GO:0070774|GO:0006665|GO:0030173|GO:0008284|GO:0030148|GO:0006672|GO:0071602|GO:0005789|GO:0030
176|GO:0044281|GO:0046512 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129285_PI430048170 0.0238474306710177 1.37460460747517 10.2609896482707
10.4433975485836 10.5528536648668 P P P 9.77463740242204 10.0000679299885
10.1013159805345 P P P LNCV6_129285_PI430048170 mRNA
TCAGCTCTCATTCCAGTTTTTTCTAACATGAATTTTCCTGGTTGACATTGATTTCAAAGG NM_003096RefSeq chr2 -
70281373 70293737 SNRPG 6637 small nuclear ribonucleoprotein polypeptide G
GO:0008380|GO:0005515|GO:0010467|GO:0000245|GO:0006369|GO:0008334|GO:0006366|GO:0031124|GO:0034
660|GO:0071013|GO:0000387|GO:0034709|GO:0005829|GO:0000398|GO:0030532|GO:0005683|GO:0005654|GO:0
005681|GO:0005687|GO:0034719|GO:0005685|GO:0005689 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_141543_PI430048170 0.1492849486923361.03687906664833 0.341396331920633
0.3585715991425640.281655742509215A A A 0.2697037739166680.28679909710175
0.269434072163843A A A LNCV6_141543_PI430048170 mRNA
TTGACTCTGTAATGGATTTATGTAGCCCACTTCAGTCTGCAAATAAAGCAAAGTAACTGG NM_001177676 RefSeq
chr14 - 91232531 91244508 GPR68 8111 "G protein-coupled receptor 68, transcript variant 1"
GO:0006954|GO:0045656|GO:0007186|GO:0005886|GO:2001206|GO:0035774|GO:0005887|GO:0004930|GO:0071
467 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138611_PI430048170 0.46176982706712 0.9739314417075180.251942333337308
0.2639367297211470.381199558994582A A A 0.37986296189059 0.319606537866198
0.31458089276055 A A A LNCV6_138611_PI430048170 mRNA
TAACCTGAACTGATGGGTTTCTCCAGAGGGAATTGCAGAGTACTGGCTGATGGAGTAAAT NM_005508RefSeq chr3
+ 32951573 32954911 CCR4 1233 chemokine (C-C motif) receptor 4
GO:0009314|GO:0070098|GO:0005886|GO:0002507|GO:0007204|GO:0050927|GO:0009617|GO:0006955|GO:0006
954|GO:0006935|GO:0007186|GO:0005887|GO:0043025|GO:0004950|GO:0016493|GO:0001764|GO:0046677|GO:0
009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127942_PI430048170 0.0607207914783711 0.7073338139097557.24970194908475
7.5856215816349 7.77446466797799 P P P 8.00446487495906 7.95007905091612

8.19070991416847 P P P LNCV6_127942_PI430048170 mRNA
AGCACAGATTTCTATGCACCTTTACTCTTTCCTCAACCCTTGTCTCTATCTGTACATAAT NM_016027 RefSeq chr8 -
70637265 70669212 LACTB2 51110 "lactamase, beta 2" GO:0005739|GO:0016787|GO:0008152|GO:0046872
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61973_PI430048170 0.0839831864802530.7225876016760437.3712295141973 7.21570674363972
7.66302955289903 P P P 7.57629462039662 8.01233559849605 8.0567519521694 P P P
LNCV6_61973_PI430048170 mRNA
CGAAGATTGGGAGAACCCTCAGCTCTGCAGTGACTACGTTAAGGATATCTATCAGTATCT NM_004701 RefSeq chr15
+ 59105084 59125045 CCNB2 9133 cyclin B2
GO:0005515|GO:0007077|GO:0005813|GO:0019901|GO:0048538|GO:0000079|GO:0001701|GO:0005829|GO:0007
067|GO:0016020|GO:0000086|GO:0015630|GO:0051726|GO:0005654|GO:0043029|GO:0000278|GO:0040007|GO:0
051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137245_PI430048170 0.3825997451181771.31083108338069 0.382179171332921
0.39230972838469 1.27132118548924 A A A 0.3456722646733130.333784076231207
0.385064403411704 A A A LNCV6_137245_PI430048170 mRNA
CCCTCCACATAGAGGGAATCAATCGACTTTTGTATACTGATTTTTGAATTTGCTTCTTTANM_001004328 RefSeq chr12
+ 8172553 8180046 ZNF705A NA zinc finger protein 705A NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144358_PI430048170 0.4191354946312951.33537412332442 0.290706486277502
0.2872384267839391.28736915735442 A A A 0.3014871714417650.271126189171142
0.285121721815563 A A A LNCV6_144358_PI430048170 mRNA
CCGAGTCCAATAGTCAATTTATTCTAAGCGAACATTCATCTCCACACTTTCCTGTCTCAA NM_014358 RefSeq chr12
- 8533304 8540962 CLEC4E 26253 "C-type lectin domain family 4, member E"
GO:0006955|GO:0030246|GO:0004872|GO:0050715|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138426_PI430048170 0.1161076626002430.7289113104288314.97804625663127
4.59601587668276 4.92909330555449 P P P 5.07752195283064 5.1255462043756
5.63042658635334 P P P LNCV6_138426_PI430048170 mRNA
TGCCACACTTGGGTACTGAAAAATCAATAAAACGAAAGTTCATCATCCCATGGCCCGTAG NM_004901 RefSeq chr8
- 23429151 23457731 ENTPD49583 "ectonucleoside triphosphate diphosphohydrolase 4, transcript
variant 1" GO:0030173|GO:0045134|GO:0000421|GO:0031410|GO:0006256|GO:0043231 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_141943_PI430048170 0.13021164769785 1.75699753935744 4.65605735531211
5.67758782602115 5.36798970517333 P P P 4.50285725731778 4.47564697474051
4.46364022016498 P P P LNCV6_141943_PI430048170 mRNA
AAGCTATTTTGAAGTATTCAAGCAGAGGAATTCCCTAACACTGACCCCCTTGTCTTTTTT NM_001077416 RefSeq
chr16 - 75538116 75556286 TMEM231 79583 "transmembrane protein 231, transcript variant 1"
GO:0042384|GO:0060170|GO:0035869|GO:0036038|GO:0016021|GO:0007224 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139404_PI430048170 0.4658494285047131.10979114884884 10.303962823672 10.567221393772
10.7854378912795 P P P 10.2041787511976 10.4091617840216 10.6046787760748 P P P
LNCV6_139404_PI430048170 mRNA
TCACTGGCTTCTGTGTCCCAAGACTAGGTTGTGTACAGTTTAATTATGGAACATTAAATA NM_000127 RefSeq chr8
- 117799364 118111819 EXT1 2131 exostosin glycosyltransferase 1
GO:0007369|GO:0005783|GO:0030176|GO:0044281|GO:0015012|GO:0015014|GO:0046872|GO:0042803|GO:0021
772|GO:0007411|GO:0033692|GO:0030203|GO:0008375|GO:0050508|GO:0050509|GO:0005794|GO:0072498|GO:0
046982|GO:0005975|GO:0016757|GO:0015020|GO:0006024|GO:0007165|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133600_PI430048170 0.3561351814214921.6683308008763 0.569661373069117

1.98635868781049 0.535481513033854 A A A 0.400224765196126 0.486944465183797
0.498006056732222 A A A LNCV6_133600_PI430048170 mRNA
CTGGTAACATCGTTGCAACCACTGCAATATCTTCGTTAGTAATCTGTATAATACTTTGTA NM_001160258 RefSeq
chr6 - 88139865 88166048 CNR1 1268 "cannabinoid receptor 1 (brain), transcript variant 4"
GO:0002866|GO:0030424|GO:0060405|GO:0005886|GO:0031999|GO:0045471|GO:0045776|GO:0007283|GO:0045
777|GO:0042220|GO:0045759|GO:0033004|GO:0043231|GO:0004949|GO:0030426|GO:0031622|GO:0007413|GO:0
008144|GO:0032496|GO:0007613|GO:0051966|GO:0060259|GO:0043065|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127396_PI430048170 0.460424511621297 1.33706882993041 0.334543153180462
0.451489665229672 1.46753329941034 A A A 0.528976983348977 0.449498955518699
0.293562742440259 A A A LNCV6_127396_PI430048170 mRNA
ATTGGAGTGGACTTTACCGTGCGTTCCCTTGATATTGACGGCAAAAAAGTGAAGATGCAG NM_001008749 RefSeq
chr7 + 140404042 140426250 RAB19 NA "RAB19, member RAS oncogene family" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137544_PI430048170 0.101389519077383 1.54083213841895 4.97538034633338 5.4620057882945
5.65513645786128 P P P 4.33479123643198 4.79945605131987 5.07476551418921 P P P
LNCV6_137544_PI430048170 mRNA
AGAGCCTAGTTTTTAATAGCTATGGAATCAATTCAATTTGGACTGGTGTGCTCTCTTTAA NM_000576 RefSeq chr2
- 112829759 112836779 IL1B 3553 "interleukin 1, beta"
GO:0032755|GO:0019221|GO:0046330|GO:0002711|GO:0005615|GO:0032757|GO:0035234|GO:0031622|GO:0009
743|GO:0030730|GO:0000165|GO:0001660|GO:0033198|GO:0034116|GO:0043123|GO:0031663|GO:0043122|GO:0
032729|GO:0045410|GO:0032725|GO:0007566|GO:0019904|GO:0030593|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135353_PI430048170 0.422285047994406 0.904045701503847 4.79136930184596 4.4008581513936
4.556715514443 P P P 4.50889880406683 4.90595999768378 4.76987591837758 P P P
LNCV6_135353_PI430048170 mRNA
GGGTCAAATATCTTTAAATAAAGTGCCAGGAACAATAAATACTGTACAGGAAGAGAGTGC NM_018111 RefSeq chr19
- 49118396 49119140 C19orf73 55150 chromosome 19 open reading frame 73 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137575_PI430048170 0.190201808425353 1.02878294553608 0.364747225921294
0.29961162586064 0.363186125560461 A A A 0.292077227997969 0.290030548232803
0.323331808070055 A A A LNCV6_137575_PI430048170 mRNA
ACCTGTTACTGAAAGTGGTTTGAAAGTGAATAAACTTCAGCACCATGGACAGAAGACAAA NM_006172 RefSeq chr1
- 11845709 11847783 NPPA 4878 natriuretic peptide A
GO:0010467|GO:0030308|GO:0048471|GO:0006367|GO:0005634|GO:0051428|GO:0005615|GO:0042629|GO:0050
880|GO:0060372|GO:0007218|GO:0060452|GO:0014898|GO:0005184|GO:0003085|GO:0001666|GO:0032868|GO:0
007565|GO:0005102|GO:0005576|GO:0035994|GO:0006182|GO:0008217|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131827_PI430048170 0.267382382596682 0.926589226125301 0.324531674614653
0.336308070594183 0.3460442976491 A A A 0.329763446341846 0.425853852432073
0.571061905619191 A A A LNCV6_131827_PI430048170 mRNA
GAGTGGAACGTTAAAGTTTATTACCTTCATGTTAAGGAATATCCAGCTTCACAGACAATT NM_001378 RefSeq chr2
+ 171687408 171750158 DYNC1I2 1781 "dynein, cytoplasmic 1, intermediate chain 2, transcript variant
1"
GO:0005813|GO:0006996|GO:0005874|GO:0003777|GO:0031982|GO:0005829|GO:0019886|GO:0005737|GO:0000
086|GO:0008152|GO:0006810|GO:0016032|GO:0005868|GO:0000278|GO:0007018 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134423_PI430048170 0.0774489004556921 1.02643525043307 0.397611502340588
0.408181598069974 0.428097177604756 A A A 0.367004007777818 0.355929775799779

0.397866836889215 A A A LNCV6_134423_PI430048170 mRNA
GGACAGGCTAGTTCTTTCAGACTGTGAAATTAATGAATGAGCAAAATATAGAGTCAAATG NM_181621 RefSeq chr21
- 30371390 30372239 KRTAP13-2 337959 keratin associated protein 13-2 GO:0005882 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139317_PI430048170 0.6964647205806650.9467494048051314.08124658675773
3.29911944487949 4.13939786603864 P P P 4.07210651525186 3.85431920293268
3.96410778415631 P P P LNCV6_139317_PI430048170 mRNA
GTCCCTGTTCATACCATCTCTGCACCCACAATCACACTGATTTTTCAAATTCATTTTGTT NM_001081573 RefSeq chrX
- 154675249 154751083 GAB3 139716 "GRB2-associated binding protein 3, transcript variant 1"
GO:0030225 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139709_PI430048170 0.00822647145789716 1.27242117158792 12.1296890398158
12.0636694930893 12.2397227758601 P P P 11.8670767637128 11.7015071833409
11.8222358759788 P P P LNCV6_139709_PI430048170 mRNA
GCTCTAGGGATTGTCTACTCCAGGGATTTTCTTCAAAATTTTTAAACATGGGAAGTTCAA NM_052935 RefSeq chr17
- 41825081 41836271 NT5C3B 115024 "5'-nucleotidase, cytosolic IIIB, transcript variant 1"
GO:0005515|GO:0005737|GO:0000287|GO:0000166|GO:0016311|GO:0008253|GO:0009117 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129676_PI430048170 0.1944248256154830.5796693222059980.524183059370145
0.5663378291021460.486362901206081 A A A 0.5879872240112 1.84618298029803
1.23482859270483 A A A LNCV6_129676_PI430048170 mRNA
GGTGGTGAATAACCTCTATCCCTAATCAAATGAATCTGACAAGAAACTTTCCAATAAATG NM_003709 RefSeq chr2
- 207074137 207166016 KLF7 8609 "Kruppel-like factor 7 (ubiquitous), transcript variant 1"
GO:0048813|GO:0003700|GO:0006357|GO:0007411|GO:0003713|GO:0008270|GO:0005634|GO:0045893|GO:0003
677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139119_PI430048170 0.7822060161191530.83924407628561 0.415175450396446
1.15601340040151 0.455524060079325 A A A 0.3347966557013930.440676562924104
1.70471559026176 A A A LNCV6_139119_PI430048170 mRNA
GAAAAAAGATACGACTCTCAGAAGCCTGTTTAAGGAAGCCCTAAAATGTGGACTGGGTTT NM_019849 RefSeq chr19
- 33208663 33225850 SLC7A10 56301 "solute carrier family 7 (neutral amino acid transporter light
chain, asc system), member 10"
GO:0005886|GO:0006865|GO:0050900|GO:0055085|GO:0003333|GO:0015804|GO:0015194|GO:0016020|GO:0042
942|GO:0005887|GO:0007596|GO:0042941|GO:0015825|GO:0015175|GO:0006811 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133291_PI430048170 0.29250800217699 1.05008390652267 0.327921395161398
0.3173179047367670.469323719126949 A A A 0.3033274101782020.277532770878047
0.326814144927719 A A A LNCV6_133291_PI430048170 mRNA
CATACTCATTTTCCCTGTATATAAAAAGTTTCTCTAATGTGATAAATAAAAACACAATAA NM_001127380 RefSeq
chr11 - 18238232 18248674 SAA2 6289 "serum amyloid A2, transcript variant 2"
GO:0034364|GO:0006953|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128411_PI430048170 0.3703113187991451.12770427824113 6.79171055277676
6.60081298150044 6.71107135107995 P P P 6.59904279838683 6.74249558479335
6.19380823733835 P P P LNCV6_128411_PI430048170 mRNA
GCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAGTGAACTGATCCCTTTG NM_144683 RefSeq
chr17 - 28897780 28903071 DHRS13 147015 dehydrogenase/reductase (SDR family) member 13
GO:0016020|GO:0016491|GO:0005576|GO:0055114 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142702_PI430048170 0.302383194498854 1.44055162297553 0.814345608433963
1.80540940753975 0.824257746009787 A A A 0.632114630110632 0.620044418324307
0.839504408540536 A A A LNCV6_142702_PI430048170 mRNA

CATCTCCTTTGTGTGAATTCATATATTATAGCAAAATACAAGAGACATGGGACTGTTTGC NM_025009 RefSeq
chr4 + 55948807 56033363 CEP135 9662 centrosomal protein 135kDa
GO:0005515|GO:0010457|GO:0005813|GO:0006996|GO:0007099|GO:0005814|GO:0000086|GO:0008022|GO:0000
278|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130351_PI430048170 0.0695489138409144 0.585733516298993 5.64475797699458
5.58833411362079 5.95784489144534 P P P 6.01966544635113 6.58340189321468
6.81890604187377 P P P LNCV6_130351_PI430048170 mRNA
GCACCACTGATCTTGGATGTACATTTATGTATACTTTGAGAAAAAGGGTTTTAGGTTGAT NM_024675 RefSeq
chr16 - 23603161 23641357 PALB2 79728 partner and localizer of BRCA2
GO:0005515|GO:0043066|GO:0006281|GO:0000724|GO:0001756|GO:0001833|GO:0009887|GO:0007498|GO:0005
654|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136400_PI430048170 0.0241273044225899 1.31569377425042 13.0516396341757
13.0545833760083 12.9492729514321 P P P 12.7777355170759 12.5587830556001
12.5204048957448 P P P LNCV6_136400_PI430048170 mRNA
GTCTGGCTGCAAAGACTATTTTTATCCTGCAACTCTTGATAAAGGGCTGTTTTGCCATGG NM_032902 RefSeq chr8
+ 144496725 144502121 PPP1R16A 84988 "protein phosphatase 1, regulatory subunit 16A"
GO:0005515|GO:0005886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66369_PI430048170 0.383294168003691 0.852481294550305 0.395646159363911 0.4960187947839
0.39519261794523 A A A 0.513813947185679 1.00066625101992 0.391214507496094 A A A
LNCV6_66369_PI430048170 mRNA
ACTCTTCTATGAGGAACGAACGTGATGGTTAAGCTACCTTCATTAAGCAGCATGACCGCT NM_033514 RefSeq chr2
- 110465050 110473075 LIMS3 96626 "LIM and senescent cell antigen-like domains 3, transcript variant 1"
GO:0005737|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_84885_PI430048170 0.512639404191177 1.17240687718557 0.341892011689192 1.13486699539065
0.672506206062533 A A A 0.274580216890625 0.919506114722814 0.277918203315508 A A A
LNCV6_84885_PI430048170 mRNA
CGGACCCAAGAATGTAAATAATATTCATAAACCTATGGGAGACTCGTGTGACTATTTTTT NM_022436 RefSeq chr2
- 43812471 43838819 ABCG5 64240 "ATP-binding cassette, sub-family G (WHITE), member 5"
GO:0042632|GO:0005515|GO:0007588|GO:0033344|GO:0046982|GO:0005886|GO:0007584|GO:0042493|GO:0017
127|GO:0044281|GO:0055085|GO:0045796|GO:0005524|GO:0043235|GO:0030299|GO:0016324|GO:0010212|GO:0
010949|GO:0015918|GO:0043190|GO:0016887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139027_PI430048170 0.517166862659906 1.02816332095276 0.284243651923568
0.310333178595117 0.44259287282313 A A A 0.328052953868621 0.298030841371776
0.295696648346752 A A A LNCV6_139027_PI430048170 mRNA
CAAAGTGGCAGCCAGTTGGTTTTGATAGGTTGCCTTTTGGAGATTTCTATTACTGCCTTT NM_004316 RefSeq chr12
+ 102957673 102960516 ASCL1 429 achaete-scute family bHLH transcription factor 1
GO:0010468|GO:0005515|GO:0060579|GO:0003700|GO:0061104|GO:0061103|GO:0061102|GO:0061100|GO:0000
989|GO:0042803|GO:0007405|GO:0071259|GO:0003690|GO:0043525|GO:0007219|GO:0050883|GO:0043025|GO:0
021892|GO:0045747|GO:2000179|GO:0070888|GO:0000122|GO:0000978|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129769_PI430048170 0.375567614964561 2.10800180072366 0.541722151059373
0.506399508610501 2.50896235941738 A A A 0.381971972723366 0.452359622380466 0.4784686501891
A A A LNCV6_129769_PI430048170 mRNA
CAGTGCTCCTGTAAGTCAAATGTGTGCTTTGTACTGCTGTTGTTGAAATTGATGTTACTG NM_005623 RefSeq chr17
+ 34319046 34321402 CCL8 6355 chemokine (C-C motif) ligand 8
GO:0008009|GO:0006874|GO:0007267|GO:0043085|GO:0009615|GO:0006887|GO:0005615|GO:0007165|GO:0006
955|GO:0016004|GO:0004672|GO:0006954|GO:0006935|GO:0060326|GO:0006468|GO:0006816|GO:0008201 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129203_PI430048170 0.0643890905736014 1.29022580803868 5.02709977834363

4.72962572812093 5.0949776395835 P P P 4.54563493379873 4.51649396914567 4.7050311794906
P P P LNCV6_129203_PI430048170 mRNA
CATTGCATTTATTTACATAGTGTCATTCCAAATCCATGCATGCTGTTGATTTTCCTGAGANM_015669RefSeq chr5 +
141135205 141138127 PCDHB5 26167 protocadherin beta 5
GO:0016339|GO:0005886|GO:0005509|GO:0007268|GO:0016021|GO:0007416|GO:0007156 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_101832_PI430048170 0.0601653105877556 1.49041974324928 1.96965084586859
1.53814577668241 2.02291957165108 A A A 0.9522124047217961.36695832873095
1.47985673157499 A A A LNCV6_101832_PI430048170 mRNA
GAAGTTTTTGAGCCTTACTGAAGAAGATCTGAATAAATTTGAGTCTCTTACCATGGGGGC NM_015144RefSeq chr16
- 87406245 87491854 ZCCHC14 23174 "zinc finger, CCHC domain containing 14"
GO:0008270|GO:0035091|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59046_PI430048170 0.0188784337358588 1.26149795667275 15.4376300656465
15.6382727549472 15.6204347281355 P P P 15.2316443301988 15.1739612104822
15.2913510129397 P P P LNCV6_59046_PI430048170 mRNA
GGTAGCCTTTCTCATCCTCTTTGCCATGTGAAGGAGCCGTCTCCACCTCCCATAGTTCTC NM_001002031 RefSeq
chr12 - 53665159 53676728 ATP5G2517 "ATP synthase, H+ transporting, mitochondrial Fo complex,
subunit C2 (subunit 9), transcript variant 1"
GO:0005215|GO:0015078|GO:0045471|GO:0005741|GO:0044281|GO:0005753|GO:0008289|GO:0022904|GO:0042
776|GO:0015991|GO:0016021|GO:0044237|GO:0045263 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138708_PI430048170 0.7178887900750520.9798025905646520.537809927908071
0.4664447542987590.288566568957675A A A 0.4003517516202470.510994822473277
0.47883499051393 A A A LNCV6_138708_PI430048170 mRNA
AGCTCCGTTTTCTATTTCTTGGGAATGCTTTATTGTGGAAACTGCTTCAGATACTTAAATNM_002976RefSeq chr2 -
166403572 166486971 SCN7A 6332 "sodium channel, voltage gated, type VII alpha subunit, transcript
variant 1"
GO:0006936|GO:0086010|GO:0005886|GO:0005248|GO:0035725|GO:0034765|GO:0001518|GO:0055078|GO:0006
814|GO:0019228 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133152_PI430048170 0.00200419668068251 0.62029055480341714.3366067434873
14.2836489624904 14.2169696202195 P P P 14.8803808570599 15.0875386702526
14.9305641039812 P P P LNCV6_133152_PI430048170 mRNA
CAACAGGATTGATCATTCTTTTATAGAGCATATTTGCCAATAAAGCTTTTGGAAGCCGGA NM_001018137 RefSeq
chr17 + 51165434 51171744 NME2 4831 "NME/NM23 nucleoside diphosphate kinase 2, transcript
variant 2"
GO:0005515|GO:0003700|GO:0006220|GO:0002762|GO:0009142|GO:0014075|GO:0051591|GO:0071398|GO:0045
618|GO:0003697|GO:0018106|GO:0070062|GO:0050679|GO:0005813|GO:0000977|GO:0015949|GO:0019901|GO:0
019215|GO:0030027|GO:0006228|GO:0006183|GO:0007229|GO:0010976|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_67421_PI430048170 0.0241861074677013 0.3962348560125685.4687233007233
4.53681415629174 5.03777527795942 P P P 6.2675735940364 6.30649876209136
6.60075315319179 P P P LNCV6_67421_PI430048170 mRNA
AGGGCAGCTCCACACCATTTCATGTATTTTTAAACCCAACTCCTAGCACTGAAGATGTTA NM_001142640 RefSeq
chr17 + 78004236 78108835 TNRC6C57690 "trinucleotide repeat containing 6C, transcript variant 1"
GO:0005515|GO:0010467|GO:0048011|GO:0001706|GO:0048015|GO:0003723|GO:0060213|GO:0016441|GO:0005
829|GO:0060964|GO:0035278|GO:0000166|GO:0007173|GO:0007219|GO:1900153|GO:0008543|GO:0045087|GO:0
035195|GO:0035162|GO:0038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131176_PI430048170 0.1077094237460550.4852189707831178.36401760003967
8.12694636421858 8.13630880969748 P P P 8.46875802305325 9.43995042848788 9.6187169842368
P P P LNCV6_131176_PI430048170 mRNA

GATTTCCCATGCCATAATTTTTCTGTCTATTAAATGGGACAAGTGTAAAGCATGCAAAAG NM_000782RefSeq chr20 - 54153448 54173977 CYP24A1 1591 "cytochrome P450, family 24, subfamily A, polypeptide 1, transcript variant 1" GO:0006805|GO:0005506|GO:0030342|GO:0042359|GO:0042369|GO:0005743|GO:0033280|GO:0044281|GO:0001649|GO:0070561|GO:0006766|GO:0016491|GO:0008202|GO:0008403|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70927_PI430048170 0.2529280868155910.8091446104794784.5758656409349 4.66800553483985 5.03913641941422 P P P 4.7723738752503 5.04077052097911 5.36743606933853 P P P LNCV6_70927_PI430048170 mRNA
AGCAACAGCATGTTTTGGATTTCCCAAATCTTTTCTCAGTGGTCTTTATGAATTCCCTCT NM_015939RefSeq chr20 - 5937832 5950558 TRMT6 51605 "tRNA methyltransferase 6, transcript variant 1" GO:0006446|GO:0003743|GO:0005634|GO:0008033|GO:0006413 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133774_PI430048170 0.0121176282667923 0.6428188081887269.83015851641891 9.60685340572606 9.44586868793332 P P P 10.151488583716 10.2111825881419 10.4421234555226 P P P LNCV6_133774_PI430048170 mRNA
TCTGGGGAAATCCGCCTCAGCTCATTCCCAATAAATTAATACTCTTGATAGCTTAAAAAA NM_032271RefSeq chr16 + 2155797 2178129 TRAF7 84231 "TNF receptor-associated factor 7, E3 ubiquitin protein ligase" GO:0005515|GO:0048471|GO:0004842|GO:0016567|GO:0005886|GO:0016874|GO:2001235|GO:0000151|GO:0006915|GO:0005634|GO:0000122|GO:0006351|GO:0043231|GO:0005829|GO:0032880|GO:0000185|GO:0033235|GO:0071354|GO:0016023|GO:0008270|GO:0043410 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140808_PI430048170 0.4854047237541490.9599983495966731 0.9798762498603 11.1956495432237 10.9730342150763 P P P 11.0789839092631 11.1202038511143 11.1367378281074 P P P LNCV6_140808_PI430048170 mRNA
CCCGCACGCGCTCATCTTTCTTCGTTTTTTGATCAGTTTATTCAGAATTGCTCTATAATT NM_194458RefSeq chr1 - 1253911 1273854 UBE2J2 118424 "ubiquitin-conjugating enzyme E2, J2, transcript variant 3" GO:0006986|GO:0000209|GO:0019787|GO:0005783|GO:0016874|GO:0005789|GO:0016021|GO:0030433|GO:0005524|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134860_PI430048170 0.2561344189430140.8572659433623310.29881033789791 0.2983117241206090.298741199727938A A A 0.7732929453018540.397189069926373 0.354073937209648A A A LNCV6_134860_PI430048170 mRNA
GCCCCATATAATGAAGTCTCAGGGTATATGAAAGTAGCTGGCTTCAAAATAAAATTTTTG NM_152852RefSeq chr11 - 60171606 60184666 MS4A6A 64231 "membrane-spanning 4-domains, subfamily A, member 6A, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136221_PI430048170 0.2781751408611491.17226215801693 7.80530180780488 7.91763374003861 8.0694625674573 P P P 7.44685584947534 7.6068499519769 8.00461271740509 P P P LNCV6_136221_PI430048170 mRNA
GCCTATGAAAATTCTCCAGAGCTTAACCCAAGGCTTTTTAAATAAAGATCATATGGTAGT NM_016013RefSeq chr15 - 41387348 41402460 NDUFAF1 51103 "NADH dehydrogenase (ubiquinone) complex I, assembly factor 1, transcript variant 1" GO:0005515|GO:0005737|GO:0006461|GO:0005747|GO:0006120|GO:0051082 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144163_PI430048170 0.6509527424491720.9586095555722480.357019174083821 0.3127614661732130.364500529197836A A A 0.6014282342390920.284306745732831 0.310075078618283A A A LNCV6_144163_PI430048170 mRNA
TTCTCTGAGGACACAGATAGGATGGGGTGTCTGTGTTATTTGTGGGGTACAGAGATGAAA NM_001030047 RefSeq chr19 + 50854914 50860764 KLK3 354 "kallikrein-related peptidase 3, transcript variant 3" GO:0005515|GO:0004252|GO:0016525|GO:0006508|GO:0008236|GO:0005634|GO:0005576|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138007_PI430048170 0.0443867582711117 0.8528753167250289.84001331814784

9.81617685335313 9.9544891341872 P P P 9.99152564885231 10.099142789353
10.2047398970958 P P P LNCV6_138007_PI430048170 mRNA
CTCCGCAGCCTTTTGTCTATTTATATGTGTACCAAGTGTTAAACATAATTATTATTGGGC NM_024640 RefSeq chr1
- 37802941 37808193 YRDC 79693 yrdC N(6)-threonylcarbamoyltransferase domain containing
GO:0005739|GO:0003725|GO:0016020|GO:0051051 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72812_PI430048170 0.0567263332243065 1.09530398503318 7.52506724479146 7.4076439349365
7.51203997838538 P P P 7.37901093127725 7.32758617559186 7.34653811029525 P P P
LNCV6_72812_PI430048170 mRNA
TACATGTTTATAGGTGGGACCAATTTTGCCTATTGGAATGGGGCCAACTCACCCTATGCA NM_000404 RefSeq chr3
- 32996607 33097202 GLB1 2720 "galactosidase, beta 1, transcript variant 1"
GO:0005515|GO:0005773|GO:0006665|GO:0048471|GO:0004565|GO:0005794|GO:0006687|GO:0005975|GO:0019
388|GO:0006027|GO:0016936|GO:0044281|GO:0042339|GO:0005737|GO:0042340|GO:0009405|GO:0006488|GO:0
044267|GO:0030203|GO:0070062|GO:0043687|GO:0043202|GO:0018279 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_141261_PI430048170 0.4263903789764571.43821518685736 0.472143563154798
1.66154759012382 0.416284710888972 A A A 0.4598979272294230.435122539801485
0.448430369099865 A A A LNCV6_141261_PI430048170 mRNA
AACTGGAAGTCGGGGAAAGGATACAATTATAGCTACAAGGTGTCAGAGATGAAGGTGCGA NM_004108 RefSeq
chr9 + 134880811 134887520 FCN2 2220 "ficolin (collagen/fibrinogen domain containing lectin) 2,
transcript variant SV0"
GO:0005515|GO:0005581|GO:0050830|GO:0043394|GO:0072562|GO:0005576|GO:0043654|GO:0003823|GO:0001
867|GO:0006956|GO:0050829|GO:0045087|GO:2001065|GO:0008228|GO:0070062|GO:0048306 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_76150_PI430048170 0.3152360518069 1.03551736360975 0.3061444216282340.257292459481586
0.385434166480805 A A A 0.27735884877271 0.2460210261763540.277119684039353 A A A
LNCV6_76150_PI430048170 mRNA
TCACATACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGT NM_032566 RefSeq chr5
+ 148312426 148315918 SPINK7 84651 "serine peptidase inhibitor, Kazal type 7 (putative)"
GO:0010951|GO:0005515|GO:0004867|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82758_PI430048170 0.0793500133558445 1.17908220989375 6.22720565753211
6.15373677941896 6.31264799160089 P P P 6.03476357095881 5.83145326903375
6.10498628548657 P P P LNCV6_82758_PI430048170 mRNA
GAGAATCTGATACCTTTACCCCAGAATAGAACAATAAATAACAGCTACCTTCTACTGACA NM_001256932 RefSeq
chr16 - 30697703 30698489 LOC730183 730183 uncharacterized LOC730183 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_129972_PI430048170 0.1861175268973461.13110262724665 4.63472084412965
4.79853349301914 4.50308143864077 P P P 4.41590634864976 4.60460916910471 4.388105595676
P P P LNCV6_129972_PI430048170 mRNA
TAGGGTTGCCAAATCGGATTTTCTAAAATGAGTAGGAAGTTGGATTTTTATGTGCAACAG NM_175872 RefSeq chr19
- 34956353 34964049 ZNF792 126375 zinc finger protein 792
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145203_PI430048170 0.0842279941430325 0.5415506940527366.74976084417177
7.12035384133921 6.77655230346471 P P P 7.16464735226631 8.12676236874544
7.87713686526916 P P P LNCV6_145203_PI430048170 mRNA
CTGTTGCCTTTTTACAGCCAACTTTTCTAGACCTGTTTTGCTTTTGTAACTTGAAGATAT NM_174936 RefSeq chr1 +
55039475 55064853 PCSK9 255738 "proprotein convertase subtilisin/kexin type 9, transcript variant 1"
GO:0005515|GO:0030134|GO:0048471|GO:0016540|GO:0010469|GO:0004252|GO:0005886|GO:0005783|GO:0070
326|GO:0043621|GO:0005764|GO:0005615|GO:0043523|GO:0005737|GO:0043525|GO:0030182|GO:0034190|GO:0

006508|GO:0001920|GO:0010989|GO:0022008|GO:0008203|GO:0009267|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133153_PI430048170 0.4612457102041021.68745005924609 2.12689341996893 0.4994833132522430.351796068453104A A A 0.3980290667438750.533789410864947 0.502820243900276A A A LNCV6_133153_PI430048170 mRNA ATTACTACTTTCTGTGCTATCGAGATACTTGGGAAGACACAGGCCAGAGTCCAGCCAATT NM_001277378 RefSeq chr19 - 14081631 14085795 C19orf67 646457 chromosome 19 open reading frame 67 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132676_PI430048170 0.0265435699677211 1.18624401651943 11.6057922378572 11.776282572508 11.6875443816962 P P P 11.3533486563279 11.5342891007437 11.4421470472646 P P P LNCV6_132676_PI430048170 mRNA TTTCTGTATGCTCTGTGCTAGTAGGGTGGATTCAGTAATAAATATGTGAAAGCTTTTGTT NM_052969RefSeq chr3 - 187120952 187139475 RPL39L 116832 ribosomal protein L39-like GO:0003735|GO:0022625|GO:0007283|GO:0006412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137413_PI430048170 0.0454293010713249 1.1554969865679 9.03540025817044 9.08054192832745 9.01173029362941 P P P 8.92851018343108 8.82506673978624 8.74342784208833 P P P LNCV6_137413_PI430048170 mRNA AATATTGCAAAAGGATGTGTGTCTTTCTCCCCGAGCTCCCCTGTTCCCCTTCATTGAAAA NM_002666RefSeq chr15 - 89664369 89679417 PLIN1 5346 "perilipin 1, transcript variant 1" GO:0006629|GO:0005811|GO:0005783|GO:0044281|GO:0019433|GO:0008289|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133969_PI430048170 0.5872329058367051.03491519607494 6.92359708026946 6.9994188224987 7.11346123850961 P P P 6.90739817466298 6.88677793826802 7.09121638684388 P P P LNCV6_133969_PI430048170 mRNA CGTAACACCAACTGTTGTGAACATCCATGTTATTGGAAAAGAACACATTTTCAGTGTATT NM_024683RefSeq chr17 - 30898982 30906268 TEFM 79736 "transcription elongation factor, mitochondrial" GO:0042645|GO:0005739|GO:0005515|GO:0006355|GO:0030529|GO:0005759|GO:0008821|GO:0006390|GO:0006259|GO:0006264|GO:0030337|GO:0006119 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126174_PI430048170 0.1862908706481421.60593054784257 1.93193180439216 0.89516170606497 1.04511266482872 A A A 0.90004717270383 0.431327348536545 0.682046909773888A A A LNCV6_126174_PI430048170 mRNA ACACACAGCAGAGTCCTCTGGACTTTGAGGAAGAACCCACAGCAGGAGGAAGTACCCCAG NM_001103150 RefSeq chrX - 152988823 152992217 PNMA5 114824 "paraneoplastic Ma antigen family member 5, transcript variant 2" GO:0043065 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69244_PI430048170 0.3951186249853091.10006172969631 12.9422214586935 13.2205961868164 13.3368292844205 P P P 13.0985836558866 12.9116854033738 13.0967132056412 P P P LNCV6_69244_PI430048170 mRNA AGCTGAAGCAGGGTTTTGAGCCACTGCTGCTGCTGCCATTGTCACCATGGTCTCAGCTCT NM_173847RefSeq chr17 + 32991863 32997874 SPACA3124912 sperm acrosome associated 3 GO:0005515|GO:0035036|GO:0050830|GO:0043032|GO:0003796|GO:0005576|GO:0009615|GO:0005764|GO:0009253|GO:0050766|GO:0042117|GO:0016998|GO:0016021|GO:0030141|GO:0002080 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138903_PI430048170 0.4700070519256811.18667789736163 0.51453234398237 1.10175830777619 0.320069649747053A A A 0.3822299055487170.473404912619626 0.456932280987932A A A LNCV6_138903_PI430048170 mRNA ACGGTCAGCGCTGGAAACTTCTATTAAATGGATGCATTCTGGAGGCATGAAGTTAAAAAA NM_020822RefSeq chr9 + 135702184 135793147 KCNT1 57582 "potassium channel, sodium activated subfamily T, member 1, transcript variant 1" GO:0008076|GO:0005249|GO:0015269|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_126919_PI430048170 0.0119123376929585 1.33153809860795 5.41354900876738
5.43608875193279 5.31769461273135 P P P 4.90389991695963 5.10954172076991
4.90758524630783 P P P LNCV6_126919_PI430048170 mRNA
GGACAGACTGCTTCCTTGAACTTTGTGTTAAAAACAGTTCTGCTTCTGAAAATAAAGTTT NM_145719RefSeq chr11
+ 65354810 65357611 TIGD3 220359 tigger transposable element derived 3 GO:0005634|GO:0003677
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115013_PI430048170 0.1946116249434211.98311241498495 2.64009883214774
2.69970164635219 1.30145546666176 A A A 1.18473361140284 1.48614430364225
1.37166395946605 A A A LNCV6_115013_PI430048170 mRNA
AAGATGACCTACTCCTCGAAAGTGTCGGCTAAGCACACCAGCCTGCGGCGGCAGCTGCAG NM_182628RefSeq
chr3 + 126394938 126436555 CCDC37 348807 coiled-coil domain containing 37 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135012_PI430048170 0.7212181685997160.9851285587881040.433829214804913
0.3979555272366810.250815862058269A A A 0.3507257782795880.409519290683017
0.39301341247797 A A A LNCV6_135012_PI430048170 mRNA
GATGCTGTCAATGAGATTTTTATGAGGTTTAACTGATGCTGTCTTCTAAGCATAAAGCTT NM_005562RefSeq chr1
+ 183186038 183245127 LAMC2 3918 "laminin, gamma 2, transcript variant 1"
GO:0048471|GO:0034329|GO:0005576|GO:0005607|GO:0005615|GO:0005610|GO:0008544|GO:0016020|GO:0022
617|GO:0030198|GO:0031581|GO:0007155|GO:0005938|GO:0008201 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_75876_PI430048170 0.1034234107883251.05501927729135 0.4354484903797770.47791041924365
0.48434259520513 A A A 0.3374195745400760.3865247697817830.440589928932734A A A
LNCV6_75876_PI430048170 mRNA
GTGCCTACAAAACCTTAAAGGAAAAGCTTTCAAAGGATATTGATTACCTTATTGGTAAGG NM_018700RefSeq chr5
- 115124761 115180546 TRIM36 55521 "tripartite motif containing 36, transcript variant 1"
GO:0004842|GO:0016567|GO:0001669|GO:0016874|GO:0051726|GO:0008270|GO:0007340|GO:0005856|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123661_PI430048170 0.1557364936086770.8482136357636844.65165448256181
4.86281685422615 4.8801537619914 P P P 4.82743179868694 5.07808681702946
5.18921711569336 P P P LNCV6_123661_PI430048170 mRNA
GAACAGCGAAAATTGGGCAATGCTCCTGCAGAAGTTGATGAAGAAGGAAAAGACATCAAC NM_006425RefSeq
chr5 - 160401640 160419161 SLU7 10569 SLU7 splicing factor homolog (S. cerevisiae)
GO:0005515|GO:0030628|GO:0005634|GO:0071013|GO:0006886|GO:0000389|GO:0043231|GO:0034605|GO:0000
386|GO:0005737|GO:0016607|GO:0016020|GO:0000398|GO:0000375|GO:0000380|GO:0030532|GO:0005654|GO:0
005681|GO:0008270. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132496_PI430048170 0.5333040473425540.8832994453471994.3417406532147 3.2530109567391
3.60459398842173 P P P 3.9107721500233 4.18807632390739 3.83307308139369 P P P
LNCV6_132496_PI430048170 mRNA
AGAAACAACTGAGGCAGCTCTTCTGCTCCCTTCAAGTTCAGAAGAAAGCTTCCAGTTGAT NM_001008409 RefSeq
chr20 + 31870701 31943055 TTLL9 NA tubulin tyrosine ligase-like family member 9 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145388_PI430048170 0.0133334850136172 0.4551424429404429.24379453422199
9.11651742080758 9.39689172195514 P P P 10.0430957017275 10.404956326673
10.6634183048605 P P P LNCV6_145388_PI430048170 mRNA
GAGCCCTTTATCAATACAGTGCTGCAATTTCTGGATATCAGCTACACTTTGTTTTTAAGT NM_002296RefSeq chr1
- 225401501 225428113 LBR 3930 "lamin B receptor, transcript variant 1"
GO:0005515|GO:0006695|GO:0031965|GO:0070087|GO:0005635|GO:0044281|GO:0016628|GO:0003677|GO:0005
639|GO:0016020|GO:0016021|GO:0005521|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134388_PI430048170 0.0437290865472943 1.94894207878413 9.89080742773923

10.2105532246348 10.70927354521 P P P 9.68757922702014 8.9033184622246
9.34584379187789 P P P LNCV6_134388_PI430048170 mRNA
TGTTGAACATCAGCTGGGGAATTGAAGCCAATAAACCTTCCTTCTTAACCATTCAAAAAA NM_000667 RefSeq chr4
- 99276365 99291028 ADH1A 124 "alcohol dehydrogenase 1A (class I), alpha polypeptide"
GO:0005515|GO:0004022|GO:0006805|GO:0017144|GO:0006066|GO:0006069|GO:0004024|GO:0008270|GO:0044
281|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128632_PI430048170 0.191892857643781 0.64737829024393 0.252704625290828
0.2649139243410120.385555835270941 A A A 0.9639566679154150.318317786257742
1.33162066991411 A A A LNCV6_128632_PI430048170 mRNA
AATGACTCCATCTGGGATTCAGAATACAGTGTTCTCAAGTGAAGAAGGCTTGGAACCCAC NM_001136503 RefSeq
chr19 - 3474406 3480542 SMIM24 284422 small integral membrane protein 24
GO:0008150|GO:0003674|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136195_PI430048170 0.100578517486337 0.839336199768923 8.51663669453879
8.47817408578529 8.48883899197729 P P P 8.58146969666868 8.76798555447419 8.8771577803225
P P P LNCV6_136195_PI430048170 mRNA
GGCTACCACTGTGGTCGCGTGCTACAGGTTTGACAAAAAGATATCATGTTTCGATTTTTT NM_006999 RefSeq chr5
+ 6714604 6757048 PAPD7 11044 "PAP associated domain containing 7, transcript variant 1"
GO:0007076|GO:0003887|GO:0042493|GO:0005634|GO:0003677|GO:0046872|GO:0006302|GO:0004652|GO:0043
221|GO:0005737|GO:0071897|GO:0007062|GO:0005654|GO:0051301 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132503_PI430048170 0.0253745868061334 0.484161010619658 8.19096870900993
7.97479113282719 8.12438767734389 P P P 8.73810673154734 9.38172192511223
9.24186039824686 P P P LNCV6_132503_PI430048170 mRNA
GTAAGCCTCCTTGTATTGAGATAATTGGGCATTAAACATTAAACTGCAGCTCTGGGCAAA NM_004091 RefSeq chr1
- 23506427 23531220 E2F2 1870 E2F transcription factor 2
GO:0005515|GO:0005667|GO:0006355|GO:0006367|GO:0003700|GO:0072332|GO:0051726|GO:0005654|GO:0001
047|GO:0000278|GO:0003677|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120173_PI430048170 0.16633507378879 1.17206713117573 7.04914862723209
6.87980383337887 7.02810386990556 P P P 6.88100184529805 6.84828954860095
6.51947897609738 P P P LNCV6_120173_PI430048170 mRNA
CAGGGGCAGTTTGCCGTTCCCTCTCCACACCACAATTTAATTCCCTTGATGTCATTGCAG NM_016651 RefSeq chr14
+ 58638038 58648320 DACT1 51339 "dishevelled-binding antagonist of beta-catenin 1, transcript variant
1"
GO:0005515|GO:0045732|GO:0030054|GO:0008013|GO:0030877|GO:0030178|GO:2000095|GO:0030177|GO:0045
202|GO:0035413|GO:0005829|GO:0035412|GO:1900107|GO:0005737|GO:0031647|GO:0046329|GO:0005080|GO:0
016055|GO:0051018|GO:0090090|GO:0070097|GO:2000134|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_118236_PI430048170 0.387041110389538 1.08087963728803 7.89554195990567
7.81156019006172 7.85130919179288 P P P 7.90704287204839 7.7597939972878
7.53164385118408 P P P LNCV6_118236_PI430048170 mRNA
TGGACTACTACACAGAGGTTCTGGACCTCTCCTACCTGCTTGACCACCTGGCTTCTGACC NM_018066 RefSeq chr1
- 26879381 26890378 GPN2 54707 GPN-loop GTPase 2
GO:0008150|GO:0003674|GO:0016787|GO:0008152|GO:0005575|GO:0005525 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140661_PI430048170 0.0227033977584072 0.63833029367613 7.88103022175649
7.60755656484534 7.76494621096356 P P P 8.23786354757108 8.27456529734782
8.65832676281149 P P P LNCV6_140661_PI430048170 mRNA
CAGGCAGAAGAGGTTCATGGCAATATAATAGTCAATGAACTTTCAGTTTAAATTGTGTAC NM_014916 RefSeq chr7
+ 98106884 98209632 LMTK2 22853 lemur tyrosine kinase 2

GO:0005515|GO:0048471|GO:0005794|GO:0004864|GO:0032456|GO:0045022|GO:0043086|GO:0005524|GO:0070853|GO:0033572|GO:0046777|GO:0001881|GO:0018105|GO:0004674|GO:0018107|GO:0006468|GO:0016021|GO:0055037|GO:0005769. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135092_PI430048170 0.00886862278784586 0.5861303976022646.64961136375793
6.28318570270819 6.56386290455303 P P P 7.18557883636398 7.11981974196453
7.49918270604783 P P P LNCV6_135092_PI430048170 mRNA
TGGTGCTGTTGACCTGCAAGAGAATATACTTTTGCATATACAGGTGAAAGTTTTGCAATT NM_194285RefSeq chr11
- 18606400 18634473 SPTY2D1 144108 "SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)"
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138528_PI430048170 0.0613649205852166 1.78837825534442 4.15248563931161
4.28822331857651 3.71535948925027 P P P 2.66350144367326 3.50562846489703
3.39509372387547 P P P LNCV6_138528_PI430048170 mRNA
CCAAGGTCATTCATATCTCGGTTTGAGCTCATATCTTATAATAACACAAAGTAGCCACAG NM_031917RefSeq chr19
- 10092336 10102749 ANGPTL6 83854 angiopoietin-like 6
GO:0001525|GO:0030141|GO:0030154|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139675_PI430048170 0.3028765349409560.9260753191836620.3687878083501
0.4232004841325070.341869074864726A A A 0.5220617771220790.597930457271079
0.334911127649043A A A LNCV6_139675_PI430048170 mRNA
CTGTTCCGAAAATTTATATGGTGGAATGCGCCATGTATAAACTGTGAATTGTATTGACAA NM_001017424 RefSeq
chr1 + 215005541 215237093 KCNK2 3776 "potassium channel, two pore domain subfamily K, member 2, transcript variant 1"
GO:0015271|GO:0007186|GO:0005886|GO:0005783|GO:0008076|GO:0042391|GO:0019870|GO:0005789|GO:0007268|GO:0034765|GO:0022841|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132882_PI430048170 0.4200528867923431.74539509309285 2.10333822666244
0.3372485945240040.484959077709332A A A 0.5796102852305220.290666464560768
0.344757079931983A A A LNCV6_132882_PI430048170 mRNA
GCTTCGCATGATTGTGGAACTCACAGACTACTAACAAATCTTCCCTATTTTCTTTCTTTT NM_001207030 RefSeq chr16
- 53369361 53371129 LOC643802 643802 u3 small nucleolar ribonucleoprotein protein MPP10-like NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127190_PI430048170 0.2974801907160230.3741007880427850.458238322495306
0.8647627441773120.499500321566397A A A 3.03566941841749 1.45567125588257
0.46059841811967 P A A LNCV6_127190_PI430048170 mRNA
TAGCCATTGGTGCACAGGATGGGGGCAATGGGAGGGGATGCTACTGATGGGAATGATTAA NM_022304RefSeq
chr5 + 175681460 175684555 HRH2 3274 "histamine receptor H2, transcript variant 2"
GO:0003382|GO:0005886|GO:0048565|GO:0001697|GO:0004969|GO:0001698|GO:0006955|GO:0045907|GO:0005887|GO:0007187|GO:0048167|GO:0048732|GO:0008542|GO:0007613 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142743_PI430048170 0.00132654464368231 0.2469762505889630.415368379507472
0.4318894570732530.414847952766738A A A 2.44794178624186 2.29756111789096
2.55758605073472 A A P LNCV6_142743_PI430048170 mRNA
GTGGCCTAGACTTCTGAGTAATTAATAAAGAAAAAGAAGTACCCTTTGGCCTACAAAAAA NM_002031RefSeq chr6
- 115941529 116060758 FRK 2444 fyn-related Src family tyrosine kinase
GO:0005515|GO:0008285|GO:0030036|GO:0005102|GO:0005634|GO:0005524|GO:0030154|GO:0031234|GO:0005622|GO:0005737|GO:0016477|GO:0045087|GO:0042127|GO:0006468|GO:0038083|GO:0004715|GO:0007169|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81052_PI430048170 0.1023206599180280.7602540185350144.39552168274758 4.55186193586023
4.66978127990726 P P P 4.63579491693692 5.1178652584541 5.01931606200145 P P P
LNCV6_81052_PI430048170 mRNA
TAATAGGGGGAAAACCCCAAGTATGTAACCCTATCCATAGCCAAAATAAAGTCTGCATGC NM_001193331 RefSeq

chr9 + 94726668 94933673 C9orf3 84909 "chromosome 9 open reading frame 3, transcript variant 4"
GO:0019370|GO:0005737|GO:0004177|GO:0006508|GO:0005730|GO:0008270|GO:0008237 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126643_PI430048170 0.1460967852199721.48307774013718 5.41272451630948
5.53705772105862 5.96085381692768 P P P 5.53789804816517 4.60883900288103
4.96206009874106 P P P LNCV6_126643_PI430048170 mRNA
CTCGAAATCCCAATGAAAAACCTACCCAGCAAAGAAGCATAGCTTTTAGCTCTAATAATT NM_020317RefSeq chr1
- 25242248 25247494 RSRP1 57035 arginine/serine-rich protein 1 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138186_PI430048170 0.7688438935802991.06694968043895 1.8987445625549
2.40125149549211 3.50835288158465 A A P 3.66390625395643 1.70709241823224
1.66513964045365 P A A LNCV6_138186_PI430048170 mRNA
CCAGAGTTTTATGAAATCATCATGTAGCCAACTTCAAATCCCATCTCTGCTCCTTCTTGC NM_001001663 RefSeq
chr22 - 24935240 24939347 TMEM211 NA transmembrane protein 211 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_136487_PI430048170 0.42577089094394 1.04557848286528 0.317009632813833
0.3232041616028440.505872980595492A A A 0.3247920392810250.289941773308527
0.34598461309933 A A A LNCV6_136487_PI430048170 mRNA
AAGTGAGATAGCACTGGAGACAAGAACTAAGCCTCTCAAGATACTTTTAGTGCTAAAAAA NM_022569RefSeq chr4
- 114827770 115113876 NDST4 64579 N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4
GO:0000139|GO:0019213|GO:0016021|GO:0015012|GO:0030210|GO:0015016 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132715_PI430048170 0.000508103391102342 0.5363324033251079.90582746874061
9.81066366118342 9.6903656138592 P P P 10.5822696509133 10.7334967048105
10.7877690005577 P P P LNCV6_132715_PI430048170 mRNA
TTTTACTCCCTTTGTACAGTATTCTGAGAAACGCAAATAAAAGGGCAACATGTTTCTGTT NM_139280RefSeq chr17
- 39921042 39927631 ORMDL3 94103 ORMDL sphingolipid biosynthesis regulator 3
GO:0005515|GO:0005783|GO:0006672|GO:0005789|GO:0035339|GO:0016021|GO:0090156 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_68831_PI430048170 0.0325360043065555 1.99321243375803 6.49827834337196
7.15757212307278 6.73149508565376 P P P 5.78015175964887 5.90902692684756
5.78799534150071 P P P LNCV6_68831_PI430048170 mRNA
CCCCGCCTACTGGGACGGCGAGAAGGAGGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCT NM_001282583
RefSeq chr1 - 1352688 1361777 MXRA8 54587 "matrix-remodelling associated 8, transcript variant
4" GO:0003674|GO:0009986|GO:0060857|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138774_PI430048170 0.2707890864282960.7206741188573 0.968118898919936
1.49345511552802 0.316276457675115A A A 1.65192475749004 1.04719052726956
1.65082673762693 A A A LNCV6_138774_PI430048170 mRNA
TTTCCTTCCCACTCACAATATATCTGAATTAGAACTGCTAAACACAGCTTGAAGACTTAA NM_152282RefSeq chr3
+ 141231824 141294903 PXYLP1 92370 "2-phosphoxylose phosphatase 1, transcript variant 1"
GO:0010909|GO:0005515|GO:0016791|GO:0050650|GO:0005794|GO:0000139|GO:0016311|GO:0003993|GO:0016
021|GO:0006024 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127313_PI430048170 0.15036867349849 0.7307421182361454.25095475405525
4.57658542323863 4.94232213317536 P P P 5.00458715738145 4.79660441587315
5.35366245637638 P P P LNCV6_127313_PI430048170 mRNA
GGTAGGAAGTAAGCTACTTAGTGGTTTCACCTGTGAAATAACTATTTTGACTGAAATGTA NM_020345RefSeq chr3
- 23892080 23917046 NKIRAS1 28512 NFKB inhibitor interacting Ras-like 1
GO:0006184|GO:0005737|GO:0016020|GO:0007264|GO:0007249|GO:0003924|GO:0005575|GO:0005525 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134923_PI430048170 0.3325354889325360.6537991523234122.04540161384253
0.49924789759053 2.40951132543004 A A A 2.52235092223094 2.85913691004801
1.84835887073271 A P A LNCV6_134923_PI430048170 mRNA
GCCTCCGATTCATTCCCTTGACACTTTTTATTTCTAAGGAAGAAATAAAAAGAGATACAC NM_001155RefSeq chr5
- 151100705 151157882 ANXA6 309 "annexin A6, transcript variant 1"
GO:0005515|GO:0042470|GO:0048471|GO:0005509|GO:0005525|GO:0005765|GO:0042803|GO:0008289|GO:0005
544|GO:0006937|GO:0034220|GO:0016020|GO:0015485|GO:0031902|GO:0051260|GO:0006816|GO:0005925|GO:0
070062|GO:0048306|GO:0015276 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102741_PI430048170 0.00807831555167607 0.5514679690439245.95353100478438
5.66142135771038 5.54520678004976 P P P 6.53226237924746 6.51678539283972
6.71015010494745 P P P LNCV6_102741_PI430048170 mRNA
AAATAAACCCAATATGTCGGATCCTGAGGAATCCAGGGGAAATGATGAACTAGTGAAGCA NM_014865RefSeq
chr12 + 6494131 6531966 NCAPD2 9918 "non-SMC condensin I complex, subunit D2"
GO:0000796|GO:0005515|GO:0000793|GO:0000797|GO:0007076|GO:0005634|GO:0000228|GO:0005829|GO:0042
393|GO:0005737|GO:0016020|GO:0005654|GO:0045120|GO:0000278|GO:0051301 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144855_PI430048170 0.6341709731377560.88781067311596 8.14109485813668
7.94239681728515 8.37286600305021 P P P 7.93700268863579 8.19839191655474
8.74694532977309 P P P LNCV6_144855_PI430048170 mRNA
ACTGGTTTGCTGACTTACTGAGGATTAATTGTTGCCTTACAATGTTACTGAAATAAACTG NM_024896RefSeq chr9
- 5784571 5833081 ERMP1 79956 endoplasmic reticulum metallopeptidase 1
GO:0016020|GO:0006508|GO:0005789|GO:0016021|GO:0046872|GO:0008237 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_68358_PI430048170 0.0171804999783881.25100062557129 8.39504415715786 8.22560592088715
8.27980052919779 P P P 8.06878812875591 8.00297933661953 7.85655324376309 P P P
LNCV6_68358_PI430048170 mRNA
TCCTACTCCCAAAACTATTTAAGGAAGCATGAAAAATAAAGATGCTGGTTATCTTCTCCT NM_145249RefSeq
chr14_KI270847v1_alt + 1195854 1217276 IFI27L1 122509 "interferon, alpha-inducible protein 27-like
1, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58554_PI430048170 0.1591300797006650.71036598104545 3.08642817112558 2.98696208813466
3.64616684388663 A A P 3.33559725418754 3.90335454825843 3.97120876387649 P P P
LNCV6_58554_PI430048170 mRNA
TGTGCATGAGCAAATGTGCAACAAAACCCTGGGACTTTGCAGTCAAATGAAGCTGAGCTT NM_199245RefSeq chr12
- 6462237 6470899 VAMP1 6843 "vesicle-associated membrane protein 1 (synaptobrevin 1),
transcript variant 2"
GO:0005515|GO:0043005|GO:0035493|GO:0030054|GO:0009986|GO:0031201|GO:0005741|GO:0006887|GO:0006
906|GO:0005829|GO:0008021|GO:0005484|GO:0005887|GO:0000149|GO:0009405|GO:0030672|GO:0035579|GO:0
070821|GO:0035577. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107237_PI430048170 0.0344841021195992 1.65630637899293 8.7759933574668
8.79283870862104 8.65664866923717 P P P 8.24445588873447 8.04515552294327 7.7051617789373
P P P LNCV6_107237_PI430048170 mRNA
ACTTCATCTTCACCATCTACCACTGGTGGCAGGCTGTGGCCATCTTCACCGTGTACCTGG NM_030930RefSeq chr11
- 67991099 68004125 UNC93B1 81622 unc-93 homolog B1 (C. elegans)
GO:0034154|GO:0005783|GO:0002224|GO:0032009|GO:0005764|GO:0006886|GO:0035325|GO:0019886|GO:0051
607|GO:0000139|GO:0045087|GO:0005789|GO:0016021|GO:0034138|GO:0034162|GO:0005768 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131132_PI430048170 0.00666647820830399 0.3251005030895545.87571110426647
5.47241363106257 5.57598646969703 P P P 6.81633756069662 7.3771816038822 7.5310949726253

P P P LNCV6_131132_PI430048170 mRNA
CAGTGCTTGAGCATCTCTGTCAGAAATGGAATGAAATACTGTTAGCCAATTAGAATTATT NM_001256126 RefSeq
chr2 + 168456248 168775134 CERS6 253782 "ceramide synthase 6, transcript variant 1"
GO:0006665|GO:0031965|GO:0016020|GO:0005783|GO:0030148|GO:0005789|GO:0050291|GO:0044281|GO:0016
021|GO:0046513|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92776_PI430048170 0.3209114425462470.8680161214676561 0.0786909498573 10.034396194108
9.99517674031585 P P P 9.99833634919929 10.1829100888353 10.4963837849473 P P P
LNCV6_92776_PI430048170 mRNA
GCCGTGCCCACACATTTCCTTGCAACTTGATCAAATTTCTTAAAGCAAACAACAAAAATG NM_001006617 RefSeq
chr9 - 125437393 125707234 MAPKAP1 79109 "mitogen-activated protein kinase associated protein 1,
transcript variant 1"
GO:0005515|GO:0070300|GO:0005886|GO:0031295|GO:0005634|GO:0005829|GO:0046580|GO:0005737|GO:0007
173|GO:0017016|GO:0048010|GO:0048011|GO:0005794|GO:0019901|GO:0043325|GO:0048015|GO:0005547|GO:0
080025|GO:0005546|GO:0008543|GO:0021762|GO:0045087|GO:0016023|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138482_PI430048170 0.0643675945432516 1.46151140961736 3.57840574307212
4.06310611783823 4.09608808488903 P P P 3.36023852106171 3.57492362612778
3.19000839526359 P P P LNCV6_138482_PI430048170 mRNA
TCATGGACAGGCTACTGGTGACCAAAGTTGGTTCCTTTTCTCCTTTCTTTCCTCCTTGAA NM_145663RefSeq chr17
+ 44708607 44752268 DBF4B 80174 "DBF4 zinc finger B, transcript variant 1"
GO:0000790|GO:0008284|GO:0016235|GO:0019901|GO:0005634|GO:0030295|GO:0003676|GO:0043231|GO:0005
737|GO:0007049|GO:0010971|GO:0010571|GO:0045860|GO:0005654|GO:0008270 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140326_PI430048170 0.00822635599955451 0.3058893715360224.48030379593273
3.88155434126493 4.79453482963083 P P P 5.74839342617492 6.24088486981965 6.3661886349029
P P P LNCV6_140326_PI430048170 mRNA
CTGCTTATCTTATTGCACTGCTAGTTGTATGTAGGTATTAATTTTATTGCTGCTTACTGC NM_203394RefSeq chr12 -
77021245 77065580 E2F7 144455 E2F transcription factor 7
GO:0005515|GO:0005667|GO:0032466|GO:0000977|GO:0003700|GO:0008285|GO:0030330|GO:0003714|GO:0060
707|GO:0032877|GO:2000134|GO:0001047|GO:0002040|GO:0005634|GO:0000122|GO:0001890|GO:0001227|GO:0
071930|GO:0006351|GO:0042802|GO:0045944|GO:0060718|GO:0070365 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_133403_PI430048170 0.3890751598183270.7849376859908133.72169182546078 2.7891301425482
3.85306847261782 P A P 3.72957996007791 3.55496627681074 4.2483255917287 P P P
LNCV6_133403_PI430048170 mRNA
GGGGTGTATTAGCAGCCAAATAAGCACATCTGATCAAAAAGAACCAGGCTTAGATTTTTT NM_015049RefSeq chr2
- 201377206 201451596 TRAK2 66008 "trafficking protein, kinesin binding 2"
GO:0005739|GO:0005515|GO:0005737|GO:0006493|GO:0006357|GO:0005886|GO:0005102|GO:0005634|GO:0050
811|GO:0006605|GO:0019899|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136481_PI430048170 0.0468316948907527 1.58623149416156 11.1881941212836
11.3158977992717 11.12275456429 P P P 10.7182668591066 10.677352609039
10.1819836069227 P P P LNCV6_136481_PI430048170 mRNA
GAGCATAGCACATTTTCCTAGAGCGAGAATTGGGGGAAAGCTGTTATTTTTATATTAAAA NM_021727RefSeq chr11
- 61873522 61891545 FADS3 3995 fatty acid desaturase 3
GO:0003674|GO:0006636|GO:0016020|GO:0005506|GO:0005789|GO:0016021|GO:0016717|GO:0055114|GO:0020
037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78925_PI430048170 0.0197613032054839 2.03069713218891 7.48790875108676 7.4569066066239
7.40795870422421 P P P 6.35423742005442 6.70571822084351 6.17701446338955 P P P
LNCV6_78925_PI430048170 mRNA

ATTCCCAGCCACTATGATGTCCAGGACCGCTTCCGCATTGAGCTGTCTGAGGAAGGAGCT NM_023948 RefSeq chr7 + 100612490 100615377 MOSPD3 64598 "motile sperm domain containing 3, transcript variant 1" GO:0007507|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_137507_PI430048170 0.0142924002834129 1.15733992680107 11.500848766111 11.6217678600968 11.6082174679232 P P P 11.3268575130379 11.4114587308576 11.3618411772218 P P P LNCV6_137507_PI430048170 mRNA
GGGGACTCGGAAATAAATTGTAGCAGCTTTCCTGCCGCTGGCCCTCCCCCTGCCAAAAAA NM_001134875 RefSeq chr14 + 105491248 105499248 C14orf80 283643 "chromosome 14 open reading frame 80, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_58998_PI430048170 0.197053971948191 0.648016130134277 0.456674925462451 0.42222205482094 0.294869829056713 A A A 1.45215575950449 0.415403356415292 1.00642717538537 A A A LNCV6_58998_PI430048170 mRNA
TCAGATTCCCAGGCTGACAAAAAGGAGAAACAGCTTTTACTTGCATCCAGGGCCAATCAT NM_007210 RefSeq chr12 - 51352048 51391416 GALNT6 11226 polypeptide N-acetylgalactosaminyltransferase 6 GO:0048471|GO:0004653|GO:0005794|GO:0006493|GO:0000139|GO:0030246|GO:0016266|GO:0016021|GO:0044267|GO:0046872|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_127894_PI430048170 0.617207328150547 1.26003429045534 1.99643219538084 1.25511324322221 0.621945734751243 A A A 1.27308326498496 1.12062178448514 0.75798756639868 A A A LNCV6_127894_PI430048170 mRNA
CTGGACTGCATGCACTTTACATATCACAAAATGCTCTCATAAGAATTATTGCATACCATC NM_001040105 RefSeq chr7 + 101020082 101058859 MUC17 140453 "mucin 17, cell surface associated" GO:0005515|GO:0019725|GO:0005796|GO:0016266|GO:0005576|GO:0030165|GO:0016324|GO:0006493|GO:0030197|GO:0016021|GO:0044267|GO:0009897|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_134813_PI430048170 0.000922552038609034 2.7904600380489 6.55063249376107 6.6342197688497 6.72129987573603 P P P 4.95574164819939 5.26022379958 5.23442173919443 P P P LNCV6_134813_PI430048170 mRNA
GTTAGCGAGCACCTTTTGACCAGTAATAAAAAACCTTGGCTTTGGAGTTTTCCACTGAAA NM_030758 RefSeq chr22 + 30694805 30907824 OSBP2 23762 "oxysterol binding protein 2, transcript variant 1" GO:0016020|GO:0015485|GO:0006869 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_115085_PI430048170 0.491525911081039 1.04181472559887 12.1924049169735 11.9718685667812 12.0295370883947 P P P 11.9762045384777 12.058352520572 11.9897683126205 P P P LNCV6_115085_PI430048170 mRNA
GAAGGCTGGAAGATGAATGAGACTGAACTTCAGCAGTCAATAAAGTCAATATGAATTTTT NM_001124767 RefSeq chr3 + 52536604 52540570 SMIM4 440957 small integral membrane protein 4 GO:0005739|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_139827_PI430048170 0.200889753381234 1.58284739983816 0.373393194362443 1.46904884879838 0.970578706408887 A A A 0.332443513169743 0.32109366811719 0.375188490545911 A A A LNCV6_139827_PI430048170 mRNA
CTTGGCTGTGCTTGAAACCTGAATTTTAGTGCTTCCCTTATTACATTCATTGTTTTCAAT NM_206855 RefSeq chr6 + 163414642 163578596 QKI 9444 "QKI, KH domain containing, RNA binding, transcript variant 4" GO:0005515|GO:0006397|GO:0008380|GO:0017124|GO:0042552|GO:0007286|GO:0005634|GO:0003729|GO:0006417|GO:0010628|GO:0042692|GO:0061158|GO:0005737|GO:0042759|GO:0051028|GO:0001570 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_60971_PI430048170 0.226397057726979 0.796565053647896 9.56922049290723 9.76377367460652 10.0979000712022 P P P 10.1680085263701 9.83126437933896 10.4087261885706 P P P LNCV6_60971_PI430048170 mRNA
GTTTCTCTTGTGTAGTGGTAAAATGGTAGCTGGTGCTTATTGAGATTTGCTGTATTTATA NM_018477 RefSeq chr14 + 58200114 58235635 ACTR10 55860 actin-related protein 10 homolog (S. cerevisiae) GO:0005737|GO:0005869|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_134319_PI430048170 0.0663493535729045 1.1581046434669 6.80938595278556
7.03468159843577 6.91555976009752 P P P 6.80467010755122 6.63502115417986
6.68820024820399 P P P LNCV6_134319_PI430048170 mRNA
CCTGTGTCTTGATGGATTGTGGTTTATTTTGTTGCAAGAGTGAGTTTGAACTATTCTAAT NM_001080507 RefSeq
chr6 - 73368556 73369792 OOEP 441161 oocyte expressed protein
GO:0009880|GO:0009566|GO:0043234|GO:0007566|GO:0003723|GO:0045177|GO:0035088|GO:0006468|GO:0005
938|GO:0001701|GO:0043623 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129262_PI430048170 0.1077921771967490.3785356150653830.525617899008537
0.5926565190474990.464196351885252A A A 1.13479308437344 2.6516822623027
1.56137119069083 A A A LNCV6_129262_PI430048170 mRNA
CCAGGAAAAATCTGAGACAGAAAATTTTTCACCCCTATGGATAGGTTTTCACCTGTAATA NM_006828RefSeq chr6
- 100508194 100881372 ASCC3 10973 "activating signal cointegrator 1 complex subunit 3, transcript
variant 1"
GO:0005515|GO:0006355|GO:0043140|GO:0005794|GO:0008283|GO:0005634|GO:0005524|GO:0006351|GO:0005
622|GO:0005737|GO:0006307|GO:0016020|GO:0032508 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140244_PI430048170 0.00157806489768624 0.5533451010703561 2.107308467362
11.8777239312374 12.1421897226367 P P P 12.9612050944083 12.7672511450441
12.9653126266298 P P P LNCV6_140244_PI430048170 mRNA
GCAGCTTCACTCACGACTTCAAGATTTGATGCTAATTCTTTTGGATTTCTACAGTTATTANM_018509RefSeq chr17 -
50381232 50397553 LRRC59 55379 leucine rich repeat containing 59
GO:0042645|GO:0016020|GO:0005783|GO:0005789|GO:0016021|GO:0005635 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_112495_PI430048170 0.1051279680315850.7998495175167313.4135691933583
3.74569699914728 3.68612715234943 P P P 3.96365090493964 4.11711651900147
3.72584293034202 P P P LNCV6_112495_PI430048170 mRNA
TACACCAGCCGCTTCCAGTAGTGCTGGTGGACGATCGGGAGTGTCCTGTCAGAAGAAATG NM_012393RefSeq chr17
+ 8249277 8270491 PFAS 5198 phosphoribosylformylglycinamidine synthase
GO:0009168|GO:0042493|GO:0055086|GO:0044281|GO:0005524|GO:0009156|GO:0046872|GO:0005829|GO:0004
642|GO:0005737|GO:0006144|GO:0070062|GO:0006164|GO:0006189|GO:0006541 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137240_PI430048170 0.5843084767801260.9802541481977170.254339987020242
0.2674043165668820.393170787808835A A A 0.3740072745313310.316288034835045
0.314247997691333A A A LNCV6_137240_PI430048170 mRNA
TGTGGCTTTGAAAACAAATTATTTGAGAAAGACCATAACACAGTGAGTAGCCTATATGTG NM_198439RefSeq chr11
- 106051097 106077738 KBTBD3 143879 "kelch repeat and BTB (POZ) domain containing 3, transcript variant
2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139024_PI430048170 0.0779884543513784 0.3589170533677311.41932566250862
1.3271500374465 2.37860340718199 A A A 3.99820799201121 2.40474656743698
2.93657468672485 P A P LNCV6_139024_PI430048170 mRNA
TATAGGTACATAGGCACTGCGTCGGCACCAAAGAGCTAAATAAAAGGATTGTTGAATTTT NM_001270601 RefSeq
chr1 - 201113952 201115372 ASCL5 647219 achaete-scute family bHLH transcription factor 5
GO:0008150|GO:0003674|GO:0006355|GO:0046983|GO:0005634|GO:0005575|GO:0003677|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144837_PI430048170 0.18374848198641 0.93133518582973 0.305330847604314
0.3546863561792710.285915263427389A A A 0.5061545530813820.417774219135752
0.325082645289963A A A LNCV6_144837_PI430048170 mRNA
ACCCCTTGTTACCTTGATTCACTGTATGTGGAAAAATAATGTAACCAAAAGGGAAGAGCT NM_001288823 RefSeq
chr1 - 101802566 101997234 OLFM3 118427 "olfactomedin 3, transcript variant 3"
GO:0005515|GO:0030054|GO:0005794|GO:0032281|GO:0045202|GO:0042462|GO:0005615 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_142728_PI430048170 0.84777993839403 0.8691042042008262.16052924400648
1.90955122752422 2.32301715893171 A A A 2.91210503129487 1.4539679862014
2.30961820467938 P A A LNCV6_142728_PI430048170 mRNA
GAGGATGGTTGTGATTAGGTCAAATAGAAAACTAGCAGGCCATTGCTGACAATTTTTACT NM_015041RefSeq chr16
+ 3500944 3539051 CLUAP123059 "clusterin associated protein 1, transcript variant 1"
GO:0005515|GO:0042384|GO:0005929|GO:0005813|GO:0006996|GO:0030992|GO:0005654|GO:0072372|GO:0043
231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137042_PI430048170 0.0281445531445548 1.69614395140161 7.80985471460551
7.72594640062284 7.6239220823827 P P P 7.2082402120356 6.95499860577132
6.66481939202341 P P P LNCV6_137042_PI430048170 mRNA
GTGTATTGCCCACCCCGCACAGCCTGAGTTTGCAATAAAACTGGGACACTGGGACTTGCA NM_001190467 RefSeq
chr19 - 7868718 7874441 PRR36 80164 "proline rich 36, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133411_PI430048170 0.1565954809534941.05055180913503 0.438543571254972
0.4404460589512120.462710065702574A A A 0.3206750415122290.370224182301532
0.435193853340792A A A LNCV6_133411_PI430048170 mRNA
GTATTTCACCTGAAAAGATGTCTAGAGATTGAAAGAAAACATGCTGGGCATATGATTTGA NM_144718RefSeq chr3
- 113442717 113515187 SPICE1 152185 spindle and centriole associated protein 1
GO:0005813|GO:0005737|GO:0005814|GO:0005819|GO:0090307|GO:0046599|GO:0051310|GO:0051301 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131584_PI430048170 0.0209540104856275 1.63632262873111 13.7492047926153
13.7412399673859 13.7500725800773 P P P 12.830569640421 13.1919717945245
13.0636548609832 P P P LNCV6_131584_PI430048170 mRNA
CATTGGAGCCCTCCTGCTGCTTTGGTGCCTCAAATAAATACAGATGTCCCCCAGAAAAAA NM_002346RefSeq
chr8_KI270817v1_alt + 8772 12698 LY6E 4061 "lymphocyte antigen 6 complex, locus E, transcript
variant 1"
GO:0042415|GO:0055010|GO:0030325|GO:0035265|GO:0005887|GO:0031225|GO:0001701|GO:0007166|GO:0048
242 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135626_PI430048170 0.432726673167333 1.03305964520866 0.334068108084599
0.337202781988205 0.474198235321275A A A 0.34032648139315 0.306677312156241
0.361646913441033A A A LNCV6_135626_PI430048170 mRNA
CAGACAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAA NM_207316RefSeq chr3
- 190428655 190449876 TMEM207 NA transmembrane protein 207 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141844_PI430048170 0.1229131838833910.7085248237551817.17708212218185
7.13953856249245 7.51245248753853 P P P 7.46213550264815 7.66959894752654
8.13455312805529 P P P LNCV6_141844_PI430048170 mRNA
GATGACTACTGCGCCTTCTCTTTCGAAAAACTCTTAATTTAGTGACTTATGGCAAAATTT NM_024835RefSeq
chr17_KI270857v1_alt + 779791 825341 GGNBP2 79893 gametogenetin binding protein 2
GO:0016023|GO:0007275|GO:0005634|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139319_PI430048170 0.2050732528207291.06298854099087 0.444119989842727
0.3576519717104230.281480565980783A A A 0.2688234116410890.285878855882418
0.268698394390368A A A LNCV6_139319_PI430048170 mRNA
TCTATGGCATTTATCACGGTACTCAAAATGGTCATTGTGGTAATTGGCATGCTGGCCACG NM_152232RefSeq chr1
- 18839598 18859661 TAS1R2 80834 "taste receptor, type 1, member 2"
GO:0043235|GO:0046982|GO:0007186|GO:0005886|GO:0032467|GO:0008527|GO:0001582|GO:0033041|GO:0016
021|GO:0050916 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_145159_PI430048170 0.1120018810451991.17140110198484 10.644356087157
10.9472595964626 10.8340704213151 P P P 10.4664245564839 10.6162973457171
10.6668895605398 P P P LNCV6_145159_PI430048170 mRNA
TTATTTCTCCAGGACCCTACAGTGCCTGGGGCTCCGCTTACAATAGTCCTCCCTCTGTTC NM_173659RefSeq chr3
- 9837848 9844018 RPUSD3285367 "RNA pseudouridylate synthase domain containing 3, transcript
variant 1" GO:0009982|GO:0001522 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115605_PI430048170 0.9873164999263450.99451241302016 7.29433064919512
7.38266754091516 7.44587841050432 P P P 7.42562462647932 7.17727683950563
7.52585302788076 P P P LNCV6_115605_PI430048170 mRNA
AGTGGGTACCGGAACTTAAGGAATACGCACCAAATGTACCCTTTTTATTAATAGGAACTC NM_012249RefSeq chr2
+ 46542727 46584688 RHOQ 23433 ras homolog family member Q
GO:0008286|GO:0032427|GO:0051056|GO:0032869|GO:0005886|GO:0007264|GO:0005884|GO:0008360|GO:0003
924|GO:0051491|GO:0005525|GO:0005829|GO:0006184|GO:0030866|GO:0046326|GO:0045944|GO:0032956|GO:0
090005|GO:0045121|GO:0005522|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134066_PI430048170 0.0214651261731517 1.24819026172959 8.40385430871503
8.37113830566405 8.55477486804816 P P P 8.0919674941081 8.12744876995632
8.15683116181525 P P P LNCV6_134066_PI430048170 mRNA
TGATAAAAAGTTGATTGCAGAAGGACCTGGGGAAACAGTATTGGTTGCAGAAGAAGAGGC NM_022915RefSeq
chr2 + 223957403 223967714 MRPL4465080 mitochondrial ribosomal protein L44
GO:0070124|GO:0070125|GO:0006396|GO:0070126|GO:0032543|GO:0006996|GO:0004525|GO:0005743|GO:0005
840|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138466_PI430048170 0.65401458573927 1.19138994146507 1.93872396081787
0.6474170566114612.61601192164914 A A A 2.76000748988949 0.630352192677802
0.43967419609099 A A A LNCV6_138466_PI430048170 mRNA
CCTCAATTCAAGTTAGAATCATGAAACAATAATGAAGCTCCTCCTATGTCTCTTTTCAAG NM_014005RefSeq chr5
+ 140847771 140854159 PCDHA9 9752 "protocadherin alpha 9, transcript variant 2"
GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_32671_PI430048170 0.3682310023924130.6814785763165830.3472785237103290.346374929918001
1.14416506611305 A A A 1.3555176611862 0.3225612798046771.66272208798533 A A A
LNCV6_32671_PI430048170 mRNA
ATAGAGGTTAATACCCTTGGGATAGGAAAGAAAACTTAAAGGGTAACTGATGGGGTTATC NM_001288760 RefSeq
chr19 - 44474427 44500523 ZNF180 7733 "zinc finger protein 180, transcript variant 5"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138156_PI430048170 0.0426243499630169 0.6120146512379427.2838498702882
7.17429571790731 7.36968647147328 P P P 7.64355968547696 8.05412673195769
8.20510427233976 P P P LNCV6_138156_PI430048170 mRNA
GGGACGTTGGATGCATTCATTTTCTGTAATAAAGTTTCTTAATCACTCTTCCCAAAAAGT NM_001301228 RefSeq
chrX + 150983384 150990775 HMGB3 3149 "high mobility group box 3, transcript variant 1"
GO:0045578|GO:0006355|GO:0003690|GO:0045638|GO:0008301|GO:0005694|GO:0003682|GO:0007275|GO:0006
338|GO:0006310|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140572_PI430048170 0.0292972986316281 0.497834175317829 5.29337330464824
4.62626886527142 4.91632551979051 P P P 5.51076374601935 6.04992131751616
6.27037510277103 P P P LNCV6_140572_PI430048170 mRNA
GGCTTCCTGCTTTTTTACCCTTGTATATTATCAGTGAAAAGGATCAACAGTTAATTTGAG NM_032217RefSeq chr4
- 73074784 73258785 ANKRD17 26057 "ankyrin repeat domain 17, transcript variant 1"
GO:0005515|GO:1900087|GO:0051151|GO:1900246|GO:1900245|GO:0005634|GO:0045787|GO:0005737|GO:0016
020|GO:0003682|GO:0045087|GO:0016032|GO:0043123|GO:0000785|GO:0001955|GO:0006275|GO:0042742 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_63271_PI430048170 0.5257813354732861.12608813004231 6.92635362235292 6.94079585390484
7.47970092035534 P P P 6.96932302697231 6.69925034556813 7.19369241269731 P P P
LNCV6_63271_PI430048170 mRNA
AATAATATTTTCCTCAGTACAATTTTGCTGGCCTTAACTGGTATCAAACGCTGTCATTGA NM_024612RefSeq chr17
+ 59565524 59608352 DHX40 79665 "DEAH (Asp-Glu-Ala-His) box polypeptide 40, transcript variant 1"
GO:0004004|GO:0006396|GO:0005737|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139726_PI430048170 0.40964752881096 0.8206660336233182.61830992704274
2.58050583171497 3.28338199378767 A A P 3.40105398328611 2.68700460733398
3.26770412763844 P P P LNCV6_139726_PI430048170 mRNA
TCATAAGGCCAGTCTTTCAGAATTTAATGTTCAGATTTTGTCATGGCAGTGAAAAAGATG NM_018665RefSeq chr6
+ 73394561 73417566 DDX43 55510 DEAD (Asp-Glu-Ala-Asp) box polypeptide 43
GO:0005622|GO:0004004|GO:0003723|GO:0008152|GO:0005524 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_119768_PI430048170 0.525184660379497 1.15193975426945 0.277997300179324
0.3105832446564290.957164028704836A A A 0.3773825501266860.33910400676678
0.322693635796816A A A LNCV6_119768_PI430048170 mRNA
CTTCCTGGAGGGGCAGCAACAGTCATTGCACAATAAGGATTTTTGAATGTATAATATCAT NM_002465RefSeq chr12
+ 101594930 101685880 MYBPC1 4604 "myosin binding protein C, slow type, transcript variant 1"
GO:0005515|GO:0032982|GO:0030049|GO:0003779|GO:0030016|GO:0008307|GO:0007155|GO:0031432|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141857_PI430048170 0.111554935119098 1.77734036767396 3.87994358227575
4.67684293073381 4.17933800141542 P P P 4.04694179559748 2.933843464356
3.12066220146106 P P P LNCV6_141857_PI430048170 mRNA
TTAAAGGTCAAGATAAAGTCAAAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCNM_002638RefSeq chr20
+ 45174898 45176544 PI3 5266 "peptidase inhibitor 3, skin-derived"
GO:0010951|GO:0004866|GO:0004867|GO:0005578|GO:0007620|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144622_PI430048170 0.1033918958325791.1158846249177 12.4208401815429
12.2937461275495 12.290337378113 P P P 12.0635103574549 12.267789608561
12.1955469198049 P P P LNCV6_144622_PI430048170 mRNA
AAGGGCGATGTGGAAGCGTTTGCCAAAGCCATGCAGAACAACGCCAAGCCCGAGCAGAAA NM_007002RefSeq
chr20 + 62302895 62308862 ADRM1 11047 "adhesion regulating molecule 1, transcript variant 1"
GO:0005515|GO:0000502|GO:0006368|GO:0005886|GO:0002020|GO:0043248|GO:0005737|GO:0016020|GO:0005
887|GO:0061133|GO:0010950|GO:0070628|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129959_PI430048170 0.2541241199130540.8298437444018818.40839966218802
8.49254261990678 8.37471051442851 P P P 8.37898536327625 8.92983966063931
8.72395656280291 P P P LNCV6_129959_PI430048170 mRNA
TTGACAGAAACCAGGTGCCTTCAGAGGCTCTCTGATTTAAATAAACCTTTCTTGTTTTTT NM_001078177 RefSeq
chr6 + 44223625 44234151 SLC29A1 2030 "solute carrier family 29 (equilibrative nucleoside
transporter), member 1, transcript variant 1"
GO:0015862|GO:0005886|GO:0005337|GO:0060079|GO:0071456|GO:0030431|GO:0055085|GO:0016323|GO:0006
139|GO:0016324|GO:0007595|GO:0016020|GO:0005887|GO:0015858|GO:0071333 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141699_PI430048170 0.000986512855934555 2.93914231465589 5.52547523722124
5.69263405175687 5.48103974859122 P P P 4.23234609217572 3.90080724779287
3.88086605489276 P P P LNCV6_141699_PI430048170 mRNA
GGAGGGTCTCTGGCTTTATTTTTCTGCTGTGCAGAATCCTATTTTATATTTTTTAAAGTC NM_003745RefSeq chr16 -
11254416 11256182 SOCS1 8651 suppressor of cytokine signaling 1
GO:0005515|GO:0016567|GO:0005159|GO:0019221|GO:0005634|GO:0060397|GO:0005829|GO:0060334|GO:0005

737|GO:0060337|GO:0060338|GO:0071230|GO:0045444|GO:0060333|GO:0042518|GO:0019901|GO:0019210|GO:0
046627|GO:0007259|GO:0046426|GO:0016023|GO:0004860|GO:0001932|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145394_PI430048170 0.9057802040128571.00993614483104 14.0301189240734
14.0232453878492 14.2611655713564 P P P 14.0628691433165 14.0060871584032
14.2081197694937 P P P LNCV6_145394_PI430048170 mRNA
AAGAGAGAGACATGTCAAAGAGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGCGGGACAT NM_033377RefSeq
chr19 - 49035568 49036934 CGB1 114335 "chorionic gonadotropin, beta polypeptide 1"
GO:0005179|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126820_PI430048170 0.00658739941220572 0.6378265620029 2.79517619586505
2.5882368657882 2.90963513123211 A A A 3.5342900152048 3.4078491558785
3.30632393068567 P P P LNCV6_126820_PI430048170 mRNA
CCTGTCTCTACATGGCCACCAAGTTCTGGCATTTCTACATCCTAAATCTTTTAATTTTAT NM_002794RefSeq chr1 -
35599540 35641844 PSMB2 5690 "proteasome (prosome, macropain) subunit, beta type, 2, transcript
variant 1"
GO:0005515|GO:0002474|GO:0010467|GO:0014070|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005
829|GO:0004298|GO:0034641|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0
005839|GO:0000502|GO:0043066|GO:0006521|GO:0051437|GO:0042590|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141160_PI430048170 0.0581258346746147 1.16932084438278 15.0732579793175
14.8570749777845 14.916055862339 P P P 14.8067042576915 14.7447246258633
14.6205015505044 P P P LNCV6_141160_PI430048170 mRNA
GCTCATGACAACTCAATAAAGCACTGCTTTTATTTTTTGCAGTCTTCAATTTGAGAAAGG NM_015379RefSeq chr7
+ 98281666 98291527 BRI3 25798 "brain protein I3, transcript variant 1" GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_137104_PI430048170 0.1117573701188221.06736740633102 0.482153867375438
0.5954022895532520.53239875545359 A A A 0.3810008978380470.454688994182197
0.492122716180442A A A LNCV6_137104_PI430048170 mRNA
TCAAAGTGTACACTACTGATGCTGTTTGTTGTACTGAGAGCACGTACCAATAAAAATGTT NM_014243RefSeq chr4
- 72280968 72568799 ADAMTS3 9508 "ADAM metallopeptidase with thrombospondin type 1 motif, 3"
GO:0005515|GO:0005578|GO:0005576|GO:1900748|GO:0005615|GO:0010573|GO:0031012|GO:0004175|GO:0016
485|GO:0030198|GO:0030199|GO:0030574|GO:0006508|GO:0008270|GO:0043206|GO:0032964|GO:0004222|GO:0
008201|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93244_PI430048170 0.1662172022975630.76229413605102811.1376688444309 11.2681261494626
11.3556475893452 P P P 11.7674277593684 11.2670644357008 11.8447187739741 P P P
LNCV6_93244_PI430048170 mRNA
GACCCTGGAATTACTGCAGTCCACAAGAATCGGAATGTCAGTTAATGCTATTCGCAAGCA NM_006756RefSeq chr8
- 53966553 54022456 TCEA1 6917 "transcription elongation factor A (SII), 1, transcript variant 1"
GO:0005515|GO:0010467|GO:0006368|GO:0006366|GO:0005730|GO:0005634|GO:0003677|GO:0050434|GO:0006
281|GO:0032784|GO:0006283|GO:0045944|GO:0030218|GO:0016032|GO:0005654|GO:0008270|GO:0006289 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143987_PI430048170 0.0938720740134744 0.8827236807734677.3032274568116
7.23203471771168 7.28419885472991 P P P 7.56805884080917 7.35242750463818
7.43151459752461 P P P LNCV6_143987_PI430048170 mRNA
CGCCAAAATTCGCTATGTTTACAGTGATACTATTAAGAAAATGAATGTGATTCTGCTCTG NM_000147RefSeq chr1
- 23845080 23868369 FUCA1 2517 "fucosidase, alpha-L- 1, tissue"
GO:0005737|GO:0004560|GO:0006027|GO:0016139|GO:0042806|GO:0006004|GO:0005764|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142014_PI430048170 0.4563142136195531.08923561538826 9.98522704811448

9.60650049466956 9.96787995951562 P P P 9.71210447596691 9.72397979227 9.78330358253 P P P LNCV6_142014_PI430048170 mRNA GAAAATAATGATCTGTACAGACAGGACAGAATGAAACTCCTGCGGGTCTTTGGCCTGAAA NM_001164317 RefSeq chr3 + 58008399 58172255 FLNB 2317 "filamin B, beta, transcript variant 1" GO:0005515|GO:0030018|GO:0001725|GO:0030036|GO:0005886|GO:0019221|GO:0003779|GO:0015629|GO:0030154|GO:0042802|GO:0005829|GO:0007165|GO:0005737|GO:0007519|GO:0016021|GO:0005925|GO:0005938|GO:0007016|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA LNCV6_141265_PI430048170 0.000490081794422074 0.5542566873045961 0.6448696275685 10.6710273486992 10.5480595891486 P P P 11.5426353953246 11.5108024019611 11.3610903470347 P P P LNCV6_141265_PI430048170 mRNA TTCTGGCAAATGGAGGCACGAACGCAGGGGCCAAATAGCAATAAATGGGTTTTGTTTTTT NM_018986 RefSeq chr4 + 8199332 8241103 SH3TC1 54436 SH3 domain and tetratricopeptide repeats 1 GO:0008150|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_134754_PI430048170 0.4060277795162534 23948545413996 3.73289018097087 0.3149237431060510.425917750408339 P A A 0.3451695158561120.313229924965663 0.302969357764464 A A A LNCV6_134754_PI430048170 mRNA CCAAGTCACCCGTTTTGGATGTGCATTTCATGTGACAATACAGATGACATGCAAATGGCC NM_032728 RefSeq chr9 + 131289693 131309262 PPAPDC3 84814 phosphatidic acid phosphatase type 2 domain containing 3 GO:0016787|GO:0008152|GO:0005789|GO:0016021|GO:0010832|GO:0005635 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_143501_PI430048170 0.0339598574849254 1.2672559517155 12.9046008806228 12.655732437413 12.6685375982546 P P P 12.358262364343 12.4882218805368 12.3674351829112 P P P LNCV6_143501_PI430048170 mRNA ACCCATGAGGAGCTGCTGTACAACAAGGAGAAGTTGCTCAACAACGGGGACAAGTGGGAG NM_002496 RefSeq chr11 + 68030616 68036647 NDUFS8 4728 "NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)" GO:0051539|GO:0005743|GO:0044281|GO:0046872|GO:0003954|GO:0005739|GO:0022904|GO:0032981|GO:0005747|GO:0006120|GO:0008137|GO:0006979|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_63829_PI430048170 0.0115037270938666 0.5353775925286136.35343927617027 6.1544090006051 6.60230919505178 P P P 7.32551399172446 7.18408403989366 7.3348200126626 P P P LNCV6_63829_PI430048170 mRNA ACACAGCAGTGATTGTCAGCTGCCAATAGCAAATGAAGTTATGGGTGACTTGAAATACCA NM_003831 RefSeq chr18 + 23452822 23483135 RIOK3 8780 RIO kinase 3 GO:0005515|GO:0007059|GO:0004674|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_145161_PI430048170 0.00504932818261892 1.39240831067595 12.8857526401447 12.7026324747424 12.710277664254 P P P 12.2778641884527 12.3993993012793 12.1883889211352 P P P LNCV6_145161_PI430048170 mRNA GCTACAGCAGGGCTCCAGGGACTCCAAATAAATGTTCAGTGACTGGCTCCAAGGAAAAAA NM_058192 RefSeq chr16 - 784973 788383 RPUSD1 113000 RNA pseudouridylate synthase domain containing 1 GO:0009982|GO:0008150|GO:0003674|GO:0003723|GO:0005575|GO:0001522 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_133245_PI430048170 0.195815950586484 0.7955394964794594 10.9926717881471 11.2600971277392 11.4488352362325 P P P 11.3340873023673 11.4721526471235 11.8670767637128 P P P LNCV6_133245_PI430048170 mRNA GTAGATGCATTAGTGTTGAACCAATGCTTTCTCATGTCTCAATTCTTTGTATATGCATTC NM_001039802 RefSeq chr1 + 22052626 22092943 CDC42 998 "cell division cycle 42, transcript variant 3" GO:0045859|GO:0005515|GO:0043497|GO:0046330|GO:0031424|GO:0035088|GO:0042802|GO:0031069|GO:0042692|GO:0051489|GO:0043525|GO:0043552|GO:0007173|GO:0007411|GO:0043025|GO:0007030|GO:0031274|GO:0

046847|GO:0051017|GO:0007088|GO:0005815|GO:0019901|GO:0032467|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142541_PI430048170 0.60964464238185 1.03164442985318 0.286680910683677 0.2964805881984590.49825784692058 A A A 0.3326043709108480.287131508547095 0.336363776591941 A A A LNCV6_142541_PI430048170 mRNA GCTTATTTGTAGTCACCTTGAACTGACTTAACCTAGAAGCTGTGCCTTCTTGTGAAAAAA NM_178423 RefSeq chr7 + 18495745 18997369 HDAC9 9734 "histone deacetylase 9, transcript variant 4"
GO:0005515|GO:0042826|GO:0046970|GO:0005634|GO:0046872|GO:0007507|GO:0005737|GO:0006954|GO:0007219|GO:0070491|GO:0005080|GO:0030183|GO:0051153|GO:0090050|GO:0004407|GO:0046969|GO:0032041|GO:0070932|GO:0005667|GO:0070933|GO:0016575|GO:0032869|GO:0034983|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52140_PI430048170 0.00295438424371901 0.4592377777872668.30154138804962 8.11613564356286 7.87756553770912 P P P 9.07603753420299 9.30059104483959 9.30601796728105 P P P LNCV6_52140_PI430048170 mRNA GACACACATCCAAGACAACCATGACGGCACGTATACAGTGGCCTACGTGCCAGACGTGAC NM_001110556 RefSeq chrX - 154348531 154374638 FLNA 2316 "filamin A, alpha, transcript variant 2"
GO:0005515|GO:0005802|GO:0031523|GO:0031267|GO:0046332|GO:0042993|GO:0042803|GO:0001948|GO:0051015|GO:0005080|GO:0043025|GO:0042789|GO:0043123|GO:0070062|GO:0034988|GO:0031532|GO:0034329|GO:0030168|GO:0017160|GO:0005925|GO:0008134|GO:0048471|GO:0005886|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135878_PI430048170 0.360688226751304 1.06252593994036 8.48211053598746 8.70647955633624 8.60787091482315 P P P 8.57822592969825 8.54974867230566 8.40910654160077 P P P LNCV6_135878_PI430048170 mRNA TATGAAAACTCTCATGAATAAACATCTCCGTGAAACGCCAAGGCCCTCGTCAAACCCTGA NM_001002244 RefSeq chr17 + 81891712 81900533 ANAPC11 51529 "anaphase promoting complex subunit 11, transcript variant 1"
GO:0007094|GO:0004842|GO:0016567|GO:0034450|GO:0051437|GO:0005730|GO:0051436|GO:0031145|GO:0051439|GO:0005829|GO:0007067|GO:0070979|GO:0005680|GO:0005654|GO:0008270|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127044_PI430048170 0.0200505457356238 0.756247506992917 8.95469796689733 8.99614635603145 8.81617253244256 P P P 9.46489727720843 9.18129817583189 9.32219534441714 P P P LNCV6_127044_PI430048170 mRNA CCTGTTGCCCTTTTGCCTAAGAAATCTTTAATGTTTCTATCTTGTAATAAACATGGGCAT NM_145294 RefSeq chr16 + 649362 667829 WDR90 197335 WD repeat domain 90 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140629_PI430048170 0.291752841763301 3.75654696336711 0.333974581572645 3.55234735281218 3.29915938424138 A P P 0.882241060154143 1.55580658613423 0.373708339773668 A A A LNCV6_140629_PI430048170 mRNA GGCATTATGCAAAAGTGGCTTGCACAAAGAAACAATTGCATTCTGCAACCTTCATTTTTT NM_006042 RefSeq chr17 - 13494031 13601942 HS3ST3A1 9955 heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1
GO:0000139|GO:0005975|GO:0033872|GO:0009405|GO:0008146|GO:0044281|GO:0016021|GO:0030203|GO:0006024 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63765_PI430048170 0.305293775799565 0.905899294096786 10.3977491364022 10.4251868742344 10.7099687789772 P P P 10.626535416586 10.5523509715582 10.7923430762755 P P P LNCV6_63765_PI430048170 mRNA GCAGTGGTCTTCCCCCTGCACTTTTCTGATCTAATTTCTGTTTTATACCTTATACCCAAA NM_020232 RefSeq chr18 + 12702987 12725741 PSMG2 56984 "proteasome (prosome, macropain) assembly chaperone 2, transcript variant 1" GO:0043248|GO:0005515|GO:0007094|GO:0043066|GO:0005634 . NA - . NA NA

NA NA NA NA NA NA NA
LNCV6_135262_PI430048170 0.000529174615397821 2.27003466551954 8.20313996579525
8.26099188216245 8.4657271260962 P P P 7.26880708407315 6.97700748413079
7.13454730985612 P P P LNCV6_135262_PI430048170 mRNA
GCATTGTTCTTTAGTTGGAGTTCTCATTCTTATTCTCCAGTACTGACTTGTGGGGAAAGC NM_001142648 RefSeq
chr10 - 70150204 70170529 SAR1A 56681 "secretion associated, Ras related GTPase 1A, transcript
variant 1" GO:0016529|GO:0005794|GO:0016192|GO:0005525|GO:0006886|GO:0070062 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_127413_PI430048170 0.0269704735985365 0.9518639641587340.404289882759499
0.3654711987451260.355285470736194A A A 0.4482812871382940.456262342555985
0.434401025584836A A A LNCV6_127413_PI430048170 mRNA
CAGACAGAAACCGAAAGCTCTATATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGC NM_017680RefSeq chr9
- 92456206 92482562 ASPN 54829 "asporin, transcript variant 1"
GO:0031012|GO:0070171|GO:0005518|GO:0005509|GO:0005578|GO:0030282|GO:0030512 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142820_PI430048170 0.00143551446665474 1.69784227548716 8.3982997722846
8.5330373995654 8.61984098430341 P P P 7.72947833623691 7.83003776837374 7.7061137813106
P P P LNCV6_142820_PI430048170 mRNA
ATTTTAAAAAATGCCAGTCTGGTCAGGGAAGTAGGGGGTTTCAATGCTGTTGGGAACCAG NM_014323RefSeq chr22
- 31325803 31346263 PATZ1 23598 "POZ (BTB) and AT hook containing zinc finger 1, transcript variant
1"
GO:0006355|GO:0005634|GO:0007283|GO:0003677|GO:0006351|GO:0046872|GO:0005737|GO:0030217|GO:0003
682|GO:0005654|GO:0045893|GO:0045892|GO:0008584 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131684_PI430048170 0.492563105750755 1.34311572010159 0.2878227705043561.4288119370208
1.5979776394109 A A A 0.4351156038826340.3410384174778171.34969137587945 A A A
LNCV6_131684_PI430048170 mRNA
GTCTGAACACTGGCCTGTGATTGGTCCATTCCAGGACCTTCATTTGCATAAGGTATCAAA NM_017912RefSeq chr4
+ 88378738 88443097 HERC6 55008 "HECT and RLD domain containing E3 ubiquitin protein ligase
family member 6, transcript variant 1"
GO:0005737|GO:0004842|GO:0042787|GO:0002244|GO:0016874|GO:0005634|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_50322_PI430048170 0.9486591972165390.9976903558529390.3101561264799640.674674267905051
0.501642615567476A A A 0.30697586569377 0.2727954464614340.861151570378092A A A
LNCV6_50322_PI430048170 mRNA
TGTGGTCGTGGACAATGCAGAGTTCCAGATGCTGGGGAGCGAAGCAGCCGTGCGTCATCG NM_001109RefSeq
chr10 - 133262415 133276903 ADAM8 101 "ADAM metallopeptidase domain 8, transcript variant 1"
GO:2000391|GO:0005515|GO:0051897|GO:0033089|GO:0051044|GO:0005886|GO:2000418|GO:2000415|GO:0035
419|GO:0071133|GO:0050714|GO:0042581|GO:0002102|GO:0032127|GO:0043621|GO:0043524|GO:0005737|GO:0
016337|GO:0051092|GO:0006954|GO:0002675|GO:0022617|GO:0045780|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129077_PI430048170 0.56892862580973 0.8965996083639540.369103868183293
0.3756431742701570.473692027380227A A A 0.9230330247388440.31753870914736
0.37188983139153 A A A LNCV6_129077_PI430048170 mRNA
ACCCAGAGAACAGAAGCGCTTTCTAAGAATGAACAAATATGTGAAATAGGATGTTTTGTG NM_032109RefSeq chr5
- 77628711 77638697 OTP 23440 orthopedia homeobox
GO:0043565|GO:0021985|GO:0006355|GO:0021879|GO:0021979|GO:0002052|GO:0005634|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145569_PI430048170 0.2720088900540981.03812861904798 0.524033410299529
0.6162060162570230.499947058171386A A A 0.4895155337670340.491220138021962

0.500100076588626 A A A LNCV6_145569_PI430048170 mRNA
TTTCCTCCAGGAATCGTGTTTCAATTGTAACCAAGAAATTTCCATTTGTGCTTCATGAAA NM_001725 RefSeq chr20
+ 38304149 38337503 BPI 671 bactericidal/permeability-increasing protein
GO:0001530|GO:0050829|GO:0006955|GO:0005737|GO:0032717|GO:0032715|GO:0005887|GO:0043031|GO:0032
720|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58587_PI430048170 0.912733263690372 1.01081280575982 9.18590671594812 9.43516319734265
9.45681939111958 P P P 9.29441378694831 9.42025661946554 9.32911488596406 P P P
LNCV6_58587_PI430048170 mRNA
GACAGAAAGCGCACAGAATCTTGGACCAGGTCTCTCTTCCTTGTCCCCCCTGCTTTTCTC NM_001007026 RefSeq
chr12 + 6924462 6942321 ATN1 1822 "atrophin 1, transcript variant 1"
GO:0005515|GO:0048471|GO:0030054|GO:0003714|GO:0019904|GO:0005634|GO:0000122|GO:0030011|GO:0051
402|GO:0007417|GO:0006351|GO:0016363|GO:0005737|GO:0050827|GO:0016477|GO:0005654|GO:0009404 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127997_PI430048170 0.352008185791724 0.880511982261491 8.26806597471225
8.58163062677612 8.48906968511913 P P P 8.35074261108225 8.7420218790644
8.77694471185202 P P P LNCV6_127997_PI430048170 mRNA
CCCTTGTCCTTGAGTGCTCTTGCTATTAACGTTATTTGTAATTTAGTTTGTAGCTCATTA NM_001798 RefSeq chr12 +
55966768 55972789 CDK2 1017 "cyclin-dependent kinase 2, transcript variant 1"
GO:0005515|GO:0032298|GO:0000793|GO:0008284|GO:0015030|GO:0071732|GO:0005634|GO:0007265|GO:0031
145|GO:0046872|GO:0005829|GO:0000082|GO:0005737|GO:0000086|GO:0006813|GO:0006977|GO:0000806|GO:0
005667|GO:0000781|GO:0005813|GO:0030332|GO:0000805|GO:0016572|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142803_PI430048170 0.630176523062503 0.557083085382378 0.439585019765231
1.33850219318081 0.43226692560083 A A A 0.391316623970458 2.75205197684754
0.430652814503141 A P A LNCV6_142803_PI430048170 mRNA
TCACCTACCTTGCCTGCACTAACTGGTGATAATAAAGACCTTATTGATCAGGTCAAAAAA NM_003433 RefSeq chr19
- 58432813 58440222 ZNF132 7691 zinc finger protein 132
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141669_PI430048170 0.00733380330197833 0.736710398142458 12.5385167432931
12.3351164734675 12.3705908334481 P P P 12.8057706705676 12.9266194713857
12.8399033098253 P P P LNCV6_141669_PI430048170 mRNA
TCATGTCCCCAACTCAAGGCTAGAAAACAGCAAGATGGAGAAATAATGTTCTGCTGCGTC NM_005628 RefSeq chr19
- 46774882 46788585 SLC1A5 6510 "solute carrier family 1 (neutral amino acid transporter), member 5,
transcript variant 1"
GO:0005515|GO:0042470|GO:0005794|GO:0005886|GO:0006865|GO:0009615|GO:0055085|GO:0003333|GO:0006
860|GO:0015804|GO:0015194|GO:0016020|GO:0001618|GO:0005887|GO:0015825|GO:0006868|GO:0015175|GO:0
006835|GO:0015186|GO:0004872|GO:0017153|GO:0070062|GO:0006811 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129360_PI430048170 0.0446724557936417 0.722202287776112 10.8927716110015
10.9563825708269 10.8530001876237 P P P 11.1546214124384 11.5319832702406
11.4009320780402 P P P LNCV6_129360_PI430048170 mRNA
GGCAAATACTAAAAATCTCGTCAATGTAATTTCTGTGGTTTCTATTCAGCTTGGGTTTCA NM_025250 RefSeq chr7
+ 2631968 2664802 TTYH3 80727 tweety family member 3
GO:0006821|GO:0034220|GO:0005886|GO:0034707|GO:0005229|GO:0055085|GO:0005254|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139210_PI430048170 0.215675569471443 1.18770987689666 8.68359084460278
8.52000539664599 8.49523098961398 P P P 8.04039850133695 8.55707427136315
8.31814018474533 P P P LNCV6_139210_PI430048170 mRNA

AGCTGCTGTGTACCTTTGGCTCTGAATTAGGAATATCTTTACTTTCTCTTTTCCAAAAAANM_001286581 RefSeq chr11_KI270832v1_alt + 106101 142116 PHRF1 57661 "PHD and ring finger domains 1, transcript variant 1" GO:0006397|GO:0016020|GO:0006366|GO:0019904|GO:0008270|GO:0070063 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126694_PI430048170 0.18504645971724 0.5309006276512620.3337084089083970.3565256230406 0.341850975574614A A A 0.3502423861677151.44060932902089 1.67062698187923 A A A LNCV6_126694_PI430048170 mRNA
TGGCTCATGTCATCACACCTCAGGTTATTGTAGAGAACTGGAAAGACAGAATCCATACTC NM_002350RefSeq chr8 + 55879826 56012447 LYN4067 "LYN proto-oncogene, Src family tyrosine kinase, transcript variant 1" GO:0005515|GO:0014070|GO:0002513|GO:0002762|GO:0001817|GO:0034605|GO:0005758|GO:0009743|GO:0007411|GO:0031668|GO:0002902|GO:0038083|GO:0031663|GO:0031625|GO:0030061|GO:0023014|GO:0032868|GO:0030335|GO:0005794|GO:0006991|GO:0030889|GO:0030168|GO:0009636|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65539_PI430048170 0.1032254494913990.8846649336649667.64913795432518 7.54415859038107 7.56604350658574 P P P 7.63939148097614 7.86914088978721 7.7741459389605 P P P LNCV6_65539_PI430048170 mRNA
TGGAACTCCTGTCCCCTTAGTCATGAGAACAGAAAGTGCAATATTTCCTTTCACCTGGCA NM_004036RefSeq chr2 - 24819169 24919186 ADCY3 109 adenylate cyclase 3 GO:0005516|GO:0007608|GO:0005886|GO:0007268|GO:0007202|GO:0044281|GO:0007193|GO:0046872|GO:0035556|GO:0005737|GO:0007173|GO:0071377|GO:0006171|GO:0006833|GO:0034199|GO:0048011|GO:0055085|GO:0005524|GO:0003091|GO:0007165|GO:0005929|GO:0006112|GO:0004016|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144270_PI430048170 0.5635064651033370.9503632922053979.1340736896484 9.21879109499493 8.85338275407345 P P P 9.21805096732449 9.18391616074142 9.04357923106802 P P P LNCV6_144270_PI430048170 mRNA
ACTCCACATGCTTTTCTTTTTCTAATAAACCAGGGTCCATCTGACCCCAGCGCTAAAAAA NM_138813RefSeq chr19 - 1782074 1812276 ATP8B3 148229 "ATPase, aminophospholipid transporter, class I, type 8B, member 3, transcript variant 1" GO:0005794|GO:0000287|GO:0005886|GO:0005783|GO:0008152|GO:0004012|GO:0007030|GO:0016021|GO:0007339|GO:0005524|GO:0002080|GO:0045332 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134134_PI430048170 0.15840105379548 1.64605069558484 1.91909379569782 0.8362603271449641.51235070936342 A A A 0.9025756849020350.303498346769847 1.00845043508118 A A A LNCV6_134134_PI430048170 mRNA
CCCAACACCTGGCTTGGGCTCACTGTCCTGAGTTGCAGTAAAGCTATAACCTTGAATCAC NM_138342RefSeq chr11 + 134331873 134376324 GLB1L2 89944 "galactosidase, beta 1-like 2" GO:0005773|GO:0004565|GO:0005975|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130384_PI430048170 0.00875720250114915 1.44468768440937 13.598527115291 13.8126454568399 13.8677521911349 P P P 13.3300569881074 13.2171551698955 13.1473067782883 P P P LNCV6_130384_PI430048170 mRNA
GGCTCCCAGCCCCTTGCACCCTCATTGCTGTTCAGATTAAAGCCTCTGTTTTGCACCTGT NM_178001RefSeq chr9 + 129111313 129148946 PPP2R4 5524 "protein phosphatase 2A activator, regulatory subunit 4, transcript variant 1" GO:0000413|GO:0043065|GO:0046982|GO:0035307|GO:0008601|GO:0035308|GO:0003755|GO:0005102|GO:0000159|GO:0005634|GO:0034704|GO:0005524|GO:0042803|GO:0008160|GO:0030472|GO:0005737|GO:0008152|GO:0032516|GO:0032515|GO:0043666|GO:0005654|GO:0051721|GO:0016887|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136954_PI430048170 0.7052651079464331.0379908401667 6.61635438846403 6.40567843727556 6.25280616324657 P P P 6.40312993474698 6.34342422723436 6.3894448325682 P P P LNCV6_136954_PI430048170 mRNA

GCCTTATAAAAATGGACCAAACCCTTTTCTAAAATAAAATAGTTCTAGGGTGGCTGGTTA NM_017875 RefSeq chr3 + 39383323 39397328 SLC25A38 54977 "solute carrier family 25, member 38" GO:0030218|GO:0006810|GO:0005743|GO:0016021|GO:0006783 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135512_PI430048170 0.6119650612451060.9847274088787840.41976628907161 0.4442683537353010.357653867021084 A A A 0.4894780266062850.390239178550199 0.408005646114859 A A A LNCV6_135512_PI430048170 mRNA
CTTCATCGCATTCTCATTTCTGTGTACATTTGCAAGATGTGTGTAATGTCATTTTCCAAA NM_000555 RefSeq chrX - 111293778 111411146 DCX 1641 "doublecortin, transcript variant 1" GO:0005515|GO:0008017|GO:0043005|GO:0019901|GO:0005875|GO:0005874|GO:0048675|GO:0021952|GO:0007417|GO:0005829|GO:0007399|GO:0035556|GO:0048813|GO:0007411|GO:0007420|GO:0001764|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99321_PI430048170 0.154127912480605 0.4704468633384 1.42255470016258 0.302636452813217 0.299783237657085 A A A 0.967372882623545 1.64892778299287 2.54721038836552 A A P LNCV6_99321_PI430048170 mRNA
CAATTGAAAAGTCTTCTGTGAATTATGAGCCTTCTAACCCTTCCGAAAAAGGAAGTAAAA NM_024997 RefSeq chr16 + 10386054 10483638 ATF7IP2 80063 "activating transcription factor 7 interacting protein 2, transcript variant 1" GO:0006355|GO:0005737|GO:0005730|GO:0005654|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130482_PI430048170 0.171384500963923 1.16305949076195 0.737530010314887 0.392236812803859 0.667858072231002 A A A 0.281724023053034 0.420623785671948 0.458185641468259 A A A LNCV6_130482_PI430048170 mRNA
AGCACTGCGGCCAAGTCGAAGACTTTAGGAGCAATAAAAGTGCTTATTGTGTTTCAGTCA NM_021615 RefSeq chr16 - 75473123 75495028 CHST6 4166 carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6 GO:0006790|GO:0005794|GO:0018146|GO:0000139|GO:0005975|GO:0009405|GO:0006044|GO:0044281|GO:0016021|GO:0001517|GO:0030203|GO:0042339 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137452_PI430048170 0.39392161776817 0.771346170600841 0.492260840502771 0.479643612380147 0.258530482305529 A A A 0.402946239159216 1.30970191656448 0.465857825619973 A A A LNCV6_137452_PI430048170 mRNA
CCTAACTAGGACCTTACTACTCTGATTCTGTAGCACCAATAAATAGATATTTTCACCTTG NM_001004308 RefSeq chrX + 112083024 112457245 ZCCHC16 NA "zinc finger, CCHC domain containing 16" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104935_PI430048170 0.0113246447274302 0.536810173485196 6.7356743228751 7.10564490681228 7.0465316219617 P P P 8.10721568041871 7.58079458632967 7.87131448938711 P P P LNCV6_104935_PI430048170 mRNA
CATTCTTTTCGGGCTGCCGAGAACAGGGAGCTAAACATCACCATCATCTAAGAGCGGGTC NM_198181 RefSeq chr15 + 82429979 82439386 GOLGA6L9 440295 "golgin A6 family-like 9, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126861_PI430048170 0.405558839245799 0.875258198707929 11.2832145543736 11.461488314888 11.8350188040299 P P P 11.6061884991231 11.5707618328533 11.9957533149751 P P P LNCV6_126861_PI430048170 mRNA
CAGGGTATGATCTGCTATTGTTATTTCTCCTCTTTATTGGAAAAAGGCCTCAGTTTTAATNM_015702 RefSeq chr2 - 149569632 149587816 MMADHC 27249 "methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria" GO:0005739|GO:0009235|GO:0006766|GO:0006767|GO:0044281|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131367_PI430048170 0.196755238830842 1.28661863092875 4.84829827143649 5.03549202319554 4.44510028731433 P P P 4.71834710320919 4.30844327663924 4.2227413310049 P P P LNCV6_131367_PI430048170 mRNA
TGGACATCCCCTTCCTGAGCTACCTGCCCACTGAGGTGCAGCTCATTAACGAAGCCTATG NM_198537 RefSeq chr19

+ 19528860 19537584 YJEFN3 NA "YjeF N-terminal domain containing 3, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117891_PI430048170 0.1360280549497531.49273504554238 4.40416685382208 4.5066732357165 4.57578246131283 P P P 4.3543099246379 3.8072369253879 3.45099338860073 P P P
LNCV6_117891_PI430048170 mRNA
GACAACAGCAGAAGCTTCTGAAAGTCCTCCAGGCCGTCGAAAGTGACTCTGCCCATCTCG NM_015202RefSeq chr16
+ 27550146 27780371 KIAA0556 23247 KIAA0556 GO:0005886|GO:0005654|GO:0005634|GO:0005615
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132220_PI430048170 0.2231688344027041.08734322144923 0.595807730621245 0.8147412663020560.622373853584562A A A 0.5008407962906810.589431293372738 0.588483665975746A A A LNCV6_132220_PI430048170 mRNA
CTACTCCACATTGCAACATTTCCATCAGACAGCATTTCAATTCCAGTATTATGTATATTG NM_003480RefSeq chr12
- 8645942 8662888 MFAP5 8076 "microfibrillar associated protein 5, transcript variant 1"
GO:0030198|GO:0001527|GO:0005576|GO:0043206|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103406_PI430048170 0.2337169089157351.20493319401028 11.7176664995064 12.0159673408848 12.2458498700351 P P P 11.7629817911126 11.5731381942976 11.8691723851922 P P P LNCV6_103406_PI430048170 mRNA
GAAGCCCAGAAAATTGGGTATGTTCTAGAGATTTACCACCATTGCTTATTGCTTTTTTCT NM_016039RefSeq chr14
+ 51989509 52004702 C14orf166 51637 chromosome 14 open reading frame 166
GO:0005515|GO:0006388|GO:0048471|GO:0005815|GO:0003723|GO:0000993|GO:0050658|GO:0005634|GO:0072669|GO:0006351|GO:0005829|GO:0042802|GO:0005737|GO:0045944|GO:0016032|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137157_PI430048170 0.3133352676982881.33626283471709 3.06200810441295 3.43868763107408 2.96025647286217 P P P 3.1631129691089 1.95513012987266 2.87837794786098 P A P LNCV6_137157_PI430048170 mRNA
AGAAACATATAGATCTGGTTTGAATTCCAGATCGAGTTTACAGTTGTGAAATCTTGAAGG NM_001289107 RefSeq chr17 - 76624755 76643838 ST6GALNAC1 55808 "ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1, transcript variant 2"
GO:0001665|GO:0009312|GO:0008373|GO:0000139|GO:0006486|GO:0016021|GO:0006488|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142617_PI430048170 0.0223515906096813 0.6098686272876097.2176656568176 7.12299153410603 7.326075286732 P P P 7.68947797187737 7.92356954864521 8.16244059272026 P P P LNCV6_142617_PI430048170 mRNA
CTTGTCCAGTCCATTGTGAAATTATCCCAGCAGCTGTAATGTACAGTTCCTTCTGAAGCA NM_012199RefSeq chr1
+ 35883208 35924298 AGO1 26523 argonaute RISC catalytic component 1
GO:0005515|GO:0010467|GO:0003723|GO:0016441|GO:0005829|GO:0010586|GO:0035068|GO:0005737|GO:0007219|GO:0007173|GO:0000932|GO:0045944|GO:0048011|GO:0048015|GO:0000956|GO:0004521|GO:0000978|GO:0006351|GO:0035278|GO:0035198|GO:0008543|GO:0030529|GO:0045087|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131251_PI430048170 0.6261135630632540.9533658033692660.463382336426609 0.4455397340584180.458689007933273A A A 0.3875045422467930.728410343279936 0.434269171495507A A A LNCV6_131251_PI430048170 mRNA
ATCAAGACTCAGAGCTGCTTTCAGATAACCACATTCTCACCACCATAGGGGACATCTTTG NM_000102RefSeq chr10
- 102830530 102837533 CYP17A1 1586 "cytochrome P450, family 17, subfamily A, polypeptide 1"
GO:0030424|GO:0006694|GO:0006805|GO:0018963|GO:0030325|GO:0006702|GO:0005783|GO:0006704|GO:0018879|GO:0044281|GO:0051591|GO:0047442|GO:0005739|GO:0010034|GO:0071371|GO:0060992|GO:0010212|GO:0043025|GO:0031667|GO:0090031|GO:0007548|GO:0032526|GO:0018958|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_78955_PI430048170 0.00927472827391827 0.2178192896979323.48984995091564 2.6764079769121
3.89842862648396 P A P 5.09682743878498 5.83541677707479 5.85960435708175 P P P
LNCV6_78955_PI430048170 mRNA
GACCTGGCTGAATCCCAGATGTATCAATAAATTGTTATAGTAGCTTATGGAAAATGCTAT NM_001122838 RefSeq
chr7_KI270806v1_alt + 95602 145153 NAPEPLD 222236 "N-acyl phosphatidylethanolamine
phospholipase D, transcript variant 1"
GO:0005737|GO:0007603|GO:0042622|GO:0070290|GO:0008270|GO:0009395|GO:0001523|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137358_PI430048170 0.2490384309677860.9268360579424798.49523098961398
8.64444198535314 8.54024759613176 P P P 8.63782769376215 8.57403381077189
8.79218549344805 P P P LNCV6_137358_PI430048170 mRNA
GTCAGAGGATAAACTCCCAACCTAGACCTTTCACTTAAAATAGTGTGAATTTGTATATGT NM_058182 RefSeq chr21
+ 34375449 34389154 SMIM11 54065 small integral membrane protein 11
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127849_PI430048170 0.7620017921128560.9776049913310250.298791367745991
0.5038505802220930.346495588040351 A A A 0.5305215972279520.438136151836798
0.275079279802797 A A A LNCV6_127849_PI430048170 mRNA
TGTTTTGCCAACACAACACCCTCTGGCAAAAGTGTCAGTTCCTCATCTTCTGTGGAAACA NM_145026 RefSeq chr6
+ 44342659 44377167 SPATS1 221409 "spermatogenesis associated, serine-rich 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136055_PI430048170 0.2548315438707880.8145583664162238.55788728947051
8.12767007568335 7.86069779124976 P P P 8.62208550635845 8.56454717685273
8.31631351584644 P P P LNCV6_136055_PI430048170 mRNA
CTCCCCTCCCCTGCTGCAGGGGCTCTGGAGAGAAACAATAAAGAGATTCACACACAAGCC NM_001927 RefSeq chr2
+ 219418376 219426739 DES 1674 desmin
GO:0005515|GO:0005882|GO:0008092|GO:0030018|GO:0030049|GO:0031594|GO:0008016|GO:0042802|GO:0005
829|GO:0005916|GO:0042383|GO:0006936|GO:0007010|GO:0005200|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144808_PI430048170 0.96001401355961 0.9793274616472587.31298805345335
7.17867165576427 7.26472469967466 P P P 7.55318204992892 6.94629800229179
7.28714380720778 P P P LNCV6_144808_PI430048170 mRNA
GGGCAGTTTTTCTGTATTTTATAAGTATCTTCATGTATCCCTGTTACTGATAGGGATACA NM_003183 RefSeq chr2
- 9489280 9555788 ADAM17 6868 ADAM metallopeptidase domain 17
GO:0005515|GO:0007220|GO:0032717|GO:0033025|GO:0030307|GO:0005112|GO:0048536|GO:0007219|GO:0007
173|GO:0030198|GO:0030574|GO:0006508|GO:0032496|GO:0006509|GO:0002467|GO:0033077|GO:0030335|GO:0
009986|GO:0045741|GO:0035625|GO:0032722|GO:0030165|GO:0055099|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144068_PI430048170 0.0366074178463968 0.9676657558194790.344053294572883
0.3730171755446560.336005944740358 A A A 0.41163648784172 0.405810514199426
0.37792591815971 A A A LNCV6_144068_PI430048170 mRNA
GGATGTTTTCAATTGGTTCTTCAACTAAGCTCTTGCAGAGTGAGATGACTTGAAATAAAA NM_133468 RefSeq chr7
+ 33904910 34155872 BMPER 168667 BMP binding endothelial regulator
GO:0030514|GO:0001657|GO:0048839|GO:0010594|GO:0002043|GO:0042118|GO:0070374|GO:0045446|GO:0005
615|GO:0060393 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127334_PI430048170 0.3046874160480821.2031777654107 5.60118661075298 5.9836674352942
5.46432710029232 P P P 5.72418675969185 5.36949434384473 5.14688021840912 P P P
LNCV6_127334_PI430048170 mRNA
AGCTTCAAATGGTACAAAAGGGTTAACAGTGATCGTGAAGTCTCTGTCCTTTCCCTCTTC NM_198150 RefSeq chr5
+ 95555120 95605102 ARSK 153642 "arylsulfatase family, member K"

GO:0006665|GO:0006687|GO:0005788|GO:0005576|GO:0004065|GO:0044281|GO:0044267|GO:0046872|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144495_PI430048170 0.1479522790604140.9305684413928150.313061144035523 0.34032571220967 0.340382678158171A A A 0.4217627920992380.517617867452097 0.361705485736067A A A LNCV6_144495_PI430048170 mRNA AAGAGTTACTTCGACAAGACGTTTCTATCTCTTCCCAGTACATTAAAATAAGGAAGCTGT NM_001007232 RefSeq chr11 - 105092468 105101431 CARD17 440068 "caspase recruitment domain family, member 17" GO:0010951|GO:0005737|GO:0004869|GO:0042981 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133067_PI430048170 0.0231287229619296 0.63584610183683 5.54924128844837 5.62663007185704 5.87591489994304 P P P 6.18065926219224 6.20248586464606 6.60766547329388 P P P LNCV6_133067_PI430048170 mRNA CAGTGTAAGCAGTAATACCATGTTGTAAGAGGGAACATTAAAGCCCATTTTATGACATAT NM_138469RefSeq chr10 + 98134623 98244897 R3HCC1L 27291 "R3H domain and coiled-coil containing 1-like, transcript variant 2" GO:0000166|GO:0035145 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141316_PI430048170 0.0604531238161987 1.96307618217507 1.08018009659052 1.60687710315621 2.06017463736829 A A A 0.3664046582685220.892964751463417 0.684296909619018A A A LNCV6_141316_PI430048170 mRNA TTACAGTTCTTAGCACTGAACTCGTCACAGTGTTTTAACATACCCCTTGGCCCACTGCAT NM_173565RefSeq chr7 + 6754108 6798765 RSPH10B 222967 radial spoke head 10 homolog B (Chlamydomonas) NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130310_PI430048170 0.0776232421569327 1.77730329720063 8.87367741650479 9.326218235934 9.07778330298914 P P P 8.77157156102468 7.78379657399595 8.08604225434148 P P P LNCV6_130310_PI430048170 mRNA GCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTTGTGCTCCTTTTTTCTGTTG NM_144717RefSeq chr3 + 136957864 137011084 IL20RB 53833 interleukin 20 receptor beta GO:0002437|GO:0032703|GO:0032753|GO:0004896|GO:0005886|GO:0032733|GO:0019221|GO:0001808|GO:0042130|GO:0048873|GO:0042015|GO:0002765|GO:0016021|GO:0032689 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141734_PI430048170 0.3301821004186771.34220647311156 3.84312225636095 3.19320338304914 2.85046600885536 P P A 3.05225975025114 3.00940671594502 2.70772727376611 P P P LNCV6_141734_PI430048170 mRNA GGGGAGGGCACCTCAGCCCCTGAAGACAAGCAGCACTGCAGTGGCAAAAATGGAAACACT NM_017781RefSeq chr7 + 983198 989640 CYP2W1 54905 "cytochrome P450, family 2, subfamily W, polypeptide 1" GO:0006805|GO:0005506|GO:0009986|GO:0008395|GO:0044281|GO:0006082|GO:0043390|GO:0043231|GO:0005737|GO:0019825|GO:0042738|GO:0005789|GO:0005788|GO:0016712|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143834_PI430048170 0.2471770166293171.1848323057391 7.53708752293914 7.79699340877339 7.82845408550035 P P P 7.23731227253349 7.39139554959869 7.76504072437807 P P P LNCV6_143834_PI430048170 mRNA CATTCTGCAGCGTTTCTCTTTCCCTTGGAAAAGAGAATTTATCATTACTGTTACATTTGT NM_002090RefSeq chr4 - 74036590 74038773 CXCL3 2921 chemokine (C-X-C motif) ligand 3 GO:0008009|GO:0006955|GO:0070098|GO:0006954|GO:0007186|GO:0042127|GO:0030593|GO:0032496|GO:0005576|GO:0045236|GO:0005615|GO:0002690 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103260_PI430048170 0.00312210326750178 1.64970450382178 13.0117290359032 13.1821349988315 13.0854495814727 P P P 12.3943735059324 12.3535601531943 12.36953782343 P P P LNCV6_103260_PI430048170 mRNA CGGGGAGGGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTC NM_031434RefSeq chr7 - 151081084 151083326 TMUB1 83590 "transmembrane and ubiquitin-like domain containing 1, transcript variant 1" GO:0005737|GO:0005654|GO:0016021 . NA - . NA NA NA NA NA NA NA NA

NA
LNCV6_142785_PI430048170 0.2335464218408411.02536359250948 0.334486966850294
0.2725414506149480.268120577768351 A A A 0.2510129155902110.264333238390076
0.252317675493121 A A A LNCV6_142785_PI430048170 mRNA
CAGGAGCTTGTAAACTAGGCCCAATAGAAATATTTTTAGGATCTATATGGCTACTTTAGC NM_207363 RefSeq chr2
- 132671798 133568460 NCKAP5 344148 "NCK-associated protein 5, transcript variant 1"
GO:0008150|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_27280_PI430048170 0.3913372806380190.80911076204826 0.4368347800861740.408450648902801
0.279152986058448 A A A 1.12559093301513 0.3977818824830390.393704307978371 A A A
LNCV6_27280_PI430048170 mRNA
AGACTTTGCATGGACTTTGCACAGGTTCCATTTCCATCGTGTGCAGACACCTGTATCTTT NM_024734 RefSeq chr14
- 95181938 95319908 CLMN 79789 "calmin (calponin-like, transmembrane)"
GO:0005737|GO:0008285|GO:0003779|GO:0016021|GO:0031175 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128453_PI430048170 0.8645279996199240.97287731511319411.0417061456818
10.9432193086246 10.97017577021 P P P 10.742594493893 11.0881409341775
11.2060109809689 P P P LNCV6_128453_PI430048170 mRNA
GGCTGCAGAGTTATAAGCCCCAAACAGGTCATGCTCCAATAAAAATGATTCTACCTACAA NM_006289 RefSeq chr9
- 35697336 35732395 TLN1 7094 talin 1
GO:0005515|GO:0005886|GO:0005158|GO:0006928|GO:0030968|GO:0005829|GO:0005737|GO:0051015|GO:0006
936|GO:0005911|GO:0007411|GO:0030274|GO:0007016|GO:0070062|GO:0005815|GO:0009986|GO:0030168|GO:0
032587|GO:0005576|GO:0001726|GO:0070527|GO:0005178|GO:0030866|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136173_PI430048170 0.0413994690293986 1.06543775996654 0.345309390919272
0.3994299807902880.322053873175979 A A A 0.2527329597194540.284424860271843
0.256182531195021 A A A LNCV6_136173_PI430048170 mRNA
GGCTATAAGTATTGTGACAGATATACAATTGTAATTTTGGCACTGAATCACATGTCTCCT NM_182559 RefSeq chr12
+ 50842917 50887880 TMPRSS12 283471 "transmembrane (C-terminal) protease, serine 12"
GO:0004252|GO:0006508|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108023_PI430048170 0.9003530607797940.9943005071113826.01097239406818
5.62957762208868 5.65858177456779 P P P 5.80194981703228 5.84159227363351
5.70919963718008 P P P LNCV6_108023_PI430048170 mRNA
CCGGAAGGAGACGTGGCGGCGGTTGGGCCGGTGATACCCGGGCGCTTTATAGTCCCGCCG NM_015701 RefSeq
chr2 + 53786930 53818819 ERLEC1 27248 "endoplasmic reticulum lectin 1, transcript variant 1"
GO:0005515|GO:0001948|GO:0005788|GO:0044322|GO:0030433 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139615_PI430048170 0.1268998429614150.4445359306363068.31814018474533
6.63264081512163 6.63741952705499 P P P 8.6006789155699 8.74173342217786
8.44643462552826 P P P LNCV6_139615_PI430048170 mRNA
CATGCTGCTGCTACTGCTAACAGCCAATTTTATAGACAGAGAAAGTATTTTGTGTTCAAA NM_001280796 RefSeq
chr12 - 56470943 56488414 GLS2 27165 "glutaminase 2 (liver, mitochondrial), transcript variant 3"
GO:0005515|GO:0006520|GO:0072593|GO:0007268|GO:0008652|GO:0042981|GO:0044281|GO:0014047|GO:0007
269|GO:0005739|GO:0034641|GO:0005759|GO:0004359|GO:0006541 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_110337_PI430048170 0.00706403266367466 2.29701898716611 3.51459695606259
3.70441920728433 3.5874151203175 P P P 2.32434273153557 2.18183373387949
2.66402606633566 A A P LNCV6_110337_PI430048170 mRNA
ATATTTGGGAATTAGTGGAGTGATCTCTGAAGACCTAGGGCTATGATCTGGAGCTGCTGT NM_198536 RefSeq chr19
- 11342775 11346305 TMEM205 374882 "transmembrane protein 205, transcript variant 1"

GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131745_PI430048170 0.14986824295836 0.5424114944003840.284295343441453
0.3160045366758260.280260822620011A A A 1.52015409396654 0.397857347064114
1.37485503270759 A A A LNCV6_131745_PI430048170 mRNA
TTGTAATTTATTGAAGTTTTACTCAATCCAAATAAAACTTAATTTATTGAAGACAAAAAA NM_005169RefSeq chr11
- 72239076 72244176 PHOX2A 401 paired-like homeobox 2a
GO:0000790|GO:0021523|GO:0000977|GO:0003700|GO:0021642|GO:0006351|GO:0048485|GO:0043576|GO:0021
703|GO:0071542|GO:0045944|GO:0021623|GO:0030901|GO:0003357 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130537_PI430048170 0.2797135094089690.9539485836557061 4.2816929381094
14.3088355348141 14.3488747396466 P P P 14.2923296621331 14.4017259620095
14.4458894215816 P P P LNCV6_130537_PI430048170 mRNA
TAGGCTGCACAAGAGCCTTGATTGAAGATATATTCTTTCTGAACAGTATTTAAGGTTTCC NM_001686RefSeq chr12
- 56638174 56646068 ATP5B 506 "ATP synthase, H+ transporting, mitochondrial F1 complex, beta
polypeptide"
GO:0042645|GO:0006629|GO:0005515|GO:0005215|GO:0042288|GO:0005886|GO:0005634|GO:0044281|GO:0006
091|GO:0005739|GO:0006754|GO:0046961|GO:0005759|GO:0006933|GO:0016887|GO:0044237|GO:0070062|GO:0
006996|GO:0031966|GO:0009986|GO:0022857|GO:0001525|GO:0005524|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142951_PI430048170 0.8371188577637060.9793839663288388.56836113897119
8.91957700594094 9.27573614396525 P P P 9.03185983189747 8.76954503330825
9.11651742080758 P P P LNCV6_142951_PI430048170 mRNA
CTGAAGATAATGCTGCATTTCTGGGTTTCTTGTGTGGATTTTAAAATAAATTGTGCCTAC NM_020319RefSeq chr7
- 16599775 16645817 ANKMY2 57037 ankyrin repeat and MYND domain containing 2
GO:0005929|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135032_PI430048170 0.0362155693791676 0.3596937413185451.32065132205427
2.28783095420618 2.41714418868462 A A A 3.3880355220436 3.7710043078609
3.49169879451542 P P P LNCV6_135032_PI430048170 mRNA
CTCTATAATCAGTGTGCTTCTGCTGTGCAGAAATGTTAGAAACGTATTGTCTAAATATCT NM_001130058 RefSeq
chr1 - 75202130 75611114 SLC44A5 204962 "solute carrier family 44, member 5, transcript variant 2"
GO:0005886|GO:0044281|GO:0016021|GO:0006644|GO:0055085|GO:0046474|GO:0006656 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_106500_PI430048170 0.1636338254411520.9335217326759070.253043169168208
0.2984353061566780.28566124938102 A A A 0.4640025222297110.362797339386334
0.303886050114836A A A LNCV6_106500_PI430048170 mRNA
ACATTGGCAGTGTGGGTGCCCAAGCCTTGGCACTGATGCTGGCAAAGAACGTCATGCTAG NM_022162RefSeq chr16
+ 50697138 50733077 NOD2 64127 "nucleotide-binding oligomerization domain containing 2,
transcript variant 1"
GO:0005515|GO:0032755|GO:0002710|GO:0002756|GO:0032500|GO:0002755|GO:0009595|GO:0032496|GO:0032
498|GO:0005856|GO:0032689|GO:0002367|GO:0009986|GO:0019901|GO:0032760|GO:0034134|GO:0032720|GO:0
006952|GO:0002224|GO:0002227|GO:0002830|GO:0035666|GO:0034166|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131226_PI430048170 0.0232014559318788 1.66814013418414 7.81930275920521
7.88548579973235 8.2932480041935 P P P 7.13467136931326 7.10445495735586
7.54744481634993 P P P LNCV6_131226_PI430048170 mRNA
GTAAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAGAA NM_025217RefSeq chr6
+ 149941937 149949232 ULBP2 80328 UL16 binding protein 2
GO:0002474|GO:0030101|GO:0009986|GO:0046703|GO:0042267|GO:0042605|GO:0046658|GO:0005615 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_34167_PI430048170 0.0743962167234376 0.76407250786374 3.72815525902465
4.00184681960106 4.02860038667776 P P P 4.11515895708515 4.5366706808696
4.25788550235332 P P P LNCV6_34167_PI430048170 mRNA
TAAGTCTTCCCTTGAAGGCAGGGAAGCAGGATGGATACACATATATCACACGCATAAAAC NM_015241 RefSeq chr22
- 17787649 18024559 MICAL3 57553 "microtubule associated monooxygenase, calponin and LIM
domain containing 3, transcript variant 1"
GO:0017137|GO:0005886|GO:0003779|GO:0005634|GO:0006887|GO:0071949|GO:0005737|GO:0007010|GO:0016
709|GO:0030042|GO:0005654|GO:0008270|GO:0005856|GO:0055114 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133309_PI430048170 0.351867394729172 1.15294482088698 3.67017411370157
3.86569615924798 3.90914696854418 P P P 3.41362492798972 3.38955439920906
3.96159662861305 P P P LNCV6_133309_PI430048170 mRNA
GCATTCCGATTCTATGTAACTGAATGGAGATGATAAGTGCTTTCCCCTCTTTATTTAAAA NM_173560 RefSeq chr6
+ 116877212 116932163 RFX6 222546 "regulatory factor X, 6"
GO:0005515|GO:0000977|GO:0003700|GO:0044212|GO:0006357|GO:0003311|GO:0003310|GO:0005634|GO:0042
593|GO:0000978|GO:0001228|GO:0006351|GO:0003309|GO:0050796|GO:0045944|GO:0031018|GO:0045893|GO:0
090104 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64505_PI430048170 0.0012130342590442 1.69153168280559 9.51124752326804
9.68769594543424 9.61946051515751 P P P 8.89021760530965 8.85023200908018
8.80723131085896 P P P LNCV6_64505_PI430048170 mRNA
AAGTTTTGTGTTTTGGGGGTTGGTGGACAAAGTTCTAGCTGATTAAATATGGTCTAACTT NM_006532 RefSeq chr19
- 18442662 18522127 ELL 8178 elongation factor RNA polymerase II
GO:0005515|GO:0010467|GO:0006368|GO:0015030|GO:0006366|GO:0019902|GO:0035327|GO:0001701|GO:0008
023|GO:0050434|GO:0042796|GO:0032786|GO:0016607|GO:0035363|GO:0010923|GO:0045945|GO:0042795|GO:0
032968|GO:0016032|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132260_PI430048170 0.985116952648509 1.20302643416032 2.69808268659198
0.366220551667952 0.276397058178908 A A A 0.911102369081486 0.387217124259726
2.09898441064835 A A A LNCV6_132260_PI430048170 mRNA
GGGAGCAGGGAGAGAAAGACTGGAGTAGATTTGCTTTTAGAAGCATCTCTGCTTTAAGAA NM_198849 RefSeq chr13
- 45780280 45851711 SIAH3 283514 siah E3 ubiquitin protein ligase family member 3
GO:0005739|GO:0006511|GO:0007275|GO:0005634|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137233_PI430048170 0.000591903416338495 0.355415422240189 5.8592160434303
5.76972815277129 6.00249021798943 P P P 7.26049007102827 7.26458475146622
7.57078546725078 P P P LNCV6_137233_PI430048170 mRNA
CGTAAAGCAAGATGGCTGTGATTTGACAGGTTTAATTGCTAGTTTTTTATAGGTGGATAG NM_032334 RefSeq chr8
+ 116766502 116774682 UTP23 84294 "UTP23, small subunit (SSU) processome component, homolog
(yeast)" GO:0000462|GO:0032040|GO:0005730|GO:0070181 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_55147_PI430048170 0.965691800978004 1.01868937177385 0.408107305835175 1.59263268154894
1.83316813221011 A A A 0.525834772187564 1.98659320999997 1.23775102809643 A A A
LNCV6_55147_PI430048170 mRNA
AATAAATTACAAGTGGTCAAGGTTGCATCCTTTTGAGCCCAGGACCTGCTTGTAAGCCGA NM_001162893 RefSeq
chr1 - 175156986 175193093 KIAA0040 9674 "KIAA0040, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128191_PI430048170 0.00411754853200743 0.73686569197869 7.64880802803994
7.49123247040634 7.63354782155433 P P P 8.14038833312261 7.97421217763456 7.9794823589356
P P P LNCV6_128191_PI430048170 mRNA
CGGCCCAAGCTCTACTTGTGTACAGTGTATATTGTATAATAGACAATTGTGTCTACTACA NM_003110 RefSeq chr17

+ 47896149 47928957 SP2 6668 Sp2 transcription factor
GO:0006357|GO:0006366|GO:0042826|GO:0000981|GO:0005634|GO:0001701|GO:0003677|GO:0048144|GO:0046
872|GO:0006955|GO:0035264|GO:0048568|GO:0005654|GO:0072358 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144122_PI430048170 0.00423806939598994 0.5341721907501394.58673772634111
4.47581793691999 4.81187703108193 P P P 5.54932914456307 5.44549458811257
5.60929671042889 P P P LNCV6_144122_PI430048170 mRNA
TGTCCCTCCAAATTTCATGTACACCTGGAATGTCACAATGTGACTTAACAGTAGCCACCC NM_005843RefSeq chr2
- 152116800 152175992 STAM2 10254 signal transducing adaptor molecule (SH3 domain and ITAM motif)
2
GO:0005515|GO:0005737|GO:0007173|GO:0031901|GO:0016197|GO:0042059|GO:0061024|GO:0005654|GO:0006
886|GO:0043231|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78390_PI430048170 0.58092797948881 0.9451986859912825.21464292173151 5.13432924736715
5.29943797633541 P P P 5.0714757346866 5.41168768791358 5.38945650607634 P P P
LNCV6_78390_PI430048170 mRNA
AACATGCAAAGACGAGTCAAAGAAGGTTATAGAGATGGAATAGATGCTGGCAAAGCAGTT NM_001282446
RefSeq chr7 + 39566375 39612089 YAE1D157002 "Yae1 domain containing 1, transcript variant 2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129314_PI430048170 0.0661946116941584 0.7757941218922124.42573857833664
4.29231206082233 4.20910356715797 P P P 4.8220455125394 4.73859816156335
4.44737829399874 P P P LNCV6_129314_PI430048170 mRNA
CCTGCAATCAAACCACCTTTGAATCTGTGTGTCATTAAAAGTAGATATAAATGGGCAAAA NM_001060RefSeq chr19
- 3594505 3606833 TBXA2R 6915 "thromboxane A2 receptor, transcript variant a"
GO:0005515|GO:0001669|GO:0005886|GO:0007584|GO:0042493|GO:0030168|GO:0045777|GO:0007204|GO:0045
766|GO:0043547|GO:0005085|GO:0006954|GO:0045907|GO:0007186|GO:0045987|GO:0005887|GO:0007596|GO:0
019932|GO:0004961|GO:0032496 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144718_PI430048170 0.00352706235511543 0.4258246213676793.07101292970268
3.00564035700313 3.30774879708458 A A P 4.40448104850188 4.36891731281389 4.322639408608
P P P LNCV6_144718_PI430048170 mRNA
CTTTGGGACAAAACAGAAGTCCATGGAGTTATCTAAGCTCTTGTAAGTGAGTTAATTTAA NM_001736RefSeq chr19
+ 47309846 47322070 C5AR1 728 complement component 5a receptor 1
GO:0021534|GO:0005886|GO:0004944|GO:0050830|GO:0007606|GO:0031100|GO:0001856|GO:0007202|GO:0007
204|GO:0000187|GO:0016323|GO:0006955|GO:0043524|GO:0006954|GO:0006935|GO:0032496|GO:0042789|GO:0
070374|GO:0004878|GO:0050679|GO:0009986|GO:0030593|GO:0045177|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144664_PI430048170 0.1220209719964920.6732328759160078.5933159201582
9.06636384160571 9.11042240779033 P P P 9.26486615866163 9.24486224990729
9.92052823121115 P P P LNCV6_144664_PI430048170 mRNA
AGTTTTTCTTCTGCATGATACGTCATGTTGTGGGATCTTTAGAAAACTTCATACTGTATG NM_000945RefSeq chr2
- 68178856 68252519 PPP3R1 5534 "protein phosphatase 3, regulatory subunit B, alpha"
GO:0005515|GO:0005516|GO:0005509|GO:0019904|GO:0033173|GO:0051533|GO:0006915|GO:0097193|GO:0005
829|GO:0042383|GO:1900740|GO:0045944|GO:0045087|GO:0016311|GO:0004723|GO:0005654|GO:0005955|GO:0
038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129447_PI430048170 0.2171817995799740.7689214136195639.78558757655725
9.12649540886178 9.02876058168024 P P P 9.82414713550137 9.67292133045739
9.69907070492112 P P P LNCV6_129447_PI430048170 mRNA
CAGTCAGCATCTTTTGACCCCTGCCCCCCAACAATAATAGAATTTCAGGAGACAAGGAAA NM_001162435 RefSeq
chr6 + 46746916 46759217 ANKRD66 NA ankyrin repeat domain 66 NA . NA - . NA NA
NA NA NA NA NA NA NA

LNCV6_120498_PI430048170 0.1615276367271311.58693949586692 4.21596670566622
5.19214556163663 4.97402813670702 P P P 4.37162507173466 4.16511549078483
3.99199643073805 P P P LNCV6_120498_PI430048170 mRNA
CTGGAGGAGCTGCACAAGGCGGAGGACAGCCTCCTGGCCGCCGAAGAGGCCGCCGCCAAG NM_001018020
RefSeq chr15 + 63042638 63071914 TPM1 7168 "tropomyosin 1 (alpha), transcript variant Tpm1.3"
GO:0008092|GO:0005862|GO:0055010|GO:0008016|GO:0006928|GO:0060048|GO:0030017|GO:0031529|GO:0005
829|GO:0006937|GO:0003065|GO:0006936|GO:0007010|GO:0005856|GO:0008307|GO:0001725|GO:0030336|GO:0
030049|GO:0045214|GO:0003779|GO:0032587|GO:0032781|GO:0001701|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140672_PI430048170 0.0278872727085898 1.26925826382097 8.01494271895915
8.05752807308438 8.06668821517655 P P P 7.67682756075206 7.82222388387924
7.59977005293154 P P P LNCV6_140672_PI430048170 mRNA
TGTCTTTTAAAAACTCCTGTTTTCACACCTTACAAAGCCAGCTCTGAGCAGACAGGGCGT NM_006651 RefSeq chr4
- 784956 826157 CPLX1 10815 complexin 1
GO:0005326|GO:0007268|GO:0045202|GO:0006887|GO:0014047|GO:0016079|GO:0007269|GO:0030425|GO:0005
829|GO:0017157|GO:0043025|GO:0017075|GO:0070032|GO:0070554|GO:0030073 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127985_PI430048170 0.00933429589037569 0.3580625843852934.95940843166092
4.873453709943 5.29873339288797 P P P 6.0611739771034 6.79308092931058
6.65844422353879 P P P LNCV6_127985_PI430048170 mRNA
GTTCTTGATCATGTGACTTGTAATCAGGATTTAGAACGACAAAAGCCTTTACTACCTAAA NM_001142725 RefSeq
chr16 - 20796340 20806473 ERI2 112479 "ERI1 exoribonuclease family member 2, transcript variant
1" GO:0005737|GO:0000175|GO:0005730|GO:0008270|GO:0003676 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140611_PI430048170 0.1651347295513770.8320838863199516.1174525647604
5.73591610273137 5.98143747631986 P P P 6.13746677281158 6.42544878619466
6.06761799576665 P P P LNCV6_140611_PI430048170 mRNA
GAAATTTATCCCAGCCCTGAGGAGGATTTGTGGAATTAAAATCTCCCCAGCCAGAAAAAA NM_016274 RefSeq chr1
+ 150149901 150160065 PLEKHO1 51177 "pleckstrin homology domain containing, family O member 1,
transcript variant 1" GO:0005515|GO:0005737|GO:0005886|GO:0005634 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_139001_PI430048170 0.00721765015268022 0.7024707011018081 4.5615301045794
14.5708049317439 14.5180884936365 P P P 15.1303562527294 14.9512269543975
15.0917622890831 P P P LNCV6_139001_PI430048170 mRNA
TGGGTCAGATTTTTATTGTGGGGTGGGATGAGTAGGACAACATATTTCAGTAATAAAATA NM_001287593 RefSeq
chr6_GL000251v2_alt - 3207868 3214610 CLIC1 1192 "chloride intracellular channel 1, transcript
variant 1"
GO:0005515|GO:0006821|GO:0048471|GO:0031965|GO:0005244|GO:0005886|GO:0051881|GO:0034707|GO:0072
562|GO:0005634|GO:0005635|GO:0031982|GO:0005254|GO:0005615|GO:0070527|GO:0045669|GO:0005739|GO:0
005903|GO:0007165|GO:0005737|GO:0016020|GO:0051726|GO:0034765|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127827_PI430048170 0.5043221854660660.9237160613594250.346155705355326
0.3679446745129110.286469694381379 A A A 0.3286011264659010.291161999065421
0.690810551568398 A A A LNCV6_127827_PI430048170 mRNA
AGCCTAAATCAATATCTTTTTCCAGTATGCCTTGAGTATGACCAGCTCCAATCTTCAGTG NM_001143832 RefSeq
chr19 + 39776593 39786135 LEUTX 342900 leucine twenty homeobox
GO:0043565|GO:0006355|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55422_PI430048170 0.4395448016298510.82496165495146 0.3053036930003740.312093519214001
0.459747228300506 A A A 0.3450213167753761.08545298410527 0.353535002653736 A A A

LNCV6_55422_PI430048170 mRNA
TGCAAAGGAAGCTCTGGAGAAGGAGGACCTCTCAGGAGGCAGAAAGGGTCACCTTAATTC NM_001170631
RefSeq chr1 - 206957966 206970625 FCAMR 83953 "Fc receptor, IgA, IgM, high affinity, transcript
variant 3" GO:0005886|GO:0016021|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127236_PI430048170 0.0842217920744919 0.67283284571842910.1786891446744
10.0870429444018 10.1262227198154 P P P 10.3415234561699 10.9201738101684
10.7854378912795 P P P LNCV6_127236_PI430048170 mRNA
TTGCTGTTTCTCCTTCTGACCCTGCTCTTGGGTCTAATAACCCCATTTATTTGTAAAAAA NM_001300868 RefSeq chr11
- 66362520 66372476 SLC29A2 3177 "solute carrier family 29 (equilibrative nucleoside transporter),
member 2, transcript variant 1"
GO:0016323|GO:0031965|GO:0006139|GO:0005886|GO:0008283|GO:0005887|GO:0005337|GO:0005730|GO:0015
858|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137574_PI430048170 0.5278303586973491.02434805302059 0.426154703069049
0.2788176012688830.325295192689955A A A 0.2825419910505070.318771277751276
0.328387141021843A A A LNCV6_137574_PI430048170 mRNA
TTTTGTGCTTGAGCCAAGGAAACATCATTAGATCCGCTAAGGGGCATCTGAAACATCCGT NM_178840RefSeq chr1
+ 16004235 16006695 C1orf64 149563 chromosome 1 open reading frame 64 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_137036_PI430048170 0.0956663180499676 1.81654758154031 2.54880226661312
3.52483759159998 3.10083639793925 A P P 2.75465497798088 1.90925762213548
1.91655855406929 P A A LNCV6_137036_PI430048170 mRNA
TGGCTTCGGGGCTGTGCTCTTTTCAAGCCATGTCCGCAAGGTGAACCGCTTCCACAAGAT NM_033054RefSeq chr7
- 44962660 44979105 MYO1G 64005 myosin IG
GO:0005516|GO:0031256|GO:0005886|GO:0043325|GO:0031589|GO:0005547|GO:0005546|GO:0001891|GO:0003
779|GO:0030175|GO:0016459|GO:0006887|GO:0005524|GO:0072678|GO:0030027|GO:0005902|GO:0003774|GO:0
071976|GO:0016020|GO:0008152|GO:0038096|GO:0002456|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142174_PI430048170 0.1077940723755010.7549396881174217.65813517978343
7.12509312303954 7.3924489482061 P P P 7.60925841359368 7.77238892015522
8.02857992595912 P P P LNCV6_142174_PI430048170 mRNA
TGACTGACAATTCATTTTACACTCTATATAATAAAATCTCCACAAGGCATCTTGTGGGCA NM_003934RefSeq chr9
+ 130579572 130638352 FUBP3 8939 far upstream element (FUSE) binding protein 3
GO:0010628|GO:0005737|GO:0001077|GO:0016020|GO:0045944|GO:0005634|GO:0045893|GO:0000978|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132588_PI430048170 0.6593793584168721.1369550067351 1.116258280804
1.56743690071485 0.518114438466085A A A 0.3997030379677530.473217945603303
1.61617527033699 A A A LNCV6_132588_PI430048170 mRNA
GAGGTTGGGGTAAGAAGATGGTGGTAAATATGAAGATAAGTAATCTTTAATAACTTCTGC NM_199261RefSeq chr21
+ 10521513 10606270 TPTE 7179 "transmembrane phosphatase with tensin homology, transcript
variant 1"
GO:0007165|GO:0034220|GO:0006470|GO:0016021|GO:0008138|GO:0005216|GO:0035335|GO:0004725 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142745_PI430048170 0.2281871707885020.8049926597800744.80423851463461
4.91882039296751 4.45199308790025 P P P 5.17629690550357 5.21770216518155
4.70609517346698 P P P LNCV6_142745_PI430048170 mRNA
TTTAGCTCTTGCCAATGGTGCTGCAGTGGCCATTCTTGTAGTTATAGCTTTGCGTACTCA NM_004914RefSeq chr22
+ 23145325 23164344 RAB36 9609 "RAB36, member RAS oncogene family"
GO:0006184|GO:0005794|GO:0000139|GO:0003924|GO:0032482|GO:0019003|GO:0005525|GO:0006886 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137123_PI430048170 0.4064455358308921.11836220568043 0.793785899297127
0.8796689143622090.947500840465827A A A 1.03831208862514 0.500989047521353
0.536825447253618A A A LNCV6_137123_PI430048170 mRNA
ATGCAAGAGGCCATAAGAAAATTACGGTTCCAATATGTTAGTTCTGCACAGAATTTCTAG NM_001004717 RefSeq
chr14 + 20060044 20060983 OR4L1 NA "olfactory receptor, family 4, subfamily L, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133909_PI430048170 0.4486119793099160.7481741054966270.321938482254262
0.2947172340896750.272126055822671A A A 0.2721704180856990.27460236049252
1.32597580730677 A A A LNCV6_133909_PI430048170 mRNA
GCTGGTAAAGGAACTACTAAGATTCAGAAGCTTGTAGTCTTCATTATTTTGTTTTACAGG NM_017952RefSeq chr2
+ 86106181 86142157 PTCD3 55037 pentatricopeptide repeat domain 3
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0005743|GO:0043024|GO:0019
843|GO:0006417 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144752_PI430048170 0.1035833063857611.30140298754307 5.45127508363409
5.35137214601752 5.01123075963951 P P P 5.12898936427059 4.81702653026585
4.73273853276882 P P P LNCV6_144752_PI430048170 mRNA
AAATGGCCTTGGTCCCGCAGCTTGTGTGCGTGAGTGCAGTGTGAGTGTGTGTGTCTCTCA NM_012476RefSeq chr2
+ 70900589 70933445 VAX2 25806 ventral anterior homeobox 2
GO:0003700|GO:0060041|GO:0005634|GO:0000122|GO:0007409|GO:0007398|GO:0006351|GO:0009950|GO:0031
490|GO:0043565|GO:0005737|GO:0030900|GO:0016055|GO:0007601|GO:0048048 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128282_PI430048170 0.0649653429072385 1.37641269278908 5.53814086082096
5.71898419349622 5.36001245674238 P P P 5.35835312300444 4.8902055748105
4.96293617280033 P P P LNCV6_128282_PI430048170 mRNA
CTGCTGTTCGTGACTCAGAAACAGAAGAAAAACACTGAGAAAAAGCATTAAAAATAAGCCNM_001670RefSeq chr22
- 19969878 20016786 ARVCF 421 armadillo repeat gene deleted in velocardiofacial syndrome
GO:0016339|GO:0005622|GO:0005515|GO:0016337|GO:0005737|GO:0030054|GO:0005886|GO:0007275|GO:0005
654|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126655_PI430048170 0.8845519701431691.01242756026385 0.28968133665731
0.5692196699555110.400279787945882A A A 0.5091220275064270.39765476090818
0.305549175005489A A A LNCV6_126655_PI430048170 mRNA
CTGCTGCTTTAAGAGATCAACTAATTCGAGCACTAACTATGATAGGAGCATATGAAATTA NM_001161528 RefSeq
chr7 - 92144883 92165276 LRRD1 NA leucine-rich repeats and death domain containing 1 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138357_PI430048170 0.3655655523360740.8558336935167970.389711808176171
0.4138413700491680.303717808776509A A A 0.3953889689752140.922807407350563
0.399023398047194A A A LNCV6_138357_PI430048170 mRNA
GAAACATGAGCTACTGTTAGAAATAAATTTCCAGTTGTATGCTGCTCTGTGTATATCATG NM_020654RefSeq chr3
- 101324188 101513241 SENP7 57337 "SUMO1/sentrin specific peptidase 7, transcript variant 1"
GO:0005622|GO:0005515|GO:0006508|GO:0005634|GO:0008234 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131123_PI430048170 0.3588875777299911.17959688041776 4.25961058299205
4.30324155429603 4.38575474440293 P P P 4.32117817949455 4.22454686807906 3.586481279667
P P P LNCV6_131123_PI430048170 mRNA
AGAAGGTGATATTTGCTTGCTGTGTCTTCATGCTTCTCTTCCCATTCTCCATCATCGTGGNM_206880RefSeq chr5 +
181154942 181155890 OR2V2 285659 "olfactory receptor, family 2, subfamily V, member 2"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_101570_PI430048170 0.8560346448926061.01558941625902 2.03619119958583

1.94008309994137 3.23871059646707 A A P 2.80707855078754 2.32534045416947
2.35081719759167 P A A LNCV6_101570_PI430048170 mRNA
TTCAACCGAACATTCTTCCCAAGCGTGAGAGAGTGACTGACACTTGGTTCCATCCATTTA NM_001005404 RefSeq
chr17 + 59331691 59401734 YPEL2 388403 yippee-like 2 (Drosophila) GO:0005730 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134283_PI430048170 0.1618084744032311.07140443944156 0.505061141494459
0.4164412797218280.530215770413207A A A 0.3032657176120070.385657432813377
0.462361073115112A A A LNCV6_134283_PI430048170 mRNA
CCTGCACGGATGGAAACAGAAAATATTCACAATGTATGTGTGTATGTACTACACTTTATA NM_052872RefSeq chr6
- 52236685 52244500 IL17F 112744 interleukin 17F
GO:0051216|GO:0045423|GO:0045414|GO:0045408|GO:0005576|GO:0006029|GO:0042089|GO:0005125|GO:0005
615|GO:0005126|GO:0042803|GO:1900017|GO:0006954|GO:0019955|GO:0045076|GO:0045944|GO:0016525|GO:0
017015|GO:0042109. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71267_PI430048170 0.6168177682681521.06653458903685 7.93977518422056 7.88234663474152
7.68277927492546 P P P 8.00986798426115 7.77456108555798 7.38695389286034 P P P
LNCV6_71267_PI430048170 mRNA
GTATTCCCTCTTGGGCTGACCACAGCTTCTCCCTTTCCCAACCAATAAAGTAACCACTTT NM_006103RefSeq chr20
+ 45469753 45481532 WFDC2 10406 WAP four-disulfide core domain 2
GO:0010951|GO:0019828|GO:0004869|GO:0004866|GO:0004867|GO:0006508|GO:0007283|GO:0005615|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145605_PI430048170 0.0186502096727715 1.4410619804851 10.0164111669677
10.2193280714515 10.2957067644403 P P P 9.63759065501963 9.46943153606554
9.83412584692815 P P P LNCV6_145605_PI430048170 mRNA
TGGAAATACTCAATGTGGCTCTTCTATAGGCTTCTAGAATAAACCGTGGGGACCCGCAAA NM_019885RefSeq chr2
- 72129237 72147862 CYP26B1 56603 "cytochrome P450, family 26, subfamily B, polypeptide 1,
transcript variant 1"
GO:0006805|GO:0071300|GO:0061436|GO:0009954|GO:0007283|GO:0030326|GO:0044281|GO:0005737|GO:2001
037|GO:0005506|GO:0001709|GO:0070268|GO:0010628|GO:0048384|GO:0006766|GO:0048387|GO:0034653|GO:0
060349|GO:0001972|GO:0008401|GO:0005789|GO:0043587|GO:0020037|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144282_PI430048170 0.33253579096232 0.9233890908804959.1137999334576
8.95595468643008 8.91813017788247 P P P 9.00118560339205 9.05641201389704
9.26876826014145 P P P LNCV6_144282_PI430048170 mRNA
CCGGTTCAGGAATCACTATGTATTTCCTTCTTGTGATAAAAATAAAATTACGAGAAGGCA NM_182501RefSeq chr2
- 241095565 241102332 MTERF4130916 "mitochondrial transcription termination factor 4, transcript variant
1"
GO:0005515|GO:0006355|GO:0042255|GO:0006364|GO:0006626|GO:0006390|GO:0019843|GO:0005762|GO:0005
739|GO:0007507|GO:0005737|GO:0003690|GO:0043010 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143202_PI430048170 0.4328287654848230.9441092047727835.18425860357181
5.29045715068535 5.26145640947465 P P P 5.16798507630181 5.42947983342131
5.37666985595644 P P P LNCV6_143202_PI430048170 mRNA
TATGCCTCTTCTTACTTCACCCATGTTTGTTGTTATGCAAATAAAGGTTTTCTCTCCAAA NM_016483RefSeq chr3 +
52410560 52423641 PHF7 51533 "PHD finger protein 7, transcript variant 1"
GO:0005815|GO:0008270|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127787_PI430048170 0.8965076475687960.9974135560297591.71442130507186
0.61777554038788 0.501556169626133A A A 0.7999832537420211.52524721006723
0.703646480964803A A A LNCV6_127787_PI430048170 mRNA
AGGGGTGGGGGGAATCAATTTGGTTTTCTCTCTTGTTTCTTTTTTAATTTAATGAGACAC NM_001389RefSeq chr21
- 40012415 40847113 DSCAM 1826 "Down syndrome cell adhesion molecule, transcript variant 1"

GO:0005515|GO:0030424|GO:0005886|GO:0048842|GO:0005576|GO:0070593|GO:0007399|GO:0030426|GO:0048813|GO:0007162|GO:0016020|GO:0005887|GO:0007626|GO:0060060|GO:0007155|GO:0042327 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2440_PI430048170 0.0158546793506523 0.7149047525127387.91389896916481 7.92499841919686 8.14939165119833 P P P 8.3707457381616 8.65738925751972 8.40798029519182 P P P LNCV6_2440_PI430048170 mRNA
CACAGAGTGTCCTCTTGGTGTATTCTAAAACGAGCATTCTTTTAAAAAACCTAAAGTTTC NM_001287585 RefSeq chr2 + 183124354 183161684 NUP35 129401 "nucleoporin 35kDa, transcript variant 4"
GO:0007077|GO:0010467|GO:0031965|GO:0005886|GO:0005975|GO:0019083|GO:0019221|GO:0019058|GO:0044281|GO:0005635|GO:0015031|GO:0055085|GO:0010827|GO:0043231|GO:0008645|GO:0015758|GO:0005643|GO:0009405|GO:0016032|GO:0005654|GO:0051028|GO:0045111|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121468_PI430048170 0.3700170351442040.9082371116054770.32113171905852 0.3563299021261040.333870575565644A A A 0.6926877107696390.339083762807006 0.369077059315071A A A LNCV6_121468_PI430048170 mRNA
AATCATTGAAAAATTAAAAAGTCTTGATGAGCACTATCATATCCGTGTAAATTTAGTAAA NM_000384RefSeq chr2 - 21001428 21044073 APOB 338 apolipoprotein B
GO:0005515|GO:0007603|GO:0048844|GO:0007283|GO:0030301|GO:0050900|GO:0009791|GO:0005615|GO:0034359|GO:0043231|GO:0034361|GO:0034360|GO:0042953|GO:0009743|GO:0034363|GO:0071356|GO:0034362|GO:0032496|GO:0019433|GO:0070062|GO:0042632|GO:0033344|GO:0005794|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127204_PI430048170 0.1185200617192290.4297198576034122.15021542493292 0.3630916262250620.474700978121801A A A 2.71675719179375 1.81473743875678 2.69261150340429 P A P LNCV6_127204_PI430048170 mRNA
GGTTGGGAGGCGGCTGCTGCACGTTTGGGCTTGAATAAAGAAGTATTTCTGGTTAAAAAA NM_139174RefSeq chr16 + 84191116 84197166 ADAD2 161931 "adenosine deaminase domain containing 2, transcript variant 1"
GO:0006396|GO:0004000|GO:0003723 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144148_PI430048170 0.0464020359166875 0.8635548379571291 1.9155560679072 11.7247519378413 11.7609860800574 P P P 11.9671347963736 11.9827334408354 12.0903958019918 P P P LNCV6_144148_PI430048170 mRNA
AAATTGGGCTGGGATCACGTCCTGTTTTGTAATAAAAGCTGAAAAGTCTGCATGAAAAAA NM_001204468 RefSeq chrX + 47145217 47186815 RBM10 8241 "RNA binding motif protein 10, transcript variant 5"
GO:0008380|GO:0006397|GO:0005515|GO:0008150|GO:0000166|GO:0008270|GO:0005654|GO:0005634|GO:0032403|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129176_PI430048170 0.0504845318715455 0.5063410169653236.01677950776869 5.10544635321075 5.34760264921096 P P P 6.39475543410688 6.71162223814082 6.44843266534383 P P P LNCV6_129176_PI430048170 mRNA
TTTCCCTGTGCCTGTGTCAAATCTTCAAGTCTTGCTGAAAATACATTTGATACAAAGTTA NM_182976RefSeq chr1 + 89995118 90028535 ZNF326 284695 "zinc finger protein 326, transcript variant 1"
GO:0005515|GO:0006397|GO:0008380|GO:0044609|GO:0000993|GO:0003677|GO:0006351|GO:0016363|GO:0043231|GO:0032784|GO:0005654|GO:0005681|GO:0008270|GO:0045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129999_PI430048170 0.0516761005249755 1.0743021863757 0.379966716472973 0.3127698871155840.410340109526871A A A 0.2530099377936540.2921414627656420.2490522555403 A A A LNCV6_129999_PI430048170 mRNA
TAAGGCGTTTTTCTCCATAGCCTCAACATTTTGGGAATCTTCCCTTAATCACCCTTGCTCNM_032192RefSeq chr17 + 39626923 39636625 PPP1R1B 84152 "protein phosphatase 1, regulatory (inhibitor) subunit 1B, transcript variant 1"
GO:0004864|GO:0004865|GO:0005634|GO:0043086|GO:0006351|GO:0005829|GO:0035556|GO:0008599|GO:0007

165|GO:0050790|GO:0001975|GO:0005737|GO:0031749|GO:0031748|GO:0008542|GO:0043025|GO:0031752|GO:0
004860|GO:0006469|GO:0007621|GO:0031751|GO:0031750 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_144360_PI430048170 0.2322716116000432.7852660857436 1.03747265851655
3.01005843022509 3.51077011667421 A A P 0.997812298463022 0.720651313947111
2.02745086597405 A A A LNCV6_144360_PI430048170 mRNA
GCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAATCCAGGAAAAAA NM_198492 RefSeq chr19
- 7728956 7732171 CLEC4G 339390 "C-type lectin domain family 4, member G, transcript variant 1"
GO:0005515|GO:0030246|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129100_PI430048170 0.0492784447630724 0.7321620485244437.52975692941935
7.27267425864083 7.24970194908475 P P P 7.62684076232802 8.03736684606048
7.72161623270346 P P P LNCV6_129100_PI430048170 mRNA
TACCTGCCTGGGACAGCCACTGGAAACTTTTGGGAACTCTCCTCGAATGTGTGGGCCCAA NM_016335 RefSeq
chr22_KI270734v1_random - 138078 161852 PRODH 5625 "proline dehydrogenase (oxidase) 1, transcript
variant 1"
GO:0071949|GO:0034641|GO:0019470|GO:0006560|GO:0005759|GO:0010133|GO:0008631|GO:0006562|GO:0005
743|GO:0004657|GO:0044281|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137604_PI430048170 0.00386658478380117 0.3755697589335456.60264779920421
6.10819758311342 6.66890840276226 P P P 7.71298925367908 7.77609806458684
8.15154107528362 P P P LNCV6_137604_PI430048170 mRNA
GTTGACCATAGCCTTCTTGTCTTTCATCACTTTATCTCCATGTATGTATCCTTAAAGAAT NM_031469 RefSeq chr6 +
79631282 79703652 SH3BGRL2 83699 SH3 domain binding glutamate-rich protein like 2
GO:0017124|GO:0005654|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130601_PI430048170 0.9828050481763451.00088119883884 13.3664694818479 13.420021780664
13.6276161470548 P P P 13.3944582955985 13.5017264703925 13.5241865476438 P P P
LNCV6_130601_PI430048170 mRNA
CCAAAGAATAGTTCCTGTGACATTCCGCCTTCCTTCCATGTAGTCCCTCTTGGTAATCTA NM_006401 RefSeq chr9
+ 97983206 98015942 ANP32B 10541 "acidic (leucine-rich) nuclear phosphoprotein 32 family, member B"
GO:0048839|GO:0006919|GO:0005730|GO:0006334|GO:0005634|GO:0046827|GO:0042393|GO:0005737|GO:0021
591|GO:0060021|GO:0045596|GO:0070063|GO:0001944|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_109229_PI430048170 0.2346031684138271.03302254850846 0.342691006215841
0.2815470645500630.376927118196305 A A A 0.2882584216049410.275276037354519
0.298534625553368 A A A LNCV6_109229_PI430048170 mRNA
ACTTCCAGGAGCTTGGTGCCAAATTTGAGGCCAAGGTCCAGGAGAACACTCAGAGAGTGG NM_024756 RefSeq
chr10 - 86935540 86957668 MMRN2 79812 multimerin 2
GO:0030948|GO:0005515|GO:0090051|GO:0001525|GO:0005615|GO:0070062|GO:0005604 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_73025_PI430048170 0.000899289615869738 0.4436957344312357.20606620769879
6.98185710463624 6.99376103707396 P P P 8.16974356779326 8.25079060328292
8.28694543140331 P P P LNCV6_73025_PI430048170 mRNA
AGGAGTATGTGGACTGTCTCACAGACAAGAGTGCCAAGACCCGGCAGGGTGCTCTTGAGA NM_006764 RefSeq
chr3 - 50287731 50292595 IFRD2 7866 interferon-related developmental regulator 2
GO:0005515|GO:0003674|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144398_PI430048170 0.00637522508717463 2.13819556978141 6.19791170642483
6.68410174602782 6.38590846263568 P P P 5.32233037037721 5.47124730041906
5.21578024686196 P P P LNCV6_144398_PI430048170 mRNA
TTTGATGTGATCTCATTGATGTACACAACCAAGTTCCAATAAAGTGCTAGAATGTGCAAA NM_032947 RefSeq chr5
+ 150777945 150796736 SMIM3 85027 small integral membrane protein 3 GO:0016021 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_140309_PI430048170 0.2872715065759230.8849343447716077.5245007091358
7.41329521054343 7.75404367958822 P P P 7.79862915779578 7.5401661482231
7.88172324188894 P P P LNCV6_140309_PI430048170 mRNA
GGGATAGGATTAACAAACATATTGATGGCATAACCTATTCAGCTATGTCCTTATTTTTGC NM_004657RefSeq chr2
- 191834305 191847280 SDPR 8436 serum deprivation response
GO:0005515|GO:0005737|GO:0005543|GO:0005901|GO:0005080|GO:0001786|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143241_PI430048170 0.1098142949405841.39028833581411 2.42563144034854
2.41379187078883 2.16416512707651 A A A 2.07889346169902 1.98391198442514
1.45449221590305 A A A LNCV6_143241_PI430048170 mRNA
CTTCCACCAACCAGAGGAAACCCATTTACTAGTTTTTCTAATAAATCAATAATGCTCCAA NM_001024858 RefSeq
chr14 - 64746282 64823148 SPTB 6710 "spectrin, beta, erythrocytic, transcript variant 1"
GO:0005515|GO:0007009|GO:0030097|GO:0008091|GO:0046982|GO:0009986|GO:0031235|GO:0030506|GO:0003
779|GO:0014731|GO:0015629|GO:0051693|GO:0005829|GO:0043234|GO:0005737|GO:0051015|GO:0006779|GO:0
007411|GO:0005200. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141181_PI430048170 0.5734624521093030.9087880062772395.63747809552035
5.56539225149006 5.18976652052855 P P P 5.92227639668888 5.45652351712292
5.40900610956382 P P P LNCV6_141181_PI430048170 mRNA
ACAGCCTCTGTTTTCCTCCCCATCTGTGGATACTATTCTAATAAATAGCACATGCCATTG NM_007058RefSeq chr6
+ 44158810 44184402 CAPN11 11131 calpain 11
GO:0005737|GO:0004198|GO:0001669|GO:0005509|GO:0006508|GO:0008233 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_72426_PI430048170 0.2655035864191491.25836665458432 2.99083091032876 3.3346842529312
3.68521245206768 A P P 2.95533673655742 3.26146416991857 2.85025079206124 P P P
LNCV6_72426_PI430048170 mRNA
GCTATTGCCTTATTTTTTCTCATGGATGTTCTTCTTCGAGTATTTGTAGAAGGGTAAGTT NM_001289912 RefSeq chr22
- 38290690 38398522 LOC400927-CSNK1ENA LOC400927-CSNK1E readthrough NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141100_PI430048170 0.0824936215947934 0.6590901845217853.33180418225169
3.31235209102787 3.48416542052805 P P P 3.62226613285141 3.96515644107258
4.27757171052757 P P P LNCV6_141100_PI430048170 mRNA
GTGATTAAGTGATCCCAGAACAAGGAATACTAGAGTAAAAAGCACCTCTTTTTCACAAAA NM_001033910 RefSeq
chr1 + 211326805 211374944 TRAF5 7188 "TNF receptor-associated factor 5, transcript variant 3"
GO:0005515|GO:0035631|GO:0004842|GO:0005813|GO:0008284|GO:0016567|GO:0006915|GO:0042981|GO:0031
996|GO:0005829|GO:0007165|GO:0051091|GO:0005737|GO:0051092|GO:0009898|GO:0008270|GO:0004871|GO:0
043123|GO:0031625. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140704_PI430048170 0.0897498316971197 1.10174182810526 0.581485747804988
0.6927531662982330.679513128633335A A A 0.6100903860144280.455693084118459
0.465926591476157A A A LNCV6_140704_PI430048170 mRNA
TGATGTCTGAAGAACGGAGAAGAAACTCAAGCTTGTTTCAGGATTTAAGATGTGTGCAAA NM_001190462 RefSeq
chr11 + 94512528 94532123 C11orf97 643037 chromosome 11 open reading frame 97 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_136120_PI430048170 0.00747272848520386 0.2784110347166053.8990289683693
3.30907048979627 3.74297433185143 P P P 5.71630275311723 5.76021411449965
4.93073032116011 P P P LNCV6_136120_PI430048170 mRNA
CTCTGAGACAGTCTCTGTGTGGAATTTGCCTTAAACTGAAGTAAATTTGGTTCTTTTAGT NM_020939RefSeq chr6
- 36740777 36839444 CPNE5 57699 copine V
GO:0043005|GO:0008150|GO:0003674|GO:0043025|GO:0070062 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_137152_PI430048170 0.30705753973215 0.9427979265400288.59434668899684
8.54012467971801 8.6971435938126 P P P 8.58540106594531 8.76036256940182
8.73898502395339 P P P LNCV6_137152_PI430048170 mRNA
GAGGAGGAGACAATATTTTTTCAAACTTTTTGGGGAGTGGGGTCATTTCTGTATATAAAA NM_001303418 RefSeq
chr2 - 127257289 127294094 ERCC3 2071 "excision repair cross-complementation group 3, transcript variant 3"
GO:0005515|GO:0010467|GO:0006368|GO:0009650|GO:0006367|GO:0006366|GO:0006363|GO:0006362|GO:0006361|GO:0006360|GO:0000439|GO:0006979|GO:0009411|GO:0008094|GO:0032564|GO:0006370|GO:0006281|GO:0006283|GO:0005654|GO:0043138|GO:0006289|GO:0008134|GO:0035315|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_99935_PI430048170 0.0677093044454227 2.21018642954244 2.84765572895134
2.3149567672682 1.85549297134452 A A A 1.84037621634024 0.582449302256528
1.04761144065399 A A A LNCV6_99935_PI430048170 mRNA
GTCTCAGCATTGAGGACACCTTTGAGAGCATCAGTGAACTGGGGCCTCTGGAGCTGATGG NM_001177880 RefSeq
chr11 + 67022718 67050863 SYT12 91683 "synaptotagmin XII, transcript variant 2"
GO:0030054|GO:0030672|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_58470_PI430048170 0.283571536217704 0.795514518243602 3.37595928777454
2.86543714315464 3.16433748428544 P A P 3.14499441787803 3.37215811868582
3.83598502716899 P P P LNCV6_58470_PI430048170 mRNA
GACTGACATTTTTTCCTAAGGAAGGAAATAATCATCTAAGACCACGAAAAAAGGCTGTTT NM_001297419 RefSeq
chr12 - 911735 990041 RAD52 5893 "RAD52 homolog (S. cerevisiae), transcript variant 2"
GO:0005515|GO:0006281|GO:0000724|GO:0000730|GO:0006310|GO:0005654|GO:0005634|GO:0003677|GO:0042802|GO:0006302 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_50213_PI430048170 0.902853546400739 0.812449047814768 1.40655372195073
1.05045793126042 1.58125233218809 A A A 2.40620366726631 0.332368921335744
1.55361887089498 A A A LNCV6_50213_PI430048170 mRNA
AGGATGGAAGTGGGGCCAGCCACCGAGACCTTCGTGCTGGAACTTCAATGTCTTGAGGAT NM_017560 RefSeq
chr7 + 6615895 6624290 ZNF853 54753 zinc finger protein 853 GO:0003676|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136203_PI430048170 0.161763468305123 0.933834535922067 0.252079875239426
0.295808741389287 0.287046989058726 A A A 0.462132611748835 0.360896678392035
0.304097020438413 A A A LNCV6_136203_PI430048170 mRNA
GTATTAGCACTGTGGTTGATTTTCTTGAATTATGTTGCATCTTGTACTACTAAGCTTGTG NM_001650 RefSeq chr18
- 26852043 26865752 AQP4 361 "aquaporin 4, transcript variant a"
GO:0005886|GO:0007605|GO:0009992|GO:0070295|GO:0016323|GO:0005737|GO:0034220|GO:0005911|GO:0071392|GO:0015250|GO:0015793|GO:0006810|GO:0005372|GO:0051260|GO:0006833|GO:0015254|GO:0009314|GO:0007565|GO:0030315|GO:0051384|GO:0042538|GO:0015670|GO:0055085|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135339_PI430048170 0.361474501709625 0.741315098246496 1.72736497356261
0.385339640603122 0.261462515029346 A A A 1.40950245498292 0.946299421710079
1.7058685991132 A A A LNCV6_135339_PI430048170 mRNA
ATCGCTTCCCCGAGAGTGAATTTTAACACTGTAACAATAAATACTACTGCACAGCACTTT NM_201628 RefSeq
chr1 + 14598716 15118048 KAZN 23254 "kazrin, periplakin interacting protein, transcript variant E"
GO:0030057|GO:0005737|GO:0031424|GO:0005634|GO:0005856|GO:0001533 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_135855_PI430048170 0.0101282070975124 1.26356002158809 7.68605212484881
7.80933351332562 7.67732852843636 P P P 7.49752002549729 7.33443047202071

7.32551399172446 P P P LNCV6_135855_PI430048170 mRNA
AAAGGGGAGTTGGTGGGCCTTTAGGTCTGCCCCATCCCCTGGAAAACTTAGGACTTATTG NM_012186RefSeq chr1
+ 47416071 47418052 FOXE3 2301 forkhead box E3
GO:0050679|GO:0043565|GO:0005667|GO:0003700|GO:0006366|GO:0006357|GO:0000981|GO:0043010|GO:0005
634|GO:0048468 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140228_PI430048170 0.6941825611465241.22345312522764 0.360030652788686
1.86523992190874 1.1952169728578 A A A 0.2739314612831781.2781731281671
1.17892440488383 A A A LNCV6_140228_PI430048170 mRNA
CAAAATTCCTAATTAAAATACTAAGTAAGTGATGGCTCCAGGCTGAAACACCGGACACTG NM_173541RefSeq chr10
+ 132445209 132448321 C10orf91 170393 chromosome 10 open reading frame 91 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131370_PI430048170 0.0422307738672948 0.2547785553911640.514122260170707
0.5756413373741042.21009086997018 A A A 2.7749075294886 3.29341320720131 3.6968104783036
P P P LNCV6_131370_PI430048170 mRNA
CATCTGGTTAACCTGTATTCACAAACTCTCAAGAGTTTCTACTTATTTCAGGAGCTTAAG NM_152546RefSeq chr5
+ 121961960 122028600 SRFBP1 153443 serum response factor binding protein 1
GO:0030490|GO:0048471|GO:0006355|GO:0005634|GO:0006351|GO:0030686 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132951_PI430048170 0.9733926579071391.17456823187053 3.08725697378212
1.71952890102768 1.11813830965504 A A A 2.38698600859472 1.71461421424236
1.75481483124968 A A A LNCV6_132951_PI430048170 mRNA
AGTTATTTTTCTGACTGTCAAGTTTCAACATTCAGGTCTGTCCCCAACAGGCACCACACC NM_024690RefSeq chr19
- 8848843 8981342 MUC16 94025 "mucin 16, cell surface associated"
GO:0005515|GO:0005886|GO:0005796|GO:0016266|GO:0005615|GO:0031982|GO:0006493|GO:0016021|GO:0007
155|GO:0044267|GO:0019898|GO:0043687|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128397_PI430048170 0.765615501580844 1.0661538223848 6.30434456739306 6.0777592027971
5.56133682983369 P P P 6.34750311366003 5.88512438744613 5.36590899052927 P P P
LNCV6_128397_PI430048170 mRNA
ACTCTCTGATGTGCCAGTGGGCCTCCCTTTTAACCTCCTAATAAATATCATTTCCTTGGC NM_002277RefSeq
chr17_GL383564v2_alt + 35368 39236 KRT31 3881 "keratin 31, type I"
GO:0005882|GO:0008544|GO:0005200|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142971_PI430048170 0.2538714421602180.6081766965514880.325904621000034
0.3296446428753790.503850580222093A A A 0.96428661335156 1.69471366981553
0.345585268449817A A A LNCV6_142971_PI430048170 mRNA
TTCCTTCACTCGTAACTTGAACTCAAGTTTTCACTTACTGACGCGCTTCCCATTAAAAAA NM_017925RefSeq chr9
+ 19230764 19374268 DENND4C 55667 "DENN/MADD domain containing 4C, transcript variant 1"
GO:0017112|GO:0032869|GO:0005886|GO:0032593|GO:0032851|GO:0015031|GO:0072659|GO:0030659|GO:0030
904|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140917_PI430048170 0.00304713309546354 0.3612287825191985.47311031383667
4.98516613079331 5.3357724619443 P P P 6.38923452115132 6.89437739123576
6.90284154565001 P P P LNCV6_140917_PI430048170 mRNA
GGAGTGGCCTAAGAAATGCGTGTTTCAGTGACTAGATTATAAATATTCTCTATTGTGAAT NM_022451RefSeq chr10
- 94333225 94362976 NOC3L 64318 nucleolar complex associated 3 homolog (S. cerevisiae)
GO:0016607|GO:0005730|GO:0045444 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135140_PI430048170 0.4123789277561490.8494694729812743.15223762052772
3.90580447870759 4.02239193172856 P P P 4.09309024347073 3.88802021868973
3.94194466511526 P P P LNCV6_135140_PI430048170 mRNA
TAAGGGCCCTAGTCAATGTAGGCCTGCTTCTTATAGCTTTTTGACTATATTATGCTGTCT NM_001145717 RefSeq

chr6 + 36270459 36308595 PNPLA1 285848 "patatin-like phospholipase domain containing 1, transcript variant 3" GO:0016042|GO:0005737|GO:0016787 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133833_PI430048170 0.0600786613486315 1.25515384828588 12.259695163248
12.4492282339204 12.2566238115794 P P P 12.1231360711104 12.0543521464726
11.7923347379149 P P P LNCV6_133833_PI430048170 mRNA
AAGGAGCCGCTTCTGCCTCCCTTGCCAAAACTCCGTTTCTAATTAAATTATTTTTAGTAG NM_138349 RefSeq chr17
+ 29568720 29573157 TP53I13 90313 tumor protein p53 inducible protein 13
GO:0005737|GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135460_PI430048170 0.579013527069858 0.907730316697109 4.45938964871654
4.58160854702282 5.16070684904139 P P P 4.88532209844498 4.64614287566056 5.1467372836549
P P P LNCV6_135460_PI430048170 mRNA
GCGAGTAAATTCAGAATTGAAACAATTTCTCCTTGTTCTACCTATCACCACATTTTCTCA NM_001286617 RefSeq
chr21 + 29077470 29175889 MAP3K7CL 56911 "MAP3K7 C-terminal like, transcript variant 3"
GO:0005515|GO:0005634|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55395_PI430048170 0.207869969838759 0.774229429472092 8.40666563036675 7.97438868033788
7.65237953170343 P P P 8.56845475493555 8.45885558689899 8.18741220486242 P P P
LNCV6_55395_PI430048170 mRNA
TGAAGACACTGCCTCCATCTTCTCCCTGAAGGAGATCCAGCTCCAGAAGGACCCAGGCTA NM_212503 RefSeq chr1
+ 205504555 205532793 CDK18 5129 "cyclin-dependent kinase 18, transcript variant 1"
GO:0005515|GO:0051726|GO:0006468|GO:0005575|GO:0005524|GO:0004693 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145620_PI430048170 0.0076031218888944 0.346994792684021 1.22622345634334
1.89792372034062 1.17433706267041 A A A 2.60105694630791 3.10762719785856
3.21716279419399 A P P LNCV6_145620_PI430048170 mRNA
CAGACATCATTCCCAGACAGCAGGGATTTATTTAAATGTTAGCTGTCTGAGTTTTTAAAT NM_181713 RefSeq chr2
+ 23940505 24000823 UBXN2A 165324 UBX domain protein 2A
GO:0010468|GO:0005801|GO:0043130|GO:0042176|GO:0005783|GO:0033130|GO:0005634|GO:0005829|GO:0008599|GO:0050790|GO:0007030|GO:0061025|GO:0043161|GO:0031396|GO:0000045|GO:0031468 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144807_PI430048170 0.181713042598888 0.899572261391755 12.2333741640546
12.1706359984772 12.0994121954247 P P P 12.465963754412 12.2094207705882
12.2768062277969 P P P LNCV6_144807_PI430048170 mRNA
TTAAGTGAATAATTTAAAGTCTTCTCCTCCCCCACTGCCCCTGCAGTAAAGTGCTTTGGC NM_001199692 RefSeq
chr7 + 151058211 151076527 SLC4A2 6522 "solute carrier family 4 (anion exchanger), member 2, transcript variant 2"
GO:0006820|GO:0008509|GO:0005886|GO:0055085|GO:0016323|GO:0005452|GO:0016020|GO:0005887|GO:0015108|GO:0015701|GO:0051453|GO:0005925|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129418_PI430048170 0.0130316794866595 0.949985374818771 0.357457623470967
0.35905016550404 0.32841561679938 A A A 0.444275334150138 0.423933803686112
0.398626003119467 A A A LNCV6_129418_PI430048170 mRNA
CAAACTTTGGATTCTGCTGTTGTTTCTACAATGACATTTTGTATGAAGCAAAGTCCTTGA NM_000718 RefSeq chr9
+ 137877788 138124624 CACNA1B 774 "calcium channel, voltage-dependent, N type, alpha 1B subunit, transcript variant 1"
GO:0005515|GO:0051899|GO:0086010|GO:0005245|GO:0005886|GO:0005509|GO:0008016|GO:0008331|GO:0007268|GO:0008022|GO:0005524|GO:0005891|GO:0030425|GO:0007269|GO:0070509|GO:0070588|GO:0051924|GO:0043025|GO:0006810|GO:0008217|GO:0048265|GO:0034765|GO:0007626 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_127575_PI430048170 0.0573701265700952 0.687111723808599 8.46105796870586
8.07757299121248 8.23190123951206 P P P 8.53718247834406 9.0797924459597

8.75141239181662 P P P LNCV6_127575_PI430048170 mRNA
GACAAAACCAAACTTCTCAGAAAACAACATGAGATTGGCATGGCTTTATTTGTTTTCTTG NM_001277083 RefSeq
chr2 + 130611532 130658037 POTEJ NA "POTE ankyrin domain family, member J"NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145762_PI430048170 0.0187834340764738 0.428649739939227 1.2834438559705
1.13570942289326 1.94054527903666 A A A 2.52812564813207 2.47238426629484
3.07755483692276 A A P LNCV6_145762_PI430048170 mRNA
AGAGGAAGAGGAAGCTGGGCATTAAATTACCTCATCCAGCAGAAATTCACGGTAGTATGGNM_001083535 RefSeq
chr6 + 109095152 109163912 CEP57L1 285753 "centrosomal protein 57kDa-like 1, transcript variant 1"
GO:0008017|GO:0008150|GO:0003674|GO:0005737|GO:0043015|GO:0034453|GO:0005815|GO:0005874|GO:0005
575|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131278_PI430048170 0.436113200456595 1.18742156199202 0.291676280285924
0.3003187266543590.957049588822874A A A 0.3149439423468120.274210682646336
0.321384433062531A A A LNCV6_131278_PI430048170 mRNA
CGGGAAAAATGAAGAACTTATTGCTCTCTGCCAGAAGTCTCTGAAATGCTGTCGGACCAT NM_152251RefSeq
chr8_KI270813v1_alt - 165610 169492 DEFB106A NA "defensin, beta 106A" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_134479_PI430048170 0.2907908974588620.2775926892425810.287644411392415
0.3224831563843460.363955723456744A A A 0.3954935323614683.34378955296167
1.04964261589609 A P A LNCV6_134479_PI430048170 mRNA
TGTGCGACCAGGGTAGAGAGTGTTGAAATTCAATACCAAATACAGTAAAAACAAATGTAA NM_014729RefSeq chr8
- 58805417 59119208 TOX 9760 thymocyte selection-associated high mobility group box
GO:0006355|GO:0003682|GO:0006338|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_126977_PI430048170 0.105195917014646 1.84575700727182 3.8402228485968
3.91565593795386 3.6483693368552 P P P 3.21956537161403 3.16856202623097
2.14501458697723 P P A LNCV6_126977_PI430048170 mRNA
GTAGCCAACCCTTGTGTTAAGTAAAATGTTCTTATTCTTTGCACCTCTTCCTATTTTTGG NM_000488RefSeq chr1 -
173903803 173917378 SERPINC1 462 "serpin peptidase inhibitor, clade C (antithrombin), member 1"
GO:0005515|GO:0005886|GO:0004867|GO:0007584|GO:0005576|GO:0072562|GO:0002020|GO:0005615|GO:2000
266|GO:0010951|GO:0007596|GO:0050728|GO:0008201|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140359_PI430048170 0.0010688966626791 3.03522268412366 3.77090584680116
3.32664242098588 3.39066383396593 P P P 1.79426002953974 1.79092609779135
2.11421680581187 A A A LNCV6_140359_PI430048170 mRNA
CAGTTCGGTGAGGAAAGAAACCAAGCTATTTTCTCTTTTCCTCATGAACATTATATTTAG NM_001243531 RefSeq
chr15 + 84172489 84182233 UBE2Q2L 100505679 ubiquitin-conjugating enzyme E2Q family member
2-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127145_PI430048170 0.579661168117864 1.00644863791415 0.374601805422916
0.3718608444592740.394074699673064A A A 0.3806790308604080.344269069691237
0.387497097859801A A A LNCV6_127145_PI430048170 mRNA
TTTGGACCTAACACTATACACAGAGTAGGCACTGTAGCTGAAGCTGTTGCTTGCATACAG NM_183375RefSeq chr4
+ 151277172 151291453 PRSS48 NA "protease, serine, 48" NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127558_PI430048170 0.152261071833128 1.18836253744351 9.85479300073464
9.93345166113254 9.73200168856532 P P P 9.35939601646363 9.76647441311861
9.62539832585008 P P P LNCV6_127558_PI430048170 mRNA
GGCCAGTGCCTAGAGTGAAGACAGCTGCTGTTTTAATATATTTTTGTGACTTTCAAATCA NM_001256440 RefSeq
chr19 - 40321059 40348527 C19orf47 126526 "chromosome 19 open reading frame 47, transcript

variant 1" GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131187_PI430048170 0.0489956867832778 0.56448156402229 3.19251560528105
2.9015461352478 3.63634069342166 P A P 4.21096766036488 4.05873325244458
4.02483116363743 P P P LNCV6_131187_PI430048170 mRNA
TGGGAACACGGCCAGTTAACAAAATGGGTTTTGGTTTTTTGTTTTGTTTTGTTTTACCATNM_020673RefSeq chr20 +
58309714 58367507 RAB22A57403 "RAB22A, member RAS oncogene family"
GO:0005515|GO:0005886|GO:0003924|GO:0005525|GO:0015629|GO:0001726|GO:0006886|GO:0006897|GO:0045
335|GO:0006184|GO:0030670|GO:0007032|GO:0032482|GO:0019003|GO:0005769|GO:0010008|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132383_PI430048170 0.148397954880572 1.91979957176484 2.24096555786896
2.24996371805583 1.77425657732019 A A A 0.48688716005534 1.98227693803059
0.453327402223271 A A A LNCV6_132383_PI430048170 mRNA
TAAATACCAACCATGCATTTGTACAGTGGGCCCTGTTCATGCGAAATCCACATCCATGGT NM_001288768 RefSeq
chr12 + 54549392 54579239 PDE1B 5153 "phosphodiesterase 1B, calmodulin-dependent, transcript
variant 3"
GO:0005516|GO:0048101|GO:0004117|GO:0046069|GO:0007202|GO:0042053|GO:0046872|GO:0005829|GO:0007
173|GO:0043025|GO:0007626|GO:0030224|GO:0097011|GO:0006198|GO:0048011|GO:0036006|GO:0004115|GO:0
006915|GO:0007165|GO:0042428|GO:0001975|GO:0007596|GO:0008543|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_125400_PI430048170 0.991437031914708 1.02804068017626 3.60831302398319
2.89290583531091 2.5123809680627 P A A 2.7000358549756 3.39009694148793 2.9366209484695
A P P LNCV6_125400_PI430048170 mRNA
TTGAAAACTTACAGAGTCCTGAGGCTTTCAGACTGAAAAAGGCTTTCTTCTGTCACTGAC NM_001134296 RefSeq
chr8 + 42152945 42171183 AP3M2 10947 "adaptor-related protein complex 3, mu 2 subunit,
transcript variant 1" GO:0048490|GO:0030131|GO:0005794|GO:0008089|GO:0030119|GO:0006886|GO:0030659
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53109_PI430048170 0.16879900133572 1.17373786590233 0.758728857910485 0.394531336393097
0.681265740134408 A A A 0.280822685188349 0.423777687421955 0.455598931054289 A A A
LNCV6_53109_PI430048170 mRNA
AAGGAAGTAACCTTCAAGGGTTTAAAACAAACTTCCTTTTTTGGGGATAGCAGCTGAAGA NM_001286554 RefSeq
chr6 - 41789895 41871637 USP49 25862 "ubiquitin specific peptidase 49, transcript variant 1"
GO:0005515|GO:0004197|GO:0042393|GO:0035616|GO:0016579|GO:0004843|GO:0061136|GO:0000398|GO:0043
161|GO:0008270|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134816_PI430048170 0.735151610391274 1.03386892071277 7.30719276251619 7.5952823499275
7.63843434518698 P P P 7.43459903986955 7.43755859051263 7.54383210705133 P P P
LNCV6_134816_PI430048170 mRNA
CTGTTTTTCTTCACGAAATACCCTTTGGATAGCTAAAGTGTTAACTTTGAAATAAAGCCC NM_080653RefSeq chr2
- 46511846 46519957 ATP6V1E2 90423 "ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E2"
GO:0008286|GO:0006879|GO:0033572|GO:0051701|GO:0008553|GO:0001669|GO:0046961|GO:0015991|GO:0090
382|GO:0055085|GO:0033178|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96079_PI430048170 0.109212682709727 1.08555122718468 8.91629077202112 8.78555469289928
8.8336311032808 P P P 8.64239177256164 8.78478913915707 8.7522268623985 P P P
LNCV6_96079_PI430048170 mRNA
CTCTACATTATCTTCTCCCGGTACATGAGAATCAACTCACTGAGCTTCCTCTGAAGCCTT NM_004278RefSeq chr17
+ 16217194 16326259 PIGL 9487 "phosphatidylinositol glycan anchor biosynthesis, class L"
GO:0006501|GO:0016254|GO:0005789|GO:0016021|GO:0044267|GO:0006506|GO:0000225|GO:0043687 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141578_PI430048170 0.436707009502283 1.14581433183382 9.03807195732414
8.92948961589907 9.22508505778782 P P P 8.43920935605756 8.81884582201815

9.24776421232063 P P P LNCV6_141578_PI430048170 mRNA
GTGAAAGTATAGGTAGCAGTAACACCTACATGAAACAATACACCTTGGATCTTTTAATCT NM_001142761 RefSeq
chr15 + 40382720 40394288 KNSTRN90417 "kinetochore-localized astrin/SPAG5 binding protein,
transcript variant 2"
GO:0005515|GO:0072686|GO:0051988|GO:0005634|GO:0035371|GO:0000070|GO:0000922|GO:0005737|GO:0007
059|GO:0015630|GO:0000777|GO:0000776|GO:0007051|GO:0051301 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145011_PI430048170 0.29622613778311 0.7848714459188788.20043225848156
8.75837597238427 9.15771665754493 P P P 8.91216067106818 9.04071479445808
9.33495364630468 P P P LNCV6_145011_PI430048170 mRNA
GAATCACAAAACAAGAATCTTTCCAAAGTTGTCTCATTCAGCAATGTTAAGGCATCTGTA NM_004282RefSeq chr6
+ 57172305 57185214 BAG2 9532 BCL2-associated athanogene 2
GO:0005515|GO:0006457|GO:0051087|GO:0019538|GO:0042802 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145674_PI430048170 0.6180282418017370.9513658524843659.00077542800731
9.05682220572449 8.9033184622246 P P P 9.23696825621958 9.05498256602742 8.8649842048171
P P P LNCV6_145674_PI430048170 mRNA
ATGCATGTGTCTGTGTATGTGTGAATGTGAGAGAGACACAGCCCTCCTTTCAGAAGGAAA NM_003627RefSeq chr11
- 57484530 57515719 SLC43A1 8501 "solute carrier family 43 (amino acid system L transporter),
member 1, transcript variant 1"
GO:0015804|GO:0005886|GO:0005887|GO:0015175|GO:0006865|GO:0015179|GO:0055085|GO:0006811 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136003_PI430048170 0.00851408012990144 0.78308616913843911.8463321613045
11.9861493424688 11.9099250141671 P P P 12.1691177994357 12.2686680673521
12.3599843176974 P P P LNCV6_136003_PI430048170 mRNA
GCTGAGCAAGAACTTTTTCTTGTTTTTAAACCATCACGTCCTCATTTCACATTGGAATAA NM_015229RefSeq chr17
- 2689385 2711633 CLUH 23277 clustered mitochondria (cluA/CLU1) homolog
GO:0005737|GO:0048312|GO:0007005|GO:0003729 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125580_PI430048170 0.1484111552958280.6900610263342264.22748592253612
4.13833051380669 4.70072952276606 P P P 4.45408923234991 4.94093042480445
5.23712364349359 P P P LNCV6_125580_PI430048170 mRNA
CTTAAAATCTGAATGGATGGAACTTAAAACTACTTTGTTGAAACATCAACCTGGGCAGAA NM_006558RefSeq chr8
+ 135457464 135647609 KHDRBS3 10656 "KH domain containing, RNA binding, signal transduction
associated 3"
GO:0005515|GO:0017124|GO:0006355|GO:0003723|GO:0005654|GO:0005634|GO:0007283|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135967_PI430048170 0.5428441629021820.9370464762996090.563067155562921
0.8390958612310560.60680684355784 A A A 0.8004409248197940.55966327855813
0.922514267646287A A A LNCV6_135967_PI430048170 mRNA
CACCTTTCTGCAACAAGTTAGTTTTCAAGCAGTTAAGTCATAGAATGTTTGTTAGCTTTG NM_002726RefSeq chr6
- 105277566 105403124 PREP 5550 prolyl endopeptidase
GO:0005515|GO:0005737|GO:0016020|GO:0004252|GO:0006508|GO:0008236|GO:0005634|GO:0070008 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130811_PI430048170 0.0992587157438191.06428654867667 0.47442479412427
0.5763850773967370.524154802801484A A A 0.3786342471207650.445621480931845
0.480984911066583A A A LNCV6_130811_PI430048170 mRNA
CCATGGTACTGATATTCTCTTCTCAGATAACCAAACAAAAACAGCTGAATAAAATCAACC NM_080817RefSeq chrX
+ 41724154 41730135 GPR82 27197 G protein-coupled receptor 82
GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_143172_PI430048170 0.7138356337856740.9740898317271150.278342055140674
0.4934212120610580.327786874131133A A A 0.5182292787130640.415624196175331
0.278204238387944A A A LNCV6_143172_PI430048170 mRNA
TCTATGGGCACTACAGAAGCCAATTCAAGAGTGAAAGTGCTAGAGAATACCACCTTGCAG NM_001080528 RefSeq
chr3 - 49177635 49191858 C3orf84 NA chromosome 3 open reading frame 84 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_101998_PI430048170 0.5247578428700291.04770066507764 6.16649040795729
6.17473790360434 5.94142718724285 P P P 5.94556627004776 6.12438011189754
6.01732233027581 P P P LNCV6_101998_PI430048170 mRNA
ATGCAAGCTCTCGAGAGTCTCACGGAGACGCAGGTCAGTGACTTCCTGTCGGGCCGTTCG NM_177401 RefSeq chr19
+ 1248552 1259143 MIDN 90007 midnolin
GO:0005730|GO:0033132|GO:0019900|GO:0046676|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134603_PI430048170 0.4831113086597821.04817613016755 0.290030548232803
0.2998425400725530.518967295277333A A A 0.3173367775696910.27585568279646
0.323346470739596A A A LNCV6_134603_PI430048170 mRNA
GCTGACAACAATGAACTGTAACCACAGTTATTTACTGCATAAACTATTTGTGTACTAACC NM_001010888 RefSeq
chrX + 65488734 65507887 ZC3H12B NA zinc finger CCCH-type containing 12B NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133010_PI430048170 0.0860391061967289 1.40941010760556 5.32807636519564
5.74748367458106 5.79852787691731 P P P 4.976770844775 4.95240058924329
5.44823703097248 P P P LNCV6_133010_PI430048170 mRNA
GAGATGAGCAACGTTGTCTTTTCTCTCAAAGCTGTAATGTGGGTTTTGTTTTATTGTTTA NM_003060 RefSeq chr5 +
132369708 132395614 SLC22A5 6584 "solute carrier family 22 (organic cation/carnitine transporter),
member 5"
GO:0005515|GO:0060731|GO:0005886|GO:0052106|GO:0015697|GO:0070715|GO:0031526|GO:0030165|GO:0055
085|GO:0005524|GO:0015651|GO:0016323|GO:0016324|GO:0006855|GO:0042891|GO:0016021|GO:0042895|GO:0
006814|GO:0015879|GO:0015893|GO:0015238|GO:0015226|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145565_PI430048170 0.76596766678415 0.94399217795258910.3240775736801
10.3574480872465 10.5448810617914 P P P 10.1382069819824 10.5195543536612
10.7610440670292 P P P LNCV6_145565_PI430048170 mRNA
AATGGCAGTCCCTTGTCTTATTCAGAATATAAAATTCAGTCTGAATGGCATCTTACAGAT NM_014321 RefSeq chr16
+ 46689645 46698394 ORC6 23594 "origin recognition complex, subunit 6, transcript variant 1"
GO:0006260|GO:0005515|GO:0006261|GO:0000082|GO:0000808|GO:0016020|GO:0005886|GO:0005654|GO:0005
634|GO:0005664|GO:0000278|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144143_PI430048170 0.1133131388233971.03255902969329 0.380395883671944
0.3359105625331110.383993793026759A A A 0.3014185711759730.30609314728245 0.3540214317878
A A A LNCV6_144143_PI430048170 mRNA
GCATCCACTGCATTTCCTTTCATTTGACATAGCTTCTGTTACAATTGCATCCATGTTTTC NM_005615 RefSeq chr14 +
20781050 20782467 RNASE6 6039 "ribonuclease, RNase A family, k6"
GO:0004519|GO:0006952|GO:0005576|GO:0004540|GO:0003676|GO:0070062|GO:0006401 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142431_PI430048170 0.5742480185119440.8370556213248067.90158918189675
8.13810767947606 8.33194924532205 P P P 7.74378646659855 8.5093846256555
8.74294005270878 P P P LNCV6_142431_PI430048170 mRNA
CTTGCCAATGTTCGGAAAGCTTTTACTGCCACGGTTTATAATTAACATACAAATAGTGTA NM_020675 RefSeq
chr2_GL383522v1_alt - 57519 77061 SPC25 57405 "SPC25, NDC80 kinetochore complex component"
GO:0005515|GO:0007067|GO:0007059|GO:0000777|GO:0005634|GO:0007052|GO:0000278|GO:0031262|GO:0051

301|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141348_PI430048170 0.0220994954870539 0.5417125948888076.46273316712322
6.47732842902778 6.71689148856062 P P P 7.09958661782007 7.4725421964315
7.69158010914869 P P P LNCV6_141348_PI430048170 mRNA
CCAGTACAAGCATATATATTGTGCCTCTTACAGCCTTTGGAATACATTGTTTCCATTTTT NM_006366 RefSeq chr6 +
17393504 17557792 CAP2 10486 "CAP, adenylate cyclase-associated protein, 2 (yeast)"
GO:0007190|GO:0007165|GO:0007163|GO:0005886|GO:0007411|GO:0007010|GO:0003779 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127285_PI430048170 0.5498014871406641.2042153220253 1.21080849840251
0.3888278378630420.294950089296125 A A A 0.5209153417449190.313351335934769
0.433775990882025 A A A LNCV6_127285_PI430048170 mRNA
AGGAGTTCCTCAGAAAAAAGGGCACAGTGGATTCCATTGATTAGAAGGATGAGATGAAAA NM_005293 RefSeq
chr8 - 141356485 141367265 GPR20 2843 G protein-coupled receptor 20
GO:0043235|GO:0007186|GO:0005887|GO:0004930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129444_PI430048170 0.895164443992245 1.0059210934443 5.22842872541651
5.14458136501958 5.30608186726527 P P P 5.4940284822302 4.99058657833965
5.12534024464036 P P P LNCV6_129444_PI430048170 mRNA
GACATGAGCCCTGCCACTCGATAGGAGAATCTATCTATTTTAATTATTTTTCTGTTTGTT NM_001277333 RefSeq chr18
+ 12093848 12129749 ANKRD62 342850 ankyrin repeat domain 62 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134524_PI430048170 0.978214171670336 1.01267838995892 4.34364292216037
4.78134388751044 4.14822776467962 P P P 4.57751871042419 4.54069159690971
4.13443891593759 P P P LNCV6_134524_PI430048170 mRNA
TGACTTCTTCACCCGAGTGGCGCTCTTCCGAGACTGGATCGATGGTGTTCTCAACAACCC NM_001700 RefSeq
chr19_KI270868v1_alt + 6673 10860 AZU1 566 azurocidin 1
GO:0008347|GO:0004252|GO:0042582|GO:0007205|GO:0045348|GO:0006955|GO:0050766|GO:0006954|GO:0016
485|GO:0006508|GO:0008201|GO:0001774|GO:0070062|GO:0043066|GO:0042535|GO:0005576|GO:0050725|GO:0
045785|GO:0050930|GO:0050829|GO:0050754|GO:0042117|GO:0015643|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141412_PI430048170 0.9773913910740220.996832670425292 9.21879109499493
9.32085217215117 9.06013603576725 P P P 9.08029572737639 9.36700183310343
9.16280905396026 P P P LNCV6_141412_PI430048170 mRNA
GAGGTACATTTGTTTTTCTGTTTTTCCTGAAAAATAAAGTCGGCCAAGTGAGTGTGAAAA NM_001145638 RefSeq
chr9 + 136327475 136359605 GPSM1 26086 "G-protein signaling modulator 1, transcript variant 1"
GO:0050790|GO:0008277|GO:0005794|GO:0005886|GO:0000139|GO:0005789|GO:0005654|GO:0005092|GO:0030
154|GO:0007399|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141099_PI430048170 0.0789460205337462 0.7180395371238197.59563754935093
7.6540275578564 7.63870403364828 P P P 8.31185039351317 8.14019905550049
7.82992353580558 P P P LNCV6_141099_PI430048170 mRNA
GTTTTAAACTCCAGTAGTCCCTAGAAATTGTAGCTCCCTCTAGTTGTGGCAATAGGTGTG NM_004295 RefSeq chr17
+ 28744004 28750958 TRAF4 9618 TNF receptor-associated factor 4
GO:0005515|GO:0004842|GO:0048471|GO:0016567|GO:0005886|GO:0030323|GO:0046330|GO:0005634|GO:0031
996|GO:0005737|GO:0045860|GO:0005856|GO:0031625|GO:0005164|GO:0090073|GO:0007585|GO:0007250|GO:0
019901|GO:0050699|GO:0006915|GO:0042981|GO:0003677|GO:0007165|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130651_PI430048170 0.16040810434812 1.89660087258459 0.367145790056381
1.27891401949994 1.64550361445899 A A A 0.260736668139846 0.280668260609408
0.258464009798505 A A A LNCV6_130651_PI430048170 mRNA
CTAATGGAATTATGTTAACATCAGCTGCCAACATATATCTCAATCTCTGTTGCCCTGAAC NM_001252634 RefSeq

chr3 - 24117153 24494822 THRB 7068 "thyroid hormone receptor, beta, transcript variant 4"
GO:0005515|GO:0010467|GO:0000790|GO:0006367|GO:0003700|GO:0007605|GO:0008016|GO:0003707|GO:0005
634|GO:0070324|GO:0060509|GO:0008050|GO:0045944|GO:0043401|GO:0009887|GO:0070062|GO:0003714|GO:0
000122|GO:0003677|GO:0006351|GO:0031490|GO:0043565|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144911_PI430048170 0.2730041502118580.8879681441946358.17269518666938
8.46985383103022 8.24515224536891 P P P 8.33104680442605 8.65986172209125
8.40705244170066 P P P LNCV6_144911_PI430048170 mRNA
ATTTTGAGGAAGAGGTGATGGCGGCAGGCAATGCAAGAGCTCAGTTTATTAAATGTGTGC NM_152482RefSeq chr19
- 1473200 1479229 C19orf25 148223 chromosome 19 open reading frame 25 GO:0005515 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135930_PI430048170 0.3018036397221591.08871652800544 6.60971148252394
6.64045986610436 6.84967854849805 P P P 6.47306584383194 6.54950704836188
6.71107135107995 P P P LNCV6_135930_PI430048170 mRNA
CGAAAAAGTTGATCTTCTGGTGTTTAATCCCCCCTATGTAGTGACTCCACCTCAAGAGGT NM_013240RefSeq chr21
- 28876063 28885373 N6AMT1 29104 "N-6 adenine-specific DNA methyltransferase 1 (putative),
transcript variant 1" GO:0005515|GO:0043234|GO:0030307|GO:0006479|GO:0008276|GO:0003676 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128288_PI430048170 0.8241315533834330.9293774278176191.86007705082957
0.4101000925357110.30749097261998 A A A 0.3224735997710561.82673490279971
0.902783911613908A A A LNCV6_128288_PI430048170 mRNA
AAATTCTCCAGAAGGAAGAGGAGGCTGAGGAAGAGTCTCTGATGAACAAAGAAGAAAGCT NM_001080516
RefSeq chr5 - 145859732 145872968 GRXCR2NA "glutaredoxin, cysteine rich 2" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_125703_PI430048170 0.0112443422010517 0.3315936295398426.09196021497783
6.07731268904906 6.40104384292882 P P P 7.41587187957435 7.63330284237455
8.20405469741152 P P P LNCV6_125703_PI430048170 mRNA
GCCCTAAGGAATATATCTCACATTCACCTCCTATATGTATGTGTATATATAAATGCCACT NM_024345RefSeq chr9
+ 37800785 37867668 DCAF1079269 "DDB1 and CUL4 associated factor 10, transcript variant 1"
GO:0016567|GO:0080008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109037_PI430048170 0.0371227109865936 1.66144475836429 3.53878459263861
3.35932725659634 3.21679569618433 P P P 2.60669142092494 2.94897053744649
2.30884225633873 P P P LNCV6_109037_PI430048170 mRNA
ACTTTCACCAAGATGTTCTAGAAACTTCTGAGCCAGGAGTGAATGGCCCTTCCTTAGTAG NM_019625RefSeq chr12
- 122928991 122966509 ABCB9 23457 "ATP-binding cassette, sub-family B (MDR/TAP), member 9,
transcript variant 1"
GO:0005515|GO:0002474|GO:0005783|GO:0030176|GO:0005765|GO:0015031|GO:0055085|GO:0005524|GO:0005
764|GO:0042803|GO:0015833|GO:0022891|GO:0008152|GO:0016021|GO:0015440|GO:0005769 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_69720_PI430048170 0.7326641376085790.8241153108555 2.37974898955311 1.74900056844995
2.14179009600661 A A A 2.65869595647569 2.76896343440156 1.38845416773387 P P A
LNCV6_69720_PI430048170 mRNA
AGAGGGGACAGTGACATTTGAGGGCCTTGGGGGAAAGTTAGCCTATGCTGAGCTGAGGCT NM_001085398
RefSeq - - 0 0 --- NA - NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109684_PI430048170 0.000213165303017553 0.49670947141497 5.52096208425326
5.34073363525832 5.5034240590996 P P P 6.49354369204787 6.528344186955
6.37406647194515 P P P LNCV6_109684_PI430048170 mRNA
TCACAAAGAAAATCCAGCTTCCTGCAGAGGTGGATCCTGTGACAGTATTTGCCTCACTTT NM_014365RefSeq chr12
+ 119178789 119194746 HSPB8 26353 heat shock 22kDa protein 8

GO:0005622|GO:0005515|GO:0008150|GO:0005737|GO:0005794|GO:0004672|GO:0005654|GO:0005634|GO:0042
802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105233_PI430048170 0.01033535323145 1.56336079761096 7.95628321768579
8.19493607229867 8.0664402214858 P P P 7.45498232975566 7.58996667619234
7.22539415965628 P P P LNCV6_105233_PI430048170 mRNA
TGGCTTGAAAAACCCTTGCCCAGTTTTGATCCCTTCAAGACTTTGTCACAGCCTCTATCA NM_006867 RefSeq chr8
+ 30384500 30572261 RBPMS 11030 "RNA binding protein with multiple splicing, transcript variant 4"
GO:0005515|GO:0006396|GO:0006355|GO:0005737|GO:0000166|GO:0008143|GO:0003713|GO:0010862|GO:0005
654|GO:0060391|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131696_PI430048170 0.00248899116861105 0.691028034938945 12.2987342461905
12.4614884001531 12.2771239590614 P P P 12.7986607661151 12.9756398283548
12.8641484772319 P P P LNCV6_131696_PI430048170 mRNA
CGACGTTTTATCAAAGGCCCCCTTTCTATGTTCATGTTAGTTTTGCTCCTTCTGTGTTTT NM_001848 RefSeq chr21 +
45981748 46005049 COL6A1 1291 "collagen, type VI, alpha 1"
GO:0048407|GO:0005578|GO:0005576|GO:0005589|GO:0035987|GO:0005765|GO:0001649|GO:0070208|GO:0042
383|GO:0031012|GO:0043234|GO:0071230|GO:0016020|GO:0022617|GO:0007411|GO:0030198|GO:0030574|GO:0
005788|GO:0007155|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131203_PI430048170 0.0161362479841644 0.191985393012668 0.271209534543808
0.289465099768949 0.361474925452339 A A A 2.51983021349391 2.15702327721238 3.1935841282855
A A P LNCV6_131203_PI430048170 mRNA
CATCTTTTGCCTGCAGGCAGGGAAAGTGTACAGTATTTATTTTGTTTCTGTTTTACTTTA NM_030647 RefSeq chr7 -
140084745 140176941 KDM7A 80853 lysine (K)-specific demethylase 7A
GO:0032454|GO:0035574|GO:0035575|GO:0005506|GO:0005730|GO:0006325|GO:0005634|GO:0035064|GO:0051
864|GO:0006351|GO:0070544|GO:0071557|GO:0016706|GO:0005654|GO:0008270|GO:0030901|GO:0045893|GO:0
071558|GO:0055114|GO:0033169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128560_PI430048170 0.417364235983597 1.02654070837627 13.1249377676701
13.1956479285761 13.177216086617 P P P 13.1519945520734 13.0575518096468
13.1732037068505 P P P LNCV6_128560_PI430048170 mRNA
CCAGGAGGGGAAAATGGTGGCAATGCCTTTTATATATTATGTTTTTACTGAAATTAACTG NM_014255 RefSeq chr12
- 56310428 56316344 CNPY2 10330 "canopy FGF signaling regulator 2, transcript variant 1"
GO:0005515|GO:0005887|GO:0005783|GO:0010629|GO:0010988|GO:0045716 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132222_PI430048170 0.241157688907409 0.726514184290865 3.05312712490324
2.23111455656664 3.28726093850644 P A P 3.21211996352287 3.36307213671979
3.55679720572782 P P P LNCV6_132222_PI430048170 mRNA
AGATGCCTTTCTGACTCTCAGCTCCTGCACTTCTGTCATCATACCTCTGATACTATTATT NM_001128128 RefSeq chr10
+ 31321134 31529814 ZEB1 6935 "zinc finger E-box binding homeobox 1, transcript variant 1"
GO:0005515|GO:0007389|GO:0003700|GO:0008285|GO:0010464|GO:0051216|GO:0008283|GO:0071560|GO:0033
081|GO:0048704|GO:0005634|GO:0048752|GO:0048596|GO:0005737|GO:0006955|GO:0003690|GO:0071230|GO:0
030857|GO:0045944|GO:0090103|GO:0031667|GO:0017015|GO:0005667|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127392_PI430048170 0.311067781799918 1.03545064549395 0.312878870969594
0.259234215559695 0.386444203378541 A A A 0.279406474439908 0.251089147395172
0.279930042316282 A A A LNCV6_127392_PI430048170 mRNA
CACGTGATCCGGGTAATCATCACATTGAATATAGTGATGATTGACCTTATTATTTTACCC NM_001297 RefSeq chr16
- 57882339 57971116 CNGB1 1258 "cyclic nucleotide gated channel beta 1, transcript variant 1"
GO:0005515|GO:0007608|GO:0060170|GO:0007603|GO:0005886|GO:0051290|GO:0045494|GO:0030552|GO:0030
553|GO:0050908|GO:0001895|GO:0005249|GO:0043195|GO:0042391|GO:0006810|GO:0071805|GO:0006812|GO:0
015276|GO:0016056|GO:0017071|GO:0005223|GO:0006996|GO:0033365|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_128500_PI430048170 0.0863608468696534 0.6879759314026844.79767345640612
4.6133289070163 4.14808876074613 P P P 5.19638783525526 5.10367450377733
4.94132099291627 P P P LNCV6_128500_PI430048170 mRNA
CACTGTTGTGTAAATACACAGTTGCTTTCCAGAAAAGTTGTAGGTACCACTTGCAAAAAA NM_006627RefSeq chr19
+ 29606262 29617255 POP4 10775 "processing of precursor 4, ribonuclease P/MRP subunit (S.
cerevisiae), transcript variant 1"
GO:0006379|GO:0005515|GO:0000171|GO:0033204|GO:0000172|GO:0004526|GO:0006364|GO:0003723|GO:0005
655|GO:0008033|GO:0030677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135681_PI430048170 0.6902532214516170.9495774731839170.9377994787231 10.303962823672
10.2948163494573 P P P 10.7330800239492 10.6649455786571 10.4452845928924 P P P
LNCV6_135681_PI430048170 mRNA
AACCACCTCTGTTGGTTAGATGATGAATAAAAAGGTTCTGAAGAAAAGGTCTGGAAAAAA NM_053041RefSeq chr20
- 32702690 32744008 COMMD7 149951 "COMM domain containing 7, transcript variant 1"
GO:0005515|GO:0051059|GO:0032088|GO:0045892|GO:0033209|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133438_PI430048170 0.2939950637871531.53034720857637 1.76945644138034
0.68285821271852 0.655708260020379A A A 0.61189724465229 0.46972207958622
0.478274484888358A A A LNCV6_133438_PI430048170 mRNA
TAGGTAAGAGATGGCAACAGTTTACTATTTGGTAAGAGTGGAATAACATCTCTAGTAATC NM_001080409 RefSeq
chr19 - 22752182 22784171 ZNF99 7652 zinc finger protein 99
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130559_PI430048170 0.9990946062388780.9902782745713141 0.1727602444274
10.5340252772009 10.3363923744776 P P P 10.6750697731462 10.0686489132168
10.2987051820798 P P P LNCV6_130559_PI430048170 mRNA
GGGATCCATTGGTGTTTGGTTTGGGGTGTTTTTTAAGTTTTTTCTTTTATATCATCCAGA NM_001193268 RefSeq chr19
- 45609399 45645517 EML2 24139 "echinoderm microtubule associated protein like 2, transcript
variant 1"
GO:0008017|GO:0072686|GO:0031115|GO:0005737|GO:0015631|GO:0007605|GO:0005875|GO:0005874|GO:0005
102|GO:0010968|GO:0008022|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138501_PI430048170 0.0955429119001758 1.81228702499516 0.803600821022228
1.84669234768208 1.37258469307154 A A A 0.8518568252373620.391062327704646
0.333829787597568A A A LNCV6_138501_PI430048170 mRNA
ATCAAAAGAGATGAAAGGTATGTAGAACAGGTTCACGTGATTACCTTTTTCTTTTGGCTT NM_006614RefSeq chr3
+ 196595 409414 CHL1 10752 "cell adhesion molecule L1-like, transcript variant 1"
GO:0008344|GO:0031103|GO:0005886|GO:0005578|GO:0045177|GO:0002020|GO:0030425|GO:0007165|GO:0043
524|GO:0050890|GO:0007411|GO:0016021|GO:0001764|GO:0007155|GO:0035640|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141288_PI430048170 0.0548469577839661 0.7626827630227569.88383184041135
9.8065952945231 9.79652753805769 P P P 10.0155571311049 10.2711433857439
10.3532867130745 P P P LNCV6_141288_PI430048170 mRNA
CGTGAGAGGAAAATGTTAATAAAAAATGCAAAGCCCCATCATTTGCACAAAACTCAGAAA NM_001159746 RefSeq
chr17_KI270910v1_alt - 42764 140753 ABR29 "active BCR-related, transcript variant 3"
GO:0043314|GO:0051056|GO:0048011|GO:0030336|GO:0043065|GO:0030036|GO:0042472|GO:0005886|GO:0007
264|GO:0097190|GO:0032855|GO:0005829|GO:0050766|GO:0016020|GO:0007420|GO:0050728|GO:0050885|GO:0
032496|GO:0005089|GO:0030675|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130276_PI430048170 0.0136752149653347 0.7082489767094295.95570697494067
6.08132091326002 5.9803604882824 P P P 6.33923993451046 6.55644441151112

6.60422382089262 P P P LNCV6_130276_PI430048170 mRNA
ACTGTGAATGCATTTAGCCACTCCCCTCTACTCAAAAATACTGGTAAACTCTGATTTTTA NM_001105573 RefSeq
chr3 + 196568853 196589059 FBXO45 200933 F-box protein 45
GO:0005515|GO:0021960|GO:0016567|GO:0030054|GO:0021957|GO:0021800|GO:0014069|GO:0006974|GO:0042
734|GO:0042787|GO:0060386|GO:0045211|GO:0021799|GO:0043161|GO:0001764 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131411_PI430048170 0.0237640172962264 0.3485179195902278.66652150763263
8.39769324134843 8.56689745731385 P P P 9.50569466508833 10.1585533298665
10.4006378998086 P P P LNCV6_131411_PI430048170 mRNA
CCAGCTCAGACCATTTCCTAATCAGTTGAAAGGGAAACAAGTATTTCAGTCTCAAAATTG NM_001165931 RefSeq
chr2 + 10122567 10131419 RRM2 6241 "ribonucleotide reductase M2, transcript variant 1"
GO:0005515|GO:0009186|GO:0015949|GO:0055086|GO:0051290|GO:0005634|GO:0044281|GO:0046872|GO:0005
829|GO:0006260|GO:0000082|GO:0005737|GO:0000083|GO:0009263|GO:0005654|GO:0004748|GO:0000278|GO:0
055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142357_PI430048170 0.00542134084314445 0.4950032430377210.0413143373449
10.0803854536785 10.4109568951993 P P P 10.959687937911 11.1701186836083
11.4359536506291 P P P LNCV6_142357_PI430048170 mRNA
ACTACTGAGAGTATTGTATCTGTTCTGGTAACCATGTACAGAATGTGAAACTGTCTTATG NM_032717RefSeq chr4
+ 83536316 83605874 AGPAT9 84803 "1-acylglycerol-3-phosphate O-acyltransferase 9, transcript
variant 1"
GO:0032006|GO:0005783|GO:0004366|GO:0044281|GO:0003841|GO:0005789|GO:0016024|GO:0019432|GO:0016
021|GO:0006644|GO:0006654|GO:0044255|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132038_PI430048170 0.0689997761794138 1.21484245234979 10.7556591543052
10.973753561686 10.677352609039 P P P 10.6463443449662 10.4632675534211
10.4635860168556 P P P LNCV6_132038_PI430048170 mRNA
AGTAGTTGGTAGAGCTGAGGAAGAGTTAGGGCCTCTCCCTCATTAAAGTTTTATAAATAA NM_015662RefSeq chr2
- 27444372 27489811 IFT172 26160 intraflagellar transport 172
GO:0097225|GO:0050680|GO:0097228|GO:0031122|GO:0009953|GO:0070986|GO:0036064|GO:0007224|GO:0001
947|GO:0045880|GO:0007219|GO:0016485|GO:0060021|GO:0021522|GO:0006996|GO:0005930|GO:0001843|GO:0
072372|GO:0031982|GO:0005929|GO:0042384|GO:0060348|GO:0008544|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127950_PI430048170 0.101350558814685 1.06783762987721 0.464670357864307
0.55180456879272 0.529657390183779 A A A 0.356197421880788 0.42743203774159
0.477280812540295 A A A LNCV6_127950_PI430048170 mRNA
GCCCATGTTTCAGTTGCCAGTAAGCTTCTCACATTTAATAAAGTGTACTTTTTAGAACAT NM_032562RefSeq chr10
- 72935179 72954752 PLA2G12B 84647 "phospholipase A2, group XIIB"
GO:0042632|GO:0016042|GO:0005509|GO:0004623|GO:0070328|GO:0005576 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127893_PI430048170 0.2220780892777290.821399604995835 5.15989104338725
4.95384839277962 5.42632341192428 P P P 5.18367348895931 5.57728288940758
5.62985637633797 P P P LNCV6_127893_PI430048170 mRNA
TATCTACCAAGAGCGCAGACTTGCATCCTGTCACTACCACTCGTTAGAGAAAGAGAAGAA NM_022746RefSeq chr1
+ 220786696 220814399 MARCH1 NA mitochondrial amidoxime reducing component 1 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_140650_PI430048170 0.0241226343580423 0.5403577865637833.13900773254048
3.42346237874151 3.71969181783119 P P P 3.95491267104234 4.41209805884731
4.56935953968568 P P P LNCV6_140650_PI430048170 mRNA
GCGATCTTCAGTGTGTCTGCATAAGCTAACTTAAGATGAATTTAAGTACAGTTTTCTGAA NM_152663RefSeq chr1
+ 178725146 178921842 RALGPS2 55103 "Ral GEF with PH domain and SH3 binding motif 2, transcript

variant 10" GO:0043547|GO:0005085|GO:0005737|GO:0005886|GO:0007264 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126020_PI430048170 0.966044106692613 1.00039746669262 6.29807589071893 6.13451842386104 6.11976600995537 P P P 6.15914291139844 6.361832651242 6.01542809930893 P P P LNCV6_126020_PI430048170 mRNA
TATGTCTGCCGGATGTGTTCTCGAGGGGATGAGGATGACAAGCTCCTGCTGTGTGATGGC NM_004187 RefSeq chrX - 53191320 53225422 KDM5C 8242 "lysine (K)-specific demethylase 5C, transcript variant 1"
GO:0034720|GO:0032453|GO:0016706|GO:0006325|GO:0008270|GO:0005654|GO:0005634|GO:0048511|GO:0045892|GO:0003677|GO:0006351|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133298_PI430048170 0.660470857401432 0.964265409835524 0.276948887344809 0.500932042690372 0.34414881240492 A A A 0.583012583478514 0.391491506851343 0.299623874755288 A A A LNCV6_133298_PI430048170 mRNA
CTGCTATTTATTCTTTATAATATCCCGTGTAGTAAATGAGAAAGAAGTGCAGAGCAGGAT NM_005450 RefSeq chr17 + 56593698 56595590 NOG 9241 noggin
GO:0005515|GO:0071773|GO:0060044|GO:0051216|GO:0048706|GO:0060302|GO:0005615|GO:0060676|GO:2000313|GO:0042803|GO:0090193|GO:0050679|GO:0030336|GO:0001706|GO:0001707|GO:0001843|GO:0030509|GO:0000122|GO:0001701|GO:0001649|GO:0008045|GO:0001501|GO:0061053|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134369_PI430048170 0.315986169613783 1.03154910457926 8.27318630676866 8.2258359631136 8.2061539798542 P P P 8.25086835542391 8.17994300124119 8.13850757897603 P P P LNCV6_134369_PI430048170 mRNA
TGTTTTCACACAACACTTGGTAGTTTTTCCAGCCTCCAAGTCACCACCTAGTAACTGGCT NM_017879 RefSeq chr19 - 57571565 57578875 ZNF416 55659 zinc finger protein 416
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141063_PI430048170 0.0655825626664353 1.20954610992494 12.5557223862932 12.3943735059324 12.6239911964917 P P P 12.3965036391489 12.1057870788103 12.2432601815297 P P P LNCV6_141063_PI430048170 mRNA
ATGGTGAAGCCATAGAAAAGTTACCCGAGGGAAAATAAATACAGTGATATTCTTACGCAA NM_001001 RefSeq chr14 - 49618688 49620685 RPL36AL 6166 ribosomal protein L36a-like
GO:0003735|GO:0022625|GO:0006412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127214_PI430048170 0.386427463520345 0.848585046585005 4.89044515237757 4.38408078387048 4.61286112718261 P P P 5.07941381179644 5.00213406035402 4.49408711559065 P P P LNCV6_127214_PI430048170 mRNA
CTGGCTCTGCCTGGCTGTTCCACGTCCTCACTCTTGTTCTATTTGACAGCAATTAAAAAA NM_022141 RefSeq chr22 + 44180889 44208469 PARVG 64098 "parvin, gamma, transcript variant 1"
GO:0005737|GO:0031532|GO:0007160|GO:0005886|GO:0003779|GO:0005856|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60074_PI430048170 0.118172723418017 0.698531742091333 3.18500915534347 2.90119321853306 3.40590300508855 A A P 3.30402599766205 3.70708501699303 3.99558612203505 P P P LNCV6_60074_PI430048170 mRNA
GCCTTGTGCCAAAGGAGAAATATGACAAAAATGATGTTATTTTAGAGGTGACAGCTGGAA NM_004294 RefSeq chr13 - 41216379 41263577 MTRF1 9617 mitochondrial translational release factor 1
GO:0005739|GO:0016149|GO:0006449|GO:0006415|GO:0003747 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143794_PI430048170 0.120750637805744 0.567809297268797 3.34151456538909 3.35152758096174 3.93484969515341 P P P 3.69848076257036 4.50623621659948 4.75784279952829 P P P LNCV6_143794_PI430048170 mRNA
CCATGTTGGGAGTAGATGGGTATATAACAGTTTGGAAATACTATCTTTGGAGAATGTATT NM_001286746 RefSeq

chr13 + 72727903 72756198 BORA 79866 "bora, aurora kinase A activator, transcript variant 2"
GO:0032880|GO:0005515|GO:0007088|GO:0007067|GO:0019901|GO:0060236|GO:0000086|GO:0000278|GO:0051
301|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110459_PI430048170 0.25197907740495 1.20834685716308 5.35876248080043
5.64636905034044 5.10259787785338 P P P 5.18918403139113 5.24883827516792
4.87463370691602 P P P LNCV6_110459_PI430048170 mRNA
AAGGCCTTCACAGAAGTCACCCAGACAGAGCTGCAGGACCCTCACCCTTCCCGGGAACTGNM_001145303 RefSeq
chr19 - 54160095 54173250 TMC4 147798 "transmembrane channel-like 4, transcript variant 1"
GO:0016021|GO:0070062|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127722_PI430048170 0.0325018924037046 2.41888230411888 2.41278495709725
3.40123390302663 3.18706818491714 A P P 1.78404862806891 1.39533147416397
2.09085162425901 A A A LNCV6_127722_PI430048170 mRNA
GGAGAAAATGCTGTCCCTGTTTCACAGTGTCTTTAATCCAATGCTGAACCCCCTGATCTA NM_001005480 RefSeq
chr7 + 144109582 144110539 OR2A2 NA "olfactory receptor, family 2, subfamily A, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145052_PI430048170 0.0741253777887808 0.4434789359518530.365584484977874
1.58331945791432 0.289245062385758A A A 2.12753203441611 2.34258110362385
1.57333404703535 A P A LNCV6_145052_PI430048170 mRNA
GAATGGCTACATTCAGATTTATTTTCACAACTATAGTCCTGCTAAACTGCCTTCATTGAA NM_001143957 RefSeq
chr6 - 96794121 96837477 GPR63 81491 "G protein-coupled receptor 63, transcript variant 1"
GO:0043235|GO:0008150|GO:0003674|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143184_PI430048170 0.38263676536877 1.1449010101998 8.45730781898159
8.79177099365866 8.95447856816431 P P P 8.51703640543881 8.32874253571355 8.7798825996806
P P P LNCV6_143184_PI430048170 mRNA
TTCAGGAAGGATGATCATTCCAGTTAGTTTGGCATTTTTTGTCGTTTGTGCACATAACTT NM_145063RefSeq chr6
- 41066791 41072449 OARD1 221443 O-acyl-ADP-ribose deacylase 1
GO:0042278|GO:0005515|GO:0001883|GO:0019213 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143165_PI430048170 0.3170473192663620.5972427596668580.279545582868855
0.29521625869728 0.285796531209559A A A 0.4769900922653820.387615100657943
1.77738233033589 A A A LNCV6_143165_PI430048170 mRNA
GATCTTCATCTTCTTCTTGATCAAGTACAAGCCACTCAAGTACAACAACATCTACACCTA NM_014229RefSeq chr3
+ 10816231 10938460 SLC6A11 6538 "solute carrier family 6 (neurotransmitter transporter), member
11"
GO:0005886|GO:0005328|GO:0042493|GO:0007268|GO:0042995|GO:0055085|GO:0007269|GO:0005737|GO:0005
887|GO:0007420|GO:0015812|GO:0042165|GO:0016021|GO:0005332 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134094_PI430048170 0.4587259462460810.6387218166957010.38450870613335
0.2587604290330540.28241414368652 A A A 0.2642604960666941.77406445076848
0.262993007907145A A A LNCV6_134094_PI430048170 mRNA
CCCGGTGAAGAAATCAAGGAACCCGGTGAAGAAATCTTATTGATGAATAAATAACTTTAA NM_020641RefSeq chr9
- 27284655 27297139 EQTN 54586 "equatorin, sperm acrosome associated, transcript variant 1"
GO:0002079|GO:0060478|GO:0005886|GO:0007342|GO:0005634|GO:0016021|GO:0002081|GO:0005769|GO:0006
897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130869_PI430048170 0.0210232602764301 1.39069375655073 12.2620842228818
12.249328003565 12.5385167432931 P P P 11.8412402618465 11.7447442267641 12.039593323602
P P P LNCV6_130869_PI430048170 mRNA
TAAATGAATTCCGGGAAAAGCACAACATTCGTCTCATGGGAGAAGATGAGAAGCCAGCAG NM_012394RefSeq
chr1 - 161100555 161118076 PFDN2 5202 prefoldin subunit 2

GO:0005739|GO:0005515|GO:0005737|GO:0006457|GO:0016272|GO:0005730|GO:0051084|GO:0005654|GO:0005634|GO:0051082|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145374_PI430048170 0.01952098041137 0.2008686716883422.8374775697085 3.96015612031036 3.72093982250054 A P P 5.88512438744613 5.93441101618426 5.86928385540528 P P P LNCV6_145374_PI430048170 mRNA
GCTGTATTCAGCAAGGCGCTAACTTGCTTAAATGTGAATTACTAACTTCTAAAACTGTAC NM_002024RefSeq chrX + 147911950 147951127 FMR1 2332 "fragile X mental retardation 1, transcript variant ISO1"
GO:0005515|GO:0008017|GO:0017148|GO:0071598|GO:0010494|GO:0003723|GO:0005874|GO:0005730|GO:0045202|GO:0003729|GO:0007417|GO:0044297|GO:0005737|GO:0043197|GO:0016020|GO:0043198|GO:0042788|GO:0045947|GO:0005654|GO:0051028|GO:0005845 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134413_PI430048170 0.00161614729060654 2.50511554662649 8.36063166952307 8.45666948035986 8.05542244967281 P P P 6.83907851808905 7.21610317021494 6.83888648629689 P P P LNCV6_134413_PI430048170 mRNA
CTGCTGTAGAGCTGAAGCTGAACATGTGTTTGCTAAATAAAGATTCCCATTCCTAGCGCA NM_194312RefSeq chr2 + 238100309 238133287 ESPNL 339768 espin-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144193_PI430048170 0.0119654477971143 0.63121627452161 7.41304368142712 7.16438907211012 7.32634933517135 P P P 7.86690952318072 7.82736652398862 8.18462371693399 P P P LNCV6_144193_PI430048170 mRNA
ATAAAGCATGCTGGTAAAACCACTACCCTCAGAGAGAGCCAAAAATACAGAAGAGGCGGA NM_000136RefSeq chr9 - 95099053 95317709 FANCC 2176 "Fanconi anemia, complementation group C, transcript variant 1"
GO:0005515|GO:0005737|GO:0006461|GO:0006281|GO:0019430|GO:0005654|GO:0005634|GO:0006289|GO:0002262|GO:0007281|GO:0043240|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141697_PI430048170 0.2514955314706260.9138574610133468.68835313027924 8.85679940846911 8.92636385273613 P P P 8.82128067129083 9.03313034888382 9.00809909903919 P P P LNCV6_141697_PI430048170 mRNA
TGCATTGCTGCATCCTGGGAAGGGGGTATATGGTCTCACAAGTTGTTGTCATTGTTTTTT NM_018416RefSeq chr12 + 8032762 8055522 FOXJ2 55810 forkhead box J2
GO:0043565|GO:0001077|GO:0045944|GO:0005730|GO:0005634|GO:0045893|GO:0000978|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134143_PI430048170 0.5151173902545540.8441083023213322.80080476948404 0.7062790121187851.00354934888511 A A A 2.17356651961396 2.35081719759167 1.56111673392144 A A A LNCV6_134143_PI430048170 mRNA
GTGACTCCCTTTCTCATTCTGTTCTGTTGTATTGCGTCCAAAAGTTGTGTGTAATTTTTT NM_199000RefSeq chr7 + 104328655 104908556 LHFPL3 375612 lipoma HMGIC fusion partner-like 3 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105831_PI430048170 0.2215633962829230.75738676386608 4.65704361754375 3.8052116156309 4.21251279198231 P P P 4.48027072390605 4.92775481557787 4.55393550055741 P P P LNCV6_105831_PI430048170 mRNA
ATGGAAAAGATGGACCAGACACAGCTAGGACATCTAGCTTTAAAACCAAAGCAGCCTTGG NM_144697RefSeq chr1 + 150282532 150287092 CIART 148523 "circadian associated repressor of transcription, transcript variant 1"
GO:0005515|GO:0045475|GO:0016605|GO:0070888|GO:0005634|GO:0001046|GO:0045892|GO:0032922|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132696_PI430048170 0.0115212768635005 0.6323901686547769.99483790773622 9.75929445390268 9.84911103226651 P P P 10.5143644318794 10.3371383211488 10.7195061884512 P P P LNCV6_132696_PI430048170 mRNA
TGTTGCTCAAGCTGTGCCTGCCAACTTGTAACTTAATAAATACAGGAAATCCTCAGAGAA NM_025090RefSeq chr17

- 78796882 78840887 USP36 57602 ubiquitin specific peptidase 36
GO:0004197|GO:0016579|GO:0004843|GO:0061136|GO:0005730|GO:0043161|GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143022_PI430048170 0.4713104154531811.25789904581874 0.515199406991513
0.5683183446980681.45139259969658 A A A 0.82106633417952 0.442152615896426
0.447479222649572A A A LNCV6_143022_PI430048170 mRNA
TTTGTTCTTCCCTTAAAGGAAGCATCTACCAAAATGTGGCACACAAACCTTGCATGGTGT NM_001040663 RefSeq
chrX + 49599012 49608536 GAGE1 2543 "G antigen 1, transcript variant 2" GO:0006968 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129171_PI430048170 0.2293117362363550.9599774104176310.250232949810088
0.26302216291143 0.351678660493026A A A 0.3994750077951480.330425501523664
0.312476664191831A A A LNCV6_129171_PI430048170 mRNA
GCTGATGATGTGCTCAAAGATGTATCAAAATCCATGTAATGACACCTTTTAGATGTTTCT NM_001146341 RefSeq
chr15 + 79282803 79298239 ANKRD34C NA ankyrin repeat domain 34C NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_75263_PI430048170 0.0383149294155784 1.33180262301059 5.57522695054974
5.65261469691231 5.87483322950536 P P P 5.26627726065721 5.27424687386775
5.33793844257149 P P P LNCV6_75263_PI430048170 mRNA
AAATTTGTTGGCAGATTGTTTGCAGGGTTGTTTTGTGGTGACGTGCACACTGTGTGCATT NM_005885 RefSeq chr5
+ 10353638 10440388 MARCH6 NA "membrane-associated ring finger (C3HC4) 6, E3 ubiquitin protein
ligase, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142649_PI430048170 0.5360465100514191.69923877711352 0.273101710636175
2.52615901903204 1.18917576678763 A A A 0.9676260648835570.49570471234687
1.05477127656731 A A A LNCV6_142649_PI430048170 mRNA
ATCAGCAATAGTGCATTGGTGGACAAGACAGACAAGACGCAGACAATGAAAACCCCTAAG NM_144702 RefSeq
chr1 + 156920631 156933088 LRRC71 149499 leucine rich repeat containing 71 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_63162_PI430048170 0.6484154471238980.8792741041050064.21933685733731 4.63403985817996
4.45377622271231 P P P 4.81523580566508 4.0516297856919 4.8880552176051 P P P
LNCV6_63162_PI430048170 mRNA
CTCTTTTAGAAAACCTGACAAGCGAGTATGACTTGGATCTTTTCCGAAGAGCACAAGCCC NM_007067 RefSeq chr17
+ 49788618 49829096 KAT7 11143 "K(lysine) acetyltransferase 7, transcript variant 1"
GO:0005515|GO:0006355|GO:0003700|GO:0005730|GO:0006325|GO:0006351|GO:0043981|GO:0006260|GO:0043
983|GO:0005737|GO:0043982|GO:0043966|GO:0043984|GO:0000123|GO:0005654|GO:0008270|GO:0004402 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132710_PI430048170 0.0352581313952148 1.70127190410826 5.71849949534437
5.88705408401368 5.82160507845879 P P P 4.75062892395655 5.33491723990392
4.98630329799481 P P P LNCV6_132710_PI430048170 mRNA
TGTGGCCCCTGGGGCAGCTTTTCTTCCAAAATGGGAACTAGTGGCCTGTGTTCTAAAAAA NM_138924 RefSeq chr19
- 1397810 1401570 GAMT 2593 "guanidinoacetate N-methyltransferase, transcript variant 2"
GO:0008168|GO:0007283|GO:0044281|GO:0032259|GO:0005829|GO:0030731|GO:0034641|GO:0006936|GO:0006
601|GO:0006600|GO:0040014|GO:0009887|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115454_PI430048170 0.4092349650303670.9494813931264290.273730671659683
0.4153953334366410.288743141008651A A A 0.5080335687606780.404798148822964
0.285027947555881A A A LNCV6_115454_PI430048170 mRNA
AATGTGATGAAGTAAATCAGATCGTGACAACCAATGTGCGTCTGAAACAGGTGACATGGT NM_001039523 RefSeq
chr2 - 174747594 174764472 CHRNA1 1134 "cholinergic receptor, nicotinic, alpha 1 (muscle),
transcript variant 1"
GO:0048630|GO:0031594|GO:0030054|GO:0005886|GO:0009986|GO:0007268|GO:0007274|GO:0046716|GO:0005

892|GO:0019228|GO:0050905|GO:0007165|GO:0034220|GO:0050881|GO:0003009|GO:0007528|GO:0045211|GO:0
015464|GO:0042391|GO:0042166|GO:0006810|GO:0070050|GO:0005216|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139146_PI430048170 0.1286921352869590.3189461905973113.64591267975198
0.65322193849434 2.08334602767589 P A A 3.90693483757807 4.16235104351618
4.61819596936151 P P P LNCV6_139146_PI430048170 mRNA
AAAGCTCATACATACCAGCGCCTTCTTAAATTGGCTCTAATGTAAAGATTGTTAATGTCA NM_001282666 RefSeq
chr11 + 12162078 12263790 MICAL2 9645 "microtubule associated monooxygenase, calponin and LIM
domain containing 2, transcript variant 5"
GO:0019417|GO:0010735|GO:0003779|GO:0005634|GO:0043914|GO:0001947|GO:0007507|GO:0071949|GO:0007
010|GO:0016709|GO:0030042|GO:0008270|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141889_PI430048170 0.6645179409496481.1894634351992 0.5322153727346611.2180551437172
1.7693363971068 A A A 0.4606185120163421.3082956303071 1.12758915085026 A A A
LNCV6_141889_PI430048170 mRNA
ACAGAAGTTACTGTCACCCTACTGACTTTCTCACCAGTAAACATTGTGGCTGTTCCTGTA NM_001145010 RefSeq
chr12 + 27466809 27502185 SMCO2 341346 single-pass membrane protein with coiled-coil domains 2
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130233_PI430048170 0.0302240392419814 0.5518813238864863.57398083430128
3.06877140031668 3.66856658733928 P P P 4.30051083241539 4.20236991828594
4.44021682511836 P P P LNCV6_130233_PI430048170 mRNA
CCTTGTATGAAAATGATCTCTTGGCATCCCGATTAAATGACACACTGTCACTGTGGGTAA NM_024567 RefSeq chr8
+ 28890707 29052725 HMBOX1 79618 "homeobox containing 1, transcript variant 1"
GO:0005515|GO:0005737|GO:0005654|GO:0005634|GO:0045893|GO:0045892|GO:0003677|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144272_PI430048170 0.0671706077089281.46517185181089 7.57408611401106
7.42133117466357 7.57529732775097 P P P 6.62202272115128 7.07971108163979
7.16438907211012 P P P LNCV6_144272_PI430048170 mRNA
AAGTAAGCTTAAACTACAACTTGTCACATAAAGGAAGTCTTAAGTGGAGTTCACAGAATG NM_014051 RefSeq chr6
+ 52671085 52686587 TMEM14A 28978 transmembrane protein 14A GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142327_PI430048170 0.11897328932312 0.7013372678280454.43255559653087
4.50149158654204 4.07415159816258 P P P 4.51511633542018 4.77617840254051
5.20304182709748 P P P LNCV6_142327_PI430048170 mRNA
TTTTTGTGTGTTTCTGTGTGTGTGGTTTTGTTTTGGATTGGTAGGTTTCACTGTGGCGTG NM_001105568 RefSeq chr6
- 17759182 17987623 KIF13A 63971 "kinesin family member 13A, transcript variant 4"
GO:0005515|GO:0008017|GO:0005813|GO:0005871|GO:0035459|GO:0043001|GO:0032438|GO:0005874|GO:0008
333|GO:0072383|GO:0030496|GO:0003777|GO:0032588|GO:0005524|GO:0006886|GO:0000910|GO:0000139|GO:0
008152|GO:0016887|GO:0010008|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_22283_PI430048170 0.0133903685369414 1.23139107218106 4.96324167104798
4.86173763703072 4.8162923288945 P P P 4.68655244459485 4.53572753167566
4.51596711942441 P P P LNCV6_22283_PI430048170 mRNA
TAATAACTTGTCATTGTTAAATTATTTATTAGCGTTTACCACACCACCACCCCCACCCTG NM_001174146 RefSeq
chr9 + 126614442 126701032 LMX1B 4010 "LIM homeobox transcription factor 1, beta, transcript
variant 3"
GO:0005515|GO:0006355|GO:0003700|GO:0008283|GO:0021954|GO:0021587|GO:0005634|GO:0007275|GO:0009
953|GO:0001701|GO:0006351|GO:0043565|GO:0035265|GO:0071542|GO:0045944|GO:0030199|GO:0030182|GO:0
002930|GO:0030901|GO:0008270|GO:0001764|GO:0035108 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_126783_PI430048170 0.55900439081366 1.02567582679533 9.33164756146001

9.25623145532591 9.19820518625421 P P P 9.31037064606319 9.17236416535827
9.19285547910747 P P P LNCV6_126783_PI430048170 mRNA
TTAGCAATTCTGGAAAAGTTAAGCCATCTCCTCCTCTGGCCCTTCCTTCTGGAATCTTCA NM_002096RefSeq chr19
- 6379568 6393280 GTF2F1 2962 "general transcription factor IIF, polypeptide 1, 74kDa"
GO:0008380|GO:0005515|GO:0010467|GO:0006368|GO:0030054|GO:0006367|GO:0006366|GO:0003713|GO:0006
370|GO:0019211|GO:0005634|GO:0043085|GO:0009615|GO:0003824|GO:0003677|GO:0050434|GO:0000398|GO:0
032968|GO:0016032|GO:0005654|GO:0005674|GO:0008134 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_139652_PI430048170 0.00536350200773195 0.6001023401020697.86120976253538
7.86087912226343 8.16464986612237 P P P 8.65859371058914 8.59040553211638 8.856279332271
P P P LNCV6_139652_PI430048170 mRNA
GTGTTTGGACTAAACAAACAATAAACTACTGATGTCTGCAGCATTTATCTATGTCCCTAA NM_203505RefSeq chr4
- 75642768 75673483 G3BP2 9908 "GTPase activating protein (SH3 domain) binding protein 2,
transcript variant 1" GO:0005737|GO:0000166|GO:0007253|GO:0030159|GO:0007265|GO:0051028 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140976_PI430048170 0.4062306423290160.91771139337242 9.78142785739696
9.64145920563461 9.95749548757641 P P P 9.79290200260793 9.85071833299591
10.1062421314051 P P P LNCV6_140976_PI430048170 mRNA
GAACTGCTTTTTATTGACTAGTAAAAGTTACTGCCTATGCTTTTTACCTTAGGCTTACAG NM_178042RefSeq chr3
+ 179562879 179588405 ACTL6A 86 "actin-like 6A, transcript variant 3"
GO:0005515|GO:0000790|GO:0005886|GO:0006325|GO:0005634|GO:0071564|GO:0016514|GO:0035267|GO:0006
338|GO:0003407|GO:0006357|GO:0043044|GO:0003713|GO:0031492|GO:0006310|GO:0000978|GO:0006351|GO:0
007399|GO:0007165|GO:0031011|GO:0043234|GO:0006281|GO:0043967|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_97870_PI430048170 0.0146775326119960.4658505273196270.6463583833354590.512422267212973
0.468967289517464A A A 1.65079427036488 1.3352253092785 1.89912612159745 A A A
LNCV6_97870_PI430048170 mRNA
GGAAGAGTAGATTCCCATAAAAAACAACCAATGCCAATCATGTTCTGGAAGTGATAATAA NM_152373RefSeq chr1
+ 40531560 40548169 ZNF684 127396 zinc finger protein 684
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130946_PI430048170 0.1182860920545810.9627516558223970.436681386095401
0.3749096408947530.394200764876939A A A 0.4771592111866410.477193930800376
0.415552629767807A A A LNCV6_130946_PI430048170 mRNA
CAAACACCGCGGGGAAGGCTGTTCTGTTTATTTAAATTTGTAAATAGAAAACAGTTGTTT NM_206808RefSeq chr13
+ 99606663 99892764 CLYBL 171425 "citrate lyase beta like, transcript variant 1"
GO:0005739|GO:0008152|GO:0046872|GO:0016829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137476_PI430048170 0.3670803011389460.7015898000306011.94352599207499
3.68491184783655 3.8794636633097 A P P 3.55084465449513 4.03943921652596
4.05553233636561 P P P LNCV6_137476_PI430048170 mRNA
GAGTTACAATGTTTGGTATTCGGATACATTCAGCAAGAACACTTGAAAACTCCTCACCAA NM_012430RefSeq chr3
+ 123201926 123274135 SEC22A 26984 SEC22 vesicle trafficking protein homolog A (S. cerevisiae)
GO:0006888|GO:0005484|GO:0005215|GO:0000149|GO:0005789|GO:0031201|GO:0048280|GO:0016021|GO:0015
031|GO:0006887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112910_PI430048170 0.0248728340283977 1.23222844879434 9.67334523819298
9.63128348010122 9.6719310694329 P P P 9.34427974224235 9.45500446168044
9.26769161033189 P P P LNCV6_112910_PI430048170 mRNA
GGTATTGGGGACATTTTAAAGGCTGAGTTATTTTTGAATGTCATGTTTATGTCATAGACG NM_000320RefSeq chr4
- 17486392 17512234 QDPR 5860 quinoid dihydropteridine reductase

GO:0043005|GO:0006520|GO:0006559|GO:0010288|GO:0051066|GO:0006729|GO:0009055|GO:0070404|GO:0044281|GO:0010044|GO:0070402|GO:0035690|GO:0042803|GO:0005829|GO:0001889|GO:0005739|GO:0034641|GO:0005737|GO:0033762|GO:0004155|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135152_PI430048170 0.8629407083258571.08998327344257 1.34969137587945 0.2976206388739030.498874453640198A A A 0.3034815326356590.779135445002802 0.857627408602767A A A LNCV6_135152_PI430048170 mRNA GAAGCTGCCATCTGTTAATACTAAAATTCCCAAATAAGGTTCTGTTTAGAATGTCCCTTT NM_001166395 RefSeq chr16 + 71526250 71538590 CHST4 10164 "carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4, transcript variant 2" GO:0005802|GO:0006790|GO:0005975|GO:0031228|GO:0006044|GO:0007267|GO:0006928|GO:0050901|GO:0006955|GO:0006954|GO:0008146|GO:0006477|GO:0001517|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143972_PI430048170 0.0276372871708041 1.36821164089031 10.255561650636 10.4314371860029 10.3542343193515 P P P 9.69326966568763 10.0253237641225 9.95052126903495 P P P LNCV6_143972_PI430048170 mRNA GGGTTATTTATTTTCCCAATAATTTTGTGTGAGCTACAGAAGACCCCATACCAAATAAAC NM_001297701 RefSeq chr19 - 36009115 36014243 ALKBH684964 "alkB, alkylation repair homolog 6 (E. coli), transcript variant 3" GO:0005515|GO:0005737|GO:0016706|GO:0005634|GO:0046872|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138222_PI430048170 0.4929601053327020.9392924243529870.307878828355018 0.2626066033697230.401531808062292A A A 0.3859657706742510.249964718935251 0.590185529377802A A A LNCV6_138222_PI430048170 mRNA CTGCCATTAAAAGAGGACCAGATTATGAATGACAACAGAGACTAACATTTACATTGACAA NM_153716RefSeq chrY - 18771814 18773735 HSFY2 159119 "heat shock transcription factor, Y linked 2, transcript variant 1" GO:0043565|GO:0006355|GO:0005737|GO:0003700|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128040_PI430048170 0.3449817989836660.78159573702472 6.02400637560637 5.60315624899249 5.40348315598545 P P P 6.38408230967577 6.12456494559293 5.53326104203222 P P P LNCV6_128040_PI430048170 mRNA TGAAGTCCCCATTTGTCCTCAGCCTGTAACTCCCCGTGTGCCTATAAAGAAGTTAATAGA NM_001193621 RefSeq chr19 + 43576799 43582104 PINLYP 390940 "phospholipase A2 inhibitor and LY6/PLAUR domain containing, transcript variant 1" GO:0004859|GO:0005576|GO:0043086 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144820_PI430048170 0.0108724466680567 1.83203622753897 1.46784531639828 1.03530906289905 1.34282209715063 A A A 0.4510164090598280.496350365716822 0.305020470470389A A A LNCV6_144820_PI430048170 mRNA CTAAGTGTATCAGACTTAGGGAAAAAGTGGCACAACCTTCGATTTAAAATTCTAGTCTTT NM_144573RefSeq chr1 + 77888514 77943893 NEXN 91624 "nexilin (F actin binding protein), transcript variant 1" GO:0030334|GO:0048739|GO:0030018|GO:0051015|GO:0051493|GO:0042981|GO:0006468|GO:0008307|GO:0005856|GO:0004683|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143821_PI430048170 0.0350279085247818 0.693632077757851 10.3453457338578 10.2172429769757 10.147499540512 P P P 10.5317818827886 10.9578528265136 10.779321834342 P P P LNCV6_143821_PI430048170 mRNA CACAGAGGCAAGGCCAGACTTTTCCGTCGTTTATTTTCAATAAATAAGCAGCTCAGCGCA NM_024816 RefSeq chr16 - 28904420 28925211 RABEP2 79874 "rabaptin, RAB GTPase binding effector protein 2" GO:0043547|GO:0005737|GO:0015031|GO:0008083|GO:0005769|GO:0043231|GO:0006897|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142188_PI430048170 0.12682437414607 1.49732630456285 1.1003012048475

0.436976790440111 1.16541782839691 A A A 0.250410698326208 0.53732224495457 0.254802471006845 A A A LNCV6_142188_PI430048170 mRNA CAGCGGGAGTCACCTAGGAAAGATGGAGGGATTGACACTATTTTCTCAATAAAATGGGAC NM_145236 RefSeq chr2 + 231395623 231401164 B3GNT7 93010 "UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7" GO:0005975|GO:0016266|GO:0044281|GO:0008378|GO:0042339|GO:0000139|GO:0006493|GO:0018146|GO:0009405|GO:0016021|GO:0030203|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145342_PI430048170 0.643728792160117 0.930268179294589 6.77262128242397 5.61047275323054 5.80781088761569 P P P 6.3693933989775 6.2789317318094 6.12804369064292 P P P LNCV6_145342_PI430048170 mRNA TTCTCTCCCTCTCCAAGCATCTGTAAGTTGCACTCAGGAGGGTTTAGGGGAGGGCCATGG NM_030570 RefSeq chr7 + 76510422 76527882 UPK3B 80761 "uroplakin 3B, transcript variant 1" GO:0005886|GO:0010629|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118486_PI430048170 0.0323837570963223 0.657354672260812 5.85792867575529 5.75476807413091 6.22009880717529 P P P 6.5749037412161 6.32832468910761 6.75605610153326 P P P LNCV6_118486_PI430048170 mRNA AAGACTGAGGATAGTTTAGAAGGATGCTTGGATTGTCTGCTTCAAGCCCTGGCTCAAAAT NM_001100426 RefSeq chr4 + 98261375 98443861 RAP1GDS1 5910 "RAP1, GTP-GDP dissociation stimulator 1, transcript variant 1" GO:0005739|GO:0031034|GO:0051561|GO:0032321|GO:0005783|GO:0032471|GO:0070062|GO:0014829|GO:0005829|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124060_PI430048170 0.442780128250017 1.12308989525487 5.26675318969678 5.44886654580507 5.79364084866422 P P P 5.19212010819406 5.34130158538512 5.50662769923468 P P P LNCV6_124060_PI430048170 mRNA ATGAAGACTGTGAGCTGAAGTTCTGGATTTTGGACTGGCTCGGCACACAGATGATGAAAT NM_139012 RefSeq chr6 + 36027676 36111236 MAPK14 1432 "mitogen-activated protein kinase 14, transcript variant 2" GO:0005515|GO:0010467|GO:0010831|GO:0042692|GO:0002756|GO:0006935|GO:0018105|GO:0002062|GO:0002755|GO:0007178|GO:0014835|GO:0031663|GO:0004708|GO:0004707|GO:0019395|GO:0038124|GO:0038066|GO:0006996|GO:0038123|GO:0034134|GO:0030168|GO:0002224|GO:0042770|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144061_PI430048170 0.398961949247851 1.05281816057733 0.308899285333061 0.312293213467061 0.511151650727591 A A A 0.311969232552062 0.276597824445706 0.329932408025549 A A A LNCV6_144061_PI430048170 mRNA TAGCGAGGACTTATTATCACAGTATCCTTTGAAAACCCATTCGGCATACTCACTCAGCAA NM_052882 RefSeq chr19 - 57134095 57145202 ZIM3 114026 "zinc finger, imprinted 3" GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137242_PI430048170 0.0907028934909409 0.680301599305225 5.36847869863705 5.48316967060435 5.59066898119016 P P P 5.66980347942658 6.06645846594632 6.31084532081441 P P P LNCV6_137242_PI430048170 mRNA GTGAATTTCAGCTTGAAATTCCATTGCTGTTCCTTGTTTTGTTTGTATTGCTCTAAGTTG NM_018181 RefSeq chr18 + 58862828 58986477 ZNF532 55205 zinc finger protein 532 GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129515_PI430048170 0.976943855979268 0.997623261237765 0.546496107913074 0.35928519983731 0.52567351918937 A A A 0.290367681910885 0.697909010290007

0.430597154036191 A A A LNCV6_129515_PI430048170 mRNA
CCCAAATGATGCAAAACATGCAGATTCTAGTTGACTTCAGTTGTAATAGACTTGTTTTTC NM_001172646 RefSeq
chr20 + 9069053 9480815 PLCB4 5332 "phospholipase C, beta 4, transcript variant 3"
GO:0043647|GO:0005509|GO:0014069|GO:0005634|GO:0044281|GO:0030425|GO:0005790|GO:0005829|GO:0016
042|GO:0035556|GO:0004629|GO:0004435|GO:0004871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136856_PI430048170 0.1293689243083120.8949788314864149.7669181297755
9.93291279627664 9.99551716570193 P P P 10.1321142311422 9.9780218571186
10.0708415081033 P P P LNCV6_136856_PI430048170 mRNA
CTTACAGAAGAATGTCAAGGACTTAATGGTGCAAGCTGGCATTGAAAATTCTATTAAAGA NM_001136180 RefSeq
chr18 + 79964581 79970822 HSBP1L1 440498 heat shock factor binding protein 1-like 1 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129412_PI430048170 0.367569558352387 1.57951922820064 1.72511268941622
0.355803149333774 0.431632943110605 A A A 0.31161002516845 0.304888079144385
0.356990769200379 A A A LNCV6_129412_PI430048170 mRNA
AACAAAGACATGAAAGATGCTCTAAAGAGAGTCCTGGGGTTAACAGTTAGCCAAAACTGANM_001004480 RefSeq
chr14 + 20223709 20224702 OR11H6 NA "olfactory receptor, family 11, subfamily H, member 6"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100179_PI430048170 0.392547462020437 0.678500775481891 0.946299421710079
3.24792146423591 3.10104294305071 A P P 3.74383286305675 3.18348341786242
2.80849608893483 P P P LNCV6_100179_PI430048170 mRNA
CTGATTACGAGAGAAGTCACTGCTTGAGGCTCAGCTGCTGTGTCAGAGCGGAGGCACATT NM_021924RefSeq chr11
- 616564 625067 CDHR5 53841 "cadherin-related family member 5, transcript variant 1"
GO:0005515|GO:0008013|GO:0005886|GO:0005509|GO:0016021|GO:0007155|GO:0007156|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136712_PI430048170 0.375951729766883 1.18693735841288 4.87646103849092
4.65393658746366 4.39901678785202 P P P 4.7653528068033 4.36966829794085
3.98762874749561 P P P LNCV6_136712_PI430048170 mRNA
GGAGGCGCGACCCCTTGTGGGTCTTTGTCTGGAAGGAATAAAAGCAAATGTTCCAAAAAA NM_003279RefSeq chr20
- 45823215 45827314 TNNC2 7125 troponin C type 2 (fast)
GO:0006937|GO:0030049|GO:0005861|GO:0003009|GO:0005509|GO:0003779|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139947_PI430048170 0.0482754946107862 0.727080756187211 10.2085302247933
10.4614751839966 10.6082304841881 P P P 10.7626389379236 10.7802273821127
11.1147973259233 P P P LNCV6_139947_PI430048170 mRNA
GACTTATGTGCAAACTGGTGCAGAAATTCTATAAACTCTTTGCTGTTTTTGATACCTGCT NM_001270439 RefSeq
chr1 - 183626192 183635941 ARPC5 10092 "actin related protein 2/3 complex, subunit 5, 16kDa,
transcript variant 2"
GO:0005515|GO:0034314|GO:0030036|GO:0048013|GO:0005885|GO:0006928|GO:0042995|GO:0015629|GO:0005
829|GO:0005737|GO:0051015|GO:0007411|GO:0045087|GO:0005200|GO:0005925|GO:0038096|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131864_PI430048170 0.497649863054599 0.963235382544406 13.0636548609832
13.2429332414275 13.0571096746295 P P P 13.1663199467999 13.2525104871574 13.111273552333
P P P LNCV6_131864_PI430048170 mRNA
GGACTAGAACTGGGATGTCTTGGCTTGTATGTTTTTTGAAGCTTCGATTATGATTTTTAA NM_002809RefSeq chr17
+ 39980767 39997960 PSMD3 5709 "proteasome (prosome, macropain) 26S subunit, non-ATPase, 3"
GO:0006511|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0034
641|GO:0005737|GO:0000082|GO:0016032|GO:0030234|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0
043066|GO:0000502|GO:0042176|GO:0006521|GO:0051437|GO:0042590|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_66842_PI430048170 0.7200888042733140.9551142513539721 0.9732411461937 10.8827409832276
11.1578254382875 P P P 11.2968040056445 10.8522165924472 11.0426371561966 P P P
LNCV6_66842_PI430048170 mRNA
TTTGCGAGAATGCAGACCACCTCACTAAACTGTAAACGGTAAAGAGATTTTTACTTTTGG NM_015530RefSeq chr2
+ 170928525 170967133 GORASP2 26003 "golgi reassembly stacking protein 2, 55kDa, transcript variant
1" GO:0005515|GO:0006996|GO:0005794|GO:0016020|GO:0000139|GO:0000278 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139102_PI430048170 0.000782302414841992 0.3684743034936794.8958477303753
4.81922118872143 4.66574758323777 P P P 6.2851710608697 6.21176920849585
6.21317062827103 P P P LNCV6_139102_PI430048170 mRNA
GTCTATCATCCTGACTTAATTCTCCTTTCAGGTCTTTTTACCCCCTCTGTGAATTGCGCA NM_001099219 RefSeq chr21
- 31038158 31038476 KRTAP19-8 NA keratin associated protein 19-8 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145595_PI430048170 0.0488438121212483 1.26262213749856 10.7340524686144
10.6750697731462 10.5134160638687 P P P 10.2522709236172 10.4843117023936
10.1666356584176 P P P LNCV6_145595_PI430048170 mRNA
CAAGCAGACCTCAGAGCGCTGCCCAGATGGAATATTAAATTATTTTTGCCAAGCAAAAAA NM_001145165 RefSeq
chr19 - 3490820 3500940 DOHH 83475 "deoxyhypusine hydroxylase/monooxygenase, transcript
variant 1"
GO:0005515|GO:0008612|GO:0019135|GO:0005575|GO:0044267|GO:0046872|GO:0055114|GO:0043687|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143513_PI430048170 0.1633162225491330.7582686408082073.125798124101
3.40268441291743 3.81994504811552 P P P 3.87100215952227 3.79682510387545
3.95922239579458 P P P LNCV6_143513_PI430048170 mRNA
TTTCTTTGGGGGTGATTGTCTCGCTTGTTTTCAGTTGTCGATTATATGGGAGGGTTCTGG NM_024017RefSeq chr17
- 48621156 48626473 HOXB9 3219 homeobox B9
GO:0043565|GO:0005739|GO:0005515|GO:0060326|GO:0045944|GO:0048706|GO:0030879|GO:0005654|GO:0009
952|GO:0060070|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137096_PI430048170 0.0231555557028081 0.42494707309646 3.87214549232766
3.00474499686694 3.50234969832949 P P P 4.51855202907394 4.77880948654187
4.88956869691008 P P P LNCV6_137096_PI430048170 mRNA
TCACATCTCAATCAGGATGCTTCTCTCCATTGGTAGCACTTTAGAGTCCATGAAATATGG NM_133498RefSeq chr19
+ 48606742 48607714 SPACA4171169 sperm acrosome associated 4
GO:0005886|GO:0001669|GO:0031225|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144487_PI430048170 0.0417134204197644 0.63758678076220612.893163948689
12.5341766938145 13.1318246806962 P P P 13.3444687204087 13.5241865476438
13.6805569537952 P P P LNCV6_144487_PI430048170 mRNA
TGGATTCTGCTAGATTTCGCTACCTTATGGCTGAAAAACTTGGCATTCATCCCAGCAGCT NM_001174097 RefSeq
chr12 - 21635340 21657794 LDHB 3945 "lactate dehydrogenase B, transcript variant 2"
GO:0005515|GO:0006089|GO:0044262|GO:0019674|GO:0044281|GO:0005829|GO:0042802|GO:0005739|GO:0005
737|GO:0051287|GO:0004459|GO:0016020|GO:0006090|GO:0019900|GO:0044237|GO:0070062|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135426_PI430048170 0.3949363840643690.62931411931986 0.388675957084066
0.47260838092544 0.820815888691562A A A 1.97293038810802 0.933611663515281
0.329394883581997A A A LNCV6_135426_PI430048170 mRNA
AGCAGGGCATGTTTCCCTTTGTTCACATTCTCTGAGAAATTGAAACTCTGGTTTCTCTTC NM_005674RefSeq chr10
- 43556344 43568459 ZNF239 8187 "zinc finger protein 239, transcript variant 1"
GO:0006355|GO:0003700|GO:0003723|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_130304_PI430048170 0.0272585790956177 0.5645776868654524.80637381352681
4.88434450730736 5.3964673261806 P P P 5.70252618604804 5.88131850391037
6.03252075974737 P P P LNCV6_130304_PI430048170 mRNA
CCAGTTGTATATTCATCACCTTTGTAGCATTTGACAAATTTTATGCTTAGCAGCTTCTTC NM_001282678 RefSeq chr7
- 92487022 92528531 PEX1 5189 "peroxisomal biogenesis factor 1, transcript variant 3"
GO:0005515|GO:0006625|GO:0042623|GO:0008022|GO:0005524|GO:0032403|GO:0043231|GO:0005829|GO:0005
737|GO:0008152|GO:0007031|GO:0016558|GO:0060152|GO:0005778|GO:0070062|GO:0005777 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137206_PI430048170 0.9651295847874330.987625624945001 0.858181432900405
0.9111023690814860.993793298435227 A A A 0.84227785690605 1.18681080513666
0.754036595536301 A A A LNCV6_137206_PI430048170 mRNA
GTTACGTATTGGTATCTTTAATTTCAACAGTGGGTAAACTGGTTTCCCAGTATACAATTC NM_001204352 RefSeq
chr4 - 166733384 167234590 SPOCK350859 "sparc/osteonectin, cwcv and kazal-like domains
proteoglycan (testican) 3, transcript variant 3"
GO:0031012|GO:0010951|GO:0019800|GO:0007165|GO:0008191|GO:0005509|GO:0005578|GO:0005539|GO:0005
615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143745_PI430048170 0.8552295483504940.992127525055864 0.497251274131315
0.4694722054785660.432452950242521 A A A 0.3828610744947280.522819927292238
0.523923379069431 A A A LNCV6_143745_PI430048170 mRNA
TGGAGGATTATCACACCCCAAATGCATAATCTCGTTAATGATTGAGGAGAGAAAAGGATC NM_001291543 RefSeq
chrX - 135777446 135785274 CT45A7 NA "cancer/testis antigen family 45, member A7" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_132983_PI430048170 0.4564468061446510.6588627865792890.313854442016687
1.56833885773008 0.388174196095733 A A A 0.2643077434590351.98632415855575
1.68292868389218 A A A LNCV6_132983_PI430048170 mRNA
CGTCTTCACCATTCTGTTATGTGACTTAAAATTCAATTTCACGAAACCCACTTCCACAAG NM_001283056 RefSeq
chr14 - 57469299 57493863 C14orf105 55195 "chromosome 14 open reading frame 105, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140050_PI430048170 0.5402386657396341.02305863363979 0.420447727784257
0.2760788935778530.320612160991862 A A A 0.2823772918093550.315535277831356
0.324034929552611 A A A LNCV6_140050_PI430048170 mRNA
ATGGCATTGACAGTGGAGTAGGTAGTATTTAATCTGTAGTGTTTACAACATAGTAGATAG NM_001205019 RefSeq
chrX + 30653358 30731460 GK 2710 "glycerol kinase, transcript variant 4"
GO:0005515|GO:0004370|GO:0019563|GO:0005634|GO:0005741|GO:0044281|GO:0042593|GO:0005524|GO:0006
071|GO:0046167|GO:0005829|GO:0016310|GO:0019432|GO:0006641|GO:0044255|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131234_PI430048170 0.8343914020274890.9932105669324020.475516070153682
0.4926954697525340.389476869955345 A A A 0.52347271529069 0.427025044742327
0.436815684444569 A A A LNCV6_131234_PI430048170 mRNA
AATATGCCATTCATTGCACACACCCACAAATGCAAATCATTCCTCTCTGTAGATGCTAGG NM_024574RefSeq chr4
- 121035626 121072518 NDNF 79625 neuron-derived neurotrophic factor
GO:0031012|GO:0019800|GO:0043524|GO:0030198|GO:0010976|GO:0010811|GO:0016049|GO:0005576|GO:0005
539|GO:0001764|GO:0008201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133612_PI430048170 0.3571739242607951.77983039808748 0.720597763913104
2.22077198340448 0.56570050031247 A A A 0.4388852463892420.607799791431549
0.582068278418545 A A A LNCV6_133612_PI430048170 mRNA
GGGAACAACCATTTTCCAACCTTGGCTTTAATAATAAAAACCAGCTGCACTGAGAAAAAA NM_152335RefSeq chr15
+ 76059957 76204963 C15orf27 123591 chromosome 15 open reading frame 27
GO:0070509|GO:0086010|GO:0005886|GO:0005245|GO:0070588|GO:0016021 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_106550_PI430048170 0.4641613942649380.82139215181142 0.26885959357169
0.2885649448669410.439278445180611A A A 1.09181682448666 0.30587293762327
0.30689139291487 A A A LNCV6_106550_PI430048170 mRNA
GGGCCATTTAACCTGGATGCCACCATTTTATGGGGATAATGATGCTTACCATGGTTAATG NM_144590RefSeq chr10
- 88819901 88851975 ANKRD22 118932 ankyrin repeat domain 22 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145199_PI430048170 0.3070279257776792.080454724484 3.05275583346253 2.7622179713397
0.954302290284686A A A 2.12476098887088 0.9464089778706110.920306132580104A A A
LNCV6_145199_PI430048170 mRNA
ACACCAAAAGGCTGGGTAAAGCATGGGAGGTTCCAGTTAATAGAAAGTAATTTTAAAATT NM_001190482 RefSeq
chr9 + 75890643 76362339 PCSK5 5125 "proprotein convertase subtilisin/kexin type 5, transcript
variant 1"
GO:0032455|GO:0004252|GO:0002001|GO:0030323|GO:0048706|GO:0007267|GO:0019058|GO:0042089|GO:0009
952|GO:0005615|GO:0007507|GO:0016486|GO:0016485|GO:0006508|GO:0030141|GO:0035108|GO:0042277|GO:0
048011|GO:0005794|GO:0007566|GO:0005796|GO:0001822|GO:0043043|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127555_PI430048170 0.29916701973298 1.20153162568056 0.295949978954264
0.8624901404004310.392629652316433A A A 0.2870737898989180.257378046162869
0.277522792795633A A A LNCV6_127555_PI430048170 mRNA
CCTGAGTTTACTGAAGAAATTGTACTTCATCCACATCCATGAAAATAAAATGCTCTCCTT NM_016521RefSeq chrX
- 133216668 133218348 TFDP3 51270 "transcription factor Dp family, member 3"
GO:0005667|GO:0006355|GO:0005737|GO:0000082|GO:0003700|GO:0046982|GO:0005634|GO:0003677|GO:0006
974|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145752_PI430048170 0.0209896852659707 0.7723923242454076.83750324109028
6.90291520744566 7.08818930985945 P P P 7.22522382837299 7.27756343494815
7.44612110877427 P P P LNCV6_145752_PI430048170 mRNA
GTCGGACTTGCTTTCTGCTTTATGATGTCCGTAGTTGTTCTAATATTAAATGCTTTGAAT NM_153348RefSeq chr12 +
116910955 117031148 FBXW8 26259 "F-box and WD repeat domain containing 8, transcript variant 1"
GO:0005515|GO:0004842|GO:0048471|GO:0005794|GO:0016567|GO:0008283|GO:0060712|GO:0005737|GO:0050
775|GO:0007030|GO:0060716|GO:0031467|GO:0019005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141204_PI430048170 0.0503854746564895 0.77011292749957911.1928880602513
11.1239541080914 11.2659449183174 P P P 11.3833623857913 11.5830156784292 11.729684607026
P P P LNCV6_141204_PI430048170 mRNA
TTTTCACCCTGTTTCTTCCCCTCCTCCAGTTCTTTGGAAATTTGTGATCGGGGGATCTTA NM_016312RefSeq chr12 -
14786477 14803467 WBP11 51729 WW domain binding protein 11
GO:0008599|GO:0008380|GO:0006397|GO:0005515|GO:0050790|GO:0005737|GO:0016607|GO:0003697|GO:0050
699|GO:0006364|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132923_PI430048170 0.5648162826504191.03746363105967 0.277430546817415
0.2903483153256310.499808307443385A A A 0.3267950889305090.283216308610333
0.309032221298897A A A LNCV6_132923_PI430048170 mRNA
CCTTGTATGTATTTCATGACTGGACTTACTGCTCTGTCAGCTTTTGTATATGAATCTTAA NM_000810RefSeq chr15 +
26866718 26949210 GABRA5 2558 "gamma-aminobutyric acid (GABA) A receptor, alpha 5, transcript
variant 1"
GO:0005215|GO:0005230|GO:0030054|GO:0005886|GO:0007605|GO:0007268|GO:0050811|GO:0005254|GO:0030
425|GO:0043524|GO:0034220|GO:0045211|GO:0090102|GO:0006810|GO:0004872|GO:0001662|GO:0008306|GO:0
004890|GO:0034707|GO:0060119|GO:0007214|GO:0055085|GO:0032809|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137898_PI430048170 0.6506705204071250.9721771480604099.36023963472835

9.16047880543378 9.4138065977859 P P P 9.27388284194688 9.39417016014201
9.39736324529406 P P P LNCV6_137898_PI430048170 mRNA
GTCTAAACTAAGGTTTAGTGCTTTTTTAAAGGAAAGTTGTCCCAGGATTCATCCTAAAGA NM_002076RefSeq chr12
- 64713441 64759446 GNS 2799 glucosamine (N-acetyl)-6-sulfatase
GO:0005515|GO:0005975|GO:0006027|GO:0008449|GO:0008484|GO:0044281|GO:0046872|GO:0042339|GO:0009
405|GO:0042340|GO:0030203|GO:0043202|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135780_PI430048170 0.0140731329706386 0.9036106702147718.31114454964292
8.3971263973651 8.3458980371464 P P P 8.49701391264198 8.52014936005438
8.47665683844732 P P P LNCV6_135780_PI430048170 mRNA
GGTTTTGCATTTACATTTGTGGACCATGTTACAGTTAAGAAAAATCCTGTTTCAGTCCTT NM_001008739 RefSeq
chr6 - 42890264 42890816 C6orf226 441150 chromosome 6 open reading frame 226 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_133012_PI430048170 0.6178034129906290.9083885046977120.292274400601571
0.2910827855086170.498602518821448A A A 0.3041298941286170.265050725406026
0.859175251177705A A A LNCV6_133012_PI430048170 mRNA
ATTTGGAGACAACTAAGGGATTATTATCCTGTCAAGCTGGTGAAAACAGCAGAGCTGCCC NM_178176RefSeq chr7
- 101195730 101201021 MOGAT3 346606 "monoacylglycerol O-acyltransferase 3, transcript variant 1"
GO:0019432|GO:0005789|GO:0003846|GO:0004144|GO:0016021|GO:0006071 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143634_PI430048170 0.00887129094306749 1.58330974993182 10.6186392364196
10.9748188271803 10.8017594113671 P P P 10.2683283385173 10.1054879012238
10.0451759365402 P P P LNCV6_143634_PI430048170 mRNA
AATTTCCTAACAAGCCGGATGCTTGAGAAACCTACATTTGGACAATGAGAGGCTGCTCCT NM_001161473 RefSeq
chr11 + 68008546 68029282 ALDH3B1 221 "aldehyde dehydrogenase 3 family, member B1, transcript
variant 3"
GO:0006629|GO:0005886|GO:0006066|GO:0006068|GO:0046185|GO:0004028|GO:0031982|GO:0005829|GO:0005
737|GO:0034599|GO:0004030|GO:0055114|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128355_PI430048170 0.63873950750726 0.9718120541560390.512907148801262
0.5214221704885570.317188219698794A A A 0.3980013301988250.56795084444847
0.513242947962255A A A LNCV6_128355_PI430048170 mRNA
CTTTTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTTATCCAA NM_022789RefSeq chr14
+ 23372860 23376403 IL25 64806 "interleukin 25, transcript variant 1"
GO:0002437|GO:0008150|GO:0045944|GO:0009620|GO:0030222|GO:0009624|GO:0005615|GO:0005125|GO:0030
380 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60888_PI430048170 0.3704712175949410.4913522047981440.4758950902070210.432995741360338
0.31657121664502 A A A 2.40080089689958 0.4628965676251190.53944057967996 A A A
LNCV6_60888_PI430048170 mRNA
GGCAGACACTGCAAGCTGTAAATTTTTGCCATAAACACAATTGCATACATAGAGACGTGA NM_001282236 RefSeq
chr14 - 50331925 50397404 CDKL1 8814 "cyclin-dependent kinase-like 1 (CDC2-related kinase),
transcript variant 2"
GO:0007507|GO:0005737|GO:0051726|GO:0006468|GO:0005634|GO:0005524|GO:0070062|GO:0004693 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144253_PI430048170 0.64606320913427 0.7278880022677491.3454447293734
0.2776126327250020.446930388895162A A A 0.2919926246186320.6631592319599962.0776666856472
A A A LNCV6_144253_PI430048170 mRNA
ATGACCTCTCAGCTTTCCAACAGGAATCTTGTAAGAGCTAATAAAAGGAAATACCTGAAA NM_152616RefSeq chr3
+ 140678023 140701150 TRIM42 287015 tripartite motif containing 42 GO:0005622|GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127987_PI430048170 8.31314129701508e-06 0.28705093995248 8.9024152139163

8.95379568389535 9.04802570096919 P P P 10.7125808783904 10.7669746783177
10.8280286880458 P P P LNCV6_127987_PI430048170 mRNA
CTCAGTTTCTAGAAAGCTCCCTTTTCTTTGAAATCTGCATGTTGAATTGAACTTTGTGAT NM_001301061 RefSeq chr7
- 73536352 73557735 BCL7B 9275 "B-cell CLL/lymphoma 7B, transcript variant 4"
GO:0008150|GO:0003779|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142243_PI430048170 0.0194707749789782 0.57595148948058 5.09896318073837
4.97182539799147 5.16607461807609 P P P 5.77889295812038 5.67128067995564
6.13881443477859 P P P LNCV6_142243_PI430048170 mRNA
ACCGAAATTTCCTACCAACCTGCTGTATCCAAAGTTTTGTAAAAAGTTGTAGAAGTTGTT NM_030753 RefSeq
chr17_KI270908v1_alt - 1281919 1338200 WNT3 7473 "wingless-type MMTV integration site
family, member 3"
GO:0005515|GO:0060064|GO:0005886|GO:0071300|GO:0048843|GO:0044339|GO:0044338|GO:0005615|GO:0009
950|GO:0005109|GO:0009948|GO:0007411|GO:0030182|GO:0060070|GO:0048018|GO:0001707|GO:0007276|GO:0
005796|GO:0061180|GO:0019904|GO:0005578|GO:0005576|GO:0010628|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_101710_PI430048170 0.0939375458861177 1.92816488692802 2.81228846310491
2.71113125027696 3.06594812961683 A A P 1.15793783924474 1.98931033994277 2.373012441037
A A P LNCV6_101710_PI430048170 mRNA
TCCAGCTGAAGAGTGAGGTGCAGCCCAAGAACACCATGAACCCCGAGAATGAGCAGCACA NM_001031737
RefSeq chr16 - 722581 726473 CCDC78 124093 coiled-coil domain containing 78
GO:0042383|GO:0048471|GO:0016529|GO:0003009|GO:0005814|GO:0030030 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134946_PI430048170 0.00190258407330922 0.57854324331352810.0056869523574
9.9672314473403 9.86114114824084 P P P 10.7346440032022 10.8567309212212
10.6039959341601 P P P LNCV6_134946_PI430048170 mRNA
GCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAAATGTCAAAAA NM_001606 RefSeq chr9
- 137007233 137028288 ABCA2 20 "ATP-binding cassette, sub-family A (ABC1), member 2, transcript
variant 1"
GO:0042632|GO:0006629|GO:0005815|GO:0006357|GO:0042493|GO:0042626|GO:0048545|GO:0005765|GO:0055
085|GO:0005524|GO:0005764|GO:0000166|GO:0016020|GO:0006810|GO:0016023|GO:0016021|GO:0032383|GO:0
043190|GO:0016887|GO:0010008|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139015_PI430048170 0.8371633190414190.9609608085241131.80649502569938
0.3061957330454520.497615260798066 A A A 1.61205755956306 1.0503797989321
0.342528756631862 A A A LNCV6_139015_PI430048170 mRNA
CCCCAACCTCTGACTGCAATGACCTTTCTGTGCAATAAAAGCTTATTGTCCATTAAAAAA NM_016347 RefSeq chr2
- 73700508 73701340 NAT8B 51471 "N-acetyltransferase 8B (GCN5-related, putative,
gene/pseudogene)"
GO:0010628|GO:0005515|GO:0043066|GO:0005793|GO:0008080|GO:0004468|GO:0033116|GO:0018003|GO:0005
789|GO:0016021|GO:0050435|GO:0001702 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131797_PI430048170 0.00286417680071369 1.74131913258142 6.17942797879458
6.48866836106385 6.27547877114444 P P P 5.66292177868047 5.46806670407448
5.41783519119231 P P P LNCV6_131797_PI430048170 mRNA
TTCAAAGCCAGTGCTCAGCTTCTCTGCTCCGTACTAGCGTTTACAGGTCTTAATTCAAAC NM_001013842 RefSeq
chr8 + 22599600 22604149 C8orf58 541565 "chromosome 8 open reading frame 58, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136320_PI430048170 0.0229669861232996 0.8406972082243215.16579318296605
5.14877571654295 5.31140248078243 P P P 5.50023533560568 5.51124900600727
5.36667075057967 P P P LNCV6_136320_PI430048170 mRNA
TCCTTGCCTCTTTTCCAGTTGCCTTCTATTGTCTGAAAAAGTAAAAGCCATTCAAAAATG NM_001243657 RefSeq

chr16 + 77722491 77742260 NUDT7 283927 "nudix (nucleoside diphosphate linked moiety X)-type motif 7, transcript variant 3"
GO:0000287|GO:0030145|GO:0015938|GO:0005102|GO:0009132|GO:0050072|GO:0003674|GO:0008150|GO:0030515|GO:0050873|GO:0003986|GO:0046356|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138991_PI430048170 0.4884100621507630.6496076970830180.25543188499045
0.2689458438026732.11803429096825 A A A 2.46152188031371 0.349856491638899
1.84500080656279 A A A LNCV6_138991_PI430048170 mRNA
AATCGTTCCTCAACCACCTCACTCGGAAGAAGCCGGCTACCAGGATCGTGCTGATTCTCC NM_080825RefSeq chr20 + 33662285 33663915 C20orf144 128864 chromosome 20 open reading frame 144 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129461_PI430048170 0.0140122278033397 16.5355594969391 8.19929951866268
10.1404853698203 9.28291145958548 P P P 5.64888377160318 5.95277001345268
3.53537459122288 P P P LNCV6_129461_PI430048170 mRNA
CTCTGCTTTTCCTGTCTGTATATAACTTATTTGCCCTAAGAACTTTGAGAATCCCAATTA NM_001956RefSeq chr1 - 41478774 41484683 EDN2 1907 "endothelin 2, transcript variant 1"
GO:0008284|GO:0001659|GO:0019722|GO:0019221|GO:0007204|GO:0005615|GO:0019229|GO:0001516|GO:0045987|GO:0042310|GO:0003100|GO:0014824|GO:0014826|GO:0048286|GO:0030593|GO:0048016|GO:0005576|GO:0060585|GO:0002690|GO:0097009|GO:0005179|GO:0003058|GO:0042116|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139976_PI430048170 0.2857707618258681.27270926226261 0.624380280044353
0.3759494906163421.11730062995547 A A A 0.3799606189033590.402177698640831
0.392443824806716A A A LNCV6_139976_PI430048170 mRNA
TTTTGCCAAGAGAAACAGGGTGAAGCTTCCAGAGGAGAAAGAAGAAACCATTGATGCTGG NM_207420RefSeq chr1 - 9003299 9026345 SLC2A7 NA "solute carrier family 2 (facilitated glucose transporter), member 7" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139721_PI430048170 0.00645951378053102 2.42122367850122 9.92832259760915
10.3527057507658 10.0708415081033 P P P 8.91829469149216 8.81139738680938
8.82537605963448 P P P LNCV6_139721_PI430048170 mRNA
TATGATCTAATTGAAACAAGACTGAAGGATCAATAAACAGCCATCTGCCCCTTCAAAAAA NM_004585RefSeq chr11 + 63536800 63546458 RARRES3 5920 retinoic acid receptor responder (tazarotene induced) 3
GO:0016042|GO:0005515|GO:0008285|GO:0004623|GO:0016021|GO:0006644 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141588_PI430048170 0.3786866517239581.0320497701443 0.293504623296922
0.2947718839560820.413015227520846A A A 0.3046434482705710.278738876405379
0.284538138479256A A A LNCV6_141588_PI430048170 mRNA
TACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCT NM_197975RefSeq chr5 + 180988844 181006727 BTNL3 10917 butyrophilin-like 3
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134289_PI430048170 0.00129853073272683 0.7019928241134712.2578304154068
12.2686680673521 12.1439637574733 P P P 12.6429973051937 12.8004301119095
12.7571780206911 P P P LNCV6_134289_PI430048170 mRNA
CTTAGCCCAAAGCTTGTGCCAGTCTCTATCGGAAATAAATGCCCCCAAAACCTCAAAAAA NM_001114403 RefSeq chr7 - 102637024 102642791 UPK3BL NA uroplakin 3B-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132431_PI430048170 0.0245533186274624 0.6534947879073197.48218046806077
7.42497973665123 7.84067355911031 P P P 8.07757299121248 8.26482328073761
8.27437993938365 P P P LNCV6_132431_PI430048170 mRNA
TAATTGGGTCTTTTGTTGATAAGAGTATGCAGCCAGGCACATCCCTAGCCAAGGCAAAAC NM_017819RefSeq chr3 + 101561835 101566446 TRMT10C 54931 tRNA methyltransferase 10 homolog C (S. cerevisiae)

GO:0042645|GO:0005739|GO:0005515|GO:0008168|GO:0000964|GO:0005654|GO:0032259|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135637_PI430048170 0.0659579921245253 0.4990185408355545.15509541731931 5.25108034093836 5.34793613626443 P P P 5.6819468980246 6.36397976677714 6.57941462837491 P P P LNCV6_135637_PI430048170 mRNA CCTGTGTAGTTTGGGTTCAGGGCTGACTTAAAATAAAGCACATCCTGCAAAGTCAAAAAA NM_022068RefSeq chr18 - 10670246 11148762 PIEZO2 63895 piezo-type mechanosensitive ion channel component 2
GO:0008381|GO:0005261|GO:0042391|GO:0050974|GO:0016021|GO:0006812|GO:0009612 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140731_PI430048170 0.6898096857166021.3595375790951 1.94864276975828 0.2967825510099910.447687626015244A A A 0.8828335703365060.474533993490507 0.59697138815443 A A A LNCV6_140731_PI430048170 mRNA AAATGACCAATGGCTTTTAAGGAAGGACTAAGTGACTTATGACCAGAACAAGGGAGCAGC NM_133509RefSeq chr14 + 67819778 68596021 RAD51B5890 "RAD51 paralog B, transcript variant 3"
GO:0000400|GO:0005515|GO:0005657|GO:0005634|GO:0006310|GO:0003677|GO:0005524|GO:0010971|GO:0003690|GO:0006281|GO:0003697|GO:0007596|GO:0000724|GO:0005654|GO:0033063|GO:0008094|GO:0007131 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134583_PI430048170 0.0507234047553488 0.6384938287183978.13585504437331 8.26295135768406 8.35323645804774 P P P 8.74207281357069 8.68359084460278 9.21544514919798 P P P LNCV6_134583_PI430048170 mRNA CAGCTGCAAAGTGTTTTGTACCAGTGAATTTTTGCAATAATGCAGTATGGTACATTTTTC NM_004456RefSeq chr7 - 148807371 148884349 EZH2 2146 "enhancer of zeste 2 polycomb repressive complex 2 subunit, transcript variant 1"
GO:0005515|GO:0010467|GO:0000790|GO:0070301|GO:0071902|GO:0021695|GO:0003723|GO:0006325|GO:0010718|GO:0005634|GO:0042054|GO:0005737|GO:0043406|GO:0042127|GO:0014013|GO:0051154|GO:0014834|GO:0034244|GO:0070734|GO:0006355|GO:2000134|GO:0001047|GO:0000122|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136851_PI430048170 0.0497532228194079 1.56264964676583 5.95936507438612 6.03731621411977 6.06917164755818 P P P 5.13329595464701 5.67270800707159 5.27455880595056 P P P LNCV6_136851_PI430048170 mRNA TCCTCTATTGCCTGCCTCTGCTGTGAATTAACTTGTTCTGTGTATTAAACTGGGCCTGAC NM_001289978 RefSeq chr19 - 38211005 38224250 DPF1 8193 "D4, zinc and double PHD fingers family 1, transcript variant 4" GO:0071565|GO:0006355|GO:0005737|GO:0006915|GO:0008270|GO:0006351|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129491_PI430048170 0.4222758027802611.05271915098481 12.3257530184347 12.3253836036397 12.2435566774042 P P P 12.0678939533098 12.303417983853 12.2906259397674 P P P LNCV6_129491_PI430048170 mRNA GGAGAGAAGCAAGGTCAAGAAATCCCACAGTTTGATGTATTAAAGAAATGACTTATTTCT NM_152743RefSeq chr7 - 2537809 2555758 BRAT1 221927 BRCA1-associated ATM activator 1
GO:0005515|GO:0016020|GO:0010212|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126725_PI430048170 0.07404928941951 1.91137491888367 4.37701011564176 4.32488703159737 3.85029520503416 P P P 2.60324648171418 3.72232921697769 3.26703166560858 P P P LNCV6_126725_PI430048170 mRNA CAGGAAGAAGCAGGGGGGAATCTATTTTTTCTCTCCTTTTCTTTTCTTCAATAAAAAGAA NM_001702RefSeq chr8 + 142464015 142545007 ADGRB1 NA adhesion G protein-coupled receptor B1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132166_PI430048170 0.9582917290807581.0078012103464 9.01493425978858 9.36180220142474 9.19285547910747 P P P 9.21544514919798 9.26235598713122 9.07223606172761 P P P LNCV6_132166_PI430048170 mRNA

TAAAAACCCTCGCTGTGTCTTCCTGTGTGTTGCGTGATCTGTGAAAAATACATCTCCCTC NM_001001563 RefSeq chr19 + 39480411 39490888 TIMM5092609 translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)
GO:0005515|GO:0005134|GO:0003723|GO:0006626|GO:0005743|GO:0001836|GO:0035335|GO:0005739|GO:0005744|GO:0006470|GO:0016607|GO:0043021|GO:0007006|GO:0004721|GO:0005654|GO:0016021|GO:0004722|GO:0044267|GO:0004725. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130571_PI430048170 0.5967446751294161.03451614321986 10.0326643317885 10.1693964591352 9.93015252845237 P P P 10.0728102815859 9.97756721734247 9.9417884300651 P P P LNCV6_130571_PI430048170 mRNA
AACAGCTACTGATAATCGAAAACTGCTGTTTGTGGCAGGAACCCCTGGCTGTGCAAATAA NM_016243 RefSeq chr1 - 202961872 202967276 CYB5R1 51706 cytochrome b5 reductase 1
GO:0005739|GO:0008150|GO:0003674|GO:0016020|GO:0004128|GO:0016126|GO:0016021|GO:0070062|GO:0055114. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71180_PI430048170 0.4627466463102110.8732898792315054.96472153116614 4.81081452686593 4.68940046250311 P P P 5.11963478341336 5.24808094982235 4.62481972290142 P P P LNCV6_71180_PI430048170 mRNA
ATGGTGTGATTGGCTCCATCCCTCCAGGCTCTCATTGTGGAAAGACCTGTCGGCACAGAC NM_001029864 RefSeq chr20 - 38210504 38260772 KIAA1755 85449 KIAA1755 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132008_PI430048170 0.00378974508507434 1.60547468705962 9.22949090990103 9.47687028725038 9.21832161650353 P P P 8.5613806845919 8.76313267604966 8.55646466999751 P P P LNCV6_132008_PI430048170 mRNA
AGCCCCTTAAGGAGCCCAGGTGTTTTAAGGAATGAATTGGTCACTGCATCTTGTATCGAT NM_019850 RefSeq chr2 - 232878685 233013241 NGEF 25791 "neuronal guanine nucleotide exchange factor, transcript variant 1"
GO:0051056|GO:0048011|GO:0043065|GO:0048013|GO:0007264|GO:0097190|GO:0043087|GO:0005829|GO:0030426|GO:0005085|GO:0043547|GO:0016020|GO:0007411|GO:0032321|GO:0005089|GO:0061002 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133239_PI430048170 0.8554003449758770.7827040443220682.09874433870684 0.3446755101994360.255655196478083 A A A 0.3179129748309130.33687125915075 2.61134072399666 A A P LNCV6_133239_PI430048170 mRNA
GCTCAACTGCAGGAACTGAGGTGAGAGGAGGCCATGTGACAATAAAGATCATTATGTACT NM_001025231 RefSeq chr1 + 152758029 152762053 KPRP NA keratinocyte proline-rich protein NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130914_PI430048170 0.00668594101007192 0.5345113154778225.28777405632944 5.04913061645336 5.31464178920307 P P P 5.917934168479 6.06870151131306 6.35580552150972 P P P LNCV6_130914_PI430048170 mRNA
GTTGCTAAGTCTATTCCATGTTAACACTGTGGAAATAAATATGAAGATGTGGACATTGCA NM_001282679 RefSeq chr9 + 125261793 125365011 GAPVD1 26130 "GTPase activating protein and VPS9 domains 1, transcript variant 1"
GO:0043547|GO:0032794|GO:0005085|GO:0007165|GO:0016020|GO:0051223|GO:0032318|GO:0006897|GO:0005829|GO:0005768|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130007_PI430048170 0.0185641629642558 0.7679434667022341 3.0799191158735 13.2371170252518 13.2781775478896 P P P 13.5643813444012 13.5672399357367 13.6133501597139 P P P LNCV6_130007_PI430048170 mRNA
TGGACTTAAGCATCTGGCTCTAATTCACAGTGCTCTTTTCTCCTCACTGTATCCAGGTTC NM_001664 RefSeq chr3 - 49359145 49412093 RHOA 387 ras homolog family member A
GO:0044319|GO:0005515|GO:0042346|GO:0033688|GO:0043931|GO:0030036|GO:0030054|GO:0005886|GO:0007264|GO:0003924|GO:0007266|GO:0032154|GO:0036089|GO:0005829|GO:0043297|GO:0043296|GO:0007411|GO:0016032|GO:0007179|GO:0090307|GO:0043123|GO:0005856|GO:0005938|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_127062_PI430048170 0.8405182107840690.9874915666612642.7795880808824
1.79321289379482 2.09172933645515 A A A 3.01938223876414 2.23643383788458
0.970390347261829P A A LNCV6_127062_PI430048170 mRNA
CAAAACCTGCCTCTCATTTATGTATTAGGAATCTTGTGACAACGGAACAGTTGAAAAATT NM_018349RefSeq chr15
+ 94298200 94483952 MCTP2 55784 "multiple C2 domains, transmembrane 2, transcript variant 1"
GO:0005544|GO:0019722|GO:0016020|GO:0005509|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130535_PI430048170 0.8332765390868641.03637950136005 0.439299458878665
0.4544317645781240.909828136036588A A A 0.4924866316146020.765632337138445
0.418330746671415A A A LNCV6_130535_PI430048170 mRNA
GAAGTAAAGGCAGCCATGAGGAAGGTGGTCACCAAATATATTTTGTGTGAAGAGAAGTGA NM_001005500
RefSeq chr14 + 19780322 19781264 OR4M1 NA "olfactory receptor, family 4, subfamily M, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138452_PI430048170 0.0104942129969878 0.6908033634691296.81197680137034
6.60089643970445 6.89349163247047 P P P 7.31984249490177 7.16169977724585
7.42892136753258 P P P LNCV6_138452_PI430048170 mRNA
ATGTACCGTTAAAAAGGACCAAAAGTTTTTGGTCTGGGTCAAAAAATACGAATGTGTTCT NM_022779RefSeq chr9
- 132594288 132670401 DDX31 64794 "DEAD (Asp-Glu-Ala-Asp) box polypeptide 31, transcript variant 1"
GO:0005794|GO:0008152|GO:0005730|GO:0004386|GO:0005524|GO:0043231 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144018_PI430048170 0.4256088050407240.8524661364938176.73705639092811
7.37481953395953 7.63607825040734 P P P 7.34045381952476 7.51567592456149
7.70128347107969 P P P LNCV6_144018_PI430048170 mRNA
TGCGCTTCTATGTTTGGGAAACATTGCTCTGATAAAAAATAGCTGTCATTATGCAGTGTG NM_017845RefSeq chr4
- 47450793 47463659 COMMD8 54951 COMM domain containing 8 GO:0005515 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143822_PI430048170 0.000397178337949908 0.2638623062223164.14165581046363
3.95131487037846 4.11688870321081 P P P 5.96714185654537 5.81552773955755
6.17786621426193 P P P LNCV6_143822_PI430048170 mRNA
CTTGTGGCAATTGATTTTCTGTTTTAACACCCTTTGGGTAAAATCTTGCAAAGAGCTTTTNM_207325RefSeq chr19 +
32406115 32485893 DPY19L3 147991 "dpy-19-like 3 (C. elegans), transcript variant 1"
GO:0000030|GO:0018406|GO:0005637|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92219_PI430048170 0.4964140750460230.93518095661738 5.31200612310118 5.25829478957662
5.11920972803601 P P P 5.52567583665037 5.18565263538134 5.25208495810237 P P P
LNCV6_92219_PI430048170 mRNA
CAGCAAACTCGAATTCATCATGTATGGAGCTATCAAAGAAAATTGCAGAAAACAAGAGTA NM_002767RefSeq chr17
+ 18858067 18931286 PRPSAP2 5636 "phosphoribosyl pyrophosphate synthetase-associated protein
2, transcript variant 1"
GO:0004857|GO:0060348|GO:0006139|GO:0000287|GO:0004749|GO:0002189|GO:0043086|GO:0009165 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132963_PI430048170 0.0187939283464915 1.29976128479282 10.4720170519761
10.5805242778443 10.4807282786362 P P P 9.98726874997951 10.2085302247933
10.1947965731246 P P P LNCV6_132963_PI430048170 mRNA
CTAAAAATGTATTTTATACCGGCTTATTCCTAGTATTGAATAAACTAGCGGGCTCACTCA NM_014026RefSeq chr11
+ 126303751 126345753 DCPS 28960 "decapping enzyme, scavenger"
GO:0005515|GO:0036245|GO:0010467|GO:0045292|GO:0000290|GO:0043928|GO:0005634|GO:0050072|GO:0005
829|GO:0005739|GO:0043069|GO:0005737|GO:0005654|GO:0000340|GO:0000288 . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_127051_PI430048170 0.0104089947979393 1.35091188643188 12.2054621102385
12.4223984559602 12.4208401815429 P P P 12.026320729395 11.8605813570693 11.864325196005
P P P LNCV6_127051_PI430048170 mRNA
GCTTAGTGTGGGGTGAACCCAGGGGTCCAAACTCTGTTTCTCTTCAGTGCTCCATTTTTT NM_001258411 RefSeq
chr16 + 24845862 24911628 SLC5A11 115584 "solute carrier family 5 (sodium/inositol cotransporter),
member 11, transcript variant 2"
GO:0005886|GO:0008643|GO:0006915|GO:0016021|GO:0006814|GO:0055085|GO:0015293 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144169_PI430048170 0.969822750632162 1.00426778306033 0.471523746490691
0.488456223678557 0.907093840992663 A A A 0.49570471234687 0.428097177604756
0.917996374226062 A A A LNCV6_144169_PI430048170 mRNA
CCTAGAACCACTGAGCCCCAAGTGAAGAATTTAACAACAAAATGGGTTAATGAAAAATAT NM_001130698 RefSeq
chr4 - 121879027 121951754 TRPC3 7222 "transient receptor potential cation channel, subfamily C,
member 3, transcript variant 1"
GO:0005515|GO:0005262|GO:0005886|GO:0010524|GO:0030168|GO:0055085|GO:0070679|GO:0051592|GO:0034
220|GO:0005887|GO:0007411|GO:0007596|GO:0070588|GO:0033198|GO:0006816|GO:0015279|GO:0007602 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143206_PI430048170 0.324359757799156 1.30553684514178 1.1961685668682
0.374080560687761 0.471427499321071 A A A 0.338403723882779 0.320685457157477
0.374612376766134 A A A LNCV6_143206_PI430048170 mRNA
GCTTAGTTGGTCATCTATCACATGATTTTAAAAAATACACCAAAGCAAACCGCCTGCTTC NM_001038704 RefSeq
chr17 - 58541586 58544372 C17orf47 284083 chromosome 17 open reading frame 47 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_143642_PI430048170 0.0407016711273018 0.741423177968717 3.350391940647
3.37078405977867 3.21382159506787 P P P 3.66122703739905 3.94823685746197 3.6010763055692
P P P LNCV6_143642_PI430048170 mRNA
ACGAGATTGTGAGTGTCAAGAGGGAATACGTAGTTTATGATCTGAAGACCCAAGTCCCAC NM_180990 RefSeq chr17
+ 76079181 76082804 ZACN 353174 zinc activated ligand-gated ion channel
GO:0005230|GO:0034220|GO:0005886|GO:0008270|GO:0016021|GO:0010043|GO:0015276 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135877_PI430048170 0.0174908303563340 .65112546230492 8.58163062677612
8.51402255187103 8.90786503738063 P P P 9.2464219830007 9.15332988939115
9.47318461466161 P P P LNCV6_135877_PI430048170 mRNA
CAGTTACAACCACCCCACTATGGAATCAGTATTTAGTTATACATTTGTATAAGAACCTGT NM_001242374 RefSeq
chr3 - 134477703 134486023 ANAPC13 25847 "anaphase promoting complex subunit 13, transcript
variant 2" GO:0007067|GO:0070979|GO:0005680|GO:0051301 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137348_PI430048170 0.547190411389299 1.21457843105389 1.60244128091043
2.62844155441701 2.39841344582729 A A A 1.80445053468219 2.31901716786743
1.78623564303885 A A A LNCV6_137348_PI430048170 mRNA
CTGGCCAAGTGCCTAATTTTAACCCAGACCTCAATAAAGACACCTTTTGTACCAATAAAA NM_016140 RefSeq chr16
- 67389806 67393535 TPPP3 51673 "tubulin polymerization-promoting protein family member 3,
transcript variant 1" GO:0005737|GO:0015631|GO:0001578|GO:0005874|GO:0070062 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_140478_PI430048170 0.00010502856772144 2.73401476225582 4.00615512387963
3.8957813395484 4.02104377339187 P P P 2.41330071181194 2.53101478742181
2.62130476408488 A P P LNCV6_140478_PI430048170 mRNA
TCAGAGAAATTATTGACCAGTTTGAGGAGAACATGCCTGTATTAAGGGCCGAGGTGGAAG NM_080571 RefSeq chr20
- 270862 290778 C20orf96 140680 "chromosome 20 open reading frame 96, transcript variant 2" NA .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135777_PI430048170 0.000886141336285262 0.40479415003102 4.9783645902567
4.70553949899942 4.86154923893665 P P P 6.08528240661367 6.17744555111607
6.20708533840876 P P P LNCV6_135777_PI430048170 mRNA
ATATGTGTGGCAGAAAGATATGGCCCTGAACTAGGGCAGGTATAGTAAACCTTTTATTAT NM_001100389 RefSeq
chr4 - 165076077 165112872 TMEM192 201931 transmembrane protein 192
GO:0048471|GO:0005794|GO:0005886|GO:0005783|GO:0005770|GO:0005634|GO:0016021|GO:0005765|GO:0005
764|GO:0042803|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134023_PI430048170 0.0515937290743938 1.05957112703197 0.342814968415609
0.38903442147876 0.310886883732089 A A A 0.2537368582144560.282590007490955
0.25686573778939 A A A LNCV6_134023_PI430048170 mRNA
TCCAAAAACCCAAGTAGTCAGTCCCTTATGTACTGTGGTAAACCTGTTTATGTTCACCCC NM_138960 RefSeq chrX
+ 89921940 89922883 TGIF2LX NA "TGFB-induced factor homeobox 2-like, X-linked" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126736_PI430048170 0.2107217970769210.8734170712580997.57372203403466
7.49955200435063 7.20893061891325 P P P 7.50342824659197 7.71930507488474
7.66185112122842 P P P LNCV6_126736_PI430048170 mRNA
GGCCCAGGGGTCAGCCTGAGAATCTCGCCCTTGGATTAAAAGCCACCAATGCTCAAAAAA NM_203425 RefSeq chr17
+ 61411750 61413280 C17orf82 NA chromosome 17 open reading frame 82 NA . NA - . NA
NA NA NA NA NA NA NA NA NA
LNCV6_132815_PI430048170 0.0079870871003136 0.4164194167926135.53484916773913
5.07333404139407 5.02504230861703 P P P 6.39193683314058 6.61713815162426 6.4632648827995
P P P LNCV6_132815_PI430048170 mRNA
ATGTTATTGGCTCCTTGAAAATGTGTGTGTGTGGCGAGGGGAATAGATCCACAAAAGCAT NM_025160 RefSeq chr1
- 224385142 224434299 WDR26 80232 "WD repeat domain 26, transcript variant 1"
GO:0005737|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98690_PI430048170 0.2528923924073410.5383793753520944.25728688193849 2.76688501431756
3.15957787150514 P A P 3.38078805910748 4.3945227163352 5.05796747012087 P P P
LNCV6_98690_PI430048170 mRNA
AAGTAGCTCAAAGGACTCCGGTTTCTGTCTACAAGTGTGATGTCTCCATGAAGAAGACTT NM_001080412 RefSeq
chr3 + 141324212 141449790 ZBTB38 253461 zinc finger and BTB domain containing 38
GO:0005515|GO:0008327|GO:0003700|GO:0045944|GO:0072562|GO:0005634|GO:0045892|GO:0046872|GO:0042
803|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127487_PI430048170 0.00609776968825705 0.6408864565068871 2.6105760761248
12.4553515390331 12.5280221085361 P P P 13.0389297317534 13.1465971008593
13.3237492632012 P P P LNCV6_127487_PI430048170 mRNA
GAGGATGCCTTCTCTACTGTGCATACCCATGAAATTTAATACACATTTTAAAACCTCTGG NM_001258310 RefSeq
chr12 - 6556869 6568332 NOP2 4839 "NOP2 nucleolar protein, transcript variant 5"
GO:0005515|GO:0008284|GO:0006364|GO:0005730|GO:0008757|GO:0032259 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145413_PI430048170 0.8481852356472810.9926339976065265.78258823532523
4.92785964336604 6.30830814308845 P P P 5.39702842323994 6.01873886987378
5.88222101971757 P P P LNCV6_145413_PI430048170 mRNA
ATTAGATATCGCTATAAGTGGACATGCGTACTTACTTGTAACCCTTTACCCTATAATTGC NM_001172438 RefSeq
chr7 + 94656324 94669694 PEG10 23089 "paternally expressed 10, transcript variant 2"
GO:0005515|GO:0005737|GO:0006915|GO:0008270|GO:0005634|GO:0003677|GO:0030512|GO:0030154 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91684_PI430048170 0.0505777195888297 0.3948369747145161 1.0976835431322
10.0828933988303 9.86093779394749 P P P 12.0001312548572 11.8154730945136 11.527346593958

P P P LNCV6_91684_PI430048170 mRNA
TTCTCCCTCTCTCCCAGGTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCC NM_001135058 RefSeq
chr14 + 30874534 30890616 COCH 1690 "cochlin, transcript variant 1"
GO:0031012|GO:0005515|GO:0045089|GO:0008360|GO:0007605|GO:0005518|GO:0005578|GO:0042742|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145194_PI430048170 0.0963317143412429 0.7276787584323458.3508974981779
8.38082993514488 8.46210318424598 P P P 8.54264782404188 8.92592027182795
9.05557175904624 P P P LNCV6_145194_PI430048170 mRNA
GGCCTTTTTGGGGCTGGAAAATGTATGAATTCTTCAACTGTCTTACAAGAGATCTGCTAA NM_000097 RefSeq chr3
- 98579445 98593611 CPOX 1371 coproporphyrinogen oxidase
GO:0010288|GO:0046685|GO:0005212|GO:0005743|GO:0044281|GO:0006782|GO:0042803|GO:0006783|GO:0005
739|GO:0005758|GO:0005737|GO:0051597|GO:0006778|GO:0010039|GO:0017085|GO:0004109|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55612_PI430048170 0.0627145286300960.6918800705997456.01177053097293 5.98373662786036
6.34374097768246 P P P 6.37202583341308 6.61222292956138 6.92427215370334 P P P
LNCV6_55612_PI430048170 mRNA
ACAAATACAATGAATGGCAGCAAGTCACCTGTTATCTCCAGACCAAAATCCACACCCTTA NM_001008493 RefSeq
chr1 - 225486831 225653143 ENAH 55740 "enabled homolog (Drosophila), transcript variant 1"
GO:0005515|GO:0050852|GO:0001725|GO:0017124|GO:0030054|GO:0005886|GO:0050699|GO:0045202|GO:0001
843|GO:0046907|GO:0003779|GO:0030175|GO:0030027|GO:0005829|GO:0005737|GO:0007411|GO:0008154|GO:0
005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137446_PI430048170 0.00122938744733348 0.6248016377737137.52678885758405
7.35734262270541 7.36232814886459 P P P 8.05059619798726 8.16146969027109
8.07412772273431 P P P LNCV6_137446_PI430048170 mRNA
TTGGGAGCTGGGACTCGGGGAGTCAAAAATAGATGAGTAATTGTCAATAAACCTGGGAAC NM_022481 RefSeq
chr5 - 141653400 141682233 ARAP3 64411 "ArfGAP with RhoGAP domain, ankyrin repeat and PH
domain 3"
GO:0005515|GO:0051056|GO:0030336|GO:0035021|GO:0005886|GO:0007264|GO:0043325|GO:0035024|GO:0008
360|GO:0005547|GO:0001726|GO:0030027|GO:0005100|GO:0005829|GO:0008060|GO:0005737|GO:0032321|GO:0
032312|GO:0007010|GO:0008270|GO:0016192|GO:0005856|GO:0030675 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140294_PI430048170 0.1528640912353261.47699461800309 2.59544263190683
1.96582509504218 2.67539589300096 A A A 1.42916244260465 1.89191484178067
2.21959887642624 A A A LNCV6_140294_PI430048170 mRNA
ATTGTTCTTCTCCGTGTCCTGGGTACAACATCGAATAATATTTCTTGGCCTCCTTTCCGCNM_003679 RefSeq chr1 +
241532133 241595647 KMO 8564 kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)
GO:0070189|GO:0006569|GO:0009651|GO:0050660|GO:0005743|GO:0019674|GO:0044550|GO:0005741|GO:0044
281|GO:0004502|GO:0043420|GO:0005829|GO:0005739|GO:0034641|GO:0019805|GO:0019441|GO:0016174|GO:0
016021|GO:0034354|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134473_PI430048170 0.0284453435920023 0.6876400237249065.62826028972478
5.69974826109252 5.9477243200137 P P P 6.52529014215151 6.2503081779777
6.10934969317818 P P P LNCV6_134473_PI430048170 mRNA
ACAAAATCAATGCTGCCAACTATGCCAGTGTGAAGACTCCAGCTCTGATTGTATATGGAG NM_032750 RefSeq chr3
- 51968509 51974630 ABHD14B 84836 "abhydrolase domain containing 14B, transcript variant 1"
GO:0005515|GO:0005737|GO:0016787|GO:0045944|GO:0008152|GO:0005730|GO:0005634|GO:0070062|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127921_PI430048170 0.7759285104940421.04831422745838 6.60624581338953
6.79837316631603 6.20879357171513 P P P 6.93770861018967 6.35838770460402 6.0230442783839
P P P LNCV6_127921_PI430048170 mRNA

TAATGTACTTCTTGGACATTTTAATAAATTTTTTAACAGTTCAACCTGCCCGTCACCACCNM_004386RefSeq chr19 + 19211972 19252252 NCAN 1463 neurocan
GO:0005796|GO:0005975|GO:0005509|GO:0005578|GO:0005576|GO:0044281|GO:0007417|GO:0030208|GO:0030207|GO:0051823|GO:0030206|GO:0001501|GO:0005540|GO:0007411|GO:0030198|GO:0009405|GO:0030246|GO:0030204|GO:0007155|GO:0030203|GO:0043202|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71129_PI430048170 0.2240489211213120.5686103014460361.62931612689901 1.66171828940158 2.02777875373176 A A A 3.26002932042228 2.31133415176356 1.86119425919598 P A A LNCV6_71129_PI430048170 mRNA
ACCCCTACAAATGGCTCCCAGTCTATACGGCCTCCGTAGTGGCTGCTTACAAGGGAAAGC NM_020884RefSeq chr20 + 34955834 35002437 MYH7B 57644 "myosin, heavy chain 7B, cardiac muscle, beta"
GO:0005515|GO:0032982|GO:0003774|GO:0016020|GO:0008152|GO:0003779|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131344_PI430048170 0.3047635271123521.34405251597606 2.84096841598785 2.56479872055064 2.09035257707408 A A A 1.42839193258457 2.46447044914908 2.22982235445381 A A A LNCV6_131344_PI430048170 mRNA
GCAAATGATGCTATTAGTTCCCTCCTTATTCTGGAAGAATTTGGATAGACTTAATTGATG NM_152510RefSeq chr22 + 30080463 30177073 HORMAD2 150280 HORMA domain containing 2
GO:0007126|GO:0005694|GO:0051177|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145563_PI430048170 0.1015874918038130.4474670493527730.607986277643474 1.84911115844659 1.98894263727395 A A A 2.51727758320185 2.18828459906512 3.32854123288875 A A P LNCV6_145563_PI430048170 mRNA
GCTGGTTGAATATCTGAGGTAAATGATGTTCAATCAAGATGCTACTTGTATCATTTTGCC NM_001190879 RefSeq chr2 - 147930396 148020747 ORC4 5000 "origin recognition complex, subunit 4, transcript variant 4"
GO:0005515|GO:0000808|GO:0005730|GO:0005634|GO:0003688|GO:0015629|GO:0005524|GO:0006260|GO:0000082|GO:0005737|GO:0000166|GO:0006270|GO:0005654|GO:0005664|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68014_PI430048170 0.6554053325780060.9719661840675960.3175316087361710.244431381639046 0.306144421628234 A A A 0.4691750437960390.2477295114763770.264642134688291 A A A LNCV6_68014_PI430048170 mRNA
TCCGATTTGAAATTGAAGATGTCAACAATAAAACTGAATGTGAAAAGCTTATGGAGGGGA NM_014191RefSeq chr12 + 51591235 51812864 SCN8A 6334 "sodium channel, voltage gated, type VIII alpha subunit, transcript variant 1"
GO:0030018|GO:0086010|GO:0005886|GO:0042552|GO:0007605|GO:0005248|GO:0009636|GO:0005524|GO:0030425|GO:0019228|GO:0007399|GO:0050905|GO:0043194|GO:0033268|GO:0007517|GO:0007422|GO:0043025|GO:0007628|GO:0016023|GO:0035725|GO:0034765|GO:0001518|GO:0016021|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137803_PI430048170 0.000456454431579623 0.2718403580639765.15009603340537 4.82146090177656 5.08873369171345 P P P 6.64759666911172 6.95271215035939 7.08415074450535 P P P LNCV6_137803_PI430048170 mRNA
CGTTCTTTCAAAAGAGGCATCTAAATGTGTTCCTAATTTTGTATATGGGCTTAGGTTTTG NM_002267RefSeq chr13 - 49699306 49792921 KPNA3 3839 karyopherin alpha 3 (importin alpha 4)
GO:0005515|GO:0006461|GO:0005643|GO:0019221|GO:0008565|GO:0008139|GO:0005654|GO:0046718|GO:0008022|GO:0006607|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78999_PI430048170 0.0746364043754605 0.8807487380848125.62070926888352 5.50246231016234 5.52803500086994 P P P 5.73815843512118 5.62463132587762 5.83317367411722 P P P LNCV6_78999_PI430048170 mRNA
AAATATCAACAGTGCATTAGACATAAAAGTTTTGACTCAGCCTTCCCAGTCAGCTGTGAG NM_001161520 RefSeq chr7 - 107207852 107564514 COG5 10466 "component of oligomeric golgi complex 5, transcript

variant 3"
GO:0005515|GO:0003674|GO:0005794|GO:0016020|GO:0000139|GO:0017119|GO:0006891|GO:0005654|GO:0015
031|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138756_PI430048170 0.2401869994634211.09080761738856 10.7102092042164
10.9032416772203 10.9509242390537 P P P 10.7964531005092 10.6463443449662
10.7523820404605 P P P LNCV6_138756_PI430048170 mRNA
CTCTGAAAACCAAGTGTCAGAGCCCCTTCCCCTTGTTTTTATTTTACTGTTATAATAATT NM_001143906 RefSeq chr12
+ 112125544 112153604 TRAFD1 10906 "TRAF-type zinc finger domain containing 1, transcript variant 1"
GO:0005515|GO:0034097|GO:0046872|GO:0045824 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62126_PI430048170 0.9157098857450210.9909056172893716.41779967134538 6.10425512147545
6.57181206892951 P P P 6.22641980364739 6.3588172386149 6.56626285221413 P P P
LNCV6_62126_PI430048170 mRNA
ATGGGAACCACATGGATCTGCCTGGTACAACTGTAACCGCTATAATGAGGATGATGCAAA NM_005744RefSeq chr15
+ 72474325 72586555 ARIH1 25820 ariadne RBR E3 ubiquitin protein ligase 1
GO:0005515|GO:0006511|GO:0005737|GO:0004842|GO:0016567|GO:0019787|GO:0016874|GO:0019221|GO:0000
151|GO:0008270|GO:0031625|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145660_PI430048170 0.8102977244357240.7097883592731830.753924814394153
0.3904499626718821.16694302367213 A A A 0.2865713095558052.30629500578175
0.287114482869824A A A LNCV6_145660_PI430048170 mRNA
AGAGTCAGCCATTCCTGTTCTCTTTGCCTTGATGTTGTGTTGTTATCATTTAAGATTTTT NM_015973RefSeq chr11 +
68684514 68691175 GAL 51083 galanin/GMAP prepropeptide
GO:0005515|GO:0007631|GO:0043627|GO:0010737|GO:0005615|GO:0006954|GO:0031765|GO:0007218|GO:0031
766|GO:0045944|GO:0031764|GO:0043025|GO:0030141|GO:0005184|GO:0051464|GO:0032868|GO:0035902|GO:0
005794|GO:0043065|GO:0042493|GO:0005576|GO:0007399|GO:0050672|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144384_PI430048170 0.0043569001432222 0.4806324835110789.00105754169988
9.42899225152405 9.16557609147879 P P P 10.1657264831028 10.3956185668885
10.2279560416419 P P P LNCV6_144384_PI430048170 mRNA
TGAGTCTCGAACAGCGGTTGTTTTTACTTTATTTATCTTAGGCCCTCAGCTCCCTGACGT NM_033229RefSeq
chr6_GL000252v2_alt + 1419106 1428597 TRIM15 89870 tripartite motif containing 15
GO:0005622|GO:0051091|GO:0051092|GO:0007500|GO:0045087|GO:1900246|GO:0032481|GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139216_PI430048170 0.3172758329450681.12199105230232 10.8296688311874
10.5741311601544 10.4413347681367 P P P 10.4241396886643 10.6039959341601
10.3328272583205 P P P LNCV6_139216_PI430048170 mRNA
GGCATCCCACCCCCAAGAAGAACTGAATAAAGATTGCTGAGCAAAGGAAGGCTTAAAAAA NM_017885RefSeq
chr16 - 3022619 3024286 HCFC1R1 54985 "host cell factor C1 regulator 1 (XPO1 dependent),
transcript variant 1" GO:0005737|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139440_PI430048170 0.0794853731107679 0.8579979938090658.66092285455919
8.75235020327547 8.50252453994433 P P P 8.78036713678229 8.9748397827783
8.82722561118928 P P P LNCV6_139440_PI430048170 mRNA
TTTGGCGGTTAAGGTTGCTGATTTCTCCACAGCTTGCATTTCTGAACCAAAGGCCCTTTT NM_003538RefSeq chr6
+ 26021678 26022050 HIST1H4A 8359 "histone cluster 1, H4a"
GO:0005515|GO:0010467|GO:0006325|GO:0005634|GO:0045653|GO:0000723|GO:0000183|GO:0000786|GO:0070
062|GO:0035574|GO:0035575|GO:0046982|GO:0006334|GO:0006335|GO:0005576|GO:0006336|GO:0000228|GO:0
003677|GO:0032776|GO:0034080|GO:0043234|GO:0016020|GO:0045814|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132394_PI430048170 0.4463196527141821.05189382872478 0.289404641282449
0.2960470411599040.51320302009418 A A A 0.3110404139674850.270360035013927

0.309342668063005 A A A LNCV6_132394_PI430048170 mRNA
CAGGCTATTGTTGGAGGACTGGTTTGGATGTGACAACTACAATTAGACCAGGAATTAAAC NM_030640 RefSeq chr12
- 12473281 12562514 DUSP1680824 dual specificity phosphatase 16
GO:0045209|GO:0005634|GO:0045204|GO:0035335|GO:0005829|GO:0000188|GO:0005737|GO:0006470|GO:0016
311|GO:0016023|GO:0004721|GO:0005654|GO:0008138|GO:0004725|GO:0017017 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136463_PI430048170 0.0128284109152401 1.89426039487686 4.92439590237474
5.291571819471 5.25198293146981 P P P 4.55467049976738 4.05880784614478
4.05809666846498 P P P LNCV6_136463_PI430048170 mRNA
GGACCAGCTGGGTGCTTGGGCATTGACAGAATGATGGTTGTTTTGTATCATTTGATTAAT NM_020672 RefSeq chr1
- 153614255 153616332 S100A14 57402 S100 calcium binding protein A14
GO:0048471|GO:0030054|GO:0034142|GO:0005886|GO:0005509|GO:0006915|GO:0042379|GO:0071624|GO:0055
074|GO:0005737|GO:0015630|GO:0032496|GO:0005654|GO:0090026|GO:0042742|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129193_PI430048170 0.6717012988015590.9798981248624838.80028710961516
8.63223834083472 8.76162569220248 P P P 8.80894037105889 8.67962547596135
8.79532495430903 P P P LNCV6_129193_PI430048170 mRNA
CCTCACTTCAAATTATGTTTGGACTTGACAAAAATGTATGCAAATGATGGGGGATGGTAG NM_007242 RefSeq chr16
+ 70299158 70333832 DDX19B 11269 "DEAD (Asp-Glu-Ala-Asp) box polypeptide 19B, transcript
variant 1"
GO:0031965|GO:0005737|GO:0006406|GO:0016020|GO:0005643|GO:0003723|GO:0004386|GO:0005635|GO:0015
031|GO:0005524|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124256_PI430048170 0.1366740242947810.499634937822 2.08059274629225
0.3955860244247311.35612493108461 A A A 2.16888460356657 2.09715662452173 2.8966480889737
A A P LNCV6_124256_PI430048170 mRNA
CCATTTTGGTTCCTAAGAATAGATAGGCCATTAAGAAGGATATTAGGTTTCTAAGGACAA NM_001030060 RefSeq
chr6 + 147508691 147570021 SAMD5 389432 sterile alpha motif domain containing 5 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_51659_PI430048170 0.0339120611763792 1.17974249470882 7.82888044153341
7.71569183847189 7.7997548860321 P P P 7.57131755763835 7.42881991922605
7.62414794038423 P P P LNCV6_51659_PI430048170 mRNA
CTGGAAACTTTCAAAGAAAACCCCCAAACTTTTAAGTCACAAAGTCTGATTAAAGAAGCT NM_015584 RefSeq chr17
- 28346627 28357589 POLDIP2 26073 "polymerase (DNA-directed), delta interacting protein 2,
transcript variant 1" GO:0042645|GO:0005739|GO:0070584|GO:0005634|GO:0003677 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_127604_PI430048170 0.6419287645027411.05634774063693 5.66533132140055
5.43991076144366 5.67258459539875 P P P 5.19970898424516 5.53943698139713
5.75917905276367 P P P LNCV6_127604_PI430048170 mRNA
GTTTGGTTTTATAGAGTATTCTGTATACTTGTTGGGATACACAAATACCAGATGTGCTGT NM_015375 RefSeq chr1
- 205142502 205211599 DSTYK 25778 "dual serine/threonine and tyrosine protein kinase, transcript
variant 1"
GO:0033674|GO:0030054|GO:0045743|GO:0018108|GO:0005524|GO:0044344|GO:0016323|GO:0005737|GO:0016
324|GO:0004674|GO:0004712|GO:0004713|GO:0070374 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74927_PI430048170 0.3624750123678110.9837506942040940.3542501578482470.365133900240924
0.351331543595035 A A A 0.4143208428846880.3451506629160510.381357489865266 A A A
LNCV6_74927_PI430048170 mRNA
GGTGACAATGAAATGTGAAGAAGTTACATTTCTCAAACTTGAAAGTTAGTGACGGCTTAC NM_001109977 RefSeq
chr4 + 151409245 151663632 FAM160A1 729830 "family with sequence similarity 160, member A1"
NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_136181_PI430048170 0.3397363114904030.94600774220503 0.322314819972965
0.4026083136666790.303010667044639A A A 0.5195893730099940.434806477024608
0.307883441588611A A A LNCV6_136181_PI430048170 mRNA
GGTGATTCATATTCTTATGGGAAGTGTCATTTACCCATCTCAATAATTGGACTATTGTGA NM_001013734 RefSeq
chr6 + 112347329 112351296 RFPL4B 442247 ret finger protein-like 4BGO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131306_PI430048170 0.8808026298572341.21665247788103 0.312902079789216
0.3264405804007742.24814992443956 A A A 1.74453428183758 0.396125504215225
0.366868457976085A A A LNCV6_131306_PI430048170 mRNA
AAATTCAAATCAACTGGAGAAGGACCAGTCCCGAGAGAACTCCATCAATCCAGTCCAAGANM_001009615 RefSeq
chrX - 143712034 143720668 SPANXN2 NA "SPANX family, member N2" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_126892_PI430048170 0.00531544580334044 0.4867532244346625.79585069915874
5.74478379630021 5.82923376357409 P P P 6.68316619919066 6.78740331794463
6.99866129822442 P P P LNCV6_126892_PI430048170 mRNA
CAGACACCATATATCCTTCTGCATCCTTTGGCCAATAAAAGTTGCTGGAGAACCAAAAAA NM_006542RefSeq chr1
+ 229304381 229305503 SPHAR 10638 S-phase response (cyclin related) GO:0006260 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131852_PI430048170 0.1162414260928361.09969953508172 6.96736224913383
6.84453291307257 6.80946323641356 P P P 6.82614424301553 6.65668849304874
6.72696437505369 P P P LNCV6_131852_PI430048170 mRNA
TACGGCTCGCCTATAGAAATATAGCCTCTTCATGCTGTATTAAAAGGACTTTTAAAAGCA NM_153367RefSeq chr10
- 79382326 79445627 ZCCHC24 219654 "zinc finger, CCHC domain containing 24" GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130383_PI430048170 0.0265859354390594 0.5248825412713376.55252232320269
7.07831219548847 7.18048704721038 P P P 7.76309991301395 7.87009177367798
8.03051743392786 P P P LNCV6_130383_PI430048170 mRNA
CTGACATCGCTATGTATTCCCAACTTTATCATTTGTCTGCCTGTTTAGTTTTGACTTATG NM_032307RefSeq chr9 -
83938311 83956748 C9orf64 84267 chromosome 9 open reading frame 64
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63457_PI430048170 0.00725979111340649 0.6073634855466291 1.8647761177534 12.140846648971
11.8743311049312 P P P 12.6945057116306 12.7454744376554 12.6123178234836 P P P
LNCV6_63457_PI430048170 mRNA
TCCCGGGCCTCGTCTGTCTGGGTCCTTTGGTCAATGTTGCACAGTTTTTATTGCTCCCAT NM_001031803 RefSeq
chr17 + 75525701 75575209 LLGL2 3993 "lethal giant larvae homolog 2 (Drosophila), transcript
variant 3"
GO:0005515|GO:0007049|GO:0005737|GO:0032878|GO:0005654|GO:0030165|GO:0006887|GO:0051301|GO:0043
231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55056_PI430048170 0.4579065426085181.05694866804311 11.1758903806023 11.1578254382875
11.1958989461384 P P P 10.9269736897299 11.0917952438229 11.2529898052765 P P P
LNCV6_55056_PI430048170 mRNA
CCAACTACTACTGGTGATGCCTAATTATGAATCCAACGTGTAACCAGTTATAAATACATA NM_012474RefSeq chr1
+ 165827494 165911618 UCK2 7371 uridine-cytidine kinase 2
GO:0007631|GO:0004849|GO:0044206|GO:0044211|GO:0071453|GO:0055086|GO:0044281|GO:0005575|GO:0043
097|GO:0019206|GO:0048678|GO:0005524|GO:0006238|GO:0005829|GO:0043231|GO:0016310|GO:0006206 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140308_PI430048170 0.00117681604629137 0.4310053323701574.90916329344337
5.07499194706811 5.28596808823425 P P P 6.12367481739717 6.36638592458368
6.42978962388335 P P P LNCV6_140308_PI430048170 mRNA

CACTGCTGCTTCTGTCATTGTTCACTTGTCAGATAAAATTTTATTATCTCAGGATGCAAA NM_001039840 RefSeq chrX + 73563147 73687102 CHIC1 53344 "cysteine-rich hydrophobic domain 1, transcript variant 1" GO:0005622|GO:0005886|GO:0006810|GO:0016023 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_93752_PI430048170 0.4524386629306161.34724220744327 2.8798416006026 3.17855512068512 1.93285192903521 A P A 1.99203934725824 2.47342513200993 2.45584135835284 A P P LNCV6_93752_PI430048170 mRNA
ACAGGAATACTCAGATCGGGAAACTCAGCTTTATGACAAAGGGGTCAAAGGTGGAACCTA NM_203351 RefSeq chr17 + 63622440 63696310 MAP3K3 4215 "mitogen-activated protein kinase kinase kinase 3, transcript variant 1" GO:0005515|GO:0001568|GO:0005524|GO:0046872|GO:0005829|GO:0005622|GO:0035556|GO:0000187|GO:0000186|GO:0046777|GO:0004672|GO:1900745|GO:0000165|GO:0043123|GO:0004709|GO:0004708 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_140018_PI430048170 0.3701515217125711.23115764545297 0.433928893124011 1.13672928828838 0.467605202314659A A A 0.3809390414285750.456616580488133 0.413502015598847A A A LNCV6_140018_PI430048170 mRNA
GCGAATGGCATTTTTACTTTTGTCAGCATTTACATAGCATTTAGCAATGCTATCTCAAGT NM_001004306 RefSeq chr17 - 20863394 20896140 CCDC144NL339184 "coiled-coil domain containing 144 family, N-terminal like" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_138909_PI430048170 0.2364473062849671.09034993942534 10.0529576752798 10.2500713552158 10.0302653048943 P P P 9.88466492001858 10.0577149089804 10.0211154079491 P P P LNCV6_138909_PI430048170 mRNA
CCCTGATGCCAGGGGCACCAGACTGATTCTGAGGCACAAATAAAAGAGGCTTCATACCGGNM_152345 RefSeq chr17 + 29593508 29614761 ANKRD13B 124930 ankyrin repeat domain 13B GO:0005886|GO:0005770|GO:0005769|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_54146_PI430048170 0.5556271805502510.9540101334783278.23996832410403 8.08309801541674 8.3931172670169 P P P 8.20671061433277 8.30003202752218 8.42176105320962 P P P LNCV6_54146_PI430048170 mRNA
TTCACCCTGATCCAGGCGTTTTGCTGCGAGAACGACATCAACATCCTGCGCGTCAGCAAC NM_001924 RefSeq chr1 + 67685176 67688338 GADD45A 1647 "growth arrest and DNA-damage-inducible, alpha, transcript variant 1" GO:0005515|GO:0043065|GO:0007098|GO:0046330|GO:0006915|GO:0001047|GO:0005634|GO:0000079|GO:0071479|GO:0042770|GO:0005737|GO:0000185|GO:0006281|GO:1900745|GO:0007050|GO:0006469|GO:0071260|GO:2000379 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_130317_PI430048170 0.00425953585199045 1.61480216524896 9.83236143009764 9.91317265930123 10.1200928876304 P P P 9.27635068122641 9.39802116610264 9.11915525552108 P P P LNCV6_130317_PI430048170 mRNA
AAAGTGACATTGTGTACACACTGCAGCTTGGGGGTTTTTTCTTTGTATTGCTGTTTATTT NM_017843 RefSeq chr20 + 50794893 50877177 BCAS4 55653 "breast carcinoma amplified sequence 4, transcript variant 1" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_28186_PI430048170 0.0325437533665038 1.39178512169897 5.65775541428957 5.97793356815618 6.01807039998353 P P P 5.50772107672992 5.46681715046126 5.26300391104601 P P P LNCV6_28186_PI430048170 mRNA
TAACAAGTGGACAGTTCAGTACAATGTTTCCCCGCTGTCTTGGAATGTGGCTGTCAAGTT NM_002833 RefSeq chr15 - 75467120 75579291 PTPN9 5780 "protein tyrosine phosphatase, non-receptor type 9" GO:0005515|GO:0005737|GO:0006470|GO:0035335|GO:0004725|GO:0004726 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_143709_PI430048170 0.692879167129741 0.946001019950083 4.40214321841181 4.50227734204732 4.0636583917998 P P P 4.6587606498342 4.33048466199331 4.21761370349985 P P P LNCV6_143709_PI430048170 mRNA

AAAGTCAGCTGTCTCCTGCTTTCTTGCCCTTAAAATCACCTCCATCTTTATATTCTTCTG NM_177478 RefSeq chr5 + 121851954 121852828 FTMT 94033 ferritin mitochondrial GO:0006879|GO:0005739|GO:0004322|GO:0008284|GO:0051353|GO:0051349|GO:0006826|GO:0051347|GO:0005634|GO:0055114|GO:0008199 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_127606_PI430048170 0.818832848669081 1.02384019268986 9.26275972599224 9.12820480071598 9.44769820406347 P P P 9.33725482654379 8.97817407911095 9.40390882974809 P P P LNCV6_127606_PI430048170 mRNA
TTTGTTGGGGGTTATGTTACTGAAGAATGAACAGATGAGTAAGTGGAGGTGTTATGTAAA NM_001134422 RefSeq chr3 + 133573589 133590274 CDV3 55573 "CDV3 homolog (mouse), transcript variant 1" GO:0003674|GO:0005737|GO:0005886|GO:0008283|GO:0005730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129079_PI430048170 0.401628056083136 1.14060211218605 6.31881199728179 6.08437574469131 5.96692294872425 P P P 6.2440032074757 5.90813430369405 5.59904552677236 P P P LNCV6_129079_PI430048170 mRNA
TACAAATGTTTGATAAGTCTTTTTCTGCCCCAGTGGCCTGTTTGCCTGCCTGAGGAGTTA NM_019845 RefSeq chr2 - 153477337 153478808 RPRM 56475 "reprimo, TP53 dependent G2 arrest mediator candidate" GO:0007346|GO:0005737|GO:0007050|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144410_PI430048170 0.159381497840737 0.953491927077784 0.261738504250905 0.330194305437989 0.305288018791742 A A A 0.431542911762191 0.337248594524004 0.333220368091418 A A A LNCV6_144410_PI430048170 mRNA
GGCTAATACATTTAAGATCTTGTTTAAACAATGTTTCTTCTGCAACTGGCTACTCCTCTT NM_198123 RefSeq chr8 - 112222929 113437013 CSMD3 114788 "CUB and Sushi multiple domains 3, transcript variant a" GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143147_PI430048170 0.531558719171215 1.02225437248142 0.394741311497255 0.257656668109316 0.298005944819079 A A A 0.274782378940514 0.299559972280564 0.28415051169091 A A A LNCV6_143147_PI430048170 mRNA
GAGGTTCTCTATTGCCTCTTGAATACAAATGCACTCCCAAAGTGGTTTTAAGAAAATAAA NM_018556 RefSeq chr20 - 1629151 1657779 SIRPG 55423 "signal-regulatory protein gamma, transcript variant 1" GO:0005515|GO:0008284|GO:0008285|GO:0022409|GO:0005886|GO:0007267|GO:0050900|GO:0035556|GO:0016020|GO:0007596|GO:0050870|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133340_PI430048170 0.0318766104559133 0.605353018723141 7.96187486743095 8.24305438877865 8.43912407766193 P P P 8.97509829772728 8.91813017788247 8.96207516075808 P P P LNCV6_133340_PI430048170 mRNA
GTAGCTCCAAAGTCTTAAATGGCTTGTTTGTTCTTAAACTGTTAATTGATGAAACTGTGC NM_001099744 RefSeq chr8 - 109574175 109691791 SYBU 55638 "syntabulin (syntaxin-interacting), transcript variant 1" GO:0005515|GO:0008017|GO:0005874|GO:0031982|GO:0043231|GO:0005739|GO:0000139|GO:0016023|GO:0005654|GO:0016021|GO:0017075|GO:0019894|GO:0061178 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133627_PI430048170 0.0140453105501148 1.31325576405605 9.15592404653687 9.09267866251668 9.13179596837946 P P P 8.83151806352384 8.63124400393307 8.73195090621018 P P P LNCV6_133627_PI430048170 mRNA
GCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTGCCTGTGATGCCTGCAAAAAA NM_033197 RefSeq chr20 + 33283134 33309878 BPIFB1 92747 "BPI fold containing family B, member 1" GO:0034144|GO:0003674|GO:0005576|GO:0005615|GO:0070062|GO:0008289|GO:0002227 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144132_PI430048170 0.432997254935756 1.07231832383215 4.74009716926463 4.70624550324156 4.72215969249268 P P P 4.81323470171044 4.4243846715381

4.60256129988417 P P P LNCV6_144132_PI430048170 mRNA
ATGGTATCGGGAACACGTTTCAGGGAGGTGCCAACTGCATCATGTTCGTCCTCTGCACCC NM_024980 RefSeq chr1
- 9104416 9129170 GPR157 80045 G protein-coupled receptor 157
GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135720_PI430048170 0.47952807175027 0.4502349915579330.644394080088229
0.24306496811075 0.289412324156125 A A A 0.2626390732697320.305898360115343
2.67331580400004 A A P LNCV6_135720_PI430048170 mRNA
CAGCAAAATGCAATGGAAGGAAGAAAAGTTCCAACAAAGAATGATTTTGTGAATTCTGTG NM_006944 RefSeq chr2
+ 234050701 234077132 SPP2 6694 "secreted phosphoprotein 2, 24kDa"
GO:0010951|GO:0043234|GO:0001501|GO:0006461|GO:0046849|GO:0004866|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129748_PI430048170 0.0333960643525587 1.33988340395132 11.2462966392473
11.5622217505329 11.4538306586828 P P P 10.9349536893683 11.0471526611853 11.029072992708
P P P LNCV6_129748_PI430048170 mRNA
GTCTAACTGTGGCCAAGTATGGTGACCTCTATTTTTCTTTATATTGACTCTTTGTATTTC NM_024319 RefSeq chr1 -
228100726 228103462 C1orf35 79169 chromosome 1 open reading frame 35 GO:0005515 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132107_PI430048170 0.364833278264055 1.05287957611642 0.303261040872758
0.293868327234547 0.483557240343001 A A A 0.299103507910505 0.263362731873559
0.302900691503049 A A A LNCV6_132107_PI430048170 mRNA
CAAGCCTCTGTACATACAATTGGTTTAAATTATTTTTTCACTTGCCCTGGAAAGCAAACA NM_001256570 RefSeq
chr1 - 165400921 165445355 RXRG 6258 "retinoid X receptor, gamma, transcript variant 3"
GO:0005515|GO:0010467|GO:0000977|GO:0006367|GO:0003707|GO:0055085|GO:0048384|GO:0007507|GO:0051
289|GO:0007519|GO:0030182|GO:0007422|GO:0043401|GO:0031641|GO:0005654|GO:0008270|GO:0032526|GO:0
004886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136111_PI430048170 0.861951313123784 0.866071696487381 0.467452697819862
1.84902038936631 1.42520576347839 A A A 0.309976337202944 1.65824903994769
2.15734283887794 A A A LNCV6_136111_PI430048170 mRNA
TTGAGGGTACTGCAGCAATTGAAGTGCTGTGAGAAAAGGAAAAATCTCAGAGTCACATAG NM_023921 RefSeq
chr12_KI270904v1_alt - 24051 24975 TAS2R10 50839 "taste receptor, type 2, member 10"
GO:0033038|GO:0007186|GO:0005886|GO:0008527|GO:0016021|GO:0001580 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134381_PI430048170 0.930549318804413 0.995654513496402 9.69106661372562
9.70712458878698 9.73260228899296 P P P 9.30287752558705 9.94755407496083 9.8220190067673
P P P LNCV6_134381_PI430048170 mRNA
GCTGGCTCCCTGGGGTGACAATGTATATATGCAAATAAATTGAGAAATCTTTTGTTGTTG NM_001303126 RefSeq
chr12 - 49064675 49070025 RHEBL1 121268 "Ras homolog enriched in brain like 1, transcript variant 2"
GO:0031929|GO:0006184|GO:0005737|GO:0051092|GO:0016020|GO:0007264|GO:0005525|GO:0046872|GO:0012
505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136736_PI430048170 0.412611666309252 0.606041936776275 0.356187635178516
0.36154763451947 0.300200773655804 A A A 0.344614254130031 0.361192101930391
1.89124632529219 A A A LNCV6_136736_PI430048170 mRNA
TCATGACCTAAGGTTAATTTCATGCATACTACTAAGTGATGCTTTAAGTCATACCATTAG NM_207404 RefSeq chr3
+ 42905909 42919333 ZNF662 NA "zinc finger protein 662, transcript variant 1" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_135446_PI430048170 0.000298741543308087 0.446667440394731 5.63077020564204
5.49020101300213 5.73821843642304 P P P 6.72026316342651 6.916669070562
6.71165529660553 P P P LNCV6_135446_PI430048170 mRNA
GTGTAATCTACTTGACATCATTTTACTCTTGGAATAGTGGGTGGATAGCAAGTATATTCT NM_001166691 RefSeq

chr6 + 80004604 80042527 TTK 7272 "TTK protein kinase, transcript variant 2"
GO:0005515|GO:0007094|GO:0008284|GO:0005819|GO:0010862|GO:0018108|GO:0005524|GO:0051304|GO:0016
020|GO:0004674|GO:0004712|GO:0004713|GO:0007051|GO:0007052 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_106542_PI430048170 0.614712982862452 1.07588200396545 11.4204500318055
11.7832726796955 11.928714891136 P P P 11.7036738454682 11.4971238206312
11.6534029013392 P P P LNCV6_106542_PI430048170 mRNA
AGACCGAAAGCTACTTCACAATCTGGCTGAACCTGGAACTGCTGCTGCCTGTCATCATTG NM_012320 RefSeq chr16
+ 68245343 68261058 PLA2G15 23659 "phospholipase A2, group XV"
GO:0005739|GO:0008374|GO:0005543|GO:0047499|GO:0006672|GO:0004622|GO:0046470|GO:0005764|GO:0070
062|GO:0009062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110990_PI430048170 0.169625771275281 1.28014366733817 6.37865198441062
6.26232875917206 6.49027558223089 P P P 5.64043853604004 6.10795611814759
6.25429581265798 P P P LNCV6_110990_PI430048170 mRNA
TTTTCTCCAGAGGAAAGCGATTCTACTTTCTCCAAAAGTACTGCCACAGAAGTAGCTCGG NM_016426 RefSeq chr22
+ 46296740 46330810 GTSE1 51512 G-2 and S-phase expressed 1
GO:0005515|GO:0005881|GO:0003674|GO:0016020|GO:0007017|GO:0006977 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139383_PI430048170 0.416181206345301 0.986528983434045 0.357412635891475
0.380464690040601 0.31623338287222 A A A 0.367693306108373 0.38830344172347
0.357374244254823 A A A LNCV6_139383_PI430048170 mRNA
TATAAGAGGATGAAGTGATATGGTGAGCAGCGGACTTCAAAAACTGTCAAAGAATCAATC NM_004054 RefSeq chr12
- 8058322 8066359 C3AR1 719 complement component 3a receptor 1
GO:0005886|GO:0004930|GO:0004943|GO:0008015|GO:0010575|GO:0007204|GO:0045766|GO:0006954|GO:0006
935|GO:0007186|GO:0004435|GO:0005887|GO:0008152|GO:0090023|GO:0010759|GO:0002430|GO:0004876 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126738_PI430048170 0.306917947029567 2.10205346350552 1.26895492352469
1.00110732427637 2.94955731251408 A A P 1.32992735782733 0.671146151190475
0.737612497834739 A A A LNCV6_126738_PI430048170 mRNA
TCTAGTAGGCTGCTATGGAATTTCTGGCATGAAAATTCTTGACCCCTCACACTTTACCCC NM_199511 RefSeq chr3
- 112604385 112641143 CCDC80 151887 "coiled-coil domain containing 80, transcript variant 1"
GO:0030198|GO:0010811|GO:0005614|GO:0001968|GO:0008201|GO:0005604 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134823_PI430048170 0.259112378155499 1.02055692392789 0.45037125738024
0.487140469260865 0.421883948279854 A A A 0.420441619267812 0.415057696868034
0.436482757947742 A A A LNCV6_134823_PI430048170 mRNA
GGCATGCAAATTGTGCTTCACTTTACAGTGTTTTATCAGAGCACTTAATAAAATGTAAGG NM_004432 RefSeq chr9
- 23690104 23826065 ELAVL2 1993 "ELAV like neuron-specific RNA binding protein 2, transcript variant
1" GO:0005515|GO:0006355|GO:0000166|GO:0003730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64362_PI430048170 0.175239266568685 0.868230391920466 5.1741616339292 5.14916179490719
5.02237506347762 P P P 5.15187315487155 5.49612462448075 5.29291540088103 P P P
LNCV6_64362_PI430048170 mRNA
AAGGAGCTGAACCGGTGGTGCTCCCTAAAGAAGACCTGCATGTACAGGTCAGAGCAGGAG NM_023008 RefSeq
chr19 - 10553084 10566026 KRI1 65095 KRI1 homolog (S. cerevisiae) GO:0005730 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131914_PI430048170 0.06380466303906 0.785432358126306 6.69572502211217
6.95379468497794 7.06654256328884 P P P 7.21965805001247 7.16011327898017
7.39571206044879 P P P LNCV6_131914_PI430048170 mRNA
CCTGCAGATACGTAATGTGACCACTGTTTTGTGTTGACAATATTGCTTTATACAGTTCTT NM_145049 RefSeq chr5

+ 159263080 159286040 UBLCP1 134510 ubiquitin-like domain containing CTD phosphatase 1
GO:0016311|GO:0005730|GO:0005634|GO:0004721 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136750_PI430048170 0.00816744178070215 1.44865537648437 11.996750337685
12.2750208257555 12.1053626489705 P P P 11.5192925726967 11.6954797405509
11.5661142285127 P P P LNCV6_136750_PI430048170 mRNA
GCACTTAGGTTTCTTTTTCCATGGTTTCCAGGTAATAAAAGGAACTTGTTTTGTTGGTAA NM_013299RefSeq chr11
+ 65040903 65044828 SAC3D129901 SAC3 domain containing 1
GO:0005515|GO:0007067|GO:0005737|GO:0005815|GO:0005819|GO:0051301 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131075_PI430048170 0.2865687531521052.34128291819533 0.430777150802478
2.61927151233103 1.11459512821282 A A A 0.5101956531880650.491560167439941
0.372676344129406A A A LNCV6_131075_PI430048170 mRNA
TGAAGGAGCCTGGAAGTGGGTGGATGGAACAGACTATGCGACCGGCTTCCAGAACTGGAA NM_182906RefSeq
chr17 - 7074536 7080281 CLEC10A 10462 "C-type lectin domain family 10, member A, transcript
variant 1" GO:0005886|GO:0045087|GO:0030246|GO:0016021|GO:0006897 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143370_PI430048170 0.0015469674485358 1.66548043809294 11.1655244640133
11.2401055909928 11.083319203674 P P P 10.5547875602815 10.39621319545
10.3246941761485 P P P LNCV6_143370_PI430048170 mRNA
GAAGGAGGGCTGGGTTCTGGGCCTGTATCGAATAAACACAAACCTGGATGGCGCAAAAAA NM_012407RefSeq
chr22 + 38057254 38075701 PICK1 9463 "protein interacting with PRKCA 1, transcript variant 1"
GO:0005515|GO:0043005|GO:0048471|GO:0030054|GO:0005886|GO:0034316|GO:0045202|GO:0007268|GO:0060
292|GO:0006605|GO:0046872|GO:0007205|GO:0042802|GO:0005739|GO:0005737|GO:0051015|GO:0045211|GO:0
005080|GO:0042149|GO:0005856|GO:0016887|GO:0043045|GO:0043046|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141750_PI430048170 0.760162166881151.04969529415667 0.270127822385183
0.7423828294674570.298415128624715A A A 0.4614627269335470.354621452442296
0.331754470959583A A A LNCV6_141750_PI430048170 mRNA
AACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATGA NM_001005284
RefSeq chr11_JH159137v1_alt - 60669 61653 OR9G4 NA "olfactory receptor, family 9, subfamily G,
member 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138424_PI430048170 0.1966694974821990.7739829957749687.78221524027572
7.42628558416036 7.11126715037361 P P P 8.04167010184265 7.87672688946058
7.54492168563621 P P P LNCV6_138424_PI430048170 mRNA
TCCCTGCCTTCCTCGTTTCCCCAGGTTTTACTAAATACATGAAATATCCCTCTGAAAAAA NM_016070RefSeq chr17
- 57838925 57850072 MRPS23 51649 mitochondrial ribosomal protein S23
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0031965|GO:0032543|GO:0006996|GO:0003735|GO:0005
743|GO:0005840|GO:0045111 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130864_PI430048170 0.1831721494997521.36850487226013 3.25639827348742
3.75292231796088 3.8892312883089 P P P 3.48770112118849 2.7786078560436
3.26033634909793 P P P LNCV6_130864_PI430048170 mRNA
TATTGAGATATTTTTACAAGCTAAGTGACTGCAGTGTGGCTGTGTATCCTGCTCCCCACC NM_001271893 RefSeq
chr2 + 238848031 238910548 TWIST2 117581 "twist family bHLH transcription factor 2, transcript variant
1"
GO:0005515|GO:0005667|GO:0010838|GO:0043066|GO:0003700|GO:0008285|GO:0006366|GO:0019904|GO:0032
720|GO:0005634|GO:0000122|GO:0048701|GO:0003677|GO:0001649|GO:0043392|GO:0061303|GO:0005737|GO:0
045668|GO:0001076|GO:0060325|GO:0045638|GO:0003682|GO:0046983|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139630_PI430048170 0.00160085908465641 1.48773112246944 10.1766790219948

10.3175834996904 10.3108787090815 P P P 9.73213621358119 9.7050309951174
9.65181076055945 P P P LNCV6_139630_PI430048170 mRNA
GGGAGGTGTTTAACTTTCTAGTGATTGATGATTGTCAGGTTTTGAAATACCAAAGCTTTT NM_138346 RefSeq chr1
- 11919587 11926428 KIAA2013 90231 KIAA2013 GO:0016020|GO:0016021 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_127087_PI430048170 0.0604825283960116 0.6745405284455530.298902516970813
0.2648994060381090.365430510579286A A A 0.7528427702051870.677647750537969
1.15721492567491 A A A LNCV6_127087_PI430048170 mRNA
TCAGAGGATTGAAAACGTGGTTGGTTTATTTGTGGTAATTGTGAAAAATTGCAAAGGTAG NM_002886 RefSeq chr3
+ 153162211 153170624 RAP2B 5912 "RAP2B, member of RAS oncogene family"
GO:0030336|GO:0032486|GO:0005886|GO:0061097|GO:0030033|GO:0019904|GO:0044291|GO:0030168|GO:0005
525|GO:0005829|GO:0070527|GO:0006184|GO:0007165|GO:0016020|GO:0045121|GO:0005923|GO:0019003|GO:0
055038|GO:0070062|GO:0031954 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142817_PI430048170 0.00615873380151764 1.29187619171748 9.94164598786257
9.98608234243263 9.88761041038808 P P P 9.59911622736367 9.4707442403112 9.6336983547326
P P P LNCV6_142817_PI430048170 mRNA
ATATTACATGTTTTATTATCCTGTCCCCAGAGGGTGGTTTATCCAGAAACCAAGAAAAAA NM_144691 RefSeq chr19
- 38730191 38744474 CAPN12 147968 calpain 12 GO:0005737|GO:0004198|GO:0005509|GO:0006508
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143767_PI430048170 0.2809773266025210.57152463039201 0.2760805119285
0.4955263267297570.315645501982648A A A 1.89698039428426 0.372896022960771
0.802289875995115A A A LNCV6_143767_PI430048170 mRNA
GATGGGGCAAGGGACAGAAAAAATATCTGTAACATCTTATATGTTCAAATATAAGCGCTT NM_207445 RefSeq chr15
+ 39250668 39254842 C15orf54 NA "chromosome 15 open reading frame 54, transcript variant 1"NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135979_PI430048170 0.186044014652213 1.14914653812309 7.42416432882351
7.22118607524787 7.27513651909888 P P P 7.31348002277786 7.00011007643776
6.98886913925566 P P P LNCV6_135979_PI430048170 mRNA
TACATACACACCACCATATATACTAGCTGTTAATCCTATGGAATGGGGTATTGGGAGTGC NM_005531 RefSeq chr1
+ 159009891 159055155 IFI16 3428 "interferon, gamma-inducible protein 16, transcript variant 2"
GO:0005515|GO:0008283|GO:0032731|GO:0005634|GO:0097202|GO:0002218|GO:0001819|GO:0042802|GO:0005
829|GO:0051607|GO:0005737|GO:0003690|GO:0006954|GO:0045944|GO:0030099|GO:0030224|GO:0032481|GO:0
042149|GO:0045824|GO:0045071|GO:0030097|GO:0005730|GO:0006914|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141066_PI430048170 0.312048543700607 1.04832562812167 0.521367223779164
0.690043205429395 0.574731262662845A A A 0.545021578089134 0.501808699519549
0.539850973191333A A A LNCV6_141066_PI430048170 mRNA
AATGTCATTCTACGACATTATGAAGACATGGTAGTCGATGAATGTGGGTGTGGGTAGGAT NM_020634 RefSeq chr12
- 7689784 7695764 GDF3 9573 growth differentiation factor 3
GO:0001654|GO:0005615|GO:0002021|GO:0060395|GO:0045662|GO:0030514|GO:0005737|GO:0032525|GO:0043
408|GO:0048468|GO:0019901|GO:0090009|GO:0010453|GO:0010862|GO:0048859|GO:0042981|GO:0005160|GO:0
005125|GO:0001701|GO:0001501|GO:0045605|GO:0007492|GO:0007498|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_51432_PI430048170 0.0846384200132244 1.24335730151005 11.0121568324802
10.7964531005092 10.8005505054529 P P P 10.3542343193515 10.5569160053706
10.7402562270112 P P P LNCV6_51432_PI430048170 mRNA
TGCTTGGGTCCTTGCTCTCAGAGTCTATAAATAAAAGAATATAATGATTTGGGAGCTTAA NM_001290185 RefSeq
chr11 + 119067751 119081978 VPS11 55823 "vacuolar protein sorting 11 homolog (S. cerevisiae),
transcript variant 2"

GO:0005515|GO:0019905|GO:0030897|GO:0005770|GO:0030139|GO:0005765|GO:0005764|GO:0006886|GO:0000166|GO:0031902|GO:0008270|GO:0016192|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139264_PI430048170 0.120449574069338 1.72240189883052 1.7679272815669 1.33025204577581 0.788155024164305 A A A 0.643093629746975 0.516872270196473 0.533255341059808 A A A LNCV6_139264_PI430048170 mRNA
ATCCAGTAACATGTGAGGGAGAAGCCCATGCAGGAAGCTCTTGAGTTACTGTACTATAAC NM_001256887 RefSeq chr6 + 116529012 116558868 FAM26D 221301 "family with sequence similarity 26, member D, transcript variant 1" GO:0034220|GO:0005261|GO:0005887|GO:0006812 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143796_PI430048170 0.0184387477168807 0.619608153622679 5.21036314633785 5.04162790659413 5.4186060629379 P P P 5.64247742075388 6.08300067208513 6.00448558692232 P P P LNCV6_143796_PI430048170 mRNA
AAACTAGGTTGCAGTGGTTTCTGTTATCAGCAAGTAAATCCTGATTGATAAAGATACTAC NM_001136194 RefSeq chr2 + 206765387 206796187 FASTKD2 22868 "FAST kinase domains 2, transcript variant 1" GO:0005739|GO:0045333|GO:0004672|GO:0006468 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95693_PI430048170 0.89824083614383 0.995939528497288 0.262849508609018 0.279474584173185 0.41836232328509 A A A 0.361403990810544 0.311460508253097 0.309942956382418 A A A LNCV6_95693_PI430048170 mRNA
GTTACATCTCATCACAGACAAATGGAGAAACGGGACAACTTGTCCATCGTTTCACTGTAC NM_001304382 RefSeq chr4 - 143996103 144019345 GYPB 2994 "glycophorin B (MNS blood group), transcript variant 2" GO:0005886|GO:0005887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136048_PI430048170 0.366604287722248 1.02441736309253 0.300401281181936 0.315447324317068 0.395533747030624 A A A 0.318321951624156 0.300299161241796 0.290031728190579 A A A LNCV6_136048_PI430048170 mRNA
AGACAGAAGAGTCCTGTCATACCACTTTCTGGAAAAGTCCTAATTTCATGTAATCCTTTT NM_000686 RefSeq chrX + 116170704 116174972 AGTR2 186 "angiotensin II receptor, type 2" GO:0005515|GO:0030308|GO:0004945|GO:0021695|GO:0006883|GO:0042990|GO:0001991|GO:0002018|GO:0061049|GO:0072300|GO:0048019|GO:0035640|GO:0010459|GO:0002033|GO:0010243|GO:0002035|GO:0010700|GO:0038166|GO:0051387|GO:0007186|GO:1900116|GO:0007420|GO:0005887|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69657_PI430048170 0.402995704747515 1.66522324426191 0.698696481637355 0.365720901896861 2.04993600134011 A A A 0.582844513172184 0.463319553254238 0.442143324461482 A A A LNCV6_69657_PI430048170 mRNA
GAGCACTGGGCTCATGCCTGGCACACAATAGGTCTGCAATAAACCATGGTTAAATCCTGA NM_000020 RefSeq chr12 + 51907417 51923361 ACVRL1 94 "activin A receptor type II-like 1, transcript variant 1" GO:0071773|GO:0005515|GO:0030308|GO:0008015|GO:0071560|GO:0046332|GO:0001946|GO:0004702|GO:0043025|GO:0007179|GO:0023014|GO:0030336|GO:0009986|GO:0019901|GO:0030509|GO:0032924|GO:0001701|GO:0043535|GO:0010596|GO:0061154|GO:0005887|GO:2000279|GO:0045893|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132518_PI430048170 0.0150199128628273 1.07733292574495 0.387856682197594 0.389304129248915 0.337848895506255 A A A 0.245702854078604 0.303481532635659 0.243215974334148 A A A LNCV6_132518_PI430048170 mRNA
AGAAGGCTTTGATTTGAATAAACCAGAGAACTCTACTGAGGCATAAATAACCAGCAATGA NM_013936 RefSeq chr6_GL000252v2_alt + 662147 663180 OR12D2 26529 "olfactory receptor, family 12, subfamily D, member 2 (gene/pseudogene)" GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130913_PI430048170 8.28833524483907e-05 3.98529462739036 6.77049149693811 6.76189192088249 6.58189275879845 P P P 4.60862189695499 4.87490186152011

4.63947731952514 P P P LNCV6_130913_PI430048170 mRNA
AAATTGAGAGTGGCAGCTGCCTGCCAAAATCTGTTCCGCTGTAACAGAACTGAATTTGGA NM_004843 RefSeq chr19
+ 14031739 14052905 IL27RA 9466 "interleukin 27 receptor, alpha"
GO:0048302|GO:0032729|GO:0006955|GO:0002829|GO:0050830|GO:0005887|GO:0002827|GO:0045509|GO:0007
166|GO:0070106|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136983_PI430048170 0.6011147947886840.8252330150402572.3260468750146
2.52430439748565 3.45118332388423 A A P 3.05022398602518 2.43577370071955 3.6561714510954
P P P LNCV6_136983_PI430048170 mRNA
CCTCACCCAAGCATTCAACCTAAATCTTTGAAAAGTTGGGTGCTGTCTTTAGTAACTTTT NM_001037277 RefSeq
chr1 + 235328437 235344529 GGPS1 9453 "geranylgeranyl diphosphate synthase 1, transcript variant
2"
GO:0006695|GO:0045337|GO:0033386|GO:0004337|GO:0004161|GO:0033384|GO:0044281|GO:0046872|GO:0006
720|GO:0004311|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138431_PI430048170 0.7031634854498860.9488554458032525.02401265712499
4.01716147264279 4.17335213732568 P P P 4.62617471572392 4.6575150119504
4.35312035378658 P P P LNCV6_138431_PI430048170 mRNA
CTCCAGTGCCCACCAGCCTTGTCCTAATAAAATTAAGTTGCATCATTTTGTCTGAAAAAA NM_000515 RefSeq chr17
- 63917192 63918852 GH1 2688 "growth hormone 1, transcript variant 1"
GO:0005515|GO:0010535|GO:0005148|GO:0042517|GO:0005131|GO:0050731|GO:0042523|GO:0060396|GO:0005
576|GO:0014068|GO:0070977|GO:0060397|GO:0005615|GO:0007259|GO:0046872|GO:0046427|GO:0005179|GO:0
015758|GO:0043568|GO:0043406|GO:0040018|GO:0008083|GO:0032355|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142337_PI430048170 0.0555894684308358 0.7414353379666175.30503303601815
5.32857769732518 5.7014917157912 P P P 5.72091921665999 5.90005975961574
6.02780303274392 P P P LNCV6_142337_PI430048170 mRNA
GCATACAGAAATTCTCAGGATCTTCTGTTTACTATCGCTGAGATCATTATCAGAAAATAG NM_138347 RefSeq chr19
+ 57681968 57689801 ZNF551 90233 "zinc finger protein 551, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133070_PI430048170 0.8412288538027 1.01141856058754 0.289272855430202
0.4135567148239620.43413677145885 A A A 0.50916409583933 0.282601571524568
0.288527521372797 A A A LNCV6_133070_PI430048170 mRNA
ATCTGTCTCTCTTGAAGACCTCATGACACCGGAGATGGCAAAGGAGAGATATGAAGATTA NM_001010859 RefSeq
chr22 - 32149531 32159256 C22orf42 NA chromosome 22 open reading frame 42 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_64733_PI430048170 0.8332425653094060.9794827925571064.51496826688539 4.94310553734795
4.5193982737074 P P P 4.8567854675193 4.698239132994 4.53773495986232 P P P
LNCV6_64733_PI430048170 mRNA
AACTTGGTGTCACTTGGACTTTCTGTTTCTAAGCCAGCCGTAATCTCCTCATTGGAGCAA NM_153257 RefSeq chr19
- 36637380 36666853 ZNF461 92283 "zinc finger protein 461, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143090_PI430048170 0.1025032737313830.7663703195580953.58146823290061
3.77892781680438 3.44209332666515 P P P 3.94323184294482 4.23797103759294
3.75079745814619 P P P LNCV6_143090_PI430048170 mRNA
TGTCCGTGGCAGAGCTAGGCCTGGGCTACGCCTCAGAGGAGAAGGTCATCTTCCGCTACT NM_004158 RefSeq chr19
- 6375293 6375849 PSPN 5623 persephin
GO:0001658|GO:0007411|GO:0005102|GO:0007417|GO:0008083|GO:0005615|GO:0007399 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_132231_PI430048170 0.5834566216960311.09630628226386 4.50872812645916
4.76109960486268 5.097479049183 P P P 4.57649754860855 4.58182092040986
4.85405891751134 P P P LNCV6_132231_PI430048170 mRNA
GGTGTATTGAAAGCTTTCCTTTAACATTTTCACCTGCTCATTGTGATTCCTCCTTTTAGT NM_178439RefSeq chr2 +
69829685 69879595 GMCL1 64395 "germ cell-less, spermatogenesis associated 1"
GO:0006355|GO:0007275|GO:0007283|GO:0005635|GO:0030154|GO:0016363 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_96690_PI430048170 0.00844033729902913 1.21670771904298 8.81289767077008
8.84039446502585 8.90767720095447 P P P 8.48308228802247 8.60716143456151
8.61952513596609 P P P LNCV6_96690_PI430048170 mRNA
AAAGAACGTTCCCTTTGGGGATAGTCTGGAAAGTTGGGATTTGCAAATAAAGGCTCTGGA NM_001271934 RefSeq
chr16 - 66508002 66550412 TK2 7084 "thymidine kinase 2, mitochondrial, transcript variant 5"
GO:0009157|GO:0046092|GO:0005743|GO:0046104|GO:0055086|GO:0044281|GO:0043097|GO:0005524|GO:0009
165|GO:0016310|GO:0006139|GO:0071897|GO:0009262|GO:0005759|GO:0004137|GO:0006264|GO:0006206|GO:0
004797 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136753_PI430048170 0.0103372277521088 0.4998375372639354.91640809090887
4.70018306206037 5.26964972690049 P P P 5.72981707719309 5.96903660557588
6.20733995982706 P P P LNCV6_136753_PI430048170 mRNA
TATCTTTGACCTCAATGGAGGTTTGCAAAGACTGAGTGTTCAAACTACTGTACATTTTTT NM_003383RefSeq chr9
+ 2621792 2654485 VLDLR 7436 "very low density lipoprotein receptor, transcript variant 1"
GO:0005515|GO:0005886|GO:0021517|GO:0005041|GO:0034361|GO:0001948|GO:0030229|GO:0045860|GO:0007
613|GO:0034447|GO:1900006|GO:0008203|GO:0005509|GO:0000122|GO:0006898|GO:0038026|GO:0007399|GO:0
038025|GO:0043235|GO:0007165|GO:0005905|GO:0016020|GO:0006869|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_94912_PI430048170 0.2849291786307881.52817980484154 1.92326634119217 2.75480866830283
2.42263085331418 A A A 2.32076245551451 1.93430286499908 0.668302968067195A A A
LNCV6_94912_PI430048170 mRNA
GACCAAGAAGCCTGGGGGGCCTGAGAGACTTGAACAAGTGTCAATAAACGCTGGCCTCTG NM_001864RefSeq
chr19 - 36150921 36152869 COX7A1 1346 cytochrome c oxidase subunit VIIa polypeptide 1
(muscle) GO:0005739|GO:0005746|GO:0004129|GO:0016021|GO:0006091 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131105_PI430048170 0.0604651332784537 1.07225544884738 0.555289360705382
0.5039694439310630.585315757454166A A A 0.3890563635116160.46485329645814
0.488041402314744A A A LNCV6_131105_PI430048170 mRNA
GGCGATTCTATGGTCAATGTGAAGGACTAGAAATAAAAACCCACATGTGGAAAGTGCGAANM_003837RefSeq chr9
- 94558713 94593832 FBP2 8789 "fructose-1,6-bisphosphatase 2"
GO:0030018|GO:0030054|GO:0005975|GO:0006094|GO:0005634|GO:0044281|GO:0046872|GO:0005829|GO:0016
311|GO:0009405|GO:0006006|GO:0070062|GO:0006000|GO:0042132 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145084_PI430048170 0.5658478357590680.9169272827916176.14956805842396
5.47040047396559 5.47533320319169 P P P 6.01455957103581 5.78488432408045
5.76844950040169 P P P LNCV6_145084_PI430048170 mRNA
CAGAGCGAGTAAGTCCCCGCCACTCAGTAAACATTGGTCCAGGGGTAGCTGTTAAAATGG NM_001001694 RefSeq
chr22 - 49994512 50012626 IL17REL NA interleukin 17 receptor E-like NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_145048_PI430048170 0.1685170555238221.13649603758163 0.670890780994561
0.3787153433039040.60840854352681 A A A 0.2821547568495960.409650892019866
0.42435349522793 A A A LNCV6_145048_PI430048170 mRNA
CTACTGTCTGTATGTGCCCAGATAAAATTTTCATGAGAGTAGTTTACAAAAGCCGTATTT NM_001171876 RefSeq

chrX - 139581770 139708222 MCF2 4168 "MCF.2 cell line derived transforming sequence, transcript variant 3"
GO:0005515|GO:0051056|GO:0048011|GO:0043065|GO:0007264|GO:0097190|GO:0016358|GO:0005829|GO:0016020|GO:0032321|GO:0005089|GO:0005856|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_14163_PI430048170 0.1814107153386061.77132808447676 1.63429958855145 0.37207637437967 1.00366123846289 A A A 0.2613035365172180.2828350068083470.263073358074045 A A A
LNCV6_14163_PI430048170 mRNA
GCTCTGGACCCCAGGTAATGTTATTGGAGTCTCTTTATTTCAATATTTAATGTTATCACT NM_001102659 RefSeq chr2 + 206642417 206649449 LOC200726 200726 hCG1657980 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136575_PI430048170 0.4634523403027981.01403221152694 0.337637571314819 0.31794050074672 0.264324499895555 A A A 0.2885319901945730.293989201565014 0.278019510377937 A A A LNCV6_136575_PI430048170 mRNA
ACAGAGCTTGTCTCACCATGTATTTCTCAATAAACCTGCATTAGTTGGCATTGCAAAAAA NM_175858 RefSeq chr21 - 30880644 30881555 KRTAP11-1 337880 keratin associated protein 11-1 GO:0005198|GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129829_PI430048170 0.1072391759833351.06446422032999 0.481944186239828 0.5913072072154180.526622406453946 A A A 0.3871693229427430.454612847768627 0.487988083976975 A A A LNCV6_129829_PI430048170 mRNA
ATTCTTGACTCCTTGGTGCTAAAGATTGTTAAATTCAATGCTTGATGTTACAAGGTGTTG NM_022726 RefSeq chr6 - 79914811 79947598 ELOVL4 6785 ELOVL fatty acid elongase 4
GO:0005515|GO:0005783|GO:0019367|GO:0030176|GO:0035338|GO:0044281|GO:0008020|GO:0009584|GO:0019432|GO:0006633|GO:0042761|GO:0016740|GO:0044255 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141791_PI430048170 0.3830903504916470.6717518081456020.422052831993046 0.4212013920909390.25698812245106 A A A 0.3777695542593770.4452796316581681.6350054966314 A A A LNCV6_141791_PI430048170 mRNA
GAAAGCCTATTCCAGCGTTCTTTACTGCCGTTTAAATAAAGAATCATACATCTGAAAGTG NM_153606 RefSeq chr1 + 212624446 212626778 FAM71A 149647 "family with sequence similarity 71, member A" GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143336_PI430048170 0.00808596223009026 1.83513633817433 8.12447099802938 7.90339223023378 7.74670778717492 P P P 7.18962411574791 7.17110789365863 6.77441843357245 P P P LNCV6_143336_PI430048170 mRNA
GATGGGATGTTCGGATCGGTTTGTAATTAAACCTGGGAATGGCCACAAGAGCACAAAAAA NM_012435 RefSeq chr19 - 416582 460996 SHC2 25759 SHC (Src homology 2 domain containing) transforming protein 2
GO:0008286|GO:0005515|GO:0048010|GO:0030971|GO:0000187|GO:0048011|GO:0019901|GO:0005886|GO:0007265|GO:0005575|GO:0007169|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129685_PI430048170 0.0615791708484646 0.8439390319238726.57181206892951 6.55932541135328 6.50485928588814 P P P 6.67366083941077 6.91061489055853 6.77715442987807 P P P LNCV6_129685_PI430048170 mRNA
GAAAAGGACTATTTGAATCCCCAAAACATCAGGAGTCGGGAAACTTCGGAAGACAGCTGT NM_019082 RefSeq chr7 - 44565416 44574538 DDX56 54606 "DEAD (Asp-Glu-Ala-Asp) box helicase 56, transcript variant 1"
GO:0004004|GO:0016020|GO:0006364|GO:0005730|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130349_PI430048170 0.2278185831600640.8495302442083744.70349665530385 4.94805654169473 4.69344002849158 P P P 4.80862779636847 5.25569433839217 4.96500078472118 P P P LNCV6_130349_PI430048170 mRNA
ATAGCTGGTTATTTCTCCCTTGTGTTAGTAATAAACGTCTTGCCACAATAAGCCTCCAAA NM_000029 RefSeq chr1 - 230702522 230714590 AGT 183 "angiotensinogen (serpin peptidase inhibitor, clade A, member 8)"
GO:0005515|GO:0030308|GO:0001658|GO:0009651|GO:0009409|GO:0006883|GO:0001819|GO:0005615|GO:0001

558|GO:0019229|GO:0002019|GO:0002018|GO:0030198|GO:0002016|GO:0014061|GO:0007565|GO:0010744|GO:0
007568|GO:0002034|GO:0014068|GO:0001543|GO:0030432|GO:0010595|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141997_PI430048170 0.467963052795956 1.049635209643 11.4452005179482
11.3690272800692 11.2360378179314 P P P 11.3943376413292 11.2667873213738
11.1790341909158 P P P LNCV6_141997_PI430048170 mRNA
CACCTCAGGACAGATTCTCTGGCCAGGCCCTTCCCTGACCCAATAAATCCTGAAGAGGTT NM_016498 RefSeq chr22
+ 30425622 30429054 MTFP1 51537 "mitochondrial fission process 1, transcript variant 1"
GO:0000266|GO:0005743|GO:0006915|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136854_PI430048170 0.424621624642123 0.540773595372628 2.79224563457469
3.45796113484455 1.7015767055608 A P A 4.34798779388219 3.86865845366849
2.06089631729734 P P A LNCV6_136854_PI430048170 mRNA
GTGAGGCAATGGGAAAGCTCACTTCAGTTCAAGAAATTGTTCTGCCTGGGCAAGAAATTA NM_001522 RefSeq chrX
- 109372905 109482056 GUCY2F 2986 "guanylate cyclase 2F, retinal"
GO:0046982|GO:0007603|GO:0022400|GO:0004383|GO:0005525|GO:0005524|GO:0042803|GO:0035556|GO:0005
640|GO:0004672|GO:0005887|GO:0006182|GO:0004872|GO:0006468|GO:0007168|GO:0007601|GO:0016056 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138778_PI430048170 0.583934658292029 0.748357005350056 0.655156860775836
0.32156356636305 0.414134540510974 A A A 1.61856107208914 0.319860270428638
0.305562151808213 A A A LNCV6_138778_PI430048170 mRNA
CATGTAGAGTTGCTCATATTAGTCTGTAAATAATTCTATGCATAGTGAATGCAGCTTCTG NM_014848 RefSeq chr15
+ 91100308 91301309 SV2B 9899 "synaptic vesicle glycoprotein 2B, transcript variant 1"
GO:0030054|GO:0016020|GO:0005886|GO:0001669|GO:0022857|GO:0009405|GO:0006836|GO:0030672|GO:0016
021|GO:0055085|GO:0008021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132694_PI430048170 0.0117064313638891 0.817630336135352 6.24284376056051
6.26159534519336 6.34842515645661 P P P 6.52436271702789 6.52416927600213
6.67282780246131 P P P LNCV6_132694_PI430048170 mRNA
GCAAAGCCTTTTAACCTGACTTCTTCATTTTGTAAATTATTATGCATTAAGTAGCAGCCC NM_001301175 RefSeq
chr12 + 109023088 109088026 USP30 84749 "ubiquitin specific peptidase 30, transcript variant 2"
GO:0005739|GO:0004197|GO:0016579|GO:0008053|GO:0004843|GO:0000422|GO:0061136|GO:0043161|GO:0005
741|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56696_PI430048170 0.0962298401687468 0.631256221882748 4.04224581957295
3.97024964472644 4.12995762827514 P P P 4.2601452481143 4.78203010490962
4.99952743998818 P P P LNCV6_56696_PI430048170 mRNA
TCAGAGATTTCAACTTCAGCAGGCTTGATGGGTCCATGTCTTACTCAGAGAGAGAAAAAA NM_001289067 RefSeq
chr10 + 94545766 94602099 HELLS 3070 "helicase, lymphoid-specific, transcript variant 2"
GO:0005515|GO:0031508|GO:0006346|GO:0004386|GO:0005634|GO:0007275|GO:0003677|GO:0005524|GO:0006
351|GO:0007067|GO:0010216|GO:0005721|GO:0046651|GO:0000775|GO:0051301 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_142583_PI430048170 0.11945080945089 1.26564487963071 5.03641834615313
4.61776286764798 4.99319791297191 P P P 4.63090874648249 4.47073532775501
4.55726180589869 P P P LNCV6_142583_PI430048170 mRNA
AACATTCACTTATAAAGAAACCCTGCTGATTAAATCTCTCTTGGGCTTCCTCCCAAAAAA NM_000997 RefSeq chr5
- 40831327 40835285 RPL37 6167 ribosomal protein L37
GO:0010467|GO:0003735|GO:0003723|GO:0006614|GO:0019083|GO:0019058|GO:0019843|GO:0006415|GO:0006
412|GO:0046872|GO:0006413|GO:0005829|GO:0006414|GO:0000184|GO:0016032|GO:0022625|GO:0044267 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140413_PI430048170 0.458297367331563 1.11049011352539 7.44989394846359
7.09341316256571 7.26705850366989 P P P 6.79974146192187 7.36098809204326

7.16310570134242 P P P LNCV6_140413_PI430048170 mRNA
ACGCACCTCCCATAGCTATTAACAACTGAGGAAGGCCAGTGCAGAATATTTTTGGAGAAC NM_012121 RefSeq chr17
- 73283623 73312004 CDC42EP4 23580 CDC42 effector protein (Rho GTPase binding) 4
GO:0005737|GO:0030838|GO:0005886|GO:0032321|GO:0008360|GO:0015630|GO:0031274|GO:0017049|GO:0007
266|GO:0015629|GO:0005100|GO:0012505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139664_PI430048170 0.0584124058577879 1.5282700355891 4.12152384753835
3.97114881844209 4.19858936103625 P P P 3.22003756795317 3.35932725659634
3.81610268126055 P P P LNCV6_139664_PI430048170 mRNA
TGCTGTCACAAAATCTCAATAAATTGATCCTGCTGCCATTCCTTCCAAATACCCAAAAAA NM_001039770 RefSeq
chr3 - 33090415 33096801 TMPPE NA "transmembrane protein with metallophosphoesterase
domain, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97103_PI430048170 0.9506175442068810.9932534726693749.75257352268329 9.85487471905608
10.0717149684988 P P P 9.71894370739018 9.92307369140516 10.0643351334708 P P P
LNCV6_97103_PI430048170 mRNA
AAACTTGTGTCTCAAGAAGAAATGGAATTTATCCAACGTGGAGGTCCTGAATAACCATGG NM_033281 RefSeq
chr5_GL339449v2_alt + 927 13338 MRPS36 92259 mitochondrial ribosomal protein S36
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0006
412|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127540_PI430048170 0.0369301065257422 1.32298129034498 8.86815793906562
8.97268365627624 8.86472968441691 P P P 8.65810053857038 8.32934234658521
8.49065683340632 P P P LNCV6_127540_PI430048170 mRNA
CTGTTCCCTAACTGTGCTTGTATTTTTTAAAAAATAAAGCCCCAATTCAGAATTGCTGGA NM_001024594 RefSeq
chr1 + 197902551 197907367 C1orf53 388722 chromosome 1 open reading frame 53 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128735_PI430048170 0.7402644037106560.9837459098609357.82625398644042
7.59671939267396 7.68288646525759 P P P 7.77432101799181 7.69142621930151
7.71917556698224 P P P LNCV6_128735_PI430048170 mRNA
AGAATGATGTCTGCTCTAGGGAAACCTTCAAAAGCAATAAAAATGCTGTGTTGAAATGCC NM_001166462 RefSeq
chrX - 154778683 154805527 MPP1 4354 "membrane protein, palmitoylated 1, 55kDa, transcript
variant 4"
GO:0005622|GO:0005515|GO:0007165|GO:0016020|GO:0005887|GO:0090022|GO:0046939|GO:0032420|GO:0004
385|GO:0030863 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145129_PI430048170 0.0149336859213765 1.31560360099657 10.2617128369792
10.3922880819563 10.4802090686759 P P P 10.0732340729145 9.83968284815302
10.0318498405669 P P P LNCV6_145129_PI430048170 mRNA
AATATTTGCCTCCTTTTCTGTGACTGAACTGGGTTTTTCTGACATGCCTAGACTCCTAAT NM_001193314 RefSeq chr14
- 77426674 77457640 VIPAS39 63894 "VPS33B interacting protein, apical-basolateral polarity
regulator, spe-39 homolog, transcript variant 1"
GO:0005515|GO:0006355|GO:0030897|GO:0005770|GO:0008333|GO:0007283|GO:0006886|GO:0006351|GO:0030
154|GO:0005737|GO:0016023|GO:0055037|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135551_PI430048170 0.1815106292241871.15882250940314 6.77569632964424 6.845410972362
6.68586242540744 P P P 6.57514960983789 6.73047758698517 6.34148765995452 P P P
LNCV6_135551_PI430048170 mRNA
TTGAACCCAGGAATCCTTGGGGGTGGTGGGAGGAGCGGACAATAAAGGTGTAAACACAGA NM_173502 RefSeq
chr16 - 31138925 31150094 PRSS36 146547 "protease, serine, 36, transcript variant 1"
GO:0005737|GO:0004252|GO:0006508|GO:0005578 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144481_PI430048170 0.9608446630830141.00684493102495 0.435459158548509
0.6176964073917830.319167156450588 A A A 0.4149509349794360.489700828809648
0.452975253983319 A A A LNCV6_144481_PI430048170 mRNA

ACCATTCACAAATGCGTCAGAAACACTACTACCGAAGCTATGAGTACGACGTACCTCCTA NM_014271 RefSeq chrX
+ 28587563 29955900 IL1RAPL1 11141 interleukin 1 receptor accessory protein-like 1
GO:0005515|GO:0030424|GO:0005245|GO:0005886|GO:0009986|GO:0005102|GO:0030425|GO:0045920|GO:0007
165|GO:0019966|GO:0005737|GO:0097105|GO:0050775|GO:0045211|GO:0010975|GO:0030182|GO:0070588|GO:0
016021|GO:0007157. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128183_PI430048170 0.00891313290924599 0.8615224837480558.73607879684171
8.69053873514984 8.62758087920955 P P P 8.93929334040756 8.83552184884539
8.92438853832915 P P P LNCV6_128183_PI430048170 mRNA
AGGATACCAACTCCCCCTCAACATTTTACCTTAATCCAACAGTACAGTAATTAGCCGAAA NM_001288654 RefSeq
chr17 - 45023337 45061109 DCAKD 79877 "dephospho-CoA kinase domain containing, transcript
variant 3" GO:0005739|GO:0016310|GO:0016020|GO:0004140|GO:0015937|GO:0005524 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_129212_PI430048170 0.5287482383637830.9904789963081290.374033249797492
0.37621016963403 0.362310344181499A A A 0.4129308895998540.351623222375405
0.388783395565627A A A LNCV6_129212_PI430048170 mRNA
GTGAGAGAATCCTGCAATGGGCAATAATCCTTAATATAGGCAATAAATGTTTGTCAACAT NM_130794 RefSeq chr20
- 23450403 23452845 CST11 140880 "cystatin 11, transcript variant 1"
GO:0010951|GO:0005737|GO:0004869|GO:0005634|GO:0042742 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129887_PI430048170 0.1991447257373070.8266564742791915.69049373550675
5.86536458655724 5.82386401910243 P P P 6.3266194669133 5.99578410703721
5.84404893632374 P P P LNCV6_129887_PI430048170 mRNA
CTCTGGGTGGATGTGTAGAAGGCACTTCAAAATGCATAAACCTGTTACAATGTTGCCAAA NM_005727 RefSeq chr1
+ 46175076 46185962 TSPAN1 10103 tetraspanin 1
GO:0005515|GO:0015403|GO:0048471|GO:0005886|GO:0008283|GO:0050821|GO:0071934|GO:0005765|GO:0031
982|GO:0045807|GO:0005737|GO:0016020|GO:0016477|GO:0016021|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_16356_PI430048170 0.2948279036684840.8913131861681670.4226831446110830.436900769124956
0.271634774027486A A A 0.3910251053846680.45994774881887 0.757187710058657A A A
LNCV6_16356_PI430048170 mRNA
TCCAGATGATCCAGGAACTTCTTGGACATGCTTGGATGAATTACACAGCCATTCTTTTTA NM_001195138 RefSeq
chr4 - 106358182 106367435 GIMD1 NA GIMAP family P-loop NTPase domain containing 1 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142134_PI430048170 0.0136002552579511 0.4211023579788994.53773495986232
4.80709873506825 4.79792933435798 P P P 5.55478933143063 6.05801839297257
6.21071013978885 P P P LNCV6_142134_PI430048170 mRNA
TTTGTGAGAAAATTATGAAGAGTTGCAAAGTCCCAGTGATTCTCTTGTTACTTAGCTAAG NM_001282735 RefSeq
chr2 + 200305880 200482263 SPATS2L 26010 "spermatogenesis associated, serine-rich 2-like,
transcript variant 5" GO:0043234|GO:0005737|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144080_PI430048170 0.0136987896645125 0.62982342948358 9.83838345523484
9.89745675309558 10.1556461976611 P P P 10.5175547355752 10.4987149342627
10.8658668904906 P P P LNCV6_144080_PI430048170 mRNA
GGACCCACATGTAACCTGCTATGAAAACCATTTGTATAGTGTGTTTCATTTTTTAATGTG NM_003592 RefSeq chr7
+ 148698840 148801110 CUL1 8454 cullin 1
GO:0005515|GO:0031461|GO:0016567|GO:0006513|GO:0008285|GO:0008283|GO:0051437|GO:0031146|GO:0031
145|GO:0097193|GO:0051439|GO:0005829|GO:0000082|GO:0007219|GO:0000086|GO:0016032|GO:0007623|GO:0
009887|GO:0005654|GO:0007050|GO:0000278|GO:0031625|GO:0019005 . NA - . NA NA NA NA NA
NA NA NA NA

LNCV6_133193_PI430048170 0.00118882462042638 1.38275271920169 8.43504395022127 8.52806035203746 8.49465294642507 P P P 8.03312718201797 8.02483686916771 7.99847139896857 P P P LNCV6_133193_PI430048170 mRNA GGAGGAAGGACCTTTCCTCACCTCCCTTTTGACAGAGATTAGAAGTACTTCTTTAAGAAA NM_001301132 RefSeq chr15 + 40439720 40468242 BAHD1 22893 "bromo adjacent homology domain containing 1, transcript variant 2" GO:0005515|GO:0006342|GO:0000976|GO:0031507|GO:0003682|GO:0005654|GO:0045892|GO:0000785|GO:0006351|GO:0005677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140690_PI430048170 0.00358267786195344 0.34423339394575 8.427701421924 8.05287005233531 8.37921473682305 P P P 9.60139453077593 9.66332967424336 10.1691061983239 P P P LNCV6_140690_PI430048170 mRNA GTGTCATTAGGATTGTTGCTGCCAGAACTGATATGCATGAATGGCACTTAAAATAAATAT NM_001198851 RefSeq chr1 - 42176538 42334965 FOXJ3 22887 "forkhead box J3, transcript variant 3" GO:0043565|GO:0006366|GO:0006357|GO:0000981|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_50762_PI430048170 0.5693920316335940.8954600852328832.21950083781078 3.13534387677899 3.16499888089247 A P P 3.21945801158549 3.06991736919932 2.87154939674856 P P P LNCV6_50762_PI430048170 mRNA TAATCACTCATAGGTTACAAGTACCTACCCTGGTCCAGTGAACTGCGGGATTCATATGTG NM_016732RefSeq chr20 + 33993651 34083185 RALY 22913 "RALY heterogeneous nuclear ribonucleoprotein, transcript variant 1" GO:0005515|GO:0000166|GO:0000398|GO:0003723|GO:0005634|GO:0071013 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141495_PI430048170 0.2868771975115510.9249131122852434.48012129783972 4.36825581967235 4.22058302349697 P P P 4.55115699105799 4.48955545898257 4.37206824614151 P P P LNCV6_141495_PI430048170 mRNA CCAGCACCTTGGAAGCACCAATAAAGAGGATGCCCACGTGGCCCCAGCAATCAGAAAAAA NM_205853RefSeq chr3 - 52833114 52835219 MUSTN1 389125 "musculoskeletal, embryonic nuclear protein 1" GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134345_PI430048170 0.0885583925273505 0.8024163820112667.64627152255927 7.38397754355993 7.59476823131327 P P P 7.89815321828206 7.64730887250941 8.02072785024043 P P P LNCV6_134345_PI430048170 mRNA TCTTCCTTACCAAGTGAACTCCATGGCCCCAAAGCACCAGATGAATGTTGTTAAGTAAGC NM_006343RefSeq chr2 + 111898613 112029368 MERTK 10461 "MER proto-oncogene, tyrosine kinase" GO:0006909|GO:0005515|GO:0060041|GO:0005886|GO:0060068|GO:0007267|GO:0007283|GO:0050900|GO:0005615|GO:0005737|GO:0050766|GO:0034446|GO:0001779|GO:0030168|GO:0043277|GO:0018108|GO:0005524|GO:0005887|GO:0007596|GO:0043491|GO:0051250|GO:0006468|GO:0004714|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129075_PI430048170 0.1261385547964630.4745022745859671.49456187800772 0.4539564885711462.1718584661883 A A A 2.42557263190526 2.52625602426722 2.84566466920221 A A P LNCV6_129075_PI430048170 mRNA AGGCAGAACTGGAAATATTAAGTAGTGAGAGTACTATAGTTTCCCTTTTGCCTACATAAA NM_144709RefSeq chr2 - 60940412 61018230 PUS10 150962 pseudouridylate synthase 10 GO:0009982|GO:0003723|GO:0001522|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119453_PI430048170 0.0811448214269336 1.28186277955909 6.22564836579491 6.5498481618147 6.36090849158031 P P P 6.20568711395623 6.05268317200729 5.7918511363164 P P P LNCV6_119453_PI430048170 mRNA TGCCAGCAAGGTCTTCAACAACACCGGCTGCCTCTTCTTCTCCATGCTGTTCCTCATGTT NM_022169RefSeq chr11 + 119149039 119162665 ABCG4 64137 "ATP-binding cassette, sub-family G (WHITE), member 4, transcript variant 1"

GO:0005515|GO:0033344|GO:0046982|GO:0005886|GO:0017127|GO:0008152|GO:0016021|GO:0055085|GO:0016
887|GO:0005524|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132402_PI430048170 0.3995031453093260.9692339798415760.260910960086069
0.2773878339398310.392707767824886A A A 0.3754376297472360.381481810189151
0.311918155125325A A A LNCV6_132402_PI430048170 mRNA
GCTGATTTAGCACTGGAGTTATTCCTTGAATGTGTAAATAATGATGTTCTATTCTGACCT NM_006581RefSeq chr6
+ 96015968 96215612 FUT9 10690 "fucosyltransferase 9 (alpha (1,3) fucosyltransferase)"
GO:0046920|GO:0042355|GO:0005794|GO:0005975|GO:0032580|GO:0008417|GO:0006486|GO:0016021|GO:0036
065|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145248_PI430048170 0.2380925296978330.8582425015258094.70301863365092
4.77319785863783 4.67039046191863 P P P 4.91108729683039 4.71193838460957
5.15318462756897 P P P LNCV6_145248_PI430048170 mRNA
CTTGGGAGGCAATGCTCCATCCCCATTATATTACAAATAAAGATGCCCTAAATGAGTGTG NM_138558RefSeq chr1
+ 27830813 27851672 PPP1R8 5511 "protein phosphatase 1, regulatory subunit 8, transcript variant 2"
GO:0008380|GO:0005515|GO:0006397|GO:0006355|GO:0008283|GO:0003723|GO:0004865|GO:0005634|GO:0043
086|GO:0003677|GO:0006351|GO:0006401|GO:0008599|GO:0005737|GO:0004519|GO:0016607|GO:0005654|GO:0
005681|GO:0008995. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135974_PI430048170 0.4336648637381320.3528887521081940.3892909112548
0.2769305900434390.321423977263835A A A 0.2864432864726433.03866063415145
0.32074198141811 A P A LNCV6_135974_PI430048170 mRNA
CCTTCATAGCCATCGACCTGAATTTCTAAGACAAATGTTTAGATGAACTCTTAGTGTTAT NM_001080465 RefSeq
chr17_KI270857v1_alt - 2870406 2876708 C17orf98 388381 chromosome 17 open reading frame
98 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129389_PI430048170 0.9477440073248651.002958191655 7.93247698262743
7.93450175846954 7.76360278794462 P P P 8.00491715583293 7.70457748097245
7.89897154850911 P P P LNCV6_129389_PI430048170 mRNA
GACCTAGTGGTTTCTACTCTCACCGACTTATTCTGATTTCAGAAATAAAATGAAATGTCT NM_001486RefSeq chr2
+ 27496838 27523683 GCKR 2646 glucokinase (hexokinase 4) regulator
GO:0004857|GO:0005515|GO:0001678|GO:0005975|GO:0070095|GO:0019904|GO:0070328|GO:0033133|GO:0044
281|GO:0033132|GO:0046415|GO:0055085|GO:0010827|GO:0005829|GO:0008645|GO:0005739|GO:0005737|GO:0
015758|GO:0009405|GO:0009750|GO:0030246|GO:0005654|GO:0019899|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136532_PI430048170 0.0347090940372755 1.56888007271227 4.05487987104071
4.59327099592007 4.30948702527323 P P P 3.85099839492746 3.57296557966247
3.61912365999047 P P P LNCV6_136532_PI430048170 mRNA
AAATTGATAAATCAGAGGTGCTACTGAGGAGTTGGTGCCCCTCATTCCAGAATCTCCTAC NM_178548RefSeq chr1
+ 35573369 35595326 TFAP2E 339488 transcription factor AP-2 epsilon (activating enhancer binding
protein 2 epsilon)
GO:0000977|GO:0046982|GO:0006366|GO:0006357|GO:0045944|GO:0042127|GO:0000981|GO:0005634|GO:0048
856|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140765_PI430048170 0.0151277814435805 0.2954094695180134.51140773596049
3.76026930167073 4.42460313317192 P P P 5.95206660891727 6.05041756680525
6.07866988881528 P P P LNCV6_140765_PI430048170 mRNA
GATTTGGGGCACTGGTTAGACTGCATTAATAGCTACTTGATTAGAATTCGAACTTTTAAA NM_004719RefSeq chr12
- 45919130 45990618 SCAF11 9169 SR-related CTD-associated factor 11
GO:0008380|GO:0006397|GO:0005515|GO:0000245|GO:0000375|GO:0005730|GO:0008270|GO:0005654|GO:0005
634. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137963_PI430048170 0.3186935658650761.1275434228429 3.75609298457452
3.50125751763544 3.39463877411945 P P P 3.16334718230511 3.5030823717731

3.46675043877025 P P P LNCV6_137963_PI430048170 mRNA
AGCCTGGGACCAGGGCATATTAAAGGCTTTTGGCAGCAAAGTGTCAGTGTTGGCAAAAAA NM_001002029 RefSeq
chr6_GL000256v2_alt + 3315983 3336608 C4B 721 complement component 4B (Chido blood group)
GO:0044216|GO:0030449|GO:0001848|GO:0004866|GO:0005886|GO:2000427|GO:0072562|GO:0005576|GO:0005
615|GO:0010951|GO:0006956|GO:0006954|GO:0045087|GO:0006958|GO:0030246|GO:0008228|GO:0032490|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138771_PI430048170 0.8518971919393280.970752433489648 1.51018957544259
0.4361867192804680.502165172027283 A A A 1.34339777788358 0.910397145135222
0.454227316800579 A A A LNCV6_138771_PI430048170 mRNA
AGAGACATGAAGGGAGCCCTGGAAAGGGTCATTTGTAAAAGGAAAAATCCCTTCCTTCTA NM_003554 RefSeq chr17
- 3432869 3433841 OR1E2 NA "olfactory receptor, family 1, subfamily E, member 2" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138786_PI430048170 0.0663911283206463 0.5867815224301862.88719971782097
3.74340779059097 3.38739652594102 A P P 4.36048625193168 4.06002936428481
4.00401621756368 P P P LNCV6_138786_PI430048170 mRNA
TGCCTATGAAGCCACAAAGATGCCACATGTTAGTATATCAGTGAGAGGTGACTCCACAGT NM_003762 RefSeq chr1
- 171700155 171742239 VAMP4 8674 "vesicle-associated membrane protein 4, transcript variant 1"
GO:0005802|GO:0035493|GO:0005794|GO:0009986|GO:0043001|GO:0090161|GO:0042996|GO:0000226|GO:0031
201|GO:0006887|GO:0005764|GO:0006888|GO:0005484|GO:0000139|GO:0000149|GO:0016021|GO:0005768 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133904_PI430048170 0.1627397134441551.14967343808705 0.701617955722037
0.4170367707021470.688420750423557 A A A 0.2846602707711850.421452585905377
0.506172668010406 A A A LNCV6_133904_PI430048170 mRNA
GTTAGATTCTTTTCCTAGGTTAAAAACATCGGGGAACTTAAATACATAGGAAAGGAGTTC NM_198506 RefSeq chr4
+ 109848183 109872315 LRIT3 NA "leucine-rich repeat, immunoglobulin-like and transmembrane domains
3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135698_PI430048170 0.7546740486060991.01841084851877 11.5716914240347
11.6187157761497 11.5061229135743 P P P 11.4359536506291 11.4749228693295
11.6951474385581 P P P LNCV6_135698_PI430048170 mRNA
GAATTTTCTTCCCCATGGGGCTGGGGTACTTTACATTCAATAAATACTGTTTAACCCAAA NM_004890 RefSeq chr17
- 4959225 4967837 SPAG7 9552 sperm associated antigen 7 GO:0005634|GO:0003676 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_139333_PI430048170 0.00184231781080261 0.4720012163615031 2.1775306739677
11.9498695606453 11.809097595256 P P P 12.9208336736301 13.1701135966533 13.107619684576
P P P LNCV6_139333_PI430048170 mRNA
CCGAATCAGAATCCCATCTCACCAGGGCGAAATTTTAATTTAAAAACTTAAAAAGAGACT NM_182565 RefSeq chr17
+ 76265204 76271298 UBALD2 283991 UBA-like domain containing 2 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_128044_PI430048170 0.00350387875441417 1.49444185511452 7.12910593243591
7.33985148713802 7.22612410672032 P P P 6.701056754462 6.66683213260017
6.59403439333405 P P P LNCV6_128044_PI430048170 mRNA
GTCACCCTTAGCCCTTCAGATAAGCCTAGCCAGTACATATTTCAGCACAGGCAGTTTTTT NM_001002901 RefSeq
chr1 + 161721543 161728143 FCRLB 127943 "Fc receptor-like B, transcript variant 1"
GO:0005737|GO:0050777|GO:0005783 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139807_PI430048170 0.0140478372548858 0.7774591614158739.43279996869748
9.26401684462951 9.29469142696514 P P P 9.65631348363643 9.60078779941121
9.82041380681786 P P P LNCV6_139807_PI430048170 mRNA
CCCTCTAAGGGAGAGAAATGCATTTGAACGAATGTGATATAAAACCACATAATCAAATAG NM_032906 RefSeq chr4
- 88520977 88523801 PYURF NA PIGY upstream reading frame NA . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_144209_PI430048170 0.0194951721889939 1.80467028683087 7.03533009930801
6.97241074958242 6.91655817192007 P P P 6.38598399307244 5.97330107651451 5.9715835196901
P P P LNCV6_144209_PI430048170 mRNA
CCAAGAAGTCAGCCCTGACTTTTGTAAAATTTTACTAAATAAAACCACCTGGATAAGCAA NM_174891 RefSeq chr14
+ 104986278 104995518 C14orf79 122616 chromosome 14 open reading frame 79 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136553_PI430048170 0.8715059525213041.01148715268445 6.33595258353492
6.41037740221272 6.56964650363866 P P P 6.46033015417216 6.31666218705754
6.49346117878448 P P P LNCV6_136553_PI430048170 mRNA
GAAAATGGCCATCAATAGATGGCTGGAGACACACCAAAAGTAAAATTGTTGATATTGTAT NM_001128213 RefSeq
chr2 - 159235792 159286592 WDSUB1 151525 "WD repeat, sterile alpha motif and U-box domain
containing 1, transcript variant 1" GO:0004842|GO:0016567 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_57946_PI430048170 0.9992626384294660.9543752029306420.4893939316653351.79154800741394
0.714600001533879 A A A 1.99520143946555 0.5274225397105450.474811021675667 A A A
LNCV6_57946_PI430048170 mRNA
CCTAAAATAGTTTCTCTAAATAGACAATCTCACTAGCTCCAGCCAAGTGGTTATTCTTTA NM_173039 RefSeq chr11
+ 77589634 77610356 AQP11 282679 aquaporin 11
GO:0005215|GO:0005886|GO:0009986|GO:0072014|GO:0005783|GO:0055085|GO:0015840|GO:0030425|GO:0005
829|GO:0003674|GO:0048388|GO:0015793|GO:0051260|GO:0006833|GO:0016021|GO:0006811 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138828_PI430048170 0.000216576835484771 0.4248724302574226.23006329548452
6.33146589383717 6.1230830597193 P P P 7.41355036268953 7.3712295141973 7.6014920013501
P P P LNCV6_138828_PI430048170 mRNA
CCCCTTCGGTCTTCCACAGCAGTATTATTGTCTTTGTGGAGTTGACTAATGATAATTTAA NM_001198533 RefSeq
chr8 + 106270177 106752693 OXR1 55074 "oxidation resistance 1, transcript variant 4"
GO:0005739|GO:0003674|GO:0043524|GO:0016491|GO:0007628|GO:0005730|GO:0071447|GO:0005575|GO:0006
979|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128129_PI430048170 0.2445515716620621.07021012914409 0.615093098629862
0.7692622637211340.577734959108805 A A A 0.5634978926755080.56025126135547
0.55185787636433 A A A LNCV6_128129_PI430048170 mRNA
ATTCAACGAGTCCACCATGGCGCAGCTCAACGGGGAGCTGCAGGCCCTGACCGAGAAGAA NM_198475 RefSeq
chr17 - 44353732 44363867 FAM171A2 NA "family with sequence similarity 171, member A2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133392_PI430048170 0.0310730672456088 1.61795914517735 8.72478934859754
8.85737974692513 8.81390894422134 P P P 8.37654189060661 7.95075106199283
7.94573839312287 P P P LNCV6_133392_PI430048170 mRNA
GGCTTAGTTCTTATAGGATGGATGCTCAGTATTCCTTAATAAAGTAGAGTTCCATTCTTA NM_181877 RefSeq chr15
+ 84601017 84623716 ZSCAN2 54993 "zinc finger and SCAN domain containing 2, transcript variant 1"
GO:0006355|GO:0003700|GO:0007275|GO:0005634|GO:0007283|GO:0003677|GO:0046872|GO:0030154|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134236_PI430048170 0.112776858896305 1.41280714520397 3.62822971212685 3.270218941438
3.14455522155158 P P P 3.22374961641272 2.56358282074269 2.71953828302332 P P P
LNCV6_134236_PI430048170 mRNA
CTAAATATTTCTTAAGGGATGTAACTTTTTATAACCATTAAGTGGGGGGAAGGGGGTGGA NM_030934 RefSeq chr1
- 185118085 185156984 TRMT1L 81627 "tRNA methyltransferase 1 homolog (S. cerevisiae)-like, transcript
variant 1" GO:0004809|GO:0008344|GO:0000049|GO:0030488|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_127438_PI430048170 0.00420904264932299 3.16373089118331 4.88909221308577
5.15989104338725 5.00152702065362 P P P 2.9903052291827 3.5305470243827
3.49690076288743 P P P LNCV6_127438_PI430048170 mRNA
TGGAGGAACCAGTGAATTCTTTCCTGGCATTTAAAACGCATTCTGTACAGTCCCCATTCC NM_001008223 RefSeq
chr12 - 49332416 49337188 C1QL4 NA "complement component 1, q subcomponent-like 4" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144938_PI430048170 0.6293431952577760.8103371562017281.1444197247246
1.99857313046354 2.06187467759948 A A A 1.44254704848306 1.79700066125037
2.72658228344461 A A P LNCV6_144938_PI430048170 mRNA
ATATCTACACCTCAACCCTCCTAGTCACCACCTGAAATAAATGTTAGGGACACTAAAAAA NM_032531 RefSeq chr11
- 126423500 127000870 KIRREL3 84623 "kin of IRRE like 3 (Drosophila), transcript variant 1"
GO:0030097|GO:0005515|GO:0030424|GO:0072102|GO:0005886|GO:0043198|GO:0048812|GO:0021740|GO:0005
576|GO:0016021|GO:0001764|GO:0002121 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133251_PI430048170 0.0547617414072343 0.5659378872157072.36402036743382
2.04979918847393 1.55842895867458 A A A 2.68615760123972 2.57144265131149
3.20741335691102 A P P LNCV6_133251_PI430048170 mRNA
CTCCTTTGTATTAGAAATCTGAACTTTGCATTTCAGCTTTGGACCTACTGACACTATTTT NM_015496 RefSeq chr8 -
94487776 94553518 KIAA1429 25962 "KIAA1429, transcript variant 1"
GO:0008380|GO:0006397|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106432_PI430048170 0.0592788130815183 1.21429928971022 7.7061137813106
7.98343857462598 7.87488629155832 P P P 7.64081406778144 7.56951754780887
7.52478877050628 P P P LNCV6_106432_PI430048170 mRNA
AGAACCGATCTTATAGGTTACTGGAAGACAGTGAAGAGAGCAGTGAGGAGACTGTGAGTA NM_003587 RefSeq
chr6_GL000253v2_alt - 1963342 1983306 DHX16 8449 "DEAH (Asp-Glu-Ala-His) box polypeptide
16, transcript variant 1"
GO:0008380|GO:0005515|GO:0004004|GO:0003724|GO:0005737|GO:0000398|GO:0005681|GO:0005654|GO:0005
634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116161_PI430048170 0.160799905244041 0.688081926393598 2.89690863211522
1.93674151097442 2.50498777738097 A A A 2.94951311345129 3.22476941468364
2.91927133109307 P P P LNCV6_116161_PI430048170 mRNA
CTAGTTCTCCACCCAAATGGATGGCTGAGATAGAACGTGATGACATCGACATGTTGAAAG NM_001024674 RefSeq
chr14 + 74084952 74200414 LIN52 91750 lin-52 DREAM MuvB core complex component
GO:0070176|GO:0000086|GO:0051726|GO:0005654|GO:0000278|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_92130_PI430048170 0.683859711525515 0.938463887419248 2.76815340577024 1.57778465899841
2.48161290368861 A A A 2.50480036850553 2.30401297295094 2.53040465151524 A A P
LNCV6_92130_PI430048170 mRNA
AGAGAAAAACATCCTTCCTGTGGACTCCAGTGTTAAAGAAGCAATTAAGGCGTTGGGAAG NM_014048 RefSeq chr16
+ 14071312 14266779 MKL2 57496 MKL/myocardin-like 2
GO:0005515|GO:0003700|GO:0003713|GO:0048514|GO:0003779|GO:0005634|GO:0001701|GO:0006351|GO:0045
844|GO:0048738|GO:0001889|GO:0003007|GO:0005737|GO:0007517|GO:0048568|GO:0045944|GO:0051145 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67186_PI430048170 0.792115539449923 1.02979049938659 12.8290990178084 12.6883401104614
13.0706620213954 P P P 12.7537963715664 12.8432051842033 12.8870362043034 P P P
LNCV6_67186_PI430048170 mRNA
ATATGCTTGGAGAGGAGAATACTTATCTCTGGCGCACATCACTATATTTGGCTGCCTCTG NM_213611 RefSeq chr12
+ 98593624 98602000 SLC25A3 5250 "solute carrier family 25 (mitochondrial carrier; phosphate
carrier), member 3, transcript variant 3"
GO:0005739|GO:0016020|GO:0015320|GO:0005887|GO:0035435|GO:0006810|GO:0005743|GO:0006091|GO:0032

403|GO:0070062|GO:0015293 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128831_PI430048170 0.3368808998432340.7031480809973082.6428033693009
1.37377087811472 2.55127327171309 A A A 2.60630442719676 2.32745455993872
3.29206488540459 A A P LNCV6_128831_PI430048170 mRNA
CACAGGCACATGGCATGTTGGCTTGTGAACCAATTGTTAAAATTTCAAGTTAATCATTAA NM_001012515 RefSeq
chr18 - 57544840 57586737 FECH 2235 "ferrochelatase, transcript variant 1"
GO:0010468|GO:0005515|GO:0046685|GO:0045471|GO:0005743|GO:0006091|GO:0010999|GO:0044281|GO:0034
379|GO:0055072|GO:0004325|GO:0005759|GO:0030350|GO:0046984|GO:0009416|GO:0008203|GO:0010288|GO:0
051537|GO:0042493|GO:0008198|GO:0006783|GO:0051597|GO:0006778|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133296_PI430048170 0.1118428073711341.42307194030163 2.46562317010343 2.5073754473291
2.44442134078206 A A A 1.74670144619941 2.3308958020679 1.72890884291549 A A A
LNCV6_133296_PI430048170 mRNA
CAGAAATAGTCCCATGTATACCTTTTCCATATTACTGTGAACTTTCAACTACTATCAAGG NM_178125 RefSeq chr7
- 73312535 73328082 TRIM50 135892 "tripartite motif containing 50, transcript variant 1"
GO:0005737|GO:0016874|GO:0008152|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63026_PI430048170 0.65382670803134 0.9721327555382168.69846031962658 8.62767638384782
8.79218549344805 P P P 8.63635454305308 8.86221683306002 8.73791779672099 P P P
LNCV6_63026_PI430048170 mRNA
ACAGGGAAGTGCCTCCTGTATTGCAATGGTGTCCTGGAGCCTCTGTACCTGTGCCCAAAT NM_001143780 RefSeq
chr17 - 44319624 44324849 SLC25A39 51629 "solute carrier family 25, member 39, transcript variant
1" GO:0006810|GO:0005743|GO:0016021|GO:0006783 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119442_PI430048170 0.7921381477101131.01676999568127 14.6164867200236
14.4083475443353 14.5230198430658 P P P 14.4717527867978 14.3986412747661
14.6053296153706 P P P LNCV6_119442_PI430048170 mRNA
GATGCTCCAGCTGCTGGTGAAGATGCATGAATAGACATTTGGAAAAATAAAACTTTATTA NM_001028 RefSeq chr11
- 119015712 119018347 RPS25 6230 ribosomal protein S25
GO:0005515|GO:0010467|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0015935|GO:0005730|GO:0005
634|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0000184|GO:0022627|GO:0
016032|GO:0005840|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139741_PI430048170 0.03848270505772 0.6523840230079183.30215997767797 2.9303014989979
3.3242991143235 P P P 3.60048021048839 4.09531838893455 3.69322878259181 P P P
LNCV6_139741_PI430048170 mRNA
CAAGAAATTAACATGAACAACAGTGGTCATAACTGATTAAAAGCTGACACGTCAGTAACA NM_031463 RefSeq chr16
- 84122138 84145195 HSDL1 83693 "hydroxysteroid dehydrogenase like 1, transcript variant 1"
GO:0005739|GO:0016491|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138552_PI430048170 0.1099376274665850.9451429980922510.265857260781296
0.2746362610127130.325485124016155 A A A 0.4309924395396190.353852088312315
0.323915835885032 A A A LNCV6_138552_PI430048170 mRNA
TGTGCGTACAGTATTATTTGGCTTCTTCAGTTGTGCTTTTAATGCTTGGATATAGTTAGG NM_001169154 RefSeq
chrX + 107206631 107244243 PIH1D3 139212 "PIH1 domain containing 3, transcript variant 1"
GO:0005737|GO:0051087|GO:0030317|GO:0070286 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136258_PI430048170 0.198485791135921 0.84767538972882 7.14973882229103
7.61402341927326 7.43208528788289 P P P 7.61060705632549 7.5854416914365
7.74716951530173 P P P LNCV6_136258_PI430048170 mRNA
CTTGTATCTCTAAATATGGTGTGATATGAACCAGTCCATTCACATTGGAAAAACTGATGG NM_031419 RefSeq
chr3 + 101849513 101861025 NFKBIZ 64332 "nuclear factor of kappa light polypeptide gene
enhancer in B-cells inhibitor, zeta, transcript variant 1"

GO:0003712|GO:0006954|GO:0006357|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119530_PI430048170 0.263475407871687 0.953695718338904 16.8946658170651 16.7490822678932 16.8613383619205 P P P 16.9570101920132 16.8728850576126 16.8829158451865 P P P LNCV6_119530_PI430048170 mRNA GAGGGGCCTAGGGAGCCGCACCTTGTCATGTACCATCAATAAAGTACCCTGTGCTCAACC NM_001289745 RefSeq chr12 + 6534404 6538375 GAPDH 2597 "glyceraldehyde-3-phosphate dehydrogenase, transcript variant 3"
GO:0050661|GO:0008017|GO:0005515|GO:0017148|GO:0048471|GO:0005886|GO:0006094|GO:0005634|GO:0044281|GO:0051402|GO:0006096|GO:0005829|GO:0042802|GO:0043231|GO:0005737|GO:0051287|GO:0015630|GO:0006006|GO:0070062|GO:0005811|GO:0035605|GO:0031965|GO:0005975|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140700_PI430048170 0.374511698536366 0.908525891832473 0.44879349366651 0.415046245591017 0.242739742150011 A A A 0.36909660749734 0.722784548029267 0.411829890761257 A A A LNCV6_140700_PI430048170 mRNA CTGAAGAGTCTTCTGGAAATTTTCCAGAAAGAAAAGATGAGAGGGATGAGAGGCAAGATA NM_000590 RefSeq chr5 - 135892245 135895827 IL9 3578 interleukin 9
GO:0008284|GO:0006955|GO:0006954|GO:0030307|GO:0045407|GO:0005140|GO:0008083|GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129698_PI430048170 0.0164518182770754 0.65660106220185 7.88021175199514 7.79202716109949 8.13786910362042 P P P 8.42322168289069 8.43991397417556 8.76422776189611 P P P LNCV6_129698_PI430048170 mRNA GATGCTGTTGTTTAGTGTAATTTCTTTGCCTGTTCAGTTAAAGTAGTGCTTGCTTGTAGA NM_206923 RefSeq chrX + 21855986 21858727 YY2 NA YY2 transcription factor NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141911_PI430048170 0.322264839195764 0.871936146288498 9.7602376103409 9.71205252967732 9.83838345523484 P P P 9.69440304510419 9.98695824203311 10.1837809874983 P P P LNCV6_141911_PI430048170 mRNA GACGGACCTTGTGATTTGTACTGTTTGCTGCGGAGCTATTTAAAGATTTTGGAATAAATA NM_024306 RefSeq chr16 - 74712957 74774831 FA2H 79152 fatty acid 2-hydroxylase
GO:0006665|GO:0042634|GO:0005506|GO:0005783|GO:0032287|GO:0001949|GO:0032286|GO:0042127|GO:0005789|GO:0006631|GO:0006633|GO:0016021|GO:0030258|GO:0080132|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127652_PI430048170 0.0612135962360699 1.48240192926149 3.79825430308801 3.75486862232705 3.62608324749773 P P P 3.13253903380397 2.85749046176036 3.43338438311897 P P P LNCV6_127652_PI430048170 mRNA CTGGGTCTTGATTTTGATGTGAGCTGGTTTTTAGCTCTCAAATGTTGTCACTTAAATAAA NM_031220 RefSeq chr17 - 6451262 6556557 PITPNM3 83394 "PITPNM family member 3, transcript variant 1"
GO:0005622|GO:0005515|GO:0030971|GO:0015914|GO:0008526|GO:0046488|GO:0005509|GO:0016021|GO:0012505|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134833_PI430048170 0.0681950285997891 0.327512218281131 0.466476252319174 2.09622372707764 0.837121377879768 A A A 2.9118007624354 2.89643555165638 2.95564990752837 P P P LNCV6_134833_PI430048170 mRNA TAGCGAGGTCTGCTGTACTGCTTATTGAAGTATTGTGATTATTTTAGGCATTGATTCTTA NM_001007189 RefSeq chr5 + 140125935 140128806 IGIP 492311 IgA-inducing protein GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134474_PI430048170 0.0444258104511434 1.14074135586496 9.3798796850837 9.38735392379573 9.25463305345679 P P P 9.12877570881672 9.2440407684699 9.07789338626536 P P P LNCV6_134474_PI430048170 mRNA

TCATTTCATCTCACAGACACAATAAAAAAGCATATTTGTCCTGCCTGGGAAGTGAAAAAA NM_015407 RefSeq chr3 + 51975025 51981200 ABHD14A 25864 abhydrolase domain containing 14A GO:0005737|GO:0016787|GO:0008152|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63043_PI430048170 0.519003097504547 1.2190708710497 0.456727661682242 1.34798793556912 1.3258487206943 A A A 0.409477653647468 1.34594832822642 0.485492433952958 A A A LNCV6_63043_PI430048170 mRNA
TCTGTGTCAGAAGGCCACCTCAAGAGGAACATCGTGGTGAAGACCGTGGAGATGCGGGAT NM_002055 RefSeq chr17 - 44905625 44915552 GFAP 2670 "glial fibrillary acidic protein, transcript variant 1" GO:0005882|GO:0045109|GO:0031102|GO:0009611|GO:0060291|GO:0051580|GO:0044297|GO:0005829|GO:0005737|GO:0005178|GO:0010625|GO:0016020|GO:0014002|GO:0030198|GO:0060020|GO:0005200|GO:0010977|GO:0019900 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53311_PI430048170 0.431674564634741 1.06749387945581 5.31807564884571 5.255364325297 5.44433648865057 P P P 5.25770608057511 5.06980511850434 5.39563038332396 P P P LNCV6_53311_PI430048170 mRNA
CTCACTGCGCTGCGAAGATGTTTTGTCACGTGACTTTCCCCGGATTTCCATTTCTTTTTT NM_001290264 RefSeq chr1 - 1661477 1692804 SLC35E2B NA "solute carrier family 35, member E2B, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126477_PI430048170 0.217056134648724 0.50984393662672 3.35619929562283 1.97538341896259 0.823052976437107 P A A 3.87340539403936 3.01624476531025 3.09113875218746 P P P LNCV6_126477_PI430048170 mRNA
CTACACATTCTCCCAAGAGTTGTCTGAGCCGCCGAGTGGACAGTGGCTGATTATGGAGAG NM_001040 RefSeq chr17 + 7630093 7633383 SHBG 6462 "sex hormone-binding globulin, transcript variant 1" GO:0007285|GO:0005576|GO:0005497|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141537_PI430048170 0.171483901753161 0.915187234143882 9.25548436740501 9.46698289690206 9.34469825274666 P P P 9.4045392215142 9.5606569423979 9.48916738562859 P P P LNCV6_141537_PI430048170 mRNA
TTGGTTTCCTCTTGGCTTTGGGGATACTTCTAAATTTTGGGAGCTCCTCCATCTCCAATG NM_001256196 RefSeq chrX + 47561099 47571921 ARAF 369 "A-Raf proto-oncogene, serine/threonine kinase, transcript variant 2" GO:0005515|GO:0032006|GO:0043066|GO:0032434|GO:0005575|GO:0005524|GO:0046872|GO:0035556|GO:0033138|GO:0004672|GO:0004674|GO:0006468|GO:0005057|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89378_PI430048170 0.115316514558358 1.53626241684714 8.36609238482109 8.51886772462297 8.8148210529303 P P P 8.43912407766193 7.62131978948374 7.66310986816751 P P P LNCV6_89378_PI430048170 mRNA
GCGCTGTGCCTTTGTCAAGATACCATCTTGTTTGATGACTTCTTTCTTTGCTGTTTTTTC NM_006134 RefSeq chr21_GL383581v2_alt - 43712 84138 TMEM50B 757 "transmembrane protein 50B, transcript variant 1" GO:0008150|GO:0003674|GO:0005886|GO:0005783|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_50770_PI430048170 0.0160137422799517 4.28700582347045 2.07835274065674 3.406392130427 2.96150041308839 A P P 0.273101710636175 1.36677895456499 0.573394725327853 A A A LNCV6_50770_PI430048170 mRNA
ATTCAGTAACCACCAGGCACAAATTCACCAGGAACAACCAAGCAAGGAAGGAAGAAGAAG NM_198279 RefSeq chrX - 19912861 19970264 CXorf23 256643 chromosome X open reading frame 23 GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98398_PI430048170 0.558823173880473 0.9815528752349 0.266914141740453 0.286142740472268 0.387627782627269 A A A 0.378459833271411 0.329504723679035 0.31548422989361 A A A

LNCV6_98398_PI430048170 mRNA
GCACAGGTTTTTGGTTTGTTAATATGGTTGTGGTCATTCTATCTGTAATAGTGTCAACAA NM_006210 RefSeq chr19
- 56810076 56840726 PEG3 5178 "paternally expressed 3, transcript variant 1"
GO:0005737|GO:0035264|GO:0006366|GO:0006357|GO:0071514|GO:0000981|GO:0006915|GO:0005654|GO:0003
676|GO:0001701|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141652_PI430048170 0.3403318967358741.64469744871817 1.78234097196294
0.4471505118270390.391965820345782 A A A 0.2935616144116570.316936246168016
0.318329028862664 A A A LNCV6_141652_PI430048170 mRNA
TGCCTCTACAGCTGTATGAAGTAGATTCTCTGATTTTATCTTGAAATCCACAACTTCCAC NM_130772 RefSeq chr5
+ 76850000 76921231 S100Z 170591 S100 calcium binding protein Z GO:0005509 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_76018_PI430048170 0.2229917867502120.724230792264615 3.23841944008971 2.98590154819645
3.95917261727781 P P P 3.77060108573003 3.70364910157577 4.23029166730702 P P P
LNCV6_76018_PI430048170 mRNA
AGCTCACCAAAATGTGTACCATTCGGATGAGTTTTGTCAAGGGTTGGGGAGCAGAATATC NM_001001419 RefSeq
chr5 + 136132844 136182734 SMAD5 4090 "SMAD family member 5, transcript variant 2"
GO:0071773|GO:0005515|GO:0030618|GO:0001657|GO:0003700|GO:0051216|GO:0005634|GO:0060048|GO:0007
281|GO:0046872|GO:0005829|GO:0005622|GO:0009880|GO:0035556|GO:0005737|GO:0001880|GO:0007179|GO:0
031625|GO:0005667|GO:0002051|GO:0030509|GO:0000979|GO:0006351|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137523_PI430048170 0.184125501926838 1.06509885892891 0.486261631226891
0.3257411535111220.392615640529323 A A A 0.2754238585859140.348418608948668
0.311409529072069 A A A LNCV6_137523_PI430048170 mRNA
CTTAAGCTGTCTTTCAATTCAGATTGTCTTGGGTATTTGCACAAAAAAGAAAGCATGTAC NM_198404 RefSeq chr13
- 45192852 45201040 KCTD4 386618 potassium channel tetramerization domain containing 4
GO:0051260 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139678_PI430048170 0.2249694824164280.666743569708694 4.74272665963784
3.39733307412737 4.32242838286412 P P P 4.6435754139994 4.86962476845134
4.98801445417057 P P P LNCV6_139678_PI430048170 mRNA
GGGTCTATTTCCATCTGTAAAATAAGAATATTTGTCTCACGTGTCTGTCATGAATAGCAA NM_018046 RefSeq chr5
+ 77030384 77065233 AGGF1 55109 angiogenic factor with G patch and FHA domains 1
GO:0005515|GO:0006396|GO:0048471|GO:0005737|GO:0001938|GO:0005576|GO:0001525|GO:0007155|GO:0003
676|GO:0001570|GO:0045766 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57196_PI430048170 0.8628842093112631.01203678842381 4.32074459965445 4.17139286457233
4.34972972721364 P P P 4.0182038887282 4.26718569355497 4.47496151773427 P P P
LNCV6_57196_PI430048170 mRNA
GTCCGCTTCTAGAAAGAGTGCAGAACAATTACGAATAGAATTGAATGCCGAAAAGTTCAA NM_003390 RefSeq chr11
+ 9573680 9589766 WEE1 7465 "WEE1 G2 checkpoint kinase, transcript variant 1"
GO:0005515|GO:0000287|GO:0000226|GO:0030010|GO:0018108|GO:0005634|GO:0005524|GO:0007067|GO:0000
082|GO:0005737|GO:0007596|GO:0004674|GO:0048812|GO:0000086|GO:0051726|GO:0005654|GO:0004713|GO:0
000278|GO:0004715|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128095_PI430048170 0.4566410077339231.1094667673501 9.07097302361112 9.0205535935483
8.88280626028882 P P P 8.45565483791675 8.97284598963562 9.03563050740637 P P P
LNCV6_128095_PI430048170 mRNA
TCATATACCCGTACTGCGAGGGCTGTTTCCAATGTAAATAAATAACTGCGCAACAAAAAA NM_152266 RefSeq chr19
+ 32972216 32977495 C19orf40 91442 "chromosome 19 open reading frame 40, transcript variant 1"
GO:0005515|GO:0006281|GO:0003682|GO:0005654|GO:0003677|GO:0043240|GO:0043231 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_92772_PI430048170 0.000345481522873947 0.5448365323861049.41457802496148

9.46359752790717 9.44539637479943 P P P 10.3347142586832 10.3646661723292
10.2505166415992 P P P LNCV6_92772_PI430048170 mRNA
GTAGCTAAAGCCACTATTTTTGCTCTCCTTAAGCTGTTCAATAAACCGGTTCCTCATTTTNM_032508RefSeq chrX -
149596555 149631912 TMEM185A 84548 "transmembrane protein 185A, transcript variant 1"
GO:0005515|GO:0016021|GO:0030425 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136088_PI430048170 0.0311762448465271 1.4532728626829 11.2573332298369
11.2148366615978 11.1655244640133 P P P 10.477196490745 10.8530001876237
10.6666123684212 P P P LNCV6_136088_PI430048170 mRNA
GCATCGTTGGGGTTTTGTTATGTGAAAATATCCTGGAAATAAATACATGTTTCTGCACTT NM_079834RefSeq chr19
+ 1905373 1926013 SCAMP4 113178 secretory carrier membrane protein 4
GO:0016021|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143490_PI430048170 0.150134648828007 0.718835134236359 8.72504950625829
8.86544547628875 9.11005367812798 P P P 9.02578581504154 9.29367464646359
9.74384047974084 P P P LNCV6_143490_PI430048170 mRNA
GAAAGCAGCCTTTTGAAGTTTATATAATGTTTTCACCCTTCATAACAGCTAACGTATCAC NM_018256RefSeq chr2
- 202880599 202912226 WDR12 55759 WD repeat domain 12
GO:0070545|GO:0005515|GO:0000463|GO:0007219|GO:0008283|GO:0043021|GO:0005730|GO:0042273|GO:0005
654|GO:0030687|GO:0000466 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137180_PI430048170 0.0539724383187298 1.28123401994493 5.04348478924091
5.33708985748691 5.2485007442732 P P P 4.87770515598228 4.84457772837139
4.84947824777204 P P P LNCV6_137180_PI430048170 mRNA
ATCCATTGGAAGAGAAAAGTTTGTGACTTGGGCCCCCAAGTTTTGAGAGAACTGGGCTTT NM_003721RefSeq chr19
+ 19192198 19201869 RFXANK 8625 "regulatory factor X-associated ankyrin-containing protein,
transcript variant 1"
GO:0003712|GO:0005737|GO:0003700|GO:0042826|GO:0006357|GO:0045944|GO:0007265|GO:0005654|GO:0003
677|GO:0006351|GO:0045171 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140623_PI430048170 0.371778768000416 0.928273819442128 0.28894337748425
0.328836100492687 0.386531759348962 A A A 0.370920032433673 0.61366098677398
0.32669549136864 A A A LNCV6_140623_PI430048170 mRNA
CCTTCTGTCAGCAGTGAAACTTATAAAATTTTTTGTGATTTCAATGTAGCTGTCTCCTCT NM_013289RefSeq
chr19_KI270889v1_alt - 38285 52629 KIR3DL1 3811 "killer cell immunoglobulin-like receptor, three
domains, long cytoplasmic tail, 1"
GO:0007165|GO:0006955|GO:0005886|GO:0005887|GO:0050776|GO:0030109 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139705_PI430048170 0.213036507315114 1.11066699064762 9.31439087211031
9.07531307623739 9.0535517456821 P P P 8.95180486576319 9.06459947597041 8.9850103218201
P P P LNCV6_139705_PI430048170 mRNA
GTTTTGTCTTGTAAATGCCTACAACCTGAGGTAATAAATCAACATTTGCTCAAACTGGAA NM_024746RefSeq chr1
- 222522259 222548102 HHIPL2 79802 HHIP-like 2
GO:0048038|GO:0016901|GO:0005975|GO:0005576|GO:0055114 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141601_PI430048170 0.172314561223153 1.04133894958863 0.42348942838978
0.408638682927907 0.426000616677892 A A A 0.315933185016916 0.351153627712047
0.414065516816958 A A A LNCV6_141601_PI430048170 mRNA
ATATCTACCTCCATAAGAAAACATAAGGACAGGCAATCTTCATAAAAATAGACTCCACCT NM_152336RefSeq chr15
+ 86142010 87029052 AGBL1 123624 ATP/GTP binding protein-like 1
GO:0035610|GO:0015631|GO:0006508|GO:0008270|GO:0035609|GO:0005829|GO:0004181 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142291_PI430048170 0.303653717230959 1.03420445591128 0.317749602438162

0.2593100543775590.380313311697638A A A 0.2794155678101840.254137701933213
0.280639648088311A A A LNCV6_142291_PI430048170 mRNA
TGTCTCGTGTCATGAATATGAAAATCGAAGAAACAACCATGACAACCCAAACCCCAGCCC NM_002218RefSeq chr3
- 52812989 52830701 ITIH4 3700 "inter-alpha-trypsin inhibitor heavy chain family, member 4,
transcript variant 1"
GO:0010951|GO:0005515|GO:0005737|GO:0005886|GO:0004866|GO:0004867|GO:0030212|GO:0072562|GO:0005
576|GO:0006953|GO:0034097|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138989_PI430048170 0.0252970131140303 1.45340910075341 9.91018274345477
9.91086924703468 9.97780933932152 P P P 9.56179240239263 9.22632460079816
9.37380834240901 P P P LNCV6_138989_PI430048170 mRNA
CTTTGGATTCTTCCCCCTTTTTTGAGAAATAAAGTTTTTTATGAAAAGCCTGTGCGTGAA NM_002860RefSeq chr10
- 95605928 95656810 ALDH18A1 5832 "aldehyde dehydrogenase 18 family, member A1, transcript
variant 1"
GO:0019240|GO:0006536|GO:0055129|GO:0005743|GO:0004349|GO:0008652|GO:0044281|GO:0005524|GO:0005
739|GO:0016310|GO:0034641|GO:0004350|GO:0005737|GO:0006592|GO:0006561|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_109701_PI430048170 0.00816911056830156 1.82488333258256 6.0126759703291
6.08371088457134 6.39015324629086 P P P 5.31433006599301 5.2042782066635
5.38715732640207 P P P LNCV6_109701_PI430048170 mRNA
TTGGTTTTATTGGAGCATTAACCTGGGAGCGATCCTGTCGTTAGGTGGCATTGCCTATAT NM_145648RefSeq chr12
- 128793193 128823996 SLC15A4 121260 "solute carrier family 15 (oligopeptide transporter), member 4"
GO:0005290|GO:0006857|GO:0016021|GO:0015031|GO:0005765|GO:0055085|GO:0015293|GO:0006811 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133441_PI430048170 0.419130557552286 1.1156356192432 2.5292064732552
2.51896414897602 2.50712799279731 A A A 2.67500159843667 2.06628073319091
2.27292362165107 A A A LNCV6_133441_PI430048170 mRNA
ACCTCCCTTCTGTCTTTTAGGCTATTTCATCACTCTTTGAGAAATAACCATTTTGACCAT NM_031958RefSeq
chr17_JH159146v1_alt - 157915 158509 KRTAP3-1 83896 keratin associated protein 3-1
GO:0005198|GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62376_PI430048170 0.93496323883535 1.0624732184513 3.1537201226981 1.95089680421732
2.18018765250732 P A A 2.21035608027246 2.04102237836951 2.91406265003712 A A P
LNCV6_62376_PI430048170 mRNA
AGGGGGAGAAGGGGAGGGGTTAAGTTAAATAAAGAAGATTATTTTTGTTTCCTGACTTTA NM_013227RefSeq chr15
+ 88803442 88875354 ACAN 176 "aggrecan, transcript variant 2"
GO:0005515|GO:0005796|GO:0005975|GO:0005578|GO:0005576|GO:0044281|GO:0046872|GO:0042339|GO:0031
012|GO:0001501|GO:0005540|GO:0018146|GO:0022617|GO:0030198|GO:0042340|GO:0006508|GO:0009405|GO:0
030246|GO:0007155|GO:0030203|GO:0043202|GO:0005201 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_128145_PI430048170 0.0692849614549456 0.6831891564997927.05052328256863
6.75754964433926 7.24396034741023 P P P 7.76699294779754 7.23102352675338
7.68813652118254 P P P LNCV6_128145_PI430048170 mRNA
CTCCACTCTATAAACTCAGACCTACTTTTTGAAGATAACTGCTTTTAACCTCTCCTTACANM_032985RefSeq chr20 +
18507543 18561406 SEC23B 10483 "Sec23 homolog B (S. cerevisiae), transcript variant 2"
GO:0006888|GO:0048471|GO:0030127|GO:0016020|GO:0000139|GO:0033116|GO:0005789|GO:0008270|GO:0016
192|GO:0006886|GO:0043231|GO:0012505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105229_PI430048170 0.7822022863493970.9676348228686245.48827044730768
5.60994856118858 5.3208463293771 P P P 5.74679143528823 5.42472836137998
5.37562247518693 P P P LNCV6_105229_PI430048170 mRNA
TTTGTAGAGCACAGTGCCCGCCTGTGCCAACCAGAGGGCATCCACATCTGTGATGGAACT NM_004563RefSeq chr14

+ 24094130 24104132 PCK2 5106 "phosphoenolpyruvate carboxykinase 2 (mitochondrial), transcript variant 1"
GO:0005515|GO:0005975|GO:0006094|GO:0006107|GO:0051384|GO:0044281|GO:0005525|GO:0046872|GO:0005739|GO:0004611|GO:0006090|GO:0004613|GO:0005759|GO:0006116|GO:0009405|GO:0006006|GO:0032024|GO:0071333|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133400_PI430048170 0.7872792734137670.78508293967764 1.92023002606871 2.5684375270139 1.30558964201074 A A A 0.9318815794151252.50886059347055 2.98649309522948 A P P
LNCV6_133400_PI430048170 mRNA
CTTTTCATCAAGGAGACGATCTCTTTATGTAAGACTTGAAAGTGTTTAGCTCTTTGCAAA NM_001042646 RefSeq
chr3 + 42091253 42225890 TRAK1 22906 "trafficking protein, kinesin binding 1, transcript variant 1"
GO:0005739|GO:0005515|GO:0005737|GO:0006493|GO:0006357|GO:0008333|GO:0005634|GO:0050811|GO:0006605|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145619_PI430048170 0.8374300284215260.9094132693926420.24535422593467 0.3027398597153841.44625570046009 A A A 0.4537344171259121.60967924863405 0.304310004506628A A A LNCV6_145619_PI430048170 mRNA
ATTCTTACAAATACAGTGACTGTGGCAAACTCCTGATGAGTTTAAGCATTAACAGACATC NM_024733RefSeq chr19
- 53163298 53193366 ZNF665 79788 zinc finger protein 665
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129821_PI430048170 0.3432302423801980.7617502138803841.45006406239581 0.4052294350614670.24301133099179 A A A 0.8454548571195631.47556155090087 1.20232065050634 A A A LNCV6_129821_PI430048170 mRNA
GGTTCATGTTTACATGCCTTTCGATAGCTGTTTGTGCATACTTAAAGATGATCAAAATGA NM_005824RefSeq chr7
+ 102912896 102945109 LRRC17 10234 "leucine rich repeat containing 17, transcript variant 2"
GO:0033687|GO:0045671|GO:0048539|GO:0005615|GO:0001649 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132888_PI430048170 0.3610048925020010.6831349243097260.469118418087371 0.4784477678864240.369673438892923A A A 1.6408614342776 0.5157580284383380.4945992532329 A A A LNCV6_132888_PI430048170 mRNA
TGAGGAGTGACACTGCCTCGGGAACCTCACTCTTGCCAACCTGTAATAAATATGAGTGCC NM_002471RefSeq chr14
- 23381989 23408277 MYH6 4624 "myosin, heavy chain 6, cardiac muscle, alpha"
GO:0005516|GO:0030018|GO:0055010|GO:0006200|GO:0008016|GO:0006941|GO:0060420|GO:0016459|GO:0030016|GO:0030898|GO:0030017|GO:0005829|GO:0007512|GO:0005737|GO:0000146|GO:0006936|GO:0043462|GO:0030239|GO:0005859|GO:0060070|GO:0016887|GO:0055009|GO:0001725|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135625_PI430048170 0.7035657768120710.9409577528806675.38928985564588 4.79205649647541 5.15509541731931 P P P 4.90878048996013 5.35092834104067 5.35758578439918 P P P LNCV6_135625_PI430048170 mRNA
GAGGCAGGGCCAATGGTTTCCCACAAAATGTAGCACAACGAAGGTCAGAATTCGTTTTTT NM_019088RefSeq chr19
- 39385629 39391195 PAF1 54623 "Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae), transcript variant 1"
GO:0005515|GO:0006378|GO:0033523|GO:0000993|GO:0000122|GO:0001711|GO:0006351|GO:0071222|GO:0045638|GO:0045944|GO:0003682|GO:0019827|GO:0032968|GO:0016593|GO:0016055|GO:0010390|GO:0031442 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143908_PI430048170 0.0761036212810196 1.40423571590432 8.020872369181 7.73016837658826 7.8360032115177 P P P 7.02731239800248 7.56785799162798 7.48141789094924 P P P LNCV6_143908_PI430048170 mRNA
AGCCGCAGTTTTTGGCTACAAACTGTCACAGTATACATTGGTAATAAAATATTTCCCCAA NM_052899RefSeq chr5
- 176595801 176610130 GPRIN1 114787 G protein regulated inducer of neurite outgrowth 1

GO:0051219|GO:0005886|GO:0031175|GO:0030426 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143768_PI430048170 0.5995236782606481.07715758324567 3.63242407243985
3.53339845045892 3.26813180412219 P P P 3.00668774729693 3.52514487378881
3.54305098386262 P P P LNCV6_143768_PI430048170 mRNA
ATATAAAACTTTTCTCAACGGAATAGCAGTGTCTGTGGTGCTGTTGACTCGATTGCTCCT NM_001080791 RefSeq
chr15 - 40552912 40565057 C15orf57 90416 "chromosome 15 open reading frame 57, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114098_PI430048170 0.2515873367629581.36405499044309 4.22044617589842
5.07829643117386 4.87748979302771 P P P 4.15571469737433 4.4010299012438
4.39457301833366 P P P LNCV6_114098_PI430048170 mRNA
GGAGTGGGAAGAAAACCTCAAAGTGGTTCATACTTGCCTGTAAAAAGTAAATGCATTTTA NM_001284350 RefSeq
chr7 - 47987148 48029119 SUN3 256979 "Sad1 and UNC84 domain containing 3, transcript variant 3"
GO:0034993|GO:0006998|GO:0090286|GO:0016021|GO:0005635 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_74519_PI430048170 0.00918556146826418 2.47685616240117 3.32433538607651
3.31884785303598 3.60188983337871 P P P 2.42432872391497 1.76136797415826
2.07619278833343 A A A LNCV6_74519_PI430048170 mRNA
GATCAAGAGTGCACCTTCTTTTTCAACTTCAAAGTGGCACAAACACTGTGCTTTCCATCT NM_004354RefSeq chr4
+ 77157203 77170060 CCNG2 901 cyclin G2
GO:0007067|GO:0005737|GO:0051726|GO:0000075|GO:0051301 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139108_PI430048170 0.4610847934663920.7763660755345890.283018664770563
0.3114719013015490.440488583592069A A A 0.3326817763519521.27810154633512
0.297579742304736A A A LNCV6_139108_PI430048170 mRNA
CATAATGGTCAATGATAATAGGAATTACATGGAGCCCAACAGAGAATATTTGCTCAATAC NM_002704RefSeq chr4
- 73986438 73988190 PPBP 5473 pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)
GO:0008009|GO:0070098|GO:0002523|GO:0030168|GO:0005576|GO:0045236|GO:0005615|GO:0002690|GO:0006
955|GO:0006954|GO:0007186|GO:0015758|GO:0060326|GO:0007596|GO:0042127|GO:0002576|GO:0032496|GO:0
051781|GO:0031093|GO:0008083|GO:0042742|GO:0005355 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_145020_PI430048170 0.00975402761399258 0.63377733976484810.0951877465011
9.76229892423584 9.78211146777248 P P P 10.6395565691273 10.5934572642521
10.3934961081936 P P P LNCV6_145020_PI430048170 mRNA
TTTCTGGACTGTTTGTATTGAAACAAAGTGGTGTCAAAATAAAGCCCCTGCAGGGCCTGG NM_032389RefSeq chr11
- 47164297 47177125 ARFGAP2 84364 "ADP-ribosylation factor GTPase activating protein 2, transcript
variant 1"
GO:0043547|GO:0008060|GO:0005737|GO:0005794|GO:0005886|GO:0000139|GO:0032312|GO:0005730|GO:0008
270|GO:0016192|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108794_PI430048170 0.9858652509104111.01105083177868 5.88258908992807
6.23350233918219 6.53767460578816 P P P 6.3317938179134 5.93382254685022
6.37475773067594 P P P LNCV6_108794_PI430048170 mRNA
ATTCTTATACCCCAAAAGTCATACAGTGTCAGAACAAAGGCTGGGATGGGTATGATGTAC NM_016127RefSeq chr8
- 30063011 30083208 SARAF 51669 "store-operated calcium entry-associated regulatory factor,
transcript variant 1" GO:0005515|GO:0030176|GO:0006816|GO:2001256 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_130526_PI430048170 0.0534934569812335 1.38169104362127 6.89977292309793
6.57527518867907 6.98598422657406 P P P 6.51519935441608 6.42329001776628
6.12703705442841 P P P LNCV6_130526_PI430048170 mRNA
TCAACCAAGTTGCTCCTCTTTTGTCTATCCTGTGGTTCCCAAGCAAGACTGCAATTGAAA NM_001085372 RefSeq

chr11 + 62671653 62673690 UQCC3 790955 ubiquinol-cytochrome c reductase complex assembly factor 3 GO:0005743|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132856_PI430048170 0.781678261380865 1.31405024126981 1.97079298871996 0.3189032108354650.344815603562886 A A A 0.7940509266620820.583424329163658 0.736746576435133 A A A LNCV6_132856_PI430048170 mRNA CTCCTCACTCCCTGCATTGGAGGGAGTGTCATTTTAAGGGACATTTTTATGACTTTTATG NM_000789RefSeq chr17 + 63477060 63498380 ACE1636 "angiotensin I converting enzyme, transcript variant 1" GO:0005515|GO:0002474|GO:0060047|GO:0007283|GO:0005764|GO:0005615|GO:0019229|GO:0003081|GO:0002019|GO:0006508|GO:0043171|GO:0051019|GO:0070062|GO:0031434|GO:0004175|GO:0042447|GO:0071838|GO:0008270|GO:0044267|GO:0008237|GO:0009897|GO:0060177|GO:0008238|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144862_PI430048170 0.0396059873994213 1.63995866335877 3.04070856150051 3.53878459263861 3.06092985625919 P P P 2.42419984351254 2.82721692940969 2.24147117652484 A P A LNCV6_144862_PI430048170 mRNA CACTCTCTTGTGTATATTCCTGTGCTATTAAATATATCAGGGCAGTGCATGTAAATCATC NM_001098627 RefSeq chr7 + 128940669 128950042 IRF5 3663 "interferon regulatory factor 5, transcript variant 3" GO:0005515|GO:0000975|GO:0032728|GO:0043065|GO:0003700|GO:0032727|GO:0019221|GO:0005634|GO:0032735|GO:0006351|GO:0005829|GO:0051607|GO:0005737|GO:0060337|GO:0045944|GO:0032494|GO:0032495|GO:0060333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126965_PI430048170 0.567872789040813 0.824243948933025 3.02998692864706 1.96625165753127 3.01484479777026 P A P 3.0145249663144 3.47168193340682 2.40106800440347 P P P LNCV6_126965_PI430048170 mRNA ATAAGAGCTTTATCAAGAACTATCCTGTGGTCTCCATCGAAGACCCCTTTGACCAGGATG NM_001976RefSeq chr17 + 4951088 4957131 ENO3 2027 "enolase 3 (beta, muscle), transcript variant 1" GO:0000287|GO:0046982|GO:0005886|GO:0005975|GO:0042493|GO:0007568|GO:0006094|GO:0044281|GO:0005615|GO:0042803|GO:0004634|GO:0006096|GO:0005829|GO:0005737|GO:0009405|GO:0006006|GO:0043403|GO:0000015|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136493_PI430048170 0.00016203419181661 4.06632864925689 11.7908226644245 11.786659385858 11.8588623296568 P P P 9.69192540009155 9.89080742773923 9.77665147645513 P P P LNCV6_136493_PI430048170 mRNA GGGAGTGACCAGAAGAAATGACGCAGAAGTGAAATGAACTTTTTATAAGCATTCTTTTAA NM_005218RefSeq chr8 - 6870575 6878007 DEFB1 1672 "defensin, beta 1" GO:0002526|GO:0005796|GO:0050830|GO:0005576|GO:0033574|GO:0005615|GO:0002227|GO:0009617|GO:0006955|GO:0006935|GO:0007186|GO:0045087|GO:0019731|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145559_PI430048170 0.1186102155906860.6565355308039919.02130829169625 8.34062961933286 8.16919821105836 P P P 9.26710474944864 9.34685730187836 8.83407790284346 P P P LNCV6_145559_PI430048170 mRNA CCCTGCCTCCCCAGGGCCTCTGCTCTCCTGGGAGACAAAGCAATAATAAAAGGAAGTGTT NM_001632RefSeq chr2 + 232378533 232382889 ALPP 250 "alkaline phosphatase, placental" GO:0000287|GO:0009986|GO:0005886|GO:0004035|GO:0016311|GO:0008270|GO:0031225|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145297_PI430048170 0.00367286180064368 1.7798630992706 5.33394413598288 5.34359661584708 5.17708122495929 P P P 4.45147170771917 4.46920103268891 4.44451788258891 P P P LNCV6_145297_PI430048170 mRNA TGTGCTTAGGTGCTTTAAAACTCAAAGGCTCTTTTCAGAGCCACTCAAGTCTCACATAAA NM_003518RefSeq chr6 - 26216200 26216644 HIST1H2BG 8339 "histone cluster 1, H2bg" GO:0046982|GO:0050830|GO:0019731|GO:0006334|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0005615|GO:0003677|GO:0070062|GO:0002227 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_142118_PI430048170 0.91281632652365 0.9967708184944540.505222258358985
0.3846378200984850.488989659457737A A A 0.4190357931212660.498222779386347
0.477370452429953A A A LNCV6_142118_PI430048170 mRNA
ACCAATTCTTTTTAAAGCATTCCATGTTCTTGTTCCTTGATGTGGTCATGTTATCACTTG NM_001130009 RefSeq chr2
+ 17754146 17785365 GEN1 348654 "GEN1 Holliday junction 5' flap endonuclease, transcript variant 2"
GO:0005813|GO:0071140|GO:0000724|GO:0071139|GO:0008821|GO:0005634|GO:0090267|GO:0010824|GO:0003
677|GO:0000737|GO:0046872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145724_PI430048170 0.6842803258877111.03196286881727 9.36324278363662
9.52642193469392 9.31838941870069 P P P 9.31086267569216 9.52582686810008
9.22690605267133 P P P LNCV6_145724_PI430048170 mRNA
GTGGTGGTGGCACATGGATGAATGAGTATTTAATAAAAGTTCCAAATTTCCACCAAAAAA NM_003427RefSeq chr6
+ 35259713 35295987 ZNF76 7629 "zinc finger protein 76, transcript variant 1"
GO:0006357|GO:0006359|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130106_PI430048170 0.2291323641032410.8304221229171350.339478231251793
0.3197500788596470.300401281181936A A A 0.4855017079695220.860829344876923
0.371257375221159A A A LNCV6_130106_PI430048170 mRNA
CCTGCTGGTTTGACGTGGAGCTATCCTGTGAAATAAAACAGCTTAACTTTTCTCAAAAAA NM_014850RefSeq chr3
- 8980590 9249685 SRGAP39901 "SLIT-ROBO Rho GTPase activating protein 3, transcript variant 1"
GO:0005515|GO:0051056|GO:0048365|GO:0030336|GO:0005737|GO:0007264|GO:0032855|GO:0030675|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97197_PI430048170 0.0340052242653369 0.5105067362828911.10676460617424
0.8471548215720251.66935949971935 A A A 1.8806607782093 2.23882399628021
2.47778861195704 A A P LNCV6_97197_PI430048170 mRNA
AATCCCGTAGACTCTGCAACAAGCCAATTCAGAGCTTGCCCAACATGGACAGCATTTTTA NM_001166415 RefSeq
chr3 - 185190623 185254098 EHHADH 1962 "enoyl-CoA, hydratase/3-hydroxyacyl CoA
dehydrogenase, transcript variant 2"
GO:0005739|GO:0050662|GO:0006635|GO:0004165|GO:0005102|GO:0003857|GO:0019899|GO:0006475|GO:0004
300|GO:0005829|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129672_PI430048170 0.6464491320438171.1968782243153 0.475641441365649
1.35037465994453 0.252633766602137A A A 0.6316284788792880.476130890027466
0.430017051305389A A A LNCV6_129672_PI430048170 mRNA
GGCGCCCTTAAGGAAAAACTTGAAGCAGTCATTGCAGAATTAAAGTAAACATGTATTCTG NM_001098529 RefSeq
chr18 + 9885725 9888159 TXNDC2 84203 "thioredoxin domain containing 2 (spermatozoa),
transcript variant 2"
GO:0031514|GO:0045735|GO:0006662|GO:0005730|GO:0015035|GO:0003756|GO:0005634|GO:0007275|GO:0007
283|GO:0001520|GO:0030154|GO:0005737|GO:0006457|GO:0004791|GO:0045454|GO:0005654|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128877_PI430048170 0.0391124952351814 0.4502909593214287.37651541060601
7.25067787497098 7.26852749725316 P P P 7.94469644579195 8.59191904095454
8.70534612365914 P P P LNCV6_128877_PI430048170 mRNA
TCATTACCCTGTATTTTTGTGCATACTGAATTGTATATCACCGGGTAAAACTGTTCAGAT NM_203434RefSeq chr9
- 129175551 129178261 IER5L 389792 immediate early response 5-like NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129761_PI430048170 0.1972995236662030.7873894549137218.66895315915325
8.22702779596629 7.99059215620746 P P P 8.7244548480736 8.7160441580608
8.55827024929533 P P P LNCV6_129761_PI430048170 mRNA
CACCCGAGGATCCCTACCCCCTGGCCCCACAATAAACATGATCTGAAGCAGCTCAAAAAA NM_013271RefSeq chrX
- 48831091 48835638 PCSK1N27344 proprotein convertase subtilisin/kexin type 1 inhibitor

GO:0010951|GO:0005802|GO:0016486|GO:0004866|GO:0007218|GO:0004867|GO:0009409|GO:0005102|GO:0030141|GO:0005615|GO:0002021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135665_PI430048170 0.0250977647264164 0.77968613679087810.164322776657 10.1164290040872 10.0441837337621 P P P 10.3175834996904 10.5561715265021 10.5195543536612 P P P LNCV6_135665_PI430048170 mRNA
GAGCCTGCCTTGTGTTCCTTTTTTGACTTGTGACATTTTTCAAACACATAATTAAAAGGA NM_018019RefSeq chr17 + 17476985 17493220 MED9 55090 mediator complex subunit 9
GO:0005515|GO:0001104|GO:0006366|GO:0006357|GO:0016592 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132950_PI430048170 0.000674574635793686 0.2306302631517494.69344002849158 4.45727744459652 4.91114835206012 P P P 6.58176682590102 6.69260387872699 7.11557327829062 P P P LNCV6_132950_PI430048170 mRNA
GGGGACTTACCTCTGTAGCATTGTGAAAATAAACTTTGATTAAGCTGATTTGAAAGGAAA NM_016275RefSeq chr3 + 150603278 150630447 SELT 51714 selenoprotein T GO:0008430|GO:0001514|GO:0045454 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143741_PI430048170 0.178486374539339 1.0869875785912 0.476592524265963 0.2904696028833290.4534776318349 A A A 0.3054150810278360.272268953977468 0.288698586655078A A A LNCV6_143741_PI430048170 mRNA
TTCTCAAAGCCCCAACATATAAGATCTGTGCAGAATAAATGCCAACAACTGGTCATACCG NM_001013630 RefSeq chr1 + 12644546 12667086 AADACL4 NA arylacetamide deacetylase-like 4NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129616_PI430048170 0.2702220938947080.4504606602116940.425937617269582 0.4481838292549730.326091470371521A A A 0.9532170552383370.481659053635552 2.44930499009662 A A P LNCV6_129616_PI430048170 mRNA
TAGCATAGGGGACTGCAAATGGTGTTCCGCAAAGCAAATCCTGTTTTTGACCATGAACTA NM_001039RefSeq chr16 + 23182718 23216879 SCNN1G 6340 "sodium channel, non voltage gated 1 gamma subunit"
GO:0005515|GO:0007588|GO:0005886|GO:0005272|GO:0050699|GO:0034706|GO:0055078|GO:0055085|GO:0015280|GO:0016324|GO:0034220|GO:0050909|GO:0050891|GO:0005887|GO:0035725|GO:0006814|GO:0050896|GO:0009897|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140304_PI430048170 0.012024091079485 1.36691354711618 9.57941723698905 9.66825778959273 9.49838764310985 P P P 9.26627514426824 9.12214124655767 8.99731103969228 P P P LNCV6_140304_PI430048170 mRNA
CTTTGACCTTCCTGTGAATAAGTGTTGACTCCAATTTCGGCTAAAGTTTATAGAAATTCT NM_032840RefSeq chr12 - 53064315 53079420 SPRYD3 84926 SPRY domain containing 3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102227_PI430048170 0.4593417188573961.18889610923522 3.25227919888435 3.25999538615505 2.57226921656661 A P A 3.08540930232413 2.4795542860733 2.80937331689377 P A P LNCV6_102227_PI430048170 mRNA
AAGATATGCAAGCAGAAGAGGGGCCTCCGGAGCCTGGGCGAGAAGATGAAGCTCCTGCCG NM_007148RefSeq chr17 + 19411177 19417276 RNF112 7732 ring finger protein 112
GO:0005737|GO:0045666|GO:0008152|GO:0003924|GO:0008270|GO:0005634|GO:0045687|GO:0016021|GO:0005525|GO:0071158 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135779_PI430048170 0.000373115475485267 2.7816062843295 4.85562374637316 5.01822651900296 4.84121745121614 P P P 3.58902583442983 3.40134305022876 3.28754107415771 P P P LNCV6_135779_PI430048170 mRNA
AAGGTGCATTGTCTTCCAGTATCTACAGCTTCAGACTTGAGCTAAGTAAATGCTTCAAAG NM_033467RefSeq chr1_KI270762v1_alt - 141831 184229 MMEL1 79258 membrane metallo-endopeptidase-like 1
GO:0005794|GO:0005783|GO:0006508|GO:0008270|GO:0016021|GO:0004222|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_143029_PI430048170 0.3944703780626330.9754633779348290.356809569302948
0.4022988732780390.33115082545048 A A A 0.4579089907471950.357973575922058
0.380889739047671 A A A LNCV6_143029_PI430048170 mRNA
TGTTCTTAATGCTGTGGTCAAACCATAGCACAAAATCATTAAAAATAATCAGCGGCATAC NM_001003674 RefSeq
chr18 + 13611463 13652754 LDLRAD4 753 "low density lipoprotein receptor class A domain
containing 4, transcript variant c1"
GO:0005515|GO:0030336|GO:0010991|GO:0031901|GO:0070412|GO:0016021|GO:0010719|GO:0060394|GO:0030
512 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142933_PI430048170 0.1831091236767010.7052537552643097.04098025911897
6.69733439922776 6.14333446852752 P P P 7.43386665060619 7.22232125091939 6.8055983594813
P P P LNCV6_142933_PI430048170 mRNA
CACTCCAGCCCTGTCCCCTGAAAAACTGATCAAAAATAAACTAGTTTCCAGTGGAAAAAA NM_000805 RefSeq chr17
+ 41712325 41715969 GAST 2520 gastrin
GO:0005515|GO:0007165|GO:0007186|GO:0005179|GO:0005576 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131200_PI430048170 0.36806594884553 1.56464145308279 0.431151878758107
1.59058285842141 1.99076170175338 A A A 0.4790330481861781.37835014334886
0.414950934979436 A A A LNCV6_131200_PI430048170 mRNA
GGAATGGTTGCCCTAAAAAAGGAAAGAGAGATAAAATCATCATGCTATGTTTCTTTGCTT NM_001206981 RefSeq
chr4 + 75556047 75565893 C4orf26 152816 "chromosome 4 open reading frame 26, transcript variant
1" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139691_PI430048170 0.000243101961956055 1.53178265011035 12.24244605425
12.3055701188439 12.1990860286199 P P P 11.6603568182569 11.6787698665732
11.5616019589329 P P P LNCV6_139691_PI430048170 mRNA
TTCGTGCCTTACTGAGTCTCTAAGACTTTTTCTAATAAACAAGCCAGTGCGTGTACCATG NM_001199039 RefSeq
chr1 + 31413812 31434680 SERINC2 347735 "serine incorporator 2, transcript variant 5"
GO:0006665|GO:0015194|GO:0015825|GO:0051347|GO:0016021|GO:0006658|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135548_PI430048170 0.7453243111913960.9732073967464351 0.1119447308987
10.0674612289648 10.2658487183729 P P P 10.063382834059 10.1422583621179 10.349426652226
P P P LNCV6_135548_PI430048170 mRNA
GATTTTTCCTGGTATACTGTTTCTTGGCTGACACTACTGGTCAAGTAAGAAATTTGTAAA NM_016500 RefSeq chrX
+ 76172935 76178198 PBDC1 51260 "polysaccharide biosynthesis domain containing 1, transcript
variant 1" GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115258_PI430048170 0.9125643844760941.02624269742148 5.09527281028197
5.40659426438755 4.82989961028125 P P P 4.97886494836479 5.05784497363141
5.22933303179168 P P P LNCV6_115258_PI430048170 mRNA
AAGAGTTCCACCAGCGATCCAACGTCACACTCACTCTACGCAACCTTAAAGGGTGCTGTC NM_014339 RefSeq chr22
+ 17084958 17115694 IL17RA 23765 "interleukin 17 receptor A, transcript variant 1"
GO:1900017|GO:0005515|GO:0030368|GO:0072537|GO:0005887|GO:0019221|GO:0032747|GO:0005576|GO:0007
166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136648_PI430048170 0.0215611794179277 0.73654115584661 8.16825725755208
8.06509484175221 8.36331981670813 P P P 8.55304435432707 8.56248221735629
8.80614830738606 P P P LNCV6_136648_PI430048170 mRNA
CACCTTTCCTCCACACACCTTCATTTTGATGTTCGGGTTTTTGTGTTAAGTTAATCTGTA NM_004655 RefSeq chr17 -
65528564 65561622 AXIN2 8313 axin 2
GO:0005515|GO:0005881|GO:0008285|GO:0005886|GO:0008013|GO:0008283|GO:0003413|GO:0090263|GO:0030
877|GO:0003139|GO:0010718|GO:0038032|GO:0005634|GO:0030282|GO:0090244|GO:0035414|GO:0009950|GO:0
005829|GO:0005737|GO:0015630|GO:0042476|GO:0048255|GO:0090090|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_66112_PI430048170 0.0465882476641334 1.33231512640339 12.6398755900529
13.0042670569831 12.9340068244904 P P P 12.3440442466593 12.4492282339204
12.5602638427586 P P P LNCV6_66112_PI430048170 mRNA
TTCCTTGTGCTCAAATGGCCAAAGCTGTTCACGTCTGTGCTCAACCATCTGCTTCAAATT NM_032827 RefSeq chr2
+ 85753785 85791383 ATOH8 84913 atonal homolog 8 (Drosophila)
GO:0006355|GO:0046983|GO:0005634|GO:0003677|GO:0030154|GO:0006351|GO:0007399 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138862_PI430048170 0.113281973814395 1.56349580276299 1.22537612477497
1.09662720406403 0.491560167439941 A A A 0.324098679042246 0.300158134022109
0.355410385347275 A A A LNCV6_138862_PI430048170 mRNA
GAGGGCAGGACCCAGCATAATGATTATATGGCTGAATAAAGTTGCACTGTGACTGGGAAA NM_001805 RefSeq chr14
- 23117305 23119611 CEBPE 1053 "CCAAT/enhancer binding protein (C/EBP), epsilon"
GO:0006909|GO:0046982|GO:0006952|GO:0042089|GO:0000978|GO:0006351|GO:0042803|GO:0001077|GO:0071
222|GO:0045944|GO:0030225|GO:0005654|GO:0042742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127004_PI430048170 0.794265747053599 0.974579090706968 8.67918543120799
8.65986172209125 8.72964951786682 P P P 8.90900909980382 8.56442097824872
8.68624009488895 P P P LNCV6_127004_PI430048170 mRNA
TTTCACCAAGGAAATATTGAGAGAGAAGTCGGCCAGGTAGGATGAACACAGGCAATGACT NM_000071 RefSeq
chr21 - 43053190 43075930 CBS 875 "cystathionine-beta-synthase, transcript variant 1"
GO:0019343|GO:0005515|GO:0070814|GO:0019346|GO:0006535|GO:0005634|GO:0044281|GO:0042803|GO:0046
872|GO:0050667|GO:0005829|GO:0042802|GO:0043231|GO:0072341|GO:0034641|GO:0004122|GO:0031625|GO:0
005730|GO:0000096|GO:0043418|GO:0030170|GO:0006563|GO:0019899|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130339_PI430048170 0.329860157540287 1.02025614115536 0.32437870934191
0.24677218624221 0.286107423241569 A A A 0.258771562661573 0.253070326723768
0.259656933500126 A A A LNCV6_130339_PI430048170 mRNA
GTCCACTAACCACGACAAGGTTGTGTCAGCCTTCTATACTATGTTCACCCCTTTACTAAA NM_001005522 RefSeq
chr1 + 247921017 247921956 OR2T8 343172 "olfactory receptor, family 2, subfamily T, member 8"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144591_PI430048170 0.00111962675797996 0.38453104043634 7.48404613336016
7.17209759299558 7.50411981114365 P P P 8.60673344477323 8.68067703972788
9.00153106455267 P P P LNCV6_144591_PI430048170 mRNA
GATGCATTCTGGCATTTTGTAAGCTGCTCTGACTAGCAATATATAGATTCATTTAATGTG NM_006624 RefSeq chr10
+ 134464 254637 ZMYND11 10771 "zinc finger, MYND-type containing 11, transcript variant 1"
GO:0005515|GO:2001237|GO:0005694|GO:0008283|GO:0003714|GO:0005634|GO:0035064|GO:0000122|GO:0003
677|GO:0006351|GO:0007049|GO:0046329|GO:0016032|GO:0005654|GO:0008270|GO:0034243|GO:0043124|GO:0
016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128993_PI430048170 0.219369799865606 0.975369108687797 0.296801459511778
0.327748481037929 0.348238671282002 A A A 0.39364802720279 0.326926251976003
0.359846480408439 A A A LNCV6_128993_PI430048170 mRNA
ACTCCTCATGAATTCCAGGAAATATGGAGGAAAACACATTTCACTGTACATGACTTTCAA NM_152279 RefSeq chr19
- 37181578 37210549 ZNF585B 92285 zinc finger protein 585B
GO:0006355|GO:0003700|GO:0005634|GO:0003676|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_77244_PI430048170 0.413863980829057 0.968335396564152 0.303196266475069 0.416778682740736
0.318477719980041 A A A 0.465342064273453 0.356593962281634 0.355654920528431 A A A
LNCV6_77244_PI430048170 mRNA

TTTTGAAAACATTGCCAAACCAGTTGCTGGGAGTGTCCTGGCAGGTTACAATGGTACCAT NM_145027RefSeq chr6
- 39335099 39725405 KIF6 221458 "kinesin family member 6, transcript variant 1"
GO:0008017|GO:0005515|GO:0005871|GO:0005737|GO:0008152|GO:0005874|GO:0003777|GO:0001673|GO:0016
887|GO:0005524|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131005_PI430048170 0.00875328432402515 1.65846652286522 7.70298403808348
8.07717426700721 7.88607677172903 P P P 7.28032614125285 7.13605617515129
7.07690358095434 P P P LNCV6_131005_PI430048170 mRNA
GTGTCCGGGAGCCAGGGAAGACTGGAAATGCTGCCGCCTTCTGCAATTTATTTATTTTTT NM_001365RefSeq chr17
- 7189890 7220050 DLG4 1742 "discs, large homolog 4 (Drosophila), transcript variant 1"
GO:0005515|GO:0030054|GO:0008328|GO:2000310|GO:0045202|GO:0031697|GO:0032403|GO:0007411|GO:0045
211|GO:0048169|GO:0050885|GO:0060997|GO:0007612|GO:0035641|GO:2000821|GO:2000463|GO:0044224|GO:0
019903|GO:0014069|GO:0030165|GO:0071625|GO:0060076|GO:0031234|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137551_PI430048170 0.1002291129301570.5561481733663512.95658027798562
2.18796142334878 1.8323748041198 A A A 3.6080597137789 3.2163302763097
2.82106966862235 P P P LNCV6_137551_PI430048170 mRNA
ACCACCTGTATAACATTTCCTTCCACTTTATTGTGAGCTGCCCAGATTTTATTCTTGAAT NM_005271RefSeq chr10 -
87050201 87095019 GLUD1 2746 glutamate dehydrogenase 1
GO:0005515|GO:0006537|GO:0006538|GO:0070728|GO:0008652|GO:0070403|GO:0044281|GO:0005525|GO:0005
524|GO:0042802|GO:0004352|GO:0005739|GO:0034641|GO:0004353|GO:0005737|GO:0072350|GO:0043531|GO:0
021762|GO:0005759|GO:0032024|GO:0055114|GO:0006541 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_144102_PI430048170 0.0169087092786084 0.4620439477460489.26520077375523
9.44811448095502 9.56305120080838 P P P 10.2892744916368 10.3635822276526
10.9006984082766 P P P LNCV6_144102_PI430048170 mRNA
CCTTGGCTGATAAAACCTCTATAGTGAATACTCACATCTTTACTTCACTCACTATCAATA NM_017812RefSeq chr7
- 132784861 133082068 CHCHD3 54927 coiled-coil-helix-coiled-coil-helix domain containing 3
GO:0005515|GO:0019902|GO:0005743|GO:0005634|GO:0000122|GO:0001227|GO:0006351|GO:0005739|GO:0005
737|GO:0032947|GO:0008053|GO:0007007|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140113_PI430048170 0.0052090448141805 0.5846162539575451 0.6701380839921
10.8661386014201 10.6557040806187 P P P 11.5213673324078 11.5285013207305 11.474553413612
P P P LNCV6_140113_PI430048170 mRNA
CGGGAAGAGACCCCAATCAGATTTTTCAAATTAAAGCCAGTCCTGGGAAATCTCAAAAAA NM_013376RefSeq chr19
- 40422500 40426025 SERTAD1 29950 SERTA domain containing 1
GO:0005515|GO:0008284|GO:0000079|GO:0045893|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141367_PI430048170 0.2620400990639271.72191537588498 0.6185432968116731.8630080613755
0.571981737671278A A A 0.2830267077948440.3996775207945690.41311942409648 A A A
LNCV6_141367_PI430048170 mRNA
CCAGCAGGAAACTGTAACTGCTATGTCTTTAGGAAAATGTAGAAGAAAGAACATTATTGT NM_024843RefSeq chr2
+ 171522355 171558133 CYBRD179901 "cytochrome b reductase 1, transcript variant 1"
GO:0006879|GO:0005886|GO:0000293|GO:0010039|GO:0016722|GO:0031526|GO:0016021|GO:0055085|GO:0046
872|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135462_PI430048170 0.1745436386478471.52402563605348 1.32275894412128
2.03277188713297 1.83698758556556 A A A 1.71584520671286 0.723700967337828
0.79424713481474 A A A LNCV6_135462_PI430048170 mRNA
ATTTATCGTCCATACCATTACTTCTTGTGAACAGTAACATGTCACTCCTCCTGGCAGGAA NM_001013615 RefSeq
chr1 + 46203333 46221256 LURAP1 541468 leucine rich adaptor protein 1
GO:0005737|GO:0042641|GO:0016477|GO:0031032|GO:0001819|GO:0043123 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_143959_PI430048170 0.000587715145964668 1.70457946495121 13.177216086617
13.3478416174073 13.2604268422821 P P P 12.6065464446112 12.4333389727352
12.4354628260606 P P P LNCV6_143959_PI430048170 mRNA
TGCTAAGATGGGAGGGCTGTTCTTAAATCACTCGTTCTTGAAGCTGCCACCTGGAAAAAA NM_181462 RefSeq chr1
- 228106678 228109312 MRPL55 128308 "mitochondrial ribosomal protein L55, transcript variant 4"
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0006412|GO:0005
762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132190_PI430048170 0.0140370453044742.96595009213657 2.21179969623939
1.62952161221084 2.57196726112901 A A A 0.2717854483776630.78465054827523
0.748423590767356 A A A LNCV6_132190_PI430048170 mRNA
AAAGAGAACCATCCAGAAAACGGTGCCTATGGAGATTTGAAAAGGGGGCGATAGTGACTT NM_013941 RefSeq
chr6_GL000254v2_alt + 705307 706346 OR10C1 442194 "olfactory receptor, family 10, subfamily C, member
1 (gene/pseudogene)" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_135556_PI430048170 0.00220157979529203 0.2901438888222314.23374595098534
3.90492960270191 4.56571495864803 P P P 5.7227222531364 6.105142323984
6.25636888995334 P P P LNCV6_135556_PI430048170 mRNA
CTTTCTAAAATGAATGTGAATGCCATCTTTTATGACTGCAACTTGCCTTTTCCATTACAG NM_173694 RefSeq chrX
- 139726345 139832288 ATP11C 286410 "ATPase, class VI, type 11C, transcript variant 1"
GO:0005515|GO:0000287|GO:0005886|GO:0005783|GO:0045579|GO:0005765|GO:0055085|GO:0005524|GO:0045
332|GO:0034220|GO:0004012|GO:0008152|GO:0005789|GO:0002329|GO:0016021|GO:0055037 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129586_PI430048170 0.00851939393142261 2.67447977242259 8.05228265333194
8.11255184234698 8.1594724386721 P P P 6.39454575258172 6.90623193513968
6.72205861508457 P P P LNCV6_129586_PI430048170 mRNA
TCCGCAGTGCGGATAAAAATTGGACTCGAATAAAACCCTTGGTGCCCGGATGGTAAAAAA NM_001291831 RefSeq
chr7 + 76201892 76287292 SRRM3 222183 "serine/arginine repetitive matrix 3, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132415_PI430048170 0.159202293486825 1.38857069935983 9.53367433496192
9.47255031938508 9.66573328466735 P P P 9.52278113439431 8.79919531630785
8.81139738680938 P P P LNCV6_132415_PI430048170 mRNA
GGGCTTTTGTTATTGTTGTTGGATATTTTTGTTTCCCATAAAAGCACATCATTTCAACCC NM_001301015 RefSeq chr5
+ 149141482 149260438 ABLIM3 22885 "actin binding LIM protein family, member 3, transcript variant 1"
GO:0042384|GO:0005737|GO:0001725|GO:0030036|GO:0007411|GO:0045944|GO:0030032|GO:0008270|GO:0003
779|GO:0030027|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137171_PI430048170 0.546131145535677 0.910432325247244 8.10348347705161
7.56149773016979 7.4322988557452 P P P 8.07257702605209 7.75176474219357
7.74519698774459 P P P LNCV6_137171_PI430048170 mRNA
ACAGGACTCGGCTTCCTCTCCTCAAATGAATAAAGGCCTCCTACCTCAACTCCCAAAAAA NM_022819 RefSeq chr1
+ 20139329 20150386 PLA2G2F 64600 "phospholipase A2, group IIF"
GO:0036149|GO:0005509|GO:0036148|GO:0005576|GO:0044281|GO:0005829|GO:0016042|GO:0008150|GO:0036
150|GO:0004623|GO:0006644|GO:0006654|GO:0036151|GO:0046474|GO:0036152 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_105696_PI430048170 0.374165155930348 0.840859877743606 3.04511962708313
3.92572287550383 3.38005965502585 A P P 3.8900724319393 3.63109950830659
3.70653570961573 P P P LNCV6_105696_PI430048170 mRNA
CAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTTGAGTTTGACCGGCTGAGGGCCTTCCA NM_001297652 RefSeq
chr6_GL000251v2_alt + 2362381 2379927 DDR1 780 "discoidin domain receptor tyrosine kinase 1,

transcript variant 7"
GO:0005515|GO:0044319|GO:0008285|GO:0005886|GO:0005518|GO:0005615|GO:0001558|GO:0046872|GO:0010
715|GO:0043583|GO:0046777|GO:0030198|GO:0007155|GO:0038083|GO:0070062|GO:0007566|GO:0014909|GO:0
038063|GO:0005524|GO:0038062|GO:0043235|GO:0061302|GO:0007595|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139421_PI430048170 0.0508176102846403 1.2370670486042 6.22248870513622
6.41270837274942 6.4728395750248 P P P 6.04458449882394 6.05481346531929
6.09895918167872 P P P LNCV6_139421_PI430048170 mRNA
TTTGAAACTTAGGTGCAATGTCCCCTGGAAAAAGCTAAAGAAATGTATATGTTCAATGAC NM_020700RefSeq chr12
- 62643983 62934885 PPM1H 57460 "protein phosphatase, Mg2+/Mn2+ dependent, 1H"
GO:0005737|GO:0016311|GO:0005634|GO:0004721 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136894_PI430048170 0.439750033891963 1.07120209636932 12.3855061756035
12.3769753953257 12.488767164726 P P P 12.1588923934001 12.2461663252287
12.5253450290623 P P P LNCV6_136894_PI430048170 mRNA
TCAGACTTGGGATGGGACGCTGATATAATAGGGTAGAAAGAAGTAACACGAAGAAGTGGT NM_006404RefSeq
chr20 + 35171936 35177362 PROCR 10544 "protein C receptor, endothelial"
GO:0005515|GO:0005813|GO:0005886|GO:0009986|GO:0005576|GO:0050900|GO:0006955|GO:0050819|GO:0005
887|GO:0007596|GO:0019882|GO:0004872|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144635_PI430048170 0.0752750539868562 0.913283426782269 8.57853484783779
8.7179477453005 8.64783614004643 P P P 8.84039446502585 8.71224273228036
8.78478913915707 P P P LNCV6_144635_PI430048170 mRNA
GGGATCCATGAACCAGGCAGGTACCTTTTTTGTTTTTGTTTTGTTTTGTTTCTTTTCTGT NM_001003722 RefSeq chr9
+ 128504691 128542301 GLE1 2733 "GLE1 RNA export mediator, transcript variant 1"
GO:0005515|GO:0005737|GO:0006406|GO:0016020|GO:0005886|GO:0016973|GO:0005643|GO:0015031|GO:0005
615|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142523_PI430048170 0.00696622937505028 1.43856100456201 12.5007649636406
12.4033276895685 12.3104756055112 P P P 11.7482998594825 12.0161423729687
11.8700320084871 P P P LNCV6_142523_PI430048170 mRNA
AATGACGCCTTTATGCAAGTTGTAAGGAGTTGAACAGTAAAGAGGAAGTTTTGCACACCC NM_001286440 RefSeq
chr16 + 397741 400754 NME4 4833 "NME/NM23 nucleoside diphosphate kinase 4, transcript variant 7"
GO:0005515|GO:0006241|GO:0015949|GO:0005743|GO:0004550|GO:0055086|GO:0042981|GO:0044281|GO:0009
142|GO:0006220|GO:0032403|GO:0005524|GO:0046872|GO:0005829|GO:0005739|GO:0006165|GO:0006228|GO:0
005758|GO:0006183|GO:0009116|GO:0006163 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57089_PI430048170 0.0168299064399069 0.939245747125529 0.367697778575352
0.337227049299922 0.323458155803522 A A A 0.463812850740203 0.43226692560083
0.40330026669968 A A A LNCV6_57089_PI430048170 mRNA
CGGGAGTGTTCTTTCAAAGGTGTCTTTACCTTAGACACTCAATAAAATGGTAACACAGTG NM_001042376 RefSeq
chr11 - 2146622 2161209 INS-IGF2 NA "INS-IGF2 readthrough, transcript variant 2" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_131568_PI430048170 0.419779471039397 1.33397043173123 0.33307494484875
1.30446635845782 0.281231488097349 A A A 0.254972907319259 0.274814019477919
0.382628891024601 A A A LNCV6_131568_PI430048170 mRNA
GTCTTTAACCTATGTGAAGCCACCTTTGTAATACTGCCTTAAGTAAAGATCCAGTATTAT NM_001144874 RefSeq
chr11 + 125833315 125840072 PATE4 NA prostate and testis expressed 4 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_63008_PI430048170 0.00339292414866607 0.450158150879551 6.0921920715988
5.61152371378444 5.83681193066591 P P P 6.88159698120935 7.22416266161875
6.90328193336069 P P P LNCV6_63008_PI430048170 mRNA

ACAGTGATGAGCAGTTTGTTCCTGATTTCCATTCAGAAAACCTAGCTTTCCACAGCCCCA NM_001079675 RefSeq chr17 - 43527842 43546432 ETV4 2118 "ets variant 4, transcript variant 2" GO:0005515|GO:0006357|GO:0006366|GO:0060762|GO:0000981|GO:0005730|GO:0000978|GO:0030154|GO:0048863|GO:0001077|GO:0008045|GO:0045944|GO:0033600|GO:0060444 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139921_PI430048170 0.000161221142447721 0.5370367888957189.23415603432914 9.2130705117987 9.21056899200052 P P P 10.1065504217669 10.0840231939681 10.157086734103 P P P LNCV6_139921_PI430048170 mRNA
GCAATAAGAACATAGATCCTAAAGGATCCTCTGGAAGCTGTATTTCTTGAATTAGAATTC NM_001002762 RefSeq chr10 - 72332829 72355149 DNAJB12 54788 "DnaJ (Hsp40) homolog, subfamily B, member 12, transcript variant 1" GO:0016020|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143551_PI430048170 0.9064208995828010.9755356787795652.27564389850754 1.24657124900775 0.542931232927207A A A 1.02720006410542 2.27420057220469 1.0100247620498 A A A LNCV6_143551_PI430048170 mRNA
CCTGCTGTGTCCGTGGTGCTGTTGTATTGGTCACTAACGGAATAAAGAGTTAATATCTCA NM_001080511 RefSeq chr7 + 139523927 139544985 CLEC2L 154790 "C-type lectin domain family 2, member L" GO:0030246|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141821_PI430048170 0.0685224818743715 1.32450000547349 8.52700261112554 8.54552183241749 8.29528106722083 P P P 8.29336335642898 7.99082442216585 7.84349367396689 P P P LNCV6_141821_PI430048170 mRNA
ACAACATTTATCATAATTTGTCATAACCACTGCTGAGTGGCCTTGAGGACGAACCCCGCA NM_016035 RefSeq chr9 + 128322507 128334072 COQ4 51117 coenzyme Q4 GO:0005739|GO:0006744|GO:0005743 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139882_PI430048170 0.1942072954738130.6972059641209440.351353199619065 0.3497625774105330.405215817467319A A A 0.3689651641460081.20904020179568 0.96625781102319 A A A LNCV6_139882_PI430048170 mRNA
CCCAATGTCACCGCACACCAGGCAGTGGGGACACGGCAGTAAGCACAAGAAAGATTTTTT NM_032753 RefSeq chr19 - 3769090 3772221 RAX2 84839 retina and anterior neural fold homeobox 2 GO:0043565|GO:0006355|GO:0005634|GO:0007601|GO:0050896|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138387_PI430048170 0.1986797561190080.8426664914175021 1.236577622154 10.8478427040201 10.7882561177907 P P P 11.1429115929086 11.3115307403386 11.1961763856898 P P P LNCV6_138387_PI430048170 mRNA
CTCTAACACTTCCCTCCCCTGTCCCCAACATGCCCTGTAATAAAATTAGAGAAGACTAAC NM_020451 RefSeq chr1 + 25800175 25818222 SEPN1 57190 "selenoprotein N, 1, transcript variant 1" GO:0005515|GO:0008150|GO:0003674|GO:0005509|GO:0005789 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70843_PI430048170 0.291154958963251 1.0353167580143 0.5114941839859240.599475227735047 0.484551670290692A A A 0.4781626338130930.4800294798577220.489605272970296A A A LNCV6_70843_PI430048170 mRNA
TTGGAATTTGCAAGAAGAAGTGCAAACCTGAAGAGATGCATACAAAGACTACAAGAATTT NM_030931 RefSeq chr20 + 142552 145751 DEFB126 81623 "defensin, beta 126" GO:0009986|GO:0030112|GO:0045087|GO:0005576|GO:0042742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139116_PI430048170 0.9746189659300040.9991434240292380.501914657204106 0.5233356233603870.409599302830084A A A 0.5360583725213660.449819121905314 0.453537069623874A A A LNCV6_139116_PI430048170 mRNA
CGCCTTAAGTGTTTCAATTGTCCTTTGTAGAAAAGCCAGATAAATGAGTTCACTTTGAAT NM_020949 RefSeq chr3 - 170459553 170586074 SLC7A14 57709 "solute carrier family 7, member 14"

GO:0015171|GO:0010923|GO:0016021|GO:0005765|GO:0003333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137226_PI430048170 0.5958076084873630.9345405189297570.434475043651883
0.2847178195870940.336600945798859A A A 0.2838500208850150.323614926907934
0.706555895713659A A A LNCV6_137226_PI430048170 mRNA
ACTAAGGAACAACGATGTGAAAAATGCCATGAGGAAGCTGTTTAGGGTCAAGAGGAGCTT NM_001004725
RefSeq chr11 + 48306222 48307152 OR4S1 256148 "olfactory receptor, family 4, subfamily S, member
1" GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134910_PI430048170 0.4666608785037581.72838967104788 2.94986265369439
0.9322821962619971.2941956824093 A A A 1.6824888005842 0.397341152542641
1.30251471187843 A A A LNCV6_134910_PI430048170 mRNA
TAAAGAGTCAATAAATAGAAACACCAGATGACTGCATTGGTGGCCACAGTGGCCTCCTGT NM_014786RefSeq chr11
+ 73308617 73369380 ARHGEF17 9828 Rho guanine nucleotide exchange factor (GEF) 17
GO:0043547|GO:0005085|GO:0051056|GO:0048011|GO:0043065|GO:0030036|GO:0032321|GO:0007264|GO:0005
089|GO:0097190|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130971_PI430048170 0.3255519639451180.6800555572863520.587799414379144
2.63966884239526 1.21240695518978 A A A 2.69707338951393 1.96547647688603
2.13454690600378 A A A LNCV6_130971_PI430048170 mRNA
TCAGTTGCCCTGGCGGCTGTAACCTATATGCCCCAGTGGGGGATCACGCACTTGAACTCC NM_080622RefSeq chr20
+ 63861212 63862988 ABHD16B 140701 abhydrolase domain containing 16B GO:0016787|GO:0008152
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128398_PI430048170 0.7578747501227171.08580456899889 3.38601736091277
2.57317959270209 3.30554484613604 P A P 3.43958067604595 2.80254755586161 2.6754529916537
P P P LNCV6_128398_PI430048170 mRNA
ACTACTACAGCGGGTCCCCATTGCTAGGTAGAATATCTTTTATTCTGCTCCTTCCCTAAC NM_213656RefSeq
chr17_JH159146v1_alt - 107811 116287 KRT39 NA "keratin 39, type I" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_98656_PI430048170 0.7167055101572980.8880435519930543.62144072945293 3.66430400943092
3.23185336349504 P P P 4.10372548192255 3.1094090106315 3.68838460467533 P P P
LNCV6_98656_PI430048170 mRNA
AGCAGTAGCATTTCTTCCTTGAAAGATGAGTTTACTCAAAGAATTGCAGAAGCAGAAAAG NM_007114RefSeq chr3
- 69019826 69052333 TMF1 7110 TATA element modulatory factor 1
GO:0003712|GO:0005515|GO:0001675|GO:2000845|GO:0043066|GO:0006355|GO:0005794|GO:0006366|GO:0005
783|GO:0007289|GO:0005634|GO:0030317|GO:0001819|GO:0003677|GO:0071407|GO:0032275|GO:0000139|GO:0
061136|GO:0010629|GO:0033327|GO:0042742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128645_PI430048170 0.4445479343783530.4699117726996940.508345824076883
0.5341605684377890.427564160604568A A A 2.6413925033698 0.447915213235282
0.451417921769609A A A LNCV6_128645_PI430048170 mRNA
CAGAGCTGTCTTCAGCAACATTATTAGTAGACAAAGAGGATGTGGATAATATTATGACAT NM_002597RefSeq chr1
- 186443565 186461108 PDC 5132 "phosducin, transcript variant 1"
GO:0001917|GO:0004859|GO:0007186|GO:0005634|GO:0007602|GO:0043086|GO:0007601|GO:0005829|GO:0001
750 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88979_PI430048170 0.00730816602369942 1.40238743789979 10.119640649097
10.3303849169349 10.3145111549235 P P P 9.64652504987758 9.88650145005793
9.76727879914996 P P P LNCV6_88979_PI430048170 mRNA
CTTTGAGAGAATACTTGTTGATTTCTGATGTGCAGGGGGTGGCTACAGAAAAGCCCCTTT NM_015670RefSeq chr17
+ 7561991 7571969 SENP3 26168 SUMO1/sentrin/SMT3 specific peptidase 3
GO:0005515|GO:0005737|GO:0071339|GO:0006508|GO:0005730|GO:0005634|GO:0008234 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_94082_PI430048170 0.1123246814376351.12390071667537 0.65291948702325 0.553959904201502
0.78303513445396 A A A 0.4324292530341910.5054356977893690.553129129257849 A A A
LNCV6_94082_PI430048170 mRNA
TCTCATTTTCTCCTGCACCAACATCGTGGGTGTCTGCACCCACTATCCGGCTGAGGTCTC NM_183357 RefSeq chr3
- 123282295 123448545 ADCY5 111 "adenylate cyclase 5, transcript variant 1"
GO:0005886|GO:0007268|GO:0007195|GO:0007202|GO:0044281|GO:0007193|GO:0046872|GO:0007191|GO:0035
556|GO:0007173|GO:0071377|GO:0050885|GO:0006171|GO:0007626|GO:0006833|GO:0034199|GO:0048011|GO:0
046982|GO:0008179|GO:0072372|GO:0055085|GO:0005524|GO:0003091|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134241_PI430048170 0.4227614277254711.77594081158504 2.14114244604253
0.4625338349976630.351091279392767 A A A 0.4841895292515070.367652401027502
0.366134552591578 A A A LNCV6_134241_PI430048170 mRNA
GGACACCTCCGAGAGAGTGGAGGGAAAATGTGTGAGAAATAAATTCTCCTAAATACTCGGNM_003802 RefSeq chr17
- 10300865 10373005 MYH13 8735 "myosin, heavy chain 13, skeletal muscle"
GO:0005516|GO:0032982|GO:0000146|GO:0006936|GO:0008152|GO:0003779|GO:0005859|GO:0030016|GO:0005
524|GO:0070062|GO:0009267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137596_PI430048170 0.5612944227801082.9569666815007 3.67197681097303
0.3337059094913960.395541972620313 P A A 1.42096236723389 0.332701499373436
0.315631852419719 A A A LNCV6_137596_PI430048170 mRNA
CTAAGGGAACGTACTCTGAATGCAAATGTTTCTGAGATTAAACACTAGTCACTTGTTAAA NM_054108 RefSeq chr11
- 63461403 63491208 HRASLS5 117245 "HRAS-like suppressor family, member 5, transcript variant 1"
GO:0016746|GO:0008152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127018_PI430048170 0.00925537562732929 2.1171792951794 4.67770817989129
5.08411211281343 5.09832641888521 P P P 3.5365098885681 3.91764625002383
4.13544649076491 P P P LNCV6_127018_PI430048170 mRNA
AGCTGCCTGTGATCTTCTTAGGTTATAGCCAAGTCAGCAACATAATTCCTCTAAATAAAA NM_003649 RefSeq chr6
- 110392179 110415550 DDO 8528 "D-aspartate oxidase, transcript variant 1"
GO:0005515|GO:0007320|GO:0048037|GO:0006531|GO:0006533|GO:0005102|GO:0042445|GO:0007625|GO:0019
478|GO:0055114|GO:0008445|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95874_PI430048170 0.5316444903141840.9232249274309198.15440304251343 7.89034991391105
7.82331999870669 P P P 7.82363866199013 8.25103442312087 8.12792323737841 P P P
LNCV6_95874_PI430048170 mRNA
AGACTAAATAGAAACCCCTCAGCCCTAAAATAGAAAAAAGAACAGTTCTGGACTATTGAA NM_032826 RefSeq chr7
- 134289337 134317075 SLC35B4 84912 "solute carrier family 35 (UDP-xylose/UDP-N-acetylglucosamine transporter), member B4"
GO:0006111|GO:0005794|GO:0015790|GO:0000139|GO:0005462|GO:0005464|GO:0008643|GO:0016021|GO:0015
788|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132249_PI430048170 0.0115257188643797 1.29305713069249 12.0877021103258
12.0953992756281 12.033022694495 P P P 11.6792855278164 11.7994169521671
11.6200349702725 P P P LNCV6_132249_PI430048170 mRNA
TTGGAGGAGAAGGACCCTGTACCCCTGTTCAAGATCTATGTGGCGGAGCTGATCCAGCAG NM_006428 RefSeq chr16
- 367383 370569 MRPL2810573 mitochondrial ribosomal protein L28
GO:0005515|GO:0070124|GO:0070125|GO:0070126|GO:0003735|GO:0006996|GO:0032543|GO:0005743|GO:0005
761|GO:0006412|GO:0005739|GO:0005737|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128051_PI430048170 0.0815182788716559 1.91657070385305 4.74150608695183
5.03154385184695 4.31934528377426 P P P 4.37635788073156 3.4747429375424
3.25602506883152 P P P LNCV6_128051_PI430048170 mRNA
ACTTGCTCCATCTACGGCCGCAGAGCGGCTGGCAGTTTCTTCGAGGACCTCAGCAAGACC NM_001014440 RefSeq

chr22 - 50530408 50532579 ODF3B NA outer dense fiber of sperm tails 3B NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143518_PI430048170 0.0163632099033065 0.853945102777797 8.96597321725094 8.90023697538204 8.88388383450035 P P P 9.13964467265017 9.21932169781866 9.07202431421436 P P P LNCV6_143518_PI430048170 mRNA AGCCTGGATGACATATTTTTCGTTTTGAATTAAAAGCACTGGCTGTGTGATTTTACCCTC NM_001204446 RefSeq
chr20 + 3820523 3825307 AP5S1 55317 "adaptor-related protein complex 5, sigma 1 subunit, transcript variant 1"
GO:0005515|GO:0005770|GO:0005634|GO:0005765|GO:0015031|GO:0030119|GO:0005764|GO:0005829|GO:0005737|GO:0000724|GO:0016197|GO:0031902|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139048_PI430048170 0.468929963302737 0.835445962367445 1.58462535158814 1.66820582905164 2.68600826476227 A A A 2.38932560823106 1.9612776450472 2.57625324513738 A A P LNCV6_139048_PI430048170 mRNA CCGGTATTTGCTGCTGAAGACAAAAATGAAAAGTAGGATGAAAATAATAGAATGGCACTG NM_006939 RefSeq
chr14 - 50117127 50231381 SOS2 6655 son of sevenless homolog 2 (Drosophila)
GO:0005515|GO:0051056|GO:0048011|GO:0043065|GO:0046982|GO:0007264|GO:0051057|GO:0003677|GO:0097190|GO:0005829|GO:0007411|GO:0032321|GO:0005089 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132535_PI430048170 0.0376635166564916 0.754145742884082 7.1592890969 7.13467136931326 7.36088745713377 P P P 7.58767739600537 7.4635589757401 7.81364802966282 P P P LNCV6_132535_PI430048170 mRNA CACTTGCCTTTGTTACTTAATGTGCTTTCAGTACAGCAGATATGCAATATTCACCAAATA NM_201553 RefSeq chr8 - 17864390 17895404 FGL1 2267 "fibrinogen-like 1, transcript variant 4"
GO:0035634|GO:0005577|GO:0060612|GO:0010906|GO:0070062|GO:0008203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141508_PI430048170 0.256819320265782 0.886341839354138 7.22254859750225 7.24643215730005 7.32926474860249 P P P 7.61402341927326 7.24230000744853 7.4424238109426 P P P LNCV6_141508_PI430048170 mRNA CTGGGTAGGCAAAGTCAGATTTTTGAGAACCTTTTTCCTGATTTGAAGTTTTAATTACCT NM_003901 RefSeq
chr10 + 70815947 70881175 SGPL1 8879 sphingosine-1-phosphate lyase 1
GO:0005515|GO:0005783|GO:0006672|GO:0001553|GO:0048705|GO:0030176|GO:0007283|GO:0044281|GO:0009791|GO:0010761|GO:0040014|GO:0006631|GO:0060021|GO:0006665|GO:0030097|GO:0001822|GO:0008209|GO:0030148|GO:0030149|GO:0097190|GO:0008210|GO:0060325|GO:0008117|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138677_PI430048170 0.0104372096991297 0.422817938420753 5.23002101230304 4.52783634485073 5.02764676723005 P P P 5.86108326564202 6.28992939399409 6.39403295186893 P P P LNCV6_138677_PI430048170 mRNA GCTTGCATCTCAATCCTTGAAAGTCTAGTATTAAATGGAAAAAACTTTTCCTAACTGTGG NM_018489 RefSeq
chr1 - 155335260 155562533 ASH1L 55870 "ash1 (absent, small, or homeotic)-like (Drosophila)"
GO:0005794|GO:0006366|GO:0005694|GO:0007267|GO:0005634|GO:0006323|GO:0002674|GO:0042800|GO:0003677|GO:0043409|GO:0005737|GO:0045944|GO:0003682|GO:0005654|GO:0008270|GO:0005923|GO:0051568|GO:0032635|GO:0070062|GO:0043124 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143912_PI430048170 0.00735388611510407 4.69069310404794 2.84733024079578 3.21880877656033 3.15262851944711 A P P 0.493549477406241 0.536604335496254 1.35413212174562 A A A LNCV6_143912_PI430048170 mRNA GCTTTAGCACTGTGCAGAGGGGAGATCCTGAGTTTTCTGTAAAAAATGACCTTTTGTTCA NM_014696 RefSeq
chr10 - 46549048 46556071 GPRIN2 9721 G protein regulated inducer of neurite outgrowth 2
GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_144109_PI430048170 0.0508923552129711 0.638867880507664 7.61257612077873 7.12760439252224 7.02699384393682 P P P 8.03825261750045 7.94103488669446 7.78616636423992 P P P LNCV6_144109_PI430048170 mRNA GTGCATCTCCCTGTATATCTTGAAGCTTTTTAAAAGGAAAAATTATTGTAGAACCACGTG NM_001193464 RefSeq chr2 + 43774038 43810010 DYNC2LI1 51626 "dynein, cytoplasmic 2, light intermediate chain 1, transcript variant 4" GO:0005515|GO:0005881|GO:0007368|GO:0006996|GO:0005930|GO:0045177|GO:0072372|GO:0031512|GO:0036064|GO:0005829|GO:0042384|GO:0019886|GO:0003774|GO:0008152|GO:0005858|GO:0030990 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131887_PI430048170 0.90656527540322 1.00118388260371 4.12717555586385 4.9346133699434 4.36515674551109 P P P 4.68437254746772 4.3704249373821 4.47169959776414 P P P LNCV6_131887_PI430048170 mRNA CACCAGGCTATAATTTGCCTGATGTCTGTGAGATTTGATAAATATATCATTCAACCTGTT NM_152683 RefSeq chr4 + 184649612 184694959 PRIMPOL 201973 "primase and polymerase (DNA-directed), transcript variant 1" GO:0030145|GO:0005759|GO:0003896|GO:0003887|GO:0003682|GO:0006269|GO:0031297|GO:0005634|GO:0006264|GO:0019985|GO:0009411 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145727_PI430048170 0.194005437983585 1.37875415574679 3.14551260903964 2.69307002576494 3.02395526519829 P A P 1.96599134078401 2.52203661858979 2.87916455613115 A P P LNCV6_145727_PI430048170 mRNA ACAGTGGTGGGCATGGAGAGGATATGACATGAAATAAAAGATCCAGCCCAACTGAAAAAA NM_014471 RefSeq chr9 + 33240197 33248567 SPINK4 27290 "serine peptidase inhibitor, Kazal type 4" GO:0010951|GO:0004867|GO:0042493|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128851_PI430048170 0.0213453822362366 0.362677485335827 6.00539253918888 5.17638075589983 5.59662908370452 P P P 7.13345940771121 7.14537448459627 7.00315840927491 P P P LNCV6_128851_PI430048170 mRNA GATGCCATCCCAGTCTCTTAAATCATCACACATCCTACCCAAGAACAGGGTTTGTTAAGA NM_001190472 RefSeq chr20 - 57358439 57359822 MTRNR2L3 NA MT-RNR2-like 3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128905_PI430048170 0.255747115834348 0.686712895527967 0.40157258288217 0.404590903975885 1.57560689119596 A A A 1.1626209331514 1.23290353886681 1.84902038936631 A A A LNCV6_128905_PI430048170 mRNA GGGTATCATTTAGATATTCCACTGTGTCTGTATTCAGACAAATGACACAATAAAACCCAA NM_001032280 RefSeq chr6 - 10396682 10412374 TFAP2A 7020 "transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha), transcript variant 2" GO:0005515|GO:0000987|GO:0044212|GO:0006366|GO:0000981|GO:0007605|GO:0000982|GO:0021559|GO:0042803|GO:0043231|GO:0009880|GO:0043524|GO:0010944|GO:0043525|GO:0014032|GO:0021623|GO:0005813|GO:0000976|GO:0001105|GO:0005794|GO:0030335|GO:0030501|GO:0042472|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112544_PI430048170 0.0168172547162689 1.52103906137761 6.08221019045291 6.05726858803543 5.93887679463906 P P P 5.29767254043836 5.32134963856076 5.62463132587762 P P P LNCV6_112544_PI430048170 mRNA AAGCCATCGATAAACCTACATATGCTACAAAGTGGCCGATACGACATGGAATCATTGAAG NM_020445 RefSeq chr7 + 152759748 152855379 ACTR3B 57180 "ARP3 actin-related protein 3 homolog B (yeast), transcript variant 1" GO:0034314|GO:0008150|GO:0003674|GO:0005737|GO:0005885|GO:0003779|GO:0042995|GO:0005524|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64398_PI430048170 0.730124258874062 1.02187746330014 7.33669994757555

7.48661181384474 7.56230692422417 P P P 7.51655849868743 7.38357542323938
7.39713096210096 P P P LNCV6_64398_PI430048170 mRNA
ATCTCCCTTGAGGATGTGGCTGTGAACTTCACCCTGGAGGAGTGGGCTTTGCTGGATCCT NM_020714 RefSeq
chr19 - 12576105 12610809 ZNF490 57474 zinc finger protein 490
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_121308_PI430048170 0.77743722155284 1.080079626151 3.77731572900819
4.46453769109497 3.69546754903791 P P P 4.13414288751895 3.45320073535476
4.05476948250524 P P P LNCV6_121308_PI430048170 mRNA
TTCAAGCACGCTGGCAGCGAAGGGGAACTCTACCCTCCAGAATCTCAGCCACCAGTTTCA NM_022835 RefSeq
chr19 + 39413109 39428415 PLEKHG2 64857 "pleckstrin homology domain containing, family G
(with RhoGef domain) member 2"
GO:0051056|GO:0048011|GO:0043065|GO:0032321|GO:0007264|GO:0005089|GO:0097190|GO:0005829 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_136150_PI430048170 0.0163022572674409 0.637082456259722 8.6416532566676
8.50144896479369 8.33786790474688 P P P 8.92788712286467 9.35599620028387
9.13260670144631 P P P LNCV6_136150_PI430048170 mRNA
GTCAGGCTCAAGCCCTGTGGTTGTAGGAATAAAGCCTGTGATCTCAAGAAGTGGAAAAAA NM_001076552 RefSeq
chr20 + 34876524 34927966 ACSS2 55902 "acyl-CoA synthetase short-chain family member 2,
transcript variant 2"
GO:0008610|GO:0006805|GO:0016208|GO:0006069|GO:0019542|GO:0044281|GO:0005524|GO:0005829|GO:0043
231|GO:0005737|GO:0019427|GO:0019413|GO:0005654|GO:0003987 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_71096_PI430048170 0.0340248694007116 1.20731930312212 8.65810053857038
8.87731230709065 8.78068083138085 P P P 8.5217531414029 8.39327661054791
8.58727778296666 P P P LNCV6_71096_PI430048170 mRNA
ATGCTATCACCCGAGGCAGAGCGAGTGCTGCGGTACCTTGTAGAAGTGGAGGAGCTCGCC NM_030815 RefSeq
chr20 - 31944954 31952080 PDRG1 81572 p53 and DNA-damage regulated 1
GO:0005737|GO:0006457|GO:0016272|GO:0051082 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134157_PI430048170 0.165049235025211 1.24825053749878 6.8072230339514
7.1708547725353 7.30980116050833 P P P 6.86779249891743 6.65532871381934
6.8413404387615 P P P LNCV6_134157_PI430048170 mRNA
ACATGACTATGCAAAAGCAGCCTTTTGTTTAGAGGAACTAATGATGACTAATCCACACAA NM_014673 RefSeq
chr8 + 108443623 108486907 EMC2 9694 ER membrane protein complex subunit 2
GO:0072546|GO:0005739|GO:0005737|GO:0005783|GO:0005730 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_134793_PI430048170 0.00197678640247565 2.31205049790421 6.91368363742704
6.84417063634895 6.55478007283645 P P P 5.46988858041479 5.80439182310148
5.40250492411826 P P P LNCV6_134793_PI430048170 mRNA
AGTCCCACTTAGCTTGGGGTCAGAACCAAGGGGTTTAATAAATAACCCTTGAAAACTGGA NM_052972 RefSeq
chr19 - 4537214 4540024 LRG1 116844 leucine-rich alpha-2-glycoprotein 1
GO:0008150|GO:0003674|GO:0016020|GO:0001938|GO:0050873|GO:0005576|GO:0005615|GO:0005160|GO:0045
766|GO:0070062|GO:0030511 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141830_PI430048170 0.0508065691223655 0.816916765451689 6.26383111201488
6.27538366271339 6.01869714825458 P P P 6.45238342281136 6.5860256706795 6.4027144468023
P P P LNCV6_141830_PI430048170 mRNA
AAATTCTTCAAATAACTGTTTGGGGGGTGGGGGGAGATGAAAGAGAGTCGCGTTTTGTTT NM_153690RefSeq chr3
+ 194685892 194689037 FAM43A 131583 "family with sequence similarity 43, member A" NA . NA -

. NA NA NA NA NA NA NA NA NA
LNCV6_100530_PI430048170 0.0142675733367948 2.05371711902387 4.28219772923515
4.43612629576154 4.43835784237341 P P P 3.59389445119827 3.05190989410469
3.35104423596732 P P P LNCV6_100530_PI430048170 mRNA
GTTCAGGGACTGGAATTGCAAGAGTATTTTCATGCGTGTTGAAGATGAACTGGAAATCCC NM_021908 RefSeq chr7
+ 116953326 117223907 ST7 7982 "suppression of tumorigenicity 7, transcript variant b" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128300_PI430048170 0.00859771220003697 0.3878326264939066.44562974033062
5.95840597355824 6.51947897609738 P P P 7.25112068553539 7.79286890575602
7.95138973157158 P P P LNCV6_128300_PI430048170 mRNA
AAGCATCTATCTATTCTGAATCATGTTTGGAAATAAAATTGCTCCATCTGGGAATGTGCT NM_001146276 RefSeq
chr3 - 172630644 172711218 NCEH1 57552 "neutral cholesterol ester hydrolase 1, transcript variant 1"
GO:0052689|GO:0016042|GO:0016020|GO:0005783|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137675_PI430048170 0.1127225950004570.6302913679525084.80545231620475
3.85771365720953 4.33324541342234 P P P 5.07391382552492 4.68721180123763 5.3184142229767
P P P LNCV6_137675_PI430048170 mRNA
GTTACAGGTTCAGTACTTCCAAAGGAAGAAACCTCCAAACCCAAAAAAGAATAAATATGA NM_005955 RefSeq chr1
- 37809566 37859620 MTF1 4520 metal-regulatory transcription factor 1
GO:0035035|GO:0005515|GO:0003700|GO:0006357|GO:0003713|GO:0055076|GO:0001047|GO:0005634|GO:0000
978|GO:0000979|GO:0003677|GO:0046872|GO:0006351|GO:0001077|GO:0045944|GO:0010038|GO:0005654|GO:0
006979|GO:0046686. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101239_PI430048170 0.4685346626314221.32107909917733 0.379398977678416
0.28929231516175 1.38775312595118 A A A 0.29003290814739 0.499130005226844
0.326983701545188 A A A LNCV6_101239_PI430048170 mRNA
ACAAGTCTTTTGACATGCTGAGGTCTGGCAGGAACATTAACCTATGTGCATCCCGAGTAT NM_145911 RefSeq chr16
- 71447599 71462223 ZNF23 7571 "zinc finger protein 23, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141090_PI430048170 0.2145169577662551.16092771045215 6.8221823636186
6.76184674412897 6.79741599825102 P P P 6.78521786877885 6.57151977132913
6.34621423020561 P P P LNCV6_141090_PI430048170 mRNA
CCAAAGCGGTCAAAAGCTTCTTCTCCCCCAGTGCTGATCTTGCTGGGCCTTAGCTTTGGA NM_001278495 RefSeq
chr10 + 79703226 79712757 NUTM2B 729262 NUT family member 2B NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_132240_PI430048170 0.1246491993911621.57030420916097 1.32433192937695
0.7146000015338791.50876955143221 A A A 0.5682043420593330.547935252437814
0.591920324658749 A A A LNCV6_132240_PI430048170 mRNA
AACTTAGAACCCAAGAAACAAGAGGAAATGAAGTCAGCCATTATAAGCGCCTGGCCAGGT NM_002980 RefSeq
chr2 - 119439842 119524452 SCTR 6344 secretin receptor
GO:0007588|GO:0005881|GO:0015055|GO:0007186|GO:0005886|GO:0005887|GO:0007586 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144744_PI430048170 0.0237819975255286 1.68346592572239 13.2278342663749
13.2525104871574 13.0879379153406 P P P 12.2711702182518 12.2893384861646
12.7140147109353 P P P LNCV6_144744_PI430048170 mRNA
GGAGGTTAGTGCCTGAAGCTCAGAGCTACACATTTTTAATAGTTTTTACATTTTTGGATA NM_006993 RefSeq chr10
- 101781324 101783413 NPM3 10360 nucleophosmin/nucleoplasmin 3
GO:0005515|GO:0009303|GO:0006364|GO:0005730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139700_PI430048170 0.5625669484472781.80021725394764 0.410850499152568

2.54594753551621 0.404247186070738 A A A 1.02898292474134 0.486339901529626
0.351822748178624 A A A LNCV6_139700_PI430048170 mRNA
GGGTTGCACCGCATGTACCCTGAGGGCTCATGGTGAATAAAGGCACCTTCCATCTCTGCA NM_133261 RefSeq chr19
+ 3585570 3593541 GIPC3 126326 "GIPC PDZ domain containing family, member 3" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133688_PI430048170 0.0673738048328210.9550601590372830.301100598734917
0.32680062938221 0.338037305055227 A A A 0.42690619758056 0.382225293421005
0.35515276295738 A A A LNCV6_133688_PI430048170 mRNA
CAAGAGAGTCTATCACTGTCATTTGAATTTGACATGACACATAAACAGATAAGTCAATGG NM_001145465 RefSeq
chr12 + 7765215 7774121 NANOGNB NA NANOG neighbor homeobox NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_142363_PI430048170 0.00104738429403125 0.3902909926982445.47692502629649
5.3164238857205 5.23884837149122 P P P 6.48116630947431 6.83305277220042
6.77627338948831 P P P LNCV6_142363_PI430048170 mRNA
TAGACGCTTGTCATGATAAGCTGGCCACATTATTAAAAGGCTCCCAAAGACAATTAAAAA NM_001031617 RefSeq
chr7 - 964849 975599 COX19 90639 COX19 cytochrome c oxidase assembly factor
GO:0033617|GO:0009060|GO:0005758|GO:0005737|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127640_PI430048170 0.1149184044007820.8568617946882651 3.2364795385168
13.1767343391342 12.9471745013908 P P P 13.3222152668747 13.3932227813297
13.3283499992198 P P P LNCV6_127640_PI430048170 mRNA
TCAGCCACACTGAACCCAATTACACACAGCGGGAGAACGCAGTAAACAGCTTTCCCACAA NM_000485 RefSeq chr16
- 88809468 88811934 APRT 353 "adenine phosphoribosyltransferase, transcript variant 1"
GO:0032869|GO:0016208|GO:0055086|GO:0044209|GO:0044281|GO:0002055|GO:0005829|GO:0005737|GO:0006
168|GO:0007595|GO:0006144|GO:0043101|GO:0005654|GO:0007625|GO:0003999|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_118812_PI430048170 0.0166056532612456 1.58080093645857 5.63822481011749
5.88512438744613 6.06527861318669 P P P 5.10188115098044 5.42033339093239
5.09119670700189 P P P LNCV6_118812_PI430048170 mRNA
ACTATGGATAAAGTTGTCGAAATCTTAAAGCCTTTATGCCGGTCTTCCCAAAGTACGGAG NM_001289079 RefSeq
chr10 - 14904610 14954432 DCLRE1C 64421 "DNA cross-link repair 1C, transcript variant h"
GO:0033151|GO:0008409|GO:0090305|GO:0000723|GO:0010212|GO:0030183|GO:0000014|GO:0005634|GO:0000
737|GO:0006302 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140200_PI430048170 0.5508880860141241.03217106732775 10.7213794955819
10.9186353141922 10.8652017622427 P P P 10.744140347708 10.7908646030465
10.8387566828596 P P P LNCV6_140200_PI430048170 mRNA
GCCGGAAGTTAAAGCACACTTACTTTATTCACCTATTTTTATAATAAACGTTCTTGCTGC NM_024309 RefSeq chr4
- 2741659 2756376 TNIP2 79155 "TNFAIP3 interacting protein 2, transcript variant 1"
GO:0005515|GO:0019901|GO:0043032|GO:0034134|GO:0023035|GO:0050821|GO:0007249|GO:0006915|GO:0005
634|GO:0006351|GO:0005829|GO:0005737|GO:0071222|GO:0006954|GO:0045944|GO:0050871|GO:0005654|GO:2
000352|GO:0043123|GO:0034138|GO:0070498|GO:0034162|GO:0031593 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_56680_PI430048170 0.0129703030948002 0.5875239256871337.02304609014989
6.82532110255671 7.27632078458784 P P P 7.72312494606897 7.77639168665803
7.95248345099462 P P P LNCV6_56680_PI430048170 mRNA
GTCGTGTACTTAGGAAGTAAATATCTTTTGAATTAGAGAAAGTGTTGGGACAGAAAGTAC NM_001130440 RefSeq
chr1 + 225777812 225790466 SRP9 6726 "signal recognition particle 9kDa, transcript variant 1"
GO:0005786|GO:0010467|GO:0005785|GO:0006614|GO:0003723|GO:0008312|GO:0005047|GO:0044267|GO:0006
412|GO:0070062|GO:0045900|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_104439_PI430048170 0.4906254435115291.12563470715649 6.21077574973485
5.68462609424018 5.75683431613825 P P P 5.49356616088358 5.98424021632449
5.67731386843851 P P P LNCV6_104439_PI430048170 mRNA
TGTGTGCCTGTGTGCCGAGGAGCAGAATTTTTCCAAGCAGAGAATGAGGGGAAAGGTGTT NM_001303465 RefSeq
chrX + 154411517 154421724 TAZ6901 "tafazzin, transcript variant 5"
GO:0030097|GO:0047184|GO:0031966|GO:0035965|GO:0005743|GO:0005634|GO:0031224|GO:0044281|GO:0060
048|GO:0005829|GO:0048738|GO:0005739|GO:0007507|GO:0032981|GO:0006936|GO:0042775|GO:0007519|GO:0
016021|GO:0032049|GO:0006644|GO:0042407|GO:0046474 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_128909_PI430048170 0.7291597835627960.9742688612822857.61263853216804
7.54791697080506 7.66201650865957 P P P 7.55313096773833 7.56727061661806
7.80332585662726 P P P LNCV6_128909_PI430048170 mRNA
CAGTGGTGTGTTTGATTCTTTTTTAGACTGGCTTCAGCATTGTGCAGTTTAAAAATAAGT NM_001242903 RefSeq
chr17 + 57085716 57121344 AKAP1 8165 "A kinase (PRKA) anchor protein 1, transcript variant 3"
GO:0005739|GO:0005515|GO:0016020|GO:0007596|GO:0003723|GO:0005741|GO:0016021|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77157_PI430048170 0.6667216537626 0.9231021813582345.78000723079566 5.66824868753104
5.54596106091413 P P P 5.84412725246161 6.03079626500682 5.40598476055459 P P P
LNCV6_77157_PI430048170 mRNA
TGCAGAGGCACTGCAGCTGCTCGGTTGCCCACCTCCTGAATGATGCCAGCCCAGTATGCT NM_019105 RefSeq chr6
- 32041154 32109374 TNXB 7148 "tenascin XB, transcript variant XB"
GO:0030036|GO:0005518|GO:0005578|GO:0005583|GO:0005615|GO:0031012|GO:0005622|GO:0016337|GO:0005
178|GO:0007160|GO:0030199|GO:0032963|GO:0006631|GO:0006641|GO:0043506|GO:0043206|GO:0007155|GO:0
008201|GO:0070062|GO:0048251 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68705_PI430048170 0.3826177917577021.18150630348061 8.96005605625832 9.47468784121988
9.53736101253511 P P P 9.14202870704614 8.80335987159807 9.323923081731 P P P
LNCV6_68705_PI430048170 mRNA
GACTAAAATTACCTGCAAATTGGGAAGCCAAAAAAGCTCGTTTGGAGTGGGAACTAAAGGNM_015484 RefSeq chr1
- 25222275 25232522 SYF2 25949 "SYF2 pre-mRNA-splicing factor, transcript variant 1"
GO:0007095|GO:0007369|GO:0000398|GO:0048568|GO:0005634|GO:0071013|GO:0001701 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143689_PI430048170 0.0253046694859657 0.4351172464564367.86254406749486
7.96604654278198 8.03176772528651 P P P 8.82506673978624 9.02163069427533
9.52692699592646 P P P LNCV6_143689_PI430048170 mRNA
CTGATTCTGATTTTGTTTTGTTTTGTTTGGGTTTTCTGAAACTTAAAATGCTGCCCCGAA NM_007011 RefSeq chr15 +
89088149 89202360 ABHD2 11057 "abhydrolase domain containing 2, transcript variant 1"
GO:0052689|GO:0008150|GO:0003674|GO:0030336|GO:0008152|GO:0009611|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133382_PI430048170 0.4961036453848020.9529620074682014.44476909071248
4.53471841217046 4.64796911965609 P P P 4.47109932190661 4.67723403461779
4.68483117130216 P P P LNCV6_133382_PI430048170 mRNA
TCATGTTATTTGTGATTTGTTTATAAGTTTGGGTGGGATGGCATACCATATTCTTGGTTC NM_001143909 RefSeq chr10
+ 103245886 103248016 RPEL1 NA ribulose-5-phosphate-3-epimerase-like 1NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_136261_PI430048170 0.8016106555705 1.04004329203834 3.241544853286
2.77802945518032 0.796517740532881 P A A 2.81296128521338 2.00919612213652
2.65676413858079 P A P LNCV6_136261_PI430048170 mRNA
GGTGGGGTGGGGATGTATATAACGAGGAAAAGTTATATGTACTTTAAAGTATGTCAAGTT NM_001029884 RefSeq
chr6 + 150599862 150843663 PLEKHG1 57480 "pleckstrin homology domain containing, family G

(with RhoGef domain) member 1" GO:0032321|GO:0005089 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127421_PI430048170 0.99122426042709 0.92013106591347 1.34712863194165 0.7687373665707410.802289875995115A A A 0.623897600322883 1.84279028050595 0.46855534035477 A A A LNCV6_127421_PI430048170 mRNA AAGACTCGACAAATCTGGGAGAAGATCTTGGGGAAGTTGCTTAATGTATGTGGGAGATAA NM_001004749 RefSeq chr11 + 4907369 4908308 OR51A7119687 "olfactory receptor, family 51, subfamily A, member 7" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145250_PI430048170 0.00098067064315374 0.2811141083928336.35366148610238 5.93805751964452 5.88936824077083 P P P 7.73001832202774 8.06601822031808 7.90432151459166 P P P LNCV6_145250_PI430048170 mRNA CAAGAAGCAACCAGCACCATCATGTGATAATGGTACTATGGCATATATGCAACATTAAAA NM_003500RefSeq chr3 - 58505135 58537202 ACOX2 8309 "acyl-CoA oxidase 2, branched chain" GO:0016402|GO:0005782|GO:0006699|GO:0033791|GO:0050660|GO:0005102|GO:0044281|GO:0003997|GO:0003995|GO:0008206|GO:0033540|GO:0044255|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139107_PI430048170 0.8868676977754471.00525806315242 0.422778932328174 0.51368258684911 0.41969079346171 A A A 0.5331970216218440.3947780722874 0.403255722557487A A A LNCV6_139107_PI430048170 mRNA GTTTTAGAAAATCCACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAAACATCAGC NM_080610RefSeq chr20 - 23564732 23568749 CST9L 128821 cystatin 9-like GO:0010951|GO:0004869|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145254_PI430048170 0.7020376740534160.95182043391029 0.429855166193245 0.4589067319151160.469778334361737A A A 0.3314605623653530.771173419744041 0.432333925745152A A A LNCV6_145254_PI430048170 mRNA TATGCAGTTTATGTGTCATCAATGTACATGCCAACATAAATATGGCGATTGTATAGCTGT NM_020547RefSeq chr12 + 53423854 53431534 AMHR2 269 "anti-Mullerian hormone receptor, type II, transcript variant 1" GO:0005515|GO:0023014|GO:0042562|GO:0005524|GO:0046872|GO:0007165|GO:0004702|GO:0005887|GO:0001880|GO:0004872|GO:0006468|GO:0007179|GO:0007548|GO:0005026 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54402_PI430048170 0.2417275974760840.5407430583871560.6854377146286790.998393025097269 0.790093617122513A A A 0.9765028267860051.26118236005654 2.45988276189528 A A A LNCV6_54402_PI430048170 mRNA GACTCCTGTGCAACTTTCCCAATGTGGCCTAAAAATGCAACTTCTTTTTATTTTCTTTTG NM_001078RefSeq chr1 + 100719639 100739046 VCAM1 7412 "vascular cell adhesion molecule 1, transcript variant 1" GO:0060710|GO:0019221|GO:0010043|GO:0005615|GO:0050901|GO:0007507|GO:0030198|GO:0071356|GO:0032496|GO:0050839|GO:0060333|GO:0070062|GO:0002526|GO:0005794|GO:0009986|GO:0007568|GO:0008131|GO:0005178|GO:0050776|GO:0009897|GO:0055114|GO:0035924|GO:0005886|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127800_PI430048170 0.8292706511551661.01169823186875 0.281170465915888 0.2861946104712590.458468101290952A A A 0.34567671132141 0.2959092406512310.3405473815141 A A A LNCV6_127800_PI430048170 mRNA CTGCCAAAACCATGCTATGAATTGAATCAAATGTGTCAAGTGTTTTCAGGAGTGTTAAGC NM_002170RefSeq chr9 + 21409146 21410185 IFNA8 3445 "interferon, alpha 8" GO:0005132|GO:0019221|GO:0005576|GO:0033141|GO:0045343|GO:0005125|GO:0005615|GO:0005126|GO:0002250|GO:0051607|GO:0060337|GO:0060338|GO:0042100|GO:0007596|GO:0045087|GO:0006959|GO:0030183|GO:0043330|GO:0002286|GO:0002323 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139737_PI430048170 0.1891460195626960.2920826029239730.285433410331689 0.3047006629471130.450033876145172A A A 0.31882673969505 2.67086536986694 2.4497207555496

A P P LNCV6_139737_PI430048170 mRNA
AATTTTTGGCCTTAGTTCCAGGTAGATTAAAAAGCTGCTAGCTCACATACAGGACAGCCA NM_015162RefSeq chr15
- 78170844 78234707 ACSBG123205 "acyl-CoA synthetase bubblegum family member 1, transcript variant 1"
GO:0000038|GO:0005737|GO:0001676|GO:0001552|GO:0005783|GO:0042552|GO:0016023|GO:0051384|GO:0031957|GO:0005524|GO:0004467 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140034_PI430048170 0.2321573225845920.7184828808846334.69169420734931
4.27823075292713 4.84381044566234 P P P 4.55059042724 5.19194652610469 5.42472836137998 P
P P LNCV6_140034_PI430048170 mRNA
CTGGATGATGTATTTTCTATTGGTTTATTGTTCCTCTAGCTTGTAAACCAGCTTGCATAT NM_001024383 RefSeq chr12
+ 77831288 78213012 NAV3 89795 "neuron navigator 3, transcript variant 1"GO:0005640 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_135677_PI430048170 0.7858335168276071.04434621050353 4.37458917071153 4.0985572547244
4.62516126987448 P P P 4.49551449468571 4.08311945524971 4.3498343273001 P P P
LNCV6_135677_PI430048170 mRNA
GGAAAAAACTGTACAAACTTAACCCCTTCAGGTGTTCAGAACAGATTAATATACCATGTA NM_025065RefSeq chr1
+ 84479236 84498350 RPF1 80135 ribosome production factor 1 homolog (S. cerevisiae)
GO:0000460|GO:0003723|GO:0000470|GO:0005730|GO:0000027|GO:0030687|GO:0042134 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130603_PI430048170 0.3601471838678240.5073086661832750.935385693845537
0.7861930478643130.612441047390638A A A 1.23764784248419 0.592456239923451
2.65917885914225 A A P LNCV6_130603_PI430048170 mRNA
ACCTAGTTTGTGTATCCCTGTAAGTCATTTTGGTATAAAGTAGGTTATAAGTGTACATGC NM_000990RefSeq chr11
+ 8682447 8689872 RPL27A 6157 ribosomal protein L27a
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0000184|GO:0016020|GO:0016032|GO:0022625|GO:0044267 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129458_PI430048170 0.2542470910222910.7052283747676553.7468754367567
3.95686794021959 3.42105541833811 P P P 4.74551549837079 3.88668946780577
3.87065092846427 P P P LNCV6_129458_PI430048170 mRNA
ATCAGGGCCGCGTTCTAAACATTCTACTGAAGTTTGCTAAGAAACCATTAGGTGAGGCTG NM_178314RefSeq chr12
- 123471361 123533718 RILPL1 353116 Rab interacting lysosomal protein-like 1
GO:0003382|GO:0005813|GO:0005737|GO:0005886|GO:0005654|GO:0072372|GO:0006886|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139639_PI430048170 0.3037645258799550.8464890532548846.14056003357154
5.78465111531462 6.14823407039416 P P P 6.00069022455192 6.53688744238252
6.23591315983418 P P P LNCV6_139639_PI430048170 mRNA
AGTGAGGGAGTTAAGTGGCTTCTCCGTGGAAACACAGCCTTCTGCTGCAGCAGAGGCTCA NM_213568RefSeq chr19
- 2734525 2740076 SLC39A3 29985 "solute carrier family 39 (zinc transporter), member 3, transcript variant 2" GO:0071577|GO:0005886|GO:0005385|GO:0016021|GO:0055085 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144156_PI430048170 0.0296982217002174 0.6551344880257640.298383219393499
0.2788330008719990.379510436218903A A A 1.15031649914737 0.762218538404545
0.847154821572025A A A LNCV6_144156_PI430048170 mRNA
CCTGGGGGGAAATTGAGGGAGGGTCTGGATACCTTTAGAGCCAATGCAACGGATGATTTT NM_012315RefSeq chr19
- 51002512 51009634 KLK9 284366 kallikrein-related peptidase 9
GO:0004252|GO:0006508|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92958_PI430048170 0.1064195906954571.60375530545156 4.730268411841 4.51618570029985
5.28241274495354 P P P 4.4036683395777 4.39137833493364 3.69311984828947 P P P

LNCV6_92958_PI430048170 mRNA
TGAGGGATTTTCTCTTGGGGGAGAAATCAGTGGTCGAGCGCCTGCCCAGCTCAAATGCCA NM_004974RefSeq chr1
- 110603153 110606353 KCNA2 3737 "potassium channel, voltage gated shaker related subfamily A,
member 2, transcript variant 1"
GO:0005251|GO:0030424|GO:0030054|GO:0005886|GO:0007268|GO:0019228|GO:0014059|GO:0030425|GO:0015
271|GO:0008076|GO:0005249|GO:0043204|GO:0051260|GO:0034765|GO:0043679|GO:0006813|GO:0071805|GO:0
031258|GO:0044224|GO:0005267|GO:0019233|GO:0030027|GO:0032809|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_102023_PI430048170 0.4292829963346760.9843099953280120.378638130964366
0.3875417636055640.349109857951178A A A 0.4340116564950190.35829715298051
0.390705467314933A A A LNCV6_102023_PI430048170 mRNA
GTAAAACCATTCAAGGCACAAGGGATCCAATTTGTGCCATAACTGCATCAGATAAGATAT NM_001006657 RefSeq
chr2 - 19910265 19990123 WDR35 57539 "WD repeat domain 35, transcript variant 1"
GO:0042384|GO:0005813|GO:0006996|GO:0005930|GO:0030991|GO:0072372|GO:0036064|GO:0035721 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132477_PI430048170 0.3763876969314111.50993032186919 1.61683608486378
0.4819052765357450.280351224752381A A A 0.2911333482735640.432348893437295
0.247892078393377A A A LNCV6_132477_PI430048170 mRNA
CCCCTGATCTACAGTCTGAGAAATAAAGATGTTAAGGATGCAATCCGAAAAATAATCAAT NM_001005496 RefSeq
chr11 + 55838751 55839738 OR5D16 NA "olfactory receptor, family 5, subfamily D, member 16"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139408_PI430048170 0.3410214189699330.9479189858077331 0.4907367465933
10.6905419360539 10.5032625928456 P P P 10.6634183048605 10.6474089566372
10.6135640353514 P P P LNCV6_139408_PI430048170 mRNA
GGACCTGAGCCTCCTGGCTCCCAGCCTGTAAATATGTATAGACCTGTTTTGTCATTTTTT NM_182958RefSeq chr16
+ 31117663 31131393 KAT8 84148 "K(lysine) acetyltransferase 8, transcript variant 2"
GO:0005515|GO:0006325|GO:0005634|GO:0035064|GO:0046872|GO:0071339|GO:0043996|GO:0000123|GO:0043
995|GO:0072487|GO:0030099|GO:0004402|GO:0031965|GO:0016573|GO:0006351|GO:0043981|GO:0043982|GO:0
043984|GO:0010506|GO:0000776|GO:0016407|GO:0005654|GO:0046972|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137508_PI430048170 0.4255919388039710.9530092334439021 6.3562729347537
16.1762377995475 16.1273862878246 P P P 16.293991131477 16.3525032782332 16.22928423518
P P P LNCV6_137508_PI430048170 mRNA
GCTAAAGAACTTGCCACTAAACTGGGTTAAATGTACACTGTTGAGTTTTCTGTACATAAA NM_000972RefSeq chr9
+ 133348213 133351425 RPL7A 6130 ribosomal protein L7a
GO:0005515|GO:0010467|GO:0003735|GO:0042254|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0005
634|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0016020|GO:0000184|GO:0042788|GO:0
016032|GO:0022625|GO:0044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_127880_PI430048170 0.4215821708752391.29500253943583 1.20566494766858
0.32668069014317 0.262054643587985A A A 0.29353695450511 0.301920978922011
0.283383312554086A A A LNCV6_127880_PI430048170 mRNA
GAGAGCTTATATAAGTGTTTTCTATAGATGCAGATTAAAAATGCTGTGTTGTCAACCGTC NM_198570RefSeq chr7
+ 49773660 49912542 VWC2 375567 von Willebrand factor C domain containing 2
GO:0030514|GO:0003674|GO:0030054|GO:0045666|GO:0032281|GO:0010811|GO:0045202|GO:0005614|GO:0005
615|GO:0005604 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145535_PI430048170 0.6085703161360510.8222747117643161.93308530018686
0.4275675573792581.87317102664242 A A A 1.01830586313589 2.11745102706693
2.12766706326453 A A A LNCV6_145535_PI430048170 mRNA

GTCCCCTATTTTAAGTCATAATTTTGTATTTAGTGCTTTCCTGGCTCTCAGAGAGTATTA NM_003326RefSeq chr1 - 173183730 173207313 TNFSF4 7292 "tumor necrosis factor (ligand) superfamily, member 4, transcript variant 1"
GO:0032755|GO:0032753|GO:0032813|GO:0002215|GO:0005615|GO:0046641|GO:0032689|GO:0002891|GO:0035709|GO:0032729|GO:0005164|GO:0002526|GO:0009986|GO:2000568|GO:0002726|GO:0005125|GO:0005887|GO:0035714|GO:0035713|GO:0035712|GO:0050871|GO:0002830|GO:0045590|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145127_PI430048170 0.000425684269802493 1.93507809552217 8.83552184884539 9.02453152696563 9.02616851155979 P P P 7.91774690272988 8.04944980240042 8.06554161608622 P P P LNCV6_145127_PI430048170 mRNA
TAACGTGACGAAGGCACGATTCCTGTAAATGTGTAAACTAAGGGGATGGTTGGATTTTTT NM_001291324 RefSeq chr17 + 81399720 81466332 BAHCC1 57597 BAH domain and coiled-coil containing 1
GO:0003682 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133128_PI430048170 0.798639866846509 0.967094084829443 7.36199083961423 7.42017049411535 7.50079302556436 P P P 7.20963190433897 7.58073404765942 7.60755656484534 P P P LNCV6_133128_PI430048170 mRNA
GCAAAACGTGGCTTTCATCGCTTTGTAAAAATTTGCATCTGTTTAGAAACTAGCCTATAA NM_173794RefSeq chrX - 44523638 44542975 FUNDC1 139341 FUN14 domain containing 1
GO:0005515|GO:0001666|GO:0000422|GO:0005741|GO:0031307 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139009_PI430048170 0.0549006346492088 0.635383800084703 5.86527578307245 6.30569874405886 6.40079014008602 P P P 6.87931500387859 6.85746909996622 6.85226288658493 P P P LNCV6_139009_PI430048170 mRNA
GGAGGATGGAGAGAGAACTCTAACACAAAACATCTTATTAAAATTGTACTTGAGAGACAA NM_020850RefSeq chr16 - 67723101 67806652 RANBP10 57610 RAN binding protein 10
GO:0005881|GO:0008536|GO:0048487|GO:0000226|GO:0005634|GO:0005087|GO:0032853|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129269_PI430048170 0.215265298368646 0.967139739220728 0.305621022613708 0.360529467608475 0.322122528222405 A A A 0.429211372661282 0.340200367808406 0.362530671898626 A A A LNCV6_129269_PI430048170 mRNA
TTCAGTTACCAGACTCCATGCTTTTACCTCCTATGTGTCAGGTATAATTTGAACCTCTAA NM_002489RefSeq chr7 - 10931952 10940186 NDUFA4 4697 "NDUFA4, mitochondrial complex associated"
GO:0005515|GO:0004129|GO:0005743|GO:0044281|GO:0005751|GO:0032403|GO:0005739|GO:0022904|GO:0005747|GO:0006120|GO:0008137|GO:0044237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133492_PI430048170 0.188847706162113 1.2502560399264 7.82845408550035 7.58531423998957 7.88413052002477 P P P 7.72421652953478 7.44824683397345 7.11131949561247 P P P LNCV6_133492_PI430048170 mRNA
AGTTTTCCTTGCTTTCCTGATACTCTTTGGCGCTGACTTGGAATTCTAAGAGCCTTGGAC NM_004584RefSeq chr11 + 67391951 67398412 RAD9A 5883 "RAD9 homolog A (S. pombe), transcript variant 1"
GO:0005515|GO:0008408|GO:0017124|GO:0030896|GO:0090305|GO:0042826|GO:0019901|GO:0031573|GO:0005634|GO:0071479|GO:0006974|GO:0006260|GO:0005737|GO:0006281|GO:0008853|GO:0000076|GO:0005654|GO:0000077|GO:0019899|GO:0000738 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140812_PI430048170 0.455862320874694 0.702622383461951 0.343501743662517 0.246141313489258 0.322471619217526 A A A 0.268915391394693 1.51722260441529 0.270567413735526 A A A LNCV6_140812_PI430048170 mRNA
TGTTGTAGGTAACTCTAATTGAGCCCGAAACCAGAATAAAAACTCTTACATTGGAAACAT NM_144992RefSeq chr2 + 98087131 98312947 VWA3B 200403 von Willebrand factor A domain containing 3B NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133835_PI430048170 0.00530736253433353 2.65340165206458 9.34843228290187

9.33970030808693 9.28311637299266 P P P 7.76175377172391 8.13345101629279
7.82539355132073 P P P LNCV6_133835_PI430048170 mRNA
TTTCTTCACGGTCACTATTTATTCTTTGTTCCTTTTTCTTTTTGTAAGAAACATTCACAA NM_001258320 RefSeq chr11
- 44932347 44950208 TP53I11 9537 "tumor protein p53 inducible protein 11, transcript variant 1"
GO:0008285|GO:0006950|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141807_PI430048170 0.0420029823223578 0.234127065542156 0.452989130777677
0.502720801431819 0.564007386102022 A A A 3.22456693263449 1.76537264622553
2.45044428466206 P A P LNCV6_141807_PI430048170 mRNA
TCTTGTTAGGGCTTCTTGAATGCACATTTTGTCATTATCTGTATACCAAAGGTGAGCTTT NM_194282 RefSeq chr4
- 82924603 83010834 LIN54 132660 "lin-54 DREAM MuvB core complex component, transcript variant 1"
GO:0005515|GO:0006355|GO:0000086|GO:0051726|GO:0005654|GO:0000278|GO:0003677|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144230_PI430048170 0.531088080403278 0.8471317340175 0.405842456780901
0.41674103730262 2.6124040479325 A A A 1.93109350524878 1.07305390504555
2.15093248708633 A A A LNCV6_144230_PI430048170 mRNA
CTTTGCCTGGCTGCAATATAGTGTGTGTTTAAATTATTTACAGGCTGTTGTTTCTCAAAT NM_015177 RefSeq chr11 +
59172338 59208587 DTX4 23220 "deltex 4, E3 ubiquitin ligase, transcript variant 1"
GO:0032479|GO:0016567|GO:0007219|GO:0045087|GO:0016874|GO:0032481|GO:0008270|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141096_PI430048170 0.450988845564081 1.66227618657457 2.20457985581872
2.43390237224368 0.496276898215711 A A A 1.74359345208713 0.438200218001168
1.11677029130735 A A A LNCV6_141096_PI430048170 mRNA
GGCCTATTGAAAGCAGGATGAGATGATAATTTAAGACACTGAATGATTTCTTTTCCAACA NM_005658 RefSeq chr9
- 120902392 120926895 TRAF1 7185 "TNF receptor-associated factor 1, transcript variant 1"
GO:2001236|GO:0005515|GO:0007165|GO:0005164|GO:0005737|GO:0051092|GO:0006461|GO:0006915|GO:0031
996|GO:0008270|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137775_PI430048170 0.216377506895707 0.802713910210455 6.48009306998109
6.53222993156411 6.07985956918019 P P P 6.95277610825596 6.67521795334629
6.40434147479838 P P P LNCV6_137775_PI430048170 mRNA
CGCAGCCTGATACGGTGTGCCAGCGTCCTCCCCACGAGGCAAATAAACACAGAAAACTCA NM_001302757 RefSeq
chr19 + 36111202 36113711 OVOL3 728361 ovo-like zinc finger 3
GO:0006355|GO:0003700|GO:0005634|GO:0003676|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_116226_PI430048170 0.16415339664599 0.577939588841622 1.48476965014766
0.483661193746546 1.81081372157689 A A A 1.61905274184468 2.15139034092157
2.54058999908424 A A P LNCV6_116226_PI430048170 mRNA
CCTACAGGCTTGCTCTCACACACGTGTATGCACAGCAGAGAGACGTATGAGCTTCTACTG NM_015205 RefSeq chr13
+ 112690328 112887168 ATP11A 23250 "ATPase, class VI, type 11A, transcript variant 1"
GO:0005515|GO:0000287|GO:0005886|GO:0005783|GO:0005765|GO:0005524|GO:0045332|GO:0043231|GO:0016
020|GO:0004012|GO:0008152|GO:0016021|GO:0055037|GO:0005769 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141584_PI430048170 0.233306177082118 1.78492353806287 2.24108824083697
3.65702701540198 3.42663956068101 A P P 2.64202861925281 2.27894414268268 2.2156282282269
P A A LNCV6_141584_PI430048170 mRNA
TGTCAGACAAGCTCAAGGAACGCAAAAGAACCCCCGTTTCTCATAAAGTGATAGAAAAGC NM_001300781 RefSeq
chr4 + 185018840 185020804 HELT NA "helt bHLH transcription factor, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62507_PI430048170 0.135966252889827 1.30449637846208 9.89398380521985 9.78390186190609
9.95842402709382 P P P 9.15243193561138 9.53826121052464 9.7401594573033 P P P

LNCV6_62507_PI430048170 mRNA
ACTAAAATTTTAATCCAGGTGCTGGTTTGCCAACTGACAAAAAGAAAGGTGGGCCATCTC NM_003090 RefSeq chr15
- 101281509 101295255 SNRPA 16627 small nuclear ribonucleoprotein polypeptide A'
GO:0008380|GO:0005515|GO:0010467|GO:0000398|GO:0030532|GO:0005681|GO:0005654|GO:0071013|GO:0005
686 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133346_PI430048170 0.3011963680657970.8947872993327741 0.1559260908948
9.79139561155692 9.77596412148683 P P P 10.0584370488974 10.1141295019722
10.0641228519496 P P P LNCV6_133346_PI430048170 mRNA
GACTTGCCCCTAAGAGGGATGTACTGTAAATAAACAGTATTTTTAGATCACCTTCAAAAA NM_001008697 RefSeq
chr22 - 26491928 26512471 TFIP11 24144 "tuftelin interacting protein 11, transcript variant 1"
GO:0006396|GO:0006355|GO:0005737|GO:0071008|GO:0016607|GO:0000398|GO:0000390|GO:0005578|GO:0005
681|GO:0071013|GO:0031214|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130833_PI430048170 0.3098115472741050.8557511594117925.81150678063173
6.15881936653405 6.38670448171849 P P P 6.22442489916066 6.276840486837
6.56357636386337 P P P LNCV6_130833_PI430048170 mRNA
GCCTATGGAATATTCTGTTGTAGTTTGGTCCTCAGGTGTTGATATAATTTCTCATTTACA NM_001199286 RefSeq chr2
+ 169694453 169701708 PHOSPHO2 493911 "phosphatase, orphan 2, transcript variant 1"
GO:0016791|GO:0016311|GO:0046872|GO:0033883 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129749_PI430048170 0.1927992299553840.9268668256784213.2147105313009
13.4019779124999 13.2901543332957 P P P 13.354658790055 13.498558461391
13.3844690816515 P P P LNCV6_129749_PI430048170 mRNA
ACACAGGCCAGCCCCAGTCTCACGGCTGAAGTGCGCAATAAAAGATGGTTTAGGGTCCCT NM_002804 RefSeq chr11
- 47418768 47426473 PSMC3 5702 "proteasome (prosome, macropain) 26S subunit, ATPase, 3"
GO:0005515|GO:0002474|GO:0010467|GO:0048471|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005
829|GO:0034641|GO:0000082|GO:0000932|GO:0016032|GO:0090090|GO:0016887|GO:0006977|GO:0000209|GO:0
043066|GO:0000502|GO:0003714|GO:0006521|GO:0003713|GO:0001824|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136501_PI430048170 0.0192078996620919 0.54732452395611 5.29133734995024
5.06164459245577 5.67044215971246 P P P 6.35876752012968 5.95518677603591
6.34888513097307 P P P LNCV6_136501_PI430048170 mRNA
TCTTGAAACATAGGAGAAACAGGATTCATGTGTATCTCTTTACCATGCACAAAATCTCAA NM_001130067 RefSeq
chr4 + 153153117 153339322 TRIM2 23321 "tripartite motif containing 2, transcript variant 2"
GO:0005515|GO:0043523|GO:0005737|GO:0004842|GO:0016567|GO:0016874|GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134489_PI430048170 0.000782445790564433 0.5141490803624176.87786150504871
6.78670205546827 7.01824655206473 P P P 7.76238425355427 7.79062924238178
8.00599359614733 P P P LNCV6_134489_PI430048170 mRNA
ATGGCAAGCAGACTGATAGCTGCACATTTGGCATGCTTTGTTTAATGGATTTTATTTTTA NM_173469 RefSeq chr15
+ 75843285 75901047 UBE2Q2 92912 "ubiquitin-conjugating enzyme E2Q family member 2,
transcript variant 1" GO:0005737|GO:0004842|GO:0016874|GO:0070936|GO:0005524 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_129699_PI430048170 0.0645569871790930.9287446349408590.325286748584944
0.3106835730061980.302235026566831 A A A 0.4737650957188310.411551888507566
0.37106161632024 A A A LNCV6_129699_PI430048170 mRNA
GAACCTTGAGGTTAGAGTTACTATATTTGCTCAAGATGACAAATGCAGGTGCTTTCTTTT NM_133478 RefSeq chr2
- 74216241 74343407 SLC4A5 57835 "solute carrier family 4 (sodium bicarbonate cotransporter),
member 5, transcript variant c"
GO:0048311|GO:0010468|GO:0060041|GO:0005886|GO:0055085|GO:0003014|GO:0003073|GO:0016324|GO:0005
452|GO:0005887|GO:0002064|GO:0051453|GO:0015701|GO:0035725|GO:0033326|GO:0016021|GO:0008510|GO:0

006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142675_PI430048170 0.1279248476414651.29869728522738 5.65107805660858
6.01851678572042 5.71154345454041 P P P 5.66897289027851 5.43716097676172 5.1191671810181
P P P LNCV6_142675_PI430048170 mRNA
GCGGAGACTTTCTTGGCAAAACCCATTCCCCAAAGCTACGCTTCCCCTGCTGAGATAGCC NM_013397RefSeq chr6
+ 41780761 41787372 PRICKLE4 29964 prickle homolog 4 (Drosophila)
GO:0008150|GO:0003674|GO:0008270|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135125_PI430048170 0.3148964054613061.21866226442224 5.34315118216483
5.52228235596509 5.30091936748422 P P P 5.41895585301099 5.18095799564887
4.60356294907601 P P P LNCV6_135125_PI430048170 mRNA
AGTACTTAGTCTACAGACCTATGTGCGTGTCCCTATCCTTCTGTCCTTTTCTCTCTTCAG NM_001281448 RefSeq chr20
+ 45306842 45317824 RBPJL 11317 "recombination signal binding protein for immunoglobulin kappa J region-like, transcript variant 2"
GO:0007165|GO:0005667|GO:0003700|GO:0006366|GO:0006357|GO:0000982|GO:0005634|GO:0045893|GO:0000978 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130790_PI430048170 0.00195414099596546 0.40798723919667 7.82401466206683
7.92068731146951 8.23656516587679 P P P 9.11895041388418 9.20148969880707
9.53886998464286 P P P LNCV6_130790_PI430048170 mRNA
CAGATTCCACACAAAATGTCACACTTGTTTCTTGTTCATCCAAGGAACCTAATTGAAATT NM_000042RefSeq chr17
- 66212028 66229438 APOH 350 apolipoprotein H (beta-2-glycoprotein I)
GO:0005515|GO:0042627|GO:0005615|GO:0008289|GO:0042802|GO:0034361|GO:0005543|GO:0001948|GO:0034364|GO:0008201|GO:0033033|GO:0034197|GO:0070062|GO:0009986|GO:0051918|GO:0051917|GO:0060230|GO:0031012|GO:0010596|GO:0034392|GO:0030194|GO:0001937|GO:0007597|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142441_PI430048170 0.8637250856724451.17575171827533 0.3675376928947321.7109856518891
0.319970790667849A A A 0.79414480484612 0.4485041994973970.883464809118922A A A
LNCV6_142441_PI430048170 mRNA
CTGAGTGCTTTTCAGATTCCATCTATGCTGAAAAAGAATCTAGGAGAATAAACACATTTC NM_024901RefSeq chr1
- 111185968 111200703 DENND2D 79961 "DENN/MADD domain containing 2D, transcript variant 1"
GO:0017112|GO:0005737|GO:0032851 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126827_PI430048170 0.4588563485236560.9224943070632595.90262027643529
6.26292748339159 6.35206249970936 P P P 6.30793547419999 6.20898594120469
6.38272229219386 P P P LNCV6_126827_PI430048170 mRNA
GACTCAGATTCTTGGCTGTCTGTTTAACCAATCACGATATGGGATTTGAGAAATAAAATT NM_003847RefSeq chr15
- 89681530 89690784 PEX11A 8800 "peroxisomal biogenesis factor 11 alpha, transcript variant 1"
GO:0005515|GO:0044281|GO:0042803|GO:0044375|GO:0007165|GO:0043234|GO:0050873|GO:0007031|GO:0005779|GO:0016557|GO:0005778|GO:0044255|GO:0005777|GO:0016559 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137900_PI430048170 0.1249867106351941.18697818724356 7.0970963093992
7.17498591833715 6.92239385429094 P P P 7.01033172375359 6.76479926623392
6.66692548807595 P P P LNCV6_137900_PI430048170 mRNA
AATATAAGTATCATTGCTATTCTGAGAAATCTATATACACCAAAGCCCTCCCTCCACAAA NM_173808RefSeq chr1
- 71402941 72282594 NEGR1 257194 neuronal growth regulator 1
GO:0005515|GO:0007631|GO:0043005|GO:0005886|GO:0009986|GO:0031225|GO:0016337|GO:0050767|GO:0005911|GO:0010976|GO:0043025|GO:0007626|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140841_PI430048170 0.0239634144303866 0.1650575983750150.452153474671089
1.74939102793574 2.17670302587394 A A A 4.52060129085298 3.89423685048309
4.18807632390739 P P P LNCV6_140841_PI430048170 mRNA
GTTTTGTTGTAAACAGTGTCCACACTCTTTGCTCCAATAAAGCTCGGTTCCTTAAGCCAC NM_001102470 RefSeq

chr4 - 99202637 99219246 ADH6 130 "alcohol dehydrogenase 6 (class V), transcript variant 1"
GO:0004022|GO:0035276|GO:0006805|GO:0045471|GO:0006069|GO:0004024|GO:0008270|GO:0044281|GO:0070
062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98985_PI430048170 0.1442566576790351.23551081825575 7.78528919869963 7.91279335291061
8.23473513728551 P P P 7.66133786019681 7.56791045587868 7.81524142115674 P P P
LNCV6_98985_PI430048170 mRNA
CCAGGGAGATTTCTCCATTTTCCTCTTGTCTACAGTGCGGCTACAAATCTGGGATTTTTT NM_002356RefSeq chr6
+ 113857334 113863475 MARCKS 4082 myristoylated alanine-rich protein kinase C substrate
GO:0005516|GO:0005813|GO:0005886|GO:0044281|GO:0015629|GO:0006112|GO:0051015|GO:0050796|GO:0005
080|GO:0042585|GO:0005925|GO:0005938|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56693_PI430048170 0.8445127326201490.9937620828785953.02654356726056 3.64327306926135
4.04983083776499 A P P 3.6324764217027 3.56007776611281 3.72713201955065 P P P
LNCV6_56693_PI430048170 mRNA
GTGGTCCATATCATGATGTCTTGCATAGTATTTTAGGGGCATACACATGCTACAGGCCTG NM_015188RefSeq chr10
+ 94402428 94536332 TBC1D12 23232 "TBC1 domain family, member 12" GO:0032851|GO:0005097
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137647_PI430048170 0.00222483564621105 0.5889887478668573.36634828161526
3.18671143707452 3.39018113412898 P P P 4.11523027348156 4.19370446861677
3.92026233053327 P P P LNCV6_137647_PI430048170 mRNA
CCAGGCACCCCCTGGCTTGAACCTTCAAAGCTTTTGTAAAATAAAACCACCAAAGTCCTG NM_002049RefSeq chrX
+ 48786573 48794310 GATA1 2623 GATA binding protein 1 (globin transcription factor 1)
GO:0005515|GO:0003700|GO:0006366|GO:0071733|GO:0050731|GO:0017053|GO:0033690|GO:0000976|GO:0010
559|GO:0000977|GO:0008301|GO:0000122|GO:0000978|GO:0030502|GO:0000979|GO:0001701|GO:0031490|GO:0
035854|GO:0045648|GO:0008270|GO:0005654|GO:0070742|GO:0001158|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129101_PI430048170 0.14354392210527 1.23898660397709 8.5264654617454
8.61452035526941 8.67891264516471 P P P 8.47651346411466 8.00616700158039
8.37268066769621 P P P LNCV6_129101_PI430048170 mRNA
CTGGTCCAAAAGAAAAAACAAGCTAAAAGCTGAATATTCTGGGAGATGATGTTCACCTTC NM_022365RefSeq chr10
- 21756547 22003721 DNAJC1 64215 "DnaJ (Hsp40) homolog, subfamily C, member 1"
GO:0005515|GO:0031965|GO:0005886|GO:0005783|GO:0051087|GO:0032781|GO:0003677|GO:0006417|GO:0045
861|GO:0016020|GO:0006457|GO:0003682|GO:0005789|GO:0050708|GO:0016021|GO:0001671 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136613_PI430048170 0.7655460512104120.9896008842074620.432824215073356
0.4717470845531090.377244454656238A A A 0.5146587461526630.398834471290893
0.412324486635761A A A LNCV6_136613_PI430048170 mRNA
ATTTTCGTGCGTTGCAAGTGTGCTGGCGTCTGACACTATGAACTTCCAACAACAAAATTG NM_171999RefSeq
chr18_KI270911v1_alt + 45389 64084 SALL3 27164 spalt-like transcription factor 3
GO:0035137|GO:0035136|GO:0021891|GO:0006355|GO:0045879|GO:0005634|GO:0003677|GO:0046872|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137697_PI430048170 0.93447219732831 0.9895203283607520.63639941687924
0.7009291156567370.604036679589091A A A 0.6022261204724760.522741770369357
0.843979959348929A A A LNCV6_137697_PI430048170 mRNA
CTAGCAACATAGGGAAATGATCCATATGGAAAATCAGAATGCGATTCTTCTGTTGTAAAA NM_182756RefSeq chr2
+ 28810833 28850609 SPDYA 245711 "speedy/RINGO cell cycle regulator family member A, transcript
variant 1"
GO:0008284|GO:0000082|GO:0019901|GO:0045737|GO:0007275|GO:0005634|GO:0006974|GO:0007140 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141765_PI430048170 0.823005890773975 1.00816645553395 0.450233639299299

0.5215384227868180.433542423230555A A A 0.5448345187215450.406673804068511
0.415951697884667A A A LNCV6_141765_PI430048170 mRNA
TTGTTTTAGCTGTTACACACACAGTAATACCTGAATATCCAACGGTATAGATCACAAGGG NM_016588RefSeq chr6
- 5997999 6007400 NRN1 51299 "neuritin 1, transcript variant 1"
GO:0030054|GO:0005886|GO:0045202|GO:0031225|GO:0007399 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128812_PI430048170 0.1602568019412992.20564661232714 1.93703359538339
2.90603453497757 1.21980489584939 A A A 0.3917321652955861.34068873072909
1.23003696473981 A A A LNCV6_128812_PI430048170 mRNA
AGGAGCCTGCTAAGGAACAATGCCGCCTGTCAATAAATGTTGAAAAGTCATCCCAAAAAA NM_002761RefSeq chr16
- 11280835 11281335 PRM1 5619 protamine 1
GO:0030261|GO:0007275|GO:0006323|GO:0005654|GO:0007283|GO:0000786|GO:0003677|GO:0030154 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142960_PI430048170 0.000816537208472049 0.2212465177462276.42858141085747
6.15668137351715 6.63459900378602 P P P 8.25368008641649 8.61332279178084
8.85811230342026 P P P LNCV6_142960_PI430048170 mRNA
CAGCAGTTGTATGTGGTTATGTTAGTCTCAAGATACTTAATTTGTTGACCTTACTTCAGA NM_003468RefSeq chr2
- 207762585 207769419 FZD5 7855 frizzled class receptor 5
GO:0005515|GO:0017147|GO:0048471|GO:2000810|GO:0008285|GO:0005886|GO:0060715|GO:0090263|GO:0060
670|GO:0044332|GO:0031076|GO:0000578|GO:0045944|GO:0030182|GO:0060716|GO:0060718|GO:0048469|GO:0
043507|GO:0008595|GO:0071219|GO:0060070|GO:0031625|GO:0032729|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_105294_PI430048170 0.2490835373410610.9703681388605620.321743119907387
0.3692490742292680.325340818788726A A A 0.4329617227107330.343877709008026
0.368696841039304A A A LNCV6_105294_PI430048170 mRNA
AAGGTCCTGGAATCTCAAAATTTGTTCAGAAAGTAAATGAAATAGGCATTTACCTGACTG NM_001776RefSeq chr10
+ 95755915 95877266 ENTPD1953 "ectonucleoside triphosphate diphosphohydrolase 1, transcript variant
1"
GO:0005515|GO:0017111|GO:0017110|GO:0005886|GO:0006200|GO:0005605|GO:0030168|GO:0005524|GO:0007
186|GO:0016020|GO:0005887|GO:0007596|GO:0009181|GO:0007155|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141014_PI430048170 0.2655070564684521.0461966468632 0.354620634427848
0.3585540645074970.483284896780919A A A 0.3306683045401920.309207160259912
0.364332897021269A A A LNCV6_141014_PI430048170 mRNA
CCAAGTGATCTGCCTTTCAGCAACTGTCTTATTTTGGTTCTTTGAAACTGTGATTTTTAT NM_020922RefSeq chrX -
54192822 54358005 WNK3 65267 "WNK lysine deficient protein kinase 3, transcript variant 1"
GO:0005515|GO:0010800|GO:0043066|GO:2000651|GO:0051928|GO:2000682|GO:0032414|GO:0005524|GO:2000
688|GO:0019869|GO:0035556|GO:0005737|GO:0046777|GO:0004672|GO:0005912|GO:0004674|GO:0010765|GO:0
006468|GO:0005923|GO:2000021|GO:0090004 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134037_PI430048170 0.1647488356684531.05599406958157 0.462785437015716
0.4254442654236960.481480817136735A A A 0.3117994517165020.374099670136876
0.445465751793517A A A LNCV6_134037_PI430048170 mRNA
GACACCCGAAGTGCATTGCGTGTTTCTGTTCAGTTTAATGACGATTAATAAATATTTATG NM_006160RefSeq chr17
- 39603767 39607922 NEUROD2 4761 neuronal differentiation 2
GO:0008306|GO:0090129|GO:0000977|GO:0003700|GO:0016567|GO:0046982|GO:0006357|GO:0021695|GO:0003
714|GO:0070888|GO:0005634|GO:0001228|GO:0006351|GO:0050850|GO:0007399|GO:0071257|GO:0051091|GO:0
031915|GO:0048666|GO:0045666|GO:0045944|GO:0071277|GO:2000297|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144172_PI430048170 0.1741944865994331.17769267765339 2.71216452148297

2.75205197684754 2.40226676117094 A A A 2.35818247704941 2.26230435772286
2.54806755994164 A A P LNCV6_144172_PI430048170 mRNA
TGCCACTGTGGCTGCTCTGTGGCCTGAAGGTCTTGGCCAAGAAATGTAGACCTTTCCCCA NM_181532 RefSeq chrX
+ 48826512 48829869 ERAS 3266 ES cell expressed Ras
GO:0006184|GO:0005886|GO:0007264|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74881_PI430048170 0.00948000227246544 0.3255069233120381.16177247710057
1.84136519437301 2.02209777443343 A A A 2.87455072624333 3.45827098464109
3.58923504110028 P P P LNCV6_74881_PI430048170 mRNA
TTGCTACAAGAAGAAAGGTCAAGCCAGCGCCTTTAGAAATAAAACCTTTGCCAGAATGGG NM_207123 RefSeq chr4
+ 143336829 143474565 GAB1 2549 "GRB2-associated binding protein 1, transcript variant 1"
GO:0005515|GO:0008286|GO:0030334|GO:0060711|GO:0048011|GO:0008283|GO:0048015|GO:0007257|GO:0005
829|GO:0007507|GO:0007173|GO:0008544|GO:0008543|GO:0045087|GO:0005070|GO:0070102|GO:0048008|GO:0
004871|GO:0006979|GO:0038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139003_PI430048170 0.0305951529529420.61566111487891 5.66324749702478
5.17869280009955 5.14093451676799 P P P 5.81777868844446 6.16998614770715
6.13018881371842 P P P LNCV6_139003_PI430048170 mRNA
TACCAGTGATGAGGAAGGTGAACCTTCCGGAAAGAGAAAAGCAGAAGATGATGATAAAGC NM_138792 RefSeq
chr15 - 51938024 51971801 LEO1 123169 "Leo1, Paf1/RNA polymerase II complex component,
homolog (S. cerevisiae), transcript variant 1"
GO:0005515|GO:0006378|GO:0033523|GO:0005730|GO:0001711|GO:0006351|GO:0045638|GO:0045944|GO:0019
827|GO:0032968|GO:0016593|GO:0005654|GO:0016055|GO:0010390|GO:0031442 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139820_PI430048170 0.0410107243800410.1798980970084520.313137814944807
2.11280692714623 2.34614156587776 A A A 3.84738162623579 4.35121688281858
4.60935438773102 P P P LNCV6_139820_PI430048170 mRNA
ATGGTAGCAAACAGTGATGTTGATGGAATGAGAATCATGAACTTTCATATTACCTCAAAG NM_176787 RefSeq chr18
- 62044224 62187056 PIGN 23556 "phosphatidylinositol glycan anchor biosynthesis, class N, transcript
variant 1"
GO:0006501|GO:0016020|GO:0016254|GO:0005789|GO:0016021|GO:0044267|GO:0016740|GO:0043687 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65802_PI430048170 0.6047247094110810.9421049490364866.70612849699717 6.39835695508993
6.88610858564878 P P P 6.59674301865436 6.88721102793833 6.79122378658633 P P P
LNCV6_65802_PI430048170 mRNA
TAAAAAGGTGGTAGAAGTATGGATTGGAATGACTATTGAGGAACTGGCCAGGGCAATGGA NM_001005369
RefSeq chr2 - 55236619 55269179 MTIF2 4528 "mitochondrial translational initiation factor 2,
transcript variant 1"
GO:0070124|GO:0005739|GO:0032543|GO:0006996|GO:0006446|GO:0003924|GO:0003743|GO:0005654|GO:0043
024|GO:0032790|GO:0005525|GO:0008135 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81407_PI430048170 0.7457794234508391.04108824240021 4.42968781822103 4.60407725579088
4.25778319382488 P P P 4.76166389565802 4.1811367487425 4.1016904118318 P P P
LNCV6_81407_PI430048170 mRNA
TTGTTGCTGTGTGAGGCGCCCTTCTGCTGCCAGTTCATCGAGTTTGCAAACACAGTGGCG NM_001242369 RefSeq
chr9 + 133459964 133470787 CACFD1 11094 "calcium channel flower domain containing 1,
transcript variant 3" GO:0008150|GO:0003674|GO:0005262|GO:0030285|GO:0070588|GO:0048488|GO:0005575
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133683_PI430048170 0.6631196529897350.9702745953134090.579997025556303
0.5013664459347060.291842808692353 A A A 0.4173819564590530.578921650155738
0.518068432644722 A A A LNCV6_133683_PI430048170 mRNA
ACCAGGGCACACAGTGTGCCTGTGAAAATTTGGCACCTACATTTGTATCAAAGTATGTCC NM_003446 RefSeq chrX

+ 47370599 47413699 ZNF157 7712 zinc finger protein 157
GO:0006355|GO:0003700|GO:0005634|GO:0000122|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138808_PI430048170 0.2447472927537651.03578975201261 0.576226715966812
0.6251559109886130.523723027102823A A A 0.5682591552632480.503088331081212
0.502349783202759A A A LNCV6_138808_PI430048170 mRNA
GAACAACTAAATTGGATTACCGAAGGCTATTGTTAAAAATTACGTTCCGTGGTGACTCAT NM_013940RefSeq chr19
- 15807006 15808126 OR10H1 26539 "olfactory receptor, family 10, subfamily H, member 1"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_44312_PI430048170 0.128667430193351 1.03673560191891 0.3350714912992550.348527104651853
0.278903377146206A A A 0.2634545295869010.27975172473806 0.26403370706578 A A A
LNCV6_44312_PI430048170 mRNA
TGGATGCAAACTCCCTTTGTGTTTCTGGCTTTAAGCAGCTCTATACTCTCATGCTGTCCT NM_001286997 RefSeq
chr1 - 103418078 103525483 LOC101928436 NA uncharacterized LOC101928436 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136273_PI430048170 0.4591477686012720.74590175984944 0.791458891827533
1.26063041698484 0.380643386555048A A A 0.4565082943725681.70859816712669
1.39914711707741 A A A LNCV6_136273_PI430048170 mRNA
GCCTCACAACTTCTGGTGCATGAAAGGACTCACACTGTAGAGCAACCCTATGAATATAAG NM_001136501 RefSeq
chr19 + 12064730 12077811 ZNF844 284391 zinc finger protein 844
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137340_PI430048170 0.1614004898120151.08663284244786 0.544533030160477
0.4301214548897830.573250095096455A A A 0.2992514970493230.400244989033486
0.486667354906085A A A LNCV6_137340_PI430048170 mRNA
TACCTTCAATGGGAACTTAAACTGTTACATGTATCACATTCCAGCTACAATACTTCCATT NM_003013RefSeq chr4
- 153780589 153789076 SFRP2 6423 secreted frizzled-related protein 2
GO:0017147|GO:0030308|GO:0030307|GO:0090263|GO:0050680|GO:0050732|GO:0005615|GO:0002063|GO:0030
199|GO:0031668|GO:0010667|GO:0061185|GO:0048018|GO:0030336|GO:0004930|GO:0001843|GO:0048546|GO:2
000035|GO:0071425|GO:0005178|GO:0060349|GO:0061056|GO:0045600|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143851_PI430048170 0.6033679898158971.0694453147811 9.40137621974967
9.16117325224896 9.00936676909214 P P P 9.29770859228126 9.13986846318363
8.83308747480771 P P P LNCV6_143851_PI430048170 mRNA
GAGAAGGTTCGTGGGAGGGGCCTCCAAAATAAAAATGGAAACTGCATTGAAAATCAAAAA NM_203397RefSeq
chr7 + 100126696 100128498 MBLAC1 255374 metallo-beta-lactamase domain containing 1
GO:0016787|GO:0008152|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128965_PI430048170 0.7988827443515020.9736666001670962.13314585745987
1.70859816712669 2.89159552706622 A A P 0.8063790554378553.30081087936722
1.95616807275252 A P A LNCV6_128965_PI430048170 mRNA
TGTCCGGAAGACATGGATTGTCTGGAAGATGTGGATTTTCTGGAAGCTCAGGATTATCTG NM_004065RefSeq chrX
- 140783259 140784558 CDR1 1038 "cerebellar degeneration-related protein 1, 34kDa" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_110503_PI430048170 0.0229697101746468 1.58701664231323 4.1256739672931
4.18860704308273 4.51698460484602 P P P 3.59854245423256 3.85332053544091
3.37145412983717 P P P LNCV6_110503_PI430048170 mRNA
GAGGCCATTTTGAGCCTTACTCTTAAGTTCTCTATGAAGAACTACATTGATTTGTTGGCT NM_152391RefSeq chr2
+ 11155371 11178872 PQLC3 130814 "PQ loop repeat containing 3, transcript variant 1" GO:0016021

. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138165_PI430048170 0.6529894446031890.7425925103990932.2928137924047
0.36021761148182 1.21310336399101 A A A 0.8137360501859921.42747164011313
2.80770281006382 A A P LNCV6_138165_PI430048170 mRNA
GTGCTTGTGGTCTGTGCTTGCTCAGAAAAACAAACAAACAAACAGTTTTTCCAATTATAA NM_207577RefSeq chr11
- 75602859 75668434 MAP6 4135 "microtubule-associated protein 6, transcript variant 2"
GO:0032418|GO:0008017|GO:0005515|GO:0048813|GO:0005516|GO:0048471|GO:0005794|GO:0005874|GO:0006
810|GO:0000226 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132334_PI430048170 0.28603278461833 1.02731086631225 0.302784372403904
0.2527734220947140.345594304190791A A A 0.2709375833125120.244724782314561
0.270211743840324A A A LNCV6_132334_PI430048170 mRNA
CAGAAGGATAGCCTTACCCTTTAAATAACACAGTTAAGGTACACTGTGGAATTAGAAATA NM_152624RefSeq chr5
+ 112976709 113022195 DCP2 167227 "decapping mRNA 2, transcript variant 1"
GO:0005515|GO:0010467|GO:0016896|GO:0030054|GO:0030145|GO:0003723|GO:0043928|GO:0006402|GO:0050
072|GO:0043231|GO:0005829|GO:0016442|GO:0000184|GO:0000932|GO:0071044|GO:0005654|GO:0000288 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142189_PI430048170 0.00048310488940197 2.48725185084584 6.3383665893425
6.64561133842367 6.46455936381103 P P P 4.99340022666827 5.28947592885973
5.22221400560546 P P P LNCV6_142189_PI430048170 mRNA
TGCCAACTTGGTTTTTTAACTCCTCTCACCCTGTTAGCTCTGATTAAAAACACTGCAACC NM_030765RefSeq chr12
+ 122203680 122207537 B3GNT479369 "UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4"
GO:0005975|GO:0030311|GO:0016266|GO:0044281|GO:0008378|GO:0042339|GO:0008532|GO:0000139|GO:0006
493|GO:0018146|GO:0009405|GO:0016021|GO:0044267|GO:0030203|GO:0043687 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143586_PI430048170 0.000134850238258137 16.3435271577487 7.14565011572972
7.75377588714177 7.25583477405164 P P P 3.75519221704502 3.18322465650013
3.11021413823498 P P P LNCV6_143586_PI430048170 mRNA
AGGGACCGGCAGCCCTGGAAGGGGCACTTGATATTTTTCAATAAAAGCCTTTCGTTTTGC NM_001306RefSeq chr7
- 73768996 73770270 CLDN3 1365 claudin 3
GO:0003382|GO:0007165|GO:0001666|GO:0016338|GO:0005887|GO:0005198|GO:0016021|GO:0005923|GO:0016
328|GO:0070062|GO:0042802|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134349_PI430048170 0.2149979637135730.8394354799326815.95394750160289
5.75137681727466 5.7082396666016 P P P 5.78311449320535 6.24375269124094
6.11798390595156 P P P LNCV6_134349_PI430048170 mRNA
TAACAACCGCTGGGGTGAATATCACCCTTATAGTAATGTGCTCTGGTTACATTACCTGAC NM_031965RefSeq chr17
+ 3723902 3726698 GSG2 83903 germ cell associated 2 (haspin)
GO:0090231|GO:0005515|GO:0005813|GO:0005694|GO:0005819|GO:2000134|GO:0005634|GO:0071459|GO:0003
677|GO:0005524|GO:0072354|GO:0035556|GO:0005737|GO:0004672|GO:2000751|GO:0006468|GO:0007064 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135955_PI430048170 0.00638723460131083 0.447856143080699 5.37719647217891
5.05931583199023 5.46562609754749 P P P 6.14421523855737 6.49760145542205
6.71195955490996 P P P LNCV6_135955_PI430048170 mRNA
TTGCCCTTTTTTAGCAAGTGTGTGAATTCACAGTGCTTTTCTATGAATAAATCATGGATC NM_020883 RefSeq chr1
- 45016403 45206578 ZSWIM5 57643 "zinc finger, SWIM-type containing 5"
GO:0008270|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144809_PI430048170 0.647185591211227 0.921234518388295 0.355786360792921
0.380176050732765 0.310697201613808 A A A 0.801657958811711 0.285448187079583
0.24651226968073 A A A LNCV6_144809_PI430048170 mRNA
CACTCACTGTGTTTGGTTACTGTCAAGAAATCAATAAATGTGTTTAACAAGTTACCCAGT NM_001082533 RefSeq

chr17 - 51630312 52159801 CA10 56934 "carbonic anhydrase X, transcript variant 1"
GO:0003674|GO:0007420|GO:0005575 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_128233_PI430048170 0.0601796501436182 0.485339627179367 10.6070946234817
9.63958632278008 9.63551912773827 P P P 11.2817608335198 11.0864200023503
10.8391050850599 P P P LNCV6_128233_PI430048170 mRNA
CCCTCTCCCAGGTGTCAGATAATGCTCGTAAATGCCTTAGTCCATCATCTCAGTAAATTT NM_001083614 RefSeq
chr16 - 23522012 23557375 EARS2 124454 "glutamyl-tRNA synthetase 2, mitochondrial, transcript
variant 1"
GO:0005739|GO:0010467|GO:0050561|GO:0070127|GO:0006424|GO:0000049|GO:0004818|GO:0005759|GO:0005
524|GO:0006418 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138738_PI430048170 0.453381114351387 0.67316959774872 0.456332355909989
0.469175043796039 1.85223993220377 A A A 1.4353227778498 0.659076954399396
2.3714746216305 A A A LNCV6_138738_PI430048170 mRNA
CTGTGCATTCAATACCTTAATGGAACTCGAGGTGGAGCTTATGAAATTTGTGTCCAAAGT NM_001012971 RefSeq
chr20 + 56524728 56526152 FAM209A 200232 "family with sequence similarity 209, member A"
GO:0008150|GO:0003674|GO:0005634|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_54679_PI430048170 7.36099446561303e-06 3.48267656224552 6.73247197943136
6.87016718836836 6.7491707324417 P P P 4.96121830440981 5.05854956524792
4.93235146434923 P P P LNCV6_54679_PI430048170 mRNA
CCATGACACTCACAGAACATTCACAACCTTTATTATGGGTGAGAGCTTCACTACAACTTT NM_001012758 RefSeq
chr1 + 145845632 145848575 NUDT17 NA nudix (nucleoside diphosphate linked moiety X)-type
motif 17 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132199_PI430048170 0.000689826086664635 2.49148986250161 6.45543772678635
6.4697927124005 6.53287080052361 P P P 5.27572666303163 5.16362264147708
5.06090016394466 P P P LNCV6_132199_PI430048170 mRNA
GTGCTTTTTTGTTTCTTTTGTTATTTTTGGTTGGGTGGGTGGGAAGGTCTCTTTAAAATG NM_005704 RefSeq chr1
+ 29236515 29326813 PTPRU 10076 "protein tyrosine phosphatase, receptor type, U, transcript
variant 3"
GO:0005515|GO:0030336|GO:0008285|GO:0005886|GO:0008013|GO:0031100|GO:0051384|GO:0035335|GO:0030
154|GO:0034109|GO:0016337|GO:0006470|GO:0005001|GO:0005887|GO:0005911|GO:0034394|GO:0007185|GO:0
007155|GO:0060070|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140683_PI430048170 0.679133282080558 1.01721807592839 0.53988835107996
0.401415120178743 0.535451486141614 A A A 0.423206849956746 0.511237354930836
0.471325348904893 A A A LNCV6_140683_PI430048170 mRNA
CACATGGAAAGAACTGTATGCAGTTGACTTTACTATGTAAATTGGAGGGAAACAAAGTTT NM_180991 RefSeq
chr5 - 102233985 102296549 SLCO4C1 353189 "solute carrier organic anion transporter family,
member 4C1"
GO:0016323|GO:0005215|GO:0005886|GO:0043252|GO:0007275|GO:0016021|GO:0007283|GO:0055085|GO:0030
154|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101033_PI430048170 0.538061943184831 1.45573238470214 2.05348714143385
3.11227017892296 1.32356741124896 A P A 2.22744489870979 1.78358425965068
1.25414360920494 A A A LNCV6_101033_PI430048170 mRNA
TTTGAGAGCAGCTTCTGGCACATGCAGGAGAAGCTGGGCATTGTGCAGGGCATCGTAGGT NM_002292 RefSeq
chr3 - 49121113 49133166 LAMB2 3913 "laminin, beta 2 (laminin S)"
GO:0072249|GO:0060041|GO:0005605|GO:0014044|GO:0045202|GO:0005576|GO:0005608|GO:0048677|GO:0043
260|GO:0005604|GO:0031012|GO:0005178|GO:0072274|GO:0005198|GO:0007411|GO:0007528|GO:0014002|GO:0
030198|GO:0007155|GO:0007601|GO:0070062 . NA - . NA NA NA NA NA NA NA NA

NA
LNCV6_141187_PI430048170 0.232456054159738 1.0192002081102 0.311758461129841
0.255622367606771 0.287916934433475 A A A 0.260981894993236 0.250875332546179
0.261652503970212 A A A LNCV6_141187_PI430048170 mRNA
TGTTCAGGGCTGTGATCGGCCTGGGGAAATAATAAAGATGTTCTTTTAAACGGTAAAAAA NM_021006 RefSeq
chr17_KI270909v1_alt - 250577 252466 CCL3L1 NA "chemokine (C-C motif) ligand 3-like 1, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131433_PI430048170 0.408448983804997 0.824869144312351 2.85731607458171
1.72759166410209 1.9926843919393 A A A 2.73645828947416 2.46697482136671
2.44139525611885 P P P LNCV6_131433_PI430048170 mRNA
TGGGAAACTAAAGTAGAAAAAGCACATCACAAAGAAACATATATAGTACAGTGTGATCCC NM_006112 RefSeq
chr1 + 39738844 39756769 PPIE 10450 "peptidylprolyl isomerase E (cyclophilin E), transcript
variant 1"
GO:0005515|GO:0000413|GO:0016018|GO:0006355|GO:0000166|GO:0006457|GO:0000398|GO:0003723|GO:0003
755|GO:0005634|GO:0071013|GO:0045070 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_133179_PI430048170 0.281943977451806 0.659676452943153 3.95522785629001
3.67661006030761 4.89520946042997 P P P 4.12105326429987 5.07974055285085
5.2011685692666 P P P LNCV6_133179_PI430048170 mRNA
GTAATAAGCAGTTTCTGCTGCTGGTCTGTCATTGAATGCCTTGTTTTCACTAAGAAAAAA NM_017858 RefSeq
chr15 - 66336669 66356716 TIPIN 54962 "TIMELESS interacting protein, transcript variant 1"
GO:0005515|GO:0000790|GO:0008284|GO:0005794|GO:0033262|GO:0048478|GO:0031573|GO:0005634|GO:0043
231|GO:0005737|GO:0007067|GO:0000076|GO:0005654|GO:0009411|GO:0051301 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_136863_PI430048170 0.678816103128273 0.841941645274861 1.42158382131839
2.26575712600277 2.55040568939135 A A A 2.69177481734765 1.53588399553727
2.69833858666379 P A P LNCV6_136863_PI430048170 mRNA
TTGAGAATGTTTTTACCTTTTCACAACTGCAGGGGTTACTGAAAGGTTTTTCATTCCAAG NM_001271420 RefSeq
chr17 + 15999379 16029409 TTC19 54902 "tetratricopeptide repeat domain 19, transcript variant 2"
GO:0005739|GO:0005515|GO:0000910|GO:0034551|GO:0005813|GO:0005743|GO:0030496 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_77809_PI430048170 0.959927498909416 0.98750164328501 0.262715314532751
0.422558467550812 1.51769814989831 A A A 0.4935966133361 1.50626264674022
0.290519951231356 A A A LNCV6_77809_PI430048170 mRNA
GAGAGTTGGCATCTTGGAAATCAAAGACGGTTGTGATGCAGTTTTTTGATATGAGGATAA NM_006734 RefSeq
chr6 - 142751466 142945201 HIVEP2 3097 human immunodeficiency virus type I enhancer binding
protein 2 GO:0006355|GO:0005654|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133423_PI430048170 0.0269517990544146 0.941327222062483 0.392291408233637
0.339152429546344 0.338407403765964 A A A 0.472560554241473 0.449091712492416
0.409864469738191 A A A LNCV6_133423_PI430048170 mRNA
ACAACAATATAATGAAGACAGAAATCCAATATCTACATAGCCCTGTTGCTTAGCAACCAC NM_003008 RefSeq
chr20 + 45221368 45224458 SEMG2 6407 semenogelin II
GO:0019953|GO:0005198|GO:0005634|GO:0030141|GO:0005615|GO:0070062 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_143191_PI430048170 0.497919253367436 1.7789268314588 2.32322050720781
0.529941186922732 0.291295262965874 A A A 0.410790180743029 0.61705770008236
0.535660168415796 A A A LNCV6_143191_PI430048170 mRNA
ATTCAAAACAGTGAATGCAGACTGGAGGAGTAACTTTTGCAAATAAGATGAATATGCTTC NM_023003 RefSeq

chr15 + 83107571 83137359 TM6SF1 53346 "transmembrane 6 superfamily member 1, transcript variant 1" GO:0008150|GO:0003674|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138889_PI430048170 0.00222079402457248 0.59837070903356 11.0573517740165 10.7957008034822 10.991428190681 P P P 11.6095369814006 11.6328082615409 11.8273906080072 P P P LNCV6_138889_PI430048170 mRNA AGAAACTGGAGGGCCTTTGACTTCAAGGAATTCTCTCATTTGGAGGACTTTCCCTTCGAT NM_001080538 RefSeq
chr7 + 134549096 134579840 AKR1B15 NA "aldo-keto reductase family 1, member B15" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127355_PI430048170 0.896648206649514 0.964455924077298 3.15262851944711 3.77183382644733 3.64958821428626 A P P 3.85679003153556 3.11194770592667 3.72924186599295 P P P LNCV6_127355_PI430048170 mRNA GATGGGTGGCCACTGTACAGATATTTATTACGCTTTCCAGACTTTCTGAATAGATTTTTT NM_021135 RefSeq chr6
- 166409365 166627238 RPS6KA2 6196 "ribosomal protein S6 kinase, 90kDa, polypeptide 2, transcript variant 1"
GO:0005515|GO:0060047|GO:0034142|GO:0008285|GO:0070613|GO:0007268|GO:0005634|GO:0001556|GO:0051403|GO:0005829|GO:0035556|GO:0007507|GO:0002756|GO:0005737|GO:0018105|GO:0007411|GO:0002755|GO:0034138|GO:0048011|GO:0031965|GO:0043065|GO:0038124|GO:0000287|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113476_PI430048170 0.00541365441015572 0.394156754458004 10.5745192621077 10.5171665878966 10.6529523497238 P P P 11.7575617584747 11.8177005274504 12.1673002686497 P P P LNCV6_113476_PI430048170 mRNA GGAGAGTCAGATCTTTCTCCTTGAATATCTTTCGATAAACAACAAGGTGGTGTGATCTTA NM_002970 RefSeq
chrX + 23783157 23786223 SAT1 6303 "spermidine/spermine N1-acetyltransferase 1, transcript variant 1"
GO:0005515|GO:0001525|GO:0032918|GO:0044281|GO:0005829|GO:0005622|GO:0034641|GO:0006596|GO:0019809|GO:0042127|GO:0006595|GO:0004145|GO:0009447 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63261_PI430048170 0.99544174180156 0.959900905535764 1.36695832873095 0.287114482869824 0.522986101281043 A A A 0.297728983257086 0.277936835147229 1.59142275011383 A A A LNCV6_63261_PI430048170 mRNA TCCCCAACCAAGTCCACCGAAAGTCCGTGAAGAAAGGCTTTGACTTTACCCTCATGGTGG NM_080415 RefSeq
chr17 - 58520249 58532084 SEPT4 NA "septin 4, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127707_PI430048170 0.00397778948177783 0.545646537047481 9.24862761221732 9.30770287529224 9.59798293886567 P P P 10.1122035779636 10.2237725055228 10.4448733982443 P P P LNCV6_127707_PI430048170 mRNA GCCAGGAATACAGGTTTTCTTGATGATTTGGGTTTTAATTTTGTTTTTATTGCACCTGAC NM_002880 RefSeq chr3
- 12583600 12664201 RAF1 5894 "Raf-1 proto-oncogene, serine/threonine kinase"
GO:0005515|GO:0031267|GO:0045104|GO:2000145|GO:0042802|GO:0007507|GO:0034220|GO:0007173|GO:0007411|GO:0000165|GO:0004709|GO:0005794|GO:0046982|GO:0030168|GO:0031434|GO:0008543|GO:0045087|GO:0042060|GO:0045595|GO:0038095|GO:0008286|GO:0008285|GO:0005886|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118503_PI430048170 0.00845427191831049 0.665199063529189 12.1706359984772 11.9071247014726 11.9597160685866 P P P 12.5325229393128 12.654032952328 12.6262375060978 P P P LNCV6_118503_PI430048170 mRNA CCAGCTCGCCCAGCGTCCGCCGCGCCTCGGCCAAGCTTCAACGGACCACACCAAAATGCC NM_002966 RefSeq
chr1 - 151982909 151994238 S100A10 6281 S100 calcium binding protein A10
GO:0005515|GO:0005509|GO:0051099|GO:0051290|GO:0006900|GO:0051894|GO:0032855|GO:0042803|GO:0008

289|GO:0044325|GO:1900026|GO:0051496|GO:0045121|GO:0090002|GO:0001765|GO:0019897|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136998_PI430048170 0.285694631656008 1.1733063366899 8.41537664772386 8.54773180289423 8.91521577569331 P P P 8.25492727065319 8.43173138339706 8.53375786948645 P P P LNCV6_136998_PI430048170 mRNA CCTGATGTGTTAACAAATAGGTGAAGAAAGTCTTGTGCTGTATTCCTAATCAAAAGACTT NM_032016 RefSeq chr7 + 38178205 38230671 STARD3NL 83930 STARD3 N-terminal like
GO:0016020|GO:0031902|GO:0016021|GO:0005765|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130474_PI430048170 0.164981570186252 1.03957314452713 0.37672999748625 0.384585144469654 0.460991508756654 A A A 0.344637128416329 0.329239370913744 0.381466674508657 A A A LNCV6_130474_PI430048170 mRNA CTTTTCTACCCACTTTTACCCATAACTTTTCCAAATTTGGTTCAAATTGTGCAGAGAAAC NM_001001786 RefSeq chr11 - 122115353 122116215 BLID 414899 "BH3-like motif containing, cell death inducer"
GO:0005739|GO:0006915 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138833_PI430048170 0.235364586900059 1.01942803533959 0.312466276244726 0.255103713305052 0.286699735219385 A A A 0.260146969767345 0.25046058445503 0.260930565358259 A A A LNCV6_138833_PI430048170 mRNA CATTCAGTATTAGTTGATGATTTCTGCTATTAAGTGATGAGAAAGTCAGCAGACTAGTCA NM_001017440 RefSeq chr7 - 71779490 72337223 CALN1 83698 "calneuron 1, transcript variant 2"
GO:0048471|GO:0005886|GO:0005509|GO:0016021|GO:0032588 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142332_PI430048170 0.121820093290072 1.06814418118146 0.462440999870736 0.516473440950038 0.530877120562073 A A A 0.336846148179546 0.410664562047367 0.474572064226533 A A A LNCV6_142332_PI430048170 mRNA CCTGTTCTATGTTAACTACCCAAGGACTAGTATAAGTAGGAGTTGTTTTTACCTTTTAAG NM_001145346 RefSeq chrX + 115189399 115192868 RBMXL3 139804 "RNA binding motif protein, X-linked-like 3"
GO:0000166|GO:0003723 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138157_PI430048170 0.440330678331869 0.817971097966576 3.59352709513825 2.51127628286529 2.42957467999425 P A A 3.37473695513793 3.42086888355532 2.85425739043613 P P P LNCV6_138157_PI430048170 mRNA TTAGGCAAGGGTGTGTGGCGTTGGTTTTAACTGCATTAAAAGTACTTTTGTAAAATCCTG NM_001105565 RefSeq chr11 + 57542640 57550274 SMTNL1 NA smoothelin-like 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136799_PI430048170 0.521113542505186 1.05805959243224 0.501667750154068 0.398538813270672 0.723872621981942 A A A 0.395550929320193 0.500188989835684 0.500936205563506 A A A LNCV6_136799_PI430048170 mRNA CAACTGTAAACATCTGTCCATTGGTGTAGCTTTACAAACCATTCACTGATTTTGTGTAAT NM_001077188 RefSeq chrX - 132626009 132961395 HS6ST2 90161 "heparan sulfate 6-O-sulfotransferase 2, transcript variant L"
GO:0000139|GO:0005975|GO:0009405|GO:0005654|GO:0044281|GO:0016021|GO:0030203|GO:0017095|GO:0015015|GO:0006024|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135059_PI430048170 0.152942870166161 1.51486160547767 9.36904858889189 9.2395916478916 9.58560180357351 P P P 9.32763942771743 8.31094255692697 8.5798529979145 P P P LNCV6_135059_PI430048170 mRNA CCTCTTTAGGCGTGGTTGAGAAAAAGCAGAAACTTTACATAAAGCTGTATTTCTTAATCA NM_012328RefSeq chr7 + 108569744 108574850 DNAJB94189 "DnaJ (Hsp40) homolog, subfamily B, member 9"
GO:0051787|GO:0005515|GO:0005737|GO:0005783|GO:0005789|GO:0005730|GO:0005788|GO:0030433|GO:0006987|GO:0044267|GO:0070062|GO:0030968 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133540_PI430048170 0.3168902529987331.2284784147843 6.88906543510341
6.35535171314928 6.22240008563349 P P P 6.3024832307343 6.33342710311072
6.00766196915681 P P P LNCV6_133540_PI430048170 mRNA
TGACCCTGCAAACAGCCAGAAGGCATCACCCAAAAAGATGCCCAAGTCAGGGGGCAAGAG NM_145288RefSeq
chr19 - 45071499 45076430 ZNF296 162979 zinc finger protein 296
GO:0003674|GO:0006355|GO:0005634|GO:0007283|GO:0005575|GO:0003677|GO:0046872|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110209_PI430048170 0.5282285570853411.03848685492693 7.60384662658833
7.81524142115674 7.66075241047917 P P P 7.72263177915168 7.60925841359368
7.58925963402787 P P P LNCV6_110209_PI430048170 mRNA
GTCTATCCAGGAAGCTTACCAGCTGCTGCTGACCGACCACACTGTGACCTTCCTGCAGTA NM_207346RefSeq chr17
+ 75516527 75524739 TSEN54 283989 TSEN54 tRNA splicing endonuclease subunit
GO:0006397|GO:0006388|GO:0005730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141283_PI430048170 0.6440351353092480.9700570737330740.551462533357786
0.4851193629662620.273342308276583A A A 0.4116059386544240.544306171641805
0.496862659170448A A A LNCV6_141283_PI430048170 mRNA
AGATGCAATGGAGATGACAAATTTGGAAAAACCACTCATCACTTACATTTCATGAAGTAC NM_152606RefSeq chr19
+ 37551370 37614178 ZNF540 163255 "zinc finger protein 540, transcript variant 2"
GO:0017148|GO:0005515|GO:0005737|GO:0003700|GO:0005654|GO:0005634|GO:0045892|GO:0003677|GO:0046
872|GO:0006351|GO:0043231|GO:0000900 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108617_PI430048170 0.3021278681815391.81686197471201 1.26642505970937
2.13855499632585 0.377097829447728A A A 0.5107383264044810.38992303636484
0.78852424221982 A A A LNCV6_108617_PI430048170 mRNA
TGGAGAATGAGACAATAGGCTGCAGCAAGATGTGGGACAACCTCACCTGCTGGCCAGCCA NM_001251882
RefSeq chr3 + 42489298 42537573 VIPR1 7433 "vasoactive intestinal peptide receptor 1, transcript
variant 2"
GO:0043235|GO:0005515|GO:0008284|GO:0006955|GO:0006936|GO:0007186|GO:0005886|GO:0004999|GO:0007
187|GO:0005887|GO:0007586|GO:0007268 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137760_PI430048170 0.2787772560245040.9457597299078787.37508896882013
7.21650466145146 7.24466653541353 P P P 7.27636840176902 7.41026491626367
7.39237080723254 P P P LNCV6_137760_PI430048170 mRNA
GGTCCCTCATCTCTTGGGGCATAATCAATGCAACTTATGAGTTCTTGTTAAAGGTTATAT NM_033412RefSeq chr9
- 37887596 37904353 SLC25A51 92014 "solute carrier family 25, member 51, transcript variant 1"
GO:0006810|GO:0005743|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141812_PI430048170 0.0183765839243234 1.37840259717638 13.2850081357041
13.1859745813469 13.2767405943442 P P P 12.6888390708653 12.7135094552707
12.9444427352714 P P P LNCV6_141812_PI430048170 mRNA
GTGTGTTCTTTCCGGGATCACAAACATTAACAAAAAAGTTAACTTATGTGACTTGGCAGT NM_014222RefSeq chr9
- 122144058 122159819 NDUFA8 4702 "NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8,
19kDa"
GO:0022904|GO:0005739|GO:0005758|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0008137|GO:0032
403|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135323_PI430048170 0.0124616145635261 0.4660789687403927.3574050885574
7.3759456111086 7.78473592881159 P P P 8.31344873163076 8.51065664572017
8.96146088476768 P P P LNCV6_135323_PI430048170 mRNA
CGATATAAGTACTTTTACAGCAAGATGGTATAGTTATGTTGCCTGGACTGGTTTTTACAT NM_018164RefSeq chr12
- 26905178 26938321 ASUN 55726 asunder spermatogenesis regulator
GO:0005515|GO:0007346|GO:0051642|GO:0007067|GO:0005737|GO:0080154|GO:0005634|GO:0030317|GO:0007
052|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_136709_PI430048170 0.9669501532360060.9353389786507390.974039398245754
0.50608259901445 1.25286511915804 A A A 0.5173709457376041.78699587037058
0.360745011631809A A A LNCV6_136709_PI430048170 mRNA
GGTTCCCAAAAAGTAGGATGTAGGTATTTATTGTGTTCTAGAAATTCCGACTCTTTTCAT NM_033195RefSeq chr15
+ 59206815 59208586 LDHAL6B 92483 lactate dehydrogenase A-like 6B
GO:0005515|GO:0005737|GO:0044262|GO:0004459|GO:0005634|GO:0055114 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142233_PI430048170 0.0912862538293019 1.40669459886867 4.60450726966104
4.62895445529221 4.49349320260359 P P P 4.21451431670198 4.26072186188647
3.71834975205623 P P P LNCV6_142233_PI430048170 mRNA
ACTTGTGACAAGTACTCAGGTGTGAGGACAAGAATGCAAATGGCTCTTCCTTGAGTGAAA NM_020396RefSeq chr15
- 52109265 52112775 BCL2L10 10017 BCL2-like 10 (apoptosis facilitator)
GO:0005515|GO:0031965|GO:0043066|GO:0046982|GO:0008630|GO:0006919|GO:0005741|GO:2001243|GO:0007
283|GO:0007292|GO:0042803|GO:0097192|GO:0005829|GO:0005739|GO:0016020|GO:2001240|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_3452_PI430048170 0.35091107675451 1.19019401984132 10.4231535619298 10.6213988277833
11.0125088486126 P P P 10.2378689238554 10.3240775736801 10.7510674056318 P P P
LNCV6_3452_PI430048170 mRNA
TGAATGTGAGTACCCCTTCTGTGAACACTGAAAGCTATTCTCTTGAATTGATCTTAAGTG NM_001199815 RefSeq
chr7 - 30496620 30504841 GGCT 79017 "gamma-glutamylcyclotransferase, transcript variant 2"
GO:0003839|GO:0006805|GO:0006750|GO:0001836|GO:0044281|GO:0042803|GO:0070062|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144985_PI430048170 0.5278320563126011.37793204153779 0.269081774236178
1.65344277364304 0.444713707220832A A A 0.3486391610997280.303893919207382
0.711453350560848A A A LNCV6_144985_PI430048170 mRNA
TGTCCAATGCCGAATGCAAGAAGTCCTGGGGCAGGAGGATCACCGACGTGATGATCTGTGNM_001906RefSeq chr16
+ 75218985 75224924 CTRB1 1504 chymotrypsinogen B1
GO:0009235|GO:0022617|GO:0004252|GO:0030198|GO:0006766|GO:0007586|GO:0006508|GO:0006767|GO:0005
576|GO:0044281|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78933_PI430048170 0.0084861310493595 0.7025483628839489.15997919858171
8.99339212145518 9.05404992354249 P P P 9.42132110990371 9.64638112983625
9.66041238300643 P P P LNCV6_78933_PI430048170 mRNA
AGAATAGGCTACTGGAAAACCAAACCCAACAGAATTCACGTCCAAAAATCCACATTCTCC NM_030961RefSeq chr7
+ 101085438 101091738 TRIM56 81844 tripartite motif containing 56
GO:0004842|GO:0032479|GO:0016874|GO:0005829|GO:0005737|GO:0051607|GO:0070534|GO:0046597|GO:0045
087|GO:0008270|GO:0032481|GO:0034340|GO:0032608 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145479_PI430048170 0.0492971296505360.2629711121327512.24810918033858
0.7442594251649880.328614108185756A A A 2.71514892060926 3.31770711660488 3.6636985125862
P P P LNCV6_145479_PI430048170 mRNA
GGGACCATAAACACATATCACCCTACATTTTCTTTGCAACTACAATTTGTGAAGGAAAAT NM_198514RefSeq chr10
+ 113854631 113912506 NHLRC2 374354 NHL repeat containing 2NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135010_PI430048170 0.4985597196738411.25887762530683 0.282361811367741
0.3080746495718511.2429914400533 A A A 0.3839759197548180.320273028710498
0.351857114555587A A A LNCV6_135010_PI430048170 mRNA
ACAAACAAGAAAGGAAATACAACCAGCTTCAGCTGGAGAAGGGACAGACACCACCAGAAA NM_178828RefSeq
chr9 + 87882856 87888899 SPATA31E1 286234 "SPATA31 subfamily E, member 1"
GO:0016021|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134099_PI430048170 0.00574734663001439 0.4613654664884185.94713580111016

5.50817323191014 6.00203434296836 P P P 6.73486047443974 6.96801940294237
7.12498236272496 P P P LNCV6_134099_PI430048170 mRNA
GTACAACTTTCTGTACAATATTGATTCCCATCTGGCATATTCTAATCAGGTTATAGGTCA NM_006421 RefSeq chr8
- 67197648 67343677 ARFGEF1 10565 ADP-ribosylation factor guanine nucleotide-exchange factor 1
(brefeldin A-inhibited)
GO:0005802|GO:0005515|GO:0034237|GO:0048471|GO:0034259|GO:0090303|GO:0090284|GO:0006887|GO:0015
031|GO:0010256|GO:0016363|GO:0005829|GO:0005085|GO:0005086|GO:0005737|GO:0030837|GO:0007030|GO:0
030532|GO:0016192|GO:0005794|GO:2000114|GO:0005730|GO:0043547|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_116817_PI430048170 0.203724868710587 1.14226476183204 4.38019170801009
4.44969507356471 4.40603126201289 P P P 4.35172007280895 4.28658511364536 3.9989105042452
P P P LNCV6_116817_PI430048170 mRNA
CCCGACGCGGCGCCCTTCCTGCTAGGGCTGCTGACCAATGAACTGCCGCTTCCGAGTCCT NM_001010867 RefSeq
chr1 + 228165727 228182257 IBA57 200205 "IBA57, iron-sulfur cluster assembly homolog (S. cerevisiae)"
GO:0016226|GO:0005759|GO:0016740|GO:0006783 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55378_PI430048170 0.476698398320339 1.21600683149005 0.937632776772532 1.61241407444687
1.18011454169138 A A A 0.587432043091182 1.7076882959066 0.243814663158833 A A A
LNCV6_55378_PI430048170 mRNA
AATATGCTGGCTACAACTACCAAGCTTTTGACATTGGCAACCATTTCAATGAGTTTGCAG NM_001297760 RefSeq
chr1 - 204131060 204152182 ETNK2 55224 "ethanolamine kinase 2, transcript variant 2"
GO:0004305|GO:0006646|GO:0001890|GO:0005575|GO:0044281|GO:0009791|GO:0001701|GO:0005524|GO:0005
829|GO:0008150|GO:0016310|GO:0035264|GO:0006644|GO:0046474 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_114806_PI430048170 0.443958468780965 1.09532547860578 4.95995565693079
5.34605270625648 5.17199798665345 P P P 4.82128554038246 5.16341627679206
5.10242711091169 P P P LNCV6_114806_PI430048170 mRNA
TTACTAGTCCAAAGCAAAGTGTTTATCTTGATTTGACACTGGATATGGCACTGGGAAAGA NM_020236 RefSeq chr4
+ 77862650 77952790 MRPL1 65008 mitochondrial ribosomal protein L1
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0015
934|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131956_PI430048170 0.0816348285691043 0.342941315500416 0.588559780502144
0.439967481727434 0.582762798566594 A A A 1.62263405276405 2.8027845489949
1.40630998982345 A P A LNCV6_131956_PI430048170 mRNA
GAAAGCATGTGATCAGTTATTGCTGCATTAAAAACATGAGTCTTTTTTATTAGGTGGCCA NM_025189 RefSeq chr19
+ 21020619 21060046 ZNF430 80264 "zinc finger protein 430, transcript variant 1"
GO:0006355|GO:0021762|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130583_PI430048170 0.0246822401196562 0.599989155244353 6.04687000453513
6.00203434296836 6.51050654952668 P P P 6.7249305942285 6.91133429886345 7.1579944447252
P P P LNCV6_130583_PI430048170 mRNA
AAAGCTGGCCTTTTTTCTACGAATGCACTACATTAAAGATGTGCAACCTATGCGCCCCCT NM_001128918 RefSeq
chr14 + 103385363 103503829 MARK3 4140 "MAP/microtubule affinity-regulating kinase 3, transcript
variant 1" GO:0005515|GO:0005886|GO:0004674|GO:0006468|GO:0005524|GO:0070062 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_136638_PI430048170 0.13343005431765 0.394111023352982 2.49347117029233
0.314112330976008 0.42813577883429 A A A 1.96267894291247 3.03722983185392
3.12931874037988 A P P LNCV6_136638_PI430048170 mRNA
GATAATTGTCTTCTTAAGATGAGGTGCTTTTTATCTGTGGATGAATGGAAATCACACTGA NM_024548 RefSeq chr3
+ 101724592 101770562 CEP97 79598 "centrosomal protein 97kDa, transcript variant 1"

GO:0005515|GO:0043234|GO:0005516|GO:0005813|GO:0005737|GO:0006996|GO:0005815|GO:0030030|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101399_PI430048170 0.4039291356377221.61638368470227 0.271284766394516 1.77803443301752 1.99504341188735 A A A 1.49456187800772 0.319847575710048 0.343247122231446 A A A LNCV6_101399_PI430048170 mRNA
TTCACAATGAAGGCTACATCTTGGAATTAGATTGCTGTTCCTCCTTAGACCACCCGACAG NM_015150 RefSeq chr3 - 16315844 16513715 RFTN1 23180 "raftlin, lipid raft linker 1"
GO:0050853|GO:0003725|GO:0050852|GO:0005886|GO:0032596|GO:0043234|GO:0005737|GO:0045121|GO:0032620|GO:0001765|GO:0002457|GO:0033227|GO:0034138|GO:0040007|GO:0043330|GO:0070062|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112069_PI430048170 0.0377680215989788 1.46522567013675 8.06408713922956 8.30033730574013 8.16266985363437 P P P 7.34107651428756 7.79071774466792 7.71291865875025 P P P LNCV6_112069_PI430048170 mRNA
AACCCTTCATGATTTGACAAAGGTCACTTTCTGTTTGCCTGGACCAAGCTACTCCAGATC NM_032818 RefSeq chr9 - 35659343 35665281 ARHGEF39 84904 Rho guanine nucleotide exchange factor (GEF) 39
GO:0030335|GO:0005886|GO:0032321|GO:0005089 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133040_PI430048170 0.2824828049284381.02942835879194 14.5032549308996 14.499982461727 14.4704652647481 P P P 14.4231614424112 14.4161809920298 14.5072627795783 P P P LNCV6_133040_PI430048170 mRNA
CTGAAGTTGCCCTACTTTTAACTTTGAACTTGGCTAGTTCAAAGATAGACTCTTCTTTTGNM_002796 RefSeq chr1 + 151399564 151401936 PSMB4 5692 "proteasome (prosome, macropain) subunit, beta type, 4"
GO:0002474|GO:0010467|GO:0002862|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0004298|GO:0034641|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0005839|GO:0000502|GO:0043066|GO:0006521|GO:0051437|GO:0042590|GO:0006915|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140383_PI430048170 0.0786390343022421 0.5570886004603011.06233957373133 0.2757241430479570.294231723808755 A A A 1.36866062011426 0.969545557771961 1.84089502099903 A A A LNCV6_140383_PI430048170 mRNA
GGATTATCATTCTTAGCAACACGTAACCGAAGCAATATTCTTAAGAATATTGAAGGGGTT NM_032236 RefSeq chr1 - 21678298 21783195 USP48 84196 "ubiquitin specific peptidase 48, transcript variant 1"
GO:0005739|GO:0004197|GO:0016579|GO:0005737|GO:0004843|GO:0061136|GO:0043161|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54279_PI430048170 0.5199267941757841.12487027045984 5.51724797303856 5.6615609291074 5.51507085433744 P P P 5.61291114491255 5.64196670563556 4.78102199592429 P P P LNCV6_54279_PI430048170 mRNA
AGGGGACACAGGCTTCTTAAAACAACCCGGCTTCCTCACCCTATGTCCTTTATTTACAAA NM_052941 RefSeq chr1 - 89181147 89198950 GBP4 115361 guanylate binding protein 4
GO:0005737|GO:0008152|GO:0003924|GO:0005634|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127367_PI430048170 0.2982644518600881.05181377579531 0.477455423830496 0.6006333949812260.54726785613126 A A A 0.5665198481465680.415043991391921 0.422691755003102 A A A LNCV6_127367_PI430048170 mRNA
CAGTTGGATGGATTTTGTCAATCAGCTGGATATGCTGTTTAGTTTTTACAACATAGTACT NM_001272077 RefSeq chr18 - 42743217 43115692 RIT2 6014 "Ras-like without CAAX 2, transcript variant 2"
GO:0006184|GO:0007165|GO:0005516|GO:0048011|GO:0005886|GO:0007264|GO:0003924|GO:0007268|GO:0005634|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129552_PI430048170 0.2952253201112130.5668365753490740.321272366027594 2.84082900594716 2.48216578798587 A A A 3.22133252716638 2.38938774861359 3.3412167214824 P P P LNCV6_129552_PI430048170 mRNA

TTTGAATTATGTATGCTGTGCCTTTCTGAGGAGGCTAAGAATATACCATTCTGCTATTAA NM_004297 RefSeq chr9 - 77423078 77648316 GNA14 9630 "guanine nucleotide binding protein (G protein), alpha 14" GO:0001664|GO:0005886|GO:0005834|GO:0003924|GO:0030168|GO:0005525|GO:0031683|GO:0046872|GO:0006184|GO:0007165|GO:0007596|GO:0060158|GO:0007188|GO:0004871|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132778_PI430048170 0.0899786892309858 0.7776803489058916.81622671892533 6.95577089706017 7.23855966944678 P P P 7.17420382161507 7.39708617000581 7.53708752293914 P P P LNCV6_132778_PI430048170 mRNA
CACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTTGTTTAACCTCATTTA NM_032801 RefSeq chr11 + 134068924 134151757 JAM3 83700 "junctional adhesion molecule 3, transcript variant 1" GO:0005515|GO:0030057|GO:0001780|GO:0031103|GO:0005886|GO:0007286|GO:0030010|GO:0050900|GO:0019226|GO:0005615|GO:0042803|GO:0033010|GO:0030198|GO:0043220|GO:0005794|GO:0046982|GO:0002523|GO:0090138|GO:0042552|GO:0044291|GO:0001525|GO:0002250|GO:0005178|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2619_PI430048170 0.0174544520995513 1.42804334752932 12.1661412139524 12.5102315051663 12.374153951825 P P P 11.7262410117586 11.8199401558757 11.9721112160391 P P P LNCV6_2619_PI430048170 mRNA
TCTTGTATGAGAAACGGATCCGGATCACCTGTTTGAAACCATCTCCCAAGCCATGCTGAA NM_002795 RefSeq chr17_KI270857v1_alt + 2788031 2799550 PSMB3 5691 "proteasome (prosome, macropain) subunit, beta type, 3, transcript variant 1" GO:0005515|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0015629|GO:0031145|GO:0004298|GO:0005829|GO:0005739|GO:0034641|GO:0005737|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0043066|GO:0000502|GO:0005839|GO:0005794|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143891_PI430048170 0.00785792900904177 0.1348562014303472.32761465281282 1.45653352681511 1.13652314174447 A A A 4.36226028413804 4.67584876208257 4.79437046189981 P P P LNCV6_143891_PI430048170 mRNA
GTGCCAGAATTTTAGGAACTTCAGAGATCGTGTATTGAGATTTCTTAAATAATGCTTCAG NM_000321 RefSeq chr13 + 48303746 48481890 RB1 5925 retinoblastoma 1 GO:0051219|GO:0005515|GO:0003700|GO:0007070|GO:0097284|GO:0050680|GO:0071922|GO:0050681|GO:0051402|GO:0043353|GO:0031175|GO:0042802|GO:0035189|GO:0045445|GO:0000785|GO:0031625|GO:0001102|GO:0003713|GO:0005819|GO:0045842|GO:0043550|GO:2000134|GO:0001047|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139970_PI430048170 0.0985021510265394 3.02405842487482 2.25437831799678 2.42634165165351 0.860485726077937A A A 0.4868139811853620.375123418088221 0.33042959383304 A A A LNCV6_139970_PI430048170 mRNA
GTTCAGTATTCAGTTCTAAAATGAAAATTCCCTCTCAGATCATCCTAAGACTCATTTCAC NM_080873 RefSeq chrX - 15281708 15315624 ASB11 140456 "ankyrin repeat and SOCS box containing 11, E3 ubiquitin protein ligase, transcript variant 1" GO:0035556|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58168_PI430048170 0.2530707758643270.8247720426518720.4101263307885340.376829163032436 0.365883988096487A A A 0.4926828241130430.4676149397964360.969415517902031A A A LNCV6_58168_PI430048170 mRNA
TTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACATCCTAATCCCCAGCATTCCC NM_001258390 RefSeq chr11 + 111540507 111561745 LAYN 143903 "layilin, transcript variant 1" GO:0009986|GO:0005540|GO:0030246|GO:0016021|GO:0005925|GO:0001726 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141313_PI430048170 0.4828580626001411.32719483447176 1.91166116193527 0.6552478592236811.74235688618645 A A A 0.6213325091724210.330228617132969 1.90571788129868 A A A LNCV6_141313_PI430048170 mRNA

GTGCATGGGGGCTGAAATGTAATATGTGTAGCTCAATTAGTCTCTCCTCTGTGATGCAAA NM_133458RefSeq chr16 + 68539212 68567136 ZFP90 146198 ZFP90 zinc finger protein GO:0001078|GO:0005634|GO:0000122|GO:0045893|GO:0003677|GO:0046872|GO:0006351|GO:0043392 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142010_PI430048170 0.0122197231341284 1.30198177305022 13.6663223986479 13.84338131332 13.7086221236711 P P P 13.4797334741849 13.342294213992 13.2509120940951 P P P LNCV6_142010_PI430048170 mRNA
CCCTGGCCCCAGATGGCACTGAGTTTTTCATTCATTGAAGATTTGATTTCCTTGAAAAAA NM_020470RefSeq chr11 - 66284579 66289167 YIF1A 10897 "Yip1 interacting factor homolog A (S. cerevisiae), transcript variant 1" GO:0005515|GO:0005793|GO:0005794|GO:0005815|GO:0015031|GO:0030968|GO:0043231|GO:0000139|GO:0005789|GO:0016021|GO:0006987|GO:0016192|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140260_PI430048170 0.0578467588834271 1.13618264230603 11.8257695977841 11.9827334408354 11.9827334408354 P P P 11.7548776921378 11.7797430168987 11.708756210041 P P P LNCV6_140260_PI430048170 mRNA
TTATTTAAGGTGAATGATAAATCCGTGGGTGGCTCCTTCTACCTGCAGTCAAAGGTGGTC NM_016069RefSeq chr16_KI270855v1_alt - 40614 53696 PAM16 51025 presequence translocase-associated motor 16 homolog (S. cerevisiae) GO:0005744|GO:0005515|GO:0043234|GO:0001405|GO:0031314|GO:0005759|GO:0006626|GO:0032780|GO:0030150|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133151_PI430048170 0.1960516191250480.8377712616498098.72794739142432 8.23645307447396 8.47522326432541 P P P 8.79283870862104 8.72336281919913 8.73035578130886 P P P LNCV6_133151_PI430048170 mRNA
TTGAAGCTATCCAAGCTTTTGAAATAAAATTTAAAAACCCCCAAGCCTGGGTGAGTGTGG NM_031266RefSeq chr5 + 178204506 178211183 HNRNPAB 3182 "heterogeneous nuclear ribonucleoprotein A/B, transcript variant 1" GO:0043565|GO:0005737|GO:0003700|GO:0000166|GO:0030529|GO:0003723|GO:0005654|GO:0005634|GO:0001837|GO:0000122|GO:0045893|GO:0003729 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127270_PI430048170 0.0401362718131752 1.17527220681356 4.07544278081357 3.89120302564126 3.996313114462 P P P 3.76240852802037 3.65269476718792 3.8481405009983 P P P LNCV6_127270_PI430048170 mRNA
TTCTCCTCACTCTGGGACAGACGATGTATGGAAACTAAAAAGAACATGCGGCACCTTAAA NM_015621RefSeq chr5 - 151181051 151224093 CCDC69 26112 coiled-coil domain containing 69 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91701_PI430048170 0.0808044996793531 0.3649985458873952.33423735791657 0.5121189859174291.77902475104869 A A A 3.08195877051529 3.56841117802992 2.76451325375359 P P P LNCV6_91701_PI430048170 mRNA
GTGGAATAGAAATCCTCAGGGCATGAGCTATACCTAAAACGTAATGGTATTAAGAATTCT NM_001167608 RefSeq chr2 + 226835954 226999207 RHBDD1 84236 "rhomboid domain containing 1, transcript variant 2" GO:0005515|GO:0045732|GO:0043066|GO:0004252|GO:0051047|GO:0031293|GO:0048515|GO:0006915|GO:0044322|GO:0030176|GO:0030433|GO:0005739|GO:2000254|GO:0034644|GO:0010954|GO:0004175|GO:0033619|GO:0005789|GO:0034620|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94062_PI430048170 0.9353588109824180.9986467449725111.48977694358309 0.794735112868339 0.613941144174429A A A 1.63350747006021 0.5686325756022840.581204519510226A A A LNCV6_94062_PI430048170 mRNA
TTGAGAATATGCTGAAACCCTTTGGACATGTCATTTCCACAAGAATACTAAGAGACGCTA NM_001003793 RefSeq chr3 + 29281311 30010395 RBMS3 27303 "RNA binding motif, single stranded interacting protein 3, transcript variant 1" GO:0005737|GO:0000166|GO:0045727|GO:0003730 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_76039_PI430048170 0.29396743668718 1.07543513784859 5.21828139375486 5.35236935490089 5.10468981126052 P P P 5.18643073087755 5.05754861471019 5.1243951393512 P P P LNCV6_76039_PI430048170 mRNA GACAAAGCAGCGCCCGTCTGCTTCGGGCCTCTGGAATTTAGCGCTCGCCCAGCTAGCCGC NM_001290307 RefSeq chr5 + 138753395 138935034 CTNNA1 1495 "catenin (cadherin-associated protein), alpha 1, 102kDa, transcript variant 2" GO:0005515|GO:0043627|GO:0031103|GO:0005886|GO:0008013|GO:2000146|GO:0016342|GO:0016264|GO:0015629|GO:0051291|GO:0007406|GO:0005829|GO:0043297|GO:0042692|GO:0071681|GO:0045880|GO:0005915|GO:0001541|GO:0051015|GO:0014704|GO:0005911|GO:2001240|GO:0042475|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131856_PI430048170 0.000337315981095509 0.51662867867633 10.6398320759406 10.5537867051467 10.7649527055045 P P P 11.5057611149375 11.6207771505213 11.692181029616 P P P LNCV6_131856_PI430048170 mRNA CCCCCCGGGTATTTATTGCTGTACATAGTGTATGTTTGTGATATATAAGGTTTTCTTTAT NM_032711 RefSeq chr17 - 81918268 81923568 MAFG 4097 "v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog G, transcript variant 2" GO:0043565|GO:0006355|GO:0003700|GO:0046982|GO:0007596|GO:0042127|GO:0030641|GO:0030534|GO:0005654|GO:0045604|GO:0001701|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129237_PI430048170 0.0811847833186276 0.4261925843003521.83213637619805 0.4580750225531341.24353036924336 A A A 3.01593104069382 1.77292965832165 2.49238587605614 P A P LNCV6_129237_PI430048170 mRNA CAAAAACAGCACCAAAGCAGTCAGCATTGGAAGGAAAATTAGATTTCTGACGGACATCCT NM_001282417 RefSeq chr17 + 18950675 19020691 SLC5A10 125206 "solute carrier family 5 (sodium/sugar cotransporter), member 10, transcript variant 5" GO:0005215|GO:0005886|GO:0016021|GO:0006814|GO:0055085|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136160_PI430048170 0.0181813903337839 2.98019934856078 3.95443937626777 4.35762648329322 4.31583416280805 P P P 2.64701642156621 3.06077169190082 2.05510528047582 P P A LNCV6_136160_PI430048170 mRNA GCACTCAGCTTCCCAGGCAATAACAGCCGTGGGGTAATAAATGGTCTCTGCACACCTGCA NM_178310 RefSeq chr16 - 88677681 88686474 SNAI3 333929 snail family zinc finger 3 GO:0005667|GO:0003700|GO:0006357|GO:0005507|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132795_PI430048170 0.000823072360803117 2.31532763935891 9.61194764857137 9.79054344970746 9.94378004695836 P P P 8.75592812697507 8.49571401420638 8.4617193990162 P P P LNCV6_132795_PI430048170 mRNA CCATCTTGTGAGATTGTTTGCCTATCTCATAATACAGTTTTATGCAGAAAGGTTGAAACT NM_016097 RefSeq chr18 - 47155018 47176374 IER3IP1 51124 immediate early response 3 interacting protein 1 GO:0005794|GO:0016020|GO:0005783|GO:2000269|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129623_PI430048170 0.66431213044901 1.46618331792258 0.304871125481694 2.12674818833543 0.326200584122348 A A A 0.281193497937431 0.499896048425474 1.0335138040349 A A A LNCV6_129623_PI430048170 mRNA CAGCGAGCTTCTTATAAATGTGGTGATTTTTACCAAGGAAACGATTGACTTAATGCTTAA NM_019605 RefSeq chr1 + 210232849 210243095 SERTAD4 56256 SERTA domain containing 4 GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136338_PI430048170 0.358928912789992 0.60387105359537 0.440277011108844 0.439106422810883 0.255495596842763 A A A 0.508145832919702 1.89032767921187 0.421666398359118 A A A LNCV6_136338_PI430048170 mRNA TGCGGAACAAAGATGTAAAGGAGGCAATCAAAAGATTGCTTGTGAGAAATTGGTTCATAA NM_001004745 RefSeq

chr11_JH159136v1_alt + 86387 87368 OR5T1 NA "olfactory receptor, family 5, subfamily T, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97097_PI430048170 0.4281183989418180.9918791735107130.3426522682141550.36866015454375
0.332697413503423 A A A 0.3619339510972690.3721243068299660.345355665948579 A A A
LNCV6_97097_PI430048170 mRNA
CAACACTGGACCTCCATATACTTTGTATTTTGGTATTAAATTCTATGCTGAAGATCCATG NM_022140 RefSeq chr5
- 112162617 112419313 EPB41L4A 64097 erythrocyte membrane protein band 4.1 like 4A
GO:0008092|GO:0008150|GO:0003674|GO:0005737|GO:0005575|GO:0005856|GO:0019898 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_29514_PI430048170 0.4751410649660331.45324015966557 1.77470905973338 0.518221555825268
0.353325719179905 A A A 0.3922639275708510.5598996421945770.518527585585229 A A A
LNCV6_29514_PI430048170 mRNA
AGGCTCACAAGTGAAATTTACCAGGAGCTGATATTGCAAAATAGATTGCTATTTCGCAAC NM_207385 RefSeq chr16
- 73126637 73144447 C16orf47 NA chromosome 16 open reading frame 47 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_128082_PI430048170 0.00289584535246274 0.3092728950960772.99911896571445
3.62589770322369 3.23090430671882 P P P 4.85657036150474 4.73428058608181
5.34116261428318 P P P LNCV6_128082_PI430048170 mRNA
TGTCTTATGTTTCCTCCCAGATTGTTTTCTGCATGAATAATAACCAACAATGTGTGTGTA NM_014388 RefSeq chr1
+ 209827966 209857565 DIEXF 27042 digestive organ expansion factor homolog (zebrafish)
GO:0000462|GO:0032040|GO:0005730|GO:0034511|GO:0007275|GO:0019843 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130151_PI430048170 0.0118914370402426 1.47179975690867 8.87876293671418
9.03033492873209 8.76122254419913 P P P 8.3331777175022 8.38508729198423
8.29040804553655 P P P LNCV6_130151_PI430048170 mRNA
ATGGAGACAGCTGAGCTGAGGCCTGACTTTTTCAATAAAACATTGTGTAGTTCTGGGCCT NM_005072 RefSeq chr16
- 67943473 67968694 SLC12A4 6560 "solute carrier family 12 (potassium/chloride transporter),
member 4, transcript variant 1"
GO:0006821|GO:0019901|GO:0016020|GO:0015379|GO:0005886|GO:0005887|GO:0006810|GO:0005765|GO:0055
085|GO:0006813|GO:0006884|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109185_PI430048170 0.14403040847203 1.23271325270318 5.995567806861
5.64501118177814 5.96807254539551 P P P 5.32094913468307 5.71544200026988 5.6615609291074
P P P LNCV6_109185_PI430048170 mRNA
TGGAACAAAAATCCCCAGATTCGAAGACACTACAGGAAGATTCACCTGGAGTGAGACAAA NM_001005368
RefSeq chr10 - 43643858 43648704 ZNF32 7580 "zinc finger protein 32, transcript variant 2"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142287_PI430048170 0.00555716022544069 1.67482448735832 5.340665340422
5.03103246239195 5.2983024239999 P P P 4.44021682511836 4.41237993061783
4.59749492265421 P P P LNCV6_142287_PI430048170 mRNA
CCAACTAATCTCGCAACCCCAAACACAAAGCGTTTTAAAAAAGAAGAAATTCTTTCCAGT NM_000535 RefSeq chr7
- 5973238 6009106 PMS2 5395 "PMS2 postmeiotic segregation increased 2 (S. cerevisiae),
transcript variant 1"
GO:0005515|GO:0032407|GO:0032389|GO:0090305|GO:0042493|GO:0005634|GO:0016446|GO:0003677|GO:0005
524|GO:0005737|GO:0004519|GO:0006281|GO:0032138|GO:0003697|GO:0015630|GO:0016447|GO:0005654|GO:0
006298|GO:0016887. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134239_PI430048170 0.66032817658269 0.9674033437816410.56269652434209
0.5387485516617750.297266802628031 A A A 0.4016230037220530.613621543533934
0.53365038902015 A A A LNCV6_134239_PI430048170 mRNA

CAGTATGTCTGTACCTTGTATCTTAGCTTGAGTATGATTGTCTTATCAAAGTAGTGTTCTNM_080874RefSeq chr4 - 176213674 176269222 ASB5 140458 ankyrin repeat and SOCS box containing 5 GO:0035556|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139544_PI430048170 0.0411948484165799 0.6940007986045457.48913212052285 7.40658598819965 7.83646426812611 P P P 7.97811591003425 7.99745914656657 8.34432653711616 P P P LNCV6_139544_PI430048170 mRNA
GCTGGGTTCTCTGTAATACCTGTAACGATTGGCAATTTGTTATATATTAGTCTAACCATA NM_001173454 RefSeq chrX + 19343892 19361707 PDHA1 5160 "pyruvate dehydrogenase (lipoamide) alpha 1, transcript variant 2"
GO:0010510|GO:0006099|GO:0005634|GO:0044281|GO:0006096|GO:0006086|GO:0005739|GO:0006090|GO:0005759|GO:0006006|GO:0004738|GO:0004739|GO:0045254|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142300_PI430048170 0.2562017924218430.83917232964775 0.532699299744404 0.6178220779645820.496960546847797A A A 0.8551494747150080.495526326729757 1.01110664554993 A A A LNCV6_142300_PI430048170 mRNA
AGAAAACTACTTGCCCATTATCTGTGGTAAAATGATAGCGGAAGCCACACTACATTTGAC NM_000283RefSeq chr4 + 625573 670892 PDE6B 5158 "phosphodiesterase 6B, cGMP-specific, rod, beta, transcript variant 1"
GO:0060041|GO:0007603|GO:0005886|GO:0051480|GO:0047555|GO:0046037|GO:0022400|GO:0007601|GO:0046872|GO:0016056 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135991_PI430048170 0.2884600501014381.26545870590475 0.387534043698973 1.13003467131791 0.743831463108086A A A 0.71839816116269 0.294965200065181 0.280222292087636A A A LNCV6_135991_PI430048170 mRNA
GCCTTAAACTTGTATGGTCTAAACTCTAAATAAATAAGCTTCTCAAGGGCATGACAACTA NM_033100RefSeq chr10 + 84194634 84218696 CDHR1 92211 "cadherin-related family member 1, transcript variant 1"
GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127844_PI430048170 0.6567263147183161.0971030949284 0.278887879202041 0.30335016911956 0.89803597998721 A A A 0.33072491700929 0.527406191063414 0.29897518495499 A A A LNCV6_127844_PI430048170 mRNA
TCCAACCTTGAGTCTCAACATCATGGGATCCTGCAGTTCTATTAAATCATTCTTGGCAAA NM_001171832 RefSeq chr20 - 31404844 31412838 DEFB121 NA "defensin, beta 121, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135785_PI430048170 0.000333757808635185 0.56764199670801911.4392173398248 11.4214941999658 11.284650137529 P P P 12.1345202827299 12.3007840076873 12.1601911996055 P P P LNCV6_135785_PI430048170 mRNA
TTTCCCCTCCCCCAACGATGTAGCGTTTTTCGTTGTTTGCTTTAGGTTTTTGAAACAGCC NM_006026RefSeq chr3 - 129314770 129316277 H1FX 8971 "H1 histone family, member X"
GO:0006334|GO:0005730|GO:0005634|GO:0000786|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136439_PI430048170 0.3802773209320421.09122433001208 6.95407854365856 6.91756227790031 7.20704084664451 P P P 6.9342141196102 6.73224158557646 7.03559935145063 P P P LNCV6_136439_PI430048170 mRNA
CAGTTTGTGCTATTTCATATCTGTACTCCAGGCAGAAATATAACTTGAAAATACTGTGTC NM_014252RefSeq chr13 + 40789410 40812460 SLC25A15 10166 solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15
GO:0034641|GO:0006520|GO:0005743|GO:0000050|GO:0000066|GO:0044281|GO:0016021|GO:0000064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_34988_PI430048170 0.3942770636430430.9690988990779610.3980100891653970.463711554555744 0.367947189838996A A A 0.5002002098560670.381155619570775 0.482988158346922A A A LNCV6_34988_PI430048170 mRNA

TTTCCAACATCAGCTAAAGAGAAGGGCCTACTTTAAGGCTGGCCAATTCTGCAAGAAAGG NM_001199818 RefSeq chrX + 102599347 102717733 ARMCX5-GPRASP2 NA ARMCX5-GPRASP2 readthrough NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101621_PI430048170 0.8051119681392661.02111354188084 1.57149867649131 1.57879343021089 1.21539541338564 A A A 1.25608111860437 1.96480953998069 0.862407880031795 A A A LNCV6_101621_PI430048170 mRNA
AATTGTAGAGTTGGCTCACGTATTACCCACAGAAGAGAATTTCCTGCTGCTCTTCCGATG NM_004929 RefSeq chr8 - 90058607 90082881 CALB1 793 "calbindin 1, 28kDa"
GO:0005515|GO:0030424|GO:0007616|GO:0071310|GO:0051480|GO:0007614|GO:0005509|GO:0035502|GO:0045202|GO:0005634|GO:0010842|GO:0072205|GO:0072221|GO:0030425|GO:0005829|GO:0048167|GO:0072286|GO:0043025|GO:0005499|GO:0007626|GO:0008270|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129017_PI430048170 0.5917185499069650.8561600950043580.352611404822817 0.4097220277716550.339675510538412 A A A 1.07853366767771 0.287349356424142 0.249505191714336 A A A LNCV6_129017_PI430048170 mRNA
ATGTCCAAGTAAGTTGTAGACATTTTTCACTTTTAATCCTTTCAGCATACATGTCATGGG NM_002092 RefSeq chr4 - 70815781 70839910 GRSF1 2926 "G-rich RNA sequence binding factor 1, transcript variant 1"
GO:0042645|GO:0005739|GO:0006378|GO:0005737|GO:0016331|GO:0000166|GO:0003723|GO:0009952|GO:0003729|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133195_PI430048170 0.0306391178615013 1.56975016431598 10.0689619614005 10.3549283211667 10.3059521346501 P P P 9.88984156676884 9.44015490868031 9.41281147534278 P P P LNCV6_133195_PI430048170 mRNA
TTTTTATAAGTATCTAGACCAAACCTTCAATAAACCACTCATCTTTTTGTTGCCCTCCCC NM_005227 RefSeq chr1 + 155063736 155069553 EFNA4 1945 "ephrin-A4, transcript variant 1"
GO:0005515|GO:0005005|GO:0048013|GO:0046875|GO:0046849|GO:0005886|GO:0007411|GO:0005887|GO:0030316|GO:0007267|GO:0005576|GO:0031225 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144734_PI430048170 0.3411794741181660.8527886048925139.5622500257027 9.67741116433965 9.85517335275137 P P P 9.68909256798456 9.80451259636918 10.2444139459988 P P P LNCV6_144734_PI430048170 mRNA
ATTCCGGGAAAGAGAATTATAGTTTTTATGCCTCCTGTTGAATAAATGGTGTCCTGATAA NM_020936 RefSeq chr12 + 123602124 123620935 DDX55 57696 DEAD (Asp-Glu-Ala-Asp) box polypeptide 55
GO:0016020|GO:0008152|GO:0004386|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133841_PI430048170 0.0271711859244925 0.6364700951255919.62169201624867 9.73414626088009 9.26876826014145 P P P 10.1444575430251 10.1396929077732 10.3276600469514 P P P LNCV6_133841_PI430048170 mRNA
TGCGTGTATGTGTTTGCACATGAGTGTTTGTAGACCATAGACCATTAAAAAATACGGAAT NM_001127649 RefSeq chr22 + 18077993 18091031 PEX26 55670 "peroxisomal biogenesis factor 26, transcript variant 2"
GO:0005515|GO:0051117|GO:0045046|GO:0016558|GO:0008022|GO:0032403|GO:0005779|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140268_PI430048170 0.4277710931641411.0214149408242 0.351760306295694 0.25167474325155 0.274273908580018 A A A 0.2585763901655060.272004510569557 0.257295064674672 A A A LNCV6_140268_PI430048170 mRNA
CTTAGGAATGCAGAGGTGAAAGGGGCTCTAAAGAGAGTCCTTTGGAAACAGAGATCAATG NM_001004135 RefSeq chr7 + 144095107 144096040 OR2A12 NA "olfactory receptor, family 2, subfamily A, member 12"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135434_PI430048170 0.2106003551694120.5494960494891011.35328367061806 0.2773025730328050.297149969675533 A A A 0.6800892151521192.15425547315421 1.60291266864079 A A A LNCV6_135434_PI430048170 mRNA
GAGCCATTTGGGAGTGCTTCAAGATACCCAATATGATATACACAATTATGATTTGTCAGT NM_001190259 RefSeq

chr3 - 112120840 112133305 GCSAM 257144 "germinal center-associated, signaling and motility, transcript variant 3"
GO:0005515|GO:0050855|GO:0005737|GO:0019901|GO:0005886|GO:0003779|GO:0045159|GO:2000402 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127195_PI430048170 0.57269928515728 1.03272827083261 12.3042258623987
12.3502842415709 12.450683143426 P P P 12.31424060836 12.2125584973602
12.4343628665284 P P P LNCV6_127195_PI430048170 mRNA
TCACGACACACTTTGATCCCTTCTGTTGGTGTCATGTTGTAAACATTTCTTTCAATAAACNM_001159936 RefSeq chr1
- 43164173 43172570 EBNA1BP2 10969 "EBNA1 binding protein 2, transcript variant 1"
GO:0016020|GO:0042254|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139923_PI430048170 0.1483112657728380.3918209677240334.11343060750265
2.11253500560139 1.50592623468718 P A A 4.56075886634592 4.25195560956976
4.30791407794143 P P P LNCV6_139923_PI430048170 mRNA
GGACAAGAAAATCCAAGTAGCAAATGACCATTATGTGTAAGACTTACTCTAAAAAGACCA NM_001029863 RefSeq
chr6 + 169702160 169706306 C6orf120 387263 chromosome 6 open reading frame 120
GO:0006915|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143296_PI430048170 0.1584056839866631.08970286174376 0.526160646970602
0.7117919317531040.591625645945995A A A 0.4001269215469460.507225482515665
0.552390843774149A A A LNCV6_143296_PI430048170 mRNA
ATCTACAGCTTGAGGAATAAAGATGTGGCTGCAGCTCTGAGGAAAGTACTAGGGAGATGT NM_001004136 RefSeq
chr1_KI270892v1_alt + 103215 104190 OR2T2 NA "olfactory receptor, family 2, subfamily T, member 2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134608_PI430048170 0.7050637531775871.01026004172738 0.294054410266967
0.3310459466520870.400824527459161A A A 0.3484531698232510.326466266238464
0.308593655024235A A A LNCV6_134608_PI430048170 mRNA
AACTCAATCACATTCAATTCCAGAGTAGTTTCAAGTTTCACATCGTAACCATTTTCGCCC NM_002190RefSeq chr6
+ 52186386 52190638 IL17A 3605 interleukin 17A
GO:0008219|GO:0072537|GO:0007267|GO:0006915|GO:0032747|GO:0045672|GO:0005125|GO:0005615|GO:1900
017|GO:0006955|GO:0006954|GO:0045944|GO:0071347|GO:0006486|GO:0009897 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134456_PI430048170 0.3441766207822420.7336946160558490.467201473682524
0.4404885835920690.245733171760289A A A 1.38289131645351 0.477121554143592
0.432980424161888A A A LNCV6_134456_PI430048170 mRNA
CTAAAGAATGTTTGAGATGGCATTTCAAGACTCTGTTTGCTGTCCAGATTATTTTGGAAA NM_182592RefSeq chr4
- 44622336 44651641 YIPF7 285525 "Yip1 domain family, member 7" GO:0005789|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118859_PI430048170 0.0887975237474113 0.4288769502827020.315213251420112
0.3499345994693880.403629305308058A A A 2.1098175911927 0.850528350713334
1.50469970667313 A A A LNCV6_118859_PI430048170 mRNA
AACCTTCTCATTTAAGTCAGTCCTTACTGTGCATCAGAAAACACACACAGGGGAGAAGCC NM_001007094 RefSeq
chr10 + 38094335 38123350 ZNF37A 7587 "zinc finger protein 37A, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_108642_PI430048170 0.6650029642659261.03724577907383 8.56010542462159
8.59844386730146 8.73926457825163 P P P 8.60166655905503 8.37005396386934 8.7490289230576
P P P LNCV6_108642_PI430048170 mRNA
ATTCAACAAAGTTGATGGATAACTTTCTTTGACTGCTCTACCTGAATTTAGACTAAGCAG NM_001127178 RefSeq
chr4 + 499199 539921 PIGG 54872 "phosphatidylinositol glycan anchor biosynthesis, class G, transcript variant 1"

GO:0006501|GO:0016780|GO:0016020|GO:0005783|GO:0051267|GO:0016254|GO:0005789|GO:0016021|GO:0044267|GO:0006506|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64217_PI430048170 0.918467642226045 0.999086812144142 6.43692936639811 6.48876702583697 6.64078568279955 P P P 6.09877440601876 6.60446009796165 6.78978364697729 P P P
LNCV6_64217_PI430048170 mRNA
TTTTATCTGTGATTTTCTCGCTGAAACCATGTTTCTCAGACAGGCCAAGGCCACCTGACT NM_032737 RefSeq chr19 - 2428164 2456968 LMNB2 84823 lamin B2
GO:0008150|GO:0003674|GO:0005198|GO:0005637|GO:0005638 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142561_PI430048170 0.111774250600121 0.592262465116227 2.56538229902062 2.16884396450462 1.47170425765057 A A A 2.8966480889737 3.09752863145582 2.64680684796095 P P P LNCV6_142561_PI430048170 mRNA
TCTTTCTGTCCTTGAGCCCAGTGAGTTCAATAAAAACCAAAATATTTGGCTCTCAAAAAA NM_001165960 RefSeq chr17 - 8095899 8118916 ALOXE3 59344 "arachidonate lipoxygenase 3, transcript variant 1"
GO:0005515|GO:0006665|GO:0019369|GO:0005506|GO:0019372|GO:0061436|GO:0035357|GO:0016829|GO:0019233|GO:0043651|GO:0005737|GO:0045444|GO:0051122|GO:0016702|GO:0046513|GO:0051120|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139730_PI430048170 0.391216423997028 1.11510719244962 11.4548285960105 11.5520270898659 11.7908226644245 P P P 11.3154752831556 11.2862190908781 11.706244610935 P P P LNCV6_139730_PI430048170 mRNA
GCTTGGACATCTGCAAATGATATTTAAACCATCTTGGCTTGTGCTTTATTCAAACTAATG NM_016355 RefSeq chr12 + 12813345 12829981 DDX47 51202 "DEAD (Asp-Glu-Ala-Asp) box polypeptide 47, transcript variant 1"
GO:0008625|GO:0008380|GO:0006397|GO:0005515|GO:0016020|GO:0006364|GO:0005730|GO:0004386|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139150_PI430048170 0.207158317911756 1.21142337076709 0.809037496919017 0.410424327661202 0.353171127278124 A A A 0.243091989085782 0.299310625926977 0.24334975999688 A A A LNCV6_139150_PI430048170 mRNA
CTAAGAAATAAGGATGTCAAATTTGCCCTGAAGAAAAATCTGGACAGCAAAGCATGTTCA NM_001291438 RefSeq chr11 + 124224638 124225663 OR8G2 26492 "olfactory receptor, family 8, subfamily G, member 2"
GO:0050911|GO:0007608|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104823_PI430048170 0.31892341868422 0.86989289626065 6.76879392212995 6.95592912117922 6.98591574874305 P P P 6.83700806658797 7.11401210358453 7.33034864904855 P P P LNCV6_104823_PI430048170 mRNA
TCGCTTTGGATGGAAGTTCTAATGTGGAGGCGGAAGTTTTGGAAAATGATGGTGTCTCAG NM_001272075 RefSeq chr16 + 84699948 84779921 USP10 9100 "ubiquitin specific peptidase 10, transcript variant 1"
GO:0005515|GO:0016579|GO:0004843|GO:0030330|GO:0006914|GO:0005634|GO:0044325|GO:0004197|GO:0002039|GO:0005737|GO:0006281|GO:0061136|GO:0010506|GO:0043161|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128164_PI430048170 0.554219456784442 0.895272176716195 5.60748439028446 5.8905879881575 5.84572755336014 P P P 5.563066280777 5.98934874162954 6.21246869426232 P P P
LNCV6_128164_PI430048170 mRNA
GATTGTGTAACAATTTTAATGCTATTTCCCCAGGGGAAAATGAAGGTTAGGATTTAACAG NM_001752 RefSeq chr11 + 34438924 34472060 CAT847 catalase
GO:0050661|GO:0001657|GO:0009650|GO:0020027|GO:0005782|GO:0005886|GO:0005783|GO:0004096|GO:0044281|GO:0005764|GO:0046872|GO:0042803|GO:0043231|GO:0005829|GO:0009060|GO:0005758|GO:0006195|GO:0051092|GO:0051289|GO:0051781|GO:0033197|GO:0004046|GO:0042744|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132296_PI430048170 0.0333914551258343 1.24511151673304 14.859161139127

14.9775809008335 15.0198140328779 P P P 14.7656189142404 14.4972395676845
14.6371772117456 P P P LNCV6_132296_PI430048170 mRNA
TGTCGTGGAACCTCTTACTGCTTTCAATACACGATTAGTAATCAACTGTTTTGTATACTTNM_001024227 RefSeq chr1
+ 228083149 228099212 ARF1 375 "ADP-ribosylation factor 1, transcript variant 1"
GO:0005515|GO:0043005|GO:0048471|GO:0005886|GO:0007264|GO:0034315|GO:0003924|GO:0060292|GO:0044
281|GO:0015031|GO:0030017|GO:0048205|GO:0005829|GO:0019886|GO:0006878|GO:0045211|GO:0061024|GO:0
016032|GO:0070062|GO:0006661|GO:0006890|GO:0006892|GO:0014069|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141688_PI430048170 0.4651242557054232.5157121698684 3.01034162369409
0.4486587201048690.376703607747221A A A 0.4625888003493250.402449872470611
0.643147055942514A A A LNCV6_141688_PI430048170 mRNA
GAGTCAGGCGGGAGACCATTTTATGTTTATTTTCTTTAGTGTATAAGTAAGGGTTTTTTC NM_153615RefSeq chr22
+ 23690860 23699176 RGL4 266747 ral guanine nucleotide dissociation stimulator-like 4
GO:0043547|GO:0005085|GO:0007264|GO:0016023 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141954_PI430048170 0.10723829292442 0.6034821080499093.77686760696974
3.19308181780946 2.73107507160129 P P A 4.28575828630993 3.78912582900861
3.95803698423729 P P P LNCV6_141954_PI430048170 mRNA
AAGATCGCCACGCTGCTGCTCGCCAAGAACTATATCCTCATGCAGGCGCAGGCCCTGGAC NM_080606RefSeq chr20
- 63005978 63007035 BHLHE23 128408 "basic helix-loop-helix family, member e23"
GO:0006355|GO:0046983|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144615_PI430048170 0.7564727314494241.01892568104043 7.37494035129735
7.43380282003423 7.21296743869981 P P P 7.2651777572862 7.36138456622918
7.32134819528642 P P P LNCV6_144615_PI430048170 mRNA
TATGAGTTATTTCTGAGTAAGTGAAGGCTGAAGGCAGTGCTGAGTCCTTTCTGCTAGCTG NM_017777RefSeq chr17
- 58205435 58219305 MKS1 54903 "Meckel syndrome, type 1, transcript variant 1"
GO:0005515|GO:0042384|GO:0005813|GO:0005737|GO:0006996|GO:0016020|GO:0005814|GO:0060271|GO:0036
038|GO:0048754|GO:0036064|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142625_PI430048170 0.1403142879873591.3713399560484 8.94369163946938
8.88435380861249 8.83552184884539 P P P 8.776182417127 8.3696277337907
8.06399450664537 P P P LNCV6_142625_PI430048170 mRNA
CCTACCCACAGGGCCCTACTTTATGGCAATAAAGGTGATGCCCCACTTGTGTCCATGCCA NM_001024675 RefSeq
chr20 + 33666497 33668525 ACTL10 NA actin-like 10NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137356_PI430048170 0.2844452021833861.50927341511232 2.9263055791077
2.97373536705704 3.26720612281434 A P P 3.28829198798472 2.08961814444951
1.37558757449328 P A A LNCV6_137356_PI430048170 mRNA
GTAGAAAAATCCTGCTCTGTCCCTAATTTTTGTTTTTATTTTGGGGGCCTTTTTTGACAT NM_181539RefSeq chr17 -
40766237 40772159 KRT26 353288 "keratin 26, type I" GO:0005882|GO:0005198|GO:0070062 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_3182_PI430048170 0.4528498653120131.24805043182329 2.29572228997 1.67519123015358
1.85147088464992 A A A 2.44968871351668 1.22071039231233 0.66982018079723 A A A
LNCV6_3182_PI430048170 mRNA
TAAAACATGCTGTCTTAGATCAGGAGAAACTCGGGCACTCCCTAAGTCCACTCTAGTTGT NM_213621RefSeq chr11
+ 113975074 113990312 HTR3A 3359 "5-hydroxytryptamine (serotonin) receptor 3A, ionotropic,
transcript variant 1"
GO:0005232|GO:0030424|GO:0030054|GO:0005886|GO:0045471|GO:0007586|GO:0007268|GO:0051378|GO:0042
220|GO:0055085|GO:0007210|GO:0004993|GO:0005737|GO:0034220|GO:0071363|GO:0005887|GO:0045211|GO:0
005249|GO:0043025|GO:0006810|GO:0004872|GO:0071805 . NA - . NA NA NA NA NA NA NA NA

NA
LNCV6_138225_PI430048170 0.45268900678837 1.20939996574068 11.5403861471265
11.9724525557687 12.0379713952708 P P P 12.2397227758601 10.9522677927794
11.2555757732122 P P P LNCV6_138225_PI430048170 mRNA
CCGGTTTCTACATGCAGAGATGAATTTATACTGCCATCTTACGACTATTTCTTCTTTTTA NM_005345 RefSeq
chr6_GL000255v2_alt + 3071341 3073770 HSPA1A 3303 heat shock 70kDa protein 1A
GO:0006986|GO:0005515|GO:0010467|GO:0030308|GO:0034605|GO:0042026|GO:0001618|GO:0031072|GO:0060
548|GO:0031397|GO:0010941|GO:0031625|GO:0070062|GO:0070370|GO:0005814|GO:0006402|GO:0045648|GO:0
005654|GO:0051082|GO:0019899|GO:0005925|GO:0003725|GO:0090084|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133319_PI430048170 0.0860425014880647 0.8471363352829487.97127711932943
8.19584166826357 8.22100025760315 P P P 8.29362790359986 8.30715898138542 8.5080498636676
P P P LNCV6_133319_PI430048170 mRNA
TGAACAAATTAGTCCACAATCAAGTGTCTACTTTTCCCTTCACTGTAGGGCCTCTCCCTG NM_031314 RefSeq chr14
- 21209135 21269479 HNRNPC 3183 "heterogeneous nuclear ribonucleoprotein C (C1/C2), transcript
variant 1"
GO:0008380|GO:0005515|GO:0010467|GO:0000790|GO:0043044|GO:0003723|GO:0031492|GO:0005634|GO:0071
013|GO:0000978|GO:0001649|GO:0042802|GO:0005829|GO:0043234|GO:0008266|GO:0016020|GO:0000166|GO:0
000398|GO:0000980|GO:0005654|GO:0005681|GO:0003730|GO:0070935|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130227_PI430048170 0.420051160762195 0.88837469470097 2.02452133977615
1.79868615621271 1.42528634287013 A A A 1.88996084842524 2.11918201381202
1.79426002953974 A A A LNCV6_130227_PI430048170 mRNA
CTTGAAGTCCAGTGAAGTCTCTCTCTTAAAGTCTTTTGCAAACATTTTTGTACCTTGTTA NM_031854 RefSeq
chr17_JH159146v1_alt - 272828 273903 KRTAP4-12 83755 keratin associated protein 4-12
GO:0005515|GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127101_PI430048170 0.0147579003690373 0.499182312819479 9.32183209987527
9.11117419376516 9.17618736401021 P P P 9.99688150023187 10.0708415081033
10.5032625928456 P P P LNCV6_127101_PI430048170 mRNA
GGGACATGTATCTTCTTCTTTGCCTTAAATCTGATACAAGAGGTCAATGACTTTGAAAAT NM_015258 RefSeq
chr9 - 113165519 113221361 FKBP15 23307 "FK506 binding protein 15, 133kDa"
GO:0005515|GO:0030424|GO:0016020|GO:0006457|GO:0010923|GO:0005884|GO:0003779|GO:0005769|GO:0030
426|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128345_PI430048170 0.352569070568509 1.02071051266032 0.324914765505694
0.242875014657768 0.300265497176401 A A A 0.263157670843985 0.25298364673458
0.264389361686036 A A A LNCV6_128345_PI430048170 mRNA
CGTGGTGATTGTTGTAAAAACTGCTATATGAGCCTTGGAAACATGAAGCTAAGTCAGAAA NM_031440 RefSeq
chr3 + 46497994 46500949 RTP3 83597 receptor (chemosensory) transporter protein 3
GO:0005515|GO:0005737|GO:0006612|GO:0016021|GO:0001580 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_141932_PI430048170 0.401578885056763 1.50050825511871 0.477900405708702
0.494104934538331 1.7660943893338 A A A 0.515407001913755 0.430574675161949
0.439803075394284 A A A LNCV6_141932_PI430048170 mRNA
TAGTAAATTTAGAACTGTAGAGGCTAATAAACTGCGATGAGACATTTAAGCTCTGCTCCA NM_001159642 RefSeq
chr1 + 151036552 151047600 BNIPL 149428 "BCL2/adenovirus E1B 19kD interacting protein like,
transcript variant 2"
GO:0005515|GO:0008285|GO:0006915|GO:0005634|GO:0042802|GO:0040009|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135366_PI430048170 0.00923867994966518 0.522270843854251 1.14046336575018

1.52532030296485 1.61541182414794 A A A 2.54300991278405 2.2855915077624
2.29146746405863 A A A LNCV6_135366_PI430048170 mRNA
CTAGTGGACTCTGCTACACTTAAACCTATGTGACAAACCGCCCATTATTTTATTGTTTAT NM_153809 RefSeq chr9
- 32629453 32635669 TAF1L 138474 "TAF1 RNA polymerase II, TATA box binding protein (TBP)-
associated factor, 210kDa-like"
GO:0010467|GO:0006368|GO:0005669|GO:0006367|GO:0016573|GO:0006357|GO:0006366|GO:0005575|GO:0003
677|GO:0004674|GO:0017025|GO:0016032|GO:0070577|GO:0005654|GO:0006468|GO:0045893|GO:0004402|GO:0
007140 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129379_PI430048170 0.2519943121216031.01995280883584 0.315695925999844
0.2539679936313540.28298945655592 A A A 0.2578762169597080.25068961807235
0.259227063401889A A A LNCV6_129379_PI430048170 mRNA
CCCTGTTTGAATTTGAGTAGCAAGAAGTTTCTGATTTGTACTAACAGAAGGAGTAAAGTT NM_017953RefSeq chr1
- 85649422 85708433 ZNHIT6 54680 "zinc finger, HIT-type containing 6, transcript variant 1"
GO:0005515|GO:0042254|GO:0070761|GO:0000492|GO:0019899|GO:0046872|GO:0070062|GO:0042802 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75419_PI430048170 0.1792866924620920.5639550913022370.4865758882519330.379140538182182
0.455330990761887A A A 1.63678518815751 1.45382886749913 0.457072589611229A A A
LNCV6_75419_PI430048170 mRNA
GTCTCCATTAAAGAAGATGTGCTACTCTTCATAATATAATAAAAGGGCTACAACAGACCA NM_001134848 RefSeq
chr5 + 42756817 42802437 CCDC152 NA coiled-coil domain containing 152 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131742_PI430048170 0.00481895160504001 1.7670923284022 2.80198867413494
3.0324596498295 3.17387668324206 A A P 2.02992393023654 2.30633554909727
2.21841696141387 A A A LNCV6_131742_PI430048170 mRNA
ACATATTTTAACCCACCTAAGGTTTTACAGACTTTAGCCTCACTCAAACTTTATCACCCT NM_152406RefSeq chr5
+ 149271837 149341804 AFAP1L1 134265 "actin filament associated protein 1-like 1, transcript variant 1"
GO:0005737|GO:0030054|GO:0005886|GO:0071437|GO:0002102|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_122801_PI430048170 0.3235428620425890.8177642653882950.276785433814078
0.3007489912510270.467972746670051A A A 0.9944694211060410.540767279230259
0.301066855784892A A A LNCV6_122801_PI430048170 mRNA
CTCTAAGTGGATCGACGACGTCAGGACAGAGAGGGGCAGTGATGTTATCATCATGCTGGT NM_016577RefSeq chr3
- 133824235 133895847 RAB6B 51560 "RAB6B, member RAS oncogene family"
GO:0005515|GO:0005794|GO:0006890|GO:0003924|GO:0006891|GO:0005525|GO:0006886|GO:0006184|GO:0031
489|GO:0000139|GO:0042147|GO:0016023|GO:0032482|GO:0019003 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_86267_PI430048170 0.00251674439426551 0.5198598044361295.9640108346156
5.81246831862283 5.89524832533694 P P P 6.68598508016759 6.81883509825411
6.98653555384192 P P P LNCV6_86267_PI430048170 mRNA
TTGTGGCTATTGGTGTGTCTCACAGGCAAAATTTGATTTGGCTAAAATAGGCTCAGATGT NM_181701RefSeq chr9
- 136206336 136245841 QSOX2 169714 quiescin Q6 sulfhydryl oxidase 2
GO:0031965|GO:0005886|GO:0016972|GO:0045454|GO:0005576|GO:0016021|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_102624_PI430048170 0.000538535804908887 1.77563220670545 8.65738925751972
8.72794739142432 8.86286146667409 P P P 7.81997030979247 7.95793113522123
7.98742499743345 P P P LNCV6_102624_PI430048170 mRNA
GTAGCAAAGTTCATGTGAATGTGGGTGAGTTTCTGTTATGAATGTGGTCAATAAATGTTA NM_001195124 RefSeq
chr16 - 87302798 87317420 C16orf95 100506581 "chromosome 16 open reading frame 95, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133642_PI430048170 0.4214910073372170.79035423192053 0.266388077006454
0.2832457098194010.437371042344227A A A 0.3526537554415761.17587744737223
0.308807238099162A A A LNCV6_133642_PI430048170 mRNA
TCATGAAATACTGCCATTGTTGCTAAATAAAGCTTGTGTGCTCTGAATATAGCCAAGCAT NM_001134450 RefSeq
chr7 - 98846487 98870050 TMEM130 222865 "transmembrane protein 130, transcript variant 1"
GO:0000139|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139564_PI430048170 0.00087513196833853 0.2800141260114 4.06436625888023
4.26080564993122 4.47512423650338 P P P 6.07574821353972 6.02864867355989
6.22693606009733 P P P LNCV6_139564_PI430048170 mRNA
GCACTACCTGGAGTTACAGTTTTCAATCTGTCAGTAAATAAAGTGTCCTTTAACTTCAAA NM_001135733 RefSeq
chr8 - 94925971 94949387 TP53INP1 94241 "tumor protein p53 inducible nuclear protein 1,
transcript variant 2"
GO:0005515|GO:0072703|GO:0048102|GO:0030336|GO:0005776|GO:0008285|GO:0016209|GO:0009408|GO:2001
235|GO:0006950|GO:0071447|GO:0006915|GO:0005634|GO:0031410|GO:0006351|GO:0005829|GO:0071361|GO:0
034644|GO:0016605|GO:0007050|GO:0045893|GO:0000045|GO:0010508 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_145641_PI430048170 0.0974539796756484 0.88535254580355213.2875650007235
13.1689221552479 13.0770436996048 P P P 13.3614622925947 13.365888908043
13.3408255005464 P P P LNCV6_145641_PI430048170 mRNA
GGACCAGGTGTGATCAGACTGCTATCTGAATAAAATAAGATTTGTCAGAAATTCCAAAAA NM_001165877 RefSeq
chr22 - 42639802 42640601 ATP5L2 NA "ATP synthase, H+ transporting, mitochondrial Fo complex,
subunit G2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98904_PI430048170 0.1016112265776851.38452053922907 9.28611745489702 9.82735064419598
9.70563342402814 P P P 9.22766278913149 9.15451367671744 9.07896890368133 P P P
LNCV6_98904_PI430048170 mRNA
TATGTGTTTTTAAACGAAGATCCGAGCGACGGCTCCTCCCCGATCCCCGACAGTGGCTCT NM_001001502 RefSeq
chr5 - 176620208 176630556 SNCB 6620 "synuclein, beta, transcript variant 1"
GO:0004859|GO:0005794|GO:0016234|GO:0043014|GO:0005509|GO:0048487|GO:0007268|GO:0043086|GO:0030
426|GO:0005739|GO:0043524|GO:0005737|GO:0042417|GO:0050808|GO:0043195|GO:0043025|GO:0005654 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132328_PI430048170 0.6479578773853021.15395404065232 1.18140282912031
0.3494870635460970.327917391512349A A A 0.4554269148966680.546322905724013
0.40676122917188 A A A LNCV6_132328_PI430048170 mRNA
GGCCACTTCTGGGGGAAAAACATGTAATTAAGTAAATGTATACATTGGTTTTCACGTTTT NM_001128174 RefSeq
chr4 + 114598454 114677046 UGT8 7368 "UDP glycosyltransferase 8, transcript variant 1"
GO:0006682|GO:0052696|GO:0002175|GO:0030913|GO:0008489|GO:0015020|GO:0007417|GO:0032870|GO:0043
231|GO:0003851|GO:0009813|GO:0048812|GO:0007010|GO:0007422|GO:0008088|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_98060_PI430048170 0.4041419478798380.5939730090956650.4773464453755290.494476884165153
0.339391231294154A A A 0.4019233079596930.5264389557206562.03003585355218 A A A
LNCV6_98060_PI430048170 mRNA
CAGCCCAATAGGATGGGAGAAACTTATAAAGGAAATGGACTATTTATGGAAAATCAATCA NM_001206631 RefSeq
chr11 - 49053713 49059112 TRIM64C NA tripartite motif containing 64C NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_132329_PI430048170 0.0106739150812188 0.3705541619906393.3976824584871
2.87379843673813 3.38447246557917 P A P 4.61624623202943 4.74812726698474
4.64413787252564 P P P LNCV6_132329_PI430048170 mRNA
CCTTTTGGGATGTGGGAAAGGTTTGGTGGGAGTTGTTATATTTATCTGTAATATTTCTTT NM_152484RefSeq chr19
- 37411157 37467437 ZNF569 148266 zinc finger protein 569

GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143135_PI430048170 0.0105578573678027 0.4710308724062984.52584316419872
4.09248485277747 4.63437642197731 P P P 5.54266340250592 5.37012410822586 5.6403540803501
P P P LNCV6_143135_PI430048170 mRNA
GCCTCACTTGCGTTTTCCTACAAGATGTAAGACTGTTTATAATTAAACTTTTTTGGTCCT NM_001257137 RefSeq chr20
+ 34363234 34511393 ITCH 83737 "itchy E3 ubiquitin protein ligase, transcript variant 1"
GO:0005515|GO:0035519|GO:0050687|GO:0006511|GO:0045732|GO:0004842|GO:0016567|GO:0005886|GO:0090
085|GO:0016874|GO:0070423|GO:0005634|GO:0046718|GO:0001558|GO:0035872|GO:0005829|GO:0070534|GO:0
051607|GO:0005737|GO:0046329|GO:0006954|GO:0007219|GO:0042787|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130230_PI430048170 0.4601528076480811.46793794796773 0.272774449362405
0.30135717741569 1.62772378973475 A A A 0.3594493899720570.318047320245143
0.30809981966317 A A A LNCV6_130230_PI430048170 mRNA
GACATCCTAGAATGGACCGACTGTACCGTGTATATGAACAATACCTCTTATGAGTATAGT NM_001946RefSeq chr12
- 89347824 89352859 DUSP6 1848 "dual specificity phosphatase 6, transcript variant 1"
GO:0014070|GO:0034142|GO:0042663|GO:0060420|GO:0051409|GO:0009953|GO:0051403|GO:0030154|GO:0035
335|GO:0005829|GO:0000188|GO:0002756|GO:0005737|GO:0002755|GO:0070373|GO:0034138|GO:0017017|GO:0
004725|GO:0048011|GO:0043065|GO:0038124|GO:0038123|GO:0034134|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141294_PI430048170 0.1702986211949780.787755821093785 5.80932924690796
5.30370775935385 5.84408589738248 P P P 5.84016291390751 5.98661196557784
6.20064398836765 P P P LNCV6_141294_PI430048170 mRNA
CTTAGTATCACGCAGCTGACTGAGCCCTTCAAAACTGACATCTTAAGGCCCAATCAAGAT NM_001252271 RefSeq
chr1 - 92842159 92877150 FAM69A 388650 "family with sequence similarity 69, member A,
transcript variant 4" GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131738_PI430048170 0.37432888109481 0.8183868188227682.98988889878809
2.41852221988427 2.79678344305705 P A A 3.27756137069511 2.57996352771363
3.17859824898989 P P P LNCV6_131738_PI430048170 mRNA
ATGGAAGTCCAGGTCAGTGGAGTCTCTCCTTGATTGATCACCCCAATAAACAACTTTCCA NM_130770RefSeq chr3
+ 184053046 184060673 HTR3C 170572 "5-hydroxytryptamine (serotonin) receptor 3C, ionotropic"
GO:0005230|GO:0034220|GO:0005886|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139859_PI430048170 0.0112165760167820.6358801069641235.21941172479013
4.87236928894528 5.10322597230303 P P P 5.64545131305536 5.81536292821037
5.70992181458551 P P P LNCV6_139859_PI430048170 mRNA
TTGAGTCATAATCTCACCTGGATACGCTGTAACAAATGCCCTGGATTATCAAATCAGTTA NM_138368RefSeq chr11
- 65773897 65780591 AP5B1 91056 "adaptor-related protein complex 5, beta 1 subunit"
GO:0005515|GO:0016197|GO:0030119|GO:0015031|GO:0005765 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142634_PI430048170 0.4674020076658110.8475763136266270.282738000355902
0.2906664645607680.495534513168299A A A 0.33384941862044 1.01529737942883
0.333585340867898A A A LNCV6_142634_PI430048170 mRNA
AACATTATCTCTTTTGGGGTAGGGAGGCAATATCTCAACAAGCGTCGGGTGAATACCTCA NM_001164379 RefSeq
chr11 + 47586677 47589194 FAM180B NA "family with sequence similarity 180, member B" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131819_PI430048170 0.9211326495125270.9967081115271690.483017748918791
0.4358110749890110.303458171769384A A A 0.3671089708829370.44229047606208
0.431963514989534A A A LNCV6_131819_PI430048170 mRNA

GACAGCTATCTGCATTCTGATCCAGATACTGTATGTTCTTAACATAAAGTGAAATTTCTC NM_005042RefSeq chr12_KI270904v1_alt + 127940 133551 PRH2 5555 "proline-rich protein HaeIII subfamily 2, transcript variant 1" GO:0005515|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130365_PI430048170 0.000111571264803168 6.62140343559935 3.61731327571856 3.75533591470554 3.32674887613338 P P P 0.7595369504471690.665700652608247 1.09010965251078 A A A LNCV6_130365_PI430048170 mRNA
ATGGACTCCACATTTGAGCTCTGCAAGATCTGTGCTGAGAGCAACAAGGATGTGAAGATT NM_012116RefSeq chr19 + 44777868 44800646 CBLC 23624 "Cbl proto-oncogene C, E3 ubiquitin protein ligase, transcript variant 1"
GO:0005154|GO:0017124|GO:0016567|GO:0016874|GO:0005509|GO:0042059|GO:0005634|GO:0042787|GO:0043407|GO:0007175|GO:0001784|GO:0008270|GO:0004871|GO:0007166|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61320_PI430048170 0.000799858891782471 1.406763369353 5.96396981109624 5.93044979476694 5.85855074715011 P P P 5.42752253829161 5.35491233294774 5.4921355697366 P P P LNCV6_61320_PI430048170 mRNA
GGAAAAAGCAAAAAGGCAGAAGAATTGTTTTTATGGGTTCCACGAAAATTGCTAATGACT NM_032233RefSeq chr14 - 99397745 99480889 SETD3 84193 "SET domain containing 3, transcript variant 1"
GO:0001102|GO:0000790|GO:0003713|GO:0010452|GO:0018027|GO:0018026|GO:0042800|GO:0006351|GO:0018023|GO:0051149|GO:0045944|GO:0046975|GO:0045893|GO:0051568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57281_PI430048170 0.00024774027529536 0.2805577923807987.12410890149589 7.20302035122778 6.90899757513306 P P P 9.00499423821254 8.91307744301874 8.82940303438009 P P P LNCV6_57281_PI430048170 mRNA
GCCAGGATTGTCACTCCAAACCTTACTCTGAGCTCATTAATAAAATAGATTTATTTTCCA NM_153676RefSeq chr11 - 17493894 17544416 USH1C 10083 "Usher syndrome 1C (autosomal recessive, severe), transcript variant b3"
GO:0005515|GO:0042472|GO:0042491|GO:0005886|GO:0007605|GO:0030046|GO:0045202|GO:0045177|GO:0032420|GO:0030507|GO:0045494|GO:0005829|GO:0005903|GO:0001917|GO:0005737|GO:0051015|GO:0000086|GO:0050957|GO:0005856|GO:0032029|GO:0050953|GO:0001750 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130998_PI430048170 0.1516285800597161.01957542600469 0.38830472769144 0.39156757612143 0.416696726102507A A A 0.3706586746609610.349120579992372 0.392722419735232A A A LNCV6_130998_PI430048170 mRNA
AAAGGCAGCAACCATTCATCTTTCCTTTGCTCTGGATACACCGAATGACCAGGTAACATC NM_020546RefSeq chr5 + 7396229 7830081 ADCY2 108 adenylate cyclase 2 (brain)
GO:0005886|GO:0007268|GO:0044281|GO:0007202|GO:0007193|GO:0046872|GO:0030425|GO:0005622|GO:0035556|GO:0005737|GO:0007173|GO:0071377|GO:0006171|GO:0006833|GO:0034199|GO:0048011|GO:0046982|GO:0008179|GO:0008294|GO:0031683|GO:0055085|GO:0005524|GO:0003091|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142507_PI430048170 0.6818817824092670.9727211844864590.272108155223449 0.4819777579287760.320354256727199A A A 0.5073905867344240.401932043147354 0.284705157268073A A A LNCV6_142507_PI430048170 mRNA
GCTTCTCTCAACCTGACATGGAAAGTCTCTTGTACTACAGTGTATTTAATAAAAATGATG NM_006180RefSeq chr9 + 84668457 85027070 NTRK2 4915 "neurotrophic tyrosine kinase, receptor, type 2, transcript variant a"
GO:0035584|GO:0048709|GO:0010996|GO:0060291|GO:2000811|GO:0042803|GO:0043524|GO:0032314|GO:0046777|GO:0045211|GO:0071356|GO:0009416|GO:0007612|GO:0005791|GO:0048786|GO:0048403|GO:0009986|GO:0007616|GO:0051968|GO:0007568|GO:0046548|GO:0046928|GO:0018108|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128463_PI430048170 0.000688948403920782 0.69370605901705510.5882060115464

10.5168086973652 10.4599656994655 P P P 10.9705817959918 11.070098688777
11.1065665389995 P P P LNCV6_128463_PI430048170 mRNA
TCTGTAAATCTGTGCACATGGCCACTCTTGGCCTAATAAAGGAGGTCTCACAGTCAAAAA NM_032451 RefSeq chr16
+ 89828498 89871319 SPIRE2 84501 spire-type actin nucleation factor 2
GO:0048471|GO:0030036|GO:0005886|GO:0070649|GO:0046907|GO:0003779|GO:0015031|GO:0032154|GO:0005
829|GO:0036089|GO:0045010|GO:0051295|GO:0040038|GO:0005856|GO:0016192|GO:0005938|GO:0030659 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139462_PI430048170 0.0116973499624718 1.56992658170938 12.662533014528
12.7928953345072 12.8332388803414 P P P 12.2871941666111 11.9270245101952
12.1053626489705 P P P LNCV6_139462_PI430048170 mRNA
CAAGTGTGAGGGTGTGAGAAACTCACAGAATACAAATTTGCCTGTATGTTTTGTGGGTTT NM_014302 RefSeq chr7
- 54752246 54759246 SEC61G 23480 "Sec61 gamma subunit, transcript variant 1"
GO:0002474|GO:0010467|GO:0006614|GO:0042590|GO:0006412|GO:0045047|GO:0015450|GO:0016020|GO:0008
565|GO:0005789|GO:0002479|GO:0016021|GO:0071806|GO:0044267 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144435_PI430048170 0.790239548264657 1.01658359122177 0.307788231169922
0.298359365217984 0.481770289604182 A A A 0.299446812437431 0.265579878205816
0.452262791106271 A A A LNCV6_144435_PI430048170 mRNA
AATGGAGAGTAAGCAGCAGCAAACTGAGAATTATCCAGCATATGAATATAACAATGTGTT NM_032291 RefSeq chr1
+ 66533955 66751139 SGIP1 84251 SH3-domain GRB2-like (endophilin) interacting protein 1
GO:0005515|GO:0008017|GO:0017124|GO:0005886|GO:0030122|GO:0097320|GO:0030136|GO:0002021|GO:0006
897|GO:2000253|GO:0005737|GO:0005905|GO:0005543|GO:0048260|GO:2000507 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129930_PI430048170 0.308602319110087 0.762716147497834 2.08118700915288
3.13579086467586 3.08651283916411 A P P 3.17824394256451 3.29025049535123
3.22869672952013 P P P LNCV6_129930_PI430048170 mRNA
CACTTGTGGGGGGTTCTCTTCATTAGCAAAACAGTCATGTCTGTCTGTATATAAGACTTT NM_001304484 RefSeq
chr12 + 32502042 32646051 FGD4 121512 "FYVE, RhoGEF and PH domain containing 4, transcript
variant 5"
GO:0030036|GO:0030035|GO:0031267|GO:0007264|GO:0008360|GO:0030032|GO:0030175|GO:0015629|GO:0046
872|GO:0005829|GO:0005085|GO:0005737|GO:0007010|GO:0046847|GO:0005089|GO:0051056|GO:0048011|GO:0
005794|GO:0043065|GO:0003779|GO:0097190|GO:0001726|GO:0030027|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135810_PI430048170 0.128302810966643 0.34997787771259 2.95198126842604
0.293326376656418 1.38633613064682 P A A 3.60014046266797 3.19654252422206
3.55909596610387 P P P LNCV6_135810_PI430048170 mRNA
CCTCTTCCAATGAGCTTAAAACATTTTTCCCAACAGTATATAAATCTTCAACATGAGAGG NM_001278438 RefSeq
chr13 + 48976608 49209779 FNDC3A 22862 "fibronectin type III domain containing 3A, transcript
variant 3"
GO:0012506|GO:0009566|GO:0016337|GO:0060009|GO:0005794|GO:0016020|GO:0001669|GO:0000139|GO:0007
286|GO:0016021|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136197_PI430048170 0.452253635384576 0.916838635414378 7.87373877364785
7.93668759826291 8.0307326031407 P P P 7.82388265401003 8.13150597356203
8.23493092664451 P P P LNCV6_136197_PI430048170 mRNA
GTACATCTATGCAAAATACTTGAATGGGCCATGGTGCCTTTTTTCCTTGTTAGTATTTAA NM_033274 RefSeq chr5
- 157477303 157575823 ADAM19 8728 ADAM metallopeptidase domain 19
GO:0007507|GO:0017124|GO:0008270|GO:0016021|GO:0006509|GO:0004222 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141148_PI430048170 0.150197687144059 0.695207898833164 4.88000703136051

5.08357449331103 5.08452680010023 P P P 5.95326395837794 5.31717772328855
5.25205378932142 P P P LNCV6_141148_PI430048170 mRNA
TTTTTCGGGAAACGGGTTAGGGAGTAAAGACTGCACCCTACATGGTCCTGGTGGTGGGGG NM_003923 RefSeq chr8
- 144473731 144476335 FOXH1 8928 forkhead box H1
GO:0005515|GO:0000790|GO:0003700|GO:0001190|GO:0044212|GO:0006366|GO:0000981|GO:0003139|GO:0046
332|GO:0003215|GO:0005634|GO:0050681|GO:0001947|GO:0045944|GO:1900164|GO:0003222|GO:0007179|GO:0
048318|GO:0005667|GO:0001104|GO:0019904|GO:0070410|GO:0035054|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130436_PI430048170 0.0249272516986131 0.5860884759456636.30020937441612
5.94302698156968 5.72729719365316 P P P 7.00624168856661 6.77748544848243
6.51664416592728 P P P LNCV6_130436_PI430048170 mRNA
TGTGTGTTGCAGCACTTATACAGGCAACTGGGCACAAGGAAAATAAAGACGGTGGAAATT NM_005523 RefSeq chr7
- 27181156 27185216 HOXA11 3207 homeobox A11
GO:0001656|GO:0060065|GO:0001658|GO:0005634|GO:0009954|GO:0007283|GO:0001759|GO:0009953|GO:0030
326|GO:0009952|GO:0009653|GO:0007338|GO:0048589|GO:0032993|GO:0060351|GO:0032332|GO:0005667|GO:0
010720|GO:0007275|GO:0006351|GO:0043565|GO:0043234|GO:0007501|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142289_PI430048170 0.0323667805585611 0.7009458321383875.16763417428474
5.2446909516318 5.57533507433728 P P P 5.96903660557588 5.69609974786097
5.88037334014111 P P P LNCV6_142289_PI430048170 mRNA
GTGTTCATGGTCGCCCATTTTTTCATCATTTAACCTATCTTCCAGAAACTACATGATTAA NM_000534 RefSeq chr2 +
189784084 189877629 PMS1 5378 "PMS1 postmeiotic segregation increased 1 (S. cerevisiae), transcript
variant 1"
GO:0032389|GO:0030983|GO:0003697|GO:0042493|GO:0005634|GO:0006298|GO:0016887|GO:0005524|GO:0003
677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138856_PI430048170 0.000597037045859556 0.43171078036935 6.69318052069154
6.9561411828485 6.96029384066336 P P P 7.91707326494821 8.12544842882948
8.20358733100721 P P P LNCV6_138856_PI430048170 mRNA
AACCATGTTTTTTGATCTAGCTCTCTGATTCCATACATTCCAGACTTCTCAGTGGATTTG NM_005760 RefSeq chr2 -
37201630 37231597 CEBPZ 10153 "CCAAT/enhancer binding protein (C/EBP), zeta"
GO:0001077|GO:0006366|GO:0045944|GO:0005634|GO:0000978|GO:0003677 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128321_PI430048170 0.0124751301309412 0.3591367060237935.6421576190881
5.96028271847563 6.2339029795492 P P P 6.91686572949448 7.50085887186222
7.78160014266294 P P P LNCV6_128321_PI430048170 mRNA
CTCCTAGGGATAACCATTTCTATCCTGTTCCAAAGTCTTATTTTATAGTTTGAAAAGCAC NM_001271512 RefSeq
chr10 - 27195213 27240879 ACBD5 91452 "acyl-CoA binding domain containing 5, transcript variant
4"
GO:0016236|GO:0005634|GO:0043231|GO:0008289|GO:0035973|GO:0003674|GO:0016020|GO:0006810|GO:0005
654|GO:0016021|GO:0000062|GO:0030242|GO:0005778|GO:0005777 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143124_PI430048170 0.8374243651852280.98369911752479910.5998674473957
10.4339207792215 10.302789753496 P P P 10.5760229003305 10.5100929295179
10.3254668075149 P P P LNCV6_143124_PI430048170 mRNA
AGAAGCCCCTGAGAAAAACCCTCTAGAAAAACAGCTGTTCCTCTGTGTGGTTTGTTTTTT NM_001303024 RefSeq
chr11 + 65570458 65571888 SSSCA1 10534 "Sjogren syndrome/scleroderma autoantigen 1, transcript
variant 2" GO:0005515|GO:0007067|GO:0051301|GO:0042802 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144773_PI430048170 0.6336288910694180.9426119102825554.53044129691231

4.41960271025668 4.35283360461238 P P P 4.47194221695683 4.75158690415248
4.30509172650286 P P P LNCV6_144773_PI430048170 mRNA
GACAGCCAGACAATAAACATGGAAAGTGCCCGACTGCTGGGCCCATGGCCGTGGAAAAAA NM_017820RefSeq
chr9 - 137306893 137423262 EXD3 54932 "exonuclease 3'-5' domain containing 3, transcript variant
1" GO:0005515|GO:0008408|GO:0005737|GO:0090305|GO:0005634|GO:0003676|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134839_PI430048170 0.000230058243269556 0.4617061147387853.65441724734408
3.8666928927679 3.6953103377299 P P P 4.74933840897021 4.93808767827802
4.87638245246907 P P P LNCV6_134839_PI430048170 mRNA
GTTTATTTGAGCCAGCTCTATCAGGGTCTTCCCATGGTGGTTCAGAATAGATGAGCATAG NM_018590RefSeq chr10
+ 43138444 43185306 CSGALNACT2 55454 chondroitin sulfate N-acetylgalactosaminyltransferase 2
GO:0050652|GO:0050653|GO:0050650|GO:0050651|GO:0005975|GO:0044281|GO:0046872|GO:0008376|GO:0030
166|GO:0030173|GO:0030206|GO:0000139|GO:0016020|GO:0032580|GO:0009405|GO:0030204|GO:0030203|GO:0
047237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98758_PI430048170 0.505189615463067 0.88501840461188911.5097289917143 11.8247441893016
12.09279760055 P P P 11.7429892150763 11.8967509215611 12.3129935822368 P P P
LNCV6_98758_PI430048170 mRNA
GACACCATTGTGTCCAACTGTATATAGCTGCCAATTAGTTTTCTTTGTTTTTACTTTGTC NM_031372RefSeq chr4 -
82422563 82430225 HNRNPDL 9987 "heterogeneous nuclear ribonucleoprotein D-like, transcript variant
2"
GO:0010468|GO:0006396|GO:0006355|GO:0005634|GO:0003677|GO:0006351|GO:0005737|GO:0034046|GO:0003
690|GO:0000166|GO:0003697|GO:0008143|GO:0005654|GO:0005681|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136767_PI430048170 0.115514355355222 0.798917040315063 6.73071605086588
6.67400229784871 6.98026024474821 P P P 7.24546302028374 6.86521166215576
7.23329035961092 P P P LNCV6_136767_PI430048170 mRNA
ATGCAATGATGTTTCTGAAACTGCTATGTACAACCTACCCTGTGTATAACATTTCGTACA NM_001204397 RefSeq
chr4 - 110617423 110642123 PITX2 5308 "paired-like homeodomain 2, transcript variant 4"
GO:0051219|GO:0005515|GO:0001191|GO:0003700|GO:0006366|GO:0033189|GO:0003350|GO:0048536|GO:0035
886|GO:0042803|GO:0042802|GO:0031076|GO:0035993|GO:0016055|GO:0055009|GO:0030334|GO:0001102|GO:0
000976|GO:0001105|GO:0003171|GO:0007520|GO:0000122|GO:0000978|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_55274_PI430048170 0.896027080719585 1.00453157646079 0.308078028915188 0.314314211566388
0.421517397225156 A A A 0.357596349801668 0.30991535503928 0.359130532883176 A A A
LNCV6_55274_PI430048170 mRNA
GTACCAAAAACTTTTGAAAACTATGCAGTCCAACAACAGTTTCTGACTACAACTCAAAAG NM_002927RefSeq chr1
+ 192636137 192660310 RGS13 6003 "regulator of G-protein signaling 13, transcript variant 1"
GO:0043547|GO:0005737|GO:0007186|GO:0005886|GO:0038032|GO:0005634|GO:0005829|GO:0005096 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135583_PI430048170 0.834496643625489 0.993166886593561 0.403745178110024
0.375237061236629 0.251214507931262 A A A 0.332041882480731 0.371419093307634
0.360639959010767 A A A LNCV6_135583_PI430048170 mRNA
GTTGGGAAGCACATGCTTGCTCTAGGAATATCTCCAATAAAGCTGTTAACTATTTGGTGG NM_004466RefSeq chr13
+ 91398618 92867234 GPC5 2262 glypican 5
GO:0005886|GO:0007603|GO:0005796|GO:0005975|GO:0005578|GO:0006027|GO:0043395|GO:0005576|GO:0044
281|GO:0031225|GO:0001523|GO:0005615|GO:0006024|GO:0005887|GO:0009405|GO:0030204|GO:0030203|GO:0
043202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139842_PI430048170 0.121039464600061 0.679960527518741 9.51654221555885
9.37729322083975 9.66547899511553 P P P 9.72875447000098 9.95537923758614

10.4596541194283 P P P LNCV6_139842_PI430048170 mRNA
GCTGCATACAGTGTAAGCATTGTGACCGCCAATAAACTTCAATGGTTTCTACTGAAAAAA NM_015024RefSeq chr8
+ 21919668 22006585 XPO7 23039 exportin 7
GO:0005737|GO:0005643|GO:0008536|GO:0006611|GO:0005049|GO:0005634|GO:0051028 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_68759_PI430048170 0.0584769121878561.28754264928743 9.41011977268376 9.26084369317716
9.61522306886505 P P P 8.99213795408257 9.09862851931944 9.12037591837636 P P P
LNCV6_68759_PI430048170 mRNA
TTATGAGATTTACTCAGACTTTGCCCTCAAGAATCCATTCTATTCCTTAGAAATGCCTAT NM_016146RefSeq chr11
+ 119018530 119023674 TRAPPC4 51399 trafficking protein particle complex 4
GO:0005515|GO:0005801|GO:0017112|GO:0005795|GO:0005783|GO:0030008|GO:0032851|GO:0045202|GO:0016
358|GO:0030425|GO:0008021|GO:0006888|GO:0030198 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138056_PI430048170 0.0142936476057571.24310177228338 10.3690854604116
10.3082341047722 10.1809385084333 P P P 9.95259983381979 10.0689619614005
9.89576730076827 P P P LNCV6_138056_PI430048170 mRNA
GGTCCAGGCTGTGAGGGACACGTATGGAGCAGATAAAGAATTCACTCAAGCAGTAAAAAA NM_001006941
RefSeq chr3 - 184242328 184249525 ALG3 10195 "ALG3, alpha-1,3- mannosyltransferase, transcript
variant 4"
GO:0052925|GO:0000033|GO:0005789|GO:0006486|GO:0016021|GO:0006488|GO:0044267|GO:0043687|GO:0018
279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139359_PI430048170 0.5406696839512890.7716192321720661.60003245697384
1.21153796987644 2.28894531604138 A A A 1.24409488123025 2.52686437050417
2.35940108140168 A P A LNCV6_139359_PI430048170 mRNA
CTGCTTGCAGTATTCATGTTGACAACAGAGTAAAAGAGAATACTGTAAAGAATTACTGCA NM_152527RefSeq chr2
- 230034973 230068999 SLC16A14 151473 "solute carrier family 16, member 14"
GO:0015718|GO:0034220|GO:0005886|GO:0008028|GO:0016021|GO:0015293 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141000_PI430048170 0.0192775998992731.9970130907636 13.5582168033812
13.7187108830953 13.6647826225386 P P P 12.9123342820059 12.3385123946731
12.6452247857505 P P P LNCV6_141000_PI430048170 mRNA
AGAAAAGAAAGCTACAGAAGAAACTGGGGCTCCTCCAGGGTGGCAGCAACAATAAATAGA NM_001042483
RefSeq chr16 - 28537340 28539174 NUPR1 26471 "nuclear protein, transcriptional regulator, 1,
transcript variant 1"
GO:0002526|GO:0006355|GO:0043065|GO:0048147|GO:0009636|GO:0005634|GO:0045786|GO:0035914|GO:0003
677|GO:0006351|GO:0031401|GO:0042771|GO:0003674|GO:0005737|GO:0006461|GO:0003682|GO:0016049|GO:2
000194|GO:0006473|GO:0008584 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133787_PI430048170 0.9091881252282170.98348337401350711.5630785061165
11.5293967965093 11.6780054219673 P P P 11.4574817752686 11.5234449120207
11.8367839462588 P P P LNCV6_133787_PI430048170 mRNA
TGTAGAGCAGTGGTGTCTCCAATGAACTTGTTTCCTGGTTTTGCATCTTGTGAAATGTTT NM_001303103 RefSeq
chr9 - 81583682 81689535 TLE1 7088 "transducin-like enhancer of split 1 (E(sp1) homolog,
Drosophila), transcript variant 1"
GO:0005515|GO:0005667|GO:0001106|GO:0030178|GO:0005730|GO:0007275|GO:0005634|GO:0000122|GO:2000
811|GO:0006351|GO:0042802|GO:0005829|GO:0010628|GO:0007165|GO:0005737|GO:0007219|GO:0003682|GO:0
009887|GO:0005654|GO:0016055|GO:0045892|GO:0043124|GO:0008134 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_141701_PI430048170 0.1557810909143941.65864104710065 1.11751752042292
0.3418464981470581.33619787112885 A A A 0.2470186634530650.289133363381103
0.245893773868261 A A A LNCV6_141701_PI430048170 mRNA

GTAGGGTGGTTGCTACCTTTAATCAGTACTATGGATTTCTAAATGCATTTAACTGTGGTT NM_001195279 RefSeq chr3 - 12539780 12545464 MKRN2OS NA MKRN2 opposite strand NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130266_PI430048170 0.464000693155631 0.748209492630025 3.20575754601967 2.71184753457575 0.276824095937592 P A A 3.0947734327867 3.14364407796989 2.41308109616178 P P P LNCV6_130266_PI430048170 mRNA
CTCCTCTGCCTGGGTTATAAGAAACGCACCTGACTTAAATAACATGTATTGTGGATATAT NM_138337 RefSeq chr12 + 9971408 9985595 CLEC12A 160364 "C-type lectin domain family 12, member A, transcript variant 1" GO:0005886|GO:0030246|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132636_PI430048170 0.155205834555745 1.09450033203466 0.667552467345854 0.842427787970886 0.661274398854353 A A A 0.563035093295126 0.624452340536671 0.599714519959736 A A A LNCV6_132636_PI430048170 mRNA
AATCGTGTCAGAACTCTTTTGGAAGAGTTGGCACTTCATTGTCTCTTCAACCTCTGTTAT NM_001171186 RefSeq chrX - 8790795 8801337 FAM9A 171482 "family with sequence similarity 9, member A, transcript variant 1" GO:0005515|GO:0005730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94708_PI430048170 0.520486754918006 1.32809249383393 1.60038021949699 0.41525569040349 0.417942324778211 A A A 0.267894584517031 0.353898955605244 0.856911346093287 A A A LNCV6_94708_PI430048170 mRNA
AAACAAAAGTTATTGCTCGTCATGTGCAGCCACGTCCTTTGGTAGTTAATCCTCCTCCTC NM_020364 RefSeq chrY + 24833819 24907040 DAZ3 NA deleted in azoospermia 3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70631_PI430048170 0.0781023130031255 0.551221615168948 3.10734294251801 4.10270697614894 3.8814411180417 P P P 4.21228671205954 4.8398134971455 4.72057635063883 P P P LNCV6_70631_PI430048170 mRNA
GCAGCAAGCAACTTTGACTGCTGTCTTGGATACACAGACCGTATTCTTCATCCTAAATTT NM_004591 RefSeq chr2 + 227813841 227817564 CCL20 6364 "chemokine (C-C motif) ligand 20, transcript variant 1" GO:0005515|GO:0008009|GO:2000406|GO:0007267|GO:0050726|GO:0005576|GO:0005615|GO:0007165|GO:0071223|GO:0006955|GO:0071222|GO:0006954|GO:0006935|GO:0060326|GO:0042060|GO:0051770|GO:0042742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127647_PI430048170 0.914919266604669 0.983311205429679 6.87508178482192 6.4661965636914 7.03447160282797 P P P 7.12665182254646 6.62421452091397 6.70344829730992 P P P LNCV6_127647_PI430048170 mRNA
GATGGGAAAAGAACACATGAATTTGTTAATAAAGCACTATGATCTGCAAACGATGGAATG NM_152261 RefSeq chr12 + 106955765 106974035 TMEM263 90488 transmembrane protein 263 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141740_PI430048170 0.237721405426976 1.22368546551153 7.79062924238178 7.92471968526006 7.53468028802602 P P P 7.16496305831758 7.78049427415381 7.38944950771917 P P P LNCV6_141740_PI430048170 mRNA
GTCACTATTTTGTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTACAAAAAA NM_024330 RefSeq chr1_GL383518v1_alt + 91992 96858 SLC27A3 11000 "solute carrier family 27 (fatty acid transporter), member 3" GO:0001676|GO:0031966|GO:0016020|GO:0000166|GO:0016021|GO:0031957|GO:0004467 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127090_PI430048170 0.000392499402057215 0.18938304309561 1.39598032869793 1.4438503508811 1.88285828014604 A A A 3.78992222370623 4.17663925840678 3.98359516142634 P P P LNCV6_127090_PI430048170 mRNA
ATGTCTATAGTGTCTTTAAATTATTGTGACCTACACTGGGTACCGGAGAGGGGGATGGCT NM_058238 RefSeq chr22 - 45920365 45977128 WNT7B 7477 "wingless-type MMTV integration site family, member 7B" GO:0060710|GO:0072236|GO:0070307|GO:0071300|GO:0046330|GO:0005615|GO:0005109|GO:0016055|GO:0060033|GO:0005796|GO:0072089|GO:0051384|GO:0072207|GO:0072205|GO:0001701|GO:0021871|GO:0045165|GO:0

050808|GO:0005788|GO:0060484|GO:0060535|GO:0032364|GO:0060482|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144847_PI430048170 0.6086653911688680.9390346520081910.414432342143313
0.4278050436138240.347511089749081A A A 0.3217591357867960.73523649828385
0.369905111654524A A A LNCV6_144847_PI430048170 mRNA
GCAGAGTGGAAGAACTTGATGAACCAATGTTTTCTGATATTGCATTAAACATTGATCAAG NM_138812RefSeq chr10
- 80336105 80356758 DYDC1 143241 "DPY30 domain containing 1, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_125082_PI430048170 0.5830188551399250.94199563086594 7.4890116639456
7.25782435691225 7.31265322485962 P P P 7.64730887250941 7.39205476539825
7.26202983647426 P P P LNCV6_125082_PI430048170 mRNA
TATTCAACATCAGAGAATCCACACTGGGGAAAAGCCCTATGAATGTAATGAGTGTGGGAA NM_001278284 RefSeq
chr7 - 100069970 100082548 ZNF3 7551 "zinc finger protein 3, transcript variant 3"
GO:0005515|GO:0006355|GO:0045321|GO:0008270|GO:0007275|GO:0005634|GO:0003677|GO:0030154|GO:0006
351|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143428_PI430048170 0.3726787116287970.5912586045595391.4211439291747
0.52857965330677 1.03530906289905 A A A 1.98115694829315 2.32402060041547
0.565673695149735A A A LNCV6_143428_PI430048170 mRNA
TGTCAGCAAAGAAATACACTTATCAAATTTTAAACCAATGGGAGCCTGAAAGTGTTACAG NM_003569RefSeq chr6
- 132457523 132513198 STX7 8417 syntaxin 7
GO:0048471|GO:0005886|GO:0031201|GO:0042582|GO:0030139|GO:0005765|GO:0006906|GO:0006886|GO:0005
764|GO:0043231|GO:0051640|GO:0000149|GO:0070925|GO:0048278|GO:0070062|GO:0001772|GO:0019905|GO:0
005770|GO:0031982|GO:0012505|GO:0019869|GO:0005484|GO:0001916|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_119620_PI430048170 0.3836954225167960.9453140661535718.49309554981767
8.27627650074995 8.36142156102863 P P P 8.37130975260563 8.44543013875099
8.55951176127305 P P P LNCV6_119620_PI430048170 mRNA
GTGGGAGCCCAACCCCATTTGATAGGAATTTTGCCACTAAGATGGGCGCCAAGGCTATGA NM_001166686 RefSeq
chr12 + 48105872 48146404 PFKM 5213 "phosphofructokinase, muscle, transcript variant 1"
GO:0005515|GO:0097228|GO:0044281|GO:0051259|GO:0006096|GO:0042803|GO:0046716|GO:0046872|GO:0005
829|GO:0042802|GO:0016324|GO:0006006|GO:0032024|GO:0019900|GO:0006002|GO:0070061|GO:0003872|GO:0
070062|GO:0005975|GO:0042593|GO:0008022|GO:0005524|GO:0009405|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139823_PI430048170 0.9497563504965181.01572265061702 0.411751086720174
0.6015687994382681.79537755040503 A A A 0.9579998828460310.3940472529580071.5676570688528
A A A LNCV6_139823_PI430048170 mRNA
GGCAGGTGTTTCTTAAAGGGATGCAAAAGATATTTTGCACTTTGTATGTTCCAAAACATT NM_145167RefSeq chr1
- 160027671 160031993 PIGM 93183 "phosphatidylinositol glycan anchor biosynthesis, class M"
GO:0006501|GO:0000030|GO:0016254|GO:0005789|GO:0016021|GO:0044267|GO:0043687 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141901_PI430048170 0.7290472961457240.9793455023318630.575388336444155
0.4879907413684410.31012212921153 A A A 0.4163587633983260.547694041656975
0.509170177906446A A A LNCV6_141901_PI430048170 mRNA
GATTTGAGGTTGTAAGCAAACTAAGTTAGTGTAATTTGGCTTCATATATGTAACGTGAGG NM_016073RefSeq chr15
- 83138051 83208018 HDGFRP3 50810 "hepatoma-derived growth factor, related protein 3"
GO:0005737|GO:0008283|GO:0005654|GO:0005634|GO:0008083 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134518_PI430048170 0.1266299735714970.3886716302150770.5985646658821
2.76280720868725 2.12902814578913 A A A 3.48128641092197 3.25171745174453

3.57527704958453 P P P LNCV6_134518_PI430048170 mRNA
TTCAAAATGTAAGGGGTGGCAAAATGTAAACACTGCTTCCTATTACTGTGCAAGTTTTTT NM_001031689 RefSeq
chr9 - 26903369 26947470 PLAA 9373 phospholipase A2-activating protein
GO:0016005|GO:0005515|GO:0007165|GO:0006954|GO:0043085|GO:0006644|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134180_PI430048170 0.7025498216545041.29174305751799 0.453460686787701
0.4393789889645091.93086000084447 A A A 0.4102629429460740.494619391080681
1.21637994756685 A A A LNCV6_134180_PI430048170 mRNA
GCTGTGTGTATATTTTGATAAAATGTTGTGACTTCATGGCAAACAGGTGGATGTGTAAAA NM_006257RefSeq chr10
- 6427142 6580301 PRKCQ 5588 "protein kinase C, theta, transcript variant 1"
GO:0005515|GO:2000318|GO:0050852|GO:0004842|GO:0032753|GO:0016567|GO:0005886|GO:0007603|GO:0070
233|GO:0001558|GO:0046872|GO:0006921|GO:0005829|GO:0035556|GO:0051092|GO:0006954|GO:0007411|GO:0
042102|GO:0006509|GO:0016056|GO:0001772|GO:0006355|GO:0032740|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_107496_PI430048170 0.3258574763498320.7645807805703763.76419963586631
3.57333782435374 3.52647601498282 P P P 3.49643473792969 3.97785169754871
4.41746763238253 P P P LNCV6_107496_PI430048170 mRNA
AAACAAGGAATTGTACAGAGTACGAGAGGACAGCACTTGAGAACACAGAATGAGCCAGCA NM_002499RefSeq
chr15 + 73052483 73305206 NEO1 4756 "neogenin 1, transcript variant 1"
GO:0042692|GO:0006355|GO:0051149|GO:0045296|GO:0005886|GO:0007411|GO:0005887|GO:0007520|GO:0004
872|GO:0007155|GO:0055072 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136115_PI430048170 0.3689013770751911.02095171324934 0.473101977506826
0.5209522080215370.432289823606523A A A 0.44558793525908 0.438711048306126
0.453628548112515A A A LNCV6_136115_PI430048170 mRNA
TTCGTGAGTATGTGCTCAGTCTATTCCAGAGAAAGAACATGTAGATGGATAGTTCTCTTT NM_001005171 RefSeq
chr11 + 4488878 4489908 OR52K1 NA "olfactory receptor, family 52, subfamily K, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132661_PI430048170 0.8811481237277911.04344121707971 1.03062317613519
0.2937744234646170.271032696353517A A A 0.24900841089109 0.934747842634067
0.249931679437602A A A LNCV6_132661_PI430048170 mRNA
GTGAGTGAAAATGAATAGAGATCCTTATTCCACTCCTTAATGGCATACCAAGATGAAATT NM_177398RefSeq chr1
- 165201866 165356715 LMX1A 4009 "LIM homeobox transcription factor 1, alpha, transcript variant 1"
GO:0021542|GO:0006355|GO:0021953|GO:0005634|GO:0021549|GO:0001558|GO:0006351|GO:0043565|GO:0045
665|GO:0007411|GO:0071542|GO:0008270|GO:0030901 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100322_PI430048170 0.0589883222977180.6362314769726347.90524428297492
8.47374200254141 8.52260905760053 P P P 8.88700528694036 8.76380066941783
9.24193859343691 P P P LNCV6_100322_PI430048170 mRNA
GAGGGAACAAGGAACAGAATCAAGATCTTCTACTCCTCTGCCAACAATTTCTTCTTCAGC NM_001032283 RefSeq
chr12 + 98515572 98550379 TMPO 7112 "thymopoietin, transcript variant 2"
GO:0005515|GO:0031965|GO:0006355|GO:0005737|GO:0016020|GO:0005637|GO:0005634|GO:0016021|GO:0005
635|GO:0003677|GO:0000785|GO:0005521 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2225_PI430048170 0.0200589227076422 0.2880601813589411.37377087811472
0.5335663382529490.430318997922213A A A 2.4911744639819 2.70299099419016
2.71487738046377 A P P LNCV6_2225_PI430048170 mRNA
GCCTTTAACAAGCCCTCAATTCTTAACAGACATAACATAATTCATACTGGAAAGAAACTC NM_182515RefSeq chr19
+ 21082146 21125080 ZNF714 148206 "zinc finger protein 714, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128465_PI430048170 0.5597863996242091.58709911465421 2.54065124377943

0.3962347645101152.2792273094884 A A A 1.21205670456216 1.8958575514353
0.600057362253597 A A A LNCV6_128465_PI430048170 mRNA
ACTGTCCTTTCAGACAAAGCTTGTACAAATTCCTGAACCGCAAATTTGCTGAAGTGACCG NM_019859RefSeq chr10
- 90740818 90857914 HTR7 3363 "5-hydroxytryptamine (serotonin) receptor 7, adenylate cyclase-
coupled, transcript variant d"
GO:0006939|GO:0004993|GO:0005886|GO:0007187|GO:0005887|GO:0008015|GO:0042310|GO:0007623|GO:0007
268|GO:0007210 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142566_PI430048170 0.0282938208713893 0.7732640524468129.99833634919929
9.95199944914705 10.0071235368203 P P P 10.3091283521704 10.261410088065
10.4902012336664 P P P LNCV6_142566_PI430048170 mRNA
CCGAAGAATTGTCTTGCAAGTTAAGGCTTCCCCCTTTACTATAAGACTATAAATAAAAAC NM_145113RefSeq chr14
- 65075123 65102544 MAX 4149 "MYC associated factor X, transcript variant 3"
GO:0003712|GO:0005515|GO:0032868|GO:0006355|GO:0003700|GO:0060041|GO:0046982|GO:0006366|GO:0003
713|GO:0005634|GO:0051402|GO:0048678|GO:0032403|GO:0042803|GO:0030425|GO:0043565|GO:0005737|GO:0
006461|GO:0071339|GO:0016605|GO:0071375|GO:0010629|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133863_PI430048170 0.3665432177671311.28938895781061 1.11475779911003
0.3228225289414520.28391434650705 A A A 0.2486110978002720.285374518851542
0.247379387699544 A A A LNCV6_133863_PI430048170 mRNA
ACTATAGGGAGCAAGTGGCAGCCACCAATTTCCTCTTTGGATAGTAAACTCACTTATTGA NM_030876RefSeq chr6
- 29355229 29356277 OR5V1 81696 "olfactory receptor, family 5, subfamily V, member 1"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141395_PI430048170 0.9747356667704051.06807093858312 3.28892711121446
2.01153279109633 2.95467945475215 P A P 2.97910974869676 2.72118619449728
2.51233461046532 P P P LNCV6_141395_PI430048170 mRNA
ACAAATAAAGGCACATCCCAGGTGGCTGGGACCTGCCAGTAGGTGTCACACCACAAAAAA NM_199350RefSeq
chr9 - 129612224 129620776 C9orf50 375759 chromosome 9 open reading frame 50 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138993_PI430048170 0.2682684934647141.16917813682765 12.7344773366566
13.0244089725752 13.2180590927874 P P P 12.8641484772319 12.618753050522
12.8453845892186 P P P LNCV6_138993_PI430048170 mRNA
AAATGGGTACAGTCTCAGGACAACTTAGCCTCCAGGACGCACTGCTGCTGCTGCTCATGG NM_080739RefSeq chr20
+ 2815010 2815830 C20orf141 128653 "chromosome 20 open reading frame 141, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98130_PI430048170 0.00359407549575306 0.5827163482936958.11415017750535
7.95390376655249 8.27627650074995 P P P 8.78570349432781 8.83464564818319
9.06384373012805 P P P LNCV6_98130_PI430048170 mRNA
AAATAGACAACAACCCTTTTGCAAAAGGTTTCCGGGACACTGGAAATGGCCGAAGAGAAA NM_016569RefSeq
chr12 - 114670253 114684164 TBX3 6926 "T-box 3, transcript variant 2"
GO:0005515|GO:0035136|GO:0008284|GO:0060596|GO:0003167|GO:0030879|GO:0005634|GO:0060931|GO:0045
662|GO:0001947|GO:0030539|GO:0046884|GO:0030857|GO:0001085|GO:0060021|GO:0009887|GO:0048332|GO:0
008595|GO:0010159|GO:0001102|GO:0043066|GO:0001568|GO:0006357|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128275_PI430048170 0.0295545082990466 0.6806995797908591 0.1488972115747
10.0665217322526 10.2826061776535 P P P 10.5004709527172 10.7102092042164
10.9286185486548 P P P LNCV6_128275_PI430048170 mRNA
GCTGTCTTACACCAGTGGAGCTACCCTTTAAATGTACAAATTATTTGTATGCTAATGTAA NM_000696RefSeq chr1
- 165662211 165698663 ALDH9A1 223 "aldehyde dehydrogenase 9 family, member A1"

GO:0001822|GO:0004029|GO:0006081|GO:0004028|GO:0044281|GO:0042803|GO:0005829|GO:0001889|GO:0005739|GO:0034641|GO:0005737|GO:0051287|GO:0047105|GO:0045329|GO:0043176|GO:0019145|GO:0042445|GO:0033737|GO:0042136|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129746_PI430048170 0.7464218696628550.9887544021995050.261335153071772
0.2779842713590550.404557934588136A A A 0.3686212323179030.317128622426624
0.310666871485752A A A LNCV6_129746_PI430048170 mRNA
ATTGTAAGATATTTTAACCCTGTATAAATGCAACTTTTCCTTTAGCTTAATGGCCTGGGG NM_021926RefSeq chr11 - 44260727 44310166 ALX4 60529 ALX homeobox 4
GO:0005667|GO:0003700|GO:0046982|GO:0048704|GO:0048565|GO:0042981|GO:0005634|GO:0009791|GO:0009952|GO:0003677|GO:0006351|GO:0043565|GO:0001501|GO:0007517|GO:0045944|GO:0035116|GO:0071837|GO:0060021|GO:0035115|GO:0001942|GO:0042733 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132226_PI430048170 0.0414273301171887 0.6802415010372816.92074706871608
7.01930679434334 6.87824168541852 P P P 7.25361745466403 7.70181621078913
7.49948038461291 P P P LNCV6_132226_PI430048170 mRNA
GCATGCCTTGCCTGAACTAACCACGTTATCTATTTGCAATAAACCCATTTCTTAAAAGGA NM_001185011 RefSeq chr22 + 50508215 50524780 NCAPH2 29781 "non-SMC condensin II complex, subunit H2, transcript variant 3" GO:0005515|GO:0016020|GO:0030261|GO:0005694|GO:0005654|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131835_PI430048170 0.0154893629731098 1.34901719185628 12.9822435204721
13.1213381931256 13.04691688484 P P P 12.4605383617051 12.6990327152789
12.6863136854935 P P P LNCV6_131835_PI430048170 mRNA
TGTTCAGGATCTCCTCCCTTGTTTAAATGTCAATAAATGCCCCAACTGCTTTGTAAGTGC NM_018285RefSeq chr15 - 75639084 75640323 IMP3 55272 "IMP3, U3 small nucleolar ribonucleoprotein"
GO:0045903|GO:0005515|GO:0030515|GO:0003735|GO:0006364|GO:0032040|GO:0015935|GO:0005730|GO:0005634|GO:0019843|GO:0034457 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135579_PI430048170 0.2659977495573940.9367820550547031 0.3549283211667
10.5285740861693 10.3428267555158 P P P 10.4243708486119 10.5340252772009
10.5547875602815 P P P LNCV6_135579_PI430048170 mRNA
GCCTTTTCCCACTGAGAGAAGGCTGCTCTTTTGTACTGCCCCCCGCTCATTAAACAGCCT NM_007165RefSeq chr19 + 2236816 2248679 SF3A2 8175 "splicing factor 3a, subunit 2, 66kDa"
GO:0008380|GO:0006397|GO:0005515|GO:0010467|GO:0000398|GO:0030532|GO:0008270|GO:0005681|GO:0005654|GO:0071013|GO:0000389 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137295_PI430048170 0.2983016507512780.7145853040821524.16371279935598
4.27096280691355 4.36637222680702 P P P 4.08311945524971 4.93522800219561
5.06254967501657 P P P LNCV6_137295_PI430048170 mRNA
TGTGTGTGTGAATGAACACTCTTGCTTTATTCCAGAATGCTGTACATCTATTTTGGATTG NM_013230RefSeq chr6 - 106969830 106975465 CD24 100133941 "CD24 molecule, transcript variant 1"
GO:0045730|GO:0005515|GO:0072112|GO:0043627|GO:0005886|GO:0061098|GO:0031295|GO:0002237|GO:0031225|GO:0007204|GO:0032597|GO:0032913|GO:0072139|GO:0042104|GO:0016337|GO:0030296|GO:0030856|GO:0043406|GO:0007411|GO:0043408|GO:0032600|GO:0004871|GO:0016055|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142531_PI430048170 0.00985510452127558 0.61304976035567 5.83872175923555
5.58500417797589 5.49433981464526 P P P 6.12138307551439 6.45304928030749 6.4586861702629
P P P LNCV6_142531_PI430048170 mRNA
ATCACGCAACGTGTTATCTTGTGGTGTAAATAAAGACTGCGTTACTTGCCCTCCCAAAAA NM_006037RefSeq chr2 - 239048167 239400949 HDAC4 9759 histone deacetylase 4
GO:0005515|GO:0030018|GO:0031594|GO:0042641|GO:0044212|GO:0010832|GO:0017053|GO:0045820|GO:0019901|GO:0034983|GO:0003714|GO:0048742|GO:0043393|GO:0001047|GO:0000122|GO:0030955|GO:0014894|GO:0033558|GO:0042113|GO:0001501|GO:0000118|GO:0002076|GO:0008270|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_140206_PI430048170 0.4262712972557280.9251268550387370.392085107273512
0.3967093478102670.356374397582234A A A 0.6963360415245640.36568040738614
0.396693823113087A A A LNCV6_140206_PI430048170 mRNA
CGTAGTACAGAAGTGCAAGAAGAGAATTTATGAAGGATGAATAGAACTACAAACCTATCT NM_001024660 RefSeq
chr3 + 124094710 124721189 KALRN 8997 "kalirin, RhoGEF kinase, transcript variant 1"
GO:0005515|GO:0051056|GO:0048011|GO:0043065|GO:0048013|GO:0007264|GO:0015629|GO:0097190|GO:0005
524|GO:0046872|GO:0005829|GO:0007399|GO:0043547|GO:0035556|GO:0005085|GO:0007165|GO:0032321|GO:0
004674|GO:0007411|GO:0006468|GO:0005089|GO:0016192|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_135501_PI430048170 0.0144739974488506 0.5479717440853811 0.9675619118149
11.0384574450526 10.9052681545459 P P P 11.762494160911 12.0710170382775
11.6508989350631 P P P LNCV6_135501_PI430048170 mRNA
TAGAAGGGACCCTCCTGTGGTCTTTGTCTTGATTTTTCTTAATAAACGGTGCTATCCCCG NM_001291860 RefSeq
chr1 - 21822231 21937297 HSPG2 3339 "heparan sulfate proteoglycan 2, transcript variant 1"
GO:0005515|GO:0005886|GO:0007603|GO:0048704|GO:0044281|GO:0005615|GO:0046872|GO:0008104|GO:0022
617|GO:0002062|GO:0030198|GO:0060351|GO:0030204|GO:0030203|GO:0070062|GO:0043202|GO:0005975|GO:0
005796|GO:0005605|GO:0006027|GO:0005576|GO:0001525|GO:0008022|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135091_PI430048170 0.23744724046474 1.40483048614954 3.42522606543259
3.24798468859303 2.58810043389255 P P A 3.02244247611361 2.5915892257322
2.18159402255225 P P A LNCV6_135091_PI430048170 mRNA
GGGACACAAGTTGCCAGCCACCAACTTTCTTGCCTCAACTACCTTCCTGAATTATTTTTT NM_005064RefSeq
chr17_KI270857v1_alt - 247623 252533 CCL23 6368 "chemokine (C-C motif) ligand 23, transcript variant
CKbeta8"
GO:0008009|GO:0008285|GO:0006874|GO:0007267|GO:0005576|GO:0005615|GO:0002548|GO:0031726|GO:0007
165|GO:0006955|GO:0006954|GO:0006935|GO:0007186|GO:2001264|GO:0008201 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144838_PI430048170 0.6639501001020091.16052993593486 0.474526379222744
0.4668574804503181.37955350164044 A A A 0.8843021235332960.50266276187471
0.451498105402187A A A LNCV6_144838_PI430048170 mRNA
GAACAGGGACATGAAAGAGGCCCTTGGGAAACTCTTCAGTAGAGCAACATTTTTCTCTTG NM_054107RefSeq chr9
+ 122510801 122511743 OR1J2 NA "olfactory receptor, family 1, subfamily J, member 2" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134285_PI430048170 0.00494530294094835 0.6293927383045518.38971335671428
8.14298636512736 8.41298202682518 P P P 8.84532324275513 8.97840391937985
9.12725696999439 P P P LNCV6_134285_PI430048170 mRNA
AGCCGGCGCCAGTAGGAAAGACCTCCTTCCTAAATAAAAGAAGTGTCTCCCATGAAAAAA NM_007357RefSeq chr1
+ 230642455 230693985 COG2 22796 "component of oligomeric golgi complex 2, transcript variant 1"
GO:0005515|GO:0009312|GO:0005795|GO:0000139|GO:0008565|GO:0007030|GO:0017119|GO:0006891|GO:0006
486|GO:0032403|GO:0006886|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127135_PI430048170 0.8366864617515180.9861830572404966.38618994939662
5.72342690908782 5.60774648973183 P P P 6.05178525112697 6.03294889002774
5.80789874992631 P P P LNCV6_127135_PI430048170 mRNA
AATGGCCCCCGGTTGCGGTAGGCAATCAATAATACTCTTTGAATAATAATGAGGTTTTCA NM_182508RefSeq chr13
+ 42781549 42791549 FAM216B 144809 "family with sequence similarity 216, member B" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_130101_PI430048170 0.0956510891180269 0.7226508416874754.82128554038246
4.83891723662596 5.3262773294535 P P P 5.44537164625597 5.48020016053298

5.52459781548747 P P P LNCV6_130101_PI430048170 mRNA
GCTGAAATTCAGTGTCAGCAAAGTGATATTACGTTGTTCTGTTTCTAATTAACCTTAGCA NM_032352 RefSeq chr14
+ 35826390 35871963 BRMS1L 84312 breast cancer metastasis-suppressor 1-like
GO:0016575|GO:0042826|GO:0004407|GO:0000122|GO:0070822|GO:0040008|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139381_PI430048170 0.2313477094327570.6802072015960863.26490278798526
3.08961455721464 3.31763365931779 P P P 4.04854746863615 3.12898120105415
4.00076142179106 P P P LNCV6_139381_PI430048170 mRNA
TCTACCTTCAGCAAGTGTTTATGTATTTTGTATGCTAGTCATGTTCTTGGTTCTGTCTTC NM_001174103 RefSeq chr17
- 28607963 28614193 SGK494 124923 uncharacterized serine/threonine-protein kinase SgK494
GO:0004674|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141458_PI430048170 0.00178222632870649 2.3669073261613 2.79288838338597
3.09669140362399 2.93049292589756 A P P 1.73533811001636 1.63007947690803
1.73909200151134 A A A LNCV6_141458_PI430048170 mRNA
GGCGGTATCTAGCCCTTTCTCTGTAAAATATCCCTATGTTTAATCTGTATTTCTTGCTTA NM_020957 RefSeq chr5 +
141181689 141186221 PCDHB16 57717 protocadherin beta 16
GO:0016339|GO:0005886|GO:0005509|GO:0007268|GO:0016021|GO:0007416|GO:0007156 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_69071_PI430048170 0.00150490998121757 0.1932868801559752.56349301160018
2.01506694220877 2.05169442423017 A A A 4.11943447999649 4.7766287563101
4.81526723505587 P P P LNCV6_69071_PI430048170 mRNA
ACCCTCTCAAGGACAAGATAAAGATTGACTTCAGAGATATATCACATCAAGCTAGAGGAA NM_144973 RefSeq chr12
- 31382222 31591018 DENND5B 160518 DENN/MADD domain containing 5B
GO:0017112|GO:0005262|GO:0050982|GO:0016020|GO:0032851|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128153_PI430048170 0.7299295933738750.9759393094005360.570550040621973
0.5287803319884020.297568297709204 A A A 0.4009799604533210.59034939295742
0.519377681949262 A A A LNCV6_128153_PI430048170 mRNA
CCAAAAATATCACATGGTTTAAAGATGGGAAGATGATCGGCTTCCTAACTGAAGATAAAA NM_000073 RefSeq chr11
+ 118344343 118353782 CD3G 917 "CD3g molecule, gamma (CD3-TCR complex)"
GO:0050852|GO:0046982|GO:0005886|GO:0031295|GO:0030159|GO:0015031|GO:0042608|GO:0042105|GO:0042
110|GO:0006461|GO:0007163|GO:0005887|GO:0070228|GO:0045087|GO:0042101|GO:0050776|GO:0038096|GO:0
007166|GO:0004888. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144275_PI430048170 0.2014293448812690.9554196991992660.269642661096996
0.3553710852115820.301774024130088 A A A 0.4420612917680790.343556490402315
0.337445836371491 A A A LNCV6_144275_PI430048170 mRNA
GGAATCTGTAGGTTACATTCCTAAATGCTGAGTCAGAGCATCTCAGCATTTAAAATTGTG NM_001286488 RefSeq
chr6 + 10747758 10759773 TMEM14B 81853 "transmembrane protein 14B, transcript variant 4"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129486_PI430048170 0.0145076964958271 1.12637067478029 9.00001920762838
8.91093473736669 9.00892180873715 P P P 8.76162569220248 8.79325122163682
8.85056181667839 P P P LNCV6_129486_PI430048170 mRNA
CCAGTTTCTCTGTGGTGTTTATGAAATAGCTAAAAGCAAATGAAGTAAAGGGCATACTAT NM_015969 RefSeq chr7
+ 55951917 55955340 MRPS17 51373 mitochondrial ribosomal protein S17
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0019843|GO:0006
412|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136801_PI430048170 0.0109779668569352 1.54599802957135 8.51233257965242
8.1634703027792 8.30172717536435 P P P 7.52836242134174 7.86160173732243
7.70429043139326 P P P LNCV6_136801_PI430048170 mRNA

GTTTTTGTCTAGGTCGAGAATGAATGTTAGCTGATGAAATAAACCCTGACAAGGAAAAAA NM_004807 RefSeq chr2 - 128265479 128318597 HS6ST1 9394 heparan sulfate 6-O-sulfotransferase 1
GO:0048286|GO:0005975|GO:0001525|GO:0044281|GO:0006024|GO:0015015|GO:0000139|GO:0005887|GO:0048666|GO:0060716|GO:0008146|GO:0009405|GO:0017095|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63384_PI430048170 0.1078285609560360.7197049225412689.23572430787933 9.38111180862515 9.75765971506482 P P P 9.67439623820865 9.87187703528731 10.2442099830561 P P P LNCV6_63384_PI430048170 mRNA
CCGTTTTGTATTGCTTCCTGATTACCAGTCTGATTATACCATGTGTGCTAATATACTTTT NM_212471 RefSeq chr17 + 68511779 68533429 PRKAR1A 5573 "protein kinase, cAMP-dependent, regulatory, type I, alpha, transcript variant 2"
GO:0005515|GO:0034236|GO:0031594|GO:0005886|GO:0008603|GO:0044281|GO:0007202|GO:0005829|GO:0035556|GO:0030552|GO:0007173|GO:0071377|GO:0006833|GO:0034199|GO:0031625|GO:2000480|GO:0048011|GO:0005952|GO:0001707|GO:0006357|GO:0031588|GO:0045214|GO:0055085|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127322_PI430048170 0.400241354569888 0.835708846298494 0.613881440484723 0.363103590874848 0.684019013089289 A A A 1.18521195231013 0.450313888778375 0.724572569272193 A A A LNCV6_127322_PI430048170 mRNA
ACGATGAAGGCATCGACAGTATTAATGTCAGGTGATCTGAAATAAACTCCCGTAACCCCA NM_178556 RefSeq chr4 + 188139443 188147495 TRIML1 339976 tripartite motif family-like 1
GO:0016567|GO:0016874|GO:0008270|GO:0007275 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132787_PI430048170 0.111041449450649 1.0411272877943 0.469104521868309 0.539113471506281 0.472804696317112 A A A 0.408891530127551 0.438014578024707 0.460298199450893 A A A LNCV6_132787_PI430048170 mRNA
CATGCTTCAAGGACAGTTTGCAAGTGGATATAAATACATACACATCACTAGTGATTATGC NM_032811 RefSeq chr11 + 124622845 124635926 TBRG1 84897 "transforming growth factor beta regulator 1, transcript variant 1"
GO:0006260|GO:0005515|GO:0008285|GO:0050821|GO:0007050|GO:0005654|GO:0005634|GO:0032066|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143814_PI430048170 0.856265206724678 1.02035285776148 10.9699209270736 11.1179839319165 11.336938299519 P P P 11.0523120697242 10.9707562513106 11.3154752831556 P P P LNCV6_143814_PI430048170 mRNA
GTCCTTCATATGTGAAAGATCCAGTGTTGGAATTCTTTGGTGTAAATAAACGTTTGGTTT NM_177559 RefSeq chr20 - 482693 543838 CSNK2A1 1457 "casein kinase 2, alpha 1 polypeptide, transcript variant 1"
GO:0005515|GO:0008284|GO:0045732|GO:0005886|GO:0030307|GO:0051879|GO:0030177|GO:0005634|GO:0005829|GO:0016581|GO:0007411|GO:0016580|GO:0071174|GO:0016055|GO:0043154|GO:0031519|GO:0006355|GO:0005524|GO:0006351|GO:0007165|GO:0047485|GO:0061077|GO:0004674|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137763_PI430048170 0.276965320147134 1.09440099567397 7.17698475366386 7.18456545244616 7.43482710570123 P P P 7.05251352984838 7.17149925129435 7.19320105647494 P P P LNCV6_137763_PI430048170 mRNA
GTCCCTCATCTCTTGGGGCATAATCAATGCAACTTATGAGTTCTTGTTAAAATTTATATG NM_001034172 RefSeq chr18 - 31759695 31760880 SLC25A52 147407 "solute carrier family 25, member 52"
GO:0006810|GO:0005743|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136593_PI430048170 0.0235452205356077 0.666082966076381 6.37915488366587 6.29315019666752 6.33457030165398 P P P 6.72887311262147 6.9421949462317 7.07486575114874 P P P LNCV6_136593_PI430048170 mRNA
TATTCCTCGTGCCCTGTGTTAGTGCTTTCTGTATAAGGGACAGACAGAACTGGGTTTTTT NM_005990 RefSeq chr5 - 172042069 172188342 STK10 6793 serine/threonine kinase 10
GO:0005515|GO:0023014|GO:0005886|GO:0042801|GO:2000401|GO:0005524|GO:0042803|GO:0071593|GO:0042

802|GO:0035556|GO:0005737|GO:0007049|GO:0046777|GO:0004674|GO:0006468|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95415_PI430048170 0.1718265149531890.5997642646275320.4951981487304550.889719746667374 0.469043029492329A A A 1.92203022211067 1.15804430015775 0.787549062330087A A A
LNCV6_95415_PI430048170 mRNA
TTTTGCTGCAGTCTTGACATCTTAACGTGGATAGAAAAAGGCCGTGCAGCATCGAAGACA NM_001199021 RefSeq
chr4 - 1166932 1208962 SPON2 10417 "spondin 2, extracellular matrix protein, transcript variant 3"
GO:0032755|GO:0002448|GO:0032760|GO:0050832|GO:0005578|GO:0003823|GO:0005615|GO:0046872|GO:0001530|GO:0051607|GO:0071222|GO:0007411|GO:0045087|GO:0060907|GO:0007155|GO:0008228|GO:0043152|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67770_PI430048170 0.2203463777017761.27348207890424 4.15316908616255 3.71788092173135 4.29914560711853 P P P 3.3974681420244 3.79543466444167 3.93924632765551 P P P
LNCV6_67770_PI430048170 mRNA
AAAGCAAGAACAACCGGACAAGTTCCAAATACAGCCATTGCCACAATCTGAAAACAAACTNM_001101802 RefSeq
chr11 - 45929318 46121434 PHF21A 51317 "PHD finger protein 21A, transcript variant 1"
GO:0006355|GO:0001967|GO:0000118|GO:0007596|GO:0003682|GO:0006325|GO:0008270|GO:0005654|GO:0000122|GO:0003677|GO:0006351|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109615_PI430048170 0.1095371296382991.39059573372343 14.9518593104834 15.4343236163935 15.4847049615393 P P P 14.8002415133615 14.7983735794686 14.9003120302304 P P P LNCV6_109615_PI430048170 mRNA
GCAAAACTGTGAGCAAAAAGCAATAGAAGCCTCGCCCCCGCCCTTCCCCTTCGCAGGATT NM_001290002 RefSeq
chr12 - 54369128 54385789 ZNF385A 25946 "zinc finger protein 385A, transcript variant 5"
GO:0000790|GO:0006355|GO:0005730|GO:0070889|GO:0006915|GO:0003677|GO:0030425|GO:0006351|GO:0006974|GO:0007599|GO:0010609|GO:0002039|GO:0035855|GO:0005737|GO:0045600|GO:0043025|GO:0007611|GO:0008270|GO:0007626|GO:0003730|GO:2000765|GO:0030220 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144264_PI430048170 0.0296688080444657 1.29004315780907 6.62687674622548 6.84900894271282 6.89096361442566 P P P 6.43420408522708 6.35032597581571 6.49034241844697 P P P LNCV6_144264_PI430048170 mRNA
CATAGCTATGGCATATTCTTCTACTATTCCTATTATACCACTTACCAGCTTACTCGAAAA NM_022773RefSeq chr16 - 853635 970984 LMF1 64788 "lipase maturation factor 1, transcript variant 1"
GO:0006888|GO:0090181|GO:0051604|GO:0009306|GO:0034382|GO:0033578|GO:0005789|GO:0016021|GO:0090207|GO:0051006 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132615_PI430048170 0.0422578853130824 1.16612328342507 0.678389713856499 0.7969223308396 0.83686980037181 A A A 0.6622478910177920.480469187780192 0.502054393981726A A A LNCV6_132615_PI430048170 mRNA
ACAATGTTAACAGCCACCTATAAGCTTGGGGCACCTACTTTCTAACAAATCTGTGATGTT NM_005460RefSeq chr5 + 122312068 122464219 SNCAIP 9627 "synuclein, alpha interacting protein, transcript variant 1"
GO:0090083|GO:0005515|GO:0042734|GO:0005737|GO:0042417|GO:0043025|GO:0046928|GO:0031625|GO:0042802|GO:0008021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135453_PI430048170 0.0467388301566942 0.8395308789951687.97171157119868 7.93501610587994 8.02999362942594 P P P 8.17095013616847 8.15543082902495 8.35986110685936 P P P LNCV6_135453_PI430048170 mRNA
GACTCTCCTCTGAGCTGTAATAAATAAAATGGTAGTAATGAATGCAATCAGTATTAGCCA NM_001512RefSeq chr6 - 52977947 52995380 GSTA4 2941 glutathione S-transferase alpha 4
GO:0006805|GO:0006749|GO:0044281|GO:0004364|GO:0042803|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131074_PI430048170 0.0660910272833218 0.3739548492625042.97071713777056 2.4965288199118 2.42111524175296 P A A 3.14834468034978 4.32176542185064

4.42706472535226 P P P LNCV6_131074_PI430048170 mRNA
CATGTCATGCTGAGATTCAGAAGGCCCATGCTTATAATTTAAAAATGAGACTATTTCAGT NM_001042683 RefSeq
chr6 - 145884808 145964097 SHPRH 257218 "SNF2 histone linker PHD RING helicase, E3 ubiquitin
protein ligase, transcript variant 1"
GO:0000209|GO:0004842|GO:0006281|GO:0016874|GO:0006334|GO:0004386|GO:0008270|GO:0005634|GO:0000
786|GO:0005524|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90647_PI430048170 0.0306371526531635 1.21673937721703 6.73526532330575
6.72444395631951 6.92688675109111 P P P 6.58794959205511 6.49591902091546
6.45974116373773 P P P LNCV6_90647_PI430048170 mRNA
TTGACTATTCTCACCCTCGTGATGTCTACAGTAACCTCAGTCACCTGCCTGGGGCCCCAG NM_001199873 RefSeq
chr1 - 161171309 161177968 B4GALT3 8703 "UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase,
polypeptide 3, transcript variant 1"
GO:0005794|GO:0005975|GO:0003831|GO:0044281|GO:0008378|GO:0046872|GO:0042339|GO:0005737|GO:0000
139|GO:0003945|GO:0018146|GO:0032580|GO:0009405|GO:0016021|GO:0044267|GO:0030203|GO:0070062|GO:0
043687|GO:0018279. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131648_PI430048170 0.1824900111076540.6220034456051533.04053454647043
2.36712127511632 3.10523624634185 P A P 2.85005085006534 3.78029592402246 3.8487265854259
P P P LNCV6_131648_PI430048170 mRNA
GCATGTTCAGCTTGTGCTAGTCATCATTCTGATTTGCTTATCTGTTTTTGGTCAAAATAT NM_012115RefSeq chr6 +
89829899 89874436 CASP8AP2 9994 "caspase 8 associated protein 2, transcript variant 1"
GO:0005515|GO:0008625|GO:0006355|GO:0032184|GO:0006919|GO:0003714|GO:0005634|GO:0005123|GO:0097
190|GO:0008656|GO:0003677|GO:0006351|GO:0005739|GO:0016505|GO:0007165|GO:0005737|GO:0007049|GO:0
016605|GO:0071260. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145389_PI430048170 0.7919164802773651.02455131024839 9.07956709420873
9.03576474522663 9.30080608181554 P P P 9.10993057322625 8.91159936347169
9.28034791192655 P P P LNCV6_145389_PI430048170 mRNA
AAATGCCTGTTTGGGAGGAGATGAACGTATTTAGTCTATTAGATTTGCACTGCTGGATTT NM_019116RefSeq chr16
+ 23557540 23574389 UBFD1 56061 ubiquitin family domain containing 1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_145185_PI430048170 0.1847412849695751.19904000805717 0.848886828299217
0.4854226193035690.454326209965665A A A 0.3475159370353240.317753914132898
0.371467233466458A A A LNCV6_145185_PI430048170 mRNA
CAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTTGTTATTTCCTCTGTATTATTTTCTNM_015696RefSeq chr1 +
52602370 52609051 GPX7 2882 glutathione peroxidase 7
GO:0004602|GO:0004601|GO:0005783|GO:0005788|GO:0005576|GO:0000302|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134042_PI430048170 0.0288445680936980.5429591920426151 1.7004868968499
11.5610204186673 11.5988190191022 P P P 12.1821164754165 12.5149473761548
12.7537963715664 P P P LNCV6_134042_PI430048170 mRNA
GGCCCCATCTCTCATCCTTTTGGATAAGTTTCTATTCTGTCAGTGTTAAAGATTTTGTTT NM_004431RefSeq chr1 -
16124336 16156087 EPHA2 1969 EPH receptor A2
GO:0051898|GO:0005515|GO:0033628|GO:0005886|GO:0014028|GO:0010591|GO:0005003|GO:0046849|GO:0007
411|GO:0016032|GO:0070309|GO:0007155|GO:0070372|GO:0060035|GO:0031256|GO:0048013|GO:0031258|GO:0
008630|GO:0009986|GO:0030316|GO:0045765|GO:0032587|GO:0007275|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141631_PI430048170 0.033661704217998 0.828939310474087 9.45823690458484
9.54853523502938 9.34269970043627 P P P 9.66597258203778 9.84181546750117
9.65321999509627 P P P LNCV6_141631_PI430048170 mRNA
GGAGATCTAAGATGTCCCAGGTCCTGGGAAGTTTACTCAATAAAGCTGGCTTTCCCCTGC NM_001040716 RefSeq

chr11 - 66848525 66958376 PC 5091 "pyruvate carboxylase, transcript variant 3"
GO:0006629|GO:0005515|GO:0005975|GO:0006768|GO:0006107|GO:0005743|GO:0006094|GO:0006767|GO:0044281|GO:0003677|GO:0005524|GO:0046872|GO:0005829|GO:0005739|GO:0006766|GO:0006090|GO:0005759|GO:0009405|GO:0009374|GO:0004736|GO:0004075|GO:0006006 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133547_PI430048170 0.560865966059535 0.960996689202657 0.280488064509122 0.458032312980941 0.307663495333643 A A A 0.518209299853251 0.41684442481048 0.279858300041748 A A A LNCV6_133547_PI430048170 mRNA TGCAATGATGGCAAGTCATTCAATCCTTCTCATCTTCATTTTTTCTCCTTATAACATGGA NM_001004470 RefSeq
chr10 - 17320676 17454255 ST8SIA6 NA "ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144643_PI430048170 0.262081658953647 1.17230130921328 0.541421167796372 0.370613669113463 0.854012275654109 A A A 0.292483757764529 0.382551795636169 0.441307469966886 A A A LNCV6_144643_PI430048170 mRNA GGTGATATCATTAGACTGTATGAATCAGTTTTATTACCTAGTGTACAAGTGTCAGTCATG NM_032383 RefSeq
chr3 + 149129583 149173196 HPS3 84343 Hermansky-Pudlak syndrome 3
GO:0031084|GO:0006996|GO:0043473 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144503_PI430048170 0.0259352659494044 0.450180952526494 5.58700487235718 5.5738325675752 5.87440095716247 P P P 6.37324099674927 6.86329744741558 7.16557215563002 P P P LNCV6_144503_PI430048170 mRNA TAGCTATATCCACTATGATTATAAACTGTGTCTCGACCTGTGTTATTTACATTAGCTGCT NM_003713 RefSeq chr1 - 56494746 56579584 PPAP2B 8613 phosphatidic acid phosphatase type 2B
GO:0006629|GO:0005515|GO:0005886|GO:0030111|GO:0050731|GO:0044281|GO:0042392|GO:0051091|GO:0042577|GO:0005912|GO:0060020|GO:0004721|GO:0070062|GO:0006665|GO:0008354|GO:0005794|GO:0001568|GO:0044329|GO:0030148|GO:0050821|GO:0008195|GO:0044328|GO:0001702|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134601_PI430048170 0.813978038867813 0.968642518368671 2.84317184845638 3.19303173226474 3.25427213174004 A P P 3.05942225338671 2.97446806700511 3.39291393399113 P P P LNCV6_134601_PI430048170 mRNA ATGGGACAGGTAAATGAAATGTTCCTAGTTGCATAGCTGTTAACCATGCTTCAAAAATAA NM_207360 RefSeq
chr6 - 149447629 149485012 ZC3H12D 340152 zinc finger CCCH-type containing 12D
GO:0030308|GO:0005737|GO:0004519|GO:0090305|GO:0000932|GO:2000134|GO:0005634|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83551_PI430048170 0.12523136369813 1.60956806818108 1.27852662291764 1.8220973304751 0.884085609808356 A A A 0.319922991101464 0.934782182107234 0.757693929555291 A A A LNCV6_83551_PI430048170 mRNA CAAAAAAGGAGGAACGAGGGTCAACCAGCAGCAGACCAGTCACAAAAAGAGATGAAATGT NM_178571 RefSeq
chr17 + 15732276 15744784 TBC1D26 353149 "TBC1 domain family, member 26"
GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143855_PI430048170 0.689197882673146 1.38933451946794 3.28064933741445 2.04304067393036 0.715951633463082 P A A 0.510476720943548 1.42561291191958 2.81401542312951 A A P LNCV6_143855_PI430048170 mRNA AACAGGCACCACTTACTAAGAGAGGATGAATGAAAAGCACACCTACCCTTTGGCGTAATC NM_002732 RefSeq
chr9 - 69012532 69014123 PRKACG 5568 "protein kinase, cAMP-dependent, catalytic, gamma"
GO:0006094|GO:0007202|GO:0007283|GO:0044281|GO:0005829|GO:0035556|GO:0007173|GO:0071377|GO:0006006|GO:0006833|GO:0019433|GO:0034199|GO:0048011|GO:0005975|GO:0055085|GO:0005524|GO:0003091|GO:0007165|GO:0006112|GO:0050796|GO:0007596|GO:0008543|GO:0045087|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_138587_PI430048170 0.25986774183242 0.9686897125887230.388901568654903
0.4140519823720580.31365700482359 A A A 0.4091575514376920.440337083837361
0.406431271432699A A A LNCV6_138587_PI430048170 mRNA
CCTAGGTGGACAGTGCTCCTCTAGAGAGCTGCGACTTTAATTAAAAACAACAGGAAAACA NM_022120RefSeq chr1
- 39769524 39771348 OXCT2 64064 3-oxoacid CoA transferase 2
GO:0005739|GO:0046952|GO:0031514|GO:0008260 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92344_PI430048170 0.0403749692235142 0.4907192973852221.52585798579071
1.26895492352469 1.88464701932231 A A A 2.9989214829848 2.09475888166782
2.59414840893334 P A P LNCV6_92344_PI430048170 mRNA
TCTCATTTGCCACATCGTAGAAACCAATTGGAGGAAACATAATCTTCATTCCTGGGTTCT NM_017439RefSeq chr7
- 77310750 77416400 GSAP 54103 gamma-secretase activating protein
GO:0030162|GO:0005802|GO:0001540 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131950_PI430048170 0.6749498750276770.8743575576750440.524309120395753
0.5525510234938330.619050471780228A A A 0.3177520524855211.25087670662294
0.538702537073951A A A LNCV6_131950_PI430048170 mRNA
GACTGGGCCCCATTGACGTCCTTGAGCAGGAAATAAATGCTGACATTTATACGTAAAAAA NM_001145113 RefSeq
chr17 - 81939644 81947233 MYADML2 255275 myeloid-associated differentiation marker-like 2
GO:0005737|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131284_PI430048170 0.1353431954749191.05738575658414 0.499226123102969
0.6142396255674180.526970548157674A A A 0.4260807937644280.474783857616373
0.499610870721102A A A LNCV6_131284_PI430048170 mRNA
GTTTCCCGTTTACAGAATGCTACAAGAATAATGTACGTACTACCTAAAAGGATGTCTAAA NM_003167RefSeq chr19
- 47870465 47886397 SULT2A1 6822 "sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA)-preferring, member 1"
GO:0005515|GO:0006805|GO:0050427|GO:0030573|GO:0007586|GO:0008146|GO:0051923|GO:0044281|GO:0047704|GO:0044255|GO:0008202|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79336_PI430048170 0.4603226078568181.05667828577961 12.5325229393128 12.8011968928163
12.6990327152789 P P P 12.6965910510394 12.5732529721245 12.5318120520943 P P P
LNCV6_79336_PI430048170 mRNA
CCCCCATGGGGGGTGGATGATTTGCACTTTGGTTCCCTGTGTTTTGATTTCTCATTAAAG NM_006712RefSeq chr7
- 151076620 151080883 FASTK 10922 "Fas-activated serine/threonine kinase, transcript variant 1"
GO:0005739|GO:0005515|GO:0004674|GO:0043484|GO:0006468|GO:0033867|GO:0097190|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129533_PI430048170 0.1647874569867650.4563783414362454.85620049007517
4.87819342740126 5.3182961709948 P P P 5.06010039539594 6.42127812171733
6.58897567106812 P P P LNCV6_129533_PI430048170 mRNA
AGTTGTATAATATGCTTGTAAAGGCTGAGGGTGAGCTGTATCTGGATGCCTTTTTACAAT NM_182751RefSeq chr10
+ 13161553 13211104 MCM10 55388 "minichromosome maintenance complex component 10, transcript variant 1"
GO:0006260|GO:0005515|GO:0005737|GO:0000082|GO:0008283|GO:0005730|GO:0005654|GO:0005634|GO:0000278|GO:0003677|GO:0046872|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136112_PI430048170 0.0888413329637985 1.2174004807075 8.12563689654976
8.22526753794116 8.16418481200333 P P P 7.71034129903594 8.05228265333194
7.88257529408423 P P P LNCV6_136112_PI430048170 mRNA
GAAAGCACAAACTTCTGTAACGGGTCGTGCTCATGTCTGTTAATAAAGAAATCCAGATCC NM_080881RefSeq chr5
- 177456612 177472870 DBN1 1627 "drebrin 1, transcript variant 2"
GO:0005515|GO:0042641|GO:0005886|GO:0003779|GO:0015629|GO:0030425|GO:0061351|GO:0005737|GO:0048168|GO:0050773|GO:0005921|GO:0007015|GO:0010643|GO:0032507|GO:0005522|GO:0005938|GO:0010644 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_144881_PI430048170 0.72400428541248 1.21297673345224 1.51066001851857
0.36896739841067 0.254825121778597 A A A 0.5318443795714620.695905348849922
0.413364626550813 A A A LNCV6_144881_PI430048170 mRNA
TCAAGCCAGGTTGAATATTTGCCATGAAATTCCAGTGAATGTGTAGCTCAAATGCAAACC NM_014689 RefSeq chr2
- 224765089 225042613 DOCK10 55619 "dedicator of cytokinesis 10, transcript variant DOCK10.1"
GO:0030334|GO:0003674|GO:0016020|GO:0032321|GO:0007264|GO:0017048|GO:0005089|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137897_PI430048170 0.5919953535169631.02772359618741 4.16752198268401
4.06914188802757 4.24424127814505 P P P 4.05530673331832 4.1045091578042
4.20405579001196 P P P LNCV6_137897_PI430048170 mRNA
TTGGGGATTATTTATCCTCCTGGGGACAGTTTGGGGAGGATTATTTATTGTATTTATATT NM_016584 RefSeq chr12
+ 56338878 56340410 IL23A 51561 "interleukin 23, alpha subunit p19"
GO:0005515|GO:2000318|GO:0042346|GO:0048771|GO:0032733|GO:0032693|GO:0042523|GO:0032735|GO:0032
819|GO:0042520|GO:2000330|GO:0032816|GO:0042104|GO:0051607|GO:0006954|GO:0042098|GO:0043382|GO:0
045944|GO:0002827|GO:0042102|GO:0051135|GO:0045519|GO:0032729|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_59582_PI430048170 0.1231476569371320.7807736806140154.39253964939852 3.93626463507843
4.38105732795792 P P P 4.65829080499151 4.52152297048152 4.64245965852857 P P P
LNCV6_59582_PI430048170 mRNA
AAACTTTCAAAGGTTGGACAAGGAATACGGAGAGAACGGTCTGGCAATACCACTTTCGGA NM_002834 RefSeq chr12
+ 112418731 112509913 PTPN11 5781 "protein tyrosine phosphatase, non-receptor type 11, transcript
variant 1"
GO:0005515|GO:0005158|GO:0019221|GO:0043560|GO:0050900|GO:0035335|GO:0060334|GO:0007507|GO:0048
609|GO:0060337|GO:0060338|GO:0007173|GO:0007411|GO:0043274|GO:0046887|GO:0070374|GO:0048806|GO:0
046676|GO:0060333|GO:0038127|GO:0048839|GO:0019904|GO:0043234|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_83866_PI430048170 0.4261968819373990.9199997838377053.55475032216697 3.19413812564333
3.5997212435297 P P P 3.56234539894757 3.67385921495758 3.50117561427524 P P P
LNCV6_83866_PI430048170 mRNA
TTACTTTTTTAAGCCGCCCATTAATCAGTTCAGCCTGAACTTCCTGGATCAGGAGCTGGA NM_001116 RefSeq chr16
- 3962648 4116185 ADCY9 115 adenylate cyclase 9
GO:0048011|GO:0005886|GO:0007268|GO:0044281|GO:0007202|GO:0055085|GO:0005524|GO:0007193|GO:0046
872|GO:0035556|GO:0003091|GO:0007165|GO:0004016|GO:0006112|GO:0007173|GO:0071377|GO:0008543|GO:0
005887|GO:0045087|GO:0006171|GO:0006833|GO:0007189|GO:0034199 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_6469_PI430048170 0.3768394408925161.22600615153091 1.04949845653266 0.32331528116034
0.417073508011827 A A A 0.2852597475420240.3566042157054530.377230014956314 A A A
LNCV6_6469_PI430048170 mRNA
CAGACCTGCGTGATTTGTACAATGTACTTTATTTCTGCTACGAGTAATTTCATGAAGTTT NM_001172673 RefSeq
chr19 + 3224703 3297075 CELF5 60680 "CUGBP, Elav-like family member 5, transcript variant 2"
GO:0006397|GO:0005737|GO:0000166|GO:0003723|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144794_PI430048170 0.1848792833016891.02608414553551 0.327696560609148
0.3197357456314040.267800762208009 A A A 0.2652072908271240.274949408098242
0.264335510590176 A A A LNCV6_144794_PI430048170 mRNA
GGAGAATAACACAAATGAGAAATGACTGTTAATTCCTGATGCATAATAACAGTTGTGAGC NM_019069 RefSeq chr3
- 122411852 122416035 WDR5B 54554 WD repeat domain 5B NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_137702_PI430048170 0.1301568732222260.8188966610685649.729724028211 9.7812710998181

9.83894110758731 P P P 9.90624304090296 9.99168346705128 10.2901076874781 P P P
LNCV6_137702_PI430048170 mRNA
GCAGCGGTTATGCTTATGAAAATACCTGGCAGCTTTGTGCAATGAATTAATGTTATAAGG NM_020135 RefSeq chr6
+ 2765431 2785745 WRNIP1 56897 "Werner helicase interacting protein 1, transcript variant 1"
GO:0006260|GO:0005515|GO:0048471|GO:0030174|GO:0016020|GO:0000731|GO:0005634|GO:0016887|GO:0005
524|GO:0003677|GO:0046872|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135442_PI430048170 0.2275148777181370.9144079632030616.20130222535033
6.29515708057217 6.4697927124005 P P P 6.48370014210027 6.4041205761464
6.47732842902778 P P P LNCV6_135442_PI430048170 mRNA
CTGCAAGATTACATATATAAAACTCCCACTATTGTTTCTCTAAGAGTGGATTAGTTCACC NM_001003702 RefSeq
chr7 - 144186082 144195698 ARHGEF35 445328 Rho guanine nucleotide exchange factor (GEF) 35
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127925_PI430048170 0.4692018795066690.7985635120920926.19362385300549
6.33204248776113 5.77970495547599 P P P 6.97137735663874 6.12558784048829
6.04500873680696 P P P LNCV6_127925_PI430048170 mRNA
AAATGGCTTTTCCTGCCCTTTGAGGATGATCTGAGGAGGGACCTCGGGCGCCAGTTCTCA NM_138454 RefSeq chr19
- 17455424 17460916 NXNL1 115861 nucleoredoxin-like 1 GO:0005739|GO:0005640|GO:0045494 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144299_PI430048170 0.6003075695561420.9005435428132640.522394782842446
0.5941437101056590.538852161871461 A A A 1.07125068024592 0.505510394130495
0.447471464244255 A A A LNCV6_144299_PI430048170 mRNA
CTGTGAACAACTCTATTCCACACTCCAAAAATACTCATTTGAAATAGATGAAGAGTTTGC NM_020651 RefSeq chr2
- 64092651 64144471 PELI1 57162 pellino E3 ubiquitin protein ligase 1
GO:0005515|GO:0034145|GO:0043331|GO:0004842|GO:0034142|GO:0034141|GO:0030890|GO:0016874|GO:0005
634|GO:0001819|GO:0005829|GO:0042130|GO:0002755|GO:0032496|GO:0031398|GO:0043123|GO:0038124|GO:0
038123|GO:0034134|GO:0032088|GO:0002224|GO:0008063|GO:0045087|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141642_PI430048170 0.165103974751221 1.27617957875957 4.23998186050399
3.88918747375749 4.24808038039792 P P P 4.01386210933254 3.43724947063077
3.83996193824769 P P P LNCV6_141642_PI430048170 mRNA
TCTCTAATAAAGATGGCCACCACTTAATGTGTGGAAAGTGATGGCCTTCTCGTGGGCAAA NM_144498 RefSeq chr20
+ 62238484 62296213 OSBPL2 9885 "oxysterol binding protein-like 2, transcript variant 2"
GO:0015485|GO:0006869 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128534_PI430048170 0.16299676563313 0.9357984832493240.345079053570355
0.3609601490072520.303392880136266 A A A 0.5070947052112340.436152242641462
0.349688130356903 A A A LNCV6_128534_PI430048170 mRNA
TTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTGTTCTGGTTCAT NM_000133 RefSeq chrX
+ 139530735 139563458 F9 2158 coagulation factor IX
GO:0004252|GO:0005886|GO:0005796|GO:0005509|GO:0005576|GO:0017187|GO:0007596|GO:0007597|GO:0007
598|GO:0006508|GO:0005788|GO:0044267|GO:0070062|GO:0043687 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132530_PI430048170 0.2066900221121761.08708502668807 0.558677768163114
0.3472413073966250.521265533342463 A A A 0.28564486715979 0.380594074069284
0.405502304553539 A A A LNCV6_132530_PI430048170 mRNA
TATCTTTGCTGTAGGCAGATACCTGGAGAAGTACCTGGAGCGCTTCCTGGAGACGGCGGA NM_001080438 RefSeq
chr1 - 33306765 33321098 A3GALT2 127550 "alpha 1,3-galactosyltransferase 2" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138026_PI430048170 0.0279218919734337 0.7077819048765666.94911151693158
6.77419534547139 6.91691438262262 P P P 7.26812876230807 7.26018518315988

7.58878658117736 P P P LNCV6_138026_PI430048170 mRNA
CCCTGTAATTAGACAAGAAAGCATAATATAGCTCTACTCATGGGTACACATACCAGTGTA NM_005877 RefSeq chr22
- 30331987 30356947 SF3A1 10291 "splicing factor 3a, subunit 1, 120kDa"
GO:0008380|GO:0006397|GO:0005515|GO:0010467|GO:0000398|GO:0003723|GO:0005684|GO:0005681|GO:0005
654|GO:0071013|GO:0000389 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140237_PI430048170 0.2630819886791231.10655206813349 0.350805724536061
0.5751885505345590.270721328758592 A A A 0.2511366462789050.274104047223577
0.250645722105235 A A A LNCV6_140237_PI430048170 mRNA
GGTTGGTCATTAAATATATCATATGTTAGGCACAGTGACCTGGTTATTTTCACATGTTAC NM_001199087 RefSeq
chr2 - 18562870 18589580 NT5C1B 93034 "5'-nucleotidase, cytosolic IB, transcript variant 4"
GO:0006195|GO:0000287|GO:0000166|GO:0006144|GO:0016311|GO:0008253|GO:0055086|GO:0005634|GO:0044
281|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131552_PI430048170 0.5222870496856110.98172300831196 0.383227254602679
0.3933371164289140.284195374559114 A A A 0.3667407274576310.405092163829864
0.37095656854217 A A A LNCV6_131552_PI430048170 mRNA
GGCAGTGCCATGCAAGCTGTTTAAAATAAAGATGTTACCTTGTAAAATGCAAGTTGATTT NM_001278543 RefSeq
chr1 - 56929209 56966140 C8B 732 "complement component 8, beta polypeptide, transcript variant 2"
GO:0030449|GO:0005576|GO:0005615|GO:0031982|GO:0032403|GO:0006957|GO:0006956|GO:0006955|GO:0005
579|GO:0016020|GO:0045087|GO:0006958|GO:0019835|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_82087_PI430048170 0.88330620092912 0.9864707115143119.35963075816806 9.19415215806725
9.34427974224235 P P P 9.15947361602103 9.32409295444023 9.46321294776382 P P P
LNCV6_82087_PI430048170 mRNA
GAATTACTCTTTTTTAGACAAAGAGAAGGGCCTTTTTATCCAACCCTAAGATTACTTCAC NM_014060 RefSeq chrX
+ 120603888 120621161 MCTS1 28985 "malignant T cell amplified sequence 1, transcript variant 1"
GO:0006355|GO:0008284|GO:0005886|GO:0001731|GO:0003743|GO:0032790|GO:0006351|GO:0006974|GO:0002
192|GO:0005737|GO:0007049|GO:0022627|GO:0040008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131958_PI430048170 0.3492171340828061.24342773938136 1.25468947381113
0.6316644842043240.519340775415111 A A A 0.4967599083018060.500909953774815
0.576863281456785 A A A LNCV6_131958_PI430048170 mRNA
AGAACCCTTTAAGCCCTTAGCCTAAGCTTTCAGACTAAATGTGATTATAGAATAAGATGA NM_004215 RefSeq chr8
+ 109540074 109565996 EBAG9 9166 "estrogen receptor binding site associated, antigen, 9, transcript
variant 1"
GO:0016505|GO:0005794|GO:0005886|GO:0000139|GO:0006915|GO:0016021|GO:0030141|GO:0005925|GO:0001
558 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135581_PI430048170 0.9123228652683161.01731188472092 6.8081344966513
6.46573783114386 6.31084532081441 P P P 6.38986123444516 6.78726016685835
6.33563870316923 P P P LNCV6_135581_PI430048170 mRNA
TTTACACAGTAGGTGCTTCATATGTGTCTGTCGAATGAATGCGCTCCAGCCAACAAAAAA NM_023007 RefSeq chr1
- 227731188 227735411 JMJD4 65094 "jumonji domain containing 4, transcript variant 1" GO:0005515
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132878_PI430048170 0.2422086687668750.9454493714004520.29297207427602
0.3194391950227980.281337518881355 A A A 0.4677922895718980.363707302957144
0.300320484013758 A A A LNCV6_132878_PI430048170 mRNA
GGAAATGGGAGGATGAAGAGGCTAGAATCATCTTTCCTAGTGATCCTGACATTTAGACAG NM_030663 RefSeq chr1
+ 152878321 152885047 SMCP 4184 sperm mitochondria-associated cysteine-rich protein
GO:0005739|GO:0003674|GO:0005737|GO:0031966|GO:0007341|GO:0030317 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140740_PI430048170 0.0318798988727065 1.27627202855977 12.4480551160795

12.3045951729911 12.3988000628098 P P P 12.1632812512001 11.8781025917661
12.0437932128455 P P P LNCV6_140740_PI430048170 mRNA
CCTTGAAATTGTGAACTCTTGGAAATGTTATTAGTGAAGTTCGCAACTAAACTAAACCTG NM_001154 RefSeq chr4
- 121667996 121696992 ANXA5 308 annexin A5
GO:0004859|GO:0043066|GO:0010033|GO:0005509|GO:0072563|GO:0043086|GO:0005544|GO:0005622|GO:0007
165|GO:0050819|GO:0005737|GO:0005543|GO:0016020|GO:0007596|GO:0005925|GO:0009897|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130773_PI430048170 0.4466175921385360.9767217590105330.438352652089905
0.4241884645714390.4155382078957 A A A 0.4990750535463040.489461927343212
0.389021109204125 A A A LNCV6_130773_PI430048170 mRNA
CCAGGAATTATCAAAACTGACTTCAGCAAAGTGGTGAGGATTGGTTTCATGGGAATGAGT NM_182908 RefSeq chr14
+ 23636363 23645639 DHRS2 10202 "dehydrogenase/reductase (SDR family) member 2, transcript
variant 1"
GO:0043066|GO:0004090|GO:0008285|GO:0009636|GO:0005634|GO:0005635|GO:0005739|GO:0005737|GO:0005
759|GO:0008207|GO:0034599|GO:0043011|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144497_PI430048170 0.0557023654916048 1.97661620542124 4.14895904379664
4.94105590340316 4.79498875813173 P P P 3.74969318777492 3.70465583904217
3.59352709513825 P P P LNCV6_144497_PI430048170 mRNA
TATTATTTCTTTGTTTCGACCCTTTGTTTGTGAACAGCTTGCCAGGCCTTGAGCCCTTGC NM_032415 RefSeq chr7 -
2906075 3043945 CARD11 84433 "caspase recruitment domain family, member 11"
GO:0005515|GO:0045577|GO:0050852|GO:0005886|GO:0030890|GO:0031295|GO:0001819|GO:0005829|GO:0005
737|GO:0051092|GO:0042101|GO:0042102|GO:0045580|GO:0043123|GO:0070062|GO:0001772|GO:0050700|GO:0
004385|GO:0042981|GO:0045086|GO:0045061|GO:0045087|GO:0046939|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139501_PI430048170 0.8914596482164190.92569349132277 1.39620023330456
0.5914280961427410.46156697495137 A A A 0.5354863239143041.63647791734001
0.485553229198197 A A A LNCV6_139501_PI430048170 mRNA
CCTTTTGAGAACAAAAGAAGAACACTTTCTGATCTCCACCTTCTTCTAATTCAAAAGGTT NM_004061 RefSeq chr5
- 21750863 22853622 CDH12 1010 "cadherin 12, type 2 (N-cadherin 2)"
GO:0005886|GO:0034329|GO:0005509|GO:0016021|GO:0007156|GO:0045216|GO:0034332 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130372_PI430048170 0.2508482089278461.04516748043634 12.2032178302837
12.1642632464433 12.2216770351764 P P P 12.2134726958834 12.0887666555374 12.09279760055
P P P LNCV6_130372_PI430048170 mRNA
AGCCCGCGTGGCCGAAGCTGGAAACCAAACCTAATAAAGTTTTCCCATCCCACCAAAAAA NM_014371 RefSeq chr19
- 15380047 15419121 AKAP8L 26993 "A kinase (PRKA) anchor protein 8-like, transcript variant 1"
GO:0005515|GO:0008150|GO:0005737|GO:0017151|GO:0005654|GO:0005634|GO:0003677|GO:0046872|GO:0016
363 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129290_PI430048170 0.3190386458099590.5518621402573980.389819169547752
0.3961302548348960.437644469126057 A A A 2.06848537489211 0.775979861817131
0.385385017478979 A A A LNCV6_129290_PI430048170 mRNA
CTGGCTACACTGCTTTTAGAATGCTCTTTCTCATGAAGCAAGGAAATAAATTTGTTTGAA NM_030625 RefSeq chr10
+ 68560359 68694482 TET1 80312 tet methylcytosine dioxygenase 1
GO:0010467|GO:0005506|GO:0035511|GO:0001826|GO:0005634|GO:0090310|GO:0006351|GO:0006493|GO:0045
944|GO:0019827|GO:0043566|GO:0044030|GO:0080111|GO:0040029|GO:0008270|GO:0070579|GO:0016568 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136927_PI430048170 0.0196987344387087 0.50217970682215 8.58288048760345
8.46286925598864 8.78644890499804 P P P 9.34177824411462 9.45897349706319

9.95537923758614 P P P LNCV6_136927_PI430048170 mRNA
ATGCCTGGGCAACTATTTTTTGTAACTCTTGTGTAGATTGTCTCTAAACAATGTGTGATC NM_001020658 RefSeq
chr1 - 30931505 31065717 PUM1 9698 "pumilio RNA-binding family member 1, transcript variant
1" GO:0006892|GO:0061024|GO:0006417|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116843_PI430048170 0.0686751542022776 0.821652896984494 15.9413306735313
15.9363632671494 15.8702519644881 P P P 16.3562729347537 16.146172071012
16.0823443653574 P P P LNCV6_116843_PI430048170 mRNA
CACTAAAAGCACTCTGAGTCAAGATGAGTGGGAAACCATCTCAATAAACACATTTTGGAT NM_001030 RefSeq chr1
+ 153990762 153992155 RPS27 6232 ribosomal protein S27
GO:0005515|GO:0010467|GO:0003735|GO:0008283|GO:0019083|GO:0006614|GO:0019058|GO:0005634|GO:0006
415|GO:0003677|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0000184|GO:0022627|GO:0016032|GO:0
005840|GO:0008270|GO:0000278|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127846_PI430048170 0.210779794190823 0.54860043272129 0.316975101792946
0.290973439680423 0.44019044173031 A A A 1.30071796323383 1.71173078452484
0.304506787702919 A A A LNCV6_127846_PI430048170 mRNA
CATCGTAGGACACTAACACCTGTCCCACAGCAGTTCTCTGTGTTCAACACAATTTGGAAA NM_001011719 RefSeq
chrX + 3006612 3033385 ARSH NA "arylsulfatase family, member H" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_141916_PI430048170 0.1181317240667080 0.8472588650372511.4167792343562
11.4711962685185 11.4673438510831 P P P 11.8561316812251 11.548025140401
11.6519739406036 P P P LNCV6_141916_PI430048170 mRNA
ACTGCTCCAGGGTCTCTTTTTGGTCCAAAGGCTAGACCTATAGAGTTGGATCACTTTTTT NM_001198845 RefSeq
chr11 + 66616581 66646473 RBM14-RBM4 NA "RBM14-RBM4 readthrough, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144217_PI430048170 0.0233508796960239 0.659985596094096 8.66182897710731
8.70398694981351 8.81607608208264 P P P 9.11452866312909 9.33123136927496
9.51178407650894 P P P LNCV6_144217_PI430048170 mRNA
GTGGGACCTACCTTTTCGTTCAGTAGTTTGAACTATATATAAACTGTACAATCTGTAAAG NM_004824 RefSeq chr6
+ 4776445 4955544 CDYL 9425 "chromodomain protein, Y-like, transcript variant 1"
GO:0005515|GO:0006355|GO:0016573|GO:0003714|GO:0005654|GO:0005634|GO:0035064|GO:0007283|GO:0006
351|GO:0004402 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129027_PI430048170 0.0272241812737141 0.28896768809245 0.409742661913606
0.413742099081814 0.363359591909296 A A A 1.6538376548289 2.06204570585662 2.6636869388996
A A P LNCV6_129027_PI430048170 mRNA
GTTAGCAGTGTCTTATGAAACGTGTATTTACCTAACGTTTGTAACAGTTTTGTGTTGAAC NM_018133 RefSeq chr3
- 136148917 136195846 MSL2 55167 "male-specific lethal 2 homolog (Drosophila), transcript variant 1"
GO:0043984|GO:0016874|GO:0006325|GO:0072487|GO:0008270|GO:0005654 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143635_PI430048170 0.193879586782778 0.844966021779492 6.06092458343282 6.4295235752038
6.46493689602837 P P P 6.41838486393145 6.56916740522934 6.71530740831829 P P P
LNCV6_143635_PI430048170 mRNA
GGCAAGCATCTTCATTTTGCTAGCTTTGCAGAATCTTAAAATGTGTACTCGTTATTTCTA NM_003794 RefSeq chr3
- 125446643 125520214 SNX4 8723 "sorting nexin 4, transcript variant 1"
GO:0005515|GO:0005154|GO:0005886|GO:0005158|GO:0032456|GO:0031201|GO:0015031|GO:0043234|GO:0016
050|GO:0005737|GO:0016020|GO:0031901|GO:0005868|GO:0035091|GO:0019898 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136347_PI430048170 0.00391821157085676 2.19767460933345 8.11580612133088
7.82810918541581 7.62843533278303 P P P 6.56357636386337 6.94444181526847
6.67117210475243 P P P LNCV6_136347_PI430048170 mRNA

CCTCTCGATCTGTATATCCTCCAGTCCAAGATTAAAGAGGCGGACTGTGGCCTGAAAAAA NM_001099781 RefSeq chr22 - 24219653 24245142 GGT5 2687 "gamma-glutamyltransferase 5, transcript variant 1" GO:0019369|GO:0006520|GO:0019370|GO:0005886|GO:0006749|GO:0044281|GO:0006691|GO:0031362|GO:0006954|GO:0003840|GO:0006750|GO:0006508|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_89939_PI430048170 0.00111116963910995 0.415644511886081 5.36417207556558 5.18099789722134 5.50323136829701 P P P 6.39441444676583 6.68586242540744 6.76050919049794 P P P LNCV6_89939_PI430048170 mRNA

GAGCTTATCAAATTTGTTCTGGCTTTTTTGGCACTAAGGCAAAAACATGTTAACCAGAAA NM_001031713 RefSeq chr6 - 13786548 13814560 MCUR1 63933 mitochondrial calcium uniporter regulator 1 GO:0005515|GO:0070509|GO:0006851|GO:0051561|GO:0031305 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_129111_PI430048170 0.00508859738988555 0.5534380316703167.7605346719064 7.50371895606401 7.63504428213895 P P P 8.30871945097388 8.44518601344696 8.69103135801489 P P P LNCV6_129111_PI430048170 mRNA

GAAACTGGTTTATGATTGTTGGTGTACTCTGTTGTAAATTCAAAGAGAGCTTGTTGAACA NM_014913 RefSeq chr18 + 80109030 80140345 ADNP2 22850 ADNP homeobox 2 GO:0005515|GO:0006355|GO:0030307|GO:0071300|GO:0005634|GO:0005575|GO:0003677|GO:0006351|GO:0046872|GO:0003674|GO:0030182|GO:0060548|GO:0034599 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_88394_PI430048170 0.197001825231879 2.06839667199869 0.280167365490101 1.50296472871911 1.85279276695519 A A A 0.32220737361397 0.279109749499724 0.310268546425495 A A A LNCV6_88394_PI430048170 mRNA

TTGTAGTGAAACGGAATAACCAGTTCTTCCGGTACAAGGACTTCCTGTACTTCCTCACTC NM_007253 RefSeq chr19 + 15615217 15629637 CYP4F8 11283 "cytochrome P450, family 4, subfamily F, polypeptide 8" GO:0006805|GO:0006693|GO:0070330|GO:0005506|GO:0018685|GO:0005789|GO:0044281|GO:0016021|GO:0006690|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_126920_PI430048170 0.480039410473265 1.06449560323762 5.57397289939872 5.4530579528746 5.67482585531057 P P P 5.33281741440788 5.41775903196804 5.66792149529649 P P P LNCV6_126920_PI430048170 mRNA

CAGTTTGGATTACTTAAATTACAACTCTTTAATGTTGACTCTAGTCATTGGGCATTGACG NM_145715 RefSeq chr4 + 89112816 89114901 TIGD2 166815 tigger transposable element derived 2 GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_141010_PI430048170 0.0058012493195416 2.32235734877706 7.01324031112538 7.2730345069888 6.86805999310052 P P P 6.14704085039884 5.759855568294 5.56895974565429 P P P LNCV6_141010_PI430048170 mRNA

AGGATCTTCTGAGCAGAAGCCCAGGCGGGCCCGGGGCCTTGGCTGGCAAATAAAGCGTTA NM_002307 RefSeq chr19 - 38770967 38773517 LGALS7 3963 "lectin, galactoside-binding, soluble, 7" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_102371_PI430048170 0.866772789513533 0.995448075513764 0.50068054888842 0.387437173740717 0.484787777852195 A A A 0.438894824899813 0.498347895081898 0.457350889310577 A A A LNCV6_102371_PI430048170 mRNA

TAAGAATCCCGAGGATGTGGTTCGAAGATACATGCAGAAGGTGAAAAACCCACCTGATGA NM_004416 RefSeq chr12 + 113057856 113098028 DTX1 1840 "deltex 1, E3 ubiquitin ligase" GO:0005515|GO:0017124|GO:0016567|GO:0006366|GO:0016874|GO:0003713|GO:0005112|GO:0005634|GO:0006351|GO:0005829|GO:0005737|GO:0045665|GO:0007219|GO:0045581|GO:0010001|GO:0008270|GO:0031625|GO:0007166|GO:0008593. NA - . NA NA NA NA NA NA NA NA NA LNCV6_100218_PI430048170 0.0102081156973763 0.351358260954704 3.47308588933668 3.30333065451841 3.58814575934296 P P P 4.5585810208188 4.99450377105029 5.26627726065721 P P P LNCV6_100218_PI430048170 mRNA

TGGCTGTTCTAAGAAGTACTTATGGAGAGCAAGAACGTTTTTGTTCATTTCTTAATGTGT NM_000538 RefSeq chr13

+ 36819201 36829603 RFXAP 5994 regulatory factor X-associated protein
GO:0003700|GO:0003713|GO:0005634|GO:0045893|GO:0003677 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_103039_PI430048170 0.00795954791846061 0.5248226634288524.69164889481183
4.33144570962178 4.80844314516465 P P P 5.76520585927319 5.38899419737722
5.48222186087172 P P P LNCV6_103039_PI430048170 mRNA
CCAGCATTTGTCCTTTTGTGAAATCAGTATCAGAATACTTGCACTCTTTAACACATTCTTNM_014781RefSeq chr8 -
52622457 52714466 RB1CC1 9821 "RB1-inducible coiled-coil 1, transcript variant 1"
GO:0005515|GO:2001237|GO:0031965|GO:0006355|GO:0019901|GO:0007254|GO:0006351|GO:0005829|GO:0001
889|GO:0007507|GO:0045793|GO:0034045|GO:0005737|GO:0007049|GO:0070969|GO:0001934|GO:0010506|GO:0
000045|GO:0034273. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66778_PI430048170 0.0106138410718795 0.2264769380876420.311994509108015
0.3113021394375150.501920430315927A A A 2.47432289898866 2.03806650515146
2.91628306190418 A A P LNCV6_66778_PI430048170 mRNA
TGATGACCTGGTAACATTTGGAAGATTTTGTTATGGTGTCACTGTCATTTTGACATACCC NM_001199148 RefSeq
chr2 - 164898198 164955525 SLC38A11 151258 "solute carrier family 38, member 11, transcript variant
1" GO:0015171|GO:0005783|GO:0016021|GO:0006814|GO:0003333 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134894_PI430048170 0.0971174641541657 0.6979694322628421 1.7360130869838
11.5296818813556 11.545473004192 P P P 11.7409505321813 12.2651188760484
12.3050491115185 P P P LNCV6_134894_PI430048170 mRNA
GGCCTGCAAACACATTTACTTCTCCTCTTATGAGACTATTTATCTTTAATAAAGCACTGG NM_001070RefSeq chr17
+ 42609339 42615238 TUBG1 7283 "tubulin, gamma 1"
GO:0005515|GO:0005827|GO:0005881|GO:0003924|GO:0031122|GO:0000212|GO:0036064|GO:0005829|GO:0005
737|GO:0000086|GO:0000930|GO:0000242|GO:0031252|GO:0005813|GO:0000794|GO:0006996|GO:0005814|GO:0
000226|GO:0045177|GO:0031513|GO:0005525|GO:0006184|GO:0007020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_116247_PI430048170 0.0137958757171223 0.7248090784294066.92576371561074
6.99386994929092 7.13195828001814 P P P 7.31180748963831 7.57418503702772
7.55190534919928 P P P LNCV6_116247_PI430048170 mRNA
GAGGAAGAGCAGATCACATTGTAAAACTATGGATGGTCTGATAAGGCTTTTACTGACCCC NM_018011RefSeq chr13
- 106543313 106568166 ARGLU1 55082 arginine and glutamate rich 1
GO:0005739|GO:0005515|GO:0006355|GO:0005654|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128765_PI430048170 0.8681247363975110.96441805151923 5.24294205438102
4.76979729996887 4.27504393411742 P P P 5.24961460636264 4.82213935467822
4.41244169564076 P P P LNCV6_128765_PI430048170 mRNA
CACACTGGCTCTTCCCCAAAATTGAAATTGTACAATATGTGAGTCTAATTCTTGCTAACA NM_173629RefSeq chr18
+ 54591158 54599493 DYNAP 284254 dynactin associated protein
GO:0005515|GO:0008284|GO:0005794|GO:0005886|GO:0000139|GO:0032148|GO:0042981|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138109_PI430048170 0.0661106635900875 1.36832028022873 10.3971048573229
10.5494322120669 10.1684337800994 P P P 9.71612775056662 9.83894110758731
10.1859107205649 P P P LNCV6_138109_PI430048170 mRNA
TCCACCCAATTCTGGGTATATCAGTGTGTCTTGCAGAATCTTGGATCATTAAAGATAAAC NM_015050RefSeq chr6
+ 37433130 37481508 CMTR1 23070 cap methyltransferase 1
GO:0005737|GO:0004483|GO:0006370|GO:0080009|GO:0005654|GO:0005634|GO:0003676|GO:0097309 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135699_PI430048170 0.0039245039385162 0.2227136787751372.78115908627213

2.49024321944503 3.24064277859153 A A P 4.56124374385077 4.91498755953012
5.48403305173083 P P P LNCV6_135699_PI430048170 mRNA
ATCATGTTCCCCTTTATGATTTTTTAAGGCTGTCTTACAAGCCTAACAGTGTACTAAGTC NM_001257273 RefSeq
chr6 + 57090009 57109714 ZNF451 26036 "zinc finger protein 451, transcript variant 3"
GO:0005515|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_105793_PI430048170 0.0797463773819842 1.35851195357245 5.88957530799991
5.96255253171847 5.69410455896006 P P P 5.45569019123871 5.10222104388775
5.62691114784132 P P P LNCV6_105793_PI430048170 mRNA
GAAAAAGGATAAAGATAAAGTTTCTCTAACCAAGACCCCAAAACTGGAGCGTGGCGATGG NM_001256182
RefSeq chr16 - 89267620 89490561 ANKRD11 29123 "ankyrin repeat domain 11, transcript variant 1"
GO:0060348|GO:0005737|GO:0060325|GO:0035264|GO:0005886|GO:0001894|GO:0048705|GO:0042475|GO:0005
654|GO:0005634|GO:0001701 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134966_PI430048170 0.3340574609480980.9519229600461359.27154290306424
9.34501286015223 9.27686022476048 P P P 9.39965187643519 9.44107251446526
9.26100983155348 P P P LNCV6_134966_PI430048170 mRNA
GCTCACTAATTTATTTCCAGGAAGGTGTGTGGAAGACATGAGCCGTGTATAATATTTTTT NM_001184940 RefSeq
chr9 - 34398183 34458570 FAM219A 203259 "family with sequence similarity 219, member A,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52958_PI430048170 0.4480222880176310.7087820121335810.3106925876757180.27570453916259
0.307447955297646A A A 1.4794625397846 0.2720402742924570.272501956921659A A A
LNCV6_52958_PI430048170 mRNA
CAGGTGTCTCTATCAGGTGAGAGAAAAATGTCAGACTCAATAAATGTACACTGAAGTCTT NM_001290211 RefSeq
chr17 - 8802722 8867677 PIK3R6 146850 "phosphoinositide-3-kinase, regulatory subunit 6, transcript
variant 2"
GO:0005515|GO:0006661|GO:0030168|GO:0001525|GO:0044281|GO:0045766|GO:0005829|GO:0046854|GO:0046
935|GO:0007186|GO:0016020|GO:0046934|GO:0007596|GO:0043406|GO:0043551|GO:0006644|GO:0005944 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129735_PI430048170 0.5570441054471110.9690618478014050.477588742852179
0.4914194104553120.294028582090011A A A 0.40700116753232 0.522538408641934
0.475471971482213A A A LNCV6_129735_PI430048170 mRNA
GCCGGTCTATGTCATGTTTCAGCTTACTTACTGCAAATCAAATGTGGTGAACAATTTTTT NM_001001656 RefSeq
chr7 + 141918875 141919820 OR9A4 NA "olfactory receptor, family 9, subfamily A, member 4" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136355_PI430048170 0.00431574109095157 2.04204664399386 10.269477216911
10.3720315886699 10.0255129716682 P P P 8.94652243046201 9.40566333495022
9.20995651525524 P P P LNCV6_136355_PI430048170 mRNA
CCCCATCCAGTGTCCAGCACTGGAGTCGAACACAGTAATAAAGATGCTGAGAAAAAGTCA NM_001136485 RefSeq
chr11 + 66975282 66977008 C11orf86 254439 chromosome 11 open reading frame 86 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_145430_PI430048170 0.1046480881685 0.4308755437982971.49186574924403
0.3438083100184180.335591080503659A A A 1.24083004515178 1.82802132639931
2.69770703480803 A A P LNCV6_145430_PI430048170 mRNA
ACTGACATGCATTATTTTCACTGTGAATTCACTTTTTTATTGCATGTTCAGATGTCCCTC NM_001130961 RefSeq chr3
- 155479881 155676316 PLCH1 23007 "phospholipase C, eta 1, transcript variant 3"
GO:0016042|GO:0005737|GO:0043647|GO:0005886|GO:0004435|GO:0050429|GO:0048015|GO:0005509|GO:0044
281|GO:0004871|GO:0043231|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139653_PI430048170 0.0176813091064158 0.57750304158784 8.86731436899734
8.49967948931642 8.89716387114326 P P P 9.26209010686891 9.5776120172738

9.78614299823439 P P P LNCV6_139653_PI430048170 mRNA
ATTTGTTATGCCTTATTCTAAAATTGAGTCTCAAACTGGAATGCCTTTGAAGACAGATGC NM_005754RefSeq chr5
+ 151771914 151805354 G3BP1 10146 "GTPase activating protein (SH3 domain) binding protein 1,
transcript variant 1"
GO:0005515|GO:0090305|GO:0005886|GO:0010494|GO:0007265|GO:0005634|GO:0003729|GO:0003677|GO:0005
524|GO:0005829|GO:0004004|GO:0005737|GO:0004003|GO:0004519|GO:0008152|GO:0006810|GO:0032508|GO:0
090090|GO:0005925. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138419_PI430048170 0.196716311324286 1.06328667571083 0.534626912531226
0.683929961142663 0.552390843774149 A A A 0.464874550676317 0.511778708999795
0.532529087657469 A A A LNCV6_138419_PI430048170 mRNA
TATGGGACTTTGGCTTTCCATTTTTATCTTGCTGAAGTTTTTGAGTTTTTGCAACACAAG NM_178173RefSeq chr3 +
49198427 49258104 CCDC36 339834 "coiled-coil domain containing 36, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128576_PI430048170 0.72545213213363 1.04854623685307 6.90414492033103
7.14704173256994 7.34802891202382 P P P 6.99766201136954 6.87579988197186
7.31779336264769 P P P LNCV6_128576_PI430048170 mRNA
CTGAGCATGAGTTAAAGCATGTGGATGGCCTGGAGCTATGTTTTTAAAATTGTTATTAAA NM_052888RefSeq chr17
+ 32021135 32053501 LRRC37B 114659 leucine rich repeat containing 37B GO:0005737|GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135017_PI430048170 5.47168071097911e-05 3.07537652797941 6.31480381757917
6.3894856177306 6.23337124980707 P P P 4.59918407236677 4.80683769187848
4.66571802678189 P P P LNCV6_135017_PI430048170 mRNA
TTTTTAATTGCCAAACTGCTCTCTTCATCAGCTCAGCACATGCTTTAAGAAAGCAAAACC NM_052854RefSeq chr11
+ 46277637 46321422 CREB3L1 90993 cAMP responsive element binding protein 3-like 1
GO:0043565|GO:0030500|GO:0001077|GO:0035497|GO:0005783|GO:0045944|GO:0003682|GO:0005789|GO:0005
634|GO:0016021|GO:0006351|GO:0030968 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140796_PI430048170 0.0367915907456750 5.58480245281659 10.4727190972433
10.1766790219948 10.4429143030891 P P P 10.816355839703 11.086068977325
11.4574817752686 P P P LNCV6_140796_PI430048170 mRNA
GCTTCTGTAAATGCCATCCCAATGTGGTTTGGTTTTGTTGAACAGAAACCAAAATAAATT NM_001206840 RefSeq
chr2 - 85318017 85328296 TGOLN2 10618 "trans-golgi network protein 2, transcript variant 2"
GO:0030133|GO:0005802|GO:0005515|GO:0005794|GO:0005886|GO:0005654|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127672_PI430048170 0.272024348911175 0.825794432894321 8.87204359836082
8.67168653776156 9.08524099860332 P P P 8.82960165988341 9.19542294179895 9.4045392215142
P P P LNCV6_127672_PI430048170 mRNA
GCTGACTTTGATTAAGGAATTATAGACTGACTACATTGGAAGCTTTGAGTTGACTTCTGA NM_000179RefSeq chr2
+ 47783081 47806953 MSH6 2956 "mutS homolog 6, transcript variant 1"
GO:0005515|GO:0000790|GO:0030983|GO:0032405|GO:0005886|GO:0035064|GO:0016446|GO:0008340|GO:0042
803|GO:0043231|GO:0005737|GO:0003690|GO:0051096|GO:0032357|GO:0006298|GO:0009411|GO:0016887|GO:0
007131|GO:0008094|GO:0000400|GO:0005794|GO:0000287|GO:0008630|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134888_PI430048170 0.108313161504105 1.15091565052664 7.63274430871036
7.59063619925907 7.39477992401884 P P P 7.35372584619691 7.43976759373943
7.21877648663655 P P P LNCV6_134888_PI430048170 mRNA
TTATTTAGCTTCTCCCATCGCCCACGATGGAATGTAAAATAAATTGGTTTTGTACTGGAT NM_005515RefSeq chr7
- 157004852 157010653 MNX1 3110 "motor neuron and pancreas homeobox 1, transcript variant 1"
GO:0003700|GO:0006357|GO:0021520|GO:0005634|GO:0021675|GO:0009791|GO:0009653|GO:0006351|GO:0043
565|GO:0008045|GO:0006959|GO:0031018|GO:0060539|GO:0021904|GO:0001764 . NA - . NA NA NA

NA NA NA NA NA NA
LNCV6_144039_PI430048170 0.28415854428366 4.45300960529379 0.463090545915377
3.84087676396099 1.44394456674776 A P A 0.568016209898558 0.407268262849117
0.411124296747207 A A A LNCV6_144039_PI430048170 mRNA
CCAAGAACCAAAGTTTGTATAAACAGGTTGCTATAAGCTTGGTGAAATGAAAATGGAACA NM_014421 RefSeq chr4
- 106921801 107036296 DKK2 27123 dickkopf WNT signaling pathway inhibitor 2
GO:0090263|GO:0007275|GO:0016055|GO:0090090|GO:0005615 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141310_PI430048170 0.415498912348254 0.884258623119225 0.264858882090191
0.283320929136962 0.395550929320193 A A A 0.789884743893191 0.32430462115928
0.312316935187427 A A A LNCV6_141310_PI430048170 mRNA
TTAAGATCGAAAAGAAATTTCTGTATACTTGATGCCTTAAGATGCCCAAAGCTGCCCAAA NM_017697 RefSeq chr8
+ 94641135 94707466 ESRP1 54845 "epithelial splicing regulatory protein 1, transcript variant 1"
GO:0008380|GO:0006397|GO:0000166|GO:0043484|GO:0005634|GO:0003729 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_98074_PI430048170 0.553478032095273 1.29960207152588 3.2505239502879 2.36919192436297
1.86293429180109 P A A 2.77277282008313 1.69850380278672 2.00634219285461 P A A
LNCV6_98074_PI430048170 mRNA
ACTTACAAAGTGTTGGATGTCCCCCGTTCGAACTGAGGGACTGCAGACCGCCTCTGGGTA NM_001144058 RefSeq
chr11 + 131910817 132336822 NTM 50863 "neurotrimin, transcript variant 3"
GO:0005515|GO:0043005|GO:0016337|GO:0050767|GO:0008038|GO:0009986|GO:0005886|GO:0005911|GO:0043
025|GO:0031225|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144722_PI430048170 0.894844717975225 1.06132184410377 3.89947809414668
3.11449660069094 3.12987497752774 P P P 3.22619434464469 3.38876089842622
3.41101507328934 P P P LNCV6_144722_PI430048170 mRNA
GTGAGGGTGGGCGGGAGGCCTCAGGGGATACTGTTAATCATAAAATGAGCAACGAAAAAA NM_005714 RefSeq
chr11 - 65592854 65595996 KCNK7 10089 "potassium channel, two pore domain subfamily K,
member 7, transcript variant C"
GO:0005244|GO:0005886|GO:0007268|GO:0005267|GO:0034765|GO:0016021|GO:0006813|GO:0071805 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135568_PI430048170 0.696350736494391 1.31354439383084 2.04210970583989
0.423518113461027 0.446034558429674 A A A 0.330607942226553 0.348382045286082
1.41298452692117 A A A LNCV6_135568_PI430048170 mRNA
CACCATTCAACCAAAGAAAGTCAACATTGAACATTAAACCTCTGTGTGTTTCTATACTGA NM_001083909 RefSeq
chr10 + 133088003 133131675 ADGRA1 NA "adhesion G protein-coupled receptor A1, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130058_PI430048170 0.124560663110438 0.33309101824675 2.83539421422736
2.82394887177988 0.67303548236558 A A A 3.93216419030634 4.59665919560398 3.0022331856596
P P P LNCV6_130058_PI430048170 mRNA
TAGCCTTCCCTGGAGAAAAAGAAGTCCCCAAGAAAAAATTCACTCTATGTAGAGAAAAAA NM_001085452 RefSeq
chr9 + 39355668 39361962 SPATA31A1 NA "SPATA31 subfamily A, member 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127229_PI430048170 0.0139508361865088 0.480945857353709 5.40759453980136
5.09940244853898 5.24859802097249 P P P 5.94298480981279 6.42167360118665
6.51317459503267 P P P LNCV6_127229_PI430048170 mRNA
CGATGTGGTTTGTCCAAGTTATTTTCTGTCTTTATTACTGAGACGGATTAATCTCCTTAT NM_020245 RefSeq chr6 +
158312659 158511824 TULP4 56995 "tubby like protein 4, transcript variant 1"
GO:0035556|GO:0006355|GO:0005737|GO:0016567|GO:0003700|GO:0007584 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_135682_PI430048170 0.000803553167869666 0.2564862841972066.34332908192836
6.168437892015 6.04813513503477 P P P 8.13058274608409 8.12358929535989
8.20866714258232 P P P LNCV6_135682_PI430048170 mRNA
CCCCACTTATTCTAGGGCACACAAACACTATTTTACTTTTTTAAAATCATAAAACGGCAG NM_004050RefSeq chr14
+ 23306761 23311759 BCL2L2 599 "BCL2-like 2, transcript variant 1"
GO:0005515|GO:0043066|GO:0051400|GO:0008630|GO:0046982|GO:0005741|GO:0007283|GO:2001243|GO:0042
803|GO:0005829|GO:0097192|GO:0060011|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138454_PI430048170 0.1027033166015141.04211603863341 0.368972984057186
0.3567192330943610.428011214674299A A A 0.3113692637401810.305998081204765
0.358225761789465A A A LNCV6_138454_PI430048170 mRNA
CCTTTTATGTCTTGGAAAGTATCTGAGCCATTCTTATGCTCAAGAAATAGCAATAGGCAT NM_022473RefSeq chr15
- 42412436 42457567 ZNF106 64397 "zinc finger protein 106, transcript variant 1"
GO:0008286|GO:0017124|GO:0016020|GO:0001515|GO:0005730|GO:0046872|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_110414_PI430048170 0.1916316229613461.17522047345895 5.66216399973256
6.02442979959099 5.9405971842728 P P P 5.84109166385014 5.54408879048638
5.54699922506041 P P P LNCV6_110414_PI430048170 mRNA
TGGAACCTCGCTCTGTGGCTGTGTTCCCTTGGCACTCCTTAGTCCCCTTCCTGGCACCCA NM_001304815 RefSeq
chr19 + 42268536 42295796 CIC 23152 "capicua transcriptional repressor, transcript variant 1"
GO:0005515|GO:0048286|GO:0003682|GO:0005634|GO:0000122|GO:0003677|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132679_PI430048170 0.0642698434271883 0.9333207913120370.281109559880966
0.2961420602220130.327318567638505A A A 0.4345883764579950.426913620225681
0.340228820300029A A A LNCV6_132679_PI430048170 mRNA
TATATACCTTCAAGCAACCCTTTGGATTATGCCCATGAACAAGTTAGTTTCTCATAGCTT NM_001243786 RefSeq
chr11 - 36591942 36598279 RAG2 5897 "recombination activating gene 2, transcript variant 4"
GO:0002358|GO:0033077|GO:0046622|GO:0033151|GO:0002331|GO:0043325|GO:0080025|GO:0005547|GO:0005
546|GO:0005634|GO:0035064|GO:0003677|GO:0003682|GO:0030183|GO:0002360|GO:0008270|GO:0035091|GO:0
002326|GO:0016568. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138977_PI430048170 0.82451104054529 0.9852410269617020.554344575565736
0.4791719138744350.429863198407686A A A 0.3960940766448930.488825005981654
0.635399651285011A A A LNCV6_138977_PI430048170 mRNA
AAAGCTATCAAGAGGACCATCTTCCAGAAGGGAGATAAAGCTAGTCTTGCTCATCTTTGA NM_001005278 RefSeq
chr1 - 158776681 158777635 OR6N2 NA "olfactory receptor, family 6, subfamily N, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139448_PI430048170 0.0183627142542249 0.7464991643317587.50138168568566
7.6640378554423 7.4736770712895 P P P 7.97546998110466 7.97647008861447
7.95987957784256 P P P LNCV6_139448_PI430048170 mRNA
GTCTACTCCTCTTTCCGTGGCTGGGGGTAGACTTAATAAAGAGAGAAATTCAAGAAAAAA NM_006244RefSeq chr11
+ 64924670 64934478 PPP2R5B 5526 "protein phosphatase 2, regulatory subunit B', beta"
GO:0005515|GO:0005737|GO:0008601|GO:0000159|GO:0006987|GO:0044267|GO:0030968|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94872_PI430048170 0.3885423426231960.9066176836516756.58088006461584 6.82490111640932
6.5901783219875 P P P 6.74829645150404 6.63637225975251 7.02145585256437 P P P
LNCV6_94872_PI430048170 mRNA
CCTCTGTATGGTTTACTTCAAGCAAAACTTCAACTCATTACACATGCATATTTTGAAGAG NM_015060RefSeq chr7
+ 32495425 32588741 AVL9 23080 AVL9 homolog (S. cerevisiase)
GO:0016477|GO:0016021|GO:0055037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115910_PI430048170 0.0109800275508195 1.35948138948203 13.2891969661643

13.4488610623782 13.5195236402692 P P P 12.9170972586879 12.8919471361227 13.11810931565
P P P LNCV6_115910_PI430048170 mRNA
ACTCTGAGCTTCACACCTGTCTGCTGCCATGGGTGCAGAGCCCTAGTCCTGATGGCCCCT NM_001086521 RefSeq
chr17 + 81239310 81241298 C17orf89 284184 chromosome 17 open reading frame 89 GO:0005739
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133797_PI430048170 0.0316765022227391 1.26279607179802 11.7426203161412
11.706244610935 11.5832989047735 P P P 11.2410505369305 11.4980572683505
11.2742065184354 P P P LNCV6_133797_PI430048170 mRNA
GGACGCCTAGGCAAGAGCGGCCCTCTGCAGCCAAGAGAAATAAAATACTGGCTTCCAGAT NM_001348 RefSeq
chr19 - 3958452 3971123 DAPK3 1613 death-associated protein kinase 3
GO:0005515|GO:0017148|GO:0008360|GO:0090263|GO:2000145|GO:0005634|GO:0006940|GO:0051893|GO:0042
803|GO:0042802|GO:0043522|GO:0035556|GO:2000249|GO:0000910|GO:0005737|GO:0046777|GO:0030182|GO:2
001241|GO:0004683|GO:0007088|GO:0006355|GO:0043065|GO:0030335|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_36446_PI430048170 0.162692865328425 1.10319381568833 8.64181898917927 8.73906251453872
8.61347474401779 P P P 8.57343815196635 8.60542550086897 8.38365260217484 P P P
LNCV6_36446_PI430048170 mRNA
GGGCGGGCTTCCGCTCCGGCCCCTCCTGGGACCCGCACTCGCGCTCCGGGCCCGCTCGAC NM_001122957 RefSeq
chr16 + 31108293 31112791 BCKDK 10295 "branched chain ketoacid dehydrogenase kinase, transcript
variant 2"
GO:0005739|GO:0005515|GO:0016310|GO:0016301|GO:0004674|GO:0047323|GO:0005947|GO:0009083|GO:0006
468|GO:0009063|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141953_PI430048170 0.486577362920633 1.00586810430799 0.337445836371491
0.339769732186733 0.315192205607833 A A A 0.328729655662936 0.331428420243274
0.306928790125702 A A A LNCV6_141953_PI430048170 mRNA
CAATCAGACTATGACAGCTATGTACGACCATTTGTATGTGTATCTATGTCAGAAAGAATC NM_152414 RefSeq chr8
+ 64580237 64583634 BHLHE22 27319 "basic helix-loop-helix family, member e22"
GO:0021960|GO:0021796|GO:0021540|GO:0006366|GO:0006357|GO:0060040|GO:0021957|GO:0003682|GO:0000
981|GO:0005634|GO:0045892|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135226_PI430048170 0.419122895949196 0.233406540671611 0.328031673126387
0.356998128615795 0.352729132324637 A A A 0.356515124914868 0.356363128284533
3.78407624106106 A A P LNCV6_135226_PI430048170 mRNA
TGGGAGCAACATGAATGTTCTACAAAAGTTTAAAGCAGAGATTGTTTCAAATGGGTGTAG NM_003855 RefSeq chr2
+ 102356282 102398775 IL18R1 8809 "interleukin 18 receptor 1, transcript variant 1"
GO:0005515|GO:0032729|GO:0042346|GO:0005886|GO:0042008|GO:0007165|GO:0006955|GO:0030101|GO:0045
063|GO:0004908|GO:0004872|GO:0016021|GO:0035655 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127960_PI430048170 0.114217017432703 1.04357264497346 0.34444151126068
0.373351800892864 0.292379995960595 A A A 0.268750925308362 0.288512658011358
0.269393116811671 A A A LNCV6_127960_PI430048170 mRNA
CTGCCTGGTTTTTATTTGAACATTGCTGGTTATACAATCTTTGTTGGTTGTTTAACACGA NM_033267 RefSeq chr5 -
2746164 2751655 IRX2 153572 "iroquois homeobox 2, transcript variant 1"
GO:0043565|GO:0006355|GO:0072272|GO:0005634|GO:0072086 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_109818_PI430048170 0.368824683797432 0.866936905080801 6.57680936849135
6.18249211896062 5.89334153943011 P P P 6.5093381056893 6.52987973046992
6.30285609225322 P P P LNCV6_109818_PI430048170 mRNA
GGCAACTGCCCTCCCTTCTGGACATAAAACCTCATATTTTAAATAAAGTTGAAATATGAA NM_001276318 RefSeq
chr14 - 23295920 23302848 PPP1R3E 90673 "protein phosphatase 1, regulatory subunit 3E"
GO:0005977 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139144_PI430048170 0.8627455990942250.9833206024150241 0.8387566828596
10.9542689038502 11.2190100614031 P P P 10.9811336471623 10.8998965108032
11.2120813910983 P P P LNCV6_139144_PI430048170 mRNA
CTAAGCCATAGACAGGCTAATTGCCCACCACTCCCAGGAATATTGAAATAGCTACATGAC NM_001285404 RefSeq
chr3 - 63833869 63863786 THOC7 80145 "THO complex 7 homolog (Drosophila), transcript variant 3"
GO:0005515|GO:0006397|GO:0008380|GO:0000347|GO:0000346|GO:0003723|GO:0005634|GO:0046784|GO:0005
737|GO:0006406|GO:0016607|GO:0000445|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141516_PI430048170 0.00287932721395629 0.6978161277210238.20945044124415
8.06130071018836 8.19482496640278 P P P 8.67714039223328 8.63795384901927
8.71136096703107 P P P LNCV6_141516_PI430048170 mRNA
CTGATAAAGATCTCATCACTGCTCCTTATAATAAACCTAATAAAGCAAGAAACCAAGCCT NM_001301138 RefSeq
chr15 - 42158700 42208326 VPS39 23339 "vacuolar protein sorting 39 homolog (S. cerevisiae),
transcript variant 1" GO:0050790|GO:0030897|GO:0005083|GO:0031902|GO:0016192|GO:0005765|GO:0006886
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137322_PI430048170 0.00356796382161412 0.5947301791431621 1.9945110167551
11.7194365249271 11.7337182735137 P P P 12.4487053028473 12.6342247794958
12.6233521152065 P P P LNCV6_137322_PI430048170 mRNA
TGCCTGTGGTCTGGGTGAGATTTACTGTGACCAGATGTAGAATAAATGTGTCTCATCCTG NM_015179RefSeq chr10
- 97356700 97401370 RRP12 23223 "ribosomal RNA processing 12 homolog (S. cerevisiae), transcript
variant 1" GO:0031965|GO:0005730|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121232_PI430048170 0.1017730002778250.6201891157463141 3.6075659269923
12.7571780206911 12.8628136804818 P P P 13.8773712154242 13.8910127944091
13.6727343420528 P P P LNCV6_121232_PI430048170 mRNA
GCCCCCTGTCCAGGTTCCCTCCCCGCCACAGTGAAATAAAGCATCCCACCCTGCAGTTTC NM_012181RefSeq chr19
- 18531751 18543596 FKBP8 23770 "FK506 binding protein 8, 38kDa"
GO:0000413|GO:0005515|GO:0010468|GO:0043066|GO:0031966|GO:0001708|GO:0003755|GO:0005528|GO:0006
915|GO:0030176|GO:0046872|GO:0042802|GO:0007224|GO:0035556|GO:0030513|GO:0061077|GO:0035264|GO:0
016020|GO:0005789|GO:0016032|GO:0043010|GO:0021904 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_126680_PI430048170 0.0835998436843265 1.11638410206685 10.2570310144271
10.3254668075149 10.1427932594419 P P P 10.0019908785876 10.1399209104007
10.1091453092958 P P P LNCV6_126680_PI430048170 mRNA
TGTGCTTCTTACCAGAGGTTTGCAAGCCTCAGACAAATAAATGTGGTGTTTACAATGTAT NM_001256677 RefSeq
chr15 - 73983217 73992348 STOML1 9399 "stomatin (EPB72)-like 1, transcript variant 7"
GO:0005515|GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142849_PI430048170 0.1654669986794111.31374949543382 5.1834388076018
4.85054000200779 4.68897265326023 P P P 4.27597398484018 4.87005822736493
4.36725025352003 P P P LNCV6_142849_PI430048170 mRNA
CCTGCCAGTTAGTACTGTATTTTGCATTCATTAATAAAAGACACCGGTGGAAAGAAAAAA NM_001159531 RefSeq
chr14 - 100537146 100568070 BEGAIN 57596 "brain-enriched guanylate kinase-associated, transcript
variant 1" GO:0005515|GO:0005737|GO:0016020|GO:0043025|GO:0030425 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127211_PI430048170 0.7286087772297781.0642761265021 11.5890873617173
11.0673416963331 11.100595546022 P P P 10.8478427040201 11.2634362725488
11.3842382751694 P P P LNCV6_127211_PI430048170 mRNA
ACTCTGGTGCCTCCAGAGGGGCTCAGGTCACATAAAACTTTGTATATCAACGAGAAAAAA NM_021913RefSeq chr19
+ 41219198 41261767 AXL558 "AXL receptor tyrosine kinase, transcript variant 1"
GO:0006909|GO:0005515|GO:0051897|GO:0070301|GO:0005886|GO:0035457|GO:0060068|GO:0031100|GO:0034

101|GO:0042698|GO:0007283|GO:0097028|GO:0005615|GO:0043524|GO:0006954|GO:0001961|GO:0031668|GO:0
034446|GO:0048469|GO:0001779|GO:0032689|GO:0070062|GO:0048010|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135550_PI430048170 0.1359741622521951.21694174123724 0.774843554169317
1.11281298656007 0.771399528802142A A A 0.617925802784219 0.620153771660284
0.598413167307366A A A LNCV6_135550_PI430048170 mRNA
CTCACTGCTATTTACCAAATCTGAAAGTGATGCTGGGAAATTTCAAGAGCAGAGTCAGAG NM_001008270 RefSeq
chr7 - 141836277 141841421 PRSS37 136242 "protease, serine, 37, transcript variant 1"
GO:0051604|GO:0016477|GO:0004252|GO:0006508|GO:0005634|GO:0005576|GO:0007339 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136071_PI430048170 0.4041647204767750.5196003792337121.41642497501459
0.4676766669466890.520216882982281A A A 2.79438754939116 0.787700193619695
0.922179830456606P A A LNCV6_136071_PI430048170 mRNA
CTAATGAAGTATGGGAACTAAATTGCTGGTTTTCTAAGATAAGATATGGGATATGGGTCA NM_198182RefSeq chr2
+ 9951662 10002284 GRHL1 29841 grainyhead-like 1 (Drosophila)
GO:0003700|GO:0005794|GO:0006357|GO:0005634|GO:0007275|GO:0044281|GO:0000978|GO:0006351|GO:0043
231|GO:0043565|GO:0001077|GO:0005737|GO:0045944|GO:0005654|GO:0044255 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141413_PI430048170 0.0109319625374354 0.6030607669633966.67675211855903
6.28113954573923 6.52730908587368 P P P 7.25067787497098 7.12028713293558
7.32315266356835 P P P LNCV6_141413_PI430048170 mRNA
CATACCTCCCAACTCTCCTGACTCTTATGTTATTGAAAAAACAAACAAACAAAAACTCCT NM_030648RefSeq chr4
- 139506037 139556769 SETD7 80854 SET domain containing (lysine methyltransferase) 7
GO:0005515|GO:0006355|GO:0070828|GO:0005694|GO:0005730|GO:0006325|GO:0034968|GO:0018027|GO:0016
279|GO:0018026|GO:0006351|GO:0006974|GO:0018024|GO:0002039|GO:0005654|GO:0016568 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127948_PI430048170 0.0156298365376581 0.5162929882799568.56544123847353
8.27030280276705 8.55055640119622 P P P 9.08559660661112 9.44586868793332
9.67474022337545 P P P LNCV6_127948_PI430048170 mRNA
CATCTTTCAGAGTGATACCATTTCTACATTTGATAATGCCTGTATTCCTGTAGGATGTAT NM_057158RefSeq chr8
- 29333061 29348805 DUSP4 1846 "dual specificity phosphatase 4, transcript variant 2"
GO:0034142|GO:0005634|GO:0051403|GO:0035335|GO:0000188|GO:0002756|GO:0006470|GO:0000165|GO:0002
755|GO:0034138|GO:0017017|GO:0004725|GO:0001706|GO:0048011|GO:0038124|GO:0038123|GO:0034134|GO:0
008330|GO:0002224|GO:0045087|GO:0005654|GO:0034166|GO:0035666|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_50311_PI430048170 0.1478248116430211.01268601496026 0.3190740851860110.291167815617606
0.299015309091566A A A 0.2921115156984880.2856979878823010.276990740060812A A A
LNCV6_50311_PI430048170 mRNA
TATATTGAAGCCCATCATCGAGTCTGTACCTACAACGAGACCAAACAGGTGACTGTCAAG NM_145171RefSeq chr14
- 63312834 63318879 GPHB5 122876 glycoprotein hormone beta 5
GO:0002155|GO:0005179|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80379_PI430048170 0.5097206673654690.9287720955121029.76324189001843 9.84799810671309
9.39736324529406 P P P 9.86423877420009 9.84848974838876 9.64397136033166 P P P
LNCV6_80379_PI430048170 mRNA
CACAGGCGTGGGGTCCTACTGACCTGTCTCCCCAGCTCCCACACAGAAAGCATCTAAAAT NM_001100878 RefSeq
chr8_KI270816v1_alt - 56232 62798 MROH6 642475 maestro heat-like repeat family member 6 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94507_PI430048170 0.1115865185010480.7020435413291744.00050350286584 4.05116644356028
4.11407198641745 P P P 4.61682561864111 4.19747594529841 4.81735481622725 P P P

LNCV6_94507_PI430048170 mRNA
ATACAGAATCAAACATTTTCCACCCCAGCAAGTCAACTCTTTTCTCCTCATGGTTCTAAT NM_025138 RefSeq chr13
- 39009864 39038076 PROSER1 80209 proline and serine rich 1 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145008_PI430048170 2.75223867811782e-05 0.4001457049585976.6245532747403
6.57316684028931 6.7247926108036 P P P 8.00810885926967 7.99893637182695 7.8803310518001
P P P LNCV6_145008_PI430048170 mRNA
TGGATAGTAGATCTCGAGCGTTTATCTCGGGCTTTAATTTGCTAAAGCTGTGCACATATG NM_015355 RefSeq chr17
+ 31937024 32001038 SUZ12 23512 SUZ12 polycomb repressive complex 2 subunit
GO:0005515|GO:0010467|GO:0008284|GO:0016574|GO:0003723|GO:0016571|GO:0005730|GO:0005634|GO:0035
064|GO:0000122|GO:0001739|GO:0046872|GO:0006351|GO:0042054|GO:0043565|GO:0035098|GO:0045814|GO:0
003682|GO:0040029|GO:0005654|GO:0045596 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143554_PI430048170 0.1797489865719420.8453401321792769.67363020805905
9.56962830268013 9.61574781848981 P P P 10.0645688271181 9.83668161962296
9.65792062301647 P P P LNCV6_143554_PI430048170 mRNA
TCTACTGACCATCTTGATACTTATTTATACGAGAGGCAGTTGCTGGACGGGGTAGTACTG NM_025194 RefSeq chr19
+ 40717102 40740861 ITPKC 80271 inositol-trisphosphate 3-kinase C
GO:0016310|GO:0005516|GO:0008440|GO:0043647|GO:0005634|GO:0044281|GO:0005524|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145391_PI430048170 0.9545405092562941.03720878750952 2.55074703160318
3.84290895740958 3.7182454386114 A P P 3.70792928661045 3.42811034636945
3.06032038585644 P P P LNCV6_145391_PI430048170 mRNA
TTTCCAGGAAAAGAACCAGCGGCCTACGCACTTGGCAGGGGCCTTCCTTGCCTTCATCTT NM_001282011 RefSeq
chr19 - 55312800 55325340 TMEM150B NA "transmembrane protein 150B, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131941_PI430048170 0.441429390562356 1.04017059301226 6.64492439842926
6.78531821362105 6.76100055415636 P P P 6.64150419552685 6.60461223289505
6.77304889393139 P P P LNCV6_131941_PI430048170 mRNA
AGTTCATTTCAGCCTCAGGTCCAAGCCATGTTCTCCAATCCAGCTCTATCAGCTATAAAG NM_001010862 RefSeq
chrX - 56990830 56995555 SPIN3 169981 "spindlin family, member 3, transcript variant 1"
GO:0007276 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129044_PI430048170 0.252071776630902 1.01969572321812 0.304609963297073
0.2589606202607810.317399318597961 A A A 0.2723407461478820.255859141692337
0.268953367004973 A A A LNCV6_129044_PI430048170 mRNA
CCTTTGTCATGTTGTAGCACACATAGAAAATATTGTACAGCATACTGGTATAAACCAGAA NM_203301 RefSeq chr14
- 39396372 39432500 FBXO33 254170 F-box protein 33 GO:0005515|GO:0016567 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_57809_PI430048170 0.0580045226967579 0.72960177031411 6.62775424189456
6.63523870200608 7.01268014137397 P P P 7.17727683950563 7.20093635731192
7.29376636535376 P P P LNCV6_57809_PI430048170 mRNA
TTTTCATGAATGTGCTGGTGAACACTGTGACCAGGCTTTTGTAGATGGCGATGTGTTATA NM_001277 RefSeq chr11
- 68052858 68121391 CHKA 1119 "choline kinase alpha, transcript variant 1"
GO:0033265|GO:0004305|GO:0006629|GO:0006646|GO:0004104|GO:0004103|GO:0044281|GO:0019695|GO:0005
524|GO:0042803|GO:0005829|GO:0016310|GO:0007165|GO:0008144|GO:0006869|GO:0004871|GO:0006644|GO:0
006657|GO:0046474|GO:0006656 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94331_PI430048170 0.102176319439483 0.744107294872618 5.54066359985012 5.27780247779168
4.95995565693079 P P P 5.60489624764991 5.86960494678362 5.62594014271416 P P P
LNCV6_94331_PI430048170 mRNA
TACTAGACAGATATAAACAGATCCCCTGCTGAACAGATACACAGAGTTCTCAGACCCCAC NM_014369 RefSeq chr2

+ 130356006 130375409 PTPN18 26469 "protein tyrosine phosphatase, non-receptor type 18 (brain-derived), transcript variant 1" GO:0005515|GO:0005737|GO:0006470|GO:0005634|GO:0035335|GO:0004726 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140798_PI430048170 0.24076443769878 1.13136008731591 6.99995780806714 7.27643044134109 7.04422707037538 P P P 6.73578015871955 7.05554889366117 6.99122428197725 P P P LNCV6_140798_PI430048170 mRNA TCACCATGTAAAGAATTAACCTCCTATCTTAGCAGACATCGTCTCCTAATATTTCCCTTT NM_018316 RefSeq chr19 + 18637027 18670492 KLHL26 55295 kelch-like family member 26 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137140_PI430048170 0.1191719190594070.8001174673942971 2.3241104451663 12.096739034517 11.8848955646722 P P P 12.4497711333852 12.4277309503252 12.4267117706234 P P P LNCV6_137140_PI430048170 mRNA CCCAGCCCCACATCCCCTCTGGAAGAGAATGTAAAATAAACCTGGACACAAGGGAAAAAA NM_005775 RefSeq chr8 + 22551737 22575495 SORBS3 10174 "sorbin and SH3 domain containing 3, transcript variant 1" GO:0005515|GO:0031589|GO:0005634|GO:0000122|GO:0005829|GO:0006936|GO:0051495|GO:0051496|GO:0017166|GO:0005200|GO:0007015|GO:0043410|GO:0005856|GO:0007155|GO:0005925|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130307_PI430048170 0.000879833690968566 0.6809494205049441 3.3401609669979 13.2441797201824 13.1956479285761 P P P 13.7244941353003 13.850455787409 13.8677521911349 P P P LNCV6_130307_PI430048170 mRNA GCTTGCACCCGCTCTCTGTTGTACACTTTCAATCAACACTTTTTCAGACTAAAGGCCAAA NM_177983 RefSeq chr2 - 27381198 27409683 PPM1G 5496 "protein phosphatase, Mg2+/Mn2+ dependent, 1G" GO:0005515|GO:0005737|GO:0035970|GO:0006470|GO:0007050|GO:0005654|GO:0005634|GO:0004722|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136807_PI430048170 0.2194764157771881.21114271563271 9.53090857546669 9.10151220128935 9.23758016912054 P P P 8.73839906716968 9.07060493779583 9.22399560264265 P P P LNCV6_136807_PI430048170 mRNA GCTGACAGACTGGGATTTTCTGTACTAAAATGTTACTTTGTATCAAAAGTTAAACAGGCT NM_004747 RefSeq chr10_KI270825v1_alt - 29482 165282 DLG5 9231 "discs, large homolog 5 (Drosophila)" GO:0005515|GO:0008092|GO:0008285|GO:0005886|GO:0008013|GO:0045186|GO:0030159|GO:0045176|GO:0042981|GO:0072205|GO:0045197|GO:0035556|GO:0007165|GO:0005737|GO:0016337|GO:0060441|GO:0005913|GO:0006461|GO:0030859|GO:0071896|GO:0030901 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131900_PI430048170 0.0875597325933114 0.62096602962692 3.94468496847431 3.89346139668356 3.90817818722796 P P P 4.95784520091866 4.23814891694138 4.52083132081829 P P P LNCV6_131900_PI430048170 mRNA TGCTCAGGTAATCAGTATTTTCTTCCACGTATGTGCATATTGCACTGTTAGATCATAGAA NM_198273 RefSeq chr5 - 90515625 90529584 LYSMD3 116068 "LysM, putative peptidoglycan-binding, domain containing 3, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133786_PI430048170 0.0136286864698214 1.31842301498045 10.4917704395585 10.5406280668217 10.5534720255061 P P P 10.145684650823 10.0192620075465 10.2182330070958 P P P LNCV6_133786_PI430048170 mRNA CACCTGATGTAAAGTTTCTGTAAATCTATTTCATATCTGACCCACCAAACAGATTTCTCT NM_004715 RefSeq chr18_KI270863v1_alt + 122433 160649 CTDP1 9150 "CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1, transcript variant 1" GO:0010458|GO:0010467|GO:0005813|GO:0006368|GO:0006366|GO:0003899|GO:0005819|GO:0030496|GO:0051233|GO:0015629|GO:0050434|GO:0000922|GO:0005737|GO:0006470|GO:0016032|GO:0005654|GO:0051301|GO:0008420 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145450_PI430048170 0.1461131895774721.3629757397755 4.5698466990288 4.83383530242213 4.82678395996864 P P P 4.64486610745744 4.26443559395075

3.90057606658135 P P P LNCV6_145450_PI430048170 mRNA
GCATCATCCAAGGAATAGACTCCTTCGTGATCTGGGGATGTGCCACCCGCCTTTTCCCTG NM_002777 RefSeq
chr19_KI270868v1_alt + 19827 27018 PRTN3 5657 proteinase 3
GO:0008284|GO:0004252|GO:0005886|GO:0097029|GO:0005615|GO:0005829|GO:0031012|GO:0050765|GO:0007596|GO:0030574|GO:0006508|GO:0008236|GO:0019899|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139243_PI430048170 0.5314370706699790.9612274635012420.267046607064579
0.44565290722289 0.300320484013758 A A A 0.5006584561219090.394843178651952
0.287089613984765 A A A LNCV6_139243_PI430048170 mRNA
CAAGGAACAGCCAATACCTGCCAACTTTCTAGGTTTTTCCAACCAATTCTCTTACAGAAA NM_173167 RefSeq chr17
+ 35148263 35189345 UNC45B 146862 "unc-45 homolog B (C. elegans), transcript variant 1"
GO:0005515|GO:0005737|GO:0007517|GO:0061077|GO:0051879|GO:0030154|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133618_PI430048170 0.200983600738539 1.06667809273126 0.438916819757481
0.276350929703267 0.401512148362368 A A A 0.286933789429579 0.264411482092798
0.290896908392585 A A A LNCV6_133618_PI430048170 mRNA
TTTTTTATACTATTTAGATTTTAAGAAGGCTAAAGAATCAAACGTTTTAAACATAAAAAA NM_021211 RefSeq
chr11 - 10852703 10858073 ZBED5 58486 "zinc finger, BED-type containing 5, transcript variant 1"
GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129057_PI430048170 0.0240137174060969 0.562671546286542 8.46249504717523
8.3213799169207 8.66946684843776 P P P 9.0947996884599 9.15691237700233
9.64645309165156 P P P LNCV6_129057_PI430048170 mRNA
CCTCCATTACAGTCAAGGCTAAGTCAAATGAAACTGAATTTTAAACTTTTTGCATGCTTC NM_006437 RefSeq
chr13 - 24420930 24512810 PARP4 143 "poly (ADP-ribose) polymerase family, member 4"
GO:0005515|GO:0008219|GO:0042493|GO:0005634|GO:0003677|GO:0006974|GO:0003950|GO:0006471|GO:0005737|GO:0006281|GO:0006954|GO:0016020|GO:0030529|GO:0006810|GO:0005876|GO:0019899|GO:0006464|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145591_PI430048170 0.506503396919786 0.985248978736111 0.289474031592178
0.328608804458866 0.37802768437496 A A A 0.378516617189459 0.351042539321433
0.331855477465726 A A A LNCV6_145591_PI430048170 mRNA
GGACTTGTTCATTTCGCTTCTCAAAGTGAAAAATCTGTTATCCAATAGCTACCATAGATG NM_001040283 RefSeq
chr19 + 41845022 41852329 DMRTC2 63946 DMRT-like family C2
GO:0000987|GO:0001741|GO:0006355|GO:0003700|GO:0007290|GO:0005634|GO:0006351|GO:0042803|GO:0046872|GO:1900114|GO:0007548|GO:0007141|GO:1900111 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97152_PI430048170 0.00181223922476299 4.03454387406692 8.80675109653783
8.88053880789291 9.19452652183664 P P P 6.55430898262302 7.1075419396907
7.14106913521157 P P P LNCV6_97152_PI430048170 mRNA
AGTCAAAGTCGAGGATATTTTTTATTCAGGCCACGGAATGGAAGAAGGTCAGCAGGGTTC NM_006681 RefSeq
chr4 - 55595228 55636298 NMU 10874 "neuromedin U, transcript variant 1"
GO:0007586|GO:0005102|GO:0005576|GO:0009648|GO:0006940|GO:0001696|GO:0019233|GO:0007165|GO:0007186|GO:0045987|GO:0007218|GO:0050806|GO:0043195|GO:0046887|GO:0042922|GO:0042755 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130498_PI430048170 0.872352431389216 1.00602048260774 7.14581550309496
7.25545918897576 7.23766441181754 P P P 7.19647393590874 7.13934499473345
7.27623904068047 P P P LNCV6_130498_PI430048170 mRNA
TCCATTCTGAGTAACTTTTGAGCAAGTAATTCTAAGCTTTGTCTTGTATCCTTGTGTGAA NM_001011658 RefSeq
chrX - 13712241 13734635 TRAPPC2 6399 "trafficking protein particle complex 2, transcript variant 1"

GO:0006888|GO:0005515|GO:0048471|GO:0006355|GO:0001501|GO:0005794|GO:0005783|GO:0005634|GO:0006351|GO:0044325|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133777_PI430048170 0.291971558194472 1.03659723866691 0.357759615781132 0.360273432126095 0.467038228460629 A A A 0.342719637158974 0.3173968679515 0.371597519816236 A A A LNCV6_133777_PI430048170 mRNA
GTCTAAGTCACAAAGCATTTGTTTTAACCTGTAATGGCACCATGTTTAATGGTGGTTTTT NM_025239 RefSeq chr9 + 5510544 5571282 PDCD1LG2 80380 programmed cell death 1 ligand 2
GO:0003674|GO:0006955|GO:0005886|GO:0032693|GO:0046007|GO:0042102|GO:0031295|GO:0016021|GO:0032689|GO:0070062|GO:0012505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117827_PI430048170 0.0550693876763065 1.22860924860861 6.1087955813032 6.23145317750545 6.10934969317818 P P P 5.87777377418827 5.68678562971017 5.98207265511733 P P P LNCV6_117827_PI430048170 mRNA
AATTCGAGGCCTGGATTGCTGCTTTCAATTACTGGCATCCAGAAATTGTGTATTCAGGGG NM_138778 RefSeq chr9 - 137554906 137578935 DPH7 92715 diphthamide biosynthesis 7
GO:0044267|GO:0017183|GO:0043687|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141863_PI430048170 0.116458716905939 0.753033748672352 5.11142838849263 5.45449100953345 5.6842192663476 P P P 5.75846375490846 5.89233649878253 5.87989548323363 P P P LNCV6_141863_PI430048170 mRNA
CAGTATGGGAAAGCCTTCAGATCTGCCAAGATTCTTTGAATACAGATAATTAATGTAAAC NM_001271848 RefSeq chr19 + 11925067 11950773 ZNF700 90592 "zinc finger protein 700, transcript variant 2"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143390_PI430048170 0.00544458229017164 0.262165497456149 2.86601258338418 2.07478975718988 2.06729480833223 A A A 3.95098289296823 4.39589201938894 4.54513448181305 P P P LNCV6_143390_PI430048170 mRNA
GGAGTGGGAAGACTGCCTCCTTTTTTGAAGAGAGAGATTAAGGATTTTTATAATTGTTTT NM_005859 RefSeq chr5 + 140114122 140119416 PURA 5813 purine-rich element binding protein A
GO:0017148|GO:0005515|GO:0008284|GO:0006357|GO:0006366|GO:0003705|GO:0046332|GO:0005634|GO:0032422|GO:0030425|GO:0007399|GO:0003691|GO:0005737|GO:0003697|GO:0006270|GO:0043025|GO:0006268|GO:0045892|GO:0005662|GO:0000784|GO:0008134|GO:0000900 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144702_PI430048170 0.0868546241461887 0.373032939336821 0.506482787402079 2.16065933746719 1.84229401748828 A A A 3.05010595409341 2.96848955062986 3.21675046188037 P P P LNCV6_144702_PI430048170 mRNA
TTTCTTCTCTCTCATGTGCATGATGGAACAATAAAAAGCTTATGGCTTTGCTAGATCTAT NM_001195150 RefSeq chr7 + 128866409 128872047 LOC100130705 100130705 uncharacterized LOC100130705 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133177_PI430048170 0.0036624659143692 0.2819563383305577.60578123633236 7.25419639933177 7.11767911420916 P P P 9.53523973007654 9.07531307623739 8.79254928283471 P P P LNCV6_133177_PI430048170 mRNA
TGTACATCTTTTGTAAATGATGAGAAATAAAGGAAGTGGACGCAAAGTGATGCGGCAAAA NM_025045 RefSeq chr22 - 38084888 38110669 BAIAP2L2 80115 BAI1-associated protein 2-like 2
GO:0012506|GO:0007009|GO:0005543|GO:0005886|GO:0071439|GO:0044291|GO:0061024|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69316_PI430048170 0.2443274218046270.5808166824400712.32814448046732 0.31496734025255 1.94837477018198 A A A 2.35925717693731 2.617157051354 2.62429710185176 A P P LNCV6_69316_PI430048170 mRNA
ACGGACACCTTCCCTGTGCACACCCAGGGATTCTTCTGCTATGACAGTACCTACGCCAAG NM_022737 RefSeq chr19

+ 11355385 11365698 LPPR2 64748 "lipid phosphate phosphatase-related protein type 2, transcript variant 1" GO:0016311|GO:0016021|GO:0008195 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137552_PI430048170 0.5789882112276820.8904126552474470.596096784438896
0.409814336113681 1.11795652129963 A A A 1.16213052903487 0.977727715392486
0.505851813876395 A A A LNCV6_137552_PI430048170 mRNA
ATCCTCTGTTCATAATGAACAAGATGAACCAATGTGGATTAGAAAGAAGTCCGAGATATT NM_000395 RefSeq chr22
+ 36913632 36940437 CSF2RB 1439 "colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)"
GO:0005515|GO:0038156|GO:0005886|GO:0007585|GO:0004912|GO:0038043|GO:0004914|GO:0036016|GO:0007165|GO:0030526|GO:0005887|GO:0032496|GO:0004872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127344_PI430048170 0.0967891479465499 1.19313577524921 8.56286256073275
8.77576532305331 8.77157156102468 P P P 8.49258754836572 8.26707520695762
8.57869333849484 P P P LNCV6_127344_PI430048170 mRNA
CCAACACCAGCCATTGCCTGTCTCTAAACATCTTATGAAATAAAACCAGTTTTGTTTAAA NM_016940 RefSeq chr21
- 29005758 29019364 RWDD2B 10069 RWD domain containing 2B
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103585_PI430048170 0.000259037780060069 0.2798545787384630.974089217259244
1.02358561417207 1.22222866615602 A A A 2.73484215243187 3.09739755076486
2.88846982923673 P P P LNCV6_103585_PI430048170 mRNA
CCAGAAGCCACATGGAAAACATATCTCTCAAGGATTGTAATTTTCATCGAAATAGTGGGA NM_005767 RefSeq chr13
- 48411045 48444704 LPAR6 10161 "lysophosphatidic acid receptor 6, transcript variant 1"
GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109406_PI430048170 0.5891736244379341.05642207568272 4.48070587820486
4.66890644138919 4.68993648964278 P P P 4.62000990146773 4.6861987902803 4.2714041361087
P P P LNCV6_109406_PI430048170 mRNA
AGTTCTTCAGAGAAGCGTTGCAATTTGAAATTGATGACTCTTCCCCCAGCATGTCCGGTT NM_001300800 RefSeq
chr11 + 63939330 63957319 NAA40 79829 "N(alpha)-acetyltransferase 40, NatD catalytic subunit, transcript variant 2" GO:0006629|GO:0008080 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138642_PI430048170 0.0209868171784876 0.6281662107434042.98943720620287
3.11194770592667 2.75614227913324 A P A 3.34312103150424 3.73279885033144
3.77796582849487 P P P LNCV6_138642_PI430048170 mRNA
AGCTCCTTGTCTCAGTCTTTGTTCTCTAAAAGAACGATTTAAGGTTACAAATGGCTCTTT NM_001277291 RefSeq
chr12 - 133119968 133130473 ZNF891 NA zinc finger protein 891 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144987_PI430048170 0.5134338310759880.9358425440950279.7422592679411
9.53056890344561 9.27474880700267 P P P 9.66370678368342 9.65043335908071
9.55575187539079 P P P LNCV6_144987_PI430048170 mRNA
TGACTGTCACATGCTGCCCCCACCCAGCCTAAAATAAAGAGCTCACTGCTGTGCAAAAAA NM_004913 RefSeq chr16
- 89707132 89720986 VPS9D1 9605 VPS9 domain containing 1
GO:0043547|GO:0005215|GO:0015986|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141323_PI430048170 0.7459078072189160.9912688014135820.292387751358197
0.3045342104106730.397708786664696 A A A 0.3669997196022790.312297948159955
0.35503489468025 A A A LNCV6_141323_PI430048170 mRNA
ATGAAAGTGGCAATGAGGAGACTGTGCAGTCGTCTTGCGCATTTTACAAAGATTTTGTAA NM_001001674 RefSeq
chr15 + 101818186 101819125 OR4F15 NA "olfactory receptor, family 4, subfamily F, member 15" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133558_PI430048170 0.7751044504322141.10800546237176 1.42174214966145
1.49427931386897 0.354538059594414 A A A 0.3982407228157330.766636431474711
1.63007947690803 A A A LNCV6_133558_PI430048170 mRNA

CATTCCTGAAGGGTGATATGAAAGTTAACCCCACCTAATAAACATAACTCTAATTCTGAA NM_018935 RefSeq chr5 + 141245348 141248233 PCDHB15 56121 protocadherin beta 15 GO:0005887|GO:0005509|GO:0007155|GO:0007156|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144720_PI430048170 0.517552476791256 0.971525087106391 0.299333145458764 0.307025388621849 0.438861299834584 A A A 0.351006796184301 0.466834167701172 0.353659711381343 A A A LNCV6_144720_PI430048170 mRNA
CACAGATGAACTCTACCTTTGCTTTCAGAACCACTTAGTCCTTTTGTAACAAAGAAAAAA NM_000168 RefSeq chr7 - 41960949 42237019 GLI3 2737 GLI family zinc finger 3 GO:0046638|GO:0001656|GO:0005515|GO:0043627|GO:0001658|GO:0003700|GO:0008013|GO:0048593|GO:0021861|GO:0046639|GO:0007224|GO:0007507|GO:0048589|GO:0021798|GO:0016485|GO:0007411|GO:0017053|GO:0035035|GO:0033077|GO:0000122|GO:0000978|GO:0001701|GO:0005929|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143832_PI430048170 0.00450835943261225 1.61988349279851 10.5108696386828 10.5736747978626 10.3460975963597 P P P 9.81454986271269 9.91449409013783 9.60650049466956 P P P LNCV6_143832_PI430048170 mRNA
TAGATTTTCTCTTTCACCACGTGTGAACTGTGGGTGAGGTTTCAAAGTAGCTTCACCCCA NM_001193452 RefSeq chr16 + 4693692 4695859 NUDT16L1 84309 "nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1, transcript variant 2" GO:0005737|GO:0030515|GO:0008152|GO:0050072|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138709_PI430048170 0.0219789196513483 0.6385935852280126.76910541426442 6.38080830910632 6.65668849304874 P P P 7.07486575114874 7.15760732126605 7.50533706008826 P P P LNCV6_138709_PI430048170 mRNA
GCTAGCCAGTTTCTTTCAAGTATGGCAAGCTAACGTTAAAATGTTTAGAGATTAACAGAT NM_004453 RefSeq chr4 + 158672100 158708713 ETFDH 2110 "electron-transferring-flavoprotein dehydrogenase, transcript variant 1" GO:0048039|GO:0051539|GO:0048038|GO:0031966|GO:0050660|GO:0043783|GO:0009055|GO:0044281|GO:0033539|GO:0046872|GO:0022904|GO:0004174|GO:0005759|GO:0016491|GO:0031305|GO:0022900|GO:0006979|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139365_PI430048170 0.0175352357670806 0.5068972650580573.97263261703788 4.14460522408939 4.51150725616328 P P P 4.81103776306683 5.40652142096679 5.33532770255199 P P P LNCV6_139365_PI430048170 mRNA
GGGAATGCAGACCTTGCACTTCTTGTTTTGCTCGCAAAAAACATCGTAGTTCCTACATGA NM_006511 RefSeq chr1 + 15659868 15661722 RSC1A1 6248 "regulatory solute carrier protein, family 1, member 1" GO:0006355|GO:0030054|GO:0005794|GO:0005886|GO:0006810|GO:0005654|GO:0005634|GO:0008200|GO:0006351|GO:0051051|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49897_PI430048170 0.00696884260236406 1.93132032191402 4.5365541289587 4.35911853055163 4.30727404654391 P P P 3.67733646920634 3.22873143366113 3.42300801676124 P P P LNCV6_49897_PI430048170 mRNA
CAGGGAAACCACTAGCAGCTGCCAATGTATTCTGAACAAATAAATTAATGCTATAGCTGA NM_001044264 RefSeq chr9 - 35752990 35754277 MSMP NA "microseminoprotein, prostate associated" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128175_PI430048170 0.312150651246986 1.02470221491931 0.301450491386883 0.28437919507015 0.369586807914507 A A A 0.295750937921435 0.276425397623515 0.27896522853637 A A A LNCV6_128175_PI430048170 mRNA
GCTGTGAGGCTACTGTGGCATCTTAGGAACTATACAAAAACACCAAACCCTTTACCTTTG NM_181429 RefSeq chr12 - 11185992 11186937 TAS2R42 353164 "taste receptor, type 2, member 42" GO:0033038|GO:0007186|GO:0005886|GO:0016021|GO:0001580 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_126788_PI430048170 0.6385514902501810.9738332989367120.490663911132652
0.4421956211872720.252478151856531A A A 0.3836473437709760.48146635059968
0.444121933959031A A A LNCV6_126788_PI430048170 mRNA
TGTTCTCACAGGACATGTACCTAATTATGGTACTTATTTATGTAGTCACTGTATTTCTGGNM_001143981 RefSeq chrX
- 110673855 110796058 CHRDL1 91851 "chordin-like 1, transcript variant 1"
GO:0030514|GO:0048749|GO:0001503|GO:0030182|GO:0001654|GO:0005576|GO:0030509 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145255_PI430048170 0.6570691830617320.9764165051258631 6.327795177967
16.1194532134202 16.1492632561172 P P P 16.1680453008796 16.293991131477
16.2439075314741 P P P LNCV6_145255_PI430048170 mRNA
TGTGTTCTAGGCCCGCCCACCCCAACCTTCTGGTGGGGAGAAATAAACGGTTTAGAGACT NM_002415RefSeq
chr22_KI270879v1_alt + 130739 131584 MIF 4282 macrophage migration inhibitory factor (glycosylation-
inhibiting factor)
GO:0005515|GO:0071157|GO:0008283|GO:0030890|GO:0043030|GO:0090344|GO:0050731|GO:0050715|GO:0048
146|GO:0005615|GO:0010739|GO:0070207|GO:0033138|GO:0005737|GO:0006954|GO:0004167|GO:0001516|GO:0
043406|GO:0002906|GO:0031666|GO:0070374|GO:0033033|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127014_PI430048170 0.2919008430496851.38831488414089 0.596633376924641
0.4470270495749441.39185284598193 A A A 0.5078539955736480.403252995320428
0.28321672355092 A A A LNCV6_127014_PI430048170 mRNA
TCCAATATGTGTAAGATATTGAATTGGCTTTGGTTGTCTCTCTTAGCATTTAGTTGCCTA NM_001257995 RefSeq chr13
+ 75871037 75883812 LMO7DN 729420 LMO7 downstream neighbor NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_140169_PI430048170 0.1782754689194051.89101833785632 1.35466955463727
2.80159433112226 2.13476548995628 A A A 1.53821581812669 0.620063817804145
1.54617882912602 A A A LNCV6_140169_PI430048170 mRNA
CCTGGGCCACTTTTAAACACTAAACATTTCATTTATCCTCTAAGCTAAAATGGTGCTGAG NM_002317RefSeq chr5
- 122063194 122078360 LOX 4015 "lysyl oxidase, transcript variant 1"
GO:0005515|GO:0005581|GO:0001568|GO:0005507|GO:0030324|GO:0042493|GO:0004720|GO:0005578|GO:0005
576|GO:0005634|GO:0048545|GO:0005615|GO:0030198|GO:0030199|GO:0042060|GO:0006464|GO:0055114|GO:0
048251 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132439_PI430048170 0.1288352902689760.7929261150711451 4.9244818326387
14.6847464292064 14.7155759619385 P P P 15.3727938846762 15.0063732002994
14.9208902919575 P P P LNCV6_132439_PI430048170 mRNA
TATTCTGGGTTAGAGAAGTGCTTACTAAGGGGTTTTCTAATAAAAACAAATGCCACATTG NM_003145RefSeq chr1
- 156009047 156020967 SSR2 6746 "signal sequence receptor, beta (translocon-associated protein
beta)" GO:0010467|GO:0005783|GO:0006614|GO:0006613|GO:0005789|GO:0016021|GO:0044267|GO:0006412
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133927_PI430048170 0.0384306428322062 0.4602361834013512.14145099344908
3.11557648252134 2.47048758138909 A P A 3.56785491974896 3.66084972469292
3.99588033888686 P P P LNCV6_133927_PI430048170 mRNA
TAAAACACATGAATAAATTTGCAAAACCAAGATCACAGTACACCATATGCACTCTGGTAC NM_003291RefSeq chr13
+ 102596935 102679173 TPP2 7174 tripeptidyl peptidase II
GO:0000209|GO:0002474|GO:0005737|GO:0004252|GO:0004175|GO:0004177|GO:0006508|GO:0008240|GO:0005
654|GO:0005634|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71863_PI430048170 0.1071759003279371.02558150292006 0.3900806574081820.396976894282948
0.428300358598265A A A 0.3645109880529950.3484278819203310.393026779519916A A A
LNCV6_71863_PI430048170 mRNA
TGCTTATCTTCAGTTTATCATCAGACATCTTAGGGAAGTTTAATAAAGAACACCAGGAGA NM_152505RefSeq chr21

- 39405843 39444202 LCA5L 150082 Leber congenital amaurosis 5-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139776_PI430048170 0.0939644227676553 1.26946687519136 13.1615329258591 13.4972369891592 13.498558461391 P P P 13.2410658354115 12.8598282326474 13.023725711615 P P P LNCV6_139776_PI430048170 mRNA
GAGTCACACTGAGATAGTCAGTTGTGTGTGACTCTAATAAACGGAGCCTACCTTTTGTAA NM_003754RefSeq chr11 + 7987319 7996171 EIF3F 8665 "eukaryotic translation initiation factor 3, subunit F"
GO:0005515|GO:0010467|GO:0016579|GO:0033290|GO:0004843|GO:0005852|GO:0016282|GO:0001731|GO:0003743|GO:0006412|GO:0006413|GO:0005829|GO:0016020|GO:0071541|GO:0006446|GO:0006508|GO:0031369|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134736_PI430048170 0.21601538003567 0.7846062910509398.91189437171867 9.50544812230543 8.80710022740545 P P P 9.59113757658822 9.35303133909397 9.4218283635361 P P P LNCV6_134736_PI430048170 mRNA
AGAAGACAGAGGAGCACTTAAGGTGCAAAGCAGCCTATTTTTTCTTCAATAAAAATTGTT NM_001172700 RefSeq chr5 - 132822140 132830898 SHROOM1 134549 "shroom family member 1, transcript variant 1"
GO:0000902|GO:0005737|GO:0051015|GO:0005874|GO:0016460|GO:0051017 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110512_PI430048170 0.0467157408795101 0.7693878820760637.06292723067132 6.73302330084681 6.77978128520537 P P P 7.09010341933688 7.26134730123765 7.36796493091487 P P P LNCV6_110512_PI430048170 mRNA
TGGTCTCATCTCCGCATCAGGAATTCACCTGGAGGTTGAAAAGAGAAAAGAAAAAGCACC NM_021907RefSeq chr2 - 25377242 25673647 DTNB 1838 "dystrobrevin, beta, transcript variant 1"
GO:0005737|GO:0045202|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139055_PI430048170 0.1859159306891181.39746543722128 5.65858177456779 6.22490785880118 6.45530272305258 P P P 5.83178149736772 5.4092275345991 5.7281710897123 P P P LNCV6_139055_PI430048170 mRNA
CCCATACCAGATAAAAACCGCATATAACTCTGTGACATTTTCTTTGTTCTGAAACATCAT NM_004882RefSeq chr2 - 174348149 174395715 CIR1 9541 "corepressor interacting with RBPJ, 1"
GO:0005515|GO:0006397|GO:0008380|GO:0003700|GO:0005815|GO:0006357|GO:0006366|GO:0003705|GO:0003714|GO:0005634|GO:0005737|GO:0000118|GO:0016607|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127347_PI430048170 0.00584363163514859 0.4969521660218984.91927826041124 5.24528451910201 5.28611026038493 P P P 6.12006030128833 6.11472702906792 6.26454381209421 P P P LNCV6_127347_PI430048170 mRNA
GTCACAAAGTCTTCAGTAACGCTACAACCATTGCAAATCATTGGAGAATCTATAATGAAT NM_198457RefSeq chr19 - 52765494 52786781 ZNF600 162966 zinc finger protein 600
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138008_PI430048170 0.1288880293274741.35798990683304 4.62664530469798 4.37345646560516 4.01336339682101 P P P 3.78839808246168 3.9751865740337 3.98201532776768 P P P LNCV6_138008_PI430048170 mRNA
TTCTTATTAGACATCCCAGGCCTCCTGGTATTCCATGGAATTTGAAAAGAGACTGGCACC NM_000137RefSeq chr15 + 80152890 80186582 FAH 2184 fumarylacetoacetate hydrolase (fumarylacetoacetase)
GO:0004334|GO:0034641|GO:0006559|GO:0044281|GO:0006572|GO:0006527|GO:0046872|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142069_PI430048170 0.00257723215991181 1.52975014916492 8.4855023010108 8.68541780791528 8.51679254835378 P P P 8.05287005233531 7.96926994975173 7.824625095292 P P P LNCV6_142069_PI430048170 mRNA
ATGCACCTTAACTTCATGGATGAAAAGGATCGGATCATCACAGCCTTCTACAACGAAGCC NM_005528RefSeq chr11

+ 64230280 64234281 DNAJC4 3338 "DnaJ (Hsp40) homolog, subfamily C, member 4"
GO:0006986|GO:0005739|GO:0005515|GO:0016020|GO:0006457|GO:0051082|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_92188_PI430048170 0.541313551399291 1.06310648110927 8.10612834353383 7.81323884968784
7.87900023402053 P P P 7.73372140827609 8.04549566634956 7.74903372924696 P P P
LNCV6_92188_PI430048170 mRNA
TTGGACGCTGTCCTGCACTTCAGGTGCAAGCTGGGCTCCTGTTACATACTGGACAGACCA NM_001078172 RefSeq
chrX - 135050932 135052191 FAM127B 26071 "family with sequence similarity 127, member B,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144131_PI430048170 0.501511478186387 0.668461981540394 0.368703545069656
0.431971357241823 0.364940669390264 A A A 1.77385239996212 0.305703653639416
0.287637398700718 A A A LNCV6_144131_PI430048170 mRNA
ATCTAAAGATGTTTAGGGAAGAGCTCGACTAAAGAACAATGAAATAAATGGTCCAAGGGG NM_007365 RefSeq
chr1 - 17066760 17119453 PADI2 11240 "peptidyl arginine deiminase, type II"
GO:0018101|GO:0005737|GO:0010848|GO:0070100|GO:0021762|GO:0030331|GO:0005509|GO:0035327|GO:0004
668|GO:0048096|GO:0070062|GO:0030520 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131804_PI430048170 0.00836211044839236 0.4916007246017887.2989689233978
6.84776568529307 7.34620122620204 P P P 8.058669422713 8.13207056309838
8.40280196154545 P P P LNCV6_131804_PI430048170 mRNA
GCTTATTGTATTAGTTTTAGATGCTGGCACTGCATGTGCTCTGTTTATTCTGATTTTACT NM_004660 RefSeq chrY +
12904785 12920478 DDX3Y 8653 "DEAD (Asp-Glu-Ala-Asp) box helicase 3, Y-linked, transcript variant 2"
GO:0005737|GO:0016020|GO:0003723|GO:0008152|GO:0004386|GO:0005634|GO:0005524|GO:0003677 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71541_PI430048170 0.000905410498501024 1.94531324337688 6.11806477592233
6.31338992662444 6.08084750906631 P P P 5.16845250092101 5.30196979068 5.16868956573739 P
P P LNCV6_71541_PI430048170 mRNA
AGATCACAGGGCCAGAGGAGGCGGACCGGCCCCCTTCAATGTCCAGTCATGATACAGCCT NM_005873 RefSeq
chr20 - 64073180 64079492 RGS19 10287 "regulator of G-protein signaling 19, transcript variant 1"
GO:0005515|GO:0005794|GO:0005886|GO:0007264|GO:0005834|GO:0030136|GO:0006914|GO:0038032|GO:0043
547|GO:0005903|GO:0001965|GO:0005737|GO:0007186|GO:0016020|GO:0005096 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_116785_PI430048170 0.153730269762064 1.31653194709542 5.55350401813753
5.61670830943393 5.81138385650778 P P P 4.86324509331157 5.35469816039128
5.51012574701704 P P P LNCV6_116785_PI430048170 mRNA
TTACGAATACGTGTTGTAGTCATCCATTAAGCAATCCAGCCGAGCTTGAGGAAAGTGACG NM_004508 RefSeq chr10
- 1040023 1049121 IDI1 3422 isopentenyl-diphosphate delta isomerase 1
GO:0006695|GO:0035634|GO:0000287|GO:0030145|GO:0044281|GO:0008299|GO:0004452|GO:0046872|GO:0050
992|GO:0005829|GO:0005739|GO:0016787|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129765_PI430048170 0.782788964848354 1.53855802831842 0.44310763314708
0.475761960383995 3.11761509387453 A A P 0.412838780456233 0.407675066597775
2.25428886402775 A A A LNCV6_129765_PI430048170 mRNA
CCATGGATTGCTTAAAGTTCTCTCAGCTGTCCTCGAGTTTAAATTGTTTTAAAAATTGTC NM_001017930 RefSeq
chrX - 27977992 27981449 DCAF8L1 NA DDB1 and CUL4 associated factor 8-like 1 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_127418_PI430048170 0.0759500165421482 0.588066831555066 2.5596253491103
2.82858873073441 2.14956450203972 A A A 3.56836078932508 2.78741710550036 3.4440742139836
P P P LNCV6_127418_PI430048170 mRNA
GGGTCAGGGACAGGGATGGAGTGGTTGTTTTATGTTTACATTTTTAATAAGTAAAATAGA NM_001136049 RefSeq
chr3 + 197960199 198043720 LMLN 89782 "leishmanolysin-like (metallopeptidase M8 family),

transcript variant 1"
GO:0005811|GO:0007067|GO:0005737|GO:0016020|GO:0006508|GO:0007155|GO:0004222|GO:0005925|GO:0046
872|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141613_PI430048170 0.00169667124702001 0.2986565274341382.38393616475029
2.52226859628064 1.95577979944339 A A A 4.34271378777075 3.84885542196489 3.9071541038363
P P P LNCV6_141613_PI430048170 mRNA
CCAAAGCAGGCTGGTTGGCATAATATGTAATTTGAAAAATAAAATCTTATCTTGCAGCAC NM_001199397 RefSeq
chr4 - 169393269 169612627 NEK1 4750 "NIMA-related kinase 1, transcript variant 1"
GO:0005515|GO:0005813|GO:0018108|GO:0005634|GO:0005524|GO:0046872|GO:0006974|GO:0042384|GO:0000
187|GO:0007067|GO:0005737|GO:0004672|GO:0000165|GO:0004674|GO:0010212|GO:0004713|GO:0000242|GO:0
004708|GO:0051301. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132186_PI430048170 0.000202096959132581 3.51214004361213 4.09213948592128
3.74808798757161 3.97202015851894 P P P 2.30941157170342 2.077185392542
1.99033482198679 A A A LNCV6_132186_PI430048170 mRNA
CCAAGGATGGAGAACAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAAT NM_017625RefSeq
chr1 - 160876539 160885170 ITLN1 55600 intelectin 1 (galactofuranose binding)
GO:0043235|GO:0046326|GO:0001934|GO:0030246|GO:0045121|GO:0031526|GO:0031225|GO:0009624|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129310_PI430048170 0.4226701685245350.7725589615238163.74902181433887
2.14435647220013 2.22586688107682 P A A 3.67853000076194 3.18093173424434
2.86949101214893 P P P LNCV6_129310_PI430048170 mRNA
TTCCTATCTCACCCCCCGAAACACCACCCTAAAGTTGGATTTTTACATATAAATAAAAAA NM_152989RefSeq chr12
- 23532296 24562449 SOX5 6660 "SRY (sex determining region Y)-box 5, transcript variant 2"
GO:0005515|GO:2000741|GO:0003700|GO:0006366|GO:0044212|GO:0046982|GO:0051216|GO:0048709|GO:0000
981|GO:0071560|GO:0021953|GO:0001701|GO:0045165|GO:0045944|GO:0061036|GO:0032332|GO:0045892|GO:0
060164 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138921_PI430048170 0.00752151854971709 1.54007853880368 8.43372354937956
8.74875080743744 8.56028098543249 P P P 8.09063866470946 7.98138870582726
7.80495702613169 P P P LNCV6_138921_PI430048170 mRNA
TTGTCATTTGATCCATGTTCAAGACCCTTGAGGTATTGTTTCATCATTTCTGTATTGTCT NM_001113411 RefSeq chr1
+ 59296952 59762731 FGGY 55277 "FGGY carbohydrate kinase domain containing, transcript variant 1"
GO:0016310|GO:0003674|GO:0016301|GO:0005975|GO:0016773|GO:0005575|GO:0070050 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136751_PI430048170 0.00676830909779856 0.6367616872195155.59192805178615
5.47533320319169 5.70550738293133 P P P 6.06500572168445 6.26288214463124
6.38923452115132 P P P LNCV6_136751_PI430048170 mRNA
GAGTGGTGTCTTACTCCTTTGTTTATAAGTGAATGATTGTGCATGTTTTGTATGTCATAG NM_017719RefSeq chr3
+ 43286511 43351142 SNRK 54861 "SNF related kinase, transcript variant 1"
GO:0000287|GO:0004674|GO:0030099|GO:0006468|GO:0005634|GO:0005524 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136921_PI430048170 0.4056770579918991.68486174831562 0.394748444261121
2.05954933150822 0.59080319472296 A A A 0.4795011705120260.375621675943847
0.542672099548773A A A LNCV6_136921_PI430048170 mRNA
TACCGCATCAGCCTAAAGAAGTTCTGCAAGAAGGACTATGCGGTGCAGGTGGCGGTGGGT NM_006181RefSeq
chr16 + 2471498 2474145 NTN3 4917 netrin 3
GO:0042692|GO:0003674|GO:0051149|GO:0005794|GO:0007411|GO:0005578|GO:0005102|GO:0005575 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106371_PI430048170 0.199852530594047 1.83245337899529 1.44811095183397 0.2945010155501
1.58574983703451 A A A 0.3067289253787550.305614310762832 0.404345659083368A A A

LNCV6_106371_PI430048170 mRNA
AGATCTTCTCCGTTTCAGAGGACTGCCTGGTCCTCAACGTCTATAGCCCAGCTGAGGTCC NM_024922RefSeq chr16
+ 66961228 66975149 CES3 23491 "carboxylesterase 3, transcript variant 1"
GO:0052689|GO:0008152|GO:0005788|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143104_PI430048170 0.5592129711932291.23421198445362 3.88280996848737
2.89892706971613 3.91197226499689 P A P 2.14695282058298 3.87217570607709
3.47505037202515 A P P LNCV6_143104_PI430048170 mRNA
CCCCCTTTAGCAGGGATTCCTTTTTAAAGCTATTTTGGCTGGAATACAGGTGACTTTTGT NM_014746RefSeq chr2
+ 6917391 7044178 RNF144A 9781 ring finger protein 144A
GO:0016567|GO:0005794|GO:0005886|GO:0016874|GO:0008270|GO:0016021|GO:0030659 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144248_PI430048170 0.1377981510970581.3470995544499 4.55293279268834
5.13060597982611 4.81343618555383 P P P 4.62677056803159 4.49177112754955 4.095861845611
P P P LNCV6_144248_PI430048170 mRNA
CCCTGCCAAGGTCTTCACTGTATATATTTTGTGTGTTCTTCTGAAACTCTTGATTTCTTA NM_025188RefSeq chr1 -
117111054 117121789 TRIM45 80263 "tripartite motif containing 45, transcript variant 1"
GO:0060348|GO:0005737|GO:0008270|GO:0005654|GO:0045171 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127142_PI430048170 0.0147885053664071 0.47936688910222 0.324726400558102
0.2430381701176280.303878999059808A A A 1.09971353085582 1.33626405657364
1.57947569008057 A A A LNCV6_127142_PI430048170 mRNA
GCTATAAGCAAATTAACAAGAAACAGCAGCACTATTTTCCTCTTTTCTTAAACACGAAGG NM_032374RefSeq chr14
+ 103562956 103592173 APOPT184334 "apoptogenic 1, mitochondrial, transcript variant 1"
GO:0043280|GO:0005739|GO:0090200|GO:0034393|GO:0097193 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138083_PI430048170 0.0256178414805961.51255655734833 11.6147210384529
11.6656981741189 11.6116806562769 P P P 11.2296906563112 10.9619690868699
10.8872336915785 P P P LNCV6_138083_PI430048170 mRNA
TGCTCCGGCATTCAGTACCTGCTTCTTCCAGAGAAATAAAGTTAGTTTCTATTTTATGTTNM_005781RefSeq chr3 -
195863364 195909009 TNK2 10188 "tyrosine kinase, non-receptor, 2, transcript variant 1"
GO:0005515|GO:0030424|GO:0005154|GO:0005886|GO:0007264|GO:0030136|GO:0050731|GO:0005634|GO:0051
427|GO:0046872|GO:0030154|GO:0030425|GO:0030426|GO:0005737|GO:0005912|GO:0042127|GO:2000369|GO:0
043025|GO:0038083|GO:0030659|GO:0070436|GO:0050699|GO:0043086|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138273_PI430048170 0.28319238921563 1.51361959174864 0.396446501290558
1.50004074137334 1.49269128303281 A A A 0.3396901600432050.532116605747043
0.915322536465272A A A LNCV6_138273_PI430048170 mRNA
TTTTCTCTGTTTTACAAATGTCCCCCGTACGGCCAAGTGCATCCTGGTATTTCAGAAATG NM_001195081 RefSeq
chrX + 9967357 9968002 CLDN34 NA uncharacterized LOC100288814 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_140240_PI430048170 0.3688081047707870.9398603937349790.349953031546007
0.3769235074907460.32575991647581 A A A 0.3693404720786250.585353418110323
0.35511603119705 A A A LNCV6_140240_PI430048170 mRNA
TAAAATATCGATCTTTACACAATACACTTGAACTGTGGAATAAAGCAGGACCAGATGTGG NM_001278674 RefSeq
chr13 + 113895102 113921317 LINC00452 NA long intergenic non-protein coding RNA 452 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134165_PI430048170 0.4730151013033310.7775346554470522.93119766515598
2.46343543839381 1.7535386465677 A A A 3.38057010980891 2.42996462357904

2.44254510224334 P A A LNCV6_134165_PI430048170 mRNA
GTACAGTCTGTAGTTAGGAGGTATAGCCTATAGCTTATGTTAAATGGTTGAAATGGTTCT NM_014722RefSeq chr6
- 24804280 24911170 FAM65B 9750 "family with sequence similarity 65, member B, transcript
variant 1"
GO:0005739|GO:0005515|GO:0005737|GO:0060171|GO:0007517|GO:0007605|GO:0030175|GO:0005856|GO:0030
154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142053_PI430048170 0.1123155090652310.8570182133301 15.9891988555118
15.8808654501598 15.8461962383639 P P P 15.9508637156938 16.1944890618724
16.2271187656887 P P P LNCV6_142053_PI430048170 mRNA
GCCTCCCCCGCCACCTGTGTGTTCTTTTGATACATTTATCTTCTGTTTTTCTCAAATAAA NM_001540RefSeq chr7 +
76302557 76304297 HSPB1 3315 heat shock 27kDa protein 1
GO:0005515|GO:0006986|GO:0043130|GO:0010467|GO:0030018|GO:0035924|GO:0005886|GO:0071901|GO:0032
731|GO:0038033|GO:0006928|GO:0005634|GO:0005615|GO:0042802|GO:0005829|GO:0035556|GO:0005737|GO:0
001895|GO:0005080|GO:0005856|GO:0043122|GO:0070062|GO:0048010|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134889_PI430048170 0.8049396541095371.06515839952998 1.97176124844568
2.74263145885993 2.45390852227781 A A A 2.44223583793819 2.01928013281249
2.49087083171146 A A P LNCV6_134889_PI430048170 mRNA
CCTCTACCACCCAACACCCTGGGCTCACTTTTGGATAGGAAATAAACTCTTTATTTTTGT NM_012285RefSeq chr17
- 42156891 42181278 KCNH4 23415 "potassium channel, voltage gated eag related subfamily H,
member 4"
GO:0023014|GO:0000160|GO:0005886|GO:0008076|GO:0005249|GO:0042391|GO:0007268|GO:0034765|GO:0006
813|GO:0000155|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130067_PI430048170 0.00859025610669259 0.60585574556668911.5821736647636
11.4633415556064 11.7198515329525 P P P 12.2447168339574 12.1517591601491
12.5228865964714 P P P LNCV6_130067_PI430048170 mRNA
GAGCTGAATTTGATAAAAACCCAAAATACAGCTATGAAGTGCTGGGCAAGTTTACTTTTT NM_021027RefSeq chr2
+ 233671897 233773305 UGT1A9 NA "UDP glucuronosyltransferase 1 family, polypeptide A9" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128789_PI430048170 0.00285404977005544 0.61100478148094111.9683910421929
12.0643013124595 11.8268661603486 P P P 12.6665830782026 12.7264888521682
12.6060387857883 P P P LNCV6_128789_PI430048170 mRNA
AAAGTCCGGTGACCGCTGCCCAGACACAGACTGGCAATAAACTCCTACTAAATCCCTCCG NM_183233RefSeq
chr11_KI270831v1_alt + 131931 157362 SLC22A18 5002 "solute carrier family 22, member 18, transcript
variant 2"
GO:0007588|GO:0005886|GO:0015695|GO:0005635|GO:0055085|GO:0005737|GO:0016324|GO:0016020|GO:0006
855|GO:0016021|GO:0015893|GO:0015238|GO:0031625|GO:0015293 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132750_PI430048170 0.4265994128448481.05330513962668 0.293319950733344
0.2977775336113930.511465340440107A A A 0.30874939014318 0.269027539289341
0.310581480366018A A A LNCV6_132750_PI430048170 mRNA
CCACAGGAACAGGAGGCCATCGGCTATGAGTACTCCGAGATCAACATCCCCAAGTGAGAA NM_053003RefSeq
chr19 - 51491226 51501789 SIGLEC12 89858 "sialic acid binding Ig-like lectin 12 (gene/pseudogene),
transcript variant 1" GO:0030246|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_137667_PI430048170 0.2332425269376060.8328412221549768.05472368976256
7.85725946721011 7.48300998037719 P P P 8.13644493710362 8.16743863613753
7.92836755923272 P P P LNCV6_137667_PI430048170 mRNA
ATCAGCCCCTCCTGAGTGGCCAGCCTTTCCCCCTGTGAAAGCAAAATAGCTTGGACCCCT NM_130760RefSeq chr19

+ 496489 505343 MADCAM1 8174 "mucosal vascular addressin cell adhesion molecule 1, transcript variant 1"
GO:0005886|GO:0007568|GO:0050901|GO:0007165|GO:0006955|GO:0007160|GO:0016020|GO:0007229|GO:0030198|GO:0030216|GO:0050776|GO:0002687|GO:0043113|GO:0034113|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136554_PI430048170 0.0466273934101311 0.7734873958389551 2.7191703892771 2.7697972517675 3.0022297687747 P P P 3.1670495058365 3.0530651934257 3.3795694997691 P P P LNCV6_136554_PI430048170 mRNA
CCCATCCTTTGGGTTGTGGGTTTTTTGTTTTCTCCAAATAAATCTGATCTTTAAAGTTCA NM_001300821 RefSeq chr12 + 53006257 53042209 EIF4B 1975 "eukaryotic translation initiation factor 4B, transcript variant 1"
GO:0005515|GO:0008286|GO:0010467|GO:0016281|GO:0003723|GO:0003743|GO:0006412|GO:0006413|GO:0005829|GO:0000166|GO:0006446|GO:0044267|GO:0000289|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132886_PI430048170 0.3843450291254112 .14523772512837 0.289010723597057 2.80764604228238 1.77479710792616 A A A 0.9391999932721780.289243084877945 1.19464949684739 A A A LNCV6_132886_PI430048170 mRNA
ACTTAATGTCCATGTGACTCTTTTTCACATGCAATAAACTTTGCTTTGTTTCAATCTGGG NM_002470 RefSeq chr17 - 10628525 10657309 MYH3 4621 "myosin, heavy chain 3, skeletal muscle, embryonic"
GO:0030048|GO:0005516|GO:0030049|GO:0042623|GO:0006200|GO:0045214|GO:0030326|GO:0005524|GO:0030017|GO:0005829|GO:0000146|GO:0032982|GO:0051015|GO:0007517|GO:0060325|GO:0003009|GO:0005859|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124816_PI430048170 0.7437029622999191.07055258131102 0.303753866317795 0.2685132236174510.867278541995553 A A A 0.3639184490955670.250468902010915 0.590408321799812 A A A LNCV6_124816_PI430048170 mRNA
CCATAGAGGACAGCAACTGGTGATTGTTTCAGAGAAATAAACTTTGGTGGAAATATTGTT NM_002118 RefSeq chr6_GL000251v2_alt - 4346823 4353265 HLA-DMB 3109 "major histocompatibility complex, class II, DM beta"
GO:0019886|GO:0006955|GO:0002399|GO:0042102|GO:0031902|GO:0002503|GO:0023026|GO:0042613|GO:2001190|GO:0016021|GO:0005765 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137352_PI430048170 0.1078748743984270.5746916856100063.68709821136424 2.54585933940137 2.91610996858813 P A P 3.70568011933227 3.80508123013507 4.22362977443566 P P P LNCV6_137352_PI430048170 mRNA
GCAGTTGCTGATATACTTCCCCCTAGTACTTCAACTGCAGATTATTAACTAGAGTTTAGT NM_025000 RefSeq chr2 + 171434250 171485052 DCAF1780067 "DDB1 and CUL4 associated factor 17, transcript variant 1"
GO:0016567|GO:0005730|GO:0080008|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95161_PI430048170 0.9066579793152741.01011549716659 3.17698324489861 2.68783230886594 2.88129688423699 P A P 2.47321171006528 3.2279110075449 2.9457829264295 A P P LNCV6_95161_PI430048170 mRNA
TAGACAAAAAGACAGATGAAAGCCTTACCAAGTACTTCCATGGCTTTGTGGCCATGTGCC NM_001170629 RefSeq chr14 - 21385193 21431708 CHD8 57680 "chromodomain helicase DNA binding protein 8, transcript variant 1"
GO:0005515|GO:0008013|GO:2000270|GO:0030178|GO:0005634|GO:0035064|GO:0002039|GO:0042393|GO:0071339|GO:0045944|GO:0045945|GO:0032508|GO:0090090|GO:0060070|GO:0008094|GO:0043044|GO:0048565|GO:0000122|GO:0005524|GO:0003677|GO:0001701|GO:0006351|GO:0003678|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131591_PI430048170 0.6909999564422231.11494558646515 0.302470512571554 1.09248361242405 0.388112646488892 A A A 0.3508188285116410.334331963993204 0.728018590782366 A A A LNCV6_131591_PI430048170 mRNA
TACAGAAAAGGAGAAAAGGGTAGTACATTTCATAATTAGAGATAACCCTGTACTAGTGAG NM_001008388 RefSeq

chr4 + 102868977 102892806 CISD2 493856 CDGSH iron sulfur domain 2
GO:0005515|GO:0000422|GO:0005783|GO:0051537|GO:0005741|GO:0010259|GO:0042803|GO:0046872|GO:0043234|GO:0016020|GO:0005789|GO:0010506|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132061_PI430048170 0.0184823677199181.23046457336812 6.73901240781224 6.89977292309793 6.91641507778519 P P P 6.65937248020999 6.5011981185202 6.49760145542205 P P P LNCV6_132061_PI430048170 mRNA
TTTTTTAAACGCTCTTGGGTTTTATGTCCGCTGCTTCTTGGTTGCCGAGACAGAGAGATG NM_139159RefSeq chr19 - 4675230 4723843 DPP9 91039 dipeptidyl-peptidase 9
GO:0005737|GO:0016020|GO:0004177|GO:0006508|GO:0008236|GO:0005634|GO:0042802|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142748_PI430048170 0.2132040569804780.7195972891108632.84258544687824 2.46704305563552 2.13070731163076 A A A 3.41398448871149 2.68539540114517 2.73250166924935 P P P LNCV6_142748_PI430048170 mRNA
GCCCTGGGGTTTCTGCATCAATTAGAATATCATTAATTTCTTTGTAACCAAGTGAAAAAC NM_178539RefSeq chr12 - 61708247 62192839 FAM19A2 338811 "family with sequence similarity 19 (chemokine (C-C motif)-like), member A2" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125425_PI430048170 0.3543336161172050.98025544539901 0.293605361657374 0.3161766623737980.364923865484432A A A 0.3821201329085080.321367219931695 0.357805952893827A A A LNCV6_125425_PI430048170 mRNA
GATACCCCTTCTACTGGTTTTTCCATCATTCATCCTACGTCTTCTGAAGGTCAAGTTCCANM_006269RefSeq chr8 + 54616066 54630834 RP1 6101 retinitis pigmentosa 1 (autosomal dominant)
GO:0005515|GO:0008017|GO:0042461|GO:0035082|GO:0060041|GO:0046549|GO:0007603|GO:0005875|GO:0005930|GO:0046548|GO:0005874|GO:0071482|GO:0045494|GO:0035556|GO:0001917|GO:0035845|GO:0032391|GO:0007601|GO:0001750. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132325_PI430048170 0.0125168046480977 0.6832992261022761 0.5561715265021 10.5895467556537 10.7675396280637 P P P 11.1716556353746 11.2007535519411 11.1979698970422 P P P LNCV6_132325_PI430048170 mRNA
ACTCATCACGGCCATCTTTGTTGTAACCATTTCTGTGTTTATAAATGCATTATCTCTGAGNM_001135734 RefSeq chr12 - 6666476 6689572 ZNF384 171017 "zinc finger protein 384, transcript variant 7"
GO:0043565|GO:0017124|GO:0045944|GO:0050714|GO:0005634|GO:0005925|GO:0046872|GO:0006351|GO:0006913 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108735_PI430048170 0.3644372211396971.37002970012299 1.3653940209041 0.34222162423464 0.452812411246024A A A 0.3476401089405860.313342666825918 0.367235177506822A A A LNCV6_108735_PI430048170 mRNA
AAAGATTCAGAATCTGGAGCAGAAGCTTTCTGGAGATTCTAGGGCCTGCAGAGCTAAATC NM_001242811 RefSeq chr6 + 89562317 89633834 ANKRD6 22881 "ankyrin repeat domain 6, transcript variant 2"
GO:0005737|GO:2000096|GO:0046330|GO:0005634|GO:0090090 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62079_PI430048170 0.5971018095457930.9235541872959881 0.1823687563076 10.0918662571445 10.2263714483218 P P P 9.9923115691995 10.269307316486 10.5355021976323 P P P LNCV6_62079_PI430048170 mRNA
AGAGCTGAAAACCGCAGGCTTGTTGTGTTAAGTTACAAGGAAAATGGATTTGGTAATTAA NM_006305RefSeq chr15 - 68778535 68820922 ANP32A 8125 "acidic (leucine-rich) nuclear phosphoprotein 32 family, member A"
GO:0035556|GO:0005515|GO:0010467|GO:0048471|GO:0006355|GO:0005737|GO:0005783|GO:0005654|GO:0005634|GO:0006351|GO:0006913 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144629_PI430048170 0.0225732661169025 1.81530589822686 3.95193353893758 4.07516905929596 3.50460145293465 P P P 3.08346069051682 3.09371467394812 2.81750360776978 P P P LNCV6_144629_PI430048170 mRNA

TTCAGAACCAGCTGGCGCTGCTGCAGAAGGAACCTTGCGGCCCAGATGAGGAAGGAACCC NM_021920RefSeq
chr11_KI270832v1_alt - 156211 157072 SCT 6343 secretin
GO:0097150|GO:0021542|GO:0043524|GO:0005179|GO:0008542|GO:0005576|GO:0030157|GO:0005575 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139806_PI430048170 0.00210993580821354 0.4245859605439574.77085238614807
4.40635990519827 4.66597634109347 P P P 5.74665687050444 5.90944838922677
5.91250756018596 P P P LNCV6_139806_PI430048170 mRNA
ATTGTGGCTTGGAATGTGGTTCAGCCATTTACTCACTTATACAAATATTCAGAAGTGTAA NM_001166304 RefSeq
chr3 + 196712373 196736005 PIGX 54965 "phosphatidylinositol glycan anchor biosynthesis, class X,
transcript variant 1" GO:0006501|GO:0016254|GO:0005789|GO:0016021|GO:0044267|GO:0043687 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133641_PI430048170 0.761189231784983 1.00402546319832 0.698816920628037
2.62450854756162 2.68885193031839 A A A 2.04176520453131 2.41941493126873
2.23689095641275 A A A LNCV6_133641_PI430048170 mRNA
GGTTAAAGAGTTTTGCTGGGCATTGAGATAATCTGACAGCATCTCCACTTCCTGTTTTTT NM_001198670 RefSeq
chr11 + 120325128 120333679 TMEM136 219902 "transmembrane protein 136, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127444_PI430048170 0.0189872935908302 1.47964596478016 7.12794120200415
7.15085022391475 7.14773491835067 P P P 6.70440410524571 6.58794959205511
6.42494850603443 P P P LNCV6_127444_PI430048170 mRNA
TTTGATGAACAGACAGCCGATGACTGGGATGTGGACATGAGTGTGTACTATGACAGAGAT NM_022078RefSeq chr1
- 26890487 26900471 GPATCH3 63906 G patch domain containing 3 GO:0008150|GO:0003676 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139244_PI430048170 0.0338973576975081 .30285068348411 10.4109568951993
10.4853699676026 10.1991487821809 P P P 9.92938728363763 10.0488796676923
9.98476667642566 P P P LNCV6_139244_PI430048170 mRNA
GTCCTGGGCCGTGTTAAGCACCTTTTGTAGAAATCGTATTTTTATTAAAACATCAAATCT NM_012318RefSeq chr4
- 1811478 1856247 LETM1 3954 leucine zipper-EF-hand containing transmembrane protein 1
GO:0005739|GO:0005515|GO:0005509|GO:0005743|GO:0016021|GO:0042407 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133778_PI430048170 0.825797926297508 1.08309133566459 1.62130468592895
2.52573176775567 1.94813339090225 A A A 2.00391190917336 1.98395605387672
1.90822604118069 A A A LNCV6_133778_PI430048170 mRNA
TACAGCATACGGAACAAGGATATGAAGGCAGCCCTGGGGAAGCTCATCGGCAAAGTGGCC NM_001004713
RefSeq chr19 + 15087065 15088133 OR1I1 NA "olfactory receptor, family 1, subfamily I, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143673_PI430048170 0.313938262894227 1.12133094039276 5.13731203972671
5.35187634165881 5.01892358016474 P P P 5.18185074482138 5.01403706446807 4.8130035934883
P P P LNCV6_143673_PI430048170 mRNA
CAGCCAGGCCTCTCGGGTTCTCTCTTTTTTAAATGTCGAAATAAACTTCTTACAAATGAC NM_020064RefSeq chr9
+ 132582605 132590253 BARHL1 56751 BarH-like homeobox 1
GO:0043565|GO:0043524|GO:0001077|GO:0045944|GO:0007605|GO:0030901|GO:0005634|GO:0001764|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135680_PI430048170 0.467662279385372 0.697932235926409 2.16171863267414
2.59380487632737 1.76119100569442 A A A 3.08396992510025 3.04047174395261
1.68282638348292 P P A LNCV6_135680_PI430048170 mRNA
CAAAGTTAGGCCCTGGCTCAAACACTGTGGGTAGCAGATTTGAAATAAATTTAAATTGCA NM_001287392 RefSeq
chr13 - 75525218 75537872 COMMD6 170622 "COMM domain containing 6, transcript variant 3"
GO:0005515|GO:0005737|GO:0051059|GO:0032088|GO:0005634 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_127835_PI430048170 0.3042609216126130.6294514920414143.53766069190075
3.54372227144935 3.47844761687694 P P P 4.75900123836429 4.12100227292952 3.3514480045086
P P P LNCV6_127835_PI430048170 mRNA
ATGTTCTTAAGCACAGGGACTGTATCATGCAGGGGCCAATAAAGCTCAAGAAAACGAGTA NM_001032296 RefSeq
chr13 - 98450198 98577151 STK24 8428 "serine/threonine kinase 24, transcript variant 2"
GO:0023014|GO:0005515|GO:0042542|GO:0030336|GO:0008631|GO:0005730|GO:0097194|GO:0006915|GO:0005
634|GO:0005524|GO:0048679|GO:0046872|GO:0006921|GO:0005829|GO:0007165|GO:0005737|GO:0046777|GO:0
004672|GO:0016020|GO:0004702|GO:0004674|GO:0005654|GO:0006468|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_108146_PI430048170 0.4549728483593571.09223721603614 8.87109728700424
9.19106489150696 9.25276527452921 P P P 8.96561134325136 8.83592128542855
9.14329251651702 P P P LNCV6_108146_PI430048170 mRNA
AACCAGGAACTGCTTTTTCTTTTCCTGCTGAGTACTGCTAATAAAAGTGCTATTATCTGC NM_015014RefSeq chr1
- 235131182 235161256 RBM34 23029 "RNA binding motif protein 34, transcript variant 1"
GO:0000166|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99943_PI430048170 0.5023918285409810.8646840393934781.68147760168128 1.54705187735907
2.40718562815189 A A A 1.76045126241878 2.28324391177879 2.31258928100189 A A A
LNCV6_99943_PI430048170 mRNA
AGATAACCTTCATTGTGGAAGACGTCAACGACAATCCTGCCACATGCCAAAAGTTCACCT NM_152750RefSeq chr7
+ 105963210 106036431 CDHR3 222256 "cadherin-related family member 3, transcript variant 1"
GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129177_PI430048170 0.9143314676782471.00387178648348 7.74989791238357
7.80092879666162 7.79474520080096 P P P 7.84168384667576 7.85245543511252 7.6239220823827
P P P LNCV6_129177_PI430048170 mRNA
GCATGGTTCAGTCTTAATAGCAGTTCAAGAGCTTCTCTGATAAAGGTTTCTTTTTAAACA NM_014347RefSeq chr19
+ 58467044 58473578 ZNF324 25799 zinc finger protein 324
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137968_PI430048170 0.2229531654936990.8408939466469665.60049644548508
5.48468075881139 5.71979027812015 P P P 5.57390652111875 5.90711323436331
6.04396325025495 P P P LNCV6_137968_PI430048170 mRNA
CCCTTTCTGTAAAGCAAAATAATGTTTACACCTAATCTGTCTCTCAGGGATACCATATTA NM_152455RefSeq chr15
- 43358171 43370060 ZSCAN29 146050 zinc finger and SCAN domain containing 29
GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0003677|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106443_PI430048170 0.0151897349599757 0.4910414590196076.93751436024133
6.434564402953 6.69703466503402 P P P 7.79509091566844 7.7073880087022
7.68620040139234 P P P LNCV6_106443_PI430048170 mRNA
AACAACCAGGTCATCAACCTCACCACCCAGTATGCCTGGTCCGGCTGTCAGGTGGTATCA NM_173633RefSeq chr19
+ 42313324 42325062 TMEM145 284339 transmembrane protein 145
GO:0007186|GO:0016021|GO:0019236 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133496_PI430048170 0.7241265905259010.9074618926097734.17315382400222
4.02747861547737 3.46586211270111 P P P 4.49559529175798 3.90198785140623
3.64604108308446 P P P LNCV6_133496_PI430048170 mRNA
CAGGCTACCCTTATCTCCTCTGCACTTATGTTATCAATAAAGAGGCAAATTCTCAAAAAA NM_139282RefSeq chrX
- 120109052 120115937 RHOXF1 158800 "Rhox homeobox family, member 1"
GO:0043565|GO:0019953|GO:0006355|GO:0003700|GO:0030518|GO:0007276|GO:0007275|GO:0005634|GO:0003
677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_94833_PI430048170 0.2704397496225231.26195145845986 3.61829140463709 3.46720714823083
2.94250674838895 P P P 3.285365694787 2.92765111783924 2.85366533263765 P P P
LNCV6_94833_PI430048170 mRNA
AGGTGGACAGCAATGGGAGGGCCACGTGCCTCTAGTGAGTCTCCTGCTCAACTACTATGT NM_001304459 RefSeq
chr12 + 51888008 51891721 ANKRD33 341405 "ankyrin repeat domain 33, transcript variant 3"
GO:0005634|GO:0000122|GO:2000678|GO:0035914|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_67191_PI430048170 0.00915673745215992 0.4617363529595084.29947558678706
4.32614049969721 4.6414442970043 P P P 5.17977310545309 5.71164912544374
5.68616768846043 P P P LNCV6_67191_PI430048170 mRNA
GATGCAAATTTATAGGAGAAAAAACACTTTCAGATAAGAGGTGTTTGCTGGGATGGAAGA NM_017915RefSeq chr12
+ 102120177 102197520 PARPBP 55010 PARP1 binding protein
GO:0005515|GO:2000042|GO:0005737|GO:0006281|GO:0005654|GO:0003677|GO:0000785 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_36866_PI430048170 0.00652720551785823 0.5418689666448132.73556171006495
2.72186576033405 3.07624721286798 A A P 3.73769198855634 3.63198391451438
3.83728732233397 P P P LNCV6_36866_PI430048170 mRNA
GCTGTATAATTGGACTTAATAAAATGTTTAGAGGTACAGTAGGCATGACTTTGGGTAGAT NM_005734RefSeq chr11
+ 33257321 33357022 HIPK3 10114 "homeodomain interacting protein kinase 3, transcript variant 1"
GO:0006355|GO:0043066|GO:0006915|GO:0005634|GO:0005524|GO:0005737|GO:0004672|GO:0018105|GO:0004
674|GO:0016605|GO:0018107|GO:0006468|GO:0009299|GO:0043508 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128800_PI430048170 0.3851269494440891.13577786416617 12.4671579497256
12.4326788211697 12.3980183772743 P P P 11.8676864674112 12.3050491115185
12.5037046803371 P P P LNCV6_128800_PI430048170 mRNA
ACATGTAACCAATCAGTATCTTGTCAATATAGTCAGCCGATCGATCGACCTCACAAAAAA NM_001252039 RefSeq
chr17 - 42124975 42155044 RAB5C 5878 "RAB5C, member RAS oncogene family, transcript variant 3"
GO:0005515|GO:0005811|GO:0042470|GO:0005886|GO:0003924|GO:0048227|GO:0030139|GO:0005525|GO:0005
765|GO:0006886|GO:0043231|GO:0006184|GO:0030100|GO:0031901|GO:0032482|GO:0019003|GO:0005769|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137456_PI430048170 0.00843208184083752 2.36726133773088 8.01430609751703
8.56640293277546 8.22013443155653 P P P 6.94532972336882 7.1701517405527
7.00072298848578 P P P LNCV6_137456_PI430048170 mRNA
CTTTTGATTGCACAAGCCTTTGTTTTCAGTCCTAGTGAATAAAGTTGTGTTTTCTGGAAA NM_014353RefSeq chr16
+ 2148649 2154140 RAB26 25837 "RAB26, member RAS oncogene family"
GO:0005515|GO:0009306|GO:0005886|GO:0043001|GO:0031226|GO:0003924|GO:0005525|GO:0006904|GO:0006
184|GO:0045055|GO:0000139|GO:0035272|GO:0017157|GO:0032482|GO:0019003|GO:0019002|GO:0030667|GO:0
005768|GO:0030658. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133132_PI430048170 0.0090000502000168 0.3307730625948588.17966779152826
8.10318524226422 8.31164600224023 P P P 9.46233918055909 9.73414626088009
10.1181451437539 P P P LNCV6_133132_PI430048170 mRNA
GGCAACAGGACCTGTACATTGTCACATTGCATTATTTTTCTTCAAGCGTTAATAAAAGTT NM_003714RefSeq chr5
- 173314722 173329503 STC2 8614 stanniocalcin 2
GO:0048471|GO:0005794|GO:0005783|GO:0007566|GO:0006874|GO:0071456|GO:0043434|GO:0033280|GO:2001
256|GO:0005615|GO:0042803|GO:0030968|GO:0046697|GO:0005179|GO:0040015|GO:0046885|GO:0010629|GO:0
019899|GO:0006979|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55440_PI430048170 0.0867559384268963 0.8627830953961375.01991032820294
5.18185074482138 5.27658531148988 P P P 5.3714611695677 5.3259073257986
5.42947983342131 P P P LNCV6_55440_PI430048170 mRNA

TTGGACCAGTCAGCACAGCATGCCTGGTTGTATTAAAGCAGGGATATGCTGTATTTTATA NM_002389 RefSeq chr1 + 207752037 207795516 CD46 4179 "CD46 molecule, complement regulatory protein, transcript variant a"
GO:0005515|GO:0030449|GO:0005886|GO:0032733|GO:0035581|GO:0071636|GO:0007338|GO:0016323|GO:0043382|GO:0042102|GO:0006958|GO:0006508|GO:0016032|GO:0004872|GO:0008593|GO:0070062|GO:0004857|GO:0045296|GO:0005794|GO:0001848|GO:0009986|GO:0043086|GO:0045916|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132197_PI430048170 0.0629173479148334 0.6758246029905057.43151459752461 7.75896025580835 7.95897333141775 P P P 8.04318371522009 8.21757373565068 8.57996315070768 P P P LNCV6_132197_PI430048170 mRNA
AGAGCATTTGGGTTACTGCTTTTACTCTTTGGAAGCTGTTATCATCTGTATCTGCTTTAA NM_138287 RefSeq chr3 + 122564337 122575202 DTX3L 151636 "deltex 3 like, E3 ubiquitin ligase"
GO:0005515|GO:0042393|GO:0005737|GO:0004842|GO:0016874|GO:0008270|GO:0005654|GO:0005634|GO:0010390|GO:0006974|GO:0006302 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134114_PI430048170 0.01730035611078 0.62091614499509711.3320746951467 11.0577726853561 11.0287510062057 P P P 11.5646347535925 12.011083200071 11.8892341458437 P P P LNCV6_134114_PI430048170 mRNA
CTCTGTTGTAAATACCCCTCACGGAGGAAATAGTTTTGCTAAGAAATAAAAGTGACTATT NM_003378 RefSeq chr7 - 101162508 101165571 VGF 7425 VGF nerve growth factor inducible
GO:0030133|GO:0032868|GO:0009409|GO:0042593|GO:0006091|GO:0031410|GO:0051591|GO:0002021|GO:0005615|GO:0003674|GO:0019953|GO:0001541|GO:0005184|GO:0008083|GO:0030073|GO:0042742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134361_PI430048170 0.5472484983156050.9312189538070818.03265060421941 7.91069928800296 7.94641116142251 P P P 7.85665698453737 8.01875822829528 8.29165857704163 P P P LNCV6_134361_PI430048170 mRNA
GTTCATGTATGTAGGAGTTAAAATAGGCCAAACTGGAGAAATAAACGCATTCTGTCCACC NM_018073 RefSeq chr11 - 4598671 4608259 TRIM68 55128 "tripartite motif containing 68, transcript variant 1"
GO:0035035|GO:0004842|GO:0048471|GO:0005794|GO:0016874|GO:0019221|GO:0060765|GO:0005730|GO:0005634|GO:0050681|GO:0051865|GO:0005829|GO:0005737|GO:0005654|GO:0008270|GO:0060333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137584_PI430048170 0.491180253944623 1.82386993592456 0.35330734896523 2.65284447597404 0.958576069019003 A A A 1.35767445256164 0.419569812496693 0.393863071991921 A A A LNCV6_137584_PI430048170 mRNA
TACGTGCTCAACAGGAACCGGTACGGGGTGGAGCCACTGTGGAGGGCATCAGACTACGTG NM_001135580 RefSeq chr19 + 3539156 3544030 C19orf71 100128569 chromosome 19 open reading frame 71
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139577_PI430048170 0.0516195880094209 0.3141817306146861.31738752844179 0.5501495784050972.18081668748532 A A A 3.44029260544985 3.00058615610571 3.02959915039252 P P P LNCV6_139577_PI430048170 mRNA
GCAGTTTGGGAAGAAAGTGCTGCTGAAATTTCCAGAATTTAATTGATTGGTTACATAAAC NM_020666 RefSeq chr5 - 178602663 178627053 CLK4 57396 CDC-like kinase 4
GO:0046777|GO:0004674|GO:0043484|GO:0018108|GO:0005634|GO:0004712|GO:0004713|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135231_PI430048170 0.758209520909675 1.04651373881972 0.607169946200371 1.06981156170142 1.00420281485278 A A A 0.624265630933501 1.29215399125586 0.472743707987892 A A A LNCV6_135231_PI430048170 mRNA
ATTGCAGCAACAGCTCCAAGAAGTGCTCGGCAGGAGCCTCTCAATGGAGTCCACTTCCGA NM_144622 RefSeq chr1 - 155018526 155033781 DCST2 127579 DC-STAMP domain containing 2 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_126701_PI430048170 0.9378822617194570.9983337753690330.251635401244145
0.2629355177221830.546405228748946A A A 0.3778048995346650.317105732405416
0.391933752285245A A A LNCV6_126701_PI430048170 mRNA
AGAGCTGACAGTGCTTCTACACATTTCATCTAATTTAATATTCCTGGCATACCTTTAAGG NM_000145RefSeq chr2
- 48962156 49154527 FSHR 2492 "follicle stimulating hormone receptor, transcript variant 1"
GO:0008406|GO:0005515|GO:0008585|GO:0007186|GO:0005886|GO:0042699|GO:0004963|GO:0016021|GO:0007
292|GO:0007283|GO:0008584 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136743_PI430048170 0.36515224670894 1.05294997308704 0.317457129491324
0.3185401151631270.503513435570112A A A 0.3114378962730990.279172008148631
0.333141273713585A A A LNCV6_136743_PI430048170 mRNA
TTGTTGTTGCGAAAGCTAATTCCCTAGTATGAATAAACTTCAGACCTTGCTCTCAAAAAA NM_201631RefSeq chr15
- 43232594 43266857 TGM5 9333 "transglutaminase 5, transcript variant 1"
GO:0005737|GO:0018149|GO:0008544|GO:0003810|GO:0046872|GO:0006464 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_119688_PI430048170 0.0309608947891974 1.07938129459248 7.79767730355595
7.77556956979456 7.85390813665407 P P P 7.66912718546072 7.74716951530173
7.68013620059895 P P P LNCV6_119688_PI430048170 mRNA
AGTGTGTCTCTCTGATTGGGCTTCTAAATCAAAAGCCTGATGTTCGTGTCCCTCTCATAG NM_005730RefSeq chr12
- 57819926 57846964 CTDSP2 10106 "CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A)
small phosphatase 2"
GO:0005515|GO:0006470|GO:0001933|GO:2000134|GO:0005654|GO:0006987|GO:0044267|GO:0046872|GO:0030
968|GO:0008420 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141145_PI430048170 0.8719086984211421.09165011646121 1.64351421128577
1.58978984828143 0.378826762210276A A A 1.67239071687501 0.584947272193129
1.08611433801398 A A A LNCV6_141145_PI430048170 mRNA
AAAGCTTTCTGGGAGTTGTAGTTCTTATCCCGCGTGGAATGTTGGGAGATTGAGTTTTCG NM_017805RefSeq chr19
- 48720584 48740713 RASIP1 54922 Ras interacting protein 1
GO:0007165|GO:0048471|GO:0005795|GO:0010507|GO:0048754|GO:0001525|GO:0032319|GO:0001570 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126825_PI430048170 0.3236988038001990.8244190294684460.304107439609697
0.3708872142242410.317780256668077A A A 0.43731404231251 0.343672230564712
0.967142656007349A A A LNCV6_126825_PI430048170 mRNA
ACTACTAGCTCCACAACATCTTACCTACATGGCTTCTCTTTACTTTTTAACATTGAGTAT NM_001304507 RefSeq chr14
- 64486237 64505213 ZBTB25 7597 "zinc finger and BTB domain containing 25, transcript variant 1"
GO:0005515|GO:0010467|GO:0006355|GO:0005737|GO:0003700|GO:0005654|GO:0003677|GO:0046872|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128844_PI430048170 0.2864611253265431.13210837837867 9.31589385673727
9.45811582329032 9.6369651965317 P P P 9.38147330215659 9.06187531647382
9.42230326783155 P P P LNCV6_128844_PI430048170 mRNA
TTCTGCACAAACTTCACTACTTAGACAGTCTGAGTCTTTTTCTGTCTATCCATCTGTTTA NM_173810RefSeq chr11 +
62728479 62738636 TTC9C 283237 tetratricopeptide repeat domain 9C NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141745_PI430048170 0.1198310510350691.17147370287552 12.0274603252123
11.9739694750624 11.7277849119876 P P P 11.6473359480799 11.7862335462058
11.6225810614612 P P P LNCV6_141745_PI430048170 mRNA
GAAATGACAGTGGGCCCTGTAGCAGTGGCAGAATAAACTCAGATGTGTTCACAGAAAAAA NM_012254RefSeq
chr19 - 58498332 58512065 SLC27A5 10998 "solute carrier family 27 (fatty acid transporter),
member 5"
GO:0015245|GO:0000038|GO:0001676|GO:0005783|GO:0006699|GO:0030176|GO:0044281|GO:0032403|GO:0005

524|GO:0004467|GO:0043234|GO:0015911|GO:0009925|GO:0047747|GO:0046951|GO:0015721|GO:0005789|GO:0
008206|GO:0031957|GO:0006642 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130097_PI430048170 0.54017892044333 1.31228146473277 0.268097885191869
1.44130410538881 0.298656399789341 A A A 0.472522570941950.364270975586467
0.321474651910064 A A A LNCV6_130097_PI430048170 mRNA
ATGAAAAAATCATTGTAACACTTGATGGAGTGAAATTCCACGCCAGGCACAGAATTTTTT NM_197941 RefSeq chr5
- 65148735 65481877 ADAMTS6 11174 "ADAM metallopeptidase with thrombospondin type 1 motif, 6"
GO:0006508|GO:0005578|GO:0008270|GO:0004222|GO:0008237 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127595_PI430048170 0.00365256423333286 3.69008116102081 7.46397468540319
8.07473581631494 8.13780396854365 P P P 6.26554975846638 5.81826819072021
5.99726797857658 P P P LNCV6_127595_PI430048170 mRNA
CGTATAACATTGTCAAGTGGAAACATGCTGAAATCTATTAAACCATCTTTGTTTGTGGAA NM_000961 RefSeq chr20
- 49503873 49568170 PTGIS 5740 prostaglandin I2 (prostacyclin) synthase
GO:0005515|GO:0019369|GO:0006805|GO:0005783|GO:0019674|GO:0006767|GO:0005634|GO:0006769|GO:0044
281|GO:0005615|GO:0006690|GO:0004497|GO:0035360|GO:0001516|GO:0045019|GO:0071354|GO:0019371|GO:0
005506|GO:0071456|GO:0032088|GO:0097190|GO:0045766|GO:0006766|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142698_PI430048170 0.2733367477549 1.95522973670077 2.33097489539208
1.02470181745893 0.616798061144875 A A A 0.490321616374343 0.578987486226809
0.584601781869198 A A A LNCV6_142698_PI430048170 mRNA
GCTATTCAAGTCTACCAAACATCCAGGCAGTGAAAGAAGAAAGTAACAGAAAATGATGAA NM_144690 RefSeq
chr19 - 56383278 56393520 ZNF582 147948 zinc finger protein 582
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127789_PI430048170 0.3113722297921840.87945615416378 0.397959176928418
0.419561542996415 0.292921870312782 A A A 0.390712436656842 0.439284829121249
0.80336440973734 A A A LNCV6_127789_PI430048170 mRNA
AATGAAATTGAAAACGCCATGTGGCACCACAAAAGAGCTCTCTGTACTTTCCCCATGCTG NM_032289 RefSeq chr5
+ 139795820 139844463 PSD2 84249 pleckstrin and Sec7 domain containing 2
GO:0043547|GO:0005802|GO:0005086|GO:0030054|GO:0005543|GO:0030182|GO:0043025|GO:0032012|GO:0016
021|GO:0016192|GO:0030425 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73174_PI430048170 0.1899187184750820.7546136599360950.3535982522329630.353429536611452
0.384406843453524 A A A 0.806496056809867 1.04674819158693 0.379897054824907 A A A
LNCV6_73174_PI430048170 mRNA
AGCTATAAGGGAATTGGCCAATATGATATACAAGACAAGGTGAAGCCTCGGAAGTTATTC NM_015123 RefSeq chr3
- 69168782 69386304 FRMD4B 23150 FERM domain containing 4B
GO:0090162|GO:0005737|GO:0005856|GO:0005615|GO:0001726 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137426_PI430048170 0.4557827381637070.9523573175523680.287945452227279
0.431131191890107 0.299150399813425 A A A 0.519021830076557 0.420916120061638
0.284430111776081 A A A LNCV6_137426_PI430048170 mRNA
GATCTCAGCACCGATCGGAACTGTAAAGCTATAATCCCCAGAATTAAAGTTTTTATTATT NM_005835 RefSeq chr6
- 25912755 25930726 SLC17A2 10246 "solute carrier family 17, member 2, transcript variant 2"
GO:0005436|GO:0016020|GO:0005887|GO:0035435|GO:0035725|GO:0006796|GO:0006814 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_94847_PI430048170 0.0132869245541293 1.64075239956859 5.89662759382275
5.49152685006564 5.63994402398243 P P P 4.72293008959444 5.06099683100238
5.10141714316282 P P P LNCV6_94847_PI430048170 mRNA

TGGCTGGACTAGTGCTCAGTGACAATGACAGAAGCCTGTTGGAACGCTGGACTCGAATGG NM_139033 RefSeq chr17 + 19377720 19383544 MAPK7 5598 "mitogen-activated protein kinase 7, transcript variant 1" GO:0005515|GO:0070301|GO:0034142|GO:0071560|GO:0005634|GO:0051403|GO:0030154|GO:0005829|GO:0002756|GO:0005737|GO:0018105|GO:0045944|GO:0002755|GO:2001240|GO:0034115|GO:0034138|GO:0051019|GO:0036003|GO:0004707|GO:0051247|GO:0071499|GO:0048011|GO:0038124|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128898_PI430048170 0.346802579886681 1.06119217380749 9.81841009827537 9.86171661610767 10.0270754478564 P P P 9.90165532108086 9.74647641980465 9.80625415206007 P P P LNCV6_128898_PI430048170 mRNA
CTAAATAAGATGACGCTACTCCTCATAGCACCACAACCTGAATGTGTGTTCATATTTTTT NM_001304958 RefSeq chr12_KI270834v1_alt - 109952 119347 CCDC92 80212 "coiled-coil domain containing 92, transcript variant 3" GO:0005515|GO:0005814 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129327_PI430048170 0.440014098260263 0.967217413116614 8.04793257645317 8.10641707147697 7.95061975621304 P P P 8.06303854324638 8.14896815872128 8.03917422682418 P P P LNCV6_129327_PI430048170 mRNA
ATGTGCCCCGCACTGTGCTGATGATGATAATAATAACTACGTCCATTGAGCACTCTCCAG NM_145065 RefSeq chr11 + 66466864 66477337 PELI3 246330 "pellino E3 ubiquitin protein ligase family member 3, transcript variant 1" GO:2001237|GO:0004842|GO:0045751|GO:0016874|GO:0070434|GO:0010804|GO:0070428|GO:0005829|GO:0050829|GO:0008063|GO:0070534|GO:0031397|GO:0032480 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137946_PI430048170 0.398303951444064 1.92201470450408 2.21320951268572 0.332995059851325 0.392608130888062 A A A 0.339655464606636 0.323058205687001 0.303985949343473 A A A LNCV6_137946_PI430048170 mRNA
GGCAGATACCATATTTTTGCTAATGCATAGAAACACAAATATAACGGTATGCCAAGACAA NM_016593 RefSeq chr6 - 46549579 46652830 CYP39A1 51302 "cytochrome P450, family 39, subfamily A, polypeptide 1, transcript variant 1" GO:0006707|GO:0006805|GO:0005506|GO:0006699|GO:0008396|GO:0007586|GO:0008387|GO:0044281|GO:0033782|GO:0043231|GO:0030573|GO:0005789|GO:0008206|GO:0016125|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57248_PI430048170 0.737649352287299 0.969354800248332 10.0797891132677 10.004385353052 10.3980376673025 P P P 10.1144825074293 10.1664020680736 10.3556473140783 P P P LNCV6_57248_PI430048170 mRNA
GTTGGTCTCCTTATTGCTGGTTATGATGATATGGGCCCTCACATTTTCCAAACCTGTCCA NM_148976 RefSeq chr11 - 14504875 14643634 PSMA1 5682 "proteasome (prosome, macropain) subunit, alpha type, 1, transcript variant 1" GO:0005515|GO:0002474|GO:0010467|GO:0003723|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0004298|GO:0034641|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0043066|GO:0005813|GO:0000502|GO:0005839|GO:0006521|GO:0051437|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68020_PI430048170 0.184638591572567 1.06671666890448 0.530719176487911 0.684947220690334 0.556657972232141 A A A 0.453739332911256 0.509251945430329 0.533420981990566 A A A LNCV6_68020_PI430048170 mRNA
TGTTCTGAATTTGACAGCATCCCTTTCCGTGGGAAATTCTACAAGTGGAAAACGTACCGG NM_030957 RefSeq chr19 - 8580239 8610735 ADAMTS10 81794 "ADAM metallopeptidase with thrombospondin type 1 motif, 10, transcript variant 1" GO:0031012|GO:0005515|GO:0008150|GO:0003674|GO:0006508|GO:0001527|GO:0008270|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135006_PI430048170 0.321656161872465 0.871408338871854 12.7689064910944 12.9675597804547 12.5159621898074 P P P 12.902541999675 12.7727784535093

13.1779690092024 P P P LNCV6_135006_PI430048170 mRNA
CACACTGTCACTGGATGTCATGGGGCCAATAAAATCTCCTGCAATTGTGTATCTCAGAAA NM_015411 RefSeq
chr7 + 56064223 56080672 SUMF2 25870 "sulfatase modifying factor 2, transcript variant 2"
GO:0005788|GO:0044267|GO:0046872|GO:0043687 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_82999_PI430048170 0.150697994870215 1.71812395919449 0.735268564166342
1.83480888865544 1.24446220303239 A A A 0.661398154675685 0.493953327743268
0.52029065029723 A A A LNCV6_82999_PI430048170 mRNA
ATAGCTTCCTGAGCCGTCCTAACGTACTGTCGTTCCTGAATCTCGCAGGCACCGACACTG NM_001013838 RefSeq
chr16 + 67645126 67657569 RLTPR 146206 "RGD motif, leucine rich repeats, tropomodulin domain
and proline-rich containing"
GO:0001772|GO:0050852|GO:0048538|GO:0030011|GO:0045184|GO:0048872|GO:0005737|GO:0016020|GO:0016
477|GO:0005911|GO:0042102|GO:0008290|GO:1900042|GO:0045591 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131346_PI430048170 0.0390558379549869 1.59049634971723 3.41177659457733
3.88735645904712 3.81558584601217 P P P 3.35396556155014 2.92872865438633
2.80925953314222 P P P LNCV6_131346_PI430048170 mRNA
TAATGATTAACCCTTGCCAAGTATGAAGCGCCAAAGAATAAATTTTATTTTGGGGGGAAA NM_153707 RefSeq
chr9 - 18927659 19033258 SAXO1 NA "stabilizer of axonemal microtubules 1, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133663_PI430048170 0.150529804316468 0.739002621216582 8.24386183740005
8.3446793179073 8.57532922456359 P P P 8.45313205179698 8.84485538690535
9.11895041388418 P P P LNCV6_133663_PI430048170 mRNA
GGAATCAAATTTCCTTGTTTGAATCCTGGGACCCTATTGCATTAAAGTACAAATACTATG NM_015895 RefSeq
chr6 + 24774930 24786097 GMNN 51053 "geminin, DNA replication inhibitor, transcript variant 1"
GO:0005515|GO:0042826|GO:0003714|GO:0005634|GO:0045786|GO:0005829|GO:0005737|GO:0006461|GO:0070
491|GO:0009887|GO:0005654|GO:0008156|GO:0000278|GO:0045892 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144118_PI430048170 0.348522607533379 1.06615674501023 11.8129079629158
12.0540105904416 11.9779668172263 P P P 11.9382663694635 11.8350188040299
11.8012058201871 P P P LNCV6_144118_PI430048170 mRNA
AGGACAAAGGGTCAATCCACAAATTTGTCCCTTACCTGATTGCTGGCATCCAACACTCAT NM_000884 RefSeq
chr3 - 49024328 49029442 IMPDH2 3615 IMP (inosine 5'-monophosphate) dehydrogenase 2
GO:0009168|GO:0060041|GO:0003938|GO:0003723|GO:0055086|GO:0005634|GO:0044281|GO:0003677|GO:0046
872|GO:0005829|GO:0005737|GO:0006177|GO:0000166|GO:0016020|GO:0051289|GO:0006144|GO:0071353|GO:0
046651|GO:0005778|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_70254_PI430048170 0.311725301319597 1.30603216300093 7.84508928150945
8.00147622231116 8.32977152709031 P P P 8.19107879588835 7.6014920013501
7.04611376293082 P P P LNCV6_70254_PI430048170 mRNA
TAAAAAACCTCGCCTTCGCCTGTCTCTGGGAACCATACGCCGCAGGTGCCGCCTGTCCTC NM_001282904 RefSeq
chr8 - 53225715 53251697 OPRK1 4986 "opioid receptor, kappa 1, transcript variant 2"
GO:0005515|GO:0043005|GO:0038048|GO:0005886|GO:0007200|GO:0007268|GO:0038003|GO:0007193|GO:0019
233|GO:0004985|GO:0051607|GO:0046877|GO:0006955|GO:0042923|GO:0005887|GO:0007218|GO:0007610|GO:0
007626|GO:0016021|GO:0031635|GO:0007600 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131539_PI430048170 0.737214528377244 0.950066432589719 6.8988636534324
6.65561718090014 6.2992682286572 P P P 6.87044836058922 6.80925024086353
6.41720943017494 P P P LNCV6_131539_PI430048170 mRNA

TCATCCCTGTTCCCCTTTCTCCAAAGAGATGAAGCTCAAATAAAATGTATAACTCTAGTA NM_052961 RefSeq chr6 - 35943513 36024636 SLC26A8 116369 "solute carrier family 26 (anion exchanger), member 8, transcript variant 1" GO:0005515|GO:0006820|GO:0006821|GO:0051321|GO:0005886|GO:0019531|GO:0019532|GO:0007275|GO:0030317|GO:0005254|GO:0015116|GO:0015301|GO:0008272|GO:0008271|GO:0016021|GO:0048240 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133847_PI430048170 0.63299618794908 1.09324925108134 11.3542355133434 11.7044858388192 11.9892223431042 P P P 11.5121881139589 11.3638222014413 11.8177005274504 P P P LNCV6_133847_PI430048170 mRNA
CTGTGATGTTTCTGAATACTACCAAACAGCCATACATGTCTGCAATGAAGAGATTTATTA NM_014886 RefSeq chr5 + 74766990 74776912 NSA2 10412 "NSA2 ribosome biogenesis homolog (S. cerevisiae), transcript variant 1" GO:0030529|GO:0006364|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_136057_PI430048170 0.252226212430417 1.34836588764005 3.98560531940784 4.15062005838124 4.36475252448921 P P P 4.1406574719432 3.09461592389756 3.80934755596804 P P P LNCV6_136057_PI430048170 mRNA
TGGCGATGGCCAACAGCGCTCTCAATCCCTTCGTCTACCTCTTCTTCCAGGCGGGCGACT NM_199243 RefSeq chr5 + 95620275 95621580 GPR150 285601 G protein-coupled receptor 150 GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137978_PI430048170 0.137929211753698 0.849831778021733 5.96206507443117 5.77767837793685 5.79292027738294 P P P 6.10118329697977 6.23474932951504 5.88725770560962 P P P LNCV6_137978_PI430048170 mRNA
TATGTGCCCACCTGCTCTGAGGATTCCTCTTCATGCTGCCAGCAGTCTAGCTGCCATCCA NM_198691 RefSeq chr21 - 44539184 44540195 KRTAP10-1 NA keratin associated protein 10-1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140022_PI430048170 0.847846686959379 1.07674931184994 3.17855512068512 3.08767481698334 2.21832736805503 A A A 2.65663765851001 2.46032183650991 3.14024823427691 A A P LNCV6_140022_PI430048170 mRNA
AGTTCCTTACAGCCCTGCTGCTGGGGTTGATTTTGAACTGGAGTCATTTTCTGAAAGGAA NM_001873 RefSeq chr4 + 165378944 165498330 CPE 1363 carboxypeptidase E GO:0005794|GO:0005886|GO:0005634|GO:0072657|GO:0003214|GO:0042043|GO:0007218|GO:0008152|GO:0004180|GO:0006508|GO:0008270|GO:0030070|GO:0050839|GO:0044267|GO:0006464|GO:0070062|GO:0030667|GO:0004181|GO:0030658 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140837_PI430048170 0.0613645447519672 0.576118849591422 0.468553428886693 0.548720614484646 0.538712468404152 A A A 1.0705615250225 1.09399819138106 1.69038312307265 A A A LNCV6_140837_PI430048170 mRNA
TTTGACTGCTGCCACCAATATGATTATGCTACATGCTTATTATCAGGCACTGACTGAATA NM_001128077 RefSeq chr21 + 30642863 30643136 KRTAP20-3 NA keratin associated protein 20-3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55533_PI430048170 0.842071654983317 1.01888101794969 8.86517886843366 9.1810236387839 9.07661253679235 P P P 8.96969272874915 8.97300409395706 9.11224383261316 P P P LNCV6_55533_PI430048170 mRNA
CTAAACCAGATTTCTTTAGGGCACAATTTTTTCTGGAATCTCACTCTTGTTTTTCACAGT NM_006085 RefSeq chr1 - 220057481 220089853 BPNT1 10380 "3'(2'), 5'-bisphosphate nucleotidase 1, transcript variant 1" GO:0046854|GO:0006139|GO:0008441|GO:0006805|GO:0000287|GO:0050427|GO:0016311|GO:0044281|GO:0070062|GO:0007399|GO:0005829|GO:0004441 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127981_PI430048170 0.946291458007091 1.05344386679629 1.46028247032456 2.62738781043671 2.43010784715848 A A A 2.28684586833873 2.46906469977418

1.66757547700032 A A A LNCV6_127981_PI430048170 mRNA
TGCTCCAGCTGCTTCTATCATAGCACTTCCTACATGGACTGTAACATTTCTTTACTGCTCNM_001018071 RefSeq chr10
- 48156558 48274898 FRMPD2 143162 "FERM and PDZ domain containing 2, transcript variant 3"
GO:0005515|GO:0016323|GO:0005545|GO:0005737|GO:0070830|GO:0005923|GO:0005856 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133442_PI430048170 0.3810653640772380.8502647687447490.260405575864822
0.26775585594897 0.408426010644253A A A 0.3638371708332790.305995338821103
0.897287675484265A A A LNCV6_133442_PI430048170 mRNA
GCTCTTGTTTCTTGTACTGGGTATTTTCATAGAAGAAAATTTCTTGGTGGGTTTTCCAAT NM_031959RefSeq
chr17_JH159146v1_alt - 148587 149281 KRTAP3-2 83897 keratin associated protein 3-2
GO:0005515|GO:0005198|GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145673_PI430048170 0.7000724981180221.02399268218296 0.350589633184891
0.5686325756022840.439228259330017A A A 0.5142867453879730.384523257357661
0.360607561561184A A A LNCV6_145673_PI430048170 mRNA
CTTGTCTGTTATCTGAGTTTTCAAAAGCTTTAAGACTCTGGGAACATCTGATTTTATGGA NM_000681RefSeq chr10
+ 111077031 111080904 ADRA2A 150 adrenoceptor alpha 2A
GO:0005515|GO:0032811|GO:0043268|GO:0045202|GO:0001819|GO:0031696|GO:0042803|GO:0019229|GO:0042
596|GO:0070473|GO:0051926|GO:0046676|GO:0007565|GO:0002526|GO:0030335|GO:0019901|GO:0046982|GO:0
035625|GO:0045741|GO:0030168|GO:0010700|GO:0004938|GO:0043235|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142591_PI430048170 0.2220662472889331.01861550962613 0.312159657742928
0.25938954525112 0.284500797926729A A A 0.2614300186381240.25344323743186
0.261815555185506A A A LNCV6_142591_PI430048170 mRNA
CCAGCAAAAGTGCAGTAGTGTCACTTTTTTCCTGTCAATATATAGAGACTTCTAAATCAT NM_130811RefSeq chr20
+ 10218828 10307418 SNAP256616 "synaptosomal-associated protein, 25kDa, transcript variant 2"
GO:0005802|GO:0005515|GO:0043005|GO:0048471|GO:0016081|GO:0016082|GO:0030054|GO:0005886|GO:0007
268|GO:0031201|GO:0060291|GO:0044281|GO:0007269|GO:0005829|GO:0030426|GO:0005737|GO:0070201|GO:0
031629|GO:0017075|GO:0014047|GO:0016079|GO:0031982|GO:0005484|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143662_PI430048170 0.00470082346307561 0.4164573075782237.92286057693605
7.74777798716265 8.06019387291871 P P P 9.30004720904983 8.855415703777
9.33577453833766 P P P LNCV6_143662_PI430048170 mRNA
GTGAAATTACTTGTCTGAACCCCGTGGGGAGAAATAAATAATTTTCCCAAAGTTCAAAAA NM_021800RefSeq chr10
- 67796668 67838179 DNAJC12 56521 "DnaJ (Hsp40) homolog, subfamily C, member 12, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98_PI430053867 0.2894535955844871.22270619141612 1.01737975652402 0.435300016842919
0.479771211796522A A A 0.3151277327789330.3748234164965570.444836484342533A A A
LNCV6_98_PI430053867 mRNA
GGTGCCTGGCATATGTGCTTAACAAAATAAACTGACTGGATTATTTATCCATATTCACTT NM_207454RefSeq chr17
- 34574122 34579369 C17orf102 NA chromosome 17 open reading frame 102 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136246_PI430048170 0.0678037076025801 0.7367815187138227.50621725071772
7.62312379999799 7.60005127973391 P P P 8.06996633296567 7.7622620998367
8.18899790157449 P P P LNCV6_136246_PI430048170 mRNA
CACAAGGATAGTGGGCATCATGAATTAATAAAACGTCCTAGGATTCTGCAAGCTAAAAAA NM_030666RefSeq chr6
- 2832331 2842049 SERPINB1 1992 "serpin peptidase inhibitor, clade B (ovalbumin), member 1,
transcript variant 1" GO:0010951|GO:0005737|GO:0016020|GO:0004867|GO:0005615|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127690_PI430048170 0.1466383384805770.5197852074431420.4344168615002312.0400436262258

1.26253448550864 A A A 1.68870220119238 2.50021899469485 2.64298808025148 A A P
LNCV6_127690_PI430048170 mRNA
TGGTATGATAGTTTCTTGGTAGATACAGGTTGAAAATTTTTTGTGGCAGCCAATCCTCAT NM_012333RefSeq chr1
- 38862489 38873378 MYCBP 26292 "MYC binding protein, transcript variant 1"
GO:0005739|GO:0005515|GO:0006355|GO:0005813|GO:0005737|GO:0003713|GO:0005634|GO:0007283|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130878_PI430048170 0.4133204138521090.8338761675703510.398622719915197
0.3708582071399860.251593573939516A A A 0.3287490498833930.364287787098563
1.01158914381952 A A A LNCV6_130878_PI430048170 mRNA
ACTGTGCCGTATAAAGGCTGTTGCCTCAGCCTTACTAATAAATACTGAAAATATCACCTT NM_033026RefSeq chr7
- 82754004 83162881 PCLO 27445 "piccolo presynaptic cytomatrix protein, transcript variant 1"
GO:0005215|GO:0030054|GO:0005509|GO:0045202|GO:0014069|GO:0016079|GO:0008021|GO:0005544|GO:0016
020|GO:0007010|GO:0017157|GO:0019933|GO:0048788|GO:0005856|GO:0030073|GO:0005522|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130777_PI430048170 0.00655347988491692 1.35576658912052 8.57822592969825
8.49990785787344 8.59899177662692 P P P 8.04549566634956 8.07653210634062
8.23260280161998 P P P LNCV6_130777_PI430048170 mRNA
GAGGGAGAAATGGAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGAC NM_016029RefSeq chr14
- 60144780 60165493 DHRS7 51635 dehydrogenase/reductase (SDR family) member 7
GO:0016020|GO:0016491|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135072_PI430048170 0.1237229321784971.05869432136238 0.445157775299926
0.47648417187667 0.495759451502562A A A 0.3301943054379890.388568143248762
0.449754161252008A A A LNCV6_135072_PI430048170 mRNA
GACCTATCACCACTGATTATTAATGTCTGCATGAATGATAACAATAAGACCAAGTCATCA NM_022469RefSeq chr1
- 240489572 240612162 GREM2 64388 "gremlin 2, DAN family BMP antagonist"
GO:0060300|GO:0010172|GO:0038098|GO:0036122|GO:0019221|GO:0048263|GO:0005576|GO:0030509|GO:0008
201|GO:0005615|GO:0005125|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144909_PI430048170 0.6634536331874671.07916821548739 0.364155531245339
0.5172635972004520.911779898307355A A A 0.30003342026235 0.849547104153035
0.297701988396832A A A LNCV6_144909_PI430048170 mRNA
GTTCACTTGATGGGGAATGACTAGAATGGGGCAATAACAAATCATTTCTAAACAGTTATT NM_033427RefSeq chr7
- 117710650 117873507 CTTNBP2 83992 cortactin binding protein 2
GO:0017124|GO:0043197|GO:0007420|GO:0005938|GO:0008021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129245_PI430048170 0.0236547471276777 1.62543657093364 6.06362294618781
5.75260432360872 5.54781497076964 P P P 4.9056744522972 5.28098711177609
5.09773340364098 P P P LNCV6_129245_PI430048170 mRNA
CTATGGGATTTTCCCCCCACTGGTCTGCATAAAAGAAAATAAAATGACATAAAAGGGAGC NM_144587RefSeq chr10
+ 122271305 122338161 BTBD16 118663 BTB (POZ) domain containing 16NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133634_PI430048170 0.5550647015487610.874613205668894 9.9379984604293
9.84345200758736 10.0745516178715 P P P 9.69106661372562 10.1831995299435
10.4671935352564 P P P LNCV6_133634_PI430048170 mRNA
CCCAATATCCAGATGAATATCCGAGATGTTGAATAAACTTAGCCATTTCGTACACATGGT NM_002388RefSeq chr6
- 52264013 52284881 MCM3 4172 "minichromosome maintenance complex component 3, transcript
variant 1"
GO:0005515|GO:0042555|GO:0048471|GO:0005813|GO:0005658|GO:0005634|GO:0003677|GO:0005524|GO:0003
678|GO:0043231|GO:0006260|GO:0000082|GO:0006271|GO:0016020|GO:0006270|GO:0005654|GO:0032508|GO:0
000278 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_126980_PI430048170 0.7611861687297171.09844628483025 6.27618899933517
6.67847110352005 7.18322844190775 P P P 6.4879634010768 6.5430080201032 6.8215610531646
P P P LNCV6_126980_PI430048170 mRNA
CGGATGGAATTCTGGTATTTATAGGCATTGGTGCTAGATGGTACATTTTATGTGTTAAAA NM_024558RefSeq chr14
- 50108631 50116579 VCPKMT 79609 "valosin containing protein lysine (K) methyltransferase,
transcript variant 1" GO:0005515|GO:0005737|GO:0005575|GO:0016279|GO:0018023 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_112542_PI430048170 0.00783573513682448 0.6512410700924726.50239385828001
6.19669880290727 6.31718713170395 P P P 6.92309516953654 7.12486780384291
6.82466393615975 P P P LNCV6_112542_PI430048170 mRNA
TCTACTTCTCCCTCACTACCGAGGCCCTCAGCTTCGCGAAGACGCCCAGCTCCAAGTGTG NM_001277335 RefSeq
chr7 - 102582317 102616756 RASA4B NA RAS p21 protein activator 4B NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_64881_PI430048170 0.00896932935496432 0.79768235616123 6.12017188949365 6.1164348351657
6.06518884012959 P P P 6.51014363276741 6.39925342536999 6.3674722686005 P P P
LNCV6_64881_PI430048170 mRNA
GAAGAAAAGAAGACCCCCAGCAAACCACCAGCCCAGCTGTCGCCATCTGTTCCCAAGAGA NM_006297RefSeq
chr19 - 43543311 43575578 XRCC1 7515 X-ray repair complementing defective repair in Chinese
hamster cells 1
GO:0005515|GO:0003684|GO:0000012|GO:0006281|GO:0006284|GO:0005654|GO:0005634|GO:0019899 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141842_PI430048170 0.00809239424145266 0.4070208878839217.20041770826713
6.64350410518083 7.10890982093719 P P P 8.22695103548754 8.21625639038465
8.44751183725079 P P P LNCV6_141842_PI430048170 mRNA
CTGTTAATGGCGAAAGAATGGAAGCGAATAAAGTTTTACTGATTTTTGAGACACTAGCAA NM_001242891 RefSeq
chr1 - 114716912 114758050 CSDE1 7812 "cold shock domain containing E1, RNA-binding, transcript
variant 4"
GO:0006355|GO:0005737|GO:0005794|GO:0005886|GO:0005743|GO:0070966|GO:0003677|GO:0008584|GO:0070
937 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134396_PI430048170 0.36360693607901 1.04763985345604 0.298977813677104
0.2805514118532090.456300109881157 A A A 0.2932365092402920.256038775681203
0.291366114577755 A A A LNCV6_134396_PI430048170 mRNA
GCTGTCACTGTTGTTTTCTTGTAACATGATATGGAATAAAGTATAGCAGAATCTCCGTAA NM_001287135 RefSeq
chr7 + 90596361 91210590 CDK14 5218 "cyclin-dependent kinase 14, transcript variant 1"
GO:0005515|GO:0005886|GO:0030332|GO:0005634|GO:0005524|GO:0060828|GO:0005829|GO:0005737|GO:0000
086|GO:0000308|GO:0051726|GO:0006468|GO:0016055|GO:0004693|GO:0051301 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138804_PI430048170 0.5983711561626911.10010740258524 0.399400448145433
0.4185868481639550.951460353610731 A A A 0.3324550090592310.673706414266719
0.397759525228876 A A A LNCV6_138804_PI430048170 mRNA
TATAAGGTACAGTAAAAGCGTCTGAAAAATGCATTCAAAACACAGATTCTGGGGCCCTCG NM_032040RefSeq chr19
- 46410328 46413662 CCDC8 83987 coiled-coil domain containing 8
GO:0007088|GO:0005813|GO:0005737|GO:0005886|GO:0010923|GO:0000226 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127255_PI430048170 0.9199344862924841.02111126569711 3.16546169961063
2.54721038836552 2.62893216242557 A A A 2.98146356015011 2.92178220480501
2.34851349828398 A P A LNCV6_127255_PI430048170 mRNA
ATTCCTATTATTGTCCTAAAGTCTCTCTGGGCTCTTGGATCATGATTAAACCTTTGACTT NM_001496RefSeq chr5 -
138252379 138274564 GFRA3 2676 GDNF family receptor alpha 3

GO:0005886|GO:0005102|GO:0031225|GO:0048485|GO:0007399|GO:0043231|GO:0007165|GO:0005737|GO:0007411|GO:0007422|GO:0001764|GO:0008046|GO:0009897|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140961_PI430048170 0.0143259491622214 0.317233281296731 4.59845404093489 4.35373413723834 4.42552465246504 P P P 5.61172976222812 6.36202404790681 6.27427262743736 P P P LNCV6_140961_PI430048170 mRNA
GCCTTCTTGATAAAGTGGTAGACATTTTGTAGCTTTCTAGAAACTTTGTATTCATACGGT NM_021961 RefSeq chr11 + 12674421 12944737 TEAD1 7003 TEA domain family member 1 (SV40 transcriptional enhancer factor)
GO:0005515|GO:0010467|GO:0006355|GO:0005737|GO:0006367|GO:0005794|GO:0003700|GO:0005654|GO:0035329|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64875_PI430048170 0.2575332850883340.8051166304943312.62833076643209 2.01943784091214 2.15569046820693 A A A 2.69739400959511 2.78819808358793 2.27970726817041 A P A LNCV6_64875_PI430048170 mRNA
TCTTCCTCTCCTTAATCCAATATAGCAGCCGTGAAGTCATTTCTGTATTTCAGGAAGACT NM_002781 RefSeq chr19 - 43167742 43186536 PSG5 5673 "pregnancy specific beta-1-glycoprotein 5, transcript variant 1"
GO:0005515|GO:0007565|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142342_PI430048170 0.4852310555139080.7883437384718053.60379141842541 3.2529349878429 2.03213100188016 P P A 3.81794740115041 3.49064371799619 2.87944902474246 P P P LNCV6_142342_PI430048170 mRNA
GTGTGGAGCCTCTTCCGTGTCAATATTCAATAAAGTTATAGAAATGTTTCAAGAGCAAAA NM_033105 RefSeq chr8 + 66021555 66100520 DNAJC5B 85479 "DnaJ (Hsp40) homolog, subfamily C, member 5 beta"
GO:0016020 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141858_PI430048170 0.00284134777053462 1.1546670343888 0.793965363232436 0.8584595588449340.802156675099278 A A A 0.6299028948864880.609026970709845 0.593852034267019 A A A LNCV6_141858_PI430048170 mRNA
CAGTACAATGTTTGGATTCTCCTTGATATTACCAATACATTTTCCCTGTTATCTTGCACT NM_054031 RefSeq chr11 + 18120954 18138480 MRGPRX3 117195 "MAS-related GPR, member X3"
GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139570_PI430048170 0.49551434621633 1.08702604105359 4.52446064237266 4.23674433458727 4.61103827715712 P P P 4.1260944374605 4.36226028413804 4.52159373984549 P P P LNCV6_139570_PI430048170 mRNA
CACATGTAGTACATTGTACCAAAGTTCTTAATAAGAATATTCCCCACAATCCTGTTCTCT NM_181093 RefSeq chr1 - 169853075 169893959 SCYL3 57147 "SCY1-like 3 (S. cerevisiae), transcript variant 2"
GO:0005515|GO:0005737|GO:0005794|GO:0016477|GO:0016301|GO:0006468|GO:0005524|GO:0030027 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129726_PI430048170 0.2661060927187140.6960099505592642.46164035440292 1.82637838754339 2.9912305188671 A A P 2.84754639476974 3.47315504770859 2.61618130976586 P P P LNCV6_129726_PI430048170 mRNA
GGAGAGGAATATGGTAAAGCCAAAATAGTTGACAGATCTAACTTTCCTAGTGGAACAGTA NM_001290318 RefSeq chr19 + 57351273 57359897 ZNF304 57343 "zinc finger protein 304, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90716_PI430048170 0.0156036343888518 0.7706736157737321 5.3759176499356 15.2913510129397 15.337554831559 P P P 15.6235508916649 15.6743911878626 15.8276440199605 P P P LNCV6_90716_PI430048170 mRNA
CGACTTCAGTCAACTACAGCTGAGTCCATAGGCCAGAAAGACAATAAATTTTTATCATTT NM_003739 RefSeq chr10 + 5094375 5107686 AKR1C3 8644 "aldo-keto reductase family 1, member C3, transcript variant 1"
GO:0019369|GO:0044598|GO:0006693|GO:0044597|GO:0007603|GO:0001758|GO:0047017|GO:0005622|GO:0016488|GO:0047020|GO:0071395|GO:0047023|GO:0047115|GO:0044259|GO:0004745|GO:0010942|GO:0070062|GO:0

000060|GO:0045550|GO:1900053|GO:2000224|GO:0004032|GO:0061370|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130782_PI430048170 0.00722039093253683 3.06215576373989 3.00304666814607 2.90975169872708 3.65844191464511 P P P 1.56310352991262 1.95591937915003 1.23953888230154 A A A LNCV6_130782_PI430048170 mRNA AAAGATTGCCAAATCATGTTTGGTAGGAGGACTTTTGAGGTAGCTTTTGAACAAATGTTT NM_020682 RefSeq chr10 + 102869452 102901898 AS3MT 57412 arsenite methyltransferase GO:0030791|GO:0005739|GO:0030792|GO:0005737|GO:0008757|GO:0009404|GO:0032259|GO:0018872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_85056_PI430048170 0.0429349877847105 0.472900452713328 3.30600623538922 3.12760469515308 3.03566941841749 P P P 3.75680412233657 4.2125386014931 4.62516126987448 P P P LNCV6_85056_PI430048170 mRNA ACCTGGAAAGTGTGATTATATTCGTTACCTTCTTTGGTAGACGGAATAGTTGGGACCACC NM_001455 RefSeq chr6 + 108560865 108684768 FOXO3 2309 "forkhead box O3, transcript variant 1" GO:0005515|GO:0003700|GO:0006366|GO:0000981|GO:0005634|GO:0001556|GO:0005829|GO:0001221|GO:0005737|GO:0043525|GO:0007173|GO:0045944|GO:0090090|GO:2000177|GO:0097150|GO:0048011|GO:0006357|GO:0019901|GO:0030330|GO:0048015|GO:0001544|GO:0001542|GO:0001047|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129879_PI430048170 0.0812537675512661 0.515637342533515 7.38452993429438 7.07497257967205 7.58115977404684 P P P 7.65732845461437 8.41029000656365 8.69634268660841 P P P LNCV6_129879_PI430048170 mRNA GTCATGTAATTTGAAAAGCAGTGTTTCATTATGAAAGAGCTCTCAAGTTGCTTGTAAAGC NM_022051 RefSeq chr1 - 231363750 231425044 EGLN1 54583 egl-9 family hypoxia-inducible factor 1 GO:0031545|GO:0005515|GO:0031543|GO:0060711|GO:0071731|GO:0061418|GO:0005634|GO:0043433|GO:0005829|GO:0005737|GO:0055008|GO:0001666|GO:0031418|GO:0005506|GO:0060412|GO:0051344|GO:0045765|GO:0071456|GO:0060347|GO:0018401|GO:0016706|GO:0019899|GO:0030821|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138537_PI430048170 0.0865004215992512 1.04186155656916 0.349168280783734 0.321167343992258 0.278082034216995 A A A 0.246829493316638 0.276451562725048 0.248339741352156 A A A LNCV6_138537_PI430048170 mRNA TGTATCTGTTGCATCTTGTCAATGTTTGACTCATGGTCAGCATCCAATAGTTGTTAAATG NM_001161429 RefSeq chr5 - 36249001 36301909 RANBP3L 202151 "RAN binding protein 3-like, transcript variant 1" GO:0046907 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135664_PI430048170 0.0363697147693411 29629797460799 10.0047414937128 9.90646253258057 10.013722156927 P P P 9.71631464405904 9.42444437105996 9.64754156190966 P P P LNCV6_135664_PI430048170 mRNA TGAGTCAGCAGAAGTGGACCAAAGGATTCCTCTGAATAAAGTTATTTAAATTGATGTTCA NM_001001653 RefSeq chr1 - 43383907 43389812 MED8 112950 "mediator complex subunit 8, transcript variant 4" GO:0005515|GO:0010467|GO:0016567|GO:0006367|GO:0001104|GO:0006357|GO:0016592|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70854_PI430048170 0.643713472926111 0.926797222197554 6.90971291060282 7.00038134331223 6.80819142115757 P P P 7.32115604649912 6.90739817466298 6.76603854084841 P P P LNCV6_70854_PI430048170 mRNA CTCTTTGTCACAGACTGCATAAGTTGTCAGCCTTGACTATCTTTTGAATAAAGATTTGAT NM_080489 RefSeq chr20 - 1309910 1329235 SDCBP2 27111 "syndecan binding protein (syntenin) 2, transcript variant 1" GO:0035556|GO:0005737|GO:0046982|GO:0005886|GO:0046907|GO:0008022|GO:0042803|GO:0070062|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127130_PI430048170 0.28433770684676 0.883041648073387 8.44946886474274 8.85854588825677 8.64268171875747 P P P 8.66256590285368 8.9489943074396

8.89092213175622 P P P LNCV6_127130_PI430048170 mRNA
TTTATTGGGTGGAGGGCACCATGTCCCAGGGCTATCAAATAAAGAATAGTTTGGTTTTTT NM_002263 RefSeq
chr6_GL000256v2_alt + 4840230 4858620 KIFC1 3833 kinesin family member C1
GO:0008017|GO:0005871|GO:0005815|GO:0005874|GO:0005819|GO:0005634|GO:0003777|GO:0051225|GO:0005524|GO:0000070|GO:0008569|GO:0016020|GO:0007596|GO:0008152|GO:0090307|GO:0007080|GO:0016887|GO:0005769|GO:0051301|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81240_PI430048170 0.0914880158260755 1.26818526269538 5.97963409826362
5.89706661392396 6.09777412989707 P P P 5.48386837959932 5.54482243525333
5.89042326369292 P P P LNCV6_81240_PI430048170 mRNA
CCCCTGGAGCTCAGTTTTTATTTGTTAAAATGGCTCGATCCTCAGACTTTACTCACATGC NM_012164 RefSeq chr9
- 120756975 120793462 FBXW2 26190 F-box and WD repeat domain containing 2
GO:0005515|GO:0005737|GO:0004842|GO:0016567|GO:0006508|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127239_PI430048170 0.6638439082513 0.8906009506724260.689268740598818
0.7548870746982080.656308880474679 A A A 0.6102030167372841.31333293336707
0.549267805024717 A A A LNCV6_127239_PI430048170 mRNA
CCTGCCTTGTTGTGATCCCCATAGAAACATAATAAATATACAAGTTGTGTTCCCTGCAAA NM_014617 RefSeq chr2
- 208160739 208163573 CRYGA 1418 "crystallin, gamma A"
GO:0005212|GO:0002088|GO:0005575|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142148_PI430048170 0.00658384783299898 1.84060325811541 14.2860674911971
14.6343139984586 14.6371772117456 P P P 13.8051214581342 13.3976447324539
13.7109203054174 P P P LNCV6_142148_PI430048170 mRNA
ATGCCTGAAAATTAGGGGGCACTTCAAGTAGATAGCTTCTATTTCCTATATTTGTCTTAT NM_001287482 RefSeq
chr6_GL000252v2_alt + 3082693 3087544 C6orf48 50854 "chromosome 6 open reading frame 48, transcript variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134187_PI430048170 0.0286392547924119 0.5122191912017695.51422895883416
5.13927342777718 5.42187603978402 P P P 5.98187616537492 6.21731645448708
6.70209167510069 P P P LNCV6_134187_PI430048170 mRNA
ATTGAAAGGTCAGTGGTGGTAAGACAAGGTGTCTTGTAAATTAAGATTTTAAGAAGTGCA NM_015151 RefSeq chr21
+ 46458948 46570013 DIP2A 23181 "DIP2 disco-interacting protein 2 homolog A (Drosophila), transcript variant 1"
GO:0005515|GO:0009986|GO:0010629|GO:0008152|GO:0042981|GO:0007275|GO:0005634|GO:0003824|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140343_PI430048170 0.6680303333577681.03356057109535 0.751007031124645
0.8210256397460330.74269382506037 A A A 0.6223619045360650.587348507471335
0.937121504289863 A A A LNCV6_140343_PI430048170 mRNA
CAGTCATGTATGTCTACTTTGTAGTTTAAGTAGACTTCATCAACTATGGTCTATTTTGGG NM_017552 RefSeq chr2
- 23748663 23927114 ATAD2B 54454 "ATPase family, AAA domain containing 2B, transcript variant 1"
GO:0070577|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132593_PI430048170 0.6029066211616661.03053582425353 0.292229748993086
0.3019022544289360.493395762587551 A A A 0.3343759416436050.289995168717209
0.34148609554551 A A A LNCV6_132593_PI430048170 mRNA
GTGAACCTCAACAATTGGACTGGAAATGAGCTTTGACCTAACTTTGTAAAATAAAAGCAT NM_001017970 RefSeq
chr14 - 61277370 61281812 TMEM30B 161291 transmembrane protein 30B
GO:0005515|GO:0070863|GO:0005886|GO:0006869|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78884_PI430048170 0.9361698317913260.9939417637920816.58293677267011 6.64934047300146
6.83641398202673 P P P 6.56843993386826 6.82432048384301 6.70301741047289 P P P
LNCV6_78884_PI430048170 mRNA

ATTACAAAGGTCGTCCTCCTTGATCCAGTTAACGAGTCAGAACTCTTCTCCCAATCAGCA NM_006693 RefSeq chr7 + 99438939 99457373 CPSF4 10898 "cleavage and polyadenylation specific factor 4, 30kDa, transcript variant 1" GO:0006397|GO:0046778|GO:0019054|GO:0019048|GO:0019058|GO:0005847|GO:0008270|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73571_PI430048170 0.3923982261132070.9031980670674470.4731414717962840.490197172101039 0.38974447624259 A A A 0.4970299757694910.42935833143062 0.835702736272491 A A A LNCV6_73571_PI430048170 mRNA
ACTTTTCCAGCATTCTCCAGACCAGATTACAATGAAATGGTTGGAGAATGCTGGCTGCAG NM_001184 RefSeq chr3 - 142449234 142578826 ATR 545 ATR serine/threonine kinase GO:0005515|GO:0032407|GO:0032405|GO:0071480|GO:0034605|GO:0034644|GO:0046777|GO:0018105|GO:0000724|GO:0046983|GO:0001741|GO:0005794|GO:0005694|GO:0042493|GO:0043393|GO:0007275|GO:0005524|GO:0003677|GO:0006974|GO:0006260|GO:0007049|GO:0006281|GO:0004672|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100016_PI430048170 0.1033740742713140.3917559597862731.90040687512766 1.8974205091521 0.43318113780724 A A A 1.92226148037591 3.25956235298193 3.18879361887121 A P P LNCV6_100016_PI430048170 mRNA
CATCACCTGCAAGATGTACATAAAAATCACATAAGCTGGAATTCAACAAAAGACCTCTGA NM_001256373 RefSeq chr12 - 91984975 92142671 C12orf79 256021 "chromosome 12 open reading frame 79, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144892_PI430048170 0.7657652548922891.01476637728194 0.271393323662436 0.2938396124537030.447302620431145 A A A 0.3461180722855330.303658158936599 0.305341958369792 A A A LNCV6_144892_PI430048170 mRNA
TCTGCATGTGTGGAGACAACTGCAAATGCACAACCTGCAACTGTAAAACATGTCGGAAGA NM_032935 RefSeq chr16 + 56565048 56568957 MT4 84560 metallothionein 4 GO:0008150|GO:0006875|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129142_PI430048170 0.2172495066711250.7822892689776197.8962977868875 7.86958911392807 7.66147610950199 P P P 7.78987506956257 8.44788241219389 8.18890825541802 P P P LNCV6_129142_PI430048170 mRNA
CTGCTACAAGTAACAGATGCACTGTGAAGATTCCAGTATTAATAAAGGTGTACTGTAATT NM_138383 RefSeq chr16 - 70661203 70686051 MTSS1L 92154 metastasis suppressor 1-like GO:0007009|GO:0097178|GO:0003779 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139420_PI430048170 0.3371618260084660.7315352427366520.367145790056381 0.3286360313264960.31826764664429 A A A 1.33179902397282 0.433249876256623 0.397044640499896 A A A LNCV6_139420_PI430048170 mRNA
GAGGTGAAGAAAGCTCTGTTGAAGCTGAAAGACAAAGTAGCACATTCTCAGAGCAAATAG NM_001004464 RefSeq chr11 + 124029622 124030558 OR10G8 219869 "olfactory receptor, family 10, subfamily G, member 8" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134856_PI430048170 0.4122898336024080.8315907199464234.18945771196985 3.77423411818229 4.37363951198959 P P P 4.04452716176647 4.77146798848088 4.28597819542971 P P P LNCV6_134856_PI430048170 mRNA
TGCCCCCAACTCAAAATAGCTGTCTGTGTTGCAATCATTGCAAAATCTAAATTCTTTTGT NM_005114 RefSeq chr4 - 11398363 11428913 HS3ST1 9957 heparan sulfate (glucosamine) 3-O-sulfotransferase 1 GO:0005975|GO:0005796|GO:0009405|GO:0008146|GO:0044281|GO:0016021|GO:0008467|GO:0030203|GO:0006024 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138534_PI430048170 0.4105059623716960.9380389775566540.641491156309535 0.5105201000975110.497158772478646 A A A 0.8023295856837280.566066950043599 0.547851371912194 A A A LNCV6_138534_PI430048170 mRNA

GAACACTGACTCTTACAAGTATGTCATGAAATACTTTATGCTGTGAGCAGGTATACATGT NM_020139 RefSeq chr4 - 103077624 103099867 BDH2 56898 "3-hydroxybutyrate dehydrogenase, type 2" GO:0005739|GO:0005737|GO:0051287|GO:0006635|GO:0030855|GO:0003858|GO:0042168|GO:0016628|GO:0055072|GO:0019290|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_113890_PI430048170 0.903353888646181 0.994920857236319 0.334708762839209 0.575259237241981 0.435563702427601 A A A 0.511836551620276 0.456062273157466 0.407950011113878 A A A LNCV6_113890_PI430048170 mRNA
GAAGGCAGAGAAGAAATCTGGATTTTGGGACAATTTGGTTTTAAAACAGAATATACAGTC NM_175075 RefSeq chr8 - 489789 545781 TDRP 157695 "testis development related protein, transcript variant 1" GO:0003674|GO:0005737|GO:0005634|GO:0007283 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_142764_PI430048170 0.000759236809346217 0.313528232569939 9.40932661454995 9.25503160002608 9.31537663107788 P P P 10.8730418552118 10.9271515226548 11.1842321426108 P P P LNCV6_142764_PI430048170 mRNA
GTGGGTCATTTGGGGACCTTGTTCTTTTCTATTTTGCTTTATTAATAAAGGAACTTGTAG NM_001034841 RefSeq chr16 + 19113931 19121630 ITPRIPL2 162073 "inositol 1,4,5-trisphosphate receptor interacting protein-like 2, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_143293_PI430048170 0.508075650192791 1.20311260339481 1.21104034082476 2.08118700915288 1.66480684147794 A A A 1.98413438464231 1.16537408985399 0.908922146290832 A A A LNCV6_143293_PI430048170 mRNA
AAGAAATGTCTGTGACAAAGTCTCAGCCTGTGTTATTTATTTGCCTCTGTGCACCCCACC NM_001042522 RefSeq chr19 + 38390199 38399883 SPRED3 NA "sprouty-related, EVH1 domain containing 3, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_128174_PI430048170 0.0327831710514285 1.9126830054381 3.77117919617976 4.01104174348302 3.60609580549238 P P P 2.7912638671606 2.46428279988073 3.24692342802159 A A P LNCV6_128174_PI430048170 mRNA
AAGTCAACCAAAATTCTGAGTCTCGGACAAGACTGGTTAAAAATCGTTCTACAATGAAAC NM_001302839 RefSeq chr6 + 158869866 158910353 C6orf99 100130967 "chromosome 6 open reading frame 99, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_140167_PI430048170 0.672769706707741 0.973476021938813 0.55828624935552 0.483859105823325 0.283987951092016 A A A 0.412426836143713 0.541798130320768 0.499011848019008 A A A LNCV6_140167_PI430048170 mRNA
TTGCAGAATGAGCTGATTCGAAAGAATGATCGAGAGAAGGAGCTGCTCCTTCTGTATCAG NM_025055 RefSeq chr15 + 74236288 74336141 CCDC33 NA "coiled-coil domain containing 33, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135326_PI430048170 0.63110311206544 0.974210495425799 0.27755344096043 0.30846254260651 0.433053980851131 A A A 0.346168766515491 0.48141175533765 0.303265717612007 A A A LNCV6_135326_PI430048170 mRNA
GTCATTGGTAAAAAGACTTCTGTGTCAGAAAAAACAAAAGGCTCTTTTCAGAGCCACCTA NM_170745 RefSeq chr6 - 25726062 25726562 HIST1H2AA 221613 "histone cluster 1, H2aa" GO:0046982|GO:0005634|GO:0000786|GO:0003677|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_138045_PI430048170 0.523069873034577 0.971062653634526 0.426273164806815 0.429092437594304 0.258898789416476 A A A 0.382376932453051 0.453701937408949 0.41087744719217 A A A LNCV6_138045_PI430048170 mRNA
GCCTAAATCTTCCTCTGAAGTAAAAGATCTCAAAAGGACAGATCATTAATGACTGGAAAA NM_001005783 RefSeq chr1 + 119368775 119394130 HAO2 51179 "hydroxyacid oxidase 2 (long chain), transcript variant 2" GO:0005739|GO:0018924|GO:0052852|GO:0019395|GO:0052853|GO:0010181|GO:0003973|GO:0005102|GO:0051260|GO:0052854|GO:0070062|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_145655_PI430048170 0.0369533483396781 0.502422807599725 6.88929710905757

6.68863003478127 6.73088242241893 P P P 7.38184285061491 7.70231446547428
8.11693278989782 P P P LNCV6_145655_PI430048170 mRNA
TGTGTATTTTGAGGGTTTTAGAAACCGGTTGCCTTAGAGGTTAGACTTTTGAAGAAAAAA NM_020823 RefSeq chr6
+ 158536435 158635435 TMEM181 57583 transmembrane protein 181
GO:0015643|GO:0009405|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_24142_PI430048170 0.00432519418414317 0.4122607150437467.34831874249037
7.51107752534996 7.53910748851674 P P P 8.46958287376976 8.85110999209801 8.8845260347454
P P P LNCV6_24142_PI430048170 mRNA
ACCTGCCAGGTTTATCTGTTATACCTGTGGCATTCTTATTATGTCAGACAAGTTATTATA NM_004041 RefSeq chr11
- 75260121 75351831 ARRB1 408 "arrestin, beta 1, transcript variant 1"
GO:0005515|GO:0032717|GO:0006366|GO:0044212|GO:0005159|GO:0032715|GO:0015031|GO:0005765|GO:0007
219|GO:0070374|GO:0031397|GO:0000785|GO:0031625|GO:0043027|GO:0006892|GO:0030168|GO:0031434|GO:0
002031|GO:0043547|GO:0005654|GO:0008134|GO:0090240|GO:0016567|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131698_PI430048170 0.5095166736018960.6908433084526462.63364091484434
2.36383712412032 3.08045099299435 A A P 3.93994461160459 2.24366014532801
3.10341066134205 P A P LNCV6_131698_PI430048170 mRNA
GTCTCCAAACTGTCTTCTGCCCTAGAATTTATTCATACTGTTAAATTACCAGTTTATGCA NM_001145127 RefSeq chr17
+ 18377764 18389646 EVPLL 645027 envoplakin-like NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_67587_PI430048170 0.8534405784796381.00759518806562 0.4017758936905340.518017387972766
0.418669237152009 A A A 0.5246691863167590.3873219139127880.392226827845738 A A A
LNCV6_67587_PI430048170 mRNA
ATATGCAGATCTCTGCACAAATAAGGATCTGAAGAAAGCCATTTTGGAAGATATGGTGAG NM_015256 RefSeq chr5
- 131949973 132011662 ACSL6 23305 "acyl-CoA synthetase long-chain family member 6, transcript
variant 1"
GO:0001676|GO:0005886|GO:0005741|GO:0005634|GO:0044281|GO:0035338|GO:0042803|GO:0007405|GO:0048
666|GO:0019432|GO:0044255|GO:0005778|GO:0006637|GO:0001666|GO:0032869|GO:0010867|GO:0007584|GO:0
010747|GO:0008654|GO:0048545|GO:0005524|GO:0004467|GO:0009629|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143913_PI430048170 0.1582624316105230.7600874201612197.25910548134 7.00353721350106
7.6847999231241 P P P 7.56489065805186 7.7582165509929 7.87776530954433 P P P
LNCV6_143913_PI430048170 mRNA
TGGGGACTCAGGCAACCAAATACAATTCTGAAGTTGTTGATAAGAAGATAGAAGAGTTTC NM_002525 RefSeq chr1
- 51789193 51878937 NRD1 4898 "nardilysin (N-arginine dibasic convertase), transcript variant 1"
GO:0005515|GO:0051044|GO:0016477|GO:0009986|GO:0008283|GO:0007528|GO:0048408|GO:0006508|GO:0004
222|GO:0052548|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137721_PI430048170 0.3134708637963930.9663688161333540.41570332970693
0.4403835100142310.317904622434452 A A A 0.4175731505821590.470957877120695
0.43589879628436 A A A LNCV6_137721_PI430048170 mRNA
GCAAACCTGCCATTTAGGAGTAGAAAATGTATGATAAAACTCAAGTATTACATGCAGATC NM_001796 RefSeq chr16
- 61652010 62036835 CDH8 1006 "cadherin 8, type 2"
GO:0005886|GO:0034329|GO:0009409|GO:0005509|GO:0035249|GO:0043679|GO:0043083|GO:0016021|GO:0007
155|GO:0007156|GO:0045216|GO:0034332 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131475_PI430048170 0.000482464502899379 0.3174355307221715.05252697008929
4.72311390771249 5.06486158799742 P P P 6.37632416137304 6.70320858292121
6.72682309004547 P P P LNCV6_131475_PI430048170 mRNA
TTTCTCCAAAAGGCAAGGAGCAGAAGACATAGACGTTGAAACAGAAACAGAAGGATGAAG NM_002894 RefSeq
chr18 + 22933331 23026486 RBBP8 5932 "retinoblastoma binding protein 8, transcript variant 1"

GO:0001103|GO:0005515|GO:0051321|GO:0006357|GO:0001106|GO:0001835|GO:0031572|GO:0005730|GO:0010792|GO:0005634|GO:0000122|GO:0003684|GO:0007067|GO:0000082|GO:0006281|GO:0000724|GO:0017053|GO:0000014|GO:0000075|GO:0005654|GO:0000737|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129611_PI430048170 0.0960343720700162 1.22856471434415 9.34921424433438 9.28006111593015 9.1363832412769 P P P 8.76669006403792 9.15473972892925 8.93504676046238 P P P LNCV6_129611_PI430048170 mRNA TTCAGGCTGAGCAGAGAGGCTCCTGTACCCTCTCTCTCGGAATCTGAAGAGCCAGATTTA NM_021128RefSeq chr11 - 839720 842529 POLR2L 5441 "polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa"
GO:0008380|GO:0010467|GO:0006386|GO:0006368|GO:0006385|GO:0006367|GO:0006366|GO:0006363|GO:0006362|GO:0006361|GO:0005634|GO:0006360|GO:0006383|GO:0005829|GO:0005736|GO:0034587|GO:0005665|GO:0016032|GO:0005666|GO:0032481|GO:0035019|GO:0003899|GO:0006356|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130519_PI430048170 0.8418375758057560.9338322248233750.3999696654298581.9586196819923 1.06582296353867 A A A 0.4474977368573151.80494016659232 1.56518534787056 A A A LNCV6_130519_PI430048170 mRNA GCTCCGTTGAAGTAAACTAAGTAACTCAATATTCTTTATTTTGGTTTGGAACCTGTCTCA NM_181342RefSeq chr2 - 178463663 178478628 FKBP7 51661 "FK506 binding protein 7, transcript variant 1"
GO:0000413|GO:0061077|GO:0005509|GO:0005789|GO:0003755|GO:0005788|GO:0005528 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131572_PI430048170 0.2043509978758030.7412822169058964.34138758298957 4.80307071877972 4.90469755601651 P P P 5.24005019272991 4.68407878331931 5.38943258532176 P P P LNCV6_131572_PI430048170 mRNA CTGTCCTAAAGCCTTTGCCATTCCTAATACTCGTTTTGTAATAATTGCTGTATTTCTGTG NM_001184996 RefSeq chr7 + 156640746 156677126 RNF32 140545 "ring finger protein 32, transcript variant 1"
GO:0005515|GO:0016235|GO:0008270|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136973_PI430048170 0.22597423262993 0.8354965220719966.4055660381516 6.00757294825528 6.54455006680906 P P P 6.46586019222091 6.60324117930049 6.70848535207424 P P P LNCV6_136973_PI430048170 mRNA TAAAATTCGTCTCTGATTTGCCAGAGAAAAACGGTGGTAGCCATGGAAATCGGGAGTGAA NM_001135565 RefSeq chrX - 7048919 7148190 HDHD1 8226 "haloacid dehalogenase-like hydrolase domain containing 1, transcript variant 1"
GO:0016791|GO:0008150|GO:0003674|GO:0016311|GO:0046872|GO:0009117|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79663_PI430048170 0.1376776658907420.7673476888675265.79465763831339 5.87161410311784 6.00607184629277 P P P 6.22900299102987 5.9944551574172 6.5489561941959 P P P LNCV6_79663_PI430048170 mRNA TTAGGTGGTTACCCCAGAAAAATGCTGCTCAGTTTTTATTGTCTACCAATGATAAAACAA NM_002717RefSeq chr8 + 26291490 26372679 PPP2R2A 5520 "protein phosphatase 2, regulatory subunit B, alpha, transcript variant 1"
GO:0005515|GO:0010467|GO:0007084|GO:0008601|GO:0000159|GO:0043278|GO:0005829|GO:0007165|GO:0050790|GO:0006470|GO:0000184|GO:0000086|GO:0005654|GO:0004722|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144289_PI430048170 0.56704949646296 0.9375948948355430.285983125743266 0.2960869236862310.503795977632419A A A 0.3300447129794470.682600562977514 0.333602418378348A A A LNCV6_144289_PI430048170 mRNA TGTCTGTAATCGCCCTACTATTCAGTGGCGAGAAATAAAGTTTGCTTAGAAAAGAAAAAA NM_000594RefSeq chr6 + 31575566 31578335 TNF7124 tumor necrosis factor
GO:0032755|GO:0005515|GO:0009651|GO:0019722|GO:0032715|GO:0001819|GO:0002020|GO:0005615|GO:0042

802|GO:0031622|GO:0043068|GO:0030730|GO:0000165|GO:0030198|GO:0034116|GO:0031663|GO:0000060|GO:0
032729|GO:0005164|GO:0002876|GO:0009986|GO:0001891|GO:0032722|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141118_PI430048170 0.4298476083060670.9371326070928538.41552615763497 8.2965575910483
8.60747124707351 P P P 8.45869532842756 8.49701391264198 8.65450368591544 P P P
LNCV6_141118_PI430048170 mRNA
GGAAATTTGCTGCCTCAATGTTTACTGTGCCTTTGTTTTTGCTAGTGTGTGTTGTTGAAANM_032264RefSeq chr1 +
21440089 21484900 NBPF3 84224 "neuroblastoma breakpoint family, member 3, transcript variant 1"
GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142964_PI430048170 3.8770282321521e-05 2.0645195465508 6.82802667224724
6.93983335307204 6.87807581088506 P P P 5.91156156570505 5.80851839853165
5.78753642090795 P P P LNCV6_142964_PI430048170 mRNA
AGTTTTGGTGTGACTGGACATACTTGCTTCAATAAAAGAATACATCACTCCCCTCAAAAA NM_001282862 RefSeq
chr10 - 43194532 43229739 RASGEF1A 221002 "RasGEF domain family, member 1A, transcript variant
1" GO:0005622|GO:0032320|GO:0016477|GO:0007264|GO:0046579|GO:0005088 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130376_PI430048170 0.0456031395467641.56376515693172 5.88418265092684
5.30864076608885 5.66164842750156 P P P 5.02613273233051 5.2008950095323
4.70704506437444 P P P LNCV6_130376_PI430048170 mRNA
TGAAAACCCCAACTTCACCGGGAAGAAGATGGAAATCATAGATGACGATGTACCCAGCTT NM_000496RefSeq chr22
+ 25219644 25231869 CRYBB2 1415 "crystallin, beta B2"
GO:0005212|GO:0005198|GO:0043010|GO:0007601|GO:0050896|GO:0042803|GO:0042802 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131504_PI430048170 0.4598349334169370.6081727059451160.410520209133222
0.4435884408718090.458200518365164A A A 2.02305079333588 0.364461681357692
0.410126330788534A A A LNCV6_131504_PI430048170 mRNA
GCCAGAGCCTTAATAAACGTCCACAGAGTATAAATAACCAATTCCTCATTTGTTCATTAA NM_001911RefSeq chr14
- 24573517 24576260 CTSG 1511 cathepsin G
GO:0002003|GO:0004252|GO:0005886|GO:0009986|GO:0050832|GO:0005576|GO:0005634|GO:0005615|GO:0031
012|GO:0006955|GO:0022617|GO:0050778|GO:0030198|GO:0016485|GO:0032496|GO:0006508|GO:0008233|GO:0
044130|GO:0030141|GO:0044267|GO:0008201|GO:0070946|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132831_PI430048170 0.1464235972905271.01806728527855 0.3942735812672540.3986334815013
0.412162139822948A A A 0.3755349380633880.3554509248246050.396354977815509A A A
LNCV6_132831_PI430048170 mRNA
CTGGGTGTTACTGGAGGGAACACACTGTATAATACCTTTTGTTTCTGTTCTAAATGGATA NM_002365RefSeq chrX
+ 30230435 30237493 MAGEB3 4114 melanoma antigen family B3 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_144917_PI430048170 0.0183972007987206 0.4580219893379396.46600160998117
6.49190062433341 6.63144470871863 P P P 7.32588961143393 7.64212018470874
7.94117391612464 P P P LNCV6_144917_PI430048170 mRNA
GACAGCATTCTAGGTACAGATGGCACTCTGTTCAACCAACTGTGGATGGAAAATATTCTG NM_020374RefSeq chr12
- 4487729 4538508 C12orf4 57102 "chromosome 12 open reading frame 4, transcript variant 1"
GO:0043304|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117069_PI430048170 0.1360036656425171.19814530064205 3.41289765874378
3.70240562226303 3.66057385331355 P P P 3.15806420683012 3.30076971689202
3.52707237957948 P P P LNCV6_117069_PI430048170 mRNA
AAGCGAGTGTTTACGGGTGTTGAAGATCCTGCAAGAGGTCACTGCTGGGCAGACTGTCTT NM_000437RefSeq chr1
- 25959766 25998157 PAFAH2 5051 "platelet-activating factor acetylhydrolase 2, 40kDa"

GO:0016042|GO:0006629|GO:0043066|GO:0005737|GO:0005543|GO:0003847 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129404_PI430048170 0.3080781694776661.51006183195461 1.81697502463936 2.62008419479944 1.75624954681447 A A A 0.5914280961427412.40414743441379 0.881046692494404A A A LNCV6_129404_PI430048170 mRNA GATTCTGCCTGAGTTACTTCCCTTTTGAGAAATCATATCTCAAATACATAACCTGGTAAT NM_153214RefSeq chr2 + 112138384 112188214 FBLN7 129804 "fibulin 7, transcript variant 1"
GO:0005509|GO:0005578|GO:0007155|GO:0008201|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135540_PI430048170 0.00395278548252401 0.1992823415083862.76047737913322 1.80176327457662 2.32070166767942 A A A 4.08838332643225 4.99753208408484 4.78715399164889 P P P LNCV6_135540_PI430048170 mRNA CTCATTCTGTAAACGGTGTCTTTTTTTCATTATGGGAAAGCTTTATTGACACATTTGTTT NM_001184819 RefSeq chrX + 54530210 54567287 GNL3L 54552 "guanine nucleotide binding protein-like 3 (nucleolar)-like, transcript variant 1"
GO:0005739|GO:0005515|GO:0005737|GO:0016020|GO:0042254|GO:0008152|GO:0005730|GO:0003924|GO:0005654|GO:0005634|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144574_PI430048170 0.00219759784722906 0.4744418034570311 1.0642165318715 11.2931555816196 11.1068285550791 P P P 12.1904754569838 12.2531316215731 12.2571339637835 P P P LNCV6_144574_PI430048170 mRNA CCAAACCCCACCCATAAATCAATGGGCCCTTTATTTATGACGACTTTATTTATTCTAATA NM_003407RefSeq chr19 + 39406846 39409412 ZFP36 7538 ZFP36 ring finger protein
GO:0005515|GO:0010467|GO:0003727|GO:0010494|GO:0005634|GO:0003729|GO:0035925|GO:0019957|GO:0046872|GO:0005829|GO:0035556|GO:0071889|GO:0005737|GO:0042594|GO:0045638|GO:0017091|GO:0000289|GO:0000288|GO:0019901|GO:0032680|GO:0060213|GO:0000122|GO:0006402|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128973_PI430048170 0.0542479409428495 1.77034326525555 8.36207648972764 8.58288048760345 8.42523933597399 P P P 7.17369478995291 7.94760625752853 7.68214533172669 P P P LNCV6_128973_PI430048170 mRNA GCAGCTGTATTGTGTAACAAGCTCATTTGTACAGTGTCTGTTCATGTAATAAAGAATTAC NM_002275RefSeq chr17 - 41513744 41519018 KRT15 3866 "keratin 15, type I"
GO:0005882|GO:0005515|GO:0008544|GO:0097110|GO:0005200|GO:0005634|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131103_PI430048170 0.4754181047428240.6884494892008791.66606468969723 0.2611968255299490.402009201674757A A A 2.24675637978863 0.893149900852211 0.736705164206815A A A LNCV6_131103_PI430048170 mRNA GGTGATTCAGCTGTTCCATTTCCATATTCTCCCTTATTAGAAATGACCACTATATTATGT NM_173644RefSeq chr20 + 60055924 60072953 C20orf197 284756 "chromosome 20 open reading frame 197, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129528_PI430048170 0.1160480062500251.44342096258818 7.31056885641742 7.3859439138432 7.01156673343999 P P P 7.05739611594819 6.70560255407766 6.27946655970421 P P P LNCV6_129528_PI430048170 mRNA ATTTCAGGCATCGTTGAGGGGAGTGTTTTGGGGCCGCAGAGCTCTCAATGCTGCCTATCG NM_001077594 RefSeq chr14 + 103100143 103110557 EXOC3L4 91828 exocyst complex component 3-like 4
GO:0000145|GO:0051601|GO:0000149|GO:0006887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133532_PI430048170 0.2227908885502180.8295512493902299.41029781627221 9.48299039083265 9.46558106295188 P P P 9.42307202268942 9.91330779179061 9.78851810306282 P P P LNCV6_133532_PI430048170 mRNA ATTTTCTCACGAAGTCCCGATGGAACCCTGTGCTGTTGAGACATCAGTGTGTAAAACTCT NM_001167942 RefSeq

chr19 + 4640016 4655568 TNFAIP8L1 126282 "tumor necrosis factor, alpha-induced protein 8-like 1, transcript variant 1" GO:0032007|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138988_PI430048170 0.1297096733333230.80343488176051911.8892341458437
11.6512505564528 11.4119767169016 P P P 12.0655027521239 12.0523143908536
11.8068451522148 P P P LNCV6_138988_PI430048170 mRNA
GGGTGGCTGGAGTGAATTAAAGCCTTTGTTTTTTAAAGAAATGGCAAAGCCTTCGACTGA NM_001018078 RefSeq
chr9 + 127803180 127814081 FPGS 2356 "folylpolyglutamate synthase, transcript variant 2"
GO:0046901|GO:0031100|GO:0005743|GO:0006767|GO:0044281|GO:0005524|GO:0004326|GO:0005829|GO:0001889|GO:0005739|GO:0005737|GO:0006139|GO:0006766|GO:0007420|GO:0005759|GO:0046655|GO:0006730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134758_PI430048170 0.912039615349665 1.00180920479622 0.388290306413553
0.393220313084681 0.423622092063464 A A A 0.366700448043713 0.437796429400107
0.392165542506459 A A A LNCV6_134758_PI430048170 mRNA
CATGGCCAATAGTCATATGTGAAGACAGAGCAGATCAGTCTTTGTCAATGCTCTAACAAA NM_003301 RefSeq chr8 + 109087423 109119583 TRHR 7201 thyrotropin-releasing hormone receptor
GO:0007186|GO:0005886|GO:0005887|GO:0004997 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119671_PI430048170 0.417879288355908 1.90633436675965 0.294095671634306
0.274178183835917 2.1670566924851 A A A 0.290746487227812 0.25495910470203
0.283126737927477 A A A LNCV6_119671_PI430048170 mRNA
AACTTCAAGCCAGAAGATATCACCGAGGCTCTGAGAGCTTTTCAGGAAGCATCTGAACTT NM_002429 RefSeq chr12 - 55835429 55842983 MMP19 4327 "matrix metallopeptidase 19, transcript variant 1"
GO:0005509|GO:0005578|GO:0001554|GO:0001542|GO:0005576|GO:0001525|GO:0051591|GO:0030154|GO:0001541|GO:0022617|GO:0030198|GO:0030574|GO:0006508|GO:0008270|GO:0009725|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77296_PI430048170 0.108305219372894 2.71646668533145 2.88653616576307 2.75018492476837
3.00449216375117 A A P 2.40402514291746 0.522946776839306 0.509483200795856 A A A
LNCV6_77296_PI430048170 mRNA
TTTGGACCCAGGGGGGTGAACATTGGTGGTGTAGGCTCCTACTTGTACAATCCCCCCACT NM_206922 RefSeq chr6 - 43305472 43308792 CRIP3 401262 cysteine-rich protein 3 GO:0005737|GO:0042098|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133592_PI430048170 0.630908490553419 1.04455234297687 6.54011734186464
6.59864387770038 6.43167061978516 P P P 6.34499009890035 6.69839975310066
6.31056697820484 P P P LNCV6_133592_PI430048170 mRNA
TACATTCTCATCTACTCATTGTCTCAGTGCTGGTGGAGTTGACATTTGACAGTGTGGGAG NM_003355 RefSeq chr11 - 73974670 73982844 UCP2 7351 "uncoupling protein 2 (mitochondrial, proton carrier)"
GO:0001666|GO:0043066|GO:0007565|GO:0032869|GO:0007568|GO:0051881|GO:0005743|GO:0044281|GO:0022904|GO:0070542|GO:0006810|GO:0000303|GO:0016021|GO:0071333|GO:0061179|GO:0006839|GO:0010942|GO:0044237|GO:0015992|GO:0034198 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134679_PI430048170 0.659302601964865 0.9543718088049 0.466843910388427
0.445631191375756 0.504663609052637 A A A 0.753959461771307 0.382768316240258
0.45580739205683 A A A LNCV6_134679_PI430048170 mRNA
CCCTACAATGGGAAATGTCACAAGAATGTGCAAAAATAAAAATCTGAGGAAAAAACCCAC NM_145728 RefSeq
chr15 + 99105079 99135595 SYNM 23336 "synemin, intermediate filament protein, transcript variant A"
GO:0005882|GO:0005515|GO:0060053|GO:0016020|GO:0005912|GO:0045104|GO:0017166|GO:0043034|GO:0005200|GO:0008307|GO:0019215 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142683_PI430048170 0.0201545882443037 1.63738430022312 9.89648875047757
9.87486698252361 9.6600853224842 P P P 9.27302315828371 9.18576291394081
8.80929744133139 P P P LNCV6_142683_PI430048170 mRNA

TGCCATGAAGGAACTTGGGATTTTCAATGGAATAAGTAAAACATAAAGTCTATACTTGGG NM_024830 RefSeq chr5_KI270791v1_alt + 8166 48346 LPCAT1 79888 lysophosphatidylcholine acyltransferase 1
GO:0045732|GO:0047184|GO:0060041|GO:0005783|GO:0044281|GO:0019432|GO:0043129|GO:0006654|GO:0044255|GO:0047159|GO:0005811|GO:0005794|GO:0036148|GO:0005509|GO:2001246|GO:0008654|GO:0047191|GO:0047192|GO:0016020|GO:0000139|GO:0005789|GO:0016021|GO:0006644|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135913_PI430048170 0.0686237351459220.2553912867634480.438959566868461 2.19667754055939 2.35948898211408 A A A 3.79465915440464 4.00598362516891 3.74504492409991 P P P LNCV6_135913_PI430048170 mRNA
TTTATACCCACACACCTGTCTACAGTGTCATTCAATAAAGTGCACGTGCTTGTGAAAAAA NM_003641 RefSeq chr11 + 313990 315272 IFITM1 8519 interferon induced transmembrane protein 1
GO:0005515|GO:0030336|GO:0008285|GO:0005886|GO:0035456|GO:0019221|GO:0035455|GO:0009615|GO:0045669|GO:0035556|GO:0051607|GO:0060337|GO:0001503|GO:0016020|GO:0046597|GO:0050776|GO:0005057|GO:0016021|GO:0034341|GO:0007166|GO:0045071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127123_PI430048170 0.1314737788352161.45242569952289 6.4118954012513 6.20786240483381 6.40088353387175 P P P 6.1242099391893 5.86574395056973 5.30848641719538 P P P LNCV6_127123_PI430048170 mRNA
GGGTACTGTGGAAAGTGTCTTCCTCACATGACTACTGGTCTCCCAATTCAAGTCATATGA NM_025003 RefSeq chr12 - 43354208 43551921 ADAMTS20 80070 "ADAM metallopeptidase with thrombospondin type 1 motif, 20"
GO:0031012|GO:0043066|GO:0030198|GO:0006508|GO:0005578|GO:0009967|GO:0008270|GO:0045636|GO:0004222|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134812_PI430048170 0.2487053398750990.8738040926062884.84742230229375 5.04689946330598 4.64580433955494 P P P 5.01559264395249 5.21012672609387 4.90986612921588 P P P LNCV6_134812_PI430048170 mRNA
TAGCAGAAAAGCTCATCAAGGCCTTTGCTGAGCAGATATTTTACACCGGCTTCATCCACT NM_174922 RefSeq chr8 + 144374014 144393238 ADCK5 203054 aarF domain containing kinase 5
GO:0005739|GO:0004674|GO:0006468|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142200_PI430048170 0.49163990761947 1.58225628058687 0.282053472798852 1.90271774276341 0.306384957899725 A A A 0.4524185790746790.349142231476996 0.346047097370837 A A A LNCV6_142200_PI430048170 mRNA
GTTTAGAAGTGAGTGTAATCCAGCAATACAGTTTACTGGTTTAGTTGGTGGGTTAATTAA NM_138691 RefSeq chr9 + 72521800 72836351 TMC1 117531 transmembrane channel-like 1
GO:0005245|GO:0050910|GO:0060005|GO:0070588|GO:0016021|GO:0009897|GO:0060117|GO:0032426 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142616_PI430048170 0.2781584395795090.8913392662781976.33439614569202 6.13604749112062 6.51121160097326 P P P 6.36074061703699 6.50072606104537 6.62984018189838 P P P LNCV6_142616_PI430048170 mRNA
GAATACGGGTCTGTGGTGATAAATACAGTACAATCCTTTTTCACTGTTATGTCTTTAATG NM_012154 RefSeq chr8 - 140531164 140635547 AGO2 27161 "argonaute RISC catalytic component 2, transcript variant 1"
GO:0005515|GO:0010467|GO:0003743|GO:0031047|GO:0003729|GO:0009791|GO:0035279|GO:0006412|GO:0046872|GO:0035087|GO:0006413|GO:0016441|GO:0035068|GO:0005829|GO:0010586|GO:0016442|GO:0070551|GO:0005737|GO:0007173|GO:0007219|GO:0000932|GO:0031054|GO:0045947|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134526_PI430048170 0.6598089760812941.32676305240175 2.38987899481138 1.41224679372374 0.423386516003162 A A A 0.5807925416210141.96998323570314 0.635814744112003 A A A LNCV6_134526_PI430048170 mRNA
TGTGTATTCCTTCTCAATGCTTTCCTTGGTGTTAACCTTAATAAAAAGGCGTCATCTCCCNM_001013635 RefSeq chr12 + 48183582 48185926 CCDC184 387856 coiled-coil domain containing 184 GO:0005737 . NA -

. NA NA NA NA NA NA NA NA NA
LNCV6_141050_PI430048170 0.1765410534177631.15411655420114 14.4017259620095
14.3697715841657 14.6617423824642 P P P 14.1522910489668 14.2281645705706
14.4354531242016 P P P LNCV6_141050_PI430048170 mRNA
GCTGGTAGCTTCTATGTAATTCGCAGTGATTCCATCTAAATAAAAGTTCTGTGATCTGCA NM_001089591 RefSeq
chr1 - 15807161 15807699 UQCRHL NA ubiquinol-cytochrome c reductase hinge protein-like NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134544_PI430048170 0.3226513478187970.8539625047804380.427329227413946
0.3744302420941590.384400672517641 A A A 0.4821881227272670.923931212882434
0.408305168386524 A A A LNCV6_134544_PI430048170 mRNA
CCCAGTGCATGTACGCCCTCTGAGATGCAATAAACACCTTGAACAAAGAAATGCAAAAAA NM_001256717 RefSeq
chr6 - 83552885 83709408 SNAP91 9892 "synaptosomal-associated protein, 91kDa, transcript variant 6"
GO:0005515|GO:0005545|GO:0005905|GO:0019901|GO:0005886|GO:0030276|GO:0030136|GO:2000369|GO:0007268|GO:0015031|GO:0048268 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139223_PI430048170 0.8298366117692521.02855819411861 7.16515271684329
7.27979348879635 7.58996667619234 P P P 6.99112998825719 7.32949095226563
7.56895072951277 P P P LNCV6_139223_PI430048170 mRNA
CTCTACTTTTGTTACCTAAAATAAAATGCATTCGTTTCTCTGGGGGAGCCTGTTTAAAAA NM_016207 RefSeq chr2
+ 9423536 9473110 CPSF3 51692 "cleavage and polyadenylation specific factor 3, 73kDa"
GO:0005515|GO:0006379|GO:0008380|GO:0010467|GO:0006369|GO:0006378|GO:0008409|GO:0006398|GO:0006366|GO:0003723|GO:0031124|GO:0004521|GO:0046872|GO:0006406|GO:0000398|GO:0030529|GO:0005847|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131389_PI430048170 0.6707982796469650.9685291786750190.600333195167769
0.5209885706533330.301332318687348 A A A 0.4173122777248330.614803586804462
0.538467806734412 A A A LNCV6_131389_PI430048170 mRNA
CTGATTTCCTTATTTTCTTTATCACTTTAAGGTACAGATTCTCCTTCTCAGTGAGGTAGA NM_033061 RefSeq
chr17_JH159146v1_alt + 233710 234813 KRTAP4-7 100132476 keratin associated protein 4-7 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132546_PI430048170 0.1253674156082830.5957034057766151.66316196511688
1.68300873676653 2.14607184660518 A A A 2.48965630537089 2.0457205556732
3.06897565310541 A A P LNCV6_132546_PI430048170 mRNA
TTAGGGGTGTCACTCTTAAAATCGCATATTCAACAAACAAATGCCTTCTAAGTACTGAAA NM_001173517 RefSeq
chrX - 136213219 136251579 MAP7D3 79649 "MAP7 domain containing 3, transcript variant 3"
GO:0008017|GO:0005813|GO:0005874|GO:0005819|GO:0000226|GO:0005634|GO:0015629|GO:0005737|GO:0046785|GO:0015631|GO:0016020|GO:0005198|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145662_PI430048170 0.1273928665620330.4703850365938714.11943447999649
2.52799379189617 2.63701531808409 P A A 4.40502899379398 4.24116926080849
4.48150421731443 P P P LNCV6_145662_PI430048170 mRNA
GACCGATTGCATAGGAATTGCACAATCCATGAACAGCATTAGAATTTACAGCAAGAACAG NM_006218 RefSeq chr3
+ 179148522 179234709 PIK3CA 5290 "phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha"
GO:0005515|GO:2000653|GO:0044029|GO:0043560|GO:2000811|GO:0050900|GO:0060048|GO:0043524|GO:0007173|GO:0016301|GO:0016303|GO:0045860|GO:0001944|GO:0036092|GO:0030168|GO:0038028|GO:0030027|GO:0008543|GO:0043542|GO:0046934|GO:0045087|GO:0043491|GO:0006644|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129835_PI430048170 0.0139920978469267 1.58657816718455 7.46320037760994
7.5598542769185 7.49752002549729 P P P 6.88921230216666 6.9676391285713
6.64885166314388 P P P LNCV6_129835_PI430048170 mRNA

AAGTTAAAGATGGTGAATCAATGCTTCGGGCTTGGAGATGGAACATGCCTCCTCTCCATT NM_001282144 RefSeq chr11 + 119168712 119184016 NLRX1 79671 "NLR family member X1, transcript variant 4" GO:0005515|GO:0032715|GO:0050728|GO:0045087|GO:0039536|GO:0016032|GO:0005741|GO:0032480|GO:0005524|GO:0032688|GO:0045824|GO:0043124 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_140965_PI430048170 0.574788065523414 1.24806408944234 0.253128493824379 1.30997144941462 0.277722708270549 A A A 0.47598913815748 0.37089558154401 0.297227715862341 A A A LNCV6_140965_PI430048170 mRNA

CTGCTGTCCTTCATGATTGATTAGCCTGTTTCAGCAATTTATACATCAGAAATCTTTAGTNM_001099850 RefSeq chr1_KI270766v1_alt - 166162 169622 LOC391003 NA PRAME family member-like NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135156_PI430048170 0.567321115467861 0.809232429514591 1.36928276738931 0.307969351870887 0.412548146589234 A A A 1.43094651278236 1.29244576826331 0.288512658011358 A A A LNCV6_135156_PI430048170 mRNA

GGGGGGAGGTTCCCTTGGATTAAGGTTCCAAATAAAGCACATGGTTTCCAGAGCAAAAAA NM_022467 RefSeq chr19 + 33684527 33773509 CHST8 64377 "carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8, transcript variant 3" GO:0016051|GO:0006790|GO:0000139|GO:0042446|GO:0001537|GO:0016021|GO:0007417|GO:0030166 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_136425_PI430048170 0.819368195414562 1.01327306917776 0.275343716544272 0.280500259089045 0.464902250375948 A A A 0.344449654614256 0.293888921500013 0.333047133536753 A A A LNCV6_136425_PI430048170 mRNA

GAATTCGGCATGGTTTCATTTTACTGCACTAGCCAAGAGACTTTACTTTTAAGAAGTATT NM_007315 RefSeq chr2 - 190969035 191014250 STAT1 6772 "signal transducer and activator of transcription 1, 91kDa, transcript variant alpha" GO:0005515|GO:0042542|GO:0000790|GO:0003700|GO:0006366|GO:0000983|GO:0008015|GO:0019221|GO:0051591|GO:0042803|GO:0042802|GO:0060334|GO:0051607|GO:0060337|GO:0003690|GO:0060338|GO:0072136|GO:0031663|GO:0060333|GO:0043124|GO:0005164|GO:0032869|GO:0000122|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_72732_PI430048170 0.0526024923163262 0.378488332304515 2.16457359042767 1.64590612962717 2.93486733544272 A A P 3.61571751394371 3.86779896349897 3.75058131640363 P P P LNCV6_72732_PI430048170 mRNA

GTAAGTGGAATGTTTGAATGACTTTGCCAGGTCAGAGCAAGTAATATTTCTGTATCTGAG NM_206831 RefSeq chr3 - 16257060 16264989 DPH3 285381 "diphthamide biosynthesis 3, transcript variant 1" GO:0005515|GO:0005737|GO:0050709|GO:0051099|GO:0005654|GO:0005634|GO:0044267|GO:0046872|GO:0017183|GO:0043687|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_136398_PI430048170 0.149552101020699 0.28084789350342 3.77796582849487 0.29133892180262 1.83628679034853 P A A 3.07494308223598 4.19908926045404 5.289902750635 P P P LNCV6_136398_PI430048170 mRNA

AGCCCTCCGCAATAATTCACCAGACCAGAAGCCACTGGTGTACAGAGAACACTTAAAAAA NM_015568 RefSeq chr20 + 38805704 38923024 PPP1R16B 26051 "protein phosphatase 1, regulatory subunit 16B, transcript variant 1" GO:0005515|GO:0005886|GO:0019903|GO:0035307|GO:0035308|GO:0005634|GO:0042995|GO:0014066|GO:0008599|GO:0007165|GO:0051489|GO:0050790|GO:0001938|GO:0061028 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_134309_PI430048170 0.258954922122932 2.25633285751599 2.44311161253721 1.53418215408319 0.35650747193965 A A A 0.387784919520315 0.588566816095951 0.535127786424277 A A A LNCV6_134309_PI430048170 mRNA

CAGTCTGAGAAATAAGGATGTAAAAGAAGCAGTCAACAAAGCAATCACCAAGACATATGT NM_001004743 RefSeq chr11 - 56462468 56463401 OR5M9 NA "olfactory receptor, family 5, subfamily M, member 9" NA

. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126098_PI430048170 0.196577716535663 1.04265680368054 0.442926338178093
0.398887449870703 0.430033113887074 A A A 0.309688860546144 0.356569811988129
0.422902155487187 A A A LNCV6_126098_PI430048170 mRNA
GGGAAAAAGGCCATTGGCTAATTGCACGTGTGTATTGCAATGGGAAATAAATAAATAATA NM_000354 RefSeq
chrX - 106033198 106038727 SERPINA7 6906 "serpin peptidase inhibitor, clade A (alpha-1
antiproteinase, antitrypsin), member 7"
GO:0051412|GO:0004867|GO:0033189|GO:0042493|GO:0007568|GO:0042562|GO:0043434|GO:0070327|GO:0005
576|GO:0009791|GO:0005615|GO:0010951|GO:0034695|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130030_PI430048170 0.580743771598089 1.23248429562324 2.52359724938225
1.48751104577124 1.52588838001575 A A A 1.9834925582347 0.497945443471377
1.96730315440209 A A A LNCV6_130030_PI430048170 mRNA
TATTGCTATATGACATATGCTTTATGCTAAGACCTGAGGTGGATGGGAGGAAGCAGACCG NM_001111298 RefSeq
chr6 - 109390214 109441171 PPIL6 285755 "peptidylprolyl isomerase (cyclophilin)-like 6, transcript
variant 2" GO:0000413|GO:0006457|GO:0003755 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139056_PI430048170 0.0348976239549841 1.35559023599296 3.69969265262435
3.80794510404534 3.50895486134123 P P P 3.24554319917302 3.40805321505756
3.03830427391901 P P P LNCV6_139056_PI430048170 mRNA
AATCTTGAAAAAGAAGTCTGTCAAAGGTATGAGAAAAGCCTTCTCCACCTGTGGAGCTCA NM_001005514 RefSeq
chr3 + 98149385 98150318 OR5H14 NA "olfactory receptor, family 5, subfamily H, member 14" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110868_PI430048170 0.233555980625773 1.11843161289381 7.70818183188322
7.67897354252113 7.84405134321652 P P P 7.53452311254758 7.42996585621022
7.76685009747924 P P P LNCV6_110868_PI430048170 mRNA
ACAAGTGCAAATTCTTACACCAGGAGAGGATGGATGTTTGCGAAACTCATCTTCACTGGC NM_000484 RefSeq
chr21 - 25880549 26170820 APP 351 "amyloid beta (A4) precursor protein, transcript variant 1"
GO:0005515|GO:0031594|GO:0046914|GO:0045202|GO:0007409|GO:0051402|GO:0005615|GO:0031175|GO:0043
231|GO:0042802|GO:0006878|GO:0007219|GO:0030198|GO:0007176|GO:0050885|GO:0006979|GO:0006378|GO:0
005794|GO:0009986|GO:0007617|GO:0050803|GO:0043393|GO:0030168|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131613_PI430048170 0.011032997748367 0.585454895967866 6.77304889393139
6.69301292759375 7.02884813908163 P P P 7.449579944653 7.48987939573285
7.85816391145853 P P P LNCV6_131613_PI430048170 mRNA
CGTGCCATATTTTGTTCCTGATGGGATCAACTTAATGTTTAAGACTTTAGATGTCTTGTA NM_001142307 RefSeq
chr11 + 18322268 18367043 GTF2H1 2965 "general transcription factor IIH, polypeptide 1, 62kDa,
transcript variant 2"
GO:0005515|GO:0010467|GO:0006368|GO:0006367|GO:0006366|GO:0006363|GO:0006362|GO:0006361|GO:0006
360|GO:0000079|GO:0000439|GO:0045944|GO:0016032|GO:0008094|GO:0006370|GO:0008353|GO:0050434|GO:0
006281|GO:0004672|GO:0006283|GO:0045814|GO:0040029|GO:0005654|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141093_PI430048170 0.035616087060954 1.62936968591311 2.86892080899085
2.7070808192584 2.6064332260655 A A A 2.31062455945569 1.99084893789163
1.71942580457436 A A A LNCV6_141093_PI430048170 mRNA
ATCTGGAAACTGTATCAGAGCCATGGGAAAGAATGAAGAAAGGCTCGGCTCTTTACGACT NM_001045477 RefSeq
chr9 + 96929003 96942290 NUTM2G NA "NUT family member 2G, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83257_PI430048170 0.00945653480958591 1.64006872625674 8.11787214837721

8.26612718458349 8.3870388638252 P P P 7.30951394603535 7.62906100732687 7.67682756075206 P P P LNCV6_83257_PI430048170 mRNA TTAAGTTTCTCTGCAGAAACTACTGACGGAGTCCTGTGTTTGTGAGTCGTTTCCCCTATG NM_003119 RefSeq chr16 + 89508387 89557768 SPG7 6687 "spastic paraplegia 7 (pure and complicated autosomal recessive), transcript variant 1" GO:0005515|GO:0031966|GO:0005524|GO:0007399|GO:0005739|GO:0006508|GO:0008233|GO:0008270|GO:0007005|GO:0008089|GO:0016021|GO:0051082|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120963_PI430048170 0.86348009707453 1.06138328551847 1.10830888670144 0.337100683509034 0.329646431839805 A A A 0.411460504807193 0.331714750367873 0.861470283060656 A A A LNCV6_120963_PI430048170 mRNA AGCAACATCTCAGAAAAAAGCAAGGTGCACTACCATGTCGCAGTCATCATCAACTACCTG NM_001256299 RefSeq chr17_GL000258v2_alt - 952321 1168475 MGC57346-CRHR1 NA "MGC57346-CRHR1 readthrough, transcript variant 5" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129156_PI430048170 0.299350275800032 1.03884491067391 0.315991035373814 0.270631158312892 0.403713643453508 A A A 0.284990826894154 0.256782263965575 0.286614263939623 A A A LNCV6_129156_PI430048170 mRNA GAAATGGATTGTTCCTGCATATATTGCTGGTGGCAGTATTCAGTCTTGTGTTCTTTTTCT NM_001008781 RefSeq chr11 + 92352095 92896469 FAT3 120114 FAT atypical cadherin 3 GO:0005886|GO:0005509|GO:0007275|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72528_PI430048170 0.137391066405105 0.803099454935449 7.25583477405164 6.80175855467068 6.91244911738304 P P P 7.1228243718918 7.47216686610108 7.3424252588296 P P P LNCV6_72528_PI430048170 mRNA AGAGTAAAGACTGTCCAAGCAACAGTAGCTGCCAAAGAGAAAATACGAAATAGACACTTT NM_001104595 RefSeq chr22 + 45309199 45341955 FAM118A 55007 "family with sequence similarity 118, member A, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139096_PI430048170 0.189336189030956 0.734391941145699 4.79286315913271 4.30844327663924 4.35810516624081 P P P 5.29479569951635 4.91108729683039 4.54278838521982 P P P LNCV6_139096_PI430048170 mRNA GGATATGGCTGCTGCCGCCCATCGTACAATGGAGGATACGGATTCTCTGGCTTTTATTAA NM_181607 RefSeq chr21 - 30480044 30480317 KRTAP19-1 337882 keratin associated protein 19-1 GO:0005882 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127939_PI430048170 0.24964261210132 1.04888020864977 0.484656325353276 0.359214382388214 0.439756453261549 A A A 0.296580140134751 0.36082515358555 0.419828839584273 A A A LNCV6_127939_PI430048170 mRNA GGAATGGTTGGATTTTAGTTACAGCTGTGATTTGGAAGGGAAACTTTCAAAATAGTGAAA NM_001172132 RefSeq chr20 + 32052187 32101854 HCK 3055 "HCK proto-oncogene, Src family tyrosine kinase, transcript variant 3" GO:0030133|GO:0005515|GO:0008284|GO:0071801|GO:0005884|GO:0008360|GO:0019221|GO:2000251|GO:0005634|GO:0042995|GO:0005764|GO:0030154|GO:0005829|GO:0050764|GO:0051090|GO:0046777|GO:0002758|GO:0006954|GO:0030838|GO:0071375|GO:0016032|GO:0007155|GO:0038083|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136691_PI430048170 0.251611210200754 1.03180302953611 0.340134647625424 0.274463877886977 0.369972652612075 A A A 0.285683292594055 0.272219597276645 0.292738526614671 A A A LNCV6_136691_PI430048170 mRNA CCAAAACAAAACTCAGCATGATACTTTGAGATTGTGTTCTGAGAGATGATATGACTACAT NM_004950 RefSeq chr12 - 90963678 91005026 EPYC 1833 epiphycan GO:0007565|GO:0005578|GO:0005539 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_135194_PI430048170 0.40946119653107 1.05104908896459 0.291439693614095
0.287600542111808 0.488746699035857 A A A 0.301789473227504 0.263147332375844
0.296366070503916 A A A LNCV6_135194_PI430048170 mRNA
TTTAAGCACCACTGGACTACACATTCTTCTGTGGCAGTTATCTTACCTTCCCATAGACAC NM_033303 RefSeq chr8
- 26748149 26865405 ADRA1A 148 "adrenoceptor alpha 1A, transcript variant 2"
GO:0030018|GO:0060402|GO:0008285|GO:0005886|GO:0035024|GO:0007267|GO:0007200|GO:0005634|GO:0007
202|GO:0007204|GO:0007512|GO:0035556|GO:0006939|GO:0003084|GO:0001985|GO:0090037|GO:0045907|GO:0
060452|GO:0045987|GO:0035265|GO:0045760|GO:0070374|GO:0009725|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_110424_PI430048170 0.0270021340126617 1.22041566541104 3.51369784968181
3.69490098825351 3.55613731115532 P P P 3.37502828373254 3.35104423596732
3.17464951059319 P P P LNCV6_110424_PI430048170 mRNA
AATGTTCTATGGGCAGACGCCCTTCTACGCGGATTCCACGGCGGAGACCTATGGCAAGAT NM_001081563 RefSeq
chr19 - 45769708 45780603 DMPK 1760 "dystrophia myotonica-protein kinase, transcript variant
1"
GO:0005515|GO:0031965|GO:0005886|GO:0008016|GO:0006874|GO:0033017|GO:0010830|GO:0005524|GO:0046
872|GO:0005829|GO:0005640|GO:0050790|GO:0017020|GO:0004674|GO:0005789|GO:0010657|GO:0006468|GO:0
006998|GO:0031307 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131087_PI430048170 0.00120989785677631 1.42173682170024 6.80739829886577
6.68244337591043 6.69096726720931 P P P 6.2290822307777 6.2554198782745
6.17560919493624 P P P LNCV6_131087_PI430048170 mRNA
ACTGAAATGTACTAGCTGGATGTGACCCAGTCTTAATAAACAGGTTTTCTAATCCAGAAA NM_014014 RefSeq
chr2 - 96274335 96305569 SNRNP200 23020 small nuclear ribonucleoprotein 200kDa (U5)
GO:0005515|GO:0008026|GO:0008380|GO:0010467|GO:0000354|GO:0005634|GO:0071013|GO:0005524|GO:0001
649|GO:0042802|GO:0004004|GO:0016020|GO:0000398|GO:0005654|GO:0005681|GO:0005682 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129454_PI430048170 0.021710870403358 1.12343858576346 13.8484966143257
13.9453921669246 13.8333290900562 P P P 13.7538273204598 13.6826409601292
13.6884785356365 P P P LNCV6_129454_PI430048170 mRNA
CCAAAGATCCCTGGAGGGCTAGTTCGTATTTTTGTGTTAAACTATTTGTTAGAATAAAGT NM_145030 RefSeq
chr7 - 100435288 100436471 PPP1R35 221908 "protein phosphatase 1, regulatory subunit 35"
GO:0019902|GO:0010923|GO:0004864 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_101114_PI430048170 0.0935392904691379 0.394965268759709 2.03904267909015
0.4787766721849471.95874438926214 A A A 2.88001436416365 3.19308181780946
2.86163169714406 P P P LNCV6_101114_PI430048170 mRNA
TAAAAAGATGTCCATCTGGGGACATGAAAGGCCAGTGGATTGTGCCTTGCCTTAGTTGTT NM_024913RefSeq chr7
+ 120988696 121297444 CPED1 79974 "cadherin-like and PC-esterase domain containing 1, transcript
variant 1" GO:0005783 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137545_PI430048170 0.4625164488219980.9481797680297380.307642067114183
0.3152410318087360.406738194440847A A A 0.3635339718593260.31343411556038
0.571866730071559A A A LNCV6_137545_PI430048170 mRNA
GTGTTTGACGCAGTTACAGATATAATAATCAAAGAGAATCTAAAAGACTGTGGGCTTTTC NM_001102386 RefSeq
chr7 - 80458670 80511926 GNAT3 NA "guanine nucleotide binding protein, alpha transducing 3"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137231_PI430048170 0.1196458380260690.87009196753148 10.7570750713103
10.6857300962716 10.7669746783177 P P P 10.7882561177907 11.0604895764177 10.951743802685
P P P LNCV6_137231_PI430048170 mRNA
AGTAAGTGATGTGTGTCTGTGTGTGTGTCTAGAAGTGCTGCACTCACCTTGTGTTATTGG NM_018129RefSeq chr17

+ 47941522 47949308 PNPO 55163 pyridoxamine 5'-phosphate oxidase
GO:0042823|GO:0010181|GO:0042816|GO:0006767|GO:0044281|GO:0005829|GO:0005737|GO:0006766|GO:0005654|GO:0004733|GO:0008615|GO:0055114|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145598_PI430048170 0.6045681671771530.891400149982394 0.256128775557761
0.265780695399211 0.722495315254879 A A A 0.3727935227152050.992848417171086
0.327250897278878 A A A LNCV6_145598_PI430048170 mRNA
TCTTGTTTCCCTGATTATGATGAGCTTCCATTGTTCTGTTAAGTCTTGAAGAGGAATTTA NM_002463 RefSeq chr21 + 41362022 41408942 MX2 4600 MX dynamin-like GTPase 2
GO:0019221|GO:0035455|GO:0003924|GO:0005634|GO:0006952|GO:0005525|GO:0009615|GO:0015031|GO:0005829|GO:0051607|GO:0005737|GO:0060337|GO:0005643|GO:0008152|GO:0051726|GO:0051028|GO:0046822 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138385_PI430048170 0.53082135747917 0.57324618446349 1.94592452197554 1.9127425290529
0.426791991347012 A A A 0.5380604970474712.78277272257412 2.86801299478979 A P P
LNCV6_138385_PI430048170 mRNA
GATGGAAGCCTTCTTTTTCTCCTTTACCTCATATTGTAATAAAGCTCTGATTTCTGACTC NM_178430 RefSeq chr1 + 152663410 152664659 LCE2D 353141 late cornified envelope 2D GO:0031424 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120436_PI430048170 0.6139372390320081.02210003852102 0.279940548373363
0.309514853086516 0.442305694733801 A A A 0.3378292617547750.304224966545188
0.30003342026235 A A A LNCV6_120436_PI430048170 mRNA
TAACTTCTATTACTGGGTTGTCAACTTCTGCGATAGCAACTAACGGGTTTGTTCGTGGAG NM_000338 RefSeq chr15 + 48206300 48304078 SLC12A1 6557 "solute carrier family 12 (sodium/potassium/chloride transporter), member 1, transcript variant 1"
GO:0048878|GO:0006821|GO:0007588|GO:0005886|GO:0001822|GO:0055085|GO:0016324|GO:0034220|GO:0016020|GO:0006810|GO:0016021|GO:0006814|GO:0006813|GO:0070062|GO:0006811|GO:0008511 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133338_PI430048170 0.6636779068143130.9407086036270120.376354662231104
0.347666374341546 0.299114354058136 A A A 0.2474988124031440.293119045264592
0.703172921166094 A A A LNCV6_133338_PI430048170 mRNA
GACACCTCCTCATTTAACATAGAAAATGACTAACCCAATAATTCAGGGAGTTAAAACTCA NM_152457 RefSeq chr16 - 3432421 3443537 ZNF597 146434 zinc finger protein 597
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136858_PI430048170 0.4200804490747081.280055818932 2.67013059461051 1.7771751862596
2.45120315362973 A A A 1.97891758988882 2.4497207555496 1.33179902397282 A P A
LNCV6_136858_PI430048170 mRNA
GGTGCTGTTTGCCCTTACAAAAGAAATAAGATCTTAGAGACCTTCTCCATGATGTACATG NM_001005180 RefSeq chr11 + 5736447 5737538 OR56B1 387748 "olfactory receptor, family 56, subfamily B, member 1"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143675_PI430048170 0.0814476259872051 0.70773006408643 6.34022075161598
5.99551723165437 6.60566230958583 P P P 6.67051927804686 6.83167924540362
6.98259146483375 P P P LNCV6_143675_PI430048170 mRNA
GGAGGTACCTATTTCTACCGTTTCAAGTGATGAAGTGAAAATAATTTACATTCGATAGTG NM_053053 RefSeq chr1 - 166856511 166876417 TADA1 117143 transcriptional adaptor 1
GO:0006355|GO:0005737|GO:0043966|GO:0030914|GO:0003713|GO:0006325|GO:0005654|GO:0005925|GO:0006351|GO:0004402 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49460_PI430048170 0.0203090920764033 1.42021030002584 4.71763749376287 4.8742927048734
5.07443628844315 P P P 4.25417236396635 4.4952035223082 4.41065113132361 P P P

LNCV6_49460_PI430048170 mRNA
TGGAAGATCAGGAAATGCACCTTACTTCCTCTGTTATGCCAGATATGGTTAGCCACTTTG NM_001195243 RefSeq
chr7 + 129502478 129512932 SMKR1 100287482 small lysine-rich protein 1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_128526_PI430048170 0.0482457667629237 0.70242909014735 8.71664532161528
8.93672229003238 8.50223524748182 P P P 8.97016783551004 9.31966617555612
9.39281215514704 P P P LNCV6_128526_PI430048170 mRNA
GATCAAGCAGTTATTTGATTTGTGCTCACTTTTGATATGGCCAATAAAACCATACCGACT NM_000107 RefSeq chr11
+ 47214941 47239218 DDB2 1643 "damage-specific DNA binding protein 2, 48kDa"
GO:0000209|GO:0005515|GO:0035518|GO:0004842|GO:0030054|GO:0003677|GO:0051865|GO:0003684|GO:0043
234|GO:0006281|GO:0006290|GO:0070914|GO:0005654|GO:0031465|GO:0006289|GO:0000718|GO:0009411 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135858_PI430048170 0.7195673979975841.06892264931409 0.313897384800848
0.3058558593701550.843780352096341 A A A 0.4716527596511020.405391020700028
0.364276392650645 A A A LNCV6_135858_PI430048170 mRNA
ACCCCAAACTTGTACACAAAAGAAAGCACAGATTGTTTACCTGTTGTGGATTTTAGATGT NM_001281740 RefSeq
chr18 + 36297695 36780059 FHOD3 80206 "formin homology 2 domain containing 3, transcript variant
3" GO:0005515|GO:0030018|GO:0051639|GO:0030837|GO:0045214|GO:0005865|GO:0055003|GO:0003779 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141666_PI430048170 0.4101385753638080.8478695566691430.263276217323764
0.4296136433911410.295856151823778 A A A 0.9420691638388390.384400672517641
0.293214747925818 A A A LNCV6_141666_PI430048170 mRNA
AAATATGTTTCCACCAAACCTTGTGGAGGCCTGCTTCAAACAGTTCAAGACGCAGTACAG NM_001272087 RefSeq
chr19 - 14961312 14979735 SLC1A6 6511 "solute carrier family 1 (high affinity aspartate/glutamate
transporter), member 6, transcript variant 1"
GO:0005794|GO:0005886|GO:0005313|GO:0007268|GO:0055085|GO:0015813|GO:0015810|GO:0016020|GO:0005
887|GO:0015183|GO:0042391|GO:0017153|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134641_PI430048170 0.6916302311760641.31074146255373 0.55937286855808
0.44985010481811 1.99299683940186 A A A 0.29930912135571 0.975546916200598
1.00456622965789 A A A LNCV6_134641_PI430048170 mRNA
TGTCCCCTTACCTAGTAAGTCTTTGGCGAGGATGAACCTGATTGTTACAAGGGTTACACA NM_002022 RefSeq chr1
+ 171314182 171342084 FMO4 2329 flavin containing monooxygenase 4
GO:0050661|GO:0042737|GO:0004499|GO:0050660|GO:0005789|GO:0016021|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136037_PI430048170 0.9075251976030030.9136474920235671.04381704252377
0.2957111146661670.913356925110138 A A A 0.58517616406409 0.276546690111943
1.56069335464127 A A A LNCV6_136037_PI430048170 mRNA
TTGGCAGGAAGAGAACATATTCTGCATCCCTCACTGAATTCAGTAATAAATAAAAATGTG NM_001012419 RefSeq
chr9 + 67859348 67902847 ANKRD20A3 NA "ankyrin repeat domain 20 family, member A3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90429_PI430048170 0.2760337541784350.8790677458655168.856279332271 8.68169223579822
8.42322168289069 P P P 8.98528215569562 8.83917869296495 8.71435657800946 P P P
LNCV6_90429_PI430048170 mRNA
GAAAAAGCTCCAGAACTCCACCAAGATCCTGCAGAAGAATAACCTGAATCTGCTCAGAGA NM_001261434 RefSeq
chr17 - 42950525 42964498 AARSD1 NA alanyl-tRNA synthetase domain containing 1 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_127577_PI430048170 0.0279722220781498 0.3983123498680414.03666318475387
3.34475051457229 4.37377312814546 P P P 5.05167690918329 5.24502509520186
5.57495171272025 P P P LNCV6_127577_PI430048170 mRNA

GGGGTTTAAAGCTACAGAGGCACTGACCTTTTTCTAGTTATTGTATTGCTACAATTTAAA NM_014278RefSeq chr4
+ 127782297 127833371 HSPA4L 22824 heat shock 70kDa protein 4-like
GO:0006986|GO:0005737|GO:0006457|GO:0005634|GO:0005524|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140423_PI430048170 0.9409944048858650.9770088570762918.48933760961338
8.06973402665291 8.11626389593967 P P P 7.8783180650969 8.56520809429853
8.28897309026039 P P P LNCV6_140423_PI430048170 mRNA
AGCACTCAGACATCAGCACTGTCTTCACAGAATAAATGCTTTATCTGGCCTTGCAAAAAA NM_016458RefSeq chr8
+ 144137768 144140843 HGH1 51236 HGH1 homolog (S. cerevisiae)
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104816_PI430048170 0.6032478349986690.9651767801277496.44293097585468
6.52039930352089 6.60139198636217 P P P 6.45944150980803 6.70625586547061 6.5458269078565
P P P LNCV6_104816_PI430048170 mRNA
ATGGCTTATCTACTGTATCTCACACTACTACTTCAGGGATTTTGAACTCTGCTCCCCACT NM_001300905 RefSeq
chr12 - 56595595 56630331 BAZ2A 11176 "bromodomain adjacent to zinc finger domain, 2A,
transcript variant 2"
GO:0005515|GO:0016922|GO:0010467|GO:0070933|GO:0006355|GO:0016575|GO:0034770|GO:0003723|GO:0005
730|GO:0070869|GO:0033553|GO:0003677|GO:0006351|GO:0006306|GO:0000183|GO:0045814|GO:0040029|GO:0
070577|GO:0006338|GO:0008270|GO:0051567|GO:0005677 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_144218_PI430048170 0.22105277772085 0.8152540384976750.461205130433636
0.3553530041583070.411850675513416A A A 0.9972243515376470.468967289517464
0.594039216966305A A A LNCV6_144218_PI430048170 mRNA
CTTTTGTGTAATGTGTAATTGTTACCACTTTTCCTTGCTATCTAGTGGAGAAGTGTCACG NM_139058RefSeq chrX
- 25003695 25015948 ARX 170302 aristaless related homeobox
GO:0021846|GO:0021831|GO:0046622|GO:0044241|GO:0021800|GO:0001206|GO:0005634|GO:0000122|GO:0006
351|GO:0021853|GO:0072148|GO:0007411|GO:0003682|GO:0042127|GO:0000980|GO:0021759 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137407_PI430048170 0.0693099166998160.5510349325500291.50235674279419
0.5344874733496731.22776160935427 A A A 2.29100452075843 1.75093116400686
1.91088856174649 A A A LNCV6_137407_PI430048170 mRNA
GGGGTTTTCTTCTTGTTGTTCTGTTTTTTAATAGGGTTTACAGCTAGAATTTTGAATGCC NM_001042475 RefSeq chr6
- 118460771 118651857 CEP85L 387119 "centrosomal protein 85kDa-like, transcript variant 1"
GO:0005813|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135565_PI430048170 0.3817690289091131.1411407913397 0.351282500640096
0.3550517765650150.820522240434142A A A 0.3333446314118910.309207160259912
0.364464109378348A A A LNCV6_135565_PI430048170 mRNA
AGGCTGTAATTAAGTCCTAGGAGATGGCATTATCTGAATAAATAGTGAAAGGAGAGTGCC NM_153270RefSeq chrX
- 21655348 21658387 KLHL34 257240 kelch-like family member 34 GO:0005615 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_135113_PI430048170 0.0627795170939690.3969328819801980.607314846002938
0.4110731218850670.613896680871946A A A 1.74561604814044 2.41780949774683
1.23045799404809 A A A LNCV6_135113_PI430048170 mRNA
CCTTTTGCATAGAATTTTACCAGTTGCGTACGATCAAAATCACGTTTGTAGTATCATATC NM_145036RefSeq - -
0 0 --- NA - NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131549_PI430048170 0.3761494675284820.7998025287516610.401620819462256
0.4053260255065760.359899692341363A A A 0.4406294375127191.15977211361232
0.401291686529445A A A LNCV6_131549_PI430048170 mRNA
CATCATTGTGTTTTATGATCTTGTATCTCTACCTGGCGCTATGGAATAAATAAAATGCCT NM_058222RefSeq chr10

+ 112283655 112305034 TECTB 6975 tectorin beta GO:0005886|GO:0005578|GO:0031225 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_137784_PI430048170 0.0124441867722255 0.2068960939596340.392476614248361
0.3889460991261860.90830899708346 A A A 3.24124544492968 2.07731308075712
3.01230934051127 P A P LNCV6_137784_PI430048170 mRNA
AGACATAGCAAGAGAAACAAAATTTTGTTTTCAAGACATTTCCACTGCAGTTTCAAGCTG NM_022780RefSeq chr2
+ 86720290 86778041 RMND5A 64795 required for meiotic nuclear division 5 homolog A (S. cerevisiae)
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130743_PI430048170 0.6410695040584150.9134773452911933.07920141531585
1.30003486548824 2.43958041010353 P A A 2.270016108954 2.65458138407597
2.75836579348567 A P P LNCV6_130743_PI430048170 mRNA
GCAGATGCAGTGTGCCATTCTGAATTTTTCAATCTAAGGGATGTGGATACATAGAATGTT NM_014245RefSeq chr3
+ 141738208 141746803 RNF7 9616 "ring finger protein 7, transcript variant 1"
GO:0005515|GO:0043066|GO:0016567|GO:0005507|GO:0045116|GO:0008631|GO:0005634|GO:0005737|GO:0019
788|GO:0051775|GO:0005654|GO:0008270|GO:0031466 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128155_PI430048170 0.94031985452054 0.9955804137824220.639251615186108
0.8013736299256690.847209220519589A A A 0.6388370469106931.11498217712106
0.484332196516385A A A LNCV6_128155_PI430048170 mRNA
TTGCAATTTGTCTTATTGTTTGGGTCTACTGGCAACAATAAACTATCTCCCCTGAAAATC NM_004588RefSeq chr11
- 118162803 118176622 SCN2B 6327 "sodium channel, voltage gated, type II beta subunit"
GO:0046684|GO:0007268|GO:2000649|GO:0086091|GO:0060048|GO:0007399|GO:0060371|GO:0086002|GO:0001
518|GO:0035725|GO:0086012|GO:0086006|GO:0017080 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132179_PI430048170 0.2870955648354031.0613035932819 10.6401013525974
10.6456123530859 10.5910407445192 P P P 10.4346289225764 10.6482607998438
10.5290123918074 P P P LNCV6_132179_PI430048170 mRNA
CAAGAGCCTGATCTCTTCCTGTTTTGTACATAGATTTATTTTTCAGTTCCAAGAAAGATG NM_130803RefSeq chr11
- 64803513 64811294 MEN1 4221 "multiple endocrine neoplasia I, transcript variant e1E"
GO:0051974|GO:0005515|GO:0010467|GO:0006367|GO:0044212|GO:0048704|GO:0046329|GO:0003690|GO:0000
165|GO:0051781|GO:0007179|GO:0030674|GO:0000785|GO:0009411|GO:0010332|GO:0000400|GO:0060135|GO:0
000403|GO:0000122|GO:0045786|GO:0032925|GO:0018024|GO:0043280|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133332_PI430048170 6.03131033842804e-05 4.88644009071109 9.02245243015989
9.10719335747251 8.93433642867179 P P P 6.73833784600342 6.86148455929121
6.59024440502105 P P P LNCV6_133332_PI430048170 mRNA
TTGTCGCTGCAGCCAACTTTGCCATTAAAACTCTTTGCCAAAGTTTGCACCTGTAAAAAA NM_031297RefSeq chr9
- 137220246 137221323 RNF208 727800 ring finger protein 208
GO:0005737|GO:0004842|GO:0008270|GO:0005654|GO:0051865 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134740_PI430048170 0.2574375619344950.9170653421475412.6262375060978
12.5699502425416 12.3532261458086 P P P 12.6094068543414 12.7045912051805
12.6224299891143 P P P LNCV6_134740_PI430048170 mRNA
TGGCGTCTTTCCTGCCTCTGATGATGGACTCAATAAACAGCACTGGACAAGGCTAAAAAA NM_001128228 RefSeq
chr9 - 137191616 137200711 TPRN 286262 taperin GO:0003674|GO:0019902|GO:0007605|GO:0032420
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127063_PI430048170 0.1320214700110670.5743399503793340.466444754298759
1.50219106145532 1.52803923217491 A A A 2.43098392313486 1.56163684357738
2.00528104583881 A A A LNCV6_127063_PI430048170 mRNA
CCTCAGATGTATCTAGTGGATAGTAACCATTAACAGATGACTAATTTGTTTCACTGTATC NM_024717RefSeq chr5
- 94705536 95284575 MCTP1 79772 "multiple C2 domains, transmembrane 1, transcript variant L"

GO:0005544|GO:0019722|GO:0005509|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94583_PI430048170 0.0134624114727692 1.50916356739322 6.63507411085253
6.81162691160971 6.91186589699179 P P P 6.00149346805168 6.19064359926175
6.37459273510232 P P P LNCV6_94583_PI430048170 mRNA
CAGCAAATATGGTCTTGCTGCATTCAGGGCTTTTTTAAAGTCGGAATTCTGTGAAGAAAA NM_002923 RefSeq chr1
+ 192809038 192812277 RGS2 5997 regulator of G-protein signaling 2
GO:0005515|GO:0005516|GO:0043005|GO:0005886|GO:0038032|GO:0007283|GO:0060087|GO:0005829|GO:0005
739|GO:0010614|GO:0005737|GO:0060452|GO:0043407|GO:0043951|GO:0031116|GO:0045744|GO:0005730|GO:0
048487|GO:0006417|GO:0010519|GO:0043547|GO:0007049|GO:0008277|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145022_PI430048170 0.3283442924774450.975380941954919 0.279632741668539
0.3104319149810830.370179535262055 A A A 0.3898087090474630.349330625319148
0.329814948082018 A A A LNCV6_145022_PI430048170 mRNA
CCACTGCCATAACTTGTTTGTAAAAGAGCTGTTCTTTTTGACTGATTGTTTTAAACAACG NM_006228 RefSeq chr8
+ 28317131 28343354 PNOC 5368 "prepronociceptin, transcript variant 1"
GO:0005515|GO:0007165|GO:0007218|GO:0001515|GO:0007268|GO:0005576|GO:0005184|GO:0007600 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141606_PI430048170 4.77068140932554e-05 0.3459646129602760.299390834889865
0.29364443879282 0.386404286393282 A A A 1.95160345998093 1.79674247310555
1.82206020127712 A A A LNCV6_141606_PI430048170 mRNA
AAGTGTGAACAAAAGTGTGAGTCCAAATGCCAGCCCAGCTGTTTAAAGAAGCTGCTGCAA NM_001010857 RefSeq
chr1 + 153203429 153205125 LELP1 149018 late cornified envelope-like proline-rich 1 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_132149_PI430048170 0.0886265010848429 1.48924601596496 5.53752572851152
5.28376981721476 5.85139188334676 P P P 5.01450169766873 5.29677992807195
4.61370903221216 P P P LNCV6_132149_PI430048170 mRNA
AGGACACACCTCCCTAAATGCCTTGTAATATATTTGAATCTGATTCTGCATTTCTTCCTCNM_005128 RefSeq chr21 +
36164540 36294274 DOPEY2 9980 dopey family member 2
GO:0003674|GO:0050890|GO:0000139|GO:0007275|GO:0015031|GO:0007029|GO:0006895|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141488_PI430048170 0.0593817219779021 1.45070785741894 4.121910727164
3.96338349028572 3.82515927233616 P P P 3.68337457203682 3.46022628098946
3.11626293928847 P P P LNCV6_141488_PI430048170 mRNA
TGTTGGGAGAGCCCTGCTCCCAGACATAAATAGAGCAACCAGTACTAACCTGGATTTTTT NM_005947 RefSeq chr16
+ 56651898 56653204 MT1B 4490 metallothionein 1B
GO:0071294|GO:0048471|GO:0005737|GO:0008270|GO:0005634|GO:0045926 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139523_PI430048170 0.1485172338642440.41239024624151 2.07166268839636 2.1626267869144
2.20094093981502 A A A 2.2921694062552 3.84958016338918 3.68771561431269 A P P
LNCV6_139523_PI430048170 mRNA
CTGACAAATGTCTGAACTATTGTCGTGCCCTTCAAAACTGGAGTTTTCTAAAATAATCTT NM_012105 RefSeq chr21
+ 41167800 41282534 BACE2 25825 "beta-site APP-cleaving enzyme 2, transcript variant a"
GO:0005794|GO:0016486|GO:0009986|GO:0005783|GO:0006508|GO:0016021|GO:0006509|GO:0004190|GO:0042
985|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137290_PI430048170 0.2196444338904970.792051566190875 7.11776446792798
7.21034437702553 7.18578231958461 P P P 7.16186803660536 7.78209256945004
7.51434611834551 P P P LNCV6_137290_PI430048170 mRNA
TAATTTTAGAGGATATTGGGCCTGGTTTTCTTGTCCCTTCATACCCTAGTCCCTGGACAG NM_024032 RefSeq chr17
+ 44141905 44162476 C17orf53 78995 "chromosome 17 open reading frame 53, transcript variant 1"

NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130250_PI430048170 0.00479798544322255 1.5460942276452 10.3814394858362
10.6082304841881 10.3812337948745 P P P 9.97756721734247 9.80578618521248 9.7000734779713
P P P LNCV6_130250_PI430048170 mRNA
AGAAGTCACACTCCGGCCTCTCAGAATTCACTTGAGGTTCAATTAAATACAGTCACACCG NM_024663 RefSeq chr20
+ 58692805 58715844 NPEPL1 79716 "aminopeptidase-like 1, transcript variant 1"
GO:0005737|GO:0030145|GO:0004177|GO:0008235|GO:0006508|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_61387_PI430048170 0.0508121544940154 1.36808102705928 4.57916817792536
4.16338024716076 4.48862436805511 P P P 4.0182369807477 4.0568657106453
3.82098596497085 P P P LNCV6_61387_PI430048170 mRNA
AGAAGATCCTCACCAAGTTCAAACAGGATCAGGAATACCTCTACTAACAACCAATTTGTC NM_014226 RefSeq chr14
- 102228820 102305200 MOK 5891 "MOK protein kinase, transcript variant 1"
GO:0007165|GO:0005737|GO:0004672|GO:0004674|GO:0051726|GO:0006468|GO:0005524|GO:0004693 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134956_PI430048170 0.8595751466476940.9742432917167385.21990001052565
4.65378433651381 4.84786674087009 P P P 5.13190290667109 5.06268709714314
4.65342465863671 P P P LNCV6_134956_PI430048170 mRNA
TTCTCGTTGTTTCTGTTCCTTCCTGGGGCCATTGGTCCTACAATCTTCCTGAAAATCTTC NM_002565 RefSeq chrX -
70258165 70259804 P2RY4 5030 "pyrimidinergic receptor P2Y, G-protein coupled, 4"
GO:0030321|GO:0016323|GO:0016324|GO:0015065|GO:0005886|GO:0045028|GO:0005887|GO:0007200|GO:0035
589|GO:0045030|GO:0007204|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130412_PI430048170 0.1214903372936570.5138874517605050.32541331861811
1.83849553030796 0.866765975947281 A A A 1.79703733392093 2.00328224189566
2.44947492036582 A A P LNCV6_130412_PI430048170 mRNA
ATACATGTGGATGTGGACACTCTTCTATAGACGAGGTGGAGCTTAATTCCTGTCCTTACC NM_198562 RefSeq chr3
- 49268596 49277075 C3orf62 375341 chromosome 3 open reading frame 62 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_127665_PI430048170 0.2691780731413030.6408813598002335.17011714761067
6.68069471262682 6.84658733630028 P P P 6.87795010964275 6.96997855960443
7.25594474045022 P P P LNCV6_127665_PI430048170 mRNA
GGTCAGAGAAGCCTTTAGGAGAAGAATCAGATCATGTATATAATTGTAACATCACATTGA NM_006660 RefSeq chr15
- 65150445 65185225 CLPX 10845 caseinolytic mitochondrial matrix peptidase chaperone subunit
GO:0042645|GO:0005515|GO:0006200|GO:0005743|GO:0009368|GO:0005524|GO:0046872|GO:0016504|GO:0005
739|GO:0010952|GO:0005737|GO:0006457|GO:0051603|GO:0005759|GO:0009841|GO:0004176|GO:0005654|GO:0
051082|GO:0016887. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126921_PI430048170 0.0585805032839197 0.6931443907255766.66538507221328
6.62764574523826 6.97402756291702 P P P 6.9703996929402 7.38235671598924
7.47754444305922 P P P LNCV6_126921_PI430048170 mRNA
GCAGAATTAACTATAACAATCACTGGCTACCGAAGTAAACTGATGTACTGAATTCCATAA NM_002858 RefSeq chr1
+ 94418376 94518663 ABCD3 5825 "ATP-binding cassette, sub-family D (ALD), member 3, transcript
variant 1"
GO:0005515|GO:0006635|GO:0005782|GO:0005743|GO:0042626|GO:0055085|GO:0005524|GO:0042803|GO:0043
231|GO:0005829|GO:0016020|GO:0007031|GO:0016021|GO:0016887|GO:0042760|GO:0005778|GO:0005777 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145758_PI430048170 0.2364932970748750.6400599583176480.413449480727282
0.3882824067989520.362715062951015 A A A 0.436979277050986 0.831266127727196
1.58574983703451 A A A LNCV6_145758_PI430048170 mRNA
GTGACTCGACGTTTATCCACTTCTGTTCATTTGATCGTTTCAGTAATATGCTTACAAATA NM_033261 RefSeq chr10 -

1018906 1025859 IDI291734 isopentenyl-diphosphate delta isomerase 2
GO:0046490|GO:0006695|GO:0016787|GO:0044281|GO:0008299|GO:0004452|GO:0050992|GO:0046872|GO:0005
829|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98216_PI430048170 0.4335409060123821.04490107421101 11.9522213125853 12.0302903220365
12.101319044979 P P P 11.9155560679072 11.8928854887507 12.0816830958454 P P P
LNCV6_98216_PI430048170 mRNA
TTACCTGGAAGTAAAGACTGGCTAGATTATCGAATGTTCACATTTTAAAGTTCTGAGAGA NM_004545 RefSeq chr14
- 92116123 92121809 NDUFB1 4707 "NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1,
7kDa"
GO:0022904|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0016021|GO:0008137|GO:0044237|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105516_PI430048170 0.0903693176882489 0.7462118791338263.27259355814194
2.84476147746245 3.34225581229343 P A P 3.63119100835929 3.45008157541206
3.68359727730861 P P P LNCV6_105516_PI430048170 mRNA
CATTAAGTATAGACAGCTATCAAGATGGGCAACAGATGCAAGTAGTAACAGAGTTAAAGANM_004571 RefSeq chr21
+ 42974509 43033931 PKNOX1 5316 "PBX/knotted 1 homeobox 1, transcript variant 1"
GO:0005667|GO:0003700|GO:0006366|GO:0046982|GO:0003705|GO:0005634|GO:0001525|GO:0043565|GO:0005
737|GO:0030217|GO:0045944|GO:0030218|GO:0043010 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134372_PI430048170 0.1967607249359233.27187167242935 3.28843795499718
2.96679284908206 0.80058132458481 A A A 1.53653811140018 0.592941900651941
0.583741945450686 A A A LNCV6_134372_PI430048170 mRNA
TCTTCCTTGTAAATATGATTTATACCTAACTGAATAAAAAGCTGTTCTGTCTTCCCACCCNM_002989 RefSeq chr9 -
34709004 34710167 CCL21 6366 chemokine (C-C motif) ligand 21
GO:0051897|GO:0031295|GO:0046330|GO:0007267|GO:0051491|GO:0005615|GO:2000147|GO:0097026|GO:0031
529|GO:0006955|GO:0006954|GO:0050921|GO:0030838|GO:0034695|GO:0043552|GO:0045860|GO:0031274|GO:0
048469|GO:0070374|GO:0043123|GO:0008009|GO:0001771|GO:2000406|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141540_PI430048170 0.0323980350526214 0.67216182898756 12.1949556934166
11.881416211615 11.7176664995064 P P P 12.3470635496789 12.6544469532805
12.5367123329437 P P P LNCV6_141540_PI430048170 mRNA
GTCTCCCCACACGGACCTTTGCTGAATTAAAGTTTGTAAGTAAATGGTTTTAAAGAAAAA NM_133452 RefSeq chr19
- 10316212 10333638 RAVER1 125950 "ribonucleoprotein, PTB-binding 1"
GO:0005737|GO:0000166|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95205_PI430048170 0.51882821894562 0.8705634290720648.00403015475157 7.63172516355934
7.11557327829062 P P P 8.14103966401177 7.73365464483753 7.54578861288611 P P P
LNCV6_95205_PI430048170 mRNA
ACCCCTCTCCAACAGGAAAAGCTGCTACCTGCCCAACTCCCTGCTGAAAAGGAAGTGGGT NM_001202858 RefSeq
chr1 + 150508010 150513789 ECM1 1893 "extracellular matrix protein 1, transcript variant 3"
GO:0005515|GO:0005134|GO:0010466|GO:0002020|GO:0005615|GO:0006954|GO:0001960|GO:0002828|GO:0004
871|GO:0043123|GO:0070062|GO:2000404|GO:0006357|GO:0005578|GO:0001525|GO:0008022|GO:0030502|GO:0
031214|GO:0045766|GO:0031012|GO:0007165|GO:0001938|GO:0001503|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128341_PI430048170 0.2309656268223950.7084942856764266.28034460961104
5.33479862417328 5.24596436622175 P P P 6.41862441736156 6.2668914289305
5.85003982010358 P P P LNCV6_128341_PI430048170 mRNA
ACACCCCTCCCTGTAACCAAGGAACACTCTGAAATAAAGGTGAATGGCTAAAATCTCAAA NM_031481 RefSeq chr22
+ 17563438 17590890 SLC25A18 83733 "solute carrier family 25 (glutamate carrier), member 18,
transcript variant 1" GO:0005743|GO:0016021|GO:0055085|GO:0015293 . NA - . NA NA NA NA NA
NA NA NA NA

LNCV6_145240_PI430048170 0.9108302008780620.9788301215822880.371871435905892
0.4591907996215630.409909715196068A A A 0.2798614490528820.306627777278206
0.707495341833156A A A LNCV6_145240_PI430048170 mRNA
AATCACTGAACTTTTTCATTTGCTCTAAATTCATTATAAGATATTAAACATGTCATTTGC NM_001207043 RefSeq
chr6_GL000256v2_alt + 1098056 1103842 LOC554223 NA histocompatibility antigen-related NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144237_PI430048170 0.251393068225635 1.44693724609233 1.28272129830156
0.8826896060912660.261368774992685A A A 0.3655536914127850.329883359140394
0.308993209385665A A A LNCV6_144237_PI430048170 mRNA
GTCCAAGAACTTAGGCAGGGGCCCCAAGACAATAAAGTTGGTCTCTACTATCTCCTAAAA NM_001135105 RefSeq
chr6 - 39314697 39322554 KCNK1683795 "potassium channel, two pore domain subfamily K,
member 16, transcript variant 1"
GO:0005244|GO:0005886|GO:0007268|GO:0005267|GO:0034765|GO:0016021|GO:0006813|GO:0071805 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138125_PI430048170 0.00338821523802092 0.4669965613103995.60573975998375
5.3001830422827 5.67021226738024 P P P 6.40457789341906 6.60319532645875
6.85488246738498 P P P LNCV6_138125_PI430048170 mRNA
CTGCAGAGATGAAAAATGTGTTTTCACGGGATTTATATTGTGAACTAAACTAAGCCTACT NM_002703RefSeq chr4
- 56393362 56435636 PPAT 5471 phosphoribosyl pyrophosphate amidotransferase
GO:0032869|GO:0051539|GO:0009168|GO:0001822|GO:0060135|GO:0031100|GO:0055086|GO:0044281|GO:0035
690|GO:0046872|GO:0005829|GO:0000082|GO:0007595|GO:0051289|GO:0006144|GO:0006543|GO:0009116|GO:0
009113|GO:0004044|GO:0006164|GO:0006189 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133308_PI430048170 0.00307385619805025 0.7976480880390848.88280626028882
8.97516762537493 8.8766848930948 P P P 9.16246241267755 9.26444377314892 9.2854296930014
P P P LNCV6_133308_PI430048170 mRNA
GCCGAGCTGTTTTCTACCTTTTTGTAGTCTTTCTTAAAACAATAAATTCCGCTGTGATAT NM_002918RefSeq chr19 -
13961529 14006322 RFX1 5989 "regulatory factor X, 1 (influences HLA class II expression)"
GO:0005515|GO:0006955|GO:0006366|GO:0006357|GO:0003705|GO:0005654|GO:0005634|GO:0000978|GO:0043
231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144309_PI430048170 0.7193217073143390.9657320483594846.81049237537541
6.59917050610152 6.68830505472809 P P P 6.54502195918754 6.85936703680233
6.83181472136338 P P P LNCV6_144309_PI430048170 mRNA
TCATCCGATTCCCCTCTATCAGTCACTGCCAGTTAATAAACCTTTGCAAACGTTAAAAAA NM_021015RefSeq chrX
- 48186219 48196763 SSX5 6758 "synovial sarcoma, X breakpoint 5, transcript variant 1"
GO:0006355|GO:0005634|GO:0003676|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127841_PI430048170 0.4462377067834870.92983401461634 7.77622914345953 7.8505307718234
7.84816001454702 P P P 7.72655094575369 7.96359530680999 8.07883155645299 P P P
LNCV6_127841_PI430048170 mRNA
TTTTTTGCCTGTTACCTGTGACGTCCTTGGAAGCAGAATCTGAAACTTTCTGAGGAGAGC NM_130902RefSeq chr4
- 46734829 46909235 COX7B2 170712 cytochrome c oxidase subunit VIIb2
GO:0005746|GO:0004129|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141368_PI430048170 0.0434464479631328 0.8846712280078441 2.9019142427781
13.0261328038161 12.9084292443961 P P P 13.1329623995984 13.107928356193
13.1292379320205 P P P LNCV6_141368_PI430048170 mRNA
GGCTGGGAAACTGTTGGTGGCCAGTGGGTAATAAAGACCTTTCAGTATCCCTATAAAAAA NM_003761RefSeq chr2
+ 85577490 85582033 VAMP8 8673 vesicle-associated membrane protein 8
GO:0070254|GO:0035493|GO:0048471|GO:0005886|GO:0043312|GO:0031201|GO:0046718|GO:0006887|GO:0005
765|GO:0015031|GO:0006906|GO:0005829|GO:0005739|GO:0005737|GO:0030100|GO:0000149|GO:0061024|GO:0
035577|GO:0070062|GO:0000046|GO:0019905|GO:0009986|GO:0006892|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_94626_PI430048170 0.07129858157238 1.04801503045068 0.4417014255145290.482308612477592
0.493958449854486 A A A 0.3763596636387950.3905603873160820.447600706782047 A A A
LNCV6_94626_PI430048170 mRNA
AGGTCCTATATGTTGATCCCATGATTACAGAGATAAAAGAAATCTTCATCCCAGAACACA NM_144701 RefSeq chr1
+ 67166485 67259967 IL23R 149233 interleukin 23 receptor
GO:2000318|GO:0038155|GO:0032693|GO:0042523|GO:0032735|GO:0032819|GO:0042520|GO:2000330|GO:0042
104|GO:0006954|GO:0043382|GO:0002827|GO:0042102|GO:0051135|GO:0032496|GO:0034341|GO:0032729|GO:0
010535|GO:0032740|GO:0072536|GO:0032725|GO:0005143|GO:0042517|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139426_PI430048170 0.0312977985091688 0.6592830302396976.81875122225144
6.9896528797332 7.20256317880872 P P P 7.32672503704604 7.68242874438496
7.79087638364391 P P P LNCV6_139426_PI430048170 mRNA
GAATCACAGATGTCTCCTGAAAGAACTCTTTTAGATGAAATCATTCTACTCAAATGTACC NM_017906 RefSeq chr6
+ 10694954 10709737 PAK1IP1 55003 PAK1 interacting protein 1
GO:0005886|GO:0008283|GO:0005730|GO:0060021|GO:0005654|GO:0009968 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142581_PI430048170 0.4545312085201350.94719728561367814.9692710141697
14.7593088707663 14.6640504629162 P P P 14.9003120302304 14.8341508654683
14.9089000613038 P P P LNCV6_142581_PI430048170 mRNA
AACCAGACTCAGAAAGAAAACCTCAGGAAATTCTACAAGGGCAAGAAGTACAAGCCCCTG NM_007209 RefSeq
chr9 - 124857878 124861961 RPL35 11224 ribosomal protein L35
GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0005730|GO:0003729|GO:0006415|GO:0006
412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0000184|GO:0016020|GO:0016032|GO:0022625|GO:0
044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118484_PI430048170 0.8725561889006520.9592221065335535.53144135061327
5.21773815570859 5.73040732183136 P P P 5.11690664985974 5.68157271747094
5.81599111720357 P P P LNCV6_118484_PI430048170 mRNA
TCGCATGTTTAAAATGTGGGAACATTGTAGTTTATCATGTGATTGTTCCATGTAGTTCCT NM_001287385 RefSeq
chr1 - 143955363 143972006 FAM72C NA "family with sequence similarity 72, member C" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133897_PI430048170 0.7930220657359251.07963706193055 8.56270015919184
8.96969272874915 9.40648859062355 P P P 8.84387071045322 8.77525410317702
9.09157660748702 P P P LNCV6_133897_PI430048170 mRNA
GCCTAGTTGGTAAGACTGTTTTATCCTTAATCTGCATTCTTCTTTCATTGTAGAATACAG NM_015420 RefSeq chr8 +
103414713 103443452 DCAF1325879 DDB1 and CUL4 associated factor 13
GO:0000462|GO:0016567|GO:0032040|GO:0005730|GO:0080008 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139751_PI430048170 0.6310021065162730.9518525845727321 3.5991552361501
13.6205610198098 13.7442169941539 P P P 13.5402799867065 13.6971022294222 13.91914250264
P P P LNCV6_139751_PI430048170 mRNA
GTCTTCCATTTTGTTGGAATTAGATCCTCCCCTTCAAATGCTGTAATTAACAACACTTAA NM_003374 RefSeq chr5
- 133971874 134005133 VDAC1 7416 "voltage-dependent anion channel 1, transcript variant 1"
GO:0042645|GO:0005515|GO:0006820|GO:0019901|GO:0005886|GO:0005743|GO:0006915|GO:0005634|GO:0005
741|GO:0055085|GO:0007270|GO:0005739|GO:0046930|GO:0044070|GO:0016020|GO:0030855|GO:0016032|GO:0
001662|GO:0015288|GO:0007612|GO:0008308|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_100672_PI430048170 0.3786080838604351.09711318677172 4.3456639106144
4.69293346976447 4.45586156244121 P P P 4.34577862095491 4.23481474925849

4.52037363401827 P P P LNCV6_100672_PI430048170 mRNA
TGAACAGGAGACCATTAAACCACTAGATGACTGCCAGAAGCTCATAGAACACGGAGTCAA NM_015986RefSeq
chr17 - 30782683 30824760 CRLF3 51379 "cytokine receptor-like factor 3, transcript variant 1"
GO:0030308|GO:0005737|GO:0000082|GO:0005886|GO:0045944|GO:0045893|GO:0071158|GO:0046427 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144910_PI430048170 0.7276067525824760.8833586983002785.86509630332802
6.21137541816103 5.37482075087525 P P P 6.3469334350551 6.23577485533905
5.32471935223309 P P P LNCV6_144910_PI430048170 mRNA
ATGGAAAAGTGTGTTCCTGTTCATAGCCAGGAAACCCAGCTCAGCAAACTCCCTTTCAAA NM_147192RefSeq chr1
+ 46506995 46514214 DMBX1 127343 "diencephalon/mesencephalon homeobox 1, transcript variant 2"
GO:0008343|GO:0005667|GO:0008344|GO:0003700|GO:0046982|GO:0005634|GO:0000122|GO:0007417|GO:0003
677|GO:0006351|GO:0042803|GO:0043565|GO:0048589|GO:0007420|GO:0045892 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139622_PI430048170 0.1175695766975440.4085922697078020.403402440311962
0.4298112559638450.859213425603067A A A 2.44625755346239 1.89048437282703
0.860766056310693A A A LNCV6_139622_PI430048170 mRNA
GCCACAGGTTCTCATTCCTTTTCCCATTATACTTCTCACAATTCAGTTTCTATGAGTTTG NM_014211RefSeq chr5 +
170783718 170814046 GABRP 2568 "gamma-aminobutyric acid (GABA) A receptor, pi, transcript variant 1"
GO:0007165|GO:0005230|GO:0030054|GO:0004890|GO:0045211|GO:0034707|GO:0005254 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127390_PI430048170 0.0171873028780105 0.3722132144664893.95617454825297
3.2993129755952 3.81680532797332 P P P 5.19063902343723 5.10620522113891
5.13106453800324 P P P LNCV6_127390_PI430048170 mRNA
GTTTAAAAAACAGGTGAGGCAAGTGAGTGATTTATTGTTCCTGAGGAAGTATATCTGATT NM_001289124 RefSeq
chr4 + 41359606 41700044 LIMCH1 22998 "LIM and calponin homology domains 1, transcript variant
7" GO:0031032|GO:0008270|GO:0003779 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138061_PI430048170 0.0422448164076162 0.6027324914648316.428475499942
6.3363251385215 6.07946273878037 P P P 6.65258876584716 7.29948095962869
7.03365535584349 P P P LNCV6_138061_PI430048170 mRNA
CTGTAGTGTCTGGGATTTGCCGGTGCTCAATAAATGTTTATTCATTGACGGTGGAAAAAA NM_021625RefSeq chr12
- 109783086 109833407 TRPV4 59341 "transient receptor potential cation channel, subfamily V, member
4, transcript variant 1"
GO:0008017|GO:0005516|GO:0043622|GO:0006884|GO:0034605|GO:0030103|GO:0034220|GO:0051015|GO:0005
080|GO:0042169|GO:0005262|GO:0007231|GO:0005261|GO:0071476|GO:0019901|GO:0009986|GO:0031532|GO:0
071470|GO:0048487|GO:0042538|GO:0030027|GO:0005929|GO:0046785|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127667_PI430048170 0.1654463318850690.8101170026007259.56816020517289
9.64652504987758 9.60304160740661 P P P 9.62214878922703 10.0449683507029
10.0249554523062 P P P LNCV6_127667_PI430048170 mRNA
TTTTGCTTTATGGGTTTGGCTTGTTTTTCTTGCATGGTTTGGAGCTGATCGCTTCTCCCC NM_145109RefSeq chr17 +
21284655 21315239 MAP2K3 5606 "mitogen-activated protein kinase kinase 3, transcript variant B"
GO:0005515|GO:0034142|GO:0060048|GO:0051403|GO:0005829|GO:0002756|GO:0000187|GO:0006954|GO:0004
702|GO:0002755|GO:0045860|GO:0034138|GO:0004708|GO:0038124|GO:0019901|GO:0038123|GO:0034134|GO:0
018108|GO:0002224|GO:0005524|GO:0042035|GO:0007165|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_108670_PI430048170 0.2725355898761010.9377811075200130.277233497587622
0.3710723995530660.278727162444486A A A 0.5026814298232430.40267234007444
0.29420150635258 A A A LNCV6_108670_PI430048170 mRNA
TTCGAGAGGAGTCTATGCTATTTTTGGATTTTATGACAAGAAGTCTGTAAATACCATCAC NM_001083619 RefSeq

chr4 + 157220583 157366074 GRIA2 2891 "glutamate receptor, ionotropic, AMPA 2, transcript variant 2"
GO:0005515|GO:0030054|GO:0005886|GO:0005234|GO:0035249|GO:0007268|GO:0030425|GO:0008021|GO:0030666|GO:0007165|GO:0035235|GO:0034220|GO:0005887|GO:0045211|GO:0004971|GO:0032281|GO:0004970|GO:0005789 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141416_PI430048170 0.844392493443631 1.02195703377431 7.07942487029332
7.28895925241917 7.44924055663812 P P P 7.15602760964623 7.07532261504677
7.48293054531066 P P P LNCV6_141416_PI430048170 mRNA
GTTAATTCCTTTTCACCTTTCAAAACGGACAGCCCCTTGAACATTAAAAACTTCGCAGAC NM_001286752 RefSeq
chr21 - 36034540 36060818 SETD4 54093 "SET domain containing 4, transcript variant 3"
GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65934_PI430048170 0.160395938550056 0.837054948603349 7.69751031778907 7.56474550292996
7.99316012699006 P P P 8.05301971662137 7.93516701445771 8.06729496969303 P P P
LNCV6_65934_PI430048170 mRNA
GCCCTCTGGGAACCAAAATCGAAAAATGCATCAAAAGTTGCCAATAAAGGAAAAAGTAAA NM_001190265
RefSeq chr2 - 68042199 68063027 C1D 10438 "C1D nuclear receptor corepressor, transcript variant 4"
GO:0005515|GO:0016922|GO:0000460|GO:0003714|GO:0003723|GO:0005730|GO:0006915|GO:0005634|GO:0003677|GO:0006351|GO:0005737|GO:0017053|GO:0000176|GO:0045892 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_135305_PI430048170 0.675998635584681 1.0440521159982 0.638899432768379
0.375046105968782 0.596829261378302 A A A 0.284526668922555 0.405467994460168
0.713386129989166 A A A LNCV6_135305_PI430048170 mRNA
CCTAAGGATGTTGGCAAAGCGCTTTGAGTTTACTAGAAGTTTCATTAAAATTTGTTGGTA NM_001282537 RefSeq
chr21 - 34400111 34401072 C21orf140 NA chromosome 21 open reading frame 140 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_140959_PI430048170 0.0130876099732832 0.74477230167866 11.5181336460396
11.6792855278164 11.5082927100728 P P P 12.1421897226367 11.9316674232487
11.9016100973903 P P P LNCV6_140959_PI430048170 mRNA
CTGAACCTGAGGTGCCCAACCCCAAATAAACCCAAGATGCTGTGTATTTTCAGAGGAAAA NM_003213 RefSeq chr12
+ 2959311 3040676 TEAD4 7004 "TEA domain family member 4, transcript variant 1"
GO:0005515|GO:0010467|GO:0001501|GO:0007517|GO:0006367|GO:0003700|GO:0006357|GO:0005654|GO:0035329|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135527_PI430048170 0.592487028149176 1.15165449735604 0.281755175472096
1.04648919759938 0.30672659261758 A A A 0.460859092851752 0.353843809708133
0.343451903183191 A A A LNCV6_135527_PI430048170 mRNA
TACTATAGCTGTAAGGAGAAGCTGAGAAATGATACCCAGGAGCAGCAGGCTTTACGTCTT NM_001300854 RefSeq
chr12 - 54644590 54648493 DCD 117159 "dermcidin, transcript variant 2"
GO:0050832|GO:0031640|GO:0006508|GO:0008233|GO:0005576|GO:0042742|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142519_PI430048170 0.17565591925308 1.06917240206432 0.506776932947202
0.392937419406605 0.517274517213145 A A A 0.299366665204085 0.378532893600738
0.448992371780393 A A A LNCV6_142519_PI430048170 mRNA
GAGGTTGTTAATAGACTCTTTGAGGATCCTGAGGAAAACTAAAGTATATACTGTGAAAAC NM_016616 RefSeq chr7
+ 37848596 37900400 NME8 51314 NME/NM23 family member 8
GO:0006241|GO:0006228|GO:0006165|GO:0005622|GO:0006183|GO:0005737|GO:0004550|GO:0045454|GO:0007275|GO:0007283|GO:0005524|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_39369_PI430048170 0.530822654572274 0.937298480578104 0.339471390029716 0.366710331522541
2.95328765385727 A A P 1.96720925578445 1.80703055401058 1.8397645955556 A A A

LNCV6_39369_PI430048170 mRNA
AAAGAGCGGCGTGAGCAGCAGCACCGCGCCGTCGGCCAGCGCCAGGTGCAGCACAAGCGT NM_014430 RefSeq
chr14 - 24305186 24311370 CIDEB 27141 cell death-inducing DFFA-like effector b
GO:0005811|GO:0005515|GO:0048471|GO:0008630|GO:0090200|GO:0097194|GO:0006915|GO:0042981|GO:0097
202|GO:0010942|GO:0042802|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142404_PI430048170 0.79333141121407 0.9630373257886828.73529104010154
8.93321734974628 8.81551512318855 P P P 8.59289426458227 9.01349231564017
9.00853077433583 P P P LNCV6_142404_PI430048170 mRNA
GCTCAACCCATTGGGTGTTGGCTGTTTTTGGTTTTAGTTGTTGTTTTGTATTTTGTTGTT NM_030636 RefSeq chr7 +
36153226 36301543 EEPD1 80820 endonuclease/exonuclease/phosphatase family domain containing 1
GO:0006281|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136889_PI430048170 0.319820558385756 1.23049205951783 1.01325630746182
0.341110322569228 0.472224856411194 A A A 0.281146167130315 0.371289348510437
0.365742361660654 A A A LNCV6_136889_PI430048170 mRNA
TGGGGATGTGGAGACAAGAAATGGAAATTCTAATAAACTAGCTGAATTAGATAAATCCCA NM_203299 RefSeq chr9
+ 35042207 35045991 C9orf131 138724 "chromosome 9 open reading frame 131, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142279_PI430048170 0.196308821602231 1.11020725391199 0.620895559775742
0.351123561360827 0.479587827197993 A A A 0.336743948300049 0.309628913863559
0.364848805648706 A A A LNCV6_142279_PI430048170 mRNA
AGGTCCCTGGAAGGTGTAACAAATCAGAGACTATCTGTTCAAGTAGAAAACCCAAGAGCT NM_198993 RefSeq chr17
- 39210535 39225787 STAC2 342667 SH3 and cysteine rich domain 2 GO:0035556|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90271_PI430048170 0.2252088972186370.897307541409123 13.5708603596486 13.3205788589555
13.2631404105165 P P P 13.5708603596486 13.5551864535193 13.515839457111 P P P
LNCV6_90271_PI430048170 mRNA
GCTGGGCCCCTCCCCTGGTCCTCCCAGTGTTTGCTGGATAATAAATGGAACTATGGCTCT NM_198573 RefSeq chr9
- 34521041 34523039 ENHO 375704 energy homeostasis associated GO:0005576 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_93903_PI430048170 0.0791591871616061 1.62412064587446 3.93515153133555
4.16652625957711 3.70949724544737 P P P 3.43646183644139 3.47674339616533
2.71611564996498 P P P LNCV6_93903_PI430048170 mRNA
AATGCAGCCCAGGACTTCCTGCCAACTTCCAGGAATGACCCCGACCTGCACTTTGATGCT NM_025258 RefSeq chr6
- 31765593 31777331 VWA7 80737 von Willebrand factor A domain containing 7
GO:0008150|GO:0003674|GO:0005576|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130150_PI430048170 0.40613678151066 0.7710623375713850.4598290482336540.5119402578009
0.443992732895614 A A A 0.5235537598532091.37612124391923 0.448037718214084 A A A
LNCV6_130150_PI430048170 mRNA
GACATCCCACAACAAAAACCCAAGTTTTCTGTGCTACATGTGCAATATTTGTTATGAATG NM_020708 RefSeq chr20
+ 46029181 46060150 SLC12A5 57468 "solute carrier family 12 (potassium/chloride transporter),
member 5, transcript variant 2"
GO:0005886|GO:0015379|GO:0019901|GO:0042493|GO:0006873|GO:0007268|GO:0055085|GO:0040040|GO:0035
264|GO:0043198|GO:0005887|GO:0043025|GO:0006810|GO:0007612|GO:0016021|GO:0006813|GO:0006811 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68320_PI430048170 0.404146063390559 1.08901739454987 8.11803590420136 8.00810885926967
8.37563637499577 P P P 8.09894611449864 7.97058191581726 8.0847920035135 P P P
LNCV6_68320_PI430048170 mRNA
AATGATGGATCCTAGGGTTCTTCATCACATGGGTGGTATGGCAGGACTTCAGTCAATGAT NM_003136 RefSeq chr14
+ 34982897 35029567 SRP54 6729 "signal recognition particle 54kDa, transcript variant 1"

GO:0005786|GO:0010467|GO:0006617|GO:0006616|GO:0042493|GO:0030942|GO:0006614|GO:0008312|GO:0003924|GO:0005730|GO:0005634|GO:0005525|GO:0045047|GO:0006412|GO:0005829|GO:0005737|GO:0016607|GO:0008144|GO:0043021|GO:0019003|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142664_PI430048170 0.00552244759760485 1.3478523840379 4.24345316318223 4.12361764233879 4.18313155352362 P P P 3.72290423117973 3.86098149750059 3.67002111109171 P P P LNCV6_142664_PI430048170 mRNA
TTTATTGGGGACACGACTCTGCAATAGGGATGACAGGAATCGTACCAAAAATAGCGACGT NM_001278529 RefSeq chr14 + 21070259 21090247 ARHGEF40 55701 "Rho guanine nucleotide exchange factor (GEF) 40, transcript variant 2" GO:0005737|GO:0032321|GO:0005089 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140348_PI430048170 0.0179765484176615 1.76128860062836 5.54781497076964 5.77970495547599 5.318230602475 P P P 4.96076305707554 4.79942427558117 4.4206126479524 P P P LNCV6_140348_PI430048170 mRNA
GTCGCGTCTTAGTGGGCGGGATTCTTTTCCCTTTGAATAAAAATGGATTCAAACCCAGCA NM_138481 RefSeq chr22 - 41229509 41240931 CHADL 150356 chondroadherin-like GO:0031012|GO:0005578 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132763_PI430048170 0.3185998408093220.8347277625146830.625870201611423 0.5079549448335120.387120600739813A A A 1.11028650696092 0.588186684981941 0.542742581833757A A A LNCV6_132763_PI430048170 mRNA
TGTGGGGTCATGGGCTCCAAAAGCCAACGTGAACAATTAAAAATGTATTGAGCATCTAAA NM_022437 RefSeq chr2 + 43838963 43878466 ABCG8 64241 "ATP-binding cassette, sub-family G (WHITE), member 8" GO:0042632|GO:0005515|GO:0007588|GO:0033344|GO:0046982|GO:0005886|GO:0007584|GO:0042493|GO:0017127|GO:0044281|GO:0055085|GO:0045796|GO:0005524|GO:0043235|GO:0030299|GO:0016324|GO:0015914|GO:0010949|GO:0015918|GO:0043190|GO:0016887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140784_PI430048170 0.36211549665601 0.8527926215383512.4492282339204 12.6487877046776 12.9178682779977 P P P 12.6840951255797 12.7746501535332 13.2249414268221 P P P LNCV6_140784_PI430048170 mRNA
CCTTCGCTTTAACATAGGTCTAATTTATTTGCCGTGTCATTTTCCATACAAATCAGTTGA NM_001198842 RefSeq chr12 + 69585681 69601577 CCT2 10576 "chaperonin containing TCP1, subunit 2 (beta), transcript variant 2" GO:0005515|GO:0005832|GO:0005874|GO:0007339|GO:0005524|GO:0044297|GO:0005829|GO:0005737|GO:0006457|GO:0051084|GO:0002199|GO:0051082|GO:0051131|GO:0044267|GO:0031625|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127825_PI430048170 0.0467532929549787 1.29991208679145 6.5796681007724 6.67761098623063 6.89947612036188 P P P 6.47258584323137 6.16002454352915 6.38986123444516 P P P LNCV6_127825_PI430048170 mRNA
GGTATGGATTTGTCAGTTTTGTGTGGAGTTTAAGAAATAGAACAGCCTTAAACTCTACAT NM_005333 RefSeq chrX + 11111285 11123084 HCCS 3052 "holocytochrome c synthase, transcript variant 1" GO:0005739|GO:0005743|GO:0004408|GO:0009887|GO:0046872|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128871_PI430048170 0.6186478072768260.8084656958689640.506828715309992 1.36813834179079 0.433525865551679A A A 0.2877899761432031.64099859510027 1.18990898371406 A A A LNCV6_128871_PI430048170 mRNA
GGCAAAGCTGAAGGTGATGAGGAAGAAGAGACGAACATTAAAGATGTCTATTTACTATGAN NM_182645 RefSeq chr6 + 117265557 117273565 VGLL2 245806 "vestigial-like family member 2, transcript variant 1" GO:0005737|GO:0007519|GO:0045944|GO:0003713|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140801_PI430048170 0.9176498742424191.00611201899873 0.61841956854846 0.7815906661419890.600393462159643A A A 0.8099259854717710.586205728322655 0.572359693851894A A A LNCV6_140801_PI430048170 mRNA

GTTGAGTCACTATTTGGCTTGCACCTTTTACAAAGCTAACATTTCTAAGACAGTTGTTTT NM_032042RefSeq chr5 - 93617724 94111699 FAM172A 83989 "family with sequence similarity 172, member A, transcript variant 1" GO:0005783|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101204_PI430048170 0.0749182652777888 0.7460368391313625.06955187806898 5.16410737502763 5.07736984169095 P P P 5.73882204941547 5.50686594331126 5.30218590201608 P P P LNCV6_101204_PI430048170 mRNA
CTCTCAGGAAGGATGAGCATTGTTACAGCAGGGACAATAAAGTACAGAGATATGCCGAGA NM_001103167 RefSeq chr19 - 10304802 10309557 ZGLP1 NA "zinc finger, GATA-like protein 1"NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132504_PI430048170 0.0432014570304571 1.23556041398061 7.3376034686769 7.59554232420379 7.56175940947783 P P P 7.14391563305522 7.29858943525074 7.14471499791617 P P P LNCV6_132504_PI430048170 mRNA
CTGTCACCCTCTACTCTCCAGCTTTAGTCTTATAAATGTAGTGATAGGATTCCTTGTTGC NM_001098426 RefSeq chr17 - 63832080 63842991 SMARCD2 6603 "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2" GO:0005515|GO:0000790|GO:0006357|GO:0043044|GO:0003713|GO:0031492|GO:0005634|GO:0006337|GO:0000978|GO:0006351|GO:0043234|GO:0016514|GO:0000980|GO:0006338 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112508_PI430048170 0.00295961496983429 1.44799640830789 9.67652238923713 9.4810764233201 9.6187169842368 P P P 9.10304808252912 9.12980225077358 8.94108243802824 P P P LNCV6_112508_PI430048170 mRNA
CATATTATTGATGGAGAAGAAACAAGAAGCATAAAAGGACTGCAGGAGGTGCTGTGGGTT NM_001042697 RefSeq chr17 - 15976560 15999692 ZSWIM7 125150 "zinc finger, SWIM-type containing 7, transcript variant 1" GO:0005515|GO:0000724|GO:0050821|GO:0008270|GO:0005634|GO:0097196 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129927_PI430048170 0.0175436637399458 2.34825900162049 4.35620861733595 4.3607933688457 4.699668687582 P P P 2.75652995682281 3.49459302409594 3.3934568391961 P P P LNCV6_129927_PI430048170 mRNA
GGGATGGAGTTAGAACCTTAATGATAATTTCTTTCGTTTGGTGTAGGTTTTAGAGATTTG NM_012244RefSeq chr14 - 23125294 23183660 SLC7A8 23428 "solute carrier family 7 (amino acid transporter light chain, L system), member 8, transcript variant 1" GO:0005515|GO:0019534|GO:0006520|GO:0015695|GO:0005886|GO:0006865|GO:0009636|GO:0050900|GO:0055085|GO:0015101|GO:0055065|GO:0016323|GO:0015804|GO:0005737|GO:0015171|GO:0005887|GO:0007596|GO:0042605|GO:0006810|GO:0015175|GO:0015179|GO:0070062|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137771_PI430048170 0.3158388686486621.18372059215965 6.25048672193505 5.88774900921874 6.46870652294151 P P P 6.1341244693128 5.8322516280327 5.95301254345627 P P P LNCV6_137771_PI430048170 mRNA
GTCTGCTTGTTGATTCAGGATGCTGTAATGGGACCTAACATTAAAAATTAATGACATGTT NM_001655RefSeq chr11 + 118572386 118603032 ARCN1 372 "archain 1, transcript variant 1" GO:0008344|GO:0030126|GO:0030131|GO:0005794|GO:0005783|GO:0006890|GO:0006886|GO:0048205|GO:0005829|GO:0043231|GO:0005737|GO:0016020|GO:0043473|GO:0061024|GO:0021691 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121598_PI430048170 0.3237451514113672.00814295337503 0.99707317119446 0.5087235846381092.47671672203852 A A A 0.3815685604164860.450958714302828 0.851672828465017A A A LNCV6_121598_PI430048170 mRNA
TGACACGTCCTAGAGCTGCAAGCAGGTTCTGCTGGGACAGGCTGCTTCTGCAGGAGGTGG NM_133637RefSeq chr2 - 74518130 74526281 DQX1 165545 DEAQ box RNA-dependent ATPase 1 GO:0004004|GO:0005737|GO:0000398|GO:0005681|GO:0005524 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_139386_PI430048170 0.9136480821116410.9973602404091470.302029644450511
0.3109409632827890.407152944664266A A A 0.3630007664279190.311933224800681
0.358450877770993A A A LNCV6_139386_PI430048170 mRNA
GCACAAGACAGATATTTTGTGCCTTGAGTGTATATATTTTGTGCCTTGAGTGTATGTATT NM_145268RefSeq chr7
+ 130207863 130216844 SSMEM1 136263 serine-rich single-pass membrane protein 1 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93027_PI430048170 0.0520068082448844 1.24805065722524 11.7398794577137
11.7021837263568 11.6887820409851 P P P 11.4916684061849 11.439033927167
11.2283653725915 P P P LNCV6_93027_PI430048170 mRNA
TGTGGTCAGCTACGGGGTGACGAGAGTGGAGTCGGAGAAATGCAACAACCTCTGGCTCTTNM_032928RefSeq chr9
+ 136791324 136793317 TMEM141 85014 transmembrane protein 141 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_102121_PI430048170 0.00860711923623728 0.2986461812082915.14107414355215
4.33418412079485 4.75938720761887 P P P 6.3383665893425 6.66711005146684 6.552227551182
P P P LNCV6_102121_PI430048170 mRNA
TTTCGGTTCCCTGCTATGAAAAGTGATGTGGTAGCAATTTTATAAATGTTGCTTTCTGAT NM_001100399 RefSeq
chr4 - 39822862 39977956 PDS5A 23244 "PDS5 cohesin associated factor A, transcript variant 1"
GO:0005515|GO:0005886|GO:0005694|GO:0005654|GO:0008156|GO:0000278|GO:0000785|GO:0000775|GO:0051
301|GO:0007064|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140651_PI430048170 0.4975070250679991.02307982445596 0.529428680007939
0.56899293267406 0.484924029042565A A A 0.56822558647724 0.456157447605937
0.458567316616888A A A LNCV6_140651_PI430048170 mRNA
GAAGGCAATCAGTACCTCTGCTTTTCAAAGGTAAATGCATTCATTTTCTTTGATTCAGTT NM_182546RefSeq chr7
+ 54542324 54571080 VSTM2A 222008 "V-set and transmembrane domain containing 2A, transcript
variant 1" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102294_PI430048170 0.99711283537195 1.0031145249202 12.6820699695331
12.8924844423516 13.2166065071283 P P P 12.7727784535093 12.8359724503163
13.1847415558667 P P P LNCV6_102294_PI430048170 mRNA
TGGGTATTCTGAGATTTTCTCTTGCATGCCCTTAGCTTTACAGCTTTTGCATTTCCTGTT NM_001303047 RefSeq chr18
+ 3247529 3256237 MYL12A 10627 "myosin, light chain 12A, regulatory, non-sarcomeric, transcript
variant 2"
GO:0005515|GO:0001725|GO:0030018|GO:0048013|GO:0008360|GO:0072661|GO:0005509|GO:0005829|GO:0070
527|GO:0007411|GO:0035254|GO:0016460|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142054_PI430048170 0.2039804783838130.7331975001244582.4509422673565
2.58677406911067 3.3276404231355 A A P 3.41545654132531 3.20346969816756
3.24222358042077 P P P LNCV6_142054_PI430048170 mRNA
CACTGGGGTCTGAAACCAATAAGAAATACAGCAATGTTTCAATATTACTTACAGAACAGA NM_006608RefSeq chr1
- 113697201 113759155 PHTF1 10745 putative homeodomain transcription factor 1
GO:0005801|GO:0006355|GO:0005737|GO:0003700|GO:0005783|GO:0005730|GO:0005634|GO:0003677|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137145_PI430048170 0.1210498395473250.5508257792790071.66635864095515
0.3921032468179040.61601823631183 A A A 1.50562192330537 2.0716360332785
1.95763735916555 A A A LNCV6_137145_PI430048170 mRNA
CTTTACCCCCCTTTTTGAAAGCCTTTATTTTGTTCGGAGTCTCTTCATAAAACATTTGAA NM_018431 RefSeq chr20
+ 54475471 54651171 DOK5 55816 "docking protein 5, transcript variant 1"
GO:0000165|GO:0005158|GO:0005057|GO:0007169|GO:0007399 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_137197_PI430048170 0.80262214031427 1.04616576552375 0.883165520080209

0.44608097812322 0.341144299705073 A A A 0.527983286233529 0.675796062934742 0.306511340288588 A A A LNCV6_137197_PI430048170 mRNA CTGCTGCTCTAGATGAGAAGAATAAAATATTGACAATCTCAAATCCAAGCACCATTCTTT NM_079420 RefSeq chr2 - 210290143 210315171 MYL1 4632 "myosin, light chain 1, alkali; skeletal, fast, transcript variant 1f" GO:0030049|GO:0006936|GO:0005509|GO:0005859|GO:0030016|GO:0008307|GO:0060048|GO:0030017|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140340_PI430048170 0.0533241880647232 1.04099280647009 0.414725843489975 0.4487015318948 0.452715786046585 A A A 0.356998128615795 0.372105542765853 0.412879598174874 A A A LNCV6_140340_PI430048170 mRNA CGTCAGTGTCCTAAGTTCCTTAACAATGCTTACCAATGTATGGCTTAGAAGTTAATAAAA NM_080868 RefSeq chr1 - 75918872 75932431 ASB17 127247 "ankyrin repeat and SOCS box containing 17, transcript variant 1" GO:0035556|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65023_PI430048170 0.0976083788940164 1.38020335877435 4.75066795561873 5.04432096266421 4.4961570154259 P P P 4.49850629556329 4.38544610833094 4.0232501765708 P P P LNCV6_65023_PI430048170 mRNA ACACTGGATTCCATGAACAGCAAGGGCTGCAAGGTGTATTTCGGGCGCTGGCTGATCGAG NM_002103 RefSeq chr19 - 48968124 48993353 GYS1 2997 "glycogen synthase 1 (muscle), transcript variant 1" GO:0005515|GO:0019901|GO:0005975|GO:0016234|GO:0005978|GO:0044281|GO:0004373|GO:0005536|GO:0005829|GO:0007507|GO:0005737|GO:0016020|GO:0009405|GO:0006006 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123638_PI430048170 0.201870360700982 1.90121650447334 2.65990405159453 2.85519662810846 1.43741809674825 A A A 1.6865487842918 1.53912373095696 1.28074117988899 A A A LNCV6_123638_PI430048170 mRNA GATGCACAGGAGGAGAAGCAGGAGCTGTCGGGAAGATCAGAAGCCAGTCATGGATGACCA NM_001025159 RefSeq chr5 - 150401636 150412936 CD74 972 "CD74 molecule, major histocompatibility complex, class II invariant chain, transcript variant 1" GO:0005515|GO:0016064|GO:0043030|GO:0050731|GO:0005765|GO:0006886|GO:0042802|GO:0005622|GO:0001516|GO:0002906|GO:0070374|GO:0070062|GO:0004896|GO:0009986|GO:0006952|GO:0019955|GO:0090023|GO:0051085|GO:0002830|GO:0035718|GO:0009897|GO:0050998|GO:0042289|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143546_PI430048170 0.326821931187602 0.728436583018321 0.243073541738093 0.27194453066542 0.319402958935198 A A A 0.420840415180066 1.27179526705883 0.312635843107444 A A A LNCV6_143546_PI430048170 mRNA GTAGATGTCATTACAACCTGGAAAATAAATCACCCTAAGTGACACAAATTGAAGCATGTA NM_004291 RefSeq chr5 + 71719162 71721048 CARTPT 9607 CART prepropeptide GO:0005515|GO:0008343|GO:0070253|GO:0001678|GO:0032099|GO:0007267|GO:0007268|GO:0045671|GO:0032812|GO:0045777|GO:0051971|GO:0005615|GO:0045779|GO:0032922|GO:0003674|GO:0007165|GO:0000186|GO:0050796|GO:0007186|GO:0007218|GO:0030141|GO:0070093|GO:0009267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_48051_PI430048170 0.229277836881684 0.967942486536759 0.310566280236189 0.365286412984255 0.322240471868607 A A A 0.431919490645559 0.341916978074529 0.364325892467391 A A A LNCV6_48051_PI430048170 mRNA CTCTGCAGTGTGAGATTGACTTTAAACCAAGAAGAAGAGAAGAGAAGAAATGCCAATATA NM_052997 RefSeq chr10 + 37125856 37232567 ANKRD30A 91074 ankyrin repeat domain 30A GO:0006355|GO:0003700|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58379_PI430048170 0.786056659844209 1.02359176268078 12.6208749542026 12.7575633904446 12.8475878488558 P P P 12.5116751232948 12.6613041717983

12.929662245069 P P P LNCV6_58379_PI430048170 mRNA
TCCTGGTCACTCCCTTTATAGCCATTACTGTCTTGTTTCTTGTAACTCAGGTTAGGTTTT NM_004879 RefSeq chr11
+ 125569386 125584689 EI24 9538 "etoposide induced 2.4, transcript variant 1"
GO:0030308|GO:0031965|GO:0005794|GO:0008630|GO:0005783|GO:0042493|GO:0006914|GO:0006915|GO:2001
244|GO:0005737|GO:0016020|GO:0005789|GO:0050885|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128892_PI430048170 0.0860741694301388 0.825549873539837 7.67382657424575
7.67389027711371 7.39835051287321 P P P 7.84930719766975 7.90158918189675
7.84129187408829 P P P LNCV6_128892_PI430048170 mRNA
CCCTCTGTACCTGCCTCAAAGGTTTCAGACATTTTTCTTAAAGCACTATAATATTTATTG NM_182492 RefSeq
chr22 - 25351417 25362557 LRP5L 91355 "low density lipoprotein receptor-related protein 5-like,
transcript variant 1" GO:0042813|GO:0017147|GO:0060070|GO:0044332 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_66730_PI430048170 0.0922566077897238 0.612903134390455 2.53089904662595
2.76901197368557 3.38372463404276 A A P 3.72993374100222 3.65837126547281
3.54669342522921 P P P LNCV6_66730_PI430048170 mRNA
GGTTGTTTCATCTCAAAGACCATTTCAAGAATCTTCTGACAATGAAGGTAGGCGGACAAC NM_001282805 RefSeq
chr2 + 159712456 159768583 MARCH7 NA "membrane-associated ring finger (C3HC4) 7, E3
ubiquitin protein ligase, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134335_PI430048170 0.323935616230259 0.469381958471171 0.306795562996782
0.340209218910654 0.383918613235169 A A A 2.3714746216305 0.334370716268768
0.745709904999591 A A A LNCV6_134335_PI430048170 mRNA
CTCTGTATCACCTTTATATAGCAGACATGTCACCCTGCTTCTACACAGATGATGGATGAA NM_002207 RefSeq
chr3 + 37452321 37819790 ITGA9 3680 "integrin, alpha 9"
GO:0008305|GO:0005886|GO:0005518|GO:0030593|GO:0034679|GO:0046872|GO:0009925|GO:0007229|GO:0007
411|GO:0030198|GO:0042060|GO:0043236|GO:0007155 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127147_PI430048170 0.406456971792719 2.94406111253195 3.03438629736664
0.25954515950987 0.367724240387944 P A A 0.279738038322085 0.260525713608537
0.282005042984149 A A A LNCV6_127147_PI430048170 mRNA
AAGGATTCTGGAATCTGGGACCAGGAGAGCAGGGATTAAACATGTGCAAACTTGAAAAAA NM_199183 RefSeq
chr3 - 46742090 46744755 PRSS45 NA "protease, serine, 45" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_126923_PI430048170 0.807768947060582 1.02709370779186 10.9634072908507
10.6458760510146 10.927923359851 P P P 10.5456008228515 10.7868685839119
11.0630072767891 P P P LNCV6_126923_PI430048170 mRNA
TGTCTAGAAGGAATGTATTTGTTGCTAAATTTCGTAGCACTGTTTACAGTTTTCCTCCAT NM_000362 RefSeq
chr22 + 32800815 32863041 TIMP3 7078 TIMP metallopeptidase inhibitor 3
GO:0005515|GO:0051045|GO:0071310|GO:0005578|GO:0005634|GO:0002020|GO:0005615|GO:0046872|GO:0005
604|GO:0048553|GO:0010951|GO:0031012|GO:0008191|GO:0009725|GO:0034097|GO:0007601|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135520_PI430048170 0.408797872458301 0.977231845782313 0.458453402143836
0.439846328040889 0.395907689774635 A A A 0.405426784962581 0.498507380583844
0.488864072190376 A A A LNCV6_135520_PI430048170 mRNA
TCCATTGCTTCATAATCTTCATGAAGTTGCATGCTTTTGCAGCTTTTCACAGTTTATTTG NM_021992 RefSeq chrX
- 102513681 102516771 TMSB15A 11013 thymosin beta 15a
GO:0003785|GO:0042989|GO:0005737|GO:0007015|GO:0005856 . NA - . NA NA NA NA NA
NA NA NA NA

LNCV6_134788_PI430048170 0.0909883301098139 0.724426084668373 5.27378211224443 5.01685715652872 5.3416159558819 P P P 5.65649565549828 5.3840956963889 5.95115425446237 P P P LNCV6_134788_PI430048170 mRNA GTGTGATCTGCATTTGAAATGTTGTAAACTTGGTCAGTATTTCCATTAAAATATCAGGGC NM_001145358 RefSeq chr15 - 75369378 75451746 SIN3A 25942 "SIN3 transcription regulator family member A, transcript variant 1" GO:0005515|GO:0010467|GO:0003700|GO:0002218|GO:0032403|GO:0016580|GO:0017053|GO:0031937|GO:0044255|GO:0001103|GO:0001102|GO:0000976|GO:0001106|GO:0007568|GO:0010243|GO:0000122|GO:0001701|GO:0033558|GO:0010971|GO:0051595|GO:0002230|GO:0000776|GO:0005654|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132462_PI430048170 0.0132293968285619 0.865818021964552 14.9578663960561 15.0233517439809 14.987602215123 P P P 15.2671760348031 15.1576490443278 15.1657312715541 P P P LNCV6_132462_PI430048170 mRNA GACCTGTTTGAATTTTTTCTGTAGTGCTGTATTATTTTCAATAAATCTGGGACAACAGCC NM_001021 RefSeq chr15 - 82536749 82540544 RPS17 6218 "ribosomal protein S17, transcript variant 1" GO:0010467|GO:0003735|GO:0019083|GO:0006364|GO:0006614|GO:0019058|GO:0034101|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0016020|GO:0000184|GO:0022627|GO:0016032|GO:0005840|GO:0042274|GO:0044267|GO:0005925|GO:0070062|GO:0000028 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141665_PI430048170 0.0850386014431194 0.692408986358226 4.10980475081583 4.52701745992064 4.73261427244982 P P P 4.91192186746786 5.01395885447984 5.09647833104397 P P P LNCV6_141665_PI430048170 mRNA AAACGGAATAAGGATGTGGACATGCTTTGTGATACTTTGTATCAAGGAGGAAATCAGCTT NM_001303143 RefSeq chr4 - 2231835 2242164 HAUS3 79441 "HAUS augmin-like complex, subunit 3, transcript variant 1" GO:0051297|GO:0003674|GO:0007067|GO:0005813|GO:0005737|GO:0005874|GO:0005819|GO:0070652|GO:0051225|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105761_PI430048170 0.445035014184287 1.15598567208233 5.72185839805069 5.35852367844941 5.2841605353654 P P P 4.77178788172927 5.50658157952096 5.3949272547855 P P P LNCV6_105761_PI430048170 mRNA TCTATGTGAGTAGCTGAAAGCATTGGGTGACCAGAAAGAAGGTCGGTGTAAGTGAAGGAA NM_014783 RefSeq chr15_KI270905v1_alt + 4830069 4854533 ARHGAP11A 9824 "Rho GTPase activating protein 11A, transcript variant 1" GO:0043547|GO:0051056|GO:0007264|GO:0005829|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140329_PI430048170 0.19994418234856 0.666505945080368 3.16586990325331 1.98366103642907 2.80009967020099 P A A 3.04589601350606 3.62871584348031 3.20491789711958 P P P LNCV6_140329_PI430048170 mRNA CAACAGAAATAAGATGATTTCTAAGTATAAAGCCATTTAAGAATTCCAGAGTAGGGTGGG NM_007109 RefSeq chr6 + 31158525 31164215 TCF19 6941 "transcription factor 19, transcript variant 1" GO:0003700|GO:0006357|GO:0008283|GO:0008270|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144205_PI430048170 0.750253454053916 1.06195390221552 1.25837912073797 0.701475719005254 0.690749923724209 A A A 0.60278323840781 0.438818017645864 1.28084954253113 A A A LNCV6_144205_PI430048170 mRNA GGAAGATGTAAGGAAAAACTCGCACACTATCTGTGGAACTCATTTAAATTCAAATACTAG NM_001199978 RefSeq chr3 - 146433287 146469301 PLSCR2 57047 "phospholipid scramblase 2, transcript variant 1" GO:0017121|GO:0005886|GO:0017128|GO:0005509|GO:0005634|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104337_PI430048170 0.857428692981195 0.97778258978893 0.612999895091462 0.344220297468746 0.367213460314429 A A A 0.701887161677977 0.332456555841357

0.373931015869477 A A A LNCV6_104337_PI430048170 mRNA
AAATAGCAAAACCCAAAACAACAGCAGATGATATCTTCCAAGTGTCTGCTCGGGACACGG NM_001258459 RefSeq
chr7 - 56080282 56092996 PHKG1 5260 "phosphorylase kinase, gamma 1 (muscle), transcript variant 1"
GO:0005516|GO:0004689|GO:0005975|GO:0005978|GO:0005964|GO:0050321|GO:0044281|GO:0005524|GO:0005829|GO:0009405|GO:0006006|GO:0006468|GO:0019899|GO:0005980 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140742_PI430048170 0.0190985451783322 1.17514685418726 7.08532107780664
7.03964033929565 6.92777885080591 P P P 6.77463127526027 6.84677274733889
6.73510345156307 P P P LNCV6_140742_PI430048170 mRNA
AGACGGAGGAATTTGTGCTGGACATGAACACACTGCAGGCGCTGCAGCAGCTCTTGCAGT NM_005481 RefSeq
chr19_KI270868v1_alt - 47187 60470 MED16 10025 mediator complex subunit 16
GO:0003712|GO:0005515|GO:0010467|GO:0006367|GO:0006357|GO:0006366|GO:0003713|GO:0005634|GO:0003824|GO:2000273|GO:0046966|GO:0030375|GO:0030518|GO:0016020|GO:0042809|GO:0016592|GO:0004872|GO:0005654|GO:0045893|GO:0030521 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143340_PI430048170 0.681070043067683 0.957740176627657 0.356246467098867
0.343390102387833 0.436969508197895 A A A 0.654525973786562 0.296699554240731
0.347498928941734 A A A LNCV6_143340_PI430048170 mRNA
GTCTGCATGCTATTTTAATCTCACATTCTTTATCTGTCTTAAAGTGGAAATCCATTTGCC NM_203349 RefSeq chr15
- 48823736 48963444 SHC4 399694 "SHC (Src homology 2 domain containing) family, member 4"
GO:0005515|GO:0010468|GO:0030971|GO:0008284|GO:0030054|GO:0005886|GO:0019901|GO:0019904|GO:0006915|GO:0035556|GO:0048863|GO:0045211|GO:0007169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58224_PI430048170 0.269762158620485 1.15278335938332 6.84319653915541
7.05909258692112 6.86483224065177 P P P 6.82954137744935 6.86836870051317
6.42306054097777 P P P LNCV6_58224_PI430048170 mRNA
AGGTTGCTTAAAAGGGACAGTATTCTCAGTGCTCTCCTACCCCACCTCATGCCTGGCCCC NM_000040 RefSeq
chr11 + 116829907 116833071 APOC3 345 apolipoprotein C-III
GO:0050995|GO:0007603|GO:0042627|GO:0070328|GO:0043434|GO:0010897|GO:0044281|GO:0010903|GO:0034379|GO:0005615|GO:0034361|GO:0042953|GO:0006954|GO:0005543|GO:0034382|GO:0010987|GO:0015485|GO:0034363|GO:0070653|GO:0030234|GO:0010989|GO:0019433|GO:0071333|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81336_PI430048170 0.23160894681507 1.17531395382354 8.96645901959402 8.78735807320055
8.95595468643008 P P P 8.52664796762318 8.95150955385479 8.49269235374482 P P P
LNCV6_81336_PI430048170 mRNA
TTGACCCTAGGCTGTTCATTCTGGGCACGGAAGGCGGCTTCCCGCTCAAGTGTTCCCTGG NM_052844RefSeq chr9
- 128633660 128656850 WDR34 89891 WD repeat domain 34
GO:0005737|GO:0006996|GO:0005814|GO:0005930|GO:0072372|GO:0036064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140821_PI430048170 0.0482501482926970.5726619058265667.53062937345213 6.9207995006347
6.79060469968201 P P P 8.11717883642837 7.90145392775486 7.72126646781773 P P P
LNCV6_140821_PI430048170 mRNA
TCCTTCTCCCTTTCCCCAACTACAAAAATGTTTGGCAACTTTGTGTTTACATTTAAAGAT NM_014458RefSeq chr1 +
173714940 173786703 KLHL20 27252 kelch-like family member 20
GO:0005515|GO:0005802|GO:0030424|GO:0048471|GO:0043066|GO:0004842|GO:0005794|GO:0016567|GO:0035455|GO:0003779|GO:0015031|GO:0015629|GO:0006895|GO:0030425|GO:0005737|GO:0019964|GO:0016605|GO:0007010|GO:0031463|GO:0043161 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92763_PI430048170 0.00594795564476218 0.5999006557056386.27967600959974
6.40507978199442 6.62662386673995 P P P 7.29563793436494 7.07350651938871 7.1667899140092

P P P LNCV6_92763_PI430048170 mRNA
TTTGTGGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCA NM_016245 RefSeq chr4
- 87336524 87391303 HSD17B11 51170 hydroxysteroid (17-beta) dehydrogenase 11
GO:0005811|GO:0006694|GO:0005737|GO:0004303|GO:0016229|GO:0005576|GO:0006710|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132928_PI430048170 5.79503500609231e-05 0.2693064315596944.47773366150518
4.22160490714428 4.32240759107202 P P P 6.11351760203051 6.37260823898835
6.21335418409886 P P P LNCV6_132928_PI430048170 mRNA
CTGGGTATTTATCCTAAGGAATTAATTAAAGAGTTAATTGTTCCTTTCTTCAGTGGGCCA NM_001002800 RefSeq
chr3 + 160399303 160434961 SMC4 10051 "structural maintenance of chromosomes 4, transcript
variant 2"
GO:0000796|GO:0005515|GO:0007076|GO:0010032|GO:0046982|GO:0005634|GO:0051383|GO:0005524|GO:0005
829|GO:0000070|GO:0005737|GO:0045132|GO:0005654|GO:0000278|GO:0051301 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130996_PI430048170 0.9254663593041540.9941881400612731 1.8283316871483
11.6703120559643 11.4515741444046 P P P 11.8041104456879 11.6028193938292
11.5825625103559 P P P LNCV6_130996_PI430048170 mRNA
CATAGCCCTGGGGTGAATGTGAATCCAGAGTCTATTTTTCTAAATAAATTGGAAAAAACA NM_006302 RefSeq chr2
- 74461056 74465410 MOGS 7841 "mannosyl-oligosaccharide glucosidase, transcript variant 1"
GO:0009311|GO:0004573|GO:0005783|GO:0015926|GO:0016020|GO:0006457|GO:0005789|GO:0006487|GO:0016
021|GO:0044267|GO:0018279|GO:0043687|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143580_PI430048170 0.116971112259316 1.59538983847034 5.45095244777453
5.70196456202766 5.50306717648638 P P P 5.17442892384287 5.04765231261994
4.26943940844292 P P P LNCV6_143580_PI430048170 mRNA
TGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTT NM_199328 RefSeq chr21 -
30214005 30216151 CLDN8 9073 claudin 8
GO:0016323|GO:0016338|GO:0005886|GO:0005783|GO:0005198|GO:0016021|GO:0005923|GO:0042802 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136304_PI430048170 0.3936636413840360.9806107182851210.471785749045171
0.3916079003728820.44012105842719 A A A 0.4668091147746870.492129725282621
0.429765737851895 A A A LNCV6_136304_PI430048170 mRNA
CCTGAGTACTTAAAATGTCGAAAGTTGTTTGTCATGTTGACATGTGCCTTTCGCTATGGC NM_004312 RefSeq chrX
+ 70268334 70281840 ARR3 407 "arrestin 3, retinal (X-arrestin)"
GO:0051219|GO:0005515|GO:0007165|GO:0001917|GO:0005737|GO:0045202|GO:0001932|GO:0002046|GO:0007
601|GO:0006897|GO:0001750 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133362_PI430048170 0.2218162355478981.02209500491614 0.322361203864419
0.2659922227462610.271939591969901 A A A 0.2537551697167460.256908901601792
0.255706754424512 A A A LNCV6_133362_PI430048170 mRNA
TTTTTGGTCAGAAGAGTAAAGTTTCTGGGATTGGGGACGTGTGTGCTATGGGAACTCAGT NM_002962 RefSeq chr1
- 153537146 153541765 S100A5 6276 S100 calcium binding protein A5
GO:0005507|GO:0005509|GO:0043025|GO:0008270|GO:0005634|GO:0042803 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139699_PI430048170 0.00127660857155317 0.5375096140284223.56123162389905
3.48171600717857 3.3849353506371 P P P 4.35077149808734 4.51150725616328
4.24538955602994 P P P LNCV6_139699_PI430048170 mRNA
TGAGGAAAAATAATACAATGTGTGTGTGTGAGAGAGAGAGTGAGTTACTGACATTGTTCC NM_003574 RefSeq chr18
+ 9913957 9960021 VAPA 9218 "VAMP (vesicle-associated membrane protein)-associated protein A,
33kDa, transcript variant 1"
GO:0008017|GO:0005515|GO:0008219|GO:0048471|GO:0034975|GO:0005886|GO:0005783|GO:0044281|GO:0031

175|GO:0015630|GO:0061025|GO:0004871|GO:0043123|GO:0006665|GO:0090114|GO:0046982|GO:0030148|GO:0
019904|GO:0070972|GO:0070971|GO:0031982|GO:0006888|GO:0007165|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136632_PI430048170 0.3743895069826291.36266922047746 1.40703190505095
2.16012200091975 1.47020737848158 A A A 1.86351066491968 1.26832379669132
0.276895899945664A A A LNCV6_136632_PI430048170 mRNA
TAAAACGTTATTTAAATGGGGAGCTGAGGAAGGAGCAAACGGGTTTTCGCGGTTAAACCC NM_024869RefSeq chr1
+ 26159019 26162628 FAM110D 79927 "family with sequence similarity 110, member D" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134795_PI430048170 0.0579208778978194 0.4509736441372050.498595541095933
1.72039872129492 1.15451840232211 A A A 2.04031342505492 2.4700179568685
2.51657904143036 A A P LNCV6_134795_PI430048170 mRNA
GCTGCATTGTTTGATTATTGTTGGCTCAATTAAAAGTTGGCTTTTCCAAATCCTCCATTA NM_001010844 RefSeq chr6
+ 78867543 78900966 IRAK1BP1 134728 interleukin-1 receptor-associated kinase 1 binding protein 1
GO:0006955|GO:0006355|GO:0005737|GO:0007249|GO:0005634|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137506_PI430048170 0.6621177574695070.8998781182389454.6496160338422
3.75989617043871 3.87802433786737 P P P 4.72496134886714 4.01905187333524 4.0554737697342
P P P LNCV6_137506_PI430048170 mRNA
GCAAGCTCTGCCCTCTCTGGCTTTGACACCCTCAGAAGATGGGGCAGGCTCTTTGTCTTA NM_198688RefSeq chr21
- 44591267 44592505 KRTAP10-6 NA keratin associated protein 10-6 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136189_PI430048170 0.3625534643115760.6180315518758343.10129546522437
2.31890715283506 0.31442976915705 P A A 3.11553747642355 3.44108218085693
2.15159340005547 P P A LNCV6_136189_PI430048170 mRNA
TGCTCTCCAGCCTCTGACACAAGATGCGTTCTTAATACAGACTTGTTTGCAAAGAAAAAA NM_014461RefSeq chr3
+ 1092657 1403608 CNTN6 27255 "contactin 6, transcript variant 1"
GO:0007219|GO:0005886|GO:0007411|GO:0031225|GO:0007417|GO:0007155 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142009_PI430048170 0.2559556318486850.7563203726966689.31757858198601
9.34522647896255 9.47455741873878 P P P 9.30720452879174 9.82134599867318
10.1111791504427 P P P LNCV6_142009_PI430048170 mRNA
GTTTGGCTGTGTCTAAACTGCATTACCGCGTTGTAAAATATAGCTGTACAAATATAAGAA NM_001130845 RefSeq
chr3 - 187721376 187736497 BCL6 604 "B-cell CLL/lymphoma 6, transcript variant 2"
GO:0005515|GO:0030308|GO:0003700|GO:0008285|GO:0030036|GO:0030890|GO:0035024|GO:0005657|GO:0005
634|GO:0048294|GO:0007266|GO:0007283|GO:0046872|GO:0042092|GO:0043380|GO:0006954|GO:0048821|GO:0
002903|GO:0030183|GO:0032319|GO:0002467|GO:2000773|GO:0002634|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_116451_PI430048170 0.7914305925344510.9521874460883767.09631808422949
7.08091343766393 6.80677418484143 P P P 7.28226619174001 7.15869181304874
6.71318231775091 P P P LNCV6_116451_PI430048170 mRNA
ATTCCAGTGTGTCTCCAGCGCCCTCCTTGTGCACTGTCCCAGTCCTACAGACCGTGCCCA NM_001144857 RefSeq
chr12 + 6312650 6328506 PLEKHG6 55200 "pleckstrin homology domain containing, family G
(with RhoGef domain) member 6, transcript variant 3"
GO:0005515|GO:0005737|GO:0000922|GO:0032321|GO:0005089|GO:0032154|GO:0005096 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_108817_PI430048170 0.0506366802459044 2.38902316128352 1.40523878573502
1.38489582922456 2.41895873057213 A A A 0.25552951626389 1.03751225199332
0.255619336437117A A A LNCV6_108817_PI430048170 mRNA

ACTAGACTTAGATTTCCTCAAATATGTGGATGACATACAGAAGGGAAATACCATCAAAAG NM_001256877 RefSeq chr9 + 504694 746106 KANK1 23189 "KN motif and ankyrin repeat domains 1, transcript variant 4" GO:0005515|GO:0006355|GO:0030336|GO:0008013|GO:2000393|GO:0090303|GO:0046627|GO:0035024|GO:2000114|GO:0030177|GO:0005634|GO:0032587|GO:0035413|GO:0006351|GO:1900028|GO:0005737|GO:1900025|GO:0030837|GO:0010977. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127385_PI430048170 0.6516659994679270.8789730834472448.33786790474688 7.712774249272 7.97716713697901 P P P 8.43716495871399 8.44852134602253 7.6256820586041 P P P LNCV6_127385_PI430048170 mRNA
TTTGCTTTGAGTTCCTTCTCTCCCATCTGGATCTCCCAGCCTTTTCCAAATTGAAAAATG NM_003196 RefSeq chr1 - 23380908 23424779 TCEA3 6920 "transcription elongation factor A (SII), 3" GO:0006357|GO:0032784|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132210_PI430048170 0.0121096683346863 0.3565138279912677.6964788971274 7.40314797572685 7.77639168665803 P P P 8.77145034783462 8.93993200952436 9.53812334469423 P P P LNCV6_132210_PI430048170 mRNA
GTCCTCTTTCTAGATTGCCAGCTCATGACATGGTGCTTATAAAGATTTAATTAAAGTAAG NM_001291981 RefSeq chr6 - 127968778 128520674 PTPRK 5796 "protein tyrosine phosphatase, receptor type, K, transcript variant 3" GO:0005515|GO:0010839|GO:0030424|GO:0008285|GO:0008013|GO:0035335|GO:0030425|GO:0034644|GO:0006470|GO:0005912|GO:0005911|GO:0005001|GO:0048041|GO:0043025|GO:0007179|GO:0007155|GO:0004725|GO:0030336|GO:0031256|GO:0045295|GO:0009986|GO:0019901|GO:0045786|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141097_PI430048170 0.7630707838687681.26721840024069 0.355304717989613 2.24497613416871 2.51440096487674 A A A 0.3457596435273961.59046118004143 2.31519111369092 A A A LNCV6_141097_PI430048170 mRNA
ACTCTATTAAGAAAGACACTGTGAATCCAGGGAGGATTCTCATAATTCTGTAAACTGTAT NM_145803 RefSeq chr11 - 36483766 36510313 TRAF6 7189 "TNF receptor-associated factor 6, E3 ubiquitin protein ligase, transcript variant 1" GO:0005515|GO:0035631|GO:0004842|GO:0016874|GO:0007249|GO:0002756|GO:0002755|GO:0031398|GO:0031666|GO:0043123|GO:0005938|GO:0031625|GO:0031624|GO:0005811|GO:0000209|GO:0005164|GO:0038124|GO:0038123|GO:0019901|GO:0034134|GO:0001843|GO:0031435|GO:0000122|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139619_PI430048170 0.9257711123795671.00143845818533 5.75736796177309 5.63359056452404 5.96629013950018 P P P 6.13209620698521 5.68035478778547 5.47909466609423 P P P LNCV6_139619_PI430048170 mRNA
AGTTTCCAGCCTGCTTCTCTCTGTGAAATCATGGTTTCTCCCTTCATATAACTGTCCTCT NM_001012264 RefSeq chr14 - 21032819 21034785 RNASE13 NA "ribonuclease, RNase A family, 13 (non-active)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136220_PI430048170 0.1925103757428081.1205486200831 11.6082174679232 11.7772512049438 11.9011121408529 P P P 11.6550209643389 11.5082927100728 11.6410478672216 P P P LNCV6_136220_PI430048170 mRNA
TGGCAAGAGCCACAATCAATGAATGCATTATGGTCAAATCTTTTCATGTATATGGATGTG NM_174889 RefSeq chr5 + 60945128 61153037 NDUFAF2 91942 "NADH dehydrogenase (ubiquinone) complex I, assembly factor 2" GO:0022904|GO:0005739|GO:0072593|GO:0008137|GO:0061179 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138560_PI430048170 0.5764568997458061.06471203625279 6.31714548693849 6.29528613423468 5.94923943819035 P P P 6.00904594477877 6.21273390875275 6.08985502343841 P P P LNCV6_138560_PI430048170 mRNA
CACGGGGAGGGGATGATACAAGGAGTAAACCTTTCTTTACACTCTGAGGTCTCCAAAAAA NM_004720 RefSeq chr19

- 19623655 19628230 LPAR2 9170 lysophosphatidic acid receptor 2
GO:0005515|GO:0005886|GO:0009986|GO:0004930|GO:0035025|GO:0030139|GO:0007202|GO:0030165|GO:0007204|GO:0008289|GO:0000187|GO:0007186|GO:0005887|GO:0070915 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100100_PI430048170 0.1289701686215271.95081134027962 2.41151261501525 2.48054467099705 2.41283575520324 A A A 0.5145761063066921.59631119091379 1.95069466125854 A A A LNCV6_100100_PI430048170 mRNA
AAAGTTTGCCAAAACTGTCGTTGATGTGGGAGAGAAAACGTCAGAGTTCAAGGCCAAAGG NM_001010854 RefSeq chr14 - 90540587 90816417 TTC7B 145567 tetratricopeptide repeat domain 7B NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144335_PI430048170 0.0142776458753835 0.4608510014682717.45799503953163 7.75404367958822 8.07622254532326 P P P 8.59191904095454 8.77680810632881 9.25528336047692 P P P LNCV6_144335_PI430048170 mRNA
CAGTACTTTGGTTGACCCTTGTATGTCACAGCTCTGCTCTATTTATTATTATTTTGCAAA NM_005261 RefSeq chr8 - 94249256 94262319 GEM 2669 "GTP binding protein overexpressed in skeletal muscle, transcript variant 1"
GO:0005515|GO:0072686|GO:0005516|GO:0051276|GO:0000287|GO:0007264|GO:0003924|GO:0030496|GO:0005634|GO:0051233|GO:0005525|GO:0006184|GO:0007165|GO:0006955|GO:0007067|GO:0009898|GO:0019003|GO:0007166|GO:0051310. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143033_PI430048170 0.8560948816869690.9897815181756727.74670778717492 7.12117482791881 6.72899300350651 P P P 7.29483560562455 7.47617508740013 7.01953420547962 P P P LNCV6_143033_PI430048170 mRNA
CTTCCTTTTGAAACGAAGCTCAGCTTCGAAGATGTGAACAAGAATAAAAGGAAAAAATTC NM_139162 RefSeq chr17 + 18260533 18265781 MIEF2 125170 "mitochondrial elongation factor 2, transcript variant 1"
GO:0032464|GO:0005739|GO:0005515|GO:0008053|GO:0090314|GO:0005741|GO:0016021|GO:0007005|GO:0090141|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131164_PI430048170 0.4997406594647590.8820485884817890.29757201476728 0.2629998809268660.379434652741958 A A A 0.2829701882962910.849266854164585 0.275448969107861 A A A LNCV6_131164_PI430048170 mRNA
CAGCTGCTATCAAAATTTTGGATATGATTTCTTAGGGTCTGTGTACTTTGGTTGTATTCT NM_001300968 RefSeq chr1 - 169394869 169460669 CCDC181 57821 "coiled-coil domain containing 181, transcript variant 1"
GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126903_PI430048170 0.0166792246260084 0.5653260110127132.03847200275331 1.59090425076971 1.55368742801191 A A A 2.41746738483663 2.71822958084586 2.55219432470771 A P P LNCV6_126903_PI430048170 mRNA
ATGAAGAAGAGAAAATTTTGTCACATTCTGAAACAAATGTCATCCCCTCTGGCAACTTGA NM_001005516 RefSeq chr3 + 98390665 98391631 OR5K3 NA "olfactory receptor, family 5, subfamily K, member 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126665_PI430048170 0.00883002449354313 0.5476316288509146.86982876775815 6.51189383334391 6.7942520050134 P P P 7.36487500468241 7.56589161481091 7.83646426812611 P P P LNCV6_126665_PI430048170 mRNA
GCCTACAGGGGAAAAACAAGCTGGATAACCACCCAAAGTGTTTGTATTTTCGTTGGAAAC NM_014840 RefSeq chr12 - 106063346 106140033 NUAK1 9891 "NUAK family, SNF1-like kinase, 1"
GO:0005515|GO:0035507|GO:0005730|GO:0005634|GO:0005524|GO:0030155|GO:0046872|GO:0006974|GO:0002039|GO:0005737|GO:0004674|GO:0042127|GO:0015630|GO:0006468|GO:2000772|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143567_PI430048170 0.0215266714023318 1.21799549597484 0.744612495183815 0.8593195929124270.92553502381211 A A A 0.6703977327705360.486710769506028 0.517832671764989 A A A LNCV6_143567_PI430048170 mRNA

TTCTGCAGTTTGCTCATTGTTTTAGCGAGGTCACGAGAGAGTCACTCATGACTTTCTTGG NM_006188 RefSeq chr7 - 97984700 97990104 OCM2 4951 oncomodulin 2 GO:0005509 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133337_PI430048170 0.1137587485186770 0.8492630889879055 0.09051924641884 4.85721948235297 5.17131119267825 P P P 5.26194546152453 5.33950911849051 5.24099455105406 P P P LNCV6_133337_PI430048170 mRNA
TTGAGTGAGGGCAGGGAGTACCTGAAATAAGACAATGTTTACTAAGGCAAATAATTGAAA NM_001303111 RefSeq chr10 + 119104064 119137984 FAM45A 404636 "family with sequence similarity 45, member A, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136900_PI430048170 0.8886175756989310 0.9958772417823590 0.284834163628311 0.2916479343646410 0.415961610095897 A A A 0.3589483641461480 0.305629135157 0.349004407715999 A A A LNCV6_136900_PI430048170 mRNA
CTCAAATAAATGGAGCTGCTTACAAGCCTGTTGACATGTGTGGCTTGCACAACACGTTAA NM_030949 RefSeq chr6 + 150143051 150250392 PPP1R14C 81706 "protein phosphatase 1, regulatory (inhibitor) subunit 14C" GO:0042325|GO:0005737|GO:0016020|GO:0004865|GO:0043086 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133061_PI430048170 0.1795341222012861 .55878566666367 6.52357465799004 5.66330590406257 5.96898190557635 P P P 4.77099699837092 5.74005726571883 5.67145728005189 P P P LNCV6_133061_PI430048170 mRNA
CAGCTGCTGTAACGGAGCCACCTCCAACTCTAACAATAAACCAAGTTCATTGCAGATAGT NM_002373 RefSeq chr15 + 43517607 43531620 MAP1A 4130 microtubule-associated protein 1A GO:0008017|GO:0005515|GO:0005198|GO:0007605|GO:0005875|GO:0005874|GO:0000226|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92055_PI430048170 0.0145450317165147 0.5569187746917371 0.2198614608682 10.0176988351821 10.3091283521704 P P P 10.858584064835 10.87440776621 11.3144642892491 P P P LNCV6_92055_PI430048170 mRNA
AAATGCTGGAGAAGTTACACAAGGCTTTGCAGCTGCGCTCAAATGTGGACTGACCAAAAA NM_001261445 RefSeq chr12 + 104286681 104350307 TXNRD1 7296 "thioredoxin reductase 1, transcript variant 6" GO:0005515|GO:0015949|GO:0050660|GO:0005730|GO:0015035|GO:0009055|GO:0055086|GO:0044281|GO:0005829|GO:0007165|GO:0004791|GO:0005654|GO:0045454|GO:0000302|GO:0044255|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133461_PI430048170 0.3730825076550232 .25685171583158 0.3101361510000332 .4956625481388 0.458398629003078 A A A 0.2949799383022480 .2623057810998620 .299734676617519 A A A LNCV6_133461_PI430048170 mRNA
GATGACAAACCATGATGCCTGTGTTTCTGAGTCTTTAAATAAAAATGAACATGGAGAAGG NM_001099289 RefSeq chr2 + 109129540 109504636 SH3RF3 344558 SH3 domain containing ring finger 3 GO:0005515|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132218_PI430048170 0.4439449277328471 9.494188816975 6.89901955972771 12.8409638532931 6.86884493823351 P M P 6.64686808391733 6.98984080287405 7.33246298881404 P P P LNCV6_132218_PI430048170 mRNA
CTACGTGATGCTGTATAAATTGGATTACAAACCATATTCTTGTTCAGCTTGCACTAATCT NM_001083621 RefSeq chr1 + 22451850 22531157 ZBTB40 9923 "zinc finger and BTB domain containing 40, transcript variant 1" GO:0003674|GO:0006355|GO:0005634|GO:0030282|GO:0003677|GO:0046872|GO:0006974|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139091_PI430048170 0.6703272063147520 .8879409227224652 .11971561622555 2.41746738483663 2.47636647848274 A A A 2.90639540975712 2.49933031445208 2.00959118424115 P P A LNCV6_139091_PI430048170 mRNA
TTCTATTTCCACATAGGCTCGTTTTCTCTGCAGTGGTCCTCTCAAGGGCATTTTGCCTTT NM_025115 RefSeq chr8 -

33498508 33513185 TTI2 80185 "TELO2 interacting protein 2, transcript variant 2"
GO:0005813|GO:0005737|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126752_PI430048170 0.00586911565008094 2.00883348754398 6.60075315319179
6.4776872023517 6.44971768561916 P P P 5.42049503422427 5.71915678451851
5.34640280463724 P P P LNCV6_126752_PI430048170 mRNA
TTTCTTCTCTGGCTAAAAATTTTTAATTGGATGTGTTTGGGGGCGGGGGGATGGAAGTGA NM_001661 RefSeq chr17
+ 43398984 43401136 ARL4D 379 ADP-ribosylation factor-like 4D
GO:0005515|GO:0005737|GO:0009306|GO:0005886|GO:0007264|GO:0008152|GO:0005730|GO:0003924|GO:0005
525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134551_PI430048170 0.00459781959326813 1.99062162668418 6.76836736337078
6.71518209517336 6.64823995637039 P P P 5.90317809674638 5.63034052311428
5.60152359662213 P P P LNCV6_134551_PI430048170 mRNA
AGCCGCTTCCATTTTCTATACTCGAACCAAACAGCAATAAAGCAGTAACCAAGGAAAAAA NM_006497 RefSeq chr17
+ 2055098 2059687 HIC1 3090 "hypermethylated in cancer 1, transcript variant 1"
GO:0005515|GO:0006355|GO:0003700|GO:0008630|GO:0042826|GO:0030178|GO:0007275|GO:0000122|GO:0046
872|GO:0006351|GO:0043565|GO:0005737|GO:0043517|GO:0005654|GO:0016055|GO:0000785 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_98420_PI430048170 0.0146933836036426 0.449814224639474.51001088250378 4.2939060243237
4.38796686909125 P P P 5.21419320737544 5.60864964063598 5.81813399369169 P P P
LNCV6_98420_PI430048170 mRNA
GAGGACACGTCGCACATTTAGAAGATGATGAAGGAGATGATGATGAATCTAAACACTCAA NM_003618 RefSeq chr2
- 39249265 39437312 MAP4K3 8491 "mitogen-activated protein kinase kinase kinase kinase 3,
transcript variant 1"
GO:0005515|GO:0007254|GO:0005524|GO:0035556|GO:0005083|GO:0005737|GO:0050790|GO:0004672|GO:0004
702|GO:0004674|GO:0006468|GO:0034612|GO:0009411 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141693_PI430048170 0.0469404102584278 1.2588162975056 7.83837331697097
8.02817359812892 8.13416479734643 P P P 7.51767122512496 7.71860559405779
7.77140770346004 P P P LNCV6_141693_PI430048170 mRNA
TCTTGTGTTTGTATCTCCTTTTTATGATTGCTGTACCTACCCATGTCTTTTTGGGGAGGG NM_014598 RefSeq
chr17_KI270857v1_alt + 2387071 2440912 SOCS7 30837 suppressor of cytokine signaling 7
GO:0005515|GO:0008286|GO:0017124|GO:0016567|GO:0005886|GO:0019221|GO:0005730|GO:0005634|GO:0046
426|GO:0043231|GO:0035556|GO:0008150|GO:0005737|GO:0045444|GO:0004860|GO:0006469|GO:0040008 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131921_PI430048170 0.3328949050318590.9598768787833528.64909632835223
8.71452721644386 8.71435657800946 P P P 8.66092285455919 8.78934002284696
8.80176407200213 P P P LNCV6_131921_PI430048170 mRNA
TAGGAAAATGCCCTTTGGTCACTGTAAATATGAATTGTGACCCCATCCCTTCCCGCATGA NM_173050 RefSeq chr22
- 43203222 43343388 SCUBE1 80274 "signal peptide, CUB domain, EGF-like 1"
GO:0009986|GO:0046982|GO:0005509|GO:0009791|GO:0005615|GO:0007512|GO:0042802|GO:0006954|GO:0007
596|GO:0051260|GO:0045446|GO:0009897|GO:0019897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136106_PI430048170 0.4478968112571061.02742284181404 0.393687561245336
0.2622042767659480.287606038156741 A A A 0.2660269760576880.297996185566125
0.26554201371752 A A A LNCV6_136106_PI430048170 mRNA
GATTACGACTCTAACTCCAACTTGTCAGTTACAAACAGTTCAAGCTACTCTCACATTTGA NM_001037731 RefSeq
chr20 - 31303211 31308585 DEFB116 NA "defensin, beta 116" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144694_PI430048170 0.1444215022688570.8294914230788731 0.3509266619333 10.133619948409
9.96427123453452 P P P 10.6067310701241 10.2683283385173 10.3884046436111 P P P
LNCV6_144694_PI430048170 mRNA

CGTGTGGGGACACAGTTTTCCAAACTGAGGAAAATGTTGCAATAAAAGAATATGTTGTAA NM_001198696 RefSeq chr10 - 70112266 70132934 AIFM2 84883 "apoptosis-inducing factor, mitochondrion-associated, 2, transcript variant 1" GO:0005811|GO:0043065|GO:0050660|GO:0005741|GO:0003677|GO:0005615|GO:0005829|GO:0005739|GO:0005737|GO:0008637|GO:0004174|GO:0016021|GO:0008137|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142756_PI430048170 0.00541672696538066 0.290871760093641 12.6650791585832 12.2583996727275 12.0568849163231 P P P 14.0301189240734 14.2367013818813 14.1184678540716 P P P LNCV6_142756_PI430048170 mRNA
CTCCGCTCACCCCGCAGTTAATGGCAAACGAATAAATAAATGAGGCGGCCTCGGAAAAAA NM_148896 RefSeq chr17 + 81902195 81902905 NPB 256933 neuropeptide B GO:0005515|GO:0001664|GO:0007186|GO:0007218|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131157_PI430048170 0.3550886299209740.943056635459822 0.496759908301806 0.5163900644775930.407150406109968 A A A 0.5402392590741370.678929452622561 0.447791816409889 A A A LNCV6_131157_PI430048170 mRNA
CAGCAGAGATGGACTCATATCAGACTCAACATTTTCCCAGATGGTGGAATTGCACGACTT NM_018436 RefSeq chr2 + 3658195 3702670 ALLC 55821 allantoicase GO:0004037|GO:0000256 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104292_PI430048170 0.0459620610668639 0.484702742412453 4.97380319353892 4.06600406176124 4.43235426127715 P P P 5.03439401593192 5.73686712686943 5.85374736120972 P P P LNCV6_104292_PI430048170 mRNA
TATAACAGACATTCAAGCAAATATCCCAGGGGCCGCATACAGTGGTCGAGAGACAGTATA NM_001817 RefSeq chr19 - 41618970 41627074 CEACAM4 1089 carcinoembryonic antigen-related cell adhesion molecule 4 GO:0016020|GO:0005887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144073_PI430048170 0.801561121964975 1.0245675495208 9.64341333465847 9.58159551114854 9.40807284953079 P P P 9.77268956540301 9.53610540037738 9.16578379694276 P P P LNCV6_144073_PI430048170 mRNA
CTTGTGCTCAGAGAAGCAGACAAAACAAAGATTCAAGGTTTTAATTAATTCCCATACTGA NM_032520 RefSeq chr16 + 1351898 1363351 GNPTG 84572 "N-acetylglucosamine-1-phosphate transferase, gamma subunit" GO:0016256|GO:0005794|GO:0003976|GO:0000139|GO:0046835|GO:0042803|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127980_PI430048170 0.231897752524566 0.720300716558223 7.46244474087541 6.81790428708423 6.3596785876425 P P P 7.63662727877327 7.41258522982512 7.19098121556555 P P P LNCV6_127980_PI430048170 mRNA
CCTCTCCCTCAGCCTCATGGAGAGGAAACATTTTCTAATGTCTGTATATAGTATATATAC NM_032428 RefSeq chrX + 107522449 107605244 FRMPD3 84443 FERM and PDZ domain containing 3 GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136206_PI430048170 0.00465682310081641 0.431812618432052 4.31838433426105 4.55201118616276 4.8203995629848 P P P 5.87561093614487 5.62932096515552 5.85168329632585 P P P LNCV6_136206_PI430048170 mRNA
TAAGCAGAGATTATTTGTGATCCCATCCATTCCCCAATAAAGCAAGGCTTGTCCGACAAA NM_001170 RefSeq chr9 - 33384949 33402519 AQP7 364 aquaporin 7 GO:0007588|GO:0005886|GO:0034219|GO:0009992|GO:0006091|GO:0055085|GO:0005737|GO:0034220|GO:0005887|GO:0005911|GO:0015250|GO:0015793|GO:0015204|GO:0006833|GO:0015254|GO:0071918 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140884_PI430048170 0.531623138943106 0.977766062948098 0.25543188499045 0.264842341988784 0.389191405245114 A A A 0.372664458606503 0.311235670898751 0.326067686352711 A A A LNCV6_140884_PI430048170 mRNA

CCAATAGAGTATACAAGTGACTTGAATGATTTTTCCTAACTTGTTTGCAACTGATAGCTC NM_001144990 RefSeq chr4 + 37245067 37449465 NWD2 57495 NACHT and WD repeat domain containing 2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67536_PI430048170 0.0431294911225753 1.57008748351674 5.40952750480409 4.98673326800663 5.38945650607634 P P P 4.39313620607448 4.46875077459835 4.94524264491572 P P P LNCV6_67536_PI430048170 mRNA
AACTATTTGCTCAGGACATGATGCTGATACCGAAGATGATCCATCCCTAGCAGATTTGCC NM_015147 RefSeq chr2 + 65056360 65087008 CEP68 23177 centrosomal protein 68kDa
GO:0051297|GO:0010457|GO:0005813|GO:0005737|GO:0030054|GO:0033365|GO:0019901|GO:0005815|GO:0019904|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143570_PI430048170 0.0046709063188576 0.673703678625578 9.02890494267139 9.08619179050037 9.24986767715967 P P P 9.58124393118342 9.66072062450002 9.83032901520714 P P P LNCV6_143570_PI430048170 mRNA
GAGTGCTAAAACCTCCTGTTTTCTGTGTTAAACATTCCGTCCCTGTTTGAGACATCAGTA NM_001012991 RefSeq chr16 - 19706351 19718170 KNOP1 400506 lysine-rich nucleolar protein 1 GO:0005730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94542_PI430048170 0.389107872855808 1.15850468573299 2.69501866259674 3.19157036210832 3.25086683041713 A P P 2.87691739131356 2.95328765385727 2.72284814232107 P P P LNCV6_94542_PI430048170 mRNA
TACCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTT NM_001286423 RefSeq chr2 - 219236597 219245429 GLB1L 79411 "galactosidase, beta 1-like, transcript variant 1"
GO:0005773|GO:0004565|GO:0005975|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137417_PI430048170 0.00940364770619684 0.589853494097495 5.4145352300015 5.49081104083038 5.70453568365076 P P P 6.0503776220793 6.39709430115824 6.43295022342428 P P P LNCV6_137417_PI430048170 mRNA
TTTATTTATGAACCTGGTTTTCGGGAGTCAGGGGAGGAGATGACTTTGCTTCTGTGCACA NM_014757 RefSeq chr5 + 179732849 179777286 MAML1 9794 mastermind-like 1 (Drosophila)
GO:0005515|GO:0010467|GO:0006367|GO:0019901|GO:0003713|GO:0010831|GO:0005634|GO:0003162|GO:0007221|GO:0043231|GO:0002193|GO:0060928|GO:0007219|GO:0016607|GO:0045944|GO:0042605|GO:0045445|GO:0005654|GO:0006468. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65678_PI430048170 0.159630744720404 0.65688503386297 2.3650823745446 3.34866872223209 2.69604420265854 A P A 3.18278272793389 3.26223559290785 3.86203440923175 P P P LNCV6_65678_PI430048170 mRNA
TACATCTAAATGACATTTACTCTGTGGTGGGGATTCCTGTGTTCAGGGTTTCCCTAGCCA NM_025264 RefSeq chr2 - 39736059 39779276 THUMPD2 80745 "THUMP domain containing 2, transcript variant 1"
GO:0003723|GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132359_PI430048170 0.18445805326812 1.55925847220661 1.59549275988685 1.69582971948108 0.748510180755421 A A A 1.21080849840251 0.498127275614647 0.450147753332821 A A A LNCV6_132359_PI430048170 mRNA
TTGATGGTCTCCATTCAGGCAAGTGTGTTTCAGCAAATCTCTAGAAATTTACATTGATTA NM_153836 RefSeq chr2 - 101348353 101387503 CREG2 200407 cellular repressor of E1A-stimulated genes 2
GO:0005794|GO:0005783|GO:0010181|GO:0016491|GO:0005576|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93074_PI430048170 0.0698545170193325 1.08734835232537 0.633692057656994 0.506328582434556 0.590538308079441 A A A 0.396391149463617 0.474737054645646 0.497931651896279 A A A LNCV6_93074_PI430048170 mRNA
CTGCAGAGTGAAGAAAGCTGGTAATAGATGTCTGACAAACTAAAGAAAGACTTGTGTTAC NM_001286548 RefSeq chr12 - 75277220 75390922 CAPS2 84698 "calcyphosine 2, transcript variant 3" GO:0005509 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_128079_PI430048170 0.2753886555624071.73132009039068 0.2567616765013651.0778570961991
1.79891573400516 A A A 0.4797800053946710.3723180640322020.298861998778086A A A
LNCV6_128079_PI430048170 mRNA
ATGTATTTTTGTACCCTTCCTACAGATAGTCAAACCATAAACTTCATGGTCATGGGTAAA NM_001775RefSeq chr4
+ 15778307 15849083 CD38 952 CD38 molecule
GO:0050853|GO:0005886|GO:0030307|GO:0030890|GO:0005634|GO:0060292|GO:0007204|GO:0045779|GO:0045
907|GO:0032024|GO:0032526|GO:0032355|GO:0033194|GO:0070555|GO:0070062|GO:0001666|GO:0007565|GO:0
043066|GO:0016849|GO:0009986|GO:0050135|GO:0042493|GO:0097190|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140750_PI430048170 0.8485445685398580.9849339429834212.46236451982966
2.63993508388938 1.3433082278922 A A A 2.64338510179319 2.11301498951505
1.97309985923337 P A A LNCV6_140750_PI430048170 mRNA
TTCCATCCAGCTGCCCCTAATAATGATGTTTTGCAGTCCCATGGCACATAAGAAATTTAG NM_001123391 RefSeq
chr17 - 38057509 38068606 TBC1D3NA "TBC1 domain family, member 3" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_32949_PI430048170 0.00759168393841629 2.86314249993548 7.65856056795329
7.51466382683394 7.45580242304938 P P P 6.30606451555804 6.01966544635113
5.69353685855173 P P P LNCV6_32949_PI430048170 mRNA
GAGAAGCCTCCCTCATTCCTCCCAGGAATTAATAAATGTGAAGAGAGGCTCTGTTTAAAA NM_130786RefSeq chr19
- 58346805 58353499 A1BG 1 alpha-1-B glycoprotein
GO:0008150|GO:0003674|GO:0072562|GO:0005576|GO:0005615|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131639_PI430048170 0.0446446805061408 0.4158119741572255.11196525525107
5.04969741242357 5.28185209227979 P P P 5.79481071217203 6.59055182103013
6.70732344392004 P P P LNCV6_131639_PI430048170 mRNA
GGACTGTTTACCATTCTTCCACTGTGCTGTTATAAAGTTGTATTTGAAAGGTAATGTTGT NM_024945RefSeq chr9
+ 83980721 84004072 RMI1 80010 RecQ mediated genome instability 1
GO:0006260|GO:0005515|GO:0035264|GO:0005654|GO:0005634|GO:0042593|GO:0002023|GO:0009749 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137051_PI430048170 0.4300799185894860.4833366629464010.389913127132532
0.3858979622405710.278264949965263A A A 2.43171334259546 0.337023571907897
0.339164793964211A A A LNCV6_137051_PI430048170 mRNA
GATGTATGGGTACTCTGGCAGACTGCATGTTGTATAATTTGAAAAATACTAAAAGTGGAA NM_004522RefSeq
chr2_GL582966v2_alt + 3213 96131 KIF5C 3800 "kinesin family member 5C, transcript variant 1"
GO:0005515|GO:0008017|GO:0005871|GO:0006996|GO:0005874|GO:0003777|GO:0005524|GO:0030705|GO:0005
737|GO:0008104|GO:0007411|GO:0008152|GO:0008574|GO:0051028|GO:0016887|GO:0007018 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141948_PI430048170 0.9489140793295490.9815311041726950.27004963884683
0.2963700647772221.6187460942415 A A A 1.61460353222082 0.378819735213985
0.317317904736767A A A LNCV6_141948_PI430048170 mRNA
GAAAATACATCTATCCCTCATTTTGAGAGCCTCCAACTGATCCAAGTGTCATCCGGAGGA NM_001137669 RefSeq
chr1 + 182450120 182560598 RGSL1 353299 regulator of G-protein signaling like 1
GO:0038032|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119399_PI430048170 9.81994476415091e-05 1.19585206711065 0.865977259998718
0.9045606542447320.893846652303257A A A 0.65322193849434 0.622831825849201
0.614196585219057A A A LNCV6_119399_PI430048170 mRNA
CCCAGAATTTAGCAACCTATAGAGAAGGTTACAACGTATATGGAACCGAAAGTATTAAAA NM_001077243 RefSeq
chr11 + 105610072 105982092 GRIA4 2893 "glutamate receptor, ionotropic, AMPA 4, transcript variant
2"

GO:0030054|GO:0005886|GO:0005234|GO:0035249|GO:0007268|GO:0007215|GO:0031982|GO:0030425|GO:0030666|GO:0035235|GO:0034220|GO:0045211|GO:0004971|GO:0004970|GO:0032281|GO:0006810 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61083_PI430048170 0.267083567039515 1.40783134491492 0.273906324334444 1.23764784248419 1.02925733272875 A A A 0.558252447712219 0.351591450964323 0.304643448270571 A A A LNCV6_61083_PI430048170 mRNA GATTGGACCCCAGAACCAAACATGCTGGTACAGTCTAAAAATAAATGACTTGAACCCACT NM_001204424 RefSeq chr14 + 71932438 72566530 RGS6 9628 "regulator of G-protein signaling 6, transcript variant 10" GO:0005515|GO:0005794|GO:0005886|GO:0005834|GO:0019904|GO:0038032|GO:0035556|GO:0043547|GO:0005737|GO:0008277|GO:0007186|GO:0045666|GO:0004871|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70115_PI430048170 0.00436531493499619 0.518275912814419 4.49134849229447 4.87942608633168 4.80771134392615 P P P 5.73987154450352 5.4602100267457 5.82692235319763 P P P LNCV6_70115_PI430048170 mRNA CGCATGTCCAGAGAAGTATTAATGCCTTAATAGACTACTGAAGGTTAACTATTTACATCA NM_001048210 RefSeq chr1 - 108929507 108963499 CLCC1 23155 "chloride channel CLIC-like 1, transcript variant 1" GO:0005794|GO:0016020|GO:0005783|GO:0034707|GO:0005634|GO:0005254|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139955_PI430048170 0.0029761626919340 .47665586270583 4.36063899927019 3.99447473129579 4.1810069776576 P P P 5.24614690134436 5.1645649288792 5.349564733759 P P P LNCV6_139955_PI430048170 mRNA ACAGGCAAAATTATGGTTCCCACACCCCAACCCCAAATGAAACCTGGGATTTTGAATGTG NM_001017395 RefSeq chr3 - 129647791 129880559 TMCC1 23023 "transmembrane and coiled-coil domain family 1, transcript variant 1" GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137947_PI430048170 0.231223326801353 1.36507292729349 0.260675655966244 1.04562352933541 0.90765047132526 A A A 0.358409522236248 0.304666751017336 0.31842185896216 A A A LNCV6_137947_PI430048170 mRNA ATGGAAAAGGTTCATGACTCTAGCTCACAAATACTCCTTAAAAAACACAAGAGCAGCCAC NM_198137 RefSeq chr1 + 26190627 26202542 CATSPER4 378807 "cation channel, sperm associated 4" GO:0035036|GO:0086010|GO:0001669|GO:0005245|GO:0005886|GO:0036128|GO:0097228|GO:0007275|GO:0030317|GO:0007338|GO:0070509|GO:0070588|GO:0034765|GO:0005227|GO:0006814|GO:0048240|GO:0032504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100367_PI430048170 0.696189237460277 1.02894044595708 5.9044719750374 5.77309075333659 5.94394878499409 P P P 5.73464942765594 5.73718022417169 6.01352732105704 P P P LNCV6_100367_PI430048170 mRNA ACAGTATCTCCTTAAGGCATAATAGTGGATCCTTGAATGTTGAAGATGTCCTTACCAGCT NM_024766 RefSeq chr2 + 44361903 44772592 CAMKMT 79823 calmodulin-lysine N-methyltransferase GO:0018022|GO:0005794|GO:0005634|GO:0018025 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131124_PI430048170 0.941119490078697 0.9932261677614 8.65471627546198 8.35650655170186 8.33148130053343 P P P 8.47706251600526 8.61483607440879 8.28414987549006 P P P LNCV6_131124_PI430048170 mRNA GGGTCACAGAGGCCAAATGTGAGAGCATTGAATAAATATCTTAAGCTAAGCTGCAAAAAA NM_003890 RefSeq chr19 - 39863322 39934626 FCGBP 8857 Fc fragment of IgG binding protein GO:0005515|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135617_PI430048170 0.395673000724076 0.808585032982651 3.37252957891782 2.61250332701359 3.81118277099371 P A P 3.66486318536767 3.43699941400081 3.82971816918684 P P P LNCV6_135617_PI430048170 mRNA TGTGTTTAGTCCCAAAGATAGCAGTGATTTTGAATAAAGGAGTTTTGTGTTGCCTGGAAA NM_001278283 RefSeq chr2 + 210002564 210022260 RPE 6120 "ribulose-5-phosphate-3-epimerase, transcript variant 4"

GO:0004750|GO:0044262|GO:0005975|GO:0044281|GO:0006098|GO:0009052|GO:0042803|GO:0046872|GO:0005829|GO:0042802|GO:0019323|GO:0009405|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135946_PI430048170 0.1090195666589461.08473091160953 14.8946420567512 15.0524945358982 14.9791962204822 P P P 14.8989096307175 14.8231697549927 14.855558114037 P P P LNCV6_135946_PI430048170 mRNA
GGCTCTCACACCATGTTTTTGTACAGAACTGATGGTTGAATCTTTGTTCTCTTGAAATAA NM_006801RefSeq chr19 - 48382569 48391553 KDELR1 10945 KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1
GO:0005801|GO:0005793|GO:0030663|GO:0016020|GO:0033116|GO:0005789|GO:0016021|GO:0006621|GO:0016192|GO:0006886|GO:0005046 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135076_PI430048170 0.6634560330649831.30166411636648 2.0439068433345 0.38320273487055 1.90752094767238 A A A 1.73699322151171 0.395803521916883 1.26485976262264 A A A LNCV6_135076_PI430048170 mRNA
GCCCCCAATAGCCAAATAATAAAGCAGCATTGGATAATAATTTCTGAGTATAATCTCCAA NM_006664RefSeq chr9 - 34661882 34662692 CCL27 10850 chemokine (C-C motif) ligand 27
GO:0008009|GO:0006955|GO:0006935|GO:0060326|GO:0007267|GO:0005576|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64452_PI430048170 0.8322599334719430.870758954218091 1.59238519474803 0.363225101228137 2.32147626823554 A A A 1.86113959080843 0.476618271882711 2.49982110333563 A A P LNCV6_64452_PI430048170 mRNA
AAGGACCCCAAAGAATTATCAGCATTGGGGCCCAAACTTCCCCCCAGGCTGGGGGAAACT NM_001302493 RefSeq chr19 - 15851993 15864904 LOC102724279 NA uncharacterized LOC102724279 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137472_PI430048170 0.2542292472287750.9387006381160470.261447490554259 0.3594209016994750.275782843869481 A A A 0.4884680494811330.384089604730112 0.293210646793725 A A A LNCV6_137472_PI430048170 mRNA
TTCCTGACCATGCACGCCAGCATCTTCACGCTGACCGTCATGAGCAGCGAGCGCTACGCT NM_018949RefSeq chr17 + 82374276 82375586 UTS2R 2837 urotensin 2 receptor
GO:0005886|GO:0046005|GO:0004930|GO:0030307|GO:0042493|GO:0008015|GO:0048146|GO:0045776|GO:0010841|GO:0045777|GO:0003105|GO:0007204|GO:0045766|GO:0042312|GO:0007165|GO:0045907|GO:0007186|GO:0016020|GO:0035814|GO:0001604|GO:0035811|GO:0016021|GO:0055037|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127092_PI430048170 0.4053248621661070.5435455097048831.03849605857919 1.68292868389218 1.34262443233624 A A A 1.36813834179079 3.18916822710806 1.40590488796633 A P A LNCV6_127092_PI430048170 mRNA
CCAGTAAGCTTCCACCGTAGTTCCGTGAGCATCAATATATCTTTTCTTGGTCTTTTAATA NM_145020RefSeq chr18 - 50227193 50266495 CFAP53 220136 cilia and flagella associated protein 53
GO:0008150|GO:0005929|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61125_PI430048170 0.00491647969797642 1.96502002336717 10.3148566148416 10.5233177291944 10.5630281228109 P P P 9.5241090701907 9.49145202479736 9.4736666549625 P P P LNCV6_61125_PI430048170 mRNA
AATCCTCAAGCACAGCAAGGCTGCTCCTGTGGGTCATCTTTCTCTATCAAACTTTGATGT NM_194279RefSeq chr14 + 74493719 74495568 ISCA2 122961 "iron-sulfur cluster assembly 2, transcript variant 1"
GO:0005739|GO:0051536|GO:0016226|GO:0005198|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131383_PI430048170 0.2999684369770580.96514911168598 0.300991658274637 0.3896640894463610.314286539022703 A A A 0.45083680895111 0.349105912673008 0.357904476466763 A A A LNCV6_131383_PI430048170 mRNA
CAAAGAAAATGCAGAGTGCATGCATAGAGTATCCTCATTTCTATGGATTTGTTTTATGGA NM_001005747 RefSeq

chr2 - 151832770 151973971 CACNB4 785 "calcium channel, voltage-dependent, beta 4 subunit, transcript variant 1"
GO:0005515|GO:0050852|GO:0051899|GO:0005886|GO:0014051|GO:0007268|GO:0045202|GO:0048538|GO:0048536|GO:0019227|GO:0005829|GO:0048747|GO:0048541|GO:0050908|GO:0007528|GO:0007411|GO:0007628|GO:0006810|GO:0005245|GO:0019901|GO:0046058|GO:0006874|GO:0035249|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139667_PI430048170 0.000331511779681036 2.48184434331123 6.74425693560694 6.71658291881659 6.65583567528369 P P P 5.33197333253455 5.34083123608077 5.50442780836191 P P P LNCV6_139667_PI430048170 mRNA GGGAGGTGCTGCCCTTAACCATGACACCATTGTAAGAGCTGTCCACATTTGTATGTTGTG NM_004823 RefSeq chr19 + 38319843 38329009 KCNK6 9424 "potassium channel, two pore domain subfamily K, member 6"
GO:0005242|GO:0005886|GO:0008076|GO:0007268|GO:0034765|GO:0060075|GO:0006813|GO:0003085|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134121_PI430048170 0.569232597150002 0.80705755262404 2.74757462633118 0.337758030087647 1.07308167684176 A A A 2.73561272198174 1.835072080362 1.18011454169138 P A A LNCV6_134121_PI430048170 mRNA ACACATAAAGCACTTGGTAGGAATTGCCCGGATGTTTGAATAAATATTTATCCTCCCCCA NM_001080456 RefSeq chr19 - 56189688 56193052 ZSCAN5B NA zinc finger and SCAN domain containing 5B NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105570_PI430048170 0.00106304155040396 0.72940649417892 7.47693922531035 7.45168355144471 7.35974721804537 P P P 7.81854969118026 7.95470281296941 7.88012500086084 P P P LNCV6_105570_PI430048170 mRNA TCCTGGCGCTGCAGAAGCAATTCCACAGCGTGGAGGTGCACAAGTGGAGGCAGATCCTGC NM_020895 RefSeq chr19 + 35000341 35026469 GRAMD1A 57655 "GRAM domain containing 1A, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138130_PI430048170 0.444940425131562 0.77521516208265 0.33093724655473 0.31334355696003 0.295474738180376 A A A 1.23488130896706 0.304938938937117 0.286429811254192 A A A LNCV6_138130_PI430048170 mRNA TTCCAAATGTGTTTTAATGGCACCTGGGTGATTCTTCAGCTAAATTTAGTCATTTCTGTT NM_178424 RefSeq chr5 - 157625678 157652420 SOX30 11063 "SRY (sex determining region Y)-box 30, transcript variant 1"
GO:0043565|GO:0006355|GO:0006366|GO:0006357|GO:0000981|GO:0031960|GO:0005634|GO:0007283|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135095_PI430048170 0.116400551897212 0.717893203203122 8.62792493375408 8.09865851887157 7.96888476478119 P P P 8.76143593412076 8.85385247844743 8.58967398978559 P P P LNCV6_135095_PI430048170 mRNA CCTCCTGTCCTGTCCTTGCCCCTCAGGACTGCTGGAAAATAAATCCTTTAAAATAGTAAA NM_002990 RefSeq chr16 + 57358782 57366190 CCL22 6367 chemokine (C-C motif) ligand 22
GO:0008009|GO:0007165|GO:0006955|GO:0006954|GO:0006935|GO:0060326|GO:0007267|GO:0005576|GO:0009615|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140665_PI430048170 0.308249666800602 0.979622704482289 0.3458787828223 0.364858515101093 0.343629255438868 A A A 0.419729440517472 0.34438999874979 0.378459833271411 A A A LNCV6_140665_PI430048170 mRNA CTTTGAATCCTCTGCATCTAGCCATGTATTCTGCAAATATTAAGTGCTCAATGGTTTTTT NM_032975 RefSeq chr18 + 34493289 34891844 DTNA 1837 "dystrobrevin, alpha, transcript variant 2"
GO:0005515|GO:0030424|GO:0030054|GO:0006941|GO:0045202|GO:0007268|GO:0007274|GO:0030165|GO:0031234|GO:0042383|GO:0007165|GO:0043234|GO:0005737|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133139_PI430048170 0.00710613126311899 0.515246435137197 3.15162040390117 3.63309746860413 3.47582640885513 P P P 4.57450502671361 4.2583690444789

4.31871199164574 P P P LNCV6_133139_PI430048170 mRNA
GTCTATCCTTTGTGACAGGGCCTTTTAATGAGTGTTTTTTCTTTTTGTATATGTTACGTG NM_173569RefSeq chr7 +
139231484 139308236 UBN2 254048 ubinuclein 2 GO:0005654|GO:0005615 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_117480_PI430048170 0.1256277324269751.39358834610899 4.32092976525574
3.87485072585741 4.31478062000167 P P P 4.07816490096797 3.50246713694505
3.44960620640786 P P P LNCV6_117480_PI430048170 mRNA
TTCCGGAGGCCGTGAGACCTGCCGGGGCTGACAGTAAAGAAGCTAAGTGGAAGAGTGTTT NM_001171907
RefSeq chrX + 149540973 149548331 CXorf40A NA "chromosome X open reading frame 40A, transcript
variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143784_PI430048170 0.0922568464424688 1.09140333561502 13.2321481224908
13.3066035954038 13.3817244482516 P P P 13.1754082161513 13.1650725139738 13.205020184511
P P P LNCV6_143784_PI430048170 mRNA
AAGCTCTTCACAGTCATTGGATTAATTATGTTGAGTTCTTTTGGACCAAACCTTTTTGTC NM_007096RefSeq chr9 +
36190855 36212062 CLTA 1211 "clathrin, light chain A, transcript variant 2"
GO:0005515|GO:0030132|GO:0005886|GO:0032050|GO:0006886|GO:0005829|GO:0030118|GO:0043231|GO:0019
886|GO:0003674|GO:0007173|GO:0007411|GO:0071439|GO:0061024|GO:0042277|GO:0048011|GO:0006892|GO:0
042059|GO:0032588|GO:0006897|GO:0016020|GO:0005198|GO:0016023|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135895_PI430048170 0.000287128485706848 0.343028928068495 3.66672876009784
3.62202631453078 3.87972487794462 P P P 5.07459555917369 5.36296694960499
5.35668477813287 P P P LNCV6_135895_PI430048170 mRNA
CGTGTAGATATTATTGCAACTTATATTTTGCCTGAGCTTGATCAAAGGTCATTTGTGTAG NM_130837RefSeq chr3
+ 193593143 193697811 OPA1 4976 "optic atrophy 1 (autosomal dominant), transcript variant 8"
GO:0005515|GO:0005743|GO:0003924|GO:0005741|GO:0030425|GO:0005739|GO:0005758|GO:0005737|GO:0008
053|GO:0090201|GO:0030061|GO:0000287|GO:0000266|GO:0006915|GO:0001843|GO:0005525|GO:0016020|GO:0
008152|GO:0007007|GO:0019896|GO:0005654|GO:0007005|GO:0016021|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_103030_PI430048170 0.0292604254128442 0.6372514598919397.73262354260288
7.31559717368975 7.73072463138935 P P P 7.97159916273768 8.33720954892154
8.42060303430224 P P P LNCV6_103030_PI430048170 mRNA
AGAGACTTTTTTCTCACCATGAATGTCACCCCAGAGGTCAAGAGTCGTGGGATGAAGTTT NM_182679RefSeq chr1
- 156594307 156601487 GPATCH4 54865 "G patch domain containing 4, transcript variant 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59443_PI430048170 0.0385701472394460.6686042315524539.67515227382558 9.66237603921318
9.66190924050863 P P P 10.1969712666141 10.0607869752996 10.455804614455 P P P
LNCV6_59443_PI430048170 mRNA
AAGACACCTTCATCTAAATATATTCAAGACTGCATGTCATCAAGCACCTGAACAGGTTCA NM_020244RefSeq chr12
+ 101697638 101729068 CHPT1 56994 choline phosphotransferase 1
GO:0006629|GO:0006663|GO:0044281|GO:0001558|GO:0046872|GO:0019992|GO:0043231|GO:0000139|GO:0016
020|GO:0004142|GO:0016021|GO:0006644|GO:0006657|GO:0046474|GO:0006656 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_107026_PI430048170 0.8313557401743541.0091076991817 0.524365626935238
0.3937712929666260.519615203231762 A A A 0.3948466533472470.50468801317666
0.500087835712485 A A A LNCV6_107026_PI430048170 mRNA
AGCTCCTGGTATTATTGCCTGCACATTCTTGGTATCTTAGTATTATTGTTGTTGCCAGTG NM_138799RefSeq chr2 -
8856570 9003747 MBOAT2 129642 membrane bound O-acyltransferase domain containing 2
GO:0005789|GO:0044281|GO:0016021|GO:0006644|GO:0003841|GO:0036151|GO:0046474|GO:0036152 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_130441_PI430048170 0.1096392325514060.7740212079058327.15912154587851
7.03238722997652 7.34572103040856 P P P 7.38823159218294 7.41009188732896
7.82222388387924 P P P LNCV6_130441_PI430048170 mRNA
ATCCTGATTAGTCTAACAGTTGTGTTAGACTTTAGGGCCAGTATTGTCAGCATTTATTTA NM_003999RefSeq chr5
+ 38845998 38935641 OSMR 9180 "oncostatin M receptor, transcript variant 1"
GO:0008284|GO:0019838|GO:0002675|GO:0004924|GO:0005900|GO:0034097|GO:0038165 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133781_PI430048170 0.2006712693875130.6663860099738984.33337352000311
3.40381544702308 3.23340250525438 P P P 4.70808236914227 4.16622053818179
4.01396674264425 P P P LNCV6_133781_PI430048170 mRNA
CTCCCCCTTCAGGTATATGTTTTCTGAGTAAAGTTGAAAAGAATCTCAGACCAGAAAATA NM_000417RefSeq chr10
- 6010693 6062370 IL2RA 3559 "interleukin 2 receptor, alpha"
GO:0002437|GO:0050687|GO:0004911|GO:0005886|GO:0008283|GO:0006915|GO:0019976|GO:0006924|GO:0042
130|GO:0042104|GO:0006955|GO:0006954|GO:0050777|GO:0007219|GO:0050728|GO:0008144|GO:0046013|GO:0
038110|GO:0016021|GO:0045582|GO:0007166|GO:0009897 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_133249_PI430048170 0.7773041290727960.90471577794806 0.619967287166842
0.30160075663243 0.517674804626717A A A 0.313078640419079 0.273134542117973
1.13268080508895 A A A LNCV6_133249_PI430048170 mRNA
TCAATGAGATGGTGGCATTTTGAGAATGGTAAAGAAATACACAGGGAGGGGATGATGACT NM_057176RefSeq
chr1 + 54998943 55008792 BSND 7809 barttin CLCNK-type chloride channel accessory beta
subunit
GO:0043234|GO:0016323|GO:0005737|GO:0034220|GO:0005886|GO:0005887|GO:0055085|GO:0005254|GO:0017
081 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132605_PI430048170 0.7349817522451180.9664372573728812.8414842831411
12.8980357675429 12.6613041717983 P P P 12.6779340188858 12.8297452935341
13.0296879678646 P P P LNCV6_132605_PI430048170 mRNA
GAGGGGCATAGCCTTTCCCTAATTCTGCCTTAAATAAAACTGCATTGCTGATTCAAAAAA NM_000178RefSeq chr20
- 34928432 34955798 GSS2937 glutathione synthetase
GO:0006520|GO:0000287|GO:0006805|GO:0007568|GO:0044281|GO:0004363|GO:0005524|GO:0042803|GO:0005
829|GO:0007399|GO:0043295|GO:0006750|GO:0016594|GO:0031667|GO:0034612|GO:0043200|GO:0006979|GO:0
046686|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65568_PI430048170 0.130783237197327 1.25332302864697 6.97473378303734
6.68283095195754 6.83210682317891 P P P 6.25846823351694 6.75391261899667
6.47171921253327 P P P LNCV6_65568_PI430048170 mRNA
AATGGCGCTGTATCTCCAGCAGGCCAAGGAGCTGATCAATAAGGTCGGGGCCATGTCGAA NM_032546 RefSeq
chr2 + 27282428 27307439 TRIM54 57159 "tripartite motif containing 54, transcript variant 1"
GO:0008017|GO:0007165|GO:0030018|GO:0005875|GO:0005874|GO:0007026|GO:0008270|GO:0007275|GO:0004
871|GO:0007017|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83337_PI430048170 0.292132107594925 0.942400592393907 6.12456494559293
5.97662735717892 6.03558051093447 P P P 6.08495454515786 6.23883382155196
6.06736401253205 P P P LNCV6_83337_PI430048170 mRNA
TCTGAGATCTTCCCCAGCAAGCTTAGCCTACTTCCTGAGGTGGATGTGTGGGTGCAGGTG NM_001383 RefSeq
chr17 + 2030136 2043431 DPH1 NA diphthamide biosynthesis 1 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_102343_PI430048170 0.364095991125661 5.34512595162767 0.567593796262537
4.12956754330804 0.523675359975192 A P A 0.281568705844889 0.383126591993386
0.379847716821884A A A LNCV6_102343_PI430048170 mRNA
GCAATGACAGATGAACAGAAAACAGCATTAAAGTGGCAATTTCTCTTGGAAAGAAGCAAANM_001163560 RefSeq

chr16 - 1833982 1872178 MEIOB 254528 "meiosis specific with OB domains, transcript variant 1"
GO:0005694|GO:0008310|GO:0005634|GO:0009566|GO:0007129|GO:0005737|GO:0007144|GO:0003697|GO:0000
724|GO:0000712|GO:0003682|GO:0000738|GO:0007141|GO:0007140 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_131233_PI430048170 0.246215209268947 1.03208958296905 0.424374817030117
0.3534749685035540.386757062783117 A A A 0.3018609426565260.333627967483015
0.391838460127877 A A A LNCV6_131233_PI430048170 mRNA
TACACCATCAAGTACATCGGGGAACTCACAGACCTCCTTAACCGCGGCAGAGAGCCCAGANM_001105569 RefSeq
chr2 + 17816518 17817100 MSGN1 NA mesogenin 1 NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_131927_PI430048170 0.00123193279844473 2.0900848629645 9.63651517576989
9.51267462990559 9.3897542203137 P P P 8.61209326270178 8.44681429767217
8.28091441396464 P P P LNCV6_131927_PI430048170 mRNA
CTTAGCCCAAGGGAGAGGCAATAAAGAACACAAAGCTGTTCCCGTCTGCTGAGTAAAAAA NM_138493 RefSeq
chr6 - 37482920 37499924 CCDC167 154467 coiled-coil domain containing 167 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145593_PI430048170 0.346594612433238 1.13201348490797 8.54498780155579 8.5858207866721
8.31157652834225 P P P 8.52883851775203 8.32887751864273 8.0175679627324 P P P
LNCV6_145593_PI430048170 mRNA
CGTCCTGTCGGAGCCCTGTCTCCTCTCTCTGTAATAAACTCATTTCTAGCAGACAAAAAA NM_001144925 RefSeq
chr21 + 41420557 41459214 MX1 4599 "MX dynamin-like GTPase 1, transcript variant 1"
GO:0005515|GO:0048471|GO:0031965|GO:0019221|GO:0003924|GO:0006915|GO:0006952|GO:0005525|GO:0009
615|GO:0005829|GO:0007165|GO:0051607|GO:0005737|GO:0060337|GO:0045087|GO:0008152|GO:0005789|GO:0
034340|GO:0045071. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134100_PI430048170 0.388110150850207 0.619485927077455 0.409529971294127
0.2648745314731380.301661310935808 A A A 0.2729445867287660.474811021675667 1.797150183027
A A A LNCV6_134100_PI430048170 mRNA
CTGTCATCTCTCTTAGCATACTTATTTCCCTTATGTGATGCCTAATAATGAGGGAACATA NM_001083602 RefSeq
chr9 - 95442981 95516965 PTCH1 5727 "patched 1, transcript variant 1a"
GO:0005515|GO:0035137|GO:0001658|GO:0050680|GO:0032403|GO:0005113|GO:0007224|GO:0043231|GO:0061
005|GO:0071397|GO:0060644|GO:0016485|GO:0009887|GO:0051782|GO:0060603|GO:0032355|GO:0005794|GO:0
030332|GO:0014069|GO:0001843|GO:0030496|GO:0072372|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131326_PI430048170 0.258657714264086 1.01891692426301 0.304915543265866
0.2606262623133870.31798177899143 A A A 0.2744410264327150.258821039949695
0.269732115504297 A A A LNCV6_131326_PI430048170 mRNA
CCCATGTATACAGATTGTCATCTGTACAAGGAACTGTATGTATGAAAGCAAATGTACTTA NM_025185 RefSeq chr17
+ 63009536 63427706 TANC2 26115 "tetratricopeptide repeat, ankyrin repeat and coiled-coil containing
2" GO:0001701 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102426_PI430048170 0.0279917454202829 0.4081652962179243.11138910314287
2.76371608767548 2.72231595452291 P A A 3.59046028178689 4.29332241318969 4.4807270940067
P P P LNCV6_102426_PI430048170 mRNA
GGATTTTCCAGGCTGGTTTCACCAACAATCAAGCATCCATAAAATATTTTATAGAATGGA NM_005646 RefSeq chr1
- 234391312 234479103 TARBP1 6894 TAR (HIV-1) RNA binding protein 1
GO:0006396|GO:0001510|GO:0006357|GO:0003723|GO:0005634|GO:0008173 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137131_PI430048170 0.0244535695988325 0.6636773740273 12.3540152510522
12.0723399808623 12.3880952497802 P P P 12.7669226904465 12.6980044888725 13.109682677968
P P P LNCV6_137131_PI430048170 mRNA

GAGAGTGAGAATAATTGTGTACAAAGTAGAGAAGTATCCAATTATGTGACAACCTTTGTG NM_002156RefSeq chr2
- 197486583 197499916 HSPD1 3329 "heat shock 60kDa protein 1 (chaperonin), transcript variant 1"
GO:0006986|GO:0005515|GO:0032755|GO:0043032|GO:0048291|GO:0003688|GO:0005615|GO:0051604|GO:0042
026|GO:0006458|GO:0003697|GO:0005759|GO:0002755|GO:0002842|GO:0031625|GO:0070062|GO:0032729|GO:0
046696|GO:0002368|GO:0019907|GO:0009986|GO:0032727|GO:0042113|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139110_PI430048170 0.2938652741462370.8336301449168296.71289612723895
6.16282043104235 6.06367507178647 P P P 6.52685092042943 6.78142069888966
6.48871926061302 P P P LNCV6_139110_PI430048170 mRNA
GTACCTGTTAGTCCTTCCCCGACCCCGAAACAGATGACATTGTACAATAAAGGACTTTGA NM_003036RefSeq chr1
+ 2228694 2310213 SKI 6497 SKI proto-oncogene
GO:0005515|GO:0010467|GO:0006367|GO:0060041|GO:0046332|GO:0048593|GO:0070207|GO:0017053|GO:0007
179|GO:0031625|GO:0014902|GO:0005813|GO:0019901|GO:0003714|GO:0019904|GO:0001843|GO:0048741|GO:0
032926|GO:0000122|GO:0030509|GO:0043234|GO:0060349|GO:0043388|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140528_PI430048170 0.1145595366005060.6852118162378885.95976358765804
5.62310121194769 6.23741725408712 P P P 6.08458232130123 6.62725419460783
6.72996074223264 P P P LNCV6_140528_PI430048170 mRNA
CACCAAAGTACATTTGAAAGGAAGGTTTTCAATAGTGTAATACTGCAGCGATGTAGATAA NM_014633RefSeq chr11
+ 10750986 10779755 CTR9 9646 "CTR9, Paf1/RNA polymerase II complex component"
GO:0005515|GO:0033523|GO:0080182|GO:0000993|GO:0035327|GO:0000122|GO:0007259|GO:0001711|GO:0006
351|GO:0071222|GO:0051571|GO:0016607|GO:0045638|GO:0045944|GO:0019827|GO:0032968|GO:2001162|GO:0
016593|GO:0070102|GO:0016055|GO:0042169|GO:0010390 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_142350_PI430048170 0.0180036735925465 0.6401035005016254.62317760984641
4.39797347906893 4.57168580909191 P P P 5.04541967123451 5.04496627492132
5.41109931984383 P P P LNCV6_142350_PI430048170 mRNA
CCACCCAGTAACACATCATTTCAGTACCTGCTATTAATGGTCTTTTGATAAATAATCACT NM_178819RefSeq chr8
+ 41578187 41625001 AGPAT6 137964 1-acylglycerol-3-phosphate O-acyltransferase 6
GO:0006637|GO:0008610|GO:0005783|GO:0004366|GO:0044281|GO:0003841|GO:0007595|GO:0016020|GO:0040
014|GO:0019432|GO:0016024|GO:0005789|GO:0006631|GO:0002071|GO:0016021|GO:0006644|GO:0006654|GO:0
044255|GO:0046474|GO:0046339|GO:0006656 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141226_PI430048170 0.71232764989492 0.9254967311744572.62287718569151
1.15051700163145 1.46176488576293 A A A 2.43648386842261 1.90455320430922
1.52272377861521 A A A LNCV6_141226_PI430048170 mRNA
GAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCTGTCCAACCTGTGGCAAAAAA NM_153370RefSeq chr6
+ 36954432 36964837 PI16 221476 "peptidase inhibitor 16, transcript variant 1"
GO:0061052|GO:0010466|GO:0016021|GO:0030414|GO:0005615|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126677_PI430048170 0.9394599712607061.04009284471548 1.37171822398686
1.62551302257816 0.288077615388025A A A 0.479708534304277 0.948161618287839
1.72451254343875 A A A LNCV6_126677_PI430048170 mRNA
ATGCGGTAGGGCAGATAGGGAGTGCAAGATTAAATCAGACAAAAGTTTAAAATATTTTCT NM_148897RefSeq chr12
- 56923153 56934405 SDR9C7 121214 "short chain dehydrogenase/reductase family 9C, member 7"
GO:0005737|GO:0005730|GO:0004745|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138399_PI430048170 0.0802510783142137 0.8693377293318978.76380066941783
8.75005819976308 8.56132219006755 P P P 8.92933747109108 8.88634554170284
8.87367741650479 P P P LNCV6_138399_PI430048170 mRNA
CTGAGCTTGACTTTCAGTCAGGGCCACAGTGAGCATTAAATTATTATTCCATACAAAAAA NM_022064RefSeq chr3

+ 49689516 49721529 RNF123 63891 ring finger protein 123
GO:0005737|GO:0016567|GO:0016874|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129523_PI430048170 0.00111899659619495 0.4186366177967837.58552018490774
7.41092630618583 7.67064126153383 P P P 8.63945111506996 8.77576532305331
9.00825418082347 P P P LNCV6_129523_PI430048170 mRNA
TGTGGTTTACTGATTGGGTAATTTGATCATTAAAATTATGTGAAATCTGCCCGGGCACAC NM_002061RefSeq chr1
- 93885199 93909598 GCLM 2730 "glutamate-cysteine ligase, modifier subunit"
GO:2001237|GO:0006805|GO:0046982|GO:0006536|GO:0042493|GO:0006534|GO:0051409|GO:0044281|GO:0005
829|GO:0034641|GO:0043524|GO:0035226|GO:0051900|GO:0050880|GO:0000096|GO:0008637|GO:0035229|GO:0
004357|GO:0006750|GO:0017109|GO:0030234|GO:0006979 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_106011_PI430048170 0.2051796120393060.8280434300319677.43549733549981
6.93373823261766 6.99319844144016 P P P 7.3677158546548 7.38701666986332
7.47577449585878 P P P LNCV6_106011_PI430048170 mRNA
CCTTCCCTCCCACCTAAGATGTGTTTACCAAAATGTTGTTAACTTGTGTTAAAATGTTAA NM_001290341 RefSeq
chr15 - 100400394 100544326 CERS3 204219 "ceramide synthase 3, transcript variant 1"
GO:0006665|GO:0031965|GO:0030216|GO:0005783|GO:0030148|GO:0005789|GO:0050291|GO:0044281|GO:0016
021|GO:0046513|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107544_PI430048170 0.1195973090682831.94427038124237 2.11871387707207 3.3934568391961
2.80350927824147 A P A 1.88478128235625 2.22554548695154 1.51572195418277 A A A
LNCV6_107544_PI430048170 mRNA
AAACATTGCTTTGCTTTTCCTGAATTGTCCAGTGACCTATCCCAGGCCTTCCTTTCCAGT NM_178544RefSeq chr19
+ 39997035 40021041 ZNF546 339327 "zinc finger protein 546, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127588_PI430048170 0.0150706840851036 0.75034831572847 9.85090381279553
9.71960426785027 9.62355509438726 P P P 10.1945629433418 10.1116541515716
10.1387666522884 P P P LNCV6_127588_PI430048170 mRNA
GGCTTCAGTATCAGGGCTGAAACTGCTGGATGAATAAACTATTTATTAAAAACGGAAAAA NM_181336RefSeq chr6
- 33771212 33789129 LEMD2 221496 "LEM domain containing 2, transcript variant 1"
GO:0043409|GO:0031965|GO:0016020|GO:0035914|GO:0005639 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_91806_PI430048170 0.0330518158211543 0.8097387202382877.14537448459627 7.1342758818983
7.17817847665522 P P P 7.33364481433227 7.5210643511192 7.50936450018046 P P P
LNCV6_91806_PI430048170 mRNA
TGAAAAATGGCAAATCCAACTGACCAGAAGGAAGGAGGAAGCTTATTGGTGGCTGTTCCT NM_002089RefSeq chr4
- 74097036 74099280 CXCL2 2920 chemokine (C-X-C motif) ligand 2
GO:0005515|GO:0008009|GO:0070098|GO:0002237|GO:0005576|GO:0045236|GO:0005615|GO:0002690|GO:0006
955|GO:0006954|GO:0006935|GO:0007186|GO:0060326|GO:0042127|GO:0032496 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139978_PI430048170 0.3101961726147730.7546548529570473.61249292760444 2.7795880808824
2.33751772093221 P A A 3.54590465278461 3.33532944160253 3.3549213457129 P P P
LNCV6_139978_PI430048170 mRNA
TGAATAAGCTAAAACACCTGCTTTTAACAATGGTACCATACAACCACTACTCCATTAACT NM_006516RefSeq chr1
- 42925374 42959176 SLC2A1 6513 "solute carrier family 2 (facilitated glucose transporter), member 1"
GO:0005515|GO:0005886|GO:0006767|GO:0072562|GO:0044281|GO:0043621|GO:0070837|GO:0055056|GO:0042
802|GO:0005829|GO:0008645|GO:0016323|GO:0042910|GO:0015758|GO:0005911|GO:0042149|GO:0019900|GO:0
005355|GO:0070062|GO:0042470|GO:0005975|GO:0030496|GO:0042908|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_142133_PI430048170 0.0334671413272096 0.7513224741721687.28312030963887
7.2718330698511 7.19280223015607 P P P 7.77171504491059 7.71511350701878
7.48430599535568 P P P LNCV6_142133_PI430048170 mRNA
CAGCCCTGCTACTGCCCAGCCTGCTGTGTGTCCAGCTGCTGCCAGCATTCTTGTTGCTGA NM_001277331 RefSeq
chr17_JH159148v1_alt - 41249 41732 KRTAP9-6 NA keratin associated protein 9-6 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139604_PI430048170 0.00498645820674006 0.2715439865720874.13138918756679
4.38333530699131 4.60925715753878 P P P 5.79347828654789 6.30839163976272
6.59340723357456 P P P LNCV6_139604_PI430048170 mRNA
CTTGTTGACTGTACTATTCAGATGGCTTTATGCTTTTGTGTATTTTATGTCACCTAGATC NM_001012968 RefSeq chrX
- 63347227 63351339 SPIN4 139886 "spindlin family, member 4" GO:0007276 . NA - . NA
NA NA NA NA NA NA NA NA NA
LNCV6_145178_PI430048170 0.0231098692246737 2.4666348180795 1.676472934033
1.95251709135203 2.06972490545084 A A A 0.2651824815929580.312603511160336
1.08625488480074 A A A LNCV6_145178_PI430048170 mRNA
GATGCGGAAGACTGGAAACTATTGTGTTCATGGGTAAATAAACTACAAAATATTTATGGC NM_001003937 RefSeq
chr2 - 54253177 54256272 TSPYL6 388951 TSPY-like 6 GO:0006334|GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130943_PI430048170 0.00240241542587474 2.323699853636 10.2543379691163
10.1905273309607 10.3475613934294 P P P 8.83756439012162 9.12710122394103 9.1614144723348
P P P LNCV6_130943_PI430048170 mRNA
CTGCCCTGTTTGAACTTCCTGTTTGACAATGTTTGCTGTTGATTTTTTGTTCAATAAAGA NM_144569RefSeq chr1 -
31790421 31816051 SPOCD1 90853 "SPOC domain containing 1, transcript variant 1"
GO:0010923|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143791_PI430048170 0.3454091128324780.9689368024685090.252049993498379
0.2663433166725560.367414122183599A A A 0.3820684723052060.316630614920423
0.325570894353151A A A LNCV6_143791_PI430048170 mRNA
GAAGTGGGCTGGAAAGGTTTGGCTTTTCAGTAACCATTAGCTAATAAAGTCTGCTTTTTT NM_001145030 RefSeq
chr3 + 44241885 44332098 TOPAZ1 NA testis and ovary specific PAZ domain containing 1 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61391_PI430048170 0.0422809630002947 0.6801156737536077.16850063906099
7.16006687764414 7.51934899558853 P P P 7.72080446592162 7.66556663518405
8.11671078371632 P P P LNCV6_61391_PI430048170 mRNA
TGAGGTTGATCAAAACAAGGAAAGCAAAAAGGAGGTTCCCCCTACTGAGACAGTTCCTCA NM_015156RefSeq chr14
+ 102592658 102730576 RCOR1 23186 REST corepressor 1
GO:0005515|GO:0070933|GO:0044212|GO:0006325|GO:0005634|GO:0000122|GO:0006351|GO:0001078|GO:0045
654|GO:0007596|GO:0003682|GO:0017053|GO:0030218|GO:0016032|GO:0005654|GO:0045892 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131297_PI430048170 0.0167798873860728 0.7717363465761299.61701242268398
9.65484731597045 9.77746831962345 P P P 10.027932643804 9.94645400321192
10.1905273309607 P P P LNCV6_131297_PI430048170 mRNA
CAGCAATCCATGAGGTGTGTCAAAGAGTGTACATATGTATGTGTGTATATTGAATGCTAA NM_001127361 RefSeq
chr1 - 32936445 32964813 RNF19B 127544 "ring finger protein 19B, transcript variant 2"
GO:0005515|GO:0072643|GO:0005737|GO:0016567|GO:0042267|GO:0016874|GO:0044194|GO:0008270|GO:0016
021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101232_PI430048170 0.1381812234384390.8875999486430966.53854175898194
6.51307076693372 6.71867522637284 P P P 6.73266066783841 6.66387663603926
6.88929710905757 P P P LNCV6_101232_PI430048170 mRNA
TATTACTACTCCATTCGAGGGGTCCTCAAAGATGGCTTCACCTATGTCCTCTACATCAAC NM_001083601 RefSeq

chr16 + 3443667 3486963 NAA60 79903 "N(alpha)-acetyltransferase 60, NatF catalytic subunit, transcript variant 1"
GO:0017196|GO:0007059|GO:0000139|GO:0043967|GO:0008283|GO:0004596|GO:0006334|GO:0010485 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135443_PI430048170 0.11664386612371 1.74451577805463 5.20636555556276
5.27424687386775 5.28655418855577 P P P 5.03566158938354 3.99335946425055
4.08693729337374 P P P LNCV6_135443_PI430048170 mRNA
CGAACCCCAGCTCAATGAGTAACTGATGTGAACTGCTGGGAATAAAGGACTTCAAAGATG NM_001001669 RefSeq
chr5 + 149581571 149634964 ARHGEF37 389337 Rho guanine nucleotide exchange factor (GEF) 37
GO:0005737|GO:0032321|GO:0005089 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57649_PI430048170 0.00015078967849289 1.22194122617012 15.6495428146863
15.6870543530976 15.6382727549472 P P P 15.3525642551554 15.3639433137383
15.3910200532982 P P P LNCV6_57649_PI430048170 mRNA
CTGGGCCTGGCCACCCCTTCTTTCCCTCCGCGCCCCGCCCCCGAGGAGCCTAATAAAGAT NM_014067 RefSeq chr11
- 63998557 64166113 MACROD1 28992 MACRO domain containing 1
GO:0042278|GO:0005739|GO:0005515|GO:0016798|GO:0019213|GO:0051725|GO:0005634|GO:0006974 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128933_PI430048170 0.000122301624282492 0.26796807403447 4.04347764410926
3.89875720113805 4.19884260570036 P P P 5.83894063500282 5.86687431651422
6.13199074872604 P P P LNCV6_128933_PI430048170 mRNA
AAAGTGTTGTCTTATTCCTAATTCCTGTATGTTATCCACTACAGGTTTTATGAGACTTCC NM_001256760 RefSeq chrX
+ 114584077 114910061 HTR2C 3358 "5-hydroxytryptamine (serotonin) receptor 2C, G protein-coupled, transcript variant 1"
GO:0007631|GO:0005886|GO:0007268|GO:0007200|GO:0032098|GO:0051378|GO:0004993|GO:0008144|GO:0051482|GO:0071886|GO:0043397|GO:0007626|GO:0001662|GO:0070374|GO:0031644|GO:0001587|GO:0051209|GO:0010513|GO:0042493|GO:0006874|GO:0007210|GO:0005887|GO:0007208|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137300_PI430048170 0.553571969010661 0.830379286085238 0.44691116181985
0.477746827357915 0.498863563618952 A A A 0.329785065052518 1.26058144328525
0.451636130383689 A A A LNCV6_137300_PI430048170 mRNA
CCTGACCACATTATTATGAAACATTATGGCTGTTTATGTAATTTAGGGAGGACTGGTCTG NM_007023 RefSeq chr2
+ 172735796 173052892 RAPGEF4 11069 "Rap guanine nucleotide exchange factor (GEF) 4, transcript variant 1"
GO:0045859|GO:0005515|GO:0005952|GO:0005886|GO:0008603|GO:0007264|GO:0030168|GO:0044281|GO:0005829|GO:0005085|GO:0030552|GO:0006112|GO:0050796|GO:0032320|GO:0007186|GO:0016020|GO:0007596|GO:0017156|GO:0019933|GO:0017157|GO:0030073|GO:0017016|GO:0005088 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_119870_PI430048170 0.886879461283193 1.00146448899243 0.37732035326667
0.375088192456477 0.382845953277607 A A A 0.390604408073709 0.348582888474367
0.389349565180056 A A A LNCV6_119870_PI430048170 mRNA
GGCTAATAGCACTTTTCTTGTTCCATTCAAACATCTGAAAATGAAATTACAACACTGCCA NM_152704 RefSeq chr13
- 25161678 25172283 AMER2 219287 "APC membrane recruitment protein 2, transcript variant 1"
GO:0005515|GO:0005886|GO:0005546|GO:0016055|GO:0007398|GO:0090090 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137416_PI430048170 0.189996578458631 0.859871995222042 8.01708621644501
8.01302605405603 8.23302330347046 P P P 8.09992731459599 8.32731281118194 8.4758764776243
P P P LNCV6_137416_PI430048170 mRNA
CCAGAAACTTTAAGAACAAACTCTGAAAGACCTATGAGCAAATGGTGCTGAATACTTTTT NM_002402 RefSeq chr7
+ 130492057 130506297 MEST 4232 "mesoderm specific transcript, transcript variant 1"

GO:0016787|GO:0005783|GO:0008152|GO:0005789|GO:0007498|GO:0032526|GO:0016021|GO:0010883|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127425_PI430048170 0.341952552797096 1.24463654870268 3.41530462109366 3.2096342240596 2.65470082782663 P P A 2.89433820775629 2.97326193144193 2.53002615686427 P P P
LNCV6_127425_PI430048170 mRNA
CCACCGTTGTGCATATTGTTGCTTCTGAACCACAAACTGTATAAATGGATGGTTTTTTGC NM_181711 RefSeq chr12 + 52006944 52015889 GRASP 160622 "GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein, transcript variant 1"
GO:0007165|GO:0048471|GO:0030054|GO:0008104|GO:0030306|GO:0045211|GO:0030165|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136469_PI430048170 0.830518813546305 1.01550052397497 4.81735481622725 4.70771490696723 4.80209324177852 P P P 5.03785462288516 4.84206055996202 4.28071176223281 P P P LNCV6_136469_PI430048170 mRNA
TTTGACCTATAGTAATAAAACAATGGTCATTTTACCCCTCTGCTTCTCAACCCCACAGCT NM_001131028 RefSeq chr5 + 81972024 82255396 ATG10 83734 "autophagy related 10, transcript variant 3"
GO:0005622|GO:0005737|GO:0016874|GO:0019777|GO:0006914|GO:0006497|GO:0032446|GO:0034263|GO:0015031|GO:0031401 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130070_PI430048170 0.101586095887915 1.19515754623566 7.21333950438072 7.26612156111326 7.27477042909094 P P P 7.16233123619364 6.96202854706636 6.84059287337132 P P P LNCV6_130070_PI430048170 mRNA
AGTTAACTGCGGAGCCAAGAGTTGGACTATAATTAAATTACCTTCCTTGTACTTTCTTTT NM_024649 RefSeq chr11 + 66510647 66533613 BBS1 582 Bardet-Biedl syndrome 1
GO:0001103|GO:0005515|GO:0060170|GO:0005813|GO:0034464|GO:0006996|GO:0043001|GO:0005930|GO:0045494|GO:0035058|GO:0005113|GO:0036064|GO:0005829|GO:0042384|GO:0005119|GO:0001895|GO:0007601|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134009_PI430048170 0.00741301751458871 0.515246933375587 7.24066287491782 7.35445700928495 7.6199856511709 P P P 8.31827171874498 8.12968356683344 8.62080747724316 P P P LNCV6_134009_PI430048170 mRNA
GTGCAACCTTTTATGTGTTGATGACTCACTCATAAAGGTTTTTGTCTACTGTCATTTGTT NM_002583 RefSeq chr12 - 79591964 79691010 PAWR 5074 "PRKC, apoptosis, WT1, regulator"
GO:0005515|GO:0043065|GO:0008285|GO:0005886|GO:0003714|GO:0005884|GO:0030889|GO:0006915|GO:0003779|GO:0005634|GO:0000122|GO:0015629|GO:0097190|GO:0050860|GO:0006351|GO:0042986|GO:0042130|GO:0043522|GO:0042094|GO:0005737|GO:0019899|GO:0051017 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136101_PI430048170 0.238561888103809 1.0201016567933 0.306761797470574 0.254046771251821 0.305893584922426 A A A 0.266200810032269 0.249488292607967 0.265441697022943 A A A LNCV6_136101_PI430048170 mRNA
AATGAGTCACTACCTGTCTTGTGACTGTACTGCACTTCATGTTCTTACCTTCGGCTTCTC NM_003268 RefSeq chr1 - 223109405 223143282 TLR5 7100 toll-like receptor 5
GO:0005149|GO:0005886|GO:0034123|GO:0002224|GO:0032757|GO:0045429|GO:0071222|GO:0006954|GO:0045087|GO:0002755|GO:0050707|GO:0034166|GO:0016021|GO:0071260|GO:0034146|GO:0008584|GO:0042742|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144727_PI430048170 0.116094182131642 0.71458869847485 3.45890913727982 3.78970386750869 4.14360974142055 P P P 4.30912754858428 4.22594750111129 4.3881421125425 P P P LNCV6_144727_PI430048170 mRNA
AGCCACCTAGCACTAAAGCATAGAACTTAAACACGAATCCCTAAATGAACAGATTATGTT NM_002245 RefSeq chr1 + 233614003 233672512 KCNK1 3775 "potassium channel, two pore domain subfamily K, member 1"
GO:0005242|GO:0016324|GO:0005886|GO:0008076|GO:0007268|GO:0034765|GO:0031526|GO:0006813|GO:0071805|GO:0035094|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_131277_PI430048170 0.2561532508794480.8980816351266174.22789635329592
4.44387304367979 4.36131639388081 P P P 4.4258959815627 4.38251958680312
4.67987921338043 P P P LNCV6_131277_PI430048170 mRNA
CAGACTCAACAGCCTACAGCAGATATTATTAAGCATTTGGTCAGAGGTTTTAGCAGGGAG NM_015421RefSeq chr16
- 8795179 8797648 TMEM186 25880 transmembrane protein 186 GO:0005739|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144680_PI430048170 0.00936435644515474 0.5445481776882938.76818460052137
8.70702407499786 8.494108148861 P P P 9.25503160002608 9.63431282605358
9.68737644167602 P P P LNCV6_144680_PI430048170 mRNA
CCCTGAACTTTTTTCCTTGTCCCATCCTGGGGTCAATAAAACTGAATGTTGCATATTCTA NM_080603RefSeq chr20
+ 45881208 45885266 ZSWIM1 90204 "zinc finger, SWIM-type containing 1"
GO:0008270|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59297_PI430048170 0.0246736128636237 0.7705378706288345.03168815514077
4.91257705773266 4.7771785886291 P P P 5.3182961709948 5.13429645470862
5.39588916397963 P P P LNCV6_59297_PI430048170 mRNA
CTCATTCCTGGAAATTGCACTGGAACTGTCTGATTAAGAAAAACAGAATAATTCTGAAAG NM_001135805 RefSeq
chr12 + 78863992 79452008 SYT1 6857 "synaptotagmin I, transcript variant 2"
GO:0060201|GO:0005515|GO:0070083|GO:0043005|GO:0005516|GO:0005215|GO:0005513|GO:0030054|GO:0005
886|GO:0031340|GO:0031201|GO:0007268|GO:0031045|GO:0060203|GO:0007269|GO:0042802|GO:0005544|GO:0
005545|GO:0030276|GO:0000149|GO:0017157|GO:0051260|GO:0030672|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_62852_PI430048170 0.24822474478483 0.8903506159706178.84913076732175 8.78862204106865
8.52664796762318 P P P 8.87170901573717 9.03162861248439 8.7716794503542 P P P
LNCV6_62852_PI430048170 mRNA
AACACCAGGGCCTGGCCCAGTGGATTTCATGGTGATCATTAAAAAAGAAAAATCGCAACC NM_024308RefSeq
chr17_KI270857v1_alt + 827290 836298 DHRS1179154 dehydrogenase/reductase (SDR family) member 11
GO:0016491|GO:0005576|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65870_PI430048170 0.00558507302760967 1.49319634550597 5.79318727629283 5.5522906301837
5.73498390940413 P P P 5.15152852652678 5.16164775056981 5.03973390921712 P P P
LNCV6_65870_PI430048170 mRNA
GAGGAGCTGATGCAAAACAGTCGGTGTGTGCTGAGCAAATGGAAGAACAAATATGTCTGT NM_015910RefSeq
chr2 - 63121399 63588733 WDPCP 51057 "WD repeat containing planar cell polarity effector,
transcript variant 2"
GO:0055123|GO:0005886|GO:0032185|GO:0001822|GO:0005930|GO:2000114|GO:0051893|GO:0045184|GO:0007
224|GO:0032880|GO:0042384|GO:0010762|GO:0016324|GO:0060541|GO:1900027|GO:0016476|GO:0060271|GO:0
060021|GO:0043010|GO:0072358|GO:0005856|GO:0002093|GO:0005938|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140997_PI430048170 0.0680439096523426 0.4348199020736882.41090317396166
2.50553135414359 3.61727310927355 A A P 3.4863815238098 4.31204262050117
4.48812816898221 P P P LNCV6_140997_PI430048170 mRNA
GCTAAACGTTGTTGAACATTGATTGTTTGGTACCGAAAACAGCAGTGGACGATGTTGTGC NM_000052RefSeq chrX
+ 77910655 78050395 ATP7A 538 "ATPase, Cu++ transporting, alpha polypeptide, transcript variant 1"
GO:0005802|GO:0005515|GO:0010468|GO:0051353|GO:0051216|GO:0018205|GO:0031526|GO:0051542|GO:0010
043|GO:0021860|GO:0010041|GO:0031069|GO:0043524|GO:0006878|GO:0034220|GO:0030198|GO:0019430|GO:0
030199|GO:0043025|GO:0060003|GO:0048251|GO:0046034|GO:0005794|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130091_PI430048170 0.0492297583874333 1.37969517248286 10.0297999943617
10.3283826566221 9.97509605204825 P P P 9.62844572241071 9.69440304510419
9.64214034643247 P P P LNCV6_130091_PI430048170 mRNA

CCTTTGCCCTGGGACATCTGTATCTCTTGGCTTTGTAATAAATGCTGCATACTTTCTAAA NM_007144 RefSeq
chr17_KI270857v1_alt - 2769215 2783624 PCGF2 7703 polycomb group ring finger 2
GO:0035102|GO:0031519|GO:0005515|GO:0000790|GO:0004842|GO:0070301|GO:0016567|GO:0003700|GO:0016
573|GO:2001234|GO:0048704|GO:0005634|GO:0000122|GO:0009952|GO:0001701|GO:0001739|GO:0003677|GO:0
006351|GO:0016604|GO:0003682|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_128365_PI430048170 0.0317504419726367 0.411813941488561 0.68902983232351
0.5121469734097840.541489067969031 A A A 1.33309527329976 2.07749385335683
2.06079315993316 A A A LNCV6_128365_PI430048170 mRNA
CTAGAAGAAAAGCCCTGTTGGAGTTTTGATGTAGAGTGCAATAATACATCAATAAAGGTA NM_001105539 RefSeq
chr8 + 80486212 80526265 ZBTB10 65986 "zinc finger and BTB domain containing 10, transcript
variant 1" GO:0006355|GO:0005654|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127447_PI430048170 0.3075827336424 1.2283325513292 0.62712881757823
0.5129042841470641.15842482291695 A A A 0.427901296189141 0.525085974925158
0.538013466898084 A A A LNCV6_127447_PI430048170 mRNA
TTTGCTCTGCAGCTTTGGGTCTGAATGCTTCCAGTTTCACAGGATCAGATGGGTATTCAA NM_001101389 RefSeq
chr11 + 113779795 113780485 CLDN25 NA claudin 25 NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_104961_PI430048170 0.0238494322791655 0.816223423957331 7.25324113421285
7.32994549493895 7.46644277477313 P P P 7.6046303190087 7.6167998692542 7.712774249272
P P P LNCV6_104961_PI430048170 mRNA
ATGGACGTATCTAGTGGTTCTTCTTATCTCCATCCCCATCGGCTTCCTCTTTAAGAAAGC NM_024298 RefSeq
chr19_KI270938v1_alt - 148219 164847 MBOAT7 79143 "membrane bound O-acyltransferase domain
containing 7, transcript variant 1"
GO:0005515|GO:0016020|GO:0036149|GO:0071617|GO:0021591|GO:0005789|GO:0044281|GO:0016021|GO:0021
819|GO:0006644|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137566_PI430048170 0.120260382812326 1.20799312980412 5.87192728593573
5.87282588727227 5.54308679375346 P P P 5.57486202337475 5.51902717857086
5.39464475280878 P P P LNCV6_137566_PI430048170 mRNA
GTAGCCCTTCTTTTTGTTTTTGTTGGCATTCTAAGTTAATAAACACGCTTATGAACACACNM_001145783 RefSeq chr19
- 19181875 19192591 MEF2BNB 729991 "MEF2B neighbor, transcript variant 2"
GO:0007507|GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130751_PI430048170 0.342322384292395 0.804562049061939 0.35569661817227
0.310054442589593 0.675297762350917 A A A 1.03525544763171 0.287059877171962
0.88483402047919 A A A LNCV6_130751_PI430048170 mRNA
GTTCCAAACCTAGCAGAATAAAAATCATAGATAGCCCCAAATTAATGAGTTTGGTAACTG NM_001271999 RefSeq
chr1 - 62454725 62688368 DOCK7 85440 "dedicator of cytokinesis 7, transcript variant 1"
GO:0043005|GO:0030424|GO:0007264|GO:0045178|GO:0000226|GO:0045200|GO:0007409|GO:0032863|GO:0031
175|GO:0030426|GO:0005085|GO:0048365|GO:0033138|GO:0050767|GO:0008180|GO:0002244|GO:0022027|GO:0
043473|GO:0005925. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145032_PI430048170 0.228074065164258 1.32818819404095 1.4179199178235
0.809694175097712 1.07296864343407 A A A 0.466048969183844 1.14804826400782
0.398302024292383 A A A LNCV6_145032_PI430048170 mRNA
TCTATACTATCCAGACGTATGTCTTCCCTGTCACTACTTGCTTGGCACACAGCAATAGCT NM_181885 RefSeq chr1
+ 155941688 155942834 RXFP4 339403 relaxin/insulin-like family peptide receptor 4
GO:0005515|GO:0004945|GO:0005886|GO:0016021|GO:0038166 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_53552_PI430048170 0.00037917524523319 0.306094299534412 7.16904843154336

7.25884269075362 7.25461089125672 P P P 9.05656560113624 8.92492045431931
8.81660866575593 P P P LNCV6_53552_PI430048170 mRNA
GTTTTGAGGTGTTGGCATTCTTCGCTGATTTGGCTGTTCCCAATGTTTACATTATTTAAT NM_018584RefSeq chr1 -
20482390 20486235 CAMK2N1 55450 calcium/calmodulin-dependent protein kinase II inhibitor 1
GO:0030054|GO:0019901|GO:0045211|GO:0043025|GO:0008427|GO:0014069|GO:0006469|GO:0030425 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144903_PI430048170 0.26623557537182 0.94551960590108813.1268959806946
13.1502982905019 13.0458965994459 P P P 13.0975321209372 13.2733905369927
13.1913402339861 P P P LNCV6_144903_PI430048170 mRNA
GGTCTGTCCTTGTCCCTTTGTCTGTCTGTGAATAAATGTGAGTTCGTGAAATCCAAAAAA NM_152600RefSeq chr19
- 55577524 55580845 ZNF579 163033 zinc finger protein 579
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142532_PI430048170 0.0192867671683563 1.23137235021056 7.53027275887951
7.4310990408322 7.32124806460462 P P P 7.04737733873707 7.16911810225375
7.16948644900876 P P P LNCV6_142532_PI430048170 mRNA
TCTCTCCCAAGGCCTGACAATGGTACCTATTAGGGATGAGATACAGACAAGGATAGCTAT NM_003883RefSeq chr5
- 141620875 141636856 HDAC3 8841 histone deacetylase 3
GO:0005515|GO:0032008|GO:0042826|GO:0005886|GO:0006325|GO:0046970|GO:0005634|GO:0044281|GO:0010
832|GO:0042993|GO:0005737|GO:0046329|GO:0031647|GO:0007219|GO:0045944|GO:0017053|GO:0040014|GO:0
005876|GO:0004407|GO:0046969|GO:0006476|GO:0044255|GO:0032041|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_70303_PI430048170 0.4740446693240350.7374016968002161.35593734729506 0.464801204877983
0.386551624249744A A A 1.1724125198746 1.81381429374215 0.42864759425328 A A A
LNCV6_70303_PI430048170 mRNA
AGCTCCCCAACATATATATCTTGCAGTTTATATGCCTTTTCATTTAACCGAAACCTCTTT NM_005019RefSeq chr2 -
182140034 182522609 PDE1A 5136 "phosphodiesterase 1A, calmodulin-dependent, transcript variant 1"
GO:0005516|GO:0048011|GO:0048101|GO:0004115|GO:0004117|GO:0046069|GO:0005634|GO:0007202|GO:0048
660|GO:0046872|GO:0005829|GO:0007165|GO:0007173|GO:0030553|GO:0007596|GO:0008543|GO:0034391|GO:0
045087|GO:0043025|GO:0006198 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141483_PI430048170 0.000193472080844933 2.4502342558325 5.58129630639923
5.33355462707677 5.4796763754693 P P P 4.23132551827669 4.04440825478607
4.24228009272495 P P P LNCV6_141483_PI430048170 mRNA
GGAAAAATAAAAGTTGACTGTACTAAAAATGTATACTTGTTGCCAGGAAGGTGACCTCAA NM_000676RefSeq chr17
+ 15944916 15975896 ADORA2B 136 adenosine A2b receptor
GO:0032755|GO:0007588|GO:0005886|GO:0007254|GO:0032722|GO:0010575|GO:0060087|GO:0043306|GO:0000
187|GO:0001609|GO:0007190|GO:0006968|GO:0001973|GO:0007186|GO:0005887|GO:0031668|GO:0031284|GO:0
007189|GO:0002882. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136869_PI430048170 0.5543392563773880.9200207406950754.56006681876219
5.28777405632944 4.75963869355308 P P P 5.02226674685128 4.97178279541011
5.07322969835419 P P P LNCV6_136869_PI430048170 mRNA
GAAAGACTTTTCCAACCCTCATCACCAACGTCTGTGCCATTTTGTATTTTACTAATAAAA NM_002996RefSeq chr16
+ 57372460 57385048 CX3CL1 6376 "chemokine (C-X3-C motif) ligand 1, transcript variant 1"
GO:0005515|GO:0008009|GO:0005886|GO:0009986|GO:0030595|GO:0060055|GO:0030593|GO:0019221|GO:0005
102|GO:0005576|GO:0006952|GO:0005615|GO:0050902|GO:0045766|GO:0051041|GO:0032914|GO:0006955|GO:0
006935|GO:0050729|GO:2001240|GO:0048247|GO:0048246|GO:0016021|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129828_PI430048170 0.5539677500855421.35395637053836 2.05753206590836
0.4209614692446541.0746083029267 A A A 0.32922440437522 1.61418260468364

0.379789322098719 A A A LNCV6_129828_PI430048170 mRNA
GGAGGGTCCTAAGAGCTGATTATTTAATTTCTATCCAGAAATCTTTCTTCTTCTTGCTCT NM_152310 RefSeq chr10 + 102226277 102229587 ELOVL3 83401 ELOVL fatty acid elongase 3
GO:0005515|GO:0005783|GO:0019367|GO:0044281|GO:0035338|GO:0005789|GO:0019432|GO:0007623|GO:0034625|GO:0016021|GO:0034626|GO:0042761|GO:0016740|GO:0044255 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128059_PI430048170 0.1480823582772810.7399207363834193.38319515302692 3.59103736494393 4.03183347301013 P P P 4.00938629100575 3.91315526247376 4.41442760630635 P P P LNCV6_128059_PI430048170 mRNA
CATCTACACAAGAAGCAAAAGCAAGGAATAGTTGTTGGGTTTTTGTTTTTTGGTTGTTGT NM_152793 RefSeq chr7 + 30134935 30162765 MTURN 222166 "maturin, neural progenitor differentiation regulator homolog (Xenopus)" GO:0007275 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141362_PI430048170 0.6200893756688690.7014204453876080.7987614191830532.0183550670677 1.59706255495092 A A A 2.80561064587463 0.7847000979527661.94659381943359 A A A LNCV6_141362_PI430048170 mRNA
GCAGAGGCCAGGGTTTTAGTTAAAAGTTTAATGTAGTTCCCAAATACATTTCATATGACA NM_004058 RefSeq chr19 + 5913643 5916211 CAPS 828 "calcyphosine, transcript variant 1"
GO:0035556|GO:0005737|GO:0005886|GO:0005509|GO:0005634|GO:0031982|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92484_PI430048170 0.2638160974373390.8444253546526986.79453539279856 6.94665634158237 6.63689102329618 P P P 7.04271017491686 7.27699844467812 6.76094770068369 P P P LNCV6_92484_PI430048170 mRNA
ATTCCACCAACTCCAGCGAAAACATGTACACTATCATGAACCCCATCGGGCAGGGCGCCG NM_032627 RefSeq chr19 + 18419335 18434562 SSBP4 170463 "single stranded DNA binding protein 4, transcript variant 1"
GO:0003697|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121895_PI430048170 0.3470483138556720.7208392371474325.23362184958781 4.83633099560971 4.96365915007927 P P P 5.02764676723005 5.14590545635206 6.06805906168324 P P P LNCV6_121895_PI430048170 mRNA
TGCTGCCTTGGCTGAAGCAGCAACTCCTTATGGTATCGAATCTTTTGATTCTGTGTTAAA NM_012433 RefSeq chr2 - 197391973 197435093 SF3B1 23451 "splicing factor 3b, subunit 1, 155kDa, transcript variant 1"
GO:0005515|GO:0008380|GO:0010467|GO:0005634|GO:0009952|GO:0071013|GO:0016607|GO:0000398|GO:0000375|GO:0003682|GO:0005654|GO:0005681|GO:0005689 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144896_PI430048170 0.1381716738119921.21190178728463 4.10392881714993 4.51606590526756 4.31267328046729 P P P 4.18054241018771 3.996313114462 3.94241863526395 P P P LNCV6_144896_PI430048170 mRNA
GCCAAATCTTGTTTTATGTCCTGTCCTCATCTCTTAAGCTAAATCTGTTTGGATCATATT NM_015529 RefSeq chr6 - 132296054 132401534 MOXD1 26002 "monooxygenase, DBH-like 1"
GO:0005507|GO:0005789|GO:0016021|GO:0016715|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88843_PI430048170 0.4494162379150031.30756724684582 1.68899112903844 2.71953828302332 2.51732483220381 A A A 2.90209529194897 1.33782705484352 0.909878942689887 P A A LNCV6_88843_PI430048170 mRNA
GGGAAGACCACCTTCGTTTGTTGAACTTTCAACACAATTTTATAACTCGGATACAAAATA NM_001199018 RefSeq chr15 + 70892442 71050097 LRRC49 54839 "leucine rich repeat containing 49, transcript variant 3"
GO:0005737|GO:0005874 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83065_PI430048170 0.3425405515133550.8300013887907386.08359870928517 5.75114888728694 6.28621677247134 P P P 6.07385732110047 6.16313546338586 6.66683213260017 P P P LNCV6_83065_PI430048170 mRNA
ACACACATGTATGTTTGTTACCAAGAACTGGTCAGACCTTGCGAGTTTATTTGTAAACAC NM_001030007 RefSeq

chr16 - 71729001 71809073 AP1G1 164 "adaptor-related protein complex 1, gamma 1 subunit, transcript variant 1"
GO:0005515|GO:0005215|GO:0048471|GO:0030131|GO:0090160|GO:0032438|GO:0030136|GO:0005765|GO:0030119|GO:0006886|GO:0005829|GO:0043231|GO:0019886|GO:0005737|GO:0061024|GO:0016032|GO:0030659|GO:0043323|GO:0017137|GO:0005794|GO:0006892|GO:0032588|GO:0050690|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128647_PI430048170 0.3162164973223570.9703190838104410.391444763503088 0.4164983897846920.306424079293056A A A 0.4002650303944370.439154307386282 0.407349306435233A A A LNCV6_128647_PI430048170 mRNA
GTGTTTGATCATAAGAAATATTTCTTACTGTAAGCTGTCAGTTTTATATGCCACACCTGG NM_144651RefSeq chr8 - 51319576 51809445 PXDNL 137902 peroxidasin-like
GO:0005737|GO:0004601|GO:0004519|GO:0090305|GO:0042744|GO:0006979|GO:0005615|GO:0046872|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135392_PI430048170 0.0240691472392560.3883851886842026.58321314964277 6.55697139725076 6.55301489305923 P P P 7.50194317763739 7.9691473235431 8.22507557558143 P P P LNCV6_135392_PI430048170 mRNA
GGTGTGTCATTTTATGTATGTTCCTAATGCTTATGGAACTCCTCCAAAATAAAGTTACTC NM_001127257 RefSeq chr2 + 195656807 195737702 SLC39A10 57181 "solute carrier family 39 (zinc transporter), member 10, transcript variant 1" GO:0046873|GO:0006829|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130077_PI430048170 0.6002497843031671.01745336582103 0.327281628179711 0.3295931637561420.441245135457086A A A 0.3511083111663720.310843560479024 0.363719075634945A A A LNCV6_130077_PI430048170 mRNA
AGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGACACCAAAGTCTTCTCTTAC NM_001001952 RefSeq chr11 + 55819629 55820571 OR5D18 NA "olfactory receptor, family 5, subfamily D, member 18" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129771_PI430048170 0.8942111777493071.00461397179461 0.510696135183718 0.3995457356373550.508419693765065A A A 0.4449703789899420.504462937269077 0.451334919982142A A A LNCV6_129771_PI430048170 mRNA
CACCTGTCATCTTCTAAATTGTGTTCCTTTCATTTATTGGGAACAGAATCTCTCAAAAGT NM_181714RefSeq chr6 - 79484990 79537430 LCA5 167691 "Leber congenital amaurosis 5, transcript variant 1"
GO:0005515|GO:0005929|GO:0005737|GO:0042073|GO:0005815|GO:0045494|GO:0015031|GO:0032403 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89116_PI430048170 0.1367940711006040.8658336297949767.73049787560973 7.6601910918533 7.64355968547696 P P P 7.8031823605968 7.7841479765163 8.05569014714149 P P P LNCV6_89116_PI430048170 mRNA
ATGTCTTCTGCTTATATGGCAATGTGGAGAAGGTGAAATTCATGAAAAGCAAGCCGGGGG NM_001533RefSeq chr19 - 38836387 38849977 HNRNPL 3191 "heterogeneous nuclear ribonucleoprotein L, transcript variant 1"
GO:0005515|GO:0008380|GO:0006396|GO:0010467|GO:0044212|GO:0003723|GO:0005634|GO:0005737|GO:0000166|GO:0016020|GO:0000398|GO:0030529|GO:0005654|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65834_PI430048170 0.6422090815413820.6783510976942412.72906015074341 0.526339959420056 1.18267534945728 A A A 0.4149056669963032.94932515893435 2.62911477108907 A P P LNCV6_65834_PI430048170 mRNA
CTAATACTTCAGGAAAACTCATGATGGTTTCCATGTTAAGAGAGACATGGAGCAGGGCAC NM_002908RefSeq chr2 + 60881494 60928156 REL 5966 "v-rel avian reticuloendotheliosis viral oncogene homolog, transcript variant 1"
GO:0005515|GO:0005667|GO:0003700|GO:0007249|GO:0001205|GO:0000122|GO:0001816|GO:0038061|GO:0006

351|GO:0005829|GO:0045084|GO:0006954|GO:0045944|GO:0045087|GO:0003682|GO:0000980|GO:0005654|GO:0
043123|GO:0034097|GO:0033256 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138542_PI430048170 0.0552313159005266 1.39343254540992 6.77917138806019
6.6319214858808 6.71914318248445 P P P 6.36241100263298 6.34494566979516
5.95518677603591 P P P LNCV6_138542_PI430048170 mRNA
ATTTGAACCCTTCGGAAATCTTGATCAGCCAGATCTTTATTACGAGTACTACCCGCACGT NM_016030RefSeq
chr2_KI270769v1_alt + 9875 89041 TRAPPC12 51112 trafficking protein particle complex 12
GO:0005793|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136434_PI430048170 0.00723710098184504 0.6036658459950815.01429532823032
5.10430261907957 5.0929492760801 P P P 5.83631159495261 5.63617366558132 5.9114160375541
P P P LNCV6_136434_PI430048170 mRNA
CAGAAAGAAAATCTCACAGCACCGACTTGGCATCTGTGTTAAAAAATAGCAACTATATTT NM_002598RefSeq chr6
- 170575571 170584692 PDCD2 5134 "programmed cell death 2, transcript variant 1"
GO:0005515|GO:0005737|GO:0043065|GO:0006919|GO:0006915|GO:0005634|GO:0019899|GO:0003677|GO:0046
872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112421_PI430048170 0.0346552652281419 0.6699682808419986.76871681038652
6.58466075554864 6.60995459227676 P P P 7.03644032618117 7.15180978190103
7.47841801871214 P P P LNCV6_112421_PI430048170 mRNA
TATGAAGACTTTATTGTGAAACCTCCCGTGAGAAAGCTGGTCCACGACAAAGAGTTGGCA NM_006141RefSeq chr16
- 66720895 66751622 DYNC1LI2 1783 "dynein, cytoplasmic 1, light intermediate chain 2, transcript
variant 1"
GO:0005813|GO:0005874|GO:0000226|GO:0003777|GO:0005524|GO:0005829|GO:0019886|GO:0051642|GO:0016
020|GO:0008152|GO:0006810|GO:0005868|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141150_PI430048170 0.0233869083291274 0.2800231029765861.60370395914986
2.16820315976592 2.96913796207191 A A P 3.78934722912043 4.22974466760448
4.47770678984273 P P P LNCV6_141150_PI430048170 mRNA
GTAATCCCTGTATAAAGTAGTGCCAAACTGATTTCAGTTGTGTAACTAGTTTAAAACCCA NM_014614RefSeq chr2
- 53864066 53970840 PSME4 23198 "proteasome (prosome, macropain) activator subunit 4"
GO:0010467|GO:0002474|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0034641|GO:0016
032|GO:0070577|GO:0090090|GO:0006977|GO:0000209|GO:0043066|GO:0006521|GO:0051437|GO:0042590|GO:0
006915|GO:0007275|GO:0042981|GO:0051439|GO:0006974|GO:0016504|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130368_PI430048170 0.7631414466454330.9876253162335160.443931221347073
0.4737891624419580.413846604146963A A A 0.4199106184914010.408227621096325
0.553389668255442A A A LNCV6_130368_PI430048170 mRNA
CAAGCTTGTAAAGGAGTTAGGACATGCAAGCTACTGAGCATAAAATATATACTTGCTATT NM_020124RefSeq chr9
+ 27524313 27526498 IFNK 56832 "interferon, kappa"
GO:0006355|GO:0008285|GO:0005132|GO:0019221|GO:0005576|GO:0033141|GO:0045343|GO:0009615|GO:0005
125|GO:0005615|GO:0002250|GO:0051607|GO:0045089|GO:0030101|GO:0042100|GO:0045087|GO:0006959|GO:0
030183|GO:0043330|GO:0002286|GO:0002323 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127260_PI430048170 0.0438244003298717 1.66478300023615 8.33906402467272
8.52087910818948 8.43492945259433 P P P 7.79027007370426 7.91694681712988 7.3218350681142
P P P LNCV6_127260_PI430048170 mRNA
AGGACTTGGTTTGTTATATCAGGGAAAAGGAGTAGGGAGTTCATCTGGAGGGTTCTAAGT NM_001188RefSeq chr6
- 33572545 33580293 BAK1 578 BCL2-antagonist/killer 1
GO:0005515|GO:0043496|GO:0014070|GO:0042542|GO:0043497|GO:0051400|GO:0010524|GO:0097202|GO:0042
803|GO:0048597|GO:0042802|GO:0034644|GO:0008053|GO:0031072|GO:0002262|GO:0010332|GO:0046982|GO:0
070242|GO:0007568|GO:0032469|GO:0010248|GO:0010046|GO:0046930|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_129752_PI430048170 0.16437599954138 0.8921633592585712.2991096884994
12.0561693840959 12.2037822858932 P P P 12.3329460604721 12.2466249209817
12.4744467328847 P P P LNCV6_129752_PI430048170 mRNA
AAGCCTGTTGAGGCTGGAGTTAGGAGGCAGATTGATAGTAGGATTATAATAAACATTAAA NM_001034996 RefSeq
chr3 + 40457338 40462372 RPL14 9045 "ribosomal protein L14, transcript variant 1"
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006364|GO:0006614|GO:0019058|GO:0006
415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0000184|GO:0016032|GO:0
042273|GO:0022625|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129116_PI430048170 0.4976949314986520.8851918379651960.320318419135659
0.2437285827869670.305972252022898A A A 0.8107023474864 0.249769433200426
0.265048304260999A A A LNCV6_129116_PI430048170 mRNA
TATTTTAGAAATATTGTTCCTTGGTGTCAGCGTAGCTGTCTGTCTTAGGAGCTGGGTCGG NM_020528RefSeq chr21
+ 45849960 45942454 PCBP3 54039 "poly(rC) binding protein 3, transcript variant 1"
GO:0016071|GO:0030529|GO:0003723|GO:0005634|GO:0003677|GO:0070062|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131632_PI430048170 0.4817940856644020.8606189506236490.401877174372589
0.4121540987992380.420801977491913A A A 1.02262892459874 0.361647661983766
0.400918954771953A A A LNCV6_131632_PI430048170 mRNA
TGAATAAGCCTTAGGAGATGCCACATTCCAGAATAAAATGTTTCCAGGGTCTTTGCATCT NM_148963RefSeq chr6
- 116792084 116829057 GPRC6A 222545 "G protein-coupled receptor, class C, group 6, member A,
transcript variant 1" GO:0019722|GO:0009986|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0043200
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141493_PI430048170 0.1217846383573421.27442016172205 5.06147092442425
5.04036235174549 4.84580163942286 P P P 4.33217789346667 4.69587748000013
4.83430476439914 P P P LNCV6_141493_PI430048170 mRNA
ATATGTGTGTAGTTTGTGGCAGTTTTGGCCAAGGAGCAGAAGGAGGATTACTTGCCTGTT NM_182484RefSeq chr21
+ 10413531 10491615 BAGE5 NA "B melanoma antigen family, member 5" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_141988_PI430048170 0.58849449629022 1.05746225644822 4.13463098699211
4.22562905528391 4.45765272862057 P P P 4.3232045555908 4.25238008172458
4.00044536334445 P P P LNCV6_141988_PI430048170 mRNA
CGTCTGTTTTCCTTTGGAGAGTGAGGCCTTGTTATTATTCTTTTCTGATAAAGAAAACAT NM_001287337 RefSeq
chr13 - 49308649 49444126 CAB39L 81617 "calcium binding protein 39-like, transcript variant 1"
GO:0008286|GO:0007050|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135040_PI430048170 0.8510211634213361.00565100287009 0.368839946699718
0.34445312026009 0.256131855991075A A A 0.3102721339455520.326603057912843
0.310521163601603A A A LNCV6_135040_PI430048170 mRNA
GCATCAACTTACAAAGTACACTATGTAAGAACTGAGGTAAGTTTGTAAGTGCACAACTAA NM_001114106 RefSeq
chr1 + 94820341 94895247 SLC44A3 126969 "solute carrier family 44, member 3, transcript variant 1"
GO:0005886|GO:0044281|GO:0016021|GO:0006644|GO:0055085|GO:0046474|GO:0006656 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_64436_PI430048170 0.2122845590376890.7929434821580474.79711442998135 4.88474784799215
4.49812233852767 P P P 5.37980582670135 4.9866685038651 4.78005020152816 P P P
LNCV6_64436_PI430048170 mRNA
AAACATTCAAGAATGAGAGCGAGAACACGTGTCAAGATGTGGACGAATGTCAGCAGAACC NM_013447RefSeq
chr19 - 14732696 14778541 ADGRE2 NA "adhesion G protein-coupled receptor E2, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68464_PI430048170 0.3208171302943011.03454511901192 0.3541501804842520.356256384887443
0.465012347068686A A A 0.3437781091426240.316336814308379 0.370613669113463A A A

LNCV6_68464_PI430048170 mRNA
TTAAAGAAGTACCGGCGCTATGAAGTAATAATGACCGCCTATAACATCATCGGCGAGAGC NM_152744 RefSeq chr7
+ 3301447 4268999 SDK1 221935 "sidekick cell adhesion molecule 1, transcript variant 1"
GO:0016021|GO:0007155|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111515_PI430048170 0.00316010685317984 0.8174487445406626.27557828063012
6.34956166722599 6.28581095537801 P P P 6.60324117930049 6.6018522108031
6.57925086082227 P P P LNCV6_111515_PI430048170 mRNA
TGAACGGCATCTACCAGTTCATCATGGACCGCTTCCCCTTCTACCGGGACAACAAGCAGG NM_001453 RefSeq chr6
+ 1610445 1613894 FOXC1 2296 forkhead box C1
GO:0005515|GO:0001657|GO:0003700|GO:0055010|GO:0044212|GO:0006366|GO:0001756|GO:0001654|GO:0000
981|GO:0003705|GO:0048844|GO:0005634|GO:0007507|GO:0001541|GO:0005737|GO:0050880|GO:0014032|GO:0
007219|GO:0045944|GO:0030199|GO:0042475|GO:0043010|GO:0030203|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130331_PI430048170 0.1067003285463611.06439060438875 0.452209012673287
0.5061073177573940.51955565884299 A A A 0.3397388386522050.404731219802406
0.46162058029584 A A A LNCV6_130331_PI430048170 mRNA
ATTTATTCTCATTCTGGGGAACAGTAAGCTGAAGCAGACATTTGTAGTGATGCTCCGGTG NM_016943 RefSeq chr7
+ 141764096 141765197 TAS2R3 50831 "taste receptor, type 2, member 3"
GO:0007165|GO:0033038|GO:0050909|GO:0007186|GO:0005886|GO:0008527|GO:0016021|GO:0001580 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127587_PI430048170 0.0127538281026037 0.4794871462254175.76965102483603
5.31562062983201 5.9420376725279 P P P 6.57768708006357 6.70511753269883
6.96811450868892 P P P LNCV6_127587_PI430048170 mRNA
GCAAGACAGATGGGAATGTGTATAATAACTAGGTATTTGAGAAGTTCTGAAGTTTGATGT NM_014319 RefSeq chr12
+ 65169570 65248361 LEMD3 23592 "LEM domain containing 3, transcript variant 1"
GO:0005515|GO:0006997|GO:0005637|GO:0032926|GO:0035914|GO:0003677|GO:0002044|GO:0005639|GO:0030
514|GO:0000166|GO:0016020|GO:0051726|GO:0016021|GO:0030512 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142491_PI430048170 0.00233314037760662 0.7282588470892325.81207754909153
5.65655996137988 5.67321186780043 P P P 6.09475259818475 6.17907669679507
6.24179430431951 P P P LNCV6_142491_PI430048170 mRNA
GCAGCCTCAACCAACAACAATGTGTTGTAAAAATGTCTTTCATGTAAAAAGTGCAGTAAA NM_181458 RefSeq chr2
- 222199886 222298996 PAX3 5077 "paired box 3, transcript variant PAX3D"
GO:0005515|GO:0060594|GO:0008284|GO:0003700|GO:0006366|GO:0008283|GO:0007605|GO:0003705|GO:0001
755|GO:0005634|GO:0007507|GO:0045944|GO:0009887|GO:0048066|GO:0006915|GO:0001843|GO:0000122|GO:0
014807|GO:0048663|GO:0021527|GO:0043565|GO:0007517|GO:0003682|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140552_PI430048170 0.3214970021360821.69282256173211 0.780863131130854
1.90370070334973 0.348106258182723 A A A 0.48238072938545 0.366665389119916
0.368294076509209 A A A LNCV6_140552_PI430048170 mRNA
GTCAGATAACAGCTAATGATAAATGACATATCATTAGCTATGCATCGCAATAAAACAGCC NM_033123 RefSeq chr12
- 18683175 18738059 PLCZ1 89869 "phospholipase C, zeta 1, transcript variant 1"
GO:0048471|GO:0043647|GO:0005509|GO:0005634|GO:0007275|GO:0044281|GO:0005829|GO:0016042|GO:0035
556|GO:0007343|GO:0004435|GO:0006816|GO:0004871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130289_PI430048170 0.4762876796419950.7626495007607650.38542367413784
0.2588471444638050.282919931511768 A A A 0.2645207779481441.30766419470806
0.263432073991992 A A A LNCV6_130289_PI430048170 mRNA
GAAGCTGGAGAGAATGGGCATTTTTAAATGTTACGGCATATGCTAATATAATATTATGGC NM_001204087 RefSeq
chr1 - 154697465 154870278 KCNN3 3782 "potassium channel, calcium activated intermediate/small

conductance subfamily N alpha, member 3, transcript variant 3"
GO:0005516|GO:0005886|GO:0043025|GO:0007268|GO:0016021|GO:0071805|GO:0016286 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132501_PI430048170 0.2578290600498721.13870076594015 7.50588246318492 7.34818947703162 7.15512669467062 P P P 7.14118905804652 7.32515776713408 6.98142335721298 P P P LNCV6_132501_PI430048170 mRNA
CTTCTCAGGGCAGAGTGGGCTGGTTGTGTTGACAATAAAACAGTGTTGGTTTGCAAAAAA NM_001168682 RefSeq chr7 - 100572229 100573647 SAP25 100316904 "Sin3A-associated protein, 25kDa"
GO:0006355|GO:0005737|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140566_PI430048170 0.6399801962591390.8961901645940473.94484775046375 3.80173706704979 4.06176842256252 P P P 4.48630516531574 3.9825170835188 3.71788092173135 P P P LNCV6_140566_PI430048170 mRNA
CACATGTAACAGATTCCTTTATATGTAGTGGAAATCACTATTTGTAGAAACTGTCAGGTC NM_017664RefSeq chr13 - 110878539 110915107 ANKRD10 55608 "ankyrin repeat domain 10, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89478_PI430048170 0.0923430005829344 1.75359771236583 3.48576081963969 4.36030925547894 3.90262417521484 P P P 3.19576520019129 3.12560569991162 3.12749659687903 P P P LNCV6_89478_PI430048170 mRNA
TATTTAAAAAGATAAAATAGAGCTTTGCAGGAAAGTGCTGCAGGCTCCCACGTTGCCGGG NM_001008737 RefSeq chr3 - 10006417 10011095 LOC401052 401052 uncharacterized LOC401052 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130968_PI430048170 0.00939929736096639 0.3289713424996516.38042039920326 6.79508691005136 7.01670022076742 P P P 8.33011346460433 8.29092136287989 8.44882670339606 P P P LNCV6_130968_PI430048170 mRNA
ACAGCTGGCCAGTAATTAGTGTTGTGCACTTCATGTCATTAATCAATTTCTCAATAGTTC NM_002979RefSeq chr1 + 52927228 53051617 SCP2 6342 "sterol carrier protein 2, transcript variant 1"
GO:0005515|GO:0006694|GO:0006701|GO:0005782|GO:0006699|GO:0033814|GO:0044281|GO:0043231|GO:0005739|GO:0036042|GO:0045940|GO:0005737|GO:0032959|GO:0015914|GO:0015485|GO:0070538|GO:0007031|GO:0008206|GO:0000062|GO:0044255|GO:0032385|GO:0070062|GO:0005777|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130446_PI430048170 0.3822062905789970.7772902998961522.68592097964326 2.82595508500447 2.5747215762127 A A A 2.46720908322495 3.14603688872393 3.41734504695442 A P P LNCV6_130446_PI430048170 mRNA
CACAGTCAAGAATTAGCAGAAACCCTCTGCATTTACAAACACTTTGTGCTATAAAAAAGT NM_004631RefSeq chr1 - 53242369 53328149 LRP8 7804 "low density lipoprotein receptor-related protein 8, apolipoprotein e receptor, transcript variant 1"
GO:0006629|GO:0005515|GO:0008035|GO:0030424|GO:0005886|GO:0007603|GO:0061098|GO:0019221|GO:0050731|GO:0030425|GO:0071397|GO:0030229|GO:0043025|GO:0006508|GO:0061003|GO:1900006|GO:0021541|GO:0042493|GO:0005875|GO:0005509|GO:0050804|GO:0014069|GO:0005576|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143145_PI430048170 0.6035087690790890.9687036244278420.471669232275134 0.5184251911915880.431158298760277A A A 0.4443737632393950.653489015560286 0.452455568557434A A A LNCV6_143145_PI430048170 mRNA
TCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGAAAATCATTAT NM_001013357 RefSeq chr11_JH159136v1_alt + 193978 194908 OR8U9 NA "olfactory receptor, family 8, subfamily U, member 9" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128459_PI430048170 0.0192577478959779 1.42135240866808 8.17436039140787 8.51270214842233 8.26958786254666 P P P 7.79998978774377 7.93191732235382 7.71611122685072 P P P LNCV6_128459_PI430048170 mRNA

CTGCCTCTGGAATTGCTCAAGTTCATTGATGACCCTCTGACCCTAGCTCTTTCCTTTTTT NM_004324RefSeq chr19 + 48954859 48961262 BAX 581 "BCL2-associated X protein, transcript variant beta" GO:0043496|GO:0005515|GO:0002358|GO:0043497|GO:0009651|GO:0007281|GO:0042803|GO:0035234|GO:0006808|GO:0042802|GO:0005757|GO:0043524|GO:0034644|GO:0043525|GO:0008053|GO:0008637|GO:0002904|GO:0002262|GO:0032461|GO:0010332|GO:0046982|GO:0006687|GO:0032469|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132688_PI430048170 0.768246325814271 0.883829011037201 4.32055507808502 4.20528328486998 4.7240358314644 P P P 3.91038889373986 4.6358820577564 5.06533340791528 P P P LNCV6_132688_PI430048170 mRNA
GTGCAACGAACTTTCTGCTGAATTAATGGTAATAAAACTCTGGGTGTTTTTCAGAAATAC NM_005130RefSeq chr4 - 15935569 15938740 FGFBP1 9982 fibroblast growth factor binding protein 1 GO:0005515|GO:0007165|GO:0008284|GO:0008285|GO:0045743|GO:0009986|GO:0005886|GO:0017134|GO:0007267|GO:0008201|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142975_PI430048170 0.0173503660167123 0.422849546283788 4.89267387004137 4.19923050498858 4.96652560094915 P P P 5.56157949732431 6.09327384675629 6.1725671874346 P P P LNCV6_142975_PI430048170 mRNA
GCGTTGTTACCTGTTGAATTTTGTATTATGTGAATCAGTGAGATGTTAGTAGAATAAGCC NM_025225RefSeq chr22 + 43923738 43947568 PNPLA3 80339 patatin-like phospholipase domain containing 3 GO:0051265|GO:0051264|GO:0004806|GO:0044281|GO:0016020|GO:0004623|GO:0005789|GO:0019432|GO:0036155|GO:0016021|GO:0019433|GO:0006644|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131953_PI430048170 0.0801915386581202 0.822020735778063 5.74209682573075 5.42845224539744 5.48576277283567 P P P 5.95510147263991 5.71532145845613 5.84388040198559 P P P LNCV6_131953_PI430048170 mRNA
CCTGGTTATGTATGTACTTGTACATAACCACCTAAAGAATGGTGAAATAAATGTTCTTGG NM_005899RefSeq chr17 + 43170969 43211689 NBR1 4077 "neighbor of BRCA1 gene 1, transcript variant 1" GO:0005515|GO:0043130|GO:0030500|GO:0005776|GO:0005770|GO:0016236|GO:0000407|GO:0031410|GO:0032872|GO:0051259|GO:0005764|GO:0031430|GO:0005829|GO:0045668|GO:0016020|GO:0008270|GO:0070062|GO:0051019 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_43589_PI430048170 0.0491629519348037 0.482231996485978 1.78121323319578 1.10156884097851 1.97808150335187 A A A 2.82136960085123 2.67456445075875 2.6540648134713 A A P LNCV6_43589_PI430048170 mRNA
GCTGAAGAAGGCATCGTCAAATCAGGTGTATGAAAACATTATAGACTGGTATTTTCAATT NM_153251RefSeq chr13 - 21372570 21459369 ZDHHC20 253832 "zinc finger, DHHC-type containing 20, transcript variant 1" GO:0018345|GO:0016020|GO:0005886|GO:0016409|GO:0008270|GO:0016021|GO:0019706 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112431_PI430048170 0.199725405892412 0.738126538708616 2.59427065271601 2.85035165288314 2.26432829358983 A A A 3.39905562801325 2.66438661956089 2.92061988660521 P P P LNCV6_112431_PI430048170 mRNA
TGCAGGGGGCACATCACTAGAGGTGGCTCGTTTCTTGTCACGGGAAGACCAAGTGATCCT NM_024939RefSeq chr16 - 68228546 68236233 ESRP2 80004 epithelial splicing regulatory protein 2 GO:0008380|GO:0006397|GO:0000166|GO:0043484|GO:0005654|GO:0005634|GO:0003729 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143495_PI430048170 0.0451907826137469 1.1121182656824 11.1494139234616 11.1136723950396 11.0343378178528 P P P 10.9417827091767 10.9526227161607 10.945459809333 P P P LNCV6_143495_PI430048170 mRNA
GTACTAAAAAAGGAGAAATTATAATAAATTAGCCGTCTTGCGGCCCCTAGGCCTAAAAAA NM_001166159 RefSeq chr1 + 161202146 161214394 NDUFS2 4720 "NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase), transcript variant 2" GO:0005515|GO:0051539|GO:0048038|GO:0005743|GO:0009055|GO:0044281|GO:0046872|GO:0003954|GO:0005

739|GO:0022904|GO:0051287|GO:0005747|GO:0006120|GO:0005654|GO:0008137|GO:0006979|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143531_PI430048170 0.39089545969390240.5412222246686 0.564366542404336 7.25020018179607 0.521821811326457A P A 0.2826043587393190.381794824760095 0.387054225581775A A A LNCV6_143531_PI430048170 mRNA ATGTCTCTCTGTATTGACATTAAGTATTCACTTTTAGAGTAAAATCCATCCCTGGGACAT NM_024870RefSeq chr8 + 67952367 68231662 PREX2 80243 "phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2, transcript variant 1"
GO:0048813|GO:0008344|GO:0007186|GO:0005886|GO:0032855|GO:0030675|GO:0014065|GO:0030676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130011_PI430048170 0.431049104655996 0.832107893496665 10.3137829600594 10.4291031403102 10.6585367071642 P P P 10.3224804586785 10.6550448236975 11.1267282379727 P P P LNCV6_130011_PI430048170 mRNA GACTGTATTTTCCAACTTGTTCAAATTATTACCAGTGAATCTTTGTCAGCAGTTCCCTTT NM_000194RefSeq chrX + 134460144 134500668 HPRT1 3251 hypoxanthine phosphoribosyltransferase 1
GO:0046040|GO:0005515|GO:0044281|GO:0042803|GO:0005829|GO:0045964|GO:0006178|GO:0005737|GO:0042417|GO:0000166|GO:0051289|GO:0032264|GO:0019835|GO:0032263|GO:0046038|GO:0043101|GO:0007626|GO:0043103|GO:0007625|GO:0021895|GO:0070062|GO:0000287|GO:0052657|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134268_PI430048170 0.0667237032843893 1.04548698686896 0.394390848180359 0.412038809082157 0.454083045225318A A A 0.334488969115848 0.340494286533014 0.392938151889049A A A LNCV6_134268_PI430048170 mRNA ACTTTCTCTGGGGCCTTTTAGGCCATACTTTTAATTTTGTTATTTGATACTACTGGTTGC NM_021216RefSeq chr19 + 56595295 56624176 ZNF71 58491 zinc finger protein 71
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133060_PI430048170 0.136758510242673 1.28062865278235 10.4433975485836 10.7598992765667 10.9457875207015 P P P 10.2772895895531 10.2226426774317 10.5940455563594 P P P LNCV6_133060_PI430048170 mRNA GGGGGTAAAACTTGTTGCTTTTATGTGTGCTTGAAAACATTTTTCAAAGTTACACAACAG NM_173685RefSeq chr8 + 125091840 125367125 NSMCE2 286053 "non-SMC element 2, MMS21 homolog (S. cerevisiae)"
GO:0005515|GO:0000781|GO:0016874|GO:0016925|GO:0030915|GO:0045842|GO:0005634|GO:0006303|GO:0007067|GO:0000724|GO:0016605|GO:0019789|GO:0000722|GO:0034184|GO:0008270|GO:0090398|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127814_PI430048170 0.0358492593065338 1.36811678664338 5.78994482238083 6.04976615923027 5.6711543620042 P P P 5.45375054698388 5.4771013433069 5.23794810026398 P P P LNCV6_127814_PI430048170 mRNA TATTAATTGTGCAAGCTTTTCCTAATAAACGTGGAGAATCACAGGCTGGGCTGGGCACTG NM_000218RefSeq chr11_KI270831v1_alt + 1030 81275 KCNQ1 3784 "potassium channel, voltage gated KQT-like subfamily Q, member 1, transcript variant 1"
GO:0005515|GO:0005251|GO:0034236|GO:0005516|GO:0034237|GO:0005886|GO:0007605|GO:0008016|GO:0060306|GO:0007268|GO:0016458|GO:0060307|GO:0086091|GO:0005764|GO:0060048|GO:0071435|GO:0016323|GO:0086008|GO:0060372|GO:0086089|GO:0060452|GO:0008076|GO:0005249|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130917_PI430048170 0.0961078088770471 1.10873224248773 11.5665056027322 11.5414311882032 11.4466018169477 P P P 11.4187384597151 11.4277107439912 11.2578590382584 P P P LNCV6_130917_PI430048170 mRNA CACTGCTGGGTTTTACATCCAGATAGTAATAAACACCATTTCATCATTTTCTCTTGGAAA NM_001243926 RefSeq chr3 + 50611861 50649297 MAPKAPK3 7867 "mitogen-activated protein kinase-activated protein

kinase 3, transcript variant 1"
GO:0005515|GO:0034142|GO:0005634|GO:0007265|GO:0051403|GO:0005829|GO:0002756|GO:0000187|GO:0005
737|GO:0018105|GO:0002755|GO:0032496|GO:0034097|GO:0034138|GO:0004708|GO:0048010|GO:0048011|GO:0
031965|GO:0038124|GO:0038123|GO:0034134|GO:0006950|GO:0002224|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_109295_PI430048170 0.194839814221599 1.39263647366447 4.08623178215972
3.62597539439359 3.37078405977867 P P P 3.49002169941973 3.38701005039422
2.76397589992799 P P P LNCV6_109295_PI430048170 mRNA
GCGTGAGCGTGGCCACCGAGCGCGCCCTGCAGACGCCCACCAACTCCTTCATCGTGAGCC NM_000797 RefSeq
chr11_KI270832v1_alt + 167177 170576 DRD4 1815 dopamine receptor D4
GO:0005515|GO:0032417|GO:0060041|GO:0060406|GO:0015459|GO:0009648|GO:0042802|GO:0042596|GO:0051
586|GO:0043025|GO:0001662|GO:0005938|GO:0050848|GO:2000463|GO:0007614|GO:0035240|GO:0046928|GO:0
007212|GO:0048545|GO:0060080|GO:0005887|GO:0035176|GO:0001591|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_92081_PI430048170 0.115301878082799 0.644588490244389 0.328025601065866 0.782853606840153
1.07511008612056 A A A 1.15566440385986 1.10868647557546 1.8076997536582 A A A
LNCV6_92081_PI430048170 mRNA
CTTCAGTTTTTCTTTGTAAGCCATCACAAGCCATAGTGGTAGGTTTGCCCTTTGGTACAG NM_003014 RefSeq chr7
- 37905932 37916923 SFRP4 6424 secreted frizzled-related protein 4
GO:0042813|GO:0005515|GO:0017147|GO:0043065|GO:0008285|GO:0009986|GO:2000119|GO:0004930|GO:0090
263|GO:0055062|GO:0005634|GO:0007275|GO:0005615|GO:0043433|GO:0030154|GO:0010628|GO:0045606|GO:0
005737|GO:0009725|GO:0016021|GO:0090090|GO:0002092|GO:0035567 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_66126_PI430048170 0.0752383069155064 0.791181567658174 8.4477477187658
8.38455008003685 8.4389953538511 P P P 8.79647489410121 8.56480265235883 8.9040549186008
P P P LNCV6_66126_PI430048170 mRNA
CTGGTCAATGAGTGGTCATTGAAGATAAGAAAGGAAATGAGAGTTGTTGACAGGCAAATA NM_016079 RefSeq chr2
- 86503429 86563497 CHMP3 51652 "charged multivesicular body protein 3, transcript variant 1"
GO:0005515|GO:0006997|GO:0019058|GO:0006915|GO:0010824|GO:0015031|GO:0005829|GO:0050792|GO:0000
920|GO:0007034|GO:0016197|GO:0031902|GO:0061024|GO:0016032|GO:0007080|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_62149_PI430048170 6.49936518045953e-05 1.76849050125932 4.17614229147993
4.28642937259281 4.20797729262985 P P P 3.43224093102355 3.33277363503035
3.43782092617044 P P P LNCV6_62149_PI430048170 mRNA
TTCGACGAGTTCAAGATGCAGCTGTATCCAAGAAAGCCAGCCCAGAGGCTGCCAGCACTC NM_033238 RefSeq chr15
+ 73994672 74047814 PML 5371 "promyelocytic leukemia, transcript variant 1"
GO:0051974|GO:0005515|GO:0030308|GO:0010522|GO:0019221|GO:0046332|GO:0006605|GO:0042803|GO:0051
607|GO:0032211|GO:0030578|GO:0030099|GO:0007179|GO:0009411|GO:0010332|GO:0031625|GO:0006977|GO:0
031965|GO:0046982|GO:0003713|GO:0032469|GO:0032922|GO:0048384|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142563_PI430048170 0.00127346753420105 3.74582331309632 11.2296906563112
11.3326463097657 11.0253112355429 P P P 9.31778635452023 9.32116296309667
9.24844557256704 P P P LNCV6_142563_PI430048170 mRNA
GAGATAGCGAAGGGTCTGGCCTCGCTGTGATCTGATTTGGGATTAAAGGTTTGGAAATTT NM_145814 RefSeq chr19
+ 53992287 54012666 CACNG6 59285 "calcium channel, voltage-dependent, gamma subunit 6,
transcript variant 1" GO:0005245|GO:0070588|GO:0034765|GO:0006816|GO:0005891 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_145068_PI430048170 0.0490216264280603 0.816158801402755 11.5968548765809
11.6078525796222 11.3704602879555 P P P 11.8680379242373 11.7733137622592

11.8237112191695 P P P LNCV6_145068_PI430048170 mRNA
CACGGGGTGTGGGCGACGCTGTTATGTAAATAGAGCTGCTGAGTTGGACCAGGCAAAAAA NM_019100 RefSeq
chr1 + 44213452 44220679 DMAP1 55929 "DNA methyltransferase 1 associated protein 1, transcript variant 1"
GO:0001103|GO:0005515|GO:0003714|GO:0005657|GO:0006325|GO:0005634|GO:0000122|GO:0042993|GO:0006351|GO:0006306|GO:0005737|GO:0006281|GO:0043967|GO:0043968|GO:0003682|GO:0035267|GO:0005654|GO:0006338|GO:0045892|GO:0040008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138666_PI430048170 0.145162657730056 1.29001408859299 6.86015111566479
6.65532871381934 7.12742727380727 P P P 6.21158084366775 6.61941374427098
6.70253946083948 P P P LNCV6_138666_PI430048170 mRNA
ACCCATTACATAGTTACTCAGTAAACAAAAGAGAAATACCAGGTAGGAAAGAAGAGTTAC NM_005836 RefSeq chr8
- 98102338 98117190 HRSP12 10247 heat-responsive protein 12
GO:0005739|GO:0005737|GO:0004519|GO:0090305|GO:0019239|GO:0005634|GO:0006449|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138585_PI430048170 0.137060345906414 1.5234875139587 1.06652069988646
1.60403715417115 1.46959280682883 A A A 0.389159826257599 0.507309051971485
1.29683894302445 A A A LNCV6_138585_PI430048170 mRNA
ATAAAAATTTTAAATCTCACTTCACTTAGCCGACATTCCATGCCCTGACCAATCCTACTG NM_178033 RefSeq chr1
+ 47023567 47050751 CYP4X1 260293 "cytochrome P450, family 4, subfamily X, polypeptide 1"
GO:0070330|GO:0005506|GO:0005789|GO:0016021|GO:0055114|GO:0020037 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_78094_PI430048170 0.00929263366297219 0.78752770018467 15.955852083754
15.7970875588038 15.7877927771788 P P P 16.0965591354373 16.2439075314741
16.235620554707 P P P LNCV6_78094_PI430048170 mRNA
GCCAGGGCTTACCTGTACACTGACTTGAGACCAGTTGAATAAAAGTGCACACCTTAAAAA NM_001101 RefSeq
chr7 - 5527147 5530601 ACTB 60 "actin, beta"
GO:0050998|GO:0005515|GO:0030424|GO:0000790|GO:0005886|GO:0006325|GO:0006928|GO:0072562|GO:0005615|GO:0005829|GO:0005737|GO:0001895|GO:0006457|GO:0007411|GO:0035267|GO:0061024|GO:0005856|GO:0070062|GO:0048010|GO:0048013|GO:0019901|GO:0043044|GO:0034329|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144353_PI430048170 0.559245858251807 0.935427198744869 0.44185012683136
0.448193169988358 0.393280912865306 A A A 0.759503146926979 0.382683851250218
0.398339241775287 A A A LNCV6_144353_PI430048170 mRNA
GTTGGGAAATACAAGAAGAGAAAGACCAGTGGGGATTTGTAAGACTTAGATGAGATAGCG NM_001462 RefSeq
chr19 + 51763388 51770526 FPR2 2358 "formyl peptide receptor 2, transcript variant 1"
GO:0004982|GO:0006954|GO:0007186|GO:0006935|GO:0005886|GO:0004930|GO:0006928|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91193_PI430048170 0.381885072749477 0.851006767858149 0.345594304190791 0.37774290594002
0.33496565805586 A A A 0.383143000846565 0.934026650673245 0.364384729663013 A A A
LNCV6_91193_PI430048170 mRNA
GCATCTTACAATGCTATCACATTGCCAGAAGAATTTCATGATTTTGACACCCAAAATATG NM_001136566 RefSeq
chr20 + 1226119 1254501 RAD21L1 642636 RAD21-like 1 (S. pombe)
GO:0030999|GO:0009566|GO:0007059|GO:0005694|GO:0000724|GO:0030893|GO:0072520|GO:0034991|GO:0005634|GO:0007283|GO:0000800|GO:0070197 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139990_PI430048170 0.267468570165784 1.95744201833182 4.19734121337286
3.42478121483403 2.30993736050978 P P A 2.0083042517285 2.29950364745291
3.07819135032109 A A P LNCV6_139990_PI430048170 mRNA
AGGACGGGTGGGAGGGACAGGGAGGGACCAATAAATCATAATGAAGAAACGCTCAAAAAA NM_005317 RefSeq
chr19 + 544033 549920 GZMM 3004 "granzyme M (lymphocyte met-ase 1), transcript variant 1"

GO:0016020|GO:0004252|GO:0045087|GO:0019835|GO:0006508|GO:0008236|GO:0006915|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129140_PI430048170 0.0205998123918131 0.5835534607070078.23465754850088 8.15921945456145 8.12862180196666 P P P 8.89118716471227 8.75235020327547 9.17893983724333 P P P LNCV6_129140_PI430048170 mRNA
GTGGTCCCTTGTTTTTACATGTTCATGCTGTGTAATTTTGAGATGTTACTGAGATATGTT NM_001145667 RefSeq chr16 - 74447427 74607144 GLG1 2734 "golgi glycoprotein 1, transcript variant 3"
GO:0005794|GO:0005886|GO:0005102|GO:0032330|GO:0050900|GO:0031012|GO:0000139|GO:0016020|GO:0007596|GO:0060349|GO:0016021|GO:0010955|GO:0030512|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145170_PI430048170 0.00241447687103246 0.29432839302681 8.29834206519482 8.0175679627324 8.46858990110704 P P P 9.70474028993689 9.98317295003079 10.3520139902482 P P P LNCV6_145170_PI430048170 mRNA
CATTTCAAGCCGTGTATAATCATCAAAATGGGGGGCTTGAGTTCTTTAGCTACTTGAATC NM_001017980 RefSeq chrX + 151397184 151409364 VMA21 203547 VMA21 vacuolar H+-ATPase homolog (S. cerevisiae)
GO:0070072|GO:0030127|GO:0033116|GO:0005789|GO:0016021|GO:0005764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130846_PI430048170 0.1108602410039790.9544993256252240.277685309907897 0.2961287634132990.341669173254579A A A 0.4215436081785950.360239527898338 0.334617737558604A A A LNCV6_130846_PI430048170 mRNA
TTCTTAAAAAGGAACAAATAAACTCATTTAACTAAAGTTAACTGATTAAAGAGGAAAAAA NM_016828RefSeq chr3 + 9749943 9766669 OGG1 4968 "8-oxoguanine DNA glycosylase, transcript variant 2d"
GO:0005515|GO:0008017|GO:0090305|GO:0045471|GO:0016363|GO:0005739|GO:0008534|GO:0033158|GO:0071276|GO:0006979|GO:0032355|GO:0009314|GO:0006355|GO:0002526|GO:0043066|GO:0042493|GO:0007568|GO:0034039|GO:0051593|GO:0003684|GO:0019104|GO:0006281|GO:0004519|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134960_PI430048170 0.0331802349920392 1.09489876668737 0.374457879079173 0.4689041408795570.428018274193236A A A 0.2812032527979080.308068531774984 0.291140678057056A A A LNCV6_134960_PI430048170 mRNA
TAAATGTGATTCCTCTTATCTGTGTTGTCAACACCGTGACCAGTGCATTCCAACTCTTGG NM_001206670 RefSeq chr15 - 41981581 42050703 PLA2G4E NA "phospholipase A2, group IVE" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129047_PI430048170 0.2826517255217650.9026427530326421 3.5929408912289 13.3317560592411 13.3709603607156 P P P 13.4992689344981 13.7515388288917 13.4863570391863 P P P LNCV6_129047_PI430048170 mRNA
TTTAAGCGACTGGTTGGGATAGAACCCTAAAGAAATAAACTTCCAGTGGATACCGGAGGC NM_001258430 RefSeq chr20 - 3753498 3767805 C20orf27 54976 "chromosome 20 open reading frame 27, transcript variant 3" GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127377_PI430048170 0.00976772624580454 1.39595789585593 9.35394747551344 9.40582484364274 9.59517398239667 P P P 8.85783858414883 8.9447323606178 9.10860364601736 P P P LNCV6_127377_PI430048170 mRNA
GGACTGTCTCATACTGCTCTGGACTATGTGGTAATAAAGGCTTTATTGTTTAAGCCGCTT NM_173548RefSeq chr19 + 58408695 58418325 ZNF584 201514 zinc finger protein 584
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59327_PI430048170 0.0943233567532397 1.44105536435884 8.71063397714728 8.83257908409837 9.11163709136411 P P P 7.98189288611497 8.3657154261071 8.6734948853084 P P P LNCV6_59327_PI430048170 mRNA
TGCAAAGAGGGTAAAATTGAAGGAATAGTGTGGCATTGCAGTGATGGCTGTTTAATAAAG NM_001009894 RefSeq

chr12 + 88035490 88050160 C12orf29 91298 chromosome 12 open reading frame 29 GO:0002244
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129456_PI430048170 0.40034615932789 0.9756989369052790.269803974191257
0.2825771189203350.372459603660482A A A 0.3772664841764010.314202918691296
0.341337650439105A A A LNCV6_129456_PI430048170 mRNA
ACAGAAAGACTGGAAGTTCTTTGAGTCCTTTTATACTTTCTGTACATATGTGGCTTGGAT NM_172365RefSeq chr14
+ 64549901 64589379 PPP1R36 145376 "protein phosphatase 1, regulatory subunit 36"
GO:0019902|GO:0010923|GO:0004864 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134263_PI430048170 0.0102060630804608 1.17859319571282 5.01473511100749
4.89057834191843 4.92467079984994 P P P 4.69174965977071 4.68155617971141
4.74747306719818 P P P LNCV6_134263_PI430048170 mRNA
TATGCAGGCAAAATAACCACACTTCAGAAAATGTGGACTTCTGAAAAATAAAATCCCCAT NM_003426RefSeq chr22
+ 20394114 20408463 ZNF74 7625 "zinc finger protein 74, transcript variant 1"
GO:0006355|GO:0003700|GO:0003723|GO:0007275|GO:0005654|GO:0015629|GO:0003677|GO:0046872|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138859_PI430048170 0.6373066376784010.9035784809976822.12183971262351
3.22574230565529 1.25087670662294 A P A 2.81527620255541 2.73917785694055
2.03161915894276 P P A LNCV6_138859_PI430048170 mRNA
CCCAGGTCTTCGGCACCACCACAATTAATTCCCTTCCCAACACTTGCCTGATGGAAAAAA NM_003052RefSeq chr5
+ 177384430 177398848 SLC34A1 6569 "solute carrier family 34 (type II sodium/phosphate
cotransporter), member 1, transcript variant 1"
GO:0005515|GO:0048471|GO:2000187|GO:0097066|GO:0005886|GO:0033189|GO:0031526|GO:0032403|GO:0042
803|GO:0016323|GO:0044341|GO:0009100|GO:0016324|GO:0035864|GO:0015321|GO:0046849|GO:0071374|GO:0
032026|GO:0006817|GO:0051260|GO:0006814|GO:0032355|GO:0015293|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126071_PI430048170 0.2815840361940231.03765635423341 0.322478474228602
0.2732408115064060.397598542770372A A A 0.2855918036609890.261467168773603
0.28884398603966 A A A LNCV6_126071_PI430048170 mRNA
TCTTGCACCCCCATGAAAGAGTCTACAACTATGGAGATCTGGATTCATCCCCAACCACAG NM_032968RefSeq chrX
+ 91835460 92623229 PCDH11X 27328 "protocadherin 11 X-linked, transcript variant c"
GO:0005886|GO:0005887|GO:0010923|GO:0005509|GO:0007156|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130653_PI430048170 0.0521638106483345 0.9631320505648570.425359576679929
0.3988207932004350.373063127311712A A A 0.4304835072478870.473181138218046
0.456316057735498A A A LNCV6_130653_PI430048170 mRNA
CTCACTACCTGTACACTCAAACGACAGTATTAACTCTGAATTTGGATAAATCATATGTGA NM_001206920 RefSeq
chr14 - 57563921 57865874 SLC35F4 341880 "solute carrier family 35, member F4"
GO:0006810|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110356_PI430048170 0.1839409236006391.11721970361963 8.48965813021672
8.24889373221891 8.35696982423006 P P P 8.31887476836268 8.22313008428273
8.07333584465542 P P P LNCV6_110356_PI430048170 mRNA
GAACACTGCACTAAGATTTGGTTTGCCAAATCAGATTCTTTGGTCAAGAGTCAGTTTGGG NM_024881RefSeq chr19
- 16549836 16572382 SLC35E1 79939 "solute carrier family 35, member E1"
GO:0006810|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128437_PI430048170 0.1130990813512451.24247970179325 8.62448934179145
8.67862237937629 8.43728663188675 P P P 8.48281944984893 8.25627105061193
8.03840371436018 P P P LNCV6_128437_PI430048170 mRNA
ATGTAAAATAATTGGCCCTCTCCATCTTTTCTCATTTCATGTGTCAGGTAGTTTTTCTGA NM_000794RefSeq chr5 -
175440671 175444160 DRD1 1812 dopamine receptor D1

GO:0005515|GO:0001659|GO:0043268|GO:0060291|GO:0060292|GO:0006606|GO:0019226|GO:0019228|GO:0051
584|GO:0046323|GO:0051482|GO:0007613|GO:0001662|GO:0001661|GO:0001588|GO:0021542|GO:0030335|GO:0
007617|GO:0060134|GO:0051968|GO:0035240|GO:0007416|GO:0030432|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136958_PI430048170 0.2744804501664170.8021372426662090.510202575033674
0.6642488954509650.572411115410089A A A 0.8749135306865771.21695931924065
0.532630984610337A A A LNCV6_136958_PI430048170 mRNA
TATCCTGATGGACTTCTGGAAAACTGTGACTGGGGTTCAAGAGTTTAAACAGGGGCTACT NM_031491RefSeq chr12
- 7123683 7128870 RBP5 83758 "retinol binding protein 5, cellular"
GO:0005215|GO:0005737|GO:0016918|GO:0006810|GO:0005501|GO:0019841|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135628_PI430048170 0.0578471317761154 1.42325412896663 5.83358719047101
6.1179216232908 5.94916701443501 P P P 5.61837067142419 5.58328960793245
5.13780548811105 P P P LNCV6_135628_PI430048170 mRNA
TTTCTGGTATGACATGGAATACGACCTCAAGTATAGTTACTTCCAGCTGCTCGACTCCCT NM_001114632 RefSeq
chr15 + 41828084 41837587 JMJD7 100137047 jumonji domain containing 7 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140038_PI430048170 0.0300238130561107 1.08967625544698 0.358558490382017
0.4487964884915510.390141022257664A A A 0.2629901625074720.296076064546333
0.267967623097562A A A LNCV6_140038_PI430048170 mRNA
TTGTTTTTCTCACTAGCATTCATTCTGTGGCCTTGATGACTTCAGTGAGCCAAGAACTCG NM_001099433 RefSeq
chr4 - 6026198 6200591 JAKMIP1 152789 "janus kinase and microtubule interacting protein 1,
transcript variant 1"
GO:0008017|GO:0005515|GO:0005737|GO:0050890|GO:0030529|GO:0003723|GO:0005874|GO:0050811|GO:0019
894|GO:0019900|GO:0015031|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140551_PI430048170 0.8858615618703840.9621313456691578.21103588766144
8.31543995939194 8.25334649177063 P P P 7.90464495705726 8.48162898853338 8.4884837447637
P P P LNCV6_140551_PI430048170 mRNA
ATCCCATTGCAAGGAGAGGAACTGAACGGAGTAATTATTCTACTCTTCTTTTTACATAAA NM_012405RefSeq chr1
- 6221192 6235984 ICMT 23463 isoprenylcysteine carboxyl methyltransferase
GO:0008284|GO:0005783|GO:0046578|GO:0001701|GO:0001889|GO:0004671|GO:0008140|GO:0035264|GO:0016
020|GO:0006481|GO:0006612|GO:0003880|GO:0005789|GO:0016021|GO:0006464 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138689_PI430048170 0.00618732070719799 1.5890927068096 4.57907945451007
4.85020601093025 4.59181652787766 P P P 4.01099044015076 4.1595356777688
3.84544020392415 P P P LNCV6_138689_PI430048170 mRNA
AGCCATGCGGGAGCATTGGTGGTTATTTTCTTTGTATTGTGTTTGTTCTTTGTTCCTGGGNM_021946RefSeq chrX +
130005187 130058083 BCORL163035 BCL6 corepressor-like 1
GO:0006355|GO:0005737|GO:0005886|GO:0005654|GO:0006351|GO:0016568 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139341_PI430048170 0.2156684029954571.07601155245031 0.537040890880168
0.3557955677393490.515217745185018A A A 0.2906182837030370.377402171198763
0.426389469738493A A A LNCV6_139341_PI430048170 mRNA
CCTGCATGTGGAAACATGAAGATGTTTTCACTTTGTGTCTAGGTTTATGTACGTGAACAA NM_033053RefSeq chrX
- 72872024 72875788 DMRTC1 63947 DMRT-like family C1
GO:0000987|GO:0006355|GO:0003700|GO:0007548|GO:0005634|GO:0042803|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_116144_PI430048170 0.3898145396164720.8560302754690082.93805790398478
3.55909596610387 3.14825388236309 A P P 3.69905573192895 3.16470787799984

3.47555941091687 P P P LNCV6_116144_PI430048170 mRNA
TCAAAATGCAGTTCAGACAAGAGCAACACAGAGATCTCAAACATTAAAACTAAGCTGTGC NM_030621 RefSeq chr14
- 95086227 95158010 DICER1 23405 "dicer 1, ribonuclease type III, transcript variant 2"
GO:0060576|GO:0005515|GO:0010467|GO:0070173|GO:0051216|GO:0045069|GO:0004530|GO:0048536|GO:0009
791|GO:0016442|GO:0031069|GO:0048608|GO:0051607|GO:0004525|GO:0048255|GO:0014835|GO:0010660|GO:0
005793|GO:0000122|GO:0004521|GO:0021889|GO:0055013|GO:0003725|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130238_PI430048170 0.9203540073011050.99617858744075 0.475152345528021
0.5027384504248150.40324135905105 A A A 0.54091305413305 0.423144983714299
0.432469698410635 A A A LNCV6_130238_PI430048170 mRNA
GTCAGATCACTCTATGACGATCTGGAAGATCATCCAAATGTGATTGAAAGACCTGGAGCG NM_001004319 RefSeq
chr1 - 156298623 156299637 VHLL 391104 von Hippel-Lindau tumor suppressor-like NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_69834_PI430048170 0.4718504879056160.9521480454327075.44934132207797 5.21068017443204
5.25966499987288 P P P 5.2723469874781 5.44528627606585 5.41947815996531 P P P
LNCV6_69834_PI430048170 mRNA
TCCCCACTTAAGCACTTTGTCACTGCCAAGAAGAAGATCAATGGCATTTTTGAGCAGCTG NM_014874 RefSeq chr1
+ 11980180 12013515 MFN2 9927 "mitofusin 2, transcript variant 1"
GO:0006986|GO:0005515|GO:0006626|GO:0003924|GO:0005741|GO:0048593|GO:0034497|GO:0005829|GO:0005
739|GO:0046580|GO:0008053|GO:0015630|GO:0007050|GO:0031625|GO:0051646|GO:0006914|GO:0001825|GO:0
006915|GO:0048662|GO:0005525|GO:0006184|GO:0007596|GO:0031306|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134475_PI430048170 0.1634508710797680.9397188753478340.244366387645801
0.30370781536003 0.292006313106261 A A A 0.4505283934325440.349925845565466
0.305558319091518 A A A LNCV6_134475_PI430048170 mRNA
ATTTGTGCACCACTGGGACCCAAGTACATGGCTGAAGCTGTCCAGCTGCAGAGAGTGGTG NM_001039617 RefSeq
chr3 - 196197451 196211429 ZDHHC19 131540 "zinc finger, DHHC-type containing 19"
GO:0005783|GO:0008152|GO:0008270|GO:0016021|GO:0019706 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132599_PI430048170 0.15356673007737 1.30905170307046 7.13104134595296
6.84408097906291 6.80390335648667 P P P 6.16527956638709 6.80909929191329
6.58934101644799 P P P LNCV6_132599_PI430048170 mRNA
AACTTTGCCTAGAGAAGTCACACTCCCCAATTCAGGATGTCCCCAAGAAGATATGCAAAG NM_005879 RefSeq chr3
- 49828594 49856559 TRAIP 10293 TRAF interacting protein
GO:0035556|GO:0005515|GO:0007165|GO:0048471|GO:0004842|GO:0016567|GO:0008283|GO:0016874|GO:0005
730|GO:0006915|GO:0008270|GO:0005057 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131259_PI430048170 0.4674196047609711.802041490641 0.400582922022941
2.22350461954544 0.29727718319059 A A A 0.3973920865937860.446079213143176
0.407762249800488 A A A LNCV6_131259_PI430048170 mRNA
GCTTAGATTGAATAGGTTTCTGCTCCTTGACAAGAGATATGGCCTGAATAAAATGAATTT NM_001039845 RefSeq
chr2 - 206737764 206765549 MDH1B 130752 "malate dehydrogenase 1B, NAD (soluble), transcript
variant 1" GO:0006099|GO:0005975|GO:0016615|GO:0006108|GO:0016616 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_64670_PI430048170 0.4631611857725121.5421363756591 0.5485120867707282.36200369037868
1.23808500522426 A A A 0.4121949358936850.565859209162501 1.58525782222751 A A A
LNCV6_64670_PI430048170 mRNA
CCTTATTGGAACAATGGAAAGAGCCTGAAGTGACAGTGAGGAAAGATGGAAGAAGATGGT NM_001099438
RefSeq chr19 + 34926902 34945172 ZNF30 90075 "zinc finger protein 30, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_142707_PI430048170 0.6408343791348831.03545821993352 11.1742298553302
11.1810782148454 11.3965889057411 P P P 11.1291842576542 11.1415862738244
11.3324506994541 P P P LNCV6_142707_PI430048170 mRNA
CAAATATGCAAACCAGGATTTCCTTGACTTCTTTGAGAATGCAAGCGAAATTAAATCTGA NM_175868RefSeq chrX
- 152766146 152769716 MAGEA6 4105 "melanoma antigen family A6, transcript variant 2"
GO:0005515|GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130028_PI430048170 0.1663859864106060.4626328106080882.63479622269894
0.3332633490284641.33709107095717 A A A 2.65290461511195 3.01634461975191
2.85375165211371 A P P LNCV6_130028_PI430048170 mRNA
CAGAAGTGTGAAGAATATGGCAAAACTTTAATTCCTATACCTTATTGCACAGGAAAGCAT NM_001160183 RefSeq
chr7 + 64794387 64833681 ZNF138 7697 "zinc finger protein 138, transcript variant 2"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135885_PI430048170 0.00511259700300871 3.95323079418505 2.53636466279945
2.13203607340881 2.09303535165958 A A A 0.2839567678532240.278641633773157
0.292692240473172 A A A LNCV6_135885_PI430048170 mRNA
GGGCATGTGGAAATGGTCAGTTATATTCAGGCAATTAAAAAACCTAATTATATGGGGTTT NM_001145434 RefSeq
chr19 + 52369916 52385793 ZNF880 400713 zinc finger protein 880
GO:0005622|GO:0006355|GO:0003700|GO:0003676|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139745_PI430048170 0.1731085019782280.9063587330440728.32490951234894
8.34996210423419 8.2901113362378 P P P 8.33589878159765 8.47410360262901 8.5714808882268
P P P LNCV6_139745_PI430048170 mRNA
TTGGTGCCAAGAAAATAAAAAAGCTATTATCAGGTCTCCTAACTACCCCAGTTTGTAAGG NM_138704RefSeq
chr15_KI270905v1_alt - 1543699 1545367 NDNL2 56160 necdin-like 2
GO:0005515|GO:0005737|GO:0000781|GO:0006281|GO:0030915|GO:0031398|GO:0006310|GO:0005634|GO:0040
008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119959_PI430048170 0.0490499502966272 2.4333314279352 2.63217230411694
2.06972490545084 1.54916066766856 A A A 0.5014439010552160.379489180279501
1.46422920621958 A A A LNCV6_119959_PI430048170 mRNA
TTTACAAGTCATTCAAACCCCCCAGGGCACCTACGTGCAAGGGGTCCCAGTGTTCCTCAC NM_198441RefSeq chr13
+ 57160631 57163653 PRR20A NA proline rich 20A NA . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_138902_PI430048170 0.0170798662100023 0.4124409401210175.37322008333255
4.74117500212132 5.28265947925247 P P P 6.453826393303 6.3363251385215
6.51185697199882 P P P LNCV6_138902_PI430048170 mRNA
ATGGATGTGTATGTGTACATTTATAAGAACCAGTATGGATACATCCATTCACTGTGGTAC NM_006947RefSeq chr4
+ 56467595 56503681 SRP72 6731 "signal recognition particle 72kDa, transcript variant 1"
GO:0005786|GO:0010467|GO:0005886|GO:0005783|GO:0006614|GO:0042493|GO:0008312|GO:0005730|GO:0006
412|GO:0005829|GO:0005737|GO:0005047|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140621_PI430048170 0.3236054795916 1.50440497312756 1.5629498888314
1.04818014176855 0.248990241375071 A A A 0.5817286849153370.411094279203654
0.380861855681873 A A A LNCV6_140621_PI430048170 mRNA
AAACATATAAGAGGCTCCCTCTTAACACGGCACTTAGATACGTGCTATTCCACCTTTCCT NM_153443RefSeq
chr19_KI270938v1_alt + 707065 719117 KIR3DL3 115653 "killer cell immunoglobulin-like receptor, three
domains, long cytoplasmic tail, 3" GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141994_PI430048170 0.0177103538434076 1.34434610664827 12.4163714017612

12.3532261458086 12.2102084809755 P P P 11.8834276070807 11.919524693441
11.9035767341738 P P P LNCV6_141994_PI430048170 mRNA
AGACTCCTTGTGTCCAACGGGAATAGGAAGAATTAGTTACTGACTTCACCTGAGAAAAAA NM_001304999 RefSeq
chr17 - 81665035 81666637 OXLD1 339229 "oxidoreductase-like domain containing 1, transcript
variant 4" GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131943_PI430048170 0.00642835173876359 0.41297549257846 5.17715871634671
4.7772890735869 5.40871718169342 P P P 6.21528975549824 6.35432996782392
6.65476912264072 P P P LNCV6_131943_PI430048170 mRNA
TCTAAACCAGATTTCATTTCTTTTATTGTTTTATGTGCCAAACCACGAAGTGCATTGGGC NM_006717 RefSeq chr9
+ 88388381 88478707 SPIN1 10927 spindlin 1
GO:0005515|GO:0051321|GO:0007276|GO:0009303|GO:0005819|GO:0005730|GO:0030177|GO:0007275|GO:0005
634|GO:0035064|GO:0016055|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_5528_PI430048170 0.5109456833777041.24891170544541 0.3213279051018981.26264382343457
0.321381036636545 A A A 0.4428954715455330.3476180569720950.367720140702274 A A A
LNCV6_5528_PI430048170 mRNA
TCCTCTGTCAACATCAAAGAGCACATTTACCAGTATAGCTTGCATAGTCAATATTTGGTA NM_001136112 RefSeq
chr11 - 104994239 105023168 CASP5 838 "caspase 5, apoptosis-related cysteine peptidase, transcript
variant f"
GO:0072559|GO:0043005|GO:0072557|GO:0072558|GO:0050727|GO:0097194|GO:0006915|GO:0042981|GO:0035
234|GO:0070269|GO:0004197|GO:0005737|GO:0021762|GO:0050718|GO:0097110|GO:0006508|GO:0043025|GO:0
008234|GO:0071260|GO:0097169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130931_PI430048170 0.0116578453006831 1.67221742603415 10.0192620075465
10.2839109718038 10.3637556879905 P P P 9.22222966617277 9.62148729425496
9.58711179194266 P P P LNCV6_130931_PI430048170 mRNA
TTTAGCATCTGACAGGTGTTTACAAAAAAGTGGTTGTCGCACTGGGAAGTGGAGTGATGG NM_016172 RefSeq chr9
- 135932968 135961380 UBAC1 10422 UBA domain containing 1
GO:0005515|GO:0005737|GO:0016567|GO:0005794|GO:0005886|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138101_PI430048170 0.4617023830119411.7067293412153 0.31919340574038
2.14788311885408 0.473039442670624 A A A 0.3008076586349860.271662639511694
0.767138075417765 A A A LNCV6_138101_PI430048170 mRNA
ATAGAGGTAGACTCAGACACAGAGACCATCTTCAAGGCCTTTCTCTGTATGAGGACATCA NM_001099694 RefSeq
chr19 + 52453575 52516878 ZNF578 147660 zinc finger protein 578
GO:0006355|GO:0005737|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132753_PI430048170 0.4473675493240882.95944901366199 0.357383187692403
3.23420696255695 0.385495646395501 A P A 0.5372349283311210.469608521597119
0.28455914273224 A A A LNCV6_132753_PI430048170 mRNA
CTTGACAATGGGTCTTCTTCCATTACACCTTCTTTATATTTTAAAGGCCTGTGAATATAC NM_021233 RefSeq chr1 +
84398531 84415008 DNASE2B 58511 "deoxyribonuclease II beta, transcript variant 1"
GO:0005622|GO:0006309|GO:0005576|GO:0004531|GO:0005764 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129413_PI430048170 0.65734779258239 0.8980267121784782.47090470434607 1.8994424850425
0.559922477209533 A A A 1.42625777606735 2.20128621341613 2.22742328243215 A A A
LNCV6_129413_PI430048170 mRNA
GTCTGCTTTCACCTTCCATCCTTCTCATAATCCCAATAAAACAACACTTGAAACTATTTA NM_001282855 RefSeq
chr7 - 123452181 123532948 IQUB 154865 "IQ motif and ubiquitin domain containing, transcript
variant 2" GO:0001669|GO:0031514|GO:0060271|GO:0007224 . NA - . NA NA NA NA NA NA NA
NA NA

LNCV6_64491_PI430048170 0.1480560216685 1.43529918624722 1.87837660716827 2.44947492036582
2.27915379846534 A A A 1.54155729533723 1.30926448532033 2.12424585050733 A A A
LNCV6_64491_PI430048170 mRNA
ATGTCGTATTTTGGGGAGCATTTTTGGGGCGAGAAAAATCATGGCTTTGAGGTCCTGTAC NM_001161357 RefSeq
chr19 + 17747717 17788568 FCHO1 23149 "FCH domain only 1, transcript variant 1"
GO:0072583|GO:0005515|GO:0005905|GO:0005886|GO:0035612|GO:0030136|GO:0048268 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140677_PI430048170 0.00499970742970302 0.7384631327707558.00566786681878
8.08635812020751 8.07119864884162 P P P 8.42565105941293 8.59008017760649
8.45559977212521 P P P LNCV6_140677_PI430048170 mRNA
ATTTTTATTTTTGTTCATCTGCTGCTGTTTACATTCTGGGGGGTTAGGGGGAGTCCCCCT NM_014203RefSeq chr19
+ 49766922 49807112 AP2A1 160 "adaptor-related protein complex 2, alpha 1 subunit, transcript variant
1"
GO:0072583|GO:0005515|GO:0035615|GO:0005886|GO:0007268|GO:0006886|GO:0005829|GO:1900126|GO:0016
323|GO:0019886|GO:0016324|GO:0007173|GO:0007411|GO:0016032|GO:0048011|GO:0019901|GO:0048013|GO:0
030122|GO:0042059|GO:0008022|GO:0006895|GO:0050690|GO:0006897|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143003_PI430048170 0.1404069842447840.69702810089138712.2328147263732 12.215914856913
12.2134726958834 P P P 12.3705908334481 13.0839177757257 12.6807493399114 P P P
LNCV6_143003_PI430048170 mRNA
ATCTCTTCCAAGGCTATGGGAATCATGAACTCCTTCGTCAACGACATCTTTGAGCGTATC NM_003521RefSeq chr6
+ 27815043 27815489 HIST1H2BM 8342 "histone cluster 1, H2bm"
GO:0046982|GO:0006334|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0003677|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128120_PI430048170 0.3792494157173190.9620326211056840.278694527363168
0.4102035951476340.306406560350961A A A 0.4666365161251450.358249340405909
0.337957028550692A A A LNCV6_128120_PI430048170 mRNA
TTGCCCTTACTGCAAAGAGAAAGTTGATTTGAAGAGGATGATCAGTAATCCCTGGGAGCG NM_173662RefSeq chr4
- 153710159 153760235 RNF175 285533 ring finger protein 175
GO:0016567|GO:0000139|GO:0005789|GO:0008270|GO:0016021|GO:0030433|GO:0030968 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_54930_PI430048170 0.5779439405110421.04992816769589 9.7793099590145 9.8156838659983
9.56050454610503 P P P 9.68769594543424 9.48210065108443 9.77255442574807 P P P
LNCV6_54930_PI430048170 mRNA
TCCTAAACGTCCCAAGGAGGCAGAAAACCCTGAAGGAGAGGAGAAGGAGGCAGCCACCTT NM_004494RefSeq
chr1 - 156742106 156751751 HDGF 3068 "hepatoma-derived growth factor, transcript variant 1"
GO:0008283|GO:0001106|GO:0000122|GO:0003677|GO:0005615|GO:0006351|GO:0030968|GO:0001222|GO:0007
165|GO:0005737|GO:0000166|GO:0017053|GO:0005654|GO:0006987|GO:0044267|GO:0008083|GO:0008201 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137402_PI430048170 0.6372734799674961.0838592234144 6.73366517355791
6.30256773536855 6.38021829381631 P P P 5.87122354564547 6.59253482608484
6.53650180703873 P P P LNCV6_137402_PI430048170 mRNA
TACGCCTTTGTGTCTGGCATTTGTTTAAGAAAATGAAATGAAGGAAACACTGTGCAATGT NM_194272RefSeq chr15
- 64739895 64775571 RBPMS2 348093 RNA binding protein with multiple splicing 2
GO:0000166|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130814_PI430048170 0.00758557389476342 0.4676161600438764.27652979215855
4.13874540089923 4.47420217314439 P P P 5.15824963007908 5.29805718959245
5.68910800009867 P P P LNCV6_130814_PI430048170 mRNA
CTCAGTCAGTGCCTAACTGCACATACAAAAATAAAACCTTCTTTCTGTAATCTACCAAAA NM_173505RefSeq chr18

- 23598925 23662885 ANKRD29 147463 ankyrin repeat domain 29 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_10483_PI430048170 0.0653313990958611 1.41668993560656 3.64621687243447 3.49935387341201 3.14347023738324 P P P 2.79211021859078 3.18535213018654 2.81444846394081 P P P LNCV6_10483_PI430048170 mRNA GGACAGAACTTCCACTTTGAATAATGGAAGTTAGAACAATGAATTTCACAGGGGAATAAA NM_001297778 RefSeq chr1 + 9942922 9985498 NMNAT1 64802 "nicotinamide nucleotide adenylyltransferase 1, transcript variant 2"
GO:0005515|GO:0000309|GO:0006766|GO:0004515|GO:0019674|GO:0006767|GO:0005654|GO:0005634|GO:0044281|GO:0009435|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128173_PI430048170 0.1862463904914690 0.8354103378344587.91236304566577 7.60827342932758 7.50421941152094 P P P 7.71990077559493 8.02705486870957 8.06389962171201 P P P LNCV6_128173_PI430048170 mRNA AAGGCAAAACTCAACAGCCCCTGGAGCTGCGCTTGTGGTGGAGCTGGACCCTGAAATTAC NM_058219 RefSeq chr16 - 70250230 70251930 EXOSC6 118460 exosome component 6
GO:0045006|GO:0010467|GO:0045190|GO:0006364|GO:0005730|GO:0043928|GO:0004532|GO:0000178|GO:0005829|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142436_PI430048170 0.0158201564191782.08818914333954 9.3049854964958 9.38606976865699 9.34486432874506 P P P 7.99668212185776 8.31742075434088 8.49309554981767 P P P LNCV6_142436_PI430048170 mRNA AGATGAAGTAAATGCAGTGTTCTACTGCCTGATGTGAAAGAGAGCTATGTATGATAATTA NM_018140 RefSeq chr5 + 612289 653551 CEP72 55722 centrosomal protein 72kDa
GO:0005515|GO:0005813|GO:0006996|GO:0000086|GO:0007051|GO:0000278|GO:0033566|GO:0042802|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131548_PI430048170 0.4260537109732311.46182291738331 0.626053120329495 1.15373217283494 2.11820593439495 A A A 1.35498994428886 0.633363937269828 0.524638766395026 A A A LNCV6_131548_PI430048170 mRNA CTTTGTTGTCCTTTGAGCTTTCTGTTATGTGCCTATCCTAATAAACTCTTAAACACATTG NM_012072 RefSeq chr20 - 23079355 23086340 CD93 22918 CD93 molecule
GO:0005515|GO:0006909|GO:0005886|GO:0009986|GO:0001849|GO:0005509|GO:0016337|GO:0042116|GO:0016023|GO:0016032|GO:0030246|GO:0004872|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144821_PI430048170 0.00588660039553886 0.4608986618508249.52752401994982 9.37651924517171 9.65011372427909 P P P 10.4117418854803 10.5660622857445 10.8982021789912 P P P LNCV6_144821_PI430048170 mRNA CCAGCAGTGGATGTTACTCCAGGAAAATGCAGGATTAAAATTGTCCTTGTGTATAAAAAA NM_003677 RefSeq chr12 + 122752820 122771064 DENR 8562 density-regulated protein
GO:0005515|GO:0003674|GO:0002192|GO:0001731|GO:0003743|GO:0032790|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90041_PI430048170 0.0276132850336816 1.32325778269805 9.41482220606492 9.40704110804491 9.54286285130348 P P P 8.87149767391928 9.105244480411 9.16351990728663 P P P LNCV6_90041_PI430048170 mRNA ACAAATTGCTGCTTGTCCAAATCAGGATCCACTGCAAGGAACAACAGGCCTTATTCCACT NM_000636 RefSeq chr6 - 159681722 159693321 SOD2 6648 "superoxide dismutase 2, mitochondrial, transcript variant 1"
GO:0042645|GO:0042542|GO:0045599|GO:0009409|GO:0006801|GO:0006749|GO:0033591|GO:0034021|GO:0009791|GO:0048678|GO:0010043|GO:0010042|GO:0042802|GO:0007507|GO:0043524|GO:0005759|GO:0019430|GO:0051602|GO:0032496|GO:0010332|GO:0001315|GO:0070062|GO:0004784|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131388_PI430048170 0.1406069250573531.03259564224878 0.331019415140847 0.334959033688876 0.273424640457926 A A A 0.2623041973422690.276280627347565

0.262766961490364 A A A LNCV6_131388_PI430048170 mRNA
TACTATTTGTCTGTCAGCCTTTCAGTCATTCTTTTCTTTTGGAAAGGTAGGAGGCTGCCC NM_031960 RefSeq
chr17_JH159146v1_alt - 246639 247812 KRTAP4-8 728224 keratin associated protein 4-8
GO:0042633|GO:0007568|GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134136_PI430048170 0.00646773908480001 0.542734166764381 10.5067003136398
10.1364890283494 10.1966229441284 P P P 10.9195543630793 11.2370286662262
11.3254430086982 P P P LNCV6_134136_PI430048170 mRNA
CCTGCTGCTTCTGAGGACTTAGGTATTTTAAGCGAATAAACTGACAGCTTTGAGGAATGA NM_001083961 RefSeq
chr19 + 36054880 36105110 WDR62 284403 "WD repeat domain 62, transcript variant 1"
GO:0005737|GO:0000922|GO:0021987|GO:0005654|GO:0005634|GO:0022008 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141376_PI430048170 0.216731326779233 1.2336255940061 1.02178185628544
0.505694323735257 0.561764072437397 A A A 0.320407597436755 0.412612817237517 0.4993506415197
A A A LNCV6_141376_PI430048170 mRNA
TTTCATCACTCCTTCCTAGTTCTACTGTTCAAGCTTCTGAAATAAACAGGACTTGATCAC NM_002060 RefSeq chr1
+ 34792997 34795747 GJA4 2701 "gap junction protein, alpha 4, 37kDa"
GO:0005515|GO:0001568|GO:0005887|GO:0007267|GO:0007043|GO:0006810|GO:0005921|GO:0003158|GO:0048
265|GO:0006816|GO:0005922 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134140_PI430048170 0.380758224887217 1.38255439785907 0.325988179669534
1.32270299869664 0.270150532901985 A A A 0.253326724536869 0.265927592958353
0.255536042236811 A A A LNCV6_134140_PI430048170 mRNA
CTCTCATCTTTAGAACATTTAGACATTAAAGCAAGTTTCTGGTGAGCAATGGAATTCACA NM_144668 RefSeq chr12
+ 121918556 122003926 WDR66 144406 "WD repeat domain 66, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137922_PI430048170 0.206143460957623 0.896921704629765 5.94556627004776
6.16789424862536 5.86796826757539 P P P 6.09045527267908 6.17934961385569
6.19724530095295 P P P LNCV6_137922_PI430048170 mRNA
CTTCTCCAACTTACTATTAGACTAAACCAGAACAAGCAACAAACTGTATTTATGCAAGCA NM_001007231 RefSeq
chr2 + 68734780 68826825 ARHGAP25 9938 "Rho GTPase activating protein 25, transcript variant 1"
GO:0043547|GO:0051056|GO:0007264|GO:0005829|GO:0005096 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139649_PI430048170 0.399879511124103 0.94215528339987 8.12862180196666
8.15395197898217 8.18281873964071 P P P 8.08998905734633 8.35124447918706
8.27030280276705 P P P LNCV6_139649_PI430048170 mRNA
GGGTGTAAATCAGTGTAAACTTGGAGGAGAGATTTTTCTATCATGTAGAGTAGGTATTTT NM_014700 RefSeq
chr16_KI270854v1_alt + 24813 125149 RAB11FIP3 9727 "RAB11 family interacting protein 3 (class II),
transcript variant 1"
GO:0005515|GO:0005813|GO:0017137|GO:0006996|GO:0005815|GO:0030306|GO:0032456|GO:0005509|GO:0030
496|GO:0032154|GO:0042803|GO:0045171|GO:0043231|GO:0005829|GO:0000910|GO:0005654|GO:0055037|GO:0
016192|GO:0055038|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130021_PI430048170 0.314458632402667 1.30326792178979 1.11653232938613
0.285760377083603 0.46354207240149 A A A 0.301584388586367 0.266304452621204
0.289144422489745 A A A LNCV6_130021_PI430048170 mRNA
GATGTAGGCTAACAATGAAAAGTATTTGCCAAACTGAATAAAACTGTCATGGTTACCTTG NM_006566 RefSeq chr18
- 69862955 69957176 CD226 10666 "CD226 molecule, transcript variant 1"
GO:0005515|GO:0008037|GO:0005886|GO:0009986|GO:0019901|GO:0033005|GO:0001816|GO:0007165|GO:0005
178|GO:0005887|GO:0050776|GO:0045954|GO:0002860|GO:0045121|GO:0007155|GO:0060369|GO:0050839|GO:0
002891|GO:0009897. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145156_PI430048170 0.269533644104572 2.273354254332 2.57875632237563

0.4594447339871451.26332862550658 A A A 0.5046805564047840.718080421626932
0.292669155735644A A A LNCV6_145156_PI430048170 mRNA
ATCTTCTGCAAAAGGTTAACCGCTGGAGTGATGCGAGATTAAACAGAGGTGATAAAAATA NM_133463RefSeq chr7
+ 2679521 2715436 AMZ1 155185 "archaelysin family metallopeptidase 1, transcript variant 1"
GO:0006508|GO:0008270|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134292_PI430048170 0.958691453803123 1.00798084949567 2.41937627578683
3.23714202937564 2.70383596470298 A P A 3.13230316526535 2.2280883095952 2.9395835081135
P A P LNCV6_134292_PI430048170 mRNA
CAGAAGAGGTGAATTCAGCCTGATAGTTCAGTATCATTGATCATTCTAGAAGTCACTACT NM_024587RefSeq chr1
- 44653246 44674608 TMEM53 79639 "transmembrane protein 53, transcript variant 1"
GO:0005634|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123985_PI430048170 0.337070249424255 1.93604813605136 0.488537202777098
2.14966545929968 0.403050619945829A A A 0.271265958799626 0.351213324998621
0.283428683311771 A A A LNCV6_123985_PI430048170 mRNA
AAGAGAAAACCGTGAGACTTCCAGATCTTCTCTGGTGAAGTGTGTTTCCTGCAACGATCA NM_000948RefSeq chr6
- 22287243 22297501 PRL 5617 "prolactin, transcript variant 1"
GO:0005515|GO:0007565|GO:0005148|GO:0007595|GO:0005179|GO:0008283|GO:0040014|GO:0005576|GO:0060
397|GO:0007166|GO:0046427 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138268_PI430048170 0.563886721688032 1.07277330826882 10.1811492745472
10.2948163494573 10.6158234851326 P P P 10.239699180268 10.2508042398117
10.3314150520651 P P P LNCV6_138268_PI430048170 mRNA
CAGTTATTCTACCCCCTACCAAGGATATCAGCCTGTTTTTTCCCTTTTTTCTCCTGGGAA NM_015913RefSeq chr1 -
52020131 52056171 TXNDC12 51060 "thioredoxin domain containing 12 (endoplasmic reticulum),
transcript variant 1" GO:0019153|GO:0005788|GO:0045454|GO:0055114 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129674_PI430048170 0.169627325784717 0.7247246136193 12.1545680413324
12.0881948320944 12.5904189440066 P P P 12.3305604540652 12.7986607661151
13.0588726120267 P P P LNCV6_129674_PI430048170 mRNA
CAGGGAACCGTGCAGTGTGCATTTTAAGACCTGGCCTGGAATAAATACGTTTTGTCTTTC NM_012112RefSeq chr20
+ 31739100 31801800 TPX2 22974 "TPX2, microtubule-associated"
GO:0005515|GO:0019901|GO:0060236|GO:0008283|GO:0005874|GO:0005819|GO:0006915|GO:0005634|GO:0005
525|GO:0005524|GO:0032147|GO:0000922|GO:0005737|GO:0007067|GO:0015630|GO:0043203|GO:0005654|GO:0
051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140448_PI430048170 0.426890229655535 1.19889558344778 9.86171661610767
10.1074564367287 9.9258002334004 P P P 10.3191248918259 9.23621243918897
9.29214184078202 P P P LNCV6_140448_PI430048170 mRNA
ACCACAGGGTTAGGGGACAGGAAGCCTGTTCTATTCTCAATAAATCTTACAAAATTCCAA NM_004055RefSeq chr11
+ 77066944 77126152 CAPN5 726 calpain 5
GO:0007165|GO:0005737|GO:0004198|GO:0009986|GO:0006508|GO:0005925|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139857_PI430048170 0.00223791308575073 0.32387374217320811.2143622309933
10.9715231970544 10.8748147648873 P P P 12.5995565011557 12.6717613756345
12.6888390708653 P P P LNCV6_139857_PI430048170 mRNA
TTGGTGATGATTTTGGCAACTTTGGGAATAAATGGCAATTCCCACGGGCTTGGCAAAAAA NM_001130071 RefSeq
chr19 + 55676624 55695767 EPN1 29924 "epsin 1, transcript variant 1"
GO:0007565|GO:0005886|GO:0042059|GO:0005634|GO:0001701|GO:0006897|GO:0008289|GO:0005737|GO:0005
905|GO:0007173|GO:0007219|GO:0048568|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127218_PI430048170 0.0381942363034291 0.53812195008296 3.49109198617437
3.51608164732282 3.49397155383958 P P P 4.5875100133068 4.50980624588951 4.0239401593464

P P P LNCV6_127218_PI430048170 mRNA
TGAGATTGAAAAGGAATCACAAAGGAAGTCCATTGATCCTGCTTTGTCAATGTTGATTAA NM_016649RefSeq chr20
- 13714321 13784886 ESF1 51575 "ESF1, nucleolar pre-rRNA processing protein, homolog (S.
cerevisiae), transcript variant 1" GO:0006355|GO:0005730|GO:0005654|GO:0005615|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129122_PI430048170 0.4500008787420041.40449717108131 1.11036290924851
0.2974633064265171.74866502790876 A A A 1.15022918357568 0.38194835425167
0.358732654642448A A A LNCV6_129122_PI430048170 mRNA
CTAATTGTAAATTGATAAACTTTGCGGATGACATCTGCTCGTAGAATAAACACTTCTTCC NM_006393RefSeq chr10
- 20779973 20897602 NEBL 10529 "nebulette, transcript variant 1"
GO:0008092|GO:0005515|GO:0071691|GO:0030018|GO:0001725|GO:0051015|GO:0031005|GO:0008307|GO:0005
523|GO:0070062|GO:0031674 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57156_PI430048170 0.00906267598932438 1.1721970559627 8.20811898690445
8.32819327548074 8.26579661227379 P P P 8.10242621853135 8.02385847489015
7.98830512474563 P P P LNCV6_57156_PI430048170 mRNA
CTATACACACTGACAGAGACAGCAATACCCCACCCCCCATATTAAATAAATGTCTTCACC NM_006458RefSeq chr11
- 6448612 6473984 TRIM3 10612 "tripartite motif containing 3, transcript variant 1"
GO:0005515|GO:0005737|GO:0004842|GO:0016567|GO:0008270|GO:0015031|GO:0008022|GO:0005769|GO:0007
399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143721_PI430048170 0.1283867175506290.8115424457270284.36041484724571
4.77366733977629 4.73697208627928 P P P 5.02676281136821 4.81000601312611
4.96464514471086 P P P LNCV6_143721_PI430048170 mRNA
AGGTTATATAGTTTTCAGTGGGAGGGGTTGGGATGGGTAATCTCATTGTTACATATAGCA NM_201999RefSeq chr4
- 139057716 139139476 ELF2 1998 "E74-like factor 2 (ets domain transcription factor), transcript variant
1"
GO:0043565|GO:0005515|GO:0005737|GO:0003700|GO:0006366|GO:0006357|GO:0000981|GO:0005654|GO:0005
634|GO:0045893|GO:0045892|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130778_PI430048170 0.7523307960430741.03994994323273 9.45381468058748
9.41206462103436 9.79309593327418 P P P 8.68984280640552 9.5413029027639
10.0006478931987 P P P LNCV6_130778_PI430048170 mRNA
GCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTTAAGTATCATCTCTTATCTAAA NM_199204RefSeq chr2
+ 169067034 169096167 DHRS9 10170 "dehydrogenase/reductase (SDR family) member 9, transcript
variant 2"
GO:0004022|GO:0008209|GO:0042904|GO:0042572|GO:0042448|GO:0030855|GO:0047035|GO:0005789|GO:0030
176|GO:0016854|GO:0004745|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131469_PI430048170 0.0245789249005536 1.33285536400215 12.5576320221553
12.5272304268431 12.526506737871 P P P 12.0089687728821 12.1010219277538
12.2479132762512 P P P LNCV6_131469_PI430048170 mRNA
CTTCCGCAAACATCTGATGATGAAAAGAAAGATTTTTGAGACTGCAGCCTATTAATAAAG NM_001267864 RefSeq
chr14 + 77708070 77717601 SLIRP 81892 "SRA stem-loop interacting RNA binding protein, transcript
variant 3"
GO:0000961|GO:0006355|GO:0048471|GO:0001669|GO:0007286|GO:0005634|GO:0036126|GO:0030317|GO:0006
351|GO:0005739|GO:0007338|GO:0070584|GO:0000166|GO:0030529 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129121_PI430048170 0.28298435583429 0.8585893209486130.486701503258393
0.4843227430979390.397183044714665A A A 0.94688666029687 0.526080166167209
0.513462784152322A A A LNCV6_129121_PI430048170 mRNA
GGCAGCTGTGAGATACTAGAAAGCAAAAATTCTTACTCCTATGTCTGTGTCATCCCAGAT NM_153183RefSeq chrX
+ 51332230 51337525 NUDT10 170685 "nudix (nucleoside diphosphate linked moiety X)-type motif 10,

transcript variant 1"
GO:0052846|GO:0052845|GO:0052844|GO:0052843|GO:0043647|GO:0008486|GO:0052848|GO:0052847|GO:0044281|GO:0052840|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131098_PI430048170 0.6955370934271811.06711520048587 2.52289151163662 2.9995016431353 2.89080649467115 A P A 2.27856884616862 3.08330628219419 2.70110054305472 A P P
LNCV6_131098_PI430048170 mRNA
ATTTCAGAGTGGGGAAGTGATAAACTATTTGCCTTCTGGAGCTCTTTGTGAAAAATTAAA NM_015101RefSeq chr1 - 183935831 184037770 COLGALT2 23127 "collagen beta(1-O)galactosyltransferase 2, transcript variant 1"
GO:0030198|GO:0050211|GO:0005788 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74948_PI430048170 0.4965838106424780.9045590771856134.21556781490985 4.67003811218302 4.30072374626656 P P P 4.50039214793995 4.79433432794784 4.32828824221485 P P P
LNCV6_74948_PI430048170 mRNA
AGAAAGCGCAGCCAGGCGGCTGCTCGGCGTTCTCTCAGGTGACTGCTCGGAGTTCTCCCA NM_003264RefSeq chr4 + 153684288 153706090 TLR2 7097 toll-like receptor 2
GO:0005515|GO:0032755|GO:0034123|GO:0042995|GO:0006691|GO:0032757|GO:0042497|GO:0042498|GO:0002752|GO:0002755|GO:0042495|GO:0042496|GO:0044130|GO:0031663|GO:0032728|GO:0032868|GO:0038124|GO:0046982|GO:0009986|GO:0032760|GO:0038123|GO:0034134|GO:0042834|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131468_PI430048170 0.4627552542909350.8863549723083537.48259165387637 7.42334355709861 7.83248129814076 P P P 7.8974535260702 7.42416432882351 7.92133813717558 P P P LNCV6_131468_PI430048170 mRNA
AAACTGTGTTTATATTTGGCCCTGCCATTATAAATAAAGACACGTGCTGCTGTCAAAAAA NM_002064RefSeq chr5 - 95813848 95822873 GLRX 2745 "glutaredoxin (thioltransferase), transcript variant 1"
GO:0015949|GO:2000651|GO:0009055|GO:0005634|GO:0055086|GO:0015038|GO:0044281|GO:0005829|GO:0005739|GO:0045838|GO:0047485|GO:0080058|GO:0045454|GO:0055114|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143214_PI430048170 0.1440329302267721.1005873532818 0.516475626155686 0.6790453957490980.621360800796745 A A A 0.3563547326005270.484276076679247 0.55888670886198 A A A LNCV6_143214_PI430048170 mRNA
GTGCAGAAATATTGACAAATGCTGGCCAGCTTTATCTTCCTATATCCTTCATTAAAAGTA NM_144969RefSeq chrX - 75368426 75523502 ZDHHC15 158866 "zinc finger, DHHC-type containing 15, transcript variant 1"
GO:0018345|GO:0005794|GO:0016188|GO:0016409|GO:0008270|GO:0016021|GO:0019706|GO:0070062|GO:0045184 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141248_PI430048170 0.0769901282512156 0.7667670383134556.20675882742882 6.11304294057193 6.24284376056051 P P P 6.32354556106196 6.66394744295534 6.69872165725449 P P P LNCV6_141248_PI430048170 mRNA
CTCATAAAAGGACTCTCAGCCTCTTGGCAATCATAAATATTAAAGTCGGTTTATCCAGGC NM_007098RefSeq chr22 - 19179473 19291716 CLTCL1 8218 "clathrin, heavy chain-like 1, transcript variant 1"
GO:0005515|GO:0005802|GO:0030132|GO:0030135|GO:0030136|GO:0005819|GO:0006886|GO:0009653|GO:0006898|GO:0007165|GO:0005905|GO:0007067|GO:0016020|GO:0005198|GO:0046326|GO:0030130|GO:0004871|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100244_PI430048170 0.0353155267039274 0.7417951488475753.1528109928209 3.47287092291092 3.14569223527251 A P P 3.81347423855355 3.71456260092838 3.54850764793442 P P P LNCV6_100244_PI430048170 mRNA
AAAGCTAAATTTCCACAAAGAACAAGAACTTGACCATCTCCTTTTTGATCTGAAGACTAG NM_152621RefSeq chr4 + 107893263 107915047 SGMS2 166929 "sphingomyelin synthase 2, transcript variant 1"
GO:0006665|GO:0033188|GO:0005794|GO:0005886|GO:0006686|GO:0030148|GO:0045203|GO:0044281|GO:0047493|GO:0016310|GO:0030173|GO:0005887|GO:0016301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138807_PI430048170 0.141285194560967 0.876214145035476 0.365159662399015

0.3702954286736480.331076071177081A A A 0.5422202378649040.679717442022054
0.403645846151962A A A LNCV6_138807_PI430048170 mRNA
CAAGCATGTAAACACCAACTGGTCCATACCCATTCATTAATAAACTTCTTAAGTGCAAGA NM_001261820 RefSeq
chr6 - 35118070 35141410 TCP11 6954 "t-complex 11, testis-specific, transcript variant 6"
GO:0007275|GO:0016021|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135924_PI430048170 0.00431368343612092 2.33008541921755 9.49126090211105
9.49090250805726 9.42948175133657 P P P 8.05655209912064 8.35335850818478
8.32336038560489 P P P LNCV6_135924_PI430048170 mRNA
AGGCTGTCGCCATGTGGAAAGAGTAACTCACAATTGCCAATAAAGTCTCATGTGGTTTTA NM_001012271 RefSeq
chr17 + 78214195 78225635 BIRC5 332 "baculoviral IAP repeat containing 5, transcript variant 3"
GO:0008017|GO:0005515|GO:0004842|GO:0042803|GO:0042802|GO:0000910|GO:0043027|GO:0048037|GO:0046
982|GO:0005814|GO:0005819|GO:0031536|GO:0030496|GO:0051303|GO:0045931|GO:0000777|GO:0008270|GO:0
000278|GO:0019899|GO:0045892|GO:0000775|GO:0051301|GO:0005881|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127878_PI430048170 0.4291304743317850.6446511093141692.16588530844161
0.5517661861214771.96689061904759 A A A 2.27846407869518 1.28100034603243
3.00312617671259 A A P LNCV6_127878_PI430048170 mRNA
GGGAAGGGGAGACTGTAAAAACAGAAAAATGTAAATGCTGCCTTTATGGTATAAAACTGT NM_020787 RefSeq chr17
- 16620733 16653853 ZNF624 57547 zinc finger protein 624
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131201_PI430048170 0.3397680674809290.8065114771738074.22445322979719 5.062807960236
4.88881661953982 P P P 5.23122546958191 5.21403644794013 4.73738337422057 P P P
LNCV6_131201_PI430048170 mRNA
CAGGGCCCTGTTTTTTCCATATTTAAAGCCAATTTTTATTACTCGTTTTGTCCAACGTAA NM_002082 RefSeq chr5 +
177426685 177442849 GRK6 2870 "G protein-coupled receptor kinase 6, transcript variant 2"
GO:0005515|GO:0008277|GO:0004703|GO:0016020|GO:0038032|GO:0006468|GO:0016055|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139429_PI430048170 0.7167278313236161.06345676025609 6.15881936653405
6.27344163325708 5.74082360771625 P P P 5.76494530448914 6.32921277505707
5.79252205061619 P P P LNCV6_139429_PI430048170 mRNA
GGAGTTCTTAAAGTGTTTTTGGAGAATGTAATCCGCGATGCAGTTACCTACACGGAGCAC NM_003546 RefSeq chr6
- 27873147 27873511 HIST1H4L 8368 "histone cluster 1, H4I"
GO:0005515|GO:0010467|GO:0006325|GO:0005634|GO:0045653|GO:0000723|GO:0000183|GO:0000786|GO:0070
062|GO:0035574|GO:0035575|GO:0046982|GO:0006334|GO:0006335|GO:0005576|GO:0006336|GO:0000228|GO:0
003677|GO:0032776|GO:0034080|GO:0043234|GO:0016020|GO:0045814|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144188_PI430048170 0.0219995565578874 1.62676382505422 6.81966120159846
7.29563793436494 6.91905786874483 P P P 6.55334987867877 6.18498364838807 6.2042367262763
P P P LNCV6_144188_PI430048170 mRNA
GGGAGCCGGACCCTGACCTCCCTGGGTTCTGGTTGGAGATGAAAAAATTAGAAGCATCAG NM_001297753 RefSeq
chr19 - 48712721 48717021 MAMSTR 284358 "MEF2 activating motif and SAP domain containing
transcriptional regulator, transcript variant 3"
GO:0001076|GO:0006366|GO:0045944|GO:0010831|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137984_PI430048170 0.9752801810791020.9544747870626141.89055084573011
0.3445754919907190.358776072885886A A A 2.01884280152494 0.336088977561098
0.314455021976433A A A LNCV6_137984_PI430048170 mRNA
CTTTCTCTGTCTTCCCTGACCACGGGAGCAGGTCAGACCCTTCTAATAAACTCCTTTCCT NM_198689 RefSeq chr21

+ 44600596 44602174 KRTAP10-7 NA keratin associated protein 10-7 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89868_PI430048170 0.0436689483256821.43320423205743 4.6148493960287 4.29057737982095 4.21975322598938 P P P 4.11474444746284 3.74340779059097 3.70421629645936 P P P
LNCV6_89868_PI430048170 mRNA
AAATCAGAACCTGTAGTTTCCACTCGGAAAAGACCAGAGACCAAACCTTCCAGTGACCTT NM_018691 RefSeq chr5 - 153991705 154038937 FAM114A2 10827 "family with sequence similarity 114, member A2"
GO:0008150|GO:0017076|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133469_PI430048170 0.2537775296681830.5957453651117342.49591692157272 0.3676045993153691.71048694409611 A A A 2.74629642582277 2.3567920789571 2.40477862439554 P A A LNCV6_133469_PI430048170 mRNA
TCTCCAGTGCCCCTGAATTTTATGTTTGATGACTATATATTTGGGCATATATCTTGTTGG NM_001080505 RefSeq chr4 + 42397838 42402487 SHISA3 152573 shisa family member 3 GO:0005789|GO:0007275|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92172_PI430048170 0.83827551424397 1.01901534665629 4.54753969658852 4.36328323563916 4.23061548974255 P P P 4.37396633934567 4.34507768116515 4.35836625238732 P P P
LNCV6_92172_PI430048170 mRNA
TTCTTCATCAAGAAAAAGTGGAACCAGCTGTCCCTCCAGCAAAAACAGCAGCCCTAATAG NM_032582 RefSeq chr17 - 60177329 60392225 USP32 84669 ubiquitin specific peptidase 32
GO:0005515|GO:0004197|GO:0016579|GO:0005737|GO:0005794|GO:0004843|GO:0016020|GO:0061136|GO:0005509|GO:0043161 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132235_PI430048170 0.2303777009314821.94643659686752 1.2526605887709 1.97427097474725 0.328198807572946 A A A 0.4202049841800530.336957345152113 0.363664322524191 A A A LNCV6_132235_PI430048170 mRNA
GCTGTGAGAAGAGGATAGTGAATATTAAAGAGGGAAAGCAGTTTTCCTGGAGGAAGCAAA NM_001012415 RefSeq chr9 - 135693408 135699528 SOHLH1 402381 "spermatogenesis and oogenesis specific basic helix-loop-helix 1, transcript variant 2"
GO:0005737|GO:0001541|GO:0003700|GO:0048477|GO:0046983|GO:0005634|GO:0007283|GO:0045893|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138367_PI430048170 0.0305264374869128 0.5943609394983276.85477274052244 6.79842609208321 7.31585284619441 P P P 7.50568322045492 7.67126352835378 8.04715109306889 P P P LNCV6_138367_PI430048170 mRNA
GATCAGCCACACAACTGTTTTGTACATACTTATTTTCTCATGCACTTTTCTGTATGCAAA NM_001343 RefSeq chr5 - 39371673 39425233 DAB2 1601 "Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila), transcript variant 1"
GO:0005515|GO:0006907|GO:2000096|GO:0071560|GO:0046332|GO:0015031|GO:0005765|GO:0043231|GO:0070022|GO:1900026|GO:0030099|GO:0016055|GO:0070062|GO:2001046|GO:0030335|GO:0038024|GO:0005546|GO:0060766|GO:0001701|GO:0060391|GO:0006898|GO:0005178|GO:0007229|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143367_PI430048170 0.3618464124276130.9128458782972788.30695961864953 8.26003538182165 8.45833066552842 P P P 8.26214998314979 8.56079149373293 8.58288048760345 P P P LNCV6_143367_PI430048170 mRNA
TTGAGTATAGGGATACATGGTGGATTCATGTACTTCAGTGTTTGTTTTGACCAAAGTTTA NM_024331 RefSeq chr20 + 44475885 44494603 TTPAL 79183 "tocopherol (alpha) transfer protein-like, transcript variant 1"
GO:0005622|GO:0005215|GO:0016020|GO:0006810 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94003_PI430048170 0.3499762028665891.65091996485605 0.5833953639570120.689313773806998 2.02841426632704 A A A 0.5475309363012730.532923835946847 0.533044316541072 A A A
LNCV6_94003_PI430048170 mRNA
AAAGCAAGGAAACCAGCTTGGTTTGGCAAACAGCTGATGAAATAAATGTGACGTAGAAGA NM_152319 RefSeq

chr12 + 48482502 48496514 C12orf54 121273 chromosome 12 open reading frame 54 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_116499_PI430048170 0.5374648202993960.8529825521352383.64637866113878
2.77185378817922 3.71581761059969 P A P 3.92552461150526 3.77892781680438 3.1968035496531
P P P LNCV6_116499_PI430048170 mRNA
CTGGTGGCTTCTAGAAGCAGCCATTACCAACTGTACCTTCCCTTCTTGCTCAGCCAATAA NM_000732RefSeq chr11
- 118339073 118342744 CD3D 915 "CD3d molecule, delta (CD3-TCR complex), transcript variant 1"
GO:0050852|GO:0005886|GO:0046982|GO:0003713|GO:0031295|GO:0045059|GO:0005737|GO:0042105|GO:0030
217|GO:0042101|GO:0045944|GO:0050776|GO:0016021|GO:0007166|GO:0004888 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138114_PI430048170 0.0015619658795565 0.6018776953233943.97739304467605
4.06287450255736 4.18859187861918 P P P 4.79353577060563 4.7621801192575
4.87596509715154 P P P LNCV6_138114_PI430048170 mRNA
GGCTTCTCTGTACTTACGCCATACCCCAGAATACAATAAATAAGCAATTAGAAAACAAAA NM_000821RefSeq chr2
- 85544854 85561534 GGCX 2677 "gamma-glutamyl carboxylase, transcript variant 1"
GO:0017187|GO:0016020|GO:0007596|GO:0008488|GO:0005789|GO:0016021|GO:0044267|GO:0006464|GO:0043
687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131057_PI430048170 0.6646838530199331.01976966582705 0.27697288979771
0.3054679651963670.444926043220298A A A 0.3413670104567140.304657737551738
0.301932096474791A A A LNCV6_131057_PI430048170 mRNA
GTCTTTGTGCCTTGTGACATCAAAACTGAAATGTTTGTATTACTGTTGTCCATGACTTTT NM_199351RefSeq chr1 -
166913203 166975324 ILDR2 NA immunoglobulin-like domain containing receptor 2 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142618_PI430048170 0.7912480824978770.5780394415349381.85885569957604
1.60562557536135 0.653489015560286A A A 0.2673439852795871.32082593587984
3.40045024038787 A A P LNCV6_142618_PI430048170 mRNA
GTAGGCAGTATGTTTGCCAGTGACATTGAAGGTGAGAGAAACAAAAATTACAAATGAATT NM_014175RefSeq chr8
+ 54135220 54148514 MRPL1529088 mitochondrial ribosomal protein L15
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0005
762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134384_PI430048170 0.4785177841601091.02347377279753 0.377594110443227
0.2543526263766910.280738784933189A A A 0.2643573715748070.287240298669222
0.263478366990305A A A LNCV6_134384_PI430048170 mRNA
GTGCCAGCTGGATAACTGATGGCATTTGTCTCAAGACAGAAAATAAAAAGCATTTCATTC NM_017539RefSeq chr16
- 20933110 21159441 DNAH3 NA "dynein, axonemal, heavy chain 3" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130747_PI430048170 0.0544272901612961 1.19345845709629 8.36550941284672
8.59289426458227 8.57310774843006 P P P 8.32370106906664 8.14515231101148
8.30154138804962 P P P LNCV6_130747_PI430048170 mRNA
GTTCTTGAATTAGAAATTCTGTGGGATCAATCTTTGATGGTGAGGGTTTTAGAAAGGAAA NM_005266RefSeq chr1
- 147756198 147773362 GJA5 2702 "gap junction protein, alpha 5, 40kDa, transcript variant A"
GO:0035922|GO:0086053|GO:0003161|GO:0003283|GO:0003284|GO:0055077|GO:0048844|GO:0003281|GO:0060
307|GO:0016264|GO:0030326|GO:0042995|GO:0045776|GO:0086091|GO:0051259|GO:0086075|GO:0060371|GO:0
086069|GO:0060373|GO:0045907|GO:0014704|GO:0045909|GO:0010643|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137283_PI430048170 0.0604679693302844 0.0455011575091566 2.93565470276606
1.90283747465114 1.91829482269794 A A A 8.0458244469901 4.42908899976076 5.5728937095775
M P P LNCV6_137283_PI430048170 mRNA
CTCTCCCATTAAACCATAAGCAACTTGAGGGCAGACAATCAGTTTTACTCCTTTTATATC NM_001290053 RefSeq

chr1 + 87212668 87251331 LOC101927844 NA uncharacterized LOC101927844 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128935_PI430048170 0.0915300144869291 1.23707726981763 12.9576773478364 12.9866433301914 13.0084485815484 P P P 12.8523206780331 12.4919963151085 12.6655813795102 P P P LNCV6_128935_PI430048170 mRNA AAAGCTTTTGAGGCCCAATAAAATAGTACGTGCTGTCTGCAGCCCTTATTGATCAAAAAA NM_014390 RefSeq chr7 + 127652147 128092607 SND1 27044 staphylococcal nuclease and tudor domain containing 1 GO:0003712|GO:0005515|GO:0042470|GO:0006355|GO:0090305|GO:0005634|GO:0031047|GO:0001649|GO:0006351|GO:0016442|GO:0005739|GO:0004518|GO:0005737|GO:0016020|GO:0016032|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143231_PI430048170 0.145189484255695 1.14032740033773 10.0000679299885 9.83457844486194 9.73235977217935 P P P 9.78438905939527 9.67082812316034 9.54636952300005 P P P LNCV6_143231_PI430048170 mRNA TGCTTCTCAGCTGTGTCCGACCCCACCATGTAATAAAACCCAAAGGAACAGCCCAAAAAA NM_001282684 RefSeq chr22 + 37051735 37063390 KCTD17 79734 "potassium channel tetramerization domain containing 17, transcript variant 1" GO:0005515|GO:0051260|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126837_PI430048170 0.184762558776753 0.742157131137799 0.285393715567957 0.557797926482025 0.389266310776653 A A A 0.97910392423045 0.398895929910253 1.07081257084694 A A A LNCV6_126837_PI430048170 mRNA CCACAGAGAATAAGCTGAACTTGTATGGTTTTTCACCAAACCATGGATAGAATCAATATT NM_001081 RefSeq chr10 - 16823965 17129817 CUBN 8029 cubilin (intrinsic factor-cobalamin receptor) GO:0005515|GO:0005215|GO:0015889|GO:0005886|GO:0005783|GO:0006767|GO:0030139|GO:0044281|GO:0031526|GO:0005765|GO:0042803|GO:0005829|GO:0042953|GO:0016324|GO:0001894|GO:0004872|GO:0008202|GO:0070062|GO:0043202|GO:0008203|GO:0005794|GO:0009235|GO:0031419|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141795_PI430048170 0.471298830731686 2.36183337449324 0.357261709863388 2.81600981140012 0.310038422311168 A A A 0.480360867634173 0.42989925357493 0.385904586814184 A A A LNCV6_141795_PI430048170 mRNA CTGCTCTAATAACATATGCTCTATTGACAGGAAGGGTAGCAATAAAACTAATGGCAATTT NM_153364 RefSeq chr12 + 99647749 99650114 FAM71C 196472 "family with sequence similarity 71, member C" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133859_PI430048170 0.934176049026765 1.0088542352015 2.24537097069224 2.39462928590007 3.00329993461535 A A P 2.5650518380511 2.69892842513326 2.44605344418863 P P P LNCV6_133859_PI430048170 mRNA AGCAGAAGGCCAGCTCTTGACTCTGAGTTCAGTTGGACAAAATGCTGTTGATAAAACCTC NM_032977 RefSeq chr2 + 201182897 201221660 CASP10 843 "caspase 10, apoptosis-related cysteine peptidase, transcript variant 1" GO:0005515|GO:0005886|GO:0031265|GO:0006915|GO:0042981|GO:0097190|GO:0005829|GO:0004197|GO:0005737|GO:0035877|GO:0045087|GO:0097199|GO:0006508|GO:0043123|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51341_PI430048170 0.368493991148535 1.062992007353 12.0042583945111 12.0377184725651 11.8825656144991 P P P 11.7471740758789 11.9982765541976 11.9081580323993 P P P LNCV6_51341_PI430048170 mRNA TGCCCTGGCCCCAGCCCTACTCTGTGTAATAGAATAAAGGCCTGCGTGTGTCTGTGTTGA NM_014387 RefSeq chr16 + 28985065 28990783 LAT 27040 "linker for activation of T cells, transcript variant 1" GO:0005515|GO:0050852|GO:0010467|GO:0019722|GO:0005886|GO:0007265|GO:0042629|GO:0035556|GO:0006955|GO:0006954|GO:0008180|GO:0005911|GO:0002260|GO:0001772|GO:0043303|GO:0050863|GO:0019901|GO:0030168|GO:0009967|GO:0042110|GO:0007596|GO:0007229|GO:0005070|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137962_PI430048170 0.1324190316789461.15983221811568 0.914877137326902
0.669032663307491 0.623670557089564 A A A 0.609201949151276 0.482010640210367
0.488346873259633 A A A LNCV6_137962_PI430048170 mRNA
GTGTGTACATATATAAAACCTGTGTAAACCTCTGTCCTTATGAACCATAACAAATGTAGC NM_015886 RefSeq chr8
+ 74824536 74855029 PI15 51050 peptidase inhibitor 15
GO:0008150|GO:0010466|GO:0030414|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112541_PI430048170 0.573804761205923 0.9351839381717036.07805823739385 5.6823329217829
6.24912173504768 P P P 6.02338133861698 6.12737237978777 6.20031474087074 P P P
LNCV6_112541_PI430048170 mRNA
ATTCCAAATATGGTGCCAAGGAGTGTAGCTTTTGTGAAGACCCTCGCTTTGCTAGAACTG NM_014660 RefSeq chr7
+ 10973871 11107749 PHF14 9678 "PHD finger protein 14, transcript variant 2"
GO:2000791|GO:2000584|GO:0048286|GO:0008270|GO:0005634|GO:0000122 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138194_PI430048170 0.00754154297180892 0.1807529803618386.92531405473892
5.84951427768363 5.75857075241686 P P P 9.00989209828477 8.88848319540611
8.23601801994155 M P M LNCV6_138194_PI430048170 mRNA
GCTCTCCCTAGCTTCACATCTTGTGTTTTCCAGAAAATAAAAACAGCAGACTGTCCTTTC NM_002299 RefSeq chr2
- 135787844 135837180 LCT 3938 lactase
GO:0017042|GO:0016324|GO:0016020|GO:0005886|GO:0005975|GO:0005887|GO:0009405|GO:0044245|GO:0000
016|GO:0044281 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51901_PI430048170 0.3623152555394030.9063618545603295.43046191869858 5.38996276436278
5.77261039643298 P P P 5.5826915754558 5.63952140657267 5.81723831695209 P P P
LNCV6_51901_PI430048170 mRNA
TTCCTAATGAGAAAGTGGGCTGGCTTGTTGAGTGGCAAGACTATAAGCCTGTGGAATACA NM_024047 RefSeq chr4
+ 87422575 87459454 NUDT9 53343 "nudix (nucleoside diphosphate linked moiety X)-type motif 9,
transcript variant 1"
GO:0005622|GO:0034656|GO:0047631|GO:0046032|GO:0005759|GO:0019144|GO:0055086|GO:0044281|GO:0043
262|GO:0046709|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71645_PI430048170 0.0896929892083791 0.9327407513293040.281795010029837
0.2862890483208640.307522506183792 A A A 0.4550843996390110.378412480803422
0.34125119908291 A A A LNCV6_71645_PI430048170 mRNA
CAATAACCTGCAGATTCTCAACATCAATAAAAGTGATGAAGGTATATACAGATGTGAAGG NM_004540 RefSeq chr21
+ 20998314 21540196 NCAM2 4685 neural cell adhesion molecule 2
GO:0030424|GO:0007608|GO:0007413|GO:0005886|GO:0016021|GO:0007158 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143381_PI430048170 0.880070896682 1.00369831052122 11.3179810246252
11.3513985577994 11.2854368986147 P P P 11.266375747406 11.3046588622608
11.3667747159804 P P P LNCV6_143381_PI430048170 mRNA
TCTGGGGACCTTTCCTACCCCCATCAGCATCAATAAAACCTCCTGTCTCCAGTGAAAAAA NM_001665 RefSeq chr11
- 3826977 3840983 RHOG 391 ras homolog family member G
GO:0005515|GO:0051056|GO:0008284|GO:0030036|GO:0005886|GO:0007264|GO:0003924|GO:0030168|GO:0007
266|GO:0032863|GO:0005525|GO:0005829|GO:0016601|GO:1900027|GO:0060326|GO:0007411|GO:0007596|GO:0
008152|GO:0045893|GO:0005925|GO:0090004|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_130840_PI430048170 0.0771375286484285 1.76895364418968 8.38253584117167
8.44937951314708 8.44971034086662 P P P 8.07062009770293 7.24643215730005
7.35077303006942 P P P LNCV6_130840_PI430048170 mRNA
GTTTCCTAGATATGAATGATGTTTGCAATCCCCATTTTCCTGTTTCAGCATGTTATATTC NM_002928 RefSeq chr1 -
182598622 182604413 RGS16 6004 regulator of G-protein signaling 16

GO:0043547|GO:0005515|GO:0005516|GO:0005737|GO:0008277|GO:0005886|GO:0038032|GO:0007601|GO:0005
096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76268_PI430048170 0.0735773006740592 1.72624394991794 3.83351015536152
4.04467753009043 3.36123981239978 P P P 3.16748502511461 3.23222993033233
2.43018569949428 P P P LNCV6_76268_PI430048170 mRNA
ACAACGGCATCCTTCTCTACAAAGGAGACAATGACCCCCTGGCACTGGAGCTGTACCAGG NM_001271946 RefSeq
chr5 - 168661732 169301129 SLIT3 6586 "slit homolog 3 (Drosophila), transcript variant 1"
GO:0030308|GO:0008285|GO:0005509|GO:0050919|GO:0061364|GO:0048846|GO:0005615|GO:0035385|GO:0048
495|GO:0032870|GO:0051414|GO:0021834|GO:0005739|GO:0070100|GO:0007411|GO:0010629|GO:0009887 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129917_PI430048170 0.2196540196960750.85628398793172 15.4673741140494
15.0690015129575 15.0493510486308 P P P 15.5198597115864 15.3549455682501
15.4172867639884 P P P LNCV6_129917_PI430048170 mRNA
CCTTCCTGGCAAATAAATTCCCGTTTCTATCCAAAAGAGCAATAAAAAGTTTTCAGTGAA NM_000975RefSeq chr1
+ 23691778 23696426 RPL11 6135 "ribosomal protein L11, transcript variant 1"
GO:0005515|GO:0010467|GO:0034504|GO:0003735|GO:0019083|GO:0003723|GO:0006364|GO:0006614|GO:0019
058|GO:0005730|GO:0019843|GO:0006605|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0
016020|GO:0000184|GO:0016032|GO:0042273|GO:0022625|GO:0044267|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128039_PI430048170 0.0751349095944742 0.5946055941699236.67680090966163
6.52677083799731 6.84330664740858 P P P 6.99133053221786 7.41683763122683
7.79527624449217 P P P LNCV6_128039_PI430048170 mRNA
GAGTTATTGTTAACAAAGAGACCCAAGAAAAGCTGCTAATGTCCTCTTATCATTGTTGTT NM_000044RefSeq chrX
+ 67544031 67730619 AR 367 "androgen receptor, transcript variant 1"
GO:0005515|GO:2001237|GO:0010467|GO:0008284|GO:0004882|GO:0000790|GO:0003700|GO:0006367|GO:0044
212|GO:0008013|GO:0008283|GO:0007267|GO:0005634|GO:0051259|GO:0005737|GO:0051092|GO:0045944|GO:0
045945|GO:0001085|GO:0046983|GO:0043401|GO:0006810|GO:0030850|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138106_PI430048170 0.00136410362939184 1.32938927581426 12.2614592185658
12.3379626064825 12.2232540977639 P P P 11.889740970803 11.8764619491632
11.8257695977841 P P P LNCV6_138106_PI430048170 mRNA
CTCGGGGGCCTGGGGAAGTTGTGTGTTGTGCAGTCAGTAAAATCCTCCCACTGCCTCCGG NM_018083RefSeq chr19
+ 7516117 7521025 ZNF358 140467 zinc finger protein 358
GO:0006355|GO:0019827|GO:0021915|GO:0005634|GO:0035115|GO:0003677|GO:0046872|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102231_PI430048170 0.0211603238985824 1.36108727484201 6.71985570167677
6.49346117878448 6.75430010775824 P P P 6.17113542228309 6.27804377388547
6.19563408764004 P P P LNCV6_102231_PI430048170 mRNA
AACCTGATCGACGCCCCCAGTGTTGTTGCTAAAACTGAGCAAGAGGTTGACATTATATTG NM_033103RefSeq chr19
- 32978591 33064918 RHPN2 85415 "rhophilin, Rho GTPase binding protein 2"
GO:0007165|GO:0048471|GO:0005737|GO:0005654|GO:0043231 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_97141_PI430048170 0.0119858905285501 0.5563220061384582.19095155510519 2.617157051354
2.64066245466059 A A A 3.24300215762573 3.17990006899705 3.57479051003407 P P P
LNCV6_97141_PI430048170 mRNA
TATTATCTGATCATTCCAAACCAACTGCTGAAACGGTAGCACCTGACAACACTGCAATCC NM_001291976 RefSeq
chr4 - 87473329 87529503 SPARCL1 8404 "SPARC-like 1 (hevin), transcript variant 3"
GO:0007165|GO:0005509|GO:0005578|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA

LNCV6_100525_PI430048170 0.4189016148660991.05212634228074 0.304735158076227
0.3099083721843050.514886948921541 A A A 0.3133068481475790.276420057343421
0.329480115631587 A A A LNCV6_100525_PI430048170 mRNA
TGACAAAACGCGTATCACAATGTGACTGCAGAGCAGCTCTTTTTGAAGGACATTATAGAA NM_006100 RefSeq chr3
+ 98732703 98795845 ST3GAL6 10402 "ST3 beta-galactoside alpha-2,3-sialyltransferase 6, transcript
variant 1"
GO:0006664|GO:0009311|GO:0005975|GO:0044281|GO:0042339|GO:0030173|GO:0052798|GO:0000139|GO:0018
146|GO:0009405|GO:0071354|GO:0016021|GO:0006488|GO:0044267|GO:0030203|GO:0006464|GO:0070062|GO:0
043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71707_PI430048170 0.114509586754526 0.869683247991083 4.38497250023808
4.56808136965454 4.62194411373519 P P P 4.80660718901474 4.58723125739015
4.78601393917094 P P P LNCV6_71707_PI430048170 mRNA
CGCTGTCGCAAGAGAAAACTTGACTGTATACAGAATCTTGAATCAGAAATTGAGAAGCTG NM_206866 RefSeq
chr21 + 29299415 29346148 BACH1 571 "BTB and CNC homology 1, basic leucine zipper
transcription factor 1, transcript variant 1"
GO:0006355|GO:0003700|GO:0001206|GO:0061418|GO:0001205|GO:0005634|GO:0000122|GO:0006351|GO:0005
829|GO:0000117|GO:0001078|GO:0005737|GO:0000083|GO:0045944|GO:0000980|GO:0005654|GO:0020037 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113305_PI430048170 0.733455181545165 1.00608660554638 0.344881110861117
0.323777742152602 0.273532042226285 A A A 0.308988531767033 0.314730453964826
0.293049280558443 A A A LNCV6_113305_PI430048170 mRNA
ATGGAACCTTGGGCATTAGGAGCATGCACATTTGTTCATCTCTTGCCAAAGTTTGACCCA NM_001010845 RefSeq
chr16 + 20451536 20487669 ACSM2A 123876 acyl-CoA synthetase medium-chain family member 2A
GO:0005739|GO:0036112|GO:0005759|GO:0006631|GO:0070328|GO:0042593|GO:0005524|GO:0047760|GO:0046
872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64937_PI430048170 0.0400498163834003 0.876057079476293 12.3204019385046
12.4292890404169 12.2667955672692 P P P 12.5904189440066 12.450683143426
12.5493215805983 P P P LNCV6_64937_PI430048170 mRNA
TTCTTGAAAGTACCCTGATGACCCCAGCTGCCAAGGAAACCCCCAGTGTAATAATAAATC NM_001983 RefSeq
chr19 - 45407332 45423919 ERCC1 2067 "excision repair cross-complementation group 1,
transcript variant 2"
GO:0005515|GO:0051276|GO:0009650|GO:0048477|GO:0010165|GO:0008283|GO:0000110|GO:0010259|GO:0007
283|GO:0006302|GO:0000720|GO:0000109|GO:0005737|GO:0035264|GO:0003697|GO:0006295|GO:0009744|GO:0
006296|GO:0048568|GO:0035166|GO:0006979|GO:0000784|GO:0005669|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131055_PI430048170 0.0548273653116854 0.6525672504021023.27208307609046
3.17129403031657 2.69514312182654 P P A 3.76329754252044 3.7407728876378
3.53420187145779 P P P LNCV6_131055_PI430048170 mRNA
CAACCAGTCGAATTAGACCCATTTGGTGCTGCTCCATTTCCTTCTAAACAGTAGATACTT NM_198892 RefSeq chr4
+ 78776377 78912187 BMP2K 55589 "BMP2 inducible kinase, transcript variant 1"
GO:0050790|GO:0030500|GO:0019208|GO:0004674|GO:0006468|GO:0005654|GO:0005524 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_52488_PI430048170 0.320024314101351 1.02446703588621 0.328575909428452 0.248956977213822
0.32712331919033 A A A 0.270725275081736 0.257836380082802 0.272857699571194 A A A
LNCV6_52488_PI430048170 mRNA
TTGTGAAAGTACCCCACAAGCATCGTTAACTATAAAGTAAGGAAAAGTATGAAAGAACCA NM_020344 RefSeq chr9
- 19507451 19787019 SLC24A2 25769 "solute carrier family 24 (sodium/potassium/calcium
exchanger), member 2, transcript variant 1"
GO:0005886|GO:0031226|GO:0060291|GO:0060292|GO:0031402|GO:0046870|GO:0034220|GO:0046983|GO:0007

613|GO:0035725|GO:0007612|GO:0006813|GO:0016151|GO:0015293|GO:0006811|GO:0005262|GO:0030145|GO:0
005509|GO:0006874|GO:0030955|GO:0055085|GO:0070588|GO:0016021|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144311_PI430048170 0.1020933355777521.62157931343021 2.88706915754695
2.75095548906813 3.44391873754097 A A P 2.74382241725318 1.85826751575803
2.35052595925855 P A P LNCV6_144311_PI430048170 mRNA
AGGGCAAGTTCTTGAACAAAAATCCTGTTGGCCCTGGAAAGTATGTATTTGATGTTGGGT NM_080860RefSeq chr21
- 42472485 42496354 RSPH1 89765 "radial spoke head 1 homolog (Chlamydomonas), transcript variant
1" GO:0051321|GO:0035082|GO:0031514|GO:0005634|GO:0005829 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_65992_PI430048170 0.994909250968805 1.0042643633151 8.84364342221299 9.20781079667801
9.31550494539157 P P P 9.00705353146257 9.01218114111672 9.34402287978999 P P P
LNCV6_65992_PI430048170 mRNA
CTCTTCACAAGAAGAAAGTATTGGGACATTATTGGATGCTATCATTTGTAGAATGTCAAC NM_016058RefSeq chr2
- 73729829 73737390 TPRKB 51002 TP53RK binding protein
GO:0005515|GO:0005737|GO:0019901|GO:0005634|GO:0008033|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143041_PI430048170 0.00473412151863434 0.5625038835051278.2424912002153
8.03736684606048 8.01587264635196 P P P 8.95572763371723 8.94799541226075
8.89239391008621 P P P LNCV6_143041_PI430048170 mRNA
AGCAGCTGCCCTCCGACCCCTCACTTTGTGCCTTTAGTAAACACTGTGCTTTGTAAAAAA NM_007162RefSeq chr6
- 41683977 41735060 TFEB 7942 "transcription factor EB, transcript variant 1"
GO:0006355|GO:0003700|GO:0044212|GO:0006914|GO:0001892|GO:0005634|GO:0006351|GO:0005737|GO:0006
959|GO:0045944|GO:0046983|GO:0007040|GO:0010508 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135709_PI430048170 0.0881382771048339 0.9388809512726329.58284643708199
9.63551912773827 9.60998578737021 P P P 9.68474824061122 9.65351529707617
9.76138085805099 P P P LNCV6_135709_PI430048170 mRNA
CCTGGACACCCTCAAATGGGGTTTTCTGTGTTATTTCATAAAATTCTTTGAAGTCCAATA NM_001277961 RefSeq
chr11 + 3855702 4093210 STIM1 6786 "stromal interaction molecule 1, transcript variant 1"
GO:0005515|GO:0032541|GO:0005513|GO:0005783|GO:0005509|GO:0005874|GO:0030176|GO:0042802|GO:0032
237|GO:0051010|GO:0005887|GO:0007596|GO:0051924|GO:0005789|GO:0006816 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144760_PI430048170 0.5133147214793711.03958971518155 5.57099210550396
5.49445476019756 5.45372958910615 P P P 5.35839632056848 5.39612859897164
5.58838144072695 P P P LNCV6_144760_PI430048170 mRNA
CCCTATAATGCTGGAGCGGCTACTAAAAAGGATAAAATGTATCACTTAAATGTTACCAAA NM_033133RefSeq chr17
+ 41966740 41977736 CNP 1267 "2',3'-cyclic nucleotide 3' phosphodiesterase"
GO:0008344|GO:0048471|GO:0005886|GO:0048709|GO:0003723|GO:0005743|GO:0007268|GO:0005741|GO:0005
634|GO:0007409|GO:0005615|GO:0031143|GO:0035749|GO:0005737|GO:0030551|GO:0032496|GO:0070062|GO:0
035748|GO:0046902|GO:0042470|GO:0009214|GO:0004113|GO:0005874|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130937_PI430048170 0.0176060248229996 2.2791475726869 5.64491560447637
5.73602262010351 5.47518450806707 P P P 4.12008204576376 4.80260321501024
4.28984577460351 P P P LNCV6_130937_PI430048170 mRNA
CTAGGGCCCCTCCAAAAGAGTCCTTTTAAATAAATGAGCTATTTAGGTGCTGTGATTGTG NM_004750RefSeq chr19
- 18593224 18606850 CRLF1 9244 cytokine receptor-like factor 1
GO:0005515|GO:0001657|GO:0008284|GO:0046982|GO:0042517|GO:2000672|GO:0005125|GO:0005615|GO:0005
127|GO:0097058|GO:0043524|GO:0019955|GO:0004872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130656_PI430048170 0.0115450775434945 0.3907456203982450.392399676951138

0.3740603377911850.260600751966967A A A 1.39847122839236 1.66424479880129 1.9767505634135
A A A LNCV6_130656_PI430048170 mRNA
TACGGAAATCAACTGCTATTTCTCTTTCAGTAAGAGAAACTGGGTTTGGAATTTATAGTC NM_001276713 RefSeq
chr5 + 75611475 75671846 ANKDD1B NA ankyrin repeat and death domain containing 1B NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137156_PI430048170 0.0720197973161303 1.71436228974671 4.75396388174723
5.53233810498886 4.98221016299769 P P P 4.31572320446534 4.22883484858985
4.49235154150074 P P P LNCV6_137156_PI430048170 mRNA
TTCTATAGTGTGATTACCTGAGGGTGCCTCCAAATGTATATCATTTCACTCCCCTCCCCT NM_207015RefSeq chr3
+ 174859320 175805640 NAALADL2 NA N-acetylated alpha-linked acidic dipeptidase-like 2 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_143763_PI430048170 0.1239956293786714.16288922100124 1.41733748489058
3.77875999691422 3.41808290023104 A P P 1.41298452692117 1.20766529175036
0.617183583060718A A A LNCV6_143763_PI430048170 mRNA
GGTTTGAGGAGCTAGCCTTGTTTTTTGCATCTTTCTCACTCCCATACATTTATATTATAT NM_001286352 RefSeq chr1
+ 113979390 113982254 OLFML3 56944 "olfactomedin-like 3, transcript variant 2"
GO:0007275|GO:0005576|GO:0031982 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94717_PI430048170 0.0696429755875435 1.62811433693753 4.41525422538718
4.96217650225149 4.69223459154589 P P P 4.34078110152863 4.0185390772733
3.54348718103664 P P P LNCV6_94717_PI430048170 mRNA
TGGGCCTGTGCATTGTTGGCTGTGTGATGGATGAGAATTGTCAAGCTGGAGAAAAATGTT NM_080614RefSeq chr20
- 45774207 45791908 WFDC3 140686 WAP four-disulfide core domain 3
GO:0010951|GO:0004867|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89124_PI430048170 0.00366164922943217 0.39235773571610410.1470156277115
9.73291111386238 9.94477966825284 P P P 11.0110801125971 11.2605265701311
11.5761808796778 P P P LNCV6_89124_PI430048170 mRNA
TCAAGGGTGTGGTTGGCCTGTGGTGCTCTTTGGAGGAATGAATAAAAATGAATAGAAATC NM_001007561 RefSeq
chr19 - 43584366 43596135 IRGQ NA "immunity-related GTPase family, Q" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_130509_PI430048170 0.1746260316876927.26848076262815 0.428122733163927
4.02990411755097 3.20128555986402 A P P 0.3171581125762630.275067039314903
0.312677602520103A A A LNCV6_130509_PI430048170 mRNA
AAGCACCAGCAGTAATATGGGAAGCTATGCTGAAAACCGCTATTTTGAATAATGTGAAAT NM_019035RefSeq chr4
- 137518919 137532498 PCDH18 54510 "protocadherin 18, transcript variant 1"
GO:0005886|GO:0007420|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130690_PI430048170 0.1271374258811730.6648837993318567.46835509487969
7.06769105606689 6.79367062805878 P P P 8.03134078833047 7.78346756795247
7.25766692532612 P P P LNCV6_130690_PI430048170 mRNA
GAGAAGAAAGTTCCCCGCTCTCCAAAGCACCACCAATAAACATGTCATTTAAGCAAAAAA NM_199046RefSeq chr16
+ 57976434 57988113 TEPP 374739 "testis, prostate and placenta expressed, transcript variant 1"
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136010_PI430048170 0.8895838892203611.02096197100241 9.188847197264
9.57471287979353 9.20746475640081 P P P 9.38524637421618 9.33164756146001
9.19114453135635 P P P LNCV6_136010_PI430048170 mRNA
CCAGAGCCCACTTGGCCCCACCCCTCAATAAACCGTGTGGCTTTGGACTCTCGTAAAAAA NM_005341RefSeq chr1
+ 6579990 6589280 ZBTB48 3104 "zinc finger and BTB domain containing 48, transcript variant 1"
GO:0006355|GO:0005737|GO:0003700|GO:0005654|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_139106_PI430048170 0.1863055282222861.04275981956812 0.390576528416506
0.30552697603635 0.290090410206508A A A 0.2568319503890060.298160851895503
0.251570428033916A A A LNCV6_139106_PI430048170 mRNA
CCCTAAGTTCTCTCAAGACATCTTTTCTGTGTTTCTGAGCCAGTGAAGAAGACAGGAGGA NM_001134878 RefSeq
chr3 - 47228025 47282847 KIF9 64147 "kinesin family member 9, transcript variant 4"
GO:0005515|GO:0008017|GO:0005871|GO:0071801|GO:0005874|GO:0002102|GO:0003777|GO:0031982|GO:0005
524|GO:0005737|GO:0022617|GO:0007596|GO:0008152|GO:0046983|GO:0016887|GO:0007018 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130333_PI430048170 0.00227421784635424 0.4464421093585839.58587041154556
9.33385043510047 9.30325417492927 P P P 10.324315957037 10.7247453308276 10.650631591632
P P P LNCV6_130333_PI430048170 mRNA
CTAACCCATCCCAGAATAAATGGAGACTTCATGTGTTCATTGTTTCATTCACTCAAAAAA NM_017620RefSeq chr19
+ 10654260 10692419 ILF3 3609 "interleukin enhancer binding factor 3, 90kDa, transcript variant 4"
GO:0003725|GO:0005515|GO:0017148|GO:0003723|GO:0005730|GO:0005634|GO:0003677|GO:0006351|GO:0005
739|GO:0051607|GO:0005737|GO:0016020|GO:0030529|GO:0005654|GO:0006468|GO:0045893|GO:0045892|GO:0
045071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134212_PI430048170 0.0103920879218434 0.6389729476007659.54152713264075
9.62760355529436 9.61353932654608 P P P 10.0708415081033 10.3137829600594
10.3240775736801 P P P LNCV6_134212_PI430048170 mRNA
CCCCCAACGTCAAGTTTTTACCTTGCATGTACTGGAGTATTTATTTCATCTATTAAAATG NM_022566RefSeq chr15
+ 81000953 81004004 MESDC1 59274 mesoderm development candidate 1 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144287_PI430048170 0.00403387082387838 0.4615028631943115.18681627110571
5.43499044038612 5.62886529147717 P P P 6.28966207765291 6.54148115367457
6.76161846800145 P P P LNCV6_144287_PI430048170 mRNA
GTCTGTGGCTAAAAAATAGTCGAACCTTTCTTGAGAACTCTGTAACAAAGTATGTTTTTG NM_005359RefSeq chr18
+ 51030212 51085041 SMAD4 4089 SMAD family member 4
GO:0005515|GO:0000987|GO:0000988|GO:0010467|GO:0000790|GO:0001658|GO:0030308|GO:0003700|GO:0006
367|GO:0044212|GO:0005518|GO:0042803|GO:0042802|GO:0007411|GO:0014033|GO:0007179|GO:0017015|GO:0
003279|GO:0005813|GO:0003360|GO:0000122|GO:0030509|GO:0000978|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127821_PI430048170 0.2462706406816881.03409644557768 0.401795549796736
0.3066724909398420.320228099064014A A A 0.3043886314385020.29741295524547
0.283550968820983A A A LNCV6_127821_PI430048170 mRNA
GGCCAGTCAGTTGTACAGAAGTTGGAATATTCTGTTCCAGAATTAAAGAAGTTTTTAGAT NM_014951RefSeq chr10
+ 62374156 62402458 ZNF365 22891 "zinc finger protein 365, transcript variant A"
GO:0005515|GO:0005737|GO:0005815 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89320_PI430048170 0.4296592964108490.9191840128087047.84701212736223 7.95941304940441
7.93183756416652 P P P 8.1021220771571 7.80092879666162 8.17562913680552 P P P
LNCV6_89320_PI430048170 mRNA
CTACAAGGATTTCCATTTTATGGTAAACCAATGGAATACAGTATGCAAAAACAGATTCGG NM_003092RefSeq chr20
+ 16729963 16741772 SNRPB2 6629 "small nuclear ribonucleoprotein polypeptide B, transcript variant
1"
GO:0008380|GO:0006397|GO:0005515|GO:0010467|GO:0000166|GO:0000398|GO:0005730|GO:0017069|GO:0005
681|GO:0005654|GO:0071013|GO:0005686 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126890_PI430048170 0.00107533208197178 1.67225027831935 9.02665982124236
8.93109727660544 8.87087871656364 P P P 8.07306908031268 8.26366607277977
8.26260103130107 P P P LNCV6_126890_PI430048170 mRNA
CCTGCTGTGTTGCCAGCTGAGGGTATTTTATAATAAATTTCCATTGCCAAGTTGAAAAAA NM_053004RefSeq chr22

- 19788410 19854939 GNB1L 54584 "guanine nucleotide binding protein (G protein), beta polypeptide 1-like" GO:0035556|GO:0003674|GO:0005737|GO:0007186|GO:0035176|GO:0009898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141279_PI430048170 0.46508412990746 0.6700097832150932.12851144971241 0.3803088781693581.31078265373254 A A A 0.8370875944723882.53020523929343 2.20431238143234 A P A LNCV6_141279_PI430048170 mRNA GTGCCAAATTAGGCAGTCAGGAAATACTAAATTCTTCATTCCAAATAATGGATCTGAATG NM_022783 RefSeq chr8 + 119873654 120050918 DEPTOR 64798 "DEP domain containing MTOR-interacting protein, transcript variant 1" GO:2001236|GO:0035556|GO:0005622|GO:0005515|GO:0045792|GO:0032007|GO:0006469 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138795_PI430048170 0.4167414700746750.9617725964881340.381095616095237 0.4280703705876820.355784369078412 A A A 0.5209522080215370.465575764271619 0.342301644833187 A A A LNCV6_138795_PI430048170 mRNA TTTTTTGTGTGTTTTGTTTTTTGTGGTGGTGAAGGAGGAGGCCTAATGTCCAGAGGACTG NM_001199633 RefSeq chr9 - 84275849 84340779 SLC28A3 64078 "solute carrier family 28 (concentrative nucleoside transporter), member 3, transcript variant 1" GO:0015860|GO:0005886|GO:0005887|GO:0001882|GO:0015389|GO:0005789|GO:0015864|GO:0006863|GO:0015390|GO:0055085|GO:0072531|GO:0015855 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144369_PI430048170 0.0986136913286463 1.20082936112723 6.80858697693012 6.56021106943431 6.82204211234732 P P P 6.38815695443239 6.36478587350909 6.64365960918305 P P P LNCV6_144369_PI430048170 mRNA GGCTTGTGTTTTGATTACTAGTGTAAACTGGTTATTGAGATAGATTATGACATTGGTGGA NM_001131007 RefSeq chr4 + 153466345 153636710 KIAA0922 23240 "KIAA0922, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142874_PI430048170 0.0329614174020647 0.5963072223197854.27731170447384 4.48130550824089 4.82080603672011 P P P 5.3281347242593 5.20078825160345 5.33701086075642 P P P LNCV6_142874_PI430048170 mRNA CCCTACCCATAAAATTATTTGAAAACTTTCACCAGAAAGGGATGTAAGTCTCGCTTATAT NM_020943 RefSeq chr2 - 179944876 180007053 CWC22 57703 CWC22 spliceosome-associated protein GO:0005515|GO:0048024|GO:0005737|GO:0005794|GO:0016607|GO:0000398|GO:0003723|GO:0005681|GO:0005654|GO:0071013 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139252_PI430048170 0.0525696804229135 0.83895712658442615.2800119186552 15.0670635132446 15.2238594282307 P P P 15.4553387267963 15.4233018609932 15.4603579278637 P P P LNCV6_139252_PI430048170 mRNA CTGCATGGAGGATTTGATTCATGAGATCTATACTGTTGGAAAACGCTTCAAAGAGGCAAA NM_000971 RefSeq chr8 - 73290638 73293634 RPL7 6129 ribosomal protein L7 GO:0005515|GO:0010467|GO:0006364|GO:0003723|GO:0019058|GO:0005634|GO:0003729|GO:0006412|GO:0006413|GO:0042803|GO:0006414|GO:0005829|GO:0000184|GO:0016032|GO:0042273|GO:0070062|GO:0003735|GO:0006614|GO:0019083|GO:0006415|GO:0003677|GO:0016020|GO:0030529|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139155_PI430048170 0.9408156695643250.9978175730240050.495014923341943 0.5145616312232650.403374988682205 A A A 0.5281968863383770.445103201506963 0.450016978609609 A A A LNCV6_139155_PI430048170 mRNA CTGTAAGCTGGCAGAAATGTTTCTTTCTTTGCTTTTGTGTCTGTTGCAGTATCTCAAACANM_007185 RefSeq chr1 - 151700057 151716820 CELF3 11189 "CUGBP, Elav-like family member 3, transcript variant 1" GO:0048026|GO:0008380|GO:0005737|GO:0000166|GO:0000398|GO:0000381|GO:0003723|GO:0005634|GO:0030317|GO:0007283|GO:0003729 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139016_PI430048170 0.1895246857711990.4243724159101361.48023728483858 0.2665269671387120.376080113922285 A A A 1.28955760244834 1.21646862720502

2.94462075627272 A A P LNCV6_139016_PI430048170 mRNA
GAAAATGGAACTTCTTTTTGAAAAGACAAGCAACCATGTTAACTGTATTGACACATCCTC NM_005202RefSeq chr1
- 36095235 36125084 COL8A21296 "collagen, type VIII, alpha 2, transcript variant 1"
GO:0005581|GO:0005578|GO:0005576|GO:0048593|GO:0001525|GO:0050673|GO:0005604|GO:0031012|GO:0016
337|GO:0022617|GO:0030198|GO:0030574|GO:0005788|GO:0030674|GO:0005201 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_91057_PI430048170 0.6638258551336640.95421716464782 3.33344842249158 0.866525977605295
3.08847155470115 P A P 2.7149583168583 3.02388410963706 2.74186153875171 P P P
LNCV6_91057_PI430048170 mRNA
CGGAATTTTAAAGAAGTAGCTTTCCAGGGATTCAGAATTAAGAAAGATAGTGATAGGACA NM_023934RefSeq chrX
+ 155026788 155056916 FUNDC2 65991 FUN14 domain containing 2
GO:0005739|GO:0000422|GO:0005634|GO:0031307 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134426_PI430048170 0.486106112680403 1.03882464300773 0.311160265125748
0.3183672492073870.498830722900905 A A A 0.33064994946339 0.292483757764529
0.347758318373997 A A A LNCV6_134426_PI430048170 mRNA
TGGCAGTCTTCTTGTTACAGACCAATCTGTGGATCTCGCTTCTATCAATTCACCTGCTAA NM_181600RefSeq chr21
+ 30430275 30430758 KRTAP13-4 284827 keratin associated protein 13-4 GO:0005882 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135861_PI430048170 0.0824152958487419 1.04474064360761 0.390560387316082
0.4070314516999740.4598926827515 A A A 0.3392246852863780.338870433128821
0.390259359390143 A A A LNCV6_135861_PI430048170 mRNA
GGAAGGTTGTTTTCTGCTGCTGTTTGAATGTGCTAATAAAAGAGACAACTCTATTGAAAA NM_014989RefSeq chr6
+ 71886702 72403143 RIMS1 22999 "regulating synaptic membrane exocytosis 1, transcript variant 1"
GO:0005515|GO:0030054|GO:0005886|GO:0048791|GO:0007268|GO:0006886|GO:0007269|GO:0046872|GO:0005
829|GO:0045055|GO:0005083|GO:0017156|GO:0048169|GO:0061025|GO:0097151|GO:0048786|GO:0017137|GO:2
000463|GO:0046928|GO:0016079|GO:0014047|GO:0046903|GO:0044325|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144129_PI430048170 0.2915984308025430.8454943077682823.85482251542311
3.80676381125864 4.25602496815642 P P P 4.18770362232292 3.98704066843593
4.47133315352125 P P P LNCV6_144129_PI430048170 mRNA
GCATCCCACCATGAAATATTTGGTAAATTTATGTTGTGACGTGTTGCAGCATGTAAATAA NM_020752RefSeq chr10
+ 25175360 25602228 GPR158 57512 G protein-coupled receptor 158
GO:0008277|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0072659 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127618_PI430048170 0.0391362788332117 0.9353382072046630.3418116268586
0.3254711930505290.313695368486088 A A A 0.4648118324099330.417851434973416
0.386699498803146 A A A LNCV6_127618_PI430048170 mRNA
TGTCCACGATTGGCGCCATGTGTTTTAAGTTGCAGCGTCAAAAACATGAAGAGATTGCTT NM_001253790 RefSeq
chr16 + 4788396 4796491 SMIM22440335 "small integral membrane protein 22, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93378_PI430048170 0.0109872474932355 0.7051964908053161 0.477196490745
10.3550966750958 10.2240460842357 P P P 10.8450644976937 10.9166299027404
10.8155639549683 P P P LNCV6_93378_PI430048170 mRNA
TTGTCTCCCTGGTTGCCTCTCTTGCCCCTTGTCCTGAAGCCCAGCGACACAGAAGGGGGT NM_005928RefSeq chr15
- 88898682 88913432 MFGE8 4240 "milk fat globule-EGF factor 8 protein, transcript variant 1"
GO:2000427|GO:0008429|GO:0005576|GO:0001525|GO:0006910|GO:0031982|GO:0005615|GO:0006911|GO:0031
012|GO:0007338|GO:0005178|GO:0016020|GO:0001786|GO:0016032|GO:0007155|GO:0019897|GO:0009897|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144666_PI430048170 0.2158174836549141.0424349443058 0.339224685286378

0.3153497421974150.426881067618991A A A 0.2988283402534420.28015586113253
0.324658320505926A A A LNCV6_144666_PI430048170 mRNA
TCAGATACAAGATCATTCCCAAGACCTAATTTATTTCTGGCAGATGCCTGCTATTTTCTG NM_020834RefSeq chr14
- 23273634 23286100 HOMEZ 57594 homeobox and leucine zipper encoding
GO:0005737|GO:0003700|GO:0003714|GO:0005730|GO:0005634|GO:0000122|GO:0003677|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127055_PI430048170 0.3810402808086690.6068400009310880.385486995188655
0.3623060420320710.333519318646753A A A 1.87843670821723 0.453406513980361
0.380039515768039A A A LNCV6_127055_PI430048170 mRNA
AGGGAGTTTCTCCAGTTAACATTTCTGTGGTCACCTCTACTCTTTCCAGTGGCTATGGAA NM_004693RefSeq chr12
- 52424069 52434326 KRT75 9119 "keratin 75, type II"
GO:0005198|GO:0002244|GO:0045095|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112281_PI430048170 0.00777323924741684 0.4762227077819928.34233954531385
7.8485143430278 7.92625576284765 P P P 8.97094762465957 9.13481436668623
9.25819410431599 P P P LNCV6_112281_PI430048170 mRNA
GCTGGTCCCTCTCTCAAAAAGCTTATTAAGCCTGAAAAGCCAACTTTGTAACATATTTAA NM_001173488 RefSeq
chrX - 119588336 119593150 NKRF 55922 "NFKB repressing factor, transcript variant 3"
GO:0005515|GO:0005783|GO:0005730|GO:0005634|GO:0045892|GO:0003677|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139906_PI430048170 0.8584844362765161.00874340649405 0.579504090461103
0.4848044448297880.405380309403183A A A 0.4128743605675990.516042050156846
0.506140670458459A A A LNCV6_139906_PI430048170 mRNA
TGTTGCTGACCTGGACCAGGAGCAGCACCAAAGGAATTAGTGGGCGAAGGACCCATTGCA NM_178356RefSeq
chr1 + 152709046 152709434 LCE4A 199834 late cornified envelope 4A GO:0031424 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137902_PI430048170 0.3423476607847360.9512596964563812.64410567179
12.7373487943623 12.6661279309116 P P P 12.8644448881039 12.699786427062
12.6947290700639 P P P LNCV6_137902_PI430048170 mRNA
GGCATCGCAGATGGGGGTTCTTTCAGTTCAAAAGTGAGATGTCTGGAGATCATATTTTTT NM_001001852 RefSeq
chr22 + 49960494 49964072 PIM3 415116 "Pim-3 proto-oncogene, serine/threonine kinase"
GO:0005515|GO:0007346|GO:0043066|GO:0007049|GO:0005737|GO:0046777|GO:0004674|GO:0016572|GO:0006
915|GO:0006468|GO:0061179|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140977_PI430048170 0.1683942546496561.02490984780723 0.32417860681905
0.2803486905604030.269048551083527A A A 0.2526223231323270.260287686624633
0.254753621512803A A A LNCV6_140977_PI430048170 mRNA
ATCTCGCCACCTGAGAGGTTGCGCAACGTTCACCCCAAAGGCTCTTTTAAGAGCCACCCA NM_003493RefSeq chr1
- 228424844 228425325 HIST3H3 8290 "histone cluster 3, H3"
GO:0005515|GO:0046982|GO:0000723|GO:0005654|GO:0005634|GO:0000786|GO:0003677|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58835_PI430048170 0.1459989785819941.68477847119205 2.57702407138462 2.47987668833407
3.29188383383853 A A P 1.7726723333271 2.66956121223776 1.52948282079778 A P A
LNCV6_58835_PI430048170 mRNA
CCCAACATAAAAGACAGACTGATTAAAATAATGAGTATGCAGGGACAGATAACAGATTCA NM_001278412 RefSeq
chr12 - 31671136 31729174 AMN1 196394 "antagonist of mitotic exit network 1 homolog (S.
cerevisiae), transcript variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131821_PI430048170 0.0774296112954321 0.7015475543232528.19775426514982
7.8443963245273 7.69837766513394 P P P 8.71117796303965 8.17305070829444
8.38563055881975 P P P LNCV6_131821_PI430048170 mRNA
AGAACCTTTTGTTCTTGCAAGGAAAACAAGAATCCAAAACCAGTGACTGTTCTGTGAAAA NM_001098RefSeq chr22

+ 41469124 41528989 ACO2 50 "aconitase 2, mitochondrial"
GO:0051538|GO:0006099|GO:0051539|GO:0005506|GO:0003994|GO:0005634|GO:0006091|GO:0044281|GO:0005
739|GO:0006102|GO:0006101|GO:0005759|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128642_PI430048170 0.39663182356481 1.0217478028186 0.352962308739078
0.349156596406491 0.265700965889059 A A A 0.289814875075033 0.302546939279884
0.283952719314903 A A A LNCV6_128642_PI430048170 mRNA
ACTGAACACTGTAGGGTACCTTCCAGTCTTTTTCAAGATTGTTAAATTGAGACAAGTAAT NM_021116 RefSeq chr7
+ 45574525 45723115 ADCY1 107 "adenylate cyclase 1 (brain), transcript variant 1"
GO:0005516|GO:0005886|GO:0007268|GO:0005634|GO:0044281|GO:0007202|GO:0007409|GO:0007193|GO:0046
872|GO:0035556|GO:0005737|GO:0007173|GO:0071377|GO:0006171|GO:0006833|GO:0034199|GO:0070062|GO:0
048011|GO:0007616|GO:0042493|GO:0008294|GO:0055085|GO:0005524|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139545_PI430048170 0.0801381705361106 1.0444335347226 0.39148545779747
0.408474199786026 0.459547554198508 A A A 0.340177119161028 0.340310318957747
0.391129985521542 A A A LNCV6_139545_PI430048170 mRNA
GAAACTGTGTTCTCAACTCAAGGAGGAATAAAACTCATAAAACAAAAGCCTTGTAAGCAT NM_005390 RefSeq chr4
+ 95840087 95841474 PDHA2 5161 pyruvate dehydrogenase (lipoamide) alpha 2
GO:0006099|GO:0006090|GO:0005759|GO:0006006|GO:0005634|GO:0004739|GO:0006096 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144016_PI430048170 0.0100255007372575 0.633628111334719 0.368685667586156
0.373135161883732 0.357617217651713 A A A 1.14638401253403 1.00166979438792
0.916913781681929 A A A LNCV6_144016_PI430048170 mRNA
TAGATACTGTCATCCCCGTGTGGCTGAATCATGCAATGCACACTTTCATATTCCCCATCA NM_001143948 RefSeq
chr6 - 11713654 11779047 ADTRP 84830 "androgen-dependent TFPI-regulating protein, transcript
variant 1" GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133686_PI430048170 0.0329338993226191 0.738623794998405 7.26049007102827
7.62101959376992 7.42817226810946 P P P 7.91399657377177 7.94794838036616
7.77590400211278 P P P LNCV6_133686_PI430048170 mRNA
TGACTCAAGATTCCAAGGAGTTCTGCTCATTCTAATGATGGCCCATTCTACTTGCTCTGG NM_001015001 RefSeq
chr15 + 43692885 43699222 CKMT1A 548596 "creatine kinase, mitochondrial 1A"
GO:0005739|GO:0004111|GO:0034641|GO:0016310|GO:0006600|GO:0005743|GO:0044281|GO:0005524|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105952_PI430048170 0.0318960838407340 8.100148615075346 .50602165217076
6.25220517874202 6.37826557537281 P P P 6.78003352973604 6.67176579473597
6.60220188618582 P P P LNCV6_105952_PI430048170 mRNA
AAGCTGAAGCCCTACTCAATATAATAATAAAGAGACAAAAGAGGCCAGCCACCCACCTCC NM_032965 RefSeq
chr17_KI270857v1_alt - 232145 236612 CCL15 6359 chemokine (C-C motif) ligand 15
GO:0008009|GO:0007165|GO:0006955|GO:0006935|GO:0060326|GO:0007267|GO:0006874|GO:0005102|GO:0042
056|GO:0008201|GO:0005615|GO:0050918 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90848_PI430048170 0.00553739657676421 2.18997554784312 4.21813844940549
3.81275063209996 4.3219515384913 P P P 2.74741260810234 3.10802635526108
3.12281198490122 A P P LNCV6_90848_PI430048170 mRNA
GGTATACTGGCAGACATCTTTGTTTCCATGAGCAAGAACGATTATGAAAAGTTTAAAAAC NM_025144 RefSeq chr4
+ 112297342 112442608 ALPK1 80216 "alpha-kinase 1, transcript variant 1"
GO:0004674|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135411_PI430048170 0.0959065195252409 1.06079158498305 0.448363759914539
0.509983592263448 0.509180483572751 A A A 0.347656378428766 0.406643058919289
0.456607294133416 A A A LNCV6_135411_PI430048170 mRNA
TTCCAGTGCAAGATTCTCATGGTTGAATTCATAGTGGGCTTCTATGACTTCTGCCTTGCC NM_001242473 RefSeq

chr16 - 52026351 52073935 C16orf97 NA chromosome 16 open reading frame 97 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68763_PI430048170 0.5742608510964971.03459671797546 5.43729827146207 5.61240622034986 5.38841791134617 P P P 5.47676013473801 5.41067882922808 5.41221805306169 P P P
LNCV6_68763_PI430048170 mRNA
TGAGTATGAATTTTTCACCCATTTGGATAAACGTAGCCTGCCTGCTCTGACAAACATCAT NM_000277RefSeq chr12 - 102838325 102917603 PAH 5053 phenylalanine hydroxylase
GO:0034641|GO:0006559|GO:0005506|GO:0008652|GO:0004505|GO:0044281|GO:0042136|GO:0016597|GO:0042423|GO:0070062|GO:0055114|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137221_PI430048170 0.0957794326983823 0.7758081109238878.55646466999751 8.5232915560772 8.92708246680567 P P P 8.96719704913021 8.89716387114326 9.25197261483163 P P P LNCV6_137221_PI430048170 mRNA
CAGTCTTTCTGAAGCCCTGAAATGGTAATTGTAGCATTTCAGAAAATGTCTTTCATTTCA NM_000158RefSeq chr3 - 81489698 81761799 GBE1 2632 "glucan (1,4-alpha-), branching enzyme 1"
GO:0043169|GO:0005975|GO:0005978|GO:0005977|GO:0009405|GO:0006006|GO:0044281|GO:0006091|GO:0004553|GO:0003844|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139911_PI430048170 0.00314552225564424 0.4352324014233086.77587613571376 6.37744290489552 6.69435219885321 P P P 7.71417784681167 7.82724128061044 7.92865378040307 P P P LNCV6_139911_PI430048170 mRNA
GCTTTTCTTTCCAAGGTTGTGTGTTTGAACACATTTCTCCAAATGTTAAACCTATTTCAG NM_001200RefSeq chr20 + 6768097 6780263 BMP2 650 bone morphogenetic protein 2
GO:0005515|GO:0001658|GO:0003181|GO:0009790|GO:0005615|GO:0010894|GO:0003308|GO:0007507|GO:0007219|GO:0002062|GO:0030198|GO:0009887|GO:0033690|GO:0004745|GO:0030335|GO:0030501|GO:0009986|GO:0019211|GO:0000122|GO:0021978|GO:0030509|GO:0005160|GO:0005125|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134613_PI430048170 0.2058997577878560.95288420457389 14.7223811688627 14.6828657789336 14.596624708638 P P P 14.7223811688627 14.7012409326551 14.7885384773236 P P P LNCV6_134613_PI430048170 mRNA
TCTTGTCCCTTTCCCTACCTTTATATTTGGGGTCCTTTTTTATACAGGAAAAACAAAACA NM_000075RefSeq chr12 - 57747726 57752447 CDK4 1019 cyclin-dependent kinase 4
GO:0045859|GO:0005515|GO:0010468|GO:0071157|GO:0048471|GO:0008284|GO:0031100|GO:0006325|GO:0005634|GO:0048146|GO:0032403|GO:0005829|GO:0000082|GO:0002088|GO:0016538|GO:0000785|GO:0005667|GO:0010288|GO:0031965|GO:0043065|GO:0042493|GO:0030332|GO:0005730|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133546_PI430048170 0.1180212028370821.02073318910386 0.3941822857610450.3999734922596 0.417589262300278A A A 0.3722201669532640.3543807857507910.396125504215225A A A
LNCV6_133546_PI430048170 mRNA
GATATTTTGTGTAGCACATTCTGTTTGCGGTTGAGGGAATAAAGTATTTCACAAGTGAAA NM_005668RefSeq chr5 - 100806934 100903285 ST8SIA47903 "ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4, transcript variant 1"
GO:0003828|GO:0009311|GO:0007399|GO:0030173|GO:0000139|GO:0007411|GO:0006491|GO:0001574|GO:0006486|GO:0033691|GO:0006488|GO:0044267|GO:0006464|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74016_PI430048170 0.6214139228372491.40077414847248 0.4848193074876022.45460811041655 1.82961917017412 A A A 0.3682712575807061.67965747206195 1.56338969163143 A A A
LNCV6_74016_PI430048170 mRNA
CAATCACAAAAATACCCAGTCCGTTAATAACTGAGGAAGGACCCAACTTGCCAGAAATCA NM_032263RefSeq chr3 - 197889074 197960015 IQCG 84223 "IQ motif containing G, transcript variant 1" GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_138967_PI430048170 0.2360349898372250.843722393842951 5.24400894954912
4.71637775587885 4.85761720770541 P P P 5.18425860357181 5.25308654333384
5.16758821491651 P P P LNCV6_138967_PI430048170 mRNA
AGCCCAAAGTTGAAACCATGTGAGTGGAAAAAGCATTACATGGTACGTATAACCCCCAAA NM_015721 RefSeq chr17
- 744420 752261 GEMIN450628 gem (nuclear organelle) associated protein 4
GO:0005515|GO:0010467|GO:0006364|GO:0005730|GO:0034660|GO:0000387|GO:0005829|GO:0005737|GO:0016
020|GO:0032797|GO:0030532|GO:0005654|GO:0034719|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145661_PI430048170 0.0480175850389948 1.36022968496623 9.3963299508544
9.73778527416435 9.4954804170572 P P P 9.32911488596406 9.02927586023527
8.93095796237254 P P P LNCV6_145661_PI430048170 mRNA
AAATAAATATTGGCAAGGGGAGTGGAAATGACACCAAGAAGCCCCTCATGCTCATGGTTG NM_003492 RefSeq chrX
+ 153972539 153983195 TMEM187 8269 transmembrane protein 187
GO:0030133|GO:0008150|GO:0003674|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2222_PI430048170 0.0438568202931864 0.63287158451291 7.38178503831574
6.81952947580047 6.94829013003239 P P P 7.83576831270514 7.73391512902206
7.61316646380856 P P P LNCV6_2222_PI430048170 mRNA
ATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGATATAAGAG NM_023944 RefSeq
chr19 + 15673017 15697174 CYP4F12 66002 "cytochrome P450, family 4, subfamily F, polypeptide
12, transcript variant 1"
GO:0019369|GO:0000038|GO:0001676|GO:0006805|GO:0017144|GO:0044281|GO:0055078|GO:0043231|GO:0036
101|GO:0016324|GO:0005737|GO:0042371|GO:0008392|GO:0070330|GO:0005506|GO:0019373|GO:0018685|GO:0
050051|GO:0003091|GO:0003095|GO:0030195|GO:0005789|GO:0016021|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136460_PI430048170 0.136561832646535 1.0418622990064 0.359512549464987
0.3428737415087630.426981227138868 A A A 0.3072285936387480.297765797172665
0.347770599808927 A A A LNCV6_136460_PI430048170 mRNA
ATGACAGAGGTTTTAGTTCTCAATAGATCAGGGTTATAATCTGCACTTACCACACTCCCT NM_001005181 RefSeq
chr11 + 6107683 6108835 OR56B4 NA "olfactory receptor, family 56, subfamily B, member 4" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114545_PI430048170 0.5091391097843490.815621268135347 2.61250332701359
3.01027131548572 3.14499441787803 A P P 2.57853542648614 3.42736465310416
3.52238858886748 A P P LNCV6_114545_PI430048170 mRNA
CCAAAATTGGATAAAAATCCAAACCTAGGAGAAGACCAGGCAGAAGAGATTTCAGATGAA NM_001287583
RefSeq chr5 - 138285264 138338355 CDC25C 995 "cell division cycle 25C, transcript variant 4"
GO:0005515|GO:0048471|GO:0007088|GO:0019901|GO:0008283|GO:0050699|GO:0005634|GO:0000079|GO:0007
283|GO:0035335|GO:0005829|GO:0006260|GO:0007067|GO:0000086|GO:0051726|GO:0016032|GO:0005654|GO:0
000278|GO:0004725|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131210_PI430048170 0.5034580498637280.966461295164393 10.50018825405
10.5975252771987 10.3941754132077 P P P 10.6091530304789 10.5406280668217
10.4946076155936 P P P LNCV6_131210_PI430048170 mRNA
AAGCCCCCATTCCCTGAGAATCCTGTTGTTAGTAAAGTGCTTATTTTTGTAGTTAAAAAA NM_001128425 RefSeq
chr1 - 45329241 45340470 MUTYH 4595 "mutY homolog, transcript variant alpha5"
GO:0005515|GO:0032408|GO:0032407|GO:0032406|GO:0051539|GO:0032405|GO:0005634|GO:0046872|GO:0005
739|GO:0006281|GO:0045007|GO:0006284|GO:0016798|GO:0006285|GO:0005654|GO:0006298 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126628_PI430048170 0.0433762225675649 0.3220636601116561.33934987691901
1.80807128271307 2.7147834372806 A A A 3.63319860885976 3.88471643135483
3.57704853083833 P P P LNCV6_126628_PI430048170 mRNA

GGCAGCAAAGATGTCTGTTACATCTAAACTTGAATAATAAAGTTTTACCACCAGTTACAC NM_014112RefSeq chr8 - 115408495 115669028 TRPS1 7227 "trichorhinophalangeal syndrome I, transcript variant 1"
GO:0005515|GO:0003700|GO:0006366|GO:0005634|GO:0032330|GO:0000122|GO:0006607|GO:0043565|GO:0001501|GO:0002062|GO:0031063|GO:0007178|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142554_PI430048170 0.7484269087022750.96661303018465 6.94453388098512 6.25241594289062 6.4019651180922 P P P 6.62653772235736 6.69777379639231 6.51043075048711 P P P LNCV6_142554_PI430048170 mRNA
ACCTGGTGTTTGCCAAGTTAAAGGGCTATGCCCACTGGCCGGCGAGGATAGAGCACATGA NM_138574RefSeq chr6 + 22569448 22570521 HDGFL1 154150 hepatoma derived growth factor-like 1
GO:0034504|GO:0045944|GO:0005634|GO:0000122 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144411_PI430048170 0.0305938024700135 0.7712174780146441 4.2935646881726 4.2387163391468 4.0409570528822 P P P 4.5591228158255 4.612410385011 4.5370858116456 P P P LNCV6_144411_PI430048170 mRNA
GTCATTGCTCCGTTTGTGTTTGTACTAATCAGTAATAAAGGTTTAGAAGTTTGACCCTAA NM_001277764 RefSeq chr15 - 90230244 90234047 CIB1 10519 "calcium and integrin binding 1 (calmyrin), transcript variant a"
GO:0005515|GO:0030307|GO:0007286|GO:0031122|GO:0045653|GO:1900026|GO:0042127|GO:0071356|GO:0043025|GO:0090050|GO:0070374|GO:0017016|GO:0070062|GO:0038163|GO:0005813|GO:0005794|GO:0030335|GO:0005509|GO:0090314|GO:0070886|GO:0030027|GO:0044325|GO:0048554|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145682_PI430048170 0.0562580295404417 0.8148870872984247.83960860990318 7.93345903807715 7.82539355132073 P P P 8.24469015890393 7.99204903729938 8.2361312615735 P P P LNCV6_145682_PI430048170 mRNA
GCCACCCGACTCTCCAGTTAACCTCTTTTACTCTTTAATTCTGATTTACTGTGATGATTT NM_020343RefSeq chr20 - 20389627 20712623 RALGAPA2 57186 "Ral GTPase activating protein, alpha subunit 2 (catalytic)"
GO:0032859|GO:0005737|GO:0017123|GO:0046982|GO:0005886|GO:0061024|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137238_PI430048170 0.48403788613244 0.9029135976502484.53506589194391 4.3187486210206 4.97066763160347 P P P 4.6173332605575 4.89608346581633 4.81688628870569 P P P LNCV6_137238_PI430048170 mRNA
GCATAATGATTTCATTTTGATAATGTGCAGAATGGCCTCATAAGCTCACAGAAAGCAAAA NM_032138RefSeq chr13 - 41191574 41194566 KBTBD7 84078 kelch repeat and BTB (POZ) domain containing 7
GO:0005515|GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127333_PI430048170 0.38995530601024 1.23279888515543 0.582219736402994 0.4992888939760161.25867891378522 A A A 0.6293121630141190.428272125836083 0.495180066067855A A A LNCV6_127333_PI430048170 mRNA
CACAACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATG NM_024590RefSeq chr4 - 113900283 113979722 ARSJ 79642 "arylsulfatase family, member J"
GO:0006665|GO:0006687|GO:0005788|GO:0005576|GO:0004065|GO:0044281|GO:0044267|GO:0046872|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143464_PI430048170 0.00365715706316131 0.6443113363329428.85370555333284 8.75182989192398 8.58763995846943 P P P 9.33474929985699 9.47722098339661 9.28938789480009 P P P LNCV6_143464_PI430048170 mRNA
GAGCCGGTCAACTTTTTGCTCATGGCTAGTGAAATAAAGTTGTTTGAGTACTAGAAAAAA NM_024836RefSeq chr1 + 248838177 248849517 ZNF672 79894 zinc finger protein 672
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131642_PI430048170 0.4528107828098133.64268484462973 0.290372027068417

3.55942067602145 0.310740723118896 A P A 0.447362842188737 0.347127658444843
0.352899737299438 A A A LNCV6_131642_PI430048170 mRNA
CCATAACAGCCTCTGAATTTATTGCACCAAGTGTAATGAGAACATTTTGTATACAAGAGT NM_173554 RefSeq chr10
+ 61662960 61766333 C10orf107 219621 chromosome 10 open reading frame 107 NA . NA -
NA NA NA NA NA NA NA NA NA
LNCV6_131810_PI430048170 0.997460933739661 1.00200703933699 0.58517616406409
0.490773257191236 0.340404831502672 A A A 0.402881679317909 0.522567701192844
0.490077510606585 A A A LNCV6_131810_PI430048170 mRNA
TGAAGAATGGAGGTTGTTTCCAAAAGAAATAAAGAGAAACTTAGAAGTTGTCTCTGGACA NM_001253826 RefSeq
chr2 - 30910464 31138726 GALNT14 79623 "polypeptide N-acetylgalactosaminyltransferase 14,
transcript variant 2"
GO:0004653|GO:0006493|GO:0000139|GO:0030246|GO:0016266|GO:0016021|GO:0044267|GO:0046872|GO:0043
687 . NA - NA NA NA NA NA NA NA NA NA
LNCV6_133302_PI430048170 0.0701840878886273 0.756202021256542 6.71702248158365
6.61090996749546 6.83449530011984 P P P 6.88984329526508 7.12838208179113
7.32904852873843 P P P LNCV6_133302_PI430048170 mRNA
GTTTGGATCATGCTAAATTCTCACATGTAAACTGTGAGAAATGTGCCTTAAGTGTTTGAA NM_007044 RefSeq chr6
- 149594874 149648804 KATNA1 11104 "katanin p60 (ATPase containing) subunit A 1, transcript variant
1"
GO:0005515|GO:0008017|GO:0030424|GO:0005886|GO:0001578|GO:0005634|GO:0031122|GO:0030426|GO:0051
013|GO:0005737|GO:0008104|GO:0043025|GO:0005811|GO:0005813|GO:0046982|GO:0005815|GO:0005874|GO:0
005819|GO:0030496|GO:0005524|GO:0008568|GO:0000922|GO:0007067|GO . NA - NA NA NA NA
NA NA NA NA NA
LNCV6_144973_PI430048170 0.491253591510058 1.25095881369983 8.83151806352384 9.5430783944439
8.79730086104884 P P P 9.73964055187748 8.60787091482315 6.15199666329384 P P P
LNCV6_144973_PI430048170 mRNA
GAGGGGGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAG NM_001216 RefSeq chr9
+ 35673917 35681157 CA9 768 carbonic anhydrase IX
GO:0005886|GO:0042493|GO:0005730|GO:0071456|GO:0061418|GO:0031528|GO:0004089|GO:0044281|GO:0033
574|GO:0046903|GO:0016323|GO:0015701|GO:0008270|GO:0016021|GO:0002009|GO:0006730 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142277_PI430048170 0.0354867471428766 0.64903397696389 4.49966467533138
4.77009923474727 5.02466393911003 P P P 5.24940912155222 5.27935800026207
5.64888377160318 P P P LNCV6_142277_PI430048170 mRNA
CTCAGATATCATTTCGCCTTCGGTTGATGTAAGAAAATTCAAAAGCTACTCAAATCATTC NM_001129899 RefSeq
chrX + 46447188 46474639 KRBOX4 55634 "KRAB box domain containing 4, transcript variant 3"
GO:0005622|GO:0006355|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137649_PI430048170 0.0788619907850434 0.783747006297989 7.20434681625848
7.2051422406253 7.23102352675338 P P P 7.35398572710348 7.69228769809048
7.62717003382755 P P P LNCV6_137649_PI430048170 mRNA
CGTGTTCTGTGTTAGTGATCACTGCCTTTAATACAGTCTGTTGGAATAATATTATAAGCA NM_001002295 RefSeq
chr10 + 8054703 8075201 GATA3 2625 "GATA binding protein 3, transcript variant 1"
GO:0000987|GO:0005515|GO:0043627|GO:0032753|GO:0000790|GO:0003700|GO:0003180|GO:0006366|GO:0003
281|GO:0009791|GO:0009653|GO:0043523|GO:0007411|GO:0032689|GO:0010332|GO:0031929|GO:0035799|GO:0
000976|GO:0042472|GO:0001709|GO:0003713|GO:0006952|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130765_PI430048170 0.474776812522836 0.908429114226336 11.2578590382584
11.1339856790273 11.3158977992717 P P P 11.1297650155433 11.3381825933378 11.619316789202
P P P LNCV6_130765_PI430048170 mRNA

TCCATGCAGTCATGTTCACGTGCTAGTTACGTTTTTCTTCTTACACATGAAAATAAATGC NM_017556RefSeq chr1
+ 15758759 15786589 FBLIM1 54751 "filamin binding LIM protein 1, transcript variant 1"
GO:0016337|GO:0001725|GO:0034329|GO:0031005|GO:0008360|GO:0008270|GO:0005938|GO:0005925|GO:0033
623|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132018_PI430048170 0.8800477923834 0.9905843059066876.08147765043606
5.71111518560228 6.10904557979128 P P P 6.06900690598787 5.89524832533694
6.00616182029618 P P P LNCV6_132018_PI430048170 mRNA
GAGGCTACTATAGGGTACAGAATAACAACATGAAAGCAATCAACCCTGTATAAATAATGT NM_004426RefSeq chr12
+ 8914719 8941464 PHC1 1911 polyhomeotic homolog 1 (Drosophila)
GO:0035102|GO:0031519|GO:0016604|GO:0071300|GO:0016574|GO:0003682|GO:0008270|GO:0007275|GO:0005
654|GO:0005634|GO:0003677|GO:0001739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132082_PI430048170 0.7817152030499651.18170631470676 0.536325494100224
2.04732136328083 1.32790375220348 A A A 1.55403655188916 1.15246835969871
0.757131800245474A A A LNCV6_132082_PI430048170 mRNA
TGTTGGAGTAGGGGCAGAGGGAGGGAGCCAAGGTCACTCCAATAAAACAAGCTCATGGCA NM_001129RefSeq
chr7 + 44104360 44114565 AEBP1 165 AE binding protein 1
GO:0005516|GO:0000977|GO:0003700|GO:0003714|GO:0005634|GO:0000122|GO:0001227|GO:0005615|GO:0006
351|GO:0031012|GO:0001501|GO:0005737|GO:0007517|GO:0006508|GO:0004180|GO:0008270|GO:0070062|GO:0
004181 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135788_PI430048170 0.0173519290445769 0.2346851708803110.359189657319819
0.3353990733694990.265802404502613A A A 2.06661070580788 2.08833520992804
2.91137744596346 A A P LNCV6_135788_PI430048170 mRNA
CAAGAGAACAATAGAGTGCGTCTCTTGGGGAAACATAATAAAAATGAACTTTTCTCACCT NM_001099435 RefSeq -
- 0 0 --- NA speedy/RINGO cell cycle regulator family member E5 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132591_PI430048170 0.2996292496750740.8874775221128274.5150869963425
4.59959858799205 4.92983075648289 P P P 4.87559119655327 4.73105314328839
4.97795554195522 P P P LNCV6_132591_PI430048170 mRNA
TTTATTATACCAAGGTGTTCTAATGCCATCATATGAAGACAGATGCTTCAAACAACCTGC NM_173348RefSeq chr10
+ 73168118 73242181 FAM149B1 317662 "family with sequence similarity 149, member B1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127091_PI430048170 0.4655762166942061.11799064130642 4.52152297048152
4.28251566929767 3.98104387824081 P P P 4.27640708375534 4.10525384955448
3.95285102953012 P P P LNCV6_127091_PI430048170 mRNA
TCTGCAGCAGGAACTCTGGACCCCTGGGCCTCATCACAGCAATATTTAACAATTTATTCT NM_004625RefSeq chr3
- 13818584 13880121 WNT7A 7476 "wingless-type MMTV integration site family, member 7A"
GO:0070307|GO:0090263|GO:0046330|GO:0071560|GO:0030010|GO:0005615|GO:0005109|GO:0000578|GO:0002
062|GO:0007548|GO:0014834|GO:0032355|GO:0048018|GO:0051965|GO:0009986|GO:0014719|GO:0005796|GO:0
031133|GO:0005125|GO:0010595|GO:0045165|GO:0050808|GO:0001502|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143399_PI430048170 0.0946715042594021 0.5800933126169824.67953940126328
4.06621436214947 5.07214496943356 P P P 5.05551332054717 5.40590644190578
5.79161514435004 P P P LNCV6_143399_PI430048170 mRNA
GCACCTAAAAGGGTATGTTAAAATCACCATTTCTCAGGTCAAAATACTGTGAATAAGTCT NM_025203RefSeq chr2
- 24029335 24047426 C2orf44 80304 "chromosome 2 open reading frame 44, transcript variant 1"
GO:0019900|GO:0051259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132717_PI430048170 0.0212558643576523 1.83545377600608 7.5620976385649
7.83155384808964 8.06771991350767 P P P 6.95021038647007 6.89266006911765
7.03082693644562 P P P LNCV6_132717_PI430048170 mRNA

AAAGTTTGGAAGATCTTTAAATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGT NM_019029 RefSeq chr7 - 28995630 29146537 CPVL 54504 "carboxypeptidase, vitellogenic-like, transcript variant 2" GO:0004185|GO:0006508|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66220_PI430048170 0.15301037466708 0.8752331254350227.51215194176518 7.28532191276863 7.29268176307111 P P P 7.45543230167191 7.7118491127104 7.49807131742605 P P P
LNCV6_66220_PI430048170 mRNA
TTGTTTGCTTTTAATTTGCCAACCTATCGCTGCTGGCAGCACTTTTTGAGCAAGCCGAGA NM_017623 RefSeq chr2 + 96816253 96835384 CNNM3 26505 "cyclin and CBS domain divalent metal cation transport mediator 3, transcript variant 1" GO:0005515|GO:0016020|GO:0005886|GO:0016021|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130501_PI430048170 0.0669696489685104 0.8819254368297928.75319278764866 8.80519925273618 8.83787177795413 P P P 9.03626140818022 8.86683932530421 9.03185983189747 P P P LNCV6_130501_PI430048170 mRNA
TTGTATGTACCACACATCTCCAGACGTTAATAAAGGACTCAAAGAGGTTTTTGTACTTGC NM_001145928 RefSeq chr2 - 127941216 128027295 SAP130 79595 "Sin3A-associated protein, 130kDa, transcript variant 1" GO:0010467|GO:0043966|GO:0030914|GO:0045814|GO:0003713|GO:0006325|GO:0040029|GO:0005654|GO:0000122|GO:0006351|GO:0004402 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98249_PI430048170 0.8773058577618281.06212443052532 0.3094412976310121.22179718685653 0.40764225824863 A A A 1.00871001447159 0.46655142713559 0.284166733175094 A A A
LNCV6_98249_PI430048170 mRNA
TGTGGCACTACCAGTGCAAAATGAAGATGAAGAGTATGACGAAGAGGACTATGAAAGAGA NM_001194998 RefSeq chr15 - 48737937 48811146 CEP152 22995 "centrosomal protein 152kDa, transcript variant 1" GO:0005515|GO:0051298|GO:0005813|GO:0006996|GO:0019901|GO:0007099|GO:0000086|GO:0030030|GO:0005654|GO:0000278|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141420_PI430048170 0.0227471447849088 1.37065796132842 9.05899909210953 9.11542931464089 9.00367194127162 P P P 8.77287729944797 8.51486906403382 8.51206744314814 P P P LNCV6_141420_PI430048170 mRNA
GCTGTCTCACTTCAGGTCCATGTATTTCACTTTTCTTAAATAAAAGAATCAGGTAACCTT NM_201522 RefSeq chr6 + 43059856 43075099 KLC4 89953 "kinesin light chain 4, transcript variant 2" GO:0005871|GO:0005737|GO:0008152|GO:0005874|GO:0003777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129874_PI430048170 0.0734758237864048 0.7897040544976326.49056304423763 6.26351750880493 6.65497173527016 P P P 6.74761534285826 6.77774753959238 6.92571816843415 P P P LNCV6_129874_PI430048170 mRNA
TGCGGGAGTAGGTGGGGAGAAACTTAAAGGTTCACTTGTAAAACAATAAAGTACTAAAGA NM_001079537 RefSeq chr14 - 39147810 39170430 TRAPPC6B 122553 "trafficking protein particle complex 6B, transcript variant 1" GO:0005515|GO:0005794|GO:0005783|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97166_PI430048170 0.0441076190780745 1.05362668855591 0.355756165354233 0.3509175664398790.292772680830517 A A A 0.2449273363342410.28239073573627 0.246573042671158 A A A LNCV6_97166_PI430048170 mRNA
TCATCCAACTGCACCTATAATATGTGAATTTCTTACAATGATGGCAGTCTGTCACACAGC NM_006095 RefSeq chr4 - 42408374 42657105 ATP8A1 10396 "ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1, transcript variant 1" GO:0005515|GO:0030335|GO:0000287|GO:0005794|GO:0005886|GO:0005783|GO:0055085|GO:0005524|GO:0045332|GO:0019829|GO:0034220|GO:0042584|GO:0016020|GO:0004012|GO:0008152|GO:0061092|GO:0007612|GO:0016021|GO:0006812|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145269_PI430048170 0.0365782018632880.6131842195116696.34942045221659 6.3153302841615 6.44802440511476 P P P 6.76281059197012 7.20489045801517 7.22016773286481 P P P

LNCV6_145269_PI430048170 mRNA
AGAGGGGAGAGTTAGAAGGAATATTCGGCTTTTCTATTTTATATCCTCCTAGGTGAAATT NM_144970 RefSeq chrX
- 40626920 40647567 CXorf38 159013 chromosome X open reading frame 38 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_126666_PI430048170 0.1113547415969660.5572301528753132.08513636039118
2.72679925364629 2.55246892746101 A A A 3.84538717684764 3.1428499382151
2.76887012574027 P P P LNCV6_126666_PI430048170 mRNA
GGTTGGGACTGTTTTTATTACCTTAGATTTCCAAGTTGTCCTAAATATAAGATGCAGTTC NM_001080480 RefSeq
chr6 - 20099685 20212464 MBOAT1 154141 "membrane bound O-acyltransferase domain
containing 1, transcript variant 1"
GO:0036150|GO:0016747|GO:0005789|GO:0044281|GO:0016021|GO:0006644|GO:0046474|GO:0036152 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135138_PI430048170 0.0836846175192397 1.29073161549846 6.17410672482495
5.84755100481089 6.13881443477859 P P P 5.90611441729405 5.657193523755
5.48273493629539 P P P LNCV6_135138_PI430048170 mRNA
TGATAAGAGAGTCGGTATTGAGAAGTTTAAATTTGTGAATTTGAAGGCTGCGTGGGTGTG NM_012453 RefSeq chr7
- 73568945 73578683 TBL2 26608 transducin (beta)-like 2 GO:0008150|GO:0005575 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133140_PI430048170 0.4471399256733240.7238091452549540.381183866496846
0.2687608345167140.317325237768663 A A A 1.44612377822823 0.294580423929609
0.303422106836901 A A A LNCV6_133140_PI430048170 mRNA
TAAATCTTGGCTGACAGTGGGAAGCACCAGGTTTGAAATCAGATGGCTTTATTTTTCTTT NM_001029870 RefSeq
chr4 - 76894928 76897849 SOWAHB NA sosondowah ankyrin repeat domain family member B
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144457_PI430048170 0.7745935402434481.08301228717668 0.39516208423896
1.17653213973694 0.414567284412598 A A A 0.31496102933063 0.327476596517347
1.02382510136645 A A A LNCV6_144457_PI430048170 mRNA
GTCATTTCAGGTAAATATGACAAGTGGTGGAGCATGAAGTTTTCTAATTTGACTTAATCC NM_173653 RefSeq chr3
- 143265221 143848531 SLC9A9 285195 "solute carrier family 9, subfamily A (NHE9, cation proton antiporter
9), member 9"
GO:0005515|GO:0015385|GO:0031902|GO:0035725|GO:0016021|GO:0055037|GO:0055085|GO:0006885|GO:0006
811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135454_PI430048170 0.00695104909331693 0.7020197569112877.17727683950563
6.96811450868892 7.04416767861699 P P P 7.59335314844191 7.52733051359824
7.60669452470667 P P P LNCV6_135454_PI430048170 mRNA
TTGAAAAAGTCTTAAAGAGCCACAGACAAGACTACCTTGTTGGCAACAAGCTGAGCTGGG NM_153699 RefSeq chr6
- 52831742 52846095 GSTA5 221357 glutathione S-transferase alpha 5
GO:0005737|GO:0006749|GO:0004364|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134844_PI430048170 0.2219440895075621.3833256805903 0.393812653728663
1.24021509292855 0.838620510608669 A A A 0.4276283404164320.365214732136232
0.397470218489083 A A A LNCV6_134844_PI430048170 mRNA
TGCTGGGCAGAGAGGAATATTTAAGAAATAAAGCTTGGACCCAGATTTTTCCACAAAAAA NM_001009606 RefSeq
chr16_KI270856v1_alt - 41593 48453 HS3ST6 NA heparan sulfate (glucosamine) 3-O-sulfotransferase 6
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_37339_PI430048170 0.1195381257219351.13571616702104 7.26452845562068 7.23787326469248
7.26378592681265 P P P 6.94188708981815 7.19120664409645 7.07168813470845 P P P
LNCV6_37339_PI430048170 mRNA
CGCTATGGACCCCTGACCCCGTGGGGTCGCTCGGACTCTTAACGTGTGGACTGACCGCTA NM_006910 RefSeq chr16
+ 24539586 24572862 RBBP6 5930 "retinoblastoma binding protein 6, transcript variant 1"

GO:0005515|GO:0004842|GO:0005815|GO:0005694|GO:0016874|GO:0005730|GO:0001701|GO:0061053|GO:0005
737|GO:0035264|GO:0042787|GO:0048568|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143355_PI430048170 0.3513167364905490.6184994726700721.94226050609806
0.3747811368441840.33169501385188 A A A 2.5497638277996 1.23362325553366
1.09610866823096 A A A LNCV6_143355_PI430048170 mRNA
GCCCCACTCATGATCACCATTTTATTTTCATAATAAAGAGTGACGTTACACGTTGTAAAA NM_022053RefSeq chrX
- 102360394 102440008 NXF2 56001 nuclear RNA export factor 2
GO:0005737|GO:0006406|GO:0000166|GO:0003723|GO:0042272|GO:0050658|GO:0007275|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139752_PI430048170 0.2228739986024960.6331221593482133.73802612613533
2.93033575520773 2.14424861562709 P A A 3.71069037069954 3.80710775348538
3.70124222521783 P P P LNCV6_139752_PI430048170 mRNA
GGAGATTGCCGCCACCCTGGAGCTCAATGAAACACAGGTCAAGATTTGGTTCCAGAACCG NM_002144RefSeq chr17
- 48529444 48530910 HOXB1 3211 homeobox B1
GO:0007389|GO:0006355|GO:0019904|GO:0048704|GO:0005634|GO:0007275|GO:0009952|GO:0003677|GO:0006
351|GO:0043565|GO:0021571|GO:0021570|GO:0048646|GO:0021754|GO:0045944|GO:0021612 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127986_PI430048170 0.0930025562596005 1.20504926448288 9.10993057322625
8.77501420580079 8.94784618051871 P P P 8.56652299643965 8.75198767818033
8.71967984062308 P P P LNCV6_127986_PI430048170 mRNA
AGAACATTGCCAACATCATGAAGACACTCGCCTATCGAGGCTTCATCTTCAAGCAGACAT NM_024066RefSeq chr1
- 44221069 44355279 ERI3 79033 "ERI1 exoribonuclease family member 3, transcript variant 1"
GO:0005737|GO:0000175|GO:0005730|GO:0046872|GO:0000467 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135929_PI430048170 0.00268359979566903 0.4781036204312266.70746741067875
6.92692655044995 7.0093925618512 P P P 7.72862348365442 7.95708733393224
8.13935804218723 P P P LNCV6_135929_PI430048170 mRNA
CAGAGTTATGGTGCCGAATTGTCTTTGGTGCTTTTCACTTGTGTTTTAAAATAAGGATTT NM_001256163 RefSeq
chr11 + 102347373 102378670 BIRC2 329 "baculoviral IAP repeat containing 2, transcript variant 2"
GO:0005515|GO:0035631|GO:0004842|GO:0034121|GO:0016874|GO:0051591|GO:0002756|GO:0042127|GO:0043
123|GO:0060544|GO:0043027|GO:0060546|GO:0000209|GO:0001741|GO:0003713|GO:0001890|GO:0002224|GO:0
038061|GO:0045087|GO:0045088|GO:0009898|GO:0008270|GO:0035666|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130745_PI430048170 0.1972639074644460.8324254977129225.75121759147994 5.3933154568051
5.51955008167225 P P P 5.59574696348956 5.80358852611058 6.04632389002252 P P P
LNCV6_130745_PI430048170 mRNA
AATAGGCGTCCACCAATGATTATCCATATGTGTTCTTAATTTTTAACTGCTGGAAGTGTT NM_001290223 RefSeq
chr10 + 126905408 127452517 DOCK1 1793 "dedicator of cytokinesis 1, transcript variant 1"
GO:0005515|GO:0048010|GO:0017124|GO:0007264|GO:0006915|GO:0005634|GO:0006911|GO:0005829|GO:0043
547|GO:0005085|GO:0007165|GO:0005737|GO:0016477|GO:0016020|GO:0007596|GO:0007411|GO:0002244|GO:0
007229|GO:0045087|GO:0005654|GO:0038096|GO:0005096 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_141779_PI430048170 0.3728653478535860.51241078769262 0.963872844578366
0.4961976309386570.384674655059851 A A A 0.5005965945757640.929790114178057
2.53290044492725 A A P LNCV6_141779_PI430048170 mRNA
CCCCTGAGCTGAATAAAGATGATTTAAGCATAATAAATCGTTAGTGTGTTCACATGAGTT NM_001098668 RefSeq
chr10 - 79555851 79560407 SFTPA2 729238 surfactant protein A2
GO:0005581|GO:0007585|GO:0005578|GO:0030246|GO:0005576|GO:0005615 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_129962_PI430048170 0.4999380032818960.9806645973985790.390272751973545
0.4200671537556760.343651482151878A A A 0.4711022924670570.372006888077578
0.394532891199118A A A LNCV6_129962_PI430048170 mRNA
TTAAATAGACGTAGATGCATATGTGTTGCATTAGGTGAAAAGAAAAACTGCCAGGGAGTT NM_001033564 RefSeq
chr6 + 112087470 112102790 FAM229B 619208 "family with sequence similarity 229, member B" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137762_PI430048170 0.0591624845997962 1.96665245860697 6.05875994502415
6.26454381209421 6.11494352963599 P P P 5.66824868753104 4.79808102435082
4.88536513564343 P P P LNCV6_137762_PI430048170 mRNA
GCTTGCTTTGCTGTTTGGGATTTGCCTCCAGAATAAAGGTCCTTTTTGTTGTTGAAAAAA NM_001013706 RefSeq
chr19 - 4522530 4535196 PLIN5 440503 perilipin 5
GO:0005811|GO:0010867|GO:0019915|GO:0031999|GO:0060192|GO:0060193|GO:0035359|GO:0010884|GO:0010
897|GO:0034389|GO:0042802|GO:0005829|GO:0005739|GO:0005737|GO:0010890|GO:0032000|GO:2000378|GO:0
035473|GO:0051646. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138999_PI430048170 0.5166133137633580.9877667493159780.394483959735623
0.3989615801426660.356619745935721A A A 0.4377392686516780.367367710539882
0.397740909128405A A A LNCV6_138999_PI430048170 mRNA
TCTTGATGTATCATTCATGGAGCAGGCAAAACCAGACGTCTGGGAAGACCGTGAACTTAA NM_018690RefSeq chr16
+ 28494648 28498970 APOBR 55911 apolipoprotein B receptor
GO:0034361|GO:0016020|GO:0005886|GO:0030229|GO:0034362|GO:0006869|GO:0042627|GO:0006641|GO:0006
898|GO:0008203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130357_PI430048170 0.0226576687158059 0.6831819794728984.58748851091032
4.24345316318223 4.31709346698744 P P P 5.06600011384989 5.0166311428257
4.71282108078654 P P P LNCV6_130357_PI430048170 mRNA
TTCTCACAACCTCAGCCCACTCTCAGTCAAGGAGGGCAGAAAATAAAAGATGACATCACT NM_001300RefSeq chr10
- 3775995 3785281 KLF6 1316 "Kruppel-like factor 6, transcript variant A"
GO:0005737|GO:0030183|GO:0019221|GO:0005634|GO:0045893|GO:0003677|GO:0046872|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133931_PI430048170 0.0372280871416356 1.72277191118831 4.47385562520082
4.98925839422509 4.98201380610825 P P P 4.34740368936164 3.68717493451046
4.03936858661149 P P P LNCV6_133931_PI430048170 mRNA
ACTACTGGGGGGATAGATGGTCATAACCAAATAAATCTGGGAATCACTGGATTAAACTAA NM_014294RefSeq chr8
- 70573217 70608459 TRAM1 23471 translocation associated membrane protein 1
GO:0005515|GO:0010467|GO:0005783|GO:0006614|GO:0006613|GO:0005789|GO:0016032|GO:0004872|GO:0016
021|GO:0044267|GO:0006412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138281_PI430048170 0.0956520243917547 1.0656968730076 0.463048159001544
0.5505662948674240.524780330577617A A A 0.36077216302599 0.428045350255668
0.473363520435729A A A LNCV6_138281_PI430048170 mRNA
CAGAAAGGCACATACTAGTGCCTTTTAGTACAATTTTATGTCATGTAGAAGAAAATGGCA NM_012161RefSeq chr4
- 15604383 15655412 FBXL5 26234 "F-box and leucine-rich repeat protein 5, transcript variant 1"
GO:0005515|GO:0048471|GO:0004842|GO:0016567|GO:0005506|GO:0000151|GO:0031146|GO:0055072|GO:0019
005. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91962_PI430048170 0.0871305797747805 1.27083790777991 3.77904937768508 3.8173814238196
3.83449228731022 P P P 3.32213106780081 3.68298765685675 3.36119877072744 P P P
LNCV6_91962_PI430048170 mRNA
TTGTGAAGCTGGCCTACGAGTCTGACGGGATCGTGGTTTCCAACGACACATACCGTGACC NM_025079RefSeq chr1
+ 37474517 37484377 ZC3H12A 80149 zinc finger CCCH-type containing 12A
GO:0005515|GO:0090305|GO:0005886|GO:0032715|GO:0043031|GO:0032720|GO:0006915|GO:0010884|GO:0032

088|GO:0001525|GO:0046872|GO:0030154|GO:0010628|GO:0005737|GO:0071222|GO:0004519|GO:0045019|GO:0010629|GO:0045600|GO:0005654|GO:2000379|GO:0010508 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145583_PI430048170 0.0374939386000497 9.12458161506015 4.4673942653724 4.85965230921763 4.82160750183047 P P P 0.338730274594955 2.61397476569116 0.399337370225094 A P A LNCV6_145583_PI430048170 mRNA
TGACATGTAAATGCACCTGCACCGTTTCTGAGCCGGGAGAGTGTTTACTTAAAATCATGC NM_144727 RefSeq chr7 - 151428831 151440170 CRYGN 155051 "crystallin, gamma N" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108441_PI430048170 0.0532001577537273 0.429396507850678 2.17653932023412 3.26576662580582 2.76929280629102 A P A 4.04826249180832 3.94921056252382 4.07158907102505 P P P LNCV6_108441_PI430048170 mRNA
TTTTTGAGCAGGATCTGTAAAAGCATAATTGAATTTGTTTCACCCCCGTGGATTCCAGTG NM_017763 RefSeq chr17 - 58352499 58417582 RNF43 54894 ring finger protein 43
GO:0005515|GO:0004842|GO:0016567|GO:0005886|GO:0016874|GO:0072089|GO:0030178|GO:0005635|GO:0005109|GO:0038018|GO:0042787|GO:0005887|GO:0005789|GO:0008270|GO:0016055 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132741_PI430048170 0.380451547761183 0.791189301137665 0.410493073514079 0.31338163870508 0.305867121703281 A A A 1.1323641789021 0.512711833761997 0.255800319335305 A A A LNCV6_132741_PI430048170 mRNA
CCAGAAGCTACGAAAAAGGGAGCTGTTTAAATTTAATAAATCTCTGTTAGTAAAAGCTGC NM_018666 RefSeq chrX + 135893633 135913061 SAGE1 55511 sarcoma antigen 1 GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141209_PI430048170 0.00261216351339511 2.2519557931221 7.61272059657865 7.50809332113645 7.26485197039211 P P P 6.37944528692879 6.45216459672268 6.02752023135954 P P P LNCV6_141209_PI430048170 mRNA
ATGGAGAAAGCCACAGTTAGAACTGTTGGATACAGGAGAAGAAACAGCGGCTCCACTAAA NM_030643 RefSeq chr22 - 36189127 36204833 APOL4 80832 "apolipoprotein L, 4, transcript variant a"
GO:0006629|GO:0003674|GO:0006869|GO:0042157|GO:0005575|GO:0005615|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111755_PI430048170 0.0020374848214988 1.35272339140541 13.6146686313356 13.7538273204598 13.71970557011 P P P 13.223685522278 13.2492771098927 13.3098933610911 P P P LNCV6_111755_PI430048170 mRNA
GGTCCTGAGGCAGTTGTCTCCACACAAGTACTACTTCCTCGTGGGCTACAGTGAAACTTT NM_032014 RefSeq chr7 - 43866557 43869546 MRPS24 64951 mitochondrial ribosomal protein S24
GO:0070124|GO:0070125|GO:0008150|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0006412|GO:0005763|GO:0005762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134160_PI430048170 0.477534664790715 0.89685222507307 0.281497153818016 0.288506358262291 0.488110490348788 A A A 0.336656212076861 0.813214637305004 0.334643592830571 A A A LNCV6_134160_PI430048170 mRNA
TTACTGAGCATTAACAACACCAATAAAGGACAGCAGAGTCCCTAAATGTCTTTAAAGTTC NM_014464 RefSeq chr6 + 54308404 54390152 TINAG 27283 tubulointerstitial nephritis antigen
GO:0004197|GO:0006955|GO:0000166|GO:0006508|GO:0030247|GO:0007155|GO:0006898|GO:0005604|GO:0005044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132193_PI430048170 0.251091421068161 0.819561973200775 1.60348700877892 1.77406445076848 1.33381307526264 A A A 2.05278231812379 1.97191620778433 1.52839911864887 A A A LNCV6_132193_PI430048170 mRNA
TATTTATTTACCCAAATTTGAACTAGTCTGTTGGGTTGGGGGAAGGAGGTGGCTGCTACC NM_031478 RefSeq chr16 - 30024426 30030865 FAM57B 83723 "family with sequence similarity 57, member B"

GO:0000139|GO:0045599|GO:0005783|GO:0005789|GO:0050291|GO:0016021|GO:0046513 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131065_PI430048170 0.8292755955314261.00538902849559 0.342581482874242 0.3311054878568290.263648802964418A A A 0.2863858951662120.34964918351683 0.278228606600992A A A LNCV6_131065_PI430048170 mRNA
CAGGTAGCAGTGACTCCATTTTAATATTACAAGTGAGGAAATCAAGGCACATCAGTATGG NM_001129820 RefSeq
chr17 - 35548124 35558091 SLFN14 NA schlafen family member 14 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142765_PI430048170 0.00431423348886292 0.4313963944234287.09022359554879 6.92581766628949 7.35059035920043 P P P 8.32079182575781 8.26806597471225 8.44297838819477 P P P LNCV6_142765_PI430048170 mRNA
TTTGCCTGTATGGTACTGTTTTGTTTGTTAATAAAGTGCACTGCCACCCCCAATGCAGAC NM_001270458 RefSeq
chrX + 43654906 43746824 MAOA 4128 "monoamine oxidase A, transcript variant 2"
GO:0006805|GO:0007268|GO:0005741|GO:0044281|GO:0007269|GO:0005739|GO:0008131|GO:0042420|GO:0016021|GO:0042136|GO:0042135|GO:0006576|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144374_PI430048170 0.24594709280836 1.02004180567679 0.316387021069987 0.2559007045547320.280500259089045A A A 0.25720885945602 0.251709964343892 0.258617231657147A A A LNCV6_144374_PI430048170 mRNA
TTGTTCACCACCTGTCTTGCTTAAGCTACAAAATAAATGCATTTGACTGCACAGAAAAAA NM_138409RefSeq chr6 + 84033700 84090886 MRAP2 112609 melanocortin 2 receptor accessory protein 2
GO:0005515|GO:0007631|GO:0005886|GO:0005783|GO:0030819|GO:0031780|GO:0042802|GO:0097009|GO:0070996|GO:0006112|GO:0031783|GO:0031781|GO:0034394|GO:0031782|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145313_PI430048170 0.7727057679661141.16973010807966 1.99119141879228 1.91888892735094 0.333346768853486A A A 2.08679519988514 0.325473706774659 1.14236278744186 A A A LNCV6_145313_PI430048170 mRNA
GACAGAGAAGTGAAGGTATGGTAAACCATCTTAATTGAATTATGGCTTGTATCATGCTTA NM_001113475 RefSeq
chr14 - 77394020 77423056 NOXRED1 122945 NADP-dependent oxidoreductase domain containing 1
GO:0008150|GO:0003674|GO:0006561|GO:0005575|GO:0055114|GO:0004735 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129804_PI430048170 0.0558701404849238 0.3090597557555890.337688983002237 0.34114569483852 0.495348345483868A A A 2.7297698381263 1.37469601747003 1.81648133720307 P A A LNCV6_129804_PI430048170 mRNA
CAGTCCTCCCAGATTTCTGTAGCTATTTATGTAGCAGGCTCAATAAAATGTCTTCTCTCT NM_001278512 RefSeq
chr15 - 82659280 82709908 AP3B2 8120 "adaptor-related protein complex 3, beta 2 subunit, transcript variant 1"
GO:0030665|GO:0005215|GO:0048490|GO:0005737|GO:0005794|GO:0030137|GO:0030123|GO:0006892|GO:0005654|GO:0008089|GO:0006886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118450_PI430048170 0.000654058566017246 0.5079171444659794.67658044348979 4.6271374384492 4.80760058867045 P P P 5.70514382711143 5.63198139317725 5.71094098714342 P P P LNCV6_118450_PI430048170 mRNA
CTTAGTAGAGGCACTAACCATGTGACCCAAGGCAAAAGTGCTTAAGAAAAAGTGCTTTCT NM_019099 RefSeq
chr1 - 111722063 111739424 FAM212B 55924 "family with sequence similarity 212, member B, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128773_PI430048170 0.0264878599531631 0.560555944014789 8.0766872627286 7.59442874296474 7.93516701445771 P P P 8.34700053290226 8.76296464692886 8.97435497821228 P P P LNCV6_128773_PI430048170 mRNA
ATGATGCCTCTGGGTCTGTATGAGACCGTGATGAAGTAGAAATAAAGCCCTTCTGAGATG NM_015210 RefSeq
chr18 + 8717370 8832777 MTCL1 23255 microtubule crosslinking factor 1

GO:0005515|GO:0008017|GO:2000576|GO:0001578|GO:0090314|GO:0030496|GO:0005615|GO:0016328|GO:0016327|GO:0042803|GO:0045197|GO:0000922|GO:0005737|GO:0016324|GO:0010506|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138747_PI430048170 0.492708652081797 0.982701690480992 0.376568873661347 0.391407001104039 0.294289176408694 A A A 0.368500175621505 0.402342901180897 0.3685657337396 A A A LNCV6_138747_PI430048170 mRNA GGCTGTATATTTTGGTGGATTCTCTGTCCTATACATTTACTTAGAAGGAATGGAGTTATT NM_002864 RefSeq chr12 - 9148839 9208370 PZP 5858 pregnancy-zone protein
GO:0010951|GO:0007565|GO:0004866|GO:0004867|GO:0072562|GO:0005576|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135351_PI430048170 0.909937582579848 0.977573519734307 0.317898141095796 0.92973596473215 0.342542419560095 A A A 0.392896399796193 0.95567460989784 0.34289888049429 A A A LNCV6_135351_PI430048170 mRNA GAGGCACTTCAGAGCTAAAATAATTATGGCTTCCTTGCTTAATAAACATTTTCGTTCACT NM_173493 RefSeq chrX + 151563534 151676739 PASD1 139135 PAS domain containing 1
GO:0007165|GO:0005654|GO:0005634|GO:0004871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134267_PI430048170 0.0114543726282202 2.1057416173646 5.071887063783 4.4676840131711 4.72658702422714 P P P 3.96523141494429 3.69709526572056 3.38744636471813 P P P LNCV6_134267_PI430048170 mRNA GATCAGAAGCTCAGCATGGCCATTATGCCTAGTTTTGATGAATAAACATGGGAAAGCCAT NM_021916 RefSeq chr22 - 23741583 23751092 ZNF70 7621 zinc finger protein 70
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91894_PI430048170 0.379235408232741 1.04803778119932 0.32598196472848 0.330431563491826 0.503088331081212 A A A 0.323101740304399 0.291878260772243 0.348062583750621 A A A LNCV6_91894_PI430048170 mRNA TACCCCTGAATTGTACCCTTGTTTCAGAGCCTAACAGGGTTTTCTGATTTGCTGTTCCCT NM_001202429 RefSeq chr14 - 93934152 93976730 ASB2 51676 "ankyrin repeat and SOCS box containing 2, transcript variant 1"
GO:0035556|GO:0005515|GO:0000209|GO:0007165|GO:0004842|GO:0042787|GO:0045445|GO:0035914|GO:0031466 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136760_PI430048170 0.00517139746065646 0.290139708704721 4.28943292310592 3.50013101834024 3.92784068487285 P P P 5.31759881041293 5.6529051885818 6.10129905155032 P P P LNCV6_136760_PI430048170 mRNA GGAAGAACCTTAATTCTAAATTTGGTTCATGTGTGGCAAAGTTCTTAGCTTCTAAGAGTA NM_015306RefSeq chr1 - 55066358 55215366 USP24 23358 ubiquitin specific peptidase 24
GO:0004197|GO:0016579|GO:0004843|GO:0061136|GO:0043161 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134394_PI430048170 0.214590414739428 1.13626180141703 5.92238959228355 6.26062593239784 6.16334076114036 P P P 6.04357081968064 5.92598688192478 5.83712880574896 P P P LNCV6_134394_PI430048170 mRNA CAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTTCTGATAATGAAAAT NM_000410RefSeq chr6 + 26087280 26095241 HFE3077 "hemochromatosis, transcript variant 1"
GO:0005515|GO:0002474|GO:0048471|GO:0007565|GO:0005886|GO:0042612|GO:0045178|GO:0005102|GO:0010106|GO:0045177|GO:0031410|GO:0060586|GO:0003823|GO:0006879|GO:0006955|GO:0006461|GO:0019882|GO:0005887|GO:0001916|GO:0042605|GO:0042446|GO:0055037|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108874_PI430048170 0.135758825479155 1.37172863181715 6.08673367169456

5.86672260282903 6.25995741622752 P P P 5.99212192774488 5.28424914349485 5.5025529024682
P P P LNCV6_108874_PI430048170 mRNA
ATACCTTTTGGGAAGTAGTCCTTCAAAAACAGGACGTTCTCCTGCTCTATTACGCTCCGT NM_001303447 RefSeq
chr16 - 11679079 11742878 TXNDC11 51061 "thioredoxin domain containing 11, transcript variant
1" GO:0005515|GO:0034976|GO:0006457|GO:0005783|GO:0005789|GO:0003756|GO:0045454|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138619_PI430048170 0.270732193669721 1.34792629237203 2.43338378217296
3.31391041729614 2.71896145065873 A P A 2.19818703749823 2.34618587541606
2.72153584213558 A A P LNCV6_138619_PI430048170 mRNA
GCCAGGGAGGGCTGGCCTCACCACCACCGTCAATAAAGGATTTGAATCCCCATGAAAAAA NM_001145829
RefSeq chr11 + 1839488 1841680 TNNI2 7136 "troponin I type 2 (skeletal, fast), transcript variant
2"
GO:0005515|GO:0031014|GO:0006937|GO:0030049|GO:0005861|GO:0003009|GO:0005634|GO:0003779|GO:0045
893|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127795_PI430048170 0.967425288060756 0.995651416464729 0.386748419137146
0.263795176751797 0.439481476121499 A A A 0.282256310601477 0.519671558474045
0.300236362675975 A A A LNCV6_127795_PI430048170 mRNA
GTGAAGAAGCTTGGTGTATACCTGTGCAGGCACTAGTCCTTTACAGATGACAATGCTGAT NM_021068 RefSeq chr9
- 21186618 21187599 IFNA4 3441 "interferon, alpha 4"
GO:0005132|GO:0019221|GO:0005576|GO:0033141|GO:0045343|GO:0009615|GO:0005125|GO:0005615|GO:0002
250|GO:0051607|GO:0060337|GO:0060338|GO:0042100|GO:0007596|GO:0045087|GO:0006959|GO:0030183|GO:0
043330|GO:0002286|GO:0002323 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134525_PI430048170 0.216714575509931 0.657422825818024 0.261286925511677
0.277571958484274 0.385913971574731 A A A 0.866027787675069 1.37258469307154
0.31325434731081 A A A LNCV6_134525_PI430048170 mRNA
GGAAATAAAGCTAATGCTCTAGTTGAAAGAAAAGGAAAACTCCTGAAATCCTAGAATGTC NM_030820 RefSeq chr6
- 56056589 56247580 COL21A1 81578 "collagen, type XXI, alpha 1"
GO:0031012|GO:0005581|GO:0030198|GO:0005578|GO:0005788|GO:0005576 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_101920_PI430048170 0.00973178342841322 0.463551899460296 5.06980511850434
5.5349225018514 5.10460860736061 P P P 6.33563870316923 6.46738869481927
6.27511329579191 P P P LNCV6_101920_PI430048170 mRNA
ACACAGCTGCAGGGACCCTCGTGGATGTTGTATTAAATAAATTTGACCTTTGCTCTTTGC NM_000442 RefSeq chr17
- 64319415 64390878 PECAM1 5175 platelet/endothelial cell adhesion molecule 1
GO:0072011|GO:0005515|GO:0006909|GO:0008037|GO:0030054|GO:0005886|GO:0030168|GO:0050900|GO:0005
615|GO:0050904|GO:0007165|GO:0007596|GO:0030198|GO:0002576|GO:0031092|GO:0016021|GO:0007155|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83182_PI430048170 0.910374073777149 0.948118410846304 1.41988914074377 1.15486810811488
1.55692522983683 A A A 0.480017757075595 1.36117403752529 2.10772340626034 A A A
LNCV6_83182_PI430048170 mRNA
ATGCCATGAGCAAGAGGTCCAAGTTTGCCCTCATCACGTGGATCGGTGAGAACGTCAGCG NM_021149 RefSeq chr16
- 84565597 84618096 COTL1 23406 coactosin-like F-actin binding protein 1
GO:0005515|GO:0008150|GO:0031965|GO:0005737|GO:0050832|GO:0003779|GO:0019899|GO:0005856|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108528_PI430048170 0.0635055346491036 2.02423117811997 2.09303535165958
1.25346421520834 1.90423076506544 A A A 0.502946488626954 1.32031560755132
0.287253657948403 A A A LNCV6_108528_PI430048170 mRNA
AAATGAAGATGTTCAAGAGCCAGCTGACCCTCATGGAGCACAACTACCTGATTGAGTATC NM_024933 RefSeq chr2
+ 70978444 70985499 ANKRD53 79998 "ankyrin repeat domain 53, transcript variant 2" NA . NA -

. NA NA NA NA NA NA NA NA NA
LNCV6_137548_PI430048170 0.1121075451450061.27881069594213 14.1939627895001
14.2627727850364 14.5632906291421 P P P 13.7855668983544 13.9229621842509
14.2367013818813 P P P LNCV6_137548_PI430048170 mRNA
ACTCAGATGATAGTGACGAATGTCTGGCAGTGAGGACACATTTTGGCATTCTTGCTGACT NM_005003RefSeq chr16
- 23581013 23596318 NDUFAB1 4706 "NADH dehydrogenase (ubiquinone) 1, alpha/beta
subcomplex, 1, 8kDa"
GO:0005504|GO:0000036|GO:0031966|GO:0009249|GO:0005509|GO:0005743|GO:0044281|GO:0022904|GO:0005
747|GO:0005759|GO:0006120|GO:0006633|GO:0008137|GO:0044237 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_135358_PI430048170 0.3646980239411580.4718086885324730.418141092525028
0.4443465501233670.871595688627805A A A 2.63204019736988 0.363569200404672
1.07621166181997 P A A LNCV6_135358_PI430048170 mRNA
CTTTTACCTTTCAATCTTTGTATCTATTACTACATATGCTGCTGAAGGGAGCAGACTTTT NM_001004351 RefSeq chr7
+ 100307701 100322196 SPDYE3 441272 speedy/RINGO cell cycle regulator family member E3 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134827_PI430048170 0.8472316719065750.8994828244129560.419452776678981
1.08291327916976 0.648002264342138A A A 0.4804314446907031.51643049258263
0.409289366831542A A A LNCV6_134827_PI430048170 mRNA
AGCATTAGTGGGAAAGGCATGCCAAAATCTTCTCTATAATGTGTTCAATCTTGGGGGAAA NM_001294348 RefSeq
chr1 + 50109615 50203785 ELAVL4 1996 "ELAV like neuron-specific RNA binding protein 4, transcript
variant 6" GO:0006397|GO:0006396|GO:0000166|GO:0003723|GO:0017091|GO:0003730 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_144526_PI430048170 0.62480173249916 0.9189536409758855.3940459606623
5.36792228093042 5.4054485244808 P P P 5.15536734226731 5.56139660945864
5.75376340974264 P P P LNCV6_144526_PI430048170 mRNA
CCTTTTTAAAAAATAACCCCTCCATCCAGGATATGGAATCCAGCACCACAGTGCACAGGT NM_014824RefSeq chr11
- 72836744 73142098 FCHSD29873 FCH and double SH3 domains 2 GO:0005515 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129656_PI430048170 0.3930764091725410.7288395114168282.9979625887142
2.81364443006914 2.89736258149321 A A P 2.78281678147745 3.10402546824889 3.9401326015967
P P P LNCV6_129656_PI430048170 mRNA
TACACGCATGTATGCATGCACAAACATGTGTGTACATGTGCTTGCCATGTGTAGGAGTCT NM_002751RefSeq chr22
- 50263712 50270393 MAPK11 5600 "mitogen-activated protein kinase 11, transcript variant 1"
GO:0005515|GO:0010467|GO:0034142|GO:0007265|GO:0051403|GO:0005829|GO:0042692|GO:0035556|GO:0051
090|GO:0002756|GO:0000187|GO:0002755|GO:0034138|GO:0004707|GO:0048010|GO:0048011|GO:0038124|GO:0
006996|GO:0038123|GO:0034134|GO:0006950|GO:0002224|GO:0005524|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142373_PI430048170 0.4004662304571531.68005627899628 1.83936499133623
0.3023967335614450.270950655998242A A A 0.2483168569490910.268763299334405
0.250497795796579A A A LNCV6_142373_PI430048170 mRNA
AACCAGAAGCTAGTATCAGTTTGGGGCCTAAATGCAGCAGGTGTTCCTGATAAGCAGATA NM_001123376 RefSeq
chr10 + 44911315 44937010 TMEM72 643236 transmembrane protein 72 GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_128208_PI430048170 0.4957005709647521.04820538388506 10.2282645090254
10.4639188807539 10.3328272583205 P P P 10.3124103914907 10.3499956716232
10.1617267512808 P P P LNCV6_128208_PI430048170 mRNA
TGGCCATTTGCTGCCTCTAATTCCCTTTTGCTTTGCCATATTGGGCTATGTATTACCTCC NM_002028RefSeq chr14 +
64986788 65062652 FNTB 2342 "farnesyltransferase, CAAX box, beta"

GO:0018343|GO:0005515|GO:0042277|GO:0014070|GO:0008285|GO:0007603|GO:0005875|GO:0005965|GO:0022400|GO:0048146|GO:0019840|GO:0045787|GO:0005829|GO:0004660|GO:0010035|GO:0008144|GO:0042060|GO:0008270|GO:0051770|GO:0034097|GO:0004311|GO:0016056 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_41257_PI430048170 0.98121259099581 0.9885126831166543.66204899028069 4.1329207509218 4.02679946928427 P P P 3.52915057256056 3.9362943992841 4.3355485213807 P P P LNCV6_41257_PI430048170 mRNA
TAAACTCGTGAGTGCTTCCACTGATAACATAGTGTCACAGTGGGATGTTCTTTCAGGCGA NM_005057RefSeq chr1 - 205086141 205122022 RBBP5 5929 "retinoblastoma binding protein 5, transcript variant 1"
GO:0005515|GO:0006355|GO:0043627|GO:0044212|GO:0005730|GO:0006325|GO:0005634|GO:0035064|GO:0042800|GO:0006351|GO:0006974|GO:0035097|GO:0071339|GO:0048188|GO:0005654|GO:0051568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54263_PI430048170 0.3180254013517020.9041674346178299.52059645234028 9.50325616509691 9.85618646031999 P P P 9.76955572206777 9.69519035281611 9.87381922085203 P P P LNCV6_54263_PI430048170 mRNA
GTAACAGACTTGCGGTTAATTATGCAAATGATAGTTTGTGATAATTGGTCCAGTTTTACG NM_004261RefSeq chr1 - 86862444 86914424 SEPT15 NA "15 kDa selenoprotein, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2289_PI430048170 0.00515536710370495 0.7091671083061818.30207506215348 8.4142988447817 8.33984844441692 P P P 8.81863852083811 8.96232247548705 8.75719080201794 P P P LNCV6_2289_PI430048170 mRNA
TCCTTAACTTTGTACTAGACTGGCCTGGGCCTGCCCAGCTCAGCGTTATCAGTCTGTTTC NM_178863RefSeq chr16 - 29906335 29926232 KCTD13 253980 "potassium channel tetramerization domain containing 13, transcript variant 1"
GO:0004842|GO:0016567|GO:0035024|GO:0045740|GO:0019904|GO:0043149|GO:0005634|GO:0042802|GO:0006260|GO:0016477|GO:0031463|GO:0051260|GO:0005654|GO:0043161|GO:0017049 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144850_PI430048170 0.00094693976828549 0.2916546264521244.96232282256565 4.59295917718124 4.65316762269776 P P P 6.45598961187196 6.47542416397321 6.63137551419829 P P P LNCV6_144850_PI430048170 mRNA
ACTTAAGTACATTACTCTTCTCATTTCAAGGACATGAAAAAGTAAAGGATGGTCTGGCAC NM_020827RefSeq chr4 - 185159661 185204028 CFAP97 57587 "cilia and flagella associated protein 97, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135992_PI430048170 0.4667277209350780.88797324684358 3.87323492194942 3.9211003420414 3.95704026850848 P P P 4.34777902670226 3.76046314984063 4.09917258968889 P P P LNCV6_135992_PI430048170 mRNA
CCCAATACTTTTGTCCAATGTGGTTGGTCAAATCAACTGAATAAATTCAGTATTTTGCCT NM_005204RefSeq chr10 + 30434020 30461833 MAP3K8 1326 "mitogen-activated protein kinase kinase kinase 8, transcript variant 1"
GO:0023014|GO:0005515|GO:0000287|GO:0031295|GO:0006915|GO:0005524|GO:0005829|GO:0035556|GO:0000186|GO:0005737|GO:0007049|GO:0004702|GO:0000165|GO:0004674|GO:0045595|GO:0006468|GO:0004709 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138284_PI430048170 0.4794525923884220.8654324018871495.64104837917159 5.12126785050483 4.66804194887871 P P P 5.37542462005472 5.62814940030945 5.18135610028524 P P P LNCV6_138284_PI430048170 mRNA
TCTTTTGGGATTGTTGCCCCCCGGGTCTTTACCGAGTTGGGAACTGTGATGGCATCGGGA NM_018378RefSeq chr16 + 67159987 67164174 FBXL8 55336 F-box and leucine-rich repeat protein 8 GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133187_PI430048170 0.4419936107169931.05322873033389 0.569584092886669

0.71074744841754 0.709864952264023 A A A 0.6089780990654650.445902174674404
0.703696530120608 A A A LNCV6_133187_PI430048170 mRNA
GGGAAACCTTACAGTATGCTACAAAGAGTAGTAATAATAGCAGCTCTTATTTCCTGAAAA NM_000766 RefSeq chr19
+ 41088450 41096195 CYP2A13 1553 "cytochrome P450, family 2, subfamily A, polypeptide 13"
GO:0008392|GO:0006805|GO:0070330|GO:0005506|GO:0008395|GO:0019373|GO:0009804|GO:0044281|GO:0043
231|GO:0005737|GO:0019825|GO:0042738|GO:0005789|GO:0016712|GO:0055114|GO:0020037 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145024_PI430048170 0.31663234042156 1.21732558073645 3.95623171109905
3.94739264525888 4.28009803599065 P P P 3.28887094541567 4.009973243445
3.95412246733158 P P P LNCV6_145024_PI430048170 mRNA
TCAAAATACTTAGGCTTGGTTTTGATGCTAGAGAGGAAAAAGGACTTGGAGAGAGAGAAGNM_016089 RefSeq chr3
+ 48241105 48270989 ZNF589 51385 zinc finger protein 589
GO:0006355|GO:0005634|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145590_PI430048170 0.1098862413176281.58595878112607 8.74404097813318
8.65832676281149 8.46257936423423 P P P 8.42897669362345 7.78731959718152
7.50764124660996 P P P LNCV6_145590_PI430048170 mRNA
GTGCGGGAGGCGGACGGGGAGCAGAGACACAATAAAAATTCCCGGTCAAACCTCAAAAAA NM_014209 RefSeq
chr19 + 35641736 35644871 ETV2 NA "ets variant 2, transcript variant 1" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_115123_PI430048170 0.3157758487884910.9748966404295940.468887897247898
0.3785576777833990.424810769829491 A A A 0.4263434856785110.486356378947019
0.470339373066474 A A A LNCV6_115123_PI430048170 mRNA
TTATGAAATTGGTCCAGTTTATGAGATGGTAATTGCGCTGCAGAACACCACCACGACCAG NM_007335 RefSeq chr3
+ 38039204 38122737 DLEC1 9940 "deleted in lung and esophageal cancer 1, transcript variant DLEC1-
N1" GO:0003674|GO:0005737|GO:0008285 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144988_PI430048170 0.0413635883532891.50182714787667 9.08038349930361
8.75198767818033 9.19233979377513 P P P 8.21436874800893 8.33444164577963
8.70481900796526 P P P LNCV6_144988_PI430048170 mRNA
GAGGAGAACTACAGTTTTTCTTTTGAATTTAGTATTTGAGATGAGTTGTTGGGACATGCA NM_003129 RefSeq chr8
+ 124998477 125022283 SQLE 6713 squalene epoxidase
GO:0006695|GO:0006725|GO:0010033|GO:0050660|GO:0016126|GO:0005789|GO:0004506|GO:0044281|GO:0016
021|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144499_PI430048170 0.4293524560708571.02260244030171 0.297820546843155
0.3211417464789070.403026980359495 A A A 0.3262428924898590.30680143349122
0.294155992688342 A A A LNCV6_144499_PI430048170 mRNA
GTCAGGCTGACACAGACCATAAGAATTGTACAGATAATCCACAGAACTGTGATAAATAAT NM_181776 RefSeq chr5
- 151314977 151347590 SLC36A2 153201 "solute carrier family 36 (proton/amino acid symporter),
member 2"
GO:0005774|GO:0005280|GO:0005886|GO:0015078|GO:0006865|GO:0055085|GO:0015180|GO:0015193|GO:0015
816|GO:0035524|GO:0015187|GO:0016021|GO:0015808|GO:0070062|GO:0006811|GO:0015992 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128770_PI430048170 0.0291732356117517 0.81830479061679 11.3561612376953
11.3866183235675 11.2080245852308 P P P 11.4767872906342 11.689768347474
11.6496136628782 P P P LNCV6_128770_PI430048170 mRNA
CCAGCACAGGGGCCCTGAATTTATGTGGTTTTTATACATTTTTTAATAAGATGCACTTTA NM_020210 RefSeq chr15
+ 90184919 90229660 SEMA4B 10509 "sema domain, immunoglobulin domain (Ig), transmembrane
domain (TM) and short cytoplasmic domain, (semaphorin) 4B, transcript variant 1"
GO:0005886|GO:0045202|GO:0004872|GO:0016021|GO:0030154|GO:0007399 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_133733_PI430048170 0.15449778904624 0.8094604646979049.01117851238367
8.98565449777949 8.96318499726102 P P P 9.01651210560116 9.41452038218624
9.40932661454995 P P P LNCV6_133733_PI430048170 mRNA
TTCCCTCTTAATCTAGTTAAGCCAGGACATCCAGAATTCATTGCTTTAATAAAGAACCCA NM_004618RefSeq chr17
- 18273920 18315007 TOP3A 7156 topoisomerase (DNA) III alpha
GO:0005515|GO:0003917|GO:0007126|GO:0005694|GO:0016605|GO:0008270|GO:0005634|GO:0006265|GO:0003
677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138145_PI430048170 0.00662934384710104 1.84297577385528 9.28747764358876
9.41538263405198 9.35458178437784 P P P 8.5922119576318 8.5342851121298
8.26729459527578 P P P LNCV6_138145_PI430048170 mRNA
AATACAGAGTTTCTTTGGCCTATGGTATCGGGGTAAAGCTGAATCCTCTGAGGATGAGAC NM_031430RefSeq
chr17_KI270861v1_alt - 76178 80126 RILP 83547 Rab interacting lysosomal protein
GO:0005739|GO:0005515|GO:0043234|GO:0019886|GO:0017137|GO:0005770|GO:0031902|GO:0008333|GO:0030
670|GO:0015031|GO:0005765|GO:0005764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131793_PI430048170 0.2979062853735810.8252567816777127.66891842226503
7.85376178890792 7.94560906865987 P P P 7.72981433604647 8.15778919298372
8.35650655170186 P P P LNCV6_131793_PI430048170 mRNA
AATACTTACCAAAGAGGAGTAACCATCTCTGAGGGTGGGATTCTGGGGGAATTTTTGTTT NM_018944RefSeq chr21
- 32268218 32279065 MIS18A 54069 MIS18 kinetochore protein A
GO:0005515|GO:0006334|GO:0005634|GO:0034080|GO:0003674|GO:0008150|GO:0005737|GO:0007067|GO:0007
059|GO:0044030|GO:0005654|GO:0000775|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136729_PI430048170 0.1634535187429251.02880708834393 0.329135118665648
0.3260357978896420.270053846230035A A A 0.2639758178018190.275398310565203
0.263665166482629A A A LNCV6_136729_PI430048170 mRNA
ATTGCCAGTTCTGTAAGTGCCATCAATTAAAATAGTTTTGTGCAGTGACAGAGATTTTCT NM_001890RefSeq chr4
+ 69931080 69946570 CSN1S1 1446 "casein alpha s1, transcript variant 1"
GO:0005215|GO:0006810|GO:0005576|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132969_PI430048170 0.0808458051370815 1.01330113987489 0.319586105160385
0.2979470167023890.306324154304517A A A 0.2968515873735480.290341040500549
0.279505052233402A A A LNCV6_132969_PI430048170 mRNA
AAGGATGGCAGTATGTAATCCAGAAGCAAACTTGTATTAATTGTTCTATTTCAGGTTCTG NM_032973RefSeq chrY
+ 5056089 5742228 PCDH11Y 83259 "protocadherin 11 Y-linked, transcript variant c"
GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121327_PI430048170 0.33464740388205 0.7908983624753922.46482420206165
3.31593849691602 2.38987899481138 A P A 3.24104427046689 2.78836254692191
3.29795453686985 P P P LNCV6_121327_PI430048170 mRNA
CATTGTAGAATCCACACAGGAGAGAAACCCTATAAGTGTGAGGAGTGTGGGAAAGGTTTC NM_003425RefSeq chr19
- 43912623 43935259 ZNF45 7596 zinc finger protein 45
GO:0010467|GO:0006355|GO:0006367|GO:0003700|GO:0007275|GO:0005654|GO:0003677|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143979_PI430048170 0.3740935383963780.9195358235275320.295516664234655
0.2727274585387780.395215472092922A A A 0.6084157195590950.260736668139846
0.43943351374762 A A A LNCV6_143979_PI430048170 mRNA
TAAAGTGTAAGGCATTAGGTTCTGAGACAGCGGCAGAGAGAGCCATGCAAATGTTTAGGA NM_206893RefSeq
chr11 + 60785347 60801305 MS4A10 NA "membrane-spanning 4-domains, subfamily A, member 10"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136641_PI430048170 0.1416878481953910.5895235678152816.83380343180557
6.67164796312228 6.91201784888418 P P P 6.8988636534324 7.82864956280111
7.80761713810654 P P P LNCV6_136641_PI430048170 mRNA

TTCTCCTAATTTCTTCTGCCCGAAGGGTAAGTGGTGCGTCCAGCTTACACAATCATAATT NM_031942 RefSeq chr2 + 173354832 173368990 CDCA7 83879 "cell division cycle associated 7, transcript variant 1" GO:0006355|GO:0005737|GO:0042127|GO:0006915|GO:0005654|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136883_PI430048170 0.00974201890899598 1.26580983157373 10.1083548473779 10.2010087743572 10.0577149089804 P P P 9.75765971506482 9.79290200260793 9.79965959804457 P P P LNCV6_136883_PI430048170 mRNA
CACTGTGGTGGTCTGGATTCAGTGATTGATTCTATTTTTCTATAGCAAAGCATTTTTGTANM_017818 RefSeq chr1 - 3630766 3650107 WRAP73 49856 "WD repeat containing, antisense to TP73" GO:0005813|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109676_PI430048170 0.0447240513017358 1.17942387637428 4.97307854628669 5.09589622670593 5.13498597048746 P P P 4.84583082126318 4.7102380582937 4.93007496485678 P P P LNCV6_109676_PI430048170 mRNA
AGATTTTACAGGCTGAATTATTGGCAGTATATGGAGCAGACCCAGGCACACAGGATTCTA NM_057169 RefSeq chr12 - 109929801 109996389 GIT2 9815 "G protein-coupled receptor kinase interacting ArfGAP 2, transcript variant 1" GO:0043547|GO:0005515|GO:0008060|GO:0008277|GO:0032312|GO:0008270|GO:0005654|GO:0048266|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140458_PI430048170 0.154205915210567 0.809072201170727 8.60973415808736 8.70973899548188 9.07694765994111 P P P 9.11789673024684 8.93504676046238 9.28254706717446 P P P LNCV6_140458_PI430048170 mRNA
TCTTGATTTTTCTGTTCTGTTGAATTGCTATGTTCAGGATGTTCTAGGGGGTGGGGGCAG NM_001270643 RefSeq chr7 + 139359845 139423457 LUC7L2 51631 "LUC7-like 2 (S. cerevisiae), transcript variant 4" GO:0005515|GO:0016607|GO:0006376|GO:0019899|GO:0003729|GO:0005685 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145187_PI430048170 0.543534611458596 0.984344104355948 0.377097088878549 0.386760373101901 0.287930307143165 A A A 0.362374687842128 0.396234764510115 0.363258561512894 A A A LNCV6_145187_PI430048170 mRNA
CAGTATTTTGTTTTTCTCAAAAATGCTCTAGAACTTTCCTTGGCACATATAAAAGCACGG NM_182701 RefSeq chr6 - 28503295 28515793 GPX6 257202 glutathione peroxidase 6 GO:0004602|GO:0005576|GO:0006979|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90986_PI430048170 0.425142269439994 1.38581022777637 0.825923582397337 1.9711839274514 0.85490048987857 A A A 0.99707317119446 1.05433785894027 0.423172779020999 A A A LNCV6_90986_PI430048170 mRNA
ACTATGGCCTGGCTCACTGCAAGTACAGAGAGGACTACTTCGTGACTGCCGACCAGCTGT NM_001080395 RefSeq chr17 - 81117295 81166072 AATK 9625 "apoptosis-associated tyrosine kinase, transcript variant 1" GO:0005515|GO:0048471|GO:0005783|GO:0044295|GO:0051402|GO:0005524|GO:0004674|GO:0007420|GO:0030517|GO:0004713|GO:0016021|GO:0032482|GO:0055037|GO:0038083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127151_PI430048170 0.427366049667348 1.10825426679438 0.28792821951182 0.754272106023095 0.504336486151244 A A A 0.308499297222747 0.518136097633175 0.302216403652113 A A A LNCV6_127151_PI430048170 mRNA
ATTACCTGTTTGAACAGCCCTCTAGCCGTAGTATGATCTGGGATTCCATGTTTTGTGCTG NM_001135086 RefSeq chr16 + 2798484 2805132 PRSS41 NA "protease, serine, 41" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131564_PI430048170 0.34786517200985 1.33965837935071 3.02740014286693 3.30809592085254 3.04691424338119 P P P 1.73078840187077 2.78306989319862 3.23975574301883 A P P LNCV6_131564_PI430048170 mRNA
CAATGCCAGACCTGGCAACCCATCCTAACTGTATTATTAAAACCAAGTAAGAGTAAAAAA NM_001163692 RefSeq

chr15 - 65093003 65106359 UBAP1L 390595 ubiquitin associated protein 1-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56737_PI430048170 0.0297035661704687 0.8086464945135325.16384279387857
5.07240340068692 5.07025206495858 P P P 5.28213593718143 5.42284425581399
5.51341147098122 P P P LNCV6_56737_PI430048170 mRNA
ATTCCAGACCTGAGGTTGGGAAAAGAGGTTTTTCTCCTGCAGGGTACTGGGCCAGGCCCT NM_144588 RefSeq chr10
+ 97737120 97760907 ZFYVE27 118813 "zinc finger, FYVE domain containing 27, transcript variant 2"
GO:0005515|GO:0030424|GO:0048011|GO:0005783|GO:0005789|GO:0032584|GO:0016021|GO:0072659|GO:0055
038|GO:0046872|GO:0031175|GO:0030425 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130723_PI430048170 0.96923997196735 1.00370242029825 7.94986006692214
7.74107153938637 7.77576466473484 P P P 7.76117688097327 7.84603670787526 7.8505307718234
P P P LNCV6_130723_PI430048170 mRNA
CCGTGAAACATGGCATCATGCTCTAACTTCAGTATACCAATAAAACAATCAGCTTGCAAT NM_001291314 RefSeq
chr12 - 10880960 11171623 PRH1 5554 "proline-rich protein HaeIII subfamily 1, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127133_PI430048170 0.1981645865981634.18950101326095 0.318272371413
3.26487121950152 2.06026728852757 A P A 0.2569621452528930.258847144463805
0.258200964110179 A A A LNCV6_127133_PI430048170 mRNA
GATCATCCCAGCTGAACAATTTGAAAACTGTTCTGCCTTTTTGTTACATGAATCTGTCAG NM_005235 RefSeq chr2
- 211375716 212538628 ERBB4 2066 "erb-b2 receptor tyrosine kinase 4, transcript variant JM-a/CVT-1"
GO:0060045|GO:0005515|GO:0021551|GO:0005154|GO:0044212|GO:0001755|GO:0042803|GO:0007507|GO:0009
880|GO:0060644|GO:0046777|GO:0007173|GO:0043552|GO:0005759|GO:0070374|GO:0023014|GO:0030334|GO:0
018108|GO:0043235|GO:0045165|GO:0008543|GO:0045087|GO:0021889|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137907_PI430048170 0.4425459000171530.8809915655791883.85500149144382
3.28085901769027 3.17924586831951 P P P 3.80022053037533 3.68508384299827
3.45229563274996 P P P LNCV6_137907_PI430048170 mRNA
CACCTCCCTTCTTCTAACTAAATATAAAAAGATCCAGGGGACATAAATGTGGAGATTAAA NM_001007226 RefSeq
chr17 - 49598883 49678163 SPOP 8405 "speckle-type POZ protein, transcript variant 1"
GO:0005515|GO:0042787|GO:0016607|GO:0001085|GO:0031463|GO:0043161|GO:0005654|GO:0005634|GO:0042
593|GO:2000676|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110323_PI430048170 0.1759770687048262.78940778824451 3.25665523281406
3.69496560078827 1.66035311822233 P P A 1.7953197759924 1.50385719343892
1.53381955541159 A A A LNCV6_110323_PI430048170 mRNA
AGCAACAGGGGCCCCTTCTTCGGCTACTACTTCTTCAACGGGCTTCTGATGTTGCTGCAG NM_024552 RefSeq chr19
+ 8209332 8262420 CERS4 79603 ceramide synthase 4
GO:0006665|GO:0031965|GO:0005783|GO:0030148|GO:0005789|GO:0050291|GO:0044281|GO:0016021|GO:0046
513|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142945_PI430048170 0.7899515434415611.01297919251582 0.271162931066802
0.2940735114458850.443369011545055 A A A 0.3478096540771620.305195118124096
0.305498891224438 A A A LNCV6_142945_PI430048170 mRNA
GGAAGTCTCTTGAATGTAAGAAAGTGTTATTGGCAAAGCAATCCAATAAAATAAGCTACC NM_001251874 RefSeq
chr6 - 73241314 73310215 KHDC1 80759 "KH homology domain containing 1, transcript variant 1"
GO:0003723|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137454_PI430048170 0.14497336114376 1.2469506850373 3.68606176912516
4.11997667361422 3.90367364891639 P P P 3.80008744898559 3.58343054738012
3.37179290405456 P P P LNCV6_137454_PI430048170 mRNA
AATGAGATTCTCTATAAAAATGATCCCTTCATGCTGTGGCCTCCACAGAAGATGCCCTGG NM_145298 RefSeq chr22
+ 39040667 39055970 APOBEC3F 200316 "apolipoprotein B mRNA editing enzyme, catalytic polypeptide-

like 3F, transcript variant 1"
GO:0005515|GO:0030895|GO:0009972|GO:0003723|GO:0016553|GO:0045869|GO:0048525|GO:0010529|GO:0051607|GO:0005737|GO:0000932|GO:0045087|GO:0002230|GO:0030529|GO:0080111|GO:0004126|GO:0008270|GO:0070383|GO:0045071. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133741_PI430048170 0.000161353166583523 2.16861479389879 6.1029423246506 6.10994432459539 6.26454381209421 P P P 4.95056818310961 5.15321638557452 5.02180497820379 P P P LNCV6_133741_PI430048170 mRNA
TGGAATGTTAGAAGGGCATCTTGTACATCCACTGGGAATAAATTGCCTTGCACTTGGAAA NM_001258397 RefSeq chr17 + 44899711 44903679 CCDC103 388389 "coiled-coil domain containing 103, transcript variant 4"
GO:0060287|GO:0001947|GO:0036159|GO:0005737|GO:0031514|GO:0005930|GO:0030030|GO:0036158|GO:0003341|GO:0070286|GO:0071907|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100473_PI430048170 0.00176932920004661 0.6827464688021467.81241639756031 7.62531530497513 7.75161892554346 P P P 8.20255615932392 8.2913289687553 8.34967628920882 P P P LNCV6_100473_PI430048170 mRNA
ATTCTGGCAAAACTTCAGCAGGTTAACCCCCTTCAAAAAATGATACCTACAGGGAGGCAG NM_015185RefSeq chrX - 63634967 63755151 ARHGEF9 23229 "Cdc42 guanine nucleotide exchange factor (GEF) 9, transcript variant 1"
GO:0051056|GO:0048011|GO:0005737|GO:0043065|GO:0034220|GO:0032321|GO:0007264|GO:0007268|GO:0005089|GO:0097190|GO:0055085|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74781_PI430048170 0.3248652199238875.09638585424609 0.3738189398639124.72481723055986 3.68935973754424 A P P 0.3135788427177882.14151044978023 1.21358524845829 A A A LNCV6_74781_PI430048170 mRNA
ACTCTGAGGAGAGACCGTTCCAATGTGAAGAATGTAAAGCTTTGTTCCGGACCCCATTTT NM_018699RefSeq chr4 - 120691912 120922866 PRDM5 11107 "PR domain containing 5, transcript variant 1"
GO:0005515|GO:0016575|GO:0044212|GO:0008168|GO:0005634|GO:0000122|GO:0000978|GO:0006351|GO:0046872|GO:0043565|GO:0001078|GO:0070491|GO:0000278|GO:0045892|GO:0051567 . NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_129278_PI430048170 0.000335026403381197 1.50471684671019 13.3691934741772 13.4422303714197 13.3123099789241 P P P 12.7376169845131 12.8409638532931 12.7777355170759 P P P LNCV6_129278_PI430048170 mRNA
GAGGGGTGCCTTTTACATGTTCTATTTTGTATCCTAATGACAGAATGAATAAACCTCTTT NM_006427RefSeq chr14 + 104753132 104759659 SIVA1 10572 "SIVA1, apoptosis-inducing factor, transcript variant 1"
GO:0005515|GO:0005634|GO:0032088|GO:0097191|GO:0009615|GO:0006924|GO:0097193|GO:0046872|GO:0005175|GO:0005739|GO:0005737|GO:0001618|GO:0016032|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_112429_PI430048170 0.0602675148517813 1.20112043785452 9.20100605750685 8.99694098834714 9.11313179951928 P P P 8.68693642135687 8.95936735434658 8.86572363223533 P P P LNCV6_112429_PI430048170 mRNA
ATAATGATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGCCTTACGTGGGAAG NM_005796RefSeq chr16 + 67846915 67871316 NUTF2 10204 nuclear transport factor 2
GO:0005515|GO:0005215|GO:0005643|GO:0006611|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58392_PI430048170 0.0822679308421636 0.7772343599432715.15275792137784 4.93019279481006 5.15364011912519 P P P 5.49645073826498 5.19820672538397 5.61291114491255 P P P LNCV6_58392_PI430048170 mRNA
CCATACATATGTCCTAGAACTACAGTTAAGTGTGTTGTGGAATTTTAGTTTTGAATCCTG NM_024556RefSeq chr11 + 126211723 126262984 FAM118B 79607 "family with sequence similarity 118, member B" GO:0015030 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128063_PI430048170 0.39576040745171 0.7882094549166220.296257271252774

1.80703055401058 0.858776745308193 A A A 1.60915576320985 1.50217018018239
1.27185381926696 A A A LNCV6_128063_PI430048170 mRNA
ATAACTGCCAATGGCCCTGAGAACTCTGTGGGATAAAATGACCTGACTTGGATCATGAAA NM_182539 RefSeq chr6
- 44280159 44297721 TCTE1 202500 t-complex-associated-testis-expressed 1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_131113_PI430048170 0.3486618160605520.9665045320470260.303971419684737
0.4018201195528930.315863278602327 A A A 0.4580920010072490.352522198941055
0.358017607978272 A A A LNCV6_131113_PI430048170 mRNA
ACACTTGCATTAATAACATCCAACATACGGGAGAATGTGCTGTGGGACTTTTGGGACCAC NM_152473 RefSeq chr19
+ 53014090 53016580 ERVV-1 147664 "endogenous retrovirus group V, member 1" GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135384_PI430048170 0.6133042978411590.9849148667476810.346171357926404
0.3306374258134230.283122410414149 A A A 0.3169109209251650.407223115789796
0.300010940954421 A A A LNCV6_135384_PI430048170 mRNA
AAGAGTTTAACTTTGGGCCCAGAAACTCAACCATCAATGGAAACAGGGCAGTGACAAGTGNM_004983 RefSeq chr1
+ 160081569 160089422 KCNJ9 3765 "potassium channel, inwardly rectifying subfamily J, member 9"
GO:0005515|GO:0005886|GO:0015467|GO:0005887|GO:0010107|GO:0007268|GO:0034765|GO:0030165 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131975_PI430048170 0.1188262351813010.6205120862544284.59842753971053
4.52419691575446 4.85562374637316 P P P 4.83506372366816 5.34712141339991
5.74239877429269 P P P LNCV6_131975_PI430048170 mRNA
ATGCAGTTCACACAGTTCACACTCTGCATGTTGAGGAGTAAGTGGACAGATCTCTTAAGC NM_001256763 RefSeq
chr8 - 129839592 129939872 FAM49B 51571 "family with sequence similarity 49, member B,
transcript variant 1" GO:0005929|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144077_PI430048170 0.0743855202762478 0.2986708722332354.52243056508267
2.6315234064789 3.01572627295282 P A P 5.34869263222262 5.44882878155927 5.3344073197168
P P P LNCV6_144077_PI430048170 mRNA
GGTAGCAGTTTCTGTATGCAGTAGGCTGAAATATTTTGATGAACTGCTTAATTTTTGGAT NM_003478 RefSeq chr11
+ 108008681 108107761 CUL5 8065 cullin 5
GO:0005515|GO:0006511|GO:0005262|GO:0016567|GO:0008285|GO:0046982|GO:0005886|GO:0008283|GO:0051
480|GO:0005634|GO:0006970|GO:0097193|GO:0005829|GO:0000082|GO:0070588|GO:0016032|GO:0004872|GO:0
007050|GO:0031466|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133954_PI430048170 0.00234019460310332 0.4578045846701986.13570613995712
5.71915678451851 5.97567760436506 P P P 6.9052005307762 7.11510678565967
7.20579048046244 P P P LNCV6_133954_PI430048170 mRNA
GCCTTCTATTTACAGTGAAAAAGAGGTTTTGTGAAGGCATTTATGGTCATTACCAAAAAC NM_152678 RefSeq chr3
- 57625453 57693089 DENND6A 201627 DENN/MADD domain containing 6A
GO:0017112|GO:0005737|GO:0032851|GO:2000049|GO:0055037 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141668_PI430048170 0.000528166009995078 0.4867975830390259.43995042848788
9.18028260846892 9.31708601064076 P P P 10.3777867701536 10.2382706548135
10.4413347681367 P P P LNCV6_141668_PI430048170 mRNA
GACAATTGCCTTAAAACCTAGCACAGTCCTCAGAAATGAATACCGTGTTTCCACTGGAAA NM_003038 RefSeq chr2
+ 64989360 65023866 SLC1A4 6509 "solute carrier family 1 (glutamate/neutral amino acid transporter),
member 4, transcript variant 1"
GO:0005882|GO:0006821|GO:0005886|GO:0006865|GO:0005254|GO:0034590|GO:0030425|GO:0015193|GO:0015
195|GO:0015194|GO:0034589|GO:0015811|GO:0043025|GO:0006835|GO:0017153|GO:0070062|GO:0006811|GO:0
042470|GO:0005813|GO:0009986|GO:0005815|GO:0035249|GO:0055085|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_145631_PI430048170 0.0708711846862761.50366253149063 4.94153572119278
4.70636791095396 4.67680231978457 P P P 3.80720016753975 4.21975322598938
4.47103015165285 P P P LNCV6_145631_PI430048170 mRNA
CCCATCATTATGGTGTGTTCTTTGATTGACAAATCAGCTCTCAATAAACCACTTATAAGA NM_001099407 RefSeq
chr20 - 18383366 18467185 DZANK1 55184 double zinc ribbon and ankyrin repeat domains 1
GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144723_PI430048170 0.778801526493392 1.02250826129777 2.75072025817678
2.64546776072539 2.62454716790748 A A A 2.8394259334295 2.39377481599809
2.65995263589657 A A P LNCV6_144723_PI430048170 mRNA
GCCTGCATCAATAAATGAAAACGGTCTGCACCGCTGCGGGCGTGACGCTCCCGGAAAAAA NM_033310 RefSeq
chr11 + 64291320 64300031 KCNK4 50801 "potassium channel, two pore domain subfamily K,
member 4"
GO:0005244|GO:0005886|GO:0007268|GO:0005267|GO:0034765|GO:0016021|GO:0006813|GO:0071805 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127529_PI430048170 0.601892671033352 0.832871258023607 3.49445559225263
3.46022628098946 2.72747048131022 P P A 4.03968909875415 3.41395168817884
2.92476310678178 P P P LNCV6_127529_PI430048170 mRNA
TTTTCTATTTTCTATCGAATGCACGCAGCTGCCTCCCTCTTTGAGGTCTATTGTAAGATA NM_177998 RefSeq chr4 -
4188802 4226894 OTOP1 133060 otopetrin 1
GO:0009590|GO:0042472|GO:0016021|GO:0031214|GO:0005615 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140186_PI430048170 0.0263377997936644 0.583554430352096 9.28207788113559
9.24995586548817 9.08463284480021 P P P 9.68415847895321 10.2177335842507 10.004385353052
P P P LNCV6_140186_PI430048170 mRNA
GCTGCACAGTCAATTCATCGGTGCCTTAGTCCAAGAAAATAAAAACCACTAAGAAGCTTT NM_001039792 RefSeq
chr9 + 35906191 35907141 HRCT1 646962 histidine rich carboxyl terminus 1 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137834_PI430048170 0.0270075493276773 1.16663553556167 12.6157824190793
12.5159621898074 12.5142371858257 P P P 12.3718948678987 12.3797452671529
12.2243948133289 P P P LNCV6_137834_PI430048170 mRNA
GTAACTATTGCCATATAAATAAAAAATCCTGTTGCACTAGTGTCCTGCCATCCCAAAAAA NM_005837 RefSeq chr7
+ 100706052 100707500 POP7 10248 "processing of precursor 7, ribonuclease P/MRP subunit (S.
cerevisiae)" GO:0030678|GO:0005515|GO:0004526|GO:0005634|GO:0005655|GO:0008033 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_71457_PI430048170 0.162664431506494 0.816298613644512 3.63733045495659 3.66579712683605
3.27751403464058 P P P 3.59439049731383 3.99158881126972 3.8762682495258 P P P
LNCV6_71457_PI430048170 mRNA
TTGTCAGAAGAAAGTGCAAGAATATTAGCCACGAACTCTGAATTGGTGGGCACGCTAACG NM_003185 RefSeq
chr20_KI270869v1_alt - 85384 118224 TAF4 6874 "TAF4 RNA polymerase II, TATA box binding protein
(TBP)-associated factor, 135kDa"
GO:0005515|GO:0006352|GO:0010467|GO:0006368|GO:0003700|GO:0005669|GO:0006367|GO:0046982|GO:0006
366|GO:0003713|GO:0003677|GO:0033276|GO:0001541|GO:0005737|GO:0071339|GO:0016032|GO:0005654|GO:0
045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133712_PI430048170 0.00524287297073156 2.69455717363164 5.58212697428984
6.06033735669968 5.61632593476993 P P P 3.93767426576772 4.41081516299895
4.59427443533886 P P P LNCV6_133712_PI430048170 mRNA
CCTGGTTCCTTCGCTTGTGTTTCTGTACTTACCAAAAATCTACCATTTCAATAAATTTTG NM_177551 RefSeq chr12 -
122701292 122703357 HCAR2 338442 hydroxycarboxylic acid receptor 2
GO:0001781|GO:0050995|GO:0070165|GO:0007186|GO:0005886|GO:0016021|GO:0070553|GO:0033031 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144876_PI430048170 0.3964374878147680.9043596221677163.91128939254823
4.30978627829229 4.39432080475674 P P P 4.41101014538043 4.34617601583395
4.33678276911444 P P P LNCV6_144876_PI430048170 mRNA
TATGAATGTAAGGAATGTGGGAGGGCCTTTAGTCGTGGCTCAGAACTTACTCTGCATCAA NM_001290314 RefSeq
chr19 - 37564252 37594792 ZNF571 51276 "zinc finger protein 571, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144053_PI430048170 0.00344442424912276 0.3338292919259883.26009020934751
2.81423560064403 3.44627670101341 P A P 4.41710695795929 4.93254776886041
4.93155353013102 P P P LNCV6_144053_PI430048170 mRNA
TGGAAGAAGAAACTTTCTCTTGTAGTGCCTCTTGACAAAGCACAATTTCCCGCCTTTTTT NM_001172509 RefSeq
chr2 - 199269499 199458096 SATB2 23314 "SATB homeobox 2, transcript variant 1"
GO:0005515|GO:0005667|GO:0051216|GO:0071310|GO:0048704|GO:0000122|GO:0006351|GO:0016363|GO:0043
565|GO:0009880|GO:0005737|GO:0000118|GO:0002076|GO:0045944|GO:0003682|GO:0060021|GO:0005654|GO:0
006338|GO:0021902|GO:0001764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140992_PI430048170 0.0401908402261793 0.9482821757085930.410472088285298
0.3487868002151480.359053680615996A A A 0.4719499315561560.459834992236033
0.416536401854136A A A LNCV6_140992_PI430048170 mRNA
TTTCTGGTGTTGCTGCTAATGTGGATTAACAAATAAAAACATTCATTGCCTTTTGCCTCA NM_006573RefSeq chr13
+ 108269628 108308484 TNFSF13B 10673 "tumor necrosis factor (ligand) superfamily, member 13b,
transcript variant 1"
GO:0005515|GO:0005164|GO:0048471|GO:0008284|GO:0001782|GO:0005886|GO:0030890|GO:0008283|GO:0031
296|GO:0031295|GO:0005102|GO:0005125|GO:0005615|GO:0007165|GO:0005737|GO:0006955|GO:0042102|GO:0
002636|GO:0016021|GO:0048305 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140219_PI430048170 0.00372909116071716 0.3150197756484381.69525431662101
1.51754068795995 1.09071310516556 A A A 2.97635428659865 3.28787268445481
3.08616584133688 P P P LNCV6_140219_PI430048170 mRNA
CTGGAGGGGCTCTTATTATTTTCTCTCTTTTTAAAAAACTTCCAGTAGAAGTAAAGTGGA NM_019590RefSeq chr10
+ 24208790 24547848 KIAA1217 56243 "KIAA1217, transcript variant 1"
GO:0003674|GO:0005737|GO:0048706 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93558_PI430048170 0.9303117126784930.9863648453246546.39601299788924 6.63548088585348
6.53033722134438 P P P 6.75416033867269 6.50498446277678 6.34194063266204 P P P
LNCV6_93558_PI430048170 mRNA
AGTTTGATAGGAACTCCAACGACTATGACACCAGTGAGAAAAAACGCAAGCCTGCATGGA NM_001135642
RefSeq chr17 - 1494576 1516888 INPP5K 51763 "inositol polyphosphate-5-phosphatase K,
transcript variant 3"
GO:0005515|GO:0005802|GO:0034595|GO:0034594|GO:0005000|GO:0071356|GO:0097178|GO:0051926|GO:2000
466|GO:0005979|GO:0032869|GO:0046030|GO:0090315|GO:0001701|GO:0010801|GO:0034485|GO:0043922|GO:0
051497|GO:0007186|GO:0016311|GO:0016312|GO:2001153|GO:0006644|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141120_PI430048170 0.0146259490606965 0.6086559772065387.64823041549658
7.31056885641742 7.54612546053137 P P P 7.96152821808957 8.27173698944402
8.40578655963508 P P P LNCV6_141120_PI430048170 mRNA
CACAGACAGAGATTGTACTTGGTAAGATACCAAACAAGACAGATATGGATCTAAATTTCT NM_014864RefSeq chr1
+ 179025938 179076567 FAM20B 9917 "family with sequence similarity 20, member B"
GO:0016310|GO:0005794|GO:0000139|GO:0016301|GO:0016773|GO:0005654|GO:0016021|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128566_PI430048170 0.4666914731976470.807203528195982 1.48722280876347

0.3431279360019052.31099068948208 A A A 1.67746787555504 1.94557368284268
2.05013213908886 A A A LNCV6_128566_PI430048170 mRNA
ACGAGTCCAAGGCACATATCCACTGCTCGGTGAAAGCAGAGAACTCGGTGGCGGCCAAAT NM_000193 RefSeq
chr7 - 155802863 155812273 SHH 6469 sonic hedgehog
GO:0005515|GO:0001656|GO:0007389|GO:0001658|GO:0001755|GO:0030010|GO:0030878|GO:0007228|GO:0009
790|GO:0005615|GO:0005113|GO:0031069|GO:0007224|GO:0007405|GO:0030162|GO:0021794|GO:0001947|GO:0
007507|GO:0009880|GO:0030539|GO:0016015|GO:0001948|GO:0003140|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132858_PI430048170 0.472342954781255 0.8164004360495473.14466748692597
2.42536597774703 3.4697030887636 P A P 2.87274794008823 3.39237980081579
3.71779905264433 P P P LNCV6_132858_PI430048170 mRNA
GGTGGGAATCAGGAGAGCTGCAGTGGCTTATATAAACACCTGACGAAGTAGTCTAAAAAA NM_182633 RefSeq
chr7 + 55887276 55942226 ZNF713 349075 zinc finger protein 713
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134508_PI430048170 0.1310090346567410.71122586157444 6.22768171950349
5.67942281281866 6.39152143096447 P P P 6.53650180703873 6.62706973987375 6.6975681880593
P P P LNCV6_134508_PI430048170 mRNA
CTGAGCTCAACAAGATTGAAGTAAGTTTTCGGGAGCTACAGAAATTAAATCAAGAAAAGA NM_015462 RefSeq chr17
+ 67717832 67744208 NOL11 25926 "nucleolar protein 11, transcript variant 1"
GO:0030490|GO:0005515|GO:0005730|GO:0034455|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128966_PI430048170 0.3307622901330350.59298707536865 0.358567951580953
0.3803763032732880.291747231044257 A A A 0.2848077751078771.84520787401791
0.687379210993133 A A A LNCV6_128966_PI430048170 mRNA
GCATTTCCAGCTGTGCAGCACGTCTCAGAGATTCTTGAAGAATGAAGACATTTCTGCTCT NM_004139 RefSeq chr20
+ 38346410 38377011 LBP 3929 lipopolysaccharide binding protein
GO:0005515|GO:0032755|GO:0034145|GO:0034142|GO:0070891|GO:0050830|GO:0043032|GO:0005615|GO:0032
757|GO:0060265|GO:0002281|GO:0032496|GO:0044130|GO:0031663|GO:0008228|GO:0070062|GO:0009986|GO:0
032760|GO:0042535|GO:0005102|GO:0032720|GO:0005576|GO:0006953|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144377_PI430048170 0.0170436140628595 0.2158434611704031.32251486388927
0.3864552401380881.55073422811096 A A A 3.16177446532934 3.4757918832465
3.47789170855191 P P P LNCV6_144377_PI430048170 mRNA
CTGTTAATGTATTTGTTCATGTTTGGTGCATAGAACTGGGTAAATGCAAAGTTCTGTGTT NM_001293228 RefSeq
chr2 + 15940437 15947007 MYCN 4613 "v-myc avian myelocytomatosis viral oncogene
neuroblastoma derived homolog, transcript variant 1"
GO:0005515|GO:0003700|GO:0006357|GO:0030324|GO:0048704|GO:0002053|GO:0005634|GO:0003677|GO:0048
712|GO:0001502|GO:0045944|GO:0046983|GO:0048754|GO:2000378|GO:0000785|GO:0010942|GO:0042733 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137176_PI430048170 0.6543203357384010.9761255448045290.392525247494716
0.2588448535553770.302222604816904 A A A 0.4649572997725460.299065047400062
0.290610843145633 A A A LNCV6_137176_PI430048170 mRNA
TTCCATCTTTCTCTACATTCGTATGTCAGAGGCTCAGTCCAAACTGCTCAACAAAGGTGC NM_001005187 RefSeq
chr11 - 123942866 123943838 OR6T1 NA "olfactory receptor, family 6, subfamily T, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131331_PI430048170 0.3714702202552511.44633020392194 0.354931399521139
1.43653641511642 0.272182722995989 A A A 0.2510083290266190.2765599304258210.2501189269499
A A A LNCV6_131331_PI430048170 mRNA

GCGCTGACTCATATTGTTACCTAAGATCCCCTTATTTCTAAAGTATCTGTTACTTATTGC NM_004179 RefSeq chr11 - 18020536 18040788 TPH1 7166 tryptophan hydroxylase 1 GO:0035902|GO:0043005|GO:0005506|GO:0009072|GO:0044281|GO:0005829|GO:0034641|GO:0004510|GO:0030279|GO:0042427|GO:0046849|GO:0046219|GO:0045600|GO:0007623|GO:0016597|GO:0060749|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142227_PI430048170 0.524891484895955 0.985639299863366 0.297663255758521 0.31423974008199 0.378641275020576 A A A 0.375949490616342 0.318779181738676 0.359098251492799 A A A LNCV6_142227_PI430048170 mRNA
CCCACAGATTCTTGATTTGTAGTTGTTTGGCAGGATTTTTCTTTGTGATATAATCACTTC NM_001003679 RefSeq chr1 + 65420651 65635428 LEPR 3953 "leptin receptor, transcript variant 3" GO:0045721|GO:0005515|GO:0004896|GO:0005886|GO:0051346|GO:0019221|GO:0005576|GO:0007275|GO:0042802|GO:0043235|GO:0006112|GO:0016021|GO:0007166|GO:0004888|GO:0008203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139779_PI430048170 0.251651155861277 0.833878323298004 5.07047298174098 5.06836577480491 4.53487577382743 P P P 5.2886390384546 5.10610553252329 5.12111772642039 P P P LNCV6_139779_PI430048170 mRNA
GAGCCCTGATCCACCCACTCTCTGAAACTTCTTTGCTAATAAAACATTCCTACTAAAAAA NM_198471 RefSeq chr19 - 8322583 8343262 KANK3 256949 KN motif and ankyrin repeat domains 3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140436_PI430048170 0.0187055577901025 0.588974839836415 6.17412723689981 6.45425621435645 6.64686808391733 P P P 7.16020624528253 7.13006237696786 7.30845325793747 P P P LNCV6_140436_PI430048170 mRNA
GAGGGCTCATGTGATGATCATTTGTGAACTTAGATTTTTGAGGATTATGTGACTAGTAAT NM_001024924 RefSeq chr4 + 55853649 55905078 EXOC1 55763 "exocyst complex component 1, transcript variant 3" GO:0005515|GO:0006996|GO:0000145|GO:0016020|GO:0005886|GO:0061024|GO:0015031|GO:0006887|GO:0044267|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137808_PI430048170 0.0304851986283565 0.651264999781782 9.88984156676884 9.63824052449297 9.78571725128278 P P P 10.1437842470265 10.3685561146807 10.6277961964484 P P P LNCV6_137808_PI430048170 mRNA
ATGGCATTGAGTGTGCTGAGTCCAGACAAATGTTATTTATATACACATCCAAATTTGAAG NM_012316 RefSeq chr1 + 32108042 32176567 KPNA6 23633 karyopherin alpha 6 (importin alpha 7) GO:0005737|GO:0016020|GO:0045944|GO:0060135|GO:0008565|GO:0005634|GO:0006607 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81501_PI430048170 0.157002471853162 2.84287437796559 0.485431292647981 2.3788801570179 2.0856821359831 A A A 0.37669582962677 0.315127732778933 0.34788999824911 A A A LNCV6_81501_PI430048170 mRNA
TGAAAGCAAAATGACAACTACTCAGAAACACGATCTCTTCACGCCGGAGCCTCACTATGT NM_001001710 RefSeq chr9 - 137243582 137247792 FAM166A NA "family with sequence similarity 166, member A" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143954_PI430048170 0.00422577119506583 0.584126914647286 7.92222748789355 7.85114352371574 8.16804292747404 P P P 8.58431408151318 8.79503808393286 8.89159715322001 P P P LNCV6_143954_PI430048170 mRNA
CAAGTTCACACCTTTCATAAGCATAAAGTAGTTGCAAGAAAGTATTTTCATCCTGTTAGG NM_019051 RefSeq chr9 - 101389966 101398637 MRPL5054534 mitochondrial ribosomal protein L50 GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0005743|GO:0005840 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136340_PI430048170 0.308522825449306 1.03905283664165 11.161506787979 11.1878541245459 11.202931490603 P P P 11.0846261574471 11.0871640168466 11.2113288275066 P P P LNCV6_136340_PI430048170 mRNA

AAATGCGAAGCCGCGTGACCCTGGACTTCTGGCACATCTGAATAAACATGTTCTTATTCT NM_178836 RefSeq chr17 - 17200994 17206332 PLD6 201164 "phospholipase D family, member 6" GO:0010467|GO:0030719|GO:0090305|GO:0007286|GO:0005741|GO:0044281|GO:0046872|GO:0042803|GO:0016042|GO:0004519|GO:0007126|GO:0008053|GO:0034587|GO:0035755|GO:0016021|GO:0006644|GO:0006655|GO:0046474|GO:0043046. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129464_PI430048170 0.00697935629006636 0.697539363552615 5.12337263983363 4.9477501479379 4.90081368685065 P P P 5.58808870742484 5.58107180089155 5.35993370994524 P P P LNCV6_129464_PI430048170 mRNA
GCTGGGTTGTCCCCCCAAACATATTTTAATATGTTATTTAAAATGATTTTACCCAAGCCT NM_006242 RefSeq chr20 - 59936831 59940297 PPP1R3D 5509 "protein phosphatase 1, regulatory subunit 3D" GO:0042587|GO:0005979|GO:0016311|GO:0005977|GO:0004722|GO:0019899|GO:0043231|GO:0005981 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110011_PI430048170 0.682780187718661 1.34392716198442 2.51100747734881 1.67139422926876 0.528549315728342 A A A 0.47677724027873 1.68056373583293 1.62652705859042 A A A LNCV6_110011_PI430048170 mRNA
TTCCAGTGCTCACAGCACTGTGACTGCCACAATGGGGGGCAGTGTTCACCCACCACGGGT NM_032445 RefSeq chr15 - 65895295 66253737 MEGF11 84465 multiple EGF-like-domains 11 GO:0016323|GO:0034109|GO:0010842|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135734_PI430048170 0.0175157722278409 0.498333987837821 3.12483376173622 3.76057722862512 3.55969064423938 A P P 4.48157773058288 4.35729405583613 4.67396311395177 P P P LNCV6_135734_PI430048170 mRNA
GTTTATCTTGGTACACATCAGAAGATTAATGGTAGAACAACCTGAAGGATTTAGGAGTTA NM_001029997 RefSeq chr19 + 34734574 34742869 ZNF181 339318 "zinc finger protein 181, transcript variant 1" GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131728_PI430048170 0.393182683942265 1.96695651013071 0.318577674373941 2.64097103291274 2.5520041750244 A A A 2.11403463370725 0.272960447149909 0.321223310507033 A A A LNCV6_131728_PI430048170 mRNA
TGCCCTACATGATGGGTAACTGTGATCTTTCTTCCCTGTTAGATTGTAAGCCTCCGTCTT NM_017564 RefSeq chr12 + 103587290 103766724 STAB2 55576 stabilin 2 GO:0005515|GO:0010468|GO:0005886|GO:0015035|GO:0044281|GO:0005041|GO:0005737|GO:0005540|GO:0007155|GO:0030203|GO:0042742|GO:0005044|GO:0005975|GO:0030169|GO:0001525|GO:0006898|GO:0006897|GO:0030666|GO:0030193|GO:0005887|GO:0009405|GO:0030212|GO:0030214|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129030_PI430048170 0.139597392561536 0.892581720851663 7.58767739600537 7.59936044700524 7.7616085180457 P P P 7.68203773505959 7.84723403016933 7.90844106008541 P P P LNCV6_129030_PI430048170 mRNA
TTTTATTTTTAAGAGGTAAAGCATTATGTTGGGGAAAGTAGGGTGGGTTTCCAAATTTGC NM_014577 RefSeq - - 0 0 --- NA - NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94431_PI430048170 0.0893566362945039 1.44198471010758 6.8931643241896 6.97669362364718 7.04712882108691 P P P 6.60752147667313 6.60770455208894 6.05421147883014 P P P LNCV6_94431_PI430048170 mRNA
CTTCTGTGGCTGTGGCTATAGGTGCGGCTCTGGCTATGGCTCCAGCTTTGGCTACTACTA NM_181605 RefSeq chr21 + 30592439 30593055 KRTAP6-3 337968 keratin associated protein 6-3 GO:0005882 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136201_PI430048170 0.542095393728037 0.933013601294586 0.313040337772246 0.31885902886106 0.360858856815727 A A A 0.665438555719161 0.305855859370155 0.289954379916559 A A A LNCV6_136201_PI430048170 mRNA
GCAATCAAAAAGGAGACCTCAAACCAGATGTTAATTTGTTCTTTGTGTAACAATGTAACC NM_182511 RefSeq chr18

- 72536679 72544488 CBLN2 147381 cerebellin 2 precursor GO:0051965|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145500_PI430048170 0.3985180518268140.8703835228581220.312664437884407
0.2993435893218720.470488622611499A A A 0.2979778990126050.461947058439985
0.868604462463387A A A LNCV6_145500_PI430048170 mRNA
GAGAGGTAGTTTTGATAGTAAAAATTTTTGGTTGTGCCTAGAATGGCTTTGGTTTTGTTG NM_001201457 RefSeq
chr17 - 58556676 58692055 TEX14 56155 "testis expressed 14, transcript variant 3"
GO:0032091|GO:0005515|GO:0043063|GO:0007094|GO:0032466|GO:0019901|GO:0005623|GO:0030496|GO:0005
524|GO:0045171|GO:0051306|GO:0005737|GO:0004672|GO:0000777|GO:0000776|GO:0006468|GO:0008608|GO:0
070062|GO:0051301|GO:0007140 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132810_PI430048170 0.5630991931024191.038368893711 0.278316985010555
0.2900252974089960.503990553508661A A A 0.3260003601090680.281792616822815
0.31259557326613 A A A LNCV6_132810_PI430048170 mRNA
GGTTTTGTGCTTTGTCGTTTTTCTTTTTTAAACAAAACATGACAACCTTGGCTTTTCCGA NM_003728RefSeq chr4 -
95162504 95549210 UNC5C 8633 unc-5 homolog C (C. elegans)
GO:0030334|GO:0005042|GO:0043065|GO:0038007|GO:0005886|GO:0007420|GO:0007411|GO:0006915|GO:0016
021|GO:0033564 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126931_PI430048170 0.9389968751367140.9916839661902781.01082076823047
1.49085119756195 0.386419738260527A A A 1.73598155703158 0.520049215964925
0.504989810616824A A A LNCV6_126931_PI430048170 mRNA
AAGGAATACAAGGTAATGGTAAATGGCCAACGCATTTACAACTTTGCCCATCGATTCCCG NM_203471RefSeq chr19
+ 39704305 39709448 LGALS14 56891 "lectin, galactoside-binding, soluble, 14, transcript variant 2"
GO:0030246|GO:0006915|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127265_PI430048170 0.2319785412933090.8909992450849245.95443840687766
5.83840317474195 5.91138607522861 P P P 5.95088583480125 6.25416924532471
5.98133658446548 P P P LNCV6_127265_PI430048170 mRNA
CTTTGAAAGTTAGACTGCTACCCTGTTCTTCCTGCTGCCTCTACATTTACCAACTCTGGA NM_001278552 RefSeq
chr2 - 219249710 219254608 TUBA4A 7277 "tubulin, alpha 4a, transcript variant 2"
GO:0005515|GO:0051258|GO:0006996|GO:0005874|GO:0003924|GO:0030168|GO:0005576|GO:0005525|GO:0005
829|GO:0006184|GO:0007596|GO:0006457|GO:0000086|GO:0002576|GO:0005200|GO:0051084|GO:0007017|GO:0
000278|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139069_PI430048170 0.7794484802527040.9740361221224553.05184071296401 2.5499789904057
3.56600001413052 A A P 3.0617945407184 3.25937617152445 3.13081750291959 P P P
LNCV6_139069_PI430048170 mRNA
TGTGTGCTGTACAGAGTGACAATAGAAATAAATGTTTGGTTTCTTGTGACCAGCAAAAAA NM_024015RefSeq chr17
- 48575506 48578381 HOXB4 3214 homeobox B4
GO:0048103|GO:0003700|GO:0002011|GO:0008283|GO:2000738|GO:0060216|GO:0005634|GO:0048704|GO:0000
122|GO:0048539|GO:0060218|GO:0009952|GO:0048536|GO:0006351|GO:0043565|GO:0045944 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144047_PI430048170 0.0210161855442706 1.20050246553618 12.4112200187029
12.5253450290623 12.4023727559852 P P P 12.1065652849587 12.2889741857505
12.1494063018132 P P P LNCV6_144047_PI430048170 mRNA
AGATGTGCACACCCTCTTAGATCGAGTGGTCCGGCAGCATGTGCGTGAGGCCTCTATCTT NM_019037RefSeq chr8
+ 144078618 144080648 EXOSC454512 exosome component 4
GO:0005515|GO:0010467|GO:0000460|GO:0030307|GO:0071028|GO:0006364|GO:0000956|GO:0005730|GO:0043
928|GO:0035327|GO:0004532|GO:0005634|GO:0000178|GO:0005829|GO:0045006|GO:0051607|GO:0005737|GO:0
000175|GO:0071044|GO:0017091|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104828_PI430048170 0.1910433775032630.86878754796665 6.23139810204641
6.26695216007331 5.91749862926383 P P P 6.34593627366188 6.41333772492954

6.28756978037162 P P P LNCV6_104828_PI430048170 mRNA
ACGAGTGGTGCACCAGAATCATGGGGAGCGGAACTTCCACATCTTCTACCAGCTGCTGGA NM_001080779 RefSeq
chr17 - 1464185 1492707 MYO1C 4641 "myosin IC, transcript variant 1"
GO:0005515|GO:0005516|GO:2000810|GO:0060171|GO:0005886|GO:0006200|GO:0006605|GO:0030898|GO:0005
829|GO:0005739|GO:0005737|GO:0003774|GO:0038089|GO:0016461|GO:0009925|GO:0005643|GO:0006612|GO:0
061024|GO:0070062|GO:0001725|GO:0030335|GO:0005730|GO:0005102|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132614_PI430048170 0.6862409198012960.8943931665988830.514901420741323
0.8621127885770410.573074903421082A A A 0.5004058947669420.543247576634147
1.27586118404662 A A A LNCV6_132614_PI430048170 mRNA
TGCTCTTCCTGGGAAAGATTGTTAACCCTATTGGAAAATAAAGGAGAATTCCTGCTTGCC NM_173850RefSeq chr14
- 94487282 94517844 SERPINA12 145264 "serpin peptidase inhibitor, clade A (alpha-1 antiproteinase,
antitrypsin), member 12, transcript variant 1"
GO:0051055|GO:0045721|GO:0010951|GO:0090181|GO:0005886|GO:0004867|GO:0046628|GO:0014068|GO:0005
615|GO:0090207 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142409_PI430048170 0.7844360432146550.99347485885194 0.309101023321264
0.3180739178033490.396851071439414A A A 0.37459865255117 0.316508668669826
0.362231407050205A A A LNCV6_142409_PI430048170 mRNA
TTGAAACAGTCAGAAAAAAGATGGATGGGTGGAGACAGACAAGGAAGAGGCTCCTTGGTT NM_001171631
RefSeq chr2_GL383522v1_alt + 1109 34979 NOSTRIN 115677 "nitric oxide synthase trafficking,
transcript variant 4"
GO:0030666|GO:0005515|GO:0007165|GO:0005886|GO:0050999|GO:0046209|GO:0005634|GO:0044281|GO:0005
856|GO:0045892|GO:0003677|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142284_PI430048170 0.0250685272704934 0.6046265338478252.54104208238284
2.68195114142875 2.31471445652845 A A A 3.05119516204619 3.09056833454868
3.54355758227171 P P P LNCV6_142284_PI430048170 mRNA
GGATGCAGCAATAATTTCTGTATGGTCCATAGCACTGTATATTATGGATCGATATTAATG NM_198159RefSeq chr3
+ 69739434 69968337 MITF 4286 "microphthalmia-associated transcription factor, transcript variant
1"
GO:0005515|GO:0006355|GO:0006366|GO:0003705|GO:0030316|GO:0044336|GO:0030318|GO:0005634|GO:0045
670|GO:0000122|GO:0000978|GO:0000979|GO:0001227|GO:0043234|GO:0001077|GO:0045165|GO:0006461|GO:0
046849|GO:0045944|GO:0042127|GO:0003682|GO:0046983|GO:0043010|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_118911_PI430048170 0.4629322089100520.9341496170299350.356793590476836
0.2555389426597440.272952268209212A A A 0.5849591344288 0.319768553872539
0.255932016869996A A A LNCV6_118911_PI430048170 mRNA
TACAAGCCATTCTTTTCTACAAGACCATACCAGTCCTGGACAACAGCTCCGATTACAGTG NM_020987RefSeq chr10
- 60026297 60389876 ANK3 288 "ankyrin 3, node of Ranvier (ankyrin G), transcript variant 1"
GO:0008092|GO:0005515|GO:0030018|GO:0031594|GO:2000651|GO:0007409|GO:0043266|GO:0005764|GO:0019
228|GO:0009925|GO:0010765|GO:0007411|GO:0045211|GO:0030674|GO:0005794|GO:0045296|GO:0009986|GO:0
000281|GO:0071286|GO:0090314|GO:0030507|GO:0044325|GO:0045838|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_100985_PI430048170 0.00135757632489746 1.96673091970291 7.69280273479813
7.38803766954897 7.58430637614262 P P P 6.70209167510069 6.56442189286312
6.47875061257637 P P P LNCV6_100985_PI430048170 mRNA
TTCACAGAACTGCAGGAGAAGTATGGGGAGATTGAAGAGATGAATGTGTGCGACAACCTT NM_001040425
RefSeq chr19 - 35742526 35745442 U2AF1L4 199746 "U2 small nuclear RNA auxiliary factor 1-like 4,
transcript variant 1"
GO:0008380|GO:0006397|GO:0005737|GO:0016607|GO:0000166|GO:0003723|GO:0005681|GO:0046872 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142559_PI430048170 0.2551177412321321.03628088930327 0.363927604291041
0.3671606106736090.462551110048125A A A 0.3445607594535940.32149735726866
0.375027750684368A A A LNCV6_142559_PI430048170 mRNA
TCCAGCTCAGACCAGTTCAAGAAACTAACCTCCATTTATTTTCTTGGTGAGTCCTTTTTTNM_006078RefSeq chr22 -
36560868 36702645 CACNG2 10369 "calcium channel, voltage-dependent, gamma subunit 2"
GO:0005515|GO:0051899|GO:0005245|GO:0005886|GO:2000311|GO:0007268|GO:0019226|GO:0005891|GO:0030
666|GO:0060081|GO:0035255|GO:0007528|GO:0032281|GO:0070588|GO:0006810 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_9918_PI430048170 0.516016742609857 1.03864919345366 0.3019655656428120.310910899954832
0.503398435622049A A A 0.32917605871555 0.2886270921020950.342903373615243A A A
LNCV6_9918_PI430048170 mRNA
AGGGTAGACACTGACAACGTTATGTGTGGTCTTTAACCTGTTGTCATGTTTTTTCCCTAG NM_152991RefSeq - -
0 0 --- NA "embryonic ectoderm development, transcript variant 2" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132032_PI430048170 0.0209040860841179 0.16790069285969 0.983025933277895
2.43198481373449 1.9737870330059 A A A 4.35745476604128 4.64905465326136
4.44084691464668 P P P LNCV6_132032_PI430048170 mRNA
GGCATGTGCTGCCATCTATTATTCATTTTTAAATGGTCATTTCTTATTCAGTGAGTGCTT NM_022145RefSeq chr5 -
65517765 65563168 CENPK 64105 "centromere protein K, transcript variant 1"
GO:0034080|GO:0045944|GO:0006334|GO:0000777|GO:0005654|GO:0000278|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140747_PI430048170 0.1347769505757721.05964206860255 0.449952378914704
0.4695038111268930.498433001599102A A A 0.3256552398055730.386890572949429
0.452246271147367A A A LNCV6_140747_PI430048170 mRNA
CGTGTTAGGAGACTACTGTTATTTGACCAATGAATTGACTTCTAATAAAATCTAGTGGTG NM_000936RefSeq chr10
+ 116545915 116567855 PNLIP 5406 pancreatic lipase
GO:0030299|GO:0016042|GO:0004806|GO:0007603|GO:0044241|GO:0005576|GO:0044281|GO:0001523|GO:0046
872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132616_PI430048170 0.0368255712110364 0.2977198082546554.2528363383295
4.87160055099592 4.74859585321339 P P P 5.51766057054372 6.47481083784418
6.88149548750679 P P P LNCV6_132616_PI430048170 mRNA
CTCACGTACTCAATTATTCAAACAGGACTTATTGGGATACAGCAGTGAATTAAGCTATTA NM_001554RefSeq chr1
+ 85580760 85583965 CYR61 3491 "cysteine-rich, angiogenic inducer, 61"
GO:0044319|GO:0060710|GO:0060591|GO:0003181|GO:0008283|GO:0010811|GO:0007267|GO:0003281|GO:0002
041|GO:0001558|GO:0009653|GO:0030513|GO:0006935|GO:0030198|GO:0045944|GO:0045860|GO:0060716|GO:0
060548|GO:0007155|GO:0033690|GO:0070372|GO:0008201|GO:0005520|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_107762_PI430048170 0.3111308381029141.08871220563373 6.73149508565376
6.70043925573876 6.71927433635199 P P P 6.76033768380984 6.57567787503685
6.42824285386439 P P P LNCV6_107762_PI430048170 mRNA
TATTGCTTGGAGATGAGGGGCAGCCAGTTTTAATGGACTTGGGTTCCATGAATCAAGCAT NM_001008910 RefSeq
chr2 + 219245469 219250337 STK16 8576 "serine/threonine kinase 16, transcript variant 1"
GO:0005515|GO:0048471|GO:0005798|GO:0071560|GO:0018108|GO:0009966|GO:0005524|GO:0001077|GO:0005
737|GO:0046777|GO:0016020|GO:0004674|GO:0045944|GO:0004715 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_135964_PI430048170 0.5481408591184311.19385137636131 3.60168667268797
4.15305488547612 4.58035033418344 P P P 4.31250508302557 3.61673355572964
3.69738741105628 P P P LNCV6_135964_PI430048170 mRNA

GAGAAAGTTTAACTCTTCACCCACTATGTTGTTTTTAGTTATTTTGGGCTGCCATATTGANM_173657RefSeq chr3 - 155762611 155806287 C3orf33 285315 chromosome 3 open reading frame 33
GO:0051090|GO:0070373|GO:0016021|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131750_PI430048170 0.7041875070693840.9735721564814524.59504160504513
4.44700319368612 4.60745973125368 P P P 4.44972434262849 4.61061689849374
4.69952525912376 P P P LNCV6_131750_PI430048170 mRNA
GTGTATCTCGTGGAATCAGTGGTTAGCATTGCCGCTATTATATTTACTCATTTTATCATT NM_002515RefSeq chr14 - 26445882 26597754 NOVA1 4857 "neuro-oncological ventral antigen 1, transcript variant 1"
GO:0008380|GO:0006396|GO:0051252|GO:0000398|GO:0003723|GO:0005730|GO:0007268|GO:0007626|GO:0005634|GO:0003729|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142508_PI430048170 0.3417777379909461.1962630640459 8.69470263011814
8.84459593026609 8.54099565543921 P P P 8.80266671206685 8.41298202682518
7.99227389219751 P P P LNCV6_142508_PI430048170 mRNA
AGTATCCCCTCAAGCAGTACCGGGAATCCCAGGCCTTCTCCTTCTGCACAGCAGGGCGCT NM_001257370 RefSeq chr16 + 1773227 1776238 EME2 197342 essential meiotic structure-specific endonuclease subunit 2
GO:0006281|GO:0004519|GO:0090305|GO:0006310|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128501_PI430048170 0.0869353404190261 0.7306777137866227.42967063606372
7.36877111320573 7.58711216708515 P P P 7.59839312213166 8.01276735813916
8.09405621447889 P P P LNCV6_128501_PI430048170 mRNA
TTAGGTGTGCTGGTTGGATGTGCAGGAACTTCAGCAAGCAGTAGGTTTTACTAAGCAGAT NM_020381RefSeq chr6 - 107152556 107459575 PDSS2 57107 "prenyl (decaprenyl) diphosphate synthase, subunit 2"
GO:0050347|GO:0006744|GO:0005737|GO:0000010|GO:0046982|GO:0005759|GO:0051290|GO:0044281|GO:0008299|GO:0050878 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110405_PI430048170 0.591229719309008 1.0884118729358 7.0181126220504 7.0913045548834
6.91094751537776 P P P 7.24631734586773 6.91891993049883 6.35934253261976 P P P
LNCV6_110405_PI430048170 mRNA
TGTCTTCGTCAACGCGAGAGCGTGGAGGAGAACGCCAATGTGGTGGTGCGGCTGCTCATC NM_000540RefSeq chr19 + 38433699 38587564 RYR1 6261 "ryanodine receptor 1 (skeletal), transcript variant 1"
GO:0005515|GO:0005516|GO:0043931|GO:0005886|GO:0002020|GO:0014701|GO:0005737|GO:0034220|GO:0006936|GO:0031000|GO:0015278|GO:0006816|GO:0005938|GO:0070062|GO:0001666|GO:0005262|GO:0051209|GO:0005245|GO:0014802|GO:0051480|GO:0030314|GO:0071313|GO:0048741|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141888_PI430048170 0.274377060425488 1.50699995784804 1.28367715501923
1.1028505898318 2.02062528763314 A A A 1.66846409546913 0.325923151646017
0.379619575914534 A A A LNCV6_141888_PI430048170 mRNA
TCTGAAATCCCTGAAGGGGGTTGTACTGGGATTTGTGAATAAACTTGATACACTAAAAAA NM_001166034 RefSeq chr19 - 35523366 35528351 SBSN NA "suprabasin, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140724_PI430048170 0.383756706260986 0.826813123815094 0.411902364990014
0.417011198101019 0.321480809330759 A A A 0.321978011272229 1.04739064513163
0.504336486151244 A A A LNCV6_140724_PI430048170 mRNA
GGGCCTCTTGGGATTTACTCTGTGGCTCTCAGGGCCAATAAAGCCATGTGATGATGAGGG NM_004118 RefSeq chr20 - 31844299 31845617 FOXS1 2307 forkhead box S1
GO:0043565|GO:0003700|GO:0001568|GO:0006366|GO:0006357|GO:0000981|GO:0050885|GO:0005634|GO:0040018|GO:0045892|GO:0003677|GO:0043433 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140164_PI430048170 0.23543436946408 1.16786176885325 4.45400706429405
4.56389658008589 4.49870924403308 P P P 4.48552600904496 4.32080776797871

3.99922193715216 P P P LNCV6_140164_PI430048170 mRNA
GTGTGGCTTTCTGAGTATTTGAACCCCAGTCCTGTGTCACCTTCCTTTTTCCTTCTATGT NM_012109 RefSeq chr19
+ 18612871 18621039 TMEM59L 25789 transmembrane protein 59-like
GO:0016020|GO:0000139|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_91748_PI430048170 0.255117360889409 1.18234215429688 4.2544845720255
4.30340559869493 4.31670740526318 P P P 3.80945543320601 4.35501826169469
3.92721760175948 P P P LNCV6_91748_PI430048170 mRNA
ACATATTGGAAGAAATATGGTGGCTTGAAAATGCCAACCCGGTTAGATGGAGAGAGGCCA NM_004689 RefSeq
chr14 + 105419848 105470720 MTA1 9112 "metastasis associated 1, transcript variant 1"
GO:0005515|GO:0045475|GO:0003700|GO:0006325|GO:0005634|GO:0005635|GO:0043231|GO:0006302|GO:0005
737|GO:0016581|GO:0010212|GO:0032496|GO:0001046|GO:0043153|GO:0001103|GO:0006355|GO:0003714|GO:0
005874|GO:0003713|GO:0050727|GO:0001047|GO:0006351|GO:0032922|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128538_PI430048170 0.459401726645957 0.746876984484484 0.290609929045445
0.28259213251263 0.967815707285291 A A A 0.820020027396615 0.265207290827124
1.5448892381564 A A A LNCV6_128538_PI430048170 mRNA
CACAAAAAGTAACGGAACAGGAGTCATAATCTTTCTTGAACTCCTGTGGTTTTTACTGAA NM_002318 RefSeq
chr8 - 23296896 23404209 LOXL2 4017 lysyl oxidase-like 2
GO:0005515|GO:0005634|GO:0002040|GO:0035064|GO:0001837|GO:0005615|GO:0070492|GO:0030199|GO:0032
332|GO:0007155|GO:0018277|GO:0005044|GO:0001666|GO:0005507|GO:0005694|GO:0004720|GO:0003714|GO:0
007568|GO:0009055|GO:0016570|GO:0006351|GO:0006898|GO:0005604|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_53294_PI430048170 0.0911987150539141 0.793010787930854 3.57047382001317
3.70783249768602 3.72474539334572 P P P 4.0777730862656 4.14197522555203
3.76440295381269 P P P LNCV6_53294_PI430048170 mRNA
TGACAGCCTACAGGAGGTGGTGAACTACCACATGATCCTGTTTGACCAGGCCCAGAGGTC NM_030649 RefSeq
chr1 - 1292383 1307889 ACAP3 116983 "ArfGAP with coiled-coil, ankyrin repeat and PH domains 3"
GO:0043547|GO:0008060|GO:0032312|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140283_PI430048170 0.987536423823843 1.09719577258299 2.57457780550245
0.3231360096773710.302388788054525 A A A 0.4339288931240110.518956220266277
2.29560651706917 A A A LNCV6_140283_PI430048170 mRNA
AAGGGTTTAGGTAAAAGAGGGTAACAGTATACTACTTGATAACATAATGGGCTAACATCT NM_016220RefSeq chr7
+ 64666082 64711582 ZNF107 51427 "zinc finger protein 107, transcript variant 1"
GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0005575|GO:0003677|GO:0046872|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142987_PI430048170 0.226706256614497 1.59563561909336 1.55082048534019
1.22365865479161 0.37884516168316 A A A 0.5253499567416320.499013974764138
0.335876176148592 A A A LNCV6_142987_PI430048170 mRNA
AACTTGGACTCAGATGAAGACCAGTCCCTTTCTGCAGTTTCCTTTAACACAGCAAGATAG NM_033036RefSeq chr11
- 66040764 66049180 GAL3ST3 89792 galactose-3-O-sulfotransferase 3
GO:0006790|GO:0030309|GO:0009311|GO:0001733|GO:0032580|GO:0050698|GO:0030246|GO:0050694|GO:0016
021|GO:0050656|GO:0005996|GO:0030166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138257_PI430048170 0.609759931941499 1.22884041755097 2.33197716496101
2.72758494812632 1.43660001937385 A A A 1.62425354155067 1.55375745611191 2.5037141122694
A A P LNCV6_138257_PI430048170 mRNA
TCATTTGTAGGAAACTGGGAAATAAAAACCTGGGGAACTTTAGGTTATTTATACAAAGGG NM_003772RefSeq chr11
+ 96389993 96393563 JRKL 8690 "JRK-like, transcript variant 1"
GO:0005634|GO:0007417|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_142639_PI430048170 0.2157429910635271.55688499912194 1.41496175580091
1.22710357016184 0.369034238561666A A A 0.503591623514991 0.386668049141012
0.401387266605334A A A LNCV6_142639_PI430048170 mRNA
GTGTTGGCATGAGATGAATCAGGAGAAAAATAAACTGGATGGTGTTTTCCTTTTTCTTGG NM_138382RefSeq chrX
- 106900062 106903331 RIPPLY192129 "ripply transcriptional repressor 1, transcript variant 1"
GO:0009880|GO:0032525|GO:0007219|GO:0001757|GO:0060349|GO:0005634|GO:0045892|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143080_PI430048170 0.7284399597883310.964013616611951 6.0940588543969
5.70864777812708 5.57079629309834 P P P 5.90171000491075 5.95932646908494
5.71177254366436 P P P LNCV6_143080_PI430048170 mRNA
ACACCCTGGTTCCCACCATTCCCTGCCTTGCTGACAATAAAGATATTTCCAAGAACCCGG NM_001297439 RefSeq
chr4 + 3441932 3449495 HGFAC 3083 "HGF activator, transcript variant 1"
GO:0004252|GO:0006508|GO:0008236|GO:0005576|GO:0005615 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129683_PI430048170 0.0105146775193291 0.7150926372357649.06746268552556
8.97877613431338 8.84427354491123 P P P 9.47145293418114 9.4736666549625
9.40442217059707 P P P LNCV6_129683_PI430048170 mRNA
ACTCTTATCTCCGTGGGTGGCTCTCCTTTTGTTTTAATTAACTTCTTTATGAATATGAAC NM_001111322 RefSeq chr12
- 113157172 113185479 DDX54 79039 "DEAD (Asp-Glu-Ala-Asp) box polypeptide 54, transcript variant 1"
GO:0006396|GO:0006355|GO:0016070|GO:0003714|GO:0030331|GO:0005102|GO:0005730|GO:0005634|GO:0005
524|GO:0006351|GO:0004004|GO:0016020|GO:0030520 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67647_PI430048170 0.00301255103027191 0.5322537281557155.90176152456344
5.97646896206905 5.63241999105639 P P P 6.83152724725814 6.60314032091146
6.81653632912312 P P P LNCV6_67647_PI430048170 mRNA
AAGGCTACAAATGCAGGCATGTAACGCTGCCATCCACAAGAAATGCATCGACAAGATCAT NM_006254RefSeq chr3
+ 53161206 53192717 PRKCD 5580 "protein kinase C, delta, transcript variant 1"
GO:0005515|GO:0010467|GO:0010469|GO:0016064|GO:2001022|GO:0019221|GO:0050732|GO:0051490|GO:0043
560|GO:0007173|GO:1900163|GO:0018107|GO:0030837|GO:2000755|GO:0042742|GO:2000753|GO:0070062|GO:0
060333|GO:0030168|GO:0018108|GO:0007049|GO:0008543|GO:0045087|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142920_PI430048170 0.4311397338987140.9128569079117911.0268095094816
10.8001918567749 10.8679187228679 P P P 11.2627400760425 10.9211168050523
10.8841992709453 P P P LNCV6_142920_PI430048170 mRNA
ACTGTATTAACTCTCGAGGAGTTTCCTCACCAATAAACAGACAACCTCAACTGCCAGTGC NM_033386RefSeq chr22
+ 37906147 37942458 MICALL1 85377 MICAL-like 1
GO:0005515|GO:0005802|GO:0070300|GO:0017137|GO:0005770|GO:0032458|GO:0097320|GO:0006898|GO:0031
175|GO:0042802|GO:0006897|GO:0006612|GO:0031902|GO:0036010|GO:0008270|GO:0055038|GO:0005769|GO:0
019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127328_PI430048170 0.1370327706372790.769428099915066 4.42923922990837 4.6440424777666
4.0523845913637 P P P 4.9377088651709 4.73383786975547 4.63246046507309 P P P
LNCV6_127328_PI430048170 mRNA
CTGCCTACCTGGAGAGCTCCAAGCGTAAGAAAATAAACCCTGCCTGTTGAAGCCAAAAAA NM_000487RefSeq chr22
- 50622753 50628173 ARSA 410 "arylsulfatase A, transcript variant 1"
GO:0043627|GO:0045471|GO:0004098|GO:0008484|GO:0044281|GO:0005764|GO:0005615|GO:0004065|GO:0009
268|GO:0070062|GO:0043202|GO:0006665|GO:0006687|GO:0001669|GO:0007584|GO:0005509|GO:0006914|GO:0
007417|GO:0007339|GO:0031232|GO:0051597|GO:0005788|GO:0016021|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140620_PI430048170 0.1829059051934881.04309909980785 0.433328761166373
0.411575750360515 0.433188795361372A A A 0.31448976805057 0.357016940012128

0.42202824547692 A A A LNCV6_140620_PI430048170 mRNA
AGTCCTACTTGAGGCTGCAATCACACTGAGGAACTCACAATTCCAAACATACAAGAGGCT NM_006737 RefSeq
chr19_KI270932v1_alt - 2176 18971 KIR3DL2 3812 "killer cell immunoglobulin-like receptor, three
domains, long cytoplasmic tail, 2, transcript variant 1" GO:0006968|GO:0005886|GO:0005887|GO:0050776 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74932_PI430048170 0.199251497689185 1.26687781363719 10.7634707781097 11.2817608335198
10.8770499290352 P P P 10.9446996176536 10.5059903087023 10.4478085251782 P P P
LNCV6_74932_PI430048170 mRNA
AGAGCAGAAAAGATGAATTTGTCCAATTGTGTAGACGATATACTCCCTGCCCTTCCCCCT NM_033632 RefSeq chr4
- 152321257 152535033 FBXW7 55294 "F-box and WD repeat domain containing 7, E3 ubiquitin protein
ligase, transcript variant 1"
GO:0005515|GO:0003700|GO:0016567|GO:0005783|GO:0030324|GO:0032876|GO:0031146|GO:2000639|GO:0097
027|GO:0042802|GO:0032880|GO:0034644|GO:0005737|GO:0007219|GO:0031398|GO:0016032|GO:0051443|GO:0
070374|GO:0030674|GO:0031625|GO:0001944|GO:0045746|GO:0006355|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127897_PI430048170 0.0916121641588576 0.74429824750374 11.7435953290905
11.3911342820697 11.6500351063677 P P P 11.8338049863576 11.8951342021463
12.3089784111789 P P P LNCV6_127897_PI430048170 mRNA
CAGAGAGCACCTGATGTATCATCTCAAACACAATAAACATGCTCCTGAAGGCATAAAAAA NM_006357 RefSeq chr2
+ 180980580 181063427 UBE2E3 10477 "ubiquitin-conjugating enzyme E2E 3, transcript variant 1"
GO:0070534|GO:0005737|GO:0004842|GO:0070979|GO:0016874|GO:0005634|GO:0070936|GO:0005524|GO:0040
008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136453_PI430048170 0.10803828516894 0.8496677418272836.0407608422687
5.96638266739683 6.10698231880436 P P P 6.10319806124543 6.41204568177308
6.29075435706308 P P P LNCV6_136453_PI430048170 mRNA
TTCCTCCTATTGTCTTGTAAATCAAACTCTAAGTGAAAACTTCCCATTTGTCCCTTCAAA NM_152259 RefSeq chr15 +
89575586 89628022 TICRR 90381 TOPBP1-interacting checkpoint and replication regulator
GO:0006260|GO:0005515|GO:0030174|GO:0006281|GO:0001731|GO:0010212|GO:0003682|GO:0000075|GO:0005
654|GO:0005634|GO:0033314 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_8053_PI430048170 0.0203162445573304 0.576281399668787.53780778513069
7.58695222249179 7.75242034451373 P P P 8.18281873964071 8.35728477339512 8.6855862972675
P P P LNCV6_8053_PI430048170 mRNA
GCTTTCTATGTTCATATACTGTTTACCTTTTTCCATGGAGTCTCCTGGCAAAGAATAAAA NM_001290276 RefSeq
chr3 + 25428262 25597931 RARB 5915 "retinoic acid receptor, beta, transcript variant 1"
GO:0005515|GO:0001657|GO:0010467|GO:0003417|GO:0008284|GO:0006367|GO:0008285|GO:0055012|GO:0003
707|GO:0005634|GO:0003708|GO:0032403|GO:0046965|GO:0005737|GO:0002068|GO:0035264|GO:0045944|GO:0
008144|GO:0043401|GO:0031641|GO:0032331|GO:0048048|GO:0003406|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_69498_PI430048170 0.174228478647446 0.893615052936635 7.85493745231977 8.05379983813302
7.77273387613853 P P P 8.00548635447054 8.04283637027346 8.13168739325904 P P P
LNCV6_69498_PI430048170 mRNA
ACAGGAAAGGCGTCAAGATTGACAAGACTGACTACATGGTAGGCAGCTATGGGCCCCGGG NM_001185077
RefSeq chr17 - 81867718 81870974 ARHGDIA 396 "Rho GDP dissociation inhibitor (GDI) alpha,
transcript variant 1"
GO:0001772|GO:0005515|GO:0051056|GO:0048011|GO:0030336|GO:0043066|GO:0007264|GO:0006928|GO:0007
266|GO:0005829|GO:0043547|GO:0032880|GO:0007162|GO:0071526|GO:0050771|GO:0050772|GO:0005856|GO:0
050770|GO:0005094|GO:0070062|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_22815_PI430048170 0.139425661842302 0.771056668077578 3.8479326183644 3.38838624653579
3.27995567854546 P P P 3.9738080906344 3.72657857799455 3.99122431977666 P P P

LNCV6_22815_PI430048170 mRNA
TCTTCATCTCCGTGAGAAAGGTGCCCCCGAAGTGAAAGAGATGGCCTGGTGGAAAGCCTG NM_001098845 RefSeq
chr10 + 46375589 46391783 ANXA8L1 728113 "annexin A8-like 1, transcript variant 1"
GO:0005544|GO:0005509 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144646_PI430048170 0.00590803765908148 0.752867985081356 14.7571594910394
14.8407157286467 14.8726953183056 P P P 15.3067090808037 15.264927876499
15.1236695909564 P P P LNCV6_144646_PI430048170 mRNA
GCTGCATTCTCTGTCCATCTGTCTGTTTCTATTAATAAAGATTTGTTGATCTGTTCCAAA NM_001282208 RefSeq chr9
- 34634721 34637826 SIGMAR1 10280 "sigma non-opioid intracellular receptor 1, transcript variant 9"
GO:0005811|GO:0030054|GO:0005637|GO:0038003|GO:0005635|GO:0004985|GO:0007399|GO:0030426|GO:0005
640|GO:0043523|GO:0005887|GO:0008144|GO:0006869|GO:0005789|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_55433_PI430048170 0.0760200927101476 1.04171907251192 0.380192677924332
0.372537425964633 0.425456261101721 A A A 0.31485997350363 0.315822847621143
0.370468414359835 A A A LNCV6_55433_PI430048170 mRNA
TGAACTTCATCCTTATTGGAGAGAGCACTCTCCGTTGTACAGTTGATAGTCAGAAGACTG NM_001006658 RefSeq
chr1 + 207454299 207489895 CR2 1380 "complement component (3d/Epstein Barr virus) receptor 2,
transcript variant 1"
GO:0001848|GO:0005886|GO:0003677|GO:0042803|GO:0043235|GO:0006955|GO:0042100|GO:0045087|GO:0006
958|GO:0030183|GO:0016021|GO:0002430|GO:0009897|GO:0070062|GO:0004875|GO:0004888 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134530_PI430048170 0.63664087063025 1.0322068288845 0.345393669034396
0.58750917321919 0.457795812096696 A A A 0.516117208182525 0.386991341036069
0.355516345658354 A A A LNCV6_134530_PI430048170 mRNA
GCAAATACATGTCACCAAATGCACAACATTTTGGGAATGATGGTAAAATTGTATGACTGA NM_130808 RefSeq chr3
- 131533559 132035442 CPNE4 131034 "copine IV, transcript variant 3" GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_106578_PI430048170 0.00214536749022747 1.27196950350704 5.93680151368105
5.8274450946306 5.85463570525462 P P P 5.53066029670393 5.58578425216235
5.46079000858891 P P P LNCV6_106578_PI430048170 mRNA
TTGAAAGACTGGTTTGCCAAAAGGAAGAAGTTTAAGCGGCCTCCACAGAGGCTGTTTGAT NM_003169 RefSeq chr19
+ 39445647 39476668 SUPT5H 6829 "suppressor of Ty 5 homolog (S. cerevisiae), transcript variant 1"
GO:0005515|GO:0010467|GO:0006368|GO:0032044|GO:0006354|GO:0010033|GO:0046982|GO:0006366|GO:0006
370|GO:0005634|GO:0000122|GO:0050434|GO:0007049|GO:0032786|GO:0032785|GO:0045944|GO:0003682|GO:0
016032|GO:0005654|GO:0006338|GO:0019899|GO:0016239 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_142181_PI430048170 0.564934642874611 0.708998783412518 0.429368866174413
0.451227467779392 0.912956891886575 A A A 0.417492859337826 0.485070059537101
1.90618921123307 A A A LNCV6_142181_PI430048170 mRNA
AAATGAAGAATTTGACAAGGACTACCAGAAGAAGATGGCAGGAAGCACCCTAACCTTCCG NM_001008743
RefSeq chr2 + 108247194 108265351 SULT1C3 NA "sulfotransferase family, cytosolic, 1C, member 3"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140943_PI430048170 0.252126164840674 1.44159751899625 1.44542911239369
0.492718197447582 0.650263281008079 A A A 0.496029876791446 0.386517412306064
0.306117749082946 A A A LNCV6_140943_PI430048170 mRNA
GAGGCCAGTTCCTTGGAGGGACATGACTAATTTATCGATTTTTATCAATTTTTATCAGTT NM_020530 RefSeq chr22
- 30262829 30266840 OSM 5008 oncostatin M
GO:0042506|GO:0008284|GO:0008285|GO:0042503|GO:0009408|GO:0008283|GO:0042508|GO:2001235|GO:0050
731|GO:0005615|GO:0046888|GO:0033138|GO:0006955|GO:0002675|GO:0045944|GO:0051781|GO:0005147|GO:0

007275|GO:0005125|GO:0038165|GO:0007422|GO:0043410|GO:0008083|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138375_PI430048170 0.6236895375326090.8842971371759432.47611969732224
2.86374868787556 3.36976653115432 A A P 3.45991702570874 2.64842985457673 3.1602049542183
P P P LNCV6_138375_PI430048170 mRNA
GCAGACAAGCAGAGAAACAACTGGGGAATTTATTGACTCATTTAGTTATTCTTTCTACTT NM_174912RefSeq chrX
+ 57286676 57489196 FAAH2 158584 fatty acid amide hydrolase 2
GO:0016884|GO:0016787|GO:0008152|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135920_PI430048170 0.00542873759710568 0.4742027640732775.8863985783472
5.54171967340739 5.69556243364153 P P P 6.74366288499957 6.78936127201147
6.83907851808905 P P P LNCV6_135920_PI430048170 mRNA
AGCAAACCTAAGCCAAAGGAAGGAAAGCCATGAAGAATGCAGAAGTCAAACCCTCATGAC NM_033138RefSeq
chr7 + 134779412 134970729 CALD1 800 "caldesmon 1, transcript variant 1"
GO:0005516|GO:0006936|GO:0005886|GO:0030478|GO:0006928|GO:0017022|GO:0003779|GO:0030016|GO:0015
629|GO:0005856|GO:0005523|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57780_PI430048170 0.4270641878115482.00364762565514 0.4540765509099712.40151424176909
0.320314702451089A A A 0.4679656192166890.3583011107177540.354762990165952A A A
LNCV6_57780_PI430048170 mRNA
ATGGAGACCATTGGCAGGGACCTGCACCGTCAATTCCCTCTGCACGAGATGTTTGTGTCG NM_198517RefSeq chr11
+ 67403912 67410090 TBC1D10C 374403 "TBC1 domain family, member 10C, transcript variant 1"
GO:0016020|GO:0005886|GO:0050869|GO:0051534|GO:0031527|GO:0042147|GO:0032851|GO:0070373|GO:0005
097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137234_PI430048170 0.8118890590628480.9867697073764292.90777133248919
2.87148447391024 1.4514371767985 A A A 2.88939861519522 2.46630509318915
2.28009103107547 P A A LNCV6_137234_PI430048170 mRNA
GGAATGAGGCCTAAACCACAATCTTCTCTTCCTAATAAACAGCCTCCTAGAGGCCACATT NM_001145643 RefSeq
chr15 + 40351032 40356433 PHGR1 NA proline/histidine/glycine-rich 1 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_135715_PI430048170 0.0255108178464322 1.58001512643235 9.74917248708905
9.83968284815302 9.76990044719339 P P P 8.90448204063449 9.31757858198601
9.12897319068133 P P P LNCV6_135715_PI430048170 mRNA
AAACCATGACGTCGGACATTTTAAAGATGCAGCTTTACGTGGAAGAGCGCGCTCATAAAG NM_001127325 RefSeq
chr1 - 11674479 11691621 MAD2L2 10459 "MAD2 mitotic arrest deficient-like 2 (yeast), transcript
variant 1"
GO:0005515|GO:0007094|GO:0005634|GO:2000048|GO:0010719|GO:2000678|GO:0001558|GO:0043433|GO:0006
302|GO:0005737|GO:0033138|GO:0010944|GO:0005680|GO:0007015|GO:0016035|GO:0008432|GO:0090090|GO:0
001102|GO:0042177|GO:0005819|GO:0060564|GO:0000122|GO:0006351|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136104_PI430048170 0.00411319248191652 1.48060875688598 12.884551943205
12.874568312598 13.0053085742043 P P P 12.2452748458275 12.4799774256138
12.3345260048664 P P P LNCV6_136104_PI430048170 mRNA
TTTCCACAATGTCTGTGAACTGGACCTGGTGTTCAACTTCTACAAGGTTTACACGGTCGT NM_001301078 RefSeq
chr19 - 46838157 46850995 AP2S1 1175 "adaptor-related protein complex 2, sigma 1 subunit,
transcript variant 4"
GO:0072583|GO:0005215|GO:0048011|GO:0035615|GO:0048013|GO:0005886|GO:0030122|GO:0042059|GO:0007
268|GO:0006886|GO:0050690|GO:0005829|GO:0030666|GO:0019886|GO:0007173|GO:0007411|GO:0030100|GO:0
008565|GO:0016032|GO:0030669|GO:0048268 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133651_PI430048170 0.3662684457961980.6431834574514331.88429788997229
0.2683744447287073.24761200963164 A A P 2.09303535165958 3.03977409855933

3.30588289660238 A P P LNCV6_133651_PI430048170 mRNA
ATTTGATTTCTAAACATTCCTTCATATGCCTTTAATGAAAGCCAGCAATTATCCCATGGG NM_017640RefSeq chr6
+ 25279427 25620530 LRRC16A 55604 "leucine rich repeat containing 16A, transcript variant 1"
GO:0030335|GO:0030032|GO:0005634|GO:0046415|GO:0032403|GO:2000813|GO:0030027|GO:0031529|GO:0005
829|GO:0005737|GO:0031941|GO:1900026|GO:0016477|GO:0030838|GO:0007596|GO:0051638|GO:0051496|GO:0
007015|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139852_PI430048170 0.0277783526950524 0.7111407265889747.68575295680295
7.53193880501019 7.66544085818008 P P P 7.99779454207903 8.01972424328132
8.32245082684673 P P P LNCV6_139852_PI430048170 mRNA
GCATTGTATTTAGTCTGTATTGATCATGGATGCCCTCCTTAATAGCCATATGCAATAAAA NM_003749RefSeq chr13
- 109753836 109786567 IRS2 8660 insulin receptor substrate 2
GO:0005515|GO:0008286|GO:0008284|GO:0005886|GO:0008283|GO:0030890|GO:0005158|GO:0030879|GO:0060
397|GO:0005829|GO:0010907|GO:0071889|GO:0007173|GO:0046326|GO:0002903|GO:0006006|GO:0032024|GO:0
004871|GO:0071333|GO:0033673|GO:0048011|GO:0032869|GO:0030335|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_59559_PI430048170 0.7476336376234161.04834793127735 9.04855871178684 9.17525424508774
9.53056890344561 P P P 9.07517025399854 9.18164338544748 9.32635697601663 P P P
LNCV6_59559_PI430048170 mRNA
TTTCCTAAAGCCAAAGTTTCTGTTGAATTATGTTTTGACACACCCCTAAGTACAAGGTGG NM_002710RefSeq chr12
- 110719807 110742978 PPP1CC 5501 "protein phosphatase 1, catalytic subunit, gamma isozyme,
transcript variant 1"
GO:0005515|GO:0005634|GO:0044281|GO:0032154|GO:0046872|GO:0005829|GO:0005739|GO:0016791|GO:0005
737|GO:0006470|GO:0004721|GO:0007179|GO:0004722|GO:0019433|GO:0043153|GO:0030512|GO:0019901|GO:0
005977|GO:0005730|GO:0030496|GO:0032922|GO:0043234|GO:0016607|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_71727_PI430048170 0.0834515742344036 0.5807599913009545.01328820281573
4.83660358723443 5.09361038623655 P P P 5.24883827516792 6.07333646954745
5.86400632287293 P P P LNCV6_71727_PI430048170 mRNA
TAAAAAACAAAACCGTGTGTGAAGACCAGGAGCTGAAACTGCACTGCCATGAATCCAAGTNM_058187RefSeq chr21
+ 32412436 32515400 EVA1C 59271 "eva-1 homolog C (C. elegans), transcript variant 1"
GO:0030246|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130619_PI430048170 0.0202725980048315 0.3376947768324690.44755213198842
0.9818981857311560.308139224734424A A A 1.53357190303021 2.18308919590176
2.61284471627257 A A P LNCV6_130619_PI430048170 mRNA
CGCTGTATGTTAACTATGACTGGAATTCTGTGATATTTTGGTAATAAATGAAGTGGGATC NM_001419RefSeq chr19
- 7958572 8005645 ELAVL1 1994 ELAV like RNA binding protein 1
GO:0003725|GO:0005515|GO:0010467|GO:0019901|GO:0003723|GO:0045727|GO:0005634|GO:0007275|GO:0003
729|GO:0035925|GO:2000036|GO:0005829|GO:0005737|GO:0000166|GO:0016020|GO:0017091|GO:0005654|GO:0
048255|GO:0003730|GO:0070935 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142628_PI430048170 0.0580692728641331.10682923361517 13.0311022525958
13.0770436996048 12.9969298050981 P P P 12.893163948689 12.9606652177078 12.80908117805
P P P LNCV6_142628_PI430048170 mRNA
TTCAGAAAGTGAAGGAGAAACTCAAGATTGACTCATGAGGACCTGAAGGGTGACATCCCA NM_001645RefSeq
chr19 + 44914663 44919349 APOC1 341 apolipoprotein C-I
GO:0032375|GO:0006629|GO:0050995|GO:0005783|GO:0010900|GO:0010873|GO:0042627|GO:0034379|GO:0060
228|GO:0034361|GO:0034364|GO:0034382|GO:0055102|GO:0034447|GO:0070062|GO:0008203|GO:0033344|GO:0
005504|GO:0004859|GO:0032374|GO:0045717|GO:0031210|GO:0034369|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144693_PI430048170 0.00157593694086757 0.3434559112496983.27895714797426

3.16554799095803 3.66074630287249 P P P 4.92624775586708 4.6858218807183 5.1320207824874
P P P LNCV6_144693_PI430048170 mRNA
TGACATTTTAGCTTTCCCAGGTAAAAGTGGTTTTCATCCTCACACCAATTTTATGGACTG NM_001199208 RefSeq
chr19 + 15640896 15660760 CYP4F3 4051 "cytochrome P450, family 4, subfamily F, polypeptide 3,
transcript variant 2"
GO:0019369|GO:0006805|GO:0052871|GO:0005506|GO:0050051|GO:0044281|GO:0006691|GO:0006690|GO:0036
101|GO:0004497|GO:0005789|GO:0016021|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_126772_PI430048170 0.5047505029149370.9137352157020090.5700153184867
0.4007410219763090.245148526441089A A A 0.3617490859325390.423439228142667
0.79952032597342 A A A LNCV6_126772_PI430048170 mRNA
CAAGGGTGTAATATACCATAGTGATAAATATGACCAAAAGCCATAAATGACTGTGAGATG NM_152357RefSeq chr19
+ 11814291 11835201 ZNF440 126070 zinc finger protein 440
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140250_PI430048170 0.2898141846522290.9140640177029996.93498837864213
6.82413524150742 7.02614531373322 P P P 6.88943064799989 7.11565719627154
7.16169977724585 P P P LNCV6_140250_PI430048170 mRNA
AAATGTCATGGGTGACTTCTGACTTTCTAAGGAAATGATGCTTCCCAAGCACCCGAGGTT NM_021089RefSeq chr19
+ 58278951 58295888 ZNF8 7554 zinc finger protein 8
GO:0008270|GO:0005634|GO:0030509|GO:0000122|GO:0003677|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_96907_PI430048170 0.8047095356209220.9631081240825998.93127455274174 8.8432967949679
8.65684986237079 P P P 9.05918666165008 8.93064780688568 8.57532922456359 P P P
LNCV6_96907_PI430048170 mRNA
ATGCTGGTCGCCACCGCCGTCTGCTGTTACCTCTTTGCCCAGCTCTCGGAATGACTGTGG NM_145230RefSeq chr7
+ 149872967 149880712 ATP6V0E2 155066 "ATPase, H+ transporting V0 subunit e2, transcript variant 1"
GO:0008286|GO:0051701|GO:0042625|GO:0055085|GO:0006879|GO:0033572|GO:0016020|GO:0046961|GO:0007
035|GO:0008152|GO:0015991|GO:0030670|GO:0016049|GO:0016021|GO:0090382|GO:0010008|GO:0033179|GO:0
015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128445_PI430048170 0.000965833694953038 1.71268665847483 13.0565740736994
13.020652871286 12.8460146313391 P P P 12.1057870788103 12.2222299379163
12.2701964663499 P P P LNCV6_128445_PI430048170 mRNA
GCTTTCAGGGCAGGCAGCTGTGCATGTTCTCTCAACTAAAGGTCTTGTGAGAGGAAAAAA NM_016209RefSeq chr16
+ 88857097 88861112 TRAPPC2L 51693 trafficking protein particle complex 2-like
GO:0006888|GO:0005515|GO:0048471|GO:0005737|GO:0005794|GO:0005783 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_113775_PI430048170 0.0426114137305119 0.30327937527707 0.508520941494682
0.5690441502148640.444019157310133A A A 1.51812686314434 2.74600082963376
2.16839017301528 A P A LNCV6_113775_PI430048170 mRNA
GCCACCCAGAAAGCTATGAATTCCAATATACACCACTGATCGTGCAAGTTAGGGTTTTTT NM_001033723 RefSeq
chr8 - 80628450 80874781 ZNF704 619279 zinc finger protein 704 GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_50487_PI430048170 0.1076235184646120.6012151733317724.68252161108537 3.66442708845385
4.06094244757536 P P P 5.2765509455859 4.59657164078035 4.83831815936496 P P P
LNCV6_50487_PI430048170 mRNA
TGGTCTCCTCCTAAGCTCTGAGGTGCTCTCATATTCCCTCCATAAGTAAAGAGATTTTTT NM_017926RefSeq chr14
+ 76151884 76212803 GPATCH2L 55668 "G patch domain containing 2-like, transcript variant 1"
GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133306_PI430048170 0.2395559724116581.08304855041474 0.580244394906716
0.4207516836430450.597012878901677A A A 0.2942799802248260.46539204651657
0.491665341398168A A A LNCV6_133306_PI430048170 mRNA
TCAGACTTGAACTCAGGCTAGCTTTCTTGTGTTTTTCAAAACAAAATGGTGTCTTGTCTT NM_134428RefSeq chr9
- 3218296 3526001 RFX3 5991 "regulatory factor X, 3 (influences HLA class II expression), transcript variant 2"
GO:0005515|GO:0005667|GO:0000790|GO:0006355|GO:0003700|GO:0044212|GO:0006357|GO:0006366|GO:0003705|GO:0005634|GO:0072560|GO:0000978|GO:0003677|GO:0060287|GO:0042384|GO:0003309|GO:0050796|GO:0060285|GO:0045944|GO:0031018|GO:2000078|GO:0048469|GO:0045893|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_89228_PI430048170 0.0540646361340320.6044851868050515.57656290083611 5.75640856519523
6.08443290169434 P P P 6.14956805842396 6.54445571102433 6.86164561201871 P P P
LNCV6_89228_PI430048170 mRNA
AATGCACATTAGTTTTGCATCTGTTTTGTGACCTGTTAGATGTGACACATTCTCTTTTTG NM_001083112 RefSeq chr2
+ 156435452 156586403 GPD2 2820 "glycerol-3-phosphate dehydrogenase 2 (mitochondrial), transcript variant 1"
GO:0009331|GO:0019563|GO:0005509|GO:0004368|GO:0005743|GO:0006094|GO:0044281|GO:0006072|GO:0052591|GO:0035264|GO:0043010|GO:0044255|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127006_PI430048170 0.0933545563910365 1.20467483888702 6.78273626202801
6.69509697532685 6.743613812899 P P P 6.60008144421915 6.51600505819188
6.28228349221979 P P P LNCV6_127006_PI430048170 mRNA
CTCCAGGAAGCCTCTGTAGATCTTCATTCTGGGTTCTTGTCCATTAAAAATACCCACCAT NM_001291931 RefSeq
chr8 - 142269461 142403249 TSNARE1 203062 "t-SNARE domain containing 1, transcript variant 2"
GO:0005484|GO:0000149|GO:0031201|GO:0016021|GO:0006906|GO:0006886|GO:0048278|GO:0012505 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135308_PI430048170 0.6867887717531821.65039652431113 4.58526072705741
2.32209952496245 2.28783095420618 P A A 3.30827553195588 2.09711104770877
2.66661617788104 P A P LNCV6_135308_PI430048170 mRNA
TTTGCTCCTGCTCTCAGATCAGATCAAGCATTCTTTCTATTTTATTATCTGGGACATATT NM_001308RefSeq chr10 -
100042307 100081885 CPN1 1369 "carboxypeptidase N, polypeptide 1"
GO:0006508|GO:0051384|GO:0008270|GO:0010815|GO:0005615|GO:0004181 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141978_PI430048170 0.00707060527128547 0.4408285884224254.36341909933367
4.40149132790195 4.90489308451184 P P P 5.485651855018 5.7461531151081
6.00253923670122 P P P LNCV6_141978_PI430048170 mRNA
GCCTGTGGATATGATCACTTAAATGATTTTGTGGTGATTCGTGCCATTGCTTTTTTATTT NM_033515RefSeq chr6 -
129577094 129710225 ARHGAP18 93663 Rho GTPase activating protein 18
GO:0043547|GO:0051056|GO:0007264|GO:0005829|GO:0005096 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143213_PI430048170 0.0608366306850492 1.39579320485851 5.16818015588988
5.45354188731374 5.42358489368301 P P P 4.68594790183672 5.15590719417257
4.72863445726389 P P P LNCV6_143213_PI430048170 mRNA
GAGAAAATGAAACAGCTCGACAAGAACAAACTACAGGCGGTTGCCAACCAGACTTATCAC NM_198046RefSeq
chr10 + 97446130 97457370 ZDHHC16 84287 "zinc finger, DHHC-type containing 16, transcript variant 5" GO:0018345|GO:0016409|GO:0005789|GO:0006915|GO:0008270|GO:0016021|GO:0019706 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139086_PI430048170 0.0687138004463771.04482535791908 0.394551457282724
0.4075189936950820.444951390729512A A A 0.3281860902530310.336908210892027
0.391790445156214A A A LNCV6_139086_PI430048170 mRNA

GTTCTGCAAAACTGCTAAGCCATGAACAGTTTTCTTAGCTACTTAGAATGGTTATACATT NM_173549RefSeq chr8 + 98064521 98093610 ERICH5 203111 "glutamate-rich 5, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135250_PI430048170 0.00733281776759352 1.59908080987262 6.96114350764754 6.70571822084351 6.70524745607655 P P P 5.91658388715256 6.25479853882486 6.1635342222517 P P P LNCV6_135250_PI430048170 mRNA
TGAGGGACATGTACTGCCTCTCATCTAGAATTTATTTTCCTAGCACTTCACCACCTCCTT NM_007186RefSeq chr20 + 35455401 35511974 CEP250 11190 centrosomal protein 250kDa
GO:0005515|GO:0048471|GO:0005813|GO:0010457|GO:0006996|GO:0033365|GO:0005815|GO:0019901|GO:0005814|GO:0019904|GO:0008022|GO:0005829|GO:0043234|GO:0005929|GO:0030997|GO:0008104|GO:0000086|GO:0031616|GO:0000278|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138142_PI430048170 0.0414533886529008 0.6809239266877186.09475259818475 6.0123738354359 5.91632157823515 P P P 6.29397368832403 6.62040005030641 6.74161697843866 P P P LNCV6_138142_PI430048170 mRNA
ATTTCATGCACTTTAAAGTCCTGTGGCTTGTGACCTCTTAATAAAGTGTTAGAATCCAAA NM_001991RefSeq chr17 - 42700274 42745053 EZH1 2145 enhancer of zeste 1 polycomb repressive complex 2 subunit
GO:0035098|GO:0003682|GO:0005654|GO:0000122|GO:0009653|GO:0046976|GO:0006351|GO:0070734 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133775_PI430048170 0.0294371872489819 1.04447567404885 0.427415230988983 0.4673006989651860.449391982807483A A A 0.3821085094340510.388703873493098 0.385227803061078A A A LNCV6_133775_PI430048170 mRNA
GTCAGAACCAAACATATTAGGGAGACAGTGCTGAGGATTTTCTTCAAGACAGATCACTAA NM_001005167 RefSeq chr11 - 5840955 5841897 OR52E6 NA "olfactory receptor, family 52, subfamily E, member 6" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144544_PI430048170 0.0478747038267753 1.09280798363895 12.0930578912282 12.148634454374 12.0302903220365 P P P 11.9175711138992 12.0170639743684 11.9538932932173 P P P LNCV6_144544_PI430048170 mRNA
CCAACCTTGTCTGGTGGATGAGAAGGCGTATTTATTTTTCACTGTACAGTATTTAAAAAG NM_004860RefSeq chr17 - 7591229 7614897 FXR2 9513 "fragile X mental retardation, autosomal homolog 2"
GO:0017148|GO:0005515|GO:0005737|GO:0016020|GO:0003723|GO:0005634|GO:0022625|GO:0003729|GO:0005844|GO:0070062|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141236_PI430048170 0.1818427144063780.9853196498024480.3350833856165160.3687878083501 0.344542267823573A A A 0.3769406351163670.3815292465980850.354011809035541A A A LNCV6_141236_PI430048170 mRNA
CCCTTTGAAGATCTGTCCATATTCAGGAATCTGAGAGTGTAAAAAAGGTACCAATCATTG NM_178839RefSeq chr2 - 80301877 80304362 LRRTM1347730 leucine rich repeat transmembrane neuronal 1
GO:0030424|GO:0030054|GO:0009986|GO:0005783|GO:0035418|GO:0060291|GO:0060076|GO:0030426|GO:0003674|GO:0008150|GO:0050808|GO:0045211|GO:0007626|GO:0016021|GO:0035640|GO:0002091 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90842_PI430048170 0.0697547014867561 2.20272941031857 3.12548499814162 2.51891422674368 2.18159402255225 P A A 1.32251486388927 0.826917363308238 2.12051960355104 A A A LNCV6_90842_PI430048170 mRNA
TCTCAGAGACAGCGAGTACGAGACTGCAGAAACCATGTGTCAGATCCTCCCCAAGGGGGT NM_001282470 RefSeq chr11 + 120564435 120988804 GRIK4 2900 "glutamate receptor, ionotropic, kainate 4, transcript variant 1"
GO:0030054|GO:0005886|GO:0005234|GO:0035249|GO:0007268|GO:0031960|GO:0005634|GO:0007215|GO:0030425|GO:0042734|GO:0035235|GO:0032983|GO:0034220|GO:0005887|GO:0045211|GO:0043195|GO:0006810|GO:0015277|GO:0043204. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143440_PI430048170 0.6030688104282610.916233815355451 5.45096668484774

5.14635014848585 4.66371056050559 P P P 5.44085217346272 5.26469311478478
5.00803525896556 P P P LNCV6_143440_PI430048170 mRNA
TAGTGTCTTCTTCCTGCCCTCAGCACCACAGCTCAAGAAAACCTAAAGTTTCAATACAAG NM_012450RefSeq chr7
- 135681238 135728185 SLC13A4 26266 "solute carrier family 13 (sodium/sulfate symporter), member 4"
GO:0005886|GO:0005887|GO:0008272|GO:0035725|GO:0055085|GO:0015382 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133541_PI430048170 0.0496152381231549 3.95298750037925 2.90977384004711
2.35378477623867 1.42128156699169 A A A 0.3133892046231460.360815042462962
0.427550573425831A A A LNCV6_133541_PI430048170 mRNA
TGAGAGAGAAGCATTGGGGGTGCAAGTGTCCACCAAACCAGATAGGCATCCCTGGCCACT NM_001278563
RefSeq chr7 + 101362819 101559024 COL26A1 136227 "collagen, type XXVI, alpha 1, transcript variant
1"
GO:0031012|GO:0005581|GO:0005794|GO:0022617|GO:0005886|GO:0030198|GO:0030574|GO:0010811|GO:0005
578|GO:0005788|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142645_PI430048170 0.0364858934794080.3874760349126510.343096517190341
0.3994261525185781.43333561664895 A A A 1.82005863918478 2.2007100838383
2.46459164357446 A A P LNCV6_142645_PI430048170 mRNA
GTTCCTGAAAATGAGGCACAGGTCATTCTTTTTGAACATTCTGCTTTATAACTCAACTAA NM_181506RefSeq chr5
+ 62578734 62581448 LRRC70 100130733 leucine rich repeat containing 70 GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_142551_PI430048170 3.74705805038809e-05 0.68076906541974 8.94160769770435
8.87482380515287 8.91281495470306 P P P 9.47741626874142 9.43516319734265
9.48127959788688 P P P LNCV6_142551_PI430048170 mRNA
AAGGGTTTTGTATTCAGAATGTTGTGCAATATTTTGGAATGGGACATTGGTGTGTTTAGA NM_016272RefSeq chr22
- 41433487 41447023 TOB2 10766 "transducer of ERBB2, 2"
GO:0010468|GO:0005515|GO:0005737|GO:0008285|GO:0042809|GO:0045671|GO:0005634|GO:0007292|GO:0045
778 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130961_PI430048170 0.476106771837771 1.42963724781793 1.65375558468771
0.4214717962123470.296181401608435A A A 0.3945432260436120.442167836022466
0.404289882759499A A A LNCV6_130961_PI430048170 mRNA
GAAGGTAGTGCATAGAAACAACTTGTATACTTGGAACAAATGTAACAATACTGCAGAAAC NM_001010977 RefSeq
chr13 - 102685746 102694521 METTL21C 196541 methyltransferase like 21C
GO:0018022|GO:0006479|GO:0005634|GO:0016279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133507_PI430048170 0.0218807216814166 0.5721629801353398.92677276154912
8.93358812850215 8.97284598963562 P P P 9.5538422748877 9.97200299256895
9.69242054308365 P P P LNCV6_133507_PI430048170 mRNA
TTATATATTAAAAAACGTATCATGCACCAACTGTGAATAGCTGCCGCTTGCGCAGAGGAC NM_015103RefSeq chr3
- 129555212 129606739 PLXND1 23129 plexin D1
GO:0005515|GO:0030334|GO:0001569|GO:0005886|GO:0019904|GO:0045765|GO:0001525|GO:0007416|GO:0003
151|GO:0030027|GO:0032092|GO:0005622|GO:0017154|GO:0043542|GO:0005887|GO:0007411|GO:0060666|GO:0
071526 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143227_PI430048170 0.971353317786661 1.30478200760189 0.484797571872667
3.08914277223312 1.41298452692117 A P A 1.67260381022473 2.09318012852809 1.1247809466432
A A A LNCV6_143227_PI430048170 mRNA
TTTTAGACTTTGCAGATCTTATCTCAAGGTGACTAGGAACCCAGAGCTAAGTATCTGTGA NM_001286522 RefSeq
chr12 - 3808860 3873448 PARP11 57097 "poly (ADP-ribose) polymerase family, member 11,
transcript variant 3" GO:0008152|GO:0003950 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98251_PI430048170 0.1288177994237780.5612938707360320.4172895908990910.42797350374751
0.345683542103066A A A 0.8150438836326470.8982398314936991.7726723333271 A A A

LNCV6_98251_PI430048170 mRNA
CAATGAAAAAGATGACAAATTTCATTCTGGGAGTGAAGAGAGAATTCGTGTCACTTTTGA NM_017672 RefSeq chr15
- 50557158 50686815 TRPM7 54822 "transient receptor potential cation channel, subfamily M, member
7, transcript variant 1"
GO:0005262|GO:0070266|GO:0005886|GO:0031032|GO:0003779|GO:0016340|GO:0055085|GO:0001726|GO:0005
524|GO:0046872|GO:0034220|GO:0046777|GO:0004674|GO:0010961|GO:0070588|GO:0017022|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55216_PI430048170 0.2324993618920591.97095026207589 2.00495387507867 1.29271373485842
0.295124696241774 A A A 0.2457693696293780.6141067304263940.245688049895504 A A A
LNCV6_55216_PI430048170 mRNA
TGATGCCTGTATGGCGGCCTTACTGATGCCACGCAGGAACAAAGGGATGAGGACTCGACT NM_001102450 RefSeq
chr1 - 182646656 182672932 RGS8 85397 "regulator of G-protein signaling 8, transcript variant 2"
GO:0043547|GO:0005737|GO:0005886|GO:0038032|GO:0005096 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140463_PI430048170 0.4554428141034520.8089819910331380.437342631394967
0.4184297923658010.306223463982183 A A A 0.3402329038892950.39126712496633
1.18700820062721 A A A LNCV6_140463_PI430048170 mRNA
GATTATTAAAAAAGCAAAAATTTTGGTCACTTCCAAGCTAGAAGGAGGAATCAGATACCC NM_004430 RefSeq chr8
- 22687660 22693302 EGR3 1960 "early growth response 3, transcript variant 1"
GO:0033089|GO:0043066|GO:0035924|GO:0006355|GO:0035767|GO:0003700|GO:0045586|GO:0002042|GO:0005
634|GO:0007274|GO:0003677|GO:0046872|GO:0044344|GO:0006351|GO:0005737|GO:0071371|GO:0007517|GO:0
001938|GO:0007422|GO:0007623|GO:0071320 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116360_PI430048170 0.00250252697751579 0.3595730970261634.41128567554578
4.60787769416618 4.95074546400363 P P P 6.27738799389229 5.83241646250228
6.29366739758755 P P P LNCV6_116360_PI430048170 mRNA
AACATTAAAAGCAGCAAGACCCTCAACTTTGTAGAGCATTCCATTAGTTGCAAGGAAAAA NM_001293640 RefSeq
chr12 + 105107713 105169134 KIAA1033 23325 "KIAA1033, transcript variant 1"
GO:0031083|GO:0016197|GO:0071203|GO:0007032|GO:0005654|GO:0005768 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142182_PI430048170 0.0284475935169968 1.06249688305142 0.358115666872207
0.3729949882079220.306583217763712 A A A 0.2438730421819750.285890176636757
0.246004076070731 A A A LNCV6_142182_PI430048170 mRNA
CAAGCTTGAGTAATGTTCATGCCTGCTTTTCATTGAAATAGAATGAAAAGGTTGCACAAT NM_001004419 RefSeq
chr12 + 9669707 9699555 CLEC2D 29121 "C-type lectin domain family 2, member D, transcript
variant 2" GO:0016020|GO:0009986|GO:0005887|GO:0005783|GO:0030246|GO:0007166|GO:0004888 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69153_PI430048170 0.1088576997988091.23691169499325 7.62620621317993 7.43572748149679
7.36726941870351 P P P 7.28064783428653 7.29090815790131 6.92004451153879 P P P
LNCV6_69153_PI430048170 mRNA
AAAGTGTCATCTATTGGGCGCAGATACCCACGTAAGAGATGTATCTGCTGCTTCTTGCTT NM_001100814 RefSeq
chr14 - 20457852 20461612 TMEM55B 90809 "transmembrane protein 55B, transcript variant 1"
GO:0016787|GO:0031902|GO:0008152|GO:0016021|GO:0005765 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145162_PI430048170 0.0445380024104105 0.8247349364692389.70644654598266
9.55027770500485 9.4941834699946 P P P 9.86093779394749 9.84902379852425
9.88319989756337 P P P LNCV6_145162_PI430048170 mRNA
AGACCCCCAACAGGAAGAGTCTAAAAATCCAGTTTGCAACCACTTCTGACCTACAAAAAA NM_080605 RefSeq chr1
+ 1232248 1235040 B3GALT6 126792 "UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6"
GO:0005975|GO:0008499|GO:0005797|GO:0044281|GO:0015012|GO:0006024|GO:0030206|GO:0035250|GO:0000

139|GO:0016020|GO:0032580|GO:0009405|GO:0006486|GO:0016021|GO:0030204|GO:0030203|GO:0047220 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134125_PI430048170 0.1059775930875961.05369226935838 0.432768994587646 0.4705861471125620.478500577092321A A A 0.33538242684701 0.381709195446423 0.437019772681985A A A LNCV6_134125_PI430048170 mRNA ATGGAGCTAGACGACATGGATGAGGTCGAATTCTTACGGATAAAATACTGGGACAGGAGA NM_152631RefSeq chrX + 34942795 34944917 FAM47B 170062 "family with sequence similarity 47, member B" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129580_PI430048170 0.7590852356512120.9532033717549389.49904105460161 9.62982718008406 9.41845298553914 P P P 9.28120648946039 9.79859322214948 9.63551912773827 P P P LNCV6_129580_PI430048170 mRNA TCTGCATTGCTTTGACTTCCCTCTCCTTGGTTAATAAACACAAATGCTTGTTTCTCAAGGNM_001289145 RefSeq chr20 + 833696 846279 FAM110A 83541 "family with sequence similarity 110, member A, transcript variant 4" GO:0005515|GO:0005737|GO:0000922|GO:0005815 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135727_PI430048170 0.3862013418973981.40157459195272 0.270156315153818 1.42454412603766 0.456079187675675A A A 0.3469651319766370.295576808362464 0.327827852458158A A A LNCV6_135727_PI430048170 mRNA TGACCCACTTTTTCCTTTGAAAATACAATAAAATTCCCCCATACCGGTGTGCATTTAAAA NM_021081RefSeq chr20 - 37251085 37256896 GHRH 2691 "growth hormone releasing hormone, transcript variant 1" GO:0021984|GO:0060124|GO:0008284|GO:0046005|GO:0030819|GO:0007267|GO:0005576|GO:0005615|GO:0032094|GO:0031770|GO:0043568|GO:0016608|GO:0043195|GO:0019933|GO:0030252|GO:0007189|GO:0040018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130080_PI430048170 0.3679138834557170.659614573539889 3.29859634481243 0.5275740061212542.47532959274643 P A A 3.3294416240531 3.25616225730042 2.56718833967252 P P P LNCV6_130080_PI430048170 mRNA CAGCACAACACTCTGTACATTTCAGTCTGATATTCTACTTTGCCATTTAAGGACACCATT NM_001031723 RefSeq chr4 - 99896249 99946726 DNAJB14 79982 "DnaJ (Hsp40) homolog, subfamily B, member 14, transcript variant 1" GO:0016020|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130623_PI430048170 0.5110108060460650.967606113553852 0.278356924525668 0.4410014383460280.313674300519353A A A 0.4780806387047510.367799896132257 0.330691582648068A A A LNCV6_130623_PI430048170 mRNA ATGCTGGGGCAAGGATTGCAGTTGAAGTATTTTGCTTTTGGAGTGTATAATAGTATGAAT NM_001039395 RefSeq chr9 - 4598315 4666674 SPATA6L 55064 spermatogenesis associated 6-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139533_PI430048170 0.0609501537289297 0.6962906430961139.46884116049812 9.23851078784423 9.49728309415926 P P P 10.0770561820098 9.60246863396058 10.0574500014078 P P P LNCV6_139533_PI430048170 mRNA CGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTGTAGAATTACTGTTTACACAC NM_012449RefSeq chr7 + 90154374 90164827 STEAP1 26872 six transmembrane epithelial antigen of the prostate 1 GO:0005215|GO:0005886|GO:0055072|GO:0055085|GO:0046872|GO:0016020|GO:0005887|GO:0005911|GO:0016491|GO:0010008|GO:0006811|GO:0015267|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136520_PI430048170 0.0426069632181935 0.7019285323249578.3157634263414 8.11868243694147 8.58288048760345 P P P 8.94834625297187 8.64087563091209 8.9745056994782 P P P LNCV6_136520_PI430048170 mRNA CTGTCCTCAAAGTATATAATGTTTCATGTACCAAGACCCTTTTCACAGTACAATAAACAG NM_016451RefSeq chr11 - 14457502 14499858 COPB1 1315 "coatomer protein complex, subunit beta 1, transcript variant 1" GO:0005515|GO:0030126|GO:0005793|GO:0005794|GO:0005886|GO:0006890|GO:0005798|GO:0006891|GO:0006886|GO:0048205|GO:0043231|GO:0005829|GO:0005737|GO:0000139|GO:0016020|GO:0005198|GO:0061024|GO:0

016032 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138103_PI430048170 0.0370812353280355 0.6615992879795225.69413158895311
5.77370100642881 6.0754391082396 P P P 6.20898594120469 6.39296165407756
6.71233322952861 P P P LNCV6_138103_PI430048170 mRNA
AACAGAGCCTGGGAATTTCTTTCCTCTGCACAGTCCCTTGATATTTGGAATCCAGGTTCT NM_012204RefSeq chr9
+ 132670340 132690083 GTF3C4 9329 "general transcription factor IIIC, polypeptide 4, 90kDa"
GO:0005515|GO:0010467|GO:0016573|GO:0043085|GO:0006384|GO:0042791|GO:0003677|GO:0006383|GO:0006
351|GO:0042797|GO:0000127|GO:0005654|GO:0008047|GO:0004402 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_99707_PI430048170 0.0479860791425498 1.23939383087053 6.76057558758681
6.98271107152948 6.70314641542359 P P P 6.42109838369834 6.48566838322576
6.61899673772458 P P P LNCV6_99707_PI430048170 mRNA
GACGAGGATGAGGAAGACGACTCTGAGGATGCTATCAATGAGTTTGATTTCCTGGGCTCA NM_001039877 RefSeq
chr19 - 46719510 46746463 STRN4 29888 "striatin, calmodulin binding protein 4, transcript variant 2"
GO:0005515|GO:0008150|GO:0005516|GO:0005737|GO:0043197|GO:0016020|GO:0000159|GO:0051721|GO:0032
403|GO:0070016 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134087_PI430048170 0.0783378370767476 0.7664068995145973.47389276163825
3.64093629995173 3.90067556275779 P P P 4.09569857695834 3.85972460709332
4.22087434569706 P P P LNCV6_134087_PI430048170 mRNA
ATTTGTATTGTTTCTCTGTCCAAGTCCTTATTCTCTATCTTGTGGGGAGGGGTGACAGGG NM_001197026 RefSeq
chr7 + 30028360 30084662 PLEKHA8 84725 "pleckstrin homology domain containing, family A
(phosphoinositide binding specific) member 8, transcript variant 1"
GO:0005802|GO:0035621|GO:0051861|GO:0016020|GO:0017089|GO:0006869|GO:0097001|GO:0070273|GO:0046
836|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134223_PI430048170 0.0813374953070555 0.7256169797726180.51310547014847
0.5098868375535930.284995504031715 A A A 1.07704207883197 0.581278126268889
1.00173055638031 A A A LNCV6_134223_PI430048170 mRNA
GTAAGTACTTGAATTTGAATTCTCTTCCTTTTCATTTTTGCCTGCAAACTGACCAGTCTT NM_014805RefSeq chr3 -
36985865 36993304 EPM2AIP1 9852 EPM2A (laforin) interacting protein 1
GO:2000467|GO:0032868|GO:0045725|GO:0005783|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143978_PI430048170 0.0462013171653555 0.9161588298040361 3.2082246529411
13.307405233388 13.1989601502063 P P P 13.4049236061206 13.3677780868071
13.3222152668747 P P P LNCV6_143978_PI430048170 mRNA
TGCTTAAGACACTCCTGCTGCCCCGTCTGAGGGTGGCGATTAAAGTTGCTTCACATCCTC NM_016579RefSeq chr19
- 8302126 8308356 CD320 51293 "CD320 molecule, transcript variant 1"
GO:0009235|GO:0005886|GO:0031419|GO:0005783|GO:0006767|GO:0044281|GO:0001558|GO:0016020|GO:0006
766|GO:0016021|GO:0008083|GO:0030656|GO:0010008|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141834_PI430048170 0.4594202003827131.09376652671233 6.82623061448168
6.51299965722313 6.54992191795592 P P P 6.31504724882627 6.74694309109988
6.42432050404535 P P P LNCV6_141834_PI430048170 mRNA
TTCACCCCGTCCCCTTTAAATAAAAAGAATCTCTGTGTTCTCTTTGGGCAAAATGTAAAA NM_152320RefSeq chr12
- 48340009 48350891 ZNF641 121274 "zinc finger protein 641, transcript variant 1"
GO:0005737|GO:0006366|GO:0006357|GO:0000981|GO:0005654|GO:0003677|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_67544_PI430048170 0.3405870150117920.7558861718831340.3083346416698370.307287474212386
0.501240232739885 A A A 0.30617648053886 1.26090666575342 0.599151294861239 A A A
LNCV6_67544_PI430048170 mRNA

AGAGATGCTCTTTTTCTACCTCCTACTTCTCTGGCTCTTAGAGAGGCAGCATGGGATAAT NM_000189RefSeq chr2 + 74832654 74893354 HK2 3099 hexokinase 2 GO:0001678|GO:0005975|GO:0005741|GO:0044281|GO:0004396|GO:0055085|GO:0005524|GO:0005536|GO:0006096|GO:0008645|GO:0005829|GO:0004340|GO:0008865|GO:0008637|GO:0046324|GO:0016020|GO:0015758|GO:0007595|GO:0002931|GO:0009405|GO:0046835|GO:0006006|GO:0019158|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142047_PI430048170 0.3584842215900771.04341491863145 0.297083335139184 0.2745841327946920.435841382544162A A A 0.2900951101708950.252804257497053 0.285725484435684A A A LNCV6_142047_PI430048170 mRNA
ATTTGTCGAGAAACGCACTGTACGTGAAATGCTTTGCCATCTTGTACGAAAGACTTTTTT NM_004976RefSeq chr11 + 17735947 17777830 KCNC1 3746 "potassium channel, voltage gated Shaw related subfamily C, member 1, transcript variant 2" GO:0005251|GO:0005886|GO:0007268|GO:0032809|GO:0032590|GO:0005249|GO:0008076|GO:0034765|GO:0051260|GO:0016021|GO:0019894|GO:0030673|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144206_PI430048170 0.1725821459107930.5730219570387831.3690016567022 2.51804874539885 2.58689213676814 A A A 2.38822605189798 3.24887485050224 3.35716174388223 A P P LNCV6_144206_PI430048170 mRNA
TGGGGAGCCAGAAGCCAATCTACAATCTCTTTTTGTTTGCCAGGACATGCAATAAAATTT NM_003722RefSeq chr3 + 189631426 189897279 TP63 8626 "tumor protein p63, transcript variant 1" GO:0005515|GO:0010838|GO:0000790|GO:0003700|GO:0044212|GO:0007283|GO:0000989|GO:0031069|GO:0042802|GO:0045617|GO:0043523|GO:0034644|GO:0003690|GO:0007219|GO:0048745|GO:0002064|GO:0048807|GO:0006978|GO:0000785|GO:0010332|GO:0045747|GO:0005791|GO:0000122|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131178_PI430048170 0.5312552654955310.690067187138145 1.4757744094076 0.2804156075741330.456243327078381A A A 0.2932605856232361.13891470717345 2.12139968152563 A A A LNCV6_131178_PI430048170 mRNA
CCCATAAGAGGGTGTAAACAATTAACTCCAGGGTTTTATTGTATCCTGCAATATTTAGTA NM_015384RefSeq chr5 + 36876758 37065819 NIPBL 25836 "Nipped-B homolog (Drosophila), transcript variant B" GO:0005515|GO:0001656|GO:0035136|GO:0042826|GO:0070087|GO:0007605|GO:0071481|GO:0048592|GO:0005634|GO:0048703|GO:0045778|GO:0035261|GO:0048589|GO:0045944|GO:0045444|GO:0040018|GO:0000785|GO:0070062|GO:0042634|GO:0042471|GO:0000122|GO:0032116|GO:0008022|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139373_PI430048170 0.0363947148889333 1.41401291358624 10.6517132233128 11.0202264581928 10.7848657346204 P P P 10.3874375787194 10.3031150031275 10.2892744916368 P P P LNCV6_139373_PI430048170 mRNA
GGTTCCTTCAGTTTCATCCCCTTTCTCTCCTTCCATGGATTATGTAATACATTGTAAAGT NM_015997RefSeq chr1 + 156728470 156736960 RRNAD1 51093 "ribosomal RNA adenine dimethylase domain containing 1, transcript variant 1" GO:0031167|GO:0016021|GO:0000179 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129126_PI430048170 0.2209593583857 0.7497547987040620.348500439449362 0.35235334800919 0.291198578107499A A A 0.8906928605001790.279207772962012 0.974844982204527A A A LNCV6_129126_PI430048170 mRNA
CTCAGGAACAAGCATATAATTTGTCCAAGATTTATTTCTTCTCAGAAGTGTAAGTGCAGT NM_001079526 RefSeq chr2 - 212999685 213151609 IKZF2 22807 "IKAROS family zinc finger 2 (Helios), transcript variant 2" GO:0005515|GO:0008150|GO:0003674|GO:0046982|GO:0045944|GO:0005634|GO:0003677|GO:0046872|GO:0042803|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136892_PI430048170 0.6999814805297720.9658520567778520.492095192303452 0.5411500308707390.473287314146152A A A 0.4503445091135350.740469393233034

0.446846070093964 A A A LNCV6_136892_PI430048170 mRNA
GTGGTCAGAAGTACATTAAAGATTTCTGCTCCAAATTTTCAATAAATTTCTGCTTGTGCC NM_001872 RefSeq chr13
- 46053186 46105076 CPB2 1361 "carboxypeptidase B2 (plasma), transcript variant 1"
GO:0009408|GO:0042493|GO:2000346|GO:0051918|GO:0005615|GO:0003331|GO:0007596|GO:0006508|GO:0008
270|GO:0010757|GO:0071333|GO:0042730|GO:0004181|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143889_PI430048170 0.0953082304621145 0.66203622049299 7.83557600819093
7.86874530037322 8.25153621973528 P P P 8.2145919279064 8.52394603554949
8.94625577005929 P P P LNCV6_143889_PI430048170 mRNA
CAACCAAACCACTCCTATCTGCATGATTCTGAACATCTGGATGCCTGTTGTTTTACTGTG NM_012329 RefSeq chr17
- 55392612 55421980 MMD 23531 monocyte to macrophage differentiation-associated
GO:0016020|GO:0005887|GO:0031902|GO:0019835|GO:0004872|GO:0005765 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136317_PI430048170 0.2926192425103241.03085412486976 0.31107596917016
0.2516855883698830.357895658215063 A A A 0.2719165113098560.245825276822358
0.27319069216916 A A A LNCV6_136317_PI430048170 mRNA
CACTCACAAAGCAAGACACAGCTGCATTTTTGATCATTCAGTTACTTTATTAAACGCACA NM_001164442 RefSeq
chr5 + 64690307 64718190 FAM159B NA "family with sequence similarity 159, member B" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140630_PI430048170 0.00575299605758784 0.8172722163465319.28596916674933
9.40862175345375 9.2869383487981 P P P 9.62237196580744 9.67090104396147
9.56305120080838 P P P LNCV6_140630_PI430048170 mRNA
ATCCACTAGTCCTAAACCGGAAGAGGATGACACCGGCCATGGGTTAACGTGGCTCCTCAG NM_014298 RefSeq chr16
+ 29679119 29697993 QPRT 23475 quinolinate phosphoribosyltransferase
GO:0005737|GO:0006766|GO:0004514|GO:0019674|GO:0006767|GO:0044281|GO:0009435|GO:0051259|GO:0042
803|GO:0034213|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130955_PI430048170 0.00433906023123374 0.5143684965851894.66753339327514
4.67160399786119 5.02992737461326 P P P 5.75607932594662 5.62036084954032
5.88835259292399 P P P LNCV6_130955_PI430048170 mRNA
GGGGGCAGGAGGAGCTAATTTCCTTTGCACATTTGTATTTTATTTCAAAATAAAGTATTC NM_002505 RefSeq chr6
+ 41072967 41102407 NFYA 4800 "nuclear transcription factor Y, alpha, transcript variant 1"
GO:0005515|GO:0006355|GO:0003700|GO:0006366|GO:0044212|GO:2000648|GO:0005634|GO:0044281|GO:0003
677|GO:2000036|GO:0001221|GO:0016602|GO:0032993|GO:0045944|GO:0005654|GO:0048511|GO:0001046|GO:0
045893|GO:0044255. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142242_PI430048170 0.0875928534116484 0.9547337065599120.286628831473735
0.3109494336237740.340404831502672 A A A 0.4238413189377210.3701276313418840.3438505219774
A A A LNCV6_142242_PI430048170 mRNA
CCAGGTTCTAATGTGTGGAATGTGCAGATTTAGGTTACTTTAGTGTATGTTCTAGTTAAT NM_004680 RefSeq chrY
+ 25622116 25624901 CDY1 NA "chromodomain protein, Y-linked, 1, transcript variant 2" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_144420_PI430048170 0.4670084236109170.8182262726809 0.410752288278485
0.2929855768421270.334181674653289 A A A 0.2893432555214551.11748759879198
0.345980167400142 A A A LNCV6_144420_PI430048170 mRNA
TGTATCCTTATGTGCTTATGGAAATGTTCACATACACACCTGCAGATGTGATGACTGAAA NM_032279 RefSeq chr3
- 193398966 193555122 ATP13A4 84239 ATPase type 13A4
GO:0008152|GO:0006874|GO:0005789|GO:0016021|GO:0016887|GO:0005524|GO:0046872|GO:0006812 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144286_PI430048170 0.2148603448422590.757626851766083 3.3934568391961
3.80953826510143 4.24971901253024 P P P 4.29515839719214 4.2552185869231

4.22940680546499 P P P LNCV6_144286_PI430048170 mRNA
ATTGGTAAATGCTGGCTGTAACTTGAGTACTTTAAACATCACTCTTCTATCTTGGAGTAA NM_001301135 RefSeq
chr7 - 91872875 91880720 MTERF1 7978 "mitochondrial transcription termination factor 1, transcript variant 3"
GO:0005515|GO:0006353|GO:0042645|GO:0010467|GO:0006355|GO:0006996|GO:0006390|GO:0006393|GO:0005739|GO:0003690|GO:0005759|GO:0032392|GO:0007005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136285_PI430048170 0.0313478943773678 0.7487563544798459.73884882852502
9.40912231526063 9.48894657974869 P P P 9.81701041362962 10.0704352388195
10.0106231402047 P P P LNCV6_136285_PI430048170 mRNA
CTTTGCACTCCTCGTGTGTTGGCAAACGCAGTTAATAAAGCAGTGTTTTCTGTGCTGAAA NM_001289984 RefSeq
chr5 + 134525649 134583230 JADE2 23338 "jade family PHD finger 2, transcript variant 1"
GO:0043981|GO:0043983|GO:0043982|GO:0043966|GO:0043984|GO:0000123|GO:0008270|GO:0005654|GO:0060395|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141531_PI430048170 0.1526466340634950.5421623035904990.452105316571403
0.4193107388940291.51764541256053 A A A 2.38143700257667 1.42288520620095
1.25050606260745 A A A LNCV6_141531_PI430048170 mRNA
TCATCCTTTAAGTAAGTTTCTCACTTTTCAAAACTCATGTATCAACACTGACTGACTTGCNM_017987RefSeq chr10 - 68343517 68407189 RUFY2 55680 "RUN and FYVE domain containing 2, transcript variant 1"
GO:0005634|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139880_PI430048170 0.6483280617451791.0632600641713 6.98897772100676
7.26814911894198 7.44214039322256 P P P 6.98769631044602 7.09107371954284
7.36409422687192 P P P LNCV6_139880_PI430048170 mRNA
AGAAGGTCTTAGACTTAAATCCTGGATTTCAAGATGCTACTTTGAGCTTAAAACAGACTA NM_001008237 RefSeq
chr2 - 19896752 19901983 TTC32 130502 tetratricopeptide repeat domain 32 GO:0042802 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142296_PI430048170 0.6996993214840120.8866673481361371.16534417964576
0.4081375667925960.285665086009198A A A 0.61353330305837 1.35739810893914
0.388114575695536A A A LNCV6_142296_PI430048170 mRNA
TGTAACCTCACAACTCCAAGTCCACAGAATATTTCAAACTGCAGGTATGCGCAGACACCA NM_002934RefSeq chr14 + 20955470 20956435 RNASE2 6036 "ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)"
GO:0006935|GO:0005576|GO:0004540|GO:0004522|GO:0003676|GO:0005764|GO:0070062|GO:0006401 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55200_PI430048170 0.9357269870768541.15206092427775 1.16213052903487 2.81792377062456
2.66921196753695 A A A 1.90872569024992 2.33015139554508 2.26337620391678 A A A
LNCV6_55200_PI430048170 mRNA
TTTCAGAACCTCCATTCTCTGCTGAGCAGCAAGGGGAACCGGTCCAGCCTCTACCTGGTA NM_020950RefSeq chr1 + 180913176 180946103 KIAA1614 57710 KIAA1614 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140941_PI430048170 0.1352700230199050.6792566879074694.28914134779056
4.58985634850269 4.84050058063997 P P P 5.43536095285347 4.66597634109347
5.23865166427091 P P P LNCV6_140941_PI430048170 mRNA
AAGAGGAGGAGCTGACACATTTCACTTGGCTGCGTCTTAATAAACATGAATGCAAGCATT NM_001144757 RefSeq
chr15_KI270905v1_alt + 4856252 4911692 SCG5 6447 "secretogranin V (7B2 protein), transcript variant 1"
GO:0005515|GO:0004857|GO:0016486|GO:0007218|GO:0046883|GO:0005576|GO:0051082|GO:0030141|GO:0005525|GO:0043086|GO:0006886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145274_PI430048170 0.7865240729565341.08461515917264 0.322240471868607
1.27593853694956 0.823910873338961A A A 0.2588534142998480.722598629739044

1.11822559537484 A A A LNCV6_145274_PI430048170 mRNA
TCATATACTGTTTCTGCAATGGCGAGGTACAAGCTGAGATCAAGAAATCTTGGAGCCGCT NM_000316RefSeq chr3
+ 46877745 46903799 PTH1R 5745 "parathyroid hormone 1 receptor, transcript variant 1"
GO:0005515|GO:0008284|GO:0008285|GO:0005886|GO:0045453|GO:0060732|GO:0007200|GO:0005634|GO:0030
282|GO:0031526|GO:0043621|GO:0007204|GO:0016323|GO:0005737|GO:0016324|GO:0004991|GO:0002062|GO:0
048469|GO:0070062|GO:0007568|GO:0043235|GO:0001501|GO:0007186|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130334_PI430048170 0.2173301935778641.71741485155576 1.32195213960434
0.2767540548094261.52495137572981 A A A 0.4028192990367920.341052882306335
0.319586105160385A A A LNCV6_130334_PI430048170 mRNA
AAACTGAGGCAGACATTTGTCAGAATGCTGACATGTAGAAAAATTGCCTGCATGATATGA NM_023918RefSeq
chr12_KI270904v1_alt - 4756 5686 TAS2R8 50836 "taste receptor, type 2, member 8"
GO:0033038|GO:0007186|GO:0005886|GO:0008527|GO:0016021|GO:0001580 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_94777_PI430048170 0.9490152532853980.9830818599312430.4932852485924870.587445005081452
0.580531759740244A A A 0.3386553796391130.8339041000829490.520415375540235A A A
LNCV6_94777_PI430048170 mRNA
CAAATCACGGCAATCCTGGGTCACAGTGGAGCTGGCAAATCTTCACTGCTAAATATTCTT NM_080284RefSeq chr17
- 69078705 69141874 ABCA6 23460 "ATP-binding cassette, sub-family A (ABC1), member 6"
GO:0005215|GO:0008152|GO:0006810|GO:0016021|GO:0016887|GO:0005524 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131932_PI430048170 0.9272882478573820.9106789131230460.760223927678274
0.8529165148597490.909048278994306A A A 1.60897084700298 0.49842381033707
0.528224230204216A A A LNCV6_131932_PI430048170 mRNA
TGGAATTTGGGATTGAAGTTAAACTACAACAGTGCCGCCAACACCAAGTCTTGCAGGAAA NM_032452RefSeq chr14
- 23568034 23578800 JPH4 NA "junctophilin 4, transcript variant 1" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129634_PI430048170 0.00693031801137273 0.73793784654053210.1512713248441
10.026793490309 10.0231471202339 P P P 10.5212899488106 10.6041156595115
10.3865068689205 P P P LNCV6_129634_PI430048170 mRNA
CTGTTACAAATGAGTCATGACATCATACTGTAATAAAAGCAGCTTGTTTTCTGCTTGAAC NM_024658RefSeq chr14
- 24180218 24188918 IPO4 79711 "importin 4, transcript variant 1"
GO:0043234|GO:0005737|GO:0000790|GO:0016020|GO:0005643|GO:0008536|GO:0006335|GO:0006336|GO:0015
031|GO:0006886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136867_PI430048170 0.00381585186332459 0.4483787583429034.52202717879435
4.83644082955143 4.94993897111364 P P P 5.70786373398488 6.18752907912584
5.87632977287978 P P P LNCV6_136867_PI430048170 mRNA
TTGAACATTCTGAGAACCCAATAAAACTAGAAGGAGCCAGCTTCCTGAGTATGCTCCACT NM_152550RefSeq chr5
+ 145936562 146063316 SH3RF2 153769 SH3 domain containing ring finger 2
GO:0005515|GO:0016567|GO:0019902|GO:0016874|GO:0010923|GO:0004864|GO:0008270|GO:0008157|GO:0005
654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120080_PI430048170 0.2338378827651632.07459944273467 0.800017157725407
2.37552363210079 2.40436310009712 A A A 0.9857731564665020.84068585668078
1.08483293023832 A A A LNCV6_120080_PI430048170 mRNA
ATTTAGGTACCAGCTCACGATGGGCAGTGTTCTCCATACTATTATTAGCTCTCATGTCCC NM_014579RefSeq chr14
+ 20999254 21001875 SLC39A2 29986 "solute carrier family 39 (zinc transporter), member 2, transcript
variant 1" GO:0071577|GO:0005886|GO:0005385|GO:0005887|GO:0016023|GO:0006829|GO:0055085 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62220_PI430048170 0.8646097550810731.25085657325296 3.30953111685367 1.34016239862278

1.85055468683858 P A A 2.11543510120766 2.48695107056876 1.5331544020801 A P A
LNCV6_62220_PI430048170 mRNA
ATTTGTAAGGAAAGAAAAGGAAGCAACAACATAATGCCCAGAGTTGGAGCCAATTAAACC NM_024776RefSeq
chr15 - 77108155 77420104 PEAK1 79834 pseudopodium-enriched atypical kinase 1
GO:0005515|GO:0005737|GO:0046777|GO:0016477|GO:0005886|GO:0034446|GO:0018108|GO:0005654|GO:0015
629|GO:0005925|GO:0005524|GO:0004715 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134520_PI430048170 0.0662915434445496 1.41120435339086 11.1267282379727
11.110696011722 11.25837935474 P P P 10.3843704132508 10.6720291062966
10.9062731854026 P P P LNCV6_134520_PI430048170 mRNA
CATTGTCCCAAAAGTGTCTGTGCATTGTGCAAAAAGTAAACTTAGGAAACATTTGGTATT NM_002208RefSeq chr17
- 3714624 3801243 ITGAE 3682 "integrin, alpha E (antigen CD103, human mucosal lymphocyte
antigen 1; alpha polypeptide)"
GO:0008305|GO:0005886|GO:0030198|GO:0007229|GO:0007155|GO:0046872|GO:0009897 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135146_PI430048170 0.2798758848727381.25742518372374 1.18462053352232
0.4605363873687860.828197191439512A A A 0.45418203603482 0.408167827115298
0.693330831327535A A A LNCV6_135146_PI430048170 mRNA
GGGAACAAGAGACAGTGTAGTTGTATATGACAGTAAATACAGTACAAGTTCACTATCAAA NM_004267RefSeq chr3
+ 143119775 143124014 CHST2 9435 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
GO:0005802|GO:0006790|GO:0005975|GO:0031228|GO:0006044|GO:0007275|GO:0044281|GO:0042339|GO:0006
954|GO:0000139|GO:0018146|GO:0008146|GO:0009405|GO:0001517|GO:0016021|GO:0030203 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_113182_PI430048170 0.140240407812796 1.22039539620183 9.59368582579321
9.35077140970371 9.37562178743249 P P P 8.99930661655518 9.40582484364274
9.02890494267139 P P P LNCV6_113182_PI430048170 mRNA
TTCTGTGCCAGCATGATCAGCGGTCTTGTCACCACTGCTGCCTCCATGCCTGTGGACATT NM_003562RefSeq chr17
- 4937130 4940167 SLC25A11 8402 "solute carrier family 25 (mitochondrial carrier; oxoglutarate
carrier), member 11, transcript variant 1"
GO:0005739|GO:0005975|GO:0005887|GO:0015367|GO:0009405|GO:0006810|GO:0006094|GO:0005743|GO:0006
006|GO:0015742|GO:0005634|GO:0044281 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143947_PI430048170 0.516545014262377 0.135916424386125 0.519028709704797 1.5321236726332
0.262851512607557A A A 0.395384947155162 5.24614690134436 0.465916668504338A P A
LNCV6_143947_PI430048170 mRNA
TGTAAAGAAGCGTCGTGTATACCTGTGCAGGCACTAGTACTTTACAGATGACCATGCTGA NM_021268RefSeq chr9
- 21227242 21228222 IFNA17 NA "interferon, alpha 17" NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_102820_PI430048170 0.204584023149066 0.674285006381743 3.36429829419414 2.7907773888886
2.13371716830764 P A A 3.3710215968076 3.58785720763882 3.27401965092331 P P P
LNCV6_102820_PI430048170 mRNA
ATGACTCCACGCTCCGAAGGCTCCAGTGTGAATCTGTCACCTCCATTGGAGCAGTGTGTC NM_000506RefSeq chr11
+ 46719192 46739506 F2 2147 coagulation factor II (thrombin)
GO:0005515|GO:0010544|GO:0008284|GO:0005886|GO:0004252|GO:0030307|GO:0008360|GO:1900738|GO:0072
562|GO:0050900|GO:0005615|GO:0006508|GO:0051281|GO:0070062|GO:0005796|GO:0051480|GO:0005509|GO:0
005102|GO:0009611|GO:0051918|GO:0030168|GO:0005576|GO:0007275|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132657_PI430048170 0.00971414593261775 5.20244831164385 6.26774314873179
6.5862709775911 6.27314553303575 P P P 4.46215497515867 3.96748281762987
3.38698541099231 P P P LNCV6_132657_PI430048170 mRNA
TGACTGTTTCTCATGCCTTTATGTTCCTTCATGTAAGTAAAGTGGACCTTTGTGCTCAAA NM_024320RefSeq chr17

- 47951967 47957877 PRR15L 79170 proline rich 15-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78598_PI430048170 0.00670924952835525 1.92715415183949 7.85220988076649 8.20937562371713 8.2777422636778 P P P 7.15878335653424 7.04258451568213 7.32015023077583 P P P LNCV6_78598_PI430048170 mRNA TGTCTGTACATGTTCTAATGTTTTGTAGAACACGTGTGCCTGTTTAAGTGTATTGATGTG NM_003596 RefSeq chr7 + 66205271 66360451 TPST1 8460 tyrosylprotein sulfotransferase 1 GO:0006954|GO:0016020|GO:0000139|GO:0016021|GO:0008476|GO:0006478 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83465_PI430048170 0.162809880705834 1.16506575828122 8.05613478389382 8.28669028171116 8.30012479255353 P P P 7.93268090685875 7.85071432264001 8.18914760153328 P P P LNCV6_83465_PI430048170 mRNA TTCTTTTACCTGAGAAATGCTACGACCAACTTTTCGTTCAGTGGGACTTGCTTCACGTCC NM_004870 RefSeq chr17 + 7583646 7588209 MPDU1 9526 "mannose-P-dolichol utilization defect 1, transcript variant 1" GO:0005739|GO:0009312|GO:0016020|GO:0006457|GO:0005783|GO:0006810|GO:0005789|GO:0016021|GO:0006488|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69336_PI430048170 0.0289312250401813 0.907585008587672 11.8196176278314 11.7575617584747 11.7842060898739 P P P 11.8647761177534 11.9706859804657 11.9441880648426 P P P LNCV6_69336_PI430048170 mRNA TCTCACCAGCCAACCAGCGGAAATGTGAGCGTGTACTGCTGGCCCTATTCTGTCACGAAC NM_005762 RefSeq chr19 + 58544468 58550715 TRIM28 10155 tripartite motif containing 28 GO:0005515|GO:0010467|GO:2000653|GO:0004842|GO:0003700|GO:0006367|GO:0016567|GO:0070087|GO:0016874|GO:0005634|GO:0045739|GO:0001837|GO:0051259|GO:0042993|GO:0060669|GO:0060028|GO:0046777|GO:0031625|GO:0043045|GO:0005719|GO:0007566|GO:0003714|GO:0016925|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127533_PI430048170 0.911292590286408 1.00378396751934 0.374513522409397 0.354135996868999 0.257408843653491 A A A 0.325002470061886 0.328446389923024 0.318939719700823 A A A LNCV6_127533_PI430048170 mRNA ACCATGTGTATACTCAAGTAGGTGATGAGATTGTAGGAAGAAGGTAGGATATAATAGCAG NM_001301203 RefSeq chr15 + 79311061 79384719 TMED3 23423 "transmembrane emp24 protein transport domain containing 3, transcript variant 2" GO:0030126|GO:0005793|GO:0005794|GO:0005783|GO:0033116|GO:0032580|GO:0005789|GO:0016021|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141163_PI430048170 0.0124208749821464 0.465005380476454 13.834941567572 13.7289298886238 14.0835832042834 P P P 14.6911003669162 14.9035109591796 15.3183585657629 P P P LNCV6_141163_PI430048170 mRNA CTGCAGCTGAACTGAATGGTACTTCGTATGTTAATAGTTGTTCTGATAAATCATGCAATT NM_001127500 RefSeq chr7 + 116672404 116798386 MET 4233 "MET proto-oncogene, receptor tyrosine kinase, transcript variant 1" GO:0005515|GO:0014812|GO:0005886|GO:0008283|GO:0000187|GO:0046777|GO:0009925|GO:0060665|GO:0007411|GO:0045944|GO:0030534|GO:0005008|GO:0014902|GO:0048012|GO:0009986|GO:0019903|GO:0005576|GO:0018108|GO:0042593|GO:0001890|GO:0005524|GO:0050918|GO:0010828|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122952_PI430048170 0.412553356472026 0.94889250452523 0.356631820715074 0.35409442340025 0.405760420999731 A A A 0.369504266364269 0.585026619075909 0.37916429510386 A A A LNCV6_122952_PI430048170 mRNA TACCTCTGTCGAGCCACCAATTTCATAGGCGTGGCCGAGAAGGCCTTTTGGCTGAGCGTT NM_001163213 RefSeq chr4 + 1793311 1808872 FGFR3 2261 "fibroblast growth factor receptor 3, transcript variant 3" GO:0005515|GO:0003416|GO:0070307|GO:0045597|GO:0050680|GO:0048678|GO:0005764|GO:0035988|GO:0061

144|GO:0046777|GO:0043525|GO:0007173|GO:0043552|GO:0000165|GO:0002062|GO:0031398|GO:0070374|GO:0
005794|GO:0009986|GO:0017134|GO:0010518|GO:0018108|GO:0000122|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130140_PI430048170 0.459426094145216 1.09438000832619 8.71544508919312
8.73485100418503 9.06145229275007 P P P 8.55226696947604 8.64221443082423
8.92677276154912 P P P LNCV6_130140_PI430048170 mRNA
CTCATAGCACAGTCTACTGCTTTGTACGAATTCTAAGTATTCTTGTTGCACTTAATTAGC NM_138777 RefSeq chr9
+ 122264602 122323463 MRRF 92399 "mitochondrial ribosome recycling factor, transcript variant 1"
GO:0070126|GO:0032543|GO:0006996|GO:0005759|GO:0032790 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_102184_PI430048170 0.170288735252226 1.3577509390074 6.15275075671863
6.49195747421162 6.74483980107511 P P P 6.21377568428963 5.60561547192765
6.22437515037437 P P P LNCV6_102184_PI430048170 mRNA
CCAAGATGCCTTTTTAAAAATTTGTGTGGAATACTAACCGGGGATCAAATTTCATCCATA NM_032930 RefSeq
chr11 + 102047437 102084560 C11orf70 85016 "chromosome 11 open reading frame 70,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127794_PI430048170 0.59292846903475 0.971094598036029 9.68828455451811
9.85269507042204 9.92025935264461 P P P 9.84848974838876 9.82755069034794
9.92025935264461 P P P LNCV6_127794_PI430048170 mRNA
GACCGAGTTCACAGATAAATCCATTGGTTTGTATCCTTGAGAAACTTTGTTTTTGTGGAA NM_138417RefSeq chr1
- 52032104 52033800 KTI12 112970 "KTI12 homolog, chromatin associated (S. cerevisiae)"
GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134591_PI430048170 0.0380272067917805 0.4891434165976224.61401718424391
4.16743661221008 4.58463525235863 P P P 4.99548165458984 5.50680227438474
5.86998759667049 P P P LNCV6_134591_PI430048170 mRNA
TCTAGGCATTCCTGAGAAATTGAAAGTGGCTACCTTTCATGTCAAAAATGTTGATCTATT NM_020854RefSeq chr18
+ 62187290 62307122 KIAA1468 57614 KIAA1468 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138189_PI430048170 0.9074750063559390.9865600253708041 1.937783604601
11.9721112160391 12.0796495554357 P P P 11.8487954432702 11.989407450689
12.1928646927023 P P P LNCV6_138189_PI430048170 mRNA
CTTTTCCCATTTCAATTCCTGTGATTTATGCCAATAAAGTTTGCCCATGATTTTCACCTG NM_001243756 RefSeq chr12
- 120210438 120265771 PXN 5829 "paxillin, transcript variant 3"
GO:0005515|GO:0005886|GO:0008013|GO:0008360|GO:0030032|GO:0006928|GO:0060396|GO:0005829|GO:0000
187|GO:0005737|GO:0006936|GO:0007172|GO:0007173|GO:0048041|GO:0007010|GO:0034446|GO:0007179|GO:0
007155|GO:0005938|GO:0048010|GO:0001725|GO:0019901|GO:0034329|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138973_PI430048170 0.0347148077541531 1.30609804791459 8.15304528950378
8.06858429365591 8.2328939128954 P P P 7.57565546450618 7.83755203858359
7.87236050521316 P P P LNCV6_138973_PI430048170 mRNA
ATATTGCTGAATGCAAGAAGTGGGGCAGCAGCAGTGGAGAGATGGGACAATTAGATAAAT NM_000291RefSeq
chrX + 78104168 78126827 PGK1 5230 phosphoglycerate kinase 1
GO:0005515|GO:0005975|GO:0006094|GO:0044281|GO:0005524|GO:0006096|GO:0005829|GO:0016310|GO:0004
618|GO:0016020|GO:0030855|GO:0009405|GO:0006006|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142218_PI430048170 0.0155543592428494 0.5725319242063985.72932018759892
5.48297920148803 5.93483916118794 P P P 6.47670200786075 6.48706578069431
6.62736459345874 P P P LNCV6_142218_PI430048170 mRNA
CTTGAATGATGTTCATTTGTCAGGAGAACTGTGAGAAATAAACTATGTGGATACTGTCTG NM_015534RefSeq chr1

- 77562415 77682658 ZZZ3 26009 "zinc finger, ZZ-type containing 3"
GO:0005515|GO:0031965|GO:0006355|GO:0003682|GO:0006325|GO:0005730|GO:0005671|GO:0008270|GO:0005
634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138629_PI430048170 0.569988230452175 1.03701434913701 0.277270977106451
0.28995275738738 0.499896048425474 A A A 0.327230074254037 0.283407346490455
0.309845234002874 A A A LNCV6_138629_PI430048170 mRNA
CTGTTAGAGCATTGACTGAGGTAAAAAGAGACTTGATTTCTAGTCCTGATTTTGACATTC NM_016161 RefSeq chr3
- 138123717 138132387 A4GNT 51146 "alpha-1,4-N-acetylglucosaminyltransferase"
GO:0008375|GO:0009101|GO:0016020|GO:0006493|GO:0000139|GO:0005975|GO:0050680|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77675_PI430048170 0.0860178801613493 0.66988564695061 3.7831330506637
3.93001801815024 3.92258622621165 P P P 4.21362840488488 4.28900125754491 4.7990545721406
P P P LNCV6_77675_PI430048170 mRNA
CAGCCGAGAAGATTCCTTGAAGAATCAAGCATTTAAGCATTTCAGTGATTGAGAACAATA NM_145062 RefSeq chr6
- 116635617 116668810 ZUFSP 221302 zinc finger with UFM1-specific peptidase domain GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134324_PI430048170 0.68563274756296 0.9660420483635556 8.8846991559823
7.24407344320157 7.12882248328034 P P P 7.05159342705391 7.1065184484832
7.26352038821841 P P P LNCV6_134324_PI430048170 mRNA
CACCTGGAAACCTGTGCCTTGTATTCAAATTCATTAAAGCCTAATCCTGCAAGTAAAAAA NM_031307 RefSeq chr11
- 125893484 125903221 PUS3 83480 "pseudouridylate synthase 3, transcript variant 1"
GO:0009982|GO:0003723|GO:0005634|GO:0031119 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141473_PI430048170 0.5840880798076950 0.9215323171538070 0.413502015598847
0.4297577050948220 0.352724867412508 A A A 0.320691521685229 0.809434887415934
0.368801308639264 A A A LNCV6_141473_PI430048170 mRNA
CCAAAGGTTGAAGTTCTGCTGTTTTGTTATAATGCCTGATACACATCTTGAATAAAGTCT NM_022912 RefSeq chr2
- 86213996 86337654 REEP1 65055 "receptor accessory protein 1, transcript variant 2"
GO:0008017|GO:0005515|GO:0032386|GO:0005737|GO:0031966|GO:0016020|GO:0005783|GO:0051205|GO:0071
786|GO:0005789|GO:0016021|GO:0031849 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88513_PI430048170 0.298481811551783 1.42891913976063 2.63125118370361 3.39928060229661
3.27529893519006 A P P 1.85531076683472 2.32081380792885 3.30464756570057 A A P
LNCV6_88513_PI430048170 mRNA
TTAGAATCGGTCAGGAAGCAGAGTTCATTTATCCTGACTCCACCTCGAAGGAAAATTCCC NM_001127181 RefSeq
chr1 - 173799549 173824639 CENPL 91687 "centromere protein L, transcript variant 1"
GO:0034080|GO:0006334|GO:0005654|GO:0000278|GO:0000775|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142714_PI430048170 0.0802649100895376 0.2787407160157090 .350097942478941
2.58421202398845 0.794692282766506 A A A 3.12269966213091 3.55612179574018
3.56532688891518 P P P LNCV6_142714_PI430048170 mRNA
GTGGGAGTATTTTGGTGACAACCTACTTTGCTTGGCTGAGTGAAGGAATGATATTCATAT NM_001005340 RefSeq
chr7 + 23246696 23275110 GPNMB 10457 "glycoprotein (transmembrane) nmb, transcript variant 1"
GO:0042470|GO:0008285|GO:0005178|GO:0005887|GO:0030282|GO:0016021|GO:0007155|GO:0008201|GO:0001
649 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133495_PI430048170 0.0386327822606238 0.2386522383390481 .74738804419243
3.38178100722713 2.97733072989732 A P P 4.66268271042974 5.11476221262112 4.9432938193079
P P P LNCV6_133495_PI430048170 mRNA
CTTATAGTAAGACTTGTGCTTGTTAGCAGGTTTTTCTGTTAGTTTTTCCCCCATAACATT NM_020648 RefSeq chr18 +
9334766 9402420 TWSG1 57045 twisted gastrulation BMP signaling modulator 1
GO:0030097|GO:0001707|GO:0030509|GO:0005615|GO:0030154|GO:0030514|GO:0030513|GO:0045668|GO:0001

503|GO:0043010|GO:0030900|GO:0007435|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67747_PI430048170 0.4110570580674871.1017464013915 6.02318041331918 6.14315981494748
6.39163670517432 P P P 6.05080998941797 5.86026722239998 6.22882878932582 P P P
LNCV6_67747_PI430048170 mRNA
GGGAGAGATTAAAGTCTCTCCTGATTATAACTGGTTTAGAGGTACAGTTCCCCTTAAAAA NM_016630RefSeq chr15
- 64963020 64989946 SPG21 51324 "spastic paraplegia 21 (autosomal recessive, Mast syndrome),
transcript variant 1"
GO:0005515|GO:0005737|GO:0042609|GO:0005654|GO:0005634|GO:0030140|GO:0050851|GO:0010008|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111380_PI430048170 0.7550373951045080.9807324105572260.275466808437813
0.4904448518432880.335134850282254A A A 0.4975539498689260.389133571108011
0.300414011497575A A A LNCV6_111380_PI430048170 mRNA
TAATGGAGATGTCAATGCTCTGACTGCAGTGATTCGGGAAGACCCTTCTATCCTAGAATG NM_024669RefSeq chr5
- 56099679 56233359 ANKRD55 79722 ankyrin repeat domain 55 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127918_PI430048170 0.0185763254882214 0.6305114458271383.8729218177495
3.70646590332257 3.87522027135406 P P P 4.23992905032823 4.5457472542058
4.64174080288966 P P P LNCV6_127918_PI430048170 mRNA
AAGCAGAACAGCCTGGCCTTTTGAATGTATTTTCCTGGGTTTTTTCCCCTTTTCTTTTTT NM_018086RefSeq chr2 -
163607607 163736003 FIGN 55137 fidgetin
GO:0005815|GO:0005874|GO:0005634|GO:0031122|GO:0008022|GO:0005524|GO:0010569|GO:0016363|GO:0008
568|GO:0005737|GO:0007067|GO:0008152|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82695_PI430048170 0.2211898396892421.26144213224833 5.61745174341407 6.17509290562503
5.72491002257804 P P P 5.73079743926562 5.57252329051515 5.22630782042395 P P P
LNCV6_82695_PI430048170 mRNA
TTCAGACCCAGTCAGAGGTTAAAGGAAGGCTGGAACCCTCACCTGCTGCTTCTCCTCCTG NM_181079RefSeq chr16
+ 27402161 27452042 IL21R 50615 "interleukin 21 receptor, transcript variant 3"
GO:0030101|GO:0016021|GO:0001532|GO:0038114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104375_PI430048170 0.6705565022176050.9567434739991724.783863631827
4.92353872844831 5.34225788678549 P P P 5.14137529343767 5.11062354870513
5.04747513423781 P P P LNCV6_104375_PI430048170 mRNA
AGTTACGATGGTTTTGGACCATTTATGCCGGGATTCGACATCATTCCCTATAATGATCTG NM_000274RefSeq chr10
- 124397302 124418976 OAT 4942 "ornithine aminotransferase, transcript variant 1"
GO:0005739|GO:0034641|GO:0055129|GO:0005759|GO:0004587|GO:0030170|GO:0008652|GO:0044281|GO:0034
214|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107158_PI430048170 0.4586193302271110.8399860622205224.99173157431394
4.24559263531875 3.97858676427058 P P P 4.91886212445154 4.84232444381938
4.34279259135298 P P P LNCV6_107158_PI430048170 mRNA
AATGGCTCGCCTGGACTCCTGCAACAACTGCACCTGTGTCTCTGGTAAGATGGCATGCAC NM_198455RefSeq chr7
+ 149776041 149833964 SSPO 23145 SCO-spondin
GO:0005737|GO:0010466|GO:0030414|GO:0007155|GO:0005615|GO:0030154|GO:0007399 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134751_PI430048170 0.0627705527728019 0.7507414368229821 3.0369773190063
12.9685783618219 13.257545481516 P P P 13.3264561956472 13.420021780664
13.7401851685402 P P P LNCV6_134751_PI430048170 mRNA
ATTCCAGACCTTTCTGCCACTTAGCACTTGTATAATCAGACTGGAAATGGGGATGAGGGT NM_001144944 RefSeq
chr18 + 3262612 3278284 MYL12B103910 "myosin, light chain 12B, regulatory, transcript variant 1"
GO:0005515|GO:0030018|GO:0001725|GO:0006936|GO:0048013|GO:0007411|GO:0008360|GO:0005509|GO:0045
177|GO:0016460|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_92953_PI430048170 0.0316070859399646 0.7719248641213914.861352213384
5.14942278146007 4.91026543699579 P P P 5.28453233215095 5.44962591478984
5.31872777612854 P P P LNCV6_92953_PI430048170 mRNA
TCAGCTATTTCCACCAAATCCTCCTGTCTTTCGTGGCCAACACCCCAGGCAAGGCTTGGG NM_001288833 RefSeq
chr22 + 24603156 24629005 GGT1 2678 "gamma-glutamyltransferase 1, transcript variant 6"
GO:0019369|GO:0005515|GO:0019370|GO:0019344|GO:0006520|GO:0006805|GO:0005886|GO:0006536|GO:0050
727|GO:0002682|GO:0006749|GO:0044281|GO:0007283|GO:0031362|GO:0005615|GO:0006691|GO:0003840|GO:0
006750|GO:0006751|GO:0006508|GO:0016021|GO:0031638|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_130850_PI430048170 0.306325469687395 1.05056537011517 0.496899463671622
0.3241288529465070.415637715878827A A A 0.2869806942533230.355606926345098
0.384033592506906A A A LNCV6_130850_PI430048170 mRNA
GATTTGGGCATCTGCCACATTGGTTCATATTCAGAAAGTGTTATCTCATTGATTATATTC NM_130782RefSeq chr1
+ 192158461 192185815 RGS18 64407 regulator of G-protein signaling 18
GO:0043547|GO:0005737|GO:0007186|GO:0005886|GO:0038032|GO:0005096 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135180_PI430048170 0.2400621017648690.9018808126468439.52151223961658
9.23504289695568 9.24042425271943 P P P 9.45897349706319 9.52360272729727 9.4796164192594
P P P LNCV6_135180_PI430048170 mRNA
GCAGCTCTTAGGGAACCAAAAACCAGCACTGAAATAAAGCTGAATGACTGACTGAAAAAA NM_001142443
RefSeq chr15 - 74630557 74696045 EDC3 80153 "enhancer of mRNA decapping 3, transcript variant
1"
GO:0005515|GO:0010467|GO:0016020|GO:0000932|GO:0003723|GO:0043928|GO:0042802|GO:0005829|GO:0000
288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108681_PI430048170 0.2747860346591630.8670969080796350.387078496076828
0.3861152691903670.339077147817729A A A 0.8250234498616930.446547739544449
0.422076161876389A A A LNCV6_108681_PI430048170 mRNA
AACTTGGAATTACCTGTGAGAGAAGAGCCTTCAAATGATAATGTTATCAAACAGCAAAGC NM_023073RefSeq chr5
- 37106227 37249428 C5orf42 65250 chromosome 5 open reading frame 42 GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_128235_PI430048170 0.0226199741085203 3.37709546227264 2.45197348873256
1.60863532042961 2.41867872597457 A A A 0.5424703724338660.401775893690534
0.410248649034887A A A LNCV6_128235_PI430048170 mRNA
TTGCAGTTTTGGTTTCTTTTGCGGTTTTCTAACCAATTGCACAACTCCGTTCTCGGGGTGNM_032108RefSeq chr19 -
4542587 4559759 SEMA6B 10501 "sema domain, transmembrane domain (TM), and cytoplasmic
domain, (semaphorin) 6B" GO:0005886|GO:0030215|GO:0004872|GO:0016021|GO:0030154|GO:0007399 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140087_PI430048170 0.2077227306818431.12127378530854 13.265436456506
13.4383622542383 13.5391924420898 P P P 13.1779690092024 13.1712002584602 13.399667967402
P P P LNCV6_140087_PI430048170 mRNA
AAGCCCCAAGTTGCTGTATATTTTCACAAGTATGTCTACACACTGGTCATGATTTTGATA NM_020531RefSeq chr20
- 24962943 24992789 APMAP 57136 adipocyte plasma membrane associated protein
GO:0008150|GO:0016844|GO:0016020|GO:0009986|GO:0009058|GO:0016021|GO:0004064|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138691_PI430048170 0.1033576410845190.6568262479229876.61842774238053
6.56973522685927 6.51074423307693 P P P 6.75654108936308 7.45645038621967
7.22185936298251 P P P LNCV6_138691_PI430048170 mRNA
GGCAAATAATGTCTCCATAGAATCACTTTCCAATACAACGGCTCTTTTCAGAGCCACCTA NM_003511RefSeq chr6
+ 27865328 27865798 HIST1H2AL 8332 "histone cluster 1, H2al"

GO:0005515|GO:0008150|GO:0046982|GO:0005634|GO:0019899|GO:0000786|GO:0003677|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128359_PI430048170 0.5300765752483470.2892623424578061.2284617299977 0.2653703208982670.379532985655752A A A 0.3811329108566293.82862802774738 0.313537883309514A P A LNCV6_128359_PI430048170 mRNA AGCAAATAACATATGCTGTTCTACCTACTGTGGGAATGTTTGCATGAGCATCCTGTGAGT NM_080753RefSeq chr20 + 45629745 45631192 WFDC10A 140832 WAP four-disulfide core domain 10A
GO:0010951|GO:0004867|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136143_PI430048170 0.0507069134896085 0.4673164812217983.51519961729322 2.46447044914908 3.07779885932471 P A P 4.37577577108919 4.01515022268431 4.12224973129507 P P P LNCV6_136143_PI430048170 mRNA GACCATCAGCCTAATTCACTGAGGTGTGTTGTGTATCACTCTATTTTATAGATGATTTTA NM_001040441 RefSeq chr1 + 32539144 32605950 ZBTB8A 653121 "zinc finger and BTB domain containing 8A, transcript variant 1"
GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0005575|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138647_PI430048170 0.2102689220880131.04112300312057 0.428506369561471 0.4774922086772550.472857192728919A A A 0.3517052858609160.387479635566739 0.463486097069504A A A LNCV6_138647_PI430048170 mRNA GCTTTGTGACTTAAGCAGGTGTGTGGGCTCCTTTAGGCAGGTTACAGTTAACTTTCTAGA NM_005068RefSeq chr6 - 100388873 100463675 SIM1 6492 single-minded family bHLH transcription factor 1
GO:0007165|GO:0001657|GO:0006355|GO:0003700|GO:0046982|GO:0005634|GO:0004871|GO:0003677|GO:0030154|GO:0006351|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134649_PI430048170 0.00808538563552797 0.4589565750584384.34115745376682 4.20467860065076 4.72814899927789 P P P 5.31245310726019 5.45755330810686 5.86802907549834 P P P LNCV6_134649_PI430048170 mRNA TGGTTACAGTTTATCCCTGTAGGATAAATGATCCATTTAACTATTCATCAGAGGTGCTGT NM_006606RefSeq chr20 - 18486540 18497243 RBBP9 10741 retinoblastoma binding protein 9
GO:0005737|GO:0016787|GO:0042127|GO:0008152|GO:0005730|GO:0005654|GO:0005634|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132601_PI430048170 0.16573448606688 0.7784746920769568.32555371670911 8.69382337287705 8.59983444619002 P P P 8.56248221735629 9.11023094117613 8.99914065491005 P P P LNCV6_132601_PI430048170 mRNA CATTGCACCATGTCAGACTTTTGTATATGCCTTGAAAATAAATGAAAGTGAGAATCCTCT NM_032564RefSeq chr11 + 75768732 75801536 DGAT2 84649 "diacylglycerol O-acyltransferase 2, transcript variant 1"
GO:0048471|GO:0019915|GO:0005783|GO:0003846|GO:0030176|GO:0035356|GO:0044281|GO:0006071|GO:0035336|GO:0042803|GO:0005739|GO:0034383|GO:0042572|GO:0019432|GO:0004144|GO:0044255|GO:0005811|GO:0042632|GO:0055089|GO:0050252|GO:0071400|GO:0005789|GO:0060613|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126640_PI430048170 0.199142693005338 1.08488185497688 0.641702312585083 0.8258358190848880.637481341472147A A A 0.5545232024436890.613528509788053 0.591865924510551A A A LNCV6_126640_PI430048170 mRNA ATTTCACAGGGGATGAACTAGCTTCAGTTATGGTTTTCATGACAATAAAATGAAATCCGA NM_001167902 RefSeq chr15 - 98968229 99007795 PGPEP1L 145814 "pyroglutamyl-peptidase I-like, transcript variant 2"
GO:0006508|GO:0008234 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_3483_PI430048170 0.00183815381545733 0.32610712627029 7.27045730419033 7.06907699508122 7.16948644900876 P P P 8.56442097824872 8.76838532848883 9.00001920762838 P P P LNCV6_3483_PI430048170 mRNA GGGATACTATATTGGTAATTATGTTTTCATATAGCAACCACCACAGTATATTCTTGGTGC NM_001193485 RefSeq

chr2 + 108654811 108687246 LIMS1 3987 "LIM and senescent cell antigen-like domains 1, transcript variant 1"
GO:0005515|GO:0048471|GO:0005886|GO:0010811|GO:0071560|GO:0001837|GO:0051894|GO:0043009|GO:0051291|GO:0005829|GO:0045184|GO:0016337|GO:1900026|GO:0005911|GO:2001046|GO:0050678|GO:0043066|GO:2000178|GO:0019901|GO:0007569|GO:0034329|GO:0045216|GO:0010628|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137930_PI430048170 0.6356229423887291.29692142654607 1.89274616691666 0.6136215435339340.489373892025426A A A 1.20226004308253 0.497521590272493 0.498450362712066A A A LNCV6_137930_PI430048170 mRNA
GACGTTCGGAAAGGGTCATGGGCTAAATGTCACCTGAGGGGTATTTTTAAAGGGTTTTTT NM_018488RefSeq chr17 + 61456445 61484303 TBX4 9496 T-box 4
GO:0006355|GO:0003700|GO:0030324|GO:0048705|GO:0007275|GO:0005634|GO:0030326|GO:0001525|GO:0035108|GO:0003677|GO:0002009|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142969_PI430048170 0.000157121296243755 3.03032534296237 8.29889601139038 8.41685634586835 8.4178610219807 P P P 6.90642090188522 6.74161697843866 6.68082779150949 P P P LNCV6_142969_PI430048170 mRNA
TTGCCATGGACTACCTTTGCTAAGAAAAGTCTGAATGAGAAGATGGCAGGACGTCTGAAA NM_138720RefSeq chr6 + 26158120 26171348 HIST1H2BD 3017 "histone cluster 1, H2bd, transcript variant 2"
GO:0003674|GO:0046982|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0003677|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134940_PI430048170 0.1886782539554 1.68517229264539 1.41048963629923 0.3377931516963951.34178749346035 A A A 0.28712721273544 0.369613514259489 0.399762728163733A A A LNCV6_134940_PI430048170 mRNA
AACAAGAGAGTATCTGTGCCCTTTACAGCTAATTGTTCTAAAAGGAGTTTCTAAAAACAC NM_001177506 RefSeq chr7 - 36512940 36724549 AOAH 313 "acyloxyacyl hydrolase (neutrophil), transcript variant 2"
GO:0006629|GO:0006954|GO:0050528|GO:0005576|GO:0003824|GO:0004465 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83047_PI430048170 0.5085043334187451.1081851109933 8.96091033144989 9.00879340504477 8.78145895004316 P P P 8.93531957720094 8.97988196453568 8.30887777840732 P P P LNCV6_83047_PI430048170 mRNA
TGGAACCCAAGTCCCCTGAAGCCCCTGTGCTCTCTGTTGTGATTGGAGTTCTAGGGCTTC NM_006927RefSeq chr16 - 70379434 70439088 ST3GAL2 6483 "ST3 beta-galactoside alpha-2,3-sialyltransferase 2"
GO:0006040|GO:0005975|GO:0016266|GO:0005576|GO:0044281|GO:0003836|GO:0042339|GO:0030173|GO:0000139|GO:0006493|GO:0018146|GO:0032580|GO:0009405|GO:0006488|GO:0044267|GO:0030203|GO:0006464|GO:0043687|GO:0018279. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139601_PI430048170 0.5226582085884641.43700987586044 1.93903859504569 0.83686980037181 0.262229518190825A A A 0.33350832737091 0.358046433519842 1.14025775211627 A A A LNCV6_139601_PI430048170 mRNA
AAAGAGGCCTGAGAGAAACTGAGGTCAAGATTTCAGGATTAATGGTCCTGTGATGCTTTG NM_001177800 RefSeq chr3 + 186842673 186858463 ADIPOQ 9370 "adiponectin, C1Q and collagen domain containing, transcript variant 1"
GO:0005515|GO:0045599|GO:0033211|GO:0006091|GO:0010739|GO:0005615|GO:0010906|GO:0032757|GO:0042803|GO:0042802|GO:0046888|GO:0045923|GO:0009744|GO:0046326|GO:0034115|GO:0033691|GO:0033034|GO:0043123|GO:0043124|GO:0019395|GO:0030336|GO:0032869|GO:0006635|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69049_PI430048170 0.0420927656651416 1.56123122387675 6.34483192860066 6.81653632912312 6.38485231874124 P P P 5.9751003809498 5.88475183606557 5.8020034736923 P P P LNCV6_69049_PI430048170 mRNA
ATCAAACCAGAAGATGCCATGGACTTTGGCATCTCCCTTCTCTTCTATGGCCTCTACTAT NM_018320RefSeq chr11

+ 71928721 71997597 RNF121 55298 "ring finger protein 121, transcript variant 1"
GO:0016567|GO:0000139|GO:0005789|GO:0008270|GO:0016021|GO:0030433|GO:0030968 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139515_PI430048170 0.00468839294288105 1.24927097831084 11.7689967149415
11.7558870097493 11.6508989350631 P P P 11.3417077418445 11.4827119250871
11.3873771717344 P P P LNCV6_139515_PI430048170 mRNA
TGTGCCTTATACACGTGCCAACCTGGAAATAAAATGTCAGCCTTTTTTATACGTAAAAAA NM_001271610 RefSeq
chr19 - 13144057 13150374 STX10 8677 "syntaxin 10, transcript variant 3"
GO:0005515|GO:0005802|GO:0019905|GO:0048471|GO:0031201|GO:0006886|GO:0006906|GO:0031982|GO:0032
880|GO:0005484|GO:0000139|GO:0034498|GO:0042147|GO:0016021 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141387_PI430048170 0.0053681758852845 0.438035099354257 10.7655911005374
10.6206406265677 11.0306165628766 P P P 11.7266942950257 11.9548802285759
12.2834759914632 P P P LNCV6_141387_PI430048170 mRNA
GATTGGGTGGGATTTTTTCCCTTTTTATGTGGGATATAGTAGTTACTTGTGACAAGAATA NM_005063 RefSeq chr10
+ 100347014 100364831 SCD 6319 stearoyl-CoA desaturase (delta-9-desaturase)
GO:0016020|GO:0005506|GO:0005783|GO:0004768|GO:0005789|GO:0006633|GO:0016021|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134559_PI430048170 0.00175051697653165 2.37581487351631 7.2522473845046
7.50079302556436 7.46307732739339 P P P 5.91844813446811 6.30768722773517
6.22833405593063 P P P LNCV6_134559_PI430048170 mRNA
TTTAAATAAGGTTGGAGATGTCAAGTTGGGTTCACTTGCCATGCAGGAAGAGGCCCACTA NM_174963 RefSeq chr1
+ 43707532 43931165 ST3GAL3 6487 "ST3 beta-galactoside alpha-2,3-sialyltransferase 3, transcript variant 1"
GO:0005975|GO:0016266|GO:0005576|GO:0044281|GO:0003836|GO:0042339|GO:0030173|GO:0000139|GO:0006
493|GO:0008118|GO:0018146|GO:0032580|GO:0009405|GO:0006488|GO:0044267|GO:0030203|GO:0043687|GO:0
018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134141_PI430048170 0.00753604654486825 1.31906127351056 12.2397227758601
12.1865127831714 12.116827053212 P P P 11.8955067432717 11.7378702353084
11.7065888275935 P P P LNCV6_134141_PI430048170 mRNA
TATATCTGAAGACGGAGAGCCTGTAATATTCTTCAGATTAAATGAAGCGTGAGACACTTT NM_001014764 RefSeq
chr17 + 3668722 3669669 EMC6 83460 "ER membrane protein complex subunit 6, transcript variant 1" GO:0072546|GO:0005515|GO:0030176|GO:0016021|GO:0000045 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127020_PI430048170 0.322729321583186 1.08656077526416 14.242784713781
14.1034580254554 13.941251227715 P P P 13.8893348975831 14.0194430460902
14.0308984293506 P P P LNCV6_127020_PI430048170 mRNA
AACTGACCTGTTTTGGGACCTGTTACCCAAATAAAAGATGTTTCTAGACATCTGTACAGT NM_014437 RefSeq chr1
- 153959098 153967732 SLC39A1 27173 "solute carrier family 39 (zinc transporter), member 1, transcript variant 1"
GO:0071577|GO:0016020|GO:0005886|GO:0005385|GO:0022890|GO:0005789|GO:0005102|GO:0016021|GO:0055
085|GO:0006812 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_5044_PI430048170 0.00107813102762766 1.84274753471433 9.05498256602742
8.82525260470326 8.84244253884376 P P P 7.96455622100829 8.17269518666938 7.9398675286267
P P P LNCV6_5044_PI430048170 mRNA
TCTGGAGAGTGCCTAGTATTCTGCCAGCTTCGGAAAGGGAGGGAAAGCAAGCCTGGCAGA NM_001007074
RefSeq chr3 - 12834944 12840450 RPL32 6161 "ribosomal protein L32, transcript variant 3"
GO:0010467|GO:0005813|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0006415|GO:0006412|GO:0006
413|GO:0005829|GO:0006414|GO:0005737|GO:0000184|GO:0016020|GO:0016032|GO:0022625|GO:0044267 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140327_PI430048170 0.0360077075891525 0.475927200775501 1.80856929744343
1.89396751083664 2.6424682267838 A A A 3.0085986054198 3.26019145094806
3.41414345019161 P P P LNCV6_140327_PI430048170 mRNA
CGAAAATCCTTTGTAAATTACAGATGTGTGTTATAAATGAAGTATCTCTCGAGTCACTCC NM_001278277 RefSeq
chr2 - 11444374 11466177 E2F6 1876 "E2F transcription factor 6, transcript variant d"
GO:0005667|GO:0003700|GO:0000083|GO:0071339|GO:0003714|GO:0005634|GO:0000122|GO:0003677|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143049_PI430048170 0.0514908029672491 0.410650465830926 0.430209433582804
1.56870431377398 1.13610485262004 A A A 2.81808730093777 1.70167724152245
2.47298942151176 P A P LNCV6_143049_PI430048170 mRNA
ATCCATCCTGTATTTTGATTGATGCTTTAATAAAGGGTTTGCACAGCTGTGTGGAAAAAA NM_021647 RefSeq chr4
- 169986596 170026430 MFAP3L 9848 "microfibrillar-associated protein 3-like, transcript variant 1"
GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93263_PI430048170 0.487216249124115 0.849812661028448 0.479176571249703 0.569856742238184
0.517309460698327 A A A 0.56199129709555 0.418100153467517 1.17553854627615 A A A
LNCV6_93263_PI430048170 mRNA
TTCTAGGATCTGCCAAGCATCCAGGTGGAGAGCCTGAGGAATCAGGAGCTCCAGGAACCA NM_175743 RefSeq
chrX + 152714585 152718607 MAGEA2 NA "melanoma antigen family A2, transcript variant 3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78892_PI430048170 0.000678184261262041 0.232866557169112 2.10462203916453 2.1209655414436
2.5321366007883 A A A 4.03073628096795 4.556715514443 4.46656143274749 P P P
LNCV6_78892_PI430048170 mRNA
TAATGAACTAGAACCTAAGGTTGCTGTGTGTCGTACAACTAGGGAACGTATGAAGGTCAA NM_001291829 RefSeq
chr7 - 99648188 99680026 CYP3A5 1577 "cytochrome P450, family 3, subfamily A, polypeptide 5,
transcript variant 4"
GO:0006805|GO:0005506|GO:0070330|GO:0070989|GO:0044281|GO:0043231|GO:0004497|GO:0042737|GO:0019
825|GO:0009822|GO:0005789|GO:0016491|GO:0008202|GO:0020037 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127832_PI430048170 0.0416789578620451 0.632352012499133 5.82293060745349
5.64445036158072 6.13222483094149 P P P 6.21561495640933 6.56271578970451
6.79048612867012 P P P LNCV6_127832_PI430048170 mRNA
TATACATTTATAAGGAGCCAGGGTCTGGAGGGTTGCTATCACTTTGTCCAGCCCAAATAC NM_004157 RefSeq chr3
- 48750659 48847837 PRKAR2A 5576 "protein kinase, cAMP-dependent, regulatory, type II, alpha"
GO:0005515|GO:0034236|GO:0005886|GO:0008603|GO:0007202|GO:0044281|GO:0005829|GO:0035556|GO:0005
737|GO:0030552|GO:0007173|GO:0071377|GO:0006833|GO:0034199|GO:0031625|GO:0070062|GO:2000480|GO:0
048011|GO:0005952|GO:0005813|GO:0031588|GO:0055085|GO:0003091|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130596_PI430048170 0.103635971956959 0.626059962020896 6.45996231256817
6.50764021600356 6.84825928955212 P P P 6.76556544308622 7.41090384086215
7.57751933983293 P P P LNCV6_130596_PI430048170 mRNA
CCATCCATTTACCACATATTTCCATCTGATAGTCTAGCAGGTAATTAAACTTATATGTCC NM_145247 RefSeq chr10
+ 104122057 104126385 SFR1 119392 "SWI5-dependent recombination repair 1, transcript variant 2"
GO:0005515|GO:0032798|GO:0000724|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131372_PI430048170 0.208545662700387 1.13168458090667 6.89387113376742
7.04110770132257 6.96954991679024 P P P 6.64289284522996 6.98507808342424
6.72227750091279 P P P LNCV6_131372_PI430048170 mRNA
ATGGTGATTTGTTAATTTCCATGGGAAGCCATGATGGCCTAGCATGGAGGGAATCTGTTC NM_024864 RefSeq
chr17_KI270857v1_alt + 837089 844472 MRM1 79922 mitochondrial rRNA methyltransferase 1 homolog

(S. cerevisiae) GO:0005739|GO:0001510|GO:0006364|GO:0008173 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57371_PI430048170 0.6088843750715680.9316876282879257.33766144363309 7.46607428553783 7.78508045281984 P P P 7.68730440723411 7.38530606148646 7.82547295030902 P P P LNCV6_57371_PI430048170 mRNA
CTTTGAGGTCATTACAATTTACGAATCCAGGAAGGCAAACTGAATTTGCTCCAGAAACTG NM_152316RefSeq chr11 + 30323098 30338223 ARL14EP 120534 ADP-ribosylation factor-like 14 effector protein GO:0005515|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128470_PI430048170 0.1325717094215241.22253037759203 8.66701500426927 9.01218114111672 8.85854588825677 P P P 8.72700435865068 8.60394081081293 8.32963064857677 P P P LNCV6_128470_PI430048170 mRNA
AGATCCGAGAGTAAGGAAGTTCCCTGTCTTCCCCGTCCTTTTCCACCAGTCTCGCCTCTG NM_032488RefSeq chr19 - 42387018 42390292 CNFN 84518 cornifelin GO:0005737|GO:0031424|GO:0001533|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140710_PI430048170 0.00859569096317349 0.4631638028945135.38191406756929 4.77676866812274 5.13382912967885 P P P 6.06632319671163 6.08937095744997 6.49056304423763 P P P LNCV6_140710_PI430048170 mRNA
CCTTAGTGCTTTTGGCTAAACATACAGAATACTACTTGTATGCAGAAGAGAATTAGTTGA NM_017747RefSeq chr5 + 140401813 140539856 ANKHD1 54882 "ankyrin repeat and KH domain containing 1, transcript variant 1" GO:0005515|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131408_PI430048170 0.190667193464075 0.8202712139500191 0.848516012214 10.7923430762755 11.2874657537982 P P P 11.1179839319165 11.2874657537982 11.4173531624846 P P P LNCV6_131408_PI430048170 mRNA
GAGCTGGATCCATACAGGTTGTGTGTCATCTGTCCTCTTGAGGTTCAGGAGATTCTAAAT NM_001494RefSeq chr10 - 5765222 5813549 GDI2 2665 "GDP dissociation inhibitor 2, transcript variant 1" GO:0005515|GO:0051056|GO:0005794|GO:0031267|GO:0007264|GO:0032851|GO:0015031|GO:0031982|GO:0005829|GO:0007165|GO:0005737|GO:0016020|GO:0005093|GO:0016192|GO:0005925|GO:0005097|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2199_PI430048170 0.0217562846848336 2.16681838551483 2.24359739121422 2.89543890174649 2.35747998536075 A A A 1.28183225256636 1.81053866337393 1.0323881777692 A A A LNCV6_2199_PI430048170 mRNA
AGTACTGGTGGTAGCCAATATGGGCAGACATTAGGAAATTGGGGTCTTCATACTGCTTCT NM_170739RefSeq chr11 - 66435074 66438848 MRPL1165003 "mitochondrial ribosomal protein L11, transcript variant 3" GO:0070124|GO:0005515|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005761|GO:0005743|GO:0006412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131687_PI430048170 0.5175005014245140.9372450406644456.99814419237337 6.75153511055846 6.58437763985368 P P P 6.76336454180962 6.87276312690667 6.99903047628198 P P P LNCV6_131687_PI430048170 mRNA
AGAAAGTGACATGAAGGAAGCAATCTACAACTTCCTTCCGCTTAGCGAGCATGCAAAAAA NM_004722RefSeq chr7 + 100101506 100107180 AP4M1 9179 "adaptor-related protein complex 4, mu 1 subunit" GO:0005802|GO:0005215|GO:0030131|GO:0005905|GO:0000138|GO:0030119|GO:0016192|GO:0006895|GO:0006886|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127079_PI430048170 0.0882559173705162 0.7210879486249 7.66201650865957 7.74946398597127 8.08800498761811 P P P 8.19606437089663 8.09026876933335 8.61047067387035 P P P LNCV6_127079_PI430048170 mRNA
GTCTGTAAAGCTTAAGGTTTTAAAAATGTTGCCCGTAATGTTGAACGTGTCTGTTAGAAA NM_017632RefSeq chr4 + 183444635 183447896 CDKN2AIP 55602 CDKN2A interacting protein GO:0005515|GO:0030308|GO:0001652|GO:0030307|GO:0003723|GO:0005730|GO:0005634|GO:0009967|GO:0006974|GO:0002039|GO:0005737|GO:0031647|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_127097_PI430048170 0.0856961597904219 0.4225569542933814.18568936831047
3.13865921140569 3.81653792905838 P P P 4.09653202380234 5.20844800285066
5.43195295461654 P P P LNCV6_127097_PI430048170 mRNA
CTTGAGTAGCACATCAACATACAGCATTGTACATTACAATGAAAATGTGTAACTTAAGGG NM_006750RefSeq chr16
+ 69187146 69309052 SNTB2 6645 "syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic
component 2)"
GO:0005515|GO:0043234|GO:0005516|GO:0005737|GO:0016020|GO:0016010|GO:0005874|GO:0045202|GO:0003
779|GO:0005925|GO:0070062|GO:0030658 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58281_PI430048170 0.0157493872417243 0.7852481531496815.6424106548327
5.43720209994844 5.62279343282007 P P P 5.85848957984504 5.90150970025556
5.99415080412568 P P P LNCV6_58281_PI430048170 mRNA
AAGAAAAGGAAAAACAGAAGTTGAAAAAACTCCCCCCAGACCGAGTTGGGGCCAACTTTG NM_198489RefSeq
chr11 + 118998132 119015792 CCDC84 338657 "coiled-coil domain containing 84, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68458_PI430048170 0.2391137605074721.06178099722209 0.51306705488818 0.350494550279118
0.473219417879181 A A A 0.2920204335191020.3685686204632550.418847670533101 A A A
LNCV6_68458_PI430048170 mRNA
AGGTGGAAACACTGCATGATTTTGAGGCAGCAAATTCTGATGAACTTACCTTACAAAGGG NM_001635RefSeq chr7
- 38383695 38631567 AMPH 273 "amphiphysin, transcript variant 1"
GO:0005515|GO:0031256|GO:0030054|GO:0005543|GO:0007268|GO:0030672|GO:0048488|GO:0007612|GO:0015
629|GO:0008021|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130862_PI430048170 0.7745484172084060.9931221747331070.304078450756859
0.31453238257156 0.395273794236995 A A A 0.3687443272497820.315698167026371
0.360487328827763 A A A LNCV6_130862_PI430048170 mRNA
ATAGCTTATAAGGCTTATGGCAATGTCCCAACTATTGCAATCATAAAACCCTAGTTTTAG NM_182606RefSeq chr4
- 67910300 67963514 TMPRSS11A 339967 "transmembrane protease, serine 11A, transcript variant 1"
GO:0007049|GO:0004252|GO:0005887|GO:0006508|GO:0005576 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145210_PI430048170 0.8692931621697881.02728524026401 8.52685841733611
9.01556307784884 8.80955753612601 P P P 8.62463061922064 8.79232282007694
8.85036746280286 P P P LNCV6_145210_PI430048170 mRNA
GAAAAATCTGTCTGCCGCCTATTTCCCATTGGTGTCGATTGAATAAATGTATGTGAACTT NM_004474RefSeq chr1
+ 47436016 47440691 FOXD2 2306 forkhead box D2
GO:0043565|GO:0003700|GO:0006366|GO:0006357|GO:0000981|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_88433_PI430048170 0.3732745873794921.07117178777848 0.3001099859457470.258445376042363
0.525716276789459 A A A 0.27896522853637 0.2459010329856730.276172874049312 A A A
LNCV6_88433_PI430048170 mRNA
AAGTGTTCAGCCAAGTGACGTTTACTAAATAGCCAATAAAGGGCTGGTGGGTGTGAATGC NM_207421RefSeq chr1
+ 17372195 17401699 PADI6 NA "peptidyl arginine deiminase, type VI" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_141460_PI430048170 0.0231156211845909 0.56954354916389 7.82901379074692
7.54450457691174 8.02559242174959 P P P 8.34445918216123 8.54475461194811
8.92505303167784 P P P LNCV6_141460_PI430048170 mRNA
GCTGGCACATCATTTTGCTGGAGAGTTTTTTATATACTGTAGCCTGATTTCATATTGTATNM_005238RefSeq chr11 -
128458760 128522310 ETS1 2113 "v-ets avian erythroblastosis virus E26 oncogene homolog 1, transcript
variant 2"
GO:0005515|GO:0008284|GO:0070301|GO:0003700|GO:0008285|GO:0006366|GO:0000981|GO:0021983|GO:0005
634|GO:0010715|GO:0006955|GO:0005737|GO:0030578|GO:0048870|GO:0045944|GO:0032355|GO:0070555|GO:0

046677|GO:0035035|GO:0005667|GO:0001666|GO:0007565|GO:0060055|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132379_PI430048170 0.653682038444762 1.02304842314627 0.29704513386431
0.3056752026433170.474618266906705 A A A 0.34082993319777 0.296331100560491
0.348050134784105 A A A LNCV6_132379_PI430048170 mRNA
CCAAAGGTTCCGTTGCAGCTTTTTACAACCATCCGGTGTGGTTTGGAGGATTTGTTTTTT NM_002523 RefSeq chr7
+ 98617284 98629869 NPTX2 4885 neuronal pentraxin II
GO:0003674|GO:0030246|GO:0007268|GO:0005576|GO:0005575|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131945_PI430048170 0.3571770559450891.19600698513188 7.66221725141666
7.02005691131181 7.54157330372799 P P P 7.10999341069219 7.34898539715972
7.04978666648703 P P P LNCV6_131945_PI430048170 mRNA
AAATTGATCAGGGATTTTGATGAAAAGCAACAGGAAGCAAATGAAACGCTGGCAGAGATG NM_006370 RefSeq
chr14 - 67651149 67674885 VTI1B 10490 vesicle transport through interaction with t-SNAREs 1B
GO:0048471|GO:0008283|GO:0031201|GO:0005765|GO:0006904|GO:0043231|GO:0005737|GO:0000149|GO:0043
025|GO:0042147|GO:0061025|GO:0016192|GO:0000046|GO:0012507|GO:0005794|GO:0006891|GO:0048280|GO:0
006896|GO:0031982|GO:0008021|GO:0019869|GO:0006888|GO:0005484|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145212_PI430048170 0.0873591994741989 0.5887214981732552.48141050668367
3.26989738214239 3.28979446351812 A P P 3.9373797057285 3.77482834160836 3.7520541897611
P P P LNCV6_145212_PI430048170 mRNA
GTAAGTAGGATATTAATTTCAGAACATTGATTTCTTATCTGTGTGTCTGACGTGCCATCT NM_207305 RefSeq chr9
- 116230 118417 FOXD4 2298 forkhead box D4
GO:0043565|GO:0003700|GO:0006366|GO:0006357|GO:0008301|GO:0000981|GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130898_PI430048170 0.8709435655036330.9851197546818043.97307992428845
4.02781637349652 3.53514130993179 P P P 4.49441048990912 3.74082504655771
3.06317663083382 P P P LNCV6_130898_PI430048170 mRNA
CAAGACCCTCCTCTTTCATTTTATGCTGGACCTGGAAAATTACAGAGCAGGTTCTGACTT NM_001288961 RefSeq
chr21 + 33948925 33963960 LOC400863 NA uncharactered LOC400863 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_137282_PI430048170 0.0477961312707757 0.7731601423527797.09615061431693
6.90379433765448 7.26439490057764 P P P 7.32359449685542 7.52393760897956
7.54270791884522 P P P LNCV6_137282_PI430048170 mRNA
TCCTGTATAGTTTAATGATGAATGTGCAGGGGACCTGTCTCAGGCTCCTATATGGTTCCT NM_025187 RefSeq chr16
+ 67110011 67148539 C16orf70 80262 chromosome 16 open reading frame 70 GO:0005515 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137536_PI430048170 0.2175985105480061.27692139878388 6.30860709468428
6.54761968830027 6.35234531153616 P P P 6.08041175752964 6.36808114208497
5.61621574187082 P P P LNCV6_137536_PI430048170 mRNA
CCCCATCTCTCTAGAAACACCTATAAAGGCTATTATTGTGATCAGTTTTGACTAACAAAA NM_016941 RefSeq chr19
+ 39498916 39508481 DLL3 10683 "delta-like 3 (Drosophila), transcript variant 1"
GO:0048339|GO:0007386|GO:0001501|GO:0050768|GO:0007219|GO:0001756|GO:0005112|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60440_PI430048170 0.0706495816795216 1.57097500678466 1.80123799868937
2.14221115229296 1.74324329271137 A A A 1.65375558468771 1.05758058541798
0.949777696222384 A A A LNCV6_60440_PI430048170 mRNA
AAGATTTGTTGGGTTTTAGATCTCTTTTCATTTGTCAACCTTTTCAGTAAAGCCCTCTGT NM_198968 RefSeq chr13 -
95578201 95644706 DZIP1 22873 "DAZ interacting zinc finger protein 1, transcript variant 2"

GO:0005515|GO:0005813|GO:0005814|GO:0005634|GO:0007275|GO:0007283|GO:0007281|GO:0046872|GO:0036064|GO:0043231|GO:0042384|GO:0043234|GO:0005737|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143284_PI430048170 0.26795871097336 0.7971398705041085.30786746031328 5.16696772049583 5.61813125227221 P P P 5.29920905651667 5.76834301250376 5.96570106761213 P P P LNCV6_143284_PI430048170 mRNA
GACATAGAAGGCATCCGCTATGAACCAAAATGTCCTCTTGGAGTAGACATATCAAAAGAA NM_022353RefSeq chr2 - 189746659 189763198 OSGEPL1 64172 O-sialoglycoprotein endopeptidase-like 1
GO:0005739|GO:0070526|GO:0016747|GO:0000408|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133747_PI430048170 0.00661788236849388 1.58084923527517 6.87206365340297 7.18188870075604 6.92759058717906 P P P 6.40527894528097 6.42306054097777 6.17762161742098 P P P LNCV6_133747_PI430048170 mRNA
TCCTATTTATGGGGTCTGACCAACTGCACCCACTCCCTAATAAATTCATTCTCCTTGGGA NM_005609RefSeq chr11 - 64746388 64760715 PYGM 5837 "phosphorylase, glycogen, muscle, transcript variant 1"
GO:0000166|GO:0005975|GO:0030170|GO:0005977|GO:0009405|GO:0008184|GO:0006006|GO:0044281|GO:0005980|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128344_PI430048170 0.8729638173552550.7037301318743630.44932894003018 2.01129232807618 1.98626310832561 A A A 3.24967881831421 1.29874129746589 0.408552277271869P A A LNCV6_128344_PI430048170 mRNA
CACTGGATGTGACAATAATTGGGGGAAGGGGAAAAGGGTGTAATAAAGGTTTTAGAGCTTNM_001004312 RefSeq chr3 - 187698258 187702557 RTP2 NA receptor (chemosensory) transporter protein 2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77709_PI430048170 0.0324411658983328 0.5968023389134680.959357067445601 0.3731383179554160.710078534983319A A A 1.36293392660726 1.19295750781101 1.72730658880862 A A A LNCV6_77709_PI430048170 mRNA
CCTACATAAGCAGTGGGAGAACACAGAGACTAACTGGCATAAGGAAAAGATGGAATTACT NM_014702RefSeq chr6 - 127438405 127459390 KIAA0408 9729 KIAA0408 GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142380_PI430048170 0.4811038765148660.7426297215172650.539657618120509 0.42019779647815 0.541581083297803A A A 0.4421292544603641.58121576969463 0.452543074341899A A A LNCV6_142380_PI430048170 mRNA
TGGAAGAATTTAAGAAATTGGTGCAGCACAAGGGACTCTCGGAGGAGGACATTTTCATGC NM_001293189 RefSeq chr9 + 135546138 135549969 OBP2A 29991 "odorant binding protein 2A, transcript variant gamma"
GO:0007608|GO:0007606|GO:0006810|GO:0005576|GO:0005549|GO:0005575|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139805_PI430048170 0.4503704947479 0.8997263838340656.8498301055622 6.48972673418297 6.66954098367584 P P P 6.54504055048741 6.89494145799164 7.0093925618512 P P P LNCV6_139805_PI430048170 mRNA
TAGGAGTGGACTAGAAGTTTAAGCCCAGAGTCAGTAAACACTGTTTTGAAGTCCAAAAAA NM_032590RefSeq chr12 - 121429095 121581015 KDM2B 84678 "lysine (K)-specific demethylase 2B, transcript variant 1"
GO:0005515|GO:0035518|GO:0032452|GO:0021555|GO:0006325|GO:0005634|GO:0019843|GO:0007283|GO:0048596|GO:0021678|GO:0043524|GO:0016577|GO:0031519|GO:2000178|GO:0021993|GO:0005730|GO:0000122|GO:0003677|GO:0051864|GO:0006351|GO:0070544|GO:0021670|GO:0021592|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91665_PI430048170 0.2594138116535421.02064831530403 0.3204840425963150.257132306513235 0.27611433802004 A A A 0.2552530215390850.2537551697167460.256997821021707A A A LNCV6_91665_PI430048170 mRNA
TGGTGGCCATATTTTATATAGACCAAAAAGAGCCACAGAGAAATTTGAAGAATTCCTAGC NM_173538RefSeq chr8

+ 86866447 87382727 CNBD1 168975 cyclic nucleotide binding domain containing 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140274_PI430048170 0.1094170363604810.7196087722222659.0413965955758 8.80816733633621 9.15184292286252 P P P 9.1106345532272 9.55353595886281 9.71652149074737 P P P LNCV6_140274_PI430048170 mRNA
TCCGGTTCAGTACCTATTGTTTCTCCTTTCAAATATGTGATTGTACTAGCTCTTTCCATA NM_013318RefSeq chr9 + 131430089 131500188 PRRC2B 84726 proline-rich coiled-coil 2B GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144228_PI430048170 0.0666147887067839 1.45697319456474 5.54314712810864 5.80574619335741 5.26094166971039 P P P 5.24638908428877 5.00616866632118 4.73433207691624 P P P LNCV6_144228_PI430048170 mRNA
GTGTGTGTTCATCAGATACAGTTCTCCCTTAACCTTGTCCTTTCTCTCCTGTGTCTCAGT NM_178502RefSeq chr12 + 57604621 57609804 DTX3 196403 "deltex 3, E3 ubiquitin ligase, transcript variant 1"
GO:0005737|GO:0016567|GO:0007219|GO:0016874|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144144_PI430048170 0.8477205017030721.03316490698908 4.79535777297386 4.30112020694901 4.70292216095375 P P P 4.55315874950493 4.44458634804002 4.69570379780596 P P P LNCV6_144144_PI430048170 mRNA
GTGGTGTCCCTAAAGGGAGGAAATGATTTCAGCAAAACTGGTTGAACAGCGGATGAAGAT NM_022768RefSeq chr1 + 110339322 110346681 RBM15 64783 "RNA binding motif protein 15, transcript variant 1"
GO:0005515|GO:0031965|GO:0001569|GO:0060674|GO:0000166|GO:0045638|GO:0060412|GO:0016032|GO:0005654|GO:0048536|GO:0007221|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92514_PI430048170 0.7790968066041340.9886595588337378.1564497936923 8.11560093361904 8.02720612895828 P P P 8.10502350641015 8.18877006748088 8.05464193923081 P P P LNCV6_92514_PI430048170 mRNA
ATGGCTTCTCCACCTTCGATGTTCCCATCTTCACTGAAGAGTTCTTGGACCAAAACAAAG NM_006339RefSeq chr19 + 3572944 3579083 HMG20B 10362 high mobility group 20B
GO:0005515|GO:0006355|GO:0046982|GO:0005694|GO:0006325|GO:0035914|GO:0003677|GO:0006351|GO:0007049|GO:0045666|GO:0007596|GO:0003682|GO:0005654|GO:0006338|GO:0033234 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143816_PI430048170 0.1754307931029341.16293040099473 9.63759065501963 9.59203537979852 9.541781039207 P P P 9.582369927661 9.30095311967826 9.20976010879532 P P P LNCV6_143816_PI430048170 mRNA
TCAAACCTCACTTCCGAATGTAAAAGGCTCACTTGCCTTTGGCTTCCTGTTGACTTCTTC NM_001896RefSeq chr16 - 58157907 58197878 CSNK2A2 1459 "casein kinase 2, alpha prime polypeptide"
GO:0005515|GO:0031519|GO:0006355|GO:0006915|GO:0005634|GO:0005524|GO:0006351|GO:0005829|GO:0047485|GO:0004674|GO:0007411|GO:0006468|GO:0071174|GO:0000278|GO:0016055 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133595_PI430048170 0.00140366491379868 1.44476408364715 6.77277449128479 6.87636871994098 6.70631368534241 P P P 6.1913701482411 6.34032711169597 6.23223440810975 P P P LNCV6_133595_PI430048170 mRNA
ACTGTCTGAAGGTTCTCCAAATTGTCTGTGAACTGCTTAGGTAGGAGTGCACTGCAGTTT NM_001242739 RefSeq chr1 + 42846572 42852475 ZNF691 51058 "zinc finger protein 691, transcript variant 1"
GO:0005634|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98691_PI430048170 0.5195826543618270.8841890094093938.82879514867822 8.66559049841566 9.12037591837636 P P P 8.65764923398721 9.19452652183664 9.26027384097023 P P P LNCV6_98691_PI430048170 mRNA
CACTGGGAAAGAAGTAACAGTTGAGTGCAAGATTGATGGATCAGCCAACCTAAAAAGTCA NM_001679RefSeq chr3 + 141876627 141926540 ATP1B3 483 "ATPase, Na+/K+ transporting, beta 3 polypeptide"

GO:0042470|GO:0005886|GO:0030007|GO:0050821|GO:0006883|GO:0010107|GO:0032781|GO:0050900|GO:0005890|GO:0072659|GO:0055085|GO:0086009|GO:0034220|GO:0007596|GO:0005901|GO:0006810|GO:0051117|GO:0001671|GO:0070062|GO:0005391 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134395_PI430048170 0.0450995315800686 0.4972604760292043.17765524031968 3.57783488072949 4.14302818143851 P P P 4.40700574646672 4.53621270717585 5.05840099671217 P P P LNCV6_134395_PI430048170 mRNA
TGGACTTTAAGTGACCATTCAAGAAAAGATGAAATCTCACGAACCTCAAAACTTCATTCA NM_018229RefSeq chr14 + 57268887 57290079 AP5M1 55745 "adaptor-related protein complex 5, mu 1 subunit, transcript variant 1"
GO:0030131|GO:0016020|GO:0005770|GO:0031902|GO:0016197|GO:0030119|GO:0016192|GO:0005765|GO:0006886|GO:0005764|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130152_PI430048170 0.5468533977102630.7769993361005390.535141724761304 0.4507864958030240.461316382835846A A A 0.3445899024631031.48180067998316 0.414905666996303A A A LNCV6_130152_PI430048170 mRNA
TAACAGCGAGGCCATAAACAATGAAATGAATAAAAACGGTGGTCATTCAGTCAACGGAAA NM_000339RefSeq chr16 + 56865206 56915850 SLC12A3 6559 "solute carrier family 12 (sodium/chloride transporter), member 3, transcript variant 1"
GO:0005515|GO:0005215|GO:0006821|GO:0005886|GO:0015378|GO:0055085|GO:0005829|GO:0016324|GO:0016020|GO:0005887|GO:0006810|GO:0035725|GO:0006814|GO:0070062|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132223_PI430048170 0.0950809403975221 1.18888895488837 5.42232552130217 5.27030460953253 5.55316463865861 P P P 5.19713751884856 5.01380986425533 5.28659552453236 P P P LNCV6_132223_PI430048170 mRNA
GAATCACACAACAAGGAGATTTTTAGCATGATACTGGAAATAAAATGTCCAAGCTGACAA NM_005926RefSeq chr15 - 43804534 43824753 MFAP1 4236 microfibrillar-associated protein 1
GO:0005515|GO:0008150|GO:0030198|GO:0001527|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140374_PI430048170 0.0296709235028016 0.2891861874044164.55497137094499 3.40980107846503 4.26076200047918 P P P 6.0431626034104 5.85656077559444 5.91737585902457 P P P LNCV6_140374_PI430048170 mRNA
GGTTTGAATATGCTGAAGTGAGCAATTATGATTTGCCCAAGTGCAATACAACAAATCTAT NM_133496RefSeq chr1 + 100896077 100981755 SLC30A7 148867 "solute carrier family 30 (zinc transporter), member 7, transcript variant 1"
GO:0048471|GO:0005737|GO:0005794|GO:0032119|GO:0008324|GO:0016023|GO:0006829|GO:0016021|GO:0055085|GO:0044267|GO:0031982|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_24045_PI430048170 0.0365905207180439 0.4678424537315351.97988596098521 2.91496564154652 2.69071897572817 A A A 3.70023495189096 3.36412835004478 3.912440215027 P P P LNCV6_24045_PI430048170 mRNA
GAGGGCACATAACAAATGTTAGATCTCTCAAATGTTTTTCTGTAACCCAAATATGCTTAC NM_001198844 RefSeq chr11 + 66638616 66668386 RBM4 5936 "RNA binding motif protein 4, transcript variant 3"
GO:0005515|GO:0008380|GO:0017148|GO:0032055|GO:0046685|GO:0010494|GO:0003723|GO:0005634|GO:0003729|GO:0051403|GO:0030154|GO:0005737|GO:0000166|GO:0000381|GO:0045947|GO:0097158|GO:0003730|GO:0097157|GO:0046822|GO:0043153|GO:0006397|GO:0006396|GO:0005730|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132203_PI430048170 0.2127798419121781.22577796664409 3.59921815859534 4.14598484418615 3.83888993103849 P P P 3.5393669992155 3.49910352915599 3.7082050810288 P P P LNCV6_132203_PI430048170 mRNA
GTTCACAGAAGACACACCTTAAAGGCAAACGGGTTCATGATGTAATCTTCTATTGACTAG NM_130469RefSeq chr14 + 75428356 75472701 JDP2 122953 "Jun dimerization protein 2, transcript variant 1"

GO:0043565|GO:0005515|GO:0003700|GO:0003690|GO:0046982|GO:0031065|GO:0045599|GO:0003682|GO:0005654|GO:0005634|GO:0000122|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58690_PI430048170 0.0636268404664227 0.5753508628748184.01799418936399 3.36253074203155 3.19191467523997 P P P 4.57970553207084 4.47299944753669 3.9816010728214 P P P LNCV6_58690_PI430048170 mRNA
GGTGGTGAGCCAATCAAGATCTGATATAGAAAAATGCAGAAAAAGGAGTATACACATGTT NM_001271592 RefSeq chr12 + 11171180 11176020 SMIM10L1 NA chromosome X open reading frame 69-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137265_PI430048170 0.0119435487053708 0.6193967804228877.68182591360245 7.76988202170151 7.91420990508051 P P P 8.28414987549006 8.45471809083236 8.6820778944931 P P P LNCV6_137265_PI430048170 mRNA
TCTCCCTGCATCACTGTTCATTCACAATGAAAGGTTAGGAAGAAGCTTTAAAATTCACTA NM_020186RefSeq chr7 + 97116592 97181763 SDHAF3 NA succinate dehydrogenase complex assembly factor 3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133047_PI430048170 0.4714485850741381.35573692431933 1.71847707365781 0.6048007126709730.533498230284836A A A 0.5457499720247970.395444359265396 0.880973970137212A A A LNCV6_133047_PI430048170 mRNA
GCTGTTATATTTTTATATAAGCTATGTTTATGACAGACTTTCCTATAATATTCTTATCAT NM_031912RefSeq chr10 - 47750085 47762793 SYT15 83849 "synaptotagmin XV, transcript variant a" GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138617_PI430048170 0.7193216175215910.8945525592370330.665011883236212 0.3926590491530120.604056770092849A A A 1.20196585191377 0.410893905143269 0.388646387140639A A A LNCV6_138617_PI430048170 mRNA
GATCATGAGTGTTGCTGCAATACTTGAAGCTTCATGTATTTTCATTAATGTATACCATGC NM_001290030 RefSeq chr2 + 170770681 170798971 ERICH2 285141 "glutamate-rich 2, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133680_PI430048170 0.0679074859261237 0.5285812654265658.56674635296289 8.45377785486123 8.71513799498911 P P P 9.0528380893476 9.3699205624508 9.94106326113571 P P P LNCV6_133680_PI430048170 mRNA
GATCAGTCAGAGCCCCTACAGCATTGTTAAGAAAGTATTTGATTTTTGTCTCAATGAAAA NM_005228RefSeq chr7 + 55019031 55207338 EGFR 1956 "epidermal growth factor receptor, transcript variant 1" GO:0005515|GO:0042698|GO:0033590|GO:0005615|GO:0006412|GO:0033594|GO:0042802|GO:0005006|GO:0016337|GO:0021795|GO:0001948|GO:0003690|GO:0007173|GO:0000165|GO:0007411|GO:0007611|GO:0042743|GO:0001942|GO:0004709|GO:0006979|GO:0031625|GO:0031965|GO:0030335|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143976_PI430048170 0.0539801117200983 0.6585600893000836.1133356889259 5.69769548058483 5.96151039146437 P P P 6.21826059568343 6.51931853667547 6.81217071521282 P P P LNCV6_143976_PI430048170 mRNA
CAAGTGCTCTTTCACTAGTACTACAGATAATCAAAGCTATCAGAATTGTGTCTTTGATCA NM_001126129 RefSeq chr16 + 58392393 58406144 GINS3 64785 "GINS complex subunit 3 (Psf3 homolog), transcript variant 1" GO:0006260|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132997_PI430048170 0.23067781822713 0.5253519149890322.17637144681797 2.0912407499753 0.274863764472478A A A 3.22089064459061 2.53251071884407 1.96667551022504 P P A LNCV6_132997_PI430048170 mRNA
GCCTCCCACACTTTTCTTTGATGGGAGGTTTCAATAAACAGCGATAAGAACTCTAAAAAA NM_004254RefSeq chr11 - 62992823 63015845 SLC22A8 9376 "solute carrier family 22 (organic anion transporter), member 8, transcript variant 1" GO:0006820|GO:0005886|GO:0015697|GO:0031427|GO:0009636|GO:0055085|GO:0015651|GO:0016323|GO:0034220|GO:0005452|GO:0034635|GO:0005080|GO:0015711|GO:0008514|GO:0016021|GO:0070062 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_134073_PI430048170 0.5916933601649210.9637768217372450.529965833300514
0.5061828258149990.269524457090264A A A 0.4087578671433830.565261320249523
0.501157839973769A A A LNCV6_134073_PI430048170 mRNA
TTTACCCTGTAATCCAAGCGTTAATAGTTTGTTAGAAGATGGGTTATTGCATGTCACTTT NM_020775RefSeq chr1
+ 109113962 109206781 KIAA1324 57535 "KIAA1324, transcript variant 1"
GO:0005802|GO:0005887|GO:0005770|GO:0031902|GO:0016236|GO:2001240|GO:2000786|GO:0044090|GO:0005
765|GO:0005764|GO:0070062|GO:0009267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136647_PI430048170 0.3028679188945311.19495507969624 0.463661601237045
0.9677361035430720.44085282666169 A A A 0.34719346724085 0.400012124448514
0.416929614871922A A A LNCV6_136647_PI430048170 mRNA
AGAAAGACATTTCAAGATAGATGCTTCAGGTGACATTGTGGAGCTGTACCCCAGGAACGT NM_001080532 RefSeq
chr15 - 81332418 81374077 TMC3 342125 transmembrane channel-like 3 GO:0016021|GO:0006811
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142546_PI430048170 0.00413372487748218 0.3502428889474385.4353879025753
4.82338881130751 5.17161116739626 P P P 6.53196432152911 6.61889418588887
6.86384840303152 P P P LNCV6_142546_PI430048170 mRNA
CAAGCTGGACTTTGTTGCCATCCTTGAGATGAACCTTTTAAGAAAAATAAGTTAATCTCA NM_001171894 RefSeq
chr15 + 99565927 99716424 MEF2A 4205 "myocyte enhancer factor 2A, transcript variant 5"
GO:0005515|GO:0000790|GO:0003700|GO:0006366|GO:0003705|GO:0000981|GO:0046332|GO:0051403|GO:0007
507|GO:0042692|GO:0002756|GO:0000165|GO:0002755|GO:0070375|GO:0055005|GO:0061337|GO:0035035|GO:0
048311|GO:0001105|GO:0000977|GO:0038124|GO:0019901|GO:0038123|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144536_PI430048170 0.2244606503457152.03530157904568 0.299939789975965
1.96861789239563 1.57160586662023 A A A 0.5099371575667750.394917608452396
0.321277023232375A A A LNCV6_144536_PI430048170 mRNA
GTGCCATATGTATCAAATGACAAATCTTTATTGAATGGTTTTGCTCAGCACCACCTTTTA NM_002988RefSeq
chr17_KI270909v1_alt + 18368 25578 CCL18 6362 chemokine (C-C motif) ligand 18 (pulmonary and
activation-regulated)
GO:0009607|GO:0005515|GO:0008009|GO:0007165|GO:0006955|GO:0007154|GO:0006954|GO:0006935|GO:0060
326|GO:0007267|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141917_PI430048170 0.5172628261564671.06890833004195 0.832139820212312
0.8732144770717520.903778200889794A A A 0.6738747767339511.03456777544004
0.571144933010696A A A LNCV6_141917_PI430048170 mRNA
CTCCTTTCTTCAGAACATATGACTTTCATTTCCCAGAAAAAAGATTAATGGTCCTGAGTA NM_018940RefSeq chr5
+ 141172620 141176376 PCDHB7 56129 protocadherin beta 7
GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129426_PI430048170 0.0256607425473989 0.3585978725651790.396652544870325
1.19446112907707 1.40861748956674 A A A 1.93343358647523 2.94986265369439
2.56318966104123 A P P LNCV6_129426_PI430048170 mRNA
AGCGGCAGCCACCACCAGTGTTGTTTTGAATAAAAGCCCAGAAGCCTATTTAAGAAAAAA NM_021096RefSeq chr22
+ 39570752 39689736 CACNA1I 8911 "calcium channel, voltage-dependent, T type, alpha 1I subunit,
transcript variant 1"
GO:0005515|GO:0086010|GO:0005245|GO:0005886|GO:0008332|GO:0030431|GO:0030317|GO:0005891|GO:0019
228|GO:0007165|GO:0070509|GO:0007411|GO:0070588|GO:0006810|GO:0034765 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138614_PI430048170 0.3593909608059712.6419518595162 2.88593196785771
0.3933856291449940.641282744046701A A A 0.2801482575136610.418970510528192
0.415866269823376A A A LNCV6_138614_PI430048170 mRNA

CAAATCTTCAACTACCTAGGAAGACAAATGCCTAGGGAGAGCTGTGAAAAGTCATCATCC NM_005201 RefSeq chr3 + 39329705 39333680 CCR8 1237 chemokine (C-C motif) receptor 8 GO:0006955|GO:0070098|GO:0007186|GO:0006935|GO:0005886|GO:0005887|GO:0004950|GO:0016493|GO:0015026|GO:0007155|GO:0007204 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_107794_PI430048170 0.1394033891218421.30974071830388 4.06090268514989 3.57089498668203 3.59020321827727 P P P 3.35721665047526 3.30860522604999 3.44040446332422 P P P LNCV6_107794_PI430048170 mRNA
TGAAACTGGATGAACTGGTGAAGAAAATTGGCAAAGCTGTGGAAGACTCCAAGCCCTACT NM_004844 RefSeq chr3 - 15254355 15332629 SH3BP5 9467 "SH3-domain binding protein 5 (BTK-associated), transcript variant 1" GO:0035556|GO:0005739|GO:0005515|GO:0007165|GO:0017124|GO:0005737|GO:0004860|GO:0006469 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_142521_PI430048170 0.0057671282888603 1.57919086148685 10.0641228519496 10.0332634427571 10.0881656302762 P P P 9.38555053778435 9.51287149424643 9.30226428465475 P P P LNCV6_142521_PI430048170 mRNA
ATCTACCTCTTCTCTGGAATGTTTATGGTGGTTCAGAAGAATGATGACTCCTCTTTGCTG NM_005793 RefSeq chr3 - 48292316 48301411 NME6 10201 NME/NM23 nucleoside diphosphate kinase 6 GO:0006241|GO:0006228|GO:0006165|GO:0005739|GO:0045839|GO:0006183|GO:0030308|GO:0006915|GO:0004550|GO:0005524|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_139729_PI430048170 0.0143381072441419 0.5079587360284719.43067566427592 9.32437173043055 9.34861316183811 P P P 10.1572427299394 10.2492878024047 10.5934572642521 P P P LNCV6_139729_PI430048170 mRNA
AGCCTGGTGTATTGTACTTCAAGATGCCTCCCTGATGTATAGAATCTCCTTGTAAAATAA NM_001048183 RefSeq chr1 + 28369581 28500369 PHACTR4 65979 "phosphatase and actin regulator 4, transcript variant 1" GO:2001045|GO:0030036|GO:0001755|GO:0001843|GO:0003779|GO:0007266|GO:0043085|GO:0030027|GO:0048484|GO:0061386|GO:0005737|GO:0051726|GO:0071862|GO:0008157 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_131357_PI430048170 0.4989225961345081.51756989899258 0.294028582090011 0.29067983146587 1.81167063748751 A A A 0.3022538052416040.276614746414402 0.568281047528973 A A A LNCV6_131357_PI430048170 mRNA
TGTATAATTTTATCTTCCAGGTCATCTGTGCTGGTGTCTATCAGTCTGCTAGTCTTTCCC NM_001079512 RefSeq chr16 - 10766675 10818764 TVP23A NA trans-golgi network vesicle protein 23 homolog A (S. cerevisiae) NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_128610_PI430048170 0.2437812099405310.7734271922386350.429712363805074 0.3948528712021510.248915274526729 A A A 1.1088394456543 0.406877394789774 0.580553305775731 A A A LNCV6_128610_PI430048170 mRNA
AGAAATAAGGAGATGAAGAAAGCTTTGAGGAAACTTATTGGTAGGCTGTTTCCTTTTTAG NM_001005192 RefSeq chr19 - 9114827 9115763 OR7G1 NA "olfactory receptor, family 7, subfamily G, member 1" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_56272_PI430048170 0.96602267482194 0.97412880932708 4.96222494309202 4.93162325866369 4.39391449497535 P P P 4.95224502616646 5.12209280506938 4.25758861163993 P P P LNCV6_56272_PI430048170 mRNA
ACATCAGCACATTCAGTAATGACTCTTGAAGCTTTTGTCTGCCCTAAATGATTTGGTATT NM_001282905 RefSeq chr10 - 45615500 45672732 ZFAND4 93550 "zinc finger, AN1-type domain 4, transcript variant 3" GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_126777_PI430048170 0.0292315279928471.53443767278333 10.2257385771581 10.5738516494667 10.1424930223468 P P P 9.76491669497942 9.76324189001843 9.59113757658822 P P P LNCV6_126777_PI430048170 mRNA
GAGCCTTAACTGGACATGAGGGGCATGAGAATAAAGCTGAACTGCAGCCTCCTGAAAAAA NM_032251 RefSeq

chr11 + 64340217 64357534 CCDC88B 283234 coiled-coil domain containing 88B GO:0016020 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64979_PI430048170 0.3288397727818890.9761224477677815.8702519644881 15.9334532671581 15.8920469077763 P P P 15.981602844932 15.9179385903177 15.9002497547656 P P P LNCV6_64979_PI430048170 mRNA
ATCCAGTTGTAGCTGCCATCAGATGCCGGAGACTCGCCCTTCAATAAAAAATCTCTTCTA NM_015710RefSeq chr19 + 47745535 47757066 GLTSCR2 29997 glioma tumor suppressor candidate region gene 2
GO:0005622|GO:0008150|GO:0005730|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142149_PI430048170 0.3433396052765890.8983885645156590.25443571680537 0.2676672675889770.361901769795819A A A 0.6762121851522570.3306873381258020.3135111149243 A A A LNCV6_142149_PI430048170 mRNA
GTCTCTGTGTACTTTGAATTATTTTGCAGTTATGTAGGTATCCTAATGAGTGAATGGTAC NM_145756RefSeq chr18 - 35366696 35377337 ZNF396 252884 zinc finger protein 396
GO:0006355|GO:0005737|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137598_PI430048170 0.0566473614736081.20942161266339 7.07035533542028 7.2739400945507 7.33647368131197 P P P 7.01568042810919 7.00544020552524 6.84353487852962 P P P LNCV6_137598_PI430048170 mRNA
TCATGCTTATAATAAAGCCGGCGTCAGAGACCGCTGCTTCCCTCACCTGCCTGCCTGTCT NM_021603RefSeq chr11 - 117820074 117828092 FXYD2 486 "FXYD domain containing ion transport regulator 2, transcript variant b"
GO:0005215|GO:0005886|GO:0005890|GO:0055085|GO:0001558|GO:0043231|GO:0016323|GO:0034220|GO:0042127|GO:0006810|GO:0035725|GO:0005216|GO:0006813|GO:0070062|GO:0005391 . NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_137256_PI430048170 0.28716847079424 4.2814763467411 0.332244382953884 3.62466889028977 1.21296406763134 A P A 0.3080006321987830.283079035762122 0.335352716090842A A A LNCV6_137256_PI430048170 mRNA
AGCAATGACAATAAACAAGAGGTATTTATCATCACCAATAAACAATCCCCCAAGAGGTAA NM_173355RefSeq chr2 + 158101869 158136154 UPP2 151531 "uridine phosphorylase 2, transcript variant 1"
GO:0046135|GO:0044206|GO:0045098|GO:0009116|GO:0055086|GO:0044281|GO:0043097|GO:0046108|GO:0009166|GO:0006206|GO:0004850|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141983_PI430048170 0.0341478900569832 1.25210562420272 10.1502529265745 10.3325093480368 10.3550966750958 P P P 9.93385900872197 9.97780933932152 9.96139494715846 P P P LNCV6_141983_PI430048170 mRNA
CGTCTTTCAGTTGTGACAATTTCTTGAGGGTTAAGCACATGTTCATATTAAAGTTGTCAT NM_001013663 RefSeq chr2 - 24790266 24793382 PTRHD1 391356 peptidyl-tRNA hydrolase domain containing 1
GO:0008152|GO:0004045|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129169_PI430048170 0.00544097559632355 1.37433599473684 10.5082719915483 10.6435539435616 10.656152656286 P P P 10.1113543189262 10.1680085263701 10.1564009146607 P P P LNCV6_129169_PI430048170 mRNA
CCCATCTAGTTGGGGATAGAACTTTATAATTACCTTTTGGATACTGTGGTTCTATTTGAT NM_015694 RefSeq chr7 - 149431362 149460962 ZNF777 27153 zinc finger protein 777
GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0005575|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140614_PI430048170 0.00727066780653975 0.440881523229765 4.18852330688102 4.03659681430126 3.66891012782312 P P P 4.8742927048734 5.08637560140776 5.46352895065328 P P P LNCV6_140614_PI430048170 mRNA
CGTTATTGTGCCAAATGTACTGTATTCAAAAGGATGTGAATGTGTATTGTTTCAGAACCT NM_005400 RefSeq chr2 + 45651903 46187990 PRKCE 5581 "protein kinase C, epsilon"

GO:0005515|GO:0050730|GO:2000650|GO:0010763|GO:0007173|GO:0018105|GO:0030838|GO:0032024|GO:0005856|GO:0043123|GO:0031663|GO:0035641|GO:0051209|GO:0005794|GO:0032467|GO:0030168|GO:0043278|GO:0032230|GO:0007049|GO:0035276|GO:0008543|GO:0045087|GO:0030546|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129355_PI430048170 0.237162097086793 1.26175146232376 5.51873948532533 5.97784902694739 5.52751938704831 P P P 5.49572932177645 5.55025616000603 4.94781403402946 P P P LNCV6_129355_PI430048170 mRNA TTAAAACTAGCTTTTTAAGCAGCTGTATGAAATAAATGCTGAGTGAGCCCCAGCCCGCCC NM_004626 RefSeq
chr11 - 76186325 76206530 WNT11 7481 "wingless-type MMTV integration site family, member 11"
GO:0030308|GO:0030325|GO:0044212|GO:0071300|GO:0048706|GO:0032915|GO:0061101|GO:0048844|GO:0030282|GO:0060675|GO:0005615|GO:0005109|GO:0005737|GO:0090037|GO:0070830|GO:0072177|GO:0030182|GO:0045860|GO:0060548|GO:0060021|GO:0031667|GO:0090090|GO:0060070|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141068_PI430048170 0.00236725846226092 6.97034630978906 4.03334194402756 3.80571257849409 3.35682740210232 P P P 0.308146662830668 1.22478037136207 1.16979098487854 A A A LNCV6_141068_PI430048170 mRNA GATAGAGTTGAGGAGTGTGAGGCTGTTAGACTGTTAGATTTAAATGTATATTGATGAGAT NM_000557 RefSeq
chr20 - 35433348 35438190 GDF5 8200 growth differentiation factor 5
GO:0005515|GO:0035137|GO:0035136|GO:0005886|GO:0050680|GO:0007267|GO:0030326|GO:0060395|GO:0005615|GO:0042802|GO:0043524|GO:0030198|GO:0002062|GO:0040014|GO:0043408|GO:0007179|GO:0032332|GO:0048468|GO:0010862|GO:0005576|GO:0042981|GO:0030509|GO:0005160|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133217_PI430048170 0.532866720627156 0.764660648615433 1.98431956030416 1.81972683010566 0.310484092066364 A A A 1.98853333595841 2.4155688542016 1.0767710259911 A A A LNCV6_133217_PI430048170 mRNA AGTTCAAACCCTGAGCCCTTCATTCACCTCTGTGAGTGAATAAATGTGCTAAGTCTCTTT NM_014433 RefSeq
chr22 - 23059414 23142054 RSPH14 27156 radial spoke head 14 homolog (Chlamydomonas)
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58458_PI430048170 0.154318711492613 1.10198317703458 0.574594031886608 0.455112287946643 0.618641645380252 A A A 0.297618477185203 0.412840947797759 0.514368560118954 A A A LNCV6_58458_PI430048170 mRNA TTATTTCACAGCCACGTTTCCGTACCTGATGCTTGTCATTTTGCTGATCAGAGGTGTCAC NM_003044 RefSeq
chr12 - 190076 213447 SLC6A12 6539 "solute carrier family 6 (neurotransmitter transporter), member 12, transcript variant 1"
GO:0071474|GO:0010033|GO:0005886|GO:0005328|GO:0006865|GO:0007268|GO:0009992|GO:0055085|GO:0007269|GO:0005887|GO:0015812|GO:0006810|GO:0016021|GO:0005332|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132832_PI430048170 0.00775768279175538 1.27169131500867 6.70440410524571 6.76594665566505 6.87620752180609 P P P 6.4112956763689 6.49527204966214 6.40321076226015 P P P LNCV6_132832_PI430048170 mRNA TTGAGTTTCCTCAATGTGGTCAAAGCTTCAGTCATCATTAAACTTCTCTGGACCAAAAAA NM_025231 RefSeq
chr6 + 28124608 28130078 ZSCAN16 80345 zinc finger and SCAN domain containing 16
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132505_PI430048170 0.163911899563425 0.719598529397888 6.61811492567954 6.48753616515812 6.79939245596759 P P P 6.70511753269883 7.08704500030861 7.4569066066239 P P P LNCV6_132505_PI430048170 mRNA TATGTTTGTCAGTTCATGCCGAGATGAAATAAATCACGCAGAAAGTGCCAGTCCTCCTGA NM_014867 RefSeq

chr8_KI270821v1_alt + 157253 190319 KBTBD11 9920 kelch repeat and BTB (POZ) domain containing 11
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128217_PI430048170 0.652756602272034 0.966040812718162 0.586667399681659
0.527151261660061 0.291772078699144 A A A 0.412540469015299 0.616206016257023
0.535668130257694 A A A LNCV6_128217_PI430048170 mRNA
TCCAGGCAACCAAATAAAGTTTGAGTGTACCAGGAACAGAATCCTGGGGCTTGCAAAAAA NM_001868 RefSeq
chr7 + 130380370 130388108 CPA1 1357 carboxypeptidase A1 (pancreatic)
GO:0006508|GO:0008270|GO:0005615|GO:0004181 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139966_PI430048170 0.92095248354979 0.991464260551102 9.85781759444259
9.71612775056662 9.49669235957042 P P P 9.87187703528731 9.66914127323007
9.57314256620201 P P P LNCV6_139966_PI430048170 mRNA
GTCTTACTGGTGATCATCTCCTCACCCCATCTCCCACCTTGTGGAATAAATACATGTTAG NM_022479 RefSeq chr7
+ 71132536 71713601 WBSCR17 64409 Williams-Beuren syndrome chromosome region 17
GO:0004653|GO:0000139|GO:0030246|GO:0006486|GO:0016021|GO:0046872 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_127562_PI430048170 0.1272280103459460.8992744203174489.12950897853419
8.96892204988474 9.00586946845632 P P P 9.13869541496454 9.30866841548796
9.11346844468942 P P P LNCV6_127562_PI430048170 mRNA
TACATGGCAGAAGTGAAAAAGTACAAAGCTCACCAGTGCGGTGACGATGATAAAACTCGG NM_024038RefSeq
chr19 - 12730639 12734715 C19orf43 79002 chromosome 19 open reading frame 43 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_127100_PI430048170 0.1773483326004960.3913985964289041.08662742042564
1.48082735329589 2.37279695807689 A A A 2.60271974606067 1.96015649108386
3.98413222705688 A A P LNCV6_127100_PI430048170 mRNA
CTTCTAGCATTTCTTCCAATTATTACAGTCCTTCAAGATTCCATTTCTTAACAGTCTCCA NM_005373RefSeq chr1 +
43337803 43354464 MPL 4352 "MPL proto-oncogene, thrombopoietin receptor"
GO:0048872|GO:0004896|GO:0005886|GO:0008283|GO:0007596|GO:0005887|GO:0019221|GO:0032642|GO:0030
168|GO:0007166|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127968_PI430048170 0.0151291314127850.4517919779330429.54578562104874
9.50237744764541 9.73567239379757 P P P 10.4446494686509 10.6545427992543
11.0642165318715 P P P LNCV6_127968_PI430048170 mRNA
CCTCGGCATGTACTGTAGTCACTCAGTATTTGTATATGTTGCTAGAATTTAGATTGTAAA NM_080927RefSeq chr3
- 98795969 98901689 DCBLD2 131566 "discoidin, CUB and LCCL domain containing 2"
GO:0005515|GO:0030308|GO:0009986|GO:0005887|GO:0042060|GO:0030522 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131339_PI430048170 0.0323621194113147 0.5422360390855074.17016209156137
4.26276475195233 4.15271479770294 P P P 4.76971206642796 5.04926728940339
5.35809191723328 P P P LNCV6_131339_PI430048170 mRNA
CAGAAAGGGTTCAGAAGAAGTTAGCATCAACTGTATGAAAATTCTAGGTAAAGCTAAGTA NM_001040157 RefSeq
chr4 + 174283676 174320331 CEP44 80817 "centrosomal protein 44kDa, transcript variant 1"
GO:0005813|GO:0005737|GO:0000922|GO:0030496 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90659_PI430048170 0.6206774061342161.05992247957322 7.65393813950008 7.37006777208313
7.31277890811656 P P P 7.25665153461512 7.60301340937469 7.21678061177489 P P P
LNCV6_90659_PI430048170 mRNA
AAGATCATCCATATCAGCAAGAAGCACCGCACGTGGTTCTTCTCGGCCTCCTCCGAGGAG NM_001145855 RefSeq
chr4 + 2812218 2841096 SH3BP2 6452 "SH3-domain binding protein 2, transcript variant 4"
GO:0005515|GO:0007165|GO:0017124|GO:0005070|GO:0009967 . NA - . NA NA NA NA NA NA NA
NA NA

LNCV6_144667_PI430048170 0.0616842164095037 1.05595800321586 0.34181991787788
0.38471369909212 0.30574078012967 A A A 0.25616408941184 0.282532008016398
0.258858960670557 A A A LNCV6_144667_PI430048170 mRNA
CAGTTAATTGCCAGTTGCCAACAAATCTAGTTCTATACAGTTTCTTGGGATGATGATAAT NM_147180 RefSeq chr9
- 101591614 101595001 PPP3R2 5535 "protein phosphatase 3, regulatory subunit B, beta" GO:0005509
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133530_PI430048170 0.302712370084594 0.945659652160796 0.255360938542049
0.378055067512651 0.280838775904013 A A A 0.482512561478258 0.375790132696605
0.294522237943455 A A A LNCV6_133530_PI430048170 mRNA
GGTGGTGAATGACTATTGATGACTGTGTTAAGTGCATCTGTATTGTAAGTGAAATGTAAT NM_012281 RefSeq chr7
+ 120273667 120750333 KCND2 3751 "potassium channel, voltage gated Shal related subfamily D,
member 2"
GO:0005251|GO:0005515|GO:0005250|GO:0005886|GO:0031226|GO:0007268|GO:0046872|GO:0043197|GO:0005
249|GO:0008076|GO:0051260|GO:0034765|GO:0001508|GO:0016021|GO:0071805 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127266_PI430048170 0.968269931950241 1.00239893291842 0.453921556277438
0.422577304344396 0.300358051940446 A A A 0.351050456985167 0.410752288278485
0.408415865356667 A A A LNCV6_127266_PI430048170 mRNA
GGAATTTCAGCTCTAAACACATTTTTGAGACAGTTATCTGTGAGTGAAAACAGGGTATTA NM_032961 RefSeq chr4
+ 133149289 133194610 PCDH10 57575 "protocadherin 10, transcript variant 1"
GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138664_PI430048170 0.573706287299902 1.29189737646784 0.637260909296788
0.705705182591973 1.87123556500711 A A A 0.617590628786673 0.499967631591829
1.23250113063606 A A A LNCV6_138664_PI430048170 mRNA
CACTCAAAAGTCAAATTAAATTCTTTCCCAATGCCCCAACTAATTTTGAGATTCAGTCAG NM_182536 RefSeq chr2
- 68945231 68952970 GKN2 200504 gastrokine 2 GO:0005576 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_78428_PI430048170 0.0238681580309545 0.606803238743446 4.25410973783058 4.512895237279
4.68311149223628 P P P 5.25498934183269 5.22269091239829 5.16506194522871 P P P
LNCV6_78428_PI430048170 mRNA
CTAGCTTTCCTTTTCTCTTTTTGGATGACCGCTACAGGTGAACCTCCTTGGCCTGGGCGA NM_001256879 RefSeq
chr7 - 44114679 44123508 POLD2 5425 "polymerase (DNA directed), delta 2, accessory subunit,
transcript variant 3"
GO:0005515|GO:0003887|GO:0005634|GO:0003677|GO:0006260|GO:0006271|GO:0006281|GO:0071897|GO:0000
723|GO:0006283|GO:0006284|GO:0000722|GO:0006297|GO:0005654|GO:0006298|GO:0006289|GO:0000278|GO:0
032201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131882_PI430048170 0.290916749019531 1.23525267482815 5.0777146324004
4.55873110804998 5.20217855865833 P P P 4.69684264949046 4.61391064453901
4.68927483582142 P P P LNCV6_131882_PI430048170 mRNA
TGTAACTCTTGGTATCTTTACTGCATCATAGTCAATAAACTTCTTTGTACCCTTTGGCTA NM_198275 RefSeq chr11 -
118226689 118252368 MPZL3 196264 "myelin protein zero-like 3, transcript variant 1"
GO:0005515|GO:0042633|GO:0030198|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139258_PI430048170 0.505986177889936 0.793082199523114 0.484068165027124
0.588186684981941 0.528169208482973 A A A 1.43621328705617 0.457134419167251
0.484011261287358 A A A LNCV6_139258_PI430048170 mRNA
TGAAGAAACCTATATCCCAAAGGACCAGAAGTATTCATTCCTGCATGACTCCCAGACCTC NM_022644 RefSeq chr17
- 63872011 63873729 CSH2 1443 "chorionic somatomammotropin hormone 2, transcript variant 2"
GO:0005179|GO:0005576|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_110460_PI430048170 0.0568829685701432 1.18710343211909 13.8677521911349
13.9811162205519 14.0251423025196 P P P 13.8532278328632 13.6081566211034
13.6632163650127 P P P LNCV6_110460_PI430048170 mRNA
CATCTGTTTTCTACAGGGTTTAAGTCTCAGGAGGTCTCAATAAACTTGGTATATAAATGT NM_001282332 RefSeq
chr19_KI270938v1_alt + 165695 169508 TSEN34 79042 "TSEN34 tRNA splicing endonuclease subunit,
transcript variant 3"
GO:0006397|GO:0005730|GO:0005654|GO:0005634|GO:0003676|GO:0000214|GO:0000379|GO:0000213|GO:0016
829. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143306_PI430048170 0.744356025996383 0.684185393330494 1.60458914559212
0.499848267660904 0.403771259567375 A A A 2.52912116342696 0.413202667599179
0.423754026536903 A A A LNCV6_143306_PI430048170 mRNA
CTTCCTTCTTTTAATGATCACTTTGGGTTATCTCCCTATAACCAGGGATCTTACCTATAT NM_030975 RefSeq
chr17_JH159148v1_alt - 50745 51726 KRTAP9-9 81870 keratin associated protein 9-9 GO:0045095
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136294_PI430048170 0.0180369280237053 1.24725830615605 6.63616991871481
6.84750110367275 6.78607372588022 P P P 6.3810026865567 6.53315034152688
6.40267954741471 P P P LNCV6_136294_PI430048170 mRNA
CAAATGATGTGTAATTATCTAGGTTGTAAAAATAAAACATACTCCCCCTTCCCTTGAGGA NM_001099692 RefSeq
chr10 + 79512600 79516436 EIF5AL1 NA eukaryotic translation initiation factor 5A-like 1 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_144540_PI430048170 0.575961419567475 0.936531724270136 12.6990327152789
12.7958486094912 12.7065584313305 P P P 12.654032952328 12.7349857081965
13.0647069831795 P P P LNCV6_144540_PI430048170 mRNA
TTTATTCTGCGTCCCCTTCTCCAATAAAACAAGCCAGTTGGGCGTGGTTATATGTTGAAA NM_001282652 RefSeq
chr11 + 64185271 64204548 STIP1 10963 "stress-induced phosphoprotein 1, transcript variant 1"
GO:0005515|GO:0005794|GO:0006950|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135719_PI430048170 0.780972929199414 0.978556462245362 9.8460787438012
9.84754275767072 9.72276846120677 P P P 9.8067453244042 9.98577966548887
9.70728808853043 P P P LNCV6_135719_PI430048170 mRNA
AGATTTCATCATCTTTGAGGCTGCTCCCCAAGAGACACGGGGCATCCCCTCCAAGAAGCC NM_001303506 RefSeq
chr16 + 30075975 30085377 PPP4C 5531 "protein phosphatase 4, catalytic subunit, transcript variant
4"
GO:0005515|GO:0005815|GO:0005886|GO:0005634|GO:0010569|GO:0038061|GO:0046872|GO:0030289|GO:0004
704|GO:0005737|GO:0016311|GO:0005654|GO:0004722 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144175_PI430048170 0.0718522338860696 0.378942049266876 2.93327128998603
1.27380062105838 2.41079800328779 A A A 3.24880344426767 3.96979271172866
3.94455644751191 P P P LNCV6_144175_PI430048170 mRNA
CACACTGATGGGTATTTACAGCAGATATATCCAAGCTGTTTATGTAATAGTCTCATTTAC NM_194291 RefSeq chr8
- 124310917 124372699 TMEM65 157378 transmembrane protein 65 GO:0005739|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143585_PI430048170 0.398002247837517 0.547137106740339 0.753587137124564 1.8385363400205
0.35023632199287 A A A 0.483972665177374 2.0567721761527 2.67557026828512 A A P
LNCV6_143585_PI430048170 mRNA
AAAGGTATTTTCCCTCACCAGTCTAGGCATGACTGGCTTCTGAAAAATTCCAGCACACCT NM_001171092 RefSeq
chrX + 106900163 106930861 CLDN2 9075 "claudin 2, transcript variant 2"
GO:0016338|GO:0005886|GO:0005198|GO:0016021|GO:0005923|GO:0070062|GO:0042802 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145271_PI430048170 0.993534983386581 1.00055088220213 0.2873976662762
0.29508041692482 0.425376944544228 A A A 0.355606926345098 0.303993739984942

0.349530260834918 A A A LNCV6_145271_PI430048170 mRNA
TGATTAGTGGGATGGATATGCTTTCTTCAGGACCCTTAGGCACTAAAATCTAGGACACAG NM_001099851 RefSeq
chr1 + 13389631 13392629 PRAMEF17 NA PRAME family member 17 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_114496_PI430048170 0.3500687225246171.03327712076817 0.296835517678609
0.26340115440956 0.391224591132065 A A A 0.2836972236916070.252182982683995
0.276774378796696 A A A LNCV6_114496_PI430048170 mRNA
AAATGGACACAGGACTCAGTGAGACTTTTCAGACCTCGAAAGTTTCATAAAGTGGTCAGA NM_001287740 RefSeq
chr5 + 147235015 147387855 STK32A 202374 "serine/threonine kinase 32A, transcript variant 3"
GO:0005886|GO:0004674|GO:0006468|GO:0005524|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138543_PI430048170 0.4583338336701970.6252993792341020.392948589723465
0.3919452968691540.42546933090603 A A A 1.91960793670731 0.328893990930238
0.386148754734357 A A A LNCV6_138543_PI430048170 mRNA
CTGTAAATCCCCATTGGAGACTGCATTAGGGAATTAAAGCTGCTTGTCACTTTTTGCTGA NM_007128 RefSeq chr22
+ 22244779 22245515 VPREB1 7441 "pre-B lymphocyte 1, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142303_PI430048170 0.9880795428061210.9967024686856120.5164661288916880.6318988072531
0.528924990002708 A A A 0.4576694056449580.7138625068656050.509975318554193 A A A
LNCV6_142303_PI430048170 mRNA
CCAAAGACACATCCATGTGATTCTCTAGTTCAGCAGAAAGAATAAAAATTGCTTCAATCT NM_001110359 RefSeq
chr14 - 20556092 20560931 RNASE9 NA "ribonuclease, RNase A family, 9 (non-active), transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141143_PI430048170 0.4124798627720690.8047572822585870.542534261241582
0.4702277729110470.287648370790367 A A A 0.4031262640192 1.21899128078324
0.483265288124319 A A A LNCV6_141143_PI430048170 mRNA
CACTATCTGCAAACTCAGGACACTTTAACAGGGCAGAATACTCTAAAAACTTGATAAAAT NM_001875 RefSeq chr2
+ 210556598 210679107 CPS1 1373 "carbamoyl-phosphate synthase 1, mitochondrial, transcript variant
2"
GO:0042645|GO:0005515|GO:0019240|GO:0005743|GO:0044281|GO:0014075|GO:0010043|GO:0032094|GO:0032
403|GO:0050667|GO:0072341|GO:0034641|GO:0042594|GO:0005543|GO:0071377|GO:0070409|GO:0045909|GO:0
005759|GO:0006508|GO:0006526|GO:0032496|GO:0046209|GO:0019433|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144957_PI430048170 0.0162327117944028 0.7966100251927971 0.2345602971998
10.1530302956692 10.0638393719312 P P P 10.3589527838311 10.5696436178274
10.5040605377087 P P P LNCV6_144957_PI430048170 mRNA
CTACCTCTCCTGTGCCTGCCACTCAATAAACAGTGTCTGCGCCCCACAGTTGTGAAAAAA NM_001170881 RefSeq
chr11 + 64284812 64289500 GPR137 56834 "G protein-coupled receptor 137, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143790_PI430048170 0.5075442676310320.9604424955951060.264809321255461
0.4382415666741620.298216916296058 A A A 0.4951981487304550.388663467989346
0.290770801759807 A A A LNCV6_143790_PI430048170 mRNA
ATTCAAGAACAAGCAATGATGACCCACTAAAGAGTGAATGCCATTTAGAATCTAGAAATG NM_001644 RefSeq chr12
- 7649399 7665903 APOBEC1 339 "apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1,
transcript variant 1"
GO:0006629|GO:0005515|GO:0010467|GO:0009972|GO:0003723|GO:0045471|GO:0010043|GO:0051607|GO:0005
737|GO:0042953|GO:0042127|GO:0080111|GO:0004126|GO:0017091|GO:0048255|GO:0010332|GO:0006397|GO:0
006396|GO:0032869|GO:0016556|GO:0042493|GO:0016554|GO:0006970|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_138986_PI430048170 0.2987519503069110.713071180869861 2.20536665352331
1.48891778650014 0.778405408824151 A A A 2.42463862586443 1.76005917100059
2.01906984829947 A A A LNCV6_138986_PI430048170 mRNA
GCCAGGGAGAGCCGCACAACATACAATTATATTTTTGGTAGTATTAAACAGTTTTGTATT NM_006942 RefSeq chr17
- 7588179 7590170 SOX15 6665 SRY (sex determining region Y)-box 15
GO:0006355|GO:0003700|GO:0046982|GO:0006357|GO:0006366|GO:0000981|GO:0014718|GO:0006325|GO:0070
318|GO:0005634|GO:0000122|GO:0003677|GO:0030154|GO:0045843|GO:0005737|GO:0045944|GO:0003682|GO:0
048627|GO:0043403|GO:2000288|GO:0008584 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90147_PI430048170 0.0600944245670377 1.10230309964838 0.540753725713121
0.5230806428929410.657832199319907 A A A 0.3795655153699130.443552903012104
0.478981638615851 A A A LNCV6_90147_PI430048170 mRNA
AGAATCGATACATAAATATCGTTGCCTATGATCATAGCAGGGTTAAGCTAGCACAGCTTG NM_002851 RefSeq chr7
+ 121873104 122062036 PTPRZ1 5803 "protein tyrosine phosphatase, receptor-type, Z polypeptide 1,
transcript variant 1"
GO:0005515|GO:0072534|GO:0048709|GO:0070445|GO:0005578|GO:0007409|GO:0007417|GO:0035335|GO:0006
470|GO:0002244|GO:0005001|GO:0005887|GO:0007611|GO:0004725 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133685_PI430048170 0.0249735753829661.26373516489263 12.6591215100599
12.8781623493341 12.8149253088919 P P P 12.4777944345373 12.4665354431626
12.4023727559852 P P P LNCV6_133685_PI430048170 mRNA
ATGGCAGGTGCCTAGGGGGTGTGGGGTTCCGTTCTCCCTTCCCCTCCCACTGAAGTTTGT NM_032843 RefSeq chr9
- 130902437 130938852 FIBCD1 84929 "fibrinogen C domain containing 1, transcript variant 1"
GO:0008061|GO:0016020|GO:0016021|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144195_PI430048170 0.319649943097073 1.02470226795009 0.34720775707819
0.3475208504472540.267767988865239 A A A 0.2837765870251670.296213496648732
0.278288385298918 A A A LNCV6_144195_PI430048170 mRNA
GGTCTTGTATCCGAAGCTTGAAGTAACCATGCCACCATTTATCATCAAATTTGAACCTTT NM_001304787 RefSeq
chr20 - 58459100 58514938 APCDD1L 164284 "adenomatosis polyposis coli down-regulated 1-like,
transcript variant 2" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129040_PI430048170 0.146653021671566 1.10740248447859 0.755904368397471
0.5580695458579050.744737914707576 A A A 0.4475945358463220.577446714322029
0.596075628363728 A A A LNCV6_129040_PI430048170 mRNA
CCACGTGAGTTATGTGCTTACAACGAGTCGTTTCTTTGCATTTTCCAACTTTCTTACATT NM_001024457 RefSeq chr2
+ 86917614 87013976 RGPD1 400966 RANBP2-like and GRIP domain containing 1 GO:0000042 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133868_PI430048170 0.989378930104275 0.979203960157242 0.81188076349666
0.8850564109119980.817407553362209 A A A 0.6231606328852071.26822327393643
0.613163545852843 A A A LNCV6_133868_PI430048170 mRNA
ATCAGCAAGATAAAAGTGAGTGTGTTTTGTCGGGAGGGAACTCCAGGGGAAGTGAGGGGA NM_178128 RefSeq
chr17 - 74877310 74893811 FADS6 283985 fatty acid desaturase 6
GO:0016491|GO:0006633|GO:0016021|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125586_PI430048170 0.332352705399334 0.898550625212139 5.26358220032852
5.38739608935583 5.42845224539744 P P P 5.73399224861979 5.36889991510979
5.41665894342501 P P P LNCV6_125586_PI430048170 mRNA
GAAGTGTATCTTCAGTGAACCATGTGCCAATTAAGCTGTAATAAAAAAGTGGTCTAGTCT NM_004580 RefSeq chr15
- 55202965 55270394 RAB27A 5873 "RAB27A, member RAS oncogene family, transcript variant 1"
GO:0005515|GO:0043316|GO:0009306|GO:0003924|GO:0032400|GO:0006605|GO:0006887|GO:0006886|GO:0005
764|GO:0032402|GO:0030425|GO:0006904|GO:0045921|GO:0050766|GO:0016324|GO:0071985|GO:0097278|GO:0
019882|GO:0032482|GO:0030141|GO:0070062|GO:0042470|GO:0043320|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_144590_PI430048170 0.0578935082201074 0.7312824574578198.2225814406474
8.03964097895438 8.2913289687553 P P P 8.40033533522307 8.62419571585148
8.85871516286896 P P P LNCV6_144590_PI430048170 mRNA
GTGTTCAGTAAAAGTATGCACTGTTAGATTACTGATAACGCGGATAGATTTTTGTTTACC NM_006029RefSeq chr14
- 73711782 73714425 PNMA1 9240 paraneoplastic Ma antigen 1
GO:0005515|GO:0002437|GO:0005737|GO:0043065|GO:0005730|GO:0005925 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145761_PI430048170 0.4791141582504151.02292274060869 0.374288710175269
0.2533420456323090.280007781366427A A A 0.2640169072038560.285203019481538
0.263035728303642A A A LNCV6_145761_PI430048170 mRNA
TGTCTTGTTTGGTAATAAACACATTCCAGTTGATGCCTTGCAGGGCATTCTTCAAAAGCA NM_006799RefSeq chr16
+ 2817162 2821722 PRSS21 10942 "protease, serine, 21 (testisin), transcript variant 1"
GO:0005515|GO:0005737|GO:0016020|GO:0005886|GO:0004252|GO:0006508|GO:0008236|GO:0031225|GO:0007
283 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63471_PI430048170 0.00481524917405489 0.5354850008132781 0.2515716640127
9.90800649931102 10.0176988351821 P P P 11.1928880602513 10.8197703537483 10.859668334317
P P P LNCV6_63471_PI430048170 mRNA
ACGCTAAGAAGTTTCAGACAAGCAGAGAGCTCTATTTTTAGAAGAAATATGTTACACTCA NM_014230RefSeq chr17
- 76038774 76072526 SRP68 6730 "signal recognition particle 68kDa, transcript variant 1"
GO:0005786|GO:0010467|GO:0005783|GO:0042493|GO:0030942|GO:0006614|GO:0008312|GO:0005730|GO:0045
047|GO:0006412|GO:0005829|GO:0005737|GO:0005840|GO:0005047|GO:0005048|GO:0044267|GO:0005925 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134826_PI430048170 0.6907434195317071.05860483584488 6.79035833734856
6.58961369774735 6.42286919835888 P P P 6.90676565681571 6.438003573758
6.12710782048427 P P P LNCV6_134826_PI430048170 mRNA
CTTTCTGATCAAGCCCTGCTTAAAGTTAAATAAAATAGAATGAATGATACCCCGGCAAAA NM_172089RefSeq chr17
+ 7549057 7561608 TNFSF12-TNFSF13 NA TNFSF12-TNFSF13 readthrough NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_133952_PI430048170 0.5263720323976890.5849044199826340.520049215964925
0.7028029136314920.614215278082831A A A 0.3693806778526542.34657112661381
0.559335013060494A A A LNCV6_133952_PI430048170 mRNA
TATTTATCTCTGAGGCATGGTGTGTGGTGCTACAGGGAATTTGTACGTTTATACCGCAGG NM_002478RefSeq chr11
+ 17719562 17722131 MYOD1 4654 myogenic differentiation 1
GO:0005515|GO:0000790|GO:0006366|GO:0003705|GO:0035257|GO:0005634|GO:0035914|GO:0030016|GO:0042
693|GO:0042692|GO:0005737|GO:0048743|GO:0000381|GO:0071392|GO:0045944|GO:0043503|GO:0043484|GO:0
031625|GO:0009267|GO:0005667|GO:0000977|GO:0046982|GO:0006357|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138181_PI430048170 0.0370099126262281.32075557894842 9.229925293978
9.03968013466699 8.88415596486283 P P P 8.67042758301064 8.74965688930183
8.54293595971909 P P P LNCV6_138181_PI430048170 mRNA
CAGCTCCATGCCTTTGTCTTTTTTAAATGTAATTAAAAAAGGAACCAACTGGCGTTTGTA NM_001136113 RefSeq
chr9 + 131502901 131523806 POMT1 10585 "protein-O-mannosyltransferase 1, transcript variant 4"
GO:0000030|GO:0001669|GO:0005783|GO:0005975|GO:0007275|GO:0035269|GO:0046872|GO:0004169|GO:0016
529|GO:0006493|GO:0030198|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77961_PI430048170 0.2319725812929231.45583589551178 3.14927229310804 2.85749046176036
3.76466108562011 P A P 2.18183373387949 3.10208354217355 2.86484784110421 A P P
LNCV6_77961_PI430048170 mRNA
TGGCTGTTTTTCAACCTGAAACTAGCACACTGCAAGGTCTCGAAGGTCGAGAGAATTTAG NM_007045RefSeq chr6

+ 166999316 167042418 FGFR1OP 11116 "FGFR1 oncogene partner, transcript variant 1"
GO:0005515|GO:0048471|GO:0005813|GO:0008284|GO:0030335|GO:0006996|GO:0034453|GO:0019901|GO:0030
307|GO:0061099|GO:0030292|GO:0005634|GO:0018108|GO:0042803|GO:0005829|GO:0000086|GO:0004713|GO:0
006469|GO:0000278. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130488_PI430048170 0.0554926156568675 1.28752392545833 12.3335036799657
12.503235382399 12.6635144832315 P P P 12.09279760055 12.1524244989068 12.17873113379
P P P LNCV6_130488_PI430048170 mRNA
CCATAAGGAGATTTCTGTTTTTCTTTTTGGCTGTTAATGCTTGTCTATAACATTGGAGCC NM_001545 RefSeq chr17 +
75012663 75021261 ICT1 3396 "immature colon carcinoma transcript 1, transcript variant 1"
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0005759|GO:0005743|GO:0016
150|GO:0004045|GO:0005762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128485_PI430048170 0.00061599863281734 0.3101579125561076.22796827574363
6.22934828677896 6.55626996727495 P P P 7.82350046290718 7.98838844948463
8.25986995483757 P P P LNCV6_128485_PI430048170 mRNA
CGGCCTTGGCATTTTCTGGCATTAATGTAGAAATAATGTTCCTATGATGACATATTTTCA NM_014181 RefSeq chr2
+ 64454192 64461383 LGALSL 29094 "lectin, galactoside-binding-like" GO:0005622|GO:0030246 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133053_PI430048170 0.6804445067815680.8711906322762052.17121334045832
3.04500315783807 2.74219629336323 A P A 2.68639123305794 3.41250332252905
2.38927929951421 A P A LNCV6_133053_PI430048170 mRNA
CATAATCAATAGCTACGTAATCAACTTCAGCAAGTTCCTAAGCTGTGGCCCTGGATCCCT NM_052971 RefSeq chr5
+ 132873665 132874890 LEAP2 116842 liver expressed antimicrobial peptide 2 GO:0005576|GO:0042742
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128604_PI430048170 0.1085272146001420.9362553933611470.266635623153043
0.2744122205605690.308586277476147 A A A 0.4465030993307820.361686211409476
0.324131349804012 A A A LNCV6_128604_PI430048170 mRNA
CTGTTTGAATCTTGTCTCACTAGTTTTTCCTGTGCAAAAATAAAATGGACAGAATTGCAG NM_000743 RefSeq chr15
- 78595304 78621295 CHRNA3 1136 "cholinergic receptor, nicotinic, alpha 3 (neuronal), transcript
variant 1"
GO:0030054|GO:0005886|GO:0007268|GO:0006940|GO:0060084|GO:0014056|GO:0030425|GO:0007171|GO:0034
220|GO:0015464|GO:0045211|GO:0042391|GO:0042166|GO:0043025|GO:0007626|GO:0006811|GO:0015276|GO:0
060079|GO:0014069|GO:0007271|GO:0005892|GO:0007399|GO:0035095|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_43649_PI430048170 0.0345264355777907 0.71269384942028 5.18773812600037
5.51747775086466 5.15055419334901 P P P 5.74811505379659 5.71106184959948
5.88557070394296 P P P LNCV6_43649_PI430048170 mRNA
TGAAAGAGGAGTCATGGCACATCCACTTCTTCGAGTACGGGCGTGGCGTGTGCATGTACC NM_198868 RefSeq chr5
- 179862070 179907856 TBC1D9B 23061 "TBC1 domain family, member 9B (with GRAM domain),
transcript variant 1" GO:0005515|GO:0005509|GO:0032851|GO:0016021|GO:0005097 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_62629_PI430048170 0.1553071193348991.09647886597658 11.3764644026777 11.4227113103803
11.245660646863 P P P 11.1612107355583 11.3243602158581 11.160157052061 P P P
LNCV6_62629_PI430048170 mRNA
CAAGACGGACAGTGTACATAAGAGTTTCTTGTTGCTTTACAATAAAACATGAGAACCTGC NM_004424 RefSeq chr16
+ 2223487 2235742 E4F1 1877 "E4F transcription factor 1, transcript variant 1"
GO:0005515|GO:0003700|GO:0016567|GO:0008283|GO:0035497|GO:0016874|GO:0010564|GO:0046872|GO:0009
794|GO:0005737|GO:0016032|GO:0000977|GO:0003714|GO:0003713|GO:0005819|GO:0000122|GO:0003677|GO:0
001227|GO:0006351|GO:0006260|GO:0071850|GO:0007067|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_130337_PI430048170 0.56733629912604 1.04555776856254 8.23160464817607 8.3508974981779
8.49309554981767 P P P 8.24787499332604 8.43016419292765 8.20671061433277 P P P
LNCV6_130337_PI430048170 mRNA
CCTGCAGGAGGCTGAGTGTAAAGAGTATCATTCATTGTTTCTCTATTAAATTATTTTCTC NM_001099436 RefSeq
chr15 - 74836115 74843211 ULK3 25989 "unc-51 like kinase 3, transcript variant 1"
GO:0005515|GO:0006914|GO:0045879|GO:0000407|GO:0005524|GO:0005829|GO:0045880|GO:0005737|GO:0046
777|GO:0016020|GO:0004674|GO:0010506|GO:0000045|GO:0034273|GO:0090398 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_82662_PI430048170 0.0199140484138724 0.626681095416297 4.31515717205623
4.19547280495853 3.85099839492746 P P P 4.65509227282435 4.76791349623381
4.98122856793796 P P P LNCV6_82662_PI430048170 mRNA
GCAACCAGAAAATAAGCTGGTACTAGTTAAACAATTGGATATCTTGGCTGCTGTACATGA NM_015092 RefSeq chr16
- 18804852 18926404 SMG1 23049 SMG1 phosphatidylinositol 3-kinase-related kinase
GO:0005515|GO:0010467|GO:0006950|GO:0005634|GO:0005524|GO:0046872|GO:0005829|GO:0046854|GO:0005
737|GO:0046777|GO:0004672|GO:0006406|GO:0000184|GO:0018105|GO:0000724|GO:0004674|GO:0046983 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141157_PI430048170 0.602954207115545 1.04875548286929 9.59835217729503 9.2993590736264
9.43428603344291 P P P 9.26054413328015 9.32239745796937 9.5430783944439 P P P
LNCV6_141157_PI430048170 mRNA
AGACAGAGTGGCTCTAACCACTGTGAGAAGCCCAAATAAAAATTGATCCCAAAAATGAAA NM_017787 RefSeq chr10
+ 102776130 102816264 WBP1L 54838 "WW domain binding protein 1-like, transcript variant 2"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131047_PI430048170 0.101258704877664 2.29917280430984 4.17360158956695
2.83664113503013 3.1198026959261 P A P 2.23643383788458 2.55676949904705
2.04979918847393 A A A LNCV6_131047_PI430048170 mRNA
AGGCTCCAAGACCTCATCAACAATTAAGAGCACCCCATCTGGGAAGAGGTATAAGTTTGT NM_001013254 RefSeq
chr11 + 1870868 1892263 LSP1 4046 "lymphocyte-specific protein 1, transcript variant 3"
GO:0007165|GO:0006968|GO:0016020|GO:0006935|GO:0005886|GO:0006928|GO:0003779|GO:0004871|GO:0015
629|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140277_PI430048170 0.486841654158296 0.884553249693182 3.41521687823824
3.67892130471436 3.17730753333018 P P P 3.86615660545373 3.64033583881439
3.28011135266141 P P P LNCV6_140277_PI430048170 mRNA
TTTTGTTTCGTGTGTTGTTTGTAAAGCTGCCATCCGACCAAGGTCTCCTGTGCTGAAGTT NM_002479 RefSeq chr1
- 203083128 203086038 MYOG 4656 myogenin (myogenic factor 4)
GO:0003700|GO:0008285|GO:0003705|GO:0010831|GO:0005634|GO:0035914|GO:0071158|GO:0042693|GO:0042
692|GO:0048743|GO:0032993|GO:0014878|GO:0071392|GO:0045944|GO:0042789|GO:0071285|GO:0014873|GO:0
005667|GO:0000977|GO:0046982|GO:0048741|GO:0014891|GO:0070888|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_96683_PI430048170 0.0445135995974143 0.8027391841326 6.37109272828411
6.17768084395369 6.21909473779554 P P P 6.73088242241893 6.53778620190567 6.4423290588429
P P P LNCV6_96683_PI430048170 mRNA
TTCTTTGCGTTTGAGCACAGTGAGGAGTACCAGCAGGCTCAGCACAAGTTCCTGGTGGCC NM_014972 RefSeq chr16
+ 89873585 89911384 TCF25 22980 transcription factor 25 (basic helix-loop-helix)
GO:0007507|GO:0005515|GO:0003700|GO:0005634|GO:0000122|GO:0003677|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127791_PI430048170 0.599885372399213 0.705991464300491 1.04626345660384
0.374885350241599 0.312528118763607 A A A 0.442470612368257 0.345113959547935
1.96045641563435 A A A LNCV6_127791_PI430048170 mRNA
ACTCAACCTGCCCGAAACCACCATCAAGGTGTGGTTCCAGAACCGGCGCATGAAGGACAA NM_001080458

RefSeq chr2 - 176080106 176083962 EVX2 NA even-skipped homeobox 2 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_136000_PI430048170 0.4859367285528310.9051879186353299.5406018184384
9.33849606192556 9.21038042168287 P P P 9.62091054668376 9.66756025159466
9.20884809471974 P P P LNCV6_136000_PI430048170 mRNA
TTTGCAATAGATGTAAATAGGACCAATAAATCCTTTGGAAGAGCCATGGGGTGAACTGAG NM_001163809 RefSeq
chr17_KI270861v1_alt + 154866 168638 WDR81 124997 "WD repeat domain 81, transcript variant 1"
GO:0010923|GO:0008152|GO:0016772 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137065_PI430048170 0.2144863676863810.7352090647465343.39958155395644
3.98874209050367 4.04151825157904 P P P 3.83282606170397 4.55829171959532
4.36003002049749 P P P LNCV6_137065_PI430048170 mRNA
TTTTAAGAAAACAATCAAAACAAGCATTGGGGGATTGGGGCAAGGATGGAAGGAGCAGTG NM_001171816
RefSeq chr16 - 88696494 88703617 RNF166 115992 "ring finger protein 166, transcript variant 3"
GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142544_PI430048170 0.0653188310745644 1.53234133426469 7.23188820293246
7.44205687806456 7.82873618631724 P P P 6.796526375423 6.96337724744957
6.95407854365856 P P P LNCV6_142544_PI430048170 mRNA
CCGGGTTCTTAGATTTTGTTAGACTTTTTAAACTCAAGGATGAGCATAAGTGCTTGAAAT NM_002787RefSeq chr7
- 42916860 42932206 PSMA2 5683 "proteasome (prosome, macropain) subunit, alpha type, 2"
GO:0005515|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0004
298|GO:0034641|GO:0000082|GO:0000932|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0
005839|GO:0000502|GO:0043066|GO:0006521|GO:0051437|GO:0042590|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135408_PI430048170 0.00807464230298345 0.5558799335956192.77109888756002
2.42391462613444 2.80485056687731 A A A 3.28739038640813 3.54275743714533
3.71007041412647 P P P LNCV6_135408_PI430048170 mRNA
CCTCAGCTCAGAGTGTATTTTGAATATGAGCAAATGTTTATGTACGTATGAGATTTCAAG NM_020776RefSeq chr18
+ 36829116 37225325 KIAA1328 57536 KIAA1328 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140688_PI430048170 0.1614600317551591.20646937574394 5.84422820745281
5.74674164106411 5.77704178600505 P P P 5.25651894666301 5.55931442259772
5.70583708003535 P P P LNCV6_140688_PI430048170 mRNA
GTGACACTTTGGAGCAAAAACCTTGCAGTGGTAAATAAAAAATTTCCAACAGGGAAAAAA NM_001247987 RefSeq
chr11 - 45240301 45286333 SYT13 57586 "synaptotagmin XIII, transcript variant 2"
GO:0030133|GO:0005887|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99295_PI430048170 0.5462342567994930.8367089707813011.07039150338228 0.293979944632183
0.406193234170027 A A A 1.04712967197384 0.2727020617597731.19184423510148 A A A
LNCV6_99295_PI430048170 mRNA
TCAGAGAGGGGTTGACGAAGGAGAAGCATTCAGAGGGCACTGGCTTCTGGACAGCAATGA NM_031941RefSeq
chr19 - 17250039 17264735 USHBP183878 "Usher syndrome 1C binding protein 1, transcript variant 1"
GO:0005515|GO:0030165 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130428_PI430048170 4.76118180648955e-05 0.3239347018293173.28699508564824
3.19324583908334 3.18902351562217 P P P 4.75153531139891 4.86843177580571
4.92474102015464 P P P LNCV6_130428_PI430048170 mRNA
GACATAGCATGTACAGGCAGTTTTCTGTCCTGTGCACAAAAAGTTTAAAAAAGTTGTTTA NM_004114RefSeq chrX
- 138631572 138711665 FGF13 2258 "fibroblast growth factor 13, transcript variant 1"
GO:0005515|GO:0008017|GO:0043005|GO:0030424|GO:0005886|GO:0007267|GO:0005634|GO:0030175|GO:0048
671|GO:0030425|GO:0030426|GO:0005737|GO:0021795|GO:0014704|GO:0000165|GO:0045860|GO:0007613|GO:0
007612|GO:0005874|GO:0048487|GO:0005730|GO:0005576|GO:0045200|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_141011_PI430048170 0.00129461646109389 0.4238832707720976.4631284292559
6.18824292005942 6.57228099146746 P P P 7.52533887841254 7.58870501758326
7.83248129814076 P P P LNCV6_141011_PI430048170 mRNA
CCAACCTTGTCAAATTAATAGTCCTGAGCAAGCAAGAAAAAGAGGTAATAACATACCCAT NM_001127192 RefSeq
chr3 - 129167814 129183967 CNBP 7555 "CCHC-type zinc finger, nucleic acid binding protein,
transcript variant 1"
GO:0005515|GO:0006695|GO:0003727|GO:0006355|GO:0008284|GO:0003700|GO:0005783|GO:0005634|GO:0006
351|GO:0005829|GO:0003697|GO:0045944|GO:0008270|GO:0045893 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139834_PI430048170 0.5834021225924810.9799715657231950.471284764219209
0.4770369085783220.378203630477295A A A 0.3988738634668740.516301976034282
0.498280997835284A A A LNCV6_139834_PI430048170 mRNA
CTTTGTGTGCGGTGAATATGTATGATACTTGTTTTCTTTTTCATGCTCACCTATCAATTC NM_173667RefSeq chr5 +
61637780 61706535 C5orf64 285668 "chromosome 5 open reading frame 64, transcript variant 1"
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56840_PI430048170 0.2747168547982980.9021013071669374.53018563372337 4.48425136778926
4.31772529947928 P P P 4.71591176094937 4.40880740358247 4.64433335437558 P P P
LNCV6_56840_PI430048170 mRNA
CTAAAGAAAAAGATCCCAAAGTACCATCAGCCAAGGAAAGAGAAAAGGAGGCAAAAGCCT NM_007373RefSeq
chr10 + 110919542 111013667 SHOC2 8036 "soc-2 suppressor of clear homolog (C. elegans), transcript
variant 1"
GO:0050790|GO:0005737|GO:0019888|GO:0008543|GO:0019903|GO:0000164|GO:0046579|GO:0007265|GO:0005
654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101355_PI430048170 0.0248940252436372 0.5968518223167728.05115908254319
7.69929030638055 7.50588246318492 P P P 8.66157153417638 8.39164665698785 8.4771958497472
P P P LNCV6_101355_PI430048170 mRNA
AAACGTTTCTCCCAGCGCAAGAACCTCTCCCAGCACCAGGTCATCCATACAGGGGAGAAG NM_138447RefSeq chr16
- 30602557 30610386 ZNF689 115509 "zinc finger protein 689, transcript variant 1"
GO:0006355|GO:0005634|GO:0035914|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_80608_PI430048170 0.0280759544224151.70647334099681 11.0380417231203 11.1965438315322
11.6211832863412 P P P 10.561082967973 10.3082341047722 10.7097538694937 P P P
LNCV6_80608_PI430048170 mRNA
CTAATCATCGAATTTAAGGTAAACTTTCCTGAGAATGGCTTTCTCTCTCCTGATAAACTG NM_001539RefSeq chr9
+ 33025210 33039064 DNAJA1 3301 "DnaJ (Hsp40) homolog, subfamily A, member 1"
GO:0006986|GO:0005515|GO:0048471|GO:0009408|GO:0051087|GO:0000151|GO:0005634|GO:0007283|GO:0046
872|GO:0005829|GO:0005739|GO:0042026|GO:0006457|GO:0042769|GO:0031397|GO:0043508|GO:0031625|GO:0
070062|GO:0043066|GO:0001664|GO:0043065|GO:0030317|GO:0005524|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93502_PI430048170 0.4279210645722350.4984321670918291.32699056390333 0.971119105433954
1.41146448206201 A A A 3.24862528004132 1.00426382986719 1.48169840046545 P A A
LNCV6_93502_PI430048170 mRNA
TTGGAGCAGAATATGGAAAGCAAGGATCTTTTTCATGTTGAACAAAGACAGTACATTGAT NM_001135597 RefSeq
chr2 - 55287841 55419921 CCDC88A 55704 "coiled-coil domain containing 88A, transcript variant
1"
GO:0031929|GO:0008017|GO:0005794|GO:0005886|GO:0005783|GO:0030032|GO:0003779|GO:0031410|GO:0043
422|GO:0042803|GO:0030027|GO:0005829|GO:0006260|GO:0016020|GO:0016477|GO:0042127|GO:0032956|GO:0
010975|GO:0032148|GO:0061024|GO:0016023|GO:0001932|GO:0035091|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_142423_PI430048170 0.0711027164051621 0.76925531957342210.1947965731246
9.96944003078446 9.76178817176894 P P P 10.4486614729588 10.4312693248905
10.2010087743572 P P P LNCV6_142423_PI430048170 mRNA
GGTGGGCTTTAGTTTAGTCCCAGAAATGGAGAAAAAATAAAAACTCACGTTGTTCTAATG NM_001136108 RefSeq
chr8 + 23288091 23296279 R3HCC1203069 "R3H domain and coiled-coil containing 1, transcript variant
1" GO:0000166|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133748_PI430048170 0.0428325671334932 0.8020003492717185.9099623074763
5.69174510084333 5.63849692705519 P P P 6.10129905155032 6.16385614146625
5.93500199669299 P P P LNCV6_133748_PI430048170 mRNA
GTGCTGTTCCTGGACATGAAGCCGCACAAGGAACGTTTTATTCCTAAGAAAAAGTTTCCT NM_001287045 RefSeq
chr9 - 129007792 129028353 SH3GLB2 56904 "SH3-domain GRB2-like endophilin B2, transcript
variant 1" GO:0005515|GO:0005737|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140900_PI430048170 0.0708122745522023 0.9091144046957421 2.0213748093212
12.0577066969219 11.9385146749093 P P P 12.2176717954567 12.0698056979458
12.1412994114645 P P P LNCV6_140900_PI430048170 mRNA
GAGTGGCCAGCAGAGGTCACGAATAAACTGCATCTCTGCGCCTGGCTCTCTACCAAAAAA NM_000709RefSeq chr19
+ 41397788 41425005 BCKDHA 593 "branched chain keto acid dehydrogenase E1, alpha polypeptide,
transcript variant 1"
GO:0005739|GO:0005515|GO:0003863|GO:0034641|GO:0005759|GO:0016831|GO:0005947|GO:0009083|GO:0044
281|GO:0046872|GO:0003826|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135174_PI430048170 0.8399200839554740.8432403595348711.38356486553114
0.3846316501504970.412786221427367A A A 0.31442976915705 1.87596061796101
0.386419738260527A A A LNCV6_135174_PI430048170 mRNA
GTGCTGAATTAAGTCTTCACAAACAACACATAAAGATCCAGACATTAGGACTGTATACCT NM_001142733 RefSeq
chr3 - 57268350 57292682 ASB14 142686 "ankyrin repeat and SOCS box containing 14, transcript
variant 1" GO:0035556|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131350_PI430048170 0.0222657079689252 0.3678105423661510.310260712026357
0.3165086686698260.414554295866138A A A 1.43019096385588 1.65170047572679
2.18391235233272 A A A LNCV6_131350_PI430048170 mRNA
TGGGGAAACAAGAAGCTAAAGCAGACTTATCTTTCAGTTTTGTGGCAAATGAGGTACTGA NM_176886RefSeq
chr12_GL877876v1_alt - 327524 328424 TAS2R45 259291 "taste receptor, type 2, member 45"
GO:0033038|GO:0007186|GO:0005886|GO:0016021|GO:0001580 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_67059_PI430048170 0.0829943086168903 0.7868467341926528.39615163813962
8.39164665698785 8.32994773665577 P P P 8.49949154636435 8.85284750707489
8.78027810661112 P P P LNCV6_67059_PI430048170 mRNA
CTGGAATTGTGGCTATCCTGATTATAGGATTTTAACTTAACTGAAATGCCTGCTTTGAAT NM_005479RefSeq chr10
+ 97319264 97321915 FRAT1 10023 frequently rearranged in advanced T-cell lymphomas 1
GO:0000578|GO:0090263|GO:0016055|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94401_PI430048170 8.11746346972421e-05 3.23980686583656 7.51799909057878
7.54181526639465 7.53708752293914 P P P 5.88597065249581 5.80139529110911
5.82055312089831 P P P LNCV6_94401_PI430048170 mRNA
ACTGCGAGAACTGCAAGACCACTTTGGGCTGGAAATATGAACAGGCCTTTGAGAGCAGCCNM_031477RefSeq chr16
- 30092313 30096200 YPEL3 83719 "yippee-like 3 (Drosophila), transcript variant 1" GO:0005730 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67603_PI430048170 0.190330006059516 1.07137546081729 0.513196955004885 0.636430198849774
0.600333195167769A A A 0.58406807319291 0.427715041199481 0.437163807140073A A A

LNCV6_67603_PI430048170 mRNA
CTTTAGGAGATTCTGGCTCAATTATTAGTCGGACAGCAAAAGTTGCAGTAGCAGAAAAGA NM_005215 RefSeq chr18
+ 52340171 53535903 DCC 1630 DCC netrin 1 receptor
GO:0005515|GO:0030424|GO:0005886|GO:0021965|GO:0007409|GO:0033563|GO:0048671|GO:0005829|GO:0033
564|GO:0042802|GO:0005042|GO:0038007|GO:0007411|GO:0070374|GO:2000171|GO:0043065|GO:0003713|GO:0
006915|GO:0032584|GO:0097190|GO:0001975|GO:0010976|GO:0010977|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145455_PI430048170 0.42258243210247 0.9774998464897760.273945461419157
0.2869513690631960.374258287346932A A A 0.3763691106949050.314234886055377
0.34445312026009 A A A LNCV6_145455_PI430048170 mRNA
GGATCTGGTTATTGATACTTTAATAAATGTGGTGTAAAGAAAATCCATGGCTACAGTCTG NM_001005473 RefSeq
chr5 - 41306945 41510628 PLCXD3 345557 "phosphatidylinositol-specific phospholipase C, X domain
containing 3" GO:0016042|GO:0007165|GO:0008081|GO:0004871 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_100161_PI430048170 0.9803081559810641.00110446818275 0.365112991484569
0.3395797625759430.25849062328961 A A A 0.3159233917552940.331424063229876
0.313126647934745A A A LNCV6_100161_PI430048170 mRNA
CCTGGAAAGGAACACTTTGAACGTGTTTTGGAAGAATATTCACATCAAGTCAAAGATTTA NM_001042784 RefSeq
chr4 - 76313038 76407305 CCDC158 339965 coiled-coil domain containing 158 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126691_PI430048170 0.00157326989828529 0.5741558304639486.51664416592728
6.26904349770513 6.47875061257637 P P P 7.11500479617423 7.24741646844704
7.30884790377525 P P P LNCV6_126691_PI430048170 mRNA
CCCTTTGATCAATATGGCTTTTTTCCAAATTGGCTAATGGATCAAAATGAAACCTGTTGA NM_012207 RefSeq chr10
+ 68332010 68343196 HNRNPH3 3189 "heterogeneous nuclear ribonucleoprotein H3 (2H9), transcript
variant 2H9"
GO:0008380|GO:0005515|GO:0006396|GO:0000166|GO:0000398|GO:0003723|GO:0030855|GO:0005681|GO:0005
654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130795_PI430048170 0.1746733704815910.7880257843711410.2818767920327
0.3148350757249210.371277823336676A A A 0.7849658226796590.833358215057965
0.330944051900945A A A LNCV6_130795_PI430048170 mRNA
TGTGAAGCAGATGTTTTTGTCCGGAAATAAAAATAATAGTCTTGGAGTCTCGCCACCAAA NM_022842 RefSeq chr3
- 45082273 45146422 CDCP1 64866 "CUB domain containing protein 1, transcript variant 1"
GO:0005886|GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140942_PI430048170 0.1885039784087590.6980458770245644.46127555926556
4.28410604730229 4.20807681996069 P P P 4.33267499829103 5.19271305019536
4.86895783773807 P P P LNCV6_140942_PI430048170 mRNA
GTTTTTCTGTCAGCAGACAAAATCAGCCTAACAGCAAAGGCTCTTTTCAGAGCCACCTAC NM_003513 RefSeq chr6
- 26033091 26033568 HIST1H2AB 8335 "histone cluster 1, H2ab"
GO:0008150|GO:0046982|GO:0005634|GO:0000786|GO:0003677|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127366_PI430048170 0.8064210869245291.01841647438239 11.0892253528063
11.2832145543736 11.0388453898543 P P P 11.2232509799562 11.0835663074753
11.0302346766994 P P P LNCV6_127366_PI430048170 mRNA
TATATTGTCATTTTATAACACTCTAGCCCCTGCCCTTATTGGGGGACAGATGGTCCCTGT NM_001014831 RefSeq
chr19 + 39125779 39179406 PAK4 10298 "p21 protein (Cdc42/Rac)-activated kinase 4, transcript
variant 2"
GO:0023014|GO:0005515|GO:0005794|GO:0008283|GO:0006915|GO:0006928|GO:0005524|GO:0035556|GO:0007
165|GO:0004672|GO:0016477|GO:0004702|GO:0007010|GO:0016049|GO:0006468|GO:0000278|GO:0005925 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137375_PI430048170 0.5296076040122361.11607980205127 8.58177472056247
8.81359416307076 9.14695088307942 P P P 8.50659043864001 8.54885741360074
9.01173029362941 P P P LNCV6_137375_PI430048170 mRNA
GGAGTGATGTTTCATTTACCTGGGTTGTGTTAATGACTGAATGTTGACAATAAATCTGTT NM_005513RefSeq chr3
+ 120742710 120783069 GTF2E1 2960 "general transcription factor IIE, polypeptide 1, alpha 56kDa"
GO:0043565|GO:0005515|GO:0010467|GO:0006368|GO:0006355|GO:0006367|GO:0006366|GO:0016032|GO:0005
654|GO:0045111|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132295_PI430048170 0.47071863955195 1.17852397237505 1.55711236241851
1.40205405727085 1.41473035287896 A A A 1.73940665975481 1.19132481381069
0.463588804037003A A A LNCV6_132295_PI430048170 mRNA
AGTCAGAGAAGCTATCTCAATACTTGGTTTGCCGGCTGGCTGTAGCCCAATGATGTAATT NM_014481RefSeq chrX
+ 55000322 55007873 APEX2 27301 "APEX nuclease (apurinic/apyrimidinic endonuclease) 2, transcript
variant 1"
GO:0003906|GO:0008311|GO:0005730|GO:0005743|GO:0005634|GO:0006310|GO:0003677|GO:0043231|GO:0007
049|GO:0006284|GO:0008270|GO:0000737|GO:0000738 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140595_PI430048170 0.1022996091611480.7221878268684855.48340574644475
4.92775481557787 5.44286743451896 P P P 5.63635094167829 5.63346724821839
6.02105995372688 P P P LNCV6_140595_PI430048170 mRNA
TCTCGGCCTTTTACTCAGACAAGTAGCATCTCATTAAACCCATTCATTTAGCATTCATAA NM_001257097 RefSeq
chr12 + 2877198 2889525 RHNO1 83695 "RAD9-HUS1-RAD1 interacting nuclear orphan 1, transcript
variant 4"
GO:0005515|GO:0034644|GO:0005694|GO:0070318|GO:0005634|GO:0000725|GO:0000077|GO:0071479 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109208_PI430048170 0.0741741159135468 0.8225028457265847.64593673823965
7.6147363423522 7.90991107985374 P P P 8.03101926165892 7.92793910833928
8.07213483778532 P P P LNCV6_109208_PI430048170 mRNA
AAACTTTCACCAGCGATTTGAATCTCCAGAATCACAGGCATCTGCCGAACAGCCTGAAAT NM_004896RefSeq chr10
+ 69124151 69172860 VPS26A 9559 "vacuolar protein sorting 26 homolog A (S. pombe), transcript
variant 1"
GO:0005515|GO:0008565|GO:0042147|GO:0031982|GO:0006886|GO:0010008|GO:0005769|GO:0070062|GO:0043
231|GO:0030904|GO:0005829|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135589_PI430048170 0.2865400441690330.9358831188272995.75861867442313
5.65667612419085 5.81372809906263 P P P 5.85883500018695 5.72352657100218
5.93025340171728 P P P LNCV6_135589_PI430048170 mRNA
CACCTTTGGAACGGAATTCTTTATCAATAAAGTTTCACAATCCGTCCCTCTTCCAAAAAA NM_001287060 RefSeq
chr7 + 66682090 66811461 RABGEF1 27342 "RAB guanine nucleotide exchange factor (GEF) 1,
transcript variant 1"
GO:0043305|GO:0005515|GO:0017112|GO:0004842|GO:0017137|GO:0016567|GO:0032851|GO:1900235|GO:0003
677|GO:0031982|GO:0006897|GO:0046580|GO:1900165|GO:0050728|GO:0048261|GO:0002686|GO:0006612|GO:0
001933|GO:0008270|GO:0055037|GO:0060368|GO:0005769 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_134011_PI430048170 0.0129948453490228 0.8697405653335171 4.350248829694
14.2588790745633 14.2341057605247 P P P 14.4363141000323 14.4717527867978
14.5398792313611 P P P LNCV6_134011_PI430048170 mRNA
ACCAGTGGATGCCCAGGATCTTTTACCACAACCCCTCTGTAATAAAAGAGATTTGACACT NM_198426RefSeq chr19
- 58551565 58555003 CHMP2A 27243 "charged multivesicular body protein 2A, transcript variant 1"
GO:0005515|GO:0006997|GO:0019904|GO:0019058|GO:0010824|GO:0015031|GO:0045184|GO:0005829|GO:0050
792|GO:0000920|GO:0007034|GO:0016020|GO:0031902|GO:0016197|GO:0060548|GO:0061024|GO:0016032|GO:0

007080|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134148_PI430048170 0.8856723724144740.9785528355685261 1.3079841912347
11.2828123697117 11.241623721767 P P P 11.4504091627403 11.046763647911 11.397474987501
P P P LNCV6_134148_PI430048170 mRNA
TGTTAAACTACAAAACTGTACAGCCTATTTTAGTGTGGACTATTAAAACCCTTGCACTGT NM_175887RefSeq chr7
+ 29563810 29567295 PRR15 222171 proline rich 15 GO:0007275 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140994_PI430048170 0.9438491808600311.02471387744873 2.67261964953556
3.33538744845702 3.21929645311503 A P P 2.97528411316626 2.90094220443257
3.29687326943404 P P P LNCV6_140994_PI430048170 mRNA
TCATTGTCATTAAAATCATACAGGATAGTAATTCCTTTCCATCTGCTACCATGCCTAGCC NM_001145191 RefSeq
chr4 + 15681728 15690447 FAM200B 285550 "family with sequence similarity 200, member B"
GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141345_PI430048170 0.00175778871488754 0.4801821592550826.3836568353776
6.159641765219 6.38467468959219 P P P 7.31005089210588 7.39917237583499
7.40331686813148 P P P LNCV6_141345_PI430048170 mRNA
GACTAGAAACTTCAGAAAGACAAAACTGTTTGCCATTTTTACTGGCAGATAAGAGGAAAA NM_032860RefSeq chr6
+ 143843370 143863806 LTV1 84946 LTV1 ribosome biogenesis factorGO:0005737|GO:0005654 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133718_PI430048170 0.6622873319142750.9771165112914070.383335468291871
0.2830287037226720.330912748954206A A A 0.2885275213727970.479102913960947
0.324395396901587A A A LNCV6_133718_PI430048170 mRNA
AATGATTCCTTCTACTAAATGCAGGCAAGGAGTAGGACCTCACAGGAAAGATAAGTGGCA NM_003967RefSeq chr6
- 132588591 132589738 TAAR5 9038 trace amine associated receptor 5
GO:0007165|GO:0007186|GO:0005887|GO:0004930|GO:0007606|GO:0007268|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129775_PI430048170 0.7724515649389471.38556983419502 2.29894946426881
0.3115281676908280.46148900792289 A A A 0.7593946294341021.3215525605864
0.320700031233569A A A LNCV6_129775_PI430048170 mRNA
CACTGTTTCTCTGCTGTTGCAAATACATGGATAACACATTTGATTCTGTGTGTTTTCATA NM_002984RefSeq
chr17_KI270909v1_alt + 57923 59718 CCL4 NA chemokine (C-C motif) ligand 4 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136125_PI430048170 0.0430790664711062 1.26002654272384 6.82449732246008
6.64444134842137 6.8928942015142 P P P 6.46142719554082 6.43248600096201
6.47845819828923 P P P LNCV6_136125_PI430048170 mRNA
TTAATTTGTGGGAAGGAGTAGGCAAAGAATATGCTTACATGATTACACCTGTAAAGTAAG NM_000692RefSeq chr9
+ 38392663 38398665 ALDH1B1 219 "aldehyde dehydrogenase 1 family, member B1"
GO:0005739|GO:0005975|GO:0005759|GO:0006068|GO:0004029|GO:0005654|GO:0055114|GO:0043231 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141766_PI430048170 0.1852442949126871.04483645879924 0.351491609556288
0.3397955332910130.442953312774687A A A 0.3080498674788410.293670371929933
0.344440166656017A A A LNCV6_141766_PI430048170 mRNA
CTTCCTTAGTGTGACATTCCAATCATTTAGTATTTTAGGACCTGTGAATAACTTCCAACA NM_001004441 RefSeq
chr5 - 80556754 80570485 ANKRD34B 340120 ankyrin repeat domain 34B GO:0005737|GO:0005634
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128860_PI430048170 0.6814079879316480.9315430385078188.17926188784995
8.04909306906665 8.48524325831052 P P P 8.15696502963407 8.17171323531736
8.66677268484997 P P P LNCV6_128860_PI430048170 mRNA
TAGGAGGACAGTTTTAATGATTGTACTTGCATGAACACAATCATATGATGGTAAAGCAGA NM_006364RefSeq chr14

- 39031918 39103233 SEC23A 10484 Sec23 homolog A (S. cerevisiae)
GO:0005515|GO:0002474|GO:0012507|GO:0048471|GO:0030127|GO:0005783|GO:0048208|GO:0044281|GO:0006886|GO:0005829|GO:0006888|GO:0019886|GO:0000139|GO:0030868|GO:0005789|GO:0061024|GO:0008270|GO:0016192|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145725_PI430048170 0.0724397503881033 0.147311425993701 0.375448751029845
0.2879827135780010.279231628887528A A A 2.26022964685034 4.08439612020011
1.83900264516711 A P A LNCV6_145725_PI430048170 mRNA
TGAGGACTGGTCTGAATTCTTCAAAGGTTTCAGCTGTATTAACATTCTCCATCTAATAAA NM_001531RefSeq chr1
+ 181033424 181061938 MR1 3140 "major histocompatibility complex, class I-related, transcript variant 1"
GO:0002367|GO:0002474|GO:0005886|GO:0005783|GO:0042612|GO:0005576|GO:0003823|GO:0050829|GO:0007165|GO:0006955|GO:0019882|GO:0045087|GO:0001916|GO:0042605|GO:0032611|GO:0005789|GO:0016021|GO:0032620|GO:0032393. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108754_PI430048170 0.411471740893274 0.929915335770843 5.28136386955713
5.48003618162603 5.48968443235694 P P P 5.55372312843441 5.65241617496701
5.35290979814541 P P P LNCV6_108754_PI430048170 mRNA
TGTCCTGGAGCTACTTCTCACCAACTGTGGTCAGTGCAGGGGGAACGAGGAGGTCTTTTG NM_002360RefSeq chr7
+ 1530731 1543043 MAFK 7975 v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog K GO:0001221|GO:0006355|GO:0000976|GO:0003700|GO:0007596|GO:0005654|GO:0006351|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131018_PI430048170 0.115539493195731 0.464620041394118 1.34390010240037
0.2800850112766661.17892440488383 A A A 1.31172688441119 1.95848296173528
2.71826962684893 A A P LNCV6_131018_PI430048170 mRNA
GCTATTTCTGTAATGTGTATTTTTCTCCCCTTGGTAAAGGGCAATAAAACCATTACACAA NM_020829RefSeq chr9
+ 5629118 5776556 RIC1 57589 "RAB6A GEF complex partner 1, transcript variant 1"
GO:0005515|GO:0043234|GO:0017112|GO:0017137|GO:0016020|GO:0034066|GO:0042147|GO:0032851|GO:0016021|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145640_PI430048170 0.290512024378984 1.32425341274997 0.482647823140827
1.18983225323305 0.389829997003254A A A 0.2827266746052430.347011675303133
0.354841302867424A A A LNCV6_145640_PI430048170 mRNA
TAGCTCTTGCAAATCAGTGAGAAGAGAGTAACGCCACATATTTTAAACAGGCAAAAATAT NM_207398RefSeq chr1
- 89131750 89176040 GBP7 388646 guanylate binding protein 7
GO:0016020|GO:0008152|GO:0003924|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104784_PI430048170 0.0791961148718227 0.614321705803923 4.94628310611453
5.07375176647782 5.2567637971445 P P P 5.42378964095071 5.68666789811251
6.18612067902445 P P P LNCV6_104784_PI430048170 mRNA
GACACAAATGTAAGCAGAGATTCACCAAGATCACCCAATACCTAATTCGAATTAGAAAAC NM_032509RefSeq chr8
+ 33485166 33501260 MAK16 84549 MAK16 homolog (S. cerevisiae) GO:0005730|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108866_PI430048170 0.145232568032855 0.487814730098322 0.391630811377274
1.93029484323108 1.97305533441474 A A A 2.77032604085259 2.6507518474167
2.44570176668385 P P P LNCV6_108866_PI430048170 mRNA
AACAATAAGCGTGTTGCAGTCAATGTATTAAGCAAAGCAAACCTGCCAGCCAGCAAATTC NM_001170704 RefSeq
chrX - 132369314 132489968 MBNL3 55796 "muscleblind-like splicing regulator 3, transcript variant 6"
GO:0008380|GO:0006397|GO:0005737|GO:0043484|GO:0007275|GO:0005634|GO:0046872|GO:0045662 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134876_PI430048170 0.57996953429765 1.18353299365683 1.46722834605868
0.4694590073105910.899247698968885A A A 0.2727124713086850.45619618163354
1.32302057072946 A A A LNCV6_134876_PI430048170 mRNA

GTGATAATTTCTATCTACCTCATAAATCTTTACATTTCCTTCTGCAACAGGCCCTCTTCC NM_001039111 RefSeq chr3 + 32818017 32892279 TRIM71 131405 "tripartite motif containing 71, E3 ubiquitin protein ligase" GO:2000177|GO:0004842|GO:0016874|GO:2000637|GO:0072089|GO:0001843|GO:0010586|GO:0051865|GO:0060964|GO:0035278|GO:0000082|GO:0035198|GO:0000932|GO:0008543|GO:0021915|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136388_PI430048170 0.5047565929614031.25543348848024 2.34603761991248 3.35169696666393 2.83857066096908 A P A 2.54623781994126 1.53019928688737 3.19371180066893 P A P LNCV6_136388_PI430048170 mRNA
GGTTTCCTTCAGCAATTCCAAATTTTCCTTCAGCCTTTCTGGATTTCACAGATTTATAAA NM_152549RefSeq chr5 - 115267187 115296290 CCDC112 153733 "coiled-coil domain containing 112, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134146_PI430048170 0.0722927725600802 1.0415332723239 0.435434710545074 0.4479088673702680.393669167068639A A A 0.3328738590875550.375317514431997 0.392599339063257A A A LNCV6_134146_PI430048170 mRNA
AACCAGAACTGGCTACCAGCTTCAGAAATGTGTTACTTATGTTCAAGTAATTTGTTATAG NM_182548RefSeq chr6 + 35805293 35824075 LHFPL5 222662 lipoma HMGIC fusion partner-like 5 GO:0016324|GO:0050910|GO:0060088|GO:0016021|GO:0032426|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54840_PI430048170 0.1928390550443680.8703317761407 5.7671886982054 5.80563825333688 5.59627981925613 P P P 6.10623157324575 5.75487815133197 5.8957632471145 P P P LNCV6_54840_PI430048170 mRNA
TATGTGACCTCACCATCCGGACGCAGGGCCTTGAATACCGCACCCACAGGGCTGTGCTAG NM_001252406 RefSeq chr1 + 155002629 155018525 ZBTB7B 51043 "zinc finger and BTB domain containing 7B, transcript variant 3" GO:0006355|GO:0006366|GO:0007275|GO:0005654|GO:0005634|GO:0007398|GO:0003677|GO:0046872|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127120_PI430048170 0.1418596727616540.8247387568378016.78117103602233 6.54663400549317 6.3894448325682 P P P 6.65165063219395 6.92056252972329 6.98493557157441 P P P LNCV6_127120_PI430048170 mRNA
GTTCCTGTAGAAAACGAACTGTAAAAGACCATGCAAGAGGCAAAATAAAACTTGAAGTGANM_012215RefSeq chr10 - 101784442 101818465 MGEA5 10724 "meningioma expressed antigen 5 (hyaluronidase), transcript variant 1" GO:0060124|GO:0046060|GO:0010524|GO:0005634|GO:0005829|GO:0010616|GO:0051901|GO:0043243|GO:0006612|GO:0046326|GO:0032024|GO:0004402|GO:0016231|GO:0070265|GO:0051054|GO:0060051|GO:0016573|GO:0007568|GO:0006044|GO:0048545|GO:0045862|GO:0031343|GO:0016020|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143672_PI430048170 0.6041302758494020.9533533420019494.75635598804616 5.00831506956504 5.10957361841661 P P P 5.08567434711634 4.88518451723838 5.12160230920132 P P P LNCV6_143672_PI430048170 mRNA
GGAAAACTGGATTTGTCGAAAACTAATTGTGCCCATTTTCTCACATTTTTGATCCATTGG NM_017774RefSeq chr6 + 20534456 21232403 CDKAL154901 CDK5 regulatory subunit associated protein 1-like 1 GO:0005791|GO:0008150|GO:0003674|GO:0051539|GO:0016020|GO:0035600|GO:0005789|GO:0035598|GO:0016021|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126911_PI430048170 0.5805297269295361.38011054588473 1.72501733744698 0.3078725349094021.84335452030819 A A A 1.1261781863213 0.795393067359122 0.981156582877679A A A LNCV6_126911_PI430048170 mRNA
TCTTTGGCTGTTGTAATTATCTGGGGTTTGTACTGTACATATCCGGGGTGTGTGTGTGTG NM_006772RefSeq chr6_GL000256v2_alt + 4868794 4902412 SYNGAP1 8831 synaptic Ras GTPase activating protein 1

GO:0007389|GO:0017124|GO:0050803|GO:0031235|GO:0032851|GO:0007265|GO:0016358|GO:0005099|GO:0046580|GO:0043524|GO:0005737|GO:0032320|GO:0048167|GO:0043198|GO:0008542|GO:0048169|GO:0043408|GO:0043113|GO:0050771|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137944_PI430048170 0.533701490864187 1.79372286624189 2.47724324503439 0.295376344309241 0.494053632445722 A A A 0.301710021750817 0.264646207758238 1.09743584239096 A A A LNCV6_137944_PI430048170 mRNA
ACAGCAACAAAAAAGACATTGGGCTGTGGCATTATTAATTAAAGATGATATCCAGTCTCC NM_001256346 RefSeq chr3 - 122909192 122993273 SEMA5B 54437 "sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B, transcript variant 2" GO:0004872|GO:0016021|GO:0030154|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131529_PI430048170 0.887658369944346 0.920358463228433 0.633986481011333 0.376238976684951 0.815207740690178 A A A 0.281161878281102 1.306526291565 0.400088110216706 A A A LNCV6_131529_PI430048170 mRNA
TGCCATGGTATTTGGGTCCTGGGAGGGTGGGTGAAATAAAGGCATGCTGTCTTCAAAAAA NM_000180 RefSeq chr17 + 8002669 8020340 GUCY2D 3000 "guanylate cyclase 2D, membrane (retina-specific)"
GO:0007603|GO:0022400|GO:0004383|GO:0005525|GO:0005524|GO:0035556|GO:0005640|GO:0004672|GO:0005887|GO:0006182|GO:0004872|GO:0006468|GO:0007168|GO:0007601|GO:0016056 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140649_PI430048170 0.307876570996387 1.03481657411514 0.318191922882682 0.260811996551921 0.385158118826026 A A A 0.280935276848756 0.255417180306224 0.282213542632217 A A A LNCV6_140649_PI430048170 mRNA
AGCAGTTATCTTTAGGATAATATGTACAAATGTTGGGGTCAAAGCCTTTTGACAAAGCAA NM_001146339 RefSeq chr19 + 29526583 29564319 VSTM2B 342865 V-set and transmembrane domain containing 2B
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127579_PI430048170 0.0335420570973818 1.09670312483841 15.5807816577061 15.6235508916649 15.5215859227363 P P P 15.38348582894 15.479263449902 15.4636449014733 P P P LNCV6_127579_PI430048170 mRNA
ATTTGTCCCAGCCTGGGGCTCCCTCTCTGGTTTCCTATTTGCAGTTACTTGAATAAAAAA NM_145901 RefSeq chr6 + 34236872 34246231 HMGA1 3159 "high mobility group AT-hook 1, transcript variant 3"
GO:0005515|GO:0003906|GO:0008285|GO:0090402|GO:0005634|GO:0035985|GO:0035986|GO:0042974|GO:0042975|GO:0005829|GO:0046965|GO:0030374|GO:0016032|GO:2000774|GO:0031936|GO:0005667|GO:0006355|GO:0006337|GO:0009615|GO:0003677|GO:0006351|GO:0051575|GO:0006461|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128619_PI430048170 0.0550625572714279 1.34497536193095 7.41774226964918 7.61257612077873 7.38157438587649 P P P 7.27696046071463 6.98383395160015 6.84500668805 P P P LNCV6_128619_PI430048170 mRNA
CCTCTGGTTCAAACCTTCGCGTGGCATTTTCACATTATTTAAAAAAGACAAAAACAACTT NM_001080434 RefSeq chr19 - 48485270 48513189 LMTK3 114783 lemur tyrosine kinase 3
GO:0003674|GO:0004674|GO:0010923|GO:0006468|GO:0016021|GO:0005575|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139234_PI430048170 0.762142868387061 1.05064446486281 7.07532261504677 7.07712761290214 7.53755984326382 P P P 6.85872385397302 7.14729109392448 7.45861085240526 P P P LNCV6_139234_PI430048170 mRNA
GAATTGAGGCCATTTGGGAAGAAAATTCTAGCACTGGTGGAGAATTATAGAATAAAGATT NM_015368 RefSeq chr11 + 94128927 94181971 PANX1 24145 pannexin 1
GO:0005886|GO:0005783|GO:0007268|GO:0055077|GO:0002020|GO:0022840|GO:0034214|GO:0035872|GO:0051015|GO:0050717|GO:0050718|GO:0097110|GO:0033198|GO:0006816|GO:0006812|GO:0005262|GO:0046982|GO:0005102|GO:0044325|GO:0043234|GO:0032059|GO:0016020|GO:0002931|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_129425_PI430048170 0.113456439769398 0.805675031375166 9.95259983381979
9.79602213626434 9.52024808916487 P P P 10.1578055476847 10.0003744087337
10.0742859480725 P P P LNCV6_129425_PI430048170 mRNA
TCTCAAGGGAGAGGGAGGGGGCGGAGCGGAATAAATAGTAACTTATTTAAGAAATGCAAA NM_021098 RefSeq
chr16 + 1153240 1221772 CACNA1H 8912 "calcium channel, voltage-dependent, T type, alpha 1H subunit,
transcript variant 1"
GO:0086010|GO:0005886|GO:0008332|GO:0008016|GO:0007520|GO:0005891|GO:2000344|GO:0046872|GO:0032
870|GO:0034651|GO:0042383|GO:0070509|GO:0035865|GO:0006936|GO:0007517|GO:0007411|GO:0005901|GO:0
097110|GO:0042391|GO:0070588|GO:0006810|GO:0032342|GO:0034765|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131019_PI430048170 0.0694488447570611 1.24893246554535 13.7690526584716
14.0260251102733 13.9597918858737 P P P 13.4300074124505 13.5708603596486
13.7821624674289 P P P LNCV6_131019_PI430048170 mRNA
ATGGAGATCAACAGTTACTGTGACTGAGTCGGCCCATTCTGTTTAGAAATATATTTTAAA NM_003769 RefSeq
chr12 - 120461667 120469755 SRSF9 8683 serine/arginine-rich splicing factor 9
GO:0005515|GO:0006397|GO:0008380|GO:0006369|GO:0010467|GO:0048025|GO:0006366|GO:0006376|GO:0005
730|GO:0031124|GO:0006406|GO:0000166|GO:0000398|GO:0005654 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139887_PI430048170 0.00116000505368344 1.58354150234662 6.50431262170907
6.38002565831728 6.30167549566756 P P P 5.70238775155318 5.83358719047101
5.66222957285936 P P P LNCV6_139887_PI430048170 mRNA
TAAGAATATCCACCAGTCGGTGAGTGAGCAGATCAAGAAGAACTTTGCCAAGAGCAAGTG NM_003656 RefSeq
chr3 - 9757344 9769984 CAMK1 8536 calcium/calmodulin-dependent protein kinase I
GO:0005515|GO:0005516|GO:0071902|GO:0043393|GO:0005634|GO:0005524|GO:0006913|GO:0046827|GO:0032
880|GO:0007165|GO:0005737|GO:0007049|GO:0051149|GO:0051835|GO:0010976|GO:0006468|GO:0004683|GO:0
060999|GO:0051147 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136192_PI430048170 0.552816661123374 0.954334510775779 11.5099021498302
11.4105959494363 11.329323022237 P P P 11.3190916712714 11.5944360367705
11.5301180619276 P P P LNCV6_136192_PI430048170 mRNA
GGCAGGTGTGCAAGGTGACAACTAGGATAATCATGGCTGGAATAAAGTAAGTTTCCACAC NM_001031703 RefSeq
chr3 - 47495639 47513709 ELP6 54859 elongator acetyltransferase complex subunit 6
GO:0008150|GO:0003674|GO:0033588|GO:0006355|GO:0030335|GO:0006325|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134719_PI430048170 0.816355866691238 0.977784671263492 0.330706017754216
0.33449079022163 0.500509576042983 A A A 0.606504767250769 0.293654305994484
0.349740322002741 A A A LNCV6_134719_PI430048170 mRNA
CCAGAAAGCCCTCTTTTTCGCACCTCATCAAACAGAACAAATAAGTTATATTTAATGTCT NM_032681 RefSeq
chr11 + 55883296 55891808 TRIM51 84767 tripartite motif-containing 51 GO:0005622|GO:0008270
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130635_PI430048170 0.328569103031213 0.544848292022582 2.64173849118864
2.90582809236396 0.393327413689938 A A A 3.91484066282659 2.94393751264486
2.27562224760707 P P A LNCV6_130635_PI430048170 mRNA
GTGTGCACACGCCCACGTTCTCTGAACCATTCCACATAAAGGAAAATCGTTTATTCACAC NM_145248 RefSeq
chr13_KI270838v1_alt + 177306 235665 SPACA7 122258 sperm acrosome associated 7
GO:0001669|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141113_PI430048170 0.795770182583682 0.979788216026741 4.75729292630913
3.82327279828637 4.25808569940489 P P P 4.36616237226806 4.38269549314338
4.32884615586849 P P P LNCV6_141113_PI430048170 mRNA
TCCTTTGATTTGAGAAGCCACATTCCATCCCCCTCCAATTGTGATCAATACCTAGGGAGA NM_001143989 RefSeq

chr1 - 108223340 108244081 NBPF4 NA "neuroblastoma breakpoint family, member 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133654_PI430048170 0.0347219002449873 1.41358088596641 9.79215091566691 9.52862038065899 9.48072807671078 P P P 9.29097045823728 9.13092542299735 8.87061105619829 P P P LNCV6_133654_PI430048170 mRNA CCACACAGTGCTTTGGAAATTCTCAGTGAATGATGTTTAATAAAGCAAAAAATGTCAAGG NM_022460 RefSeq
chr2 - 20617803 20651104 HS1BP3 64342 HCLS1 binding protein 3 GO:0035091 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127274_PI430048170 0.151699135197105 2.29637398264495 1.87497194065736 1.66751151833599 3.17480861145147 A A P 0.370759839031168 2.00991975288894 0.671288540841741 A A A LNCV6_127274_PI430048170 mRNA CTTAAAATATAATTGAAGCAGCCCAGATGATCTTCCACAACCTGTGATCTAAGGAAAAAA NM_033124 RefSeq
chr12 + 48904109 48921576 CCDC65 85478 "coiled-coil domain containing 65, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133528_PI430048170 0.00993983649940416 0.240970505256541 3.1313067285594 3.24842310795406 3.1406574719432 A P P 4.79241871317305 5.24405977066117 5.54809651343828 P P P LNCV6_133528_PI430048170 mRNA CTCTCACTCCAAACTGTGTATAGTCAACCTCATCATTAATGTAGTCCTAATTTTTTATGC NM_012206 RefSeq chr5 - 157029412 157058241 HAVCR1 26762 "hepatitis A virus cellular receptor 1, transcript variant 1" GO:0001618|GO:0016032|GO:0016021|GO:0009615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128084_PI430048170 0.00248517274285646 0.460890492834332 9.51794182773371 9.8581340142557 9.82461104147081 P P P 10.719722501844 10.7346440032022 11.0911376041423 P P P LNCV6_128084_PI430048170 mRNA GGACCAACTACAAATTAATGTTGGTTGTCAAATGTAGTGTGTTTCCCTAACTTTCTGTTT NM_021960 RefSeq chr1 - 150574550 150579738 MCL1 4170 "myeloid cell leukemia 1, transcript variant 1" GO:0005515|GO:2001020|GO:0005741|GO:0005634|GO:2000811|GO:0042803|GO:0005829|GO:0005739|GO:0005737|GO:0008637|GO:0005759|GO:0097136|GO:2001240|GO:0034097|GO:0071806|GO:0019725|GO:0008630|GO:0046982|GO:0001709|GO:0051434|GO:0007275|GO:2001243|GO:0097192|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143938_PI430048170 0.00401818963575125 0.482686328030458 4.99450377105029 4.55218840084505 4.77463843459368 P P P 5.58158620332414 5.94945532580308 5.94654602833794 P P P LNCV6_143938_PI430048170 mRNA CCTACTGGTTTGGGAGATGTATATAGTAATATGATTCTCATACCCAGGAACTGTAAATTT NM_005445 RefSeq
chr10 + 110567690 110604634 SMC3 9126 structural maintenance of chromosomes 3 GO:0005515|GO:0030893|GO:0008280|GO:0032876|GO:0005634|GO:0016363|GO:0005829|GO:0005737|GO:0007052|GO:0000785|GO:0006275|GO:0046982|GO:0005694|GO:0000800|GO:0003777|GO:0005524|GO:0005604|GO:0007165|GO:0000922|GO:0007067|GO:0008278|GO:0045502|GO:0006281|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139059_PI430048170 0.000844905800676289 0.204041409231347 8.06567686887401 7.52631208418332 7.59389341070396 P P P 9.88061614755856 9.98996772653643 10.2334182765344 P P P LNCV6_139059_PI430048170 mRNA TACGGGCAACAGTATGCGGAAAGTACGTTTTTTAAGTAAAAAACAAAGGCAAACTTTGTA NM_014279 RefSeq
chr9 + 135075242 135121184 OLFM1 10439 "olfactomedin 1, transcript variant 1" GO:0005515|GO:0030054|GO:0001540|GO:2001223|GO:0032281|GO:0045202|GO:0051259|GO:0005615|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145541_PI430048170 0.92966640370468 1.00254563891713 0.361168515200863 0.336246620098536 0.260287686624633 A A A 0.314186905734486 0.327593633851919 0.306744788054717 A A A LNCV6_145541_PI430048170 mRNA

CCAAGAATATATGCTACAGATATAAGACAGACATGGTTTGGTCCTATATTTCTAGTCATG NM_002019 RefSeq
chr13 - 28300345 28495128 FLT1 2321 "fms-related tyrosine kinase 1, transcript variant 1"
GO:0005515|GO:0030949|GO:0008284|GO:0035924|GO:0005886|GO:0048514|GO:0002040|GO:0048598|GO:0005
615|GO:0030154|GO:0042802|GO:0046777|GO:0043552|GO:0019838|GO:0043406|GO:0005021|GO:0038084|GO:0
048010|GO:0001569|GO:0030335|GO:0014068|GO:0018108|GO:0005524|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137879_PI430048170 0.0402619435901996 0.542298936271246 4.60873286847799
4.73347889875587 4.86832476226058 P P P 5.66281157584406 5.20950678334828
5.91274817268884 P P P LNCV6_137879_PI430048170 mRNA
CAATTAGAGGCTCCAGAGTCTTCATAGTGGAAAGAATGCTTTGTATTTAATTGTTCTTAG NM_017644 RefSeq
chr3 + 183635622 183684516 KLHL24 54800 kelch-like family member 24
GO:0030424|GO:0005737|GO:0043204 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106163_PI430048170 0.0996946103664584 0.78021527046576 6.95836072997058
7.16850063906099 7.43737437726466 P P P 7.43040237009573 7.55590662736022
7.68132685687469 P P P LNCV6_106163_PI430048170 mRNA
TGCCTTAATAAGCATCTGAATGTTTGGTTGTGGGGCGGGTTCTGAAGCGATGAGAGAAAT NM_001083926 RefSeq
chr11 + 62337301 62393415 ASRGL1 80150 "asparaginase like 1, transcript variant 1"
GO:0008798|GO:0033345|GO:0005737|GO:0006508|GO:0004067|GO:0003948|GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132345_PI430048170 0.0274100435726495 0.898610659970341 14.2751362134804
14.212989510495 14.1927403761144 P P P 14.3135993282208 14.4312998643549
14.3974152667537 P P P LNCV6_132345_PI430048170 mRNA
CGGTGTGGGTGGTGGTTCTATAGAGGGATAAATGAATAATAAACATTGTTAAAATATACG NM_002668 RefSeq chrX
+ 49171836 49175119 PLP2 5355 proteolipid protein 2 (colonic epithelium-enriched)
GO:0005515|GO:0005886|GO:0005783|GO:0015075|GO:0019221|GO:0019956|GO:0034220|GO:0006935|GO:0016
020|GO:0005789|GO:0016021|GO:0006811|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131662_PI430048170 0.216963208750661 0.884537896730411 7.81997030979247 7.7922266602668
8.02905453623827 P P P 7.89789414992202 8.05163158003765 8.21689230249434 P P P
LNCV6_131662_PI430048170 mRNA
GCCCCAGTCTTTGATTTTACAGGTAACTTTCAAAACATCATGATGCTGCCAAATGTACTT NM_007198 RefSeq chr8
+ 37762582 37779768 PROSC 11212 proline synthetase co-transcribed homolog (bacterial)
GO:0005739|GO:0005622|GO:0008150|GO:0005737|GO:0030170|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132957_PI430048170 0.3375072255975770 0.8828368808985436.36626692444914
6.66446956629562 6.83174871589022 P P P 6.70354801082606 6.71150784679567 7.0039196651214
P P P LNCV6_132957_PI430048170 mRNA
AATCTGACAAAGTCATGAAGCTCAGTTTGGCTGTAATTTAATTCCCCTTCCCTTATTTTT NM_003885 RefSeq chr17 +
32487086 32491253 CDK5R1 8851 "cyclin-dependent kinase 5, regulatory subunit 1 (p35)"
GO:0005515|GO:0031594|GO:0009790|GO:0071158|GO:0031175|GO:0043231|GO:0007413|GO:0043525|GO:0018
105|GO:0016301|GO:0007411|GO:0018107|GO:0021722|GO:0032956|GO:0043025|GO:0061001|GO:0045296|GO:0
019901|GO:0005509|GO:0090314|GO:0014069|GO:0021549|GO:0007213|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145497_PI430048170 0.00768520385490325 0.4033705229310364.56525423101763
4.74296849525075 5.1178652584541 P P P 6.00690006858113 6.20613261539824
6.19031462962747 P P P LNCV6_145497_PI430048170 mRNA
GCATTTCAAATGTTTTTGGTTATCTGTAAACTAAATGTGCCCTTATTGGCTCACTTGTCA NM_001288645 RefSeq chr17
+ 15699576 15720786 ZNF286A 57335 "zinc finger protein 286A, transcript variant 6"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_49314_PI430048170 0.1527627453197777 1.25158346857861 4.63666956813117 4.7014276259243
4.31587605672027 P P P 4.50565839918077 4.09569857695834 4.06717044757277 P P P
LNCV6_49314_PI430048170 mRNA
GACAGGGCTCTGAAGAGTCTGAAGATCACTTCCCGCTTCTTCCTCGGAAACCCTCCTTCC NM_152762 RefSeq chr11
+ 65945643 65959963 TSGA10IP 254187 "testis specific, 10 interacting protein" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_80979_PI430048170 0.0303229589927124 1.44158166738596 12.2461663252287
12.3961237134502 12.4760305847334 P P P 11.6398595031704 11.807847476995 12.064979433984
P P P LNCV6_80979_PI430048170 mRNA
TCATGAGCCAGACCACATATTCTTCTCTTTAGACGACCTCTTCCAAAAGATCAACAAAAA NM_001827 RefSeq chr9
+ 89311194 89316703 CKS2 1164 CDC28 protein kinase regulatory subunit 2
GO:0007127|GO:0008283|GO:0016538|GO:0000079|GO:0051301 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131566_PI430048170 0.0152335205599209 1.82459241734109 4.73544274745511
5.14821976384086 4.88705079300568 P P P 4.11787619922117 4.05839298699755 4.0205851687186
P P P LNCV6_131566_PI430048170 mRNA
TTTTGGGTTATTTATTTTGTGCATCTGTGGCAATAAATGAGATCTCAGTGGTGGTATGGA NM_025236 RefSeq
chr6_GL000256v2_alt - 1369184 1374770 RNF39 80352 "ring finger protein 39, transcript variant 1"
GO:0008150|GO:0005737|GO:0008270|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93912_PI430048170 0.6202814091056361 1.04780271108645 8.12694636421858 8.41249836300559
8.09840885446979 P P P 8.19642204989638 8.20699462843571 8.0482973176589 P P P
LNCV6_93912_PI430048170 mRNA
ATTGAGGGCAAGAAGGACATCCGTGCAGCACTGGCAGCTGAGAGGAAGTTCTTCCTCTCC NM_001005361 RefSeq
chr19 + 10718052 10831910 DNM2 1785 "dynamin 2, transcript variant 2"
GO:0005515|GO:0008017|GO:0017124|GO:0005886|GO:0050999|GO:0003924|GO:0044281|GO:0005829|GO:0030
426|GO:0031623|GO:0033572|GO:0019886|GO:0005737|GO:0030516|GO:0045211|GO:0000086|GO:0061024|GO:0
046209|GO:0070062|GO:0006355|GO:0043065|GO:0005794|GO:0005874|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133606_PI430048170 0.0352150218302556 0.7724468083522871 3.1650725139738
13.11810931565 13.3408255005464 P P P 13.5929408912289 13.4127519583595
13.7282087591897 P P P LNCV6_133606_PI430048170 mRNA
GTAGCTTCTGAAAGGTGCTTTCTCCATTTATTTAAAACTACCCATGCAATTAAAAGGTAC NM_005080 RefSeq chr22
- 28794559 28800572 XBP1 7494 "X-box binding protein 1, transcript variant 1"
GO:0005515|GO:0031670|GO:0006511|GO:0034976|GO:0003700|GO:0044212|GO:0006366|GO:0000981|GO:0010
832|GO:0002020|GO:0042993|GO:0030968|GO:0045348|GO:0051602|GO:0031625|GO:0042632|GO:0032869|GO:0
000977|GO:0046982|GO:0019901|GO:0006990|GO:0001047|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_111757_PI430048170 0.0105521614630664 0.4645411804532983 .93199374822299
4.30183014823226 3.71058329797517 P P P 4.93822320786504 5.23497405579621
5.13657544670011 P P P LNCV6_111757_PI430048170 mRNA
CCTCAGAGCTCAAATAGGTTGTTTAAAATCACATTCAATTTTCAGATGAAGGGGAACTTT NM_006989 RefSeq chr7
- 102579645 102616758 RASA4 10156 "RAS p21 protein activator 4, transcript variant 1"
GO:0035556|GO:0005099|GO:0046580|GO:0005737|GO:0032320|GO:0005886|GO:0071277|GO:0031235|GO:0046
872|GO:0005829|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72303_PI430048170 0.6969871357920850.8964197808215863.08288927161688 2.87274794008823
3.29094499641889 A A P 2.69215629535468 3.39129577043038 3.53433614998962 P P P
LNCV6_72303_PI430048170 mRNA
GGTCTTTTCTATTATATCTGAGTAACTAGTCAGTTTTTCTTACAGTGCTCATAGCAGTTG NM_021090 RefSeq chr22 +
29883168 30030868 MTMR3 8897 "myotubularin related protein 3, transcript variant 3"

GO:0006661|GO:0044281|GO:0046872|GO:0035335|GO:0005829|GO:0005737|GO:0006470|GO:0016020|GO:0004438|GO:0046856|GO:0052629|GO:0005654|GO:0004722|GO:0006644|GO:0004725|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143460_PI430048170 0.0434573436679652 0.4901278261853683.43084682885308 2.86985716335883 3.79063547572665 P A P 4.2288033016667 4.53764396192988 4.5345978638131 P P P LNCV6_143460_PI430048170 mRNA
CATTTCCCTGCTGGTAACAATACCATTCTGTCACCATCTACTGTTTTAGGCTTCCGTTTT NM_023077 RefSeq chr1 - 52686341 52698366 COA7 65260 cytochrome c oxidase assembly factor 7 (putative) GO:0005758 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91159_PI430048170 0.3919286641681081.14126768949843 4.47569755226157 4.59312744812457 4.47991970434032 P P P 4.6562740189738 4.27769407198197 3.96202067832605 P P P LNCV6_91159_PI430048170 mRNA
AAAGAGAACTTACAAAGCAATAATGGAAAACCTCCCACTTTGGTGACCAGCATGATTGAC NM_003787 RefSeq chr18 - 33851099 34223551 NOL4 8715 "nucleolar protein 4, transcript variant 1" GO:0003723|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145357_PI430048170 0.0625828425893976 1.34696952076189 10.0296243916468 10.3579194125508 10.4217247323748 P P P 9.77094769687523 9.88061614755856 9.89524151799384 P P P LNCV6_145357_PI430048170 mRNA
GGTTTTTTAAAACACAAAAATTATAGAATATGGGATCCCGTGTGTGTGTGTGTGTGTTTG NM_031905 RefSeq chr7_KI270806v1_alt - 144965 158099 ARMC10 83787 "armadillo repeat containing 10, transcript variant A" GO:0005739|GO:0005789|GO:0016021|GO:0040008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67724_PI430048170 0.0190917274637483 1.45176009956214 7.17420382161507 7.54373430228068 7.37879236080749 P P P 6.97393055087458 6.84108327483943 6.67661431473706 P P P LNCV6_67724_PI430048170 mRNA
AGAAGAAAGCAGTGAAGCCAGGTAGCAGTAGCCCGGCCACCCCACCAGGCTCTGCTGTAG NM_178520 RefSeq chr17 - 81311270 81330674 TMEM105 284186 transmembrane protein 105 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143478_PI430048170 0.0099140784201711 0.7257923507630794.73883384624293 4.69760972441631 4.77277079704696 P P P 5.30503303601815 5.09598108614701 5.18867231438883 P P P LNCV6_143478_PI430048170 mRNA
TCCCCGCAGGTTTATTAAAGCAAGAACAGATGCCAAGCTCAGGGATAATAAATCTATTTT NM_018127 RefSeq chr17 - 12991611 13018064 ELAC2 60528 "elaC ribonuclease Z 2, transcript variant 1" GO:0005739|GO:0072684|GO:0004519|GO:0005654|GO:0005634|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128289_PI430048170 0.7174150648629640.9860694001860340.355660313666943 0.4600150489359160.355090671826019 A A A 0.4864143916897260.369306966410995 0.375270058711997 A A A LNCV6_128289_PI430048170 mRNA
GTTAATTGGAGCTTCTACCCAGGAAAAACCTCATTTTATTAATCAAAGGCAATACTTTGG NM_001080476 RefSeq chr4 + 42893265 43030658 GRXCR1389207 "glutaredoxin, cysteine rich 1" GO:0060122|GO:0042491|GO:0007605|GO:0015035|GO:0048563|GO:0060118|GO:0009055|GO:0032420|GO:0060119|GO:0003674|GO:0060091|GO:0010923|GO:0045454|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69231_PI430048170 0.0352577106851269 1.63637937926317 10.1927306532376 10.1200928876304 10.0903914240231 P P P 9.11321242958803 9.58346555443569 9.53242469763337 P P P LNCV6_69231_PI430048170 mRNA
ACAGTCCTGGACCTGAAGAAGGCCATCCAGAGATACGTGCAGCTCAAGCAGGAGCGTGAA NM_024571 RefSeq chr16 + 53828 57669 SNRNP25 79622 small nuclear ribonucleoprotein 25kDa (U11/U12) GO:0008380|GO:0006397|GO:0005737|GO:0005654|GO:0005634|GO:0005689|GO:0045171 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_142914_PI430048170 0.00786331522914262 0.33209996429347 3.38211681192536
3.94557727218232 4.14456729410114 P P P 5.22368138286485 5.4458554623734
5.64646601949561 P P P LNCV6_142914_PI430048170 mRNA
TCTGTTAGACAGCTGATGGGTGTTTTTGAGCAACGTCTTAATAATTCAGTTGTTTCTGTT NM_001195432 RefSeq
chr3 + 158571163 158606460 MLF1 4291 "myeloid leukemia factor 1, transcript variant 4"
GO:0005515|GO:0005737|GO:0019904|GO:0007050|GO:0005654|GO:0005634|GO:0002318|GO:0003677|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129438_PI430048170 0.306228271667055 1.03461842640509 0.317390480813995
0.259835593218885 0.383011909180043 A A A 0.279994057772863 0.254244976638389
0.281177332029507 A A A LNCV6_129438_PI430048170 mRNA
CTGATGTGTCTGTACTAAAAAATTGGGAATTTTTGGAACATCTTATTGACCTCTGTGTCT NM_001145194 RefSeq
chr18 - 5143672 5197256 C18orf42 NA chromosome 18 open reading frame 42 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134030_PI430048170 0.00334345654540251 1.14468031423632 5.57017068889154
5.63203729794492 5.56621157136088 P P P 5.35017731991925 5.42476804923203
5.40852709729142 P P P LNCV6_134030_PI430048170 mRNA
TGTGGAGAAGACCGCCACTCCATCTGATTTGCATAAATGACTCAGTGGGCTTTTGTATCT NM_021100 RefSeq chr20
- 35668687 35699365 NFS1 9054 "NFS1 cysteine desulfurase, transcript variant 1"
GO:0005515|GO:0006534|GO:0005730|GO:0006767|GO:0005634|GO:0044281|GO:0042803|GO:0043231|GO:0005
829|GO:0032324|GO:0005739|GO:0005737|GO:0000096|GO:0006461|GO:0006766|GO:0005759|GO:0031071|GO:0
030170|GO:0006777|GO:0005654|GO:0018283 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134198_PI430048170 0.531668582841157 1.24539950014188 0.383555926265498
0.388953811480541 1.35760652103967 A A A 0.660853640888226 0.34082993319777
0.388542244687834 A A A LNCV6_134198_PI430048170 mRNA
GGAGAAACACCGGGTTTCAGCTTTCTCGACCTTAGCTTGGGTGAGACTGTTTACAAAAAA NM_001194958 RefSeq
chr17 + 21692522 21704612 KCNJ18 NA "potassium channel, inwardly rectifying subfamily J, member
18" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104913_PI430048170 0.201468659107367 0.895948016233537 8.7711543974079
8.54608268343894 8.56652299643965 P P P 8.69587042920713 8.93419580479849 8.7283821678475
P P P LNCV6_104913_PI430048170 mRNA
ACTGCAAGTCCCTGGGCCACTTTGAGAACCTGCAGAAATACAAGGCGGCCAAGAACCCCA NM_001257975
RefSeq chr9 - 128166064 128192104 CIZ1 25792 "CDKN1A interacting zinc finger protein 1,
transcript variant 6" GO:0005515|GO:0008270|GO:0005634|GO:0003676 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_135910_PI430048170 0.868538099846939 1.01364292215663 2.22737424668243
0.523087168545537 0.471439985802843 A A A 0.390159828419674 1.70222688672913
1.50626264674022 A A A LNCV6_135910_PI430048170 mRNA
GGTACCCAAAACATAGGCCATACACAGAAGAAATTAAGTGTGGTAAATAAACTAGTTTGA NM_213589 RefSeq chr2
- 203433681 203535335 RAPH1 65059 "Ras association (RalGDS/AF-6) and pleckstrin homology domains 1,
transcript variant 1"
GO:0005515|GO:0007165|GO:0005737|GO:0007160|GO:0005886|GO:0048675|GO:0030175|GO:0005856|GO:0030
027 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138605_PI430048170 0.380975944693119 1.19972517990511 5.90486736070438
5.88764540909319 5.33561080666483 P P P 5.8340493990665 5.2041662199258
5.28681894007785 P P P LNCV6_138605_PI430048170 mRNA
GATCAGAGACCCTGCCTCTGTTTGACCCCGCACTGACTGAATAAAGCTCCTCTGGCCGTT NM_001077191 RefSeq
chr2 + 218261014 218263859 GPBAR1151306 "G protein-coupled bile acid receptor 1, transcript variant 1"
GO:0005737|GO:0007186|GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_140840_PI430048170 0.3132827455910090.9001700867753997.65657383276946
7.50956640206231 7.24477910025362 P P P 7.59661579153575 7.58738486986491
7.70866318063928 P P P LNCV6_140840_PI430048170 mRNA
GTGGTGCTTTCCCCCTTTCCCTTGAATTCTGCTTTGAAAAGAATAAATTTGTACTTGTTT NM_001939RefSeq chrX +
101219943 101264496 DRP2 1821 "dystrophin related protein 2, transcript variant 1"
GO:0005737|GO:0005886|GO:0008270|GO:0007417|GO:0005856 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_80352_PI430048170 0.4286357884447011.10003429659137 11.7096056968168 11.6683462361825
11.4904124373621 P P P 11.2273800874154 11.7373718584916 11.4548285960105 P P P
LNCV6_80352_PI430048170 mRNA
GAAAGCTGCAACCTTTCTGTTTTATTTAAAGAAAGCCCAACATTAAAGGGTTTTCATTGC NM_016647RefSeq chr8
+ 142727202 142736932 THEM6 51337 thioesterase superfamily member 6 GO:0005576 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131153_PI430048170 0.0800993215666598 0.7430171521590180.33139025770951
0.3139444849883950.299163707885793A A A 0.4817310308298770.828136382618215
0.888016483256506A A A LNCV6_131153_PI430048170 mRNA
AAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAG NM_002001RefSeq chr1
+ 159289713 159308224 FCER1A 2205 "Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide"
GO:0001812|GO:0045401|GO:0019370|GO:0045425|GO:0001820|GO:0005886|GO:0009986|GO:0050731|GO:0007
257|GO:0050850|GO:0043306|GO:0019863|GO:0005887|GO:0045087|GO:0019767|GO:0009897|GO:0038095 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127267_PI430048170 0.0664977452284828 0.9432389286049460.309499273069632
0.3216389498278660.321763810658614A A A 0.4453659844980260.394629194447044
0.364700541662482A A A LNCV6_127267_PI430048170 mRNA
GAGTGATCTCCTTACAGAATCTGTGATTTTCAGGCTGGATCACAGAACTGTTGGGTTCTG NM_016580RefSeq chr5
- 141943584 141959062 PCDH12 51294 protocadherin 12
GO:0016339|GO:0060711|GO:0008038|GO:0005886|GO:0005911|GO:0005887|GO:0005977|GO:0005509|GO:0007
156|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127828_PI430048170 0.1038609765223421.25584213501666 10.344312554301
10.1133795370138 9.95508940437944 P P P 10.0166598560681 9.7584984278116
9.65386143108646 P P P LNCV6_127828_PI430048170 mRNA
TGACTGTGTTTCATAGCCCCAGTCCAGGGCTGTCTAAGAAATAAAGATCATCAGACTCCA NM_024589RefSeq chr16
- 4796961 4802950 ROGDI 79641 "rogdi homolog (Drosophila), transcript variant 1"
GO:0030097|GO:0005622|GO:0008284|GO:0005635 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137627_PI430048170 0.2396572545814010.7507732496965720.475785302215132
0.5835070493081260.535182709329323A A A 0.9602614779483161.28026507952732
0.489469120653171A A A LNCV6_137627_PI430048170 mRNA
CTGGTGGCCGCATAGTAGAATATGGTCCCTGATATTTAAAACCGATCATCTTAAGTAAAT NM_001195555 RefSeq
chr5 - 157785742 157859175 CLINT1 9685 "clathrin interactor 1, transcript variant 1"
GO:0005515|GO:0048471|GO:0005794|GO:0030136|GO:0006892|GO:0005829|GO:0006897|GO:0008289|GO:0043
231|GO:0016020|GO:0030276|GO:0061024|GO:0005654|GO:0048268 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_51174_PI430048170 0.0115544568052457 0.2481169674665411.35127562092238
0.3186478542623170.390422997230622A A A 3.03082489905851 2.43420857863184
2.81042620546502 P P P LNCV6_51174_PI430048170 mRNA
CCTTGTAAGTTTGGATCAAATTTTGCTGGTTCTTTGGATAATGGAGTTCTTGTGTTAACA NM_001278524 RefSeq
chr10 + 96129714 96163761 ZNF518A 9849 "zinc finger protein 518A, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_127318_PI430048170 0.8700057340650380.9920890157809651 0.5602527353437
10.5532966582124 10.5882060115464 P P P 10.4739269053252 10.620134428388
10.6368060032725 P P P LNCV6_127318_PI430048170 mRNA
CCTCCATGGACCCTTGGTGGCTTTTGTAAATTAATTTTTGATGACATTTTGAGTTTTAAGNM_001261411 RefSeq chr12
+ 131711086 131799738 SFSWAP 6433 "splicing factor, suppressor of white-apricot family, transcript
variant 1" GO:0006397|GO:0006355|GO:0048025|GO:0003723|GO:0006376|GO:0005634|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133113_PI430048170 0.0915635117877590.8820537338797541 0.0002871719874 9.776556541813
9.89648875047757 P P P 10.1021589826535 10.0288982681354 10.0930291619344 P P P
LNCV6_133113_PI430048170 mRNA
CCCCTCATTTGTAAGAATAGCTACACACTAACATTTTGGGAAGGAGAGGCACATAACTTT NM_019613RefSeq chr17
- 82614561 82648535 WDR45B 56270 WD repeat domain 45B
GO:0006995|GO:0034045|GO:0000422|GO:0080025|GO:0006497|GO:0032266|GO:0000045|GO:0034497|GO:0019
898|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136168_PI430048170 0.0228800694817068 0.7891844736630281 2.4444648472381
12.2944974081257 12.2304523186754 P P P 12.5294150989406 12.7640464690612
12.6990327152789 P P P LNCV6_136168_PI430048170 mRNA
GTGTTTGAGCCTACAGTGGGATACATAGGGTCAAATTGAGAATAATAAACTGAGTCATTC NM_001040431 RefSeq
chr17 - 42797617 42798725 COA3 28958 cytochrome c oxidase assembly factor 3
GO:0033617|GO:0005739|GO:0005515|GO:0031305|GO:0070131 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142733_PI430048170 0.8782010734137481.02312086569104 7.72669057737652
8.05969749706822 8.15865479013659 P P P 7.9386428727466 7.85629863228369
8.07707837515875 P P P LNCV6_142733_PI430048170 mRNA
TAGGATTCACATTTAACTGCTGGCATAATTTGCAACTGTTGGATTTTCTCATGTTTGGAA NM_001010851 RefSeq
chr19 + 52269570 52292723 ZNF766 90321 zinc finger protein 766
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131638_PI430048170 0.2733223617434321.2899403714073 1.18134377507081
0.7985049975565060.4074772988889 A A A 0.4108870326150910.491515615833668
0.484700487855595A A A LNCV6_131638_PI430048170 mRNA
ATACCTGGATTGGCTTAGCTTACTGAAGAAGGTAGGAAGAAATAAAATGTTTATGAACCA NM_173699RefSeq chrX
+ 26138342 26140736 MAGEB18 286514 melanoma antigen family B18 GO:0005515|GO:0005737 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141805_PI430048170 0.00519966208635721 0.4800325414328258.57092141680061
8.43629033028379 8.6670950979788 P P P 9.44753628807536 9.51722617846759
9.86050852273775 P P P LNCV6_141805_PI430048170 mRNA
GGGAGGAAGTACGACTAATGTTGGAGCCTGAAACTATGGAAATGCTGCTAAAATTTTTAT NM_001257180 RefSeq
chr8 - 42416461 42501460 SLC20A2 6575 "solute carrier family 20 (phosphate transporter),
member 2, transcript variant 1"
GO:0005886|GO:0035435|GO:0009615|GO:0055085|GO:0005436|GO:0016020|GO:0001618|GO:0005887|GO:0006
810|GO:0016032|GO:0004872|GO:0005315|GO:0035725|GO:0070062|GO:0006811 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129451_PI430048170 0.5872003719641580.3609105060542431.80817805386316 1.6353602561448
0.396329127319412A A A 4.18057701925722 1.13249447893732 0.706675827726765P A A
LNCV6_129451_PI430048170 mRNA
CTATGGCTGCCTTTGATTAAACTTCTTCCAAAAAATAAATTCTGCCCAGATGTTGTTGAC NM_053002RefSeq chr3
+ 151086797 151436677 MED12L 116931 mediator complex subunit 12-like
GO:0001104|GO:0008013|GO:0006366|GO:0006357|GO:0016592|GO:0008134 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_129615_PI430048170 0.4393936834758871.13187043678286 5.7238933949579
5.77388224785726 5.73793917491028 P P P 5.94945532580308 5.45822602751075
5.18694321043135 P P P LNCV6_129615_PI430048170 mRNA
AGGCCCCACGGACACACTTGGGCTGCTCTGAAATAAAGCTGTTGACTCCACCTGAAAAAA NM_001130413 RefSeq
chr1 + 1280435 1292029 SCNN1D 6339 "sodium channel, non voltage gated 1 delta subunit,
transcript variant 1"
GO:0005515|GO:0015280|GO:0034220|GO:0050909|GO:0016020|GO:0005886|GO:0035725|GO:0016021|GO:0015
629|GO:0006814|GO:0055085|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129686_PI430048170 0.7660677136068240.9711495078158373.73207378739096
4.25588703666708 4.07811407926757 P P P 4.0295185550403 3.992280804443
4.20962803812962 P P P LNCV6_129686_PI430048170 mRNA
CATGTGTTCTCTGATTGTGAGGTCACTGTGAATGATTAAATTGGTAAGGGTAAAGTAAAA NM_005527RefSeq
chr6_GL000255v2_alt - 3065447 3070886 HSPA1L 3305 heat shock 70kDa protein 1-like
GO:0005515|GO:0006986|GO:0072562|GO:0007339|GO:0005524|GO:0044297|GO:0005829|GO:0034605|GO:0042
026|GO:0008180|GO:0005759|GO:0002199|GO:0005654|GO:0051082|GO:1900034 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134659_PI430048170 0.0786902656971829 0.90960565777302812.1831302567536
12.1217099582552 12.1211729604108 P P P 12.361022473419 12.2048372948951
12.2667955672692 P P P LNCV6_134659_PI430048170 mRNA
TGGGCCAGGCATAGACTGAACCAATAAAGAGATGTCACGTCACCTTCTCCCGATAAAAAA NM_017722RefSeq chr19
- 13104899 13116649 TRMT1 55621 "tRNA methyltransferase 1 homolog (S. cerevisiae), transcript
variant 1" GO:0004809|GO:0000049|GO:0030488|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131822_PI430048170 0.1045038398578760.6342716647816326.59112829894839
6.36280349239992 6.66433459052289 P P P 6.69118233483174 7.41071944243872
7.39386376969146 P P P LNCV6_131822_PI430048170 mRNA
AGGGTGCTCTGAGTTTTGGGATGGTCACATGACACAATCCAGCACTTGAACCTGAAAAAA NM_005811RefSeq chr12
+ 55743279 55752881 GDF11 10220 growth differentiation factor 11
GO:0001656|GO:0001657|GO:0021512|GO:0008285|GO:0010862|GO:0042981|GO:0048593|GO:0005575|GO:0060
395|GO:0005125|GO:0005160|GO:0005615|GO:0007399|GO:0001501|GO:0031016|GO:0043408|GO:0060021|GO:0
048469|GO:0007498|GO:0048468|GO:0045596|GO:0040007|GO:0008083 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129113_PI430048170 0.00323330309032766 2.61811354006702 8.03377922613956
8.47450269794421 8.33576631461167 P P P 7.20740891206172 6.65990727125874
6.78726016685835 P P P LNCV6_129113_PI430048170 mRNA
CATATCAGCCCCTTCATTCCATGTATTCCAGTTGTAAAACAAGTATCAAAATATTGGGAA NM_001004323 RefSeq
chr7 - 100456614 100464271 C7orf61 402573 chromosome 7 open reading frame 61 GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132207_PI430048170 0.1910667116170580.3687903400917730.367337327811877
0.2547700459290760.307447955297646 A A A 2.27126246223351 2.01584055168139
0.283484197081227 A A A LNCV6_132207_PI430048170 mRNA
GATAATGACTTTGGAATTATCTCTCCTGGGTCTCAGTTAATAAACTGAAGAATGACCTAA NM_030667RefSeq chr12
+ 15322256 15598331 PTPRO 5800 "protein tyrosine phosphatase, receptor type, O, transcript variant
1"
GO:0005515|GO:0072112|GO:0043005|GO:0017147|GO:0030424|GO:0090260|GO:0036060|GO:0005886|GO:0030
032|GO:0010812|GO:0042803|GO:0032835|GO:0035335|GO:0030426|GO:0016791|GO:0016324|GO:0006470|GO:0
043197|GO:0007411|GO:0005001|GO:0090090|GO:0004725|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_132357_PI430048170 0.0588477690089872 0.5616099195401544.08925618421794
3.99555672719839 4.29781087435687 P P P 4.48458436507268 5.25770608057511
5.04814309289143 P P P LNCV6_132357_PI430048170 mRNA
CATCAGATGGCCAAACTGTATTTATAATCCACTTAGGCATTTTGAAAAACTTTCAACCTG NM_016228RefSeq chr4
- 170060221 170090032 AADAT 51166 "aminoadipate aminotransferase, transcript variant 1"
GO:0070189|GO:0006569|GO:0006536|GO:0009058|GO:0033512|GO:0047536|GO:0044281|GO:0042803|GO:0034
641|GO:0097052|GO:0019441|GO:0005759|GO:0006103|GO:0030170|GO:0016212|GO:0006554 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_98303_PI430048170 0.0057798160487717 1.66707154013569 10.6831020797635
10.6940535570462 10.8841992709453 P P P 9.98451966702557 9.85295606481314
10.1995319328613 P P P LNCV6_98303_PI430048170 mRNA
AGAACACAGTCACGAGGATAATGGGAATTTACCGAAACCCGTGGAAGCCTTTAAGGAATG NM_016627RefSeq
chr17 + 68248003 68257164 AMZ2 51321 "archaelysin family metallopeptidase 2, transcript variant 1"
GO:0006508|GO:0008270|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129597_PI430048170 0.4485979650342810.9086438948012785.94998685220403
5.99080154699974 6.41580136184123 P P P 6.21212364792156 6.15134779202758
6.43909784886556 P P P LNCV6_129597_PI430048170 mRNA
GTCCTTCTTAGAATGTTCTAAAATGTCAAGGCAGTTGCTTGTGTTTAACTGTGAACAAAT NM_000368RefSeq chr9
- 132891347 132944633 TSC1 7248 "tuberous sclerosis 1, transcript variant 1"
GO:0045859|GO:0005515|GO:0008286|GO:0017148|GO:0032007|GO:0008285|GO:0021987|GO:0005886|GO:0005
884|GO:0051492|GO:0051087|GO:0051894|GO:0051291|GO:0043231|GO:0005829|GO:0030426|GO:0006407|GO:0
005737|GO:0046323|GO:0051726|GO:0007050|GO:0055007|GO:0006813|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140052_PI430048170 0.6805096666551291.1416542053385 6.32754036895837 5.4125421287296
6.24721652622835 P P P 5.66830618322652 6.03753245830455 5.84926888950956 P P P
LNCV6_140052_PI430048170 mRNA
GCTGAGGGTCCTGCCTCATTAAGATGCAATAAATATGTAAGTACATAAAAACAGCAATAG NM_139075RefSeq chr11
+ 69048881 69090604 TPCN2 219931 two pore segment channel 2
GO:0005515|GO:0051209|GO:0086010|GO:0005245|GO:0005886|GO:0019901|GO:0006874|GO:0005765|GO:0055
085|GO:0042802|GO:0006939|GO:0034220|GO:0072345|GO:0070588|GO:0006816|GO:0034765|GO:0016021|GO:0
010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129839_PI430048170 0.0260398308428686 1.14819637072315 9.39802116610264
9.45211666830751 9.52798137243333 P P P 9.17754665068288 9.323923081731 9.2776456462288
P P P LNCV6_129839_PI430048170 mRNA
GAGAGAAGATCAGTTTGGGCTTCACAGTGTCATTTGAAAACGTTTTTTGTTTTGTTTTGT NM_198057RefSeq chrX
- 107713221 107775787 TSC22D3 1831 "TSC22 domain family, member 3, transcript variant 1"
GO:0007589|GO:0006355|GO:0034220|GO:0003700|GO:0070236|GO:0043426|GO:0006970|GO:0005634|GO:0000
122|GO:0048642|GO:0055085|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143431_PI430048170 0.2879927276797921.12717657699956 11.0852513573575
11.3405597655816 11.2007535519411 P P P 11.2360378179314 11.0361001019334
10.8173629072898 P P P LNCV6_143431_PI430048170 mRNA
AGGTTGTTTCCACTAGGAGATTTTTATAAACCCTCTCCAGCCTCTCCCAAAGGAAGCGTT NM_001244666 RefSeq
chr11 - 62806859 62832091 STX5 6811 "syntaxin 5, transcript variant 2"
GO:0005515|GO:0045732|GO:0005794|GO:0005783|GO:0031201|GO:0048280|GO:0090166|GO:0006886|GO:0006
906|GO:0031982|GO:0006888|GO:0005484|GO:0047485|GO:0000139|GO:0034498|GO:0033116|GO:0000149|GO:0
042147|GO:0005654|GO:0016021|GO:0048278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105101_PI430048170 0.2999877873936780.8925856602672435.73199027682875
5.74095781847061 5.83998061824335 P P P 5.72076329567277 5.94972004365983 6.1104314910556
P P P LNCV6_105101_PI430048170 mRNA

CGAGCTTGCAGTTATCTATTTCTTTGTGCCATTCCTCAAATGATAAGAAATCCCAAAAAT NM_004268 RefSeq chr11 + 93784238 93813330 MED17 9440 mediator complex subunit 17
GO:0003712|GO:0005515|GO:0005667|GO:0010467|GO:0001104|GO:0006367|GO:0006357|GO:0003713|GO:0005634|GO:0046966|GO:0030374|GO:0030518|GO:0016020|GO:0042809|GO:0045944|GO:0019827|GO:0016592|GO:0004872|GO:0005654|GO:0045893|GO:0030521 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141935_PI430048170 0.75039857499854 0.9880335238138520.415247486292987 0.3842040176780620.248743311558003 A A A 0.3408341669699130.389711808176171 0.374696388371442 A A A LNCV6_141935_PI430048170 mRNA
TGCTTGGTGTTTGTTTTTAACGCACAACTTGCTTGTACAGTAAACTGTCTTCTGTACTAT NM_001031680 RefSeq chr1 - 24899510 24965010 RUNX3 864 "runt-related transcription factor 3, transcript variant 1"
GO:0005515|GO:2001238|GO:0000790|GO:0006355|GO:0000977|GO:0003700|GO:0005794|GO:0006366|GO:0000981|GO:0050680|GO:0005730|GO:0005634|GO:0000122|GO:0045786|GO:0005524|GO:0043231|GO:0031069|GO:0005737|GO:0007411|GO:0002062|GO:0048935|GO:0048469|GO:0006468|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130834_PI430048170 0.9147814064591681.0120463565357 8.16837577744037 8.4198489702069 8.52788506031873 P P P 8.21197417248734 8.30361036922459 8.55034001628221 P P P LNCV6_130834_PI430048170 mRNA
TATCTGATCAGGAACTTGTCATGATTTCCTTTCTTAGACTTCATAGGAGATAGTGCTTTA NM_022087 RefSeq chr7 + 152025673 152122347 GALNT11 63917 "polypeptide N-acetylgalactosaminyltransferase 11, transcript variant 1"
GO:0007368|GO:0007220|GO:0005112|GO:0016266|GO:0046872|GO:0061314|GO:0004653|GO:0000139|GO:0006493|GO:0060271|GO:0030246|GO:0018243|GO:0016021|GO:0044267|GO:0008593|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139480_PI430048170 0.000978820973184574 1.33127336141584 12.9367973811168 12.9748083432933 12.8940553607465 P P P 12.4754484604218 12.5877359566132 12.5027965068231 P P P LNCV6_139480_PI430048170 mRNA
TCATTTGGGGATGGAAGGAATCTGTCCCGCATCGGGAATAAAATTTATGATGCAAATTTG NM_021177 RefSeq chr6_GL000255v2_alt - 3053217 3062802 LSM2 57819 "LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)"
GO:0008380|GO:0005515|GO:0010467|GO:0019901|GO:0000398|GO:0043928|GO:0005654|GO:0071013|GO:0017070|GO:0017160|GO:0005829|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140410_PI430048170 0.0416049871401226 0.5910622611663528.28308024797292 8.23465754850088 8.5736453573016 P P P 8.80781615650058 9.03726401523171 9.46698289690206 P P P LNCV6_140410_PI430048170 mRNA
CCAATAAGTGGAGATTCCTCCTTATGATGTATGCTAGGTTATGGAAGATGTAAAATATTC NM_005109 RefSeq chr3 + 38165534 38255488 OXSR1 9943 oxidative stress responsive 1
GO:0005515|GO:0023014|GO:0000287|GO:0071476|GO:2000687|GO:0005524|GO:0035556|GO:0005737|GO:0004702|GO:0004674|GO:0018107|GO:0006468|GO:0006979|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119237_PI430048170 0.1944567632450891.02507851013586 16.8216623879831 16.7777793187243 16.7576247876299 P P P 16.7576247876299 16.739255850033 16.7536629512591 P P P LNCV6_119237_PI430048170 mRNA
AAGAAAGCCGAGGCTGGGGCTGGGTCAGCAACCGAATTCCAGTTTAGAGGCGGATTTGGT NM_001203245 RefSeq chr6 - 34417453 34426041 RPS10 6204 "ribosomal protein S10, transcript variant 1"
GO:0005515|GO:0010467|GO:0019083|GO:0006614|GO:0019058|GO:0005730|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0000184|GO:0022627|GO:0016032|GO:0005840|GO:0044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139443_PI430048170 0.0531582830619607 0.6835361120866269.99989860390457 10.0451759365402 10.0643866719335 P P P 10.3357963812193 10.7938864019379

10.5910407445192 P P P LNCV6_139443_PI430048170 mRNA
AATTTCCGGTTTGATTTATGAGGAGACTCGTGGCGTTCTCAAGGTGTTTCTGGAGAACGT NM_003544RefSeq chr6
- 26026895 26027252 HIST1H4B 8366 "histone cluster 1, H4b"
GO:0005515|GO:0010467|GO:0006325|GO:0005634|GO:0045653|GO:0000723|GO:0000183|GO:0000786|GO:0070
062|GO:0035574|GO:0035575|GO:0046982|GO:0006334|GO:0006335|GO:0005576|GO:0006336|GO:0000228|GO:0
003677|GO:0032776|GO:0034080|GO:0043234|GO:0016020|GO:0045814|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131028_PI430048170 0.177344204723651 1.08362939979333 8.56236964039689
8.49336973352469 8.43028074224355 P P P 8.28424868072279 8.483836396641
8.36634713330858 P P P LNCV6_131028_PI430048170 mRNA
AAGGGACCTCCTGAAAACTCGCTCTTTATAAACGAGGCAAAAGCATTTAATTCCCACCCC NM_015649RefSeq chr19
- 45883606 45886170 IRF2BP1 26145 interferon regulatory factor 2 binding protein 1
GO:0005515|GO:0006355|GO:0016235|GO:0016874|GO:0005654|GO:0046872|GO:0006351|GO:0043231 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127106_PI430048170 0.56582770963624 0.8805631736785660.340548539859218
0.3133521099598120.420235531513638A A A 0.2977775336113930.280184908963759
0.944983848653404A A A LNCV6_127106_PI430048170 mRNA
CTCAATTAAGTATGAGTTTGAATTTAGTTTGAAATCTGGAATTGGCCAGACTGTGGTCAT NM_001714RefSeq chr12
+ 32107250 32378207 BICD1 636 "bicaudal D homolog 1 (Drosophila), transcript variant 1"
GO:0005802|GO:0005515|GO:0005881|GO:0048471|GO:0034452|GO:0031871|GO:1900737|GO:0072385|GO:0009
653|GO:0005829|GO:0016032|GO:0005856|GO:0072517|GO:0008093|GO:0006396|GO:0045298|GO:0017137|GO:0
008298|GO:0005794|GO:0033365|GO:0031410|GO:1900275|GO:0072393|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144683_PI430048170 0.00594894979746676 0.5537566917358096.17888079513042
6.44220670413317 6.55327960036548 P P P 7.27742317680364 7.13454730985612
7.33809826204208 P P P LNCV6_144683_PI430048170 mRNA
GAGTATTTTTCTGATCAAGTGATAACCAAAGTGTCACTGCAAGAGATATTCAAGTTCTAC NM_017909RefSeq chr6
- 151404761 151452181 RMND1 55005 "required for meiotic nuclear division 1 homolog (S. cerevisiae),
transcript variant 1" GO:0005739|GO:0006412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128734_PI430048170 0.00216502748011296 0.3360017613903735.60225212633953
5.09511559508394 5.31403501796568 P P P 6.68337260683729 7.22753748947403 6.8081344966513
P P P LNCV6_128734_PI430048170 mRNA
GAGATGAAGATCCTGGCTCTGTGCTGTGCACATAGGTGTTTAATAAACATTTGTTGGCAG NM_013389RefSeq chr7
- 44512535 44541315 NPC1L1 29881 "NPC1-like 1, transcript variant 1"
GO:0042632|GO:0005515|GO:0006695|GO:0017137|GO:0005886|GO:0042493|GO:0044281|GO:0031526|GO:0030
301|GO:0030299|GO:0031489|GO:0007165|GO:0016324|GO:0008144|GO:0042157|GO:0015918|GO:0008158|GO:0
016021|GO:0030659. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63430_PI430048170 0.0236859568539089 0.8230195612006271 3.797512757143
13.9072642140079 13.8418095260872 P P P 14.2367013818813 14.1129898881203
14.0347998221427 P P P LNCV6_63430_PI430048170 mRNA
TTCTCTGGAGATTCCTGCAACCTCAAGAGACTTCCCAGGCGCTCAGGCCTGGATCTTGCT NM_022036RefSeq chr17
+ 74431527 74447429 GPRC5C 55890 "G protein-coupled receptor, class C, group 5, member C, transcript
variant 1"
GO:0043235|GO:0005739|GO:0007186|GO:0005887|GO:0004930|GO:0031982|GO:0030659|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134422_PI430048170 0.00842973116699692 0.5406700651891522.37908766145021
2.05999444928367 1.94257405731029 A A A 2.88168275892686 3.09408182499959
3.09326488021737 P P P LNCV6_134422_PI430048170 mRNA
GATAAATCAGGAGATGGCTGATTCATAATGGGTAATAAAATAAATAGCACTTTCGAGCTG NM_207352RefSeq chr4

+ 186191519 186213463 CYP4V2 285440 "cytochrome P450, family 4, subfamily V, polypeptide 2"
GO:0004497|GO:0010430|GO:0005506|GO:0005789|GO:0016705|GO:0016021|GO:0007601|GO:0050896|GO:0020
037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144849_PI430048170 0.0240504587802101 0.79072146869801 6.06532281538755
5.91270454768684 6.15607400620546 P P P 6.38910405070682 6.32292807692012
6.44611887503317 P P P LNCV6_144849_PI430048170 mRNA
TAGGCAAAACTTTCAGTACTAAGCAATTTTAGTCTCTGCAGGCTCTTGTCTTGAATTAAT NM_001297734 RefSeq
chr19 - 57905773 57916616 ZNF417 147687 "zinc finger protein 417, transcript variant 2"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128949_PI430048170 0.0123167956824981 8.8688488592719 4.68956418946591
4.15428439878871 4.50029791384514 P P P 3.31191514795083 3.72181630110499 3.6230302743889
P P P LNCV6_128949_PI430048170 mRNA
CTTGACATCTGTTGCTCTACAGTTGTCAACTAGAAAATTAGGCATAGAGTTTCACATTAT NM_025152 RefSeq chr14
+ 31561384 31861223 NUBPL 80224 "nucleotide binding protein-like, transcript variant 1"
GO:0005739|GO:0032981|GO:0051539|GO:0070584|GO:0005524|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_108885_PI430048170 0.142946683676306 1.1787921445506 9.94529341367805
10.1661974650033 9.86439296255723 P P P 9.64754156190966 9.6719310694329
9.94265884093068 P P P LNCV6_108885_PI430048170 mRNA
TATTTCTCTTGACAACCAAGGGCCTCCGTCTGGATTTCCAAGGAAGAATTTCCTCTGAAG NM_000034 RefSeq chr16
+ 30053089 30070420 ALDOA 226 "aldolase A, fructose-bisphosphate, transcript variant 1"
GO:0005515|GO:0008092|GO:0008360|GO:0006094|GO:0006941|GO:0005634|GO:0044281|GO:0015629|GO:0005
615|GO:0046716|GO:0006096|GO:0042802|GO:0005829|GO:0004332|GO:0006754|GO:0015631|GO:0051289|GO:0
006006|GO:0031093|GO:0007015|GO:0070061|GO:0070062|GO:0006000|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_122531_PI430048170 0.472276052750306 0.946471176161239 8.73485100418503
8.60930711566348 8.68486098147994 P P P 8.81390894422134 8.85485799664948
8.58694934607799 P P P LNCV6_122531_PI430048170 mRNA
TTCTTTGACGTGAAGACAACGCGTCGCGTTTACAACTTCTGTGCCCAGGACGTGCCCTCG NM_002972 RefSeq chr22
- 50445000 50475071 SBF1 6305 SET binding factor 1
GO:0017112|GO:0006470|GO:0032851|GO:0005634|GO:0016021|GO:0008138|GO:0007283 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_70352_PI430048170 0.893520369772862 1.0098864421541 5.05796747012087 4.66106538476775
5.10476500115769 P P P 4.41746763238253 5.04445641620836 5.23805214361207 P P P
LNCV6_70352_PI430048170 mRNA
ATTCTGTGCAAACACTCTTCCAGCAGGCTAGAGCTAAGAGTGAAGAACTTGCAGCTCTTA NM_005966 RefSeq chr2
+ 190649121 190692766 NAB1 4664 NGFI-A binding protein 1 (EGR1 binding protein 1)
GO:0014037|GO:0006355|GO:0001958|GO:0042552|GO:0045682|GO:0005634|GO:0045892|GO:0006351|GO:0008
134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141305_PI430048170 0.0213772130503803 1.16422029782732 9.16712288585226
9.06969773659926 9.20473704463982 P P P 8.87959861581571 8.88783087688968
9.01532737289333 P P P LNCV6_141305_PI430048170 mRNA
TACCTTTTGCGTAGTTAAACAGACGTGTATCCAGTCTAGTTAAGGAAGAAACATTAAGAT NM_145914 RefSeq chr7
+ 100049793 100065041 ZSCAN21 7589 zinc finger and SCAN domain containing 21
GO:0005515|GO:0006355|GO:0001077|GO:0045944|GO:0005634|GO:0000978|GO:0046872|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127831_PI430048170 0.0334376404523052 1.10124532644747 0.672470904013066
0.730931182468892 0.67807085314712 A A A 0.621126948391701 0.516738162930819

0.524563716702025 A A A LNCV6_127831_PI430048170 mRNA
GTGTGTTGCAGATTTATTTGGCCATTTAGAATAACCAAATCAATCTGGCTAACTAGGAAT NM_002736 RefSeq chr7
+ 107044732 107161811 PRKAR2B 5577 "protein kinase, cAMP-dependent, regulatory, type II, beta"
GO:0034236|GO:0005886|GO:0008603|GO:0044281|GO:0007202|GO:0005829|GO:0035556|GO:0005737|GO:0030
552|GO:0043197|GO:0007173|GO:0071377|GO:0043198|GO:0000086|GO:0006631|GO:0006833|GO:0007612|GO:0
034199|GO:0031625|GO:0070062|GO:2000480|GO:0048011|GO:0005952|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129846_PI430048170 0.0575467128460183 1.79795521271109 9.75541052344752
9.88949962847521 9.77549626521443 P P P 8.49630728018712 9.28120648946039
9.00118560339205 P P P LNCV6_129846_PI430048170 mRNA
TGAGTGAGCCCCTAAGCTTCAGTCTGCAATAAAGAATGCATTGGTTTCATCTGCAAAAAA NM_207119 RefSeq chr10
- 70298969 70381914 LRRC20 55222 "leucine rich repeat containing 20, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131110_PI430048170 0.0395576616149865 1.51357134461521 4.35881023652766
4.58319150787583 4.14234399731331 P P P 3.9212250971211 3.89957009369087 3.4576431644133
P P P LNCV6_131110_PI430048170 mRNA
ACAGCCTCCGTATACATATGTACACATATAAATAAAGTGCGTCCGTGCTGCGTGAAAAAA NM_014975 RefSeq chr19
+ 12838444 12874952 MAST1 22983 microtubule associated serine/threonine kinase 1
GO:0035556|GO:0005515|GO:0005737|GO:0000287|GO:0005886|GO:0004674|GO:0007010|GO:0006468|GO:0005
856|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142672_PI430048170 0.4108056774726530.81805559930802 2.50853932251989
3.03960131592112 3.24755990841416 A P P 3.62148867279928 2.85187074728217
3.18434102705769 P P P LNCV6_142672_PI430048170 mRNA
CTGCCGTTGCTAAATGATTTAATAATATTGTAATTCTGTATTTCTTTGGGGGGAAAAGGC NM_194449 RefSeq chr18
+ 62715438 62980443 PHLPP1 23239 PH domain and leucine rich repeat protein phosphatase 1
GO:0005515|GO:0048011|GO:0048015|GO:0006915|GO:0005634|GO:0046872|GO:0005829|GO:0007173|GO:0016
020|GO:0008543|GO:0009649|GO:0016311|GO:0045087|GO:0004721|GO:0038095 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141815_PI430048170 0.1130775510588380.3372101459301292.59377950439944
0.38940509604159 0.345976497323256 A A A 2.8586426921466 3.03735492593125
3.33521756635525 P P P LNCV6_141815_PI430048170 mRNA
GCCAAAGTGTGCACAATGGCTTTTTGTTAATAAAGAACAGATTAGTTTTGAAGAAGGCAA NM_003816 RefSeq
chr8_KI270822v1_alt + 7545 10943 ADAM9 8754 "ADAM metallopeptidase domain 9, transcript
variant 1"
GO:0005515|GO:0042542|GO:0051044|GO:0033627|GO:0017124|GO:0051549|GO:0005518|GO:0050714|GO:0051
088|GO:0005615|GO:0010042|GO:0016323|GO:0005737|GO:0000186|GO:0022617|GO:0030198|GO:0005080|GO:0
030574|GO:0007179|GO:0006509|GO:0007155|GO:0070062|GO:0034241|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135218_PI430048170 0.0439785398873766 1.24248250854812 10.3283826566221
10.2731183563841 10.2939372404075 P P P 9.83646121734575 10.0707079012882
10.0381541948121 P P P LNCV6_135218_PI430048170 mRNA
TTAGTCTAAAAAGCTGTCTGGTTGTATAAACGGTGCAAACAATGTCGCCACAGCACCCAC NM_015160 RefSeq chr9
+ 136410572 136423761 PMPCA 23203 "peptidase (mitochondrial processing) alpha, transcript variant 1"
GO:0005739|GO:0005759|GO:0006626|GO:0006508|GO:0005743|GO:0004222|GO:0044267|GO:0005615|GO:0046
872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133080_PI430048170 0.155219652236804 1.07307249809387 0.49505911110957
0.458817511918583 0.542412589421854 A A A 0.311395422769921 0.396845410066559
0.479151214246894 A A A LNCV6_133080_PI430048170 mRNA
GAGGTCAAAGAGGCTGTAAAGAAAGTCCTGAGCAGACATCTGCATTTATTGAAAATGTGA NM_001004484 RefSeq

chr9 + 104694421 104695462 OR13D1 286365 "olfactory receptor, family 13, subfamily D, member 1"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128052_PI430048170 0.1179900731105491.22040415861159 4.84298327213208
5.18339652517078 4.84546320402165 P P P 4.83243030335179 4.60162699449296
4.58974052031135 P P P LNCV6_128052_PI430048170 mRNA
GTATAAAATAAACTCTCTCTTTTCCCTGGACCCTCCTACTGTATTCTTTCCTCTGTGGCA NM_001040107 RefSeq chr12
- 110648685 110689812 HVCN1 84329 "hydrogen voltage gated channel 1, transcript variant 1"
GO:0071294|GO:0035036|GO:0005886|GO:0022843|GO:0010043|GO:0071467|GO:0007338|GO:0030171|GO:0034
220|GO:0005887|GO:0034765|GO:0016021|GO:0009268|GO:0015992|GO:0032504 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_91913_PI430048170 0.807887634823468 1.04260489702586 7.67775111401005 7.96217900918204
8.26440944522789 P P P 7.53531789207461 7.91314642432624 8.24770025525732 P P P
LNCV6_91913_PI430048170 mRNA
TCTAGGATGATCACTTGTGCTTAGCTTAGCATTGTAACTCTTTAAGTCTATATTTTCCTC NM_015550 RefSeq chr7 -
24796536 24980212 OSBPL3 26031 "oxysterol binding protein-like 3, transcript variant 1"
GO:0005515|GO:0031965|GO:0016020|GO:0005886|GO:0015485|GO:0006869|GO:0097038|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134962_PI430048170 0.0795649513520337 0.6025823514632835.16894457082823
5.09124163872101 4.85767136286396 P P P 5.53419968180475 6.20014073575446
5.47656519932109 P P P LNCV6_134962_PI430048170 mRNA
TTGTGACCAAAGCAATTGTAAAACGTGGGGGAGGAAATTAAAAGCCTGCCACCTTAGTCC NM_176072 RefSeq chr11
+ 73218297 73242427 P2RY2 5029 "purinergic receptor P2Y, G-protein coupled, 2, transcript variant 1"
GO:0042312|GO:0005886|GO:0045028|GO:0005887|GO:0007200|GO:0006873|GO:0004872|GO:0035589|GO:0070
257 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143853_PI430048170 0.0232334062112295 0.7433041490888891 1.3639096952614
11.1914207685792 11.1186689200007 P P P 11.4821604806098 11.7927020546173
11.6772617907632 P P P LNCV6_143853_PI430048170 mRNA
GACGAGACTTCCTCTTGAACAGTGTGCTGTTGTAAACATATTTGAAAACTATTACCAATA NM_001304349 RefSeq
chr19 - 14091694 14108390 PRKACA 5566 "protein kinase, cAMP-dependent, catalytic, alpha,
transcript variant 3"
GO:0005515|GO:2000810|GO:0031594|GO:0035584|GO:0006094|GO:0071158|GO:0046777|GO:0007173|GO:0018
105|GO:0018107|GO:0006833|GO:0019433|GO:0031625|GO:0070062|GO:0005813|GO:0006996|GO:0001707|GO:0
019901|GO:0031588|GO:0005975|GO:0043393|GO:0050804|GO:0001843|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141589_PI430048170 0.0208407104679391 0.5128453256784790.814402352491793
0.48647068584892 0.292499345931908 A A A 1.32286265850794 1.25223791512778
1.87394263490426 A A A LNCV6_141589_PI430048170 mRNA
ACAAAGTGAAGACAGTAGGTCAACAACAGAGCCATTCTTGATAATACAGAATATTTCACA NM_015038 RefSeq chr1
+ 39409503 39416482 KIAA0754 643314 KIAA0754 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_81741_PI430048170 0.4331979886532261.02880711645899 0.3394651853933070.341157662560486
0.461288788848545 A A A 0.3449711880053280.3112806101674160.365634126553486 A A A
LNCV6_81741_PI430048170 mRNA
AAGTTGGAGAGGGAAAAGTTAGCCCAGAAGGAAAGCATTTTCTGCAGATCAGCCTGAATCNM_020717 RefSeq chrX
- 50591644 50814044 SHROOM4 57477 "shroom family member 4, transcript variant 1"
GO:0001725|GO:0030036|GO:0015629|GO:0000902|GO:0005737|GO:0016324|GO:0051015|GO:0009925|GO:0031
941|GO:0050890|GO:0007420|GO:0009898|GO:0007015|GO:0030864|GO:0016460 . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_144179_PI430048170 0.5722958030889350.8054181185334010.485965676174629
0.73812058616962 0.446189343761672A A A 0.3969810942756880.498609496513214
1.47084476335474 A A A LNCV6_144179_PI430048170 mRNA
CGGGGAGGAAGTTAAAGGCTCCTAGCAGGTCCTGAATCCAGAGACAAAAATGCCGTGCCT NM_182532RefSeq
chr1 + 54980663 54992293 TMEM61 199964 transmembrane protein 61 GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_140017_PI430048170 0.2390126736476441.04829252280216 0.57755789437152
0.4716527596511020.587874765132556A A A 0.4524522298782130.540923466062495
0.44032521125454 A A A LNCV6_140017_PI430048170 mRNA
TGTCTAAGACTGTAAAGTTTATTGGGGAGAGGCCATGACTACCTCTGAATTTAGTAAATT NM_001874RefSeq chr12
- 68851175 68963240 CPM 1368 "carboxypeptidase M, transcript variant 1"
GO:0009986|GO:0005886|GO:0006508|GO:0004180|GO:0008270|GO:0031225|GO:0009653|GO:0070062|GO:0004
181 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141590_PI430048170 0.9583588483872260.9874916150035677.94708585712971
8.19355731052437 8.3686350106033 P P P 7.89175778509564 8.21184677287706
8.43920935605756 P P P LNCV6_141590_PI430048170 mRNA
CACCAAAAGGAAGGGTTTTAATCCATTGGATGACGCTTTGTCAAACACAAATGAAATTAA NM_001193538 RefSeq
chr11 + 85628572 85636539 TMEM126B 55863 "transmembrane protein 126B, transcript variant 3"
GO:0008150|GO:0003674|GO:0031966|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129210_PI430048170 0.2117195168118150.5617681414766863.24185985654473
2.12632127243506 1.78306867054342 P A A 3.58231999027272 3.71969181783119
2.48168626074838 P P P LNCV6_129210_PI430048170 mRNA
TTCAGACCCCCCATTTATTTGTATGAAGGCTTCAGTTGCCTTAATAAAGTGCTCTGTGGG NM_080827RefSeq chr20
- 45534196 45539495 WFDC6 140870 WAP four-disulfide core domain 6
GO:0010951|GO:0004867|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79694_PI430048170 0.1107514029015972.42923411011697 2.62372970100216 3.11764285206644
2.20402111340562 A P A 2.31305357639681 0.7842718208685190.395472876209275A A A
LNCV6_79694_PI430048170 mRNA
ATCTTCTGATAAGCACCCAACAGATATCATTCGTTTTAATTACCTAGACAACCGTGACCC NM_172366RefSeq chr8
- 28428408 28490318 FBXO16 157574 "F-box protein 16, transcript variant 1" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_137515_PI430048170 0.3655607674292860.7266846162881422.25835680713197
2.62357036582646 0.914638952392429A A A 2.21127899988276 2.78083874535819
2.62183112638146 A P P LNCV6_137515_PI430048170 mRNA
CCCCCGGAACAAGCCTAAAAATTGTTTCAAAATAAAAACCAAGAAGATGTCTTCACATAT NM_001716RefSeq chr11
+ 118883765 118896271 CXCR5 643 "chemokine (C-X-C motif) receptor 5, transcript variant 1"
GO:0005515|GO:0070098|GO:0005886|GO:0004930|GO:0032467|GO:0006928|GO:0048535|GO:0042113|GO:0006
955|GO:0006935|GO:0007186|GO:0005887|GO:0016494|GO:0009897 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139134_PI430048170 0.3202245726799931.08686463544089 9.81530712932561
9.87121459575671 9.74647641980465 P P P 9.5169630885437 9.8481837017622
9.69106661372562 P P P LNCV6_139134_PI430048170 mRNA
TTTGGGGACTCAATAAACCCTCACTGACTTTTTAGCAATAAAGCTTCTCATCAGGGTTGC NM_032319RefSeq chr2
- 73228005 73233228 PRADC1 84279 protease-associated domain containing 1
GO:0005576|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139077_PI430048170 0.00269202210469541 1.21587664068193 0.876539341929511
0.9041469961467640.93069987430689 A A A 0.6775733377822030.588221711768514
0.59844095911794 A A A LNCV6_139077_PI430048170 mRNA

TGATTTCAAACTCAATGCTACAGAGCACTTTGAATACATCACACCTTATAGGAAAGATAG NM_001002912 RefSeq chr1 - 74568110 74673738 ERICH3 127254 glutamate-rich 3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110681_PI430048170 0.0414222999324447 0.5054108105630414.16003422769363 3.44186692115074 4.06196537692757 P P P 4.95425254337184 4.81916821121491 4.93958853842359 P P P LNCV6_110681_PI430048170 mRNA
AGACCATAAATAAGGGCGAAAACATTACCATGTGAAAAGAATGTATTTCACCTGCAAGTT NM_004490 RefSeq chr2 - 164492812 164621850 GRB14 2888 "growth factor receptor-bound protein 14, transcript variant 1" GO:0007165|GO:0005737|GO:0005886|GO:0000139|GO:0007596|GO:0005070|GO:0009967|GO:0050900|GO:0010008|GO:0043231|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143015_PI430048170 0.1983895210766281.62201809490229 1.90455320430922 0.9147418199473720.931629987091827A A A 0.6718516199047350.60942954700608 0.611319868986276A A A LNCV6_143015_PI430048170 mRNA
AGGCATATGTGGAGCAAGAGAAACTTAAGGATAGTAGAATCGCCACTGTCTGCGCTTTTG NM_033126 RefSeq chr8 - 86048461 86069622 PSKH2 85481 protein serine kinase H2 GO:0004674|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141695_PI430048170 0.00061025134205825 0.1153757350991410.798504997556506 0.3457658306124460.380141872014953A A A 3.49038036848556 3.29901860223101 4.02582938031505 P P P LNCV6_141695_PI430048170 mRNA
TCTGAATCCCATTGTAGCCTGTCAACTAAATTTGAGTGTTAACGGTCTTTTTAAAGTGCA NM_144949 RefSeq chr2 + 46699209 46762788 SOCS5 9655 "suppressor of cytokine signaling 5, transcript variant 2" GO:0005515|GO:0030971|GO:0005154|GO:0016567|GO:0019221|GO:0032436|GO:0007259|GO:0046426|GO:0005737|GO:0007173|GO:0045629|GO:0007175|GO:0045627|GO:0004860|GO:0016049|GO:0009968|GO:0040008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140753_PI430048170 0.46686579444196 1.10270236856056 8.73273901884622 8.82295693189016 8.84792729567476 P P P 8.98289558595248 8.57024407127057 8.3587953533172 P P P LNCV6_140753_PI430048170 mRNA
GGTATAGGGTTGAGGGGAAATAAGTTTTGAGTGAGAAATAAACGTTTTAGCTGAAATTGT NM_130898 RefSeq chr1 + 153967838 153974364 CREB3L4 148327 "cAMP responsive element binding protein 3-like 4, transcript variant 1" GO:0000977|GO:0005794|GO:0005783|GO:0035497|GO:0005634|GO:0007283|GO:0001228|GO:0006351|GO:0030968|GO:0000139|GO:0045944|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133486_PI430048170 0.00173436310135674 0.3394342913194024.75110910967971 4.42706472535226 4.92944195709251 P P P 5.99603390469067 6.27586578288699 6.5105855883337 P P P LNCV6_133486_PI430048170 mRNA
GGAATGCTGAGCAAAATGTGGATGTACTGGTTGTAAATGTTTATATATTGTACAGTACCT NM_152900 RefSeq chr1 + 113390852 113685923 MAGI3 260425 "membrane associated guanylate kinase, WW and PDZ domain containing 3, transcript variant 2" GO:0005515|GO:0005886|GO:0004385|GO:0006915|GO:0005634|GO:0005524|GO:0005109|GO:0035556|GO:0032947|GO:0016020|GO:0046939|GO:0016032|GO:0005923|GO:0043507 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145071_PI430048170 0.0087490983399018 0.63439113321474 4.08476120054294 4.14242678097115 3.81775541323804 P P P 4.81382521946052 4.70771490696723 4.49543657132311 P P P LNCV6_145071_PI430048170 mRNA
GCAGCCCATGGGTATGACATAGGCCAAGGCCCAACTAACAGTCAAGAAACAGCTAAAAAA NM_001441 RefSeq chr1 + 46394266 46413848 FAAH 2166 fatty acid amide hydrolase GO:0005737|GO:0016884|GO:0017064|GO:0031090|GO:0047372|GO:0016021|GO:0005856|GO:0012505|GO:0009062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133283_PI430048170 0.5111897939297040.8095004266819980.562630429017737

0.6242501877039320.575165794487695A A A 0.5933736920667420.4612519378272571.4241852390285
A A A LNCV6_133283_PI430048170 mRNA
GGAGCTAACCAGGATAATCTTTGTCCCCAAAGGCAAACCTTTAAAATAAATAGATCATTA NM_020482RefSeq chr6
+ 96562547 96616636 FHL5 9457 "four and a half LIM domains 5, transcript variant 1"
GO:0005515|GO:0045944|GO:0003713|GO:0008270|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127531_PI430048170 0.3175283694210641.08535676549312 7.6152509986057
7.53338801003774 7.53642453807971 P P P 7.48620941648032 7.57114738087053
7.25665153461512 P P P LNCV6_127531_PI430048170 mRNA
AGAATATCTGCTCCCACTCCTCACATGCTAAGGAAAGTAAAAGCTCTCCCCTGTAAAAAA NM_006858RefSeq chr19
- 10832066 10836307 TMED1 11018 "transmembrane emp24 protein transport domain containing 1,
transcript variant 1"
GO:0005515|GO:0007165|GO:0005793|GO:0005794|GO:0005886|GO:0005783|GO:0033116|GO:0007267|GO:0005
789|GO:0005102|GO:0016021|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144761_PI430048170 0.1357029260978651.21928307014218 10.2599488860338
10.1025401237964 10.3660360149117 P P P 9.78906334755016 9.85681431912013
10.2018562840109 P P P LNCV6_144761_PI430048170 mRNA
CTCTAGTAGTATTCTGTTGTGTCTAGAGAACTGATTTTTTCCTACATACGCAAATTGTAC NM_001267062 RefSeq
chr2 + 131104846 131149852 PLEKHB2 55041 "pleckstrin homology domain containing, family B
(evectins) member 2, transcript variant 4" GO:0055038 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131789_PI430048170 0.0209316764581168 0.6522942994659449.04291765283922
8.96833439751582 9.25693964182505 P P P 9.53072436476357 9.62047574216319
9.94783651522274 P P P LNCV6_131789_PI430048170 mRNA
GTGCTGTAACTGGGTGGTCCTTTTTAAACAAAACATTATTTGCAAAACAGAGGGTATTAT NM_013354RefSeq chr8
- 17229230 17246878 CNOT7 29883 "CCR4-NOT transcription complex, subunit 7, transcript variant 1"
GO:0005515|GO:0010467|GO:0008284|GO:0003700|GO:0008285|GO:0003723|GO:0004532|GO:0000290|GO:0005
634|GO:0031047|GO:0046872|GO:0030014|GO:0005829|GO:0000932|GO:0045944|GO:0004871|GO:0000289|GO:0
000288|GO:0033962|GO:0005975|GO:0060213|GO:0043928|GO:0006351|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131765_PI430048170 0.00922415808449695 0.5945723002445891 1.3379107279789
11.1928880602513 11.1725515825846 P P P 12.0766073040505 12.0949470445285
11.7644198486825 P P P LNCV6_131765_PI430048170 mRNA
TGTAGTTTTGGCGTGGCACTATTGTAATGGAAATAAAATACTTGTACGGAGGGCAAAAAA NM_001113347 RefSeq
chr1 - 21217246 21279690 ECE1 1889 "endothelin converting enzyme 1, transcript variant 3"
GO:0048471|GO:0005886|GO:0034959|GO:0010814|GO:0010815|GO:0005765|GO:0010816|GO:0046872|GO:0042
803|GO:0043583|GO:0019229|GO:0007507|GO:0016486|GO:0016485|GO:0006508|GO:0001921|GO:0003100|GO:0
070062|GO:0033093|GO:0031982|GO:0060037|GO:0004175|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136116_PI430048170 0.0512649701978377 0.9638951191716850.359181428033242
0.3829154726846780.33044603944525 A A A 0.4212179122557680.419142792635535
0.391627512215066A A A LNCV6_136116_PI430048170 mRNA
GTATGCAATATCCATATATACTTTCACAGAACAAAGAGTAAAGAGGCTGAGTGTGACTTT NM_004677RefSeq chrY
+ 18135448 18137029 XKRY NA "XK, Kell blood group complex subunit-related, Y-linked" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134061_PI430048170 0.0472126922405207 1.17060079024947 12.6709347671106
12.6179997683865 12.5116751232948 P P P 12.2549678659475 12.4686714277656
12.3916925937409 P P P LNCV6_134061_PI430048170 mRNA
ACAACCTGGAAAAGTACGGCTTCGAGCCCACACAGGAGGGAAAGCTCTTCCAGCTCTACC NM_032477 RefSeq

chr9 + 137551856 137552555 MRPL41 64975 mitochondrial ribosomal protein L41
GO:0005515|GO:0070124|GO:0070125|GO:0070126|GO:0003735|GO:0006996|GO:0032543|GO:0005743|GO:0006
915|GO:0006412|GO:0005762|GO:0005739|GO:0007049|GO:0030529 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_27317_PI430048170 0.0517063941160829 1.32941695156826 5.54230293979405
5.43996100110472 5.37932423971943 P P P 4.94988521481969 5.26252812140533
4.89351276680812 P P P LNCV6_27317_PI430048170 mRNA
ATCATAGCTACGCTGGGGAACATCGTGGTGGTGGGCGTGGTGTATGCCTTCACCTTCTGA NM_001282463 RefSeq
chr14 + 96039323 96093971 C14orf132 56967 "chromosome 14 open reading frame 132,
transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142450_PI430048170 0.0331507368388922 0.632003146686041 5.84042848791612
5.64247742075388 6.19358025825349 P P P 6.49107300192537 6.46805312365312
6.74184322905699 P P P LNCV6_142450_PI430048170 mRNA
TGAGGGGATTAATATGAAAACTTATGACCTCTTCCTTTAGGAGGGAGTTATCTAAAAGAA NM_005611 RefSeq
chr16 + 53434438 53491648 RBL2 5934 retinoblastoma-like 2
GO:0005515|GO:0005667|GO:0006357|GO:0005730|GO:0043550|GO:0005634|GO:0003677|GO:0006351|GO:0005
737|GO:0051726|GO:0005654|GO:0000278|GO:0070062|GO:0016568 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137591_PI430048170 0.0378041028753413 0.799553119387056 9.37009909443609
9.43548670928496 9.172932988431 P P P 9.56200475435104 9.78695728997192
9.60034617434306 P P P LNCV6_137591_PI430048170 mRNA
GGTGAAATAACACATGTGGGCATTTTCACAACAATCTCTCCCCAGCCTCCCAAATCAAGT NM_020370 RefSeq
chr12 - 54362444 54364486 GPR84 53831 G protein-coupled receptor 84
GO:0043235|GO:0008150|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_131143_PI430048170 0.0212314728948086 0.784853964040172 10.588375624874
10.4404835324723 10.4745682004171 P P P 10.7695147296935 10.7837020538216
10.9919900318737 P P P LNCV6_131143_PI430048170 mRNA
CTTCTCATTCCCATGTGGAACAGGATGCCCACATACTGTCTAATTAATAAATTTTCCATT NM_170695 RefSeq
chr18 + 3451404 3458408 TGIF1 7050 "TGFB-induced factor homeobox 1, transcript variant 1"
GO:0005515|GO:0010467|GO:0007368|GO:0006367|GO:0003700|GO:0008285|GO:0060041|GO:0009953|GO:0048
146|GO:0010470|GO:0007179|GO:0003714|GO:0042493|GO:0070410|GO:0001843|GO:0007275|GO:0000122|GO:0
000978|GO:0006351|GO:0001078|GO:0045666|GO:0048387|GO:0003682|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145448_PI430048170 0.00898319281327512 0.938720645986893 6.8924997704184
6.92813948913954 6.92253035080809 P P P 6.98172802903571 7.03186952457042
7.00308341253546 P P P LNCV6_145448_PI430048170 mRNA
CTATTAGGTGACTATGCATTTCCAGAGAAATGTGGACTTTTCATATTATGTGGTAAGGAT NM_138386 RefSeq
chr4 - 163128670 163166921 NAF1 92345 "nuclear assembly factor 1 ribonucleoprotein, transcript
variant 1"
GO:0005515|GO:0005737|GO:0042254|GO:0006364|GO:0003723|GO:0005732|GO:0005634|GO:0001522 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_112269_PI430048170 0.0488274214665063 1.69281330200163 4.03698796035566
4.19826481814479 3.99719634521944 P P P 2.9596640198857 3.2689786702198
3.6502605807575 P P P LNCV6_112269_PI430048170 mRNA
TCAGAGGAAGAGATCCGAAAAATTCCTATGTTTTCTTCATATAATCCAGGGGAACCAAAC NM_001171080 RefSeq
chrX - 107061887 107118827 RBM41 55285 "RNA binding motif protein 41, transcript variant 2"
GO:0000166|GO:0003723 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137722_PI430048170 0.0852387507840446 1.03164221211054 0.392487788133642

0.403828691636926 0.439435730158632 A A A 0.358630577714714 0.348412319913601
0.393902325644826 A A A LNCV6_137722_PI430048170 mRNA
GTGTATATGTACTAGAACTTTTTTATTAAAGAAACTTTTCCCAGAGGTGCCTGGGGAGTG NM_001793 RefSeq
chr16 + 68644247 68699054 CDH3 1001 "cadherin 3, type 1, P-cadherin (placental)"
GO:0010838|GO:0005886|GO:0048023|GO:0031424|GO:0032912|GO:0003674|GO:0016337|GO:0005737|GO:0005
913|GO:0001895|GO:0007155|GO:0060070|GO:0007156|GO:0060901|GO:0034329|GO:0042493|GO:0005509|GO:0
045216|GO:0022405|GO:0010628|GO:0043568|GO:0032773|GO:0042060|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143698_PI430048170 0.505017971023653 0.880762897738199 6.13335141156571
5.62601181373234 6.33065474976872 P P P 5.94778548041258 6.22136310351762
6.50485928588814 P P P LNCV6_143698_PI430048170 mRNA
TTAGAAAACCACCAGGAAAACTCAAGGAATCAGAAGCCTAAGAAGCGCAAAAAGGGACAG NM_017816 RefSeq
chr4 - 4267700 4290169 LYAR 55646 "Ly1 antibody reactive, transcript variant 1"
GO:0005515|GO:0005730|GO:0005634|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144221_PI430048170 0.183234280871094 0.760295640397144 8.24214277846439
8.2057280965835 8.29582899764153 P P P 8.26240590763701 8.70217453275297
8.89584546893754 P P P LNCV6_144221_PI430048170 mRNA
CTGTTCAACGTGTAAAGAGACCTGATGTTTTCCCTAATAAAGCTGATAACAGATTTTGCA NM_173551 RefSeq
chr9 - 98732008 98796512 ANKS6 203286 ankyrin repeat and sterile alpha motif domain containing
6 GO:0005929|GO:0005737|GO:0042803 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_132318_PI430048170 0.173450114513715 0.495095251179479 0.393217475268212
0.382068472305206 0.257742243243128 A A A 0.38471369909212 1.79173962548255
1.55182490791397 A A A LNCV6_132318_PI430048170 mRNA
CAGCAATAGAGAGGTTTCCTAAATTATCACATGAAGAGGATAGGCTAATCATGAGTAATT NM_001145373 RefSeq
chr10 + 23439268 23442381 OTUD1 220213 OTU deubiquitinase 1
GO:0004843|GO:0070536|GO:0006508 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_139397_PI430048170 0.532201008759376 0.971205735182211 0.428881330491851
0.427277730095881 0.255580917572151 A A A 0.380464967106593 0.45305113558256
0.410535676207761 A A A LNCV6_139397_PI430048170 mRNA
AGGAACCAACAGGTAAAACAACCCTTCAAGGATATGGTCAAAAAGCTTCTGAATCTTTAA NM_001258285 RefSeq
chr12 + 55574414 55575344 OR2AP1 121129 "olfactory receptor, family 2, subfamily AP, member 1"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_135633_PI430048170 0.0010834124695467 0.558288088774587 7.18720985885851
7.23211420694958 7.41998839963543 P P P 8.1100122091806 8.00599359614733
8.24664504894148 P P P LNCV6_135633_PI430048170 mRNA
AATCCCGTGAAACCATCATCAGAGTCACCATAATGAATTTATCTAATCTATCACCTTTGT NM_001204818 RefSeq
chr19 + 57830293 57846238 ZNF587B 100293516 zinc finger protein 587B
GO:0006355|GO:0005634|GO:0003676|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129319_PI430048170 0.0433685483491962 0.59471752693725 0.500961607325008
0.611805830432871 0.913596662051846 A A A 1.71926924743 1.04482132699526
1.46506434393045 A A A LNCV6_129319_PI430048170 mRNA
GTGGTAGTAGTGTGAACATTAAAAAGATAATGTATGTGAAGTACCATTCGAGTGGTGAAT NM_001304420 RefSeq
chr3 + 57757255 57930003 SLMAP 7871 "sarcolemma associated protein, transcript variant 1"
GO:0042383|GO:0005515|GO:0006936|GO:0005815|GO:0005887|GO:0005790 . NA - . NA NA

NA NA NA NA NA NA NA
LNCV6_144267_PI430048170 0.014133151209916 0.612096124073792 8.2547573208014
7.89726785911228 8.31060361805562 P P P 8.74268826574037 8.78145895004316
9.07364044742389 P P P LNCV6_144267_PI430048170 mRNA
CAAAACACACCAAAACCTAGAGCGGTAGTTTTATGTAAATGCTCATGAGTTTGTATCAAT NM_030940 RefSeq
chr9 - 86264547 86282575 ISCA1 81689 iron-sulfur cluster assembly 1
GO:0005739|GO:0051536|GO:0016226|GO:0005198|GO:0046872 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_133105_PI430048170 0.359560416387659 1.51681149412318 0.302865567729539
1.71600660046369 1.42379426773516 A A A 1.19842563185524 0.270211743840324
0.318552435771773 A A A LNCV6_133105_PI430048170 mRNA
ACACAAAAGGATTGATCTGAACATATTCTCATTGTTTCCTTCGGAGGCTTCTTCTGCGGA NM_001005173 RefSeq
chr11 - 5985891 5986985 OR52L1 NA "olfactory receptor, family 52, subfamily L, member 1" NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_134299_PI430048170 0.0226495258860278 0.611225580090355 12.2094207705882
11.8829804410964 11.9600946927354 P P P 12.4665354431626 12.9835808567941
12.7070922332593 P P P LNCV6_134299_PI430048170 mRNA
ACATGTTCTCCAGCAACGACAAGGTGATTAAGAAGATGATTGCAGAGACATCCAGTGGTG NM_001135168 RefSeq
chr17 - 19737984 19745459 ALDH3A1 218 "aldehyde dehydrogenase 3 family, member A1,
transcript variant 1"
GO:0001666|GO:0008284|GO:0005886|GO:0005783|GO:0007584|GO:0042493|GO:0007568|GO:0004029|GO:0006
081|GO:0004028|GO:0051384|GO:0051591|GO:0005615|GO:0043231|GO:0005829|GO:0005737|GO:0008106|GO:0
005654|GO:0055114|GO:0004030 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137136_PI430048170 0.128574959432523 0.850180724840672 9.96038182071167
9.97865831715404 9.67318594501722 P P P 10.1910799065876 10.162290676495
9.9714760158491 P P P LNCV6_137136_PI430048170 mRNA
CAGGAGGAATATTTTTCCTGCACTTTTTCTCAGGTATCAATAAAGTTGTTTCCAACTCAT NM_052902 RefSeq chr2
+ 219597850 219616451 STK11IP 114790 serine/threonine kinase 11 interacting protein
GO:0005737|GO:0008104|GO:0019901|GO:0005765|GO:0043231 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_101678_PI430048170 0.628202974368337 1.12677876295983 3.22700901911746
4.0256255108181 3.78921801071677 P P P 3.39712263144714 3.19314052479346
3.94040561343715 P P P LNCV6_101678_PI430048170 mRNA
ATCTGCTGATGTCCAATACCTGCTTCATGTGTTCTCAGAGCCCTCATCACTTCCCATGCC NM_005449 RefSeq chr1
- 206903285 206922033 FCMR NA "Fas apoptotic inhibitory molecule 3, transcript variant 1" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59620_PI430048170 0.940830557493362 1.23184455183183 2.19711507661191
0.332901807371204 0.35424033911761 A A A 0.648244995268728 1.37249507926488
0.701617955722037 A A A LNCV6_59620_PI430048170 mRNA
TGGTTGCCTTCCTTTTCTGCACCTTGCGATGTGAACTTTGATATTCTGTAATGTCTGGGG NM_003806 RefSeq
chr12 - 116860419 116881427 HRK 8739 "harakiri, BCL2 interacting protein, transcript variant 1"
GO:0032464|GO:0005739|GO:0005515|GO:0043065|GO:0090200|GO:0006915|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126744_PI430048170 0.664942803755693 1.0210149972598 8.80699586744315
8.6889837695174 8.78537786568161 P P P 8.63436692209831 8.82568971167859
8.72765916926673 P P P LNCV6_126744_PI430048170 mRNA
TTTCAATACTGAAAGATTAAAATGGGGAGGTTGCAGGGAGCAGAGCTTTTCCCTAGCACC NM_024098 RefSeq
chr11 + 60841955 60851088 CCDC86 79080 coiled-coil domain containing 86
GO:0005515|GO:0005730|GO:0016032|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA

NA NA NA NA
LNCV6_127341_PI430048170 1.93287719513891e-05 0.257056263209315 6.88432962916508
6.71867522637284 6.80880285854885 P P P 8.69426861208059 8.71393902691591
8.88053880789291 P P P LNCV6_127341_PI430048170 mRNA
CTTCTGTGGCAAATGCCAGTTTTGTTTAATAATGTACCTATTCCTTCAGAAAGATGATAC NM_007127 RefSeq chr2
+ 218419114 218449525 VIL1 7429 villin 1
GO:0005515|GO:0008360|GO:2000392|GO:0030175|GO:0032432|GO:0032433|GO:0042803|GO:0042802|GO:0051
014|GO:0061041|GO:0009617|GO:0005737|GO:0051015|GO:0007173|GO:0035727|GO:0032233|GO:0035729|GO:0
030855|GO:0030041|GO:0030042|GO:0043154|GO:0043027|GO:0070062|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143723_PI430048170 0.000512124115678079 7.73758017497828 3.10838946438764
3.74087684389472 3.35803345600024 P P P 0.3551945315095660.351862276977894
0.689062643543856 A A A LNCV6_143723_PI430048170 mRNA
TCAGAGCCACATTGAGTTGCTTTTTCTGGGATGAGGAAGTAGGGTTAAACTCCCCAGTTT NM_024046 RefSeq chr3
- 49857988 49869936 CAMKV 79012 CaM kinase-like vesicle-associated
GO:0005516|GO:0004672|GO:0005886|GO:0006468|GO:0005524|GO:0030659 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144098_PI430048170 0.84866688379019 0.9743362788735883.41609131861985 4.0330565912328
3.5292571652315 P P P 3.46119626654909 3.96220627659132 3.70127180220197 P P P
LNCV6_144098_PI430048170 mRNA
CTGTCTGAAAACAAATAAAGCAGATGCCTTTGTTTTCAGTCGTTGACTCACTGGCAAACA NM_032343 RefSeq chr3
+ 126704219 126960420 CHCHD6 84303 coiled-coil-helix-coiled-coil-helix domain containing 6
GO:0005739|GO:0005515|GO:0005743|GO:0042407|GO:0006974 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_92156_PI430048170 0.9191149893853750.9625103739229279.36447905095397 9.65603189734133
9.32574569289275 P P P 9.90828079881733 9.16497206431054 9.35485296861656 P P P
LNCV6_92156_PI430048170 mRNA
ATTACCATTTGGACTCCAGTGGTAGCTATGTATTTGAGAACACAGTGGCTACGGTGATGG NM_001605 RefSeq chr16
- 70252393 70289509 AARS 16 alanyl-tRNA synthetase
GO:0010467|GO:0002161|GO:0000049|GO:0006419|GO:0004813|GO:0005524|GO:0006400|GO:0008033|GO:0030
968|GO:0005829|GO:0006418|GO:0043524|GO:0005737|GO:0016020|GO:0021680|GO:0006457|GO:0050885|GO:0
008270|GO:0006450|GO:0043200|GO:0016597|GO:0001942|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_143839_PI430048170 0.2862397333487630.8875937865835629.54964273339537 9.5575068764968
9.49681191033623 P P P 9.47042691261697 9.81559386695263 9.80854905221307 P P P
LNCV6_143839_PI430048170 mRNA
GGGGCGTATCCACAAAATCACCGAATTCATACAGATCGTTTAAATAAATGAACATCATTA NM_018390 RefSeq chrY
+ 281393 303355 PLCXD1 55344 "phosphatidylinositol-specific phospholipase C, X domain containing 1,
transcript variant 1" GO:0006629|GO:0008081 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136318_PI430048170 0.0518494382363065 1.81600623841298 6.57577971378289
7.05346870685373 6.99071752964084 P P P 6.20848201395852 6.26979840866139
5.47879857418588 P P P LNCV6_136318_PI430048170 mRNA
CCCGTAAAATCCAGGATTTTTTGTTTTTTGCTACAATCTTGACCCCTTTGCTACATTCCT NM_001301267 RefSeq chr16
- 56666734 56668065 MT1G 4495 "metallothionein 1G, transcript variant 2"
GO:0071294|GO:0005515|GO:0071280|GO:0048471|GO:0035924|GO:0005737|GO:0042117|GO:0030224|GO:0008
270|GO:0005634|GO:0071276|GO:0045926 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131988_PI430048170 0.0791561657523374 0.6307449919845629.9825586335234
9.90582746874061 10.2120886887289 P P P 10.4322426127777 10.4851799162662
11.0969563520575 P P P LNCV6_131988_PI430048170 mRNA

CTCTGTGTCAAACCTGTGGCCACTCTATATGCACTTTGTTTACTCTTTATACAAATAAATNM_002227RefSeq chr1 - 64833222 64966504 JAK1 3716 Janus kinase 1
GO:0005515|GO:0005131|GO:0019221|GO:0005634|GO:0030154|GO:0005829|GO:0060334|GO:0035556|GO:0005737|GO:0060337|GO:0060338|GO:0042127|GO:0038110|GO:0005856|GO:0038083|GO:0046677|GO:0060333|GO:0019903|GO:0005524|GO:0012505|GO:0031234|GO:0016477|GO:0045087|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136778_PI430048170 0.2359555483979420.8862622602934079.49043819424118 9.39340815582478 9.12489239600881 P P P 9.51848458554609 9.54578562104874 9.49090250805726 P P P LNCV6_136778_PI430048170 mRNA
CCCACGTGTCCAAATACACTCCAGATGCAAAATAAAAAGCTCTACGACATTGGCAAAAAA NM_198476RefSeq chr19 - 40740855 40749923 C19orf54 NA chromosome 19 open reading frame 54 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140098_PI430048170 0.1423800328105572.24479205743204 2.69633711735319 2.53351779089015 1.26741514396797 A A A 0.3130113633410841.91556232943817 0.607935793062139A A A LNCV6_140098_PI430048170 mRNA
CAGGCTAGGTCCGGTGCCAATAAATCCTTGTGGAATCTGACTTGAGGGGCAGTGAAAAAA NM_002975RefSeq chr19 + 50723347 50725724 CLEC11A 6320 "C-type lectin domain family 11, member A"
GO:0008284|GO:0005737|GO:0030246|GO:0005576|GO:0008083|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140455_PI430048170 0.6951255552781250.9408501359135981.80092819285504 3.60609580549238 3.36467117648973 A P P 3.46937273867963 2.93768468490434 3.14674723389267 P P P LNCV6_140455_PI430048170 mRNA
TGAACTGCAGCAAGGACAAAAACCTGATTTCCATTGCCTAGAATACTTCAAGTCTTTCAA NM_173487RefSeq chr4 + 129093673 129112688 C4orf33 132321 "chromosome 4 open reading frame 33, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140258_PI430048170 0.4411294184345 1.07573281921143 9.48299039083265 9.51508225760486 9.74150299714803 P P P 9.28963757322562 9.52601248790612 9.60373373955927 P P P LNCV6_140258_PI430048170 mRNA
TTTCTCCATGGTTGAAATAAAACAGGGTGACTGGGAGTTACTTAGAATTCATGAAGATTT NM_001145001 RefSeq chr9 + 124257916 124352440 NEK6 10783 "NIMA-related kinase 6, transcript variant 1"
GO:0005515|GO:0007077|GO:0031572|GO:0005634|GO:0005829|GO:0000910|GO:0005737|GO:0046777|GO:0007059|GO:0018105|GO:0004871|GO:2000772|GO:0043123|GO:0000287|GO:0005815|GO:0019901|GO:0005874|GO:0006915|GO:0051225|GO:0005524|GO:0007165|GO:0007346|GO:0000922|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136562_PI430048170 0.5727715876810820.8745923533494470.328655541684247 0.3331438504568710.498626515132085A A A 0.3273438928999330.296047041159904 1.00668652069363 A A A LNCV6_136562_PI430048170 mRNA
CAAGTTACAAAAGGAATCATGAATCCTGGTAAACAATAAAGAAGATTCAGACACTGAGGGNM_153343RefSeq chr4 - 184088705 184217961 ENPP6 133121 ectonucleotide pyrophosphatase/phosphodiesterase 6
GO:0016042|GO:0006629|GO:0008081|GO:0005886|GO:0047390|GO:0005576|GO:0031225|GO:0019695|GO:0008889|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112282_PI430048170 0.6406848625479630.8340964382540761.18742634904891 1.02406513999166 0.326944213598635A A A 0.36427891438048 1.52225842553979 1.32929316878736 A A A LNCV6_112282_PI430048170 mRNA
CTGGGTATCCCACAGATGCAAAAGGGAGAATAAACCTGAATATTATTACCAGCCTAGAGT NM_145799RefSeq chrX - 119616945 119693370 SEPT6 NA "septin 6, transcript variant I" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135754_PI430048170 0.00402027860353036 0.3308890260150323.10308373919332 3.1202491872663 3.25338468966799 P P P 4.5041749100745 4.98846519867375

4.73487460633712 P P P LNCV6_135754_PI430048170 mRNA
CCATTCTTCACCCCATGTCTTACATAATAAATTGTGGTCTTGATCCTGGATTTAAAAACA NM_032221 RefSeq chr20
- 41402102 41618494 CHD6 84181 chromodomain helicase DNA binding protein 6
GO:0008026|GO:0001221|GO:0036091|GO:0003682|GO:0005665|GO:0005654|GO:0005524|GO:0003677|GO:0006
351|GO:0016568|GO:0008094 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143419_PI430048170 0.0107232068991505 0.6825494176499715.56018418756382
5.40243477326253 5.46961587969636 P P P 5.86330465499157 6.15720190058541
6.05382255028372 P P P LNCV6_143419_PI430048170 mRNA
TTATTTAAGACTTCCCCCTTAATTTATCTGCCCCCAGGATGCGTCAGTCTGTTCAGTGGT NM_032482 RefSeq chr19
+ 2164148 2232578 DOT1L 84444 DOT1-like histone H3K79 methyltransferase
GO:0005515|GO:0006342|GO:0031151|GO:0051726|GO:0046425|GO:0005634|GO:0034729|GO:2000677|GO:0003
677|GO:0018024|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131053_PI430048170 0.6490053105906540.92717141689634 4.59336542484926
4.49120373744457 5.44762994123132 P P P 4.94993897111364 5.23744306805309 4.8444292592843
P P P LNCV6_131053_PI430048170 mRNA
ACATTATGAGTGCTTGTATTTTATCTATTTGAGCTCTTCTCCTATCTTTGCCGACCCCCC NM_001102396 RefSeq chr1
- 114769483 114780687 SIKE1 80143 "suppressor of IKBKE 1, transcript variant 1"
GO:0005515|GO:0045087|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110146_PI430048170 0.1537007523971110.7501998792519234.01412866373512
4.59632683672638 4.01670133490067 P P P 4.36309559887369 4.81056666509265 4.7396682945454
P P P LNCV6_110146_PI430048170 mRNA
TCTGAGTACCTGATCCAGCACGACTCGGAGGCCATCATCAGCACCTGGCATAAGGCCATT NM_001282290 RefSeq
chr17_KI270908v1_alt - 84404 120802 ARHGAP27 201176 "Rho GTPase activating protein 27, transcript
variant 4"
GO:0005622|GO:0007165|GO:0017124|GO:0005737|GO:0016020|GO:0043089|GO:0032855|GO:0030675|GO:0006
898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142035_PI430048170 0.0374798258508762 0.5877268306257694.31864282706652
3.97567787182768 4.3410133077477 P P P 4.64934729978585 4.9319213593794
5.30679568934873 P P P LNCV6_142035_PI430048170 mRNA
CTAGCTAAGCGGATGCTGTATCAACTAGTAACTTGCCATTAAGGATTATTTTATAGCATG NM_001099270 RefSeq
chr9 + 126860664 126885877 ZBTB34 403341 zinc finger and BTB domain containing 34
GO:0006355|GO:0005654|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135110_PI430048170 0.0581479156898212 1.42487002619569 7.07746323954638
7.3032274568116 7.08894155279813 P P P 6.79627712817662 6.77884752232756
6.32599937105162 P P P LNCV6_135110_PI430048170 mRNA
ACTGAACAGCTTCAAAATGGTGCAAGGCACTGCCCAGTCCCTGGCTTCTTCCTCTCTCCT NM_017793 RefSeq chr15
- 74955101 74957434 RPP25 54913 ribonuclease P/MRP 25kDa subunit
GO:0005515|GO:0005815|GO:0004526|GO:0005654|GO:0008033 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135296_PI430048170 0.1019649771402761.20803752708837 8.35828789926547
8.33544789757455 8.22917827749302 P P P 8.00540962588944 8.2197097523179
7.86024752009714 P P P LNCV6_135296_PI430048170 mRNA
GTTTTCATAATAAACTTTATTGTGACAGGCGGGGCTGATCCCTCCCATGTTGGGAAAAAA NM_006284 RefSeq chr11
- 6610816 6612244 TAF10 6881 "TAF10 RNA polymerase II, TATA box binding protein (TBP)-
associated factor, 30kDa"
GO:0005515|GO:0010467|GO:0006368|GO:0048471|GO:0003700|GO:0006367|GO:0006366|GO:0006325|GO:0005
634|GO:0005737|GO:0000125|GO:0016032|GO:0051260|GO:0070063|GO:0004402|GO:0006352|GO:0016578|GO:0
006355|GO:0005669|GO:0030914|GO:0003713|GO:0030331|GO:0033276|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_87124_PI430048170 0.00612155762669023 0.5257839174225676.46033015417216
6.77101577840154 6.57979881699747 P P P 7.32226198003827 7.76704604388498
7.48588765920415 P P P LNCV6_87124_PI430048170 mRNA
CATGTCCTGACCTGTGCACGGGGATGGGGGGACAACTCCTACCCTTCTTTCCCCACATGC NM_001172630 RefSeq
chr19 + 35775514 35788822 ARHGAP33 115703 "Rho GTPase activating protein 33, transcript variant 2"
GO:0005515|GO:0051056|GO:0005886|GO:0007264|GO:0035091|GO:0015031|GO:0032855|GO:0030675|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144515_PI430048170 0.00291546479839655 0.6243544682909677.53213627342889
7.34504990742587 7.60711241335157 P P P 8.07213483778532 8.18501448273045
8.27140661073307 P P P LNCV6_144515_PI430048170 mRNA
CCCTCAAAGAATGGGGTCTGTGGGCTAGTTAAAATAGAAATAAACTTTTAAAATATCCAC NM_018184RefSeq chr3
+ 5122244 5180916 ARL8B 55207 ADP-ribosylation factor-like 8B
GO:0007264|GO:0043014|GO:0048487|GO:0003924|GO:0030496|GO:0051233|GO:0005525|GO:0005765|GO:0005
737|GO:0007049|GO:0007059|GO:0016020|GO:0008152|GO:0031902|GO:0019003|GO:0070062|GO:0051301 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133474_PI430048170 0.1863420749607180.7912470356747146.79301620666768
6.68820024820399 6.83410356102982 P P P 6.78936127201147 7.35905417624609
7.12816501045271 P P P LNCV6_133474_PI430048170 mRNA
AGATTTTCTCGTCTATGATGTCCTTGACCTCCACCGTATATTTGAGCCCAAGTGCTTGGA NM_000561RefSeq chr1
+ 109687795 109693745 GSTM1 2944 "glutathione S-transferase mu 1, transcript variant 1"
GO:0043295|GO:0005737|GO:0006805|GO:0018916|GO:0070458|GO:0042178|GO:0006749|GO:0044281|GO:0019
899|GO:0004364|GO:0042803|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64282_PI430048170 0.1354342677507491.14751115825054 8.75759113365016 8.68693642135687
8.75025805932117 P P P 8.35568783280536 8.62049575044548 8.60891492804152 P P P
LNCV6_64282_PI430048170 mRNA
AGGGCTCTGGGGACACTTCCATAGGAAAGGGGCCTGGCACTTTGTGATTGCCACGTGTTT NM_005934RefSeq chr19
- 6210380 6279948 MLLT1 4298 "myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog,
Drosophila); translocated to, 1"
GO:0005515|GO:0006355|GO:0005737|GO:0006366|GO:0005730|GO:0005654|GO:0005634|GO:0006469|GO:0008
023|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140971_PI430048170 0.6937650782318870.8800344408791931.78869239167495
2.38113360320076 1.90370070334973 A A A 1.8281516189221 2.74707787989904
1.93848027125742 A P A LNCV6_140971_PI430048170 mRNA
CTGGCTCAGGCTTCTGGGCTCTGAGAAATAAACTATGAGAGCAATTTCCTCAGGAAAAAA NM_004345RefSeq chr3
+ 48223346 48225491 CAMP 820 cathelicidin antimicrobial peptide
GO:0005515|GO:0008284|GO:0051873|GO:0050830|GO:0042581|GO:0005618|GO:0042995|GO:0005615|GO:0005
829|GO:0071356|GO:0071354|GO:0044130|GO:0090382|GO:0042742|GO:0070062|GO:0051701|GO:0045766|GO:0
002227|GO:0050829|GO:0071222|GO:0071347|GO:0019731|GO:0001934|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140655_PI430048170 0.4567125037929790.9198873166941965.93571710761618
6.40085479358838 5.98676007526362 P P P 6.30347501053028 6.20828437415294
6.21750426585684 P P P LNCV6_140655_PI430048170 mRNA
TACCTCATTCTGACACCTGCATATAGTGTGGGAAATTGCTCTGCATTTGACTTAATTAAA NM_052880RefSeq chr22
- 31281592 31292534 PIK3IP1 113791 "phosphoinositide-3-kinase interacting protein 1, transcript variant
1" GO:0005886|GO:0043553|GO:0016021|GO:0014067|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_136674_PI430048170 0.3642224025534580.7767254778744720.353347081789068
0.4192152600679540.333700738927978 A A A 0.4681064233571640.361292996364926

1.21473139740736 A A A LNCV6_136674_PI430048170 mRNA
TACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTAATGCCTCCTTTTGGCTCCAAG NM_012131 RefSeq chr21
- 30165922 30166653 CLDN17 26285 claudin 17
GO:0016338|GO:0070830|GO:0005886|GO:0005198|GO:0034329|GO:0016021|GO:0005923|GO:0045216|GO:0042
802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144780_PI430048170 0.1135972767919560.5250828877303491.12146218030702
0.5152831887642991.16223001988737 A A A 1.1678467189922 2.37410560700157
1.88628603549849 A A A LNCV6_144780_PI430048170 mRNA
ATCCTCTCTGCTGTTCACATTATCCTTTGTTTAACGTATGAACCAGGTTACTAAAATAGG NM_031435 RefSeq chr12
+ 71663896 71680648 THAP2 83591 "THAP domain containing, apoptosis associated protein 2"
GO:0005730|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139982_PI430048170 0.3336794520561350.5094491709144491.86818912353354
0.3314727349083451.32452299562319 A A A 2.56538229902062 2.79062647537616
0.777069673746469 A P A LNCV6_139982_PI430048170 mRNA
GATTTACACTGGGAGAGGTGCCAGCAACTGAATAAATACCTCTTAGCTGAGTGGAAAAAA NM_004131 RefSeq chr14
- 24630955 24634226 GZMB 3002 "granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated
serine esterase 1)"
GO:0001772|GO:0005515|GO:0004252|GO:0006915|GO:0005634|GO:0097193|GO:0043231|GO:0005829|GO:0005
737|GO:0006955|GO:1900740|GO:0007219|GO:0016020|GO:0016485|GO:0019835|GO:0006508|GO:0008236|GO:0
008626 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137457_PI430048170 0.0636295010406785 1.49133288543082 7.84736454529049
7.81364802966282 7.73100013189011 P P P 7.53173754129122 7.01556372827247
7.05861179497153 P P P LNCV6_137457_PI430048170 mRNA
AGAGTGCATGAGTTGCTTCGAAATAAAAGGGTCAAGCATTCCTACCTGAGACAGGTTAAA NM_001031677 RefSeq
chr5 - 177301189 177303744 RAB24 53917 "RAB24, member RAS oncogene family, transcript variant 1"
GO:0005515|GO:0005776|GO:0003924|GO:0006914|GO:0030139|GO:0005525|GO:0006886|GO:0005829|GO:0005
739|GO:0006184|GO:0016020|GO:0032482|GO:0019003|GO:0005768 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143881_PI430048170 0.9938310307358950.9985607630361089.79965959804457
9.89576730076827 9.91394370958346 P P P 9.82316297648738 9.77435229163607
10.0098359870815 P P P LNCV6_143881_PI430048170 mRNA
GGTCATCTGCTGGGATCTAGTTTTCCAAGTAACATTTTGTGGTGACAGAAGCCTAAAAAA NM_004628 RefSeq chr3
- 14145147 14178672 XPC7508 "xeroderma pigmentosum, complementation group C, transcript
variant 1"
GO:0005515|GO:0000404|GO:0005886|GO:0000405|GO:0042493|GO:0031573|GO:0005730|GO:0071942|GO:0005
634|GO:0003684|GO:0005737|GO:0006281|GO:0003697|GO:0010224|GO:0000715|GO:0005654|GO:0006289|GO:0
000718|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145196_PI430048170 0.2631747804585651.04224679957251 0.567231466684264
0.65929453533256 0.530569538068734 A A A 0.5401106137437520.519208742946831
0.521660862844968 A A A LNCV6_145196_PI430048170 mRNA
TCTCGCTAGTGATGTTTTTATGATATCCCTGATCCTAACTGAAGAGACAGTTATTTATAG NM_002594 RefSeq chr20
+ 17226951 17484577 PCSK2 5126 "proprotein convertase subtilisin/kexin type 2, transcript variant 1"
GO:0005515|GO:0030133|GO:0016540|GO:0004252|GO:0005615|GO:0032403|GO:0030425|GO:0007399|GO:0034
230|GO:0034231|GO:0016020|GO:0006508|GO:0043204|GO:0030070|GO:0044267|GO:0034774 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140681_PI430048170 0.1393886994404340.5455456840722861.18256602969347
0.6374244589737272.13013513695544 A A A 2.66154120560941 2.06764089651794
2.17540036588567 P A A LNCV6_140681_PI430048170 mRNA
CCCCTTATTGCTGAAAGTAGATTGCAATAAAACCCCAATAAAACGTTTGGTCGGATATCT NM_001278351 RefSeq

chr12 + 69470348 69579791 FRS2 10818 "fibroblast growth factor receptor substrate 2, transcript variant 3"
GO:0005515|GO:0008286|GO:0005886|GO:0070307|GO:0005158|GO:0046619|GO:0003281|GO:0001759|GO:0007405|GO:0000187|GO:0000186|GO:0007173|GO:0005911|GO:0005068|GO:0008595|GO:0070372|GO:0060527|GO:0050678|GO:0048011|GO:0005168|GO:0048015|GO:0042981|GO:0005104|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101440_PI430048170 0.00991907544351066 0.5879319063113771 0.3777867701536 10.3410556410122 10.0753200966289 P P P 10.8519773719934 11.2685227993263 10.9578528265136 P P P LNCV6_101440_PI430048170 mRNA
TGCAAGCATCCCATGGGGCGGGGGCGGGACCAGGGAGAATTAATAAAGTTCTGGACTTTTNM_001256849 RefSeq
chr19 + 50384322 50418018 POLD1 5424 "polymerase (DNA directed), delta 1, catalytic subunit, transcript variant 1"
GO:0043625|GO:0005515|GO:0003887|GO:0005634|GO:0044281|GO:0046872|GO:0000109|GO:0005737|GO:0006271|GO:0000723|GO:0000166|GO:0000722|GO:0006297|GO:0006298|GO:0009411|GO:0008296|GO:0051539|GO:0016235|GO:0055089|GO:0003677|GO:0006260|GO:0045004|GO:0006281|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145501_PI430048170 0.5107041614708070.8648364796818010.629211430048841 0.5061247560678380.445103201506963A A A 0.4287591528792291.1395800559465 0.541601567060667A A A LNCV6_145501_PI430048170 mRNA
AAGCTGGCCATTAACATGAACTACGTCACTTTTCTTTTGAGGGTCAAATATTTAGTGCAT NM_031275RefSeq chr11 + 112167371 112172556 TEX12 56158 testis expressed 12 GO:0000711|GO:0000801|GO:0007130 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132127_PI430048170 0.4039904737458112.18992197261864 0.411758678122498 2.62107641347132 0.54829308789541 A A A 0.5458491277382180.394988194346948 0.389230878007491A A A LNCV6_132127_PI430048170 mRNA
AATGAAAAATCTTTCTTTGGAAGCAGCATAGGGGAAGAGCATGAGCTTCAGAGTCAAACA NM_152489RefSeq chr1 + 64203806 64244344 UBE2U 148581 ubiquitin-conjugating enzyme E2U (putative)
GO:0000209|GO:0005737|GO:0000790|GO:0006281|GO:0019787|GO:0033503|GO:0016574|GO:0016874|GO:0043161|GO:0005524|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136337_PI430048170 0.288319392058025 1.06662557383246 10.9591776270917 10.94366863945 10.8567309212212 P P P 10.9265085035784 10.8464955359598 10.7004772878353 P P P LNCV6_136337_PI430048170 mRNA
AGGGCAAAAAGGGCCCAGGGTTATAATAAGTAAATAACTTGTCTGTACAGCCTGAAAAAA NM_012268RefSeq chr19 + 40348424 40378490 PLD3 23646 "phospholipase D family, member 3, transcript variant 2"
GO:0016042|GO:0005515|GO:0070290|GO:0005789|GO:0004630|GO:0044281|GO:0016021|GO:0006644|GO:0006655|GO:0070062|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142677_PI430048170 0.0734386899690444 1.36834878970007 3.90572362467422 4.35766248971489 4.32870221038521 P P P 3.93388544005286 3.60581222431172 3.71840692943086 P P P LNCV6_142677_PI430048170 mRNA
TTAAAAAATACTGTCTCAAAGGTGGCTGAAACTTTCTTTTCTAGACCTTTCCCCTCCCCT NM_198557RefSeq chr2 - 151248213 151261875 RBM43 375287 RNA binding motif protein 43 GO:0000166|GO:0003723 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130897_PI430048170 0.1112963040413391.88361452856632 5.05216922136866 4.78928436050833 5.15232730272384 P P P 4.75645464646765 3.5455649839314 3.64022603763721 P P P LNCV6_130897_PI430048170 mRNA
CCTGGTAACGAATTTCAACTGACAGTGAAATGAATAGGCCTTTAAACTTTATAACATTGC NM_033411RefSeq chr6 + 83193312 83196537 RWDD2A 112611 RWD domain containing 2A NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91013_PI430048170 0.0426427131072308 1.45486459376196 10.7989777222108

11.2378458056908 11.0206215348656 P P P 10.5480595891486 10.5014300221274
10.4154755950184 P P P LNCV6_91013_PI430048170 mRNA
AAGTTGCCTTAAAGAATAGACAAGAGCTGTATGCACTACCTCCTCCTCCCCAGTTCTACT NM_001114636 RefSeq
chr2 - 58159242 58241380 FANCL 55120 "Fanconi anemia, complementation group L, transcript
variant 1"
GO:0004842|GO:0006513|GO:0007276|GO:0016874|GO:0005635|GO:0006974|GO:0043240|GO:0005737|GO:0006
281|GO:0042127|GO:0005654|GO:0008270|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124715_PI430048170 0.0205580645740344 0.6657574180451769.23538924759175
9.24909511760683 9.25528336047692 P P P 9.65921637688937 9.89113533188439
9.93532073142936 P P P LNCV6_124715_PI430048170 mRNA
TTCTGGTGCCCATTCCATTTGTCCAGTTAATACTTCCTCTTAAAAATCTCCAAGAAGCTG NM_001293212 RefSeq
chr6_GL000256v2_alt + 2022334 2026212 TUBB 203068 "tubulin, beta class I, transcript variant 1"
GO:0005515|GO:0051258|GO:0042288|GO:0042267|GO:0003924|GO:0006928|GO:0005634|GO:0032403|GO:0005
829|GO:0000086|GO:0005641|GO:0005856|GO:0007017|GO:0031625|GO:0070062|GO:0006996|GO:0009987|GO:0
005874|GO:0019904|GO:0005525|GO:0051225|GO:0044297|GO:0006184|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138077_PI430048170 0.5378824740553590.9315222302830078.59386285518364
8.53291750264761 8.89384432302437 P P P 8.62758087920955 8.7224948279908
8.98050382405473 P P P LNCV6_138077_PI430048170 mRNA
CTCATAGCCAAAGAGGAGATGATACATAATCTACAATAAGGGTCTTAGTGCTTTAGAAAA NM_002816RefSeq chr17
- 67340502 67366605 PSMD12 5718 "proteasome (prosome, macropain) 26S subunit, non-ATPase,
12, transcript variant 1"
GO:0010467|GO:0002474|GO:0090263|GO:0044281|GO:0031145|GO:0005829|GO:0034641|GO:0000082|GO:0016
032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0000502|GO:0043066|GO:0005838|GO:0006521|GO:0
042590|GO:0051437|GO:0006915|GO:0042981|GO:0051436|GO:0051439|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144202_PI430048170 0.4364307350950580.9784530126245520.463249790969247
0.4312524555099790.405777300424362A A A 0.4035006074292180.497807862350761
0.491902253989868A A A LNCV6_144202_PI430048170 mRNA
ACATATGTGCTTGTCGAGTGATCTTAAGACAGCTGGATGTCCGAACCATGCAGTAATAGC NM_182560RefSeq chr14
+ 98711612 98717766 C14orf177 283598 chromosome 14 open reading frame 177 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134171_PI430048170 0.0365961036579551.15312884375117 0.660626712149779
0.7732377968552090.803217666465361A A A 0.6388643796605920.480875337446291
0.499338904586727A A A LNCV6_134171_PI430048170 mRNA
GGTACCTGTGTTGAGTTGATAAACATTTCCATCTTCATTAAAACTGCTTCCAAACTAGTA NM_014376RefSeq chr5
+ 157269341 157395598 CYFIP2 26999 "cytoplasmic FMR1 interacting protein 2, transcript variant 3"
GO:0005515|GO:0043005|GO:0048010|GO:0048471|GO:0030054|GO:0006915|GO:0045202|GO:0097202|GO:0045
862|GO:0005829|GO:0005737|GO:0016337|GO:0016020|GO:0045087|GO:0038096|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143308_PI430048170 0.5211771837015731.10231787394882 8.44183652140853
8.67962547596135 8.86651460924842 P P P 8.29969013383154 8.37193175747337
8.85945651533582 P P P LNCV6_143308_PI430048170 mRNA
GTGAGCTCAGAATTACTTTAAAAGGAGGTAACAGCCAGCCATTACACCTAAATTTAATTT NM_014160RefSeq chr3
+ 12557013 12583711 MKRN2 23609 "makorin ring finger protein 2, transcript variant 1"
GO:0005622|GO:0005515|GO:0008150|GO:0016567|GO:0016874|GO:0008270 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136234_PI430048170 0.67591169411676 0.9785684074480110.386151330513241
0.28990929259324 0.33597893280405 A A A 0.2900305482328030.478898309817154

0.331586047374219 A A A LNCV6_136234_PI430048170 mRNA
CCAGTCTAAGCTCTGCTTATGCCTATCTTGAGATGCAATTACACCCAATTTCCAATGTGA NM_017481 RefSeq chr11
- 5507299 5509923 UBQLN3 50613 ubiquilin 3 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134622_PI430048170 0.6392522443627590.9017544166154831 0.2720909577018
10.3328272583205 10.5815834919304 P P P 10.1102287657675 10.601388092348
10.8470151820208 P P P LNCV6_134622_PI430048170 mRNA
TGAGCTGATTGTTCTAATCAGAGCTGGTACCTACTTTCAATAAATTCTGGTTTTGTGTTT NM_001256875 RefSeq chr1
+ 37692400 37709719 CDCA8 55143 "cell division cycle associated 8, transcript variant 1"
GO:0005515|GO:0051276|GO:0010369|GO:0005730|GO:0005819|GO:0030496|GO:0005634|GO:0005829|GO:0045
171|GO:0032133|GO:0043234|GO:0007080|GO:0000278|GO:0000775|GO:0051301 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129886_PI430048170 0.1658131428528981.86979613259654 2.98930610078204
2.32663384096286 2.55708364036987 A A A 1.14155399140519 0.902851684919079
2.58527921766515 A A P LNCV6_129886_PI430048170 mRNA
AGAGGAGGGTGGCTCTGTGAATGAAAATCACTCAGGCCCCAGGTTATTACTGGATTTATA NM_198479 RefSeq chr19
- 47801242 47803604 TPRX1 284355 tetra-peptide repeat homeobox 1 GO:0005634|GO:0003677 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138714_PI430048170 0.13584324498965 1.29173843064419 6.90291520744566
7.02088792192612 6.90949979329083 P P P 6.45579828676221 6.87805618675815
6.33701460844002 P P P LNCV6_138714_PI430048170 mRNA
GGAGGCTTTTGCTGGGATGAATGTTTTTATAGGGTTTTTGTTGTAACATAAGCTATTTTC NM_001039775 RefSeq
chr1 - 26321858 26354130 AIM1L 55057 absent in melanoma 1-like GO:0030246 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138179_PI430048170 0.64168061179394 1.01345047154722 9.59070689528387
9.60515300731574 9.6819834360888 P P P 9.6369651965317 9.55613709523872 9.627250272484
P P P LNCV6_138179_PI430048170 mRNA
CGATGATGATGTCCATTGCTGTGTGATGGCTTGGAATTTAATTTATTAAAGTCAAATTGG NM_014807 RefSeq chr11
+ 119107349 119117124 C2CD2L 9854 "C2CD2-like, transcript variant 1"
GO:0008150|GO:0003674|GO:0035774|GO:0016021|GO:0005575|GO:0043559 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_99535_PI430048170 0.1190373737254731.33526582757998 6.73414636251801 7.06301750420949
7.28435449740206 P P P 6.60971148252394 6.55309399283389 6.7149532264225 P P P
LNCV6_99535_PI430048170 mRNA
GAAATATTCTCATCCTTAGTGGGGATGTTAATTTGGCAGAGAGTGATTTGGCATATACCC NM_004595 RefSeq chrX
+ 21940572 21994837 SMS 6611 "spermine synthase, transcript variant 1"
GO:0034641|GO:0004766|GO:0006597|GO:0016768|GO:0006595|GO:0006555|GO:0044281|GO:0070062|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134881_PI430048170 0.12399009857387 1.04431077405396 0.476569541105811
0.557813444299912 0.483833315171115 A A A 0.415761009728432 0.447282957438823
0.468441429812936 A A A LNCV6_134881_PI430048170 mRNA
ATTTGTAGTTTCCTCTCACGCATCTTCTATTTTCCTCTCAGACCTTTCATTTGCCACGGA NM_001146162 RefSeq chr11
+ 89710298 89717872 TRIM77 NA "tripartite motif containing 77, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137105_PI430048170 0.36926117477308 0.681538303604848 0.3685657337396
0.393346819102636 0.326372916787102 A A A 0.416277863992976 0.42451814869731
1.57756240584481 A A A LNCV6_137105_PI430048170 mRNA
TTCTGGCTTACCGATACAACAACCAATACATCTTTGTTCTGTAATGTAAAATTTGACTCC NM_014244 RefSeq chr5
- 179110850 179345430 ADAMTS2 9509 "ADAM metallopeptidase with thrombospondin type 1 motif, 2,

transcript variant 1"
GO:0030324|GO:0005578|GO:0005576|GO:0007283|GO:0016485|GO:0030198|GO:0030199|GO:0030574|GO:0006508|GO:0008270|GO:0043588|GO:0004222|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99261_PI430048170 0.4434148512549890.9306998741988060.2598443489043640.268468628980263 0.416537843050332 A A A 0.6119474334731590.3050890553774260.323094513456643 A A A
LNCV6_99261_PI430048170 mRNA
AAATATATCCCAAGCCCTGGAAATGGCATTGGAACAGAAGGAATTAGACCAGGAACCTGG NM_012278 RefSeq
chrX + 71301747 71305371 ITGB1BP2 26548 "integrin beta 1 binding protein (melusin) 2, transcript variant 1"
GO:0005515|GO:0007165|GO:0030018|GO:0017124|GO:0007517|GO:0005178|GO:0005509|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_44052_PI430048170 0.5534783274753631.28493551939174 0.4001606300710581.54133492501376 0.433299914363293 A A A 0.8012584200774670.3576790312563460.399578181786201 A A A
LNCV6_44052_PI430048170 mRNA
TCTCAAGCATCTTGGTCTCTGCTAAGAAGAGGCTCAGAGGCTTAGAAGCCCTGCCTCGCC NM_199001 RefSeq chr9
+ 137224634 137226311 CYSRT1 NA cysteine-rich tail protein 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126693_PI430048170 0.1294510017234050.7593501415865575.78022351549288 5.99884406604868 5.99668984145771 P P P 6.00841689370594 6.34483192860066 6.57020776011161 P P P LNCV6_126693_PI430048170 mRNA
TAGTCTCAGTTACCCAGATAACCTCGGTTGTCACCTTGGAGTATCTTGTTGTAGTCCCTT NM_014777 RefSeq chr1
+ 229626233 229660199 URB2 9816 URB2 ribosome biogenesis 2 homolog (S. cerevisiae)
GO:0016235|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134109_PI430048170 0.00906215475243142 1.64531614232048 8.48975184445256 8.77334193921777 8.76615457646967 P P P 8.17232390758687 7.78247867967041 7.90929498621121 P P P LNCV6_134109_PI430048170 mRNA
CACAGCAATAAAAGCTTCCCCCTGATATCCATCCCTTTGTAGTTTGAACAAATATATTTA NM_020898 RefSeq chr12
- 53711117 53727523 CALCOCO1 57658 "calcium binding and coiled-coil domain 1, transcript variant 1"
GO:0003712|GO:0005515|GO:0000790|GO:0044212|GO:0008013|GO:0003713|GO:0005634|GO:0008022|GO:0006351|GO:0043231|GO:0043565|GO:0007165|GO:0005737|GO:0030374|GO:0030518|GO:0045944|GO:0003682|GO:0045893|GO:0016055|GO:0070016 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129725_PI430048170 0.0108013448623592 0.5437675858258396.48753616515812 6.7925122030765 6.96880957742286 P P P 7.4021044954044 7.61520120909698 7.87054576439572 P P P LNCV6_129725_PI430048170 mRNA
GGGCATGTGAAGATATTTAGTCACCCAGAGGAGCCAGTAAATGTTATAATGTTAAAAATT NM_018675 RefSeq chr19
+ 34677638 34686397 ZNF302 55900 "zinc finger protein 302, transcript variant 15"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132725_PI430048170 0.0435617234478552 1.59437292611282 7.90365312480207 7.94216786501181 7.89789414992202 P P P 6.93730250520198 7.44303345420031 7.2989689233978 P P P LNCV6_132725_PI430048170 mRNA
GTTACCTGGGGGAAGTAGAATGAGAGGTCTGTTGGGAATAAAGGTTTTTCTTAGATTCTG NM_001160042 RefSeq
chr1 + 32205634 32208687 IQCC 55721 "IQ motif containing C, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142775_PI430048170 0.4404931485384680.8196577767267648.08629238687563 8.30924812697624 8.64828968535566 P P P 8.1447563733444 8.67134020174601 9.01503948462322 P P P LNCV6_142775_PI430048170 mRNA
CTTGCATCTAGAGCTACGTTGTAAAATTCTTTTAGGCATGTGTTAGATTTCTGTGTAAAC NM_006807 RefSeq chr17
- 48070051 48101198 CBX1 10951 "chromobox homolog 1, transcript variant 1"

GO:0005515|GO:0010369|GO:0005819|GO:0042803|GO:0005720|GO:0001939|GO:0005721|GO:0003682|GO:0005654|GO:0001940|GO:0019899|GO:0045892|GO:0000785|GO:0000775 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136669_PI430048170 0.0021731131924113 0.7219982638458919.58470953728559 9.43538888192426 9.43636390720953 P P P 9.98476667642566 9.88224806262308 10.0015534887524 P P P LNCV6_136669_PI430048170 mRNA CCACATTGCCCAAGTCACACAGGCTTCTGTATTATGTATTTAGATAAAATGTGTGAAAAT NM_001291379 RefSeq chr10 - 45825591 45853877 AGAP4 NA "ArfGAP with GTPase domain, ankyrin repeat and PH domain 4, transcript variant 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133953_PI430048170 0.0102394901911755 0.4548307223193375.0951387387992 5.43667901000346 5.74951688192724 P P P 6.73493293845496 6.32849981884605 6.66931125480267 P P P LNCV6_133953_PI430048170 mRNA TATGGTTAATACTATTAAGCAAGAATGCAGTACAGAATTGGATACAGTACGGATTTGTCC NM_001093726 RefSeq chr5 - 42799879 42811922 SEPP1 6414 "selenoprotein P, plasma, 1, transcript variant 3" GO:0019953|GO:0008430|GO:0001887|GO:0007420|GO:0007626|GO:0005576|GO:0009791|GO:0040007|GO:0006979|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139163_PI430048170 0.2328933825857460.7473731092943483.51230253856483 3.67750053734683 4.38448941172036 P P P 4.45150116055663 3.99615837292603 4.49166040352411 P P P LNCV6_139163_PI430048170 mRNA TTGGTGGTATTTAAAACCTACACCTACCATGTTGCTATTTCACTTTCATTGCTTTAGTTG NM_052927 RefSeq chr5 - 160075884 160119445 PWWP2A 114825 "PWWP domain containing 2A, transcript variant 1" GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131369_PI430048170 0.6101702808932320.8984922737838963.08847155470115 2.90804387377942 3.71364523166097 P A P 3.04301841498128 3.69448855099144 3.48980091590853 P P P LNCV6_131369_PI430048170 mRNA GCCCTTGAAAAGTCTTGAGATATAAGTGTGAGTACTATACAAGCATTAAACTGGAGTGCA NM_017515 RefSeq chr11 - 107790990 107859188 SLC35F2 54733 "solute carrier family 35, member F2" GO:0008150|GO:0003674|GO:0006810|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133142_PI430048170 0.0233348719254680.3722466562059472.29430230390862 1.2990068270242 2.16839017301528 A A A 2.98066830513226 3.76415061585176 3.37611575535568 P P P LNCV6_133142_PI430048170 mRNA AGGCAGTCTTTCATGGAATGTTTTGATTGAGCAATGAAATAAACAGTCCTCCATTTTGTT NM_175873 RefSeq chr5 + 132813323 132816797 SOWAHA 134548 sosondowah ankyrin repeat domain family member A NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134362_PI430048170 0.8278009163567870.9902060179828631 0.1567083404344 10.0682991359136 10.1241523802857 P P P 10.0329037397902 10.1674865154115 10.1878873341844 P P P LNCV6_134362_PI430048170 mRNA TTCAGGGAGGAGTCTGCCACCAGTGTAATGTATCAATAAACTTCATGCAAGCATAAAAAA NM_012189 RefSeq chr18 + 24138955 24161600 CABYR 26256 "calcium binding tyrosine-(Y)-phosphorylation regulated, transcript variant 1" GO:0017124|GO:0003351|GO:0046982|GO:0031514|GO:0005509|GO:0005730|GO:0005634|GO:0097228|GO:0097229|GO:0005737|GO:0035686|GO:0005856|GO:0019899|GO:0048240 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126850_PI430048170 0.1264505651620820.7346029905505046.05639263030547 5.84762691804391 5.65384322343215 P P P 6.51755730100539 6.40885321987852 5.92919791775522 P P P LNCV6_126850_PI430048170 mRNA GCTTTCTCCCCCTAAGAGAATATTTCAAGTATTTTTCAACAGAACTCACTTCCTCTTTAT NM_013369 RefSeq chr21 - 44246338 44262216 DNMT3L 29947 "DNA (cytosine-5-)-methyltransferase 3-like, transcript variant 1"

GO:0005515|GO:0010467|GO:0005634|GO:0007283|GO:0043085|GO:0046872|GO:0005829|GO:0006306|GO:0032776|GO:0006349|GO:0040029|GO:0008047|GO:0019899|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142593_PI430048170 0.2087486408766790.7432500594622397.30378181345786 7.15321726397751 7.45339466066376 P P P 7.46673668283828 7.49015011220832 8.14578366665171 P P P LNCV6_142593_PI430048170 mRNA
CATTTGTCATTTTAACCGACAACCACCCAATAAATTTACTCTGCAGTTCTGAACTCAAAA NM_013441RefSeq chr1 + 24502896 24537020 RCAN3 11123 "RCAN family member 3, transcript variant 1"
GO:0031013|GO:0019722|GO:0003723|GO:0009653 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73705_PI430048170 0.000954851629359861 0.3823670565331054.96652560094915 4.66642276437334 5.05363190190078 P P P 6.15202224284042 6.21182724430394 6.48876702583697 P P P LNCV6_73705_PI430048170 mRNA
GTAAACACCGTGAAGGTACCATGAGTTCTATGGGTACTCAATAAATGCTTGTGATAATGA NM_002268RefSeq chr3 - 160494994 160565588 KPNA4 3840 karyopherin alpha 4 (importin alpha 3)
GO:0005515|GO:0042542|GO:0019221|GO:0008565|GO:0005654|GO:0006607|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136430_PI430048170 0.0967103143875607 1.29862285037149 11.7847285549895 11.5178532396679 11.6616488134423 P P P 11.2874657537982 11.0090445540364 11.5064263543005 P P P LNCV6_136430_PI430048170 mRNA
GGAGTTTATTGTATTCATTGGAATATGTGACGTAAGCAATAAAGGGAATGTTAGACGTGT NM_013232RefSeq chr5 + 271620 314974 PDCD6 10016 "programmed cell death 6, transcript variant 1"
GO:0051898|GO:0005515|GO:0030948|GO:0032007|GO:0005783|GO:0005634|GO:0006886|GO:0042803|GO:0034605|GO:0005737|GO:0060090|GO:0006508|GO:0046983|GO:0070062|GO:0031965|GO:0006919|GO:0005509|GO:0001525|GO:0031410|GO:0097190|GO:0070971|GO:0045766|GO:0010595|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133985_PI430048170 0.2958137496831581.7289112746653 0.37060288245136 1.9830391927886 1.18791139719223 A A A 0.3547025558019770.6836924125093 0.552985075236495A A A LNCV6_133985_PI430048170 mRNA
CTGGACACTCAGCATTTAGTGAAGGTAATTCCAAAATACTGGTATCAGTACTCTTATTTA NM_001284269 RefSeq chr14 - 89794990 89954557 EFCAB11 90141 "EF-hand calcium binding domain 11, transcript variant 5" GO:0005509 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136086_PI430048170 0.2122658063507591.07053623306254 8.29986334160944 8.19980188714639 8.13455312805529 P P P 8.15557056089071 8.16176023196905 8.02246269485141 P P P LNCV6_136086_PI430048170 mRNA
TTGGATTGCAGCCCTGTCTACACTGGATAATCATTCCCTGGCCATATCAGTCATCATGAT NM_005697RefSeq chr15 - 74844855 74873329 SCAMP2 10066 secretory carrier membrane protein 2
GO:0030133|GO:0005515|GO:0005794|GO:0006892|GO:0005654|GO:0016021|GO:0015031|GO:0055038|GO:0032588|GO:0070062|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131015_PI430048170 0.0113137981345302 1.45352890295931 9.32539488516707 9.32773971450762 9.25156967189777 P P P 8.62724063435147 8.88262802121023 8.76615457646967 P P P LNCV6_131015_PI430048170 mRNA
AGTTGCCCTATGGAAAACTTGTCCAAATAACATTTCTTGAACAATAGGAGAACAGCTAAA NM_001297650 RefSeq chr12 - 7354960 7444185 CD163L1 283316 "CD163 molecule-like 1, transcript variant 1"
GO:0005886|GO:0005576|GO:0016021|GO:0006898|GO:0005044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137518_PI430048170 0.00112786079733606 0.7155689447218831 2.5137959299234 12.4610203038949 12.5522303951769 P P P 12.9279504814549 12.9798263050151 13.0658575264447 P P P LNCV6_137518_PI430048170 mRNA
CTGTGTGTCTGCGTTGTGTGTGATTTTCATGGAAAAATAAAATGCAAATGCACTCATCAC NM_000350RefSeq chr1

- 93992837 94121149 ABCA4 24 "ATP-binding cassette, sub-family A (ABC1), member 4"
GO:0005215|GO:0006649|GO:0007603|GO:0042626|GO:0045494|GO:0055085|GO:0001523|GO:0005524|GO:0045
332|GO:0016020|GO:0005887|GO:0004012|GO:0006810|GO:0007601 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140148_PI430048170 0.3852531154489841.37725937825165 2.49176841298877
1.82683508271131 1.28051017700742 A A A 1.29866984925925 1.78085333488721
1.33759597635873 A A A LNCV6_140148_PI430048170 mRNA
TGGCCCCCACAGAGAGAGGTCCTACAGCTGTCATAAATTAAATTTATTCTCTGGAAAAAA NM_170604RefSeq chr19
- 38409057 38426305 RASGRP4 115727 "RAS guanyl releasing protein 4, transcript variant a"
GO:0005886|GO:0007264|GO:0008283|GO:0005509|GO:0009991|GO:0046579|GO:0007202|GO:0019992|GO:0030
742|GO:0005737|GO:0008277|GO:0032320|GO:0016020|GO:0030099|GO:0016049|GO:0007169|GO:0005088 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72986_PI430048170 0.3817292421454190.9534180525798466.93170076368501 6.72717430210897
6.87572938849798 P P P 6.91133429886345 6.86072776984893 6.97441307922941 P P P
LNCV6_72986_PI430048170 mRNA
AGACAAAGAAGAACCCCTCTAATCCCAAGGATAAAAGCACGAGTATCCGGTACTTGAAGG NM_017730RefSeq
chr3 - 49029708 49094071 QRICH1 54870 "glutamine-rich 1, transcript variant 1"
GO:0008150|GO:0003674|GO:0005654|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140924_PI430048170 0.6649726153711190.8334625191846611.19686970985506
0.5142274857307910.38168520356344 A A A 1.64035809114308 0.555780005447288
0.525950251995332A A A LNCV6_140924_PI430048170 mRNA
AGATAGAGAATGCAATGATATGATGGCACACAAGATGAAGGAGCCCAGTCAGAGTTGCAT NM_001012975
RefSeq chr14 + 20510471 20511122 RNASE10 NA "ribonuclease, RNase A family, 10 (non-active)"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127235_PI430048170 0.3642970353585810.96613461295403 0.299892054550108
0.40592231014056 0.315277759077074A A A 0.4607928803414140.353780777868533
0.355291109606564A A A LNCV6_127235_PI430048170 mRNA
CTGAGGAGAGTCATAGATTTCTCCTGAAATATGTCCTCTTTTGTTGTTTCTTAATTTGGA NM_006891RefSeq chr2 -
208121606 208124589 CRYGD 1421 "crystallin, gamma D"
GO:0005515|GO:0005737|GO:0005212|GO:0070306|GO:0002088|GO:0034614|GO:0005634|GO:0007601 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69318_PI430048170 0.1787458813004641.28241363410227 12.4148962959885 13.0149106307849
12.7680655429589 P P P 12.3292645710493 12.3089784111789 12.5341766938145 P P P
LNCV6_69318_PI430048170 mRNA
AAAGGACACTGTCTGTGAAGATATGACTTTCTCCACCTGGACCCCGCCCCCTGGAGTCCA NM_078481RefSeq chr19
+ 14381143 14408725 ADGRE5 NA "adhesion G protein-coupled receptor E5, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113479_PI430048170 0.00199758565820749 0.6821663069150575.85728086943764
5.96519623775045 5.82005643452716 P P P 6.39809063380973 6.43820936294789
6.46483326690192 P P P LNCV6_113479_PI430048170 mRNA
ATTCTCAAGATACAGAGTTTTCATGGAGTGATAATGAAAGGAGCAGCAGCCGCATTAATA NM_001166703 RefSeq
chrX - 55145244 55161102 FAM104B 90736 "family with sequence similarity 104, member B,
transcript variant 6" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133390_PI430048170 0.000347038841075809 7.70990784747774 9.16825826058211
9.59618394683098 9.32219534441714 P P P 6.73650742066045 6.35732350116216
6.11724503059118 P P P LNCV6_133390_PI430048170 mRNA
TTTTGAGCAGGTGGCTTTTGACGAAACCAAGAATGTGTTTGTCAAGTTCTATGCCCCGTG NM_006849RefSeq chr16
+ 283117 287209 PDIA2 64714 "protein disulfide isomerase family A, member 2"
GO:0031545|GO:0005515|GO:0034976|GO:0006457|GO:0005783|GO:0005788|GO:0003756|GO:0045454|GO:0019

511|GO:0006621|GO:0005496 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137471_PI430048170 0.0108222306265390.3470821602503363.98435100802682
3.45103617513991 3.45802364838477 P P P 4.71046583942323 5.58565733167053
5.11134777168565 P P P LNCV6_137471_PI430048170 mRNA
CCAGCGTTTTCATTTGGTCCATAACACAATGTATGGAAATGTGAAAGACAATTTTGTACA NM_001076786 RefSeq
chr11 + 32893177 32980268 QSER1 79832 glutamine and serine rich 1 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_132799_PI430048170 0.0698175928341292 0.5751524849773074.16770822800311
4.02725831513404 3.38777226190441 P P P 4.92650047823352 4.8418102951316
4.22562905528391 P P P LNCV6_132799_PI430048170 mRNA
GGCTCTCCTGCCTGTTCATCTAACCAAAGTCGAGAGAGATGATAAATACAAAAAGTCACA NM_001012728 RefSeq
chr19 + 53632055 53637009 DPRX NA divergent-paired related homeobox NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_128963_PI430048170 0.7757972792954240.9679481171784357.88829819710514
7.90158918189675 8.25069216385094 P P P 7.89581417189027 8.02720612895828
8.26416592030698 P P P LNCV6_128963_PI430048170 mRNA
CTGGAGAGAAGATTGTATTTTTTACAGTTTTTTGGGTTTGGCTTCCTTCTCACATTTCTT NM_022491 RefSeq chr12 +
118376552 118418035 SUDS3 64426 suppressor of defective silencing 3 homolog (S. cerevisiae)
GO:0005515|GO:0010467|GO:0016575|GO:0043065|GO:0042826|GO:0006325|GO:0006915|GO:0005634|GO:0000
122|GO:0042803|GO:0006351|GO:0005737|GO:0021762|GO:0016580|GO:0045814|GO:0040029|GO:0005654|GO:0
004407|GO:0070822|GO:0019899|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132744_PI430048170 0.6459851315126641.11573415964083 0.523422446974076
0.3552895965118451.10744885084775 A A A 0.78955232000699 0.373041219177047
0.424748076694857 A A A LNCV6_132744_PI430048170 mRNA
AACACGCTTTCTTTACATCACTAGTGTAGACTCAAAAGATATGCAAGTGTCAAATATGCA NM_004975 RefSeq chr20
- 49371967 49482644 KCNB1 3745 "potassium channel, voltage gated Shab related subfamily B,
member 1"
GO:0005251|GO:0005515|GO:0005886|GO:0007268|GO:0044281|GO:0030425|GO:0032809|GO:0015271|GO:0047
485|GO:0006112|GO:0032590|GO:0050796|GO:0045211|GO:0008076|GO:0051260|GO:0034765|GO:0016021|GO:0
071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68172_PI430048170 0.23182785799851 1.31850829950803 4.8610927801826 4.88272814140733
4.64812812281711 P P P 4.8844888437819 4.06209580120384 4.10372548192255 P P P
LNCV6_68172_PI430048170 mRNA
AAGGCTGCTAACTCTACCTTGATTCTGTTCTGCCCTCGGCTGCAGCAGCCTTTGATATAG NM_020653 RefSeq chr17
- 16550316 16569206 ZNF287 57336 zinc finger protein 287
GO:0042035|GO:0003700|GO:0005634|GO:0045893|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129671_PI430048170 0.0809273641074021 1.04420421197137 10.7081837865736
10.656152656286 10.7203819363069 P P P 10.6649455786571 10.6020727881909
10.6306043212725 P P P LNCV6_129671_PI430048170 mRNA
GTCCTGTTGACTTGTATGATATCCACAAATAAATATTTTCATGGCGGTCGTGTTGAAAAA NM_003681 RefSeq chr21
+ 43719096 43762307 PDXK 8566 "pyridoxal (pyridoxine, vitamin B6) kinase"
GO:0042823|GO:0000287|GO:0008283|GO:0042816|GO:0006767|GO:0008478|GO:0005634|GO:0044281|GO:0030
955|GO:0031402|GO:0031403|GO:0005524|GO:0042803|GO:0005829|GO:0016310|GO:0005737|GO:0006766|GO:0
030170|GO:0005654|GO:0008270|GO:0009443|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_129880_PI430048170 0.92185214381881 1.00333851276898 0.425808567278751
0.5060346840805450.457795812096696 A A A 0.5260801661672090.501658069993512
0.341749167580039 A A A LNCV6_129880_PI430048170 mRNA

GATAGAAGTTTACTTTTTCCTCTTCTGGTTTTGGAAAATTTCCAGATAAGACATGTCACC NM_022073RefSeq chr14 - 33924214 33951078 EGLN3 112399 egl-9 family hypoxia-inducible factor 3 GO:0031545|GO:0005515|GO:0001666|GO:0031418|GO:0005506|GO:0006919|GO:0071456|GO:0061418|GO:0006915|GO:0005634|GO:0006974|GO:0005829|GO:0043523|GO:0005737|GO:0042127|GO:0018126|GO:0018401|GO:0016706|GO:0005654|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138976_PI430048170 0.00278983879254114 3.00332029866799 8.99248662687294 9.18958338961237 8.81507353413659 P P P 7.09993791899299 7.69570551431883 7.40497292608408 P P P LNCV6_138976_PI430048170 mRNA
CATTTTTGAAGCACCTGCTCCTTTTCTTGCAGTGTATTTTCTACAACCAGATTGTATTAA NM_018419RefSeq chr20 - 64047725 64049626 SOX18 54345 SRY (sex determining region Y)-box 18 GO:0000790|GO:0044212|GO:0005634|GO:0060836|GO:0048866|GO:0001947|GO:0001946|GO:0061028|GO:0045944|GO:0060956|GO:0042789|GO:0048469|GO:0001942|GO:0001944|GO:0035050|GO:0046982|GO:0060214|GO:0001525|GO:0000122|GO:0000978|GO:0001701|GO:0003151|GO:0022405|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138445_PI430048170 5.32313722746761e-05 0.0872324486796228 0.258745095032179 0.274265140620737 0.390283942941041 A A A 3.72874917636539 3.9913162450208 3.74873833121989 P P P LNCV6_138445_PI430048170 mRNA
CTCTGTATCTGCCATGTGAAGAGAATTAACAATAAAAGTGTGAAGAGCGATTGTGAGGAA NM_012231RefSeq chr1 + 13704854 13825079 PRDM2 7799 "PR domain containing 2, with ZNF domain, transcript variant 1" GO:0006355|GO:0005794|GO:0003700|GO:0034968|GO:0008270|GO:0005634|GO:0003677|GO:0006351|GO:0018024 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126961_PI430048170 0.147645036419546 1.15252693443771 9.96244308027378 9.92307369140516 10.1119447308987 P P P 9.68138325975728 9.71057844806298 9.97902317595047 P P P LNCV6_126961_PI430048170 mRNA
CTCCACCTGTTAGAAGCTATGTGTTTGAAGGAATGAATCAGTGCAGTATAAATAAAATTC NM_022745RefSeq chr1 - 46635038 46668427 ATPAF1 64756 "ATP synthase mitochondrial F1 complex assembly factor 1, transcript variant 1" GO:0005739|GO:0005515|GO:0006461 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129639_PI430048170 0.0328978910644496 0.773294742728173 9.41348291184587 9.34735782844384 9.52332089869068 P P P 9.72849707707246 9.68722621517178 9.9701864376381 P P P LNCV6_129639_PI430048170 mRNA
GGTTTTGGTGGTACTAATGCAACACTTTGTATTGCTGGACTGTAGAACATATAATTTGTA NM_017897RefSeq chr3 + 25790071 25794534 OXSM 54995 "3-oxoacyl-ACP synthase, mitochondrial, transcript variant 1" GO:0005739|GO:0006637|GO:0005737|GO:0051792|GO:0051790|GO:0004315 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136335_PI430048170 0.000248069482991726 2.81919146268024 6.60089643970445 6.8900447395976 6.65476912264072 P P P 5.08362054940517 5.3523141457951 5.22809786824866 P P P LNCV6_136335_PI430048170 mRNA
GAGGCTCTGCCTAATGTGAATTTATTTATTTGTGAATAAACTGTACTGGTGTCAGTTGGC NM_018670RefSeq chr15 - 89749866 89751309 MESP1 55897 mesoderm posterior basic helix-loop-helix transcription factor 1 GO:0090082|GO:0003700|GO:0003259|GO:0007369|GO:0044212|GO:0003236|GO:0003139|GO:0042662|GO:0005634|GO:0060913|GO:0042664|GO:0003143|GO:0001947|GO:0007219|GO:0008078|GO:0060975|GO:0045944|GO:0046983|GO:0051155|GO:0035481|GO:0045446|GO:0055007|GO:0003241|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133765_PI430048170 0.0108004664255937 0.822315651966238 8.84270175453467 8.73607879684171 8.70398694981351 P P P 8.97397057487068 9.02453152696563 9.1302232531965 P P P LNCV6_133765_PI430048170 mRNA
AAGTTTCCACCGCATTTCTCCTTGACTTTACTAAAAGTTAAATAAACGTGCCACTCGCCC NM_001286198 RefSeq chr12 - 121002421 121016502 C12orf43 64897 "chromosome 12 open reading frame 43, transcript

variant 7" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127039_PI430048170 0.0627978895207479 0.80786020056493311.2911705074231
10.9901530222205 11.0169362817376 P P P 11.3108701529148 11.4821604806098
11.4428026223756 P P P LNCV6_127039_PI430048170 mRNA
ATTGTATCAACGCCAGGAAAGGGGGGTGAAAAGCCTCTTTTACCCCCCAAATAAATTGTC NM_014292RefSeq chr22
- 38861426 38872334 CBX6 23466 "chromobox homolog 6, transcript variant 1"
GO:0031519|GO:0005515|GO:0000792|GO:0003727|GO:0005654|GO:0005634|GO:0000122|GO:0006351|GO:0016
568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129921_PI430048170 0.1270482130468210.5743347970443091.7883113825604
3.03992809129874 2.14966545929968 A P A 3.52049877114896 2.98432220376231
3.11617999937726 P P P LNCV6_129921_PI430048170 mRNA
CCCTCCTACCCAATTCTATGGAATATTTTATACGTCTCCTTGTTTAAAATGTCACTGCTT NM_001039348 RefSeq chr2
- 55865961 55924163 EFEMP12202 "EGF containing fibulin-like extracellular matrix protein 1, transcript variant 2"
GO:0005515|GO:0005154|GO:0006355|GO:0005509|GO:0005578|GO:0005576|GO:0018108|GO:0005615|GO:0031
012|GO:0005006|GO:0007173|GO:0030198|GO:0032331|GO:0007601|GO:0008083|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130934_PI430048170 0.0200959835543725 0.3676936208786624.70755387126284
3.87377514587346 4.6940926228741 P P P 5.67222617973316 6.01851678572042
6.03365741125962 P P P LNCV6_130934_PI430048170 mRNA
GGTAGATATTGAGGCCAAGAATATTGCAAAATACATGAAGCTTCATGCACTTAAAGAAGT NM_002345RefSeq chr12
- 91103454 91111765 LUM 4060 lumican
GO:0005515|GO:0014070|GO:0051216|GO:0005518|GO:0044281|GO:0005583|GO:0005615|GO:0030198|GO:0030
199|GO:0045944|GO:0030203|GO:0043202|GO:0070062|GO:0005975|GO:0005796|GO:0005578|GO:0005576|GO:0
070848|GO:0042339|GO:0031012|GO:0018146|GO:0009405|GO:0042340|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_121356_PI430048170 0.5745467802359670.9217229353966267.25566359365107
6.76295404206299 6.56012978527914 P P P 7.07781516303871 7.10146816611515
6.82755448510805 P P P LNCV6_121356_PI430048170 mRNA
TATCACCTCCTGGTGGCCTTGCCGCCCCCACAACCCCGAGGTATAAAGCCAGGTACACGA NM_000737RefSeq chr19
- 49022868 49024375 CGB 1082 "chorionic gonadotropin, beta polypeptide"
GO:0007165|GO:0016486|GO:0005179|GO:0007267|GO:0006915|GO:0005576|GO:0007292|GO:0044267 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129391_PI430048170 0.9763713405728880.9808524422843310.460800218025261
0.4183064564982871.45555825222441 A A A 0.4489166286983621.517867013977
0.414780496334681A A A LNCV6_129391_PI430048170 mRNA
TATTCTGTTCAAGGTAAAATTCCTGCATTCCTGCAAAGATGTCCTGCCAGCAAAACCAGC NM_178434RefSeq chr1
+ 152600661 152601086 LCE3C 353144 late cornified envelope 3C GO:0031424 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_100588_PI430048170 0.0776016992429214 1.08112012400351 12.7264888521682
12.7803135853553 12.8467615841794 P P P 12.6578129605813 12.6863136854935
12.6742342799202 P P P LNCV6_100588_PI430048170 mRNA
GGGGACTAGTGAATGACTTGACCTGTGACCTCAATACAATAAATGTGATCCCCCACCCAA NM_001289103 RefSeq
chr19 + 11435256 11450967 PRKCSH 5589 "protein kinase C substrate 80K-H, transcript variant 4"
GO:0051219|GO:0005783|GO:0005509|GO:0044325|GO:0005622|GO:0035556|GO:0006457|GO:0006491|GO:0045
087|GO:0005080|GO:0005788|GO:0044267|GO:0018279|GO:0043687 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141438_PI430048170 0.595156175347617 1.01046729793767 0.380902110964524
0.343288914689212 0.301071754318798 A A A 0.329706203023053 0.337206169919769

0.314292901240811 A A A LNCV6_141438_PI430048170 mRNA
GAGTAGCTGAATCCGCTTCTCTTTGAGTTAATCCATGAATACTTATTTCTAGAATTGTGA NM_019090 RefSeq chr1
+ 232804891 232810346 MAP10 54627 microtubule-associated protein 10
GO:0051256|GO:0008017|GO:0005881|GO:0005813|GO:0032467|GO:0032886|GO:0030496|GO:0031122|GO:0051
301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127472_PI430048170 0.022555562414066 0.775982661519174 12.0345284032365
11.871591618846 11.7685845812759 P P P 12.1652822131552 12.3763736420906
12.235224989768 P P P LNCV6_127472_PI430048170 mRNA
GTCATGTCAGGCATTTTGCAAGGAAAAGCCACTTGGGGAAAGATGGAAAAGGACAAAAAA NM_030981 RefSeq
chr11 + 66268584 66277492 RAB1B 81876 "RAB1B, member RAS oncogene family"
GO:0005515|GO:0005793|GO:0005794|GO:0003924|GO:0006914|GO:0019068|GO:0005525|GO:0006886|GO:0005
739|GO:0006184|GO:0006888|GO:0034045|GO:0000139|GO:2000785|GO:0005789|GO:0032482|GO:0019003|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128431_PI430048170 0.994402547062576 1.00120865209984 0.491879769911405
0.442932086904903 0.322936811165009 A A A 0.369945301696182 0.447549575375029
0.438974111239837 A A A LNCV6_128431_PI430048170 mRNA
CCTACATGTTCATTATGCATAATGAGCTTGTCACCTATCTCAGCAATAAAGGTTCTGACC NM_001858 RefSeq
chr6 + 69866555 70212454 COL19A1 1310 "collagen, type XIX, alpha 1"
GO:0005581|GO:0005578|GO:0005576|GO:0030154|GO:0001501|GO:0016337|GO:0022617|GO:0007519|GO:0030
198|GO:0030574|GO:0005788|GO:0030674|GO:0007155|GO:0005201 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141712_PI430048170 0.723020167734752 1.02292614968749 7.45316923704421
7.34034298787685 7.42648072340428 P P P 7.32263273941703 7.24525352001968
7.53998915594771 P P P LNCV6_141712_PI430048170 mRNA
CAGGAACTTGTATAGTTCAGCTTCCAACACTTTGGAACAGATTAAAAAGGGAATCTTTTA NM_173475 RefSeq
chr16 - 20858073 20900239 DCUN1D3 123879 "DCN1, defective in cullin neddylation 1, domain
containing 3" GO:0003674|GO:0048471|GO:0030308|GO:0010225|GO:0043065|GO:0010332 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_59399_PI430048170 0.128763004490119 0.412462882711141 0.337724867350486
2.36946373831647 1.65102604303911 A A A 2.20975949642987 2.87817248034396
3.48907277148574 A P P LNCV6_59399_PI430048170 mRNA
GCTACATTGCTTCTGGATCTCTTAGTGGTGAAATTATTTTACACAGTGTAACCACTAATT NM_152905 RefSeq
chr12 + 96907222 96953691 NEDD1 121441 "neural precursor cell expressed, developmentally
down-regulated 1, transcript variant 2"
GO:0005813|GO:0006996|GO:0005886|GO:0005814|GO:0005730|GO:0045177|GO:0036064|GO:0005829|GO:0000
922|GO:0007067|GO:0000086|GO:0005654|GO:0000278|GO:0000242|GO:0051301 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_143130_PI430048170 0.0148234849815588 1.50106030102694 6.75732268758365
6.78105299893219 6.50498446277678 P P P 6.21705835169844 6.18409141438806
5.87629334220189 P P P LNCV6_143130_PI430048170 mRNA
GATACAAAATCATCGCCTCATCACTTTCTAGAATGAAAGGCTGGGGGCATTGCTCACCTT NM_001135570 RefSeq
chr12 - 103950202 103957215 C12orf73 728568 chromosome 12 open reading frame 73
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134811_PI430048170 0.0052664118991 1.72904916943875 14.7692967831865
14.5896128200302 14.6427416155582 P P P 13.6890949128143 13.9026299567941
14.0260251102733 P P P LNCV6_134811_PI430048170 mRNA
AAGCTACATCTCTCAACCTTGGGCAATGACAATAAAGTTTGAGAAGCTGATGGCTGTGTA NM_032417 RefSeq
chrX - 141697400 141698739 SPANXD 64648 "SPANX family, member D"
GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_52045_PI430048170 0.723710577179993 1.07419499961816 1.60938880584571
1.79707393646823 2.54598549688995 A A A 2.22524695604183 0.484009198269738
2.44301066528175 A A A LNCV6_52045_PI430048170 mRNA
ATTTTATGCTATGCAACTGCCTTGCAGTTGACTTTTTCTTGCCTGGCCTCTGTAAGGCCT NM_001293289 RefSeq
chr5 - 142310426 142324417 SPRY4 81848 "sprouty homolog 4 (Drosophila), transcript variant 3"
GO:0005515|GO:0005737|GO:0005794|GO:0043407|GO:0032587|GO:0007275|GO:0005925 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138586_PI430048170 0.454220293155984 0.86746835662944 2.66228352007194
2.53048618157332 3.26996520942632 A A P 2.77345693616714 3.26952670616846
3.10385042320719 P P P LNCV6_138586_PI430048170 mRNA
GGTAAACAACATTTGTGCAGAAGTATGTATGTATTTAGTTCAGGTTGACTTGTGTCCTTA NM_015028 RefSeq chr3
- 171062502 171460408 TNIK 23043 "TRAF2 and NCK interacting kinase, transcript variant 1"
GO:0005515|GO:0031532|GO:0030033|GO:0007256|GO:0005634|GO:0072659|GO:0005524|GO:0048814|GO:0035
556|GO:0016324|GO:0005083|GO:0005737|GO:0046777|GO:0004672|GO:0004702|GO:0004674|GO:0007010|GO:0
001934|GO:0005654|GO:0006468|GO:0055037|GO:0016055|GO:0005856|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133887_PI430048170 0.00723300591065693 0.483444530633617 9.54656808072502
9.48998279295174 9.22570998258997 P P P 10.4701504352744 10.4486614729588
10.5084461499628 P P P LNCV6_133887_PI430048170 mRNA
ATAGTCTGCTCTCCCCGGGAATCTCTAACATGCTCTGTTTACATCGATAAATGCACTTAA NM_005370 RefSeq
chr19 + 16111679 16133635 RAB8A 4218 "RAB8A, member RAS oncogene family"
GO:0005515|GO:0009306|GO:0005886|GO:0003924|GO:0005634|GO:0007409|GO:0006886|GO:0036064|GO:0030
425|GO:0005829|GO:0006904|GO:0048210|GO:0000086|GO:0048169|GO:0017157|GO:0043025|GO:0030670|GO:0
061024|GO:0032482|GO:0030140|GO:0030659|GO:0070062|GO:0032869|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_126856_PI430048170 0.185569927726641 3.31342192310092 0.461668596421423
2.43920799829319 2.78591367321524 A A A 0.552161773909415 0.411176012254891
0.419900733375305 A A A LNCV6_126856_PI430048170 mRNA
AATCTTTATGTGGCAGTGCCACCAATGCTGAACCCCATTGTCTATGGTGTGAAGACTAAG NM_001004052 RefSeq
chr11 - 6169354 6170326 OR52B2 255725 "olfactory receptor, family 52, subfamily B, member 2"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_139634_PI430048170 0.813623624364526 0.994425463766956 0.287006570085323
0.326569110474191 0.391299207847842 A A A 0.367876852215546 0.33967423748752
0.323089160568678 A A A LNCV6_139634_PI430048170 mRNA
CTGCTCTTGCAGTCCAAAGGGATACCTGATTAAAGAAGTTTCTTATTTAAACATCTCAGA NM_014395 RefSeq
chr4 + 99816823 99870189 DAPP1 27071 dual adaptor of phosphotyrosine and 3-
phosphoinositides GO:0007165|GO:0006470|GO:0005543|GO:0005886|GO:0043325|GO:0005547|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142193_PI430048170 0.234029816898965 0.793491637707547 12.3705908334481
12.4820820158407 12.2187560467929 P P P 13.0458965994459 12.4893841684641
12.4727220160771 P P P LNCV6_142193_PI430048170 mRNA
TCACACCACGACGGACTCCCCTTCCTAATAAAACTCAAAGACAAGATGCAGCTTAAAAAA NM_002220 RefSeq
chr15 + 41493857 41503559 ITPKA 3706 inositol-trisphosphate 3-kinase A
GO:0005516|GO:0006020|GO:0008440|GO:0030036|GO:0043647|GO:0044281|GO:0005524|GO:0005829|GO:0097
062|GO:0048365|GO:0007165|GO:0043197|GO:0048167|GO:0006468|GO:0004683|GO:0061003 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141380_PI430048170 0.587007810808758 1.33396437116894 1.74237686471008
0.527185132493749 0.375188490545911 A A A 0.623033240761102 0.627039453280599

0.562011818850959 A A A LNCV6_141380_PI430048170 mRNA
TAAAAGTCTCTTTCCAGATTCCAAAAGGACAAGAGATCAGAGAGTCACATATACGCCTCT NM_004852 RefSeq
chr18 + 57435684 57491298 ONECUT2 9480 one cut homeobox 2
GO:0030335|GO:0000978|GO:0015629|GO:0006351|GO:0030154|GO:0001889|GO:0042384|GO:0001077|GO:0045
165|GO:0045944|GO:0031018|GO:0002064|GO:0048935|GO:0001952|GO:0009887|GO:0005654|GO:0030512 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130400_PI430048170 0.0288619683163934 1.46957756257453 10.6882236408875
11.0856280290435 10.9641294062508 P P P 10.4442065101475 10.3772472300588
10.2734327433637 P P P LNCV6_130400_PI430048170 mRNA
TTTTATTTTTAAAGGATGAGCTTTGGTCCTTTTCAGGCCGCCGGTTGTTTCCGTTCCCGA NM_001004431 RefSeq
chr17_KI270860v1_alt - 8451 24134 METRNL 284207 "meteorin, glial cell differentiation regulator-like"
GO:0003674|GO:0005179|GO:0050873|GO:0014850|GO:0050728|GO:0009409|GO:0045444|GO:2000507|GO:0090
336|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130494_PI430048170 0.638754087353085 0.9253207963363 2.7656443587338
2.30344176633111 3.00950086400989 A A P 2.87851459388233 2.55689335767678
3.02654356726056 P P P LNCV6_130494_PI430048170 mRNA
GTACCTATTTTCATTCCCTCTCTGTGGGTCATTAAAAAACACAATGTGGTGGATAAAAAA NM_005941 RefSeq
chr8 - 88037231 88327488 MMP16 4325 matrix metallopeptidase 16 (membrane-inserted)
GO:0005886|GO:0009986|GO:0005796|GO:0005509|GO:0005578|GO:0043085|GO:0048701|GO:0035988|GO:0001
958|GO:0022617|GO:0005887|GO:0030198|GO:0030574|GO:0006508|GO:0008270|GO:0004222|GO:0008047|GO:0
097094 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138406_PI430048170 0.293439800912207 1.04832830536934 0.470848493474627
0.30798348200054 0.372222210413688 A A A 0.279015147670182 0.340527366682741
0.331163210852235 A A A LNCV6_138406_PI430048170 mRNA
CATTGTGTTCATGACCATGTAGCTCATGTTGAAATTAAAGTTTTTGGCTTTTCTAACCTG NM_001205317 RefSeq
chr20 - 44751803 44810338 RIMS4 140730 "regulating synaptic membrane exocytosis 4, transcript variant 1"
GO:0048786|GO:0030054|GO:2000300|GO:0097060|GO:0042391|GO:0006836|GO:0006887|GO:0044325 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_129587_PI430048170 0.142135219329524 0.832229474341084 11.160157052061
11.1806236274776 11.1669157286724 P P P 11.2133677375912 11.4912865102115
11.5737681958803 P P P LNCV6_129587_PI430048170 mRNA
CCCCAACTTTTCATGTTTCTTAAAGGCATTTTGGTTTTTTAAAATCTGTACAGCAAGAGC NM_016333 RefSeq
chr16 + 2752328 2771412 SRRM2 23524 serine/arginine repetitive matrix 2
GO:0047485|GO:0015030|GO:0016607|GO:0000398|GO:0070742|GO:0005654|GO:0071013 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135890_PI430048170 0.00226551060548428 1.72058650448596 9.65484731597045
9.68109094241541 9.86271963996706 P P P 8.93640512616172 9.01013251684489
8.91056333633978 P P P LNCV6_135890_PI430048170 mRNA
TATATGGTAGGTGCCGCTACAGTTTTTATTTAGCATGGGGATTGCAGAGTGACCAGCACA NM_001167820 RefSeq
chr20 - 37517416 37527931 BLCAP 10904 "bladder cancer associated protein, transcript variant 2"
GO:0005515|GO:0007049|GO:0030262|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_89077_PI430048170 0.026543744310927 0.818797808235316 13.4149755731886
13.533717347736 13.365888908043 P P P 13.7352804682294 13.7344377840421
13.7152352418852 P P P LNCV6_89077_PI430048170 mRNA
TGTCGCCGTCCTGTCCCCAGCCTGCTTGTGTCCCGTGAGGTTGTCAATAAACCTGCCCTC NM_024407 RefSeq
chr19 + 1383883 1395589 NDUFS7 374291 "NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)"

GO:0005515|GO:0043005|GO:0051539|GO:0048038|GO:0005743|GO:0044281|GO:0002020|GO:0046872|GO:0003954|GO:0022904|GO:0032981|GO:0005747|GO:0016655|GO:0097060|GO:0006120|GO:0043025|GO:0008137|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129448_PI430048170 0.844440466829632 0.972546878106782 8.71405629465787 8.7219136370386 8.78315224100781 P P P 8.99248662687294 8.76818460052137 8.54534549600854 P P P LNCV6_129448_PI430048170 mRNA GAGAGCATCTTATTTTGTTTAAAGGCAAGAAATAAAATTTCCTTTTGTGGAGCTCTGGCA NM_001202560 RefSeq chr7 + 73683567 73698221 WBSCR22 114049 "Williams Beuren syndrome chromosome region 22, transcript variant 1"
GO:0008150|GO:0006355|GO:0005737|GO:0006364|GO:0008168|GO:0005730|GO:0005575|GO:0032259|GO:0006351|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145337_PI430048170 0.0136656082306678 0.659560877944697 5.47668632157201 5.28732305327559 5.62851596891255 P P P 5.89598760956284 6.04500873680696 6.25082072582788 P P P LNCV6_145337_PI430048170 mRNA GAGAACAAAACAGTCCTTTAAATTTTGCACTGCTCAATTCTGTTTTTCGTTTGCATTGTC NM_002381 RefSeq chr2 - 19992051 20012694 MATN3 4148 matrilin 3
GO:0005515|GO:0001501|GO:0030198|GO:0005578|GO:0005576|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114754_PI430048170 0.240245637083335 0.561425997913262 2.83456135702298 0.417102681091347 0.775661072387253 A A A 2.20693740042999 2.71206651178422 2.79985626208771 A P P LNCV6_114754_PI430048170 mRNA TTCTTGAGTAGGCCAAGTTGCGTATAAAGAGAAAATGACAACAGGAGATTTTAAGGTATG NM_152778 RefSeq chr4 - 127917804 127965984 MFSD8 256471 major facilitator superfamily domain containing 8
GO:0005654|GO:0016021|GO:0005765|GO:0055085|GO:0007040|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144257_PI430048170 0.00268463472482683 0.519943316479245 7.24561545143006 7.22982598110489 7.25868113084585 P P P 8.16092867337198 8.10861348992046 8.28940084471285 P P P LNCV6_144257_PI430048170 mRNA TTTGGAGACAGAGCCATTTGGATATTTTCCCCTTGAACTTCTCCATGACCTGAAGCGTTC NM_015299 RefSeq chr14 + 24429934 24441341 KHNYN 23351 "KH and NYN domain containing, transcript variant 1"
GO:0008150|GO:0003674|GO:0003723|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107995_PI430048170 0.186652551275319 0.891166262558384 8.83257908409837 8.66714981232148 8.81318042411332 P P P 8.76707772398762 9.01223525197497 9.0236279560357 P P P LNCV6_107995_PI430048170 mRNA CGGGGAGTCCCTGTCTCTCACAGCATCTAGCAGTATTATTAAATGGATTCATTTTAAAAA NM_001556 RefSeq chr8 + 42271301 42332653 IKBKB 3551 "inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta, transcript variant 1"
GO:0005515|GO:0035631|GO:0007249|GO:2001259|GO:0042501|GO:0042803|GO:0002756|GO:0010765|GO:0002755|GO:0071356|GO:0043123|GO:0038124|GO:0019901|GO:0038123|GO:0046982|GO:0034134|GO:0002224|GO:0045087|GO:0009898|GO:0034166|GO:0035666|GO:0045121|GO:0045893|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128525_PI430048170 0.673809094149326 1.02192378885129 12.3418259076265 12.1372113112696 12.2368000731531 P P P 12.2108572994527 12.1985075057258 12.2197887742193 P P P LNCV6_128525_PI430048170 mRNA TTCGGAAAGAAGAAGGTGGGAGGATGTGAATTGTTAGTTTCTGAGTTTTACCAAATAAAG NM_001923 RefSeq chr11 - 61299446 61333212 DDB1 1642 "damage-specific DNA binding protein 1, 127kDa"
GO:0005515|GO:0035518|GO:0043066|GO:0046726|GO:0051702|GO:0005634|GO:0080008|GO:0003677|GO:0005615|GO:0003684|GO:0005737|GO:0006281|GO:0042787|GO:0070914|GO:0016032|GO:0043161|GO:0031465|GO:0

005654|GO:0006289|GO:0031464|GO:0000718|GO:0016055|GO:0045070|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131148_PI430048170 0.400118921702396 1.40805032191689 0.320536223238002 0.562666895778045 1.53738404271064 A A A 0.507437441764297 0.385972670946776 0.343789325601912 A A A LNCV6_131148_PI430048170 mRNA
AATGATCTTGCCTGCTGGATATTTCAGTTATATCTGTGATACAATGTCTTCTGTCATTTC NM_031957 RefSeq chr17_JH159146v1_alt - 175420 176597 KRTAP1-5 83895 keratin associated protein 1-5
GO:0008150|GO:0003674|GO:0005575|GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91334_PI430048170 0.0207011364153838 0.7547591167589735.52465250349268 5.41523320787403 5.54768903485188 P P P 5.90192729194564 5.75898973850131 6.03468332229069 P P P LNCV6_91334_PI430048170 mRNA
GAAGGCAATGCAGTATGGCTTCCTTAATTTCAACTCATTTAACCTTGATGAATATGAACA NM_033331 RefSeq chr9 - 96500112 96619830 CDC14B 8555 "cell division cycle 14B, transcript variant 2"
GO:0005515|GO:0031965|GO:0031572|GO:0005730|GO:0005634|GO:0035335|GO:0051488|GO:0006281|GO:0006470|GO:0005654|GO:0004722|GO:0008138|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67891_PI430048170 0.6603502118900760.9675056729160245.11806903393301 5.28117936761815 5.33272696658859 P P P 5.39402137251462 5.14654810748489 5.33165040508293 P P P LNCV6_67891_PI430048170 mRNA
AGACATCCATCTGGTCTGGGATTTCGGGAGTTAGAATGGAAAGCTCTTTGCTAAAGACTG NM_001115016 RefSeq chr2 - 96593154 96638379 KANSL3 55683 "KAT8 regulatory NSL complex subunit 3, transcript variant 1"
GO:0043981|GO:0043982|GO:0043984|GO:0043996|GO:0043995|GO:0000123|GO:0006325|GO:0005730|GO:0046972|GO:0005654|GO:0005634|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131556_PI430048170 0.9894997211071310.961276488315053 1.98461122302102 0.9900340243165172.92816613603063 A A P 2.75183377404106 2.5342429242426 0.653343940907037 P P A LNCV6_131556_PI430048170 mRNA
AAGGGCTCACTTGTATGCTAGAAATAGAAAGAAAAGAAAATTGAACATACTCCGCCACAT NM_014895 RefSeq chr6 - 84124240 84227635 CEP162 22832 "centrosomal protein 162kDa, transcript variant 1"
GO:0005515|GO:0042384|GO:0005813|GO:0005737|GO:0006996|GO:0005814|GO:0005819|GO:0005879|GO:0005654|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94149_PI430048170 0.2657219830937492.91271737221312 0.3807933452559922.65130045447545 3.00024511710821 A A P 1.37449182176589 0.5328982429112040.391033723445665 A A A LNCV6_94149_PI430048170 mRNA
ATCAAGACTGTGTTACCTACTACAAAGCAGCAAGCCCTAGAACCAAGATAGATGCCATCC NM_032604 RefSeq chr2 + 27123788 27130812 ABHD1 84696 abhydrolase domain containing 1
GO:0052689|GO:0008150|GO:0003674|GO:0008152|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134639_PI430048170 0.5131771016784850.9595802720222570.331042983863433 0.4422524286804040.323372509582284 A A A 0.5273628162038490.44611415934617 0.295329652874519 A A A LNCV6_134639_PI430048170 mRNA
CAACTGCAGTTTACAATTTTTGTTCTTCTCCTGTAAAGAATGTCAATGGTTATCACCTTC NM_001460 RefSeq chr1 + 171185207 171212683 FMO2 2327 "flavin containing monooxygenase 2 (non-functional), transcript variant 1"
GO:0050661|GO:0006805|GO:0072592|GO:0017144|GO:0050660|GO:0006739|GO:0006082|GO:0044281|GO:0070995|GO:0004497|GO:0004499|GO:0016020|GO:0005789|GO:0009404|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136367_PI430048170 0.0301470605370102 1.46690248082073 8.59040553211638 8.4841835235956 8.52429383357544 P P P 8.04338551977816 8.12047878168234

7.75330746504163 P P P LNCV6_136367_PI430048170 mRNA
GCACGCCTGTCTCGTCTTCCTTGTTTTGCTGCACTCACTTTTTTATACTCTGACAAAAAA NM_080621 RefSeq chr20 -
63974112 63979642 SAMD10 140700 sterile alpha motif domain containing 10 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_140804_PI430048170 0.1658362468084730.7716900106677241 2.4303713106628 11.889740970803
11.8289564631992 P P P 12.5318120520943 12.4520616217837 12.3606726337001 P P P
LNCV6_140804_PI430048170 mRNA
TTTGGTGCCCTCTCCCTTGGTTCATCAAGCACCAGTCATATAATACCACATACTTGAACT NM_199340 RefSeq chr17
- 64854311 64919480 LRRC37A3 374819 "leucine rich repeat containing 37, member A3, transcript
variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139270_PI430048170 0.000788303523657301 1.62005929075393 14.0354208675472
14.0534719990836 13.9805292133763 P P P 13.2483491029949 13.3317560592411
13.3982707087753 P P P LNCV6_139270_PI430048170 mRNA
TTTCCTCTAAACCTACGAGGGAGGAACACCTGATCTTACAGAAAATACCACCTCGAGATG NM_201397 RefSeq chr3
- 49357175 49358358 GPX1 2876 "glutathione peroxidase 1, transcript variant 2"
GO:0019369|GO:0042542|GO:0060047|GO:0009650|GO:0001659|GO:0006982|GO:0007605|GO:0006749|GO:0004
602|GO:0043523|GO:0006195|GO:0005759|GO:0047066|GO:0045444|GO:0009410|GO:0042744|GO:0010332|GO:0
032355|GO:0070062|GO:0051702|GO:0007568|GO:0009636|GO:0048741|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138947_PI430048170 0.0585806704907892 0.8019424187658778.61918561511592
8.71305296951252 8.59401015047986 P P P 9.11117419376516 8.95834714694992
8.79777012914542 P P P LNCV6_138947_PI430048170 mRNA
CCTTCTAGTTAGTATAGCGGACTTAATAAAAGAGGAAAAAACTCTTGCTTCAGTACTGAC NM_001278216 RefSeq
chr17 + 47970955 47981786 CDK5RAP3 80279 "CDK5 regulatory subunit associated protein 3,
transcript variant 1"
GO:0005515|GO:0019901|GO:0071569|GO:0032088|GO:0000079|GO:0012505|GO:0007346|GO:0043234|GO:0005
737|GO:0016020|GO:0007420|GO:0045944|GO:0045664 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133555_PI430048170 0.3887374065179811.13002008543791 5.20285630159027
5.66343499847578 5.26707292782882 P P P 5.3840956963889 5.14471452213433
5.10367450377733 P P P LNCV6_133555_PI430048170 mRNA
CTGCTTGGGTGTATTTTTCTACACAGGTCTGTACTTCTGCCACTTTCTCCTTTTAAAAAA NM_032510 RefSeq chr18 -
80157233 80247514 PARD6G 84552 par-6 family cell polarity regulator gamma
GO:0005515|GO:0043234|GO:0007049|GO:0070830|GO:0005886|GO:0034329|GO:0005923|GO:0045216|GO:0051
301|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72982_PI430048170 0.24418908507316 1.13212679287657 7.88307120949763 7.72539011798253
7.78309394872892 P P P 7.63907849723728 7.79545830254907 7.39667455969959 P P P
LNCV6_72982_PI430048170 mRNA
TTCTGGGATCTCACCACCATGCTAGACCATGACTCCACTGTCCTGGAGCCTCCAGTGGAT NM_018031 RefSeq chr3
+ 49007203 49015953 WDR6 11180 WD repeat domain 6
GO:0005515|GO:0005737|GO:0008285|GO:0008180|GO:0005886|GO:0010507|GO:0007050 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136580_PI430048170 0.4970004361436241.2488833414949 2.04986730617887
1.29579745902376 1.96737116097964 A A A 0.2927298897883251.82317305020404
1.86752355489176 A A A LNCV6_136580_PI430048170 mRNA
GTTTCCAACACTTAAGGAGACTCTAATGAAAGCTGATGAATTTTCTTTTCTGTCCAAACA NM_001258311 RefSeq
chr1 - 230321645 230425928 PGBD5 79605 piggyBac transposable element derived 5 GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143962_PI430048170 0.40441383236784 0.8235972294348311.29271373485842
1.47512181477717 1.41208308286883 A A A 1.83148855272856 1.17354216201729

1.91328313223994 A A A LNCV6_143962_PI430048170 mRNA
TTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAACATTGTCAGGGTGGT NM_001178045 RefSeq
chr6_GL000250v2_alt - 3195808 3210286 SLC44A4 80736 "solute carrier family 44, member 4,
transcript variant 3"
GO:0005886|GO:0030307|GO:0008292|GO:0044281|GO:0016021|GO:0006644|GO:0055085|GO:0070062|GO:0046
474|GO:0006656 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71521_PI430048170 0.00945101164941487 1.88017852563497 5.64655107816059
6.00272775757233 5.52228235596509 P P P 5.00213406035402 4.77646452902344
4.68574592642524 P P P LNCV6_71521_PI430048170 mRNA
ACGTCCTGTACTCCAGGGTCTGCAAGCCTAAAAGGAGGGACCCAGGACCCACCACAGACC NM_017806 RefSeq
chr20 + 63736459 63739107 LIME1 54923 Lck interacting transmembrane adaptor 1
GO:0050853|GO:0050852|GO:0005886|GO:0016021|GO:0005615 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_64535_PI430048170 0.1660994405563470.8351152693303046.61941374427098 6.43143497816403
6.50897655813226 P P P 6.9387781933948 6.84459881744208 6.53180679788914 P P P
LNCV6_64535_PI430048170 mRNA
AATGTCCGTGCTTGCCTCGTATGAGAAGCTGGGCTCCACCGACCTCTGCTACATCGCGGC NM_020410 RefSeq chr19
- 19645200 19663694 ATP13A1 57130 ATPase type 13A1
GO:0008150|GO:0003674|GO:0016020|GO:0008152|GO:0005789|GO:0016021|GO:0016887|GO:0005524|GO:0046
872|GO:0006812 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105281_PI430048170 0.0989002748107319 0.7566834152232115.72748930560819
5.65410419775096 5.41461454730306 P P P 5.79207402798335 5.90539731496045
6.27784400330255 P P P LNCV6_105281_PI430048170 mRNA
AATGGCCTTTCCTATGAATGTAGGACGCTGCTCTTCAAAGCGATCCACAATCTGTTAGAA NM_015335 RefSeq chr12
- 115958575 116277186 MED13L 23389 mediator complex subunit 13-like
GO:0001104|GO:0006366|GO:0006357|GO:0016592 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138137_PI430048170 0.9966177373327111.03429012116829 4.14270722976762
2.99705407677333 3.24542852614486 P A P 3.89407076310533 3.05059729350426
3.43473289845318 P P P LNCV6_138137_PI430048170 mRNA
TCAAAGAAAGAAATGCCAGACCTGTATCCCAGAAAATAAAGCCACATGATATAGCAAAAANM_152474 RefSeq chr19
- 57958436 57974534 C19orf18 147685 chromosome 19 open reading frame 18
GO:0008150|GO:0003674|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126647_PI430048170 0.3234809336943161.31710552762065 1.17378390760713
0.2997346766175190.479316889191104 A A A 0.3263699635629180.2885103743555
0.29941049077878 A A A LNCV6_126647_PI430048170 mRNA
TTGAGGAACAAGGATGTCAAAGTTGCCCTGAGGAGAACTTTGGGCAGAAAAATCTTTTCT NM_001005195 RefSeq
chr11 - 124542721 124543654 OR8B12 NA "olfactory receptor, family 8, subfamily B, member 12" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107805_PI430048170 0.1291348901226 0.9021943742204612.3988000628098 12.286679473039
12.202051870989 P P P 12.4652282228976 12.3440442466593 12.5246666681054 P P P
LNCV6_107805_PI430048170 mRNA
GTGTGGCTACCCTCGCCACCCCAAATTCCATGTCAATAAAGAACAGCTAAATTCTCCTAG NM_005051 RefSeq chr3
- 49095931 49105129 QARS 5859 "glutaminyl-tRNA synthetase, transcript variant 1"
GO:0005515|GO:0010467|GO:0006425|GO:0005737|GO:0007420|GO:0005759|GO:0004819|GO:0005524|GO:0006
418|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139930_PI430048170 0.5085962196703290.9193379215204160.257202320927057
0.4816025714086870.372854800911375 A A A 0.3869707466708940.745763964926285
0.313646954265306 A A A LNCV6_139930_PI430048170 mRNA
AGCAGTATCTAAAGACGTAGGCGATGAGACTAGACCACATTAAATGCATTTTGATCTCTT NM_021012 RefSeq chr17

+ 21376386 21419867 KCNJ12 3768 "potassium channel, inwardly rectifying subfamily J, member 12"
GO:0005242|GO:0006936|GO:0005886|GO:0051289|GO:0005887|GO:0008016|GO:0010107|GO:0007268|GO:0034
765|GO:0031224|GO:0006813 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145299_PI430048170 0.4970443444032050.9776307806302170.262201209271193
0.2720297802407270.384025301039084A A A 0.3734698526741470.311252298009944
0.333963021480765A A A LNCV6_145299_PI430048170 mRNA
AACCACCATCAAGAAGAACACTCTGAACCCCTATTACAACGAAGCTTTCAGCTTCGAGGT NM_003180RefSeq chr19
- 55173100 55180352 SYT5 6861 "synaptotagmin V, transcript variant 1"
GO:0019905|GO:0005215|GO:0043005|GO:0048471|GO:0030054|GO:0046982|GO:0007268|GO:0031045|GO:0044
281|GO:0046872|GO:0005544|GO:0006112|GO:0050796|GO:0030276|GO:0017156|GO:0043025|GO:0030672|GO:0
016021|GO:0055038. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141381_PI430048170 0.00331183586370276 1.57225000246196 8.26758401818357
8.45745838166033 8.25842870634047 P P P 7.82557672424101 7.62759030229075
7.56791045587868 P P P LNCV6_141381_PI430048170 mRNA
TGGATTTCCAAACCATCCTTGTATAAACTGCTCAGAACTAGCATCTTGCTCCTTCTTACC NM_001014445 RefSeq
chr17 - 35131321 35142251 NLE1 54475 "notchless homolog 1 (Drosophila), transcript variant 2"
GO:0007219|GO:0045930|GO:0090263|GO:0005730|GO:0001826|GO:0042273|GO:0005634|GO:2001268 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141200_PI430048170 0.5002607430925460.9768351384955730.396215215198951
0.4061251903871120.275594835909168A A A 0.3742924202323970.422183743649554
0.386090430510058A A A LNCV6_141200_PI430048170 mRNA
CCACCGCATGAGTTGAATCAAAATTTTCAGATCTTTTCAGGAGTGTAAGGAAACATCATG NM_002175RefSeq chr9
- 21165636 21166660 IFNA21 3452 "interferon, alpha 21"
GO:0005132|GO:0019221|GO:0005576|GO:0033141|GO:0045343|GO:0005125|GO:0005615|GO:0005126|GO:0002
250|GO:0051607|GO:0060337|GO:0060338|GO:0042100|GO:0007596|GO:0045087|GO:0006959|GO:0030183|GO:0
043330|GO:0002286|GO:0002323 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142098_PI430048170 0.0918487462690631.16783029073182 6.17134045229924
6.36483675626747 6.10353204912235 P P P 5.95811136207187 5.96730446875488 6.0537606203745
P P P LNCV6_142098_PI430048170 mRNA
AAGCTGGAGCACTACGACTTGCAGGCCACCCATTCCAACTGAGTGTAGTCGGCTCAACAC NM_152657RefSeq chr19
- 38384351 38388028 GGN 199720 gametogenetin
GO:0048471|GO:0008104|GO:0007276|GO:0046983|GO:0005730|GO:0007275|GO:0007283|GO:0030154 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139817_PI430048170 0.2323381920444531.06498622371615 0.62219132693603
0.4679138137414830.619390941538361A A A 0.4276503289432180.551034587800375
0.460800218025261A A A LNCV6_139817_PI430048170 mRNA
TTATTGAATGTATGTTTTGGATGCCACATCCTCCTGGAAGCAAATTTTGCCAAGATACTG NM_173801RefSeq chr11
+ 60040274 60048043 OOSP2 219990 oocyte secreted protein 2 GO:0005576 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_135413_PI430048170 0.5691186139892940.8185913958209210.522207445190438
0.6654749398570050.63806564836635 A A A 0.5896027525373510.42861820707886
1.45541113257062 A A A LNCV6_135413_PI430048170 mRNA
CTCTACTACTATGCTCATGACAAAATGAAACAAAGCATATTGTGAGCAATACTGAACATC NM_018930RefSeq chr5
+ 141192378 141195640 PCDHB10 56126 protocadherin beta 10
GO:0016339|GO:0005886|GO:0005509|GO:0007268|GO:0016021|GO:0007416|GO:0007156 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140300_PI430048170 0.0676804650445058 1.51198441116558 4.63582267490574
4.82249137830109 5.03015109428983 P P P 4.30710667600669 3.84207623674933
4.50025222881046 P P P LNCV6_140300_PI430048170 mRNA

GATTTCAATAGTCAAACTGCTGTGTTTGTTGATGTAAAGATGTTTTGAATGGCTAGATGG NM_001284238 RefSeq chr2 - 143946013 144332534 GTDC1 79712 "glycosyltransferase-like domain containing 1, transcript variant 7" GO:0009058|GO:0016757 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143964_PI430048170 0.00347817816610427 0.5670917426858824.13128998921703 4.13657544670011 3.9751865740337 P P P 5.03663505460372 4.92439590237474 4.72582484783635 P P P LNCV6_143964_PI430048170 mRNA
GCGTTTTGTTGTAGATGCTAACGTGTCAGAATCCTTTACATTCAACTTTTCTAAGAAAAG NM_016374RefSeq chr1 - 235166894 235328217 ARID4B 51742 "AT rich interactive domain 4B (RBP1-like), transcript variant 1" GO:0005515|GO:0010467|GO:0044212|GO:0006357|GO:0006325|GO:0005634|GO:0005575|GO:0007283|GO:0006351|GO:0003674|GO:0008150|GO:0005737|GO:0045944|GO:0045814|GO:0036124|GO:0006349|GO:0040029|GO:0005654|GO:0034773. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134858_PI430048170 0.0165311954026601 0.4519061851431954.29895237155021 4.017585982175 4.47279252484654 P P P 4.96998160923575 5.53128397782829 5.67087530971124 P P P LNCV6_134858_PI430048170 mRNA
TAGCCCTGAGTATTTTAGTCATTTGTGCCTATAGAAAACAACATGCTCTTTTATTGTGGA NM_001031720 RefSeq chr4 + 105710812 105847725 GSTCD 79807 "glutathione S-transferase, C-terminal domain containing, transcript variant 1" GO:0005515|GO:0008150|GO:0003674|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114173_PI430048170 0.7157289775017691.03834027632158 8.00587554881051 7.86340710606771 8.16743863613753 P P P 7.71318910110885 8.05655209912064 8.09083499801336 P P P LNCV6_114173_PI430048170 mRNA
TCTGTTCCTCATAGCTATACTGTGTACACATAAGACGCATATAGGGTTTTACTGAAATCT NM_007353RefSeq chr7 - 2728105 2844325 GNA12 2768 "guanine nucleotide binding protein (G protein) alpha 12, transcript variant 1" GO:0005515|GO:0032006|GO:0005886|GO:0008360|GO:0003924|GO:0032434|GO:0007266|GO:0031526|GO:0030154|GO:0046872|GO:0010762|GO:0004871|GO:0042493|GO:0005834|GO:0030168|GO:0005525|GO:0031683|GO:0001701|GO:0006184|GO:0007186|GO:0007596|GO:0031752|GO:0007188|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137048_PI430048170 0.1731714016824580.7403552870835131.4570139103864 2.14850616623281 2.00180896678996 A A A 2.08009929257875 2.62183112638146 2.23961876740981 A P A LNCV6_137048_PI430048170 mRNA
AAATAGAGTATTTTTCCTCGTAGTTCGAGAATAAAATGTGTGGGGTTGGGTCCCCTGCGC NM_014360RefSeq chr14 - 36580010 36582581 NKX2-8 26257 NK2 homeobox 8 GO:0003700|GO:0006366|GO:0030324|GO:0050680|GO:0005634|GO:0005575|GO:0007409|GO:0000978|GO:0006351|GO:0001889|GO:0043565|GO:0001077|GO:0003690|GO:0045944 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139287_PI430048170 0.5557186931435170.9290876371973060.297346782884356 0.2617514098674330.395472876209275A A A 0.2828741198305750.678389713856499 0.277292920724315A A A LNCV6_139287_PI430048170 mRNA
TAGATCACCTGGATACTCGAGTATAGACCCTAGAAGTGTATCTAGGCGCGGCCAGGGCCC NM_001001712 RefSeq chr9 - 136738166 136742959 LCN10 NA lipocalin 10 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142510_PI430048170 0.2914162193398530.6287150160378612.91137744596346 1.12168386060439 2.60451909076088 A A A 2.42162511042957 3.2877270788058 3.31865593726236 A P P LNCV6_142510_PI430048170 mRNA
CTTTGTCTACCTGCTCGTTCCCAATGTATCTTAATGAAAAGTGCAAAAGAAAAACCTACC NM_030762RefSeq chr12 - 26120025 26125070 BHLHE41 79365 "basic helix-loop-helix family, member e41" GO:0001191|GO:0005515|GO:0001102|GO:0046982|GO:0042826|GO:0006366|GO:0008283|GO:0003705|GO:0003714|GO:0043426|GO:0043425|GO:0070888|GO:0005634|GO:0010832|GO:0000122|GO:0000978|GO:0042803|GO:0

032922|GO:0030154|GO:0001078|GO:0010944|GO:0007623|GO:0009887|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136082_PI430048170 0.1164286449116561.16450855278751 10.9337152405478 11.2171426457909 11.1202038511143 P P P 10.8827409832276 10.9023122998549 10.8403814032961 P P P LNCV6_136082_PI430048170 mRNA
GGCGCTGGATTTTGGGACAAAACTATTTTTCAGAGCGTTGTACCGGCACTTTATATATAT NM_152326RefSeq chr14 - 102506860 102509791 ANKRD9 122416 ankyrin repeat domain 9NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143056_PI430048170 0.1345937371998570.8222417731720649.60765685609221 9.60703289679022 9.629912885496 P P P 9.68494943847581 9.90800649931102 10.0728102815859 P P P LNCV6_143056_PI430048170 mRNA
GATCTGGGAAACTGATTGAATAATACACTTTTCTTGCTTTGGTGCTCAAAGTGGTTTTTT NM_016495RefSeq chr6 - 13304950 13328583 TBC1D751256 "TBC1 domain family, member 7, transcript variant 1"
GO:0005515|GO:0032007|GO:0017137|GO:0033126|GO:0031398|GO:0032851|GO:0016023|GO:0032862|GO:0031410|GO:0070848|GO:0036064|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141963_PI430048170 0.0257845390900671 0.3540633147897312.41985584510966 2.08530403002936 2.07699398149773 A A A 3.06491931503432 3.91239023306636 3.96258418760775 P P P LNCV6_141963_PI430048170 mRNA
TCAGTCTTTTCCGCTACCAGATCAGGTTAGCACAGTATAGAGCACTTAACTATTAAAAAA NM_015559RefSeq chr18 + 44680897 45068510 SETBP1 26040 "SET binding protein 1, transcript variant 1"
GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139314_PI430048170 0.9619656222832380.9515970197062810.488318420224372 1.21003344635049 0.688250047990779A A A 1.4909967149095 0.442575710982077 0.514696782454278A A A LNCV6_139314_PI430048170 mRNA
AACAAGGAATTTAAGGACGCCTTGAAAAAGGCCTTGGGCTTGGGTCAAACTTCACACTAA NM_001005853 RefSeq chr2 - 240029490 240030429 OR6B2 NA "olfactory receptor, family 6, subfamily B, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94673_PI430048170 0.0425787950944157 0.7796795678594496.4889008082398 6.65234546912668 6.80229553348605 P P P 7.05635628311115 6.94265083162451 7.03613001044448 P P P LNCV6_94673_PI430048170 mRNA
GCTGCTGATCTACAGAGAACTTCTTGTAATTAAAAGATTTCAATTCATAGCAAACTGGTG NM_005642RefSeq chr5 - 141318489 141320784 TAF7 6879 "TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa"
GO:0035035|GO:0005515|GO:0006352|GO:0008024|GO:0000296|GO:0003700|GO:0005669|GO:0005794|GO:0006367|GO:0044212|GO:0006366|GO:0003713|GO:0000122|GO:0035067|GO:0033276|GO:0046966|GO:0042809|GO:0071339|GO:0045944|GO:0005654|GO:0006469|GO:0045892|GO:0030520|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136450_PI430048170 0.0398768009594165 1.25928882512759 8.29787944039597 8.2962151023611 8.49663684097997 P P P 7.87373877364785 8.16959877187992 8.04371678628953 P P P LNCV6_136450_PI430048170 mRNA
GAATCGGGGGTGGGACTTGCAGTTACTTAAAATTTTTTAATAAACTGTGCCCTGAAACCT NM_152735RefSeq chr6_GL000256v2_alt + 4903301 4906266 ZBTB9 221504 zinc finger and BTB domain containing 9
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145558_PI430048170 0.2968206097792430.9850270882877730.350693704255555 0.3792176312033280.326529371494602A A A 0.3735032618018810.389487149302846 0.359066231839198A A A LNCV6_145558_PI430048170 mRNA
ATTTATTCTTTAACAGCATCTTGCCATCTATATGTTAGTAGCAGTTGGCCCAGAAAGGAC NM_207407RefSeq chr4 - 68053197 68129869 TMPRSS11F 389208 "transmembrane protease, serine 11F"

GO:0004252|GO:0005887|GO:0006508|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132552_PI430048170 0.0667013291308893 1.86826119867035 12.1429356773868
12.9194972577931 12.1155170448771 P P P 11.4198982213655 11.432892788237
11.7474501318228 P P P LNCV6_132552_PI430048170 mRNA
GTTTTTAATTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAACTGTATCATTTTCTGC NM_016022 RefSeq chr1
- 150265398 150269209 APH1A 51107 "APH1A gamma secretase subunit, transcript variant 2"
GO:0042987|GO:0001656|GO:0005515|GO:0048011|GO:0043065|GO:0005794|GO:0007220|GO:0048013|GO:0005
886|GO:0031293|GO:0005783|GO:0043085|GO:0097190|GO:0004175|GO:0007219|GO:0016020|GO:0016485|GO:0
005887|GO:0007411|GO:0032580|GO:0005789|GO:0006509 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_127733_PI430048170 0.1107799462241661.18531150555325 9.86805553664281
9.58631702116832 9.58420717365187 P P P 9.36067234110299 9.48238036095725
9.47538068402991 P P P LNCV6_127733_PI430048170 mRNA
GTTGTAACTTTTTGTGTCTTGTCATGTCAGAGAATAAATAAATATTCTAAGTAGAAAAAA NM_001191060 RefSeq
chr11 - 790474 797995 SLC25A22 79751 "solute carrier family 25 (mitochondrial carrier: glutamate),
member 22, transcript variant 1"
GO:0005739|GO:0015813|GO:0005313|GO:0005743|GO:0005654|GO:0016021|GO:0015293 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133097_PI430048170 0.3944072767780520.9322505658548231 0.6355492973004 10.862499434899
10.9574904815912 P P P 10.9113838729731 10.8513387361905 11.0106215784944 P P P
LNCV6_133097_PI430048170 mRNA
TGCTCTTTGCTGTGTCCTTTCAGAATTTTTACCAGGAACATAATGTGGATGTGACTTATG NM_001003690 RefSeq
chr6 + 43629541 43640951 MAD2L1BP 9587 "MAD2L1 binding protein, transcript variant 1"
GO:0005515|GO:0007093|GO:0005737|GO:0007096|GO:0005819|GO:0005730|GO:0005634|GO:0043231 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139326_PI430048170 0.12200396130313 1.06590612933402 0.456591524714886
0.3307457374498150.361427386526411 A A A 0.26854823562982 0.3346394743227
0.271366867441141 A A A LNCV6_139326_PI430048170 mRNA
CCCTTCATTCAATAACGATTTTCCTTGATTCTTAGATAAGTCCATTCCATAATGTACTCC NM_052952 RefSeq chr2 -
188733737 188790104 DIRC1 116093 disrupted in renal carcinoma 1 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140790_PI430048170 0.0883650194815277 1.19500542804886 9.3322100940992
9.56892765071966 9.38385942424359 P P P 9.18129817583189 9.31645494646846
9.01089855751238 P P P LNCV6_140790_PI430048170 mRNA
ATGCTATAAAAGGACTTGGATTTCTGACTTGGCTCAGGGACTGGGGTTAGCAGTCTCTTT NM_212550 RefSeq chr19
+ 45178744 45181800 BLOC1S3 NA "biogenesis of lysosomal organelles complex-1, subunit 3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143441_PI430048170 0.0646508167393328 0.82083001083138 8.32105462432054
8.26503191265213 8.11115158414287 P P P 8.35471301247721 8.65557574145535
8.53382534238662 P P P LNCV6_143441_PI430048170 mRNA
GTGACGTTTGGTGTTTTCTGTACTGTGTTTCAATAAAAACTCCTTCAAGGTTGCAAAAAA NM_020421 RefSeq chr14
+ 77800082 77933954 ADCK1 57143 "aarF domain containing kinase 1, transcript variant 1"
GO:0005739|GO:0004674|GO:0006468|GO:0005576|GO:0005524 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_106821_PI430048170 0.7095088409567080.8727752990923482.27061296010136
2.41877127244986 1.77530540563211 A A A 2.91771425153085 2.1209655414436
1.87618739328802 P A A LNCV6_106821_PI430048170 mRNA
CAATCAAGAATAAAATTAAGAAGAACCTTATATCAAAGGTGGGTGGATCCTTAGGAAAGC NM_001135993 RefSeq
chr18 + 24014419 24135610 TTC39C 125488 "tetratricopeptide repeat domain 39C, transcript variant 1"

NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132933_PI430048170 0.00840529825669592 1.43304647053842 2.76529473690863
2.80511332876608 2.64573155111941 A A A 2.22400532837757 2.22077198340448 2.2188299282962
A A A LNCV6_132933_PI430048170 mRNA
CATAGACTTGTATTTTTATGTTTTGGGGATGGGATGGGGTTATCTTCTGTTGTAAATTAG NM_001145312 RefSeq
chr1 - 157124666 157138591 ETV3 2117 "ets variant 3, transcript variant 1"
GO:0043565|GO:0008150|GO:0003674|GO:0006366|GO:0006357|GO:0017053|GO:0000981|GO:0005634|GO:0000
122|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127346_PI430048170 0.3395964723253590.8461807328064969.90787532462349
9.37502255635142 9.18655919796255 P P P 9.82829000374877 9.85152775395646 9.5992094498687
P P P LNCV6_127346_PI430048170 mRNA
CCCAGAAATCACTGAAATTTCATGATTGGCTTAAAGTGAAGGAAGTAAAGGTAAAATCAC NM_032689RefSeq chr19
- 37696362 37719790 ZNF607 84775 "zinc finger protein 607, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130038_PI430048170 0.7610941868825610.8092747960584291.43839745648624
1.20592649076987 1.38058400820493 A A A 0.6143770633384541.68089914467267
2.22639657274056 A A A LNCV6_130038_PI430048170 mRNA
CTGTAAGTAATCTGAAAGCAATAGTGCATGAATTTCATAGGTAGTGTTGTTTTAGGTCAG NM_003437RefSeq chr19
+ 12163056 12189249 ZNF136 7695 zinc finger protein 136
GO:0005515|GO:0006366|GO:0003714|GO:0005634|GO:0000122|GO:0003677|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139175_PI430048170 0.34431474193979 1.02211041054306 0.339107998499968
0.2568750145964830.271239779175685A A A 0.2543142443202560.26523187955841
0.254339987020242A A A LNCV6_139175_PI430048170 mRNA
CTGAAACTCACCAATCTCTATACACCATAAAGACCTCACCTTGGTAGGCACCAGAAAAAA NM_152794RefSeq chr19
+ 46303598 46343433 HIF3A 64344 "hypoxia inducible factor 3, alpha subunit, transcript variant 1"
GO:0003700|GO:0006357|GO:0006366|GO:0003714|GO:0003713|GO:0061418|GO:0071456|GO:0003677|GO:0005
829|GO:0007165|GO:0046983|GO:0005654|GO:0004871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144187_PI430048170 0.5656055578709111.12610400926312 4.67160399786119
4.98081142186446 4.29027804782907 P P P 4.81858643792504 4.25181009438362
4.37695642012641 P P P LNCV6_144187_PI430048170 mRNA
ATACTTGTGAGTTCTTGGGGTTGCTCACAAATACTAGGGGTTTTTGTTGTATTTTTAACA NM_025202RefSeq chr2
+ 232633496 232682781 EFHD1 80303 "EF-hand domain family, member D1, transcript variant 1"
GO:0005509|GO:0005743|GO:0031175|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141661_PI430048170 0.00024131950223141 8 0.2752992557583551.96077826775953
1.7804041756526 2.14556018730742 A A A 3.67297346195083 3.91018563226105
3.89734386342377 P P P LNCV6_141661_PI430048170 mRNA
TAGCAGTCTGCATCCTAAGTTTAAAATATTTGAGAATCCTCTATGGGACTCTCTGTAAAT NM_017645RefSeq chr9
- 19053136 19102942 HAUS6 54801 "HAUS augmin-like complex, subunit 6, transcript variant 1"
GO:0051297|GO:0003674|GO:0007067|GO:0005813|GO:0005737|GO:0005815|GO:0005874|GO:0005819|GO:0070
652|GO:0005654|GO:0051225|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144238_PI430048170 0.2800943458999331.8994058671408 1.23318939231121
2.24096555786896 0.43976159417899 A A A 0.8789218719996730.384064731149423
0.374643533958704A A A LNCV6_144238_PI430048170 mRNA
TATCCAGAGGGACCCATGGGAATCATACAGCATCTGGAACCTTCTGCTCACGCTGCAGGC NM_001135111 RefSeq
chr6 - 39299000 39314461 KCNK1789822 "potassium channel, two pore domain subfamily K,
member 17, transcript variant 2"
GO:0005244|GO:0005886|GO:0007268|GO:0005267|GO:0034765|GO:0016021|GO:0006813|GO:0071805 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_9161_PI430048170 0.1346141052483831.26582318186612 7.41041262471028 7.89109418334527
7.69039730629939 P P P 7.26452845562068 7.39777387497571 7.34620122620204 P P P
LNCV6_9161_PI430048170 mRNA
GCCACCCGAGCCGGAGCGGGCTGGGCCGCCAAGGCAAGATGGTGGACTACAGCGTGTGGG NM_007065RefSeq
chr19 - 10391132 10403595 CDC37 11140 cell division cycle 37
GO:0005515|GO:0051879|GO:0051087|GO:0050821|GO:0031435|GO:0032587|GO:0000079|GO:0006605|GO:0043
422|GO:0005829|GO:0060334|GO:0043234|GO:0005737|GO:0060338|GO:0006457|GO:0031072|GO:0051082|GO:0
019900|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143215_PI430048170 0.000362122033385698 0.5433239296551178.73552330552983
8.79812603129046 8.71452721644386 P P P 9.63651517576989 9.61582201412997
9.63739931736368 P P P LNCV6_143215_PI430048170 mRNA
TCCGTGTGTGATGAAACTTCCCGTGGACAGCCAATAAAATGACGTCCTCTGTTATTTTGG NM_024630RefSeq chr6
+ 157381524 157673945 ZDHHC14 79683 "zinc finger, DHHC-type containing 14, transcript variant 1"
GO:0018345|GO:0005783|GO:0016409|GO:0008270|GO:0016021|GO:0019706 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_52910_PI430048170 0.4450249395543490.2736026020306680.4090490844096420.43826410386387
0.455050547069538A A A 0.3376126449297753.61167595642581 0.409005713424178A P A
LNCV6_52910_PI430048170 mRNA
TTCGATGCGTGGATTACAATGTTCTCTTTGCCAACCAACCAAGTAACCATACCAGACCTG NM_173681RefSeq chr7
- 151012208 151024499 ATG9B 285973 "autophagy related 9B, transcript variant 1"
GO:0000421|GO:0031410|GO:0016021|GO:0000045 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140600_PI430048170 0.0208198540973169 2.05957176157557 7.93904258475913
7.90781763001426 7.84248790102336 P P P 6.84417063634895 7.11756258870822
6.54594706202205 P P P LNCV6_140600_PI430048170 mRNA
GGGCTCCTCCCGGCGGGGGCTTGGCCAAAGCTTTCTTAATAAAATGCCTTTCCCCTCAAA NM_153334RefSeq chr22
- 20424583 20437859 SCARF2 91179 "scavenger receptor class F, member 2, transcript variant 1"
GO:0005515|GO:0016021|GO:0005925|GO:0007157|GO:0006898|GO:0005044 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135164_PI430048170 0.1613363995423990.6512217017108892.92054862383916
2.50982836788413 3.58576984336817 A A P 3.28210026960331 3.92496400831474
3.79625320059851 P P P LNCV6_135164_PI430048170 mRNA
GGTCTTTCTTAGAATGGTCTAGTTAAGTTCCACATGTAGCATAATTCTTAAATAGGCACT NM_001086RefSeq chr3
+ 151814072 151828488 AADAC 13 arylacetamide deacetylase
GO:0004806|GO:0008152|GO:0019213|GO:0005789|GO:0010898|GO:0017171|GO:0016021|GO:0003824|GO:0016
298 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140627_PI430048170 0.9513274869367441.09506454865948 1.80751807477103
0.4071640054558640.248462537656465A A A 0.4645199823928191.48385583903288
0.395589131762637A A A LNCV6_140627_PI430048170 mRNA
CTCAAGGGTGTAGGTAAAAGATGGTAAAAATACACTATTTGGTAAGATAATGGACTGACA NM_003430RefSeq chr19
- 23357695 23395560 ZNF91 7644 "zinc finger protein 91, transcript variant 1"
GO:0003700|GO:0070895|GO:0008270|GO:0005634|GO:0045892|GO:0003677|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_101405_PI430048170 0.0325538623048487 2.1216643185239 4.3527218075892
4.38742216934427 4.77998710149909 P P P 2.87620481591426 3.74623177829059
3.54622540860582 P P P LNCV6_101405_PI430048170 mRNA
TGAAAAAGTCTGTCTGATTCCAGGGTGTTTTTCCTGGGTTTCATCATCAGGTACCTCCTC NM_001440RefSeq chr8
+ 28701472 28753690 EXTL3 2137 "exostosin-like glycosyltransferase 3, transcript variant 1"
GO:0001888|GO:0030307|GO:0005783|GO:0005789|GO:0016021|GO:0015012|GO:0006987|GO:0044267|GO:0046

872|GO:0006024|GO:0030968 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120720_PI430048170 0.5514248038554481.12809359545152 1.19936872536191
0.9452253807881011.07294818446937 A A A 0.3102180681028491.65417253513787
0.286908533112389A A A LNCV6_120720_PI430048170 mRNA
CTGACAAATGTGTATCGGATGCTTTTGTTCAGGGCTGTGATCGGCCTGGGGAAATAATAA NM_002983RefSeq
chr17_KI270909v1_alt - 149003 150906 CCL3 6348 chemokine (C-C motif) ligand 3
GO:0005515|GO:0019722|GO:0051928|GO:0008360|GO:0006887|GO:0005615|GO:0042802|GO:0005622|GO:0031
726|GO:0043525|GO:0006935|GO:0000165|GO:0016301|GO:0071356|GO:0007610|GO:0070374|GO:0031663|GO:0
008009|GO:0030335|GO:0032760|GO:0023052|GO:0030593|GO:0071621|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144090_PI430048170 0.3482983957429590.9197959163213090.292774113719601
0.33257681784853 0.377058763904675A A A 0.3774965707396450.636009867665315
0.333078896034893A A A LNCV6_144090_PI430048170 mRNA
TGGGTCCTAATGATATCTCTGTATAACAAAGCAGTTACGAAGCCTACAGATTTTGTGCAA NM_001012417 RefSeq
chr11 + 60515412 60542718 MS4A13 NA "membrane-spanning 4-domains, subfamily A, member 13,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137103_PI430048170 0.0102189395391684 0.5093641162118771 0.8144960831896
10.2562413247591 10.4715106158502 P P P 11.3492099862723 11.4105959494363
11.7283389824019 P P P LNCV6_137103_PI430048170 mRNA
TACTGTTGATTTTGCCCTCGGAGCAAACTGAATAAAGCAACAAGATGAAAACTGAAAAAA NM_006839RefSeq chr2
- 86143931 86195770 IMMT 10989 "inner membrane protein, mitochondrial, transcript variant 1"
GO:0005739|GO:0005515|GO:0008150|GO:0016020|GO:0051560|GO:0009409|GO:0005743|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133484_PI430048170 0.9105282289169350.96341846177657 2.3182387866497
1.89822112480264 1.63219258837406 A A A 2.06204570585662 2.3853226124011
1.51743713162176 A A A LNCV6_133484_PI430048170 mRNA
TTTTCATTTCAACCAGTTTGCAAAGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAA NM_014439RefSeq chr2
+ 112912970 112918881 IL37 27178 "interleukin 37, transcript variant 1"
GO:0006955|GO:0005737|GO:0005149|GO:0006954|GO:0019221|GO:0005730|GO:0005654|GO:0005634|GO:0005
576|GO:0005615|GO:0005125|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142211_PI430048170 0.3258525303507610.8719927989946 0.380779125703299
0.4462253461789230.352105624663649A A A 0.4858217967416420.856370911649997
0.388023992067089A A A LNCV6_142211_PI430048170 mRNA
TGAAGTAACTGGTATGTGTACACAAGCATATTGCTTTTTTCTTCAAACCAAACAGCCAAT NM_001002255 RefSeq
chr6 + 149400358 149401046 SUMO4 NA small ubiquitin-like modifier 4 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_130451_PI430048170 0.2679793134460950.8246210003882525.84684538018737
5.15068808642418 5.54463926508826 P P P 5.69501823558508 5.88258908992807
5.87465231216052 P P P LNCV6_130451_PI430048170 mRNA
CACAACTTAGAACAGACTGAATTAATAAATGAGAAGCGACATGAACGCAGCCTTAAAAAA NM_015245RefSeq chr6
+ 34889260 35091413 ANKS1A 23294 ankyrin repeat and sterile alpha motif domain containing 1A
GO:0016322|GO:0005515|GO:0043005|GO:0005737|GO:0048013|GO:0006929|GO:0005654 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132821_PI430048170 0.5684864634532410.9771017820920270.417023984458244
0.4469413252823880.403762899012185A A A 0.5149293543085090.486237600018775
0.362664385811473A A A LNCV6_132821_PI430048170 mRNA
ATCCTTCCCAAATAAATGTTTCTTCTTGCCATTTTGAGCCATCTTATTTGGCTAATGTAG NM_182974RefSeq chr9 -
135623655 135639540 GLT6D1 NA glycosyltransferase 6 domain containing 1 NA . NA - . NA NA
NA NA NA NA NA NA NA

LNCV6_137058_PI430048170 0.2568597180374020.9387508431517570.313595887835069
0.3811766663525240.293423164273598A A A 0.5139127121768010.426466046943555
0.316051703322882A A A LNCV6_137058_PI430048170 mRNA
GTTAAAATATCCAAGATGTATTCCAAGACAAAGCACTCTGTCTTATCAAGAACCCTTAAG NM_001994RefSeq chr1
- 197039190 197067267 F13B 2165 "coagulation factor XIII, B polypeptide" GO:0007596|GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136614_PI430048170 0.3217104673466441.10318904307712 0.685755549392069
0.3812925104664660.619155204138237A A A 0.2822443483522140.412067722729413
0.569869539129487A A A LNCV6_136614_PI430048170 mRNA
GGACATGATGTAAGGGAAAAGGCCTCAAATTCTTGTGAATGTCTGGACATTCTCGTTAAT NM_005407RefSeq chr14
- 21521080 21537216 SALL2 6297 "spalt-like transcription factor 2, transcript variant 1"
GO:0005515|GO:0016581|GO:0001654|GO:0021915|GO:0000122|GO:0003677|GO:0046872|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139044_PI430048170 0.0933556805684127 0.7903755658262845.96872569004203
6.05916002204038 5.66808857642286 P P P 6.09845549218422 6.43238360585778
6.19077994558934 P P P LNCV6_139044_PI430048170 mRNA
GCTGCTTTTGTCTTTGTACCTTTGCATCCTTTGTAATGAAACGTAATAAAAATCCAACGT NM_001098482 RefSeq
chr19 + 18683614 18782333 CRTC1 23373 "CREB regulated transcription coactivator 1, transcript
variant 3"
GO:0005515|GO:0005886|GO:0005634|GO:0006351|GO:0032793|GO:0060081|GO:0005737|GO:0008140|GO:0051
289|GO:0045944|GO:0016032|GO:0005654|GO:0007613|GO:0048511|GO:0043153 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145094_PI430048170 0.2346091905328020.3824009714589590.337678613286805
0.3260676863527110.409236678331919A A A 1.22996623452076 0.449918581736506
2.66541270726374 A A P LNCV6_145094_PI430048170 mRNA
TCTTGCGTGCAGGGATGCTTGCTGATGGATGAAAGACCACAATAAAACAAGATTAGCAGC NM_173509RefSeq chr1
+ 179743162 179816198 FAM163A 148753 "family with sequence similarity 163, member A" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139522_PI430048170 0.4634201231792440.9591161411256481 1.0831192734824
10.8748147648873 10.8740727834334 P P P 11.0365567918455 11.0202264581928
10.9651414208128 P P P LNCV6_139522_PI430048170 mRNA
GTTTTGCGACATTGTCCCATTCACACAGATATTTTGGGATAATAAAGGAAAATAAGCTAC NM_001172818 RefSeq
chr1 + 63623215 63660246 PGM1 5236 "phosphoglucomutase 1, transcript variant 2"
GO:0000287|GO:0005975|GO:0005978|GO:0006094|GO:0019388|GO:0044281|GO:0015629|GO:0006096|GO:0005
829|GO:0005737|GO:0004614|GO:0009405|GO:0006006|GO:0005980|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137467_PI430048170 0.1175631813609720.7780499936593912.58281890761983
3.04181659299749 2.95910156397221 A P P 3.29744387833756 3.00266402999868
3.38306275240428 P P P LNCV6_137467_PI430048170 mRNA
AACTGGCAGCCACCTGGCCTTATCATTGTTCTATTTGATTTGCACCCTGGTTCTCTTTCT NM_152429RefSeq chr10 -
91906587 91909501 FGFBP3 143282 fibroblast growth factor binding protein 3
GO:0031012|GO:0045743|GO:0017134|GO:0005576|GO:0043117|GO:0008201 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131922_PI430048170 0.1147636451997870.9265007260411930.275666303867953
0.2847051572680730.291024379673925A A A 0.4691236291350120.379822030826605
0.329415407475851A A A LNCV6_131922_PI430048170 mRNA
TTTTGCCATTTTGGGCTGGATCTTGCTCAGTTTTTTAAATTGCAGGTTTAAACAAAGCCG NM_001144981 RefSeq
chr13 - 36230774 36297855 CCDC169 728591 "coiled-coil domain containing 169, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133176_PI430048170 0.3252894272499241.10038981727028 9.16314332321424
8.97988196453568 9.09073895150079 P P P 9.07290308657181 8.71704729143336
9.01117851238367 P P P LNCV6_133176_PI430048170 mRNA
TGGAGTTGAGATATCAGTCTCGGAAACTTCTGAAAAATGCTAATAATTACCCAAGGATTA NM_173216RefSeq chr3
+ 186930525 187078553 ST6GAL1 6480 "ST6 beta-galactosamide alpha-2,6-sialyltranferase 1, transcript variant 1"
GO:0008373|GO:0006054|GO:0016266|GO:0003835|GO:0030173|GO:0000139|GO:0006493|GO:0006959|GO:0032580|GO:0006488|GO:0044267|GO:0070062|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134126_PI430048170 0.5385846204665881.04947578796049 10.4828993614833
10.7110779894564 10.4917704395585 P P P 10.4552241180433 10.6303356931301
10.3922880819563 P P P LNCV6_134126_PI430048170 mRNA
GCTAAGATACTGCTGATGCTGAAATAAACTAGGGTTTTGGCCTGCCTGCGTCTGAAAAAA NM_001823RefSeq chr14
- 103519657 103522859 CKB1152 "creatine kinase, brain"
GO:0005739|GO:0005515|GO:0004111|GO:0034641|GO:0016310|GO:0030644|GO:0021762|GO:0006600|GO:0044281|GO:0005524|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130515_PI430048170 0.3138548367780650.8088122011118232.46211746988721
3.02612702823319 2.32933058305924 A A A 3.24648625011319 2.65694257216009
2.86805712779534 P P P LNCV6_130515_PI430048170 mRNA
CCAATGAGCCACTAATAAAGGTGAACATAAGGTTAATATTACTAATTGATCCCCCCAAAA NM_002013RefSeq chr14
- 45115598 45134529 FKBP3 2287 "FK506 binding protein 3, 25kDa"
GO:0005515|GO:0000413|GO:0061077|GO:0005789|GO:0003755|GO:0005528|GO:0005634|GO:0004872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134890_PI430048170 0.0460871786720244 1.05653655899081 8.72426138782081
8.7905956861078 8.7405803104643 P P P 8.70973899548188 8.66256590285368
8.64515907625379 P P P LNCV6_134890_PI430048170 mRNA
CCATGCCCTAACTTTTAATATGCTTGTTCAGCTCTAATAAAGTAATAAAGCTTGGTTGTC NM_016437RefSeq chr17
+ 42659247 42667006 TUBG2 27175 "tubulin, gamma 2"
GO:0005881|GO:0005874|GO:0003924|GO:0031122|GO:0005525|GO:0005829|GO:0006184|GO:0005198|GO:0000086|GO:0007020|GO:0015630|GO:0000930|GO:0005876|GO:0000278|GO:0000242 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61702_PI430048170 0.00598689257635936 0.6208438206968985.48468075881139
5.59403033629341 5.75263879756599 P P P 6.23924113256482 6.33588019230149
6.32994663074257 P P P LNCV6_61702_PI430048170 mRNA
AATATCCAAAAGGAGCAGCTTCAATTTCATTGAGGTGAAAGTGCACTATGAAGATTGTTC NM_024713RefSeq chr15
- 34140673 34210096 KATNBL1 79768 katanin p80 subunit B-like 1 GO:0005730 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138351_PI430048170 0.1967641816047841.05112612953023 0.575411411709538
0.6421954039563380.600281331819842A A A 0.6004036121421450.464865317324921
0.534420736972861A A A LNCV6_138351_PI430048170 mRNA
TGGATTCTTCAGCAGGTCAGAATGGTCTGATATACAGTAACCCCCAATTTTCTTAATAAA NM_001128326 RefSeq
chr19 - 47968045 47992170 BSPH1 NA binder of sperm protein homolog 1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_133880_PI430048170 0.7100156595383380.9864819772134960.483562657454729
0.4602025986701170.416422002313296A A A 0.3898199036150990.514628703497647
0.511958637468233A A A LNCV6_133880_PI430048170 mRNA
TTCCAGAATAGGGAGATGCAGGCAGGAATTAGGAAGGTGTTTGCATTTCTGAAACACTAG NM_001005487 RefSeq
chr1 - 247672117 247673041 OR13G1 NA "olfactory receptor, family 13, subfamily G, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_143169_PI430048170 0.3970227712580010.8739293094598658.66932717755172
8.52394603554949 8.83795469681055 P P P 8.55055640119622 8.92534930792897
9.10207862940547 P P P LNCV6_143169_PI430048170 mRNA
CTTAATGTTGACTTCTATTACTCCTGCATGGAGCAGTTGTTATGAATACTAATACATCAC NM_007280RefSeq chr15
- 41309267 41332621 OIP5 11339 Opa interacting protein 5
GO:0005515|GO:0015030|GO:0010369|GO:0006334|GO:0005634|GO:0034080|GO:0005737|GO:0007067|GO:0007
154|GO:0005654|GO:0000785|GO:0000775|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142435_PI430048170 0.2817590788557290.7109364814598291.2145208702667
2.26337620391678 1.29130286700771 A A A 2.61759196086177 1.93752430973816
1.80420111229744 P A A LNCV6_142435_PI430048170 mRNA
TTAGTTGAACTGGGACCAGAACTCTAGCCCCCAAATCTAAACTTTAAACTTCTTTGTTCC NM_001199237 RefSeq
chr6_GL000256v2_alt - 2960505 2965567 GPANK1 7918 "G patch domain and ankyrin repeats
1, transcript variant 1" GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_39334_PI430048170 0.0946127805619210.8023963472506897.73016837658826 7.7642035954428
7.44466679079351 P P P 7.86371507632788 8.17130925758547 7.8546649998184 P P P
LNCV6_39334_PI430048170 mRNA
TGACCATGAACCCCCAGGATGGCGTGGGGTTTAAGGTGAAAGCGTCTCACGCACAAGTCANM_001170543 RefSeq
chr12 + 132710806 132722737 PGAM5 192111 "phosphoglycerate mutase family member 5, transcript
variant 1"
GO:0043547|GO:0005739|GO:0016791|GO:0070266|GO:0016311|GO:0005741|GO:0004721|GO:0016021|GO:0032
403|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106658_PI430048170 0.0244896953016478 1.52603378342996 5.59998328959608
5.922015319115 5.92740129149863 P P P 5.40401677247594 4.95330264863363
5.25069830565752 P P P LNCV6_106658_PI430048170 mRNA
GGAGAAAGCCATGACCGACACTTTCACTCTTCAGGCACATGATCAATTCTCTCCATTTTC NM_020166RefSeq chr3
- 183015217 183099587 MCCC1 56922 "methylcrotonoyl-CoA carboxylase 1 (alpha), transcript variant 1"
GO:0005515|GO:0005743|GO:0006768|GO:0006767|GO:0009083|GO:0044281|GO:0005524|GO:0046872|GO:0005
829|GO:0005739|GO:0034641|GO:0004485|GO:0006766|GO:0005759|GO:0009374|GO:0004075|GO:0006552 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138545_PI430048170 0.0632792442903922 1.26211405427677 13.4118750583853
13.6902670325324 13.7015089882626 P P P 13.2151830269063 13.2994282940421
13.2981423491844 P P P LNCV6_138545_PI430048170 mRNA
AGAGGAATGATTTGTCCTCACGCTCCCAAGACTGGTTTTTCTACTCTCATGCATTCCAGA NM_002455RefSeq
chr1_GL383519v1_alt + 15376 18867 MTX1 4580 "metaxin 1, transcript variant 1"
GO:0006626|GO:0005741|GO:0016021|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134721_PI430048170 0.1857966358739413.61217863856343 0.45149546785358
2.44301066528175 2.97007756767499 A A P 0.45719694664655 0.4138031064126
0.43099814684033 A A A LNCV6_134721_PI430048170 mRNA
CTCTGACATCATATTGTTGTCTGTTTACACAGATACATTTATTGCTGGGGATTGCAAAAA NM_001134438 RefSeq
chr3 + 111859179 111976517 PHLDB290102 "pleckstrin homology-like domain, family B, member 2,
transcript variant 1" GO:0005515|GO:0005737|GO:0005886|GO:0045111 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_143966_PI430048170 0.0286409350323838 0.6023160565623595.37137868872016
5.27058369647729 5.50514981305725 P P P 5.80139529110911 6.18042309535441
6.32053657583601 P P P LNCV6_143966_PI430048170 mRNA
GGGTAAACATAGATGACACAGCTTTCGAGTGATTTCATTGAATAAAATTCTACTGACTTC NM_001221RefSeq chr4
- 113451031 113761927 CAMK2D 817 "calcium/calmodulin-dependent protein kinase II delta, transcript
variant 3"
GO:0005515|GO:0005516|GO:2000650|GO:0008016|GO:0019221|GO:0001558|GO:0051259|GO:0042803|GO:0034

605|GO:0046777|GO:0018105|GO:0018107|GO:0086003|GO:0061049|GO:0070374|GO:0004683|GO:0060333|GO:0010389|GO:0032469|GO:0031432|GO:0044325|GO:0002026|GO:0005654|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95534_PI430048170 0.981580706623359 1.00424311593447 10.5738516494667 10.6402884755473 10.9161563915045 P P P 10.5805242778443 10.6734700040914 10.866369174159 P P P LNCV6_95534_PI430048170 mRNA AAGCCTGACTGGACCATTGCACGGATTGAACACTCAAAATTATTAGAATAATTTTCTTGG NM_024520 RefSeq chr2 + 199955316 199964124 C2orf47 79568 chromosome 2 open reading frame 47 GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53954_PI430048170 0.118850625060449 2.99743228162258 3.1619066495278 5.04964231098113 4.74210190215121 P P P 3.28443484502339 3.00844873188538 2.37107249251162 P P P LNCV6_53954_PI430048170 mRNA TACAAAAGGGTGGAATAGTTGTTACAAGAAGGTCACATCATCCTGGCACTGCTCCCAGAA NM_001243766 RefSeq chr1 - 46188680 46220305 POMGNT1 55624 "protein O-linked mannose N-acetylglucosaminyltransferase 1 (beta 1,2-), transcript variant 2" GO:0006493|GO:0000139|GO:0047223|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109278_PI430048170 0.232732701885319 0.768604704982844 4.55633294642758 4.35881023652766 4.74890324111079 P P P 4.76663809213325 5.32789115680023 4.63827921830082 P P P LNCV6_109278_PI430048170 mRNA GGGTGATTGACATCCTCCCAAACTGTGTATCATCTGTGTATTTGTACTACGATCCTGATT NM_001288736 RefSeq chr10 - 121740420 121928801 ATE1 11101 "arginyltransferase 1, transcript variant 5" GO:0005515|GO:0005737|GO:0004057|GO:0005634|GO:0016598 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137532_PI430048170 0.0177831622706074 0.711389294489901 5.37497442169606 5.23523580389169 5.50164820932459 P P P 5.67074645456736 5.9300834041359 5.97858630668677 P P P LNCV6_137532_PI430048170 mRNA CTTAAATACAGCTTTTGGATTGGACAAAATGACTTGAAGACTTACAGCAAATCCTTTGTG NM_001281439 RefSeq chr6 + 70667770 70862013 SMAP1 60682 "small ArfGAP 1, transcript variant 3" GO:0043547|GO:0008060|GO:0005737|GO:0005886|GO:0045648|GO:0032312|GO:0030276|GO:2000369|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129906_PI430048170 0.0409107510705237 1.10996870083204 0.643781706316064 0.69415781034904 0.575738459873913 A A A 0.416383626892158 0.503881611207686 0.541459496267189 A A A LNCV6_129906_PI430048170 mRNA GTTGAATCCCTTGATATATAGTCTGAGGAACAATGAAGTAAGAAATGCTCTGATGAAACT NM_001005197 RefSeq chr11 + 123906431 123907376 OR8D4 NA "olfactory receptor, family 8, subfamily D, member 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134993_PI430048170 0.223091361320895 1.29902018531431 3.44711960316181 2.74985766684299 3.24270891949908 P A P 2.88508127796874 2.89513009519958 2.59319012876603 P P P LNCV6_134993_PI430048170 mRNA GAACTGTACAAATTGTGATGTGGCTACATAGAAAGCCATGTGCTAAGAATAAACTCCATT NM_002141 RefSeq chr7 - 27128506 27130780 HOXA4 3201 homeobox A4 GO:0043565|GO:0006355|GO:0003700|GO:0048704|GO:0005634|GO:0009952|GO:0009653|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53533_PI430048170 0.0449644461359757 0.775637768943729 5.72772059569985 5.7654768871204 6.03122266455972 P P P 6.10977459915625 6.14361511506283 6.37527716674211 P P P LNCV6_53533_PI430048170 mRNA AAAGATTACTGACACCAATTCTCGAATCCCACCTCCTGTCTTTGACCACTCGTGGTTTTA NM_020765 RefSeq chr1 - 19074505 19210252 UBR4 23352 ubiquitin protein ligase E3 component n-recognin 4

GO:0005515|GO:0005516|GO:0005813|GO:0005737|GO:0004842|GO:0042787|GO:0016020|GO:0016874|GO:0016032|GO:0008270|GO:0005654|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137465_PI430048170 0.148068363216018 0.705860640610262 5.67416613340884 5.84453140665179 6.45373707801626 P P P 6.27495994427791 6.46777393618554 6.8070684155954 P P P LNCV6_137465_PI430048170 mRNA TAATATGAAAACTCTCCAAGTCTTGATCATCAGCCAGGATTTTGCCACAGCAATTTCATT NM_004249 RefSeq chr4 - 13367722 13484365 RAB28 9364 "RAB28, member RAS oncogene family, transcript variant 2"
GO:0005737|GO:0005886|GO:0007264|GO:0035253|GO:0008152|GO:0003924|GO:0019003|GO:0005525|GO:0036064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126956_PI430048170 0.356368068479889 1.4812732575395 0.444241580438617 1.62019616535922 0.485962242465084 A A A 0.325443426661313 0.405528626558822 0.445460278014595 A A A LNCV6_126956_PI430048170 mRNA AACAGATATTTTCGCCCACCTAAAGGGAAGCCCTGACAACAACTATCACCAAAAGACGAG NM_000787 RefSeq chr9 + 133636362 133659344 DBH 1621 dopamine beta-hydroxylase (dopamine beta-monooxygenase)
GO:2001236|GO:0007268|GO:0044281|GO:0050900|GO:0003824|GO:0001816|GO:0042596|GO:0004500|GO:0034641|GO:0005737|GO:0045907|GO:0042127|GO:0007626|GO:0007613|GO:0002443|GO:0030658|GO:0034466|GO:0042711|GO:0031418|GO:0005507|GO:0005576|GO:0042593|GO:0001975|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141251_PI430048170 0.0240799975059289 0.573542720770063 3.76219890365464 3.92050752864745 4.29644835225945 P P P 4.86459425197837 4.6899035119739 4.87652873364229 P P P LNCV6_141251_PI430048170 mRNA CTAAGAGTTACCACTTCCGTAGCCTATAACATCAAAACGTAGTTTTTGCATGTTTTCAAT NM_001300979 RefSeq chr19 + 36687611 36721336 ZNF567 163081 "zinc finger protein 567, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135504_PI430048170 0.58637331948099 0.916041857108042 0.88483402047919 0.36425210910072 0.342906615478632 A A A 0.6558744628056 0.917503426877655 0.42344406895688 A A A LNCV6_135504_PI430048170 mRNA GAAGGAAGAGTCCATTTCTAATCAAATAATTCGCCTGTTTTACTAGCTTATAGTGATCTG NM_024761 RefSeq chr9 - 27325208 27529852 MOB3B 79817 MOB kinase activator 3B GO:0005515|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144087_PI430048170 0.307649167277021 0.833206543264662 11.2758426256218 11.1461777735576 11.1753419364768 P P P 11.147450548095 11.7652497649524 11.4105959494363 P P P LNCV6_144087_PI430048170 mRNA AACAGCAGCTATTTTGTTGAGTGGATCCCCAACAATGTGAAAACGGCTGTCTGTGACATC NM_006088 RefSeq chr9 + 137241258 137243707 TUBB4B 10383 "tubulin, beta 4B class IVb"
GO:0003725|GO:0051258|GO:0042288|GO:0006996|GO:0042267|GO:0005874|GO:0003924|GO:0006928|GO:0005634|GO:0005525|GO:0055085|GO:0051225|GO:0031982|GO:0005829|GO:0006184|GO:0006457|GO:0000086|GO:0005200|GO:0051084|GO:0051082|GO:0000278|GO:0005856|GO:0044267|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128056_PI430048170 0.695616744101473 1.05842918563432 13.0341950772722 13.1519945520734 13.4952286240612 P P P 13.0173574331304 13.0022297687747 13.417170905471 P P P LNCV6_128056_PI430048170 mRNA GGACACCTGTGGTATCTTTAATTGTATCTCCTTCAGAAGTTTGCTTCTTATGGTATAATA NM_001011546 RefSeq chr20 + 17569953 17608007 DSTN 11034 "destrin (actin depolymerizing factor), transcript variant 2"
GO:0051014|GO:0008154|GO:0030836|GO:0030042|GO:0006928|GO:0003779|GO:0030864|GO:0015629|GO:0070

062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130130_PI430048170 0.0344770118280714 0.446826457354433 1.59039650428453
0.642138398882432 0.963087873909702 A A A 2.49709054232088 2.21427849808162
2.10737480511454 A A A LNCV6_130130_PI430048170 mRNA
ACACAGCTTGGAATGTAGTGGTGCCTACCACAGTTTGAATAAATAACACTACACCTTTCA NM_022111 RefSeq chr1
- 35732111 35769950 CLSPN 63967 "claspin, transcript variant 1"
GO:0005515|GO:0010997|GO:0031572|GO:0006915|GO:0003677|GO:0006921|GO:0006260|GO:0032147|GO:0006
281|GO:0018105|GO:0005654|GO:0000077|GO:0033314 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134347_PI430048170 0.174835012629902 1.10440417611882 0.600630382192519
0.401305341213697 0.598604681717464 A A A 0.290606351271398 0.404386172780925
0.478508170413948 A A A LNCV6_134347_PI430048170 mRNA
TTTTCATCCCTTCTGAGAAATGTACCCTATTATTTCCTTCATAAAGAATGCCACCCATCT NM_001080554 RefSeq chr12
- 13083536 13103696 GSG1 83445 "germ cell associated 1, transcript variant 3"
GO:0005789|GO:0016021|GO:0070063 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69217_PI430048170 0.546912185792674 1.47608601869699 0.37018251177434 1.20747851175399
2.2453229468966 A A A 0.265549834726014 1.19801317512458 1.10833966846643 A A A
LNCV6_69217_PI430048170 mRNA
TTTCCAAAATGTTTGCAGTTGATGCTAAGGCCTTGCCTCAGAATAAGCCAAGGCCTCTCA NM_024580 RefSeq chr15
- 82130219 82262763 EFTUD1 79631 "elongation factor Tu GTP binding domain containing 1, transcript
variant 1" GO:0006184|GO:0042256|GO:0003924|GO:0043022|GO:0005525|GO:0003746|GO:0006414 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144345_PI430048170 0.182676752159663 1.23419175106191 0.452829978768838
0.399188050514966 0.861946500241643 A A A 0.258798612599613 0.340014919030733
0.248403372457066 A A A LNCV6_144345_PI430048170 mRNA
CAGCAGGTAACATTTACAGTCTGCTTTAAAACATGCTTTGGACATATATTTTAGTGCTCA NM_024532 RefSeq chr2
+ 213284378 214410501 SPAG16 79582 "sperm associated antigen 16, transcript variant 1"
GO:0042384|GO:0019901|GO:0031514|GO:0005930|GO:0015630|GO:0005634|GO:0007283 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_93955_PI430048170 0.00613691849121422 0.521612107296497 12.120237877342
12.0082918747129 11.8047292632357 P P P 12.871768711498 12.9359889790009
12.9584922998008 P P P LNCV6_93955_PI430048170 mRNA
CTGTGCCTGCTCTCAAGAGCACTTACTGCCTCGCAAATAATAAAAATTTCTAGCCAGTCA NM_001270448 RefSeq
chr17 + 7219830 7225267 ACADVL 37 "acyl-CoA dehydrogenase, very long chain, transcript
variant 4"
GO:0042645|GO:0090181|GO:0001659|GO:0006635|GO:0050660|GO:0045717|GO:0005730|GO:0005743|GO:0046
322|GO:0005634|GO:0044281|GO:0033539|GO:0004466|GO:0030968|GO:0005739|GO:0005737|GO:0005759|GO:0
030855|GO:0003995|GO:0006987|GO:0044267|GO:0044255|GO:0015980 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_139953_PI430048170 0.142392594480782 0.772422975518231 9.2135516247545
8.93242329025261 9.19985545080086 P P P 9.23621243918897 9.40755393765985
9.78174765889004 P P P LNCV6_139953_PI430048170 mRNA
GCTGAAAACTCCTGATAACACTTGCTACATATCATGTTTTAATTGCTTGTACAGTTAACC NM_020773 RefSeq chr4
+ 6909767 7033118 TBC1D14 57533 "TBC1 domain family, member 14, transcript variant 1"
GO:0005515|GO:0005794|GO:0005776|GO:0019901|GO:2000785|GO:0010507|GO:0032851|GO:0055037|GO:0071
955|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136649_PI430048170 0.886130381144587 0.995521501267059 0.486137866227252
0.503024537635995 0.396263083135923 A A A 0.525143620646536 0.436548230085798
0.443738362106007 A A A LNCV6_136649_PI430048170 mRNA
GACCATTGTATTCAGTTCATTACCAAAGAAATGTTTGCACTTTGTAATGATGCCTTTCAG NM_012293 RefSeq chr2

- 1631886 1744547 PXDN 7837 peroxidasin
GO:0005783|GO:0005578|GO:0005152|GO:0005615|GO:0046872|GO:0031012|GO:0006955|GO:0004601|GO:0001960|GO:0030198|GO:0042744|GO:0006979|GO:0070062|GO:0055114|GO:0005201|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140476_PI430048170 0.5530164971786030.8150705876363871.20547790849918 0.4310593205518530.448967007098112A A A 1.47982130010442 0.353232566978361 1.06467962783674 A A A LNCV6_140476_PI430048170 mRNA
ACTTCCAAGTTCCCAAATAGATCTGTAGGAGAAGAGGGATGGAAAATATATTCCACAGTT NM_001010915 RefSeq chr9 - 21006365 21031636 HACD4 NA 3-hydroxyacyl-CoA dehydratase 4 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133427_PI430048170 0.0835449011616379 0.90099198586534313.3006774447531 13.1362869965007 13.2382685845274 P P P 13.3646235204574 13.3769537873746 13.389540417392 P P P LNCV6_133427_PI430048170 mRNA
ATATAAATCTCAGGTAATAAGGCTTTAGAACTGCTGATAAAGCGGATCGTTCTCAGGCCC NM_014214RefSeq chr18 + 11981427 12030886 IMPA2 3613 inositol(myo)-1(or 4)-monophosphatase 2
GO:0052833|GO:0052832|GO:0006021|GO:0043647|GO:0006796|GO:0044281|GO:0042803|GO:0046872|GO:0005829|GO:0007165|GO:0046854|GO:0005737|GO:0046855|GO:0008934 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128461_PI430048170 0.00376731893027278 2.67199735857814 1.78577100185343 2.17372789829042 2.14866966752657 A A A 0.5192537058048940.944375593037144 0.357205584853109A A A LNCV6_128461_PI430048170 mRNA
AGGAGGACACCTTGTGGGACATCTGAGGACATCCGCAGATTCTTGTCAGCCTGTGAACTA NM_013385RefSeq chr22 + 37282453 37315348 CYTH4 27128 cytohesin 4
GO:0043547|GO:0005802|GO:0005086|GO:0005886|GO:0032012|GO:0016192|GO:0030155|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58940_PI430048170 0.0497574286077378 1.61587640339465 7.00117800165953 6.95807239444383 7.04359786717414 P P P 6.61116827252875 6.21981497409542 6.03507201731445 P P P LNCV6_58940_PI430048170 mRNA
CATCATTGGTCACTGCCGATGTCTATTTTTGAAGGGTTGAGATGGACAGATTTCCCAAGA NM_001143782 RefSeq chr12 - 48923125 48925547 FKBP11 51303 "FK506 binding protein 11, 19 kDa, transcript variant 3"
GO:0000413|GO:0061077|GO:0016020|GO:0005789|GO:0003755|GO:0005528|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136193_PI430048170 0.7181159223672650.962322886268791 7.90325352919465 7.85816391145853 7.99351737446481 P P P 8.15418132662313 7.76779238350816 7.97669461638011 P P P LNCV6_136193_PI430048170 mRNA
GGCATTTTACAAAGGTTTAAAGGAATTGATTCCTCTGAAAGGGCCTGAAAATAAAAAGTC NM_018091RefSeq chr8 + 28093066 28191152 ELP3 55140 "elongator acetyltransferase complex subunit 3, transcript variant 1"
GO:0045859|GO:0005515|GO:0006368|GO:0030335|GO:0051536|GO:0006357|GO:0010484|GO:0000993|GO:0005730|GO:0006325|GO:0007417|GO:0008023|GO:0046872|GO:0002098|GO:0033588|GO:0005737|GO:0043966|GO:0043967|GO:0000123|GO:0010485|GO:0008607|GO:0001764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136241_PI430048170 0.0161646985060518 1.24250617948907 10.1782663225179 10.1272246998643 10.1984990238398 P P P 9.84799810671309 9.94674830507458 9.76464831502011 P P P LNCV6_136241_PI430048170 mRNA
GAGAAAGAACTCACTTACGAGAAGTTCGTAGAATGGACGAGGCTGGACATGATGGATGAA NM_001297699 RefSeq chr6 - 2948158 2972165 SERPINB6 5269 "serpin peptidase inhibitor, clade B (ovalbumin), member 6, transcript variant 7"
GO:0010951|GO:0043234|GO:0005737|GO:0004867|GO:0002020|GO:0005615|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_136109_PI430048170 0.4224484153001731.27060567347883 3.96140169058704
4.45864743195028 3.47001146879199 P P P 3.91935597456687 3.24222358042077
3.77541740376331 P P P LNCV6_136109_PI430048170 mRNA
AGGTACATGTTCAAAGATGGGGAGCCCTCAGGTCACAAAGAATTTAGAGAATCATCTTGA NM_023922RefSeq
chr12_KI270904v1_alt - 136959 137913 TAS2R14 50840 "taste receptor, type 2, member 14"
GO:0033038|GO:0007186|GO:0005886|GO:0008527|GO:0016021|GO:0001580 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131724_PI430048170 0.5704920132224871.02162755050298 0.28539969352718
0.3164289037586060.428715566548556A A A 0.3357113577826360.307276922523946
0.298658667441311A A A LNCV6_131724_PI430048170 mRNA
GCTCTAATGTATTAGGAAGCACTAAATGGCCTAAAAAAGCTACTACATTGCCTAAATATG NM_014258RefSeq chr20
- 59863562 59932154 SYCP2 10388 synaptonemal complex protein 2
GO:0009566|GO:0043066|GO:0000795|GO:0046982|GO:0048808|GO:0005634|GO:0000800|GO:0007143|GO:0007
130|GO:0003677|GO:0051301|GO:0007140 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91406_PI430048170 0.2875783805405191.21071174449871 4.22326048220831 4.23797103759294
4.67340820848121 P P P 3.8692581469086 3.97739304467605 4.44120779101429 P P P
LNCV6_91406_PI430048170 mRNA
AGAAATTACATCTTATCAACTCAAGATCGCCTTGTAGGGGGATTTGCCAAGTGGCCAGAC NM_005023RefSeq chr5
- 115210829 115262872 PGGT1B5229 "protein geranylgeranyltransferase type I, beta subunit"
GO:0042277|GO:0004661|GO:0008284|GO:0018344|GO:0008144|GO:0004662|GO:0008270|GO:0034097|GO:0019
840|GO:0051771|GO:0045787|GO:0005953 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142026_PI430048170 0.3987661594676250.7483554050404981.72968581346616
0.4041159994023490.387806604905429A A A 1.29778578818277 0.883493222708164
1.86594315611504 A A A LNCV6_142026_PI430048170 mRNA
CTGATCTTACCTTCCCACTTTACCTCATACAACAATAAAGCTCTTTTGCCTCTTCGTGAANM_178428RefSeq chr1 +
152698363 152699442 LCE2A 353139 late cornified envelope 2A GO:0031424 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_81962_PI430048170 0.4457056016977590.7712555663058080.3269101304145640.300717611858944
0.281928588199575A A A 0.2917066292516351.24092934100171 0.277676622162219A A A
LNCV6_81962_PI430048170 mRNA
AAAGGCCAAGAAATTATTGTGCCTGAAATTTCCCGAGAGAATTAAGACAGACTGAATTTG NM_001287344 RefSeq
chrX - 101349446 101390796 BTK695 "Bruton agammaglobulinemia tyrosine kinase, transcript variant 3"
GO:0005515|GO:0019722|GO:0007249|GO:0030154|GO:0042802|GO:0043231|GO:0002755|GO:0042127|GO:0002
902|GO:0038083|GO:0038124|GO:0038123|GO:0034134|GO:0005547|GO:0002224|GO:0002721|GO:0031234|GO:0
042113|GO:0045087|GO:0045121|GO:0038095|GO:0050853|GO:0050852|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143801_PI430048170 0.0625308341137434 1.02779783425876 0.402954240741139
0.4194588893837120.434796070854306A A A 0.3764871010667230.360398365137484
0.401531808062292A A A LNCV6_143801_PI430048170 mRNA
TGAAAAGAGTGAATGTGACATTGGCTTCAAACACAGCTCACCTGAGACTGATTTCTTCTG NM_001304561 RefSeq
chr6_GL000255v2_alt - 3616377 3630176 BTNL2 56244 butyrophilin-like 2 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76128_PI430048170 0.2124324563590821.36861312653679 4.72174777704251 4.58427615565796
4.03851563656476 P P P 4.22669540528371 4.20839135924515 3.53677694728549 P P P
LNCV6_76128_PI430048170 mRNA
AAGATGATGTGTATCTGAGGCACAGCTCTTCCCTGACTTATAGGCTTTGACACTGCTGTT NM_021182RefSeq chr5
+ 143812160 143820719 HMHB1 57824 histocompatibility (minor) HB-1 GO:0002376 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145267_PI430048170 0.0286926135807343 0.897436416966001 0.312487303773071

0.3049218593559330.297438801165448A A A 0.4757619603839950.406064038969498
0.499781780049431A A A LNCV6_145267_PI430048170 mRNA
ACTGCTGTACAGTGGGTATAGTATTTTGGTTTTGGTTCCAGATTGTGCAATCTTTAAGAA NM_021620RefSeq chr6
+ 99606773 99615578 PRDM13 59336 PR domain containing 13
GO:0003682|GO:0008168|GO:0005634|GO:0000122|GO:0032259|GO:0003677|GO:0046872|GO:0006351|GO:0022
008. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143754_PI430048170 0.3297366367543461.3674103467971 0.531160843879567
0.3360355563277891.32464347916562 A A A 0.2836198313485990.369540186942845
0.381239066409532A A A LNCV6_143754_PI430048170 mRNA
TATTAGTTTAGATGGGCGTAGGGATAGAGCTCTTAAAGTTGACAGCTTGGGTCGGTTGAC NM_001349RefSeq chr2
- 135905880 135985684 DARS 1615 "aspartyl-tRNA synthetase, transcript variant 1"
GO:0005515|GO:0010467|GO:0004815|GO:0005524|GO:0006412|GO:0005829|GO:0006418|GO:0006422|GO:0005
737|GO:0006461|GO:0016020|GO:0004046|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68029_PI430048170 0.0688828201094650.7013439107164575.65186908247049 5.77418143976369
5.80789874992631 P P P 6.03677819033958 6.15509086230866 6.53420549319888 P P P
LNCV6_68029_PI430048170 mRNA
TAAACCAGAAAATCTTCTGTTGGATGAAAGGGATAACCTCAAAATCTCAGACTTTGGCTT NM_001114122 RefSeq
chr11 + 125625135 125657147 CHEK1 1111 "checkpoint kinase 1, transcript variant 1"
GO:0005515|GO:0005657|GO:0031572|GO:0005634|GO:0005615|GO:0010569|GO:0043231|GO:0005829|GO:0042
127|GO:0000086|GO:0018107|GO:2000615|GO:0010767|GO:0000785|GO:0005813|GO:0000794|GO:0000781|GO:0
046602|GO:0071313|GO:0035407|GO:0005524|GO:0006974|GO:0035402|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93179_PI430048170 0.55465162517262 0.9690628313332470.4536522508054090.442177746715894
0.250040116521918A A A 0.38615822989831 0.4748451057908880.42844401548803 A A A
LNCV6_93179_PI430048170 mRNA
ACTATTCTGACTTCTCAGCCTGGAAAAGAGGTGGTCAAACAGTTGGAGGAAGGGTTGAAA NM_138804RefSeq chr2
- 74557882 74648037 M1AP 130951 "meiosis 1 associated protein, transcript variant 1"
GO:0006396|GO:0003674|GO:0005737|GO:0051308|GO:0031497|GO:0016021|GO:0007292|GO:0007283|GO:0030
154. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65456_PI430048170 0.0172144250336951 0.3662064094781560.335477196068508
0.2731504402458140.375810701975625A A A 2.02775298539577 1.86170808050208 1.3655149652388
A A A LNCV6_65456_PI430048170 mRNA
CACTCAAATTAAGGGCAAGCGAAAAAGTAATAATTTGGCATTCTTTAAGCCTACAGAATG NM_001261428 RefSeq
chr2 + 11677578 11827407 LPIN1 23175 "lipin 1, transcript variant 3"
GO:0007077|GO:0006646|GO:0042826|GO:0045598|GO:0031100|GO:0005741|GO:0005634|GO:0044281|GO:0005
635|GO:0042975|GO:0031529|GO:0005829|GO:0009062|GO:0003674|GO:0005737|GO:0045944|GO:0001085|GO:0
019432|GO:0044255|GO:0006656|GO:0005667|GO:0032869|GO:0031965|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137122_PI430048170 0.7544180529001581.06904470570058 0.963666840363297
0.5304749865498280.295536529705973A A A 0.4126251910395360.621491310223204
0.539949708257691A A A LNCV6_137122_PI430048170 mRNA
GTTGAACAGAGGGACAATTGTTTTACTTTTCTTTGGTTAATTTTGTTTTGGCCAGAGATG NM_002852RefSeq chr3
+ 157436790 157443628 PTX3 5806 "pentraxin 3, long"
GO:0050766|GO:0006954|GO:0046597|GO:0045087|GO:0001849|GO:0046790|GO:0005576|GO:0001872|GO:0005
615|GO:0001878|GO:0008228|GO:0045429 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140086_PI430048170 0.5433107630241091.12476606449947 7.37149185182047
6.81388583090245 6.75782013673264 P P P 6.80790424382563 6.9259474323501
6.77911402936285 P P P LNCV6_140086_PI430048170 mRNA
CTCTGGTCTGTGTCTGTGTGTGCCTGTAAGTGTGAAATAAACCTCTCTGATGGCAAAAAA NM_001012508 RefSeq

chr10 - 133420665 133424617 SPRN 503542 shadow of prion protein homolog (zebrafish)
GO:0005886|GO:0005730|GO:0031225|GO:0006606|GO:0003676|GO:0031982|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_115847_PI430048170 0.0112780375674176 1.7043892575345 11.9103198679096
12.2734897612873 12.1963973152676 P P P 11.441126286925 11.3657524011342
11.2862190908781 P P P LNCV6_115847_PI430048170 mRNA
GAAAATGCTGTATCAAGGGTGGGCTTAGCTGTGCCTTTCCAATAAAGATGTGAGAAGCTT NM_198969RefSeq chr19
- 3052909 3062966 AES 166 "amino-terminal enhancer of split, transcript variant 1"
GO:0005515|GO:0032091|GO:0060761|GO:0003714|GO:0005634|GO:0007275|GO:0000122|GO:0006351|GO:0001
501|GO:2000210|GO:0031668|GO:0010629|GO:0009887|GO:0016055|GO:0090090|GO:0045892|GO:0070555|GO:0
040008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127502_PI430048170 0.370011571413045 1.47055820568986 0.479736554152499
0.321361331435096 1.55822035991229 A A A 0.288916020918116 0.348814630733433
0.384375712194248 A A A LNCV6_127502_PI430048170 mRNA
AAAGACTGTGACCAGCTTCACAAAAGGCAGCAAAGGACTATCAGAGAAAGAGAACTCCGA NM_032298RefSeq
chr19 - 50621976 50638045 SYT3 84258 "synaptotagmin III, transcript variant 1"
GO:0019905|GO:0005215|GO:0030054|GO:0031340|GO:0046872|GO:0005544|GO:0051592|GO:0030276|GO:0017
156|GO:0001786|GO:0030672|GO:0016021|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135336_PI430048170 0.930877774325484 0.995848638008978 0.307994455820188
0.512587283446372 0.377055801545466 A A A 0.496378575561323 0.379024058897416
0.343319561722152 A A A LNCV6_135336_PI430048170 mRNA
CAACAGGTTTTCACTGGGATTTTGCCTGTTTTAATCTACTTGTCTGTCAAAGTAATGTAA NM_001010870 RefSeq
chr6 + 46687874 46704319 TDRD6 221400 "tudor domain containing 6, transcript variant 1"
GO:0033391|GO:0010467|GO:0005737|GO:0005783|GO:0034587|GO:0007275|GO:0043186|GO:0007283|GO:0007
281 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143944_PI430048170 0.0654001241847641 0.0717856263081 0.444955365037259
0.347661442529341 0.358551635896853 A A A 0.263550718108664 0.330247637394928
0.258180798980389 A A A LNCV6_143944_PI430048170 mRNA
ATTATTTCACTGAAGATATTCCAATTTCCATACTATTTCCTCCAATAGACCCTTGTTGCC NM_033226RefSeq chr16 -
48082972 48146770 ABCC1294160 "ATP-binding cassette, sub-family C (CFTR/MRP), member 12"
GO:0005739|GO:0008152|GO:0042626|GO:0016021|GO:0055085|GO:0005524 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126584_PI430048170 0.159098068260334 0.82406734114045 11.3601966276937
11.3891333272588 11.4357248600948 P P P 11.439033927167 11.6850586438343
11.8676864674112 P P P LNCV6_126584_PI430048170 mRNA
TGTGGACATCTAATTGAGGCCCACAAGGAATGCATGAGAGCCCTAGGATTTAAAATATGA NM_005694RefSeq chr3
- 119669524 119677396 COX17 10063 COX17 cytochrome c oxidase copper chaperone
GO:0007507|GO:0005739|GO:0005758|GO:0005737|GO:0007420|GO:0005507|GO:0016531|GO:0006091|GO:0006
825 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140990_PI430048170 0.0904726638308578 1.47032494851014 5.85435536151666
6.11668181558334 5.97633048575175 P P P 5.56941407609056 5.64168888504503
4.99781740070204 P P P LNCV6_140990_PI430048170 mRNA
TAAGCACAAAGTGCTCCTCTCTGTGGCTCTGTTCTCCTTTGTTTGCTCACCTATGACAAA NM_005913RefSeq chr18
+ 13825543 13826862 MC5R 4161 melanocortin 5 receptor
GO:0005515|GO:0005886|GO:0007187|GO:0005887|GO:0042562|GO:0030819|GO:0004977 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_101135_PI430048170 0.787066155464992 1.31279032724835 3.08068281649694
0.788009928464012 1.70931820990634 A A A 2.17492243435317 0.591643037969077
2.07998652332796 A A A LNCV6_101135_PI430048170 mRNA

CTTAGTCAAGGACCTGTAGTTCATAAACATCAATTCAACAGTAATGCTGTTACAGACATT NM_014709RefSeq chr2 - 61187454 61470714 USP34 9736 ubiquitin specific peptidase 34 GO:0071108|GO:0005515|GO:0004197|GO:0016579|GO:0005737|GO:0004843|GO:0061136|GO:0090263|GO:0043161|GO:0005634|GO:0016055|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_128366_PI430048170 0.3554086084130080.96856393161031 0.24976317431801 0.2626987197743830.368909678796987A A A 0.3826637485917570.317826381471992 0.321182548315259A A A LNCV6_128366_PI430048170 mRNA
CAGATGCAGGGGAAATGTTTCAGGACAATAATTTATCAAAACTAGTATTAAAACAGCGGA NM_001001711 RefSeq chr11 + 104036579 104039194 DDI1 414301 DNA-damage inducible 1 homolog 1 (S. cerevisiae) GO:0006508|GO:0004190 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_136752_PI430048170 0.4711883718798470.8987236721035830.325120130527087 0.3004397353738480.289793003080066A A A 0.2946315111727070.752407641285111 0.278924919408417A A A LNCV6_136752_PI430048170 mRNA
AAATATAGACGTGCACGATGGTGGTGTGGCTTACCCAGGATGGAAACACTGCAGTTTTTA NM_020697RefSeq chr8 + 98427021 98430795 KCNS2 3788 "potassium voltage-gated channel, modifier subfamily S, member 2" GO:0005251|GO:0005886|GO:0008076|GO:0007268|GO:0051260|GO:0034765|GO:0016021|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_136538_PI430048170 0.1828869098785730.472804760336202 1.97758088867044 0.6275662179886982.31871384723512 A A A 1.8381675315865 3.23086153594695 3.19930417181294 A P P LNCV6_136538_PI430048170 mRNA
CTGGCAGCTGAAACTGCACACAACTGATACACATATTTAATTTGTATTCCTTTGTAGTAA NM_024838RefSeq chr10 + 25016578 25026666 THNSL1 79896 threonine synthase-like 1 (S. cerevisiae) GO:0005739|GO:0008150|GO:0003674|GO:0005737|GO:0030170|GO:0005654|GO:0005634|GO:0005575|GO:0004795|GO:0009088 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_141075_PI430048170 0.0106511674035278 1.08255544630469 0.379179177645378 0.4037312738651640.34726493391325 A A A 0.2434869048464530.299996712992508 0.243179102888647A A A LNCV6_141075_PI430048170 mRNA
GCACAGCATAACTACTGAGAGGAAAGTGATTGATCTGTTTGTAATTACTTGTTTGTATTG NM_022788RefSeq chr3 - 151336842 151384812 P2RY12 64805 "purinergic receptor P2Y, G-protein coupled, 12, transcript variant 1" GO:0005886|GO:0031224|GO:0007193|GO:0005739|GO:0005085|GO:0043270|GO:0009925|GO:0051924|GO:0071805|GO:0009986|GO:0030168|GO:0010700|GO:0070527|GO:0007599|GO:0043547|GO:0001609|GO:0007186|GO:0001973|GO:0007596|GO:0005887|GO:0005901|GO:0030030|GO:0070588|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_125004_PI430048170 0.0172404896134165 0.75696911958197710.9680091276126 11.0881409341775 10.9459542738017 P P P 11.5293967965093 11.4036942300138 11.2662026697391 P P P LNCV6_125004_PI430048170 mRNA
ACAACAAAGACTTACAGCAGGCCTAGGTCCTCCCACACCTGCCCCCTAATAAAGTGGGCG NM_001024943 RefSeq chr7 + 66075846 66093342 ASL 435 "argininosuccinate lyase, transcript variant 1" GO:0042450|GO:0034641|GO:0005737|GO:0000050|GO:0044281|GO:0006527|GO:0006475|GO:0004056|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_145349_PI430048170 0.0337133935669897 0.6551100209748046.31781829020581 6.22287094316677 6.29096757935313 P P P 6.68330375297805 6.8449289007242 7.1041264262158 P P P LNCV6_145349_PI430048170 mRNA
CTTGTGGTATTTGGTACTATTAGAGGAAAAACTTTGGATTCAGACCTTCTTGCAGTTTTT NM_001003681 RefSeq chr22 + 35257451 35295807 HMGXB4 10042 "HMG box domain containing 4, transcript variant 1" GO:0006355|GO:0003682|GO:0008333|GO:0030178|GO:0006338|GO:0016589|GO:0016055|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_93479_PI430048170 0.84129737081559 0.9460301953445875.11293528121555 5.20662271325223

5.02058590947676 P P P 4.7350033672809 5.30522314803772 5.45140010624287 P P P
LNCV6_93479_PI430048170 mRNA
AATACATCAGGATGGCAGCATCATTAAATGCTGGGGAGACAACCTACAGTCTGGAACATG NM_022340 RefSeq chr3
- 15070068 15099157 RBSN 64145 "rabenosyn, RAB effector, transcript variant 1"
GO:0000011|GO:0005515|GO:0017137|GO:0005886|GO:0034058|GO:0006896|GO:0015031|GO:0006895|GO:0043
231|GO:0006897|GO:0010009|GO:0045324|GO:0007596|GO:0031901|GO:0016197|GO:0008270|GO:0010008|GO:0
070062|GO:0005768. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136165_PI430048170 0.179209504219785 0.601775561072238 3.13068145087126
1.68568857968606 2.58957395105882 P A A 3.49852195382008 2.92461126428753
3.46044801078389 P P P LNCV6_136165_PI430048170 mRNA
GATCTTCTCAAGTGGGAAACAGGCGTGGTAAATAAATACTGTTGTTTCAGCTGGTGTAAA NM_018235 RefSeq chr18
+ 74496264 74523454 CNDP2 55748 "CNDP dipeptidase 2 (metallopeptidase M20 family), transcript
variant 1"
GO:0006805|GO:0034701|GO:0044281|GO:0016805|GO:0046872|GO:0005829|GO:0034641|GO:0000096|GO:0006
750|GO:0004180|GO:0006508|GO:0008237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127408_PI430048170 0.224420500032078 1.14236840433461 0.742488897419977
0.396663321162663 0.455661349787056 A A A 0.32984760443653 0.329024159355874
0.383389479924491 A A A LNCV6_127408_PI430048170 mRNA
GCAGCTTTCTCTCAAGTGAAATAAGTGATGTGACATGTTTATCAGTTATGGCTAAAATGT NM_001080415 RefSeq
chr3 + 143001529 143060725 U2SURP 23350 U2 snRNP-associated SURP domain containing
GO:0005515|GO:0006396|GO:0000166|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131400_PI430048170 0.345738460045466 0.650488141940417 0.71074744841754
2.03176505709315 1.76964784266922 A A A 2.50853932251989 2.56074774077313
1.29475610470579 A P A LNCV6_131400_PI430048170 mRNA
ACCCGACAAGCACCCAGACTCTTTCACATAACAAATAAAATAGCAGAGTTCCCTTTCAAA NM_173506 RefSeq chr19
- 41837073 41844673 LYPD4 147719 "LY6/PLAUR domain containing 4, transcript variant 1"
GO:0005886|GO:0031225 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140297_PI430048170 0.32417350461135 0.873372343607669 0.358178584641861
0.385623475735178 0.329588743794452 A A A 0.411965257380049 0.81917807437717
0.386752465105537 A A A LNCV6_140297_PI430048170 mRNA
TGACACTGCCATTTTTCCTTTTTGGAGGAAATGGACATAGATAAAGAAGATATTTCTTCG NM_014618 RefSeq chr9
- 119166629 119369461 BRINP1 1620 bone morphogenetic protein/retinoic acid inducible neural-specific
1 GO:0005515|GO:0008219|GO:0005737|GO:0071300|GO:0045930|GO:0045666|GO:0007050|GO:0045786 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138002_PI430048170 0.068367667653476 0.584711872573661 4.48839910711518
4.09705155965301 3.76500707610145 P P P 5.0130278970631 5.20431290317827 4.4428533936897
P P P LNCV6_138002_PI430048170 mRNA
GGGCTCCGTCCCCTTAAAAAATACCCCAATAGCTAAAATAATACATTCATAGAAAACAAC NM_017584 RefSeq chr22
+ 50486783 50490321 MIOX 55586 myo-inositol oxygenase
GO:0050661|GO:0019310|GO:0050113|GO:0005737|GO:0004033|GO:0016234|GO:0016651|GO:0070062|GO:0055
114|GO:0016701|GO:0008199 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135314_PI430048170 0.152779496069958 0.781545436820373 8.1159373498809
8.33576631461167 8.50323403221738 P P P 8.51164441464082 8.50638170598144
8.97732200149164 P P P LNCV6_135314_PI430048170 mRNA
TATCTTGAGACGCCTTACAAATGATGGAGGATTCCAAAGAGTTTTTGTTTATTTGGGTTA NM_078476 RefSeq chr6
+ 26457903 26469653 BTN2A1 11120 "butyrophilin, subfamily 2, member A1, transcript variant 2"
GO:0006629|GO:0003674|GO:0005887|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127696_PI430048170 0.00509969223914029 2.35393038160853 6.36705931594304

6.32172021160027 6.32935628088688 P P P 5.24645451675326 5.12852794638169
4.91956573420997 P P P LNCV6_127696_PI430048170 mRNA
ATTGGTTGAGGTGACACCATCTGTTGTAACAGATAAACCCCGAAATCCCAGTGCTGAACT NM_030907 RefSeq chr1
- 16231686 16237164 RSG1 79363 REM2 and RAB-like small GTPase 1
GO:0042384|GO:0005737|GO:0007264|GO:0017157|GO:0005654|GO:0034613|GO:0015031|GO:0006887|GO:0005
525|GO:0036064|GO:0031338 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134802_PI430048170 0.95649396497816 0.9975848639828330.381663610527619
0.4911010745746220.386736465073342 A A A 0.5057823848578590.378761853653006
0.384488076297982 A A A LNCV6_134802_PI430048170 mRNA
ACGTGACATTCAGTGTGTATTTCTGAATATGACCTACCGACGTGTAGGTTTGCGTGTGAG NM_001256894 RefSeq
chr4 + 9234384 9236334 USP17L15 NA ubiquitin specific peptidase 17-like family member 15
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142751_PI430048170 0.23497906584581 0.8527836487347920.244724782314561
0.2740102500520210.325622440448181 A A A 0.4124213258961820.329381009455717
0.756568882533523 A A A LNCV6_142751_PI430048170 mRNA
AGCAAGTGTAGACACCTTCGAGGGCAGAGATCGGGAGATTTAAGATGTTACAGCATATTT NM_015381 RefSeq chr22
+ 48576305 48751935 FAM19A5 25817 "family with sequence similarity 19 (chemokine (C-C motif)-like),
member A5, transcript variant 2" GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_54642_PI430048170 0.2568499771833540.8708668076726089.96107172728365 9.99307403372859
10.0661943831361 P P P 10.0121752037002 10.1502529265745 10.4270149148343 P P P
LNCV6_54642_PI430048170 mRNA
TGTTTACTCATTGGAGGAACAGTACCTTGGCTTGGCTCTTGACGTGGACAGAACTAAAAA NM_001278267 RefSeq
chr1 - 145289899 145405778 NBPF20 NA "neuroblastoma breakpoint family, member 20" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_136961_PI430048170 0.2245771970936931.06527233813338 0.617550039085154
0.75505035721155 0.58750917321919 A A A 0.5579529338216110.572591399791704
0.561444757243119 A A A LNCV6_136961_PI430048170 mRNA
GTTGAAAACAAGCAGCTACTGTATGTATGTAGCTAACTGAATTTGTTCAGTGTTTTAACC NM_152688 RefSeq chr6
- 61679959 62286195 KHDRBS2 202559 "KH domain containing, RNA binding, signal transduction
associated 2"
GO:0005515|GO:0008266|GO:0017124|GO:0006355|GO:0046982|GO:0008143|GO:0005634|GO:0042169|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144605_PI430048170 0.2907921229619841.0301180605817 0.305020470470389
0.2519243622729030.355401852553706 A A A 0.2712907433330770.242733036107622
0.271559162039237 A A A LNCV6_144605_PI430048170 mRNA
GTCTTTGCAGAGGTCCAAATGATATTCATGATGGTAATAAACGAGATGTTTGCCAAATAA NM_005187 RefSeq chr16
- 88874854 88977096 CBFA2T3 863 "core-binding factor, runt domain, alpha subunit 2; translocated to,
3, transcript variant 1"
GO:0005515|GO:0003700|GO:0008283|GO:0003714|GO:0005730|GO:0005634|GO:0046872|GO:0006351|GO:0000
139|GO:0003682|GO:0045944|GO:0005654|GO:0030851|GO:0045892 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128556_PI430048170 0.2872649572648371.1528539365891 6.30276776680733
6.17152320307109 6.20031474087074 P P P 5.74209682573075 5.99345438606193
6.27705481413734 P P P LNCV6_128556_PI430048170 mRNA
TGGGCCAGCTGAGGCAAGCTGTCTTTTTTCCCTTTTCTTTTTAATAGATGCAACATTTTT NM_014957 RefSeq chr8 +
141128620 141195801 DENND3 22898 DENN/MADD domain containing 3
GO:0017112|GO:0008333|GO:0032851|GO:0044257 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138942_PI430048170 0.6402135935561580.9522606566406317.40190716819648

7.53100904116444 7.78259782323324 P P P 7.54513527999712 7.56117820323457
7.82920305990223 P P P LNCV6_138942_PI430048170 mRNA
CCATTCCCTTTAAACAGTGGTGATATCAAATATACTTCCATCCATTGAATGGGGTATTTT NM_003795 RefSeq chr6
- 108211216 108261260 SNX3 8724 "sorting nexin 3, transcript variant 1"
GO:0005515|GO:0042541|GO:0030111|GO:0030136|GO:0070273|GO:0032009|GO:0005829|GO:0043231|GO:0050
765|GO:0016050|GO:0009617|GO:0033572|GO:0005737|GO:0070676|GO:0022615|GO:0033157|GO:0010314|GO:0
070062|GO:2000642|GO:0042177|GO:0019903|GO:0080025|GO:0032268|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140717_PI430048170 0.1923326774785021.27537165237653 0.821468045047866
0.5130547550491811.11758201605024 A A A 0.3998326217885580.553075376993563
0.505228357066661 A A A LNCV6_140717_PI430048170 mRNA
TAGGATGTGAGTGTATAGAAAGACTCTCTCTAACGTTAGCTACGCGTGCAGAAATGTGGG NM_015155 RefSeq chr10
- 806913 931705 LARP4B 23185 "La ribonucleoprotein domain family, member 4B"
GO:0005737|GO:0016020|GO:0042788|GO:0010494|GO:0005730|GO:0045727|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127525_PI430048170 0.0321117748638945 0.6352601618793919.07019077370031
9.04979319971114 9.23621243918897 P P P 9.58455465004494 9.65386143108646
10.0449683507029 P P P LNCV6_127525_PI430048170 mRNA
CTTTTCATCAAGGCGCCTTTCCTAATAATATGGTTCAACTGTGAATGTAGAAGTGGGGGG NM_002265 RefSeq chr17
+ 47649837 47683638 KPNB1 3837 "karyopherin (importin) beta 1, transcript variant 1"
GO:0005515|GO:0019221|GO:0019058|GO:0005635|GO:0044281|GO:0006606|GO:0006607|GO:0006921|GO:0005
829|GO:0005737|GO:0006610|GO:0005643|GO:0008536|GO:0016032|GO:0070062|GO:0000060|GO:0031965|GO:0
071782|GO:0019904|GO:0006915|GO:0016020|GO:0006309|GO:0008565|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138955_PI430048170 0.5539520183271730.8783916947076150.450780338479081
2.88807218893124 1.46501138898497 A A A 1.75810187663905 2.40146650223893
2.15724106983489 A A A LNCV6_138955_PI430048170 mRNA
GCAGTCCTTCAAAGATGACCACCATATATAGTTGTGTACGTGTTATTCCAAGCCTTTAAA NM_022774 RefSeq chr1
+ 40508760 40516542 EXO5 64789 exonuclease 5
GO:0005737|GO:0051539|GO:0045145|GO:0008310|GO:0005654|GO:0005634|GO:0003677|GO:0046872|GO:0042
803|GO:0000738|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137698_PI430048170 0.3878897196708371.2068589756391 6.45173593751547 6.8537586913307
7.20480260895231 P P P 6.66334646970384 6.35790266591523 6.74446602108293 P P P
LNCV6_137698_PI430048170 mRNA
CCTTTAGTGAGTACCCCTTTAGTGCTATATTTGTGCCATTCATTATCTGGTTCATATTTC NM_006416 RefSeq chr6 +
87472924 87512339 SLC35A1 10559 "solute carrier family 35 (CMP-sialic acid transporter), member A1,
transcript variant 1"
GO:0005794|GO:0005975|GO:0008643|GO:0055085|GO:0005456|GO:0015782|GO:0000139|GO:0005887|GO:0005
351|GO:0006488|GO:0044267|GO:0006464|GO:0015992|GO:0018279|GO:0043687 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137430_PI430048170 0.0627301909264077 0.7566419835498431 1.6024600196863
11.2991022932102 11.2308012337275 P P P 11.7645922142597 11.8406961764265
11.7603041252864 P P P LNCV6_137430_PI430048170 mRNA
TTCCCTCGGAATGTTTCCGTAACAGGACATTAAACCTTTGATTTTACTTCCGTGAAAAAA NM_012227 RefSeq chrY
- 304749 318819 GTPBP6 8225 GTP binding protein 6 (putative) GO:0005525|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129459_PI430048170 0.2886790754089340.8725727444923926.33503444601996
6.18737530131102 5.87052377719131 P P P 6.50740466349007 6.22504380169996
6.27257249590003 P P P LNCV6_129459_PI430048170 mRNA

CCCCCAGGGGAACACCCCTGCCCAGCTACTTTCCTAATGAAATAAAGAGCATTGAAGCAG NM_145017 RefSeq chr11 + 61481112 61490928 PPP1R32 220004 "protein phosphatase 1, regulatory subunit 32, transcript variant 1" GO:0005515|GO:0019902 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144952_PI430048170 0.2899078575357510.72875357618659 4.69894279307107 3.54590465278461 3.55625619580792 P P P 4.1690579216606 4.7373665175059 4.53267945793874 P P P LNCV6_144952_PI430048170 mRNA
CTTTCCCTCTTGTCCTCATTAATGGTGATGTTTCTGGGTTGAAAGAAGTAAAAATGTTTT NM_016188 RefSeq chr7 - 100643102 100656461 ACTL6B 51412 actin-like 6B GO:0071565|GO:0006357|GO:0016514|GO:0003713|GO:0006325|GO:0005730|GO:0005200|GO:0006338|GO:0005634|GO:0006351|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131323_PI430048170 0.46848531273501 0.39329404511412 0.395380011269774 0.4569054789121430.412136028919516A A A 0.3030362082371052.94774874552855 0.343081722152518A P A LNCV6_131323_PI430048170 mRNA
TACATGGGGGCATCCTCAACAAGACGGTGCACGAACTCATACGCGGGCTGCGCATGCAGG NM_001029886 RefSeq chr5 - 177400106 177400636 PFN3 345456 profilin 3 GO:0005737|GO:0030036|GO:0005634|GO:0003779|GO:0005856|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145224_PI430048170 0.00220441094243163 1.96805584489023 7.39798531187306 7.63919224060801 7.65730094060643 P P P 6.40974251485114 6.77062980295974 6.57536618868323 P P P LNCV6_145224_PI430048170 mRNA
CTGCATTCATGGTTAGAAGCTTTCCATGCCTAGGTTCTAGGGAATTTATTTTTCTATGTG NM_015305 RefSeq chr14 - 76787242 76812940 ANGEL1 23357 angel homolog 1 (Drosophila) NA . NA - . NA NA NA NA NA NA NA NA NA NA NA
LNCV6_139049_PI430048170 0.4036032668984790.7046191561488521.28845749489942 0.6693424906291671.35534127578637 A A A 1.76353452056109 2.08866566051389 0.770613418352701A A A LNCV6_139049_PI430048170 mRNA
CAGACTGATTGTTCACCAACGATCTTGTAAACCCAAAGCCGCCAAGTAAAGCCCTTTTCT NM_001195535 RefSeq chr5 + 122160175 122182663 LOC100505841 100505841 zinc finger protein 474-like NA . NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_129511_PI430048170 0.0094144664778648 3.39069849251866 5.63392030878616 5.75524145335719 5.63086119280739 P P P 3.68080442507743 4.2769332046666 3.698074905511 P P P LNCV6_129511_PI430048170 mRNA
GACAAGGTCAGCATCATTTGCTCTCCTGAATTTATGAGGTTTATTTATTTTTCTCTTTCC NM_004573 RefSeq chr15 - 40287896 40307973 PLCB2 5330 "phospholipase C, beta 2, transcript variant 1" GO:0043647|GO:0005509|GO:0007268|GO:0007202|GO:0044281|GO:0005829|GO:0016042|GO:0035556|GO:0004629|GO:0050913|GO:0004435|GO:0008152|GO:0004871|GO:0006644 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138645_PI430048170 0.6578331558060440.8136826550064272.16650272012662 0.3517380251566850.450507454678224A A A 2.15720538428615 1.59804300874829 0.352995744327852A A A LNCV6_138645_PI430048170 mRNA
AATGCTCCCTGGGGGAGCCCTCGGAATCTATTTAATAAATTATATTGAATTTTTCTCATA NM_001014336 RefSeq chr12 - 122172029 122174199 IL31 386653 interleukin 31 GO:0005615|GO:0005125|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55036_PI430048170 0.3340768847217831.05036586725462 0.3331330662783710.335883243998699 0.498530016905047A A A 0.3198357092256520.2925908886595240.348201309729568A A A LNCV6_55036_PI430048170 mRNA
GAAAAGTGTCGAGTTGTGCACATCCATTTCTTGTTTCACAATGTTTAAAAGTGACAGTAA NM_002585 RefSeq chr1 + 164559359 164851823 PBX1 5087 "pre-B-cell leukemia homeobox 1, transcript variant 1" GO:0005515|GO:0006694|GO:0001658|GO:0008284|GO:0003700|GO:0030325|GO:0048706|GO:0048538|GO:0005

634|GO:0009954|GO:0030326|GO:0048536|GO:0009952|GO:0043433|GO:0005737|GO:0030278|GO:0045944|GO:0
007548|GO:0035019|GO:0035162|GO:0005667|GO:0046982|GO:0000978|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133409_PI430048170 0.00119665471719467 1.67359738390244 11.1250049504234
11.1556954816948 10.9623998430264 P P P 10.4224334545259 10.3834780437381
10.2066774078874 P P P LNCV6_133409_PI430048170 mRNA
GCTGACATCAGACGGGATATCCGAATATCTGATAGCAATTAAAAGGCAGCCTTGTTTCGT NM_138496RefSeq chr8
- 144449931 144465035 CYHR1 50626 "cysteine/histidine-rich 1, transcript variant 1"
GO:0048471|GO:0008270|GO:0005654|GO:0005635 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139275_PI430048170 0.441361408808394 0.906915524590984 5.54876242736228
5.43855124475459 5.95751027326905 P P P 5.72245213482129 5.74147691894029
5.94614723963981 P P P LNCV6_139275_PI430048170 mRNA
CTTCACTGGGGAATACTGACTTCCTAAAATCTCAAGATGGAAGATATACCACATGTAAAT NM_000367RefSeq chr6
- 18128313 18155165 TPMT 7172 thiopurine S-methyltransferase
GO:0006139|GO:0006805|GO:0008119|GO:0044281|GO:0032259|GO:0070062|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_95407_PI430048170 0.207046274679142 1.06990821717904 0.415909525170172 0.392033435805998
0.561314730094795 A A A 0.333195804254424 0.376336694067844 0.372750626429179 A A A
LNCV6_95407_PI430048170 mRNA
GAAGTACCAGCACAATTTGAGCATTCCCATTAACAAAGGTGTTCACAGTTGAGAAACTCT NM_054110RefSeq chr3
+ 16174676 16229746 GALNT15 117248 polypeptide N-acetylgalactosaminyltransferase 15
GO:0030133|GO:0004653|GO:0006493|GO:0000139|GO:0030246|GO:0016266|GO:0016021|GO:0044267|GO:0046
872|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139221_PI430048170 0.0645168318767026 0.702205928785257 5.81188614808713
5.43904356080857 5.9915773986855 P P P 6.21446814301589 6.12599205124714
6.46422064956762 P P P LNCV6_139221_PI430048170 mRNA
GCAAATATTACCATAAGTGGGTAAAAGTAAAATTCCTCTTCTGAAAATGTGTCCTGTGCT NM_003932RefSeq chr22
- 40824534 40857008 ST13 6767 "suppression of tumorigenicity 13 (colon carcinoma) (Hsp70
interacting protein), transcript variant 1"
GO:0005515|GO:0032564|GO:0019904|GO:0051087|GO:0061084|GO:0032403|GO:0005829|GO:0042802|GO:0043
234|GO:0005737|GO:0070389|GO:0006457|GO:0030544|GO:0051260|GO:0051082|GO:0030674|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145689_PI430048170 0.989057989252143 0.968006606058732 4.54760663083018
4.38820021609131 4.27110939199502 P P P 3.98269930332447 4.35732748972584
4.87929153638631 P P P LNCV6_145689_PI430048170 mRNA
GGGATGCATTGAGCAGTCTGACAGTGAGAATAAAGAATGCTGAGTCAAGATTTATATTAA NM_025243RefSeq chr2
- 227685209 227718029 SLC19A3 80704 "solute carrier family 19 (thiamine transporter), member 3"
GO:0015403|GO:0005886|GO:0006766|GO:0006767|GO:0071934|GO:0044281|GO:0016021|GO:0042723 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135714_PI430048170 0.0011223762409866 2.41268723889243 12.3871697671375
12.728893371401 12.5576320221553 P P P 11.3897653142227 11.1897693862681
11.2955247344623 P P P LNCV6_135714_PI430048170 mRNA
TAATCACGGAGGGAAGTGGCTGCCCCCTTAACACACCTTTAATAAACAGTCTACAGACCC NM_007108RefSeq chr16
- 2771413 2777296 TCEB2 6923 "transcription elongation factor B (SIII), polypeptide 2 (18kDa,
elongin B), transcript variant 1"
GO:0005515|GO:0070449|GO:0010467|GO:0006368|GO:0016567|GO:0006366|GO:0071456|GO:0061418|GO:0005
829|GO:0050434|GO:0006461|GO:0016032|GO:0031462|GO:0005654|GO:0031466|GO:0031625|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93662_PI430048170 0.908051003776335 1.14049886300934 2.43138645778732 1.62724650845127

0.408167827115298 A A A 0.5306234696104581.98091551030344 1.6824888005842 A A A
LNCV6_93662_PI430048170 mRNA
TTGTCCTTTGCTGATTGGTTTTGGAAACGGTCTTAACAGGAGGGAGAGTGAAGAGAAGAC NM_001134649 RefSeq
chr3 - 71679288 71754383 EIF4E3 317649 "eukaryotic translation initiation factor 4E family member 3,
transcript variant 3" GO:0019221|GO:0003743|GO:0006417|GO:0006413|GO:0005845|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141558_PI430048170 0.1931000459040711.04167518406309 0.344620199964499
0.3218347014055140.424527285608276 A A A 0.3005944692114250.284633918549179
0.330685053344006 A A A LNCV6_141558_PI430048170 mRNA
TTGGGCCCTTGGCCTTACTATGATGATATGAGATTCTTTATGAAAGAACATGAATGTAAG NM_182617 RefSeq chr16
- 20536760 20576373 ACSM2B 348158 "acyl-CoA synthetase medium-chain family member 2B,
transcript variant 1"
GO:0005739|GO:0003674|GO:0006805|GO:0005759|GO:0006631|GO:0044281|GO:0005524|GO:0047760|GO:0046
872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63558_PI430048170 0.4044716235516120.8662665570947045.35531955502203 5.86624494253912
5.42259794604827 P P P 6.06413204277833 5.64372225336812 5.56079870171345 P P P
LNCV6_63558_PI430048170 mRNA
ACAGGCAGATCCAGAATCAGCTGGAAGAAATGCTGAAGTCTTTTCACAACGAGCTGCTTA NM_006340 RefSeq chr17
+ 81035146 81117432 BAIAP2 10458 "BAI1-associated protein 2, transcript variant 3"
GO:0008286|GO:0007009|GO:0005515|GO:0043005|GO:0005886|GO:0008360|GO:0007409|GO:0030175|GO:0015
629|GO:0005829|GO:0042802|GO:0009617|GO:0005737|GO:0048167|GO:0032956|GO:0051764|GO:0070064|GO:0
051017|GO:0008093|GO:0070062|GO:0048010|GO:0008022|GO:0001726|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129312_PI430048170 0.8582001297898770.8716181128907130.351139018748181
0.3272129403110111.32122128974562 A A A 1.72256824817984 0.314628434643312
0.293633453359687 A A A LNCV6_129312_PI430048170 mRNA
AAGATTCAAAAGGGACCCGACAACACTAAGGCGCGCAAAGGCACCACCGTGACGCTGACT NM_001286811
RefSeq chr2 + 219496354 219498287 LOC100996693 NA CAVP-target protein-likeNA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132371_PI430048170 0.1008856339917781.03356620924606 0.330042857560686
0.31071389309012 0.271268668383499 A A A 0.2500816249622410.266811772023897
0.252804257497053 A A A LNCV6_132371_PI430048170 mRNA
GGGTTGAACTTGCTAAAGTAAATCATACTTTAGAATCTCTTCAGGGAATGTGACATACAA NM_030960 RefSeq chr6
+ 88047788 88066832 SPACA181833 sperm acrosome associated 1
GO:0001675|GO:0016021|GO:0002080 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136458_PI430048170 0.1323424841101940.9074197466094631 4.868521318949
14.7155759619385 14.7960789111859 P P P 14.8588297182165 14.8928522779702
15.0460496015513 P P P LNCV6_136458_PI430048170 mRNA
CTCATGCAGGCCCCACCTGCCAATAGTAATAAAGCAATGTCACTTTTTTAAAACATGAAA NM_005620 RefSeq chr1
- 152032505 152037035 S100A11 6282 S100 calcium binding protein A11
GO:0005515|GO:0008285|GO:0005509|GO:0005634|GO:0001726|GO:0005615|GO:0042803|GO:0007165|GO:0044
548|GO:0005737|GO:0005654|GO:0008156|GO:0070062|GO:0048306 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_95326_PI430048170 0.9952895374949770.9997421497352726.1014736990379 5.98439232959609
6.34043827096633 P P P 6.24340165421022 5.90982037730642 6.27013657066215 P P P
LNCV6_95326_PI430048170 mRNA
CCTATGTTTTTGAACGAGACCAATCTGTTGGAGACCCTAAAATTGACTTAATTAGAACAT NM_005506 RefSeq chr4
- 76158738 76213899 SCARB2 950 "scavenger receptor class B, member 2, transcript variant 1"
GO:0005515|GO:0016020|GO:0006622|GO:0004872|GO:0016021|GO:0019899|GO:0007155|GO:0005765|GO:0005

925|GO:0070062|GO:0043202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53039_PI430048170 0.9870505876541941.07890128188736 0.3297717877588612.06813501679256
1.78162605416072 A A A 1.92508839809253 0.7684021508710661.45280099224148 A A A
LNCV6_53039_PI430048170 mRNA
AGAAACGGGCTTATCTTGGGCTTCAGCTCGCTGGTTGGTGGAGGCATCAGAGCTAGCTTC NM_001242757 RefSeq
chr16 - 89195760 89200121 SLC22A31 146429 "solute carrier family 22, member 31"
GO:0022857|GO:0016021|GO:0055085|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138876_PI430048170 0.6217550385785931.58892474120441 0.41318172174705
0.4217692540190622.4033776702386 A A A 1.25417193554729 0.37669582962677
0.408181598069974A A A LNCV6_138876_PI430048170 mRNA
GATGAGATGGCTTGTCTCATCCACACCACAGAAGGAAATAAACCATGTGGCTTAAATTTT NM_001098835 RefSeq
chr11 + 60756866 60776731 MS4A15 219995 "membrane-spanning 4-domains, subfamily A, member
15, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135547_PI430048170 0.1545412033159971.22836448382882 11.9242582756108
11.8764619491632 11.8041104456879 P P P 11.2914872016422 11.775521807016
11.6090144782996 P P P LNCV6_135547_PI430048170 mRNA
TATATTGCCCTTGGAACACATGGTGCCATATTTAGCTACTAAAAAGCTCTTCACAAAAAA NM_002168RefSeq chr15
- 90083979 90102554 IDH2 3418 "isocitrate dehydrogenase 2 (NADP+), mitochondrial, transcript
variant 1"
GO:0000287|GO:0006099|GO:0005975|GO:0005743|GO:0044281|GO:0006097|GO:0004450|GO:0005739|GO:0006
102|GO:0051287|GO:0005759|GO:0006103|GO:0044237|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_126767_PI430048170 0.4181936903821180.8765746343901673.78414431128754
4.14000844036774 4.5194500663415 P P P 4.22361561718727 4.39739192685719
4.47487285260735 P P P LNCV6_126767_PI430048170 mRNA
GAAAATGGTTGAGGGCCATAGGGAACCAGATGGTAAATACATTCTTCAAAATTGTGTGAG NM_014177RefSeq chr18
+ 74148510 74158969 TIMM2129090 translocase of inner mitochondrial membrane 21 homolog (yeast)
GO:0033617|GO:0005744|GO:0005515|GO:0032981|GO:0003674|GO:0006626|GO:0016021|GO:0030150|GO:0044
267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131550_PI430048170 0.8531356400856061.01835185543524 0.642652903637605
0.3557109179880160.360967450757339A A A 0.3725717853119640.366304680294082
0.552923614365265A A A LNCV6_131550_PI430048170 mRNA
GGCTGTTGCTTTGCTTCATGTGTATGGCTATTTGTATTTAACAAGACTTAATCATCAGTA NM_198196RefSeq chr3
+ 111542078 111652359 CD96 10225 "CD96 molecule, transcript variant 1"
GO:0006955|GO:0005886|GO:0005887|GO:0050776|GO:0007155 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137839_PI430048170 0.0633745585424044 0.5939048009412344.18218721288527
4.24765109696764 4.8589386598796 P P P 5.14362450188362 5.21427326471448
5.28319709524854 P P P LNCV6_137839_PI430048170 mRNA
GCCCATTAATAGACGCAGTAAAATATTTTTGAATCAGACATTTGGGGTTTGTATGTGCAT NM_173552RefSeq chr3
+ 143971797 143992368 C3orf58 205428 "chromosome 3 open reading frame 58, transcript variant 1"
GO:0030126|GO:0000139|GO:0014066|GO:0005615|GO:0060038 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_108003_PI430048170 0.9676776643165050.9986247178422755.42845224539744
5.03399967060799 4.99189276091916 P P P 5.51837058137395 4.99632283233952
4.90900307737451 P P P LNCV6_108003_PI430048170 mRNA
TGACTTCTTGCTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAG NM_001145772 RefSeq
chr16 + 57628225 57665039 ADGRG1 NA "adhesion G protein-coupled receptor G1, transcript variant
6" NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_136155_PI430048170 0.1840082384766282.03146773340606 0.469652105307384
1.73242702973839 1.95236034482756 A A A 0.3258224387450370.401957156517272
0.720490803808134A A A LNCV6_136155_PI430048170 mRNA
CAGTCAGTCAGGCTTCAGTTTATTTTTTGAACACTTGGGCAATTAATTAAAGCCATATGT NM_001284274 RefSeq
chr10 + 91410284 91514828 HECTD2 143279 "HECT domain containing E3 ubiquitin protein ligase 2,
transcript variant 3" GO:0005737|GO:0004842|GO:0042787|GO:0016874|GO:0005634 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_134941_PI430048170 0.4067631896542811.08201943108157 7.16415069598696
7.06117368902006 7.32487029453282 P P P 7.20606620769879 7.11803071138448 6.8775287701342
P P P LNCV6_134941_PI430048170 mRNA
TTGAGAAGTTATCTTTCTGTGATTTTGGTTTCCCTTCTCCTCCCATAATTTCTCCCGCAA NM_001143685 RefSeq
chr16_GL383556v1_alt - 70050 99287 CES5A 221223 "carboxylesterase 5A, transcript variant 1"
GO:0052689|GO:0008152|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143522_PI430048170 0.4308888505926040.5358365112568420.403731273865164
0.26035170634468 0.299513240216801A A A 0.3333489062919142.17766478028416
0.283235622980181A A A LNCV6_143522_PI430048170 mRNA
GGCAGCCTGTCTGACCTCATCTATGCCTTGGCCATTGTCGTCAATGTGGACCACTCCTAG NM_001080837 RefSeq
chr17 - 28364267 28365151 SEBOX NA SEBOX homeobox NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_111679_PI430048170 0.10606661771497 0.6672513648370694.13727917815811
4.24006049954454 3.74819678624032 P P P 4.59619333491837 4.98864235195009
4.23992905032823 P P P LNCV6_111679_PI430048170 mRNA
CACCTTCTTCTCCCAGTTCTCGAGAAGAAAAGGAGAGTAAGAAGGAAAGAGAAGAAGAAT NM_014739RefSeq
chr6 - 136256862 136289851 BCLAF1 9774 "BCL2-associated transcription factor 1, transcript variant 1"
GO:0005515|GO:0043065|GO:2001022|GO:0005730|GO:0006915|GO:2001244|GO:0005634|GO:0043620|GO:2000
144|GO:0003677|GO:0006351|GO:0005737|GO:0005654|GO:0045892 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_97993_PI430048170 0.5664960152200740.9128308392485243.82446984865626 3.17900702748072
4.01622841943087 P P P 3.77824800812162 3.86247651883063 3.89745116630333 P P P
LNCV6_97993_PI430048170 mRNA
ACACTAGGAAGAAAATAGAAATGGAGACCAAAACTTCTATTAGCATTCCTAAACCTGGAC NM_001198799 RefSeq
chr10 - 72096031 72216441 ASCC1 51008 "activating signal cointegrator 1 complex subunit 1,
transcript variant 1" GO:0005667|GO:0006355|GO:0005737|GO:0003723|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_138835_PI430048170 0.2624880591208031.12518403550137 10.5024650351749
10.7897645663726 10.8468158324077 P P P 10.5058447930717 10.488691233953
10.6514798903338 P P P LNCV6_138835_PI430048170 mRNA
AAGTTTCTTCATCGTTGTCCTCCCTGCTGGTCACATGAGTTTACGATTCCTTTGAAGTGT NM_203288RefSeq chr7
- 33094797 33109390 RP9 6100 retinitis pigmentosa 9 (autosomal dominant)
GO:0008380|GO:0005515|GO:0005737|GO:0005785|GO:0050890|GO:0008270|GO:0005654|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132538_PI430048170 0.0230246207575709 0.4871652891975734.26080564993122
3.91535134942364 4.6847628311023 P P P 5.14127752881638 5.32985839407134
5.57297468187351 P P P LNCV6_132538_PI430048170 mRNA
GCTGCTAGAACTCATCTGTAGTCCTTTATTATTTACACTGAATTCCAATTTCATTTCTGC NM_006055RefSeq chr2 -
210431248 210476767 LANCL1 10314 "LanC lantibiotic synthetase component C-like 1 (bacterial), transcript
variant 1"
GO:0005515|GO:0017124|GO:0004930|GO:0005634|GO:0003824|GO:0005737|GO:0043295|GO:0007186|GO:0005
887|GO:0008152|GO:0008270|GO:0050750|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_93040_PI430048170 0.0202677733581388 0.5452478824632594.36146051421112
4.44329622206511 4.32848321340183 P P P 5.32227231692314 4.96834784842778
5.43068425636584 P P P LNCV6_93040_PI430048170 mRNA
ATTTGAGAGATGTATCAGTTTCTTCTGAAGTACAATCAACTGTAGAAGCCTTTGTAGCAG NM_015878RefSeq chr8
- 102826301 102864200 AZIN1 51582 "antizyme inhibitor 1, transcript variant 1"
GO:0042978|GO:0004857|GO:0034641|GO:0006596|GO:0042177|GO:0006521|GO:0005634|GO:0044281|GO:0043
085|GO:0003824|GO:0043086|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143037_PI430048170 0.6548082055642370.8648394238225260.37263437293903
1.69150029319838 0.322838369440202A A A 1.33765686518282 1.51747106330884
0.364843950898008A A A LNCV6_143037_PI430048170 mRNA
TCTGTGGTTCAGCTTGTGACATGATATATAACACAGAAATAAATTATGCTTGTCCCTGAA NM_002112RefSeq chr15
- 50241948 50265965 HDC 3067 histidine decarboxylase
GO:0001694|GO:0034641|GO:0006547|GO:0030170|GO:0006548|GO:0044281|GO:0004398|GO:0042423|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136296_PI430048170 0.1746753062219811.25283551429349 0.323190631414665
0.8399958559033890.541337568547285A A A 0.2614189255666260.251826365552854
0.262621355217349A A A LNCV6_136296_PI430048170 mRNA
AGTCCAGTGAGAATACTATGGTACCATACAGTATAAACAACTGCTCAGTGATATTTCCAT NM_207377RefSeq chr14
+ 58395925 58408701 TOMM20L 387990 translocase of outer mitochondrial membrane 20 homolog
(yeast)-like GO:0005742|GO:0016021|GO:0006605 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138561_PI430048170 0.000444540999482588 1.71045747472937 13.2419014671353
13.365888908043 13.3691934741772 P P P 12.5385167432931 12.4649595426425
12.6480670661894 P P P LNCV6_138561_PI430048170 mRNA
TGAAAGAAACCGTCTTTGCGTTACACCCGAGTCTGCCTCTCGGAGCAGGGAGCTCACCTT NM_001300900 RefSeq
chr16 - 1771894 1773139 MRPS34 65993 "mitochondrial ribosomal protein S34, transcript
variant 1"
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0005743|GO:0005840 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139543_PI430048170 0.8169267726852630.876009748174572 3.52219486724919
3.12913173213318 3.63342332453121 P P P 2.74673444046213 3.87408019360683 3.9904517953706
P P P LNCV6_139543_PI430048170 mRNA
CCAGAATGTTTTTAAATCACCCTACTTCTATTGAACTTGCACTATCATCTGTTAACCTCT NM_024928RefSeq chr10 -
103877559 103918287 OBFC1 79991 oligonucleotide/oligosaccharide-binding fold containing 1
GO:0005515|GO:0070188|GO:0045740|GO:0005730|GO:0005634|GO:0010833|GO:0043231|GO:0000723|GO:0003
697|GO:0005654|GO:0045111|GO:0043047|GO:0000784 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131392_PI430048170 0.3072228153821921.06017734029343 0.496276898215711
0.6665916381085760.475373047206011A A A 0.43608399779248 0.49599867646035
0.460335773891868A A A LNCV6_131392_PI430048170 mRNA
CCACATTTTACCTCTCTACCAAATGAACATAAGTTGTAATTTGCTCTGAAATCTGTCAAC NM_032524RefSeq chr17
- 41159653 41160731 KRTAP4-4 84616 keratin associated protein 4-4 GO:0045095 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141790_PI430048170 0.0231694282001254 1.09953416635714 0.454446592496052
0.3989683273583680.407044054803975A A A 0.2590784271088450.340823648965987
0.248729267077649A A A LNCV6_141790_PI430048170 mRNA
TATTTGGAAACAGCAGCACTGTATTGGAGGACTCGAAGTCCAACGAGAAAGCTGAGGAATNM_006512RefSeq chr11
- 18231354 18236837 SAA4 6291 "serum amyloid A4, constitutive"
GO:0034364|GO:0005576|GO:0006953|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127996_PI430048170 0.0890758195689321.2164841414928 10.625355583026
10.6820370032811 10.5745192621077 P P P 10.1827285638728 10.5224195336277 10.310033372147

P P P LNCV6_127996_PI430048170 mRNA
CACTCCCTTTGTGGACTTTATTTAATTTCATAAATTGGCTCCTTTCCCACAGTCAAAAAANM_004935RefSeq chr7 -
151053811 151057965 CDK5 1020 "cyclin-dependent kinase 5, transcript variant 1"
GO:0008092|GO:0005515|GO:0031594|GO:0030054|GO:0021697|GO:0009790|GO:0006886|GO:0031175|GO:0046
777|GO:0043525|GO:0018105|GO:0048167|GO:0007411|GO:0016301|GO:0045211|GO:0018107|GO:0045860|GO:0
043025|GO:0031397|GO:0005856|GO:0043125|GO:0030334|GO:0014069|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106214_PI430048170 0.0392470157494545 0.69018601526117 6.43052977211604
6.2027333663761 6.26959914480796 P P P 7.08806613643699 6.73550033452609
6.65619298847537 P P P LNCV6_106214_PI430048170 mRNA
AATGCACCAACACCAACCGCTGTATTCCCGGCATCTTCCGCTGCAATGGGCAGGACAACT NM_002332RefSeq chr12
+ 57128498 57213342 LRP1 4035 low density lipoprotein receptor-related protein 1
GO:0005515|GO:0005886|GO:0007603|GO:0008283|GO:0097242|GO:0030136|GO:0030178|GO:0070325|GO:0005
765|GO:0002020|GO:0032403|GO:0007205|GO:0010875|GO:0014912|GO:0030425|GO:0043524|GO:0042953|GO:0
005737|GO:0032956|GO:0043025|GO:0004872|GO:0042954|GO:0008203|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144427_PI430048170 0.3891268088544440.8723219042836680.408618757554367
0.3860492157562760.247091621869891A A A 0.3513181804032270.853937113410095
0.375348656399933A A A LNCV6_144427_PI430048170 mRNA
TCCCTTCAGTGGTTCAACACTAATAATAGCACCAAGGAACATGTCACTGGTGCATATAGG NM_001178085 RefSeq
chrX + 24149728 24216255 ZFX7543 "zinc finger protein, X-linked, transcript variant 3"
GO:0006355|GO:0003713|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128586_PI430048170 0.0739178053289918 0.4238940353692440.402770647820097
1.52367987587587 0.308262948497811A A A 2.13815368294804 2.07328063526964
2.07462879544466 A A A LNCV6_128586_PI430048170 mRNA
ACTTCCAGTCCCCTTTGTATTCCTTAAATAAACTCAATGAGCTCTTCCAATCCTAAAAAA NM_001178098 RefSeq
chr16 + 28931938 28939347 CD19 930 "CD19 molecule, transcript variant 1"
GO:0050853|GO:0048011|GO:0005886|GO:0048015|GO:0043234|GO:0006968|GO:0007173|GO:0005887|GO:0008
543|GO:0045087|GO:0050776|GO:0005057|GO:0051281|GO:0007166|GO:0009897|GO:0038095|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141049_PI430048170 0.7909995590713831.06593511698741 0.360896678392035
0.2727787980757790.949300845705263A A A 0.3609596809450890.709881563753992
0.298345687994364A A A LNCV6_141049_PI430048170 mRNA
ATGTAGCAGTGATAGACATATTCCCCTCCTTTGAAACCTAGCATTAAATGGAAAAACAAA NM_004164RefSeq chr3
- 139452883 139476510 RBP2 5948 "retinol binding protein 2, cellular"
GO:0005215|GO:0008544|GO:0007603|GO:0006776|GO:0016918|GO:0006810|GO:0005501|GO:0019841|GO:0001
523|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130728_PI430048170 0.3205202197504881.02095890096544 0.463249790969247
0.5062317515719330.427870553260472A A A 0.4340397771619070.428300358598265
0.446247582517226A A A LNCV6_130728_PI430048170 mRNA
TTACTAGGAGAGGAAAACTTTTTCTTGATACCGGCAATCTTTTACTTATAATGGCTTGAG NM_033364RefSeq chr3
+ 119703021 119767102 MAATS1 89876 "MYCBP-associated, testis expressed 1"
GO:0005739|GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83659_PI430048170 0.6366136605202410.961524972999552 0.460200413934725 0.438821210638575
0.351956064047118A A A 0.3505287974424550.408332888719582 0.646807039927253A A A
LNCV6_83659_PI430048170 mRNA
GAAACTCCCAGTAAAAAAGACTTGGGAGACATGTTAATAAACTCAAGCATTTGATCGACC NM_014683RefSeq chr17
- 19770829 19867926 ULK2 9706 "unc-51 like autophagy activating kinase 2, transcript variant 1"

GO:0005515|GO:0048675|GO:0005524|GO:0048671|GO:0005829|GO:0007165|GO:0034045|GO:0042594|GO:0046777|GO:0004674|GO:0010506|GO:0000045|GO:0030659|GO:0034273 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136557_PI430048170 0.0215690242207898 3.22292243234243 3.07126449775506 2.89433820775629 2.47565082215272 A A A 0.957617735599177 0.509934455865688 1.71130385621454 A A A LNCV6_136557_PI430048170 mRNA CCAAGTATGAACAAGGGTGAAATTTGTGTTTTAAAAATAAAACTCCTTATCATGCCCAGC NM_198085 RefSeq chr7 - 122701665 122702967 RNF148 378925 ring finger protein 148 GO:0008270|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144085_PI430048170 0.562347490674855 0.919797639767899 0.315835906198574 0.27433331457397 0.410302748028373 A A A 0.286639811236465 0.741253253951264 0.288750512471051 A A A LNCV6_144085_PI430048170 mRNA TTCACCCTCTATGAGTCCCATTTTACTTCTACACCTGCAAGTCCTGGTTTATATTGGACC NM_006087 RefSeq chr19 - 6494318 6502584 TUBB4A 10382 "tubulin, beta 4A class IVa, transcript variant 3" GO:0005515|GO:0051258|GO:0006996|GO:0005874|GO:0003924|GO:0005634|GO:0005525|GO:0055085|GO:0005829|GO:0006184|GO:0005929|GO:0033269|GO:0006457|GO:0043209|GO:0000086|GO:0043025|GO:0005200|GO:0051084|GO:0007017|GO:0000278|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142963_PI430048170 0.699369254982509 1.19929542600705 1.63710182476322 1.44729759448999 0.337670964384721 A A A 1.35760652103967 0.923669610709532 0.54746693934975 A A A LNCV6_142963_PI430048170 mRNA CTGTCTGAACTATTTTACATTTTATGGTGTCTCATAGCCAATCCCACAGTGTAAAAATTC NM_003505 RefSeq chr7 + 91264467 91268817 FZD1 8321 frizzled class receptor 1 GO:0005515|GO:0017147|GO:0005886|GO:0090263|GO:0007267|GO:0044339|GO:0044338|GO:0035414|GO:0005109|GO:0030514|GO:0051091|GO:0030182|GO:0030855|GO:0090090|GO:0060070|GO:0060022|GO:0042813|GO:0003150|GO:0009986|GO:0004930|GO:0042493|GO:0090179|GO:0005102|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130572_PI430048170 0.00506954971727326 0.72077718178345 10.0146017332603 10.1759639202951 9.98890462420141 P P P 10.4843117023936 10.5948816043682 10.5224195336277 P P P LNCV6_130572_PI430048170 mRNA TGTGTGTGTCCATGTCTGCAAGCAGTTCTTCAATAAATGGCCTGCCTCCCCCTCAAAAAA NM_031466 RefSeq chr8 - 139730342 140458579 TRAPPC9 83696 "trafficking protein particle complex 9, transcript variant 1" GO:0005794|GO:0005783|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127816_PI430048170 0.493214186441056 1.74770825624141 0.365936044912453 2.29749856196813 0.449607857036443 A A A 0.856145781560341 0.307300610276525 0.360699321235748 A A A LNCV6_127816_PI430048170 mRNA GGAACACAACTATTCCACAAGTGGCCTTTAGTGCTCTTTATAATATGATTTCCTGTAATT NM_004519 RefSeq chr8 - 132120857 132480757 KCNQ3 3786 "potassium channel, voltage gated KQT-like subfamily Q, member 3, transcript variant 1" GO:0005251|GO:0005886|GO:0005267|GO:0007268|GO:0043194|GO:0060081|GO:0033268|GO:0007411|GO:0005249|GO:0008076|GO:0034765|GO:0016021|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76399_PI430048170 0.477594471100849 1.09012473463289 8.43299802055893 8.26868904984379 8.22033704966068 P P P 8.36936643843583 8.27389255252136 7.86612030859721 P P P LNCV6_76399_PI430048170 mRNA CGAGGAGGACCACTGCTCCCCGTCTGCCCGCGTGACTTTCTTCACAGACAACAGCTACTA NM_182925 RefSeq chr5 - 180601505 180649624 FLT4 2324 "fms-related tyrosine kinase 4, transcript variant 1" GO:0005515|GO:0008284|GO:0035924|GO:0005886|GO:0048514|GO:0046330|GO:0005634|GO:0002040|GO:0001

946|GO:0005737|GO:0046777|GO:0090037|GO:0060312|GO:0019838|GO:0005021|GO:0070374|GO:0038084|GO:0
001945|GO:0001944|GO:0048010|GO:0043066|GO:0019903|GO:0005576|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127650_PI430048170 0.0107169316770731 1.40833460675041 12.8453845892186
13.0884298112167 12.9818434093305 P P P 12.5380971638978 12.4435265795269
12.4605383617051 P P P LNCV6_127650_PI430048170 mRNA
CAGAAGTTTTCCTTTACACCAACTGTCAATGCCGGAATTTTGTATTCTGTTTTGTAAAGA NM_199054 RefSeq
chr19 - 2037470 2051244 MKNK2 2872 "MAP kinase interacting serine/threonine kinase 2, transcript
variant 2"
GO:0005515|GO:0030097|GO:0005730|GO:0005634|GO:0005524|GO:0046872|GO:0006417|GO:0097192|GO:0035
556|GO:0005737|GO:0004674|GO:0016605|GO:0005654|GO:0006468|GO:0071243|GO:0007166 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127098_PI430048170 0.0307393537034344 0.77400218380886 9.86588570190499
9.90903143359338 9.6427265682719 P P P 10.1280323325031 10.2470442251511
10.1626347787394 P P P LNCV6_127098_PI430048170 mRNA
TAAATTGTTCCGTGAAGCCGCGCTCTGTTTTGGGAATAAACTTCTATAGAAAACAAAAAA NM_001407 RefSeq
chr3 - 48636462 48662915 CELSR3 1951 "cadherin, EGF LAG seven-pass G-type receptor 3"
GO:0032880|GO:0005515|GO:0042384|GO:0007413|GO:0007186|GO:0005886|GO:0004930|GO:0005509|GO:0016
021|GO:0001764|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129173_PI430048170 0.0137815987370974 0.942569617572328 0.364836668741329
0.34513101471032 0.325584670858156 A A A 0.457456485530193 0.430057564362556
0.403792887735361 A A A LNCV6_129173_PI430048170 mRNA
AAGCTGAATCAGTGAGTGTGTACAATGATACATAATAAATCCTGGAAGTCTTGGGATCCT NM_005547 RefSeq
chr1 + 152908562 152911886 IVL 3713 involucrin
GO:0005737|GO:0018149|GO:0030216|GO:0010224|GO:0005198|GO:0031424|GO:0018153|GO:0030674|GO:0001
533|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128631_PI430048170 0.410378823935263 0.757226682538804 0.545491015001099
0.518594389813097 0.28000340488107 A A A 0.40784670916794 1.41529977542915
0.514929354308509 A A A LNCV6_128631_PI430048170 mRNA
GGAGCACACTTTGGAGCTACATTTCTTGTCTCCTCATTGTTGACATTAATTAAACATTTA NM_001171610 RefSeq
chr10 + 86668448 86736067 LDB3 11155 "LIM domain binding 3, transcript variant 5"
GO:0008092|GO:0005515|GO:0051371|GO:0048471|GO:0030018|GO:0005080|GO:0045214|GO:0008270|GO:0005
856|GO:0031143 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137597_PI430048170 0.024222402115716 1.56837242025625 8.73456449677085
9.08559660661112 9.1302232531965 P P P 8.26603142639071 8.13810767947606
8.59146206939429 P P P LNCV6_137597_PI430048170 mRNA
CCAGCAGGAGTGGAGTTTGGTTTACTGATTTTACTGTTTTGTGTTCATGAATCTTTATTT NM_017878 RefSeq chr11
- 63552769 63563383 HRASLS2 54979 HRAS-like suppressor 2
GO:0016042|GO:0005737|GO:0016746|GO:0016787|GO:0016021 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_127103_PI430048170 0.296753377044023 0.881185835484496 11.5673197268568
11.6809188513604 11.2634362725488 P P P 11.7007929791118 11.5296818813556
11.843224129831 P P P LNCV6_127103_PI430048170 mRNA
GCTAAACTGGTGTCAGTCCTTTTTTCCTTTGTTCCAAATAAAAGATTAAACCAATGGCAA NM_021939 RefSeq
chr17 + 41812709 41823217 FKBP10 60681 "FK506 binding protein 10, 65 kDa"
GO:0000413|GO:0061077|GO:0005509|GO:0005789|GO:0003755|GO:0005788|GO:0005528 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141285_PI430048170 0.535934036908907 0.888565031223853 4.84337036730772
4.23298813979296 3.82809094361868 P P P 4.65118490104853 4.61119963200472

4.3137246145314 P P P LNCV6_141285_PI430048170 mRNA
TTAGCAGAACGGGTAAACTCTGTTTCCTTTGTCCGTCCTGTTGTGAGTAACTGAAGCCTA NM_020469 RefSeq
chr9 - 133255175 133275214 ABO 28 "ABO blood group (transferase A, alpha 1-3-N-
acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)"
GO:0004381|GO:0032580|GO:0004380|GO:0006486|GO:0005576|GO:0016021|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128388_PI430048170 0.0128071370205538 0.578345446326642 6.90218185779318
6.95451076036525 6.7960755702737 P P P 7.51530573688062 7.89871403766306
7.58359354535634 P P P LNCV6_128388_PI430048170 mRNA
ATGCAACAGGAGCAAACCAAGTGTTGCTGTGACATTGATTCAGATGTTTGGCAAGAGGTG NM_006779 RefSeq
chr11 + 65314817 65322429 CDC42EP2 10435 CDC42 effector protein (Rho GTPase binding) 2
GO:0005515|GO:0030036|GO:0005886|GO:0008360|GO:0005100|GO:0012505|GO:0005737|GO:0031334|GO:0016
020|GO:0030838|GO:0032321|GO:0001515|GO:0015630|GO:0031274|GO:0007015|GO:0017049 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138727_PI430048170 3.49258981004977e-05 2.90419032622037 7.33781885618622
7.17727683950563 7.20231437436005 P P P 5.73615818039576 5.73840184835281
5.63108050894664 P P P LNCV6_138727_PI430048170 mRNA
GTTAGGAATACACAAGCCGTAAAATCGAGTCCTTACAGCCATACCACAAGGTACGTCCAT NM_001130921 RefSeq
chr22 - 50767491 50783659 RABL2B NA "RAB, member of RAS oncogene family-like 2B, transcript
variant 5" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144713_PI430048170 0.429360734134017 0.921432293641858 9.17236416535827
9.61535461904423 9.29367464646359 P P P 9.51871602840218 9.50403003908747
9.44887452791706 P P P LNCV6_144713_PI430048170 mRNA
GGTGGGCACTGCCCAGCACCGCATGCCACGTGTCCGGAATAAATTCTTTTTGATTGTTGG NM_138465 RefSeq chr8
+ 143267436 143276931 GLI4 2738 GLI family zinc finger 4
GO:0008150|GO:0003674|GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136200_PI430048170 0.398871565525265 0.978143275777135 0.369620586240179
0.397518683694865 0.336486588815385 A A A 0.452455568557434 0.359479377019684
0.386391409710823 A A A LNCV6_136200_PI430048170 mRNA
GTTCGTCCAGGAGTTTTGATTGTATCGGAACATAATGTGAAAGCAAAAATGAAATAAACG NM_004352 RefSeq chr16
- 49277917 49281831 CBLN1 869 cerebellin 1 precursor
GO:0051965|GO:0021707|GO:0030054|GO:0009306|GO:0045211|GO:0007268|GO:0005576|GO:0042803|GO:0007
157|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140542_PI430048170 0.948284181509174 0.995418495827897 13.3509792021545
13.1663199467999 13.4374270739494 P P P 13.2733905369927 13.2364795385168
13.4670855232404 P P P LNCV6_140542_PI430048170 mRNA
CCAGGCCATTATCATATCCAGATGGTCTTCAGAGTTGTCTTTATATGTGAATTAAGTTAT NM_000688 RefSeq chr3
+ 52198082 52214327 ALAS1 211 "5'-aminolevulinate synthase 1, transcript variant 1"
GO:0006996|GO:0044281|GO:0006782|GO:0006783|GO:0005739|GO:0005737|GO:0006778|GO:0005759|GO:0030
170|GO:0005654|GO:0007005|GO:0003870|GO:0044255 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143248_PI430048170 0.350933486778359 0.634114217406861 0.324657187731129
0.367991906015203 0.295137345825827 A A A 0.510708961445364 1.70559372146433
0.332048606212405 A A A LNCV6_143248_PI430048170 mRNA
CTGTACTCACCCTGTACCACAAACACATTACATTATTAAATGTTTCTCAAAGATGGAGTT NM_022555 RefSeq
chr6_GL000251v2_alt - 3934020 3947089 HLA-DRB3 3125 "major histocompatibility complex,
class II, DR beta 3"
GO:0005515|GO:0002437|GO:0050852|GO:0005886|GO:0019221|GO:0031295|GO:0042088|GO:0005765|GO:0042
130|GO:0019886|GO:0006955|GO:0002381|GO:0042605|GO:2001179|GO:0071556|GO:0032689|GO:0060333|GO:0

030658|GO:0012507|GO:0051262|GO:0035774|GO:0042613|GO:0032588|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62372_PI430048170 0.251627831432382 1.20844572823665 11.0057859311495 10.9414807411991 10.899469086214 P P P 11.02627571019 10.4529893393677 10.4739269053252 P P P LNCV6_62372_PI430048170 mRNA
GACTAGAGGCTTTCGGCTTTTTGGGACAGCAACTACCTTGCTTTTGGAAAATACATTTTT NM_001303236 RefSeq chr15 + 88638742 88656344 ISG20 3669 "interferon stimulated exonuclease gene 20kDa, transcript variant 5"
GO:0030619|GO:0015030|GO:0008283|GO:0008310|GO:0006364|GO:0019221|GO:0005730|GO:0034511|GO:0030620|GO:0005634|GO:0008859|GO:0009615|GO:0046872|GO:0006401|GO:0051607|GO:0004527|GO:0005737|GO:0060337|GO:0000175|GO:0016605|GO:0005654|GO:0000738|GO:0045071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108098_PI430048170 0.850116638263874 1.01922312247355 9.18782336732739 8.84715216505983 9.14245721945027 P P P 8.84792729567476 8.83290920778688 9.37009909443609 P P P LNCV6_108098_PI430048170 mRNA
GTTACCAGAACACATCAAGGAGCCAATCTGGGAAACACTATCAGAAGAAAAAGAAGAAAG NM_018141 RefSeq chr6 - 42206800 42217895 MRPS10 55173 mitochondrial ribosomal protein S10
GO:0070124|GO:0070125|GO:0008150|GO:0003674|GO:0070126|GO:0032543|GO:0006996|GO:0005743|GO:0005840 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51362_PI430048170 0.394807322848875 0.836894276664289 5.39256117184848 5.29061405477799 5.2212303262946 P P P 5.94239814670548 5.38655478559472 5.25585569820381 P P P LNCV6_51362_PI430048170 mRNA
AATGAACCCTGCCCAGAGGTGTCTGTAGTGAGCTTCTGCCCTAGTGACTTTTGAGCCGGC NM_001174100 RefSeq chr3 - 51957453 51967466 PCBP4 57060 "poly(rC) binding protein 4, transcript variant 5"
GO:0005737|GO:0030529|GO:0003723|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129056_PI430048170 0.807546545789077 0.907621074373029 2.16786614305625 2.1384544600004 1.87213761037592 A A A 2.42536597774703 2.47506477330042 1.53791567571104 A P A LNCV6_129056_PI430048170 mRNA
CTTTGACTTCACCCTGTTTGTAAATAAAACAATAAAATGGAAGGTGCTGTGGACTGGAAA NM_020214 RefSeq chr15 - 72241180 72271287 PARP6 56965 "poly (ADP-ribose) polymerase family, member 6"
GO:0008152|GO:0003950 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136905_PI430048170 0.281989720426956 0.843938800276361 7.23505750113822 6.99415923515028 6.88487204281872 P P P 6.96811450868892 7.4645438444369 7.390385523373 P P P LNCV6_136905_PI430048170 mRNA
CGGAGGAGGAGGAGGAAGATTACAGATCTATTCTGAGTATTTTTTAGAGAGTTAATATTT NM_001085375 RefSeq chr1 + 162381729 162386818 C1orf226 400793 "chromosome 1 open reading frame 226, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94617_PI430048170 0.266249027413978 0.867171813906109 4.6473003089674 4.70642842018567 5.01567121139536 P P P 5.21846501092315 4.89369493398528 4.87535733145982 P P P LNCV6_94617_PI430048170 mRNA
AGCTTCTTTGACAGAGAGCAAGTCTGCTCATGTGCAGACTCAGACTGGCCAAAATTCAAT NM_183013 RefSeq chr10 + 35126840 35212958 CREM 1390 "cAMP responsive element modulator, transcript variant 19"
GO:0005515|GO:0005667|GO:0006355|GO:0003700|GO:0006687|GO:0005634|GO:0007275|GO:0007283|GO:0051591|GO:0003677|GO:0032922|GO:0030154|GO:0006351|GO:0007165|GO:0008140|GO:0005737|GO:0045944|GO:0001046|GO:0045892. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132457_PI430048170 0.41960451691117 0.937604601520914 16.6599274146178 16.4587715345757 16.3189804638986 P P P 16.5675448485282 16.5817996676127 16.5875856490733 P P P LNCV6_132457_PI430048170 mRNA
CAGCTGCCAACAAGAAGCATTAGAACAAACCATGCTGGGTTAATAAATTGCCTCATTCGT NM_001022 RefSeq chr19

+ 41859917 41871416 RPS19 6223 ribosomal protein S19
GO:0005515|GO:0000462|GO:0010467|GO:0006364|GO:0009991|GO:0019058|GO:0060266|GO:0006412|GO:0042
803|GO:0006413|GO:0060265|GO:0005829|GO:0006414|GO:0030490|GO:0005737|GO:0000184|GO:0016032|GO:0
042274|GO:0070062|GO:0000028|GO:0051262|GO:0003735|GO:0019901|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138054_PI430048170 0.9692856150416141.12202277017175 2.20540481692788 2.1123640207085
0.360337866694374A A A 1.79068801719266 1.28013221849869 1.68702633804903 A A A
LNCV6_138054_PI430048170 mRNA
ATTATTTTAGCTTTAAAAGGAAATAAGGGGTTCAGATTTGAAAGGGGGTGGTATGGGTGG NM_022143RefSeq chr7
- 128027070 128030949 LRRC4 64101 leucine rich repeat containing 4
GO:0005515|GO:0030054|GO:0050808|GO:0043197|GO:0050807|GO:0045211|GO:0016021|GO:0060076|GO:0097
119 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145629_PI430048170 0.0880150326524524 0.7327393099051485.51612170577019
4.95798917617875 5.13463933732749 P P P 5.80901191012598 5.69012949636166
5.49579566602513 P P P LNCV6_145629_PI430048170 mRNA
CAGTCCCCTTGATCTTTCTATATAATAAATAACACAGGAGTGAACATCCTGAATCAGAAA NM_000195RefSeq chr10
- 98416197 98446947 HPS1 3257 "Hermansky-Pudlak syndrome 1, transcript variant 1"
GO:0005515|GO:0060041|GO:0030318|GO:0005764|GO:0032816|GO:0005737|GO:0031085|GO:0005887|GO:0007
596|GO:0033299|GO:0048069|GO:0046983|GO:0016023|GO:0007040|GO:0007601 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143604_PI430048170 0.2574526049612 2.30668193187388 3.32321683162495
1.21437031208829 3.15585277967193 P A P 2.45360247470054 0.448742404517034
1.24258045505971 A A A LNCV6_143604_PI430048170 mRNA
TCAGCATCTGGCATCCAAAGCAACATCAGAGAGAGAGAACACAGAAGAAAAGCAATTGCC NM_001004334
RefSeq chr17_KI270857v1_alt - 2360557 2378758 GPR179 NA G protein-coupled receptor 179 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108784_PI430048170 0.00120030936556585 1.87920987277823 6.96560628358539
7.19786015051655 6.96337724744957 P P P 6.28839609343419 6.03439768443706
6.07329347634502 P P P LNCV6_108784_PI430048170 mRNA
TGGTTAGAGTTATGGGAAGCGCGGTTATGGACACCAAGAAGAAAAAAGATGTTTCCAGCCNM_016203RefSeq chr7
- 151556114 151877231 PRKAG251422 "protein kinase, AMP-activated, gamma 2 non-catalytic subunit,
transcript variant a"
GO:0008286|GO:0004679|GO:0008603|GO:0071901|GO:0044281|GO:0005615|GO:0005829|GO:0035556|GO:0006
754|GO:0046324|GO:0045860|GO:0061024|GO:0006633|GO:0007050|GO:0044255|GO:0010800|GO:0006996|GO:0
031588|GO:0016208|GO:0019901|GO:0006853|GO:0005977|GO:0046320|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139868_PI430048170 0.8517006264421230.8478157301608391.98944368546899
0.2953023975450181.80467410385582 A A A 0.4758950902070211.51304245510532
2.58657841573405 A A P LNCV6_139868_PI430048170 mRNA
CCTCGTGGTGCTGCGGTGACTTTGTAGCCAACTTTATAATAAAGTCCAGTTTGCCTTTTT NM_178864RefSeq chr11
+ 66421003 66426706 NPAS4 266743 neuronal PAS domain protein 4
GO:0007165|GO:0005667|GO:0001077|GO:0046982|GO:0045944|GO:0005634|GO:0004871|GO:0000978|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107906_PI430048170 0.000755178337792115 0.6947868477164 11.1573359866724
11.0486689590424 11.0502092915251 P P P 11.5391963808022 11.6082174679232
11.6839498480556 P P P LNCV6_107906_PI430048170 mRNA
GAAGCTCTGAGAATTTTTTGTACGATCAGCCTTACTGCTAATAAAAGCACTTCCACAGGG NM_015908RefSeq chr7
+ 100875078 100888664 SRRT 51593 "serrate, RNA effector molecule, transcript variant 1"
GO:0097150|GO:0005515|GO:0046685|GO:0006355|GO:0005737|GO:0008283|GO:0031053|GO:0005654|GO:0005

634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131823_PI430048170 0.460022669257181.03235778587251 10.7710856839812 10.802116323944
10.8480219531264 P P P 10.66152990913 10.8300516637629 10.7875765289639 P P P
LNCV6_131823_PI430048170 mRNA
TTGTTGATTTTGGAGCCTCTTAGTGACCTGGTTGCGTCTGTGTCAGGAACTTAAACTTTC NM_014239RefSeq chr14
+ 75002908 75009591 EIF2B2 8892 "eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa"
GO:0005515|GO:0005851|GO:0010467|GO:0051716|GO:0009408|GO:0042552|GO:0043434|GO:0003743|GO:0005
525|GO:0007417|GO:0005524|GO:0006412|GO:0006413|GO:0009749|GO:0005829|GO:0043547|GO:0005085|GO:0
001541|GO:0005737|GO:0019509|GO:0014003|GO:0006446|GO:0044267|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127924_PI430048170 0.0022784954175663 0.2544906250431919.0394038288851
8.66895315915325 8.73552330552983 P P P 10.9494877567404 10.9822583779929
10.3894047633217 P P P LNCV6_127924_PI430048170 mRNA
TCCCCCCGCACCATCCGTGTCCTGCATTCTGCGAGTCTGTGCTCATTAACAATGTGCTGT NM_145283RefSeq chr9
+ 88535100 88575789 NXNL2 158046 "nucleoredoxin-like 2, transcript variant 2"
GO:0007608|GO:0045494|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129002_PI430048170 0.0764871507807243 0.4491259824752640.557238029978099
1.10041312629465 1.67627192232341 A A A 1.90910257028594 1.88235363364087
2.94932515893435 A A P LNCV6_129002_PI430048170 mRNA
ATGCATCCCATGTCTTTGGGTACTAGTGTATGAATTCTAATCTCTGTAAATGAAATGTTG NM_005118RefSeq chr9
- 114784634 114806128 TNFSF15 9966 "tumor necrosis factor (ligand) superfamily, member 15,
transcript variant 1"
GO:0005164|GO:0005886|GO:0007250|GO:0006919|GO:0005102|GO:0050715|GO:0005123|GO:0005125|GO:0005
615|GO:0007165|GO:0006955|GO:0005887|GO:0016021|GO:0042107 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129377_PI430048170 0.2917340001737241.02878818040171 0.358800130024155
0.2736899574399280.271983920139862A A A 0.2538247634053030.277677534576324
0.251708368911628A A A LNCV6_129377_PI430048170 mRNA
GCTTGCAGATGTTAAATGGAAAAGTTATATATGCATAAACCTTTTCTTCCTGGATTTGGC NM_001270524 RefSeq
chr14 - 56800706 56810476 OTX2 5015 "orthodenticle homeobox 2, transcript variant 4"
GO:0005515|GO:0005634|GO:0009953|GO:0042706|GO:0030426|GO:0005737|GO:0032525|GO:0007411|GO:0048
852|GO:0045944|GO:0040019|GO:0042472|GO:0001708|GO:0046982|GO:0090009|GO:2000543|GO:0048664|GO:0
000978|GO:0022037|GO:0043234|GO:0001077|GO:0006461|GO:0007492|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130594_PI430048170 0.7746011324278221.01051531401389 0.459917331631976
0.5269081358353220.441449926086148A A A 0.5486298753444790.411170225996486
0.420479707242325A A A LNCV6_130594_PI430048170 mRNA
AGACAAGCTGAAGCTACACACATGGCTGATGTCACATTGAAAATGTGACTGAAAATTTGA NM_007003RefSeq chrX
+ 49829302 49834034 PAGE4 9506 "P antigen family, member 4 (prostate associated)"
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139345_PI430048170 0.3957176718915676.00345735026401 0.879811742976594
4.58327797269158 0.425358860474851A P A 1.03476178851859 0.353190835702304
0.259513202407049A A A LNCV6_139345_PI430048170 mRNA
CTGTCAAGCCCCAGAACAATGTAGAATGGGCAATAATTCTGTAACCTTCTTAACTGTGTC NM_001195581 RefSeq
chr5 + 116051465 116059130 ARL14EPL NA ADP-ribosylation factor-like 14 effector protein-like NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93750_PI430048170 0.1214949451791741.32971650206505 3.91226742658235 3.95329007538451
3.47039712232349 P P P 3.34879636347618 3.37078405977867 3.42963631576549 P P P
LNCV6_93750_PI430048170 mRNA

CAAAACGCTCCTGGTTCGGGAACTTCATCTCCTTGGACAAAGAAGAACAAATATTCCTCG NM_032430 RefSeq chr19 + 55284165 55312535 BRSK1 84446 BR serine/threonine kinase 1
GO:0005813|GO:0030054|GO:0000287|GO:0043015|GO:0019901|GO:0031572|GO:0050321|GO:0030010|GO:0005634|GO:0007409|GO:0005524|GO:0006974|GO:0007269|GO:0008021|GO:0051298|GO:0005737|GO:0004674|GO:0030182|GO:0010212|GO:0005654|GO:0006468|GO:0009411 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120843_PI430048170 0.349620956149073 0.629845397281959 0.380293545445688 0.379851412610908 0.852733318921197 A A A 0.35427387676668 1.89888603099053 0.994300450317383 A A A LNCV6_120843_PI430048170 mRNA
TACACCAACACGCAGCTGCTGGAACTGGAGAAGGAATTCCACTTTAATAAGTACCTGTGC NM_002145 RefSeq chr17 - 48542655 48545031 HOXB2 3212 homeobox B2
GO:0006355|GO:0003700|GO:0002011|GO:0008015|GO:0021569|GO:0048857|GO:0048704|GO:0005634|GO:0007275|GO:0009953|GO:0009952|GO:0006351|GO:0043565|GO:0005737|GO:0021570|GO:0021612 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98123_PI430048170 0.00699171466530743 0.592294444529155 5.90845823363265 5.93263225110833 6.24652159303377 P P P 6.66321020258579 6.81308656406019 6.8939561322563 P P P LNCV6_98123_PI430048170 mRNA
GGCGAACAGCTGCTTGGAGAACTACAAGTGAAGAAAAGAAAGCATTAGATCAGGCAAGTG NM_006838 RefSeq chr12 + 95474045 95515837 METAP2 10988 methionyl aminopeptidase 2
GO:0070084|GO:0005886|GO:0007603|GO:0018206|GO:0022400|GO:0046872|GO:0005829|GO:0005737|GO:0016485|GO:0004177|GO:0070006|GO:0006508|GO:0008235|GO:0031365|GO:0016056 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121820_PI430048170 0.029613574415075 0.658234609977271 7.37934847308052 7.28675657569563 7.31501427022402 P P P 7.73239041408272 7.90432151459166 8.12848776978867 P P P LNCV6_121820_PI430048170 mRNA
TGGTAACCTACAATTAAGGAACAAAGAAGTGACTTGGGAAGTACTAGAAGGAGAGGTGGA NM_001294145 RefSeq chr2 + 169799027 169812061 SSB 6741 "Sjogren syndrome antigen B (autoantigen La), transcript variant 2"
GO:0005515|GO:0000049|GO:0008334|GO:0000166|GO:0030529|GO:0005634|GO:0003729|GO:0006400 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134958_PI430048170 0.0281123130605213 0.841739030387256 8.65607496283336 8.83419797079709 8.76444413592084 P P P 9.04127159772186 8.98262434768192 8.9812265696702 P P P LNCV6_134958_PI430048170 mRNA
ATGAATGTGATAGTTCAGACCAATGCCTTCCACTGCTCCTTTATGACTGCACTTCTAGCC NM_001159323 RefSeq chr19 - 48047842 48110852 PLA2G4C 8605 "phospholipase A2, group IVC (cytosolic, calcium-independent), transcript variant 3"
GO:0019369|GO:0007567|GO:0036149|GO:0044281|GO:0005635|GO:0005829|GO:0035556|GO:0005543|GO:0006954|GO:0016020|GO:0047499|GO:0005789|GO:0005654|GO:0046475|GO:0006644|GO:0005938|GO:0036151|GO:0046474|GO:0036152. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134228_PI430048170 0.261555261088082 1.05052771696601 0.344566326779652 0.343455181716296 0.480733534071626 A A A 0.315290629342933 0.295002868504714 0.348966726170948 A A A LNCV6_134228_PI430048170 mRNA
GCTACAGGAAATGGTTGTTTCTCCTATACTTTGTCCTTAACATCTTTCTTGATCCTAAAT NM_001925 RefSeq chr8 - 6935819 6938338 DEFA4 1669 "defensin, alpha 4, corticostatin"
GO:0005796|GO:0045087|GO:0050832|GO:0031640|GO:0019731|GO:0005576|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141298_PI430048170 0.166540949286609 1.38422441327473 4.68812402261471 5.21895045369831 5.41799559614078 P P P 4.6426305326583 4.48913645677209 4.85698925751915 P P P LNCV6_141298_PI430048170 mRNA

TCTTGGGAGTCCATAGAATACTGTTTCCTTCTAATAAAGGTTTCAAACAAATCCCTGCAG NM_001023560 RefSeq chr6 + 28267009 28278223 ZSCAN26 7741 "zinc finger and SCAN domain containing 26, transcript variant a" GO:0006355|GO:0003700|GO:0005634|GO:0003676|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133077_PI430048170 0.0117259760224479 0.3515600379589268.14176953783378 7.86299258974275 8.11448892767146 P P P 9.12386403412934 9.56200475435104 9.8767224903858 P P P LNCV6_133077_PI430048170 mRNA
CTTGTAAGATTGCGCTTTGTGCTTCAGTTTGTTACCTTTGTAGACTTATTTAATGAAACC NM_001184985 RefSeq chr12 + 752922 911452 WNK1 65125 "WNK lysine deficient protein kinase 1, transcript variant 4" GO:0005515|GO:0019902|GO:0005524|GO:0019869|GO:0035556|GO:0005737|GO:0048666|GO:0004674|GO:0050794|GO:0010923|GO:0018107|GO:0004860|GO:0006468|GO:0006469|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138404_PI430048170 0.0585636429778381 0.6348856572464667.33679335945688 6.67651596604489 6.84469093206041 P P P 7.89364787768285 7.58158562589813 7.38728943797732 P P P LNCV6_138404_PI430048170 mRNA
TCCTGTCTCCCTAGAGGTACTAGTATCTAGAGTTTACCCAGAAAATTTTATGATTGTAAC NM_001079519 RefSeq chr14 + 35044906 35083383 FAM177A1 283635 "family with sequence similarity 177, member A1, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145214_PI430048170 0.47713831399969 1.53879436075927 1.12266885396428 2.96737629516164 2.5821409577496 A P A 2.01143993847488 2.33804649281577 0.37986028246594 A A A LNCV6_145214_PI430048170 mRNA
GCTCATGTGCAAGCTCATCGTGGCTATCGACCAGTACAACACCTTCTCCAGCCTCTACTT NM_005285 RefSeq chr8 + 52939907 52940894 NPBWR1 2831 neuropeptides B/W receptor 1 GO:0005515|GO:0043005|GO:0005886|GO:0019222|GO:0007268|GO:0038003|GO:0008188|GO:0004985|GO:0007186|GO:0042923|GO:0005887|GO:0007187|GO:0007218|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128387_PI430048170 0.0894653929967596 1.06352199745906 0.460609426115119 0.5446706776421490.520348320298199 A A A 0.3634856596967880.426415413405753 0.468537094419834 A A A LNCV6_128387_PI430048170 mRNA
CATGTTAATCATTTTCCTAAGCTGTCCTTTTGAGGCTTAGTCAGTTTATTGGGAAAATGT NM_006636 RefSeq chr2 + 74198562 74215297 MTHFD2 10797 "methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase, transcript variant 1" GO:0000287|GO:0004329|GO:0004477|GO:0005615|GO:0005829|GO:0005739|GO:0004488|GO:0004487|GO:0042301|GO:0046653|GO:0009396|GO:0006730|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135071_PI430048170 0.0894742800755936 0.9271674114775930.290343675171167 0.2916748659496230.298882404609279 A A A 0.46720416963929 0.390765255837871 0.347692412518843 A A A LNCV6_135071_PI430048170 mRNA
GGGGAGTTGATAGTCTCATAAAACTAATTTGGCTTCAAGTTTCATGAATCTGTAACTAGA NM_013372 RefSeq chr15_KI270905v1_alt + 4932597 4949251 GREM1 26585 "gremlin 1, DAN family BMP antagonist, transcript variant 1" GO:0005515|GO:0030308|GO:0001658|GO:0033689|GO:0005615|GO:0060676|GO:0051973|GO:0016015|GO:0030297|GO:0007171|GO:0030199|GO:0090191|GO:0048018|GO:0009986|GO:0090291|GO:0030502|GO:0005125|GO:2000727|GO:0072331|GO:1900155|GO:0043184|GO:1900158|GO:0060173|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136454_PI430048170 0.0373396477649962 0.5680039696478383.92954027138135 3.40299658928375 4.05992081074705 P P P 4.79055146447966 4.79772947681092 4.2722549076982 P P P LNCV6_136454_PI430048170 mRNA
GGGCAAAGGGAAAAAATGATAAATCCTCTGTAATCACAAACCCCAATTTCGTTTTGTTTA NM_015323 RefSeq chr6 + 96521825 96555275 UFL1 23376 UFM1-specific ligase 1

GO:0005515|GO:0071568|GO:0034976|GO:0008284|GO:0005783|GO:0071569|GO:0016874|GO:0005634|GO:0032088|GO:0032434|GO:0001649|GO:0032880|GO:0005737|GO:0016020|GO:0033146|GO:0005789|GO:0005654|GO:0031397 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142440_PI430048170 0.4705751380891310.8342901371357322.48459849964389
2.06537125312477 1.12890979155516 A A A 2.11367872079425 2.46014286681321 2.1749959152459
A P A LNCV6_142440_PI430048170 mRNA
TGTCGTCAAAAGACTTGCTCTTGCCGCCTCTACGAGCTGCTGCACGGCGCGGGCAATCAC NM_001524RefSeq chr17
- 42184059 42185452 HCRT 3060 hypocretin (orexin) neuropeptide precursor
GO:0005791|GO:0048471|GO:0030054|GO:0051928|GO:0060079|GO:0043267|GO:0046928|GO:0007200|GO:0007268|GO:0005576|GO:0051970|GO:0051971|GO:0007204|GO:0007205|GO:0008021|GO:0031771|GO:0031772|GO:0007218|GO:0042755|GO:0008156|GO:0030141 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88342_PI430048170 0.00476791481707218 0.4134864876734623.67241289513706
3.13166734561754 3.50183474392655 P P P 4.57953830292498 4.68288000597836 4.8988255507407
P P P LNCV6_88342_PI430048170 mRNA
ACAGTTTCTTGTTAAGTTTCAGCCAAGTCTGTGACAATCTCACCAAATAAGAATGAAATG NM_014911RefSeq chr2
- 69457994 69643845 AAK1 22848 AP2 associated kinase 1
GO:0045747|GO:0005515|GO:0035612|GO:0030136|GO:0050821|GO:0005112|GO:0005524|GO:0006897|GO:0032880|GO:0005905|GO:0046777|GO:0004674|GO:0043195|GO:2000369|GO:0006468|GO:0031252|GO:0019897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140139_PI430048170 0.2570197643298980.89832211938524 8.66946684843776
8.75364709736643 8.56723987234575 P P P 8.73120564771238 9.00280582882576
8.70740796889741 P P P LNCV6_140139_PI430048170 mRNA
GCTGCTTAAGCTCCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAGC NM_030968RefSeq chr17
+ 79024075 79049788 C1QTNF1 114897 "C1q and tumor necrosis factor related protein 1, transcript variant 1"
GO:0005515|GO:0010544|GO:0051897|GO:0005581|GO:0005518|GO:0090331|GO:2000860|GO:0005615|GO:0007204|GO:0010906|GO:0010628|GO:0070208|GO:0005887|GO:0051260|GO:0043410 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134999_PI430048170 0.1116712674863881.21201064466726 6.31192867655487
6.53321901110988 6.35127375373306 P P P 5.92661128729959 6.10683153805939
6.31441300339015 P P P LNCV6_134999_PI430048170 mRNA
CCTGAGAGCAGTATGAGGCCTGCAAGAAAGTGATCATATAATTGTATCTTCACTTTCTTT NM_006735RefSeq chr7
- 27100353 27102775 HOXA2 3199 homeobox A2
GO:0003700|GO:0007379|GO:0071300|GO:0001709|GO:0021658|GO:0021568|GO:0048703|GO:0000122|GO:0009953|GO:0009952|GO:0006351|GO:0043565|GO:0008045|GO:0045668|GO:0045665|GO:0002076|GO:0045944|GO:0035284|GO:0042474|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144992_PI430048170 0.1127682691515810.6806444649365316.21710037007491
6.51981353226767 6.36124108177155 P P P 7.3048944500983 6.76519047400917
6.61471028575648 P P P LNCV6_144992_PI430048170 mRNA
CACCCCATTGTCTAATCTGTAGAAGCTAATAAATAATCATCCCTCCTTGCCTAGCATAAA NM_001185RefSeq chr7
- 99966726 99976112 AZGP1 563 "alpha-2-glycoprotein 1, zinc-binding"
GO:0002474|GO:0008285|GO:0005886|GO:0042612|GO:0004540|GO:0005576|GO:0005634|GO:0008320|GO:0003823|GO:0005615|GO:0006955|GO:0001948|GO:0019882|GO:0001895|GO:0001916|GO:0042605|GO:0007155|GO:0071806|GO:0001580|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68601_PI430048170 0.5179185783171221.04427608350414 0.2866110902083480.297299470328936
0.516798663992537 A A A 0.3213794202043720.2782924497639020.324955230428298 A A A
LNCV6_68601_PI430048170 mRNA
AAAGGACTTTCTTCCCCGAAACATGGATTTGGCATTGTCTCAACATCAGTGACCCATCTG NM_015692RefSeq chr19
- 16892950 17026815 CPAMD8 27151 "C3 and PZP-like, alpha-2-macroglobulin domain containing 8"

GO:0010951|GO:0005886|GO:0004867|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129762_PI430048170 0.226739497231571 0.482381108028521 0.347515937035324
0.278901405230329 0.768526648488053 A A A 0.346260862780771 1.61494183437858
2.12104817906254 A A A LNCV6_129762_PI430048170 mRNA
GCTGCTTCTCAAAGAGTCTGATACAGGGTAATTTCATACAATATTTGATGTTGTTAAAGC NM_147188 RefSeq chr15
+ 75903858 75935267 FBXO22 26263 "F-box protein 22, transcript variant 1"
GO:0000209|GO:0006511|GO:2000060|GO:0030018|GO:0004842|GO:0048742|GO:0032436|GO:0005634|GO:0006
464|GO:0009267|GO:0006913 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132564_PI430048170 0.554108173562526 0.978559170774645 0.253192186429765
0.264858882090191 0.390851633039748 A A A 0.374548205666134 0.315436020587747
0.316000055570998 A A A LNCV6_132564_PI430048170 mRNA
ATTTATGGGGTGAGGACCAAACAGATTCGAGAACGAGTGCTCTATGTTTTTACTAAAAAA NM_001001916 RefSeq
chr11 + 5046525 5047461 OR52J3 NA "olfactory receptor, family 52, subfamily J, member 3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138199_PI430048170 0.320442244140948 1.18841805637897 3.10998898953064
2.79250212988485 2.83578151520117 P A P 2.89836651456269 2.24432174063758
2.78831086046572 P A P LNCV6_138199_PI430048170 mRNA
GGTGGGGACGGGGGTAACATTTGCCTATCAGCAGAGCTGGGCTTTTATTTAATTTTTCTT NM_032420 RefSeq chr5
- 141853110 141878410 PCDH1 5097 "protocadherin 1, transcript variant 2"
GO:0005886|GO:0005911|GO:0005887|GO:0005509|GO:0007267|GO:0007156|GO:0007399 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_102994_PI430048170 0.571006396170405 0.968973595886773 4.96822587354363
5.20913730281279 5.02324078627131 P P P 5.09527281028197 5.13009591828809
5.12260156233406 P P P LNCV6_102994_PI430048170 mRNA
TGATGCTGTGAGATTTTATCCCTGGACCATTGATAATAAATACTATTCAGCAGACATCAA NM_001271886 RefSeq
chr15 - 67200674 67254736 AAGAB 79719 "alpha- and gamma-adaptin binding protein, transcript
variant 3" GO:0005737|GO:0005654|GO:0015031|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145135_PI430048170 0.013683583758296 0.49172509669488 3.24845018056845
3.32672105284249 3.36838949297574 P P P 4.10347372047732 4.29708867775735
4.57802220001657 P P P LNCV6_145135_PI430048170 mRNA
GTTTCTTTCTATCCAGGGTTTCTCTTGGGATACTCATATGGTATATTACTGGCTTATATT NM_203390 RefSeq chr8 -
93731500 93740996 RBM12B 389677 RNA binding motif protein 12B GO:0005515|GO:0000166 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116005_PI430048170 0.195864248077028 0.964324828313759 0.429741193175936
0.390141022257664 0.392125508674307 A A A 0.489122516487401 0.478425159432841
0.400417699987352 A A A LNCV6_116005_PI430048170 mRNA
ATCAACATTGCTGTGCTCCATAGTTTCCAAAGCAGAATGTGACCATCATGGACCACCACT NM_000625 RefSeq chr17
- 27756765 27800529 NOS2 4843 "nitric oxide synthase 2, inducible"
GO:0050661|GO:0005515|GO:0005516|GO:0048471|GO:0007263|GO:0051712|GO:0010181|GO:0050660|GO:0006
801|GO:0005634|GO:0045776|GO:0043457|GO:0042803|GO:0005829|GO:0006809|GO:0005622|GO:0009617|GO:0
005737|GO:0006954|GO:0045909|GO:0042127|GO:0006527|GO:0090382|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_110000_PI430048170 0.101664286731946 0.900612825779847 8.33953686548932
8.26469850928276 8.44424775744895 P P P 8.44751183725079 8.4565406014572
8.59814824229424 P P P LNCV6_110000_PI430048170 mRNA
CAGAGAGGTGACAGAACTTATTAAAGTGGATAAAGTGAAAATTGTAGCCTGTGATGGTAA NM_004492 RefSeq chr15
- 59638061 59657538 GTF2A2 2958 "general transcription factor IIA, 2, 12kDa"
GO:0001103|GO:0005515|GO:0010467|GO:0006368|GO:0006367|GO:0030054|GO:0046982|GO:0006366|GO:0003

713|GO:0042803|GO:0051091|GO:0045944|GO:0016032|GO:0017025|GO:0005654|GO:0005672|GO:0051123|GO:0
008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138133_PI430048170 0.6471490057028531.00687475148074 0.341206054422314
0.3222031329053170.281566094663832A A A 0.30988393192573 0.313813645187747
0.292174884922298A A A LNCV6_138133_PI430048170 mRNA
ATACTTCAGCTGTTTGTTCCTGGGAGAATTCTGAGCACAGATTCCAGAGGTCACAGTAAG NM_005972RefSeq chr10
- 46461098 46465881 NPY4R 5540 "neuropeptide Y receptor Y4, transcript variant 1"
GO:0042277|GO:0007631|GO:0007186|GO:0005886|GO:0007218|GO:0005887|GO:0004930|GO:0008015|GO:0007
586|GO:0001602|GO:0001601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130017_PI430048170 0.3056857231849511.35422001235912 1.90690713841681
1.82467628610623 1.68872897830163 A A A 1.72061023964358 0.503122601926911
1.60992150221651 A A A LNCV6_130017_PI430048170 mRNA
TGAGTTTATCAGCTGACTGCAAATTATTCTGCAATTATGCACCTCCCTTGTGTATACATA NM_001170798 RefSeq
chr12 - 16188484 16277685 SLC15A5 NA "solute carrier family 15, member 5" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_68016_PI430048170 0.00177353440144009 1.42337372473074 14.348153423405
14.4804776169622 14.4189713867499 P P P 14.006845867083 13.8636723252512
13.8467556108743 P P P LNCV6_68016_PI430048170 mRNA
AGAACAGGGTCCAGAACATGGCTCTCTATGCTGACGTCGGTGGAAAACAATTCCCTGTCA NM_001204527 RefSeq
chrX + 153794174 153798512 SSR4 6748 "signal sequence receptor, delta, transcript variant 3"
GO:0010467|GO:0005784|GO:0006614|GO:0016021|GO:0044267|GO:0006412|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138212_PI430048170 0.4805121886545431.22322807556522 0.38750297984777
1.23414484358076 0.424509728355576A A A 0.2951263325613710.685021702764401
0.327690879902707A A A LNCV6_138212_PI430048170 mRNA
CTGGAAAACAACCATGTCATTGACACCTATTCTAGGATTTTATTCCCCATTGTGTATATT NM_001105580 RefSeq
chr3 - 97986682 98035304 GABRR3200959 "gamma-aminobutyric acid (GABA) A receptor, rho 3
(gene/pseudogene), transcript variant 1"
GO:0005230|GO:0030054|GO:0005886|GO:0004890|GO:0019904|GO:0034707|GO:0007268|GO:0007214|GO:0005
575|GO:0005254|GO:0055085|GO:0034220|GO:0045211 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139332_PI430048170 0.5540572452096875.42638209283409 4.75720321646782
0.3130238764183150.431216790797476P A A 1.37166395946605 0.71431776968849
0.301834844241573A A A LNCV6_139332_PI430048170 mRNA
GCCTCCATTCTTCTGGGAAACACAAAGCAATAATAAAAGGAAGTGTTAGACAATGTAAAA NM_031313RefSeq chr2
+ 232406841 232410714 ALPPL2 251 "alkaline phosphatase, placental-like 2"
GO:0005886|GO:0004035|GO:0016311|GO:0031225|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132142_PI430048170 0.4398571549039130.8890109574982630.306518670127464
0.3143342646433650.406827610670301A A A 0.8115236406717750.31315177842416
0.360189606687308A A A LNCV6_132142_PI430048170 mRNA
GAACTAGATTCTCCTCTGAGAACCAGAGAAGACCATTTCATAGTTGGATTCCTGGAGACA NM_173799RefSeq chr3
+ 114293985 114310288 TIGIT 201633 T cell immunoreceptor with Ig and ITIM domains
GO:0005515|GO:0032733|GO:0009986|GO:0005886|GO:0032695|GO:0050868|GO:0005102|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126745_PI430048170 0.4691757232690280.7971272903264910.324693820065393
0.3111956720281110.267781369905601A A A 0.2633616000158720.271478605814102
1.15749617962458 A A A LNCV6_126745_PI430048170 mRNA
CCTCTCAAAATAGATTGTAATGTAATATTTTTCTCACCCATTTTGCTGAAGGCTACCAAG NM_152723RefSeq chr11
- 85683843 85686277 CCDC89 220388 coiled-coil domain containing 89 GO:0005737|GO:0005634

. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126638_PI430048170 0.4927469597128081.12384820965254 0.359392787721082
0.85835279771522 0.306730363912933A A A 0.3575444228251990.378281883521301
0.349646051118701A A A LNCV6_126638_PI430048170 mRNA
CCTAGTGGAAAAGGGGAAGACTAATGTTTTCAAATAAACAAACAGAAACCTAACAGAACT NM_001042537 RefSeq
chrX + 135985426 136047269 SLC9A6 10479 "solute carrier family 9, subfamily A (NHE6, cation proton antiporter 6), member 6, transcript variant 1"
GO:0015385|GO:0005886|GO:0045202|GO:0048675|GO:0031547|GO:0030425|GO:0006885|GO:0043231|GO:0005739|GO:0006810|GO:0035725|GO:0043679|GO:0060996|GO:0006811|GO:0005770|GO:0051386|GO:0031410|GO:0055085|GO:0044308|GO:0050808|GO:0031901|GO:0048812|GO:0005789|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_82930_PI430048170 0.0259896511346978 0.6998117569722294.68594790183672
4.34398608733434 4.37556531081517 P P P 4.95333695286713 5.08789855421494
4.92935444700558 P P P LNCV6_82930_PI430048170 mRNA
AGAAAGTGAACTTGAGTAGCATTAGGGCCATGCTGAATAGCAATGATGTCAGCGAGTACC NM_133368RefSeq chr16
+ 57186283 57240475 RSPRY1 89970 ring finger and SPRY domain containing 1
GO:0008270|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140815_PI430048170 0.2933907940510297.7812924020633 4.8049645096396
0.6325688232103181.377527573163 P A A 0.56115112039186 0.404633590493646
0.407474760905269A A A LNCV6_140815_PI430048170 mRNA
CTGTCTGTATATCAAGACTGAATCCTGACCCTCTAAATAAACAAAGTCTCTAAGCACAAA NM_001001480 RefSeq
chr11_KI270903v1_alt + 106538 107617 KRTAP5-5 NA keratin associated protein 5-5 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_61577_PI430048170 0.4726613941954771.28353715380131 0.2752825044156130.434550125407324
1.31708762857326 A A A 0.4773903140794820.3676524010275020.327196151149317A A A
LNCV6_61577_PI430048170 mRNA
TGAAAAGTCTGAGATCCAGCTCAACGTAAAGGAGCTAAAAAGGAAACTGGAGAGGGCCAA NM_001271664
RefSeq chr15_KI270851v1_alt + 103078 112828 GOLGA6L22NA golgin A6 family-like 22 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141123_PI430048170 0.0908393803434005 1.01665255406248 0.315099708618613
0.3033436805196140.33249016452496 A A A 0.3033520591867290.293629343609185
0.28254603366546 A A A LNCV6_141123_PI430048170 mRNA
CAGCATGTTCATTTTGAACTGTTTACCTCCCATGAAATAAAAAGTCTCTTGACTCTGAAA NM_001243746 RefSeq
chr17 - 68535115 68600954 FAM20A 54757 "family with sequence similarity 20, member A, transcript variant 3" GO:0005794|GO:0070166|GO:0005623|GO:0070062|GO:0055074 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_130047_PI430048170 0.1906383260939851.28770469527969 5.67208575005637
6.09922018477033 5.62746647201451 P P P 5.54997231838333 5.66123326175609
5.07765816984099 P P P LNCV6_130047_PI430048170 mRNA
CAGAAAGTCTATCCTATGGCAAGTCTGACCTCTCCTGGCAATGCTCAGTTCTGATTTTTT NM_001080426 RefSeq
chr1 + 167094849 167129165 DUSP2792235 dual specificity phosphatase 27 (putative)
GO:0006470|GO:0008138 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138518_PI430048170 0.3871366356845841.14011026582376 0.714655239831949
1.05595151726813 0.63736881088112 A A A 0.5243960526167330.904333156968545
0.397608399355503A A A LNCV6_138518_PI430048170 mRNA
ACAGCTGAATAGCTTTGCGGAGGAGTTTAATAGTTACACATTCATGCTAATATACATTTC NM_015429RefSeq chr3
- 100749334 100993490 ABI3BP 25890 "ABI family, member 3 (NESH) binding protein"
GO:0031012|GO:0030198|GO:0010811|GO:0005518|GO:0005614|GO:0008201|GO:0005615 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_95248_PI430048170 0.6503884447298670.9259302942845085.20801164009246 5.44863642179445
5.77435010058106 P P P 5.30762615358977 5.59767036185781 5.86213258943618 P P P
LNCV6_95248_PI430048170 mRNA
CTGATCAAGAGAAGCTTTTTATCCAGAAGTTACGTCAGTGTTGCGTCCTCTTTGACTTTG NM_001161725 RefSeq
chr14 + 101761797 101927991 PPP2R5C 5527 "protein phosphatase 2, regulatory subunit B', gamma,
transcript variant 5"
GO:0005515|GO:0042771|GO:0007165|GO:0050790|GO:0008285|GO:0008601|GO:0000159|GO:0043161|GO:0005
634|GO:0000775|GO:0006977 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137168_PI430048170 0.0210441792970967 1.5811570320706 5.34673591916276
4.87539886473698 5.11690664985974 P P P 4.66343077616576 4.33816373624778
4.37011021334447 P P P LNCV6_137168_PI430048170 mRNA
CCAAAGAAGCTGTACTCCGGGGGGTCTCTTCTGAATAAAGCAATTAGCAAATCATGTAAA NM_000300RefSeq chr1
- 19975430 19980439 PLA2G2A 5320 "phospholipase A2, group IIA (platelets, synovial fluid),
transcript variant 1"
GO:0050830|GO:0005783|GO:0050680|GO:0044281|GO:0005615|GO:0005739|GO:0005543|GO:0004623|GO:0047
498|GO:0030141|GO:0006654|GO:0035019|GO:0070062|GO:0010744|GO:0036149|GO:0005509|GO:0036148|GO:0
005576|GO:0016042|GO:0036150|GO:0034374|GO:0050729|GO:0005789|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_102473_PI430048170 0.4805604978263311.05592453835777 5.63898223656253
5.68543323850394 5.41269967998841 P P P 5.54482243525333 5.53416232228353
5.43455773122027 P P P LNCV6_102473_PI430048170 mRNA
CAAAAATGTCACAGGGATCCTGTGGAACCTTTCATCCAGCGACCACCTGAAGGACCGCCT NM_007183RefSeq chr11
+ 394182 404908 PKP3 11187 "plakophilin 3, transcript variant 1"
GO:0030057|GO:0016337|GO:0005886|GO:0005911|GO:0005634|GO:0002159|GO:0090002|GO:0050839 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133189_PI430048170 0.0130736488563273 0.53402791651046 4.98287876277358
4.45239468037723 4.54678047990539 P P P 5.41417275024701 5.80594030172348
5.50437822811097 P P P LNCV6_133189_PI430048170 mRNA
AGGCCTTTGTATGTGTGTACATATATATATATATAACAAAACATCAGCCTTGGGTGGTGT NM_001620RefSeq chr11
- 62515901 62546860 AHNAK 79026 "AHNAK nucleoprotein, transcript variant 1"
GO:0005515|GO:0005886|GO:0044291|GO:0030315|GO:0005634|GO:0005765|GO:0015629|GO:0051259|GO:0031
982|GO:0005829|GO:0042383|GO:0044548|GO:0005737|GO:0016020|GO:0043034|GO:0045121|GO:0043484|GO:0
005925|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140783_PI430048170 0.00588448324631989 0.52309456042642 6.9306387894539
6.79367062805878 6.993988549173 P P P 7.60549149417105 7.91353949996109
7.98368073450742 P P P LNCV6_140783_PI430048170 mRNA
TCATCCAACTTCCATTTTTCACTTTTTACATGATTACTCAATCCTTGGGGCTGTCCATGT NM_018401RefSeq chr4 +
5051516 5501001 STK32B 55351 serine/threonine kinase 32B
GO:0004674|GO:0006468|GO:0005524|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139908_PI430048170 0.19569480754471 0.9098783505874419.51420719752472
9.75943982977275 9.64754156190966 P P P 9.86771240982021 9.77463740242204
9.69269770245991 P P P LNCV6_139908_PI430048170 mRNA
TCATTGTAATGTTCATTTCCCACCCCTGCTCCAGCCTCGATTTGGTTTTATTTTGAGCCC NM_006129RefSeq chr8 +
22165139 22212326 BMP1 649 "bone morphogenetic protein 1, transcript variant 3"
GO:0005794|GO:0031988|GO:0005509|GO:0005578|GO:0005576|GO:0007275|GO:0044281|GO:0005125|GO:0005
615|GO:0030154|GO:0001501|GO:0022617|GO:0001503|GO:0030198|GO:0001502|GO:0061036|GO:0042157|GO:0
006508|GO:0008270|GO:0008233|GO:0004222|GO:0008083|GO:0008237 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_135264_PI430048170 0.7616143986105161.11071187919102 3.05343072189759

3.34299904817635 4.11299364546491 P P P 2.74059323069011 3.81066040006156 3.5202003686462
P P P LNCV6_135264_PI430048170 mRNA
GAGAAATGTCGGTTGTTCCTAATGGCAAACTACTTTAGCTGGGAAAATTCATTTCAACTT NM_013341 RefSeq chr2
- 174072446 174248637 OLA1 29789 "Obg-like ATPase 1, transcript variant 1"
GO:0005515|GO:0005813|GO:0006200|GO:0005730|GO:0005525|GO:0005524|GO:0046872|GO:0005737|GO:0016
020|GO:0043022|GO:0043023|GO:0016887|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134797_PI430048170 0.455033114769008 0.72444207245369 0.372051478602695
0.2521165804769680.298345687994364 A A A 0.2738642627167641.43586297962164
0.279096849615514 A A A LNCV6_134797_PI430048170 mRNA
ATTCCTACAGCCATTTTTCACTCCCAACAGCTGTTTTTATTTTACCTCTTTGGCCTAAAG NM_003719 RefSeq chr5 +
77210880 77428255 PDE8B 8622 "phosphodiesterase 8B, transcript variant 1"
GO:0009187|GO:0004115|GO:0004114|GO:0005575|GO:0046872|GO:0005829|GO:0000160|GO:0008542|GO:0050
885|GO:0090032|GO:0001662|GO:0004871|GO:0035106|GO:0046676|GO:0006198 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131039_PI430048170 0.6419193055728060.9705992367272790.538403075360127
0.4767399188374850.266074665516554 A A A 0.4067967781137430.529455001014932
0.485366885381053 A A A LNCV6_131039_PI430048170 mRNA
TTTGCACTGATATATCATGAGTGAATAAATGTCTTGCCTACTCACGTCTCATCCAAAAAA NM_000459 RefSeq chr9
+ 27109140 27230178 TEK 7010 "TEK tyrosine kinase, endothelial, transcript variant 1"
GO:0005515|GO:0043627|GO:2000251|GO:0050900|GO:0051591|GO:0051259|GO:0007507|GO:0016337|GO:0046
777|GO:0009925|GO:0043552|GO:0034446|GO:0070374|GO:0009986|GO:0014068|GO:0018108|GO:0060347|GO:0
010595|GO:0001958|GO:0005887|GO:0042307|GO:0045121|GO:0005925|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130987_PI430048170 0.0105431194760017 0.22856924516549 0.315521385706221
0.3350479882974931.07858376303052 A A A 2.64845447512859 2.77551408252058
2.82499223229719 A P P LNCV6_130987_PI430048170 mRNA
CTCATGGTGAATTGCTTCAGTACCATGGTTTTGTTTTTTCCTTTTGAAAAGTTGGTCTAT NM_001286259 RefSeq chr6
- 143422831 143442677 ADAT2 134637 "adenosine deaminase, tRNA-specific 2, transcript variant 2"
GO:0008270|GO:0002100|GO:0008251 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81445_PI430048170 0.000390043133489911 0.6074205331075197.69145995317466
7.63128754287136 7.75352988422153 P P P 8.38520372866607 8.40482324072963
8.44587165297965 P P P LNCV6_81445_PI430048170 mRNA
CAGCTGTAACTACTGTTTCAGAATGTTGCTGCTGCATACTTTTGTCATGTCAGCCAGCCA NM_144653 RefSeq chr9
- 136006536 136095285 NACC2 138151 "NACC family member 2, BEN and BTB (POZ) domain containing"
GO:0005515|GO:0000790|GO:0008284|GO:0016575|GO:0008285|GO:0042826|GO:0006366|GO:0005634|GO:0000
978|GO:0042803|GO:0016604|GO:0001078|GO:0010608|GO:0001076|GO:0016581|GO:0034629|GO:1900477|GO:0
051260|GO:0004407|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127483_PI430048170 0.00855274981828812 0.4992451085246874.12315367502371
3.79991326815264 4.1714526476031 P P P 4.9744479368045 5.06142772017416
5.09021194895311 P P P LNCV6_127483_PI430048170 mRNA
AACAATTGGTAGAGAGCCACAGGTAGAAAAGATACTCCCAGCTGACAGGGTGATAAAAGG NM_014758 RefSeq
chr11 - 130875870 130916487 SNX19 399979 "sorting nexin 19, transcript variant 1"
GO:0005515|GO:0005737|GO:0002062|GO:0035091|GO:0015031|GO:0030073|GO:0030659 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129721_PI430048170 0.0139156935245850.2620806155996590.272618583616886
1.21320997937012 0.30032476024602 A A A 2.15180909201986 2.20374883785813
3.18648957046995 A A P LNCV6_129721_PI430048170 mRNA
GCTGGTTTTTTCATACTATTGGTTGTCTCTGTAATGCGAGCAGCTTTTGATCTATTAATT NM_001256165 RefSeq chr1
- 165724290 165768922 TMCO1 54499 "transmembrane and coiled-coil domains 1, transcript variant 3"

GO:0000139|GO:0005783|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79052_PI430048170 0.27956426890786 0.5710331394045272.21494624431902 2.30936548754353
2.58615439568968 A A A 3.60794285312156 3.4301140710384 2.12265764581214 P P A
LNCV6_79052_PI430048170 mRNA
GGTGGTCATTGCCTTTCTCCATTGTCTAGTAGACATGTCTAAAGTTCAAACTTTATAGGA NM_012252RefSeq chr7
- 115935147 116030813 TFEC 22797 "transcription factor EC, transcript variant 1"
GO:0034605|GO:0006355|GO:0005737|GO:0003700|GO:0003714|GO:0003713|GO:0046983|GO:0005654|GO:0003
677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136379_PI430048170 0.6580548620057930.9479408356348088.68040629385624 8.1211622194944
8.40333362845234 P P P 8.3870388638252 8.42117069124144 8.66577055538542 P P P
LNCV6_136379_PI430048170 mRNA
CCCACAGTCCAGCCTAACTATGGGACAGCTTTACGAGAAGGAAAAAGATGAAGATGGATTNM_007285RefSeq chr16
+ 75566350 75577881 GABARAPL211345 GABA(A) receptor-associated protein-like 2
GO:0008017|GO:0006995|GO:0005515|GO:0005776|GO:0005794|GO:0000422|GO:0000421|GO:0048487|GO:0006
914|GO:0006891|GO:0050811|GO:0032781|GO:0031410|GO:0000407|GO:0015031|GO:0005829|GO:0005622|GO:0
005737|GO:0000139|GO:0000149|GO:0051117|GO:0061025|GO:0000045|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140993_PI430048170 0.2456675616037461.06985372083258 0.601724562009812
0.7740463826671540.5925302316281 A A A 0.5361043056993910.576814114041609
0.570153795233257A A A LNCV6_140993_PI430048170 mRNA
ATTTTCCATTGGCGCAAAATCAAAAACCCCAAAGAATCGGGAGAAAGGGCATTCCCGAAGNM_033482RefSeq chr6
- 27309062 27312232 POM121L2 NA POM121 transmembrane nucleoporin-like 2 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142839_PI430048170 0.3980254536170740.5618048997122611.91516960141841
1.67051738495559 1.52340329269542 A A A 1.15581301289355 2.81635025948347
3.03992809129874 A P P LNCV6_142839_PI430048170 mRNA
AGCATTTCCTAACCTGCTCTGTGAAAAACAAAGAAATAAAACTTAGTGCTCTCTTTCTCT NM_004531RefSeq chr5
- 53095678 53109772 MOCS2 4338 "molybdenum cofactor synthesis 2, transcript variant 3"
GO:0006767|GO:0005634|GO:0044281|GO:0005829|GO:0042802|GO:0030366|GO:0032324|GO:0005737|GO:0000
166|GO:0006766|GO:0006777|GO:0019008|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137863_PI430048170 0.00505973313516532 0.4100788994817043.74993359043238
3.53038421625582 3.39689706927032 P P P 4.61325552247991 4.73062854472445
5.15563139104249 P P P LNCV6_137863_PI430048170 mRNA
GACTTGTAATAAACCAAGCTGTACAATTTAGTTTATAATAGCAGTATCTGAGCTGCTCCA NM_014688RefSeq chr10
- 11460509 11611789 USP6NL 9712 "USP6 N-terminal like, transcript variant 1"
GO:0035526|GO:0017137|GO:0005794|GO:0005886|GO:0033126|GO:0007030|GO:0032851|GO:0016023|GO:0048
227|GO:0031410|GO:0019068|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58617_PI430048170 0.2348228374593990.9514834251339959.06657660086866 8.92438853832915
9.01223525197497 P P P 9.10151220128935 9.10405166619528 9.01465614855621 P P P
LNCV6_58617_PI430048170 mRNA
TAAGAGACTCATCAGATTCTGAGCTGCTGCGGGATATTTTGCAGAAGACGTGCTGTATTG NM_018172RefSeq chr11
+ 71787510 71801234 FAM86C1 55199 "family with sequence similarity 86, member C1, transcript
variant 1" GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130929_PI430048170 0.1119038801527250.5467790350988564.5700603046418
3.47216410356784 3.42661037855687 P P P 4.80215564088272 4.98995884536471
4.56842648076766 P P P LNCV6_130929_PI430048170 mRNA
CCAAGTCTCCCAATATCCAATTTTAAAATGAAATGCATTTTGCTAGACAGTTAAACTGGC NM_000129RefSeq chr6
- 6144077 6320691 F13A1 2162 "coagulation factor XIII, A1 polypeptide"
GO:0018149|GO:0007596|GO:0003810|GO:0002576|GO:0030168|GO:0072562|GO:0031093|GO:0005576|GO:0046

872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128093_PI430048170 0.0819313944810715 0.5557588806487351.3577842246416
0.4583449038065081.39620023330456 A A A 2.07744924627643 2.18288151966535
1.61286578509552 A A A LNCV6_128093_PI430048170 mRNA
GTAGTTGAACATTTGGAAGACTTCTCCTTTTATCTCCTCACAATCTCTACAAACTAATCTNM_001261459 RefSeq chr9
- 92845030 92878038 ZNF484 83744 "zinc finger protein 484, transcript variant 4"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138496_PI430048170 0.3679085556422031.2332024404633 6.51642042768734
6.27207552189937 6.60575007980573 P P P 5.49994918353833 6.33451267906583
6.49063877127639 P P P LNCV6_138496_PI430048170 mRNA
GGGCCACGTTGTTGCAATTGTTTCAGTAGAACTGGTTTGATTTCTAAAATGTTCCTGTAA NM_031476RefSeq chr16
+ 84819980 84909510 CRISPLD2 83716 cysteine-rich secretory protein LCCL domain containing 2
GO:0031012|GO:0030133|GO:0060325|GO:0030324|GO:0030198|GO:0008201|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_103295_PI430048170 0.2701842622749371.22845856939723 2.05862336038553
2.48208496689931 2.40350119822961 A A A 1.61630107347741 2.11429316684883
2.27810625577532 A A A LNCV6_103295_PI430048170 mRNA
ACGAGTCCGGCCCTTTTATGCTGTCAAGTGCAACAGCAGCCCAGGTGTGCTGAAGGTTCT NM_052998RefSeq chr1
+ 33081112 33120531 AZIN2 113451 "antizyme inhibitor 2, transcript variant 1"
GO:0005802|GO:0005515|GO:0030133|GO:0042978|GO:0005801|GO:0030424|GO:0048471|GO:0005634|GO:0007
283|GO:0044281|GO:0003824|GO:0030425|GO:0005829|GO:0005739|GO:0015489|GO:0034641|GO:0006596|GO:0
033116|GO:0006595|GO:0043204|GO:0006591|GO:0042177|GO:0031410|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_62433_PI430048170 0.5049254056821940.7698124674584988.21939378277179 7.71298925367908
8.50601646688768 P P P 7.77966190880467 8.59270344548052 9.0394038288851 P P P
LNCV6_62433_PI430048170 mRNA
GAAGAGGAAAGCCTGAAGGAAAGACTCATCAAAAGCATATCCGTCTGTCAGAAAGAGCTG NM_003981RefSeq
chr15 - 90966037 90994651 PRC1 9055 "protein regulator of cytokinesis 1, transcript variant 1"
GO:0005515|GO:0008017|GO:0019901|GO:0005886|GO:0000022|GO:0005819|GO:0005634|GO:0042802|GO:0000
910|GO:0000922|GO:0005737|GO:0015630|GO:0005654|GO:0005876|GO:0019894 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133278_PI430048170 0.2171732363809740.7984195175111257.43821188625531
6.86290977547235 6.82054156952072 P P P 7.57022812989869 7.28722755256021
7.30669803664214 P P P LNCV6_133278_PI430048170 mRNA
CAGCAGTTCTGGTTCTCAAGAAAATCATCATAAATCAGACATGAAAATTCTAGCTCCAAA NM_001137610 RefSeq
chr8 - 12425614 12436343 FAM86B2 653333 "family with sequence similarity 86, member B2"
GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142846_PI430048170 0.00997114156375481 0.64820861406523710.0061818485688
9.93015252845237 10.2259647635122 P P P 10.5714236866998 10.5837746374969
10.8786704282024 P P P LNCV6_142846_PI430048170 mRNA
GAATGTGTGGTGAATGTAAAATACCTAGTTTACTTGCCAGTCTCTTGTGTAAATTACAGT NM_012399RefSeq chr22
- 27851668 27919306 PITPNB 23760 "phosphatidylinositol transfer protein, beta, transcript variant sp1"
GO:0006629|GO:0015914|GO:0000139|GO:0005789|GO:0044281|GO:0006644|GO:0001701|GO:0070062|GO:0046
474|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137151_PI430048170 0.1444880686329221.31696143499971 4.58009763504854
4.78492732423617 4.21693878656099 P P P 4.14548644168217 4.08826232535116
4.21015543633307 P P P LNCV6_137151_PI430048170 mRNA
TCTTATGAAGTCAGGTGACATTTCTCACTGTCACGTCCACAGCCTTTAATCGCAGGAGAA NM_000400RefSeq chr19

- 45351390 45370587 ERCC2 2068 "excision repair cross-complementation group 2, transcript variant 1"
GO:0005515|GO:0010467|GO:0006368|GO:0009650|GO:0006367|GO:0006366|GO:0006363|GO:0006362|GO:0006361|GO:0006360|GO:0009791|GO:0000439|GO:0030198|GO:0032508|GO:0006979|GO:0008094|GO:0019907|GO:0007568|GO:0005819|GO:0006370|GO:0001701|GO:0006281|GO:0006283|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_6295_PI430048170 0.1355000871145040.6867339606614298.91439146106281 8.25791689101556 8.08693119150867 P P P 9.16454545361318 9.08808469264689 8.73537318633882 P P P LNCV6_6295_PI430048170 mRNA
CTCTCCAGACCCCACCCCCAGATGCATTTATTAGAAATAATAAAGTTCTTTCTTAGCTAG NM_001204513 RefSeq chr7 + 5045820 5073223 RBAK-RBAKDN 100533952 RBAK-RBAKDN readthrough NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144273_PI430048170 0.8110225345316660.9604436650562060.437002366804439 0.4938133163277041.62185847071861 A A A 1.30986049992398 1.16660319528398 0.439539454385539A A A LNCV6_144273_PI430048170 mRNA
CTGTTCTGCTGCACCTGAATGCTTTCTGTTATCCTAATTCTTGTAAAATTAAATGAATCGNM_023036RefSeq chr17 + 74274246 74314884 DNAI2 64446 "dynein, axonemal, intermediate chain 2, transcript variant 1"
GO:0005515|GO:0042384|GO:0005930|GO:0008152|GO:0005874|GO:0005858|GO:0003777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134955_PI430048170 0.3657694933213641.10490603280346 9.07202431421436 9.05641201389704 8.94160769770435 P P P 8.6087717951871 9.04666289421467 8.95058816717699 P P P LNCV6_134955_PI430048170 mRNA
TGGGCTCATCACAAGGACACTTCCAGCTTGTGCAGACACCACCCTGCCATTGAGTCTGGA NM_001105198 RefSeq chr2 + 119679166 119682118 TMEM177 80775 "transmembrane protein 177, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137572_PI430048170 0.6328598189575470.8410568692032262.460250137693 2.08334602767589 0.464331598881095A A A 2.76229119174374 1.76908259260534 1.59892683227067 P A A LNCV6_137572_PI430048170 mRNA
TGTTAGTGCCAGTGATGTAGAACCTCATCACTTTGCCTCTGTGCTTTGCTTCTCTACCAA NM_001024679 RefSeq chr1 + 152719521 152720429 C1orf68 NA chromosome 1 open reading frame 68 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98177_PI430048170 0.3980347846727341.08557582365619 3.76692161272195 3.59773156441315 3.65768948506482 P P P 3.5063152093281 3.76642060026276 3.3710215968076 P P P LNCV6_98177_PI430048170 mRNA
CAGAGGCCCTATGGACAGCGATGACAGCCATGGATCTGTGCTAAGACTCAGCCAAGCCCTNM_018210RefSeq chr13 + 110615583 110639995 CARKD 55739 "carbohydrate kinase domain containing, transcript variant 1"
GO:0005739|GO:0008150|GO:0003674|GO:0047453|GO:0046496|GO:0005575|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144155_PI430048170 0.4739866973527761.1398767691854 3.14701055767337 2.88719971782097 2.66364656308235 A A A 2.97533190187654 2.27088391630493 2.83387378230243 P A P LNCV6_144155_PI430048170 mRNA
TGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCTCTGGTTCAAAAAA NM_144505RefSeq chr19 - 50996007 51001702 KLK8 11202 "kallikrein-related peptidase 8, transcript variant 2"
GO:0005515|GO:0008219|GO:0004252|GO:0009611|GO:0005615|GO:0043616|GO:0005737|GO:0050808|GO:0048681|GO:0050807|GO:0048812|GO:0006508|GO:0007613|GO:0031642 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134252_PI430048170 0.0185233187928095 3.16809513473539 4.96469373374074 5.96621922050318 5.80854761500113 P P P 4.51643282493874 3.65748513390961 3.55777705883746 P P P LNCV6_134252_PI430048170 mRNA

TAAATTGGAGATTCTCTACATTTCACTTGCAGTTTCCTGTTCTCCTCATTGCCTGCCTTC NM_080832 RefSeq chrX + 91434597 91438584 PABPC5 140886 "poly(A) binding protein, cytoplasmic 5" GO:0000166|GO:0005759|GO:0003723 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_143738_PI430048170 0.0274824290729031.18386373651916 8.99581872524388 9.09210795826728 9.04463778126706 P P P 8.81456671179335 8.88402552987697 8.69905126545761 P P P LNCV6_143738_PI430048170 mRNA
CTCTGTCTAGATTGGCTTTTTTAACATTCTCATTTTCCCAGGAGTTATCACTGTAAAAGT NM_080656 RefSeq chr5 - 134402064 134411907 CDKN2AIPNL 91368 CDKN2A interacting protein N-terminal like NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_136759_PI430048170 0.305442646182237 1.24654720077696 0.953217055238337 1.21205670456216 0.890323593016573 A A A 1.18011454169138 0.317409931585765 0.47160923633948 A A A LNCV6_136759_PI430048170 mRNA
TGCTACATTCAACCTCGTGACTTCATGATCCTGGGCCTGAGAACACAGGAATGATTCATA NM_015725 RefSeq chr19 + 10013248 10022278 RDH8 50700 retinol dehydrogenase 8 (all-trans) GO:0006694|GO:0005737|GO:0004303|GO:0007603|GO:0005887|GO:0006703|GO:0042572|GO:0052650|GO:0004745|GO:0007601|GO:0001523|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_13622_PI430048170 0.241942515771673 1.02004174078704 0.305589739285832 0.255836507149338 0.310940963282789 A A A 0.268585482368122 0.251613407221139 0.266860884414714 A A A LNCV6_13622_PI430048170 mRNA
GTGTAAGAGTATTATGGGAAGTAGAAATTCACTTCCTTAAATCCATCGTAAGATTGAGCC NM_001001664 RefSeq chr2 + 138501779 138573236 SPOPL 339745 speckle-type POZ protein-like GO:0016567|GO:0031463|GO:0043161|GO:0005634|GO:0031397 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_138823_PI430048170 0.127216987601029 0.962092727118532 0.393744572551836 0.409146686994379 0.332144654736489 A A A 0.428000312564531 0.451990011815313 0.423282879038516 A A A LNCV6_138823_PI430048170 mRNA
CTGTGGGCTGTAGTATGCCATCATTGTGACTGAATTTGTGCAATGGTTTCTTAATTTTTT NM_001269041 RefSeq chr20 - 57497167 57524867 CTCFL 140690 "CCCTC-binding factor (zinc finger protein)-like, transcript variant 3" GO:0005515|GO:0044212|GO:0016571|GO:0005634|GO:0000978|GO:0003677|GO:0046872|GO:0006351|GO:0043565|GO:0010628|GO:0042393|GO:0001077|GO:0005737|GO:0007049|GO:0045944|GO:0006349|GO:0045893|GO:0051569|GO:0043046. NA - . NA NA NA NA NA NA NA NA NA LNCV6_144119_PI430048170 0.982941086322115 1.00196303054142 12.3674351829112 12.1679558676845 12.2089943271248 P P P 12.1846920507419 12.3375202556777 12.2169262848217 P P P LNCV6_144119_PI430048170 mRNA
GTCATTGTGTATTAAATACTTGGAATAAATCAAGCAGGTCTCAACGCCTCCACTAAAAAA NM_000883 RefSeq chr7 - 128392276 128409982 IMPDH1 3614 "IMP (inosine 5'-monophosphate) dehydrogenase 1, transcript variant 1" GO:0009168|GO:0030054|GO:0003938|GO:0003723|GO:0055086|GO:0005634|GO:0044281|GO:0003676|GO:0003677|GO:0046872|GO:0005829|GO:0005737|GO:0006177|GO:0000166|GO:0006144|GO:0046651|GO:0005654|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_127206_PI430048170 0.857523530971736 1.04626292018123 1.56946208870084 3.22442619189875 3.27723363151564 A P P 2.76794461453885 2.96167413346933 2.68583992978515 A P P LNCV6_127206_PI430048170 mRNA
GCTTTTATGATATTTGTGTGCAATATCCCCTCTTCCATTGAGGATATTTGATGTAAAGGA NM_005909 RefSeq chr5 + 72107290 72209570 MAP1B 4131 microtubule-associated protein 1B GO:0005515|GO:0008017|GO:0032387|GO:0030054|GO:0005886|GO:0009987|GO:0001578|GO:0005875|GO:0005874|GO:0045773|GO:0014069|GO:0048675|GO:0016358|GO:0005829|GO:0005737|GO:0047497|GO:0043197|GO:0005198|GO:0061162. NA - . NA NA NA NA NA NA NA NA NA LNCV6_142034_PI430048170 0.704424465669417 1.07673542437485 4.70113528087466

5.16442594816118 4.54226878222229 P P P 4.51613757331561 4.99756557840726
4.60155182378776 P P P LNCV6_142034_PI430048170 mRNA
TGATGAGGAGGAGAAATTTCTCCTCTTCCTTCCCTGGCATAACATGCATTTTTGTGTTTC NM_001122770 RefSeq
chr1 + 173868354 173886636 ZBTB37 84614 "zinc finger and BTB domain containing 37, transcript
variant 1" GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_2829_PI430048170 0.6835153366432241.00276015675801 1.30850504429414 3.48207035578832
1.49558797970257 A P A 2.78815223935539 2.18461651375258 2.31375960550661 P A P
LNCV6_2829_PI430048170 mRNA
AACCTGCCAGGCCCGCAACCTAAATGCAGATTCAAACCCAGCAAAGAAAATTTGAATGAC NM_004498 RefSeq chr15
- 52756962 52790012 ONECUT1 3175 "one cut homeobox 1, transcript variant 1"
GO:0006355|GO:0030335|GO:0005634|GO:0048536|GO:0003677|GO:0048731|GO:0006351|GO:0030154|GO:0001
889|GO:0042384|GO:0001077|GO:0045165|GO:0007492|GO:0045944|GO:0031018|GO:0002064|GO:0030183|GO:0
001952|GO:0006006|GO:0030512 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136810_PI430048170 0.00254501939105731 0.3873336213148234.57860476197386
4.25597274199961 4.74359951952244 P P P 5.9843159521279 5.61152371378444
6.08706873366203 P P P LNCV6_136810_PI430048170 mRNA
CTGTTTCTAAGTGCCAAGCACAGAAAGCCGCTAAATAAAATCTTTGCAATTGTTTTCAAA NM_152380 RefSeq chr1
- 118883042 118989556 TBX15 6913 T-box 15
GO:0000976|GO:0003700|GO:0046982|GO:0001106|GO:0070722|GO:0000122|GO:0048701|GO:0042803|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143819_PI430048170 0.1526127834427071.06854118111609 0.515749283247091
0.6601884196302460.555253688792601 A A A 0.4257285540669590.494998203293143
0.525617899008537 A A A LNCV6_143819_PI430048170 mRNA
TCAGGCAATTGAAACATTTCTGTATAATACCAAGCATTGTTGCAGTATTGTCTGAAATGG NM_001039585 RefSeq
chr1 + 78491042 78540701 PTGFR 5737 "prostaglandin F receptor (FP), transcript variant 2"
GO:0043066|GO:0008284|GO:0005737|GO:0035584|GO:0007567|GO:0007186|GO:0005886|GO:0005887|GO:0071
799|GO:0032496|GO:0005576|GO:0004958 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136393_PI430048170 0.5845294734926291.34898614968801 0.277711452169506
0.304624720142803 1.63097782268202 A A A 0.383100226815974 0.654928728698069
0.300434805406524 A A A LNCV6_136393_PI430048170 mRNA
CCTGTCCCATGTGTTGTTCAGAGCTATTTTGTACTGATAATAAAATAGAGGCTATTCTTT NM_198464 RefSeq chr8
+ 10525545 10538823 PRSS55 NA "protease, serine, 55, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_106330_PI430048170 0.428835415123148 1.11582301178195 3.52428264264257
3.99497745136377 3.60400614781544 P P P 3.65248058645321 3.50304780305899
3.53424991845802 P P P LNCV6_106330_PI430048170 mRNA
AGAAAAATCCTCCAGAACTGCCACGACGACGCGGCCAAGTTCGTCCATCTGCTCATGAGC NM_013239 RefSeq
chrX_KI270913v1_alt - 6752 59448 PPP2R3B 28227 "protein phosphatase 2, regulatory subunit B", beta"
GO:0005515|GO:0008601|GO:0005509|GO:0000159|GO:0005634|GO:0000082|GO:0050790|GO:0006470|GO:0004
721|GO:0005654|GO:0007050|GO:0004722|GO:0000278 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133141_PI430048170 0.00144836437496818 0.383745628289764 7.46194962785294
7.07781516303871 7.42334355709861 P P P 8.46115171706326 8.75025805932117
8.89405595460585 P P P LNCV6_133141_PI430048170 mRNA
CTTGGAGTCTAGGTTGCCTTGTCTCTCCTATTTTTAAATAAGTGAAATTTGGGAGATTGT NM_023016 RefSeq chr2
+ 109614333 109618987 SOWAHC 65124 sosondowah ankyrin repeat domain family member C
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_20272_PI430048170 0.160167081924221 1.05478969910487 0.452231156976708

0.438440662576297 0.478080638704751 A A A 0.316556861453529 0.374784103877758
0.444001747298771 A A A LNCV6_20272_PI430048170 mRNA
ATTTTTGCTGTATCACAGGGTGGAAGACTGTTTGGTCCCAAGGGAATAATGGCTACAATC NM_001243523 RefSeq
chr7 + 137953347 137957966 LOC100130880 NA uncharacterized LOC100130880 NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_64547_PI430048170 0.340065746459762 1.52700460124977 0.475597000679074
1.68564403115095 1.78653495892563 A A A 0.571938226732099 1.29539292009088
0.41738789790083 A A A LNCV6_64547_PI430048170 mRNA
GGACAGGCTGTTCGTATTTGACCTATATTAAGTAATGTATAAGGTAGTGTTCAGAGTAAT NM_007138 RefSeq
chr19 + 20077993 20121168 ZNF90 7643 zinc finger protein 90
GO:0006355|GO:0003700|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_136394_PI430048170 0.497308212050038 0.719362747865328 0.319619109472085
0.318736480413731 0.498291296468391 A A A 1.56587001112618 0.278587697559104
0.331947288479543 A A A LNCV6_136394_PI430048170 mRNA
GTGGGAAGGTCACTTTCACTATGCTTGTGAACTAAATGCTGGCTAACAAGTGTCAAACCA NM_001080492 RefSeq
chr16 - 58279996 58295047 PRSS54 221191 "protease, serine, 54"
GO:0005737|GO:0004252|GO:0006508|GO:0005576 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129320_PI430048170 0.355011534899102 0.400945146098026 0.373664821138565
0.378477035150314 0.32620486104452 A A A 2.75690604055926 0.451945012337341
0.559032133315449 A A A LNCV6_129320_PI430048170 mRNA
CAGCAACTCGAGATTGGGCTCATTTTTATCTAAAAGCAAGTGATGTAATTTAGTTAGAGT NM_017639 RefSeq
chr4 - 154234374 154391297 DCHS2 54798 "dachsous cadherin-related 2, transcript variant 1"
GO:0008150|GO:0003674|GO:0005886|GO:0005509|GO:0016021|GO:0005575|GO:0007156 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137394_PI430048170 0.161286057450502 0.745096301753847 0.305824124015556
0.480411107822169 0.332521786526001 A A A 0.529753993932561 1.14746648279093
0.643870193466624 A A A LNCV6_137394_PI430048170 mRNA
CTTCAGAGGAGCAGTTCTTGGATGACCCAGATTTGAATCATTAAAGTAGACTCTCATGCA NM_001007089 RefSeq
chr2 - 219327408 219333177 RESP18 389075 regulated endocrine-specific protein 18
GO:0005794|GO:0048237|GO:0043204|GO:0005576|GO:0030141|GO:0001701 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_140267_PI430048170 0.21407200198656 0.753566669242949 0.511724237006567
0.492122716180442 0.550169940871637 A A A 0.636612092966491 0.736728251309995
1.31064152319065 A A A LNCV6_140267_PI430048170 mRNA
CCCCTGGATACATTGTTTTATCAGTCGGAATTCTTAAATAAAGACATACTTCCCTTCAAA NM_003128 RefSeq chr2
+ 54456316 54671446 SPTBN1 6711 "spectrin, beta, non-erythrocytic 1, transcript variant 1"
GO:0007009|GO:0005515|GO:0005516|GO:0008091|GO:0043001|GO:0072661|GO:0032437|GO:0032403|GO:0005
829|GO:0005737|GO:0005543|GO:0007411|GO:0030673|GO:0070062|GO:0000281|GO:0071709|GO:0005730|GO:0
030506|GO:0003779|GO:0014731|GO:0031430|GO:0051693|GO:0007182|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140161_PI430048170 0.152352162477809 1.0704792493279 0.485350826054648
0.46174297460996 0.53451536226417 A A A 0.313968276285041 0.39499404587231
0.474377373758979 A A A LNCV6_140161_PI430048170 mRNA
ACACCAGAAGCTTCCTAAGCTGCTGGTCTGATAATGTGTATAAATATGTATGCAAGTATG NM_152677 RefSeq
chr19 + 57668934 57679152 ZSCAN4 201516 zinc finger and SCAN domain containing 4
GO:0006355|GO:0003700|GO:0010833|GO:0003677|GO:0046872|GO:0006351|GO:0000784 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_140322_PI430048170 0.0380674223941046 3.83411971175117 3.63498290997967 4.18299388670534 3.67271064677815 P P P 2.54447054870651 1.86175578083369 0.875973195689261 P A A LNCV6_140322_PI430048170 mRNA TCGGGGGACCTGAAGAATCAATCTGTGTGAGTCTGTTTTTCAAAATGAAATAAAACACAC NM_012261 RefSeq chr20 + 9514357 9530524 LAMP5 24141 "lysosomal-associated membrane protein family, member 5, transcript variant 1" GO:0032590|GO:0005886|GO:0033116|GO:0031901|GO:0032584|GO:0016021|GO:0055038|GO:0030659|GO:0030425|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2953_PI430048170 0.036420878847658 0.594771893128028 10.7534098200105 10.6804364476153 11.0625867658907 P P P 11.2605265701311 11.5434451337864 11.8991096545213 P P P LNCV6_2953_PI430048170 mRNA CCCCGAACACTTTCATACTAAGACTGTAAGTAGATCTCAGTTCTGCGTTTATTGTAAGTT NM_004642 RefSeq chr12 - 123260969 123272140 CDK2AP1 8099 "cyclin-dependent kinase 2 associated protein 1, transcript variant 1" GO:0006261|GO:0048471|GO:0007049|GO:0070182|GO:0001934|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127726_PI430048170 0.771675670792472 0.988420886570132 0.490015193680753 0.473070104134 0.416079650285914 A A A 0.386811865971631 0.521980899879136 0.517764488716037 A A A LNCV6_127726_PI430048170 mRNA CTGGTTAGCTGTTTCCTGTCATAGAATGGAGTCTTTCTTGCTTTATCTTTTTGTGTATAC NM_207413 RefSeq chr8 - 52534036 52565461 FAM150A 389658 "family with sequence similarity 150, member A" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126762_PI430048170 0.00128318031371994 0.631792794479359 8.31703794681393 8.10672336183115 8.22679958908939 P P P 8.79855496360689 8.86824088484561 8.97348566941334 P P P LNCV6_126762_PI430048170 mRNA GGCCTAACTGTGTAGGTCAATACTCTTTTACATTGCCTTCTAATAAAAGCAGAATGATAC NM_022071 RefSeq chr8 + 19313569 19396218 SH2D4A 63898 "SH2 domain containing 4A, transcript variant 1" GO:0005515|GO:0005737|GO:0019902|GO:0010923 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129347_PI430048170 0.0274113120199393 0.451531491001803 3.73477139063477 3.55904266010591 4.42386329804508 P P P 4.93583648089585 4.94508935221606 5.38235167191719 P P P LNCV6_129347_PI430048170 mRNA GCTCATATCTTACGGTTTTGTGCAATCATTGTCGTATTGTAGTCTTAAGACTCATTATAG NM_001289003 RefSeq chr16 - 71644925 71715840 PHLPP2 23035 "PH domain and leucine rich repeat protein phosphatase 2, transcript variant 2" GO:0048011|GO:0042622|GO:0048015|GO:0005634|GO:0046872|GO:0005829|GO:0001917|GO:0005737|GO:0006470|GO:0007173|GO:0008543|GO:0045087|GO:0004722|GO:0038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135506_PI430048170 0.227561244074667 1.15972133035426 7.82707197832302 7.77845424038257 7.93345903807715 P P P 7.47856349583149 7.49802197048353 7.8875169443526 P P P LNCV6_135506_PI430048170 mRNA CAAGACAATGCTTAGTTCAGATACTCAAAAATGTCTTCACTCTGTCTTAAATTGGACAGT NM_015907 RefSeq chr4 + 17577303 17607967 LAP3 51056 leucine aminopeptidase 3 GO:0005802|GO:0005739|GO:0005737|GO:0030145|GO:0004177|GO:0008235|GO:0006508|GO:0005654|GO:0005634|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136730_PI430048170 0.0775609291223319 0.926365404439449 0.320821835488768 0.30927061745327 0.29673009134311 A A A 0.480129292041311 0.411605938654424 0.363855108498725 A A A LNCV6_136730_PI430048170 mRNA AGAGCTTATCTCTACTTGATAAAATTTCTACTGTATTCTTGGCTTAACTCAGGTCCTGTG NM_002000 RefSeq chr19_KI270920v1_alt + 160112 177440 FCAR 2204 "Fc fragment of IgA, receptor for, transcript variant

1" GO:0006955|GO:0019862|GO:0005886|GO:0005887|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145384_PI430048170 0.000222044531456481 0.346536726152181 0.34110107837201 0.57978548951228 0.325287583402072 A A A 1.8323748041198 1.99896942751509 2.00919612213652 A A A LNCV6_145384_PI430048170 mRNA TTACTCAGGACAACAGTATGTACAAAAGTCTCCGGAAAAGGAAAATAAAACAACCTGAAA NM_005819 RefSeq chr1 - 180972712 181023121 STX6 10228 "syntaxin 6, transcript variant 1"
GO:0005515|GO:0005802|GO:0019905|GO:0048471|GO:0005794|GO:0005886|GO:0090161|GO:0030136|GO:0031201|GO:0032588|GO:0006886|GO:0006906|GO:0032880|GO:0005484|GO:0000139|GO:0042147|GO:0048193|GO:0007032|GO:0016021|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135177_PI430048170 0.0371683636515298 0.223038356360085 0.383971313205542 1.30621012364016 2.35689825702012 A A A 3.55571263143543 4.20277502058541 3.28274462182688 P P P LNCV6_135177_PI430048170 mRNA CATCCCTCAGTTCCCAGCATGTACCCTAAGAATAAAGATTTTCTTCTGCATAATTACAAT NM_007086 RefSeq chr14 - 54938937 55027101 WDHD1 111169 "WD repeat and HMG-box DNA binding protein 1, transcript variant 1"
GO:0005515|GO:0006396|GO:0005737|GO:0070829|GO:0003723|GO:0003682|GO:0005654|GO:0070063|GO:0003677|GO:0000775|GO:0033044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101686_PI430048170 0.0204294723229265 2.5335048560309 4.55628184793402 4.37458917071153 4.74023770013487 P P P 3.66501882108481 3.06502358564433 2.8012069176098 P P P LNCV6_101686_PI430048170 mRNA TCGGCATCATTTGGGGAAGAGTCCACTCCAGGCCAGACTAACTCAGAGACAGCTGTGGTG NM_006044 RefSeq chrX + 48802079 48824970 HDAC6 10013 histone deacetylase 6
GO:0008017|GO:0005515|GO:0032418|GO:0070301|GO:0010469|GO:0051354|GO:0008013|GO:0045598|GO:0051879|GO:0006886|GO:0051787|GO:0034605|GO:0051788|GO:0070201|GO:0031625|GO:0000209|GO:0006996|GO:0034983|GO:0060765|GO:0048487|GO:0009636|GO:0001047|GO:0070848|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133661_PI430048170 0.0104694778985199 0.412645643330753 7.85245543511252 7.63137873995421 8.04419910554219 P P P 8.73537318633882 9.13395163311876 9.43516319734265 P P P LNCV6_133661_PI430048170 mRNA GCTTTTGGAATAATAGGAAGTTTTGTGAAATGCTGGCCTTGTGTATATCTTAGAATGCAA NM_001166599 RefSeq chrX - 134769565 134797155 FAM122B 159090 "family with sequence similarity 122B, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77141_PI430048170 0.0208903482997425 2.55832130786665 3.87065092846427 4.61325552247991 4.3292659447495 P P P 3.20546325920136 3.15413058121743 2.32646472260828 P P A LNCV6_77141_PI430048170 mRNA AAACTTTGGTGTAAAATTCCACCAGTTTCCAGCCACCTTCCTGACTTCTATCTGGGCTTG NM_025262 RefSeq chr6_GL000256v2_alt - 2975967 2979658 LY6G5C 80741 "lymphocyte antigen 6 complex, locus G5C" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137173_PI430048170 0.78957225895624 1.13560076917984 0.335166814633734 1.41187308656285 0.343909139229306 A A A 0.986949319568773 0.386758717943458 0.358599372818242 A A A LNCV6_137173_PI430048170 mRNA TTGGCTCAGGGTGAATTACAAGGGGCTACTGAATGGCTATTACTTTCATCACGACTGATC NM_012400 RefSeq chr1 - 20112649 20119566 PLA2G2D 26279 "phospholipase A2, group IID, transcript variant 1"
GO:0036149|GO:0005509|GO:0036148|GO:0005576|GO:0044281|GO:0016042|GO:0036150|GO:0006954|GO:0004623|GO:0006644|GO:0006654|GO:0036151|GO:0046474|GO:0036152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145632_PI430048170 0.0501792850933211 0.506609830962427 3.75972665445792 2.77516431564881 3.38965039296171 P A P 3.96435473146193 4.55059042724 4.45239468037723 P

P P LNCV6_145632_PI430048170 mRNA
GGTAAGTGTGGCTTTGAGTAATAACTGAGCTGTTTCCCCGCATATAAAATAGAAATAAAT NM_005870RefSeq chr13
+ 21140513 21149085 SAP18 10284 "Sin3A-associated protein, 18kDa"
GO:0005515|GO:0006397|GO:0008380|GO:0010467|GO:0048025|GO:0043065|GO:0006357|GO:0003714|GO:0006
325|GO:0006351|GO:0005737|GO:0000118|GO:0016607|GO:0000381|GO:0045814|GO:0040029|GO:0005654|GO:0
035145 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58105_PI430048170 0.4324282513669530.8029415083258980.6021187262247170.537237827924322
0.302241442154029A A A 0.411833144046579 1.28771311820912 0.547664185625718A A A
LNCV6_58105_PI430048170 mRNA
CTCAAAAAAGATGTGAAACAGTTTGTTAGGAGAAAGGACAGTGGTCCTGTTGTTAAAAAA NM_002422RefSeq chr11
- 102835796 102843611 MMP3 4314 matrix metallopeptidase 3
GO:0051898|GO:0030334|GO:0071732|GO:0005509|GO:0005578|GO:0005576|GO:0010727|GO:0005615|GO:0005
829|GO:0005739|GO:0030163|GO:0071230|GO:0004175|GO:0022617|GO:0030198|GO:0030574|GO:0006508|GO:0
008270|GO:0032461|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128613_PI430048170 0.0325548092739274 0.7531228521966661 0.7894725125294
10.7678401546352 10.5472547671953 P P P 11.1239541080914 11.1018962483355
11.1179839319165 P P P LNCV6_128613_PI430048170 mRNA
TGCCCTCCACCACCACCCAAAGTGTGGGATTAAAGTACTGTTTTCTTTCCACTTAAAAAA NM_000263RefSeq chr17
+ 42535932 42544448 NAGLU 4669 "N-acetylglucosaminidase, alpha"
GO:0045475|GO:0005975|GO:0004561|GO:0046548|GO:0060119|GO:0006027|GO:0044281|GO:0005764|GO:0007
399|GO:0021680|GO:0009405|GO:0042474|GO:0007040|GO:0030203|GO:0070062|GO:0043202 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134067_PI430048170 0.14833353461669 1.21955384113975 10.1411835646402 10.39621319545
10.5639862167112 P P P 10.0035523452374 9.97488673463811 10.2754739406005 P P P
LNCV6_134067_PI430048170 mRNA
GCTGAAGCCCAAAAGTCAAGTCTTGTCTAAGATGTCTGAACTATTAAATTTACCATTTTG NM_020409RefSeq chr3
- 179588465 179604646 MRPL4757129 "mitochondrial ribosomal protein L47, transcript variant 1"
GO:0070124|GO:0005739|GO:0070125|GO:0008150|GO:0003674|GO:0070126|GO:0032543|GO:0006996|GO:0003
735|GO:0005743|GO:0005575|GO:0005762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137535_PI430048170 0.00732336638168808 0.6215395429956585.2829660159431
5.1191671810181 5.39901279892649 P P P 5.89912373636097 5.97148343082498
6.00052062878975 P P P LNCV6_137535_PI430048170 mRNA
GTAGCAATGTACAGATAAAGAGTACTTTAACGCCCATGCGTGTTCAAGACTGTTCAAGAC NM_032494RefSeq chr2
- 112215862 112255087 ZC3H8 84524 zinc finger CCCH-type containing 8
GO:0005515|GO:0003700|GO:0015030|GO:0033085|GO:0070245|GO:0006915|GO:0035327|GO:0005634|GO:0008
023|GO:0046872|GO:0042796|GO:0043565|GO:0035363|GO:0045945|GO:0042795|GO:0043029|GO:0045892|GO:0
046677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143071_PI430048170 0.428646450875342 1.07454251458517 14.0769519564572 13.904104112329
13.9146581033509 P P P 14.0609168330814 13.8013720613204 13.7049834246037 P P P
LNCV6_143071_PI430048170 mRNA
ACCTTCAAGAGTGGCTGAAAAGATTGCAGAGTTATCATAATAAATTGCTAACTTGCGTAT NM_001037330 RefSeq
chr17 + 18722088 18736118 TRIM16L 147166 tripartite motif containing 16-like GO:0005737 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135872_PI430048170 0.0951504568532758 0.3068955649209592.53723169734898
2.49087083171146 1.64217938113612 A A A 2.86007890539455 3.61097083728987
4.80335965631597 P P P LNCV6_135872_PI430048170 mRNA
CTTTCAGTTTTGTGGCATGTGAGGTACTGGGTGAAAGGAGAGAAGCCTTCATCTTCATAG NM_176887RefSeq
chr12_KI270904v1_alt - 262228 263158 TAS2R46 259292 "taste receptor, type 2, member 46"
GO:0060170|GO:0033038|GO:0007186|GO:0005886|GO:0016021|GO:0001580 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_50666_PI430048170 0.3875407885134650.8982508981980428.40482324072963 7.88975754718937
8.1301421951038 P P P 8.2922466199136 8.43390058117672 8.19938737624486 P P P
LNCV6_50666_PI430048170 mRNA
AGAGTGACATCCTTCAGAGACCTCATTCATGACCAAGATGAAGATGAGGAGGAAGAGGAA NM_001206736
RefSeq chr20 - 1442161 1467692 NSFL1C 55968 "NSFL1 (p97) cofactor (p47), transcript variant 4"
GO:0005515|GO:0043130|GO:0005795|GO:0005886|GO:0005694|GO:0005829|GO:0008289|GO:0008599|GO:0050
790|GO:0005737|GO:0007030|GO:0061025|GO:0043161|GO:0005654|GO:0045111|GO:0000045|GO:0031468 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132173_PI430048170 0.00513272556494363 0.39306788405726 1.05477127656731
0.5381548839183221.11252455247244 A A A 2.38525670676279 2.39824788391129
1.99432742662439 A A A LNCV6_132173_PI430048170 mRNA
CTGAGCACTTCTAGTCAGATACAGATTCATCAGTGTATGCAACATCCTTTGTAATTTAAA NM_153607RefSeq chr5
+ 173056351 173139288 CREBRF 153222 "CREB3 regulatory factor, transcript variant 1"
GO:0005515|GO:0006986|GO:0032388|GO:0042711|GO:0045732|GO:0006355|GO:0034976|GO:0003700|GO:0005
634|GO:0000122|GO:0051222|GO:0006351|GO:1900170|GO:0043565|GO:0016604|GO:0005737|GO:1900102|GO:0
006810 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130769_PI430048170 0.0127212626136730.186640156994984 0.391731065652945
0.3671152162266330.251067044021157A A A 3.15109801439064 2.17299200785623
2.79146865105142 P A P LNCV6_130769_PI430048170 mRNA
GTTGACTGCTTCTCTGCAGTCGTTGATGCTAATAAATATTGTCCTGTTTCTTCATATAAT NM_021083RefSeq chrX +
37685879 37732130 XK 7504 X-linked Kx blood group
GO:0005515|GO:0008361|GO:0005215|GO:0010961|GO:0042552|GO:0031133|GO:0006874|GO:0006865|GO:0006
810|GO:0048741|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145442_PI430048170 0.9537133781078571.00155553389704 2.90886307781991
2.93546509111036 3.39035890642551 A A P 3.16877968828271 3.16681258530417
2.93220312766837 P P P LNCV6_145442_PI430048170 mRNA
CTGGGCTTGTTGCGGGAAATTTGTAAATTGTGCACAGAGAAGAATATGAAATTGCACATA NM_007105RefSeq
chr11_KI270831v1_alt - 119555 136161 SLC22A18AS 5003 "solute carrier family 22 (organic cation
transporter), member 18 antisense, transcript variant 1" GO:0008150|GO:0003674|GO:0005575 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129815_PI430048170 0.3461495047993291.14145817157618 5.90021585879882
5.76382406820012 5.96903660557588 P P P 5.44656161213585 5.55562496894419
6.00357248003857 P P P LNCV6_129815_PI430048170 mRNA
CTCTGTCTTCTCACAAGGTTTGCCAAGTTGTGTTCTGTTTTAAATAAAGGTTGCAATATTNM_007314RefSeq chr1 -
179099326 179229684 ABL2 27 "ABL proto-oncogene 2, non-receptor tyrosine kinase, transcript variant b"
GO:0005515|GO:0006909|GO:0051353|GO:0071300|GO:0046632|GO:2000145|GO:2000096|GO:0030155|GO:2000
249|GO:0051015|GO:0007173|GO:0007411|GO:0030100|GO:0042127|GO:0050885|GO:0070374|GO:0043123|GO:0
038083|GO:0051017|GO:0035640|GO:0022408|GO:0000287|GO:0021587|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145373_PI430048170 0.9504151586974091.01088007831051 4.52613455799035
4.39612020542868 4.79483319109087 P P P 4.56470506516645 4.4452462104857
4.67981964415397 P P P LNCV6_145373_PI430048170 mRNA
TGTCAAAAAAGAATCTGTATTCAGACCCTGGGTCAGGAAATTACTGCCCACTTGTCAAGT NM_198219RefSeq chr13
+ 110713262 110721074 ING1 3621 "inhibitor of growth family, member 1, transcript variant 1"
GO:0005515|GO:0030308|GO:0007049|GO:0008285|GO:0008270|GO:0005634|GO:0035064|GO:0045893|GO:0006
606|GO:0010941|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137193_PI430048170 0.0165813359833645 0.7247372315866248.38233985430788
8.58232485574057 8.67951634236464 P P P 8.94077958946859 8.99743341244191

9.10993057322625 P P P LNCV6_137193_PI430048170 mRNA
CAAGTGTGATATTTCCTGCTGAATTAAATTATACTTCAGTTGTTGCCTCAAGTAAAGGTG NM_001098817 RefSeq
chr18 - 35468326 35497991 INO80C 125476 "INO80 complex subunit C, transcript variant 1"
GO:0031011|GO:0008150|GO:0003674|GO:0006355|GO:0006281|GO:0071339|GO:0005730|GO:0006338|GO:0006
310|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135240_PI430048170 0.407153142166376 1.95462949760301 2.5312575133911
0.681144276809122 0.561572817640937 A A A 0.579885872460266 0.527764817817342
0.67484462611178 A A A LNCV6_135240_PI430048170 mRNA
ATTTATTTGAACCTCTTAGCCACATTTCCAGCAGGGCAAACCAACTGATGCCCTGGAAGA NM_016529 RefSeq chr13
+ 25372070 26021282 ATP8A2 51761 "ATPase, aminophospholipid transporter, class I, type 8A, member
2"
GO:0008285|GO:0005886|GO:0010996|GO:0007409|GO:0045332|GO:0048666|GO:0050908|GO:0050884|GO:0040
018|GO:0060052|GO:0005794|GO:0000287|GO:0042472|GO:0007568|GO:0010842|GO:0003011|GO:0005524|GO:0
008152|GO:0004012|GO:0010976|GO:0042755|GO:0043588|GO:0061092|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141110_PI430048170 0.288971550391729 1.18935406745271 0.337313704062918
0.834189238152922 0.360734712693448 A A A 0.2823650340021 0.268798784259217
0.286790385224688 A A A LNCV6_141110_PI430048170 mRNA
AACTTCCTTTCAAAGAGCAAAATCATGACTAAGTGTGCAAAGGACTCGGGGAATTAATCT NM_001030013 RefSeq
chr10 + 127549348 127552671 NPSNA neuropeptide S NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133579_PI430048170 0.285221143884753 0.640629893244808 1.5544466624703 2.1820594172504
0.300044552370309 A A A 2.36354784845799 2.39195116074941 1.67598111293185 P P A
LNCV6_133579_PI430048170 mRNA
GTGGCTATAATGACGTGGAAATGTAATCTGTGTTTTCTGGTTTTTCATTTATTTGGCCAA NM_018934 RefSeq chr5
+ 141222325 141226288 PCDHB14 56122 protocadherin beta 14
GO:0016339|GO:0005886|GO:0005509|GO:0007268|GO:0016021|GO:0007416|GO:0007156 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137990_PI430048170 0.113596616574407 1.25637791906671 8.88150168704559 8.6070587655903
8.51835907947495 P P P 8.29675434377718 8.56591769260607 8.15058988471736 P P P
LNCV6_137990_PI430048170 mRNA
TGTAAATATTCTGTGGAGAAAAGAGGACTTCAGGGAGTAAAAAAGCCACTGATGTCAAAA NM_153253 RefSeq chr11
+ 65640120 65650920 SIPA1 6494 "signal-induced proliferation-associated 1, transcript variant 1"
GO:0005515|GO:0030133|GO:0042631|GO:0048471|GO:0030308|GO:0005794|GO:0005886|GO:0008283|GO:0005
730|GO:0005634|GO:0045786|GO:0032854|GO:0008022|GO:0005829|GO:0043547|GO:0035556|GO:0043234|GO:0
007165|GO:0007162|GO:0046582|GO:0007010|GO:0005096 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_136979_PI430048170 0.0629700714920155 0.386540876316629 1.44518400177667
1.80229814893704 0.367228653062775 A A A 2.56999717785806 2.97745462405475
2.48294751333079 A P P LNCV6_136979_PI430048170 mRNA
GCCTTCTCTGCTCTGTAATACTCCACTGTGACCATGAATAAAATGCCCTTGCAAACTGTC NM_001004341 RefSeq
chr1 - 157092042 157099808 ETV3L 440695 ets variant 3-like
GO:0043565|GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0030154 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132880_PI430048170 0.159300366359105 0.790987070130503 5.24196898079484
5.53627348512836 5.80222493175303 P P P 5.6711543620042 5.90655472917025
6.04697732612388 P P P LNCV6_132880_PI430048170 mRNA
CCTGTCTTCACATTGCTTGTCCCTTATCCCCACCTGAAATAAAATCTATTGGGTCCTGAG NM_002853 RefSeq chr5
- 34905260 34915675 RAD1 5810 "RAD1 checkpoint DNA exonuclease, transcript variant 1"

GO:0005515|GO:0008408|GO:0030896|GO:0090305|GO:0005694|GO:0005634|GO:0071479|GO:0006974|GO:0043231|GO:0003684|GO:0006260|GO:0006281|GO:0008853|GO:0021762|GO:0051598|GO:0005654|GO:0000077|GO:0000738 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126908_PI430048170 0.984582597266829 0.999856911840097 0.341035010059442 0.353460383027178 0.32183275844911 A A A 0.341908099500675 0.348774980578883 0.326348840163032 A A A LNCV6_126908_PI430048170 mRNA CCTCTTTCCTACCAATTTCACATTTTGCAGAAACTTGTTCACATTTCCAACAATATCAGA NM_020872 RefSeq chr3 - 74262568 74521140 CNTN3 5067 contactin 3 (plasmacytoma associated)
GO:0005886|GO:0031225|GO:0007155|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130954_PI430048170 0.227833584438452 1.39644529230373 2.72857244166971 2.86163169714406 2.81730067849551 A A A 2.57200025772865 2.57972322927073 1.62014641912079 A P A LNCV6_130954_PI430048170 mRNA GACTTGTCTCAATCAAACCCAAGGCACTGGAAGAGAGCAGGCCCCATCTATTAATTTTTT NM_001005212 RefSeq chr11 + 58023880 58181566 OR9Q1 NA "olfactory receptor, family 9, subfamily Q, member 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104538_PI430048170 0.0145831805024015 1.31389750424829 5.30999146354215 5.27991201053573 5.13020075992505 P P P 4.90099702696153 4.93323151574715 4.69975409014227 P P P LNCV6_104538_PI430048170 mRNA CGCGAGCCCCTCGGAGAAGGGTGCCCACCCGTCGGGCGGCGCGGATGACGTGGCGAAGAA NM_006825 RefSeq chr12 - 106237880 106247935 CKAP4 10970 cytoskeleton-associated protein 4
GO:0005811|GO:0048471|GO:0016020|GO:0005886|GO:0005783|GO:0005789|GO:0016021|GO:0005856|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144541_PI430048170 0.0601906377418828 0.747809320701007 5.25585569820381 5.31090204898625 5.65234307874022 P P P 5.8265962373762 5.75911436726491 5.91942506354485 P P P LNCV6_144541_PI430048170 mRNA CCAAAACTGTAAAATAATCTCCTCCCTCAAATGCAAAGGTTGTTTTTGTTCTGTTTCTGT NM_017757 RefSeq chr18 + 74630962 75065672 ZNF407 55628 "zinc finger protein 407, transcript variant 1"
GO:0006355|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_39321_PI430048170 0.0761040541042549 0.729345132740192 3.43927886634423 3.91357623873166 3.88745849581094 P P P 4.18745131796712 4.1133164127111 4.34330654581537 P P P LNCV6_39321_PI430048170 mRNA GTGGCCTTATATGATTATGAAGCTAGAACTACAGAAGACCTTTCATTTAAGAAGGGTGAA NM_005433 RefSeq chr18 - 721591 812326 YES1 7525 "YES proto-oncogene 1, Src family tyrosine kinase"
GO:0005515|GO:0005154|GO:0005886|GO:0005884|GO:0031295|GO:0050900|GO:0030154|GO:0005829|GO:0005737|GO:0036120|GO:0015758|GO:0007411|GO:0042127|GO:0071375|GO:0038083|GO:0070062|GO:0005794|GO:0048013|GO:0005815|GO:0005102|GO:0005524|GO:0044325|GO:0031234|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134035_PI430048170 0.764806738347754 1.00505486652041 0.350667786188477 0.349310826341736 0.400380536084921 A A A 0.371631715710442 0.329588743794452 0.377434193696075 A A A LNCV6_134035_PI430048170 mRNA CTGTACAGGTTTGTTATCACAATGTATAATTGTGTTTTTCCACCCCACATTTTTAAGGCA NM_022728 RefSeq chr7 - 31337460 31340924 NEUROD6 63974 neuronal differentiation 6
GO:0021542|GO:0001077|GO:0045944|GO:0046983|GO:0005634|GO:0000978|GO:0030154|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145445_PI430048170 0.00232571243359122 1.31136271606845 8.68400879390928 8.74173342217786 8.75546296258775 P P P 8.31814018474533 8.27962319345601 8.40819923058895 P P P LNCV6_145445_PI430048170 mRNA CTTGTTTAAAAGAAAATCAGGTGGGTGGGAATCTCTTGGAGAACTGAGGCTGAGGGTAGA NM_032345 RefSeq chr12

- 55901412 55927913 WIBG 84305 "within bgcn homolog (Drosophila), transcript variant 1"
GO:0005515|GO:0005737|GO:0000184|GO:0005730|GO:0043022|GO:0045727|GO:0005654|GO:0035145 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90168_PI430048170 0.4905937668778470.7946785558093063.58161979405706 3.43569643823565
3.85707662283569 P P P 3.54467957894335 3.61753078208507 4.52187343329791 P P P
LNCV6_90168_PI430048170 mRNA
AGCACCTACGAAAAATTTAGAACAGCAGGTGAATCACAGCCAGCAGGGACATACAAATGC NM_007349RefSeq
chr7 - 154943689 155002972 PAXIP1 22976 PAX interacting (with transcription-activation domain)
protein 1
GO:0005515|GO:0000416|GO:0030330|GO:0005634|GO:0006310|GO:0060261|GO:0035066|GO:0006351|GO:0016
363|GO:0035097|GO:0006281|GO:0051571|GO:0043542|GO:0010212|GO:0045830|GO:0031398|GO:0060717|GO:0
060612|GO:0001570|GO:0051568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139165_PI430048170 0.00175177069323791 0.4362043025384458.27222541603964
8.26281601261383 8.03265060421941 P P P 9.44405852790623 9.34835098326872
9.37689689995754 P P P LNCV6_139165_PI430048170 mRNA
GACAAAAACCTAATAGAAGAGTCACCACCAAATGAAGAATAAAACTCCCAGGGTGCTGTG NM_012067RefSeq
chr1 - 19282562 19288786 AKR7A3 22977 "aldo-keto reductase family 7, member A3 (aflatoxin
aldehyde reductase)"
GO:0004033|GO:0006805|GO:0006081|GO:0009055|GO:0044281|GO:0070062|GO:0055114|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131046_PI430048170 0.5586116221573931.19247026520271 0.505718879781054
1.19928474759257 0.252765178356195A A A 0.3966367455843470.507920788588187
0.46156697495137 A A A LNCV6_131046_PI430048170 mRNA
GTGGTACCCTCTTAGCATATATCTTTGCTATCCTTAAGATCCTAAACAAATCATCTTTGTNM_032228RefSeq chr11 +
13668658 13732346 FAR1 84188 fatty acyl CoA reductase 1
GO:0005782|GO:0008611|GO:0044281|GO:0035336|GO:0080019|GO:0050062|GO:0016021|GO:0005778|GO:0044
255|GO:0005777|GO:0010025|GO:0046474|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134078_PI430048170 0.860908926344455 1.01409946482485 7.68302898329931
7.60085474836454 7.84834094579277 P P P 7.90752143637204 7.49377981081901
7.65091291781763 P P P LNCV6_134078_PI430048170 mRNA
TCCTGTACTATTGTGTTTTGAGTGTGTTTTGGAACCTTCATAGAACACACTTTCTTTTGG NM_002408RefSeq chr14 +
49620770 49623481 MGAT2 4247 "mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-
acetylglucosaminyltransferase"
GO:0009312|GO:0005794|GO:0009311|GO:0005795|GO:0008455|GO:0000139|GO:0016020|GO:0030246|GO:0006
487|GO:0016021|GO:0044267|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138009_PI430048170 0.241522761901537 1.81798293739011 0.327531188295774
1.85871522295066 1.42084023556708 A A A 0.6902640641469770.358854636802636
0.335696496341024A A A LNCV6_138009_PI430048170 mRNA
ACTCGGTTACATTCCAAAATGTATGTCAGTATTGTAAAATCATCCAGCCTTTCAAGAAGC NM_001039763 RefSeq
chr5 - 110419495 110726749 TMEM232 642987 transmembrane protein 232 GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_128157_PI430048170 0.0198758317302501 0.771932758348795 9.51349150225536
9.51965869240764 9.69550688398723 P P P 9.9223557534804 9.83236143009764
10.0898695896831 P P P LNCV6_128157_PI430048170 mRNA
ACTTGTGGCTCAGACCTGAGTGCAAGGTGGAAATAAACATCAAACATCTTTTCATTATCC NM_001300981 RefSeq
chr7 + 44796635 44803123 PPIA 5478 "peptidylprolyl isomerase A (cyclophilin A), transcript
variant 2"
GO:0005515|GO:0000413|GO:0019076|GO:0030260|GO:0050714|GO:0019058|GO:0045069|GO:0005634|GO:0050
900|GO:0005615|GO:0005829|GO:0006457|GO:0016032|GO:0006278|GO:0045070|GO:0070062|GO:0042277|GO:0

019061|GO:0003755|GO:0030168|GO:0046790|GO:0005576|GO:0019068|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52818_PI430048170 0.3235045905167671.12813597191808 4.61291134144245 4.53580118396419 4.90860454076287 P P P 4.38704402081988 4.43780100038701 4.71587433943727 P P P LNCV6_52818_PI430048170 mRNA
TCAGTTCACGTAGATTCTGGTGCATCTGCAATAACTCGAGAAAGCCACACACATAGGGAT NM_022048RefSeq chr15 - 64165516 64356243 CSNK1G1 53944 "casein kinase 1, gamma 1"
GO:0005737|GO:0018105|GO:0004674|GO:0008360|GO:0005634|GO:0016055|GO:0005524|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122503_PI430048170 0.1104251236288170.86852253526698 6.55542100063415 6.62624116627514 6.39957310642728 P P P 6.63152609837566 6.87218592770506 6.68565772847704 P P P LNCV6_122503_PI430048170 mRNA
TCCAACCCTATCATCAGGACAGTGAAGTCTGTGGGCATGATCGCGGGAGGGACAGCATCANM_001129819 RefSeq chr22 - 42617839 42646989 CYB5R3 1727 "cytochrome b5 reductase 3, transcript variant 3"
GO:0005811|GO:0006695|GO:0016208|GO:0004128|GO:0005833|GO:0005783|GO:0008015|GO:0050660|GO:0005743|GO:0006767|GO:0005741|GO:0044281|GO:0019852|GO:0005739|GO:0071949|GO:0005737|GO:0051287|GO:0043531|GO:0016020|GO:0006766|GO:0005789|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93364_PI430048170 0.5592649160184181.03088033077192 0.3056952010772790.313245097057564 0.486697213308778A A A 0.3362836545011150.2952634240765050.349273039550638A A A LNCV6_93364_PI430048170 mRNA
ATAACCTTGGTCCTTTGGAACTGATTCTTAATACTCCTAGCCATCATAGGGTTCATCATG NM_001004320 RefSeq chr7 - 15200317 15562015 AGMO 392636 alkylglycerol monooxygenase
GO:0005506|GO:0050479|GO:0005783|GO:0005789|GO:0046485|GO:0006633|GO:0016021|GO:0055114|GO:0006643 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55855_PI430048170 0.36747602761621 1.07286699247523 6.32354556106196 6.28851040388556 6.25928880986565 P P P 6.01139604459674 6.20879357171513 6.32973317362386 P P P LNCV6_55855_PI430048170 mRNA
TGGGAAGTCTTTCAACTTTAAGAAACACCTGAAGGAGCACATGAAGCTGCACAGTGACAC NM_001136036 RefSeq chr1 - 248850003 248858926 ZNF692 55657 "zinc finger protein 692, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136360_PI430048170 0.1035372222626981.38900774622417 5.05611201777297 5.11200926668268 5.06447914910269 P P P 4.48343552193793 4.92139991067572 4.34115745376682 P P P LNCV6_136360_PI430048170 mRNA
TTTATCTGAGCTGCTTGTCAGTTTGTTCGTCTGTCCCTAGGTCTGTCTGCTATCAGCTAT NM_005710RefSeq chrX + 48898255 48903143 PQBP1 10084 "polyglutamine binding protein 1, transcript variant 1"
GO:0006355|GO:0071598|GO:0010494|GO:0003713|GO:0005634|GO:0003677|GO:0006351|GO:0031175|GO:0048814|GO:0005737|GO:0016607|GO:0000380|GO:0043021|GO:0005654|GO:0043484 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132250_PI430048170 0.5992762818862041.23813115427444 1.65494522138326 1.23121139947771 0.325914500204274A A A 0.43967419609099 1.4769573544945 0.391797592524221A A A LNCV6_132250_PI430048170 mRNA
TAATGAATATGGTCACTATTTCTAGGGCCTGTTGCTCCAGTGTAGTGGTCAAGAGTGTAC NM_001242815 RefSeq chr2 - 41935367 41953803 C2orf91 NA chromosome 2 open reading frame 91 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143183_PI430048170 0.0271105682531017 0.8778635324911657.89699763620339 7.93690270322463 8.0274802189459 P P P 8.11470624469202 8.16547576585433 8.14764877587378 P P P LNCV6_143183_PI430048170 mRNA

ACATTAAAAACAGGAAGGAAGAGATCTGTGATTAAACTAAAGGCCCTTTCACACCTAAAA NM_032492 RefSeq chr3 + 9890586 9894347 JAGN1 84522 jagunal homolog 1 (Drosophila) GO:0038158|GO:0002446|GO:0005783|GO:0050832|GO:0005789|GO:0030223|GO:0016021|GO:0016192|GO:0015031|GO:0006887|GO:0007029 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92589_PI430048170 0.0641922852245729 4.27954859252286 3.44766118055535 3.89381310385407 4.37451741736214 P P P 2.79146865105142 1.42825809859373 0.327944324937365 P A A LNCV6_92589_PI430048170 mRNA
CCATCAGTTCACTTCCTGTGTCCTTAACCAAGTTAATGTTGTCAAATGCCTTATTTGTGG NM_018004 RefSeq chr3 + 100492618 100577441 TMEM45A 55076 transmembrane protein 45A GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128528_PI430048170 0.0355471342603581 0.608783977623505 2.24687386015474 2.5807205177985 2.587518934207 A A A 3.11147501759017 3.50445149610253 2.90792563043733 P P P LNCV6_128528_PI430048170 mRNA
TTTGGAAGAGAAAAGCAAATAAATGAAAATCCCTTCCTGTTAAGATGATGGGGTATTTGG NM_001098615 RefSeq chr12 - 43728608 43758758 PUS7L 83448 "pseudouridylate synthase 7 homolog (S. cerevisiae)-like, transcript variant 1" GO:0009982|GO:0003723|GO:0001522|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132115_PI430048170 0.847898187734888 1.04433804143007 1.38449516783716 0.532558344289121 0.534099130602354 A A A 0.342402977657633 0.417982638422816 1.41558471791601 A A A LNCV6_132115_PI430048170 mRNA
AGGTGCAATTTTTAATCCTTTGAAATTAGCCAGCCAGACCTAATGCTAAGGTAAATGTAA NM_014548 RefSeq chr15 + 51751560 51816361 TMOD2 29767 "tropomodulin 2 (neuronal), transcript variant 1" GO:0045745|GO:0006936|GO:0030239|GO:0007611|GO:0005865|GO:0007015|GO:0003779|GO:0005523|GO:0051694|GO:0030426|GO:0007399|GO:0007270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132131_PI430048170 0.145533268142818 0.738599707670763 10.4909579804228 10.3487008637293 10.6649455786571 P P P 10.6368060032725 10.8403814032961 11.2798193872467 P P P LNCV6_132131_PI430048170 mRNA
GACACATGCCTCCTCTGACTATAACCTCTTAATAGTTGTGTATAATGAAAACTGTAAACT NM_003344 RefSeq chr7 - 129830732 129952960 UBE2H 7328 "ubiquitin-conjugating enzyme E2H, transcript variant 1" GO:0005515|GO:0006511|GO:0005737|GO:0004842|GO:0070979|GO:0019787|GO:0016874|GO:0070936|GO:0005524|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140471_PI430048170 0.137703821411699 0.790274507419417 6.7816354386589 6.84882755285978 7.22358392375258 P P P 7.12708879621244 7.22089339758966 7.53316890470438 P P P LNCV6_140471_PI430048170 mRNA
AGGGGAAAGGATTCAGATATGACCTTTTCTTTAGTCCCAACCACTAGTTTTAACAAATGT NM_015891 RefSeq chr6 + 110180420 110232219 CDC40 51362 cell division cycle 40 GO:0008380|GO:0005515|GO:0010467|GO:0006369|GO:0006406|GO:0006366|GO:0000398|GO:0031124|GO:0005681|GO:0005654|GO:0071013 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140978_PI430048170 0.0070958908837302 6.09842929067598 4.60235651137026 4.73131015983769 5.07825863881974 P P P 2.71293416701024 2.1240929609556 1.56691303480965 A A A LNCV6_140978_PI430048170 mRNA
AACAAATGCTTGTTGGGCAAGAATGGGATTGAGGATTATCTTCTCTCAGAAAGGCATTGT NM_021181 RefSeq chr1 + 160739056 160754818 SLAMF757823 "SLAM family member 7, transcript variant 1" GO:0030101|GO:0042267|GO:0004872|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134565_PI430048170 0.00333277985591518 0.282239745331862 4.48314827566603 4.38560164247616 4.86984213094712 P P P 6.02923402804587 6.37243548067991 6.76469284024973 P P P LNCV6_134565_PI430048170 mRNA
CCTAAACCTTTTCTTTATTCCACATTTGCTACGGTAAAATCCTGTTACAAAACTACCCTA NM_004697 RefSeq chr9 +

113275633 113292905 PRPF4 9128 "pre-mRNA processing factor 4, transcript variant 1"
GO:0005515|GO:0008380|GO:0006396|GO:0010467|GO:0015030|GO:0005634|GO:0030621|GO:0071001|GO:0016
607|GO:0000398|GO:0000375|GO:0005654|GO:0005681|GO:0046540|GO:0017070 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134738_PI430048170 0.9582553123402050.9989230149670270.466107978337505
0.48385188448718 0.389611229933886A A A 0.4830975716206290.424731328210628
0.437479353955852A A A LNCV6_134738_PI430048170 mRNA
TCACCTATCAACAGATCATCCTGCTTGACTGTAACAAAATAAATAGTGTCTCTTCAAGTG NM_001649RefSeq chrX
+ 9786455 9949441 SHROOM2 357 shroom family member 2
GO:0005515|GO:0008013|GO:0005886|GO:0032438|GO:0048593|GO:0043583|GO:0032401|GO:0030835|GO:0016
324|GO:0051015|GO:0005913|GO:0002089|GO:0043025|GO:0043482|GO:0035725|GO:0043010|GO:0005856|GO:0
051017|GO:0070062|GO:0008057|GO:0005874|GO:0019904|GO:0045176|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_92002_PI430048170 0.3744710004938481.10708951666401 7.23911890358724 7.18962411574791
7.50239067562607 P P P 6.97577335281242 7.14341314758169 7.36504654116501 P P P
LNCV6_92002_PI430048170 mRNA
ACTGCATGCAGCCATCCGGGAGGTGGATATCAAGGGCGTGTTTCGATACTGCAACACGTG NM_003104RefSeq chr15
+ 45023103 45075089 SORD 6652 "sorbitol dehydrogenase, transcript variant 1"
GO:0031966|GO:0031514|GO:0046370|GO:0051160|GO:0003939|GO:0006062|GO:0030317|GO:0005615|GO:0051
287|GO:0016020|GO:0006006|GO:0030246|GO:0051164|GO:0008270|GO:0070062|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143450_PI430048170 0.00268833412424312 2.05245827325628 4.99216091194971
5.3226517855834 4.96850229930545 P P P 4.11273321150499 3.9033140530982 4.1696265464324
P P P LNCV6_143450_PI430048170 mRNA
AATTACAAGTCAGGGTCTGAACCCAGTGTGATGGGGGGAGTCTCTGGGGCCCTGAGTTCA NM_032129RefSeq chr1
+ 966496 975104 PLEKHN1 84069 "pleckstrin homology domain containing, family N member 1, transcript
variant 1" GO:0005886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142762_PI430048170 0.0478090515670593 1.3258966986253 12.8359724503163
12.846942991138 12.7135094552707 P P P 12.5405381891485 12.4387960101949
12.1758575380363 P P P LNCV6_142762_PI430048170 mRNA
GGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTTTAAATATGAAAATG NM_019015RefSeq chr7
+ 151232488 151238827 CHPF2 54480 "chondroitin polymerizing factor 2, transcript variant 1"
GO:0030206|GO:0016020|GO:0000139|GO:0005975|GO:0032580|GO:0009405|GO:0044281|GO:0016021|GO:0030
204|GO:0050510|GO:0030203|GO:0008376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145175_PI430048170 0.0479026980113052 0.4669181832472999.46206871730414
8.52501026181201 8.52806035203746 P P P 10.3616603593731 9.99568486357401
9.55723449879153 P P P LNCV6_145175_PI430048170 mRNA
CCTCTCCCCGTGGACCCTGTTAATCCCAATAAAATTCTGAGCAAGTTCAGAGTGCAAAAA NM_022117RefSeq chrX
+ 53082359 53088546 TSPYL2 64061 TSPY-like 2
GO:0045859|GO:0030308|GO:0005813|GO:0006355|GO:0005886|GO:0005730|GO:0006334|GO:0005634|GO:0009
966|GO:0045786|GO:0006351|GO:0030968|GO:0005737|GO:0007049|GO:0000182|GO:0005654|GO:0008156|GO:0
006987|GO:0044267|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129183_PI430048170 0.1558178464565011.09902792482332 0.529617914031604
0.7278536716621680.611781284492494A A A 0.3876536976092320.510388608296432
0.563815452486892A A A LNCV6_129183_PI430048170 mRNA
CAAGGTGTTCTTTTGTGTCCTCTATTTTCTTCTTGTGAACTGTTAAAGCTACATGCATTA NM_003817RefSeq chr8 +
24440995 24509564 ADAM7 8756 ADAM metallopeptidase domain 7
GO:0005886|GO:0006508|GO:0008270|GO:0016021|GO:0004222 . NA - . NA NA NA NA NA NA NA
NA NA

LNCV6_128376_PI430048170 0.17447525298626 1.06720704599583 7.40821550961793
7.36525305803269 7.33020013169399 P P P 7.18095408497026 7.29624110926751
7.34130843572703 P P P LNCV6_128376_PI430048170 mRNA
CCGGATCAGAAATATATCTATATTCTCGACTAAAGTCTCATCAGGAAATATTTCCTGTCT NM_001294340 RefSeq
chr16 + 88570380 88631964 ZC3H18 124245 "zinc finger CCCH-type containing 18, transcript variant 1"
GO:0005654|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140776_PI430048170 0.9298811580738570.9866005173940060.285683292594055
0.3215569859961960.980591539856088A A A 0.3867524651055370.952287091207223
0.333290564536967A A A LNCV6_140776_PI430048170 mRNA
ATACGCTGCTCTCATACTTGGGCTGTAGTTTGGAGACAAAATATTTTCCTGCCACTGTGT NM_001017986 RefSeq
chr1 + 121087344 121097161 FCGR1B 2210 "Fc fragment of IgG, high affinity Ib, receptor (CD64),
transcript variant 1"
GO:0002474|GO:0005886|GO:0019221|GO:0042590|GO:0006955|GO:0019864|GO:0031901|GO:0038093|GO:0002
479|GO:0016021|GO:0030669|GO:0019763|GO:0060333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141924_PI430048170 0.1228250205933780.8823672859726177.68883810946072
7.59989276330199 7.48544078174229 P P P 7.65732845461437 7.89815321828206
7.75733133357445 P P P LNCV6_141924_PI430048170 mRNA
ACTGGGCTCTGTTTCTGTCCCCTAGAAAATGGGAATAAAATTTCTTTTGCTGTCAAAAAA NM_014948RefSeq chr20
- 3107572 3159910 UBOX5 22888 "U-box domain containing 5, transcript variant 1"
GO:0000209|GO:0016604|GO:0016874|GO:0034450|GO:0008270|GO:0005634|GO:0031625 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139491_PI430048170 0.4759099514310581.04384238389294 0.282150011172341
0.2956991361330660.490720381963002A A A 0.3163014368024110.2780679948468
0.297814923312511A A A LNCV6_139491_PI430048170 mRNA
CAAACCACCAGAAGCCCAGAATAAACTGGCAGCTCAGCTGTTTTATATAAGCTCAAAAAA NM_000174RefSeq chr3
+ 129060766 129062411 GP92815 glycoprotein IX (platelet)
GO:0005886|GO:0007596|GO:0005887|GO:0007597|GO:0030168|GO:0007155 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136214_PI430048170 0.5748531564458020.9832095414507930.276720908630012
0.2857850716528730.388798821972752A A A 0.37009600438176 0.31090820566081
0.345683542103066A A A LNCV6_136214_PI430048170 mRNA
CAACTGCTTTGTGCTGATATCAGAACAGCAGAAATTAAATGTGAAATGTTTCTGATGACT NM_020980RefSeq chr15
+ 58138208 58185911 AQP9 366 aquaporin 9
GO:0005886|GO:0009992|GO:0006863|GO:0005275|GO:0043231|GO:0030104|GO:0016323|GO:0046942|GO:0006
955|GO:0034220|GO:0046943|GO:0005350|GO:0015791|GO:0015250|GO:0015793|GO:0015837|GO:0006810|GO:0
005372|GO:0015204|GO:0006833|GO:0015254|GO:0015855|GO:0007588|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132344_PI430048170 0.1952536870733791.15577969283262 0.560093402128749
0.4468418363840570.812818286720769A A A 0.2988917474126770.407730168444576
0.503918237085963A A A LNCV6_132344_PI430048170 mRNA
CATCTTTGATAAGGGAAATGGTTTCGTGACATGTACACAGTTGCTATTAAAATGTAACTC NM_001143773 RefSeq
chr10 - 59246128 59362903 FAM13C 220965 "family with sequence similarity 13, member C,
transcript variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133126_PI430048170 0.6179172107156131.21951410564597 4.00543457248314
2.86235828349168 3.04141591884851 P A P 3.32308700307052 3.37388425674022
2.46175310092122 P P A LNCV6_133126_PI430048170 mRNA
ACCTCTGCACAGCTCTCCAGGTGCTGAGATATAATGCACCAGCACAATAAACCTTTATTC NM_181724RefSeq chr12
- 108589845 108598118 TMEM119 338773 transmembrane protein 119
GO:0008150|GO:0003674|GO:0005783|GO:0016021|GO:0005575|GO:0001649 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_91469_PI430048170 0.2028619952219430.9076219762763785.79663923854782 5.66681821750243
5.91263453737843 P P P 5.8651395768605 5.88430082904192 6.04941603905505 P P P
LNCV6_91469_PI430048170 mRNA
ATATTGATGAAAAGACTCTGAAACGAGAAGGTGTTTGTGCAGCCAGTCTTCCTACCACTA NM_024818RefSeq chr3
+ 132660295 132678100 UBA5 79876 "ubiquitin-like modifier activating enzyme 5, transcript variant 1"
GO:0005515|GO:0034976|GO:0005737|GO:0071566|GO:0071569|GO:0033146|GO:0005634|GO:0005524|GO:0046
872|GO:0043231|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107293_PI430048170 0.7278485175831981.0314916817687 12.0577066969219
12.0745004189693 12.3147038414398 P P P 11.9597160685866 12.0860601287098
12.2651188760484 P P P LNCV6_107293_PI430048170 mRNA
AGGCTGGGGTTTCTGGTTTTGTTTCTGTTGTGTTTTGTTTTGGTTTCTGTATTATGTATT NM_001242795 RefSeq chr16
+ 56781791 56844949 NUP93 9688 "nucleoporin 93kDa, transcript variant 2"
GO:0007077|GO:0010467|GO:0031965|GO:0005975|GO:0019083|GO:0019221|GO:0019058|GO:0044281|GO:0005
635|GO:0051292|GO:0006606|GO:0055085|GO:0010827|GO:0008645|GO:0015758|GO:0016020|GO:0034399|GO:0
016973|GO:0005643|GO:0009405|GO:0017056|GO:0016032|GO:0000278 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_137314_PI430048170 0.0140781847025956 0.4490253996275616.05777913739657
5.76732436346187 6.01977136433549 P P P 6.70395708248423 7.27908370191899
7.27223070467256 P P P LNCV6_137314_PI430048170 mRNA
CTTCACCAAGTTAGGGCCTCCTGGGTTTATTGCAGATTAAAGCCATCTCAGTGAAGATAT NM_001281521 RefSeq
chr20 + 5950651 5995206 MCM8 84515 "minichromosome maintenance complex component 8,
transcript variant 4"
GO:0005515|GO:0004386|GO:0005634|GO:0007292|GO:0003677|GO:0005524|GO:0006974|GO:0006260|GO:0048
232|GO:0000082|GO:0006271|GO:0000724|GO:0005654|GO:0000278 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_80284_PI430048170 0.2687887441578661.37997258650507 3.48708383668265 3.91826950373639
3.3549983338189 P P P 3.67887587083415 3.02221590034054 2.47626545498278 P P A
LNCV6_80284_PI430048170 mRNA
ACCCAGGCTCCAGCTAGATCATCAGTTAATTTAAAGTGGTTATTCTTGGAAGTAGCATTT NM_001145095 RefSeq
chr8 - 132061485 132105265 HHLA1 10086 HERV-H LTR-associating 1 GO:0005576 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_92276_PI430048170 0.5285001232859591.10825760394889 4.74434554777136 4.31780113936864
4.66507578221419 P P P 4.39709843804277 4.75431921776179 4.0885732889643 P P P
LNCV6_92276_PI430048170 mRNA
TTGAGAAAAGCATCTGCAAAATGCTAAAGAGCAGAGCTTAACTCATTGCCTGTCCCCACC NM_001083537 RefSeq
chr8 - 12182103 12194115 FAM86B1 NA "family with sequence similarity 86, member B1, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139241_PI430048170 0.4192680069396270.733094582751055 1.12923267287963
0.2866919097615960.442575710982077 A A A 0.292774113719601 1.4313903804875
1.36711791942672 A A A LNCV6_139241_PI430048170 mRNA
CAAGTCCAAGATAGGAATGAAGTAATTGAAGCTGCAAATGAAGCATTACTTACTAAAGGA NM_206886RefSeq chr1
+ 93180715 93278730 CCDC18 343099 coiled-coil domain containing 18 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_127679_PI430048170 0.0209487903748175 1.52634714185732 8.2131175891212
8.45599696580967 8.09847149394201 P P P 7.87469308713257 7.6069078011847
7.44633922658613 P P P LNCV6_127679_PI430048170 mRNA
CAGAGCCACCAGGGCACTGTCTGCGTGACTATTTTTTAATAAAAGTACTGAAGACCCGTT NM_003353RefSeq chr2
- 27307396 27308262 UCN 7349 urocortin

GO:0032755|GO:0005515|GO:0030307|GO:0007605|GO:2000252|GO:0030157|GO:0031175|GO:0046888|GO:0007218|GO:0035483|GO:0060547|GO:0005184|GO:0032355|GO:0006979|GO:0008306|GO:0051966|GO:0007565|GO:0045740|GO:0051384|GO:0045792|GO:0032967|GO:0007186|GO:0035176|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130874_PI430048170 0.0162813025825174 0.6206285382301793.50770265356701 3.58773047939095 3.92859504060636 P P P 4.3602682809826 4.56418313341968 4.17307651706984 P P P LNCV6_130874_PI430048170 mRNA CACAGAAGAACGTTTTAGAAACCAAGAGATGTGCAGAAAGAAATGTTTAGTGTTTTTTCG NM_002623RefSeq chr20 + 54207962 54219953 PFDN4 5203 prefoldin subunit 4
GO:0005739|GO:0005515|GO:0005737|GO:0006457|GO:0016272|GO:0051087|GO:0051084|GO:0005634|GO:0051082|GO:0044267|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138633_PI430048170 0.0145946004181243 0.4176367605048413.06491931503432 2.37444707475041 2.75972211009048 P A A 3.8987033574256 4.15184461370749 3.99807993847148 P P P LNCV6_138633_PI430048170 mRNA TGCATTTGGACTCCTCATCATATACTTGGTATATAATACTCTAATAAAAGCTGCCTGAGT NM_012420RefSeq chr10 + 89414567 89421002 IFIT5 24138 interferon-induced protein with tetratricopeptide repeats 5
GO:0051607|GO:0003727|GO:0000049|GO:0045087|GO:0003723|GO:0045177|GO:0032587|GO:0015629 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134619_PI430048170 0.2972355635539630.83865964665588 13.0985836558866 13.1175633191862 13.1441175291465 P P P 13.029051159047 13.4452353557503 13.5908035860569 P P P LNCV6_134619_PI430048170 mRNA TGGGACTCACAGCTTTATTGGGCTTTCTTTGTGTCTTGTGTGTTTCTTTTATATTAAAGG NM_031299RefSeq chr12 - 6848807 6852066 CDCA3 83461 "cell division cycle associated 3, transcript variant 1"
GO:0008150|GO:0003674|GO:0007067|GO:0016567|GO:0005575|GO:0051301|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145296_PI430048170 0.48674162095655 0.8065842985702621.45541113257062 3.25701844032843 2.47154152116645 A P A 2.78620235477332 3.25619474673329 2.50490263305699 P P P LNCV6_145296_PI430048170 mRNA CCACCCGTGTCACAGCCTGGAGTTTTTATTCAATTAAATCTCTGTCTCTTGCCCAAAAAA NM_001270805 RefSeq chr1 - 114089291 114153850 SYT6 148281 "synaptotagmin VI, transcript variant 3"
GO:0019905|GO:0005215|GO:0030054|GO:0005886|GO:0046982|GO:0097038|GO:0042803|GO:0046872|GO:0005829|GO:0005544|GO:0060478|GO:0030276|GO:0030672|GO:0016021|GO:0048306|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126964_PI430048170 0.00889940207284252 0.3775112749297113.83076507290075 3.81926692497181 3.8367171027943 P P P 5.03492167124757 5.15175844572505 5.47890818703283 P P P LNCV6_126964_PI430048170 mRNA TCAAGGTTCTTGCTGCCTTCTTTAGCAGCATTTGATGGAAGATCTTTTATACATTTGTAANM_005612RefSeq chr4 + 56907875 56935844 REST 5978 "RE1-silencing transcription factor, transcript variant 1"
GO:0005515|GO:0003700|GO:0008285|GO:0006366|GO:0044212|GO:0006325|GO:0005634|GO:0046872|GO:0005829|GO:0071257|GO:0015271|GO:0050768|GO:2000798|GO:0002244|GO:0017053|GO:0060379|GO:0001046|GO:0046676|GO:0071805|GO:0070933|GO:0006355|GO:2000706|GO:0043065|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145607_PI430048170 0.2131195325968380.8745826269393161 1.2049399216919 11.2277974219929 11.2347699391296 P P P 11.2103867334643 11.4562865572154 11.5591156640129 P P P LNCV6_145607_PI430048170 mRNA CACATCCTCATTCTTATACTGCTTTTCGTGGCCACTTTGGACAAGTCCTGGTGGACTCTC NM_001425RefSeq chr19 + 48325371 48330553 EMP3 2014 epithelial membrane protein 3
GO:0005515|GO:0008219|GO:0008285|GO:0005886|GO:0032060|GO:0016049|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_134174_PI430048170 0.15063901199281 0.5035444171665390.368016778788338
0.5483263837862241.96836365524927 A A A 1.74686823682247 1.76025835312973
2.69925977706754 A A P LNCV6_134174_PI430048170 mRNA
CCTATAAGCTATTTGGGAAAAATTATAGTGTATGTTTCCCATCCAGAAACATGCCTTTCT NM_003454RefSeq chr16
- 3222324 3235186 ZNF200 7752 "zinc finger protein 200, transcript variant 1"
GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0003676|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_111368_PI430048170 0.9827076285458860.9046436697399420.352957329104521
1.07246348503788 0.893095394304283A A A 0.2997391694613191.72171096223942
0.333670573758699A A A LNCV6_111368_PI430048170 mRNA
GAGTTTTGGTTTACACATCAAGAAACAGACACACATACCTAGGAAAGATTTACACAATAG NM_001465RefSeq chr5
- 39105251 39219578 FYB 2533 "FYN binding protein, transcript variant 1"
GO:0005515|GO:0050852|GO:0005102|GO:0005634|GO:0015629|GO:0006607|GO:0032403|GO:0005829|GO:0035
556|GO:0007165|GO:0008150|GO:0006955|GO:0006468 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127047_PI430048170 0.00763044186960704 0.3097096989146612.79336714420782
3.00286586057139 3.15963171516349 A P P 4.25049108024114 4.6819872239108
5.01860079451794 P P P LNCV6_127047_PI430048170 mRNA
CTGTTGAAAAGGCATAGAAAGTTCTGGGAACATAAACATTTTTACCCTTTTCTATGCCAT NM_173630RefSeq chr18
- 70003805 70205726 RTTN 25914 rotatin GO:0007368|GO:0005737|GO:0036064 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136827_PI430048170 0.0316845818005423 0.3544698936796272.97329432532828
2.29582160043616 3.5627899235938 A A P 4.11004594140957 4.69169420734931
4.71334334514353 P P P LNCV6_136827_PI430048170 mRNA
GCCTTAAGCCTCTGTTGAACAGGAGAAGTGAAGCTGTTTGCAATTATATAATTTTCTAAT NM_001282730 RefSeq
chr2 - 27650809 27663840 SUPT7L 9913 "suppressor of Ty 7 (S. cerevisiae)-like, transcript variant 3"
GO:0005515|GO:0006355|GO:0043966|GO:0051457|GO:0030914|GO:0003713|GO:0006325|GO:0005634|GO:0006
351|GO:0004402 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131560_PI430048170 0.1892028933725450.6722964676635154.07328069240482
2.99184246477224 3.12397569052907 P P P 3.87578202859173 4.26076200047918 3.9990099114298
P P P LNCV6_131560_PI430048170 mRNA
GGTTTGTAAGTACGATCTGTAAAATAACTGGGATGAATTCCCATGTATACCTGTGTAAAT NM_014810RefSeq chr1
+ 179954772 180114880 CEP350 9857 centrosomal protein 350kDa
GO:0008017|GO:0005515|GO:0005813|GO:0005737|GO:0034453|GO:0016020|GO:0005819|GO:0005654 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132320_PI430048170 0.0459054501968049 0.7674593900487243.54496618385043
3.67985970121178 3.33813839097947 P P P 3.84170481038244 3.9725762535304
3.91157047348455 P P P LNCV6_132320_PI430048170 mRNA
GCAATAGAAGCTGCAAAGATGTGCCACTTTATCTATGAAATGGAGTTTTGTATACCAATA NM_015207RefSeq chr1
+ 19882394 19912944 OTUD3 23252 OTU deubiquitinase 3
GO:0004843|GO:0006508|GO:0044313|GO:0035871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144941_PI430048170 0.2400730339663570.9360143689952161 2.2790764354772
12.2390129992429 12.272615740888 P P P 12.2521186518855 12.4480551160795 12.370329730649
P P P LNCV6_144941_PI430048170 mRNA
TTCCACAGGAGGTATTTCTTTTTTATGTTGGTCCTGAGTATTTTGCAAATGCACAGAGAA NM_005850RefSeq chr1
- 149923316 149928252 SF3B4 10262 "splicing factor 3b, subunit 4, 49kDa"
GO:0048026|GO:0008380|GO:0006397|GO:0005515|GO:0010467|GO:0000166|GO:0000398|GO:0000375|GO:0005
681|GO:0005654|GO:0005689 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128249_PI430048170 0.0666165749464244 0.48515207365416 0.446449458669916
0.3728000220412180.564164492411508A A A 1.71065327264498 1.76344309102773

0.893095394304283 A A A LNCV6_128249_PI430048170 mRNA
CTCTAGCTCAATATATCCTCTGGGGACCATCAACATTTCCTATTAAAGATAACTACACCT NM_173687 RefSeq chr8
+ 143039208 143054303 C8orf31 286122 "chromosome 8 open reading frame 31, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135667_PI430048170 0.836656675841273 0.912255822905057 1.20003220819935
0.565137162245596 0.579475931445933 A A A 1.50904109742425 0.433328761166373
0.66151293099166 A A A LNCV6_135667_PI430048170 mRNA
CTGGGGACACCTGATTGCATGAACTGAAGTATACAATAACACAAATATTACAGTAAACAT NM_001017923 RefSeq
chr14 + 44897303 44907257 C14orf28 122525 chromosome 14 open reading frame 28 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_143901_PI430048170 0.00674461862630168 2.01799972665005 4.8962405206367
4.66071265115949 5.08877219985093 P P P 3.59598000460129 4.10642077072876
3.89120302564126 P P P LNCV6_143901_PI430048170 mRNA
AGAACACCAGGAGTATGATTCTGTTTCTGAAAGGTGAGTGGTGTATTGCTGTCATTGGGC NM_005982 RefSeq chr14
- 60644698 60649437 SIX1 6495 SIX homeobox 1
GO:0005515|GO:0007389|GO:0001657|GO:0001658|GO:0034504|GO:0003700|GO:0044212|GO:0007605|GO:0048
538|GO:0048704|GO:0001759|GO:0030878|GO:0048701|GO:0072075|GO:0043524|GO:0090191|GO:2001014|GO:0
030910|GO:0050678|GO:0048839|GO:0042472|GO:0072107|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131318_PI430048170 0.00244364563163905 0.3950457578454385.17589128272304
5.06254967501657 5.39596363120627 P P P 6.29026612733009 6.55975184299494
6.78246439488701 P P P LNCV6_131318_PI430048170 mRNA
GTGTTGGCTGCTGTATAGAACATGAACAAATGTCAAGGGATAGAAAATTACTTTGGATAT NM_000333 RefSeq chr3
+ 63864556 64003460 ATXN7 6314 "ataxin 7, transcript variant SCA7a"
GO:0005515|GO:0016578|GO:0006997|GO:0005730|GO:0006325|GO:0000226|GO:0005634|GO:0006351|GO:0016
363|GO:0042326|GO:0005737|GO:0043569|GO:0045944|GO:0003682|GO:0015630|GO:0005654|GO:0007601 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134908_PI430048170 0.417452341344468 0.851663281926067 6.62467496736728
6.33930232790005 6.61520211660586 P P P 6.33342710311072 6.93216556856828
6.94586078229548 P P P LNCV6_134908_PI430048170 mRNA
AAGAGGGGTTTCACTTGTATCTCCTTAGTTAACAACCCAGTTCCAGGATCGAGCCTAAAG NM_198236 RefSeq chr1
- 156934839 157045370 ARHGEF11 9826 "Rho guanine nucleotide exchange factor (GEF) 11, transcript
variant 2"
GO:0005515|GO:0030036|GO:0007264|GO:0006941|GO:0006928|GO:0038032|GO:0030010|GO:0007266|GO:0001
558|GO:0005829|GO:0005622|GO:0000910|GO:0005737|GO:0007411|GO:0005089|GO:0051056|GO:0048011|GO:0
001664|GO:0043065|GO:0097190|GO:0007186|GO:0016020|GO:0032321|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140302_PI430048170 0.1122370430939 0.680454924476549 0.342643242470619
0.371031125363682 0.334549836662434 A A A 0.619146594141525 0.756372606546741
1.25829197510244 A A A LNCV6_140302_PI430048170 mRNA
AACGTCAGGAGACTGACCCTTTTGATATCATTGCTAAGCCTCATTAAATGAATGAATGAA NM_138277 RefSeq
chr6_GL000256v2_alt + 3022639 3026004 C6orf25 80739 "chromosome 6 open reading frame 25,
transcript variant 7"
GO:0035855|GO:0005794|GO:0005886|GO:0007596|GO:0007229|GO:0005783|GO:0016021|GO:0008201|GO:0030
220 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134495_PI430048170 0.371220848222604 1.1274001176386 10.6435539435616
11.0803882964008 11.0454555987653 P P P 10.7597167802038 10.7224942018334
10.8064277140719 P P P LNCV6_134495_PI430048170 mRNA
GTGCGCTTCTGATTATTTTACTGGGGTCCATTGTCCAGATTTTTCTTTGATTGTAAAATA NM_019009 RefSeq chr11 -

1274367 1309662 TOLLIP 54472 toll interacting protein
GO:0005515|GO:0048471|GO:0007267|GO:0005150|GO:0005829|GO:0035556|GO:0045323|GO:0005737|GO:0006954|GO:0045092|GO:0030855|GO:0033235|GO:0004871|GO:0019900|GO:0031625|GO:0070062|GO:0031624|GO:0032183|GO:0006914|GO:0035325|GO:0016604|GO:0016310|GO:0007165|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137632_PI430048170 0.99922128867105 1.00569530264538 9.13481436668623 9.02876058168024 9.42962471602301 P P P 9.16367747309799 9.12447819250611 9.3046227213218 P P P LNCV6_137632_PI430048170 mRNA
TTCTAGTTTTCCTGTTCCCACCCTGGTCTTTGCCTGATGACAGAGAAACTTTCTAAAAAA NM_015983 RefSeq chr7 + 43926435 43956136 UBE2D4 51619 ubiquitin-conjugating enzyme E2D 4 (putative)
GO:0035519|GO:0005515|GO:0085020|GO:0070534|GO:0004842|GO:0016567|GO:0070979|GO:0016874|GO:0070936|GO:0044314|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139839_PI430048170 0.289300821162987 2.80531046457621 3.37859582424749 0.724496608888933 1.79507313497409 P A A 0.610152924718282 1.10300541125565 0.894595967257289 A A A LNCV6_139839_PI430048170 mRNA
CCATCAACATGCCAAGTCAGTAAAACTGATAGTTGATCAGATTTCAAGGTCTGGGGAGTA NM_001012414 RefSeq chr4 - 164954445 164977666 TRIM61 NA tripartite motif containing 61 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126773_PI430048170 0.0194505597815867 1.19098296782372 10.4669208886242 10.3854348121831 10.2964742134775 P P P 10.218765913644 10.0758414045286 10.0986730579038 P P P LNCV6_126773_PI430048170 mRNA
GTTTCTCCTGCTCCCTGTGTGTGTTAGAATTTTAACATAAATTCCACTTTCATAATATGG NM_017908 RefSeq chr19 + 58476163 58481234 ZNF446 55663 "zinc finger protein 446, transcript variant 1"
GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0005615|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134511_PI430048170 0.761909337570182 0.974143633889658 0.333520940616133 0.347030806405628 0.279584963451347 A A A 0.260085229904517 0.535368369771925 0.261151021043841 A A A LNCV6_134511_PI430048170 mRNA
GAGAGTGAAAAGCAAATAGACATATGTTCCTTACCAAGAAAAATTTGCTGCACTGAGAAA NM_001037499 RefSeq chr6 - 49960291 49964105 DEFB114 245928 "defensin, beta 114"
GO:0001530|GO:0005576|GO:0031665|GO:0042742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141646_PI430048170 0.203492950103717 0.895071281072764 9.43958331607588 9.46957870219015 9.23786382634187 P P P 9.43516319734265 9.68828455451811 9.50211803536387 P P P LNCV6_141646_PI430048170 mRNA
GAGGGCGAATTGCTATGACATTCCAAGCTCCAATAAAGACTGTCCCAGACTTTGAAAAAA NM_145798 RefSeq chr17 - 47807366 47821781 OSBPL7 114881 oxysterol binding protein-like 7
GO:0005515|GO:0071397|GO:0005776|GO:0005886|GO:0015485|GO:0006869|GO:0097038|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138754_PI430048170 0.629847551097555 1.0754715430536 7.21997726803527 7.04772831743945 7.26228202330041 P P P 6.53958798782218 7.22740463749071 7.33546449748742 P P P LNCV6_138754_PI430048170 mRNA
AGTCCAGGCAAGTTACAATGCCTTGTTGTGCCTCAATAAAAAAGTTACATGCACAAAAAA NM_032156 RefSeq chr12 - 30709551 30754514 CAPRIN2 65981 "caprin family member 2, transcript variant 3"
GO:0005515|GO:0017148|GO:0005813|GO:0030308|GO:0003723|GO:0090263|GO:0005102|GO:0005634|GO:0032092|GO:0005739|GO:0043235|GO:0005737|GO:0033138|GO:0050775|GO:0045944|GO:0005654|GO:0061003 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2134_PI430048170 0.115616553200875 0.442197643636116 0.243655372861864 0.281219101832204 0.312747024626582 A A A 1.91713809425726 1.569128671389 0.575819121431863 A A A LNCV6_2134_PI430048170 mRNA

CAAGTTGGACTCTTCCTCTCATCAGTACTAGTTGTCAAATTTAAAATGTGACAGTTAAAG NM_024726RefSeq chr2 - 236324146 236507535 IQCA1 79781 "IQ motif containing with AAA domain 1, transcript variant 1" GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137328_PI430048170 0.174525692609006 1.28671035751153 4.8748512175551 4.94799811922582 4.86039598439661 P P P 4.16538888392132 4.81829882970133 4.53676816283665 P P P LNCV6_137328_PI430048170 mRNA
GCCACCCACTGGGAGTCTTGTTTTTATTTATAATAAAATTGTTGGGGACACCTCAAAAAA NM_024036RefSeq chr11 + 66857404 66860475 LRFN4 78999 leucine rich repeat and fibronectin type III domain containing 4 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100827_PI430048170 0.282040670397657 0.832339958328645 0.409624826133494 0.362210830311062 0.360691549979316 A A A 0.449590778441351 0.4588437536668 0.958152614395986 A A A LNCV6_100827_PI430048170 mRNA
AGTGGAGAAGTTGAAAACAATTCAGACAACTCGGGAAGGTACCAAGGATTGGAGCACAGA NM_012452RefSeq chr17 - 16939083 16972088 TNFRSF13B 23495 "tumor necrosis factor receptor superfamily, member 13B" GO:0005515|GO:0001782|GO:0005887|GO:0002244|GO:0030889|GO:0004872|GO:0009897|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143610_PI430048170 0.745189198855426 1.14480418873597 1.55720101719824 0.921320671895211 0.390052033678844 A A A 1.02738067887563 0.50266955024758 0.93690913232822 A A A LNCV6_143610_PI430048170 mRNA
CTGGTGAGAAATTCTAAAAATGTGAAGACTATGGCAAAGTCTTTAAATGGTTGTCACACT NM_001256171 RefSeq chr19_GL383573v1_alt + 266528 293973 ZNF85 7639 "zinc finger protein 85, transcript variant 3" GO:0006355|GO:0003700|GO:0003714|GO:0005654|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139071_PI430048170 0.0321632595497910 0.400586774691656 0.469802120443401 0.392637802901232 0.416003420855586 A A A 1.3284085314197 2.14883954824655 1.64113635959551 A A A LNCV6_139071_PI430048170 mRNA
CTCGTGATCATTGAGAAAGTGTTTGAAACTTTCTCATGAAGTGTATATATAATGGCGTGA NM_017643RefSeq chr17 - 51177424 51260066 MBTD1 54799 mbt domain containing 1 GO:0006355|GO:0048706|GO:0008270|GO:0005634|GO:0006351|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143285_PI430048170 0.57999572158555 0.933777296852936 0.330454090077762 0.33462771935015 0.274077759973289 A A A 0.663584479264063 0.274785181302551 0.26089125421136 A A A LNCV6_143285_PI430048170 mRNA
TGCACTACACATGTGTAAGCATGATATAAAAAACAGTGGTATACAACAGTTATGTGATGC NM_001172780 RefSeq chr3 - 169795640 169812786 LRRC34 151827 "leucine rich repeat containing 34, transcript variant 1" GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143376_PI430048170 0.00228475205441989 1.71741776893346 9.27500867761021 9.27195076935378 9.40286238326406 P P P 8.64909632835223 8.39175519173451 8.56042155882153 P P P LNCV6_143376_PI430048170 mRNA
TATTATGGGGGCCCTTCGGTCTTAGAAGCTGTTTGACATGTATAATAAATGGCATTGACT NM_144723 RefSeq chr5 + 140700446 140706654 ZMAT2 153527 "zinc finger, matrin-type 2" GO:0005515|GO:0008270|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131342_PI430048170 0.0143708920014337 0.571652561413519 6.13759471394931 5.64823024769171 6.00455674691728 P P P 6.87276312690667 6.48742822426345 6.86148455929121 P P P LNCV6_131342_PI430048170 mRNA
ATGTTCATGTCTATCTCAACCAGGACCAGACCCTGTGACTTACTCGGTAATAACAGTCCA NM_020781 RefSeq chr7 + 149126415 149183026 ZNF398 57541 "zinc finger protein 398, transcript variant 2"

GO:0006355|GO:0005634|GO:0045893|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135817_PI430048170 0.0190990237389132 0.526788665820404 8.66812355791397 8.51952480329491 8.65629846549882 P P P 9.30615915731736 9.45157098500712 9.81617685335313 P P P LNCV6_135817_PI430048170 mRNA GGTCTCATTGAAGCCAACACAGAACTTGCTGCTGTGTTTTTTCTTCAGTGATAAATAAAA NM_003750 RefSeq chr10 - 119035028 119080822 EIF3A 8661 "eukaryotic translation initiation factor 3, subunit A"
GO:0005515|GO:0010467|GO:0033290|GO:0016282|GO:0005852|GO:0001732|GO:0001731|GO:0005730|GO:0003743|GO:0005634|GO:0006412|GO:0006413|GO:0005829|GO:0005737|GO:0016020|GO:0005198|GO:0071541|GO:0006446|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139605_PI430048170 0.61458000057811 0.782009977303749 0.880412696574185 1.94737497042208 0.523189065291703 A A A 0.519038777394308 2.03103912522303 1.84944521956261 A A A LNCV6_139605_PI430048170 mRNA TGTATTGAATGTCTGTGGATTTCCGTTTTCAGAAGTAGTACATTAGATCCTCCGGTTCTG NM_004099 RefSeq chr9 - 121338987 121370304 STOM 2040 "stomatin, transcript variant 1"
GO:0042470|GO:0005737|GO:0016020|GO:0005887|GO:0072562|GO:0051260|GO:0045121|GO:0005856|GO:0031982|GO:0005615|GO:0042803|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127223_PI430048170 0.114675364828234 1.99729610695178 2.50344075599047 3.03625181458114 3.74030031383507 A P P 2.34290817005381 2.21271209686306 1.97408713640122 A A A LNCV6_127223_PI430048170 mRNA TTTGAAAACATGCAGTAAAGTTGACTCTTGGGGTGCAGTTTTTGCACACGTAGGGCACAC NM_013284 RefSeq chr7 - 44072061 44082540 POLM 27434 "polymerase (DNA directed), mu, transcript variant 1"
GO:0005515|GO:0006281|GO:0071897|GO:0003887|GO:0030183|GO:0006310|GO:0005654|GO:0016446|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139191_PI430048170 0.379343673335535 1.04110386400286 0.292570707746679 0.277667140955406 0.435647083186141 A A A 0.293635885855663 0.258519387016848 0.284489476135536 A A A LNCV6_139191_PI430048170 mRNA TGTGTGTTCGATCATGAACAGATCAACAGTGTTTATTTGTTTTCCTACTGGATGAAGTAT NM_175883 RefSeq chr19 + 9185593 9188817 OR7D2 162998 "olfactory receptor, family 7, subfamily D, member 2"
GO:0050911|GO:0006355|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138606_PI430048170 0.34840890570831 1.04925525478037 0.331817689213057 0.335302841046884 0.499845206917427 A A A 0.321924959426733 0.29341788654335 0.349451819714733 A A A LNCV6_138606_PI430048170 mRNA GGTAAAGAGTTAGTTTGAGTTACTATCATGTCAAACGTGAAAATGCTGTATTAGTCACAG NM_001123041 RefSeq chr3 + 46353743 46360922 CCR2 729230 "chemokine (C-C motif) receptor 2, transcript variant A"
GO:0043310|GO:0019221|GO:2000451|GO:0090265|GO:0042803|GO:0006935|GO:0031727|GO:0004950|GO:0043025|GO:0035705|GO:0046641|GO:0032729|GO:0070098|GO:0042535|GO:2000464|GO:0007186|GO:0005887|GO:0045087|GO:0050870|GO:0016493|GO:0090026|GO:2000473|GO:0048471|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111993_PI430048170 0.0490877173950107 0.720763919801321 7.26196169147484 7.58925963402787 7.27636840176902 P P P 7.91694681712988 7.59830937008695 8.0209811423067 P P P LNCV6_111993_PI430048170 mRNA GATCTTCAGTCCTCTGCTTCATCTGTGAGCTTGCCTTCAGTCAAAAAGGCACCCAAAAAA NM_183419 RefSeq chr8 - 100257058 100310166 RNF19A 25897 "ring finger protein 19A, RBR E3 ubiquitin protein ligase, transcript variant 1"
GO:0005813|GO:0005737|GO:0016567|GO:0016874|GO:0000226|GO:0008270|GO:0016021|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_128117_PI430048170 0.690854929871947 0.963001899871403 8.0172700804266
7.88448457006668 7.63806092142935 P P P 7.89326350348695 8.04606190868073
7.77622914345953 P P P LNCV6_128117_PI430048170 mRNA
CATCATCCCAGCTGCTCCCAAATAAACTCCAGAAGAGGAATCTGTGGGCCTGTGAAAAAA NM_199173 RefSeq
chr1 + 156242159 156243332 BGLAP 632 bone gamma-carboxyglutamate (gla) protein
GO:0043627|GO:0045471|GO:0045124|GO:0033280|GO:0030282|GO:0005615|GO:0010043|GO:0071305|GO:0030
425|GO:0033594|GO:0005737|GO:0046848|GO:0042476|GO:0043204|GO:0008147|GO:0007155|GO:0005791|GO:0
014823|GO:0030500|GO:0005794|GO:0042493|GO:0007569|GO:0005509|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138379_PI430048170 0.00988549326848553 1.14342260777606 0.793577005119211
0.88483402047919 0.796422632191317 A A A 0.614043577380627 0.665340768801721
0.616671203633808 A A A LNCV6_138379_PI430048170 mRNA
GAAAGTCTAGGGACCATGAATGAATAGGCCAGCTGGGACAAATGAATTTAAAAAATCAGA NM_020828 RefSeq
chr19 + 56538947 56556801 ZFP28 140612 ZFP28 zinc finger protein
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_135350_PI430048170 0.000964105789557552 0.705039007526352 12.272615740888
12.1632812512001 12.1399439473606 P P P 12.641454057478 12.7189078067619
12.7300552708726 P P P LNCV6_135350_PI430048170 mRNA
GCCCTTGGCTTGTGTTATCGGACATTCTAATGCATATTTATAAGAGAAGTTTAACAAGTA NM_001040427 RefSeq
chr16 - 1809102 1827194 HAGH 3029 "hydroxyacylglutathione hydrolase, transcript variant 2"
GO:0005737|GO:0006750|GO:0005759|GO:0008270|GO:0004416|GO:0070062 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_128068_PI430048170 0.0153808100199815 1.35733733344785 5.30834479483994
5.29196448130851 5.48504409725454 P P P 4.8305466432841 5.08532153817174
4.84050058063997 P P P LNCV6_128068_PI430048170 mRNA
GCATTTTTTAAAACAAGAAAGTTTCCCCACCAGTGAATGAAAGTCTTGTGACTAGTGCTG NM_001885 RefSeq
chr11 - 111908619 111913213 CRYAB 1410 "crystallin, alpha B, transcript variant 1"
GO:0005515|GO:0008017|GO:0042542|GO:0005212|GO:0030018|GO:0030308|GO:0005886|GO:0005634|GO:0071
480|GO:0031109|GO:0032432|GO:0051403|GO:0046872|GO:0042803|GO:0042802|GO:0005829|GO:0005739|GO:0
005737|GO:0006936|GO:0006457|GO:0002088|GO:0015630|GO:0051260|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135641_PI430048170 0.131665036261378 1.1608328826146 11.2854368986147
11.161506787979 11.1424888528335 P P P 10.7875765289639 11.0590062824994
11.083319203674 P P P LNCV6_135641_PI430048170 mRNA
AGGAACCTTTGGTGTGTGGTGGGAAGCTATCAGAACAAGAAATGTAGGCATTTCCCGTTT NM_032758 RefSeq
chr22 - 41459716 41468704 PHF5A 84844 PHD finger protein 5A
GO:0008380|GO:0010467|GO:0003700|GO:0016607|GO:0000398|GO:0005654|GO:0045893|GO:0003677|GO:0016
363|GO:0006351|GO:0005689|GO:0005686 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_144124_PI430048170 0.153531631695434 0.954180399043998 0.262009548086246
0.325927496530116 0.30798348200054 A A A 0.428064294261229 0.335426258147529
0.334154571317988 A A A LNCV6_144124_PI430048170 mRNA
CATTTGTACCTCGAGTTTTAAACTGGTTCCTAGGGATGTGTGAGAATAAACTAGACTCTG NM_000588 RefSeq
chr5 + 132060653 132063203 IL3 3562 interleukin 3
GO:0008284|GO:0005135|GO:0045740|GO:0019221|GO:0007267|GO:0050731|GO:0042523|GO:0005576|GO:0005
125|GO:0005615|GO:0007399|GO:0006955|GO:0002763|GO:0008083|GO:0035162|GO:0070668 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138583_PI430048170 0.118246667376704 1.33793980344816 12.6094068543414

12.5843898331379 12.788566599788 P P P 12.5732529721245 12.0145790460548
12.0758645075124 P P P LNCV6_138583_PI430048170 mRNA
AGGGAGGGGAGGATAAGTGGGATCTACCAATTGATTCTGGCAAAACAATTTCTAAGATTT NM_001280790 RefSeq
chr9 - 133361448 133376166 SURF4 6836 "surfeit 4, transcript variant 4"
GO:0010638|GO:0005515|GO:0005793|GO:0000139|GO:0034498|GO:0033116|GO:0007030|GO:0005789|GO:0032
527|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143123_PI430048170 0.00764819930532375 1.73937457397528 6.34795795076407
6.66038788129564 6.30379560116351 P P P 5.74319879857563 5.76390872104987
5.40944309852127 P P P LNCV6_143123_PI430048170 mRNA
AGGGAGCTGGAGTTGAGCTGTTCCCCTAAATAAAAACCCTTCGGAAAGGAGACCAAAAAA NM_000951 RefSeq
chr19 + 49581329 49591008 PRRG2 5639 proline rich Gla (G-carboxyglutamic acid) 2
GO:0005515|GO:0005887|GO:0005509|GO:0005576 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130355_PI430048170 0.00430539143769518 0.539626128927947 10.2978911300686
10.1330424964167 10.5048011151816 P P P 11.0471526611853 11.1478024255306
11.4100994683818 P P P LNCV6_130355_PI430048170 mRNA
GTTTATTCCCAAGTATGCCTTAAGCAGAACAAATGTGTTTTTCTATATAGTTCCTTGCCT NM_004235 RefSeq chr9
- 107484851 107489766 KLF4 9314 Kruppel-like factor 4 (gut)
GO:0000987|GO:0005515|GO:0000790|GO:0001190|GO:0003700|GO:0070301|GO:0006366|GO:0044212|GO:0051
973|GO:0001221|GO:0003690|GO:0043551|GO:0034115|GO:0045444|GO:0046985|GO:0070373|GO:0051247|GO:0
045415|GO:0060761|GO:0014067|GO:0000122|GO:0031077|GO:0032270|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137012_PI430048170 0.019459453685191 0.694943027163181 9.14791324914993
9.4104708911796 9.40566333495022 P P P 10.0520879555893 9.72849707707246
9.75072708166304 P P P LNCV6_137012_PI430048170 mRNA
AGACATTGGCCAACTCTTTCAAAGTCTTTCTTTTTCCACGTGCTTCTTATTTTAAGCGAA NM_207627 RefSeq chr21
+ 42199688 42297244 ABCG1 9619 "ATP-binding cassette, sub-family G (WHITE), member 1,
transcript variant 5"
GO:0005515|GO:0019534|GO:0005886|GO:0033993|GO:0017127|GO:0010872|GO:0044281|GO:0042803|GO:0010
875|GO:0043231|GO:0005739|GO:0005543|GO:0015485|GO:0046983|GO:0009720|GO:0008203|GO:0042987|GO:0
042632|GO:0033344|GO:0006355|GO:0005794|GO:0010033|GO:0046982|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129856_PI430048170 0.0530488439401237 0.406921790168451 2.23628835606161
1.04896362839856 1.6210578483808 A A A 2.92923094538075 2.97617239416638
3.12714390742817 P P P LNCV6_129856_PI430048170 mRNA
CTGTATTGAACGGCAATGGGAACAAGAATGACTATCAAAGCAAACAAATGCATGGAATTA NM_004721 RefSeq
chr3 + 185363047 185489094 MAP3K13 9175 "mitogen-activated protein kinase kinase kinase 13,
transcript variant 1"
GO:0005515|GO:0019901|GO:0008385|GO:0007254|GO:0005524|GO:0046872|GO:0042803|GO:0042802|GO:0000
186|GO:0051092|GO:0046777|GO:0016020|GO:0004674|GO:0006468|GO:0004709 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_65020_PI430048170 0.00110270655842769 1.70010230298475 10.0825477459227
10.0283681883657 10.1396929077732 P P P 9.36207020499458 9.38501148442422
9.20201057558143 P P P LNCV6_65020_PI430048170 mRNA
TCAAGACCTTCCCCTACCTTTTGTGGAACCAGTGATGCCTCAAAGACAGTGTCCCCTCCA NM_006184 RefSeq
chr19 + 48900049 48923283 NUCB1 4924 nucleobindin 1
GO:0005515|GO:0005793|GO:0005794|GO:0016020|GO:0015630|GO:0005509|GO:0005615|GO:0003677|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137955_PI430048170 0.0877142047505478 0.641863868705627 6.54349077954278

6.3606669426751 6.71846109057278 P P P 6.75690541804397 7.20543291747798
7.50526228595144 P P P LNCV6_137955_PI430048170 mRNA
GGGGCTTCTGTGTTTGTTATGTATGCTGGGTGGGATATTGTGCTTTTATTTCTATATTGT NM_001286074 RefSeq chrX
+ 71366238 71466005 TAF1 6872 "TAF1 RNA polymerase II, TATA box binding protein (TBP)-
associated factor, 250kDa, transcript variant 3"
GO:0005515|GO:0010467|GO:0006368|GO:0006367|GO:0006366|GO:0044212|GO:0032436|GO:0060261|GO:0002
039|GO:0046777|GO:0018105|GO:0071339|GO:0018107|GO:0045944|GO:0016032|GO:0070577|GO:0004402|GO:0
006352|GO:0005669|GO:0016573|GO:0003713|GO:0005524|GO:0006974|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_98024_PI430048170 0.1879953150521590.7032827585126362.73211493469632 2.61895900086669
3.11086167999601 A A P 3.73619643270967 2.87506817100723 3.29330806515287 P P P
LNCV6_98024_PI430048170 mRNA
TTTACAAAGTGTTGGACTTACACTTCGTCTTGTCCAGTCAACTGATGGGTATGCTGGGCA NM_173791 RefSeq chr10
- 117280488 117375467 PDZD8 118987 PDZ domain containing 8
GO:0035556|GO:0016020|GO:0022604|GO:0007010|GO:0016032|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132126_PI430048170 0.0246844079126661 0.4940935859768210.421926305669981
0.2972444269295540.517386064608164 A A A 1.03074557847341 1.57739120165558
1.61729464254581 A A A LNCV6_132126_PI430048170 mRNA
GTCTATACAAATCAACCCACGGGAGACTATTTCACACAATTTAATACAGGAAGTCGATAA NM_015653 RefSeq chr22
+ 45413690 45432422 RIBC2 26150 RIB43A domain with coiled-coils 2 GO:0005515|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138102_PI430048170 0.1945825447863361.28423473742494 8.33194924532205
8.86472968441691 8.30416252485852 P P P 8.16155862239768 8.3349383436648
7.97041520502199 P P P LNCV6_138102_PI430048170 mRNA
TCTACCAGTTATGCGACTTGAATGTGGAAGAGTTGCAGAAGATCATTCACCGCAATGACG NM_001122823 RefSeq
chr9 + 133030674 133058503 GTF3C5 9328 "general transcription factor IIIC, polypeptide 5, 63kDa,
transcript variant 1"
GO:0005515|GO:0042797|GO:0010467|GO:0000127|GO:0005654|GO:0042791|GO:0035914|GO:0006383|GO:0003
677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126816_PI430048170 0.8168253301117660.8933214563629120.276869623824424
0.2809310417089231.27720875541301 A A A 0.34963652179342 1.53153542295413
0.338304487110926 A A A LNCV6_126816_PI430048170 mRNA
GTCTGTCTACCCTAGCAAAAGAAACACAGAAATTTAAATGTACTGGGAGTTATGTTGTTA NM_016383 RefSeq chrX
+ 115289716 115307556 LUZP4 51213 leucine zipper protein 4 GO:0005634 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_128638_PI430048170 0.5458909405929040.96656592104188 0.46912666890411
0.4700318008940830.262069581538097 A A A 0.4010152879370810.503139228083524
0.452231156976708 A A A LNCV6_128638_PI430048170 mRNA
TGTCCTTTTGGAAATGCCTCTGCATGAATTTATGGTAGCTCTGACTCATCTTTAAACAAT NM_001766 RefSeq chr1
+ 158179946 158186426 CD1D 912 CD1d molecule
GO:0071723|GO:0030882|GO:0030881|GO:0009986|GO:0030884|GO:0030883|GO:0005765|GO:0045058|GO:0042
393|GO:0005737|GO:0045089|GO:0005887|GO:0045087|GO:0042102|GO:0048007|GO:0048006|GO:0016032|GO:0
004872|GO:0034113|GO:0050839|GO:0016045|GO:0010008 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131721_PI430048170 0.21617359163522 1.16995214842976 5.33694203251856
5.17092338826492 5.21960081235078 P P P 5.26599115293887 4.94024373915739
4.80771134392615 P P P LNCV6_131721_PI430048170 mRNA
TTTTATCTCTGACATCTCTCTATTGCCCCATCTACCCTAATGCATCAATAAAACCTTAAG NM_016190 RefSeq chr1 -

152409242 152414274 CRNN 49860 cornulin
GO:0016337|GO:0005737|GO:0016020|GO:0009408|GO:0005509|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143711_PI430048170 0.3817425576988780.9280344096540811.9729440771277
11.8680379242373 12.0704811818292 P P P 11.9319874517587 12.0611580131485
12.2328147263732 P P P LNCV6_143711_PI430048170 mRNA
CTGGGCAATCCAGTTGACTTTTAAATGTAAGAATGGAATTCCAAACACTTAACACATTCA NM_022170RefSeq chr7
+ 74174375 74197099 EIF4H 7458 "eukaryotic translation initiation factor 4H, transcript variant 1"
GO:0005515|GO:0010467|GO:0048471|GO:0016281|GO:0003723|GO:0003743|GO:0006412|GO:0006413|GO:0005
829|GO:0019953|GO:0048589|GO:0000166|GO:0016020|GO:0006446|GO:0016032|GO:0044267|GO:0008135 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135438_PI430048170 0.0219128433551841 1.76006843735514 12.5522303951769
12.5373051683662 12.4435265795269 P P P 11.4055075874299 11.8310281664394
11.8132276511906 P P P LNCV6_135438_PI430048170 mRNA
CCTACTGTAATATGCACCCATCTCATCCACGTAGTAAAGTGAACTTAAAAATTCAATCAA NM_015894RefSeq chr20
- 63639704 63653610 STMN3 50861 "stathmin-like 3, transcript variant 1"
GO:0043005|GO:0030424|GO:0005794|GO:0035021|GO:0031110|GO:0019904|GO:0031122|GO:0031175|GO:0007
399|GO:0030426|GO:0005737|GO:0032314|GO:0051493|GO:0015631|GO:0007019 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_25281_PI430048170 0.7305908148062480.9646860342106850.33075369081702 0.311353151479522
0.442136864666686A A A 0.62219132693603 0.2759033860803170.320069649747053A A A
LNCV6_25281_PI430048170 mRNA
GAAAAATTTGACTCAGATGGGTTGAGAGGGCAATGGCAAGCAATCTTGGTACATGTCAGC NM_001292023 RefSeq
chr12 - 65855946 65882167 LOC100129940 NA "uncharacterized LOC100129940, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138825_PI430048170 0.0805387652319115 1.76305099265254 3.30865640634065
3.9393862935988 3.0314762750113 P P P 2.29166376729024 2.73551001037264
2.88818102803975 A P P LNCV6_138825_PI430048170 mRNA
ACCTGAATCCCAAGTGAGAAGAAAATCCTAAACCTCGTACCCAAACCTGTCTCCTTGATG NM_001193623 RefSeq
chr19 - 51388288 51390574 C19orf84 NA "chromosome 19 open reading frame 84, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134316_PI430048170 0.3646113928089661.11180952839819 5.07911303084607
4.86803891486039 5.25038338200889 P P P 5.00119724053461 4.72041081566868
5.02317305600167 P P P LNCV6_134316_PI430048170 mRNA
ATTATGGGATTTCCTTGCTTGTTCTGATACAATACAACTAGATGACCTTAAAAACCCTCA NM_004888RefSeq chr9
+ 114587713 114598872 ATP6V1G1 9550 "ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1"
GO:0008286|GO:0005886|GO:0006200|GO:0051701|GO:0005765|GO:0055085|GO:0005829|GO:0006879|GO:0033
572|GO:0008553|GO:0051117|GO:0090382|GO:0016471|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_60851_PI430048170 0.18165314647765 0.9261833215488787.58115977404684 7.6112414927684
7.57684810824882 P P P 7.64017912757922 7.64715054670865 7.80774946237295 P P P
LNCV6_60851_PI430048170 mRNA
ACAAGTTTTTCAAAGCCTACCAAAATCTCCCTACTGCCAATAAAGGGAAAATAAGAGATG NM_001190233 RefSeq
chr3 - 180983709 180989518 DNAJC19 131118 "DnaJ (Hsp40) homolog, subfamily C, member 19,
transcript variant 2"
GO:0005739|GO:0005515|GO:0043234|GO:0006457|GO:0006626|GO:0005743|GO:0048806|GO:0016021|GO:0044
267|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135397_PI430048170 0.0487998782787728 1.64274391135973 7.73839698409379
7.1024829973183 7.34419750535977 P P P 6.84917078928918 6.62421452091397

6.62379732730036 P P P LNCV6_135397_PI430048170 mRNA
AATCTTTCCAGAGCAGCTGAAAATCTCAGCATGGAGACAGTAAGAAAAGAGACGGGGTGT NM_024565 RefSeq
chr5 - 160251651 160312600 CCNJL 79616 cyclin J-like GO:0005634 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_75987_PI430048170 0.3571128935852821.15956507131805 3.31418025295621 3.44339681779267
3.1718487810276 P P P 3.02322391315437 2.7587726269758 3.4373688671507 P P P
LNCV6_75987_PI430048170 mRNA
GAAAACAGATTATTATTGCAACAAAGGAGCTTTTTTCCCCCTCGTGTTTATCAGCATTGG NM_001300825 RefSeq -
- 0 0 --- NA "zinc finger, CCHC domain containing 10, transcript variant 7" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_142428_PI430048170 0.1789369530603931.13129711962499 0.667232564857309
0.3806952828938590.615976817896141 A A A 0.2838570125100330.409817050975509
0.447150511827039 A A A LNCV6_142428_PI430048170 mRNA
GGGGATTTGCTTGTATGTATTAAACTTTTGACCTCTGAATATTTTACAGTCGTATGTGCTNM_032787 RefSeq chr3 +
100609588 100695481 ADGRG7 NA adhesion G protein-coupled receptor G7 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_131182_PI430048170 0.6449517252032431.3281163832212 0.575231963557463
1.96255482207043 0.536194509561903 A A A 0.9490652258662040.822015318553314
0.535883746767605 A A A LNCV6_131182_PI430048170 mRNA
GGTTTTTTAAAAAATCCTGGCCTGCTGAACGAATAGTTTCTTCTGCAACATTTGTTGTTA NM_001013743 RefSeq
chr11 - 123882925 123885642 TMEM225 338661 transmembrane protein 225 GO:0010923|GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56923_PI430048170 0.8913943334982990.9932909401524925.97670505912559 6.24652159303377
6.45738643367717 P P P 6.18296178462098 6.2463917447179 6.31714548693849 P P P
LNCV6_56923_PI430048170 mRNA
CCGATAGCCAGCAGTGGGACTTACAACTTGGACTTTGACAACATTGAGCTTGTGGATACC NM_206862 RefSeq chr10
+ 121989173 122254545 TACC2 10579 "transforming, acidic coiled-coil containing protein 2, transcript
variant 1"
GO:0021987|GO:0005815|GO:0008283|GO:0019904|GO:0005730|GO:0035257|GO:0032886|GO:0000226|GO:0030
953|GO:0005634|GO:0005737|GO:0015630|GO:0022027|GO:0005654|GO:0022008 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128073_PI430048170 0.2049689379610861.05560308963053 0.643719377326144
0.5179863237193430.586738006520145 A A A 0.43177787286522 0.535002833174203
0.547432883259381 A A A LNCV6_128073_PI430048170 mRNA
TGATTTATGTTGGCGAGTCTGAGAGCAAGCCCAAATGTGTTCTTCAAAGGACAATGGGAA NM_006138 RefSeq chr11
+ 60056627 60071115 MS4A3 932 "membrane-spanning 4-domains, subfamily A, member 3
(hematopoietic cell-specific), transcript variant 1"
GO:0005515|GO:0048471|GO:0051726|GO:0016021|GO:0012505 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130989_PI430048170 0.0531572861962609 1.67356235113543 10.3214766184993
10.1617267512808 10.2321006125212 P P P 9.84950701130688 9.18972948774388
9.36891538540299 P P P LNCV6_130989_PI430048170 mRNA
GACATGAAATACAGCAGCAGGTTACCAATGCGAACAGGTAGTTCGCATTTATGTAAAACA NM_001282705 RefSeq
chr2 - 10783390 10837977 PDIA6 10130 "protein disulfide isomerase family A, member 6, transcript
variant 2"
GO:0005515|GO:0042470|GO:0005793|GO:0034976|GO:0005886|GO:0005783|GO:0003756|GO:0043277|GO:0030
968|GO:0006457|GO:0005789|GO:0005788|GO:0045454|GO:0006987|GO:0044267|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139149_PI430048170 0.0270156720785209 0.63056704949121 9.03690219564464

8.91307744301874 8.54780344423503 P P P 9.48072807671078 9.64682973376411
9.39845829506986 P P P LNCV6_139149_PI430048170 mRNA
TCTGGGCTGCCTGGCAGAGAGCCTTGCTGTTTACAATTAAAATGTTTCTGCCACAAAAAA NM_001286613 RefSeq
chr6 - 109444062 109465968 MICAL1 64780 "microtubule associated monooxygenase, calponin and LIM domain containing 1, transcript variant 3"
GO:0005515|GO:0005882|GO:0017124|GO:0017137|GO:0019417|GO:0003779|GO:0071949|GO:0007165|GO:0005737|GO:0007010|GO:0016709|GO:0001933|GO:0030042|GO:0008270|GO:0043154|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119268_PI430048170 0.5413302860719191.15711811050617 2.83421310950285
2.54413880764569 2.40174240489279 A A A 1.47998629472621 2.83896201667066
2.54254878853431 A P P LNCV6_119268_PI430048170 mRNA
ACCCCTTCCAAGATTGTGAGAAGATGGGTAGCTGGGCATCAATAAATATTGAATCAATTG NM_004177RefSeq chr11
+ 59755058 59805882 STX3 6809 "syntaxin 3, transcript variant 1"
GO:0005515|GO:0043005|GO:0008284|GO:0005886|GO:0050544|GO:0042581|GO:0031201|GO:0042582|GO:0060291|GO:0006886|GO:0030425|GO:0031175|GO:0030426|GO:0016324|GO:0050921|GO:0005911|GO:0000149|GO:2000010|GO:0031629|GO:0048278|GO:0070062|GO:0005773|GO:0030027|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130906_PI430048170 0.6698257999708311.25928843560736 0.345480487567481
1.34501185150657 1.94406074596507 A A A 0.2471576682405891.35658049751 1.222916436657 A A A LNCV6_130906_PI430048170 mRNA
ACTCAATTCCTATTGGAGTGCAATCCTTACTTGAGAACTTTATTACTCTTGTTCTGTGTA NM_001008224 RefSeq chr15
- 70654553 70702281 UACA 55075 "uveal autoantigen with coiled-coil domains and ankyrin repeats, transcript variant 2"
GO:0005515|GO:0048471|GO:0042347|GO:0008630|GO:0008631|GO:0005576|GO:0005634|GO:0005635|GO:0043280|GO:0005739|GO:0003674|GO:0008150|GO:0005737|GO:0043293|GO:0016020|GO:0050728|GO:0042307|GO:0005654|GO:0005856|GO:0009411|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139958_PI430048170 0.0757395599827111 0.4517054173304991.77395617938359
0.59717294887834 0.522753151084035A A A 1.90232722686904 2.39613358939513
2.35010290369691 A A A LNCV6_139958_PI430048170 mRNA
AAAGAATCCGAGCATGGAAGCTCTAGAACGTATGGTCCAGTGTGGCAGCCACTATAATAT NM_001136156 RefSeq
chr19 + 32345607 32387667 ZNF507 22847 "zinc finger protein 507, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128760_PI430048170 0.5727876214465431.1498995869206 1.03429637157066
0.4123244866357610.246437153686119A A A 0.3699341379080270.439341928667317
0.402526639494034A A A LNCV6_128760_PI430048170 mRNA
CCCTTGTTAAAAACGTGGTGCAGCTATTGCGGTAATAAAATCTTTAATGCACTCGGAAAA NM_005396RefSeq chr10
+ 116620952 116645143 PNLIPRP2 5408 "pancreatic lipase-related protein 2, transcript variant 1"
GO:0004806|GO:0044241|GO:0005509|GO:0047372|GO:0006641|GO:0005576|GO:0044281|GO:0019376|GO:0004620|GO:0047714|GO:0009395|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138093_PI430048170 0.2654012421009370.9259350664542889.90489837669693
9.85415820830602 9.66041238300643 P P P 9.95671330334666 9.95552238876625
9.84902379852425 P P P LNCV6_138093_PI430048170 mRNA
TTGGAGATGTTTTTCCAAGAGCATAATGTACATTAAAGTCTTCGAGTTGAGACAATCCCC NM_015511RefSeq chr20
+ 36236416 36256941 AAR2 25980 "AAR2 splicing factor homolog (S. cerevisiae), transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141848_PI430048170 0.1109784914751070.7460709112291290.257920758152035
0.3056122193826280.452017608457077A A A 0.4709418300787091.0209622543261
0.746393033365187A A A LNCV6_141848_PI430048170 mRNA

GGTAAATTGACCTAAAGGTGACCTCTGACGATTTCCTGAAATAAATATGCAATGTTACAT NM_152577 RefSeq chrX
+ 22272912 22274459 ZNF645 158506 zinc finger protein 645
GO:0005737|GO:0016567|GO:0016874|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135165_PI430048170 0.144974035650406 1.87211994616504 3.581292348976
3.21245951139106 3.6734199871301 P P P 2.95280929148475 1.5652436885138
2.89881191331914 P A P LNCV6_135165_PI430048170 mRNA
ATCTACTGCAGGAGAACCTGCTACCACCCCACGAGTGTCTACCTGCCTGGTTGCCTAAAC NM_001277332 RefSeq
chr17_JH159148v1_alt - 35274 41732 KRTAP9-7 NA keratin associated protein 9-7 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129198_PI430048170 0.546204370218323 1.23342712895013 0.584452337683674
1.38110577070499 0.315433276763169 A A A 0.395591142389481 0.635106445158811
0.553641314085251 A A A LNCV6_129198_PI430048170 mRNA
GGTGCAAAGCGAAACTGGTTGCTCAAGTTGATAGAAAACAAAATTCTGAATATCTTCAAA NM_005924 RefSeq chr7
- 15611211 15686683 MEOX2 4223 mesenchyme homeobox 2
GO:0005515|GO:0003700|GO:0001757|GO:0008015|GO:0001205|GO:0005634|GO:0007275|GO:0001525|GO:0000
978|GO:0006351|GO:0043565|GO:0001077|GO:0005737|GO:0016607|GO:0007519|GO:0070997|GO:0045944|GO:0
060021|GO:0060173|GO:0000980 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132156_PI430048170 0.00214342209543894 0.522867547996289 4.72082502780975
4.50546796505066 4.84003036042301 P P P 5.45291484885029 5.68510730379247
5.73873856834548 P P P LNCV6_132156_PI430048170 mRNA
GTAGAAGGAGAGAAATTTGTGTGTGGCTTTTGTAAATTTTGACCGATTGCAGCAATTAAA NM_182978 RefSeq chr18
+ 11689014 11885684 GNAL 2774 "guanine nucleotide binding protein (G protein), alpha activating
activity polypeptide, olfactory type, transcript variant 1"
GO:0007608|GO:0001664|GO:0005886|GO:0005834|GO:0003924|GO:0007268|GO:0031683|GO:0005525|GO:0007
193|GO:0046872|GO:0007191|GO:0006184|GO:0007165|GO:0007190|GO:0001975|GO:0031000|GO:0004871|GO:0
007189|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143263_PI430048170 0.47959742778084 1.03894214519476 0.312878870969594
0.319860270428638 0.498106080070106 A A A 0.330864058379709 0.293183998962463
0.348639161099728 A A A LNCV6_143263_PI430048170 mRNA
GCTTTATGAAACAATGTCCTTCATTTGCTGGCAAGAAGATAAAATATGACAGAACCTGTT NM_175856 RefSeq chr5
+ 129904829 130186634 CHSY3 337876 chondroitin sulfate synthase 3
GO:0030206|GO:0000139|GO:0005975|GO:0032580|GO:0009405|GO:0044281|GO:0016021|GO:0030204|GO:0050
510|GO:0047238|GO:0030203|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129207_PI430048170 0.0771558953669137 0.94053470438654 0.290274208701798
0.303503392920208 0.319074085186011 A A A 0.445008001502687 0.381531646063709
0.350173254949689 A A A LNCV6_129207_PI430048170 mRNA
CCAGGTATCTGATGACTATATGTAGCTCCTATTTACAGGCTCAGTGAGAGAAGAGAAGCA NM_013340 RefSeq chr5
+ 141051375 141053962 PCDHB1 29930 protocadherin beta 1
GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126718_PI430048170 0.0258434367929515 0.843633837291991 11.083319203674
10.9526227161607 10.9309765350966 P P P 11.2927875955966 11.2791098646767
11.1301356081291 P P P LNCV6_126718_PI430048170 mRNA
GTGACACTCCATGAAAAGAAGTTCTTGCATACCGGAAAGTTGAATAAATGGATGAATTCA NM_024602 RefSeq chr1
- 45002547 45011355 HECTD3 79654 HECT domain containing E3 ubiquitin protein ligase 3
GO:0019905|GO:0005515|GO:0048471|GO:0005737|GO:0004842|GO:0042787|GO:0016874|GO:0043161|GO:0005
634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143603_PI430048170 0.851199724273851 0.957797840131295 7.67908723417416
7.51473758936801 7.8356525330907 P P P 7.33842129476496 7.8733576712677
7.94887510322867 P P P LNCV6_143603_PI430048170 mRNA

GAGTAATTCTAATCTCTTCTGTGTTTTCCTTGCCTTAACCACAAATTGTGGTGCTTTTTG NM_001258038 RefSeq chr4
+ 123396794 123403760 SPRY1 10252 "sprouty homolog 1, antagonist of FGF signaling (Drosophila),
transcript variant 1"
GO:0001656|GO:0005515|GO:0001657|GO:0008285|GO:0005886|GO:0000132|GO:0042059|GO:0001759|GO:0051
387|GO:0005829|GO:0046580|GO:0007173|GO:0043407|GO:0040037|GO:0070373|GO:0060449|GO:0034261 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127171_PI430048170 0.2127283269117191.08181625880373 0.570831572656511
0.7719228951811930.598223374632324A A A 0.4798681108407780.556123144913339
0.571316637271193A A A LNCV6_127171_PI430048170 mRNA
GACTTGCGATCAAAAAGTAAAACACATTCTGAAAGACTATTGAGCCATTGATAGAAAAGC NM_001971RefSeq chr12
- 51328442 51346679 CELA1 1990 "chymotrypsin-like elastase family, member 1"
GO:0004252|GO:0005576|GO:0061113|GO:0000122|GO:0009791|GO:0046872|GO:0006954|GO:0035264|GO:0042
127|GO:0045944|GO:0031017|GO:0006508|GO:0045595|GO:0016055 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127730_PI430048170 0.6975597515324391.03769048361376 9.71274101012343
9.80043634080289 9.75565228401244 P P P 9.40163277739091 9.74198251169245
9.91941748040651 P P P LNCV6_127730_PI430048170 mRNA
CTAAAGCTACTAGAAAGGCTTTGGGAACTGTCAACAGAGCTACAGAAAAGTCTGTAAAGA NM_001282382 RefSeq
chr5 + 160421909 160428744 PTTG1 9232 "pituitary tumor-transforming 1, transcript variant 1"
GO:0005515|GO:0051276|GO:0017124|GO:0006355|GO:0003700|GO:0004869|GO:0006366|GO:0005634|GO:0007
283|GO:0031145|GO:0005829|GO:0010951|GO:0005737|GO:0007067|GO:0006281|GO:0007059|GO:0000278|GO:0
051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141088_PI430048170 0.8656700695449281.01336645521994 9.40226821527127
9.40257190249559 9.18372787804387 P P P 9.30884957191822 9.53868533295161
9.05386851641095 P P P LNCV6_141088_PI430048170 mRNA
AATTTGATACATTCGTCAGACACAAGATCCCAGTGATGGCCTTGGTAGGGAATGATGCTG NM_006844RefSeq chr19
- 15114973 15125799 ILVBL 10994 ilvB (bacterial acetolactate synthase)-like
GO:0008150|GO:0003674|GO:0000287|GO:0016020|GO:0008152|GO:0016021|GO:0030976|GO:0016740 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127818_PI430048170 0.0476265452365868 0.9640210503240440.357685880506133
0.3817221139873880.330858332780146A A A 0.4207204287250560.417862054077711
0.390530672545338A A A LNCV6_127818_PI430048170 mRNA
CGTCAGTGGCCACTCTGGGTGGTTCTAAGCCAGGAGCCGAGATGGAAATTTAGACAACTT NM_178510RefSeq chr11
+ 113387790 113400418 ANKK1 255239 ankyrin repeat and kinase domain containing 1
GO:0004674|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130774_PI430048170 0.9086463934584171.01072326409667 14.4471618092667
14.3397338089349 14.1494434834321 P P P 14.4417596574525 14.2249760337651
14.2281645705706 P P P LNCV6_130774_PI430048170 mRNA
TCAGCTTGCACAAACTGGTTGAACGGCAGGAATGAAAAATAAAGAGAGATGGCTTTTGTG NM_004753RefSeq chr1
- 12567909 12617731 DHRS3 9249 dehydrogenase/reductase (SDR family) member 3
GO:0007603|GO:0042622|GO:0060411|GO:0009055|GO:0052650|GO:0001523|GO:0003151|GO:0030278|GO:0000
166|GO:0048387|GO:0060349|GO:0042572|GO:0005789|GO:0060021|GO:0016021|GO:0004745|GO:0007601|GO:0
055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139427_PI430048170 0.1963421925787080.7390130800546 4.46121355762313
3.84008014286204 4.60551863142011 P P P 4.45405270160247 4.797083640485
5.01824840696379 P P P LNCV6_139427_PI430048170 mRNA
CGCAAGTCTTTCTCGACAATCAAGAATGTTATTAATGTGTAATACTGAGCACTTTACTTC NM_000297RefSeq chr4
+ 88007646 88077779 PKD2 5311 polycystic kidney disease 2 (autosomal dominant)
GO:0071464|GO:0051219|GO:0005515|GO:0008092|GO:0001658|GO:0060674|GO:0042805|GO:0042994|GO:0071

158|GO:0042803|GO:0042802|GO:0061333|GO:0007507|GO:0001947|GO:0009925|GO:0050982|GO:0042127|GO:0
043398|GO:0051117|GO:0070062|GO:0051209|GO:0071470|GO:0031587|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142229_PI430048170 0.2883451055666741.7980925213291 1.43621328705617
1.59621615933452 2.94702292486275 A A P 0.7940789382220130.315714588235227
2.16884396450462 A A A LNCV6_142229_PI430048170 mRNA
GGACTTCCTCATTCTTTGTGGTAGTACAATGATTGGTAGCAGGTAAAATAAATACATAGA NM_030766RefSeq chr12
+ 12071467 12099693 BCL2L14 79370 "BCL2-like 14 (apoptosis facilitator), transcript variant 2"
GO:0005515|GO:2001238|GO:0005737|GO:0019901|GO:0016020|GO:0043229|GO:0006915|GO:0042981|GO:0012
505|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91759_PI430048170 0.475083783194775 1.12860050821872 4.33384612772416 3.74175801290497
4.01706850634982 P P P 3.66430400943092 3.91398098140543 4.02809657449907 P P P
LNCV6_91759_PI430048170 mRNA
TGTACAGCAGAGAGCCTGGAGGAAATAAAATTGGCCTGAAAGACGTCATTACTCTACGGA NM_130464RefSeq chr16
- 21402133 21425337 NPIPB3 23117 "nuclear pore complex interacting protein family, member B3"
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129798_PI430048170 0.9289895488847691.03816034939035 0.353965180577204
1.71831098706473 0.372401466359778A A A 0.4284423181331660.83430252240476
1.33273428137892 A A A LNCV6_129798_PI430048170 mRNA
TGGGCCATGAACTCATACCTGCCAATGAGTCAAACATAGTATCTTTATGTAGATACTTAG NM_207391RefSeq chr19
+ 32675406 32678300 RGS9BP 388531 regulator of G protein signaling 9 binding protein
GO:0007603|GO:0050908|GO:0022400|GO:0016021|GO:0009968|GO:0016056 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_122951_PI430048170 0.5482587106082440.7303577230879990.3869944669408 0.7869286313524
0.25268288974298 A A A 1.68767101636367 0.3674141221835990.347925752564809A A A
LNCV6_122951_PI430048170 mRNA
GTCGGTGTGCGAGCGCCTCAACCTGGCGCTGTCGCTCAGCCTCACCGAGACGCAGGTGAANM_001290079 RefSeq
chr4 - 1402931 1406442 NKX1-1 NA NK1 homeobox 1 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140262_PI430048170 0.3586915659898450.7093425456146880.399452038729394
0.3769789632284020.350407033391337A A A 0.4434553019984441.47368466839693
0.433366688492693A A A LNCV6_140262_PI430048170 mRNA
GTTCCAGTTTCTCTTCCATTCTGTGTCACAGACACCAACACACCACTCATTGGAAAATGG NM_006317RefSeq chr5
+ 17217560 17276845 BASP1 10409 "brain abundant, membrane attached signal protein 1, transcript
variant 1"
GO:0005515|GO:0008406|GO:0072112|GO:0030054|GO:0044212|GO:0005886|GO:0003714|GO:0007356|GO:0019
904|GO:0060231|GO:0060421|GO:0005634|GO:0031982|GO:0072075|GO:0030426|GO:0005737|GO:0008180|GO:0
016607|GO:0021762|GO:0060539|GO:2001076|GO:0005856|GO:0045892|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139899_PI430048170 0.1905412082436140.2487346008808940.487523565324042
1.19883713273344 0.477149019698607A A A 0.6476215149301933.09564173094286
3.37113358822512 A P P LNCV6_139899_PI430048170 mRNA
CTGTTTCAAGCCAGTGTGTTTTTTCTTCGTTCTGTAATAAACAGCCAGGAGAAAAGTGCC NM_005491RefSeq chrX
+ 150445453 150514178 MAMLD1 10046 "mastermind-like domain containing 1, transcript variant 2"
GO:0003674|GO:0006357|GO:0005634|GO:0005575|GO:0008584|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142838_PI430048170 0.00675817471588542 0.6438069881644274.42281740706465
4.19326382008589 4.49356877599849 P P P 4.96284427169776 4.88885281651277 5.1661682390056
P P P LNCV6_142838_PI430048170 mRNA

AAGATGAAGCAGGTCTCTTATGACTGTTCCTGCCAACGAGTTATGGAGGTAAATGACTGT NM_014484 RefSeq chr20 + 50958813 50961862 MOCS3 27304 molybdenum cofactor synthesis 3
GO:0005515|GO:0002143|GO:0016779|GO:0034227|GO:0006767|GO:0032447|GO:0044281|GO:0005524|GO:0046872|GO:0005829|GO:0032324|GO:0002098|GO:0016783|GO:0018192|GO:0006766|GO:0018117|GO:0006777|GO:0004792|GO:0042292|GO:0070733 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130674_PI430048170 0.744955727696372 0.99594289591269 0.365577766437912 0.364978010702497 0.373961260054669 A A A 0.392886694092746 0.343884690403253 0.384880913465385 A A A LNCV6_130674_PI430048170 mRNA
CAGGAAAGAGTGGTTTCTGCGTGTGTATATTTGTAATATATGATATTTTTCATGCTCCAC NM_007197 RefSeq chr12 + 130162458 130165740 FZD10 11211 frizzled class receptor 10
GO:0005515|GO:0042813|GO:0017147|GO:0009986|GO:0071300|GO:0004930|GO:0034259|GO:0038031|GO:0032855|GO:0005737|GO:0007186|GO:0005887|GO:0030182|GO:0032956|GO:0043507|GO:0060070 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106022_PI430048170 0.671564203991585 1.05118146018754 5.60180619001383 5.20304182709748 5.53699697613618 P P P 5.30846760782881 5.48984972618458 5.35209387692655 P P P LNCV6_106022_PI430048170 mRNA
AGATCTCAGTGAAGAGAAGGGGTCTGTCCAGATGGACTCCACCCTGCAGGGAGACATGAG NM_006893 RefSeq chr1 - 206591642 206612551 EIF2D 1939 "eukaryotic translation initiation factor 2D, transcript variant 1"
GO:0002192|GO:0005737|GO:0022627|GO:0001731|GO:0003743|GO:0005654|GO:0005634|GO:0004872|GO:0032790|GO:0006886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136775_PI430048170 0.203632196438821 1.21036708450179 4.93705604405987 4.94232213317536 5.04348478924091 P P P 4.65224497386297 4.97137647520929 4.42235568734863 P P P LNCV6_136775_PI430048170 mRNA
TCAGTAGGTCAGATGCCACCTCACAGGACCAAGGTGCCGATTAAACCGGAATACATTCAG NM_014047 RefSeq chr19 + 13774442 13778772 C19orf53 28974 chromosome 19 open reading frame 53 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139506_PI430048170 0.0404692301735257 0.674539492844471 8.12074737542459 7.66688284584257 8.01107813194998 P P P 8.44435074974589 8.49421277715516 8.59780296990549 P P P LNCV6_139506_PI430048170 mRNA
CTGGACTTCCAGACTTCTATCACATGAGAAAAAATAAAACTGATTATTGGTTTAAGCTGC NM_020933 RefSeq chr19 + 9140379 9163415 ZNF317 57693 "zinc finger protein 317, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126819_PI430048170 0.00503005957356416 0.488570646680237 8.09334220333778 8.04039850133695 8.20547975594232 P P P 8.96759358765902 9.10007353447045 9.35013442819539 P P P LNCV6_126819_PI430048170 mRNA
AGGATAGAGCTTCATTCCATACCAAAGACTTATCACACCATGTGCCTATACACCCAGCAG NM_032367 RefSeq chr5 - 77076706 77087205 ZBED3 84327 "zinc finger, BED-type containing 3"
GO:0016020|GO:0045944|GO:0090263|GO:0050821|GO:0001933|GO:0016055|GO:0003677|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145227_PI430048170 0.00715779154854181 0.622664162988739 5.8738784347141 5.70505316582592 6.0545972638633 P P P 6.51937908689526 6.69810218542603 6.47804928513298 P P P LNCV6_145227_PI430048170 mRNA
AGAGAGGCGTCAAGTCATTTGCACTTTGTACCTGTAAGTTAGGTAATAAACTATTATACT NM_001300755 RefSeq chr1 - 212992181 213015509 ANGEL2 90806 "angel homolog 2 (Drosophila), transcript variant 3"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_30348_PI430048170 0.191793096671249 0.860891877036563 6.0722248407827 6.3096650325231 6.48314932391789 P P P 6.60779801638352 6.44350559519318 6.48617894717073 P P P

LNCV6_30348_PI430048170 mRNA
AGGTATTCCAGAAAAAGACATGGATGAAAGACGACGACTTCTTGAACAGAAAACACAAGA NM_001098507
RefSeq chr17 + 32350137 32370449 ZNF207 7756 "zinc finger protein 207, transcript variant 3"
GO:0005515|GO:0008017|GO:0007094|GO:0006355|GO:0003700|GO:0005874|GO:0051983|GO:0050821|GO:0005
730|GO:0005634|GO:0003677|GO:0000070|GO:0000777|GO:0000776|GO:0008270|GO:0008608|GO:0008201|GO:0
051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116598_PI430048170 0.1433095400172581.7759914561813 5.58265926400946
5.75456508613614 5.8423992077255 P P P 5.58921678092997 4.25417236396635 4.4896468653691
P P P LNCV6_116598_PI430048170 mRNA
AGTGAAAAAACATTGAGCTAGGAGCCAAGACCCATCTCTTCACTATTTTGGTATTGTGCA NM_005013RefSeq chr11
+ 17276738 17331523 NUCB2 4925 nucleobindin 2
GO:0005515|GO:0005793|GO:0005794|GO:0005886|GO:0005783|GO:0005509|GO:0005635|GO:0005615|GO:0003
677|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143857_PI430048170 0.4905918657918750.5773388348012160.500107557072917
0.6711461511904750.637448263335633A A A 0.5825402673562922.33902917873374
0.427680897801688A A A LNCV6_143857_PI430048170 mRNA
AAACAAGGACATGAAAGAGGCTATTGGAAGGCTTTTCCACTATCAGAAGAGGGCTGGTTGNM_001005184 RefSeq
chr1 + 158754815 158755847 OR6K6 NA "olfactory receptor, family 6, subfamily K, member 6" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119388_PI430048170 0.0241019855839054 0.6685721631889677.48496974032414
7.47727566865656 7.69296856282298 P P P 7.89449696036338 8.16944786471092
8.31344873163076 P P P LNCV6_119388_PI430048170 mRNA
AGGACTCATGGGGACTCCTACCCATTTGATGGGCCAGGAAACACGCTGGCTCATGCCTTT NM_002423RefSeq chr11
- 102520507 102530747 MMP7 4316 matrix metallopeptidase 7
GO:0002780|GO:0050830|GO:0042493|GO:0005578|GO:0005576|GO:0005615|GO:0050829|GO:0022617|GO:0030
198|GO:0042127|GO:0030574|GO:0006508|GO:0008270|GO:0004222|GO:0002779|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_83453_PI430048170 0.2377463108766650.8349287471285736.03400524825649 5.94001800894562
5.69238074608796 P P P 6.42127812171733 5.92901615363585 6.07288629862117 P P P
LNCV6_83453_PI430048170 mRNA
GATTTCTGTGTCCTGACACCACCTCCCCATCCACCACCAAAGTAGCCGGGGTGAGCCCCA NM_001002914 RefSeq
chr17 + 7351888 7354943 KCTD11 147040 potassium channel tetramerization domain containing 11
GO:0007049|GO:0005737|GO:0016567|GO:0045666|GO:0051260|GO:0045879|GO:0040008|GO:0007406 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143112_PI430048170 0.2081147339602460.5997812739710140.4314887119640370.4575146214433
0.417130863166607A A A 1.20513327172644 1.64113635959551 0.421744303668758A A A
LNCV6_143112_PI430048170 mRNA
ACTGTATGTTCACCCTCTGAAGTGGGTACCCAGTCTCTTAAATCTTTTGTATTTGCTCAC NM_021804RefSeq chrX
- 15561032 15602069 ACE2 59272 angiotensin I converting enzyme 2
GO:0005515|GO:0002003|GO:0005886|GO:0046718|GO:0005615|GO:0001817|GO:0019229|GO:0042312|GO:0003
081|GO:0005737|GO:0001948|GO:0001618|GO:0042127|GO:0004180|GO:0006508|GO:0008241|GO:0070062|GO:0
009986|GO:0060135|GO:0050727|GO:0005576|GO:0009615|GO:0004175|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139707_PI430048170 0.0035123346123372 0.60950812452632711.3113798377676
11.1633189418828 11.0106215784944 P P P 11.7733137622592 12.010639001958
11.8496060477252 P P P LNCV6_139707_PI430048170 mRNA
TATACCAGTGTGTGTTCATCTACCCATGAGGAATAAAACCATGCAGCAGCATGCAAAAAA NM_182612RefSeq chr11
- 767222 777487 PDDC1 347862 Parkinson disease 7 domain containing 1
GO:0008150|GO:0003674|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_144918_PI430048170 0.0227303816808453 0.55210495151809 8.80816733633621
9.08768488604578 9.33789008752555 P P P 9.9569242094885 9.87203767108798
10.0202876772727 P P P LNCV6_144918_PI430048170 mRNA
GTGCTGAATGCAAGTAGAGCCAAGAAATGACAATCTTTGTTGTGTGTGCATTTTTATAAT NM_014377 RefSeq chr7
- 103312473 103344873 DNAJC2 27000 "DnaJ (Hsp40) homolog, subfamily C, member 2, transcript
variant 1"
GO:0043130|GO:0030308|GO:0031965|GO:0005634|GO:0003677|GO:0006351|GO:0005829|GO:0006260|GO:0042
393|GO:0005737|GO:0003682|GO:2000279|GO:0030544|GO:0051083|GO:0045893|GO:0016568 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130973_PI430048170 0.211347992251213 0.794838978247148 0.474027903366102
0.509112735138974 0.414772560076486 A A A 1.03657975967862 0.846896565661803
0.449127994805922 A A A LNCV6_130973_PI430048170 mRNA
CTGCATGCAGCCAAATGGAGCATCTCTGTTCTTTTTAATAATTTCAGAATAAAGTCTCAT NM_002143 RefSeq chr1
+ 32886496 32894646 HPCA 3208 hippocalcin GO:0048839|GO:0005509|GO:0003779 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132398_PI430048170 0.169826366161437 2.31467985866785 0.394881582713987 1.9743070787275
1.82158505360019 A A A 0.34407374359269 0.311898107176965 0.358441500202644 A A A
LNCV6_132398_PI430048170 mRNA
TTATTGCTGTTGTTAACCACCCATGAGGGGTGCAAACAGATAATGCTGTTAACATTTTCA NM_002034 RefSeq chr19
- 5865825 5870540 FUT5 2527 "fucosyltransferase 5 (alpha (1,3) fucosyltransferase)"
GO:0017060|GO:0046920|GO:0042355|GO:0005794|GO:0005975|GO:0032580|GO:0008417|GO:0006486|GO:0016
021|GO:0036065 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127863_PI430048170 0.550424233690041 2.4644961772253 0.318332480691193 3.1465299963158
0.271677796993678 A P A 0.259452017946046 0.314714649852 1.10306932761978 A A A
LNCV6_127863_PI430048170 mRNA
GGAAGCTGTCTTAAACTTCCTTCCCTGGTTTTATATTAACCCAACTGATAGATTAAGTAT NM_052898 RefSeq chr8
+ 55102456 55526151 XKR4 114786 "XK, Kell blood group complex subunit-related family, member 4"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61639_PI430048170 0.168158396398822 0.698384696282718 0.333647772975016 0.339034320730889
0.381256973619795 A A A 0.379249983162506 1.0300201930531 1.09619583486652 A A A
LNCV6_61639_PI430048170 mRNA
GTAGTCCTGGATTCAAGGTCCGTAGAAATCAGTCAACTGAAGAACACCATCAAATCTTTG NM_001282468 RefSeq
chr15 - 28698695 28712421 GOLGA8M 653720 "golgin A8 family, member M" GO:0005794 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140584_PI430048170 0.646370761716609 1.11127818795909 5.22977946188548
4.82524926507147 4.49377252690981 P P P 5.09773340364098 4.73220840745895
4.22729465631559 P P P LNCV6_140584_PI430048170 mRNA
CAGGACCCTGCTCTTTCTATCCCAGAGAGTTTGAGAAAACTACTTTTAAATAAATCATTA NM_001001481 RefSeq
chr8 - 73786219 73878910 UBE2W 55284 "ubiquitin-conjugating enzyme E2W (putative), transcript
variant 1"
GO:0004842|GO:0006513|GO:0016874|GO:0005634|GO:0005524|GO:0005737|GO:0006281|GO:0019787|GO:0070
979|GO:0006515|GO:0043161|GO:0031625|GO:0071218 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133578_PI430048170 0.0532321698908947 0.480933246786852 4.43996847874373
3.75109375192622 3.3467612556476 P P P 5.21178877029513 4.60810467283332
5.03711853850639 P P P LNCV6_133578_PI430048170 mRNA
GGCCATAATCTACATTTTCTTACCAGGAGCAGCATTGAGGTTTTTGAGCATAGTACTTGA NM_006813 RefSeq chr6
+ 89080709 89085160 PNRC1 10957 proline-rich nuclear receptor coactivator 1
GO:0005515|GO:0006355|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144802_PI430048170 0.00662252441314163 0.242621901592678 1.90546893693842

1.95869137761793 2.46401821085027 A A A 3.6355887948938 4.1062514329923
4.61776286764798 P P P LNCV6_144802_PI430048170 mRNA
GCTGGTACATATTCGTACGCATTACTTTTCAGAATCAATACGCACTTTCAGATATTCTTA NM_001098484 RefSeq
chr4 + 71187285 71572087 SLC4A4 8671 "solute carrier family 4 (sodium bicarbonate cotransporter),
member 4, transcript variant 1"
GO:0005515|GO:0005886|GO:0055085|GO:0016323|GO:0005452|GO:0005887|GO:0006810|GO:0015701|GO:0051
453|GO:0035725|GO:0008510|GO:0006811|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130396_PI430048170 0.801816309888034 1.03696794490947 6.80171876891371
6.95791742243808 7.27487647744188 P P P 6.80089043287694 6.80285337464438
7.26368187655766 P P P LNCV6_130396_PI430048170 mRNA
TGTCATTCAAAGGCATAGGGGCCTTTGAATGGAACAAATGCTTTCACATCATTTAAAGTA NM_017832 RefSeq chr9
+ 108934392 108940957 FAM206A 54942 "family with sequence similarity 206, member A"
GO:0005515|GO:0016607 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138905_PI430048170 0.0658651912901915 0.680557692267573 6.02864867355989
5.92901615363585 6.08521366707173 P P P 6.24088486981965 6.68109267054488
6.74106223344539 P P P LNCV6_138905_PI430048170 mRNA
TTTTAACATGCAAAATGTCCCTGGGGGTTTCTTCTTTGCTTGCTTTCTTCCTCCTTACCC NM_001429 RefSeq chr22 +
41092609 41180077 EP300 2033 E1A binding protein p300
GO:0005515|GO:0043627|GO:0008013|GO:0001756|GO:0006325|GO:0050681|GO:0018076|GO:0007507|GO:0034
605|GO:0004468|GO:0007219|GO:0000123|GO:0009887|GO:0001102|GO:0006990|GO:0003713|GO:0060765|GO:0
001047|GO:0000122|GO:0000979|GO:0043923|GO:0031490|GO:0018393|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132452_PI430048170 0.168247098698775 1.03949898107098 0.349113803218559
0.32105507724017 0.413281211836351 A A A 0.299464806852656 0.28637502190811
0.331132572079687 A A A LNCV6_132452_PI430048170 mRNA
CTGCACACATCCTTATCTTTGTTACATATGAAATATCTGTATCACGGGTATATTGAGAGA NM_017852 RefSeq
chr19_GL949748v2_alt + 946328 981128 NLRP2 55655 "NLR family, pyrin domain containing 2, transcript
variant 1" GO:0043280|GO:0005515|GO:0032090|GO:0005737|GO:0050718|GO:0005524 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_140809_PI430048170 0.0183032745103813 1.73583624657069 5.78999566810445
6.26155040331864 5.9636674722285 P P P 5.200731437213 5.32457271430433
5.13652356555073 P P P LNCV6_140809_PI430048170 mRNA
AATAGACATAACTGAGCTGAAGTAATTCCATAAAGGGCCCAGACAGCCTCCTCCACCATT NM_025216 RefSeq chr2
+ 218880532 218893929 WNT10A 80326 "wingless-type MMTV integration site family, member 10A"
GO:0005578|GO:0071560|GO:0005576|GO:0005615|GO:0048730|GO:0031069|GO:0005109|GO:0010628|GO:0045
165|GO:0014033|GO:0030182|GO:0048733|GO:0042476|GO:0043588|GO:0042487|GO:0016055|GO:0043586|GO:0
001942 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136213_PI430048170 0.00269429424844324 5.18144010547414 4.16302540451424
3.79688444424306 3.79113040855387 P P P 1.09983649219251 1.5448892381564
1.90704114099602 A A A LNCV6_136213_PI430048170 mRNA
GCTTCTCAAGCTGACAATTCTCACTTTGCAATAAATAGTCCAGTGTTTCCTTCCAAAAAA NM_001169 RefSeq chr16
+ 25216963 25228932 AQP8 343 aquaporin 8
GO:0005886|GO:0046691|GO:0009992|GO:0045177|GO:0055085|GO:0043231|GO:0034220|GO:0005887|GO:0015
250|GO:0015722|GO:0015793|GO:0006810|GO:0006833|GO:0015254|GO:0071320|GO:0000302 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134568_PI430048170 0.161842419630828 0.549759221935601 0.691676938509025
0.797210997493094 1.2188718692827 A A A 1.98931033994277 0.93834489129231
2.15250356770529 A A A LNCV6_134568_PI430048170 mRNA
GGGCTCTGAGATAATAGTAGATCCAACAGCATGCTACTATTAAATACAGCAAGAAACTGC NM_013960 RefSeq chr8

+ 32548209 32765040 NRG1 3084 "neuregulin 1, transcript variant ndf43"
GO:0060045|GO:0005515|GO:0043496|GO:0043497|GO:0031594|GO:0030307|GO:0055012|GO:0046579|GO:0030
879|GO:0009790|GO:0005615|GO:0043624|GO:0007171|GO:0030297|GO:0030296|GO:0007173|GO:0014032|GO:0
000165|GO:0060956|GO:0060379|GO:0051155|GO:0010667|GO:0055007|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131262_PI430048170 0.4368530768869340.7753308616331710.344451387438214
0.3234096069150450.262602494472262A A A 0.2953252442472150.302814966161793
1.22527873509099 A A A LNCV6_131262_PI430048170 mRNA
CTCTGCCAGGGTGGGAAAGGAGTAATAATATTACAATTCTATGGCTTTATACCATAAATA NM_001300987 RefSeq
chr1 + 96721604 96815049 PTBP2 58155 "polypyrimidine tract binding protein 2, transcript variant
3" GO:2000177|GO:0000166|GO:0033119|GO:0006376|GO:0005681|GO:0003729 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_64291_PI430048170 0.5483567948260131.04769522708548 12.136019699307 12.1105224053868
12.0038671243149 P P P 12.1990860286199 11.8670767637128 11.9655446571611 P P P
LNCV6_64291_PI430048170 mRNA
ACCCCGGGACCACCCCTCCCTTCCAGCTATGTGTACAATAATGACCAATCTGTTTGGCTA NM_001080452 RefSeq
chr19 - 6729913 6737622 GPR108 56927 G protein-coupled receptor 108 GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_105753_PI430048170 0.000236175686289078 0.3985969311160126.04326845105065
6.0443367018678 6.26529404726513 P P P 7.44642015066122 7.3551842774608
7.53801700145753 P P P LNCV6_105753_PI430048170 mRNA
TCGTCGATGCCAGCTTCTTCTTGAAATCTACCCAGAATGGAATCCTGACAATGATACAGG NM_199189RefSeq chr5
+ 139273751 139331677 MATR3 9782 "matrin 3, transcript variant 1"
GO:0005515|GO:0016020|GO:0000166|GO:0005198|GO:0005637|GO:0008270|GO:0005654|GO:0016363 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124038_PI430048170 0.1416287286955551.22312046531569 5.45778507804562
5.66456395175483 5.71810909815434 P P P 5.28505438878448 5.55838923130394
5.10123404800896 P P P LNCV6_124038_PI430048170 mRNA
ATCCTAAACAAAGCTCTGCTGCTGGGGGCCCTCGCTCTGACCACCGTGATGAGCCCCTGT NM_002122RefSeq chr6
+ 32637405 32643652 HLA-DQA1 3117 "major histocompatibility complex, class II, DQ alpha 1"
GO:0050852|GO:0012507|GO:0005886|GO:0031295|GO:0019221|GO:0042613|GO:0005765|GO:0032588|GO:0030
666|GO:0019886|GO:0006955|GO:0000139|GO:0016020|GO:0005887|GO:0042605|GO:0071556|GO:0032395|GO:0
030669|GO:0045582|GO:0009897|GO:0010008|GO:0060333|GO:0030658 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132898_PI430048170 0.3355026637417320.5841210139707620.523675359975192
0.6317093344084250.52406618393748 A A A 0.4735413771821042.09755337981677
0.93143168226387 A A A LNCV6_132898_PI430048170 mRNA
CTTTACTGAAGTGATTCCATCCGTATTCTGTTCTAATACTTGGAGAATGACCTTCATATTNM_001010883 RefSeq chr1
+ 108560348 108639327 FAM102B 284611 "family with sequence similarity 102, member B" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_128597_PI430048170 0.0102785244333004 1.40582471704879 13.7244941353003
13.7916799583624 13.6315056271022 P P P 13.3795694997691 13.1473067782883 13.137802293176
P P P LNCV6_128597_PI430048170 mRNA
TTGGGCAAATTGTTGACCACCTCTGAGCCTTGAAAAAGTAGGAGGTTACTTTGTTAGAGC NM_001271765 RefSeq
chr17 + 75087726 75106160 SLC16A5 9121 "solute carrier family 16 (monocarboxylate transporter),
member 5, transcript variant 2"
GO:0015718|GO:0035879|GO:0016020|GO:0005887|GO:0008028|GO:0015355|GO:0015129|GO:0015293 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140447_PI430048170 0.0685870957044527 0.7448542294571396.4535805983493

6.325616704801 6.63156293562937 P P P 6.65398799479729 6.89479442540528
7.11641431798273 P P P LNCV6_140447_PI430048170 mRNA
CTGCCTCTGTAAATTCATGTATTCAAAGGAAAAGACACCTTGCCTATAATTAAAATGTGG NM_001748 RefSeq chr1
+ 223712416 223776018 CAPN2 824 "calpain 2, (m/II) large subunit, transcript variant 1"
GO:0005515|GO:0008092|GO:0016540|GO:0005886|GO:0005783|GO:0005634|GO:0030425|GO:0005829|GO:0031
143|GO:0005737|GO:0071230|GO:0051603|GO:0006508|GO:0000785|GO:0070062|GO:0001666|GO:0005794|GO:0
046982|GO:0005509|GO:0001824|GO:0007520|GO:0097038|GO:0004198|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139007_PI430048170 0.2964172165180441.02835948112388 0.301450491386883
0.2545616535813980.353569911645668 A A A 0.2728793919994290.245940430295912
0.271271377962282 A A A LNCV6_139007_PI430048170 mRNA
CAAAGATTGAACTTCAGCTTCAGATTTGTAAACCATTCACATCTCTGCAACTTAAAACAG NM_001098808 RefSeq
chr9 - 93318198 93346414 C9orf129 445577 chromosome 9 open reading frame 129 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_142333_PI430048170 0.0682085916506114 1.16739724213386 0.649260431934275
0.4894780266062850.729944831501644 A A A 0.4898472327375820.375390919424079
0.339538185574006 A A A LNCV6_142333_PI430048170 mRNA
CAAATTTATTAAGAAACAAGTAGAAAATAAATCAGTGGTCGACTTGGGGACCGTAATGGC NM_014469 RefSeq chr11
+ 7088933 7091148 RBMXL2 27288 "RNA binding motif protein, X-linked-like 2"
GO:0000166|GO:0030529|GO:0003723|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143197_PI430048170 0.2142061573900151.25180422936616 9.27533357616776
8.82277735550149 8.70277879014722 P P P 8.77964795720575 8.60599279653299 8.4938000214734
P P P LNCV6_143197_PI430048170 mRNA
GATCCCGGACTCTGTATGATTGAAATAAAGAGAAATAAACAAATCTAGCAGCTCTGAAAA NM_024165 RefSeq
chr6_GL000256v2_alt + 4859722 4865178 PHF1 5252 "PHD finger protein 1, transcript variant 2"
GO:0010467|GO:0006355|GO:0003700|GO:0061087|GO:0005815|GO:0061086|GO:0035861|GO:0005634|GO:0035
064|GO:0006351|GO:0006974|GO:0005737|GO:0035098|GO:0045814|GO:0040029|GO:0005654|GO:0008270|GO:0
016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139184_PI430048170 0.2606794097151990.6823627559842442.76167355716052 1.3542699079661
1.81439893423823 A A A 2.82695941677647 2.8394259334295 2.19747463473717 P P A
LNCV6_139184_PI430048170 mRNA
AGCCCCTTCTGTGTTAACAGTTTTTCTCACAATGTAGCAACTTTTATCCACCCTTCAGGA NM_001288980 RefSeq
chr18 + 54357916 54382035 C18orf54 162681 "chromosome 18 open reading frame 54, transcript
variant 1" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138710_PI430048170 0.3564306615807411.63647675119562 0.3821494679276252.0259462269167
1.54405858146719 A A A 0.4245564875043281.05604808280265 0.718613845091893 A A A
LNCV6_138710_PI430048170 mRNA
CATAATCAGAAGCAAAATTCACAGAAACTAAACTCCACCCTTGGGACTCCACAACAACAA NM_007252 RefSeq chr7
+ 38978008 39464791 POU6F211281 "POU class 6 homeobox 2, transcript variant 1"
GO:0006355|GO:0003700|GO:0006366|GO:0007402|GO:0005634|GO:0007417|GO:0007601|GO:0003677 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100280_PI430048170 0.2728108924451410.8483388743640956.37622896143706
6.01525227189075 6.1529644983467 P P P 6.20857536155002 6.69096726720931
6.33570780200613 P P P LNCV6_100280_PI430048170 mRNA
ATGATTATGGGCCTCGGAGGAGGCATGGACTTTGACTCCAAGAAGGCCTACAGGGACGTG NM_012237 RefSeq
chr19 - 38878554 38899823 SIRT2 22933 "sirtuin 2, transcript variant 1"
GO:0005515|GO:0043130|GO:0045599|GO:0003950|GO:0034979|GO:0051781|GO:0035035|GO:0005813|GO:0017
136|GO:0034983|GO:0044224|GO:0005694|GO:0005814|GO:0048487|GO:0005819|GO:0030496|GO:0000122|GO:0
014065|GO:0010801|GO:0033558|GO:0045843|GO:0045836|GO:0005720|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_132254_PI430048170 0.0172499936727451 0.6045757648653473.94294654540042
3.61890001333785 3.45955363050378 P P P 4.18568936831047 4.54052515621922
4.49095963119427 P P P LNCV6_132254_PI430048170 mRNA
TGGGAATTCTTTTTGCCTCACTCACTGTTTCCTAAGCATCAGATAATCTATGCTAAAAAA NM_001042474 RefSeq
chr19 - 36182059 36215084 ZNF565 147929 zinc finger protein 565
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145072_PI430048170 0.1424396562450560.58247468753449 4.69280489637923
4.29815741502017 4.50700014651252 P P P 4.57929863770831 5.53031040135477 5.5573803732615
P P P LNCV6_145072_PI430048170 mRNA
TGCGTTTTTCTAGTTTTAATACCTTAAGCTTTTTCAAGACCTAACTGCAGCCGCTTTGGGNM_021224RefSeq chr9 +
106863096 107011515 ZNF462 58499 zinc finger protein 462
GO:0045944|GO:0006325|GO:0005634|GO:0003677|GO:0046872|GO:0006351|GO:0043392 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141037_PI430048170 0.3546287932299160.6215931672746830.470245650344003
1.07276895610731 0.263450523261954A A A 0.3663929074853131.99653174334273 1.1790348504779
A A A LNCV6_141037_PI430048170 mRNA
CTGGGTCTATATTAAACAGCAACCAGAGCAACAAATGGCAAACAATTTCTATTTTCAAGT NM_005761RefSeq chr12
+ 94148722 94307675 PLXNC1 10154 "plexin C1, transcript variant 1"
GO:0005622|GO:0005515|GO:0007165|GO:0016020|GO:0005886|GO:0007411|GO:0005102|GO:0004872|GO:0016
021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132346_PI430048170 0.0843348656359427 1.24598027442848 7.94536882208922
8.24615287246945 8.20918657235179 P P P 7.61272059657865 7.89941050055035
7.93393727866765 P P P LNCV6_132346_PI430048170 mRNA
ATTAATTTTCTATGTGTTGTGTTTGTAGTCTTGTCTTAGCTCTGGACGTGAAATACTTCG NM_018952RefSeq chr17 -
48595736 48604972 HOXB6 3216 homeobox B6
GO:0043565|GO:0006355|GO:0003700|GO:0034101|GO:0048704|GO:0005634|GO:0009952|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140234_PI430048170 0.81038869463831 1.01269902516027 15.2598072480328
15.0702816310656 15.1091771591063 P P P 15.1458658244667 15.1391448843491
15.1063498054941 P P P LNCV6_140234_PI430048170 mRNA
GCCTCCTCCCAGTAACTTCAGGTGTTTAATAAAGATGTGTTGACTCAGCCCTACAAAAAA NM_013234RefSeq chr19
+ 38619073 38636959 EIF3K 27335 "eukaryotic translation initiation factor 3, subunit K, transcript
variant 1"
GO:0005515|GO:0010467|GO:0033290|GO:0005852|GO:0016282|GO:0001731|GO:0003743|GO:0005634|GO:0006
412|GO:0006413|GO:0005829|GO:0005737|GO:0016020|GO:0006446|GO:0043022|GO:0044267|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139274_PI430048170 0.1872599409915420.8628485732062015.4211852134286
15.1138333081637 15.057358247685 P P P 15.4172867639884 15.4435119567437
15.3968197624887 P P P LNCV6_139274_PI430048170 mRNA
GCCCCCACCCCTGGCTACCTTGTGGGAATAAACAGACAAATTAGCCTGCTGGATAAAAAA NM_001039848 RefSeq
chr19 + 1104649 1106789 GPX4 2879 "glutathione peroxidase 4, transcript variant 3"
GO:0019369|GO:0007568|GO:0019372|GO:0050727|GO:0006749|GO:0005634|GO:0007275|GO:0044281|GO:0005
829|GO:0004602|GO:0005739|GO:0043295|GO:0008430|GO:0047066|GO:0042744|GO:0006644|GO:0006979|GO:0
032355|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98511_PI430048170 0.1415722292542420.7525745313709 7.63375970770792 7.93818520910033
8.29939341950312 P P P 8.34359184893633 8.28514995637782 8.53772179968018 P P P
LNCV6_98511_PI430048170 mRNA

AAAGGAGCAAAGCAACAGAAGTTTATCAAGGCTGTCACACATCAAGTTAAATTTGGTCAA NM_018471 RefSeq chr2 + 186486157 186509360 ZC3H1 555854 zinc finger CCCH-type containing 15 GO:0005515|GO:0005737|GO:0019221|GO:0005730|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135189_PI430048170 0.265664611497162 1.0206151473351 0.314186905734486 0.2489953604266790.293579417542805 A A A 0.2603591741232390.247243848129694 0.261565716307116 A A A LNCV6_135189_PI430048170 mRNA
GTCAAAAACCCCCAATGACTTTAGCAACAATTAAACACTGAAGCACTTGCAAAAATACAA NM_207317 RefSeq chr5 + 122129512 122153571 ZNF474 NA zinc finger protein 474 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137097_PI430048170 0.1531884232534941.7608217913275 1.13085291387868 0.53788296676441 1.69215190513594 A A A 0.4690079394478710.362294818973177 0.303020460649569 A A A LNCV6_137097_PI430048170 mRNA
GACTTTGCTTCACAGCTCTCATGCTTTACATGTTGATTTGTACAATCTTGTCATTTTGTA NM_001164431 RefSeq chr20 + 38601933 38650652 ARHGAP40 NA Rho GTPase activating protein 40 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139925_PI430048170 0.4596486518617720.794729983158393 0.316706005601489 0.27981956070089 0.274336137689503 A A A 1.14813701358039 0.263583337020604 0.262896481602679 A A A LNCV6_139925_PI430048170 mRNA
GATGCAGAAGTATTTAGGGATGTTTTTTCCATTCATTGCACTAAAGACTAAACCAGGTCA NM_002241 RefSeq chr1 - 160037466 160070261 KCNJ10 3766 "potassium channel, inwardly rectifying subfamily J, member 10"
GO:0005515|GO:0021554|GO:0005886|GO:0022010|GO:0055075|GO:0007268|GO:0042802|GO:0016323|GO:0016324|GO:0006954|GO:0015272|GO:0051289|GO:0048169|GO:0007628|GO:0034765|GO:0006813|GO:0009637|GO:0005102|GO:0010107|GO:0051385|GO:0051384|GO:0060075|GO:0005524|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90393_PI430048170 0.027036503327923 0.467047414068511 5.1578599820349 4.5082257988981 5.249081460962 P P P 5.91856727558926 6.14276491241418 6.23736023864166 P P P LNCV6_90393_PI430048170 mRNA
ATGCTATATGACTGTAAGGAATTATTGCATTTGTTCCAAGGTTAATAAAAATTTGAGCTT NM_015975 RefSeq chrX - 78129747 78139682 TAF9B 51616 "TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa"
GO:0005515|GO:0010467|GO:0006368|GO:0043066|GO:0005669|GO:0006367|GO:0046982|GO:0006366|GO:0030307|GO:0003714|GO:0050821|GO:0000122|GO:0033276|GO:0016032|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141941_PI430048170 0.203335677882228 1.18589579488666 7.85231070877354 7.97613008018717 8.16812669052266 P P P 7.59769752248798 7.62717003382755 8.01314398314809 P P P LNCV6_141941_PI430048170 mRNA
CGAAGTAGCCTGTTGCCTCCAAATTTGCCACTTGAATATAATTTTCTTTAAATCGTTAAG NM_138785 RefSeq chr6 + 149566391 149590931 GINM1 116254 glycoprotein integral membrane 1
GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143325_PI430048170 0.0126318816385953 1.1841419892118 0.771779678418765 0.833320834750948 0.858644415955728 A A A 0.660188419630246 0.523311699943604 0.546341840435717 A A A LNCV6_143325_PI430048170 mRNA
TGCTGCGCAGGCCTTGGTCTGTGCCTGTCAATAAACAGAGGCCCGAACCATCTGAAAAAA NM_001003938 RefSeq chr16 + 165973 166768 HBM 3042 "hemoglobin, mu"
GO:0019825|GO:0005833|GO:0005506|GO:0005344|GO:0070062|GO:0020037|GO:0015671 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142403_PI430048170 0.195702674242462 1.24774609013015 3.96957585574638

4.50912563884217 4.31345338755456 P P P 4.02281534899107 4.1159865098415
3.71652619497132 P P P LNCV6_142403_PI430048170 mRNA
ATCTTCAAGACCAAGTTCCTCTCTGAGATCGAAAGTGACAGCCTGGCCCTGCGGCAGGTC NM_002115 RefSeq
chr5 - 176880868 176899332 HK3 3101 hexokinase 3 (white cell)
GO:0001678|GO:0005975|GO:0042562|GO:0019318|GO:0044281|GO:0004396|GO:0055085|GO:0005524|GO:0006
096|GO:0005829|GO:0008645|GO:0005739|GO:0043234|GO:0004340|GO:0008865|GO:0015758|GO:0009405|GO:0
046835|GO:0019899|GO:0019158|GO:0051156 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_65007_PI430048170 0.139254313566052 1.08334067188131 16.6738594784235
16.625927732223 16.5817996676127 P P P 16.5096481929429 16.6005405537255
16.4208096445976 P P P LNCV6_65007_PI430048170 mRNA
GCCGAGGCTACAAAAACTAACCCTGGATCCTACTCTCTTATTAAAAAGATTTTTGCTGAC NM_000979 RefSeq
chr19 - 48615326 48619418 RPL18 6141 "ribosomal protein L18, transcript variant 1"
GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0005730|GO:0005634|GO:0006
415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0000184|GO:0016032|GO:0
022625|GO:0044267|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114625_PI430048170 0.0985436842024853 0.474297617108526 0.723820792876233
0.624521278158355 0.571566470117356 A A A 1.54870869707893 1.08937475717067
2.26680372802435 A A A LNCV6_114625_PI430048170 mRNA
CAAAAACTAATGGGCAGCATTCTCTCTGTTTGGAATGGGATCAGTATACAATTAATACAA NM_152405 RefSeq
chr5 + 79236101 79327215 JMY 133746 "junction mediating and regulatory protein, p53 cofactor"
GO:0034314|GO:0005515|GO:0070060|GO:0043065|GO:0030054|GO:0005886|GO:0006357|GO:0003713|GO:0003
779|GO:0005634|GO:0070358|GO:0051091|GO:0005737|GO:0006281|GO:0072332|GO:0005654|GO:0007050|GO:0
005856|GO:0031252 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69067_PI430048170 0.269879315028981 0.788908538622405 5.49768080526039
5.75307386570022 5.56691904054624 P P P 5.50278672949963 6.17639787780424
6.08864953549048 P P P LNCV6_69067_PI430048170 mRNA
AAACACAGAAGGTTGGTGCCATCCATTTTCCTTTTCGAAGACTTCATGGCAGAGCTGTAC NM_030653 RefSeq
chr12 + 31073844 31104791 DDX11 1663 "DEAD/H (Asp-Glu-Ala-Asp/His) box helicase 11,
transcript variant 1"
GO:0005515|GO:0000790|GO:0051539|GO:0003723|GO:0004386|GO:0005730|GO:0030496|GO:0005634|GO:0005
524|GO:0046872|GO:0030968|GO:0000922|GO:0005737|GO:0003690|GO:0004003|GO:0003697|GO:0016032|GO:0
007062|GO:0005654|GO:0032508|GO:0006987|GO:0044267|GO:0070062|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143002_PI430048170 0.46950441169929 0.736263972789154 0.438995218054578
0.490556781604707 0.460001676565186 A A A 1.55692522983683 0.403828691636926
0.435664327645684 A A A LNCV6_143002_PI430048170 mRNA
AGACTCTTCAACCCACAAAGAAGCAACTAAATGTTTCTCTAAGTTTAATTTTCTAGCGTG NM_023943 RefSeq
chr3 + 133038287 133397775 TMEM108 66000 "transmembrane protein 108, transcript variant 1"
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144292_PI430048170 0.76439852152009 0.922895093048395 1.4071261989571
2.019361509735 0.29075355361949 A A A 0.735376889579612 1.8610694984044
1.71996369423992 A A A LNCV6_144292_PI430048170 mRNA
TTTACAGAAGAAAAGAGATCGAGAATCCTGCTGGGCCCAGATTAACTTCGACAGCACAGA NM_001136482 RefSeq
chr19 + 10848429 10869684 C19orf38 255809 chromosome 19 open reading frame 38
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140019_PI430048170 0.323082590586762 1.02499862814316 0.355463498033281
0.26708742927076 0.338273200818401 A A A 0.283484197081227 0.279507389808324

0.292449734139141 A A A LNCV6_140019_PI430048170 mRNA
GTCAAATTCCCCTAATGGTGTATAACCAGGCATTTATATATTTTGATCAGTATGCTGCAA NM_001034842 RefSeq
chr10_GL383545v1_alt - 159833 176014 PTCHD3 NA patched domain containing 3 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_131405_PI430048170 0.00139898257984713 0.334669725799792 5.26041181634859
4.83102385018211 5.26475834776693 P P P 6.50718583185237 6.81157780724764
6.79658938346504 P P P LNCV6_131405_PI430048170 mRNA
CGTGATGGTGTTGATTTCTTTCAATGATGCTTACCATCTATTTTAGCCACTGAGCCTTTT NM_001001323 RefSeq
chr12 - 89588048 89656067 ATP2B1 490 "ATPase, Ca++ transporting, plasma membrane 1,
transcript variant 1"
GO:0005515|GO:0005516|GO:0005886|GO:0005634|GO:0055085|GO:0005524|GO:0046872|GO:0005388|GO:0034
220|GO:0016020|GO:0005887|GO:0007596|GO:0008152|GO:0070588|GO:0006810|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_95093_PI430048170 0.266202913412124 1.15541141527503 9.0376088151064
9.21773370540257 9.22555868700851 P P P 8.66038988994051 9.01465614855621
9.14578383644794 P P P LNCV6_95093_PI430048170 mRNA
GAACACGAAAGAAATGTACCTTCTTTCACTCTGTCATCTTTCTTTTCTTTGAGTCTGTTT NM_001005735 RefSeq
chr22 - 28687742 28741834 CHEK2 11200 "checkpoint kinase 2, transcript variant 3"
GO:0005515|GO:0046872|GO:0042803|GO:0006302|GO:0042802|GO:0046777|GO:0000086|GO:0090307|GO:0044
257|GO:0010332|GO:0031625|GO:0072428|GO:0006355|GO:0000781|GO:0005794|GO:0008630|GO:0019901|GO:0
042176|GO:0050821|GO:0005524|GO:0006974|GO:0006351|GO:0006975|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128069_PI430048170 0.357030255334813 1.05314189736411 0.316348593743941
0.314634892020976 0.498045045377161 A A A 0.307893318714932 0.276024067153996
0.328335588285264 A A A LNCV6_128069_PI430048170 mRNA
CCTATACATTGCCATCAACTTTGTTTCCTCATCTCAAATAAAGTCCTTTCAGCAAGTTAA NM_001926 RefSeq chr8
- 6924693 6926076 DEFA6 1671 "defensin, alpha 6, Paneth cell-specific"
GO:0005796|GO:0045087|GO:0050832|GO:0031640|GO:0019731|GO:0005576|GO:0005615 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138433_PI430048170 0.00119716729414645 0.249913343754843 2.73222541501464
2.83145318458156 2.31535788717531 A A A 4.59227662681565 4.50799512388648
4.81305234996951 P P P LNCV6_138433_PI430048170 mRNA
ATGGCTTAACTCGAACTTGAAGACACATACTTCAACTGTCCTTATTGTCCATTAAACTGA NM_016353 RefSeq
chr8 + 17156326 17222732 ZDHHC2 51201 "zinc finger, DHHC-type containing 2"
GO:0018345|GO:0005794|GO:0005887|GO:0005783|GO:0016409|GO:0008270|GO:0055038|GO:0019706 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_144288_PI430048170 0.337160712345695 1.02033008789606 0.327548969938343
0.248644349699019 0.280887541749307 A A A 0.257308684024493 0.255622367606771
0.258133410821176 A A A LNCV6_144288_PI430048170 mRNA
CTTCACAGAAAATATAGGATTTAAATCCTCTGGCATTTATCCTACTTACTGAACACATGG NM_001286643 RefSeq
chr8 - 96239397 96261613 MTERF3 51001 "mitochondrial transcription termination factor 3,
transcript variant 2" GO:0005739|GO:0003690|GO:0044212|GO:0045892|GO:0006351 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_128130_PI430048170 0.21535230269353 1.58795714634162 1.43181815825527
1.2447520157359 0.349934599469388 A A A 0.460937880032623 0.375451531337102
0.400779087234262 A A A LNCV6_128130_PI430048170 mRNA
GGAAAGCACTTGGACAAATACTGTTGAATCTGAACTTAATAGCATTACCAGAAATGGAAT NM_001080462 RefSeq
chr15 + 72398326 72408367 TMEM202 338949 transmembrane protein 202 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_136144_PI430048170 0.610068634611059 0.968752529733838 0.509489281517851 0.466754657954725 0.253696201008428 A A A 0.398959574207588 0.513283548585258 0.465608848395593 A A A LNCV6_136144_PI430048170 mRNA CGGCATTAATTCACCAATGCATTTGGACAACTTGATGTAACTGACTTTATTTTATGTGAC NM_032918 RefSeq chr12 - 15107781 15221477 RERG 85004 "RAS-like, estrogen-regulated, growth inhibitor, transcript variant 1" GO:0006184|GO:0030308|GO:0008285|GO:0016020|GO:0007264|GO:0030331|GO:0003924|GO:0005634|GO:0009725|GO:0019003|GO:0005525|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134123_PI430048170 0.100505289157642 1.06134599847113 0.58321995557283 0.504304956398267 0.575038773647031 A A A 0.406735111023743 0.489420650752218 0.50801852064167 A A A LNCV6_134123_PI430048170 mRNA CGGAAGAAGATTAGGCAGTTTTCAATTTACTACTCAATTGGGTATTTCTTGCTCTCATTT NM_203408 RefSeq chrX - 34129751 34132330 FAM47A 158724 "family with sequence similarity 47, member A" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115990_PI430048170 0.00495036916532078 2.45867709749628 2.59180438286714 2.05659110018345 2.32085023960175 A A A 1.20091881815345 0.956171666813775 0.953818864403995 A A A LNCV6_115990_PI430048170 mRNA AATCAACTTCAAGGACTTTTGCCGGGGGGTGTTCGCCATGAAAGGGTGCGAGGAGCTGCT NM_032932 RefSeq chr17 + 31391623 31538217 RAB11FIP4 84440 "RAB11 family interacting protein 4 (class II), transcript variant 1" GO:0005515|GO:0017137|GO:0030306|GO:0005509|GO:0030496|GO:0030139|GO:0005615|GO:0032154|GO:0042803|GO:0000910|GO:0006810|GO:0016032|GO:0055038|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138964_PI430048170 0.0106640218585856 0.457428756282146 11.0479325310251 10.4211866491992 10.5696436178274 P P P 11.5902793606736 11.8818714444116 11.9982765541976 P P P LNCV6_138964_PI430048170 mRNA ACCGGCATGTTTCCAGCAGAAGACAAAAAGACAAACATGAAAGTCTAGAAATAAAACTGG NM_053056 RefSeq chr11 + 69641104 69654474 CCND1 595 cyclin D1 GO:0005515|GO:0071157|GO:0043627|GO:0006325|GO:0032403|GO:0030968|GO:0005622|GO:0007219|GO:0017053|GO:0010039|GO:0032026|GO:0045444|GO:0016538|GO:0033197|GO:0070064|GO:0051412|GO:0019901|GO:0003714|GO:0010243|GO:0000122|GO:0070141|GO:0001889|GO:0051592|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141407_PI430048170 0.0421951873630123 0.666820998777756 6.32064442706969 6.62250964991005 6.85226288658493 P P P 6.98194951453107 7.18344102425218 7.40203924393272 P P P LNCV6_141407_PI430048170 mRNA GATATTTAACAAAATATGGACAGGCCACTTATGCTCAGTTTTACCTTAGTTATTCCTTGG NM_198076 RefSeq chr1 + 244835336 244845058 COX20 116228 COX20 cytochrome c oxidase assembly factor GO:0005739|GO:0031966|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102077_PI430048170 0.883115298067047 1.03790820320587 2.19272279353044 2.79086599066469 2.76167355716052 A A A 2.40554069821441 2.7191087295103 2.51690243421119 A P P LNCV6_102077_PI430048170 mRNA AAACACAAATCAAGCAGCAAGATCATCTGCTGCAGCTGGACAAATGATGGTCAGTACCTG NM_052985 RefSeq chr3 + 129440035 129520507 IFT122 55764 "intraflagellar transport 122, transcript variant 1" GO:0005515|GO:0050680|GO:0060830|GO:0007227|GO:0045879|GO:0048593|GO:0060831|GO:0036064|GO:0005737|GO:0060971|GO:0035720|GO:0035721|GO:0010172|GO:0006996|GO:0035050|GO:0072594|GO:0001843|GO:0072372|GO:0005929|GO:0042384|GO:0016020|GO:0060271|GO:0030991|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137383_PI430048170 0.283538765719355 1.07399650591984 12.2341873366608 12.4636114738658 12.2893384861646 P P P 12.2046202521005 12.2238267549148 12.2592457069978 P P P LNCV6_137383_PI430048170 mRNA TGTGAGACATGGGAGTCTAACTGAAGTCTCTCCTTCCTAATAAATGTTACCACTCTAAAA NM_024068 RefSeq chr12 + 56224340 56229854 NABP2 79035 nucleic acid binding protein 2 GO:0005515|GO:0007093|GO:0005737|GO:0006281|GO:0003697|GO:0000724|GO:0010212|GO:0070876|GO:0005654|GO:0005634|GO:0006974 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138210_PI430048170 0.234429298846128 0.644426088190143 4.21860488788394 2.63160481109642 3.30150221877431 P A P 4.10520551005886 4.45327337807847 3.87674415825703 P P P LNCV6_138210_PI430048170 mRNA CTTCTCTCTCTAATAATACTTCCTCTGATGTAATTAACGGTTGGTAGACAATATCAGACA NM_024790 RefSeq chr8 + 67064367 67196614 CSPP1 79848 "centrosome and spindle pole associated protein 1, transcript variant 1" GO:0005813|GO:0005737|GO:0000922|GO:0032467|GO:0005874|GO:0005819|GO:0051781|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128959_PI430048170 0.405662313163815 1.02334994754566 0.36513109997863 0.364488015825074 0.271192728375828 A A A 0.295677833099535 0.311830232634306 0.295353635571074 A A A LNCV6_128959_PI430048170 mRNA TTTCGCATCTTCAGTTAAGCATATAAAAGGCACTTTTGGTGGAATAGTCTTTTGAAGAGT NM_001004313 RefSeq chr17 - 10713321 10730329 TMEM220 388335 transmembrane protein 220 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133092_PI430048170 0.141816428820671 0.931480800719368 0.332087362566191 0.346928919020108 0.295441431567908 A A A 0.502939192525521 0.427304373035073 0.347733774085398 A A A LNCV6_133092_PI430048170 mRNA CTACTGTCCTTAAAGCCATTGTTTCCATTACAAAATCCAACTCTCTGAGAGAAAAGGGTG NM_000542 RefSeq chr2 - 85657316 85668741 SFTPB 6439 "surfactant protein B, transcript variant 1" GO:0006665|GO:0007585|GO:0009887|GO:0005764|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143659_PI430048170 0.978601962207046 1.18104718254476 0.388595878071523 0.403024616379557 2.50761571378026 A A A 1.77938713704611 1.20306831573898 0.387332208625985 A A A LNCV6_143659_PI430048170 mRNA GTTTCTAGCTGTCTGGCTCTAAATTTTTGGTTCTTAGAACCTTCTTAATCCCCTTCAGTT NM_021186 RefSeq chr1 - 237877863 237890922 ZP4 57829 zona pellucida glycoprotein 4 GO:2000360|GO:0005886|GO:0005578|GO:0005576|GO:0010737|GO:0007339|GO:0032190|GO:2000344|GO:0070528|GO:0007338|GO:0035556|GO:0060478|GO:0045860|GO:0042102|GO:0004871|GO:0016021|GO:0002922|GO:0032504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135961_PI430048170 0.0401556672053416 0.711699762871365 5.79114934083595 5.44599860640969 5.86591056867222 P P P 6.11476377400152 6.35648603987169 6.12438011189754 P P P LNCV6_135961_PI430048170 mRNA TGGGGACAAATGAAAGAGATGATGTAGATTTTTCGGATGGGTGGGTATATTTTATTTTCC NM_017824 RefSeq chr10 + 92291162 92353964 MARCH5 NA membrane-associated ring finger (C3HC4) 5 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142780_PI430048170 0.323159760919868 0.871525475645201 11.1510820952249 11.0846261574471 11.2316024083116 P P P 11.0818400177631 11.3670289070561 11.575295940917 P P P LNCV6_142780_PI430048170 mRNA GCCGAGCAGTGTGGACATCAGCCACTTTTTATATTCATGTACATTCACCTGGGGAAAAAA NM_006023 RefSeq chr10 + 12195961 12250590 CDC123 8872 cell division cycle 123 GO:0007346|GO:0008284|GO:0005737|GO:0007050|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137777_PI430048170 0.0595905129517094 0.946452569291559 0.316839112179022 0.330471434161905 0.325176481309007 A A A 0.441978457907902 0.39828232053038 0.369528647787129 A A A LNCV6_137777_PI430048170 mRNA CTGTCAAAGGAAGAGCTTCCTCAGAGAAAAATGTGCTTAAAAGCCATGTTTAAACTCTGA NM_030946 RefSeq chr6_GL000256v2_alt + 616122 617088 OR14J1 NA "olfactory receptor, family 14, subfamily J, member 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128819_PI430048170 0.2160992666565180.6590208401082290.6049757301445990.5113565394193 0.31483252406494 A A A 0.4208572987006871.18689350541122 1.45569860687278 A A A LNCV6_128819_PI430048170 mRNA CCACATTCCCATGATGGAAGTCTGCGTAACCAATAAATTGTGCCTTTCTCACTCAAAAAA NM_001017915 RefSeq chr2 + 233059966 233207903 INPP5D 3635 "inositol polyphosphate-5-phosphatase, 145kDa, transcript variant 1" GO:0005515|GO:0050852|GO:0017124|GO:0006661|GO:0043647|GO:0006915|GO:0004445|GO:0006796|GO:0044281|GO:0050900|GO:0005829|GO:0007165|GO:0016020|GO:0007596|GO:0046856|GO:0006644 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66289_PI430048170 0.5733878296333171.06139550694391 8.4136517622058 8.20255615932392 8.60119539052077 P P P 8.32448900880452 8.32641023607873 8.33604172810993 P P P LNCV6_66289_PI430048170 mRNA ACATGTCTTTTAGGTGTCTTGCTGATGACTATCCATAGGAGGAATGGCTATCCCAAAAAA NM_017546RefSeq chr2 + 101252882 101270316 CNOT11 55571 "CCR4-NOT transcription complex, subunit 11" GO:0005515|GO:0010467|GO:0006355|GO:0008283|GO:0005634|GO:0031047|GO:0006351|GO:0006417|GO:0030014|GO:0005829|GO:0003674|GO:0000289|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92551_PI430048170 0.39188241241202 0.7759342855386160.3861242846055910.473128566982904 0.381387855654746A A A 0.30185797783794 1.26562282209364 0.599248434744659A A A LNCV6_92551_PI430048170 mRNA ATTTAGAATCCCCGGCTAACAGTTCTGGAAAGGGTAGAAGGGTATGGAGAACAAGAATGG NM_031936RefSeq chr1 + 109539871 109545833 GPR61 83873 G protein-coupled receptor 61 GO:0043235|GO:0008150|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129423_PI430048170 0.4022249269878370.2881360613156930.249636575261402 0.2615272849738490.373381778793247A A A 0.3822319348802393.35516895734381 0.317137616214157A P A LNCV6_129423_PI430048170 mRNA CTGCAGCAATATCCATGGGTCCTAATAATTGTAGTTCCCCACTAAAATCTAGAAATTATT NM_000720RefSeq chr3 + 53495048 53812465 CACNA1D 776 "calcium channel, voltage-dependent, L type, alpha 1D subunit, transcript variant 1" GO:0086052|GO:0030018|GO:0005886|GO:0086010|GO:0051928|GO:0007605|GO:0044281|GO:0086091|GO:0046872|GO:0060372|GO:0007411|GO:0006816|GO:0086007|GO:0086046|GO:0005245|GO:0030506|GO:0008331|GO:0005891|GO:0070509|GO:0006112|GO:0050796|GO:0051393|GO:0086059|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55195_PI430048170 0.1216890057226321.06968437522015 0.4885372027770980.609988459445683 0.539850973191333A A A 0.3828221647006170.4624701423677840.501583173924435A A A LNCV6_55195_PI430048170 mRNA TATTTTGAAATTTCTGAATCGAGCTAGAGCGAGAGAGCGAGAGATCTCCGTAGACTGCGA NM_033343RefSeq chr1 + 180230297 180275053 LHX4 89884 LIM homeobox 4 GO:0043565|GO:0043066|GO:0008045|GO:0006355|GO:0009887|GO:0008270|GO:0005634|GO:0001890|GO:0006351|GO:0021526 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137418_PI430048170 0.2253069586379261.19743324077837 8.8120216336911 8.5219684926494 8.34375956958418 P P P 8.36083113947716 8.46499383852074 8.08500728711087 P P P LNCV6_137418_PI430048170 mRNA

TTGGCCCCTGCACCTCTTCTCAATGCACTTTAATAATGTAACATATTACTAATAAACAAG NM_003612 RefSeq chr15 - 74409288 74433958 SEMA7A 8482 "semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group), transcript variant 1"
GO:0005515|GO:0005886|GO:0050727|GO:0045773|GO:0048675|GO:0031225|GO:0021988|GO:0001649|GO:0006955|GO:0005178|GO:0006954|GO:0016020|GO:0007229|GO:0007411|GO:0060907|GO:0001934|GO:0004872|GO:0070374|GO:0009897. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142629_PI430048170 0.727367426717706 1.05695440087713 2.93480029490667 1.27678884755457 0.465857825619973 A A A 1.78570607683154 1.81467236893346 1.95156622385122 A A A LNCV6_142629_PI430048170 mRNA
ACATATGGATATATTTGCCAATTTTTGTCCTCAGCTTTGGGTCTCAGCCAAAATGGAGAT NM_018100 RefSeq chr6 + 52420195 52495785 EFHC1 114327 "EF-hand domain (C-terminal) containing 1, transcript variant A"
GO:0072686|GO:0005813|GO:0021795|GO:0005930|GO:0005509|GO:0043025|GO:0008022 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143731_PI430048170 0.145312399263156 1.0778175741959 0.484685366217114 0.539428668088697 0.561798769270199 A A A 0.331167568653491 0.423205594726021 0.503161791846745 A A A LNCV6_143731_PI430048170 mRNA
GCTCGGGGTTTGAGAAGTTCTATATTAGGATGTCATTTACATACTTTTCAACAGAAGATT NM_033196 RefSeq chr19 - 20004417 20039468 ZNF682 91120 "zinc finger protein 682, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141062_PI430048170 0.0589817195273699 1.46423303129229 9.19919328891913 9.6912287149115 9.45644453367063 P P P 9.12037591837636 8.97094762465957 8.59804803245391 P P P LNCV6_141062_PI430048170 mRNA
TTGGATTATTTTTTATCGAAGAGATCATAGAAACCAGAGCCTTCTCCCCAGGCCTGCCCT NM_005281 RefSeq chr1 + 27392643 27395813 GPR3 2827 G protein-coupled receptor 3
GO:0040020|GO:0005515|GO:0005887|GO:0004930|GO:0030816|GO:0007189|GO:0007204 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67196_PI430048170 0.934439816294646 1.00363834537891 10.9099411977971 11.0549494065991 11.0637514413746 P P P 10.9574904815912 10.8730418552118 11.1709528059258 P P P LNCV6_67196_PI430048170 mRNA
GTAGAACGAATCGAATACAAAAAACCTTAAAGCCAGGCCTGTCTTGATGATTTTTGGTTT NM_001282150 RefSeq chr12 - 110491522 110502140 VPS29 51699 "vacuolar protein sorting 29 homolog (S. cerevisiae), transcript variant 3"
GO:0005515|GO:0005770|GO:0006886|GO:0005829|GO:0043231|GO:0005737|GO:0008565|GO:0042147|GO:0008270|GO:0005769|GO:0010008|GO:0070062|GO:0005768|GO:0030904 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143366_PI430048170 0.725371870522182 0.987910774629416 0.398169748507301 0.370234413720148 0.247949462489592 A A A 0.337351443792111 0.377230014956314 0.358521113819937 A A A LNCV6_143366_PI430048170 mRNA
TGCAATATGCCTATCCTTTTGTAAATGGTATTTGTGATGCTTGCCCTTCAACTTCCATAA NM_001290261 RefSeq chr20 - 25673194 25686939 ZNF337 26152 "zinc finger protein 337, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129373_PI430048170 0.103876835843096 0.66910655254474 10.3570547096149 9.67171590143941 9.71523651481918 P P P 10.4398686213711 10.5573293501504 10.5882060115464 P P P LNCV6_129373_PI430048170 mRNA
CTGCCCCCACCTCCTAAATAAATAAAGGAATCGGCGAACACCTTCTTCTTTTATGACATT NM_004998 RefSeq chr15 - 59135968 59372872 MYO1E 4643 myosin IE
GO:0005515|GO:0006807|GO:0005516|GO:0072015|GO:0042623|GO:0016459|GO:0015629|GO:0032836|GO:0005

737|GO:0003774|GO:0000146|GO:0051015|GO:0005912|GO:0005911|GO:0035166|GO:0005856|GO:0070062|GO:0
030048|GO:0005524|GO:0001701|GO:0006897|GO:0045334|GO:0003094|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137633_PI430048170 0.611057956595021 0.935565472586177 0.276859105303391
0.288103550322592 0.499736886425365 A A A 0.329406001923441 0.284286675665292
0.711195764208826 A A A LNCV6_137633_PI430048170 mRNA
CCTGCATCACAGCAGTTTTAAGGTCCCATTATTGTACTGATTTATCCTTGTAATAAATGT NM_001105579 RefSeq
chr14 - 74405892 74426102 SYNDIG1L 646658 synapse differentiation inducing 1-like
GO:0009607|GO:0005794|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143081_PI430048170 0.312482594018226 0.967681628252771 0.428593642871944
0.448293446882388 0.334860293655136 A A A 0.418542593621034 0.48447433408595
0.452691716581016 A A A LNCV6_143081_PI430048170 mRNA
TGCCTGCTTTAGAATGTTTTCCTTCTACTTACACATCTTCCACAGGTCTCAGAATCTTTC NM_206809 RefSeq
chr6_GL000254v2_alt + 922361 937746 MOG 4340 "myelin oligodendrocyte glycoprotein, transcript
variant alpha1" GO:0005886|GO:0034126|GO:0016021|GO:0007417|GO:0007155 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131422_PI430048170 0.155227640122323 0.910121745434591 0.28046430853796
0.437896277758573 0.298635335869028 A A A 0.591353249935205 0.414793663212206
0.416420741165443 A A A LNCV6_131422_PI430048170 mRNA
AATGTTCTTTAAAATTCAACACCCACCAGGCTCTAAGCGGCGATCTGTGCTAAGAGGTCA NM_023002 RefSeq chr19
- 19255640 19262787 HAPLN4 404037 hyaluronan and proteoglycan link protein 4
GO:0001501|GO:0005540|GO:0005578|GO:0007417|GO:0007155|GO:0005201 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135578_PI430048170 0.379075084963816 0.391430471014884 0.350042962364255
0.492951947246416 0.368744327249782 A A A 0.535141724761304 0.463416168447751
2.87232505779568 A A P LNCV6_135578_PI430048170 mRNA
CAGCACATGTTTTGCTGTTACGGTGTACTGTTCGTATTTAGACAAGAAGAACAAAATTTA NM_017516 RefSeq chr11
+ 107928474 107963482 RAB39A 54734 "RAB39A, member RAS oncogene family"
GO:0045335|GO:0006184|GO:0005794|GO:0005886|GO:0030670|GO:0003924|GO:0032482|GO:0090383|GO:0019
003|GO:0005525|GO:0006886|GO:0090385 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79154_PI430048170 0.0419704287094784 0.744430644016291 8.26707520695762
8.18942858686422 8.48030397098623 P P P 8.68046759704663 8.57778272329225
8.94638298945011 P P P LNCV6_79154_PI430048170 mRNA
TACCCTAAAATGTCCAATCTGTATTTATGTACCTTGTCAGTGTTTTGCTGTTGGTTTTCT NM_014997 RefSeq chr7 +
130070508 130135720 KLHDC10 23008 kelch domain containing 10 GO:0005515|GO:0005737|GO:0005634
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141573_PI430048170 0.00575998894534612 0.63684192739128 4.86332348951872
4.64524800744498 4.86583528160832 P P P 5.44628209448853 5.49689200913205
5.39327231966006 P P P LNCV6_141573_PI430048170 mRNA
TTACTGGAAACTTTTTGTACAATAAAGCAATCACGCAGATTAAAGAACATCCTGCAATCC NM_001001433 RefSeq
chr20 + 58651252 58679526 STX16 8675 "syntaxin 16, transcript variant 1"
GO:0005802|GO:0005515|GO:0048471|GO:0005783|GO:0090161|GO:0031201|GO:0006886|GO:0006906|GO:0005
829|GO:0043231|GO:0005737|GO:0000149|GO:0042147|GO:0048278|GO:0019905|GO:0005794|GO:0005730|GO:0
031985|GO:0006891|GO:0012505|GO:0005484|GO:0000139|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136940_PI430048170 0.00753938681788028 0.414950904517941 8.37339467640761
8.14690753457441 8.36516271054059 P P P 9.33869597912001 9.43792871450689
9.87009444583849 P P P LNCV6_136940_PI430048170 mRNA
GCTTAACTGAAGTAGAACTATTCATGATGCTTTTCACACATTGTGGCATAAGATGTAAAG NM_001204803 RefSeq

chr12 + 45215986 45432351 ANO6 196527 "anoctamin 6, transcript variant 5"
GO:0006821|GO:0017121|GO:0005886|GO:0017128|GO:0042803|GO:0097045|GO:0005622|GO:0044070|GO:0034
220|GO:0005229|GO:0034765|GO:0005227|GO:0006812|GO:0070062|GO:0005244|GO:0009986|GO:0005247|GO:0
002407|GO:0034707|GO:0002543|GO:0055085|GO:0016020|GO:0007596|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144130_PI430048170 0.58273086420136 1.13755394715072 0.428510657421641
1.01458846221816 0.259904271710777 A A A 0.3847187636886950.457984000629351
0.414149066645559 A A A LNCV6_144130_PI430048170 mRNA
GATGGCTGGAGAAAAGTTCAGGATCATAAATGTTATCATCATTCTTCAAGAAAAGATGAG NM_001033045 RefSeq
chr2 - 174431571 174487088 GPR155 151556 "G protein-coupled receptor 155, transcript variant 1"
GO:0035556|GO:0003674|GO:0050890|GO:0016021|GO:0055085|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133601_PI430048170 0.0912958757230736 1.29797954172904 7.40506187864848
7.64173892463286 7.84990368942652 P P P 7.25154758093406 7.08019448986333
7.44694280808254 P P P LNCV6_133601_PI430048170 mRNA
ATTTTCCAGTCATTGGATCGTGTTTTCTTTTGTCCATTATTGTACTGTGCTGTACCACAT NM_005780RefSeq chr13 -
39342891 39603219 LHFP 10186 lipoma HMGIC fusion partner GO:0016021|GO:0003677 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_133357_PI430048170 0.0902317059519741 1.26057065699566 8.82323888861916
8.79454962354093 9.08359939179392 P P P 8.46139390623575 8.42917112044447
8.79703514137119 P P P LNCV6_133357_PI430048170 mRNA
TTTTAAAATTGCACTTGTTCACCTACCAGTGTTTACGAAATCCTGTATTTGGGATGCTTT NM_173562RefSeq chr6 +
36442766 36491143 KCTD20 222658 "potassium channel tetramerization domain containing 20, transcript
variant 1" GO:0005737|GO:0051260|GO:0042327 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100908_PI430048170 0.0890917478357919 0.8634044362844961 1.1874155866784
11.1372550268192 11.2439388732772 P P P 11.2513385087168 11.4792100106548
11.4646288756258 P P P LNCV6_100908_PI430048170 mRNA
AAGAAGTTCATGGATCAACATCCGGAGATGGATTTTTCCAAGGCTAAATTCAACTAGCCC NM_006600RefSeq chr1
+ 26921721 26946871 NUDC 10726 nudC nuclear distribution protein
GO:0005515|GO:0007067|GO:0005737|GO:0008283|GO:0005874|GO:0007275|GO:0005654|GO:0000278|GO:0051
301|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142761_PI430048170 0.000975958955556421 0.2987866967891543.1170568247652
3.50698496070889 3.57583805607901 P P P 5.31566391854495 4.97561505496058
5.15809899570701 P P P LNCV6_142761_PI430048170 mRNA
CAAATTTGGATTCTGTCCCAGGCCTTACTGTAAAACTAGGGGATTGCCTTTCCATATCTG NM_001969RefSeq chr14
+ 103334001 103345024 EIF5 1983 "eukaryotic translation initiation factor 5, transcript variant 1"
GO:0010467|GO:0005737|GO:0005886|GO:0006446|GO:0003924|GO:0003743|GO:0005525|GO:0044267|GO:0006
412|GO:0008135|GO:0006413|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134065_PI430048170 0.912565017724225 1.01354087018064 0.391379045293265
1.44368382298821 1.61953281935277 A A A 1.05305258454957 0.304416319248697
1.88744585534234 A A A LNCV6_134065_PI430048170 mRNA
TACGAAGCCAATGATTACGAGGAGATTGTCTTTCTCATGTTCACCCTGAAGCAAGCCTTC NM_005383RefSeq chr2
+ 233032671 233035057 NEU2 4759 sialidase 2 (cytosolic sialidase)
GO:0006665|GO:0009313|GO:0006687|GO:0006689|GO:0044281|GO:0005829|GO:0052794|GO:0005737|GO:0052
796|GO:0052795|GO:0006488|GO:0044267|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127676_PI430048170 0.0232570846426928 0.615254004668177 9.24193859343691
9.0633104047395 9.55213219724419 P P P 9.76772505442461 9.96557207265968
10.2314960507428 P P P LNCV6_127676_PI430048170 mRNA

CTAAGCAGCAAAATCTTGGTGTTGTGATGTACAGAAATGGAGAAGAGTATTAAACCATAT NM_001256302 RefSeq chr5 - 138506092 138543300 ETF1 2107 "eukaryotic translation termination factor 1, transcript variant 2"
GO:0005515|GO:0010467|GO:0003723|GO:0006449|GO:0006415|GO:0003747|GO:0006412|GO:0005829|GO:0005737|GO:0000184|GO:0016149|GO:0006479|GO:0043022|GO:0008079|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75440_PI430048170 0.1423437323738410.8820797734625518.05820932863863 7.89022789247241 8.12987826345915 P P P 8.14677782060248 8.12914406498127 8.34565251299352 P P P LNCV6_75440_PI430048170 mRNA
GAAGAGGTCGAATTGATGACTTGCGATACCAGATAGATGATAAACCAAACAACCAGATTC NM_016640RefSeq chr5 + 44808924 44815516 MRPS30 10884 mitochondrial ribosomal protein S30
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0006915|GO:0005840 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143270_PI430048170 0.5701591522037360.95289157937727 0.346928701607288 0.3456929840444030.266889801488047A A A 0.2842436519235680.29632287682247 0.570680371366377A A A LNCV6_143270_PI430048170 mRNA
ATAAAATTTCCATTCTGAACTACAAGTGCCGGAAAGTCTAGGGGTCTGTGCAAGGCCTGT NM_001900RefSeq chr20 - 23875934 23879743 CST5 1473 cystatin D
GO:0010951|GO:0005515|GO:0004869|GO:0005576|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129036_PI430048170 0.3679160984578840.6742423538568270.368128933832156 0.3936094987717550.326493226767663A A A 1.60038021949699 0.502110250948349 0.349286232953289A A A LNCV6_129036_PI430048170 mRNA
TGAAACCTTGTGAGCAGAAGGCAAGAGCGGCAAGATGAGTTTTGAGCGTTGTATTCCAAA NM_005601RefSeq chr19 - 51371619 51372706 NKG7 4818 natural killer cell granule protein 7 GO:0005887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136597_PI430048170 0.6638487921527520.9517102139357577.42933992334355 7.12435140075384 7.51767122512496 P P P 7.3352015562406 7.32226198003827 7.6347891524959 P P P LNCV6_136597_PI430048170 mRNA
GAAGAGGAATATTAAGACATCTTAACAACAAACCACAACATTGCCTGCATGTCTAAAAGA NM_018128RefSeq chr17 - 2322687 2337384 TSR1 55720 "TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)"
GO:0042255|GO:0005730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136880_PI430048170 0.4830735610919990.9598871986168850.40661993160533 0.4233810474566550.442372584201385A A A 0.5414211677963720.349153538443996 0.550391446233296A A A LNCV6_136880_PI430048170 mRNA
GGGTTCATAGAAACCCAATGACTTGATTGTGGCTACTACTCAATAAATAATAGAATTTGG NM_002160RefSeq chr9 - 115019575 115118257 TNC 3371 tenascin C
GO:0008284|GO:0071300|GO:0045471|GO:0071799|GO:0005614|GO:0005615|GO:0071305|GO:0071774|GO:0007528|GO:0030198|GO:0014012|GO:0042475|GO:0007155|GO:0060739|GO:0009611|GO:0060740|GO:0005576|GO:0001649|GO:0009612|GO:0005604|GO:0010628|GO:0031012|GO:0007162|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134536_PI430048170 0.000845573632046093 0.2938474648813362.67508758898646 2.22443208316814 2.26838453619262 A A A 4.13210669753481 3.99315654085644 4.36288024217326 P P P LNCV6_134536_PI430048170 mRNA
CTCTTAGCTTGAGCTTATGCAATGATTGGTTAAGATTTTGGCATTGTAAGAATTAGGAGA NM_001300907 RefSeq chr11 - 68154862 68213345 SUV420H1 51111 "suppressor of variegation 4-20 homolog 1 (Drosophila), transcript variant 3"
GO:0000780|GO:0006355|GO:0042799|GO:0007517|GO:0006351|GO:0034773|GO:0018024 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_129199_PI430048170 0.8520761222801391.15487456319479 1.78212440151059
0.8541133726737060.29355565055882 A A A 1.05016163292701 0.520245216783485
1.07015172164274 A A A LNCV6_129199_PI430048170 mRNA
GGGGCCAAGAAGATGTACTTCCATCATTACTTCCAAAAAGTAAGTTGAAAAAGATACAGT NM_001145101 RefSeq
chr11 - 57743513 57751781 BTBD18 NA BTB (POZ) domain containing 18 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_130403_PI430048170 0.1798937387666780.8173136594408891 2.3993993012793
12.5223812792627 12.4882218805368 P P P 12.4686714277656 12.8651052087476
12.9123342820059 P P P LNCV6_130403_PI430048170 mRNA
CCCTAACTGTTCCCTTATCTGTTTTCTACCTCCTCCTTTGTTTAATAAAGGCTGAAGCTT NM_001284526 RefSeq chr17
- 8204730 8210626 AURKB 9212 "aurora kinase B, transcript variant 3"
GO:0051256|GO:0043146|GO:0005515|GO:0032091|GO:0031577|GO:0008283|GO:0034501|GO:0005634|GO:0051
233|GO:0031145|GO:0046872|GO:0036089|GO:0005829|GO:0009838|GO:0034644|GO:0046777|GO:0002903|GO:0
005876|GO:0000780|GO:0032466|GO:0010369|GO:0032467|GO:0007568|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_78813_PI430048170 0.2931411033702570.8004852350228425.13199349156123 4.85322387497021
5.4015417857126 P P P 5.08240228042598 5.46286458792179 5.77435010058106 P P P
LNCV6_78813_PI430048170 mRNA
CTTTTACAAGTGGTGCCTATTAAAGTCAGTAATGGCCATTATTGTTCCATTGTGGAAATT NM_001145306 RefSeq
chr7 - 92604920 92836627 CDK6 1021 "cyclin-dependent kinase 6, transcript variant 2"
GO:0005515|GO:0010468|GO:0008285|GO:2000145|GO:0050680|GO:0048699|GO:0005634|GO:0048146|GO:0005
829|GO:0005737|GO:0000082|GO:0007219|GO:0045638|GO:0043697|GO:0007050|GO:2000773|GO:0021542|GO:0
033077|GO:0030332|GO:0003323|GO:0060218|GO:0045786|GO:0009615|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137125_PI430048170 0.4299246916276850.9686351348915820.442439824455704
0.4655169074809420.317701121511446 A A A 0.4134451478689740.495512512009381
0.457795812096696 A A A LNCV6_137125_PI430048170 mRNA
CCTCCGGTATACCTTTATCCCTTTGAAAGGGTGCTTGTACAATTTGATATATTTTATTGA NM_002449 RefSeq chr5 +
174724571 174730899 MSX2 4488 msh homeobox 2
GO:0005515|GO:0003416|GO:0008285|GO:0035313|GO:0044212|GO:0006366|GO:0045599|GO:0000982|GO:0032
792|GO:0005634|GO:2000678|GO:0009952|GO:0045617|GO:0030513|GO:0090427|GO:0002063|GO:0071392|GO:0
061312|GO:0003712|GO:0005667|GO:0043066|GO:0003198|GO:0023019|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129912_PI430048170 0.0245594107962263 1.33041861805633 14.1927403761144
14.4116448221343 14.3579344138166 P P P 13.91914250264 13.904104112329
13.9123061790258 P P P LNCV6_129912_PI430048170 mRNA
GGCCGACTCTTTTCCCTGCTTTGGTTTGTTTGAAATCTAAATAAAACTACTTTATGAGAA NM_004359 RefSeq chr19
+ 531732 542087 CDC34 997 cell division cycle 34
GO:0000209|GO:0005515|GO:0004842|GO:0016567|GO:0090261|GO:0016874|GO:0005634|GO:0070848|GO:0005
524|GO:0000082|GO:0005737|GO:0043525|GO:0019787|GO:0006270|GO:0043161|GO:0005654|GO:0070936|GO:0
043951|GO:0031625|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134917_PI430048170 0.7762609833431821.00610711565232 0.34954673547592
0.3260095960745870.264420069924025 A A A 0.3066685445289430.314732039199617
0.293478206514028 A A A LNCV6_134917_PI430048170 mRNA
AAGCAGGACACAGGCTGCACATCACAGGTTCCAAAGTGTGCAGCAAGGCTTCTGACCAGG NM_152698 RefSeq
chr2 + 130755503 130768134 AMER3 205147 "APC membrane recruitment protein 3, transcript variant 1"
GO:0005515|GO:0005886|GO:0016055|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143333_PI430048170 0.9894667247659971.00617271928297 9.68769594543424 9.9258002334004
10.0953807143561 P P P 9.82911797115729 9.85127110856219 10.0227643609402 P P P

LNCV6_143333_PI430048170 mRNA
CTTCAGCTCAGTAGCTTTGGTCATAGGCAAGTTTGTTTTCCATTATCATAATTTGATGATNM_207356RefSeq chr1 -
3889132 3900293 C1orf174 339448 chromosome 1 open reading frame 174 GO:0005634 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_144074_PI430048170 0.4865179670137531.19728772195443 0.428180633595302
1.08560628479323 0.256337525468514A A A 0.3438982647154480.397752589846973
0.386668049141012A A A LNCV6_144074_PI430048170 mRNA
CTTCCAGTGAAACACACGCATCTTAATAATAAGGGTAAATAAACGCTCCATATGAAACTA NM_001102445 RefSeq
chr1 + 163068605 163076802 RGS4 5999 "regulator of G-protein signaling 4, transcript variant 1"
GO:0043547|GO:0000188|GO:0043234|GO:0005516|GO:0001965|GO:0005737|GO:0008277|GO:0005886|GO:0038
032|GO:0005829|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136015_PI430048170 0.7297712711567881.09673518491288 1.00504037708997
0.3020765583578781.0956833319825 A A A 0.9823474676094530.764948638543471
0.296076906646669A A A LNCV6_136015_PI430048170 mRNA
TCCTTCTGGTGCTCCTTACTCCAAGTCTATTTCATTTTTCCACACTGAGCAATGAATGTGNM_005181RefSeq chr8 +
85438826 85449038 CA3 761 carbonic anhydrase III
GO:0045471|GO:0015701|GO:0008270|GO:0044281|GO:0004089|GO:0006979|GO:0006730|GO:0016151|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122983_PI430048170 0.0197059643741237 0.4054008452876515.5122625530517
4.84470660121143 5.4745666456973 P P P 6.5311743474272 6.72159151269346
6.57164816913643 P P P LNCV6_122983_PI430048170 mRNA
GGAGATATTTTCCACCTATGGGAAAATTAAAATGATTGACATGCCCGTGGAAAGGATGCA NM_080594RefSeq chr16
- 2253115 2268412 RNPS1 10921 "RNA binding protein S1, serine-rich domain, transcript variant 2"
GO:0008380|GO:0005515|GO:0010467|GO:0006369|GO:0048025|GO:0043065|GO:0006366|GO:0003723|GO:0031
124|GO:0005634|GO:0006351|GO:0005829|GO:0005737|GO:0006406|GO:0016607|GO:0000166|GO:0000184|GO:0
000381|GO:0000398|GO:0005654|GO:0003730|GO:0035145 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_128922_PI430048170 0.2639767174525131.03902644805083 0.533874112948137
0.6263702906597260.510458913170037A A A 0.5016704673804440.499051234830198
0.506894709745198A A A LNCV6_128922_PI430048170 mRNA
TGATGGCCAGGAGTAGATGACAGGGAGTTGCCTTGGGGAACCTTTGGTGTGCCAAGAGGA NM_030776RefSeq
chr20 - 57603845 57620576 ZBP1 81030 "Z-DNA binding protein 1, transcript variant 1"
GO:0005515|GO:0003726|GO:0003723|GO:0005634|GO:0003677|GO:0005829|GO:0003692|GO:0008150|GO:0005
737|GO:0045087|GO:0008152|GO:0060340|GO:0032481 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135940_PI430048170 0.0502997876496432 0.2012609971916112.39195116074941
0.4449880422636490.3570847866634 A A A 3.68540179310256 3.37650057580528
3.99603767204667 P P P LNCV6_135940_PI430048170 mRNA
CCAGTTACACTCCTGTGAGTCAGCTTATTTTTACCCTAACATAAATAGTATGTTTTGTAG NM_032427RefSeq chr11
- 95976592 96343180 MAML2 84441 mastermind-like 2 (Drosophila)
GO:0010467|GO:0006367|GO:0005794|GO:0016607|GO:0007219|GO:0045944|GO:0003713|GO:0005654|GO:0005
634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137744_PI430048170 0.7556141822793990.8128198371301950.881451102925265
0.9112335533511420.97029891978796 A A A 0.6943703133258281.95316638602612
0.58517616406409 A A A LNCV6_137744_PI430048170 mRNA
AGACTCACACTTGAGAAAACCTAAGACTTGTACTGGAGCCTCAGGGCAGAATTGTAACCT NM_052929RefSeq chr1
+ 15247271 15398126 FHAD1 114827 forkhead-associated (FHA) phosphopeptide binding domain 1
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68791_PI430048170 0.1606606090132312.36134073597304 2.05020384057958 3.33865074967608
3.59179116084289 A P P 1.3341869579324 0.66928806019295 2.81404612691712 A A P

LNCV6_68791_PI430048170 mRNA
GTTTTCTAAAACAATAGAGAAGGAAATTTCACCGGAAATTAGGAGTTTGAGCCCAGAATA NM_152347 RefSeq chr17
+ 47323960 47441311 EFCAB13 124989 "EF-hand calcium binding domain 13, transcript variant A"
GO:0005737|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140256_PI430048170 0.0382988855754202 0.8419773074626354.13720265767559
4.29313918907315 4.25725456797544 P P P 4.45665416333211 4.37861658474773
4.59312744812457 P P P LNCV6_140256_PI430048170 mRNA
CTTTTGAAAGCAACTTGAGGAAAAACACATAACAGAATCTATAGGTGTGGACAATATGTG NM_001291605 RefSeq
chr2 + 95165416 95184316 ZNF2 7549 "zinc finger protein 2, transcript variant 5"
GO:0006355|GO:0003700|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_48590_PI430048170 0.4224853429141481.13250042426947 0.2784972244972210.814205447883301
0.410433735181903 A A A 0.3687545691686980.3056210226137080.344856934091867 A A A
LNCV6_48590_PI430048170 mRNA
ATTTATAGCTGTGACACAAGATGATAGAAATTGCTCATGCTCACATATATTCCAACTGGC NM_001010852 RefSeq
chr6 + 122995970 123072919 CLVS2 NA clavesin 2 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137046_PI430048170 0.0629358060806009 1.22511586155457 8.71117796303965
8.95850070980812 8.97094762465957 P P P 8.64073274259336 8.53739320911783 8.5964654075821
P P P LNCV6_137046_PI430048170 mRNA
CCAACGGGCACAAGCATTCTATATATAAGTGGCTCATTAGGTGTTTATTTTGTTCTATTT NM_144635 RefSeq chr3
+ 184337487 184346275 FAM131A 131408 "family with sequence similarity 131, member A, transcript
variant 1" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145532_PI430048170 0.0638573174660033 0.6099742512817049.4112747211748
9.3868733705315 9.73477656062581 P P P 9.79995650243616 10.2778426320501
10.5291812984247 P P P LNCV6_145532_PI430048170 mRNA
GCTAGAAGCACTTTATGTTTCCTTTTTGGGTGAAATGGATTTATGTGAGTGCTTTAAACA NM_006708 RefSeq chr6
- 38675925 38703176 GLO1 2739 glyoxalase I
GO:0043066|GO:0005737|GO:0006357|GO:0005975|GO:0030316|GO:0006749|GO:0008270|GO:0004462|GO:0009
438|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138335_PI430048170 0.000278928368055656 0.4315544210768892.83619985723966
2.98114939635468 2.75778447988013 A P A 4.02510456057692 4.1554448618526
4.03707291439378 P P P LNCV6_138335_PI430048170 mRNA
AAGACCTTGACTGGTGGGCTTTTTACGTGTAAGGAAGAGGAAGTTTAAGAAGTAGGACTC NM_024759 RefSeq chr8
- 98192158 98294393 NIPAL2 79815 NIPA-like domain containing 2
GO:0015693|GO:0015095|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133544_PI430048170 0.0106793789663692 0.5367186353452757.01115058924278
6.89926857591862 7.16127148375005 P P P 7.71579649683771 7.83578473160728
8.18362578828427 P P P LNCV6_133544_PI430048170 mRNA
ATGTTAAGCATGGAGAGGGATGCTTGACAGCATGCTAATTGAAGCCAGAGCAAGTATGTC NM_001240 RefSeq chr12
- 48688457 48716998 CCNT1 904 "cyclin T1, transcript variant a"
GO:0005515|GO:0010467|GO:0008024|GO:0006368|GO:0006367|GO:0044212|GO:0019901|GO:0006366|GO:0005
730|GO:0005634|GO:0000079|GO:0003677|GO:0006351|GO:0050434|GO:0007049|GO:0045944|GO:0003682|GO:0
017069|GO:0016032|GO:0007179|GO:0005654|GO:0006468|GO:0051301 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_138499_PI430048170 0.3610657779670380.7438947470759270.919682423645001
0.2722517818598310.351371142397079 A A A 1.02154226652961 1.38136062800078
0.317535158946134 A A A LNCV6_138499_PI430048170 mRNA
AATCCTCCTCACAAACTGGGGGGAAACCGAAGGTTGTTAAAATACAGCTAAAGTTGGTGG NM_032962 RefSeq

chr17_KI270857v1_alt - 218219 221292 CCL14 6358 "chemokine (C-C motif) ligand 14, transcript variant 2" GO:0008009|GO:0008284|GO:0006955|GO:0060326|GO:0006874|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137172_PI430048170 0.2873506496970341.04757594165095 0.460369153155814 0.3033814913049410.357990404693596A A A 0.2768240959375920.33498594082059 0.31259557326613 A A A LNCV6_137172_PI430048170 mRNA AAGTATCTTTTCTCTGTCAGCGAACGTGGCATTTTCTGCGCCGGCAGGACCACCTGCCAG NM_014589RefSeq chr1 - 19920306 19923617 PLA2G2E 30814 "phospholipase A2, group IIE" GO:0036149|GO:0005509|GO:0036148|GO:0005576|GO:0044281|GO:0016042|GO:0036150|GO:0006954|GO:0004623|GO:0006644|GO:0006654|GO:0036151|GO:0046474|GO:0036152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55339_PI430048170 0.00151105851205757 2.45880284313215 7.19766475196843 7.42422172756234 7.50681004806706 P P P 6.07648819280626 6.28636538944408 5.85768977349619 P P P LNCV6_55339_PI430048170 mRNA TTTAACTGCGAGTTCTTCACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGG NM_198149RefSeq chr1 + 201888676 201892587 SHISA4 149345 "shisa family member 4, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127742_PI430048170 0.00557731913825797 0.5406295356986694.53698402931737 4.29446011377512 4.70645724637007 P P P 5.18279159854806 5.48159984841009 5.53996985343316 P P P LNCV6_127742_PI430048170 mRNA CCATTGCAATTTGATTTAAGCCTACTAGAGCCATTGTATGTGACAGCTATATTGTATTAC NM_001164384 RefSeq chr8 - 73549601 73747708 STAU2 27067 "staufen double-stranded RNA binding protein 2, transcript variant 6" GO:0005515|GO:0003725|GO:0016020|GO:0005783|GO:0005874|GO:0006810|GO:0005730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132071_PI430048170 0.427533141803313 1.01546480169591 13.9903471705811 14.0159087889289 14.0386642609619 P P P 14.0105607404028 14.0159087889289 13.9515550431602 P P P LNCV6_132071_PI430048170 mRNA ATTAGATCTAAAGCCCCTTCCTCCCCAGCCCCTGCTTTCATTAAGGTATTTAAACTTGGG NM_018426RefSeq chr6 + 44127638 44155519 TMEM63B 55362 transmembrane protein 63B GO:0000166|GO:0016021|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145067_PI430048170 0.4994901833245790.8208285443293 1.62607228338456 0.4680834784344740.457373567757377A A A 1.51579586759724 1.40810114484392 0.682579289837899A A A LNCV6_145067_PI430048170 mRNA CGATCACTGGTTTACTTTCTATGGATACAATCTCTCCTCCATTGAGAATTGATTTTACAA NM_001010897 RefSeq chr13 + 44373841 44397714 SERP2 387923 stress-associated endoplasmic reticulum protein family member 2 GO:0005789|GO:0016021|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140141_PI430048170 0.0746185442705249 0.9349383452797730.304472316318064 0.3087869042246410.311448165682408A A A 0.4573958956096220.395493532361468 0.361349149765568A A A LNCV6_140141_PI430048170 mRNA TGTGGAAAAGATAATATCTGATGGCCAGAGACAATTTCTTGCTTTGGTATGTTTGAAGTG NM_181435RefSeq chr5 - 34017857 34043266 C1QTNF3 114899 "C1q and tumor necrosis factor related protein 3, transcript variant 2" GO:0005515|GO:0045721|GO:0005581|GO:0042347|GO:0070165|GO:0035356|GO:0050715|GO:0071638|GO:0005615|GO:0003674|GO:0070206|GO:1900165|GO:0016020|GO:0050728|GO:0010629|GO:0045444|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139878_PI430048170 0.2312411098787881.18870670118642 5.68122932095459 5.7135394319341 5.39076041874505 P P P 5.48954491583596 5.47924597729677 5.04737668432105 P P P LNCV6_139878_PI430048170 mRNA GCAGCTGAGCCTAGGTCTGTGCTGTAAATCCTAAGATTAAACATTCCAGATAGTAAAAAA NM_012163RefSeq chr16

- 67207138 67226818 LRRC29 26231 "leucine rich repeat containing 29, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136152_PI430048170 0.0917168549035559 0.9324505345500930.280530923250938
0.2847178195870940.306712090534327A A A 0.455390615288641 0.377318687242474
0.339666162138537A A A LNCV6_136152_PI430048170 mRNA
TTTGGAAGCTTTGGTTATGAAACATGTGGAGTGTATTAAGTGCAGCTTGACATTATGTTT NM_000780RefSeq chr8
- 58490177 58500161 CYP7A1 1581 "cytochrome P450, family 7, subfamily A, polypeptide 1"
GO:0042632|GO:0006707|GO:0006805|GO:0005506|GO:0006699|GO:0044281|GO:0055085|GO:0043231|GO:0071
397|GO:0070857|GO:0005789|GO:0008206|GO:0016125|GO:0071333|GO:0008123|GO:0044255|GO:0055114|GO:0
020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116554_PI430048170 0.0616548183449359 0.6181273436216359.74384047974084
9.67660095790193 9.90205827472009 P P P 10.1497824244619 10.3742708032185
10.8102623378968 P P P LNCV6_116554_PI430048170 mRNA
CAAAGGATAAAACTGTTCTAAAGGCTTCCAGGGTCATGATGGGATTTTTTAAATAAATGC NM_001172640 RefSeq
chr11 - 47465936 47489024 CELF1 10658 "CUGBP, Elav-like family member 1, transcript variant 5"
GO:0017148|GO:0005515|GO:0006397|GO:0016246|GO:0042835|GO:0003723|GO:0006376|GO:0007286|GO:0005
634|GO:0009790|GO:0003729|GO:0007281|GO:0005737|GO:0016020|GO:0000166|GO:0030529|GO:0043484|GO:0
031369|GO:0005654|GO:0040018|GO:0000900 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132397_PI430048170 0.6164482718611791.08687794646697 9.0725430850886
9.20533825840901 8.70339779193027 P P P 9.16985900164391 8.8803404402454
8.55000415135093 P P P LNCV6_132397_PI430048170 mRNA
TCATGTTTATCTGGTTTGCATGTCCCTGTCCTCTCTAAACAGTAGTGCCAACCCCATCAT NM_054032RefSeq chr11
+ 18172836 18174280 MRGPRX4 117196 "MAS-related GPR, member X4"
GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128582_PI430048170 0.3380863044609681.11069617438401 8.54773180289423
8.43788416596627 8.81568738793396 P P P 8.33064795321521 8.49087366826789 8.5435450524848
P P P LNCV6_128582_PI430048170 mRNA
ACAAGTAAACTCAGCCTGAAGACACCAGAGAGAAGGACTGCAAACCCAAATCATGACATG NM_001201475
RefSeq chr18 + 35972624 35979287 C18orf21 83608 "chromosome 18 open reading frame 21,
transcript variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143026_PI430048170 0.0190836659912908 2.18935849861855 7.7806367640597
8.05797322655034 7.69781632280483 P P P 6.28969757721384 7.04588395255494
6.73637141960228 P P P LNCV6_143026_PI430048170 mRNA
CTTCTCTTGCCGACATGTTTTTTGTAAGGCTGGTAAATAAATTATTTTGGACAAAACTGG NM_018957RefSeq chr22
+ 37639676 37656043 SH3BP1 23616 SH3-domain binding protein 1
GO:0043547|GO:0007165|GO:0017124|GO:0005737|GO:0005096 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138685_PI430048170 0.0261363781840661 0.8236389977213256.91756227790031
6.70792314549092 6.84509509571007 P P P 7.0244452770943 7.08772748786728
7.20041770826713 P P P LNCV6_138685_PI430048170 mRNA
CAGCTCTTTGATACCCTGTGTTAGAGTAATAGCTAAAGGAAGTTCATGTCAATAAATTCA NM_001135629 RefSeq
chr2 + 48440768 48515392 PPP1R21 129285 "protein phosphatase 1, regulatory subunit 21,
transcript variant 1" GO:0016020|GO:0019902 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137336_PI430048170 0.2550160013727881.05389083802195 0.582996050209726
0.7068710274352170.553568904874433A A A 0.54082578929413 0.539458446882454
0.540604132706205A A A LNCV6_137336_PI430048170 mRNA
CTCAGTTAAATCTTTGAAGAATATTTGTAGTTATCTTAGAAGATAGCATGGGAGGTGAGG NM_003012RefSeq chr8
- 41261956 41309471 SFRP1 6422 secreted frizzled-related protein 1
GO:0005515|GO:0001657|GO:0014070|GO:0017147|GO:0030308|GO:0033689|GO:0030307|GO:0050732|GO:0050

680|GO:0010564|GO:0005615|GO:0032855|GO:0042802|GO:0005109|GO:0005622|GO:0014034|GO:0006508|GO:0
046676|GO:0050679|GO:0030336|GO:0009986|GO:0004930|GO:0001843|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145292_PI430048170 0.11169612972046 1.03404958420591 0.335792426156627
0.3047790155341870.271134348582919A A A 0.2483776653022680.268266159177892
0.250788702447145A A A LNCV6_145292_PI430048170 mRNA
TTAGAACATAAATACTTGACTCCCATGGCCAGCACGAGGATCAGGAATCAGTTGCTGGAT NM_001142807 RefSeq
chr2 + 110732572 111118222 ACOXL 55289 acyl-CoA oxidase-like
GO:0008150|GO:0003674|GO:0006635|GO:0003997|GO:0003995|GO:0005575|GO:0005777 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127056_PI430048170 0.0540604344935232 3.40987407723326 2.32997307678042
3.5030823717731 3.66593296040319 A P P 2.30656537024231 1.1042198974447
0.51100055936394 A A A LNCV6_127056_PI430048170 mRNA
TGATTTGTCTTCCACAGTCTCTCTGGGGCTGTGTCCTACATAGCTTCTGACTCTCAATTT NM_175053 RefSeq chr12 -
52565818 52573825 KRT74 121391 "keratin 74, type II"
GO:0005737|GO:0005198|GO:0045104|GO:0045095|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128938_PI430048170 0.3868031420013250.9754015162741580.272004510569557
0.2949670521524450.374292420232397A A A 0.3876936719345220.340289180270137
0.322290896686489A A A LNCV6_128938_PI430048170 mRNA
GCAAATAGCAAGTATGGTGCTAAAGTCTACACCAATGGAATTAGATGAGTGCTATGCACT NM_001134375 RefSeq
chr10 + 96043401 96060868 CCNJ 54619 "cyclin J, transcript variant 1" GO:0005634 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_144483_PI430048170 0.7237899698260260.9914618440884570.440306073154158
0.4504080354372250.370622781920323A A A 0.4742591621942530.403667112672608
0.420881545964445A A A LNCV6_144483_PI430048170 mRNA
AGCTATGTATTAGGTAATACATAATGCCTAATACATAACTAATATATGGACAGGAAGTTA NM_032025 RefSeq chr3
+ 150546786 150586016 EIF2A 83939 "eukaryotic translation initiation factor 2A, 65kDa"
GO:0005515|GO:0005850|GO:0000049|GO:0042255|GO:0003743|GO:0072562|GO:0009967|GO:0005615|GO:0006
413|GO:0006417|GO:0005737|GO:0032933|GO:0043022|GO:0006468 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134935_PI430048170 0.00682386108037866 4.45869954253477 6.58028181125616
6.56419784582285 7.0846679196811 P P P 4.77539062544633 3.95051351710635
4.92032482507195 P P P LNCV6_134935_PI430048170 mRNA
TTTGAAGACTTACTGTTGGCCATAGTTAATTGTGTGAGGAACACGCCGGCCTTTTTAGCC NM_005139 RefSeq chr4
+ 78551587 78610451 ANXA3 306 annexin A3
GO:0006909|GO:0005886|GO:0043312|GO:0005509|GO:0042581|GO:0019834|GO:0043086|GO:0045766|GO:0005
544|GO:0010595|GO:0051091|GO:0005737|GO:0016020|GO:0030670|GO:0042742|GO:0070062|GO:0048306 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127360_PI430048170 0.4695160215146380.6142346020263740.482878908827749
0.5944359639881660.529088129506777A A A 2.10646652899108 0.455901706818387
0.490251607092942A A A LNCV6_127360_PI430048170 mRNA
ATGTAGTCAAGGTCTTCCCAGTGAAGTTTTCAGGTTTCTAAGGGCAAGTCAAGGATCCCA NM_001005272 RefSeq
chr11 + 54706831 54707902 OR4A5 NA "olfactory receptor, family 4, subfamily A, member 5" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129437_PI430048170 0.2998755667414381.31148684079472 5.24849113009501
6.09965166056775 5.84207409901564 P P P 5.35818495083308 5.41249713511866
5.37175457728652 P P P LNCV6_129437_PI430048170 mRNA
CTCCTCTAGCTATCCTTGATGAGCTTCTCACTTTAAGAATAAATGTGTTTGATATAAGGA NM_005398 RefSeq chr10

- 91628439 91633101 PPP1R3C 5507 "protein phosphatase 1, regulatory subunit 3C"
GO:0005515|GO:0005975|GO:0019903|GO:0016311|GO:0005978|GO:0009405|GO:0006006|GO:0044281|GO:0004
722|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140811_PI430048170 0.1549554725012991.09174029950106 0.435479605651415
0.5801596378838980.384354527817154A A A 0.2982297050100530.336071719928445
0.391491506851343A A A LNCV6_140811_PI430048170 mRNA
CTGGTGCATCTTTGAAAAGTGTGCCTTTAGAAACAAGACACCCTTTTAAAGTAATATGTC NM_001256598 RefSeq
chr8 + 49072340 49076083 C8orf22 492307 "chromosome 8 open reading frame 22, transcript variant
4" GO:0007275|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142801_PI430048170 0.4273381125083291.40358427205133 1.7015767055608
0.5514625333577860.519676925525168A A A 0.3686383656758870.771096069632532
0.470093077556151A A A LNCV6_142801_PI430048170 mRNA
TGTTCCTCTCACCTCATGGTGGTGGGAATGTACTATGGAGCAGGTTTGTTCATGTACATA NM_001004690 RefSeq
chr1 + 248145147 248146086 OR2M5 NA "olfactory receptor, family 2, subfamily M, member 5"NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124590_PI430048170 0.3974982720291371.13399139739681 7.1312614152597
6.69609304600235 6.84734591889469 P P P 6.56964650363866 7.00240314659939
6.54543276591792 P P P LNCV6_124590_PI430048170 mRNA
TTTCTGTGAAAACAGCAGTGAACAGGTTCAGTTTTGAACTGGCCCTGAGGAAATGGGTCA NM_025263RefSeq
chr6_GL000256v2_alt + 1857463 1865451 PRR3 80742 "proline rich 3, transcript variant 1"
GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141330_PI430048170 0.0627004411080355 0.39929670197903 1.63855998404921
0.4529292312542260.553129129257849A A A 2.2450469438913 2.33249899622242
2.35698279019992 A A A LNCV6_141330_PI430048170 mRNA
TGTGGCAAATCATTTATCTGGTCCTCAACCCTTTTTAAGCATAAGAGGATTCATACTTGA NM_001244038 RefSeq
chr19 + 23914881 23933967 ZNF726 730087 zinc finger protein 726
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_80536_PI430048170 0.8039634757332060.9836074034172294.69543785281868 5.06270767336101
4.76028216654384 P P P 4.92373908756964 4.84999267294458 4.84201981628496 P P P
LNCV6_80536_PI430048170 mRNA
GAACTCATGAGACTGCTTTTTTAGGACCAAAGGATATATTTCCTTACTCAGAAAATAAGG NM_033222RefSeq chr9
- 15464065 15511005 PSIP1 11168 "PC4 and SFRS1 interacting protein 1, transcript variant 2"
GO:0005515|GO:0001105|GO:0006355|GO:0009408|GO:0005730|GO:0035327|GO:0005634|GO:0006351|GO:0005
829|GO:0000395|GO:0005720|GO:0097100|GO:0034399|GO:0045944|GO:0003682|GO:0016032|GO:0005654|GO:0
033613|GO:0006979. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134596_PI430048170 0.00828113327345966 0.7236358569285056.72974261130123
6.74889979822819 6.620892144366 P P P 7.02793381838989 7.24803950779046
7.21713698970805 P P P LNCV6_134596_PI430048170 mRNA
AGTGACTATGGGCGCACTGCCTAACATTTAGCCCTGCCCCATATGGAACATGTTAAAAAA NM_213566RefSeq chr1
- 10460545 10472556 DFFA 1676 "DNA fragmentation factor, 45kDa, alpha polypeptide, transcript
variant 2"
GO:0005515|GO:0005811|GO:0000790|GO:0043065|GO:0070242|GO:0006915|GO:0005634|GO:0006921|GO:0005
829|GO:0005737|GO:0006309|GO:1900118|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80658_PI430048170 0.1923130035219140.8810248574813745.8677529696359 5.7887247700265
5.55410418845349 P P P 6.04954204854445 5.81723831695209 5.90050015185768 P P P
LNCV6_80658_PI430048170 mRNA
TACCCTTCCTGGGCAAACTAAGCTCCTTGCAGAGGATCCTGGAGATTCAGCCCCACCATG NM_032634RefSeq chr9
- 35088687 35096549 PIGO 84720 "phosphatidylinositol glycan anchor biosynthesis, class O, transcript

variant 1"
GO:0006501|GO:0003674|GO:0016020|GO:0016254|GO:0005789|GO:0016021|GO:0044267|GO:0016740|GO:0006506|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77645_PI430048170 0.3077093867026350.9207822786367589.44769820406347 9.65393712470722 9.62311538440504 P P P 9.72898764841154 9.5446827546547 9.80451259636918 P P P
LNCV6_77645_PI430048170 mRNA
GCCAGATGCTTGTGTATCCTCAGACCAAACTGATTCATGTACAAATAATAAAATGTTTAC NM_147686RefSeq chr6 - 111555377 111606274 TRAF3IP2 10758 "TRAF3 interacting protein 2, transcript variant 2"
GO:0035556|GO:0005515|GO:0001783|GO:0006959|GO:0005575|GO:0043123|GO:0048305 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103066_PI430048170 0.00661316063657902 1.54181756122864 8.02046414224653 7.92330817011427 8.22226279838087 P P P 7.33859808517762 7.53328131716596 7.42996585621022 P P P LNCV6_103066_PI430048170 mRNA
AATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGATGGAGAGTA NM_020536RefSeq chr20 + 18142223 18188387 CSRP2BP 57325 "CSRP2 binding protein, transcript variant 1"
GO:0005515|GO:0005737|GO:0043966|GO:0000086|GO:0030274|GO:0006325|GO:0005671|GO:0005634|GO:0004402 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132780_PI430048170 0.476789222641822 1.03466768374324 10.8423854412322 10.8337769251183 10.8257933110502 P P P 10.8076474031212 10.8702665842113 10.6693220983556 P P P LNCV6_132780_PI430048170 mRNA
GGAAGGGGTCAGGTGGTTTGGGTTTTGTTTTTTAAAATAAAATAGACATGTTATATTGCC NM_015164RefSeq chr1 + 15684331 15734769 PLEKHM2 23207 "pleckstrin homology domain containing, family M (with RUN domain) member 2" GO:0005515|GO:0005737|GO:0007030|GO:0019894 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138697_PI430048170 0.102150974718925 1.06453825410907 0.477411902518838 0.5827032354957030.525186895196223 A A A 0.3817291268611830.449367681727994 0.483594815762708 A A A LNCV6_138697_PI430048170 mRNA
TGAGGGGAGGATAACATTTTTGCTTTCTTATGTGACTCTCTTTGAAAATGTGCAGTAAGA NM_003651RefSeq chr12 - 10699076 10723354 YBX3 8531 "Y box binding protein 3, transcript variant 1"
GO:0048471|GO:0003700|GO:0009409|GO:0005634|GO:0007283|GO:0005737|GO:0003690|GO:0003697|GO:0071356|GO:0003730|GO:0060546|GO:0071474|GO:0000977|GO:0046622|GO:0003714|GO:0000122|GO:0048642|GO:0001701|GO:0001227|GO:0006351|GO:2000767|GO:0009566|GO:0017048|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83495_PI430048170 0.324823680641896 0.718036810782058 2.14957544890107 3.25338468966799 2.48625442190649 A P A 3.67055315027003 3.03298335675698 2.66562429470821 P P P LNCV6_83495_PI430048170 mRNA
TCATCACTCAGCCTAAGAGGCCCAGCAGGTTCCGGATCCATCTGGACCCCCTACCTTCCG NM_173728 RefSeq chr17 + 8310237 8322516 ARHGEF15 22899 "Rho guanine nucleotide exchange factor (GEF) 15, transcript variant 1"
GO:0005515|GO:0050790|GO:0005737|GO:0032321|GO:0051496|GO:2000297|GO:0061299|GO:0005089|GO:0030425|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131476_PI430048170 0.0151353708544244 0.279475323110538 3.56303086167356 2.74769366680391 3.75425328940705 P A P 5.47091175223677 5.0368296102534 5.22599587867901 P P P LNCV6_131476_PI430048170 mRNA
CCTAGTGAGGGAATCTAATTAAGATTTCATGCTGTTCTTTGTAATGATAAATGTTTCCGG NM_203403 RefSeq chr9 + 12775012 12823060 LURAP1L 286343 leucine rich adaptor protein 1-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135483_PI430048170 0.349326447492616 1.15956982641087 9.3896086115711 9.11360574592581 9.29917095820533 P P P 8.95595468643008 9.39604311244944

8.74518617301627 P P P LNCV6_135483_PI430048170 mRNA
CTGGGCACAACAGTTTCAGTGAGTGCTTTTGAGCACACTTTTATTTTTATATAGTAACTA NM_016399 RefSeq
chr12 - 120443960 120446412 TRIAP1 51499 TP53 regulated inhibitor of apoptosis 1
GO:0005515|GO:0043066|GO:0048471|GO:0030330|GO:0097035|GO:0005739|GO:0002039|GO:0005758|GO:0043
234|GO:0034644|GO:0090201|GO:0015914|GO:0045944|GO:2001140|GO:0043154|GO:0006977 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138654_PI430048170 0.33304882987584 0.549315448863302 1.89651269773315
0.516993090503857 0.624616256951686 A A A 2.07340661284925 2.66318105911014
0.719354611150875 A A A LNCV6_138654_PI430048170 mRNA
AGAGTATCTCCCACACTGAACATATTTATTCCTAGTTCTAAGGCAACAAATAGGCGGTAA NM_001005274 RefSeq
chr11 + 55343200 55344187 OR4A16 NA "olfactory receptor, family 4, subfamily A, member 16"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141198_PI430048170 0.043714755119182 0.706833971393192 9.2198904135315
8.80151609453128 8.82637634930954 P P P 9.58587041154556 9.51937989290377
9.26383712773578 P P P LNCV6_141198_PI430048170 mRNA
AGCCCCTTTCCCCACTGCCTTGTGTCCAAGGCCCTTTCCTTCATGTATCCATGGAGGAGA NM_001025 RefSeq
chr5 - 82273319 82278416 RPS23 6228 ribosomal protein S23
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0005730|GO:0006415|GO:0006
412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0000184|GO:0022627|GO:0016032|GO:0
005840|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145764_PI430048170 0.403282226966309 1.18066150623466 6.08568829623885
5.80180836075382 5.67974571860713 P P P 6.07086377917409 5.21570900831956
5.4530579528746 P P P LNCV6_145764_PI430048170 mRNA
TGGGCTGAGGGGAACAAGCATTTGCTGAAACTTGAAAAAACAAAGCAAATCAAAAACAGG NM_025182 RefSeq
chr9 - 35104120 35115896 FAM214B 80256 "family with sequence similarity 214, member B"
GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130323_PI430048170 0.190184956653658 0.689199013763488 7.30787064711317
6.65491005489491 6.29357863038421 P P P 7.49687148232581 7.53791207362287
6.94796956925213 P P P LNCV6_130323_PI430048170 mRNA
GCTCCTCTCTCCACCAAATTAGGATAGAATAATTGCTGGATAAACAAATTCAGAATATCA NM_004833 RefSeq
chr1 - 159062484 159076857 AIM2 9447 absent in melanoma 2
GO:0005515|GO:2001056|GO:0035458|GO:0032731|GO:0005634|GO:0002218|GO:0035872|GO:0005829|GO:0042
802|GO:0006955|GO:0005737|GO:0006954|GO:0003690|GO:0051092|GO:0050718|GO:0032461|GO:0050702|GO:0
006915|GO:0032088|GO:0035690|GO:0033209|GO:0070269|GO:0002230|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127203_PI430048170 0.197146785061622 1.2541827595832 12.9891730460733
12.9519118716641 13.2875650007235 P P P 12.5602638427586 12.5415720292838
13.0985836558866 P P P LNCV6_127203_PI430048170 mRNA
GCCTACTATCCTGAATTTGCCTACTATCTAATCAGCAATTAAATAAATTGTGCATGATGG NM_007193 RefSeq chr4
+ 168092536 168187742 ANXA10 11199 annexin A10 GO:0005739|GO:0005544|GO:0005509 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145120_PI430048170 0.388560826452771 0.872428833418234 0.488380981881621
0.442418944922738 0.25050856891728 A A A 0.384063257145996 0.898694007115062
0.443371663992433 A A A LNCV6_145120_PI430048170 mRNA
TTCGGCAATTGAAACATGCTTCTCTGAGGGCTTTTCCATGGAAATTGCAGCCTTCCAATG NM_032730 RefSeq
chr6 - 106571027 106629498 RTN4IP1 84816 reticulon 4 interacting protein 1
GO:0005739|GO:0016491|GO:0008270|GO:0055114 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127854_PI430048170 0.279696922150706 0.567965921976248 0.406997177953862

0.396250476848565 0.253770839176787 A A A 0.775856286610286 1.90143093027263
0.381767143425832 A A A LNCV6_127854_PI430048170 mRNA
GCTCAGCTGTCCACCTTTTCAAATACCAGGCTAAAATCAATCTCATATTTTTGCTAAATT NM_001191016 RefSeq
chr11 - 104885717 104898670 CASP12 100506742 -
GO:0072559|GO:0004197|GO:0005737|GO:0070059|GO:0072557|GO:0050727|GO:0006508|GO:0097194|GO:0042
981|GO:0097169|GO:0030968 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65742_PI430048170 0.583745436068801 1.04416837044797 5.87079857261954
6.11806477592233 6.04201947926417 P P P 5.80390417425024 6.06008691741234
5.97907023487298 P P P LNCV6_65742_PI430048170 mRNA
ACTGTGAAATGAGTAACTTAATCCTGACAACCGTAGTGCAAGGTATGGCCCATCTCCTGT NM_173074 RefSeq
chr2 - 46581273 46617112 PIGF 5281 "phosphatidylinositol glycan anchor biosynthesis, class F,
transcript variant 2"
GO:0006501|GO:0004307|GO:0016254|GO:0005789|GO:0016021|GO:0044267|GO:0006506|GO:0043687 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_145301_PI430048170 0.0665091469027577 0.645921246314654 13.089343328836
12.884551943205 12.8535774039145 P P P 13.2061024052 13.8450373408877
13.6088827644191 P P P LNCV6_145301_PI430048170 mRNA
AATCATGAACTCCTTCGTCAACGACATCTTCGAACGCATCGCGGGTGAGGCTTCCCGCCT NM_080593 RefSeq chr6
- 27138292 27146858 HIST1H2BK 85236 "histone cluster 1, H2bk"
GO:0003674|GO:0046982|GO:0050830|GO:0019731|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0005
615|GO:0003677|GO:0002227 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136311_PI430048170 0.23987582307837 1.07443476328956 0.600403612142145
0.786236549305495 0.600643463992568 A A A 0.527554156252623 0.581114514876566
0.575363163006434 A A A LNCV6_136311_PI430048170 mRNA
CTGCCGCAACAGAAATTGTTTTTATTTCATGTAAAATAAGGGATCAATTTCAAACCCTGC NM_005461 RefSeq chr20
- 40685847 40689240 MAFB 9935 v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog
B
GO:0005515|GO:0005667|GO:0033077|GO:0042472|GO:0003700|GO:0007379|GO:0007585|GO:0048538|GO:0005
634|GO:0006351|GO:0043565|GO:0007423|GO:0021572|GO:0021571|GO:0045647|GO:0045944|GO:0035284|GO:0
008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128616_PI430048170 0.0306585646310258 1.18590849949445 10.5352361653737
10.5413447891899 10.5636845572633 P P P 10.3380512647096 10.2058673367871
10.3539907243545 P P P LNCV6_128616_PI430048170 mRNA
GCACTTCTTGTATTTCTAATAAGATGACTTTCCAGAAAGTGAGATTTGTTATGTTCTGGC NM_018683 RefSeq chr20
+ 49936376 49953885 RNF114 55905 ring finger protein 114
GO:0005622|GO:0005737|GO:0016567|GO:0016874|GO:0008270|GO:0007275|GO:0005634|GO:0007283|GO:0030
154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143932_PI430048170 0.730360107983565 0.747406926017044 0.395142703227852
0.365657080539123 1.15949162597608 A A A 0.308738092050157 0.321815079349326
1.99408075870172 A A A LNCV6_143932_PI430048170 mRNA
CCTGTCATCATGTGTGCAGAATATTGGTCGAGTTATAAGAGCTGCCTTTACTGGGACTAC NM_001001670 RefSeq
chr9 + 81988771 81995256 SPATA31D1 NA "SPATA31 subfamily D, member 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_100727_PI430048170 0.148176233834239 0.66188852099445 2.31829938907889
1.73279125425545 2.39392003061429 A A A 2.52418694669501 3.21778625367549
2.44395185805692 A P P LNCV6_100727_PI430048170 mRNA
TGCATTCTCCTGTGCCTACCACGTAACCAAAAATGAAGGAGAACTACTGTTTACAAGCCG NM_001797 RefSeq chr16
- 64946779 65122016 CDH11 1009 "cadherin 11, type 2, OB-cadherin (osteoblast)"
GO:0005886|GO:0021957|GO:0034329|GO:0005509|GO:0045216|GO:0001501|GO:0005737|GO:0001503|GO:0016

021|GO:0007155|GO:0007156|GO:0034332|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128469_PI430048170 0.3664582598645840.9533504230203281 1.1725515825846
11.3598701458499 11.238589841466 P P P 11.3905848446525 11.2529898052765
11.3371709428643 P P P LNCV6_128469_PI430048170 mRNA
CTTCCCTGTGCGTAAACATAAGACAATCCCTCTTCAGAATAAACTTGCTTTATAATCAAT NM_001177802 RefSeq
chr17 + 8288650 8290091 RANGRF 29098 "RAN guanine nucleotide release factor, transcript
variant 3"
GO:0005791|GO:0005886|GO:0005634|GO:2000649|GO:0044325|GO:0043547|GO:0005085|GO:0006888|GO:0005
737|GO:0002027|GO:0014704|GO:0005901|GO:0042391|GO:0008536|GO:0008565|GO:2000010|GO:0032527|GO:0
005654|GO:0003254|GO:0090004|GO:0017080 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141427_PI430048170 0.0112939580401757 1.41700345661562 8.17542879082226
8.40482324072963 8.32162081320601 P P P 7.96063526555445 7.75616154270433 7.6702138728347
P P P LNCV6_141427_PI430048170 mRNA
TATATTTTCTGCTGGGGCTTAATAAAGCAGTAGACAGGGCTTGTTCCATCCCTCTGTGCT NM_005262RefSeq chr16
+ 1984148 1987749 GFER 2671 "growth factor, augmenter of liver regeneration"
GO:0005739|GO:0005515|GO:0005758|GO:0005737|GO:0016972|GO:0050660|GO:0006626|GO:0015035|GO:0005
576|GO:0044267|GO:0008083|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55601_PI430048170 0.482747738429255 1.31898424965642 0.3822775018454870.277830137633539
1.40081387326634 A A A 0.3455943041907910.4778125253256810.317270200524623 A A A
LNCV6_55601_PI430048170 mRNA
CTTTGATGAGTTAAGGACAGATTTTAAGAGCCCCATAGACCAGTGCAATCCTGTTCATGC NM_152495RefSeq chr1
+ 224616476 224740547 CNIH3 149111 cornichon family AMPA receptor auxiliary protein 3
GO:0035556|GO:0016247|GO:0030054|GO:0043198|GO:0045211|GO:0042391|GO:0032281|GO:2000311|GO:0035
249 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134496_PI430048170 0.1985552458746440.7495564241434476.10996294965853
5.91533624978409 6.26868047366482 P P P 6.07019498750176 6.64551805849671
6.75782013673264 P P P LNCV6_134496_PI430048170 mRNA
TGCTCTAGCCATTTTGGATTGTGTAAGTTGCAGATGTGGCTTTTACTTTTTAAATGGCAT NM_003626RefSeq chr11
+ 70270699 70384501 PPFIA1 8500 "protein tyrosine phosphatase, receptor type, f polypeptide
(PTPRF), interacting protein (liprin), alpha 1, transcript variant 2"
GO:0005515|GO:0048786|GO:0007268|GO:0014047|GO:0007269|GO:0005829|GO:0051497|GO:0007165|GO:0005
737|GO:0007160|GO:0090005|GO:0004871|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125055_PI430048170 0.00190659918651793 2.40780239872098 5.90416180381336
5.59113583080033 5.72198263155011 P P P 4.22840069722555 4.50378186032231
4.66576577152504 P P P LNCV6_125055_PI430048170 mRNA
AAGATGCCAAAGCTTCGCTTTGCCAGTAGAATCCGGAAAATTCGGAAGAAGCAATTTTAA NM_006528RefSeq chr7
- 93885396 93890991 TFPI2 7980 "tissue factor pathway inhibitor 2, transcript variant 1"
GO:0010951|GO:0007596|GO:0004867|GO:0005578|GO:0005634|GO:0005201 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144004_PI430048170 0.3052564910661961.0223446495607 0.365942015466612
0.3653227187216780.431458758570417 A A A 0.3582711554413270.329258911390839
0.380104182111687 A A A LNCV6_144004_PI430048170 mRNA
TTGTGGAGAGGTCTTAAACTCCCCATTTCCTTGTTTTGCTGCAATAAACTGCATTTGAAA NM_006121RefSeq chr12
- 52674735 52680407 KRT1 3848 "keratin 1, type II"
GO:0005515|GO:0005886|GO:0061436|GO:0045765|GO:0072562|GO:0005634|GO:0005615|GO:0001867|GO:0031
012|GO:0016020|GO:0001895|GO:0005198|GO:0050728|GO:0030246|GO:0004872|GO:0045095|GO:0005856|GO:0
042730|GO:0006979|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136913_PI430048170 0.0632548674426687 1.28735865812899 9.75391842262854
9.7722799840204 9.77825255365381 P P P 9.23445098394119 9.38120707633284

9.57531308713388 P P P LNCV6_136913_PI430048170 mRNA
CCCCGAACGGCATTCTCGGTACTTCTGTTTGTTTTTGTACATTTTATTAGAAAGGACTGT NM_020328 RefSeq chr12
+ 51951666 51997079 ACVR1B 91 "activin A receptor, type IB, transcript variant 3"
GO:0005515|GO:0016361|GO:0030308|GO:0005886|GO:0046332|GO:0046872|GO:0000082|GO:0046777|GO:0004
702|GO:0019838|GO:0048185|GO:0045944|GO:0018107|GO:0005024|GO:0007178|GO:0001942|GO:0031625|GO:0
070062|GO:0046545|GO:0023014|GO:0006355|GO:0009986|GO:0010862|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93382_PI430048170 0.0582460736224067 0.8125517121247387.26416717166405
7.25776528280185 7.23991527482593 P P P 7.46999122320177 7.70033648314378
7.47798918708411 P P P LNCV6_93382_PI430048170 mRNA
GCTGTCACTTTCTCTCTTATAAATTCTGTTAGCTGCTCACTTAAACAATGTCCTCTTTGA NM_054033 RefSeq chr2 +
24049713 24063680 FKBP1B 2281 "FK506 binding protein 1B, 12.6 kDa, transcript variant 2"
GO:0005515|GO:0000413|GO:0042542|GO:0030018|GO:0035584|GO:0019227|GO:0005829|GO:0022417|GO:0051
284|GO:0006939|GO:0042026|GO:0005737|GO:0030551|GO:0034220|GO:0042098|GO:0006458|GO:0048680|GO:0
010880|GO:0060314|GO:0060315|GO:0033197|GO:0051280|GO:0010459|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139374_PI430048170 0.2794163154333330.6891587840641920.295941028377637
0.3039988428323020.447176966649367 A A A 0.348375680545577 1.42372373286761
0.673776203421125 A A A LNCV6_139374_PI430048170 mRNA
CCAAATCTGTGGCCATCACAACCGACCTTGAACCATAATACTAAGAATGATAACAATAAT NM_001278081 RefSeq
chr16 + 57810636 57816927 LOC388282 NA uncharacterized LOC388282 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_128972_PI430048170 0.0632189930185313 0.9282648268359790.297089910666423
0.3064951834034780.314663099209077 A A A 0.451921281578616 0.430992439539619
0.355801787092359 A A A LNCV6_128972_PI430048170 mRNA
TGTGAAATGTATGCCTTGATTCCAACAAGAATGTCAAGAGCATAGAGAGAAGTTTTTGAA NM_000223 RefSeq chr17
- 40861177 40867210 KRT12 3859 "keratin 12, type I"
GO:0061303|GO:0005882|GO:0060429|GO:0005198|GO:0007601|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135669_PI430048170 0.2881009420478460.3716879941659850.412845101859917
0.3512363682067420.317670388428865 A A A 0.338844596462933 1.07935762905609
2.80511332876608 A A P LNCV6_135669_PI430048170 mRNA
AACCTTGCCTTGTCCGTATACTAGGAATATTGATCCATGTGTATACATTCTTGAAAGATT NM_014166 RefSeq chr13
- 48075727 48095141 MED4 29079 "mediator complex subunit 4, transcript variant 1"
GO:0003712|GO:0005515|GO:0010467|GO:0001104|GO:0006367|GO:0006357|GO:0006366|GO:0005634|GO:0046
966|GO:0030374|GO:0030518|GO:0016020|GO:0042809|GO:0016592|GO:0004872|GO:0005654|GO:0045893|GO:0
030521 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130772_PI430048170 0.00797657408039635 1.24460501485642 8.16402906205109
8.27244612221178 8.24228285602838 P P P 7.85591621563105 8.00566786681878
7.86740374726863 P P P LNCV6_130772_PI430048170 mRNA
AAACAGCAGCCTTTCTTGTTTACCCATACCCTTGATATGAAGAGAAGCCCTCTGCTGTGT NM_001136050 RefSeq
chr14 - 24290597 24299833 DHRS1 115817 "dehydrogenase/reductase (SDR family) member 1,
transcript variant 1" GO:0005783|GO:0016491|GO:0005743|GO:0055114 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_128689_PI430048170 0.9333617361667171.00467205488376 4.95591759730059
4.66124072144633 4.81346466126387 P P P 4.62818450081838 5.05708081407863
4.70292216095375 P P P LNCV6_128689_PI430048170 mRNA
AGACAGCACGTCTTCAGGGTGTGGTTTCTAAGCAGAAAATAGCAAATGTTTATATTGAAT NM_022755 RefSeq chr9
- 92613183 92670265 IPPK 64768 "inositol 1,3,4,5,6-pentakisphosphate 2-kinase"

GO:0005622|GO:0052746|GO:0043647|GO:0005654|GO:0044281|GO:0035299|GO:0005524|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136467_PI430048170 0.73998016106188 0.850219788286371 1.8630494394317
1.57970110773695 2.48750448582519 A A A 2.84561850780985 1.44440265452483
2.16370690974989 P A A LNCV6_136467_PI430048170 mRNA
TCAGCTGTTTGCCCGTTCTTATTACATAAACTGAAAACAGGATAAAAACGGAGTGAAATG NM_018359 RefSeq chr4
- 185399539 185425985 UFSP2 55325 "UFM1-specific peptidase 2, transcript variant 1"
GO:0071567|GO:0005515|GO:0005737|GO:0005783|GO:0033146|GO:0006508|GO:0005634|GO:0016790 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131901_PI430048170 0.7969155396455420.9574381987319557.18628991153797
7.25705148895627 7.57775799183737 P P P 7.15073550108839 7.34147834938311
7.69444309397176 P P P LNCV6_131901_PI430048170 mRNA
CAATCCTGATTATGTGAAAATATGGTTGCTGTTTAAGTGATGCTGAATTTGCTGTGTGTT NM_153374 RefSeq chr15
- 51723063 51738123 LYSMD2 256586 "LysM, putative peptidoglycan-binding, domain containing 2,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140828_PI430048170 0.0922482274788171 1.0646437975869 0.43754557983684
0.33693724237931 0.34349494044381 A A A 0.2636262702763530.325575422578224
0.258911810887027 A A A LNCV6_140828_PI430048170 mRNA
TTCTATGGGAGCATCCTTTCCATGTATGTGCAGCTGAAGAAGAGCTACTCACTGGACTAT NM_001005185 RefSeq
chr1 - 158765743 158766682 OR6N1 128372 "olfactory receptor, family 6, subfamily N, member 1"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144925_PI430048170 0.1157799804751121.07718154686526 11.6283752871679 11.633682085314
11.6918845253989 P P P 11.474553413612 11.5301180619276 11.6243590332346 P P P
LNCV6_144925_PI430048170 mRNA
GTGAGTGTGGGCTGTGGTGTGTCCGTGTGTGTACATATGTGTATATGTATATATCACGCA NM_025219 RefSeq chr20
+ 63895101 63936031 DNAJC5 80331 "DnaJ (Hsp40) homolog, subfamily C, member 5"
GO:0042470|GO:0043008|GO:0005886|GO:0007268|GO:0005765|GO:0006887|GO:0016079|GO:0007269|GO:0008
021|GO:0005739|GO:0045055|GO:0043524|GO:0001948|GO:0016020|GO:0061202|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142245_PI430048170 0.9287178887522070.912769302606701 1.84877468352116
1.41836124375415 1.90198473100743 A A A 2.46997837697791 1.12092607270987
1.70204960708666 A A A LNCV6_142245_PI430048170 mRNA
TTGTGACGTCCCATGACATAGTCTGATGCACGATAAAACAATTATTTCTTTATCTTGCAA NM_030761 RefSeq chr1
- 22117304 22143026 WNT4 54361 "wingless-type MMTV integration site family, member 4"
GO:0018345|GO:0001658|GO:0072034|GO:0072033|GO:0006702|GO:0038030|GO:0033080|GO:0071560|GO:0010
894|GO:0005615|GO:0048599|GO:0005109|GO:0072174|GO:0061045|GO:0072273|GO:0061184|GO:0048018|GO:0
022407|GO:0030336|GO:0030501|GO:0009986|GO:0005796|GO:0061369|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129430_PI430048170 0.3755382785137480.9265622281744280.501395746880479
0.5121827156828590.313124122281835 A A A 0.4006007728853340.552525776284713
0.697045024108045 A A A LNCV6_129430_PI430048170 mRNA
GTGAACTCTTTACTGATACACACAAGACAACTGTTAAAAAGTGAATCCAGCACTTAAATG NM_001100829 RefSeq
chr6 + 11538226 11583524 TMEM170B 100113407 transmembrane protein 170B GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137163_PI430048170 0.0170292257407182 2.17512913534805 1.71288238353191
1.64633027045484 2.20678380905701 A A A 0.65291948702325 0.75545819779861
0.854501466215748 A A A LNCV6_137163_PI430048170 mRNA
ATGGTGAACTTCTACAACAATTACATTTCCTGCACCAACAAGGCCAACCTGTCCCAAGTG NM_004413 RefSeq chr16

+ 89620591 89638431 DPEP1 1800 "dipeptidase 1 (renal), transcript variant 1"
GO:0005515|GO:0019369|GO:0006805|GO:0030054|GO:0034235|GO:0071732|GO:0005886|GO:0006749|GO:0031
528|GO:0005634|GO:0031225|GO:0044281|GO:0006691|GO:0005615|GO:0050667|GO:0072341|GO:0072340|GO:0
016324|GO:0070573|GO:0071277|GO:0006508|GO:0043154|GO:0043027|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141585_PI430048170 0.000784707448216505 0.2526207456295032.84068508467671
2.63446490701734 3.17021626285477 A A P 4.58182092040986 5.08595620651091
4.93822320786504 P P P LNCV6_141585_PI430048170 mRNA
CAGTGTGCTCATTGTCTCAGTGAAGTTCTTTTGTTTTCAAAGATTCATGGTAACAAAATG NM_014877RefSeq chr17
- 67070437 67245203 HELZ 9931 helicase with zinc finger
GO:0016020|GO:0008152|GO:0004386|GO:0005634|GO:0005524|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141973_PI430048170 0.4749467130965060.8285153855214333.1733682357594
2.13706993967203 3.6737565331696 P A P 3.22739208972666 3.40460196172164
3.54170358921315 P P P LNCV6_141973_PI430048170 mRNA
TGTTAGGGATCTTTGTTCTCTGAAACGCAACCCTGTCTAGGACAATATACACGTGAGTGA NM_017924RefSeq chr14
+ 23095473 23100456 C14orf119 55017 chromosome 14 open reading frame 119 GO:0005739 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116008_PI430048170 0.00444802266648189 2.76243675137688 8.13359220825321
8.21799209925006 8.25791689101556 P P P 6.94552415294523 6.72903280625612
6.50659890103128 P P P LNCV6_116008_PI430048170 mRNA
GCGGAAGATATAACCTTATATTTGGTAAGTGTTTCTTGTGCTATTTTATCACGTGACCTG NM_153350RefSeq chr16
- 692499 705825 FBXL16 146330 F-box and leucine-rich repeat protein 16 GO:0005737 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130044_PI430048170 0.9544532198010431.00375265848009 9.36476942521527
9.50122780776611 9.68240553848125 P P P 9.37710317397379 9.40648859062355
9.73778527416435 P P P LNCV6_130044_PI430048170 mRNA
GTGGGGGAAAGAGTTATAGGACCACAGTCTTCACTTCTGATACTTGTAAATTAATCTTTT NM_016026RefSeq chr14
- 67676800 67695793 RDH11 51109 "retinol dehydrogenase 11 (all-trans/9-cis/11-cis), transcript variant
1"
GO:0005622|GO:0016062|GO:0001917|GO:0007603|GO:0042574|GO:0042572|GO:0005789|GO:0016021|GO:0052
650|GO:0004745|GO:0001523|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140105_PI430048170 0.9466447359134550.9972469858737755.13409516402426
5.04771083414116 5.34559188678082 P P P 5.08174751521759 5.20274485731259 5.2653237434723
P P P LNCV6_140105_PI430048170 mRNA
GAAAACCATTTACCAACTGAAAGGACACGAAGTCTAGCTCCGGACAAAAGCTGTTAGAGG NM_020764RefSeq
chr16 - 2177182 2196464 CASKIN1 57524 CASK interacting protein 1
GO:0005515|GO:0007165|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131520_PI430048170 0.1372324824903430.80501303318953 6.61858191077818
6.98507808342424 6.51642042768734 P P P 6.97191249566684 7.18125961622273
6.93644358409406 P P P LNCV6_131520_PI430048170 mRNA
CTTTGGTGAGCTGGGCGGTCATGGTTTTGAAATAAATGTATTTTGTTACTTTCTGAAAAA NM_152889RefSeq chr3
+ 126524287 126543291 CHST13 166012 carbohydrate (chondroitin 4) sulfotransferase 13
GO:0047756|GO:0016051|GO:0030206|GO:0000139|GO:0005975|GO:0009405|GO:0001537|GO:0044281|GO:0016
021|GO:0030204|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137689_PI430048170 0.0131553837892378 0.4348077552944756.25510673926205
5.60496689677682 5.87187822087582 P P P 6.70479691433436 7.22909518054927
7.39177602431714 P P P LNCV6_137689_PI430048170 mRNA
ACGCTGTGTCTCATGCTGTATACTTAAGAGGAGAAGAAAAAGTCCTATATTTGTGATCAA NM_004380RefSeq chr16

- 3725054 3880120 CREBBP 1387 "CREB binding protein, transcript variant 1"
GO:0005515|GO:0000987|GO:0001191|GO:0010467|GO:0000790|GO:0006367|GO:0003700|GO:0006325|GO:0018
076|GO:0034605|GO:0007219|GO:0000123|GO:0044255|GO:0001102|GO:0001105|GO:0003713|GO:0000122|GO:0
045087|GO:0005654|GO:0008270|GO:0016407|GO:0048511|GO:0045893|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_125296_PI430048170 0.2138443049165731.06040585515723 0.525406589585083
0.6203325676279370.578087734881716A A A 0.5848037955377130.436969508197895
0.444926043220298A A A LNCV6_125296_PI430048170 mRNA
ATGTGAGGACAATTACGTGCTCCAGGGATCTAAAAGCATCACCTGTCAGAGAGTTACAGA NM_033225RefSeq chr8
- 2935352 4994806 CSMD1 64478 CUB and Sushi multiple domains 1 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135450_PI430048170 0.3138168693246880.9789445888138820.349520466543367
0.3697530864162310.341334661263529A A A 0.4253090833508250.346737138727634
0.379732773057162A A A LNCV6_135450_PI430048170 mRNA
ATTGTTGGACCTCCTTGAGATAGTAACAACAAAATAAAGCAAGCTATCTGCACCTCAAAA NM_001267550 RefSeq
chr2 - 178525990 178807423 TTN7273 "titin, transcript variant IC"
GO:0045859|GO:0005515|GO:0030240|GO:0005516|GO:0007076|GO:0030018|GO:0042805|GO:0006941|GO:0043
621|GO:0002020|GO:0060048|GO:0042802|GO:0005829|GO:0003300|GO:0051015|GO:0006936|GO:0055003|GO:0
008307|GO:0048769|GO:0055008|GO:0070062|GO:0000794|GO:0030049|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144142_PI430048170 0.1693038132251090.79690274528799 9.29969581873404
9.28867239482915 9.22373232989916 P P P 9.28393222557538 9.74272576154664
9.72415566444636 P P P LNCV6_144142_PI430048170 mRNA
TGTCATGCACCACGGTGTCTGTGTCCACACAGTAATAAACGGTTTACTGTCCGCAAAAAA NM_016337RefSeq chr14
+ 100065413 100144236 EVL 51466 Enah/Vasp-like
GO:0005515|GO:0017124|GO:0003779|GO:0030027|GO:0005829|GO:0007399|GO:1900028|GO:0005737|GO:0030
838|GO:0016020|GO:0051289|GO:0007411|GO:0008154|GO:0051496|GO:0009887|GO:0007015|GO:0005856|GO:0
005522|GO:0005925|GO:0007166|GO:0010633 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133757_PI430048170 0.906620641165555 1.29464507912069 0.452725800231484
0.4574692686276753.2304499497271 A A P 1.9875592941833 1.96385990083488
0.585564940549139A A A LNCV6_133757_PI430048170 mRNA
GAAGACACAAACTCAAAGAAAGCACAACTGAGGAGATTGAGCTGGAAGATGTTGAGTGTT NM_001144871
RefSeq chr11 - 93820568 93850502 VSTM5 NA V-set and transmembrane domain containing 5 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137319_PI430048170 0.8238459054639870.9498809282417060.383902673878945
0.5640779722127030.286158219834651A A A 0.2681225045742870.851411648654207
0.269499303081086A A A LNCV6_137319_PI430048170 mRNA
CACACTTCTAGATTCTTCCCAGCTCAGAGGCTTGGCATTTGCCATATCATCATCTTTTTT NM_000750RefSeq chr15 -
78624293 78641245 CHRNB4 1143 "cholinergic receptor, nicotinic, beta 4 (neuronal), transcript variant
1"
GO:0030054|GO:0005886|GO:0046928|GO:0007268|GO:0006940|GO:0060084|GO:0005892|GO:0007271|GO:0035
095|GO:0006939|GO:0007165|GO:0034220|GO:0005887|GO:0045211|GO:0015464|GO:0007626|GO:0016021|GO:0
001508|GO:0004889|GO:0006812|GO:0015276|GO:0006811 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_69314_PI430048170 0.5146662344914332.2223121921455 4.01858343680974 3.90354077922226
6.43185124580117 P P P 4.25043574772543 4.10270697614894 4.05849415147822 P P P
LNCV6_69314_PI430048170 mRNA
TGCTATATTTCCGCATAAGGTTTTATTTCCGGAACTGGCATGGCATGAATCCTCGGGAAC NM_003331RefSeq chr19
- 10350527 10380572 TYK2 7297 tyrosine kinase 2

GO:0005515|GO:0005131|GO:0019221|GO:0005634|GO:0031702|GO:0005524|GO:0030154|GO:0031234|GO:0005829|GO:0035556|GO:0005737|GO:0060337|GO:0060338|GO:0016477|GO:0045087|GO:0042127|GO:0006468|GO:0004713|GO:0005856|GO:0038083|GO:0004715|GO:0007169|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137975_PI430048170 0.1481846801193310.7788969931454428.68237407969297 8.25807877214608 8.18667098349315 P P P 8.99713360194118 8.5613806845919 8.66464745237596 P P P LNCV6_137975_PI430048170 mRNA
CAGTGTGTGCCATGTCTCCCATACTAGAGATAAATAAATGTAGCCACATTTACTGTGAAA NM_000185RefSeq chr22 + 20774094 20787720 SERPIND1 3053 "serpin peptidase inhibitor, clade D (heparin cofactor), member 1"
GO:0010951|GO:0006935|GO:0004866|GO:0007596|GO:0004867|GO:0005576|GO:0008201|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140042_PI430048170 0.0291465284003583 0.4169897841436642.70271021224845 3.73221256890068 3.0907636260986 A P P 4.82962972317678 4.49405083681339 4.08265249488274 P P P LNCV6_140042_PI430048170 mRNA
GTACTAAGGAGATGGAAGGCGACACACAAAAGCTTGAAGTAGAACATGTGATGATGAGAA NM_025190RefSeq chr2 - 97504797 97589965 ANKRD36B 57730 ankyrin repeat domain 36B NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136514_PI430048170 0.0226625727850693 0.4358762513810662.56761687485573 3.27914138939551 3.3869198341158 A P P 4.01203195786674 4.49972823488935 4.40019850566895 P P P LNCV6_136514_PI430048170 mRNA
CTGCCCATACAAGTGTTGATTCATTTTAATGCTGTTTATGATTTCTGCATTGGCAGAAAT NM_018847RefSeq chr9 - 21331018 21335430 KLHL9 55958 kelch-like family member 9
GO:0000910|GO:0007067|GO:0004842|GO:0016567|GO:0031463|GO:0030496 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75924_PI430048170 0.2320646909979710.9479363971184479.34541319390149 9.46087536708087 9.303648038479 P P P 9.4876870156425 9.42833801212405 9.42915040236424 P P P LNCV6_75924_PI430048170 mRNA
AGGAACTGGGTCTTCATCGTCTGGAGTTTTAATGGTTGGACCTAACTTTAGAGTTGGAAA NM_001031812 RefSeq chr5 + 123512098 123617044 CSNK1G3 1456 "casein kinase 1, gamma 3, transcript variant 2"
GO:0007165|GO:0005737|GO:0004672|GO:0018105|GO:0004674|GO:0008360|GO:0005634|GO:0016055|GO:0005524|GO:0006464|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144304_PI430048170 0.00118921505348454 2.85746864764591 6.45588213328713 6.50666123030273 6.07571769813123 P P P 4.63926487245705 5.03461088193109 4.83030434629621 P P P LNCV6_144304_PI430048170 mRNA
CTTGTAGCCCTTTCCAAGCTTCTAGAAGGTGCTTAGTAAATACTTGATAAGCCCCACGTG NM_007101RefSeq chr9 - 133663561 133739955 SARDH 1757 "sarcosine dehydrogenase, transcript variant 1"
GO:0005739|GO:0005759|GO:0055114|GO:0008480 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137836_PI430048170 0.8528037722198380.9746116591465150.36334604060185 0.3806825398376731.56996194875352 A A A 0.8943623655704541.35797485168865 0.35621144436248 A A A LNCV6_137836_PI430048170 mRNA
TCAAAATACAAGTGTCGGATGAAGAACCATCATCCTGAACAGCAAAGCTCCCTGCTAAAC NM_001256852 RefSeq chr4 + 9210656 9212249 USP17L10 NA ubiquitin specific peptidase 17-like family member 10 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138205_PI430048170 0.0288837459542021.09226271855667 0.464155740453907 0.3795851067756790.400222761016623A A A 0.2628706907327810.343435851529182 0.255388717251889A A A LNCV6_138205_PI430048170 mRNA
GCCTTGCCAAGTATAACTTGTATATCTTGACTCTGTGGTAGATTTCAAGTTCAATGTTAT NM_002590RefSeq chr13 - 52843973 52848640 PCDH8 5100 "protocadherin 8, transcript variant 1"

GO:0042734|GO:0030054|GO:0016331|GO:0005886|GO:0005887|GO:0045211|GO:0001756|GO:0005509|GO:0007267|GO:0007268|GO:0007156|GO:0030425 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137335_PI430048170 0.1891047211100451.22735968476938 1.12092607270987 0.8183468109985910.623317671910031A A A 0.5294706601203770.600307184425102 0.589131310670711A A A LNCV6_137335_PI430048170 mRNA
AGCGCATGCGTAAAGCAACTCCTTATCATTATTAAAGTTTTATTTGTTGCCCAGGGTAAA NM_001010912 RefSeq chr10 - 122697708 122699822 C10orf120 NA chromosome 10 open reading frame 120 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133384_PI430048170 0.0316768185263610.6332251057517965.57091987400316 5.27567377969259 5.41644862128398 P P P 6.07932800778111 6.32855795135488 5.79969529670512 P P P LNCV6_133384_PI430048170 mRNA
GTCTGGGTTTCTGTTGGCTGTTTTTCTTTTCTTGAGTGGTGATTTTTCTCTAAATAAAAG NM_194248RefSeq chr2 - 26457202 26558698 OTOF 9381 "otoferlin, transcript variant 1"
GO:0016323|GO:0003674|GO:0030054|GO:0035612|GO:0007605|GO:0005509|GO:0005789|GO:0061025|GO:0030672|GO:0016021|GO:0016079|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139441_PI430048170 0.311104903672818 1.29609743021649 1.09694142862053 0.28509804202221 0.465678844936164A A A 0.3009916582746370.265165835157965 0.289462522514521A A A LNCV6_139441_PI430048170 mRNA
GTCATTATTAGCCCTTTGCTTTTCTGTATTGTTTCACTCCGTATGTAACATAACCCTAAA NM_032756RefSeq chr1 + 45326872 45328674 HPDL 84842 4-hydroxyphenylpyruvate dioxygenase-like
GO:0003868|GO:0009072|GO:0046872|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93872_PI430048170 0.0843070895132664 0.5689406801080716.3933151421489 5.6783073100675 5.38191406756929 P P P 6.98685818102691 6.63379329183299 6.40766197620124 P P P LNCV6_93872_PI430048170 mRNA
ACACGTCTCCCGAGAAGAAGAAGGCCAAGGAGCTCCCTGAAATGGACGCCACCTCCAGCC NM_015133RefSeq chr16 + 1706219 1770317 MAPK8IP3 23162 "mitogen-activated protein kinase 8 interacting protein 3, transcript variant 1"
GO:0010468|GO:0048286|GO:0007585|GO:0060425|GO:0031434|GO:0030159|GO:0031435|GO:0007257|GO:0009791|GO:0001701|GO:0030425|GO:0005790|GO:0046328|GO:0005737|GO:0008104|GO:0000139|GO:0045666|GO:0007411|GO:0030900|GO:0030673|GO:0019894|GO:0008432|GO:0016192|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54114_PI430048170 0.410662977355006 1.4976096834162 3.01459024744217 4.13390418577725 4.49296952393947 P P P 3.48400288025992 3.36457420648284 3.41488359608506 P P P LNCV6_54114_PI430048170 mRNA
GAAGAACTGCAGTTGAAATCCTTTTCCATTTCTGTGAGGAAATATCTTCCATGTTTTACA NM_013339RefSeq chr1 + 63367589 63438562 ALG6 29929 "ALG6, alpha-1,3-glucosyltransferase"
GO:0006490|GO:0016020|GO:0005789|GO:0042281|GO:0046527|GO:0016021|GO:0006487|GO:0006488|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142537_PI430048170 0.485000714570857 1.04826205611268 0.287693243207738 0.2974446902921310.51801394575061 A A A 0.3166464463249220.274893475506827 0.319141099414502A A A LNCV6_142537_PI430048170 mRNA
TAGCTTGTTGTTTGGGGGACCAAATTTTCTAGAGAGAACTAGAGCACTTTTGTTGTGTTT NM_023067RefSeq chr3 - 138944223 138947140 FOXL2 668 forkhead box L2
GO:0005515|GO:0003700|GO:0006366|GO:0000981|GO:0005634|GO:0042703|GO:0030154|GO:0001541|GO:0045944|GO:0031624|GO:0043028|GO:0048048|GO:0043065|GO:0006357|GO:0030331|GO:0000122|GO:0003677|GO:0043280|GO:0043565|GO:0019101|GO:0006309|GO:0002074|GO:0045893|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134089_PI430048170 0.0226223420376726 0.5672191773389295.75187951084086 6.03547985295768 5.97516058286999 P P P 6.85839838352899 6.3974352262373

6.92144186515743 P P P LNCV6_134089_PI430048170 mRNA
AATCCCAGTGAGTTCTGCATTTGTATCTTGCAAGTTTGTATAAACCCAATACAGGAAATA NM_014935 RefSeq chr1
- 204218850 204359929 PLEKHA6 22874 "pleckstrin homology domain containing, family A member 6"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71163_PI430048170 0.0531783583630526 1.20192193467833 14.0327216165805
14.0835832042834 14.1889495001395 P P P 13.7827805327767 13.7322547113031
13.9859387121785 P P P LNCV6_71163_PI430048170 mRNA
CATAGCACAGTACATGCAGCATCTAATAAGAGTTTCCATTGTAGAATGTTTTCACATACT NM_001199535 RefSeq
chr20 + 36574553 36612557 TGIF2-C20orf24 NA TGIF2-C20orf24 readthrough NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144153_PI430048170 0.32087541925824 0.599105713710015 3.22485521405256
1.16121329992705 2.75904057697077 P A A 2.70908701164118 4.00781772383459
3.00209753562848 P P P LNCV6_144153_PI430048170 mRNA
TGTTTCTGAGATGCGTCCATGGAAAAATGGAAAAAACTGTGGTGCGTTGACTTGCTGGAA NM_006987 RefSeq
chr17_KI270907v1_alt + 49795 122927 RPH3AL 9501 "rabphilin 3A-like (without C2 domains), transcript variant 1"
GO:0008092|GO:0017137|GO:0045744|GO:0042493|GO:0050714|GO:0042593|GO:0006887|GO:0006886|GO:0046872|GO:0017158|GO:0005737|GO:0030274|GO:0030658|GO:0030667 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_131693_PI430048170 0.388265041707204 1.68590872343632 0.414941196170713
0.268273546171786 1.86988897103093 A A A 0.275326412112999 0.311008899056932
0.289648132079922 A A A LNCV6_131693_PI430048170 mRNA
GACGTGGACTTTATTGACTGTGAATTCATTTACATGTAACTTCTGACATTTCACTCTGTG NM_001287763 RefSeq
chr4 + 4386255 4419058 NSG1 27065 "neuron specific gene family member 1, transcript variant 3"
GO:0005737|GO:0000139|GO:0032051|GO:0045211|GO:0005634|GO:0016021|GO:0007212|GO:0016328|GO:0048268|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136309_PI430048170 0.276388857766282 0.89008878271549 9.27302315828371
9.04740842315579 8.87490329558709 P P P 9.35125088488547 9.24454246610174
9.12214124655767 P P P LNCV6_136309_PI430048170 mRNA
CAAGGTCACGCAGGTCTCCCCAGCACGTGTTAATTTGGTTAATAAAACTGTGGATCAAGG NM_052924 RefSeq chr8
+ 143368854 143384220 RHPN1 114822 "rhophilin, Rho GTPase binding protein 1"
GO:0007165|GO:0050790|GO:0005083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127764_PI430048170 0.570015473519436 0.98194605106309 0.266534642887379
0.285515637361706 0.388532325966909 A A A 0.377895756975079 0.328760000897641
0.315030129039375 A A A LNCV6_127764_PI430048170 mRNA
TTCTCTTCCTGACCAGTTCCTCAAGAGAAATGCAAAACTAGTGATTAACAGTAAGAGTCA NM_001144931 RefSeq
chr22_KI270879v1_alt + 267291 268218 LOC391322 NA D-dopachrome tautomerase-like NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_140293_PI430048170 0.661161959058805 1.25643768607719 1.76407554298355
1.05865475897084 0.283307750727175 A A A 0.831323426389364 0.500428501319708
1.09479468222276 A A A LNCV6_140293_PI430048170 mRNA
AAGGGGCTGTGGAGGTTGATATTATTAATAGTGTTATGCAGAAAATATGAATGGCAGGGA NM_205850 RefSeq chr15
+ 48120971 48142392 SLC24A5 NA "solute carrier family 24 (sodium/potassium/calcium exchanger), member 5" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92191_PI430048170 0.0083485785200675 0.719610794645632 7.54440153673274
7.30017193565357 7.45563463367267 P P P 7.8546649998184 8.04103238762736
7.82978318961159 P P P LNCV6_92191_PI430048170 mRNA
TGACAGAGACTGTCGCTCTGATCCAGCACAGCAAAAACATCTTCACCAATAAGTGTGAAC NM_138802 RefSeq chr2

+ 219206783 219209651 ZFAND2B 130617 "zinc finger, AN1-type domain 2B, transcript variant 1"
GO:0005515|GO:0005783|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69022_PI430048170 0.0210897058203411 0.5992899219806335.41734891799557
5.17790112007118 5.35802344254701 P P P 5.77802906080869 6.27143902947659
6.08806567694686 P P P LNCV6_69022_PI430048170 mRNA
TCTTTGGCCACACTCATGTGGATGAATTTGAGGTCTTCTATGATGAAGAGACTCTGAGCC NM_000543 RefSeq chr11
+ 6390413 6394998 SMPD1 6609 "sphingomyelin phosphodiesterase 1, acid lysosomal, transcript variant 1"
GO:0005515|GO:0006665|GO:0006685|GO:0043065|GO:0006684|GO:0005886|GO:0006687|GO:0042493|GO:0035307|GO:0004767|GO:0044281|GO:0042220|GO:0005615|GO:0005764|GO:0007399|GO:0007165|GO:0043407|GO:0042599|GO:0016798|GO:0046513|GO:0023021|GO:0070062|GO:0043202|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_78781_PI430048170 0.1648863234845 0.6855763108452483.65288901664436 2.82163171831755
3.45432671450525 P A P 3.47902692398784 4.19062934502675 3.92949687504932 P P P
LNCV6_78781_PI430048170 mRNA
ACATATGAATTTGGAAAGGCTTTTTTCCAGAAACAAAATGTTCGAAGGCAGCAATACTAG NM_018843 RefSeq chr7
- 87834498 87876377 SLC25A40 55972 "solute carrier family 25, member 40"
GO:0005743|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142871_PI430048170 0.5145042197994630.86614033142458 3.53497080490149
4.11244395519301 2.77049635989702 P P A 3.78796366047574 3.86831043830681
3.67959532283969 P P P LNCV6_142871_PI430048170 mRNA
TGTCAGTGACCTCGCTGCAGCAGCACCACAGTTGCTGTCAAAGTTTCAAATACGTTTTTT NM_001281432 RefSeq
chr17_KI270857v1_alt + 721530 734214 ZNHIT3 9326 "zinc finger, HIT-type containing 3, transcript variant 2" GO:0046966|GO:0005622|GO:0006355|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_63312_PI430048170 0.4344112748262880.6246042276067961.91391771693999 0.365901900331151
0.249606015901349 A A A 0.3990069864723971.85523753301042 2.33999998787613 A A A
LNCV6_63312_PI430048170 mRNA
AAACCCAAGGACAGAGTATTGAGAACAATCTAGGGCCACACTCAAAATGGCGGAAAACCT NM_017647 RefSeq
chr17 - 63819432 63827671 FTSJ3 117246 FtsJ homolog 3 (E. coli)
GO:0008649|GO:0005515|GO:0005730|GO:0005634|GO:0030688|GO:0000453 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130114_PI430048170 0.0396108201120414 1.23374123675873 10.5264449536578
10.6845516899185 10.7601704823118 P P P 10.2136756948433 10.3845702614718
10.4624618847505 P P P LNCV6_130114_PI430048170 mRNA
CCTGAAAGTAATATAATGATGCTGTCTGAACAGGTTTTACTGCTTGCTTTCCAAGTAAAG NM_020642 RefSeq chr11
+ 8911153 8920079 AKIP1 56672 "A kinase (PRKA) interacting protein 1, transcript variant 1"
GO:0005515|GO:0034446|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126714_PI430048170 0.4272044095890651.18985233641259 1.05634039989459
0.461325464285855 0.349499462376019 A A A 0.4834187101465590.36722380631381
0.364958686694082 A A A LNCV6_126714_PI430048170 mRNA
TATCCTATGAGAGAGCCAAGGAAATATGGGAGATCACGGAGACCTTCAAGAGCCGAATAT NM_001205201
RefSeq chrX - 154271264 154295211 TEX28 1527 "testis expressed 28, transcript variant 1"
GO:0008150|GO:0003674|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112309_PI430048170 0.7856676379569821.02689623969856 7.70398210650482 7.8655638898513
7.5210643511192 P P P 7.76331662225167 7.59186401508392 7.63552635277103 P P P
LNCV6_112309_PI430048170 mRNA
ACATTGACAAGAAGTTCTCTGCGCACTACGACGCGGTGGAGGCAGAGCTCAAGTCCAGCA NM_004699 RefSeq
chrX + 154444125 154450654 FAM50A 9130 "family with sequence similarity 50, member A"

GO:0005654|GO:0005634|GO:0007283 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130983_PI430048170 0.6092287639669741.44742542474171 2.10284795895544
2.14704630627911 0.312044111851241 A A A 1.63495865845094 1.20280552271696
0.563483574807727 A A A LNCV6_130983_PI430048170 mRNA
CCAGGAAAATATGAAAGTGGCCTTTATATTTTATGGCACAGTTATTCCCATGTTAAATCC NM_001005323 RefSeq
chr11 + 56988913 56989843 OR5AK2 390181 "olfactory receptor, family 5, subfamily AK, member 2"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133052_PI430048170 0.1923434625945251.96281073778218 0.371794692612199
1.06652069988646 1.87816639730079 A A A 0.2517115597743920.287078933238512
0.24895390165653 A A A LNCV6_133052_PI430048170 mRNA
GCCTGAGCATTAGGATGCTCAAACATCCTATCTTTCTTCTTCTATTCATGCTTTTATCCA NM_001612 RefSeq chr11 -
125672333 125680898 ACRV1 56 "acrosomal vesicle protein 1, transcript variant 1" GO:0001669|GO:0007275
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55817_PI430048170 0.6245285863282570.9431301530578590.30239304841153 0.256427909298651
0.380290404988203 A A A 0.2762928575431930.2446081314114460.640004018578045 A A A
LNCV6_55817_PI430048170 mRNA
TAGCCCATTTACAAACAACAGCTTATATAATAGTCATTCACATACCTCAACACTCACCAT NM_001143943 RefSeq
chr1 + 244970328 245125228 EFCAB2 84288 "EF-hand calcium binding domain 2, transcript variant 2"
GO:0005509 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135363_PI430048170 0.1643345284857371.52820021520418 4.17470867952227
4.97689599340491 5.01574107856387 P P P 3.785060503199 4.10620633805917
4.49738520362888 P P P LNCV6_135363_PI430048170 mRNA
CCTTTTCTTCCCTTTTGGTAGCAAAGGACACCAACTTTTTCTTAATAAATGGGTATTTTG NM_016237 RefSeq chr12 -
121308244 121352462 ANAPC5 51433 "anaphase promoting complex subunit 5, transcript variant 1"
GO:0007094|GO:0019903|GO:0051437|GO:0005634|GO:0051436|GO:0031145|GO:0051439|GO:0005829|GO:0007
067|GO:0070979|GO:0005680|GO:0005654|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134025_PI430048170 0.0311619872076839 0.6882952714762575.94289604576645
5.85499135504786 6.09190846688174 P P P 6.73655806543219 6.42339056697251
6.32374609721256 P P P LNCV6_134025_PI430048170 mRNA
GTATTGTATGCAAATCTGTGATTGTTGGCAGTGTCATCTCTGAGAAACAGATAAATAAAG NM_002078 RefSeq chr3
+ 37243190 37366879 GOLGA4 2803 "golgin A4, transcript variant 2"
GO:0005515|GO:0005802|GO:0005794|GO:0043001|GO:0045773|GO:0043231|GO:0005737|GO:0051020|GO:0000
139|GO:0005654|GO:0016192|GO:0000042|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101198_PI430048170 0.7707624656149011.05018469422063 3.10683385466203 3.0641028762946
3.55455187319042 P P P 2.70179222094021 3.35086157586927 3.41231908892043 A P P
LNCV6_101198_PI430048170 mRNA
AAATCGTCATCCAAGCATGTTTCTCTTACTTTTGGTGTTGGAGAGACTCTACGCTTCCCC NM_001083953 RefSeq
chr2 - 43230835 43595974 THADA 63892 "thyroid adenoma associated, transcript variant 3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129085_PI430048170 0.7528297221878471.0455153665834 0.446475926350522
0.7666618711405850.291477188990656 A A A 0.4083385051927610.494320537032693
0.449371203648936 A A A LNCV6_129085_PI430048170 mRNA
GATGCCTGTTATTTCACATCACTGTCTTTTTGTGTATCATAGTCTGCACCTTACAAATAT NM_000800 RefSeq chr5 -
142592177 142686495 FGF1 2246 "fibroblast growth factor 1 (acidic), transcript variant 1"
GO:0005515|GO:0008286|GO:0008284|GO:0030324|GO:0001759|GO:0005615|GO:0009653|GO:0005829|GO:0034
605|GO:0007173|GO:0043406|GO:0045944|GO:0051781|GO:0070374|GO:0005938|GO:0008201|GO:0050679|GO:0
048011|GO:0030335|GO:0060681|GO:0048015|GO:0005730|GO:0005578|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_74911_PI430048170 0.2020331794192451.83817202630489 1.29860338263435 2.10877249536719
0.70231252590556 A A A 0.5850562728512530.631646171263362 0.604516086075787 A A A
LNCV6_74911_PI430048170 mRNA
GCCAAGGCCCTGAGTTGGCAGTGGCCCATAAGTGTAAAATAAAAGTTTACAGAAACCTTG NM_001957 RefSeq chr4
+ 147480916 147544954 EDNRA 1909 "endothelin receptor type A, transcript variant 1"
GO:0005515|GO:0007507|GO:0006939|GO:0014032|GO:0015758|GO:0051482|GO:0032496|GO:0070374|GO:0050
678|GO:0031965|GO:0007568|GO:0060137|GO:0043278|GO:0043084|GO:0001701|GO:0048484|GO:0007186|GO:0
005887|GO:0090023|GO:0045121|GO:0008284|GO:0090184|GO:0005886|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137727_PI430048170 0.2543261003657190.5570710985567170.356970267773762
0.3606507267881270.297848008917908 A A A 0.3434409494174 0.915285690737594
1.87026008546158 A A A LNCV6_137727_PI430048170 mRNA
GCTCTACAGATAATGTCTATATATTGGCCAAACTGGTGCATGACAAGTACTGTATTTTTT NM_001795 RefSeq chr16
+ 66366621 66404786 CDH5 1003 "cadherin 5, type 2 (vascular endothelium)"
GO:0005515|GO:0048010|GO:0030054|GO:0008285|GO:0005886|GO:0008013|GO:0034329|GO:0019903|GO:0005
509|GO:2000114|GO:0005102|GO:0045216|GO:0044325|GO:0005912|GO:0016020|GO:0005911|GO:0005923|GO:0
016021|GO:0001955|GO:0007156|GO:0034332 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134737_PI430048170 0.0377417223013824 0.2686114396851443.51814109262751
3.21587127955255 3.75011945052977 P P P 4.48784603499328 5.49445476019756
5.90245768392708 P P P LNCV6_134737_PI430048170 mRNA
CCACTACCAATCATCTGTACAGTTCCTACTGTTATGATCACAATAAGACTAACATGAATT NM_020859 RefSeq chr4
+ 76435099 76783252 SHROOM3 57619 shroom family member 3
GO:0007389|GO:0030036|GO:0008360|GO:0005874|GO:0001843|GO:0045176|GO:0000902|GO:0002066|GO:0043
296|GO:0005737|GO:0016324|GO:0051015|GO:0005912|GO:0043482|GO:0005856 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133299_PI430048170 0.4930480593472830.7279793769089320.98410369192629
0.3889729085615020.246416499142367 A A A 0.6095693348138781.72941086855432
0.382698974166454 A A A LNCV6_133299_PI430048170 mRNA
GCCAAACCTCTGTCAGTCAGAGGCATTCATTAGTTTTATACATGTAATTTGAAAATCACT NM_005565 RefSeq chr5
- 170248083 170297818 LCP2 3937 lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte
protein of 76kDa)
GO:0005515|GO:0050852|GO:0050663|GO:0045576|GO:0006955|GO:0007596|GO:0005911|GO:0045087|GO:0030
168|GO:0007169|GO:0038095|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53671_PI430048170 0.7344829449567931.08627296365401 4.94383773718731 4.16801590825573
4.4575025829488 P P P 4.26392642186562 4.73918662586313 4.26215750177465 P P P
LNCV6_53671_PI430048170 mRNA
AAGGAGGCGGTCTCACCGAGGTCAGAGGAGCTGAGTAATGAAGGGGACTCCCAGCAGAGC NM_004672 RefSeq
chr1 - 27355178 27366866 MAP3K6 9064 "mitogen-activated protein kinase kinase kinase 6,
transcript variant 1"
GO:0007165|GO:0005737|GO:0000186|GO:0000287|GO:0006468|GO:0007257|GO:0005524|GO:0004709 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112140_PI430048170 0.2033393760985130.9024759298906434.26108821055697
4.00339070385156 4.22094900446678 P P P 4.41853472300628 4.25066944367597
4.26744191247059 P P P LNCV6_112140_PI430048170 mRNA
ATTTGAGGAGGAGCTAAAGAGGATCCAGGATGACTGTACATCTCAGATAAAGGAGGCTCA NM_020893 RefSeq
chr9 + 97307627 97377295 CCDC180 100499483 coiled-coil domain containing 180
GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144023_PI430048170 0.2082218640305981.10595142845565 0.432216851652761

0.6211774424605860.357101156489951A A A 0.2915648184769430.327289753983568
0.367748092873503A A A LNCV6_144023_PI430048170 mRNA
ATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACT NM_173160RefSeq chr10
+ 43371643 43376335 FXYD4 53828 "FXYD domain containing ion transport regulator 4, transcript
variant 1" GO:0034220|GO:0005886|GO:0051117|GO:0005267|GO:0016021|GO:0055085|GO:0071805 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137996_PI430048170 0.1269419755307211.57915245620761 9.57657337480473
9.34324413286342 9.13668174083662 P P P 9.23590249634339 8.39998359173846
8.27859201701528 P P P LNCV6_137996_PI430048170 mRNA
CAGAGCCAGAGTGTACACATTCCTAAACCATTAAACAGATTTCTATAACAAGCCAAAAAA NM_001204887 RefSeq
chr3 - 129087568 129121804 RAB43 339122 "RAB43, member RAS oncogene family, transcript variant 6"
GO:0005515|GO:0005794|GO:0003924|GO:0019068|GO:0005525|GO:0006886|GO:0045335|GO:0006184|GO:0035
526|GO:0007030|GO:0030670|GO:0032482|GO:0019003|GO:0090382|GO:0070062|GO:0005768 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137195_PI430048170 0.0508602346146942 1.03645896417568 0.411090662589984
0.4389006784027450.444510704571183A A A 0.3615707471876590.368965164146008
0.408750984432257A A A LNCV6_137195_PI430048170 mRNA
ACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAAATGGAATAG NM_022144RefSeq
chrX + 100584792 100599885 TNMD 64102 tenomodulin
GO:0071773|GO:0005737|GO:0035990|GO:0001937|GO:0001886|GO:0016525|GO:0016021|GO:0005635 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144095_PI430048170 0.2136191017165090.7995098630643985.54128359200202
5.45119599780511 6.08212160681832 P P P 5.95086437772923 6.0407608422687
6.12956417767952 P P P LNCV6_144095_PI430048170 mRNA
GTAGTAGAATTAGACAGTGAGATCATCTGAGTAAATTGATTGGTGATTCCAGAGATAAGA NM_018710RefSeq chr8
- 90994270 91040975 TMEM55A 55529 transmembrane protein 55A
GO:0016787|GO:0031902|GO:0008152|GO:0016021|GO:0005765 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140579_PI430048170 0.8015449278836470.9534553665539091 0.6238103287122
10.6699612869088 10.6401013525974 P P P 10.9672620495278 10.3795632050451
10.7340524686144 P P P LNCV6_140579_PI430048170 mRNA
CACCCATCCAGCCTATTACCTTTTGCTTTGTGTATTAAAAGTGCTGCAAAATCTGCCTTG NM_001124756 RefSeq
chr20 + 44910061 44939321 PABPC1L 80336 "poly(A) binding protein, cytoplasmic 1-like"
GO:0006378|GO:0000166|GO:0003723|GO:0001556|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_125846_PI430048170 0.0332839704395372 0.6539785831029992.95376508179495
3.28261564591563 3.45772028907518 A P P 3.70479175103747 3.94692857003727
3.91320250474593 P P P LNCV6_125846_PI430048170 mRNA
GTGTCCATCAGCTACTAAATGTAGAACTTAAATAAGTTGCTCACATCTGTTCTTTTAGTG NM_014007RefSeq chr9
+ 126805005 126838208 ZBTB43 23099 "zinc finger and BTB domain containing 43, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_54209_PI430048170 0.6890435319261590.8514360522240983.52975784545656 2.6102482634575
3.27446429535254 P A P 3.96929050157532 2.74200567174293 3.28510237841344 P P P
LNCV6_54209_PI430048170 mRNA
CTTACCATTGAGATTAAAAAAGGGTGGAAAGAAGGCACCAAAATTACTTTTCCAAGAGAA NM_007034RefSeq chr1
+ 78004951 78017311 DNAJB411080 "DnaJ (Hsp40) homolog, subfamily B, member 4"
GO:0006986|GO:0005515|GO:0005737|GO:0009408|GO:0005886|GO:0006457|GO:0051087|GO:0005654|GO:0051
082|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_58370_PI430048170 0.8536994974684310.853382596505283 1.16665728615444 0.274673539732846
1.38316106880608 A A A 0.8129024655824740.3439415728326052.02812095132917 A A A
LNCV6_58370_PI430048170 mRNA
CTTCTGTCTTGTGAACCATACGGAGCCTATTATTTTAAAATATGATCAGACAAGTAAGGC NM_025004RefSeq chr11
+ 124954120 125041491 CCDC15 80071 coiled-coil domain containing 15 GO:0005813 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_140212_PI430048170 0.3605976446445461.0250353952226 0.458649378459121
0.4432698065111280.370002979892165A A A 0.3484699400476550.404562021743231
0.412573617777194A A A LNCV6_140212_PI430048170 mRNA
CTGTTGCACTCAGCAATTGTGACTATACTTAACAAAATTCTTGTAGTCTGTAGAGATATC NM_014980RefSeq chr3
+ 120908202 121424761 STXBP5L 9515 syntaxin binding protein 5-like
GO:0019905|GO:0005737|GO:0005886|GO:0017157|GO:0050714|GO:0042593|GO:0016021|GO:0015031|GO:0006
887|GO:0046676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131291_PI430048170 0.871952750721263 1.00200607751022 3.17256189388837
3.37985025767786 3.10292495208673 P P P 2.617157051354 3.26294756600315
3.61197427748238 A P P LNCV6_131291_PI430048170 mRNA
CTTTTCATTTTTCTCCCCCACATTTCAGTGTTAGAAAGAAAACGAGAGGAGCTAGGGAAA NM_001145652 RefSeq
chr6 + 49550399 49552095 C6orf141 135398 chromosome 6 open reading frame 141 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_136984_PI430048170 0.0172606574240726 0.57795541642486 5.29877945141147
5.15298135977733 5.4274600746345 P P P 5.84170053381101 6.03452497578786
6.34397256002504 P P P LNCV6_136984_PI430048170 mRNA
CACCAATATCTGAGGAGAAGATGGAGTGAAGGGAATTCTTACTTTTTGCTTTATACCTTT NM_153705RefSeq chr11
- 108472105 108498432 KDELC2 143888 KDEL (Lys-Asp-Glu-Leu) containing 2
GO:0008150|GO:0003674|GO:0005788|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110161_PI430048170 0.1801977091660590.662017767669778 0.365804033378864
0.4036220345474390.334340240895385A A A 1.08598963516298 1.275567523011
0.384441289685342A A A LNCV6_110161_PI430048170 mRNA
ATGATTTTCTCTTCAACGAGGAGACCAAGATTGAGGTGCTGGTGGATGTCCTGGAGAAAA NM_153446RefSeq chr17
+ 49132966 49169989 B4GALNT2 124872 "beta-1,4-N-acetyl-galactosaminyl transferase 2, transcript
variant 1"
GO:0030173|GO:0022408|GO:0019276|GO:0006486|GO:0016021|GO:0006047|GO:0030259|GO:0008376 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134485_PI430048170 0.52903898027185 1.09381029372049 10.1148287909837
10.5755676088436 10.1935421980052 P P P 10.3273913376416 10.2146626712367
9.97488673463811 P P P LNCV6_134485_PI430048170 mRNA
TATGAGAAGAAGCAGTGGAAGAAGTGACTTGCATCCCCAGCTGTCTCCCTGAGGCTCCGC NM_032609RefSeq chr20
+ 31637887 31644997 COX4I2 84701 cytochrome c oxidase subunit IV isoform 2 (lung)
GO:0045333|GO:0004129|GO:0006091|GO:0005751|GO:0055114 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141465_PI430048170 0.3591992440087150.698607242294234 2.98061316858132
1.80128498124773 0.510964619055047A A A 2.4875499760791 2.77350789157417
2.55613034048221 A P P LNCV6_141465_PI430048170 mRNA
GTTTTGGAGAATAGTTGTAAGGTGGAAAAAGAATTAGGAACTCGACAGATAGTGAGTTTT NM_032151RefSeq chr5
+ 134905119 134962646 PCBD2 84105 pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of
hepatocyte nuclear factor 1 alpha (TCF1) 2
GO:0005739|GO:0005515|GO:0051289|GO:0006729|GO:0004505|GO:0005634|GO:0005575|GO:0045893|GO:0008
124|GO:0051291|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142236_PI430048170 0.3243091442136291.09837036293807 10.0840231939681

10.2404501719503 10.2997206374587 P P P 9.91059264122683 10.032192377397
10.2615776303015 P P P LNCV6_142236_PI430048170 mRNA
TGTAAAATACTTTCTCAGGGTGTTCTTGTCCTCATCTACCCTCTACCCCTTACTGTGCAANM_001185012 RefSeq chr5
- 140645362 140647785 NDUFA2 4695 "NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2,
8kDa, transcript variant 2"
GO:0022904|GO:0031966|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0008137|GO:0044237 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134549_PI430048170 0.0174966290701116 0.4280718084500885.29822872972794
5.00103356113079 5.30597118957395 P P P 6.07510729004174 6.31451699319984
6.80904692780655 P P P LNCV6_134549_PI430048170 mRNA
CTAGTTCAGACAACTTTCCCTGTTACTTGTTCTTGATAAGTGAAAACTGCAGGGAAATAA NM_015630RefSeq chr2
+ 148644990 148787567 EPC2 26122 enhancer of polycomb homolog 2 (Drosophila)
GO:0006355|GO:0032777|GO:0006281|GO:0006351|GO:0016568 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144588_PI430048170 0.0267121956950939 3.00346648211423 3.58846831466027
4.01136324259309 4.07055491344426 P P P 2.36007566184263 2.77083559891816
1.58956288570544 A P A LNCV6_144588_PI430048170 mRNA
CTCTTCAACGTTTTCAGTACGTGTTTCTCTTCAATAAACTTCATTCAGTGTTCCAGCCGGNM_013364RefSeq chrX +
153056408 153060467 PNMA3 29944 "paraneoplastic Ma antigen 3, transcript variant 1"
GO:0043065|GO:0005730|GO:0008270|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145424_PI430048170 0.280496656855173 1.44284240898297 0.282653183542814
1.37810936969771 0.93490921847419 A A A 0.50838816860564 0.399547376190486
0.296338589995404 A A A LNCV6_145424_PI430048170 mRNA
TTTCTTGATGGTAACACTATTTCATAGAAATGCTTTGCCTTGCAATTCGTGTCTACGTTT NM_001286631 RefSeq chr13
- 79318867 79406221 RBM26 64062 "RNA binding motif protein 26, transcript variant 1"
GO:0006397|GO:0005515|GO:0000166|GO:0010923|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143705_PI430048170 0.0673018692109603 1.34148582456177 9.03626140818022
9.34427974224235 9.40880617255012 P P P 8.85023200908018 8.613395546667
9.04835213442433 P P P LNCV6_143705_PI430048170 mRNA
CTGGCACTGCTTTCTCTTTTTAGCTTTACTACTCTTTTGTGAGGAGTACATGTTATGCAT NM_001195156 RefSeq chr1
- 34981525 34985347 ZMYM6NB 100506144 ZMYM6 neighbor GO:0016021 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_70544_PI430048170 0.6078306237169881.12563530985737 0.2772369896326270.984692878016496
0.354805634920465 A A A 0.5131265307123160.4079065164592360.28311121612425 A A A
LNCV6_70544_PI430048170 mRNA
TTTCTTTTTGGAAAAGAAGGGGGAAAGTTCCAGGAAACATAGGTACCCCCAGAGCATGTG NM_198483RefSeq chr2
+ 218069014 218090581 RUFY4 NA "RUN and FYVE domain containing 4, transcript variant 1"NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_130920_PI430048170 0.00915634093741046 0.2661669780761673.7288413077897
3.20068591870727 3.02596122321822 P P P 5.16901267596351 5.28755940729353
5.31907986979117 P P P LNCV6_130920_PI430048170 mRNA
AGGTCTGAGCTGCCTCTTCAATAAAGAAGCTAATGTGTAACATTTCATATTTCCCTAAAC NM_021163RefSeq chr7
+ 5045921 5069488 RBAK 57786 "RB-associated KRAB zinc finger, transcript variant 1"
GO:0006355|GO:0008270|GO:0005634|GO:0003676|GO:0045892|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141946_PI430048170 0.0351741723241692 0.7347261853463696.12794670308882
6.30547051158437 6.105142323984 P P P 6.44216436836979 6.59875358506339
6.81572858327022 P P P LNCV6_141946_PI430048170 mRNA

GGGATTATTCATACTCTCATTGTGGATAATAGAGAAATCCCAGAGATTGCAAGTTAATGA NM_001033030 RefSeq chr3 + 138608699 138633371 FAIM 55179 "Fas apoptotic inhibitory molecule, transcript variant 1" GO:0043066|GO:0005737|GO:0006915 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142316_PI430048170 0.00195394527720123 0.417641119733112 5.44622650433 5.22339983065588 5.64679844941001 P P P 6.58719647163326 6.67629533877013 6.85035884624097 P P P LNCV6_142316_PI430048170 mRNA
GGGGAGCTGTTTAAGAAACTGAAAAGTAATTGCAAACTACATTGGATAATTGTGACTTTC NM_003588 RefSeq chrX - 120524590 120575829 CUL4B 8450 "cullin 4B, transcript variant 1" GO:0005515|GO:0006511|GO:0035518|GO:0045732|GO:1900087|GO:0005886|GO:0003684|GO:0005737|GO:0007049|GO:0070914|GO:0005654|GO:0031465|GO:0031625|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136279_PI430048170 0.284158085174135 1.05383541060703 0.496208370631258 0.319928480956866 0.406973421599151 A A A 0.283189455772884 0.353540328446731 0.363495752119744 A A A LNCV6_136279_PI430048170 mRNA
CCCGTTGATGAAGAGATGATCATGTTGCAGTGCACAGAGACCTTTGACGATGAAGATTTG NM_182489 RefSeq chr7 + 135231978 135258492 STRA8 346673 stimulated by retinoic acid 8 GO:0046620|GO:0010032|GO:0071300|GO:0005634|GO:0007283|GO:0048599|GO:0006260|GO:0007129|GO:0009566|GO:0001541|GO:0005737|GO:0046983|GO:0042138|GO:0033315|GO:0007066|GO:0007131 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129801_PI430048170 0.00850854740706088 0.262978541075612 3.4043385281915 2.8586426921466 3.82251738146793 P A P 5.11269909033927 5.59151312127159 5.27884149585298 P P P LNCV6_129801_PI430048170 mRNA
ATTGCAGTTTCCTAGAGAGTATTGAGGTGCTAGGTAGAAAGTTAGGAAAGGTCCTGAGGA NM_032869 RefSeq chr8 - 109240918 109334121 NUDCD1 84955 "NudC domain containing 1, transcript variant 1" GO:0005515|GO:0005737|GO:0005654|GO:0005634|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137466_PI430048170 0.0790765207469814 1.32088016697636 6.30801440999207 6.1768394529935 6.48001207343141 P P P 5.66808857642286 6.14961273263731 5.91873175923979 P P P LNCV6_137466_PI430048170 mRNA
CACAGTCTTCTGAAACCTTGTATTAATAGTTCTCTTTTGTATTACCATTTTCAGGTAGGG NM_001135663 RefSeq chr1 - 205767985 205775482 RAB29 8934 "RAB29, member RAS oncogene family, transcript variant 3" GO:0005515|GO:0005773|GO:0005802|GO:0042470|GO:0048471|GO:0005886|GO:0032438|GO:0003924|GO:0090316|GO:0005525|GO:0015031|GO:0030154|GO:0005739|GO:0006888|GO:0035526|GO:0005737|GO:0008152|GO:0007030|GO:0032482|GO:0019003|GO:0005856|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109216_PI430048170 0.0828509841015714 1.28674998860256 7.9720110608303 7.97748572186334 8.32448900880452 P P P 7.79949080523274 7.72882695798175 7.68098066004209 P P P LNCV6_109216_PI430048170 mRNA
AGTTAAGTGGAAATATGGAAGAACTGATCCTGGCCCTCTTCATGCCTCCTACGTATTACG NM_004034 RefSeq chr10 - 73375430 73414083 ANXA7 310 "annexin A7, transcript variant 2" GO:0005515|GO:0014070|GO:0009651|GO:0005886|GO:0008283|GO:0008360|GO:0009992|GO:0005634|GO:0005635|GO:0005829|GO:0005544|GO:0030855|GO:0061025|GO:0070062|GO:0005509|GO:0006914|GO:0006874|GO:0007599|GO:0051592|GO:0005178|GO:0016020|GO:0042584|GO:0010629|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129781_PI430048170 0.00684122883034998 0.476320789767241 5.27008391819407 4.89028770859011 5.39825527302995 P P P 6.08325248503997 6.15202224284042 6.53761549154584 P P P LNCV6_129781_PI430048170 mRNA
GGAGAGAGATTTAATGGGATTTGAAATGTGCAAGCTGTCTAAATAAGATGCAGTCAAATA NM_001011713 RefSeq chr14 + 57390552 57412748 NAA30 122830 "N(alpha)-acetyltransferase 30, NatC catalytic subunit"

GO:0005515|GO:0031417|GO:0005737|GO:0017196|GO:0004596|GO:0005844|GO:0006474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129984_PI430048170 0.6649401322033130.9746728652298 0.274113392802291 0.4714573279593570.322154868723833A A A 0.4916839811860290.382376932453051 0.306054454511088A A A LNCV6_129984_PI430048170 mRNA CAGGTTTTGTTTTCCTCCTTTACCTCATGTTATAATAAAGCTCTGATTTCTGACTCACAA NM_014357RefSeq chr1 + 152686122 152687400 LCE2B 26239 late cornified envelope 2B
GO:0003674|GO:0008544|GO:0031424|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109980_PI430048170 0.0718815274715276 0.4255034225076591.38181549314334 0.2941345786107061.37541047492198 A A A 1.56846436194604 2.41504602017127 2.76640377905434 A P P LNCV6_109980_PI430048170 mRNA GACTATAAGAAGAGTGTACTTTTAGTAAGGGAGAAGTCTTGGAGGGTTGCTTCTGCAGGA NM_024908RefSeq chr15 + 43826913 43868419 WDR76 79968 "WD repeat domain 76, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143996_PI430048170 0.0292997495498424 0.6461071827113665.34580510946924 5.00550583539485 5.47411513825611 P P P 5.73802076504559 5.82538530375206 6.15743435346459 P P P LNCV6_143996_PI430048170 mRNA TCCTGTGTGAATTCGCTGGTTAAGTGATAATTAACTGCAGTTAAAATTCAGGTCAAGCAT NM_032856RefSeq chr15 - 84641494 84654343 WDR73 84942 "WD repeat domain 73, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132537_PI430048170 0.5042087112064110.8242981709912512.57725531149218 1.62252434064481 2.72204302694233 A A A 3.04004783582577 2.62797536306704 2.19323561294537 P P A LNCV6_132537_PI430048170 mRNA GTTTTTCAATAAAAGTGTCCTCCTCTTTCTGTGAGAGTCCTGAGTCCCTCAGTGGAGCAA NM_021155RefSeq chr19 - 7739994 7747578 CD209 30835 "CD209 molecule, transcript variant 1" GO:0005515|GO:0019062|GO:0005886|GO:0009986|GO:0009988|GO:0046790|GO:0019079|GO:0005537|GO:0046872|GO:0006897|GO:0035556|GO:0046968|GO:0005737|GO:0016020|GO:0019882|GO:0045087|GO:0019048|GO:0042605|GO:0042129|GO:0007159|GO:0030246|GO:0016021|GO:0007157|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143222_PI430048170 0.6172669327461290.9800868558829180.331012610150121 0.44949270465666 0.34125119908291 A A A 0.4788434447505920.364748626425719 0.365210811987144A A A LNCV6_143222_PI430048170 mRNA ACACAGGCACATACAGGGCACACTGGTATGGCTTGTCATTTTGTGACAAATTCTTGTCAG NM_001145399 RefSeq chr11 - 30384492 30586383 MPPED2 744 "metallophosphoesterase domain containing 2, transcript variant 2" GO:0016787|GO:0008152|GO:0046872|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129627_PI430048170 0.0446697286823039 1.0598947026307 0.382643830085081 0.3535249908624470.305635487032555A A A 0.2480787607005230.297263407649328 0.245148526441089A A A LNCV6_129627_PI430048170 mRNA CATTTGTATATCTGCATGTAGTCTGTCTCTGATTTAGGGTTTAGGTTCCTCTGTATTTTT NM_024058RefSeq chr13 - 44143150 44161257 SMIM2 79024 small integral membrane protein 2 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142464_PI430048170 0.48677221944228 0.9422959689163919.42915040236424 9.1280325258888 9.30287752558705 P P P 9.23504289695568 9.40495118365428 9.48210065108443 P P P LNCV6_142464_PI430048170 mRNA ATTTAAAAGGACGCATATCAAGATGAAGAAACAACCCAAAGGTTACGGCCTCCGCTGCCA NM_031902RefSeq chr2 - 95087206 95122009 MRPS5 64969 mitochondrial ribosomal protein S5 GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0022627|GO:0005743|GO:0006412|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_56054_PI430048170 0.610921801351631 0.971476847182277 0.482074681036892 0.44199509585981 0.247329556966048 A A A 0.384141377252414 0.48142002226085 0.440194251955538 A A A LNCV6_56054_PI430048170 mRNA ATCCGTTGCCAGAATTACTACTTCCAAATCCTTCCCAGCAAGCCTTGGAATGTGTACTGT NM_001142308 RefSeq chr10 + 19048770 19734478 MALRD1 NA MAM and LDL receptor class A domain containing 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111238_PI430048170 0.72699378437439 1.06988089453686 3.91952108338646 4.41081516299895 3.8173814238196 P P P 3.66189512349732 3.88961112092319 4.30183014823226 P P P LNCV6_111238_PI430048170 mRNA AGTCAGCAAAGTAAATAAATACTGTGCTTCTTCCAACTTTCATTCCACTTGGGGAAAAAA NM_015030 RefSeq chr4 - 48497362 48780299 FRYL 285527 FRY-like GO:0006355|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126803_PI430048170 0.0041492971454194 2.02622789021801 7.33147921048738 7.65237953170343 7.54695309229143 P P P 6.72547887404155 6.28092013468233 6.45111349990574 P P P LNCV6_126803_PI430048170 mRNA TACTGTACTCAGAATCACGACATTCCTTCCCTACCAAGGCCACTTCTATTTTTTGAGGCT NM_024119 RefSeq chr17 - 42101405 42112733 DHX58 79132 DEXH (Asp-Glu-X-His) box polypeptide 58 GO:0003725|GO:0005515|GO:0003727|GO:0004386|GO:1900246|GO:1900245|GO:0039534|GO:0009615|GO:0003677|GO:0005524|GO:0051607|GO:0005737|GO:0045087|GO:0045088|GO:0039536|GO:0008152|GO:0016032|GO:0008270|GO:0032481|GO:0032480|GO:0045824 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129298_PI430048170 0.867397042339467 0.929403216904059 2.97751287322442 1.92774503547564 3.08606297443039 P A P 2.38960301634621 3.48770112118849 2.39152725074286 A P P LNCV6_129298_PI430048170 mRNA GGCAACCTGTTCTTCCTACCAAATATAAACTTGTGTATGATCCAAGTATTTTATCTGTGT NM_000818 RefSeq chr10 + 26216306 26304562 GAD2 2572 "glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa), transcript variant 1" GO:0005515|GO:0030424|GO:0048471|GO:0030054|GO:0046982|GO:0005886|GO:0042493|GO:0007268|GO:0031225|GO:0007269|GO:0005829|GO:0042734|GO:0004351|GO:0000139|GO:0030170|GO:0030672|GO:0061202|GO:0042136|GO:0016595|GO:0006540 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95288_PI430048170 0.243290892060431 1.0209931406975 0.309246690343946 0.312044886577944 0.365933619367767 A A A 0.312026409232701 0.298986813838105 0.286893505246038 A A A LNCV6_95288_PI430048170 mRNA GGCAAAATCCATTCCATTGGTGATGCCTTCAGAAATTTTAAAAATCTCCGATCCTTAGAT NM_018296 RefSeq chr16 + 67326843 67385206 LRRC36 55282 "leucine rich repeat containing 36, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66504_PI430048170 0.000834170020704102 2.90896542050246 7.06041132706712 7.24334395436087 6.90134983879623 P P P 5.67057821756355 5.62758889187219 5.27387328667778 P P P LNCV6_66504_PI430048170 mRNA GCAGACCTGGTGTTTGTTTGTTGGGCTCACGCTTGCACAATGAAGGCTTGTTCACACAAC NM_001161404 RefSeq chr2 - 127638420 127681786 LIMS2 55679 "LIM and senescent cell antigen-like domains 2, transcript variant 5" GO:2001046|GO:0043066|GO:0016337|GO:2000178|GO:0005886|GO:0034329|GO:2000346|GO:0008270|GO:0005634|GO:0005925|GO:0045216|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130278_PI430048170 0.322622560183162 0.7049262866491 0.437745304365599 0.448531334302587 0.366880391344704 A A A 0.625155910988613 1.48925296316216 0.418866915557106 A A A LNCV6_130278_PI430048170 mRNA TCCCCTCAACAATGAAGCAAGCTTAGCTGTCAAGGGAAACTTTTTACAAATCTGAAAAAA NM_177454 RefSeq

chr2 + 186694061 186763785 FAM171B 165215 "family with sequence similarity 171, member B" GO:0016021|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_140634_PI430048170 0.0915650280326647 1.11831607951981 9.09111313522002 8.98270167978717 8.89118716471227 P P P 8.86329285230894 8.86703193639731 8.75485733438231 P P P LNCV6_140634_PI430048170 mRNA GTGTCTTCTGCTTATGAAGCGCCTTTCTTAAAGTTTGGCAATAAATCCATTTTTATGGAA NM_025201 RefSeq
chr15 + 64841882 64868002 PLEKHO2 80301 "pleckstrin homology domain containing, family O member 2, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_138010_PI430048170 0.650988282292793 1.05005244510942 11.4357248600948 11.5673197268568 11.5414311882032 P P P 11.7599168870764 11.2828123697117 11.2330754680064 P P P LNCV6_138010_PI430048170 mRNA CTGGGATGCCCCTGCTCTGGACCTCTCATTTCTCTTCATTGGTTTATTTTTCAATGCATC NM_004922 RefSeq chr10 + 73744372 73772175 SEC24C 9632 "SEC24 family member C, transcript variant 1" GO:0005515|GO:0002474|GO:0012507|GO:0048471|GO:0030127|GO:0048208|GO:0044281|GO:0006886|GO:0005829|GO:0006888|GO:0003674|GO:0019886|GO:0000139|GO:0005789|GO:0061024|GO:0008270|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_15139_PI430048170 0.0373290192240103 0.471685844826753 3.8924431627719 3.32880939908562 4.26541826711911 P P P 4.86119247224754 4.7987114689217 5.1961691178026 P P P LNCV6_15139_PI430048170 mRNA CAATGTTGTTTTCTGCCACAACTTGAATAGATACTTGAAGCAGAGATGATGTTGAGTTAA NM_000373 RefSeq
chr3 + 124730365 124749272 UMPS 7372 "uridine monophosphate synthetase, transcript variant 1" GO:0007565|GO:0044205|GO:0004588|GO:0006222|GO:0055086|GO:0005634|GO:0044281|GO:0004590|GO:0035690|GO:0005829|GO:0005737|GO:0046134|GO:0007595|GO:0006207|GO:0006206 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_115690_PI430048170 0.308580112153494 1.03072780472321 0.300954555749129 0.255388717251889 0.365365743104191 A A A 0.274508178261632 0.245382299409521 0.272764478121155 A A A LNCV6_115690_PI430048170 mRNA GAAAAAATCAGCATCTTGGATTACACGGATACGACCAGAGCTTGTGAAGAACGGCCAGTT NM_005874 RefSeq
chr19_GL949753v2_alt - 248816 256172 LILRB2 10288 "leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2, transcript variant 1" GO:0005515|GO:0032755|GO:0042288|GO:0005886|GO:0007267|GO:0005615|GO:0042130|GO:0006955|GO:0005737|GO:0042102|GO:0002774|GO:0051926|GO:0004872|GO:0034113|GO:0050839|GO:2001198|GO:0009986|GO:0002666|GO:0007165|GO:0006968|GO:0071222|GO:0002767|GO:0016020|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_128258_PI430048170 0.00657029909952401 2.02150573187618 7.29310956933531 7.2798826131011 7.35958324920787 P P P 6.46870652294151 6.12703705442841 6.2713204321632 P P P LNCV6_128258_PI430048170 mRNA TAAACAGTATCTCGGAGAAGCCTGGGATGAGAAAATGAGGAGGATGGGTCCAAGAAACAT NM_021944 RefSeq
chr14 - 22986900 23010201 C14orf93 60686 "chromosome 14 open reading frame 93, transcript variant 1" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_137519_PI430048170 0.50648100978094 1.27483002193066 1.31376042767551 0.336702575090496 0.283359041131864 A A A 0.464410022388038 0.358661144356748 0.302476049744624 A A A LNCV6_137519_PI430048170 mRNA GACTATCAGTTTTGGCCCTGTAAGATCGTGGAGATCTGTAAGATAGATACTTATATAACT NM_018672 RefSeq
chr17 - 69244434 69315633 ABCA5 23461 "ATP-binding cassette, sub-family A (ABC1), member 5, transcript variant 1" GO:0005215|GO:0033344|GO:0010745|GO:0005770|GO:0043691|GO:0005765|GO:0005524|GO:0005764|GO:0000139|GO:0008152|GO:0031902|GO:0034375|GO:0016021|GO:0016887 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_140758_PI430048170 0.223796853596095 0.741567127201185 4.98756849519616
5.23272534408526 5.52528818431337 P P P 5.30971977624961 5.57236523226817
6.09480079665482 P P P LNCV6_140758_PI430048170 mRNA
GGAAATGAAAGCTAGCGCACCTGCACTTTGAATTCTTGCTTCTTTTTTATTACTGTTATG NM_015130 RefSeq chr4
- 140620781 140756317 TBC1D9 23158 "TBC1 domain family, member 9 (with GRAM domain)"
GO:0005515|GO:0005509|GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_122189_PI430048170 0.49805414844347 2.20818070595716 0.351964654924211
0.41105323010597 2.85519662810846 A A P 0.246152301649968 1.05775374055473
0.250141590721792 A A A LNCV6_122189_PI430048170 mRNA
AGGAGGTTGCAGAATACCGTACAGAGTGGATTTGCAGGGCAGTGGCATGGAGCCCCTCTT NM_182647 RefSeq
chr20_KI270870v1_alt + 2740 5589 OPRL1 4987 "opiate receptor-like 1, transcript variant 1"
GO:0005515|GO:0043005|GO:0005886|GO:0004930|GO:0007268|GO:0038003|GO:0007193|GO:0007204|GO:0019
233|GO:0042923|GO:0005887|GO:0007218|GO:0007610|GO:0016023|GO:0001626|GO:0007600 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_99356_PI430048170 0.722649467894311 1.07679529441203 4.97880882782288 4.31609347503527
4.80367565585768 P P P 4.59834743754496 4.70704506437444 4.54701768804068 P P P
LNCV6_99356_PI430048170 mRNA
GAGTGAACAGAAGAATAATTCCATGAATAGTAATATGGGTACAGGTACATTTGGACCAGT NM_001031716 RefSeq
chr2 + 191678134 191688522 NABP1 64859 "nucleic acid binding protein 1, transcript variant 1"
GO:0007093|GO:0005737|GO:0006281|GO:0003697|GO:0000724|GO:0010212|GO:0003723|GO:0070876|GO:0005
654|GO:0005634|GO:0006974 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145759_PI430048170 0.412404216710731 2.13150313942693 0.458567316616888
0.494021108876434 2.58562903213557 A A A 0.534971966561115 0.412825505418339
0.423790413949633 A A A LNCV6_145759_PI430048170 mRNA
AGCTTTTATATTCAAGGGCCTCTGTTGAATATGGGGTATTCAATAAATATCTGACTACAC NM_022901 RefSeq chr9
- 26993136 27005693 LRRC19 64922 leucine rich repeat containing 19 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141616_PI430048170 0.0194705801828309 2.25490314441681 11.3419263710375
11.529105065083 11.6448909522899 P P P 10.6876296710607 9.9362307618407
10.2910671662143 P P P LNCV6_141616_PI430048170 mRNA
TCTGTATAAAAGGGAACAGTGTGGAGATGTTTTTGTCTTGTCCAAATAAAAGATTCACCA NM_033280 RefSeq chr18
+ 59139856 59158837 SEC11C 90701 SEC11 homolog C (S. cerevisiae)
GO:0010467|GO:0050796|GO:0006614|GO:0006508|GO:0005789|GO:0008236|GO:0016021|GO:0044267|GO:0006
412|GO:0006465 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142632_PI430048170 0.192786816623394 0.8238707080372468.97119725600274
8.81863852083811 9.17387535273188 P P P 9.07559266199073 9.1777857300707
9.53056890344561 P P P LNCV6_142632_PI430048170 mRNA
CGGAAAGCGGCATGTATCGTACATATTGTATGATTCAACATTTTTAAAGGCAGATTGTTT NM_017615 RefSeq chr10
- 121957087 121975228 NSMCE4A 54780 "non-SMC element 4 homolog A (S. cerevisiae), transcript
variant 1" GO:0005515|GO:0000781|GO:0006281|GO:0030915|GO:2001022|GO:0006310|GO:0005654 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141692_PI430048170 0.151883016701953 0.4755854643348662.32168656752111
0.510748620875087 0.538433537545113 A A A 2.32916379022035 2.34855159767908
2.68775580726636 A A P LNCV6_141692_PI430048170 mRNA
GACATAGTTTGGAGTTCTGATTATATGGTACATTTTTCTACCAGTAATATAGGGTTGCCA NM_001134479 RefSeq
chr1 + 89821013 89936430 LRRC8D 55144 "leucine rich repeat containing 8 family, member D,
transcript variant 1" GO:0005515|GO:0016020|GO:0005886|GO:0005789|GO:0016021|GO:0006811 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_136835_PI430048170 0.2873678836378481.60247208618207 1.71814824311505
0.3263245521857240.909631675340498A A A 0.3082902901927860.282886768585082
0.635072538389114A A A LNCV6_136835_PI430048170 mRNA
CGTGGACACCCCAGACCTGCGAAGGATGATCGCCCGATAAAGACGGATTCTAAGGACTCTNM_139355RefSeq chr19
- 3777968 3786417 MATK 4145 "megakaryocyte-associated tyrosine kinase, transcript variant 1"
GO:0005515|GO:0008284|GO:0008283|GO:0005102|GO:0005524|GO:0030154|GO:0031234|GO:0005829|GO:0016
477|GO:0045087|GO:0042127|GO:0006468|GO:0007498|GO:0004713|GO:0038083|GO:0002009|GO:0004715|GO:0
007169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141005_PI430048170 0.1799654905864250.9089627713585860.28899783321968
0.2957437980236850.309428336270529A A A 0.5643877621096570.384697492263603
0.348916998617614A A A LNCV6_141005_PI430048170 mRNA
CGACAGCTTAGTGGTGTCTGATTTTATACATGACAAAATGAACGAGTTAACCATTTAAGC NM_024979RefSeq chr13
+ 113001713 113099739 MCF2L 23263 "MCF.2 cell line derived transforming sequence-like, transcript
variant 2"
GO:0051056|GO:0048011|GO:0043065|GO:0005886|GO:0007264|GO:0007266|GO:0097190|GO:0005615|GO:0030
027|GO:0005829|GO:0005545|GO:0032321|GO:0045944|GO:0005089 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_136534_PI430048170 0.9096826958160130.9717486952371193.62450254289201
3.64124613005559 3.82220701243332 P P P 3.36695459976531 3.91355996369139
3.87791402651818 P P P LNCV6_136534_PI430048170 mRNA
TCAAAAGGCTATCAAAGGAAGGGGGTTATGATAAGGAAAGGCTCAAGACCTGCCTCAGAA NM_015476RefSeq
chr18 - 36794105 36829216 TPGS2 25941 "tubulin polyglutamylase complex subunit 2, transcript
variant 1" GO:0005737|GO:0005874 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128253_PI430048170 0.3545450828834810.5955736741555610.410087063708725
0.3955266181482910.436684406169228A A A 1.94303694002151 0.642565111917682
0.385234430712638A A A LNCV6_128253_PI430048170 mRNA
TCTATGCCATTGTTATGCCTCTGCTGAACCCTGTGATTTATAGTCTAAGGAATAAAGAGG NM_001004685 RefSeq
chr7 + 143935232 143936186 OR2F2 NA "olfactory receptor, family 2, subfamily F, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75380_PI430048170 0.0451446465841031 0.6669548188702646.3994995088682
6.22985843474091 6.68027573164999 P P P 7.03685000924137 7.03580936622747
7.02620821910102 P P P LNCV6_75380_PI430048170 mRNA
CTGCCTGTGCTTTTGTTTGACTGTCTCTAGATTTTGAAACCAAAAAACTGAACTGAAATC NM_194283RefSeq chr5
+ 34929592 34958964 DNAJC21 134218 "DnaJ (Hsp40) homolog, subfamily C, member 21, transcript
variant 1" GO:0005515|GO:0006457|GO:0005840|GO:0008270 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144114_PI430048170 0.8832501104684680.9982514100615920.348760045404798
0.3533892037867850.305799935429401A A A 0.3387267951743670.349792681572284
0.327393124012692A A A LNCV6_144114_PI430048170 mRNA
ACTATCCTGTTCACGAAGACATGTGAACTTGGTTCAGTCCAAATGGGGATTTGTATAAAC NM_004473RefSeq chr9
+ 97853254 97856715 FOXE1 2304 forkhead box E1
GO:0003700|GO:0006357|GO:0006366|GO:0000981|GO:0048538|GO:0005634|GO:0000122|GO:0030878|GO:0003
677|GO:0009653|GO:0048562|GO:0031069|GO:0043565|GO:0016477|GO:0060465|GO:0006590|GO:0045893|GO:0
045892|GO:0060022|GO:0060023 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130764_PI430048170 0.2060889431007150.6738298204749380.39259677477093
0.2579164348008510.28902072094021 A A A 0.2686046243423861.15923929119507
1.06898155560401 A A A LNCV6_130764_PI430048170 mRNA
ATGAAGACGGCAATAAGACAGCTGAGAAAATGGGATGCACATTCTAGTGTAAAGTTTTAG NM_001005484 RefSeq

chr1 + 69090 70008 OR4F5 NA "olfactory receptor, family 4, subfamily F, member 5" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141489_PI430048170 0.4391753702434260.8779698448694810.330015523331493
0.5804969477417660.436869506861033A A A 0.5117711201457180.38757778929013
0.958112267113948A A A LNCV6_141489_PI430048170 mRNA
GGGAATTCTGTTTTCAGTCTTGGGTGGTATCTTTCTGAAAATTAAGGAAGTTCTTCATGA NM_033185RefSeq
chr17_JH159146v1_alt - 142824 143528 KRTAP3-3 85293 keratin associated protein 3-3
GO:0005198|GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134139_PI430048170 0.2148131470936391.26025088461638 5.6031024786473
6.10984405844194 5.89277346751486 P P P 5.74088255407761 5.66658277642149
5.17968785981392 P P P LNCV6_134139_PI430048170 mRNA
TGACAACATCTTCAAGACACCCAAGGAGCTCTCCTGCACCCACGTCTTCTGCCTGGAGTG NM_001205252 RefSeq
chr1 - 1071745 1074307 RNF223 NA ring finger protein 223 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106905_PI430048170 0.4888528336486420.9137002905744885.37476506144291
4.81682938632609 5.28755940729353 P P P 5.21926540692945 5.29178329437789 5.4120929765191
P P P LNCV6_106905_PI430048170 mRNA
TGGTTAATGTGTTGCTAACAACTCCACTCTGGGTGGTAAACACCAGACTGAAGCTTCAAG NM_001282726 RefSeq
chr22 - 40769629 40819399 SLC25A17 10478 "solute carrier family 25 (mitochondrial carrier;
peroxisomal membrane protein, 34kDa), member 17, transcript variant 2"
GO:0005515|GO:0043132|GO:0015230|GO:0051087|GO:0044281|GO:0043231|GO:0005739|GO:0001561|GO:0015
228|GO:0005779|GO:0005778|GO:0044255|GO:0051724|GO:0005777|GO:0006635|GO:0044610|GO:0035349|GO:0
035350|GO:0016020|GO:0015866|GO:0015867|GO:0080122|GO:0015217|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135034_PI430048170 0.1494585574414210.8776769724173655.81018296511661
5.58565733167053 5.87908507135986 P P P 5.88424098807846 5.95860324995414
6.01007327173103 P P P LNCV6_135034_PI430048170 mRNA
GTCATTTATGGAGATTAATTCATTATGGAAATAAAACATTGCCTAAGCCCTTGCCTGCTG NM_001204747 RefSeq
chr4 - 39287448 39366381 RFC1 5981 "replication factor C (activator 1) 1, 145kDa, transcript
variant 2"
GO:0005515|GO:0030054|GO:0003689|GO:0005634|GO:0006271|GO:0003690|GO:0000723|GO:0000722|GO:0005
663|GO:0006297|GO:0070062|GO:0005794|GO:0019904|GO:0005730|GO:0000122|GO:0043085|GO:0005524|GO:0
003677|GO:0006351|GO:0043565|GO:0006261|GO:0006281|GO:0006283|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134863_PI430048170 0.0129277109484369 0.4698189607482732.61994980300966
3.09531872654882 3.16167585662755 A P P 3.69372613232868 4.11004594140957
4.33016265628792 P P P LNCV6_134863_PI430048170 mRNA
GGTGTACTGGTCCCTCTGGGATGAATTTATAAGGCTCATGATATAGGAAAAGGAATATAG NM_138775RefSeq chr11
- 107502726 107565735 ALKBH891801 "alkB, alkylation repair homolog 8 (E. coli), transcript variant 2"
GO:0005515|GO:0000049|GO:0005506|GO:0030488|GO:0005634|GO:0006974|GO:0005829|GO:0002098|GO:0016
300|GO:0015630|GO:0016706|GO:0005654|GO:0008270|GO:0055114 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_53423_PI430048170 0.9742343748717891.0019279839168 6.04391328661931 5.72712884206732
5.7711399230054 P P P 5.77818517973267 5.68215483824986 6.06614316490436 P P P
LNCV6_53423_PI430048170 mRNA
AATTCGCAGACTCAAAATCACCAGCACAATCAGTGTTTTAACGAGGCCACCTGCATTTCG NM_001009566 RefSeq
chr1 - 9729020 9824526 CLSTN1 22883 "calsyntenin 1, transcript variant 1"
GO:0005515|GO:0042988|GO:0030054|GO:0005509|GO:0005634|GO:0042995|GO:0001540|GO:0000139|GO:0045
211|GO:0005789|GO:0016021|GO:0019894|GO:0007155|GO:0007156|GO:0070062 . NA - . NA NA NA

NA NA NA NA NA NA
LNCV6_70829_PI430048170 0.193085465730807 1.12463439660865 11.5697776975312 11.669971396508
11.3796598564897 P P P 11.4266376997792 11.4403825651977 11.2513385087168 P P P
LNCV6_70829_PI430048170 mRNA
CAGCTGGATGCACATCTCATTCTGTCATGAATGTCCAGTAAAAATCTGAATTGGTTGCAA NM_152783 RefSeq chr2
+ 241734578 241768816 D2HGDH 728294 "D-2-hydroxyglutarate dehydrogenase, transcript variant 1"
GO:0008762|GO:0050660|GO:0044281|GO:0010043|GO:0051990|GO:0010042|GO:0005739|GO:0051592|GO:0005
759|GO:0006103|GO:0032026|GO:0032025|GO:0044267|GO:0044237|GO:0055114 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139306_PI430048170 0.324018223087183 1.0093071726487 0.332773572981778
0.319922991101464 0.300220193946006 A A A 0.311414179471118 0.310995525362849
0.290498384817124 A A A LNCV6_139306_PI430048170 mRNA
CTGCAGTTCTGCGCTTTTTACCAGTGAAAAAATGTAATTATTTTCCCCTCTTAAGGATTA NM_006665 RefSeq chr4
- 83292460 83335153 HPSE 10855 "heparanase, transcript variant 1"
GO:0005515|GO:0051897|GO:0030305|GO:0005634|GO:0044281|GO:0005765|GO:0005764|GO:0043231|GO:0061
042|GO:0030200|GO:0046983|GO:0033690|GO:0030203|GO:0043202|GO:0004566|GO:0005975|GO:0006027|GO:0
005576|GO:0006029|GO:0010575|GO:0051798|GO:0007160|GO:0030194|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144648_PI430048170 0.000619451729945413 0.350765801644218 12.5677682419714
12.4116120102016 12.5107405595382 P P P 13.925989531632 13.9062755658641 14.179965314642
P P P LNCV6_144648_PI430048170 mRNA
ACACCCTGCTTTGTATTCTGGGCTAAGATTCATTAAAAACTAGCTGCTCTTAACTTACAA NM_000690 RefSeq chr12
+ 111766886 111809985 ALDH2 217 "aldehyde dehydrogenase 2 family (mitochondrial), transcript variant 1"
GO:0006805|GO:0005975|GO:0006066|GO:0006069|GO:0006068|GO:0004029|GO:0007268|GO:0009055|GO:0044
281|GO:0005759|GO:0042136|GO:0004030|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133875_PI430048170 0.0211526358210742 0.335368152042741 0.424275193133221
0.410388144317562 0.367162474891411 A A A 1.51445264264683 2.00391190917336 2.3052133328865
A A A LNCV6_133875_PI430048170 mRNA
GTGGTGTGAAGGAAGAGGAGGTACATTAAGAGCTATTTTATTTGAGGTAGTCATTTTTAT NM_033051 RefSeq chr9
- 112878919 112890913 SLC46A2 57864 "solute carrier family 46, member 2"
GO:0009986|GO:0005886|GO:0070233|GO:0045580|GO:0048538|GO:0016021|GO:0043029|GO:0055085|GO:0015
293 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141982_PI430048170 0.226072817176316 0.496716368915035 2.7098281637481
0.275566291435411 2.4700179568685 A A A 3.09752863145582 3.13865921140569
3.23204955390268 P P P LNCV6_141982_PI430048170 mRNA
GTCTTTTTCCTCAATGAATGGGATGTCTAATGTATTTCAAAATCACCCAAAACTTTTGGC NM_005670 RefSeq chr6
- 145625303 145735855 EPM2A 7957 "epilepsy, progressive myoclonus type 2A, Lafora disease (laforin),
transcript variant 1"
GO:0005515|GO:0005886|GO:0005783|GO:0019203|GO:0005634|GO:0044281|GO:0035335|GO:0005829|GO:0005
737|GO:0006470|GO:0006006|GO:0004722|GO:0004725|GO:0005975|GO:0005978|GO:0005977|GO:0006914|GO:0
007399|GO:0004439|GO:0046855|GO:0009405|GO:0008138|GO:0005844|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141808_PI430048170 0.906931345912455 1.00450544199906 4.2726591439688 4.2805112163063
4.32828824221485 P P P 4.47526596527344 4.19580519292134 4.17139286457233 P P P
LNCV6_141808_PI430048170 mRNA
TTTTCCTTTTCTTCGTGGCCAATGCCATAATCCACCTCTTCTGCTTCAGTTGAGGTGACA NM_001803 RefSeq chr1 +
26317919 26320523 CD52 1043 CD52 molecule
GO:0045730|GO:0016020|GO:0005887|GO:0031225|GO:0007204 . NA - . NA NA NA NA NA NA NA
NA NA

LNCV6_134127_PI430048170 0.00200709230519705 0.6079265723163246.82348812836704
6.58255196374328 6.70077103755106 P P P 7.38068674136501 7.55949627445825
7.31990389683644 P P P LNCV6_134127_PI430048170 mRNA
GGGGCAGAATAATCTATCACGTTAGAAGGGTGTCCATTAAAGAACAGTATTTCCCTGAAA NM_173793RefSeq chr22
- 19443149 19448232 C22orf39 128977 "chromosome 22 open reading frame 39, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138476_PI430048170 0.75486735233788 1.1228920377644 1.26253448550864
1.07858376303052 0.262183666283723A A A 0.9247601935829360.746435888348957
0.594021535213863A A A LNCV6_138476_PI430048170 mRNA
CCTGCATTTACCCTTTGATTAAAATATGATAGATGAAGCTGTTCCTGCATTTAGTCTTGT NM_017581RefSeq chr4
+ 40335328 40355217 CHRNA9 55584 "cholinergic receptor, nicotinic, alpha 9 (neuronal)"
GO:0005262|GO:0030054|GO:0042472|GO:0005886|GO:0022848|GO:0007268|GO:0007204|GO:0005892|GO:0005
887|GO:0045211|GO:0050910|GO:0070588|GO:0004889 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136383_PI430048170 0.4850658069120940.835941634352654 0.454208888753456
0.4358413825441620.346229748557202A A A 0.3472825117906 0.403192994800744
1.12645090787666 A A A LNCV6_136383_PI430048170 mRNA
AATTGTAGAAGGTATGGAAAGTTAGGACTGTGGTGGACCCAGTTAAATCACTGGACAGAA NM_001134233 RefSeq
chr1 - 159834473 159855347 C1orf204 284677 chromosome 1 open reading frame 204 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_131497_PI430048170 0.4085664773851080.9747061889887470.26418808042875
0.2765194647069150.37377143482368 A A A 0.3770428411524030.313584201987492
0.336533147702167A A A LNCV6_131497_PI430048170 mRNA
CTTTAGTAAAAATTCCATCCTAGTACAACATTGCAGTATTCATACCAGAGAGAAGCCTTA NM_001143939 RefSeq
chr19 + 52431413 52439446 ZNF534 NA "zinc finger protein 534, transcript variant 2" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_31337_PI430048170 0.3555236584292920.8473901863649214.30363415804394 3.95338444969003
4.4271713545984 P P P 4.79846955456745 4.26929302765139 4.31194371827664 P P P
LNCV6_31337_PI430048170 mRNA
CATCTGTGAAAGTAAACAGATACTTCCCAGTAAAACACCTCTTCCATCTGCCCTTGATGA NM_001204056 RefSeq
chr18 + 9137562 9285985 ANKRD12 23253 "ankyrin repeat domain 12, transcript variant 3"
GO:0005737|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131484_PI430048170 0.36532071269595 0.9063546993498776.71969104216739
6.86513307972561 6.84561794332716 P P P 6.76910541426442 6.90495831498137
7.15878335653424 P P P LNCV6_131484_PI430048170 mRNA
CATTGAAGTTGGATCTAAGAGGAAAGTGGTTATCGGTTGCTTTTTATTTATAAAGGATGC NM_032177RefSeq chr5
+ 126600914 126627252 PHAX 51808 phosphorylated adaptor for RNA export
GO:0010467|GO:0015030|GO:0003723|GO:0005730|GO:0005634|GO:0034660|GO:0000387|GO:0015031|GO:0043
231|GO:0005829|GO:0006408|GO:0015643|GO:0043025|GO:0005654 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127739_PI430048170 0.0648180702916410.8447243230046689.85269507042204
9.78614299823439 9.81646379152781 P P P 9.92754655439686 10.0860537134298
10.1629235967771 P P P LNCV6_127739_PI430048170 mRNA
ATAGAGGGATAAGCAGCTCATTCCCCTGGTTCCTAATAAAAAGCCTTTAAATTAAATGGT NM_031212RefSeq chr10
- 99610517 99620464 SLC25A28 81894 "solute carrier family 25 (mitochondrial iron transporter),
member 28" GO:0005743|GO:0044281|GO:0016021|GO:0055072|GO:0006811 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139561_PI430048170 0.1324007637732074.3767249316841 3.57572720722813
1.36473863613108 1.51637409464371 P A A 0.5010805393892910.402278678211941
0.29800204308158 A A A LNCV6_139561_PI430048170 mRNA

AATATGAATAGAAAGAATACCCCGTACCAACAAGGAACACCTTGTGCCGGTTGCCCTGAT NM_003296RefSeq chr6 - 49692357 49713590 CRISP2 7180 "cysteine-rich secretory protein 2, transcript variant 1" GO:0016337|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_144741_PI430048170 0.0951080257008825 0.8649430731694717.79409230678994 7.75436888476897 7.81524142115674 P P P 7.85336133552888 8.03942402699925 8.08900107242307 P P P LNCV6_144741_PI430048170 mRNA
GCTGCTTCTGAGAGGCAATGTGAAAGAGGGAGTATTACTTTTATGTACAAAGTTATTTAT NM_015541RefSeq chr3 - 66378796 66500421 LRIG1 26018 leucine-rich repeats and immunoglobulin-like domains 1 GO:0060384|GO:0007605|GO:0032474|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_132993_PI430048170 0.0127726000891008 0.5303724053499585.62139125079596 5.12003212632158 5.59175754684045 P P P 6.11631796649804 6.41757145726614 6.56161577174167 P P P LNCV6_132993_PI430048170 mRNA
GGATCTGTATGTGTTCTATTCAGCACAAGGAAATAAAATTTTAGTTGAGGATTCAGCACT NM_006469RefSeq chr1 - 185296387 185317329 IVNS1ABP 10625 influenza virus NS1A binding protein GO:0008380|GO:0005667|GO:0005737|GO:0016032|GO:0005681|GO:0005654|GO:2001243|GO:0015629|GO:0009615|GO:0006383 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_130024_PI430048170 0.00805417271995359 1.56004529251809 7.78731959718152 7.86133932968863 7.64975615328789 P P P 7.14537448459627 7.11189968754776 7.12410890149589 P P P LNCV6_130024_PI430048170 mRNA
GTTGTTAAAAGTATACCCTGGACCACCCATCTGACCATCTCCTTAAGGTTTCACCCAAAG NM_019034RefSeq chr12 - 121777753 121793688 RHOF 54509 ras homolog family member F (in filopodia) GO:0051056|GO:0005886|GO:0007264|GO:0008152|GO:0003924|GO:0007015|GO:0005856|GO:0005525|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_132634_PI430048170 0.1823848561323270.8211600302705835.72683276070083 5.67482585531057 6.14611318653399 P P P 6.02819701205523 6.07850274146793 6.3238793422729 P P P LNCV6_132634_PI430048170 mRNA
AATCCACCACTTCTCTGTGAAACACTCTACCTTGTTTTTGGTTTGATTCTACTGATGTCA NM_014569RefSeq chr7 + 99504949 99533822 ZKSCAN5 23660 "zinc finger with KRAB and SCAN domains 5, transcript variant 1" GO:0005515|GO:0006355|GO:0003700|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_138107_PI430048170 0.18622039326099 0.88221143732445 10.3728786601149 10.3185155070715 10.4604552137 P P P 10.4331373328668 10.5082719915483 10.7385958761251 P P P LNCV6_138107_PI430048170 mRNA
CATCTGACCCTACTTGAACACTCCTGAACAGTCATGTTTTTTAAAATCTTCCTTTATATC NM_001521RefSeq chr2 - 27325848 27357034 GTF3C2 2976 "general transcription factor IIIC, polypeptide 2, beta 110kDa, transcript variant 1" GO:0042797|GO:0010467|GO:0000127|GO:0005654|GO:0042791|GO:0006383|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_2531_PI430048170 0.4934590510322671.74410731953018 1.45435209481228 2.71650033126701 0.406422563444482A A A 0.7560290948966240.4857967279740431.58999544986414 A A A LNCV6_2531_PI430048170 mRNA
TGTGTTGTGTGACTTGTTTTAGCAGTTAATGATATGTGGCCTTGTGCTTACTTAACCATCNM_001286401 RefSeq chr6 - 37212177 37258155 TMEM217 221468 "transmembrane protein 217, transcript variant 3" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_141816_PI430048170 0.5119745765973230.9468654181759241 5.0006265228572 15.041235123712 15.1677581322621 P P P 14.9886198989383 15.1508320135442 15.2954972797084 P P P LNCV6_141816_PI430048170 mRNA
TGAAGATGTGTGGGCACATGTTATGGCAGATTGAAAAGGATCTCATTCCATGGGAAAAAA NM_006886RefSeq chr20 - 59028677 59032367 ATP5E 514 "ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon

subunit"
GO:0022904|GO:0046961|GO:0046933|GO:0042776|GO:0005759|GO:0022857|GO:0044281|GO:0000275|GO:0016
887|GO:0044237|GO:0005753 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145564_PI430048170 0.0404083621397291 0.6176851682631549.48751632881068
9.42604634182034 9.84490117006581 P P P 9.98695824203311 10.2285320666483
10.5981350261627 P P P LNCV6_145564_PI430048170 mRNA
GCTTGCCAAAGCAGATTTTCCTAAGGCCACTGTTTTAAAAGATCATAGTTGCAAAATATA NM_002553RefSeq chr7
- 104126340 104208047 ORC5 5001 "origin recognition complex, subunit 5, transcript variant 1"
GO:0005515|GO:0000808|GO:0005634|GO:0003688|GO:0005524|GO:0006260|GO:0003674|GO:0000082|GO:0005
737|GO:0000166|GO:0006270|GO:0005654|GO:0005664|GO:0000278 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_137252_PI430048170 0.5647274194900531.04517041403809 9.20519902823465
9.16512503193861 9.10405166619528 P P P 8.89074843861633 9.15044933109634
9.22302575584623 P P P LNCV6_137252_PI430048170 mRNA
ACTAAGATGGGTTTATAACTGGAACCTCCAATGACCAGATGTATATAGAGATTTACAAAG NM_004366RefSeq chr3
- 184346184 184361651 CLCN2 1181 "chloride channel, voltage-sensitive 2, transcript variant 1"
GO:0044070|GO:0034220|GO:0060041|GO:0005886|GO:0005247|GO:0034707|GO:0006810|GO:0034765|GO:0060
689|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111083_PI430048170 0.9806096952001570.9996201548283170.3615104850421
0.3598179999760270.3834316923866 A A A 0.3839978467277340.339194407312071
0.382881727608385A A A LNCV6_111083_PI430048170 mRNA
GTACATCACATTTACTGTGACACTATCCCATTGTCTAAGATTTCTTGTACTGATTCTTCT NM_001005515 RefSeq chr3
+ 98168699 98169641 OR5H15 NA "olfactory receptor, family 5, subfamily H, member 15" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126988_PI430048170 0.3969677509699520.8041597548230044.38999889020101 4.8931147825582
4.57860476197386 P P P 4.53773495986232 4.78963475505926 5.38722822405049 P P P
LNCV6_126988_PI430048170 mRNA
CTCGAGTGGAAGAACTCATTGAAATAAAAACAAAGTCTACCTCTGAAGAAAATATTGGGA NM_053274RefSeq chr1
- 92246397 92299009 GLMN 11146 "glomulin, FKBP associated protein"
GO:0005515|GO:0031461|GO:0001843|GO:0032434|GO:0050715|GO:0042130|GO:0042692|GO:0005622|GO:0045
086|GO:0031463|GO:0031462|GO:0040029|GO:0055105|GO:0031397|GO:0031464|GO:0005171|GO:0001570|GO:0
031625|GO:0042327. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143454_PI430048170 0.2603256297505680.8595776267037920.462970010315611
0.4828657467131130.304954733720273A A A 0.8926376392995850.511944473341624
0.46887000298206 A A A LNCV6_143454_PI430048170 mRNA
GTGTCCTATATCATATTTATTGTTCAACAAAACACTGCTCCACGGCTTCAATTCAGTTTA NM_001126334 RefSeq
chr9 - 65282100 65285209 FOXD4L5 NA forkhead box D4-like 5 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132265_PI430048170 0.3376143119199220.7486973501187371.24446220303239
1.45627215689798 0.339818294117753A A A 1.83137633103437 1.04624337221008
1.53409473022454 A A A LNCV6_132265_PI430048170 mRNA
GCATCTCTGGTGTATACTGATTGAGAAAATAATTAAACTGAAGTTAGGGGAGGGGAAAAA NM_000860RefSeq chr4
- 174490176 174522898 HPGD 3248 "hydroxyprostaglandin dehydrogenase 15-(NAD), transcript variant
1"
GO:0019369|GO:0019371|GO:0007565|GO:0006693|GO:0007567|GO:0019372|GO:0070403|GO:0044281|GO:0045
786|GO:0003824|GO:0004957|GO:0042803|GO:0005829|GO:0016323|GO:0051287|GO:0070493|GO:0007179|GO:2
001300|GO:0097070|GO:0030728|GO:0070062|GO:0055114|GO:0016404 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_137239_PI430048170 0.0283866076361814 0.4137229487180484.24367783885464

3.91593019585306 4.17419346626735 P P P 4.84568716398315 5.49508047941904
5.70196456202766 P P P LNCV6_137239_PI430048170 mRNA
GCTTATCTCAAACAGATTACCCATCTGCAGAACTAAGGAAAGCAATTTATGTATGAAAGA NM_152903 RefSeq chr13
- 41127572 41132800 KBTBD6 89890 kelch repeat and BTB (POZ) domain containing 6
GO:0005515|GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141892_PI430048170 0.273542341833147 1.25483301301376 4.50359382831968
4.67723403461779 3.99704380664105 P P P 4.30386109857471 3.97324634660041
3.97580792920153 P P P LNCV6_141892_PI430048170 mRNA
AATACCTTTTTCTATGAAAAAAGACCCAGCGCCGTGTGCAATAAAGGTTATGTTTCTAAA NM_020693 RefSeq chr11
- 117427771 117797261 DSCAML1 57453 Down syndrome cell adhesion molecule like 1
GO:0005886|GO:0009986|GO:0001709|GO:0048704|GO:0007409|GO:0009953|GO:0007417|GO:0005615|GO:0042
803|GO:0070593|GO:0007162|GO:0007420|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142324_PI430048170 0.425196955594141 0.958186107429958 0.495128034500755
0.520491982339952 0.407488719759988 A A A 0.511673473328646 0.449793067577254
0.642195403956338 A A A LNCV6_142324_PI430048170 mRNA
ACAGAAGTTTCTGCTGACGTCTTGATGTCCTACCCAGGCAATGATATGGTCATCATTGTG NM_001080442 RefSeq
chr16 - 84009666 84042157 SLC38A8 NA "solute carrier family 38, member 8" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131965_PI430048170 0.628895084170611 1.04984169133086 11.4683693173907
11.3151706061239 11.2419123633745 P P P 11.4657439249602 11.3043272670377 11.019341570923
P P P LNCV6_131965_PI430048170 mRNA
TCCCTCTCGGAATGTTGGACAAAGGGAATAAAATTGGGGATATGTCTACTTCCCAAAAAA NM_001042631 RefSeq
chr19 + 35995187 35996318 SDHAF1 644096 succinate dehydrogenase complex assembly factor 1
GO:0034553|GO:0005739|GO:0016226|GO:0005759 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140195_PI430048170 0.296165934587883 1.14818295042559 6.47167556659924
6.62034591679877 6.90823518177775 P P P 6.56459380466626 6.28274802520173
6.57110095174692 P P P LNCV6_140195_PI430048170 mRNA
GTACTTCTGCTGTGAGATTCCCTAGTGTCAAAATTAAATCAATAAAACTGAGCATTTGTC NM_000282 RefSeq chr13
+ 100089014 100530437 PCCA 5095 "propionyl CoA carboxylase, alpha polypeptide, transcript variant 1"
GO:0006635|GO:0004658|GO:0006768|GO:0006767|GO:0044281|GO:0005524|GO:0046872|GO:0005829|GO:0006
766|GO:0005759|GO:0009374|GO:0004075|GO:0019626|GO:0019899|GO:0044255 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_102799_PI430048170 0.196655517591743 0.674884654496866 1.64633027045484
1.65883695304515 2.69670685810029 A A A 2.5123809680627 2.87136582447464
2.56079409676044 A P P LNCV6_102799_PI430048170 mRNA
ACTTCAGGTTACAAGGCTCTGGTACTTGACCATGATGACTCCATGAGAAAACAGCAGAAC NM_024805 RefSeq chr18
+ 80034345 80050652 RBFA 79863 "ribosome binding factor A (putative), transcript variant 1"
GO:0005739|GO:0008150|GO:0003674|GO:0006364|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129097_PI430048170 0.987839280455648 0.989779304672897 12.4893841684641
12.3462704471593 12.4430761513627 P P P 12.103124293708 12.4965331289929
12.6702617405273 P P P LNCV6_129097_PI430048170 mRNA
TAGGGTTTGGAGCTATTCAAGAGGAAATGTCACAGAAGCAGCTAAACCAAGGACTGAGCA NM_021873 RefSeq
chr20 + 3795738 3806121 CDC25B 994 "cell division cycle 25B, transcript variant 1"
GO:0005515|GO:0008284|GO:0005813|GO:0019901|GO:0032467|GO:0001556|GO:0035335|GO:0005829|GO:0045
931|GO:0000922|GO:0005737|GO:0007067|GO:0007144|GO:0000086|GO:0045860|GO:0005654|GO:0006468|GO:0
000278|GO:0004725|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145097_PI430048170 0.284111386013665 1.25758200664232 4.41587176692897

5.14573097791712 4.75421693843105 P P P 4.29081338560156 4.4926108999304
4.61462642056146 P P P LNCV6_145097_PI430048170 mRNA
TGATGATTCTGTCTCAGACCCAACAACCTGGCCTTCCCAGGAGGTCTCCATGTGTCACCC NM_001080515 RefSeq
chr9 - 133578414 133580246 FAM163B 642968 "family with sequence similarity 163, member B"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100667_PI430048170 0.6729038819342221.04920945421623 11.6839498480556
11.8981545538253 12.0896668029442 P P P 11.7277849119876 11.7874436881846
11.9662662446297 P P P LNCV6_100667_PI430048170 mRNA
GAACATCTGAAGACATCAGACTGCACTGCGTATACATGTTGAATTCTTCATTTTTGCCAT NM_031420RefSeq chr1
- 151759642 151763916 MRPL9 65005 "mitochondrial ribosomal protein L9, transcript variant 1"
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005761|GO:0005
743|GO:0006412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132016_PI430048170 0.0467023769505338 0.2918967826276181.90335409831845
2.81930153706598 3.52949371118044 A A P 4.46961685643238 4.59254892828476
4.91998087303921 P P P LNCV6_132016_PI430048170 mRNA
CTGAAGACAAATCAGAAGATAAATTTGCTATCTTGACAATGGACTTAGTACCCATGCTTT NM_024629RefSeq chr4
- 184694064 184734132 CENPU 79682 "centromere protein U, transcript variant 1"
GO:0034080|GO:0006355|GO:0005815|GO:0006334|GO:0000777|GO:0016032|GO:0005654|GO:0005634|GO:0000
278|GO:0043009|GO:0006351|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144991_PI430048170 0.46322506327024 1.05746777510035 8.69613075224811
8.53165931501906 8.69088881376735 P P P 8.60433632978275 8.67405629170343
8.38940820524771 P P P LNCV6_144991_PI430048170 mRNA
TCTACAGCCTAATTTATTGGATTCCCTATTCGTAGCCATCTCCGTGGCCAATGTGACTAC NM_000033RefSeq chrX
+ 153724867 153744762 ABCD1 215 "ATP-binding cassette, sub-family D (ALD), member 1"
GO:0005515|GO:0005215|GO:0048471|GO:0042626|GO:0044281|GO:0042803|GO:0005829|GO:0042802|GO:0015
910|GO:0005739|GO:0005737|GO:0007031|GO:0015919|GO:0005779|GO:0016887|GO:0044255|GO:0005778|GO:0
042760|GO:0005777|GO:0006635|GO:0005325|GO:0036109|GO:0055085|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126946_PI430048170 0.0039302824431387 0.2035991963672640.385349489255255
0.3800871843821721.24724569160188 A A A 3.16852354422863 2.49888321664448
3.29621145523744 P P P LNCV6_126946_PI430048170 mRNA
CTCTGAATACAATACTGCTGACCACATTTGGCTACTTCAGCTTAAATGTATGTTAATTGA NM_024794RefSeq chr19
- 15226918 15232420 EPHX3 79852 "epoxide hydrolase 3, transcript variant 1"
GO:0008150|GO:0003674|GO:0016787|GO:0008152|GO:0005576|GO:0005575 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129908_PI430048170 0.00070643915169156 2.74155225504916 2.34947497599974
2.38891368842446 2.03228431362029 A A A 0.6328468838612220.855686779257662
0.926915365636789A A A LNCV6_129908_PI430048170 mRNA
TGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGAAGGCAGTCATCCT NM_001002918
RefSeq chr11 - 124319261 124320197 OR8D2 283160 "olfactory receptor, family 8, subfamily D, member
2 (gene/pseudogene)" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_139560_PI430048170 0.00437662572266812 0.4010888275972826.44316137609471
5.92961092570732 6.27264598847721 P P P 7.22271699120791 7.57261774832655
7.79400834492911 P P P LNCV6_139560_PI430048170 mRNA
CTCTTTGCCATGGGTCTTATTTTCACCCTCTTTTCTGTAAGAAAAAAGAACAATGTCTTA NM_001130963 RefSeq
chr12 - 57055642 57078791 TMEM194A 23306 "transmembrane protein 194A, transcript variant 1"
GO:0008150|GO:0003674|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117058_PI430048170 0.0508807885175437 1.22490329684888 10.2002301772017

10.2720909577018 10.2098049593907 P P P 10.0740295090209 9.81266280276349
9.90624304090296 P P P LNCV6_117058_PI430048170 mRNA
CGTGTATGGTGTATTCCAGTTTAAAGTGGATTACAACCGGCTAGGCTACACACACCTGTA NM_005216RefSeq chr1
- 20651766 20661544 DDOST 1650 dolichyl-diphosphooligosaccharide--protein glycosyltransferase
subunit (non-catalytic)
GO:0004576|GO:0005515|GO:0010467|GO:0005783|GO:0006614|GO:0006412|GO:0043231|GO:0043234|GO:0042
110|GO:0016020|GO:0045087|GO:0004579|GO:0005789|GO:0006486|GO:0006487|GO:0016021|GO:0034097|GO:0
008250|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145665_PI430048170 0.6692759197888131.16007624812844 0.368003177999232
1.26779774653237 0.339913494318149A A A 0.7534681897365230.36586514269286
0.383709452763253A A A LNCV6_145665_PI430048170 mRNA
AAAGAACAATCGTGTGCAGGTGGTCACACTTCCTTTTTCTGTACCACTTTTGCAACAAAA NM_002192RefSeq chr7
- 41689002 41703108 INHBA 3624 "inhibin, beta A"
GO:0005515|GO:0042541|GO:0030308|GO:0042701|GO:0035987|GO:0030154|GO:0042802|GO:0071397|GO:0045
077|GO:0001942|GO:0046982|GO:0046882|GO:0006952|GO:0046881|GO:0046880|GO:0032924|GO:0045786|GO:0
005125|GO:0005160|GO:0045650|GO:0032270|GO:0005179|GO:0045648|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_76221_PI430048170 0.2710732770014070.6269510709397130.5539130619431990.679840826689847
0.661864804106864A A A 1.5375348810766 0.4428201152730211.65902906391676 A A A
LNCV6_76221_PI430048170 mRNA
TCGCACCTTTGGGTATATTAAACAGCTGGTATCATAACAAAGAATCCAAATGAACCTTCA NM_000337RefSeq chr5
+ 156326756 156767787 SGCD 6444 "sarcoglycan, delta (35kDa dystrophin-associated glycoprotein),
transcript variant 1"
GO:0048738|GO:0042383|GO:0060047|GO:0005737|GO:0007517|GO:0016010|GO:0005886|GO:0016012|GO:0061
024|GO:0055001|GO:0016021|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138503_PI430048170 0.18191380011044 1.28422747072829 4.23274222583224
3.80528574777556 3.76182760063454 P P P 3.35229108447908 3.89984573496003
3.45273695630298 P P P LNCV6_138503_PI430048170 mRNA
TAACTTGGTGAAGAGCTGCCTGCCACTCTGAACATCCACATGTGACAATAAACATCTCCT NM_198478RefSeq chr19
- 45149749 45160150 NKPD1 284353 "NTPase, KAP family P-loop domain containing 1" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62789_PI430048170 0.0793462791949238 0.6945236119839982.67882300051776
2.85553765511481 3.26748288829286 A A P 3.26856851086935 3.3910042934719
3.74186189820352 P P P LNCV6_62789_PI430048170 mRNA
ATTTATTTAAAGTTTTCCCTTACATACCTTGGGGGCCAGATGTGAATAACACAGTTTGTA NM_001288758 RefSeq
chr17 + 32142453 32225771 RHOT1 55288 "ras homolog family member T1, transcript variant 7"
GO:0005515|GO:0051056|GO:0019725|GO:0005886|GO:0007264|GO:0005509|GO:0003924|GO:0005525|GO:0005
829|GO:0003674|GO:0016020|GO:0047497|GO:0008152|GO:0031307 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_98461_PI430048170 0.0144129775168475 0.5679747825014626.13609285947568
5.64863023908897 5.76649547169716 P P P 6.40957505187945 6.81593112768356 6.78549791438 P
P P LNCV6_98461_PI430048170 mRNA
ACTAGAAGGGAGCACAAGCTTTGCTGAACTGCTCTTCAAATTTAAGCAGCTAAAAATGCC NM_022662RefSeq chr2
- 111767636 111884164 ANAPC1 64682 anaphase promoting complex subunit 1
GO:0007094|GO:0007067|GO:0070979|GO:0005680|GO:0051437|GO:0005654|GO:0051436|GO:0000278|GO:0031
145|GO:0051439|GO:0051301|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116816_PI430048170 0.0455880618305136 0.70153948916204 8.25781815110213
8.19422341821187 8.26680067091804 P P P 8.60137215092444 8.6499797390704
8.97371702298105 P P P LNCV6_116816_PI430048170 mRNA

GGTGTTTACGTGATCCACACTTGAAATACTAGATCAGTAGACATTCACTAATATACCAAA NM_004578RefSeq chr1 + 229271061 229305893 RAB4A 5867 "RAB4A, member RAS oncogene family, transcript variant 1" GO:0005515|GO:0048471|GO:0003924|GO:0005525|GO:0006886|GO:0031982|GO:0006184|GO:0016020|GO:0019882|GO:0030100|GO:0032593|GO:0008565|GO:0061024|GO:0032482|GO:0019003|GO:0070062|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130388_PI430048170 0.0283849459054218 0.5610127461731565.51140736696391 5.10388309019835 4.98486903718121 P P P 6.09354214799545 5.97963409826362 6.08022370243483 P P P LNCV6_130388_PI430048170 mRNA
GACTAAGGCTGGTATTCTAGAACACGCCTTTCACTGATTGTGTTAAATAAAAGAGAAAGA NM_173520RefSeq chr9 + 135343248 135346558 C9orf62 157927 chromosome 9 open reading frame 62 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_12361_PI430048170 0.3892375635732660.7012999754426190.2993154522683740.332571414102376 0.351175116757796A A A 1.48496139707636 0.3740603377911850.349480477214112A A A LNCV6_12361_PI430048170 mRNA
CCAAAGACGAGGTTTCATAATTGAGCTCCATTTCTTCTTATTCCCTTTCTCAGTGATATT NM_001287444 RefSeq chr2 + 3703591 3847410 DCDC2C NA doublecortin domain containing 2C NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128784_PI430048170 0.00674366227968432 0.3996481476789275.65198987952023 5.29767254043836 4.99249435007176 P P P 6.7348094991293 6.80862509369832 6.41423156284241 P P P LNCV6_128784_PI430048170 mRNA
AGGCTCATGTCTTTACACCTTCACTCAGCCACGCCAACCAGAGACTGGGTTCCAATCTCA NM_018484RefSeq chr11 + 64555600 64572875 SLC22A11 55867 "solute carrier family 22 (organic anion/urate transporter), member 11" GO:0005515|GO:0016324|GO:0005886|GO:0005452|GO:0015347|GO:0005887|GO:0015711|GO:0008514|GO:0046415|GO:0055085|GO:0009897|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135789_PI430048170 0.3042804761056771.80506739496422 0.783900814520163 0.6191880781984922.18569050463797 A A A 0.5289423213263310.715197693545799 0.311035093694169A A A LNCV6_135789_PI430048170 mRNA
CATGTGCAACAAATACCTCCATTAAATGGTCTAAAATGTAAATTGAATTCCCTGGCTCTC NM_005559RefSeq chr18 - 6941743 7117814 LAMA1 284217 "laminin, alpha 1" GO:0030334|GO:0005515|GO:0002011|GO:0005102|GO:0005578|GO:0005606|GO:0005576|GO:0005608|GO:0030155|GO:0005615|GO:0045198|GO:0005604|GO:0045995|GO:0031012|GO:0061304|GO:0060441|GO:0043208|GO:0030198|GO:0007411|GO:0005911|GO:0007155|GO:0007166|GO:0060445|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138897_PI430048170 0.7491174909037181.00957823305895 0.32249961591597 0.3257021879245030.425199854145865A A A 0.3569287383501250.313011363341084 0.36405689186854 A A A LNCV6_138897_PI430048170 mRNA
CCTGCCAGCTCAGGATATTATGTTTCTTTTTTCATTTTTGCCAGTCTGTTAAGTAAAATG NM_003687RefSeq chr5 + 132257657 132273454 PDLIM4 8572 "PDZ and LIM domain 4, transcript variant 1" GO:0005515|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144825_PI430048170 0.1158938611871661.68515006724515 3.52296302967736 3.39756411264247 3.44430601664903 P P P 2.99825292091216 2.89795181833035 2.03232034656883 P P A LNCV6_144825_PI430048170 mRNA
TTCTTCTATATTGGCTGGTAAATTGCCATGGCCCTGAGCCACTGAGTATGTTCATTGCCA NM_080680RefSeq chr6_GL000252v2_alt - 4406190 4435967 COL11A2 1302 "collagen, type XI, alpha 2, transcript variant 1" GO:0005515|GO:0005592|GO:0051216|GO:0007605|GO:0005576|GO:0046872|GO:0001501|GO:0022617|GO:0030020|GO:0030198|GO:0030199|GO:0030574|GO:0060021|GO:0005788|GO:0030674|GO:0060023 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_141595_PI430048170 0.00140111751012902 0.1985387002193820.714925832977562
0.46708606461585 0.504068461284106A A A 2.67736725454751 2.75267520616538
3.20735267670223 P P P LNCV6_141595_PI430048170 mRNA
GAATGCCTGTAAATGTAGGCTGAACACTTCTAACATGAGAAAACCTAAGTATCCTAAAAA NM_001282531 RefSeq
chr20 - 50888917 50930990 ADNP 23394 "activity-dependent neuroprotector homeobox, transcript variant 3"
GO:0005515|GO:0043524|GO:0006355|GO:0003682|GO:0005634|GO:0005615|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139746_PI430048170 0.0454195426391211 0.5342737341121344.84126895418203
4.02386329737624 4.60296079631007 P P P 5.04599243925914 5.43503951777591
5.73570137481337 P P P LNCV6_139746_PI430048170 mRNA
TCTGAAAAAATATCAGCCACCAAAATAGTTATGTTGGCACTGTGTTCACACGCATGGTCC NM_015282RefSeq chr2
- 121337775 121649476 CLASP1 23332 "cytoplasmic linker associated protein 1, transcript variant 1"
GO:0005828|GO:0005515|GO:0008017|GO:0005881|GO:0034453|GO:0030981|GO:0001578|GO:0051294|GO:0005829|GO:0051010|GO:0007411|GO:0000086|GO:0031023|GO:0005876|GO:0005938|GO:0070062|GO:0010458|GO:0005813|GO:0005794|GO:0006996|GO:0031111|GO:0000226|GO:0007163|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128594_PI430048170 0.0286515377154968 0.4603108441372443.63181332642457
3.52831478221844 4.22685207946635 P P P 5.00893120868938 4.8471227593151
4.98604543655433 P P P LNCV6_128594_PI430048170 mRNA
CTTACCTTCTATAAAAATGAGGATTACTGTTGGTGAGGGAATAAGGAATGTAAGTAAAGG NM_001166496 RefSeq
chr1 - 112911847 112956063 SLC16A1 6566 "solute carrier family 16 (monocarboxylate transporter), member 1, transcript variant 2"
GO:0006629|GO:0005886|GO:0015129|GO:0044281|GO:0050900|GO:0032094|GO:0042803|GO:0015130|GO:0005739|GO:0015718|GO:0006090|GO:0051780|GO:0097159|GO:0044237|GO:0070062|GO:0015293|GO:0005813|GO:0008028|GO:0042593|GO:0055085|GO:0051297|GO:0015728|GO:0071407|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145326_PI430048170 0.9370374772603950.998215644442737 0.386148754734357
0.3590335365649880.252565609005776A A A 0.3213172824089740.348396398900475
0.339060952371122A A A LNCV6_145326_PI430048170 mRNA
GCTGGACTTGGTAAAGATACAAATGGGCTTATAATGTTGGTCAGGTGAGACATGTTGCAT NM_001282456 RefSeq
chr11 + 76381312 76408131 LOC100506127 NA putative uncharacterized protein FLJ37770-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127200_PI430048170 0.2259957190587861.07042195865104 0.505872980595492
0.4624871564277220.555840199778616A A A 0.3097005197895590.401048065241134
0.513210432946471A A A LNCV6_127200_PI430048170 mRNA
GACCTTGGAGTGCAGAGAGGAGAACTGAAAATAAAACTGGAAAGATGTTCCAACTGCAAA NM_152670RefSeq
chr2 + 88524650 88529585 TEX37 200523 testis expressed 37 GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136749_PI430048170 0.00718502120642503 0.6984638690055141 1.548025140401
11.5024705879522 11.6473359480799 P P P 11.9368759763136 12.1345202827299
12.1725660103056 P P P LNCV6_136749_PI430048170 mRNA
TTAGTTTCGTTTGGCAGTCTGGCCCTGTTGACTTTGATTTGCAGACCAATTCTCCCTTGA NM_001013642 RefSeq
chr1 + 26993703 27000886 TRNP1 388610 TMF1-regulated nuclear protein 1
GO:0061351|GO:0007049|GO:0006355|GO:0005719|GO:0042127|GO:0021696|GO:0051726|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139032_PI430048170 0.0052374943160011 1.36661202590149 12.2452748458275
12.4321333225242 12.2643611286636 P P P 11.8611266571256 11.9330774161239
11.8001004949783 P P P LNCV6_139032_PI430048170 mRNA

CCTGTAGGGGGTGCACCCCCCACCCTATGGACCAGTCAAATAAAAGCCTTCAGGCCCCTC NM_004146 RefSeq chr19 - 14566077 14572077 NDUFB7 4713 "NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa" GO:0022904|GO:0005739|GO:0005758|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0008137|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111670_PI430048170 0.1049459222721550.7120085858094966.05174976632112 5.8541755155577 6.21940456091748 P P P 6.28697051278435 6.38272229219386 6.87697245932276 P P P LNCV6_111670_PI430048170 mRNA
CACCAAACCTTTCCTTACCAGCTCTGGTCTATATTGCTCCCATGCATTTAATATATTATT NM_001431 RefSeq chr6 - 130839347 131063322 EPB41L2 2037 "erythrocyte membrane protein band 4.1-like 2, transcript variant 1" GO:0008091|GO:0030054|GO:0005886|GO:0003779|GO:0005634|GO:0008180|GO:0005198|GO:0030866|GO:0005654|GO:0042731|GO:0005925|GO:0019898|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60621_PI430048170 0.3265019993666111.76450425368655 1.93419131601206 0.394432008253341 0.510590820512994 A A A 0.27033451677973 0.3767182379077820.27938900074398 A A A LNCV6_60621_PI430048170 mRNA
TTCAAAGGGAAGAGTCCAGATGAAGTCCTGGAGAACATTTATGGACTCATGGAGGGCAAA NM_173846 RefSeq chr14 + 21030185 21032173 TPPP2 122664 tubulin polymerization-promoting protein family member 2 GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141447_PI430048170 0.0211525687541349 0.82909466955226414.4352130529517 14.6053296153706 14.54240971327 P P P 14.703028021652 14.8014593007758 14.8887644909552 P P P LNCV6_141447_PI430048170 mRNA
GGAAGAGAAATTTTTATTTTTGAACCCCTGTGTCCCTTTTGCATAAGATTAAAGGAAGGA NM_000597 RefSeq chr2 + 216633403 216664435 IGFBP2 3485 "insulin-like growth factor binding protein 2, 36kDa" GO:0005515|GO:0007565|GO:0007584|GO:0042493|GO:0007568|GO:0031994|GO:0031995|GO:0051384|GO:0005576|GO:0031410|GO:0001558|GO:0005615|GO:0032870|GO:0009612|GO:0042104|GO:0007165|GO:0016324|GO:0010226|GO:0043567|GO:0032526|GO:0044267|GO:0032355|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82743_PI430048170 0.00726215216469068 1.66435289441071 9.33834247491392 9.41582192752259 9.29097045823728 P P P 8.5088808764739 8.78829821266452 8.52865459595509 P P P LNCV6_82743_PI430048170 mRNA
AGTTTCCCTGAAGGAACATTCCTTAGTCTCAAGGGCTAGCATCCCTGAGGAGCCAGGCCG NM_002746 RefSeq chr16 - 30114104 30123309 MAPK3 5595 "mitogen-activated protein kinase 3, transcript variant 1" GO:0005515|GO:0010467|GO:0051216|GO:0019221|GO:0006361|GO:0006360|GO:0051403|GO:0034605|GO:0002756|GO:0007173|GO:0000165|GO:0007411|GO:0002755|GO:0009887|GO:0005856|GO:0038083|GO:0031663|GO:0004707|GO:0038124|GO:0005794|GO:0038123|GO:0019902|GO:0034134|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141419_PI430048170 0.2306924779147261.14380642565712 6.73697526469899 6.57395503056521 6.90388548007819 P P P 6.36975250489359 6.54838370435608 6.71356442776229 P P P LNCV6_141419_PI430048170 mRNA
CTGTGCATGAAAAGCTGAAGAAATGAATTGTTTCTGAGAACTATAGTAATATGGCTTGGA NM_017421 RefSeq chr6 - 99369471 99394206 COQ3 51805 coenzyme Q3 methyltransferase GO:0005739|GO:0006744|GO:0005759|GO:0008689|GO:0004395|GO:0008425|GO:0044281|GO:0032259|GO:0008171|GO:0006071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56394_PI430048170 0.0586645078769611 0.6258937258139183.17962038946085 3.03374633456649 2.6961664586442 P P A 3.34078720083113 3.54760827587229 4.0081099053383 P P P LNCV6_56394_PI430048170 mRNA
CCATGCACACTCTTAGGGAAAAATATGGTATTAAATCCCATTGTCATTGTACTAACAAAC NM_032776 RefSeq chr10 - 63167220 63466001 JMJD1C 221037 "jumonji domain containing 1C, transcript variant 1" GO:0046966|GO:0005622|GO:0005515|GO:0006355|GO:0007596|GO:0051213|GO:0005654|GO:0046872|GO:0006

351|GO:0055114|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131801_PI430048170 0.0304428486699539 0.7776186584619175.14046879202612
5.20769259354518 5.19142407520827 P P P 5.42559223498604 5.51932603350719
5.67321186780043 P P P LNCV6_131801_PI430048170 mRNA
GGAGCTGGGCTGGCTATGGCTTTACCACAACAAGTAGGTTTGCTTAAGAAATTACTAAAC NM_001113482 RefSeq
chr1 + 37794101 37801606 MANEAL 149175 "mannosidase, endo-alpha-like, transcript variant 3"
GO:0016787|GO:0000139|GO:0008152|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113214_PI430048170 0.2842432412179130.7617894064919664.67684293073381
4.20412754106548 3.87462829741665 P P P 4.9597501433966 4.77003076296042
4.21897395330008 P P P LNCV6_113214_PI430048170 mRNA
TAATGGCCTCAGCCCTATCTGGGCTCCAACACAGGAGAAGGTGACATTTGAAATTTATGA NM_002661 RefSeq chr16
+ 81779257 81962693 PLCG2 5336 "phospholipase C, gamma 2 (phosphatidylinositol-specific)"
GO:0050853|GO:0010468|GO:0005515|GO:0050852|GO:0019722|GO:0005886|GO:0043647|GO:0044281|GO:0005
829|GO:0004629|GO:0043069|GO:0032237|GO:0032959|GO:0030183|GO:0032496|GO:0004871|GO:0016055|GO:0
070062|GO:0051209|GO:0006661|GO:0030168|GO:0007596|GO:0004435|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134255_PI430048170 0.000231745494621415 0.7016012770422858.34565251299352
8.2991935150309 8.24241672697572 P P P 8.77478623614486 8.78756083085475
8.85915529784529 P P P LNCV6_134255_PI430048170 mRNA
CACATCTTCCTCTAACAAATCTCTCAGTATGCGATTGGTCTCAAGCTAAAACAAAAATAA NM_001281723 RefSeq
chr3 + 15601351 15645821 BTD 686 "biotinidase, transcript variant 1"
GO:0047708|GO:0005730|GO:0006768|GO:0006767|GO:0045177|GO:0005576|GO:0044281|GO:0007417|GO:0005
615|GO:0008544|GO:0006766|GO:0005759|GO:0004075|GO:0043204|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127361_PI430048170 0.395274595610835 1.08272498199553 5.34787939930943
5.18279159854806 5.17495583401275 P P P 4.91821733764086 5.29045715068535
5.13561380431837 P P P LNCV6_127361_PI430048170 mRNA
AAAGAAAATCCTGGAGAGACACTTCACTGCTCCAAGGCTTTTGAGACACAAGGGAATCTC NM_153335 RefSeq chr17
- 63702831 63741970 STRADA 92335 "STE20-related kinase adaptor alpha, transcript variant 3"
GO:0005515|GO:0008286|GO:0071902|GO:0005634|GO:0030295|GO:0005524|GO:0005829|GO:0035556|GO:0032
147|GO:0005737|GO:0004672|GO:0004702|GO:0006611|GO:0005654|GO:0006468|GO:0007050|GO:0043539|GO:0
019900|GO:0000278. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139954_PI430048170 0.54727657468175 1.34335945027463 0.431903003450333
1.61131624884056 0.304900575287161 A A A 0.4122952167740720.484423977395263
0.554186559938195 A A A LNCV6_139954_PI430048170 mRNA
GAAATCTGTGTGAACACACCAAGAGAGCCGACTTGACTTTGAAGAATTGCTAAACCAGGA NM_002871 RefSeq chr1
- 202878281 202889257 RABIF 5877 RAB interacting factor
GO:0043547|GO:0005515|GO:0005085|GO:0007264|GO:0061025|GO:0008270|GO:0015031 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_124141_PI430048170 0.7693493875364591.01297372209855 0.274518216972824
0.3025976087354290.435667794290502 A A A 0.3483218718694360.309128368545316
0.304325426471501 A A A LNCV6_124141_PI430048170 mRNA
CATAAATTAACACCCTCATAAAGGTAAACCAAGAAGGTTATCCTCAATCATCTGGTATCA NM_001563 RefSeq chr6
- 75921113 76072678 IMPG1 3617 "interphotoreceptor matrix proteoglycan 1, transcript variant 1"
GO:0005578|GO:0007601|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114489_PI430048170 0.0009172246616844 2.14691527004592 4.46857071889215
4.58943073405973 4.73690121246348 P P P 3.52117610852238 3.32213106780081
3.63967773590898 P P P LNCV6_114489_PI430048170 mRNA
GCAAGAGACTTAAATGACTGATAAGAACCGTGAGAAACATGTTGCTTCCAGGCTTGATTT NM_000405 RefSeq chr5

+ 151253051 151270392 GM2A 2760 "GM2 ganglioside activator, transcript variant 1"
GO:0006665|GO:0009313|GO:0032428|GO:0051345|GO:0006687|GO:0019915|GO:0006689|GO:0044281|GO:0005
739|GO:0016004|GO:0045179|GO:0005889|GO:0006869|GO:0050885|GO:0007611|GO:0009898|GO:0005319|GO:0
070062|GO:0043202. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127387_PI430048170 0.5037760168156481.35891375906276 0.377297584102797
1.83100541711007 1.37516976629333 A A A 0.3271992368432331.37588371128283
0.707543196260884A A A LNCV6_127387_PI430048170 mRNA
CAGCTGGTGATTCTCCATCATGATAATGAACAGTTAATTGACAGAAAACCAAAGTTGTTT NM_152761RefSeq chrX
+ 23908005 23939507 CXorf58254158 "chromosome X open reading frame 58, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141439_PI430048170 0.1974456358200450.5335425187061250.392728280457706
0.4391959834082920.263825406991784A A A 0.3217455535629811.53258419269445
1.63662052202729 A A A LNCV6_141439_PI430048170 mRNA
GAATGCAGATGCCTGTGCCCAAATAATAATTCATATAGCATAAATTGGAGTTGTGTGTTA NM_018933RefSeq chr5
+ 141213918 141217421 PCDHB13 56123 protocadherin beta 13
GO:0016339|GO:0005886|GO:0005509|GO:0007268|GO:0016021|GO:0007416|GO:0007156 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129349_PI430048170 0.80606496316113 1.015842506154 6.12102158491392
6.14096518266632 5.93055072116797 P P P 5.96635886298956 6.07914066491132
6.08513911584983 P P P LNCV6_129349_PI430048170 mRNA
TAAAATGATACCTTTCATGTACAGAGCCCTCAATGGGGCCGATTTTCAGTTGTGTAAAAA NM_013324RefSeq chr3
- 50606453 50611831 CISH 1154 "cytokine inducible SH2-containing protein, transcript variant 1"
GO:0005515|GO:0016567|GO:0005886|GO:0046627|GO:0019221|GO:0060397|GO:0005575|GO:0001558|GO:0046
426|GO:0007205|GO:0005829|GO:0035556|GO:0003674|GO:0005737|GO:0004860|GO:0006469 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131979_PI430048170 0.7695616562814631.31753071384007 2.96184431470931
1.46155204542102 0.829680863557754A A A 2.25905931906172 1.55296573583134
0.70642578619889 A A A LNCV6_131979_PI430048170 mRNA
CCCTCCTTGCATCCGAATTTTTTCATCAAGCTTTGTTAACACTAATGATGATTCTTGAAANM_001284246 RefSeq chr14
+ 71586280 71741229 SIPA1L126037 "signal-induced proliferation-associated 1 like 1, transcript variant
3"
GO:0030054|GO:0048013|GO:0031532|GO:0014069|GO:0032861|GO:0005575|GO:0003674|GO:0008150|GO:0005
737|GO:0046875|GO:0043197|GO:0048167|GO:0045211|GO:0061001|GO:0005856|GO:0050770|GO:0032317|GO:0
005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135705_PI430048170 0.4581573615055662.09515617152078 0.274265140620737
2.49982110333563 0.338675743694371A A A 0.4234338494411570.35749602227265
0.331273011963335A A A LNCV6_135705_PI430048170 mRNA
CGTGTTTCTGTACACCCTTTCTATCGTGTCAAATGTTAATGAATCTGTGATCAATTGAAA NM_022150RefSeq chr7
- 25224571 25228486 NPVF 64111 neuropeptide VF precursor GO:0007218|GO:0005576|GO:0032277
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128681_PI430048170 0.9828800186308991.08498849460865 3.60298111947774
3.70952463188194 2.34565709866193 P P A 3.09482747047361 3.07587244309029
3.45492453573792 P P P LNCV6_128681_PI430048170 mRNA
GAAGTATCATCCCTACCCCCTAACTAATCTGTTATTAAAGCTACAAATTCTTCACACCAT NM_213653RefSeq chr1
- 146017467 146021822 HFE2 148738 "hemochromatosis type 2 (juvenile), transcript variant a"
GO:0005515|GO:0009986|GO:0005886|GO:0007411|GO:0045944|GO:0031225|GO:0030509|GO:0015026|GO:0055
072|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128375_PI430048170 0.9800263397104560.99007135785116 12.074944502282
12.1751758340332 12.0213748093212 P P P 12.2750208257555 12.1729864342729

11.8351334499288 P P P LNCV6_128375_PI430048170 mRNA
GTGGTGATGTTTTCGTTCTGTTTTATTTTTCTAACTCTGCTGACCATGAATAAAAGACCANM_020246RefSeq chr7 +
100852718 100867012 SLC12A9 56996 "solute carrier family 12, member 9, transcript variant 1"
GO:0006821|GO:0005886|GO:0015377|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_109885_PI430048170 0.0404186572971253 1.11323096586897 7.44779860901857
7.37391003707259 7.36273974053073 P P P 7.2774958647708 7.1583484732349
7.28244521077804 P P P LNCV6_109885_PI430048170 mRNA
AACCTTACACTACAAGGGCGAGACCCTGCCCCCTGTGGGCGTCAACAGAAATCGCATCAA NM_006821RefSeq chr14
+ 73569058 73575658 ACOT2 10965 "acyl-CoA thioesterase 2, transcript variant 1"
GO:0052689|GO:0047617|GO:0005739|GO:0006637|GO:0000038|GO:0001676|GO:0016290|GO:0005102|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143119_PI430048170 0.0157950344952636 0.945923186464339 0.356787168854092
0.35063638029665 0.32599800075637 A A A 0.450682785369182 0.424393450952144
0.398675432680714 A A A LNCV6_143119_PI430048170 mRNA
CATTGGAGCTCTTTTATTACAAGTCTGCTTGTTAATTTTAGAACTGTAAAACCGCTCTGA NM_001035RefSeq chr1
+ 237042401 237833988 RYR2 6262 ryanodine receptor 2 (cardiac)
GO:0005515|GO:0005516|GO:0005513|GO:0030018|GO:0060402|GO:0019722|GO:0035584|GO:0043621|GO:0060
048|GO:0042802|GO:0003143|GO:0034220|GO:0097050|GO:0015278|GO:0086029|GO:0086005|GO:0070062|GO:0
005262|GO:0051209|GO:0005509|GO:0071313|GO:0014808|GO:0035994|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127152_PI430048170 0.151075166566083 1.07032062018892 0.482490188734219
0.467410264968303 0.534373588019867 A A A 0.315583831593421 0.396196761867801
0.474830226529979 A A A LNCV6_127152_PI430048170 mRNA
ATAAAAGGGATGGTCTGTGGCTATAAAGAACAAGGAAAGGATTCTTGTCAAGGAGATTCT NM_182702RefSeq chr3
- 46830403 46834095 PRSS42 339906 "protease, serine, 42"
GO:0005737|GO:0004252|GO:0006508|GO:0005576|GO:0007283|GO:0046658|GO:0007281 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_61456_PI430048170 0.976669016308723 1.00581147913283 12.4143568487957 12.788566599788
12.4998722067285 P P P 12.5107405595382 12.7300552708726 12.4487053028473 P P P
LNCV6_61456_PI430048170 mRNA
ACACTTTCAAGTAAACCAGGTGGTGGAGACCCCATCCTTGGCTGCTTGCAGGGCCACTGT NM_001311RefSeq chr14
+ 105486919 105488787 CRIP1 1396 cysteine-rich protein 1 (intestinal)
GO:0010468|GO:0042277|GO:0010033|GO:0008630|GO:0008283|GO:0008301|GO:0060741|GO:0071493|GO:0010
043|GO:0007507|GO:0005737|GO:0006955|GO:0003680|GO:0008270|GO:0071236 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_72465_PI430048170 0.906729681650271 1.0088685302713 7.94144009906349 8.19788258771704
8.16437993676089 P P P 8.30467682783 7.91894510690157 8.02720612895828 P P P
LNCV6_72465_PI430048170 mRNA
TGCAGAAGCTACGAAGTAGAGTGCAGATCGGTGTGGTGGGCGGCTCTGACTACTGTAAGA NM_002676RefSeq
chr22 - 41576885 41589867 PMM1 5372 phosphomannomutase 1
GO:0004615|GO:0043025|GO:0019307|GO:0009298|GO:0006488|GO:0044267|GO:0046872|GO:0043687|GO:0018
279|GO:0006013|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129247_PI430048170 0.40855241829369 1.53209562765939 0.386717522277089
0.376770275630958 1.72853144715477 A A A 0.349373393202831 0.38722567317446
0.358331590557859 A A A LNCV6_129247_PI430048170 mRNA
CACAAACACCTGTATATGCGTGCATATACAACCAAGTGGGTAGACCTAGGTGTTCTCTCA NM_019854 RefSeq
chr12 + 3491197 3593972 PRMT8 56341 "protein arginine methyltransferase 8, transcript variant 1"
GO:0005515|GO:0019919|GO:0006355|GO:0046982|GO:0005886|GO:0016571|GO:0043393|GO:0034969|GO:0035

241|GO:0018216|GO:0005634|GO:0008757|GO:0008469|GO:0042803|GO:0042802|GO:0005829|GO:0035242|GO:0044020|GO:0043985 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141880_PI430048170 0.0923771116525144 2.28141652684499 2.65402405285671 2.69552920386107 2.31477163084012 A A A 0.390093592945702 1.92646758571314 1.4154301294032 A A A LNCV6_141880_PI430048170 mRNA
GAAGTCCAGGCAGAATTCTAATGCAATAAGCTAAATGTTCTTGCAATTTAAGAAGTGTTC NM_006177 RefSeq
chr14 - 24080106 24084623 NRL 4901 neural retina leucine zipper
GO:0005515|GO:0006366|GO:0046548|GO:0005634|GO:0000978|GO:0003677|GO:0045872|GO:0043522|GO:0001077|GO:0045944|GO:0007468|GO:0007601|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137738_PI430048170 0.0106269356133438 0.619046324161372 6.48467281127042 6.10580254994458 6.37771401902224 P P P 7.21594904422423 6.87890862942327 6.95277610825596 P P P LNCV6_137738_PI430048170 mRNA
CCAACTTCGTGTGAAATTGTGATGTTGAAGTGAATAAATGTCTATTGTGTAACTCTCATG NM_052831 RefSeq
chr6 - 132769367 132798608 SLC18B1 116843 "solute carrier family 18, subfamily B, member 1"
GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127159_PI430048170 0.173421978138564 2.1185358073743 0.916720576220957 2.40993564020396 1.13704965919827 A A A 0.340927705483442 0.48329315297765 0.826433304361168 A A A LNCV6_127159_PI430048170 mRNA
TGAAGACAGTGTGTGCGGCAAGAACGCAAGGGGGCAAGTCCCAGAAGTAACGCCACTGCT NM_005303 RefSeq
chr19 + 35351541 35352464 FFAR1 2864 free fatty acid receptor 1
GO:0005886|GO:0051928|GO:0004930|GO:0045125|GO:0042593|GO:0044281|GO:0008289|GO:0005085|GO:0043547|GO:0070542|GO:0006112|GO:0007186|GO:0050796|GO:0005887|GO:0030073 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_3294_PI430048170 0.89321065647179 0.969998845805798 4.92197855667657 4.95349418310173 5.19297114089193 P P P 4.7229811677066 5.11200926668268 5.31884019038919 P P P LNCV6_3294_PI430048170 mRNA
AGATCAAAGAGAAGATGTACGGCAAGCAGAAGATCTATTTTGCGGATCAGGACCAGTTTG NM_001256015 RefSeq
chr17 - 42572309 42577831 PSMC3IP 29893 "PSMC3 interacting protein, transcript variant 4"
GO:0051321|GO:0030374|GO:0006310|GO:0005634|GO:0005575|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141337_PI430048170 0.0292828572284318 0.470266075592829 3.30326574196998 2.52342771644718 3.28552162467952 P A P 3.92771413054881 4.43966502164386 4.09027688634785 P P P LNCV6_141337_PI430048170 mRNA
CATGGAAGTAGAAGGTAAGGAGTTTAGGAAAATACTAGAATCTACTCTGCTTACATTCTT NM_014812 RefSeq
chr1_KI270763v1_alt - 136535 267514 CEP170 9859 "centrosomal protein 170kDa, transcript variant alpha" GO:0005515|GO:0031965|GO:0005813|GO:0005737|GO:0005814|GO:0005874|GO:0005819 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132735_PI430048170 0.0992874406999928 0.771629103010494 1.37789742233301 1.51946491182251 1.67091268026999 A A A 2.10485124110133 1.63384377066799 1.92789569541323 A A A LNCV6_132735_PI430048170 mRNA
GTGCAGTTGTGCCACAAACCTTCCCTAAATTATCTAGGTTTGCTTTGATGAATTAAATTA NM_001042702 RefSeq
chr2 + 178451435 178461383 DFNB59 494513 "deafness, autosomal recessive 59"
GO:0007605|GO:0043025 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134647_PI430048170 0.28415036764562 0.794468104371562 0.28691096711929 0.326405612793744 0.396736743927177 A A A 0.362882789716582 1.04733945483235 0.504193071068667 A A A LNCV6_134647_PI430048170 mRNA
GGTTCACACGTTCCAAACTTTGAGTGATTTCTGGAGTTAGACATAGATTTTCTATTTTGT NM_001304536 RefSeq
chr2 - 221418026 221574202 EPHA4 2043 "EPH receptor A4, transcript variant 1"

GO:0005515|GO:0030424|GO:0097161|GO:0030054|GO:0031594|GO:0005886|GO:0008347|GO:0005783|GO:0005741|GO:0030175|GO:0030425|GO:0042802|GO:0005005|GO:0005737|GO:0005004|GO:0046777|GO:0032314|GO:0048681|GO:0043197|GO:0007411|GO:0045211|GO:0007628|GO:0043204|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103817_PI430048170 0.164308769044595 0.519550773671276 1.25846013029846 1.70532247815688 1.6865487842918 A A A 1.68085197314169 3.09603249152651 2.41142990669608 A P P LNCV6_103817_PI430048170 mRNA ACTTCCTTTGATTGATGTGTACATAAATTCTATACTTACTCCTGCGTCGAAATCTAATCC NM_020748 RefSeq chr17 - 61865366 61928016 INTS2 57508 "integrator complex subunit 2, transcript variant 1" GO:0005622|GO:0005515|GO:0031965|GO:0016020|GO:0032039|GO:0016021|GO:0016180 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138793_PI430048170 0.662522236884278 0.970660072205216 2.50150568381955 2.63927334392447 2.44588085975443 A A A 1.91403671436716 3.62942773299158 0.783639782238315 A P A LNCV6_138793_PI430048170 mRNA GTTCCATGATGGACTAGGTTTGGAACCACTGGGTTAAATAAACTTAGAGAGGGCTGTTTA NM_004213 RefSeq chr15 + 84884660 84945796 SLC28A1 9154 "solute carrier family 28 (concentrative nucleoside transporter), member 1, transcript variant 1" GO:0006139|GO:0016020|GO:0005886|GO:0005887|GO:0005337|GO:0001882|GO:0005415|GO:0015858|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134891_PI430048170 0.243885218337303 1.0423417212385 0.362242350014663 0.366740727457631 0.474192177110877 A A A 0.337693283082554 0.316889147037783 0.37138972516317 A A A LNCV6_134891_PI430048170 mRNA CTACGAAGCCATTTCTCTTGATTTTTAGTAAACTTTTATGACAGCAAATTTGCTTCTGGC NM_020661 RefSeq chr12 - 8602165 8612846 AICDA 57379 activation-induced cytidine deaminase GO:0005515|GO:0006397|GO:0009972|GO:0045190|GO:0005634|GO:0016445|GO:0016446|GO:0090310|GO:0000178|GO:0005737|GO:0071222|GO:0030183|GO:0080111|GO:0004126|GO:0008270|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145177_PI430048170 0.00194429557052458 0.259662841424527 0.290638865441333 0.327343892899933 0.406533858461814 A A A 2.50135154044262 2.10678565181393 2.22586688107682 A A A LNCV6_145177_PI430048170 mRNA GGACAGCATGTCTCGACTTCCTGAGGAATATCTGAAAGCATATAAAATATCTGTAAAAAT NM_003309 RefSeq chr6 - 116274858 116280117 TSPYL1 7259 TSPY-like 1 GO:0008150|GO:0006334|GO:0005730|GO:0005634|GO:0019899 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128186_PI430048170 0.00416960251960888 1.5695784130532 10.6035688585629 10.5336772222553 10.3283826566221 P P P 9.84785395014283 9.94836513860452 9.72348111532887 P P P LNCV6_128186_PI430048170 mRNA CTGTCAAGACGTGTCATGTACATTTGTATCAAAAATAAAGAAGTGACCATGAGCTGTTAA NM_001085454 RefSeq chr17 - 29573468 29589592 GIT1 28964 "G protein-coupled receptor kinase interacting ArfGAP 1, transcript variant 1" GO:0005515|GO:0032465|GO:0048013|GO:0016235|GO:0005829|GO:0043547|GO:0008060|GO:0005737|GO:0008277|GO:0016020|GO:0007411|GO:0032312|GO:0008270|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138613_PI430048170 0.0557744683594176 1.30807610505348 9.48733382965619 9.35981356888782 9.25100565468205 P P P 8.83495292129439 9.20290007392105 8.8790312851064 P P P LNCV6_138613_PI430048170 mRNA TAAGTTTTCTGAGATGAGGGTCTAGCCCTGTTGGGGACAGAAAAGTGTGTAGACCTTCTT NM_004475 RefSeq chr17 - 28879338 28897697 FLOT2 2319 flotillin 2 GO:0005515|GO:0048471|GO:0005886|GO:0050821|GO:0030139|GO:0002020|GO:0031982|GO:0016600|GO:0035

255|GO:0008544|GO:0016020|GO:0005901|GO:0010629|GO:0007155|GO:0090002|GO:0002080|GO:0005925|GO:0
070062|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128854_PI430048170 0.0541210479053529 0.889634166695705 0.265953889152726
0.278749202847016 0.294809341833036 A A A 0.460800218025261 0.367823561030778
0.513431116329633 A A A LNCV6_128854_PI430048170 mRNA
ACTATTTAACATTTCTCCTAGTACAAAAGGACAAGAGAAGCAGGGCCCATTTCACAAAGC NM_001190476 RefSeq
chr16 - 3371052 3372283 MTRNR2L4 NA MT-RNR2-like 4 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_121705_PI430048170 0.670112420382733 0.96817095312817 0.489081487156671
0.332223364489948 0.41787699268533 A A A 0.616616160625709 0.355184869584753
0.3977923765849 A A A LNCV6_121705_PI430048170 mRNA
TGGTGCTATACTACTGATCCAGAACAGAGATATGACTACTGCGACATTCCTGAGTGTGAA NM_002665 RefSeq
chr2 + 87748086 87759475 PLGLB2 NA plasminogen-like B2 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_126935_PI430048170 0.629128107676315 1.01618939452007 0.535093935616566
0.57056202182779 0.461323193928712 A A A 0.559899642194577 0.469077597562972
0.468710508361068 A A A LNCV6_126935_PI430048170 mRNA
CCCTTCGTGGAACAACAGCGGGGGTAATCATATCACTAATTTTGTATGAATAAATGAAAA NM_152665 RefSeq
chr1 + 66752456 66779047 TCTEX1D1 200132 Tctex1 domain containing 1 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_139844_PI430048170 0.0109302549160715 0.406113910819842 6.80281796940713
6.72512893080685 6.61345105894019 P P P 7.70330619017948 7.99518411457687
8.28985905077308 P P P LNCV6_139844_PI430048170 mRNA
GGTTCCTCAGGTGACCAAAACTGAAAATCAATATTTCCATGTTTCATTAATCAAGGCATA NM_001042440 RefSeq
chr5 + 96662156 96774681 CAST 831 "calpastatin, transcript variant 6"
GO:0010951|GO:0005515|GO:0005737|GO:0004869|GO:0016020|GO:0004866|GO:2000675|GO:0005829 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_135081_PI430048170 0.0253234769908323 1.35694860480393 11.4016898353539
11.5655182414051 11.7021837263568 P P P 11.0778638416998 10.9782182765053
11.2900579289965 P P P LNCV6_135081_PI430048170 mRNA
AATGTGGTCCCCCTGACTGCTGTTTTCAGATTGCTTTGAAATAAAGCTTATTTTTCTATA NM_016305 RefSeq chr3
+ 42590805 42594998 SS18L2 51188 synovial sarcoma translocation gene on chromosome 18-like 2
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135916_PI430048170 0.754772135726674 1.09578327873298 0.453511433536632
1.23389634092562 1.29317299039955 A A A 1.0322901330318 1.16207798736059
0.432403773646625 A A A LNCV6_135916_PI430048170 mRNA
AGCACCAAGTTTGATGACGCGGACTATGACTGACAGGCTGGGTCCTGATCTGGGGCACTA NM_001025295 RefSeq
chr11 - 298200 299526 IFITM5 387733 interferon induced transmembrane protein 5
GO:0009607|GO:0030500|GO:0005887|GO:0060349|GO:0030282 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_135915_PI430048170 0.847173360226977 1.02344029679884 9.03248168474213
8.72802292537128 8.65386465471279 P P P 8.89384432302437 8.94504018622092
8.4553331116398 P P P LNCV6_135915_PI430048170 mRNA
CTTTTCTACAATGGCATTCAATAAAGTGTATATGTTTCTGGTGCTGCTGTGACTTCAAAA NM_006435 RefSeq
chr11 + 308106 309410 IFITM2 10581 interferon induced transmembrane protein 2
GO:0051607|GO:0006955|GO:0060337|GO:0005886|GO:0046597|GO:0035456|GO:0035455|GO:0019221|GO:0034
341|GO:0016021|GO:0009615|GO:0045071 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_128152_PI430048170 0.123462610179074 0.612413208033396 3.53183668764591

2.48617031050642 2.70020942343748 P A A 3.60624679565316 3.43465791515986
3.9686468276167 P P P LNCV6_128152_PI430048170 mRNA
ACACTGTACAAGTGGATTGCATATAGGCATATAGGCAGAACCAATGTGCAATAATTAAGA NM_015984 RefSeq
chr1 - 193012365 193059393 UCHL5 51377 "ubiquitin carboxyl-terminal hydrolase L5, transcript
variant 1"
GO:0005515|GO:0006511|GO:0016579|GO:0000502|GO:0006355|GO:0004843|GO:0004866|GO:0005634|GO:0006
310|GO:0048853|GO:0006351|GO:0005829|GO:0010951|GO:0031011|GO:0006281|GO:0021670|GO:0061136|GO:0
070628|GO:0030901|GO:0007179|GO:0008242|GO:0030512 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_142990_PI430048170 0.00947089171998873 1.93948550876936 5.00980772076096
5.12155389278141 5.14069877646507 P P P 4.35789398836984 4.07129888361122
3.94816146250908 P P P LNCV6_142990_PI430048170 mRNA
CTATCCTGGTGGAAATGACCCTATTTGATATGCTGTCCCTTAAAATAACTTGTATCAATA NM_001130142 RefSeq
chr11 + 124115403 124146911 VWA5A 4013 "von Willebrand factor A domain containing 5A, transcript
variant 3" GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143238_PI430048170 0.185603534108493 2.12921397208898 0.448303491811077
1.84511538666834 1.92797746481576 A A A 0.408175618592643 0.495669923766654
0.462963381437664 A A A LNCV6_143238_PI430048170 mRNA
TAGGGAGCCTATACTGTTTCTAGAATTTTTATGCCCATTTTAGGGGACTTGTAGCATATA NM_001145395 RefSeq
chr3 + 12484510 12531013 TSEN2 80746 "TSEN2 tRNA splicing endonuclease subunit, transcript
variant 5"
GO:0006397|GO:0006388|GO:0005813|GO:0005737|GO:0005730|GO:0005654|GO:0003676|GO:0000214|GO:0000
379|GO:0000213|GO:0016829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142325_PI430048170 0.497978427141835 0.559455625381582 0.456067181017369
0.335678319446617 0.316371804743687 A A A 0.257910683718266 2.18517721633127
0.250824773694261 A A A LNCV6_142325_PI430048170 mRNA
CATGTAGTGAGAAGGGACTTAATTACAAACTTAAGACGTAAGTGTGCAATAAAGTAAGCT NM_004202 RefSeq chrY
+ 13703566 13706022 TMSB4Y9087 "thymosin beta 4, Y-linked"
GO:0003785|GO:0042989|GO:0005737|GO:0008064|GO:0007015|GO:0005856 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_121720_PI430048170 0.431302423833578 0.915741900081044 0.275437933643542
0.306186281847048 0.423051462024548 A A A 0.354061878627195 0.315493601054632
0.690158854966704 A A A LNCV6_121720_PI430048170 mRNA
CCATAAACTGCTGGGGCAAAAATCATCTTGGAAGGCTCTGAACCTCAGAAAGGATTCACA NM_173843 RefSeq chr2
+ 113117892 113134016 IL1RN 3557 "interleukin 1 receptor antagonist, transcript variant 4"
GO:0006629|GO:0002439|GO:0005886|GO:0014050|GO:0045352|GO:0045353|GO:0005152|GO:0005615|GO:0005
151|GO:0005150|GO:0005622|GO:0005737|GO:0006955|GO:0042594|GO:0001960|GO:0070670|GO:0001660|GO:0
032496|GO:0034115|GO:0007613|GO:0043507|GO:0070555|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137895_PI430048170 0.427085162012644 1.9002152016577 0.24965696129122
1.56683171142859 2.59197332693578 A A A 1.27042976926121 0.34128490718724
0.747112942801256 A A A LNCV6_137895_PI430048170 mRNA
GGGGAGAATCAAAGCTTTCATTTCAGAAATGTTGCGTGGAAAAGTATCTGTAATTAAAGT NM_153000 RefSeq chr18
+ 10454627 10488701 APCDD1 147495 adenomatosis polyposis coli down-regulated 1
GO:0017147|GO:0005887|GO:0030178|GO:0016055|GO:0001942|GO:0043615 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_49692_PI430048170 0.878566246211883 1.02337422912068 0.550595516328254 0.711990990971384
0.268843967399691 A A A 0.412190779959031 0.551236105586797 0.498927541316644 A A A
LNCV6_49692_PI430048170 mRNA

TGCCCAAGTGGATTAGCCTTTTTAGAGTTTATTAATTAAAAGAGAGCAGCAAGAATGGCA NM_001145712 RefSeq
chr7 - 56114680 56116397 NUPR1L 389493 "nuclear protein, transcriptional regulator, 1-like" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133995_PI430048170 0.00334892303371819 1.7209399973711 11.7572529704437
11.7862335462058 11.6235078159129 P P P 11.0380417231203 11.005412620252
10.7638789127948 P P P LNCV6_133995_PI430048170 mRNA
GCATTTCCCCCAGGGAAGTTTCTGGGTGCCCCACTAAGTAGAATAAAGAAAAACGGTTAT NM_004159 RefSeq
chr6_GL000252v2_alt - 4084286 4088505 PSMB8 5696 "proteasome (prosome, macropain)
subunit, beta type, 8, transcript variant 1"
GO:0005515|GO:0002474|GO:0010467|GO:0090263|GO:0019221|GO:0044281|GO:0031145|GO:0005829|GO:0004
298|GO:0034641|GO:0000082|GO:0060337|GO:0016032|GO:0045444|GO:0090090|GO:0070062|GO:0006977|GO:0
000209|GO:0005839|GO:0000502|GO:0043066|GO:0006521|GO:0051437|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134173_PI430048170 0.5626206918066341.09967412250822 2.85815865125382
2.81199745651048 3.3028579805313 A A P 2.6825111237917 3.14418943522113
2.74271864864464 P P P LNCV6_134173_PI430048170 mRNA
CGTCTCCACCTAGAAAATAAAAATACATTAAGATGTGCTTTCATTGCTGGTTGTCAGTTT NM_001014279 RefSeq
chr5 - 43039079 43040345 ANXA2R 389289 annexin A2 receptor NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_54927_PI430048170 0.3401462154245471.34908101515734 0.9404882743025941.2945975185577
0.265370320898267 A A A 0.3639134977921750.4371348593222330.576309769189898 A A A
LNCV6_54927_PI430048170 mRNA
ATCGAGGACGAGAGCGTGGCGCTGACCTTGAGCTTGGAGGTTCAATTACTACGAGGCGAA NM_021817 RefSeq
chr1 + 156619293 156625725 HAPLN2 60484 hyaluronan and proteoglycan link protein 2
GO:0085029|GO:0001501|GO:0008065|GO:0005540|GO:0005578|GO:0007417|GO:0007155|GO:0005201 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142196_PI430048170 0.1102759273245730.91267410624694 11.6090144782996
11.6410478672216 11.4810685669314 P P P 11.6996787935455 11.7149982992723
11.7167952447661 P P P LNCV6_142196_PI430048170 mRNA
ACACCAAGGTCTACAACTATGTGGACTGGATTAAGGACACCATAGCTGCCAACAGCTAAA NM_001303414 RefSeq
chr7_KI270803v1_alt + 793915 797537 PRSS2 NA "protease, serine, 2 (trypsin 2), transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134168_PI430048170 0.1835490235863311.13162744874736 13.0266733984724
13.2017769372595 13.1913402339861 P P P 12.9417866208977 12.8057706705676
13.1256873133023 P P P LNCV6_134168_PI430048170 mRNA
CTTGACTTTCTTCTGTGCACCTGATGGGAGGGTAATGTCTAATGTATTATCAATAACAAT NM_016816 RefSeq chr12
+ 112906933 112919907 OAS1 4938 "2'-5'-oligoadenylate synthetase 1, 40/46kDa, transcript variant 1"
GO:0003725|GO:0005515|GO:0035457|GO:0005783|GO:0001730|GO:0019221|GO:0005576|GO:0005634|GO:0042
593|GO:0009615|GO:0051259|GO:0005524|GO:0046872|GO:0005829|GO:0005739|GO:0051607|GO:0005737|GO:0
060337|GO:0006006|GO:0008270|GO:0060700|GO:0060333|GO:0045071|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141338_PI430048170 0.6688561609286291.02536402112167 8.0383281679084
7.97491968365682 8.03495390529699 P P P 7.82039183998142 8.02272807188257
8.08452088290942 P P P LNCV6_141338_PI430048170 mRNA
AGATAGGATGTGAGGTGAGCATGAGCTTGAGCTGAGAGACAGACACAACAGTATCTGAAA NM_006753 RefSeq
chr9 - 133330706 133336210 SURF6 6838 "surfeit 6, transcript variant 1"
GO:0001652|GO:0042254|GO:0003723|GO:0005730|GO:0005654|GO:0003677 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135923_PI430048170 0.1187231023431370.3272364193931520.355373584965151

0.4060718418169030.325262903317018A A A 0.7257453729912332.15672257232617
2.50454073479546 A A P LNCV6_135923_PI430048170 mRNA
ACTCTACAGTGGGTGTGCTATGTTCTTATTACCCTGATTAAATGTGTGATGTGACTCAAA NM_033341RefSeq chr19
- 53289600 53291622 BIRC8 112401 baculoviral IAP repeat containing 8
GO:0004842|GO:0043066|GO:0048471|GO:0016567|GO:0090263|GO:0005634|GO:0002020|GO:0051402|GO:0005
829|GO:0005737|GO:0043524|GO:0097110|GO:0005876|GO:0008270|GO:0090307|GO:0043027 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135014_PI430048170 0.3612151074980081.02752319442801 0.297707524340505
0.30683071757109 0.40021219347866 A A A 0.3117173337705870.290905389139773
0.286737442686676A A A LNCV6_135014_PI430048170 mRNA
TAGTCTTGCCCAAATCCAAATCACTTCAACATTCATGTGAAAGATCTATCCCACTTCCCA NM_207422RefSeq chrX
+ 72144183 72161750 FLJ44635 NA TPT1-like protein NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128805_PI430048170 0.5692187378071150.9778385536420570.328559538222847
0.44177551255072 0.336174462657642A A A 0.4755350926938580.362906815867201
0.364958686694082A A A LNCV6_128805_PI430048170 mRNA
CACAAATGCCTTCTATGTTGTTTGCTCTGTAGACATGAAAATAAACAATATCTCTCGATG NM_001184697 RefSeq
chr4 + 87832968 87846816 MEPE 56955 "matrix extracellular phosphoglycoprotein, transcript
variant 5" GO:0005515|GO:0001501|GO:0046850|GO:0005578|GO:0030502|GO:0031214|GO:0005201 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92138_PI430048170 0.5820106036295490.9492734808151340.2691897990670950.719565333494074
0.396329127319412A A A 0.5508934429477870.5151427085334650.581657832483841A A A
LNCV6_92138_PI430048170 mRNA
GCATAAGGACATGTAATTTTTGAAGACCAAATGTGATGCATGGTGGATCCAGAAAACAAA NM_007036RefSeq chr5
- 54977866 54985586 ESM1 11082 "endothelial cell-specific molecule 1, transcript variant 1"
GO:0008284|GO:0005178|GO:0005576|GO:0002040|GO:0001525|GO:0005171|GO:0001558|GO:0005520 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77165_PI430048170 0.29742140933767 1.21463694952655 6.14287571107541 6.57935772798403
6.18752907912584 P P P 6.195546886997 6.21852587779555 5.61921373118588 P P P
LNCV6_77165_PI430048170 mRNA
TGTGCAGACAGACTCTGATGGACTTATGTGCCCAGAAGCCCTGCCCACGCAATTCCCACT NM_004557RefSeq
chr6_GL000256v2_alt - 3511047 3540275 NOTCH4 4855 notch 4
GO:0005515|GO:0010467|GO:0006367|GO:0007220|GO:0005886|GO:0005634|GO:0030879|GO:0009790|GO:0007
221|GO:0030154|GO:0005829|GO:0007219|GO:0004872|GO:0030097|GO:0001569|GO:0046982|GO:0009986|GO:0
001709|GO:0005509|GO:0005576|GO:0000139|GO:0001886|GO:0005887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128977_PI430048170 0.67402870965229 0.969463402280889 15.2073281337525 15.319866896558
15.2025789317142 P P P 15.1360681118687 15.4103523571617 15.3074643990533 P P P
LNCV6_128977_PI430048170 mRNA
AAGGGACCCTTACCCCCGGCTCTTCTCCTGACCTGCCAATAAAAATTTATGGTCCAAGGG NM_002276RefSeq chr17
- 41523616 41528389 KRT19 3880 "keratin 19, type I"
GO:0005515|GO:0005882|GO:0030018|GO:0043627|GO:0060706|GO:0045214|GO:0032403|GO:0071944|GO:0042
383|GO:0016010|GO:0005200|GO:0043034|GO:0016032|GO:0008307|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127507_PI430048170 0.4247752389719751.06436489455533 12.0508228901586
12.1010219277538 11.8283316871483 P P P 11.839115585704 11.9808101202355
11.9011121408529 P P P LNCV6_127507_PI430048170 mRNA
CCACCAAATCATCCTGAATCTGATCTTTTTATACACAATATACGAAAAGCCAGCTTGAAA NM_013258RefSeq chr16
- 31201485 31202776 PYCARD 29108 "PYD and CARD domain containing, transcript variant 1"

GO:0005515|GO:0032755|GO:0046330|GO:0002218|GO:0002020|GO:0042803|GO:0051607|GO:0032314|GO:0030
838|GO:0071356|GO:0043025|GO:0070374|GO:0032688|GO:0043124|GO:0032729|GO:0032760|GO:0010803|GO:0
008656|GO:0033209|GO:0044325|GO:0043280|GO:0042771|GO:0050870|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137194_PI430048170 0.00812198700187596 0.3080145697010864.1101608130532
3.39844692077604 3.39762811232374 P P P 5.14012967873482 5.50832802167711 5.4507459119569
P P P LNCV6_137194_PI430048170 mRNA
CGATTGACTTTTGGTTTGTAATTTCCCTTTAAACAAGAAGAGATGGCTCACATTTTCCAT NM_017759RefSeq chr2
- 205993720 206086182 INO80D 54891 INO80 complex subunit D
GO:0006355|GO:0006281|GO:0006310|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144631_PI430048170 0.0514107165865175 0.8772409995133491 3.3227944848908
13.2744803186862 13.3925171570935 P P P 13.4107073912519 13.5643813444012
13.5781015905063 P P P LNCV6_144631_PI430048170 mRNA
CTCTGAAGCTAGACATGTGCTTTGAAATGATTATCATCCTAATATCATGGGGGAAAAAAT NM_001212RefSeq chr17
- 5432778 5439151 C1QBP 708 "complement component 1, q subcomponent binding protein"
GO:0005515|GO:0008380|GO:0051897|GO:0050687|GO:0030984|GO:0030449|GO:0048025|GO:0005886|GO:0070
131|GO:0005634|GO:0003729|GO:0005615|GO:2000510|GO:0005829|GO:0005739|GO:0005737|GO:0006955|GO:1
900026|GO:0005540|GO:0005759|GO:0039536|GO:0005080|GO:0006958|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145736_PI430048170 0.7101718987986010.83062836186591 0.593170962247359
0.73037751188723 2.53010171387758 A A A 2.70287611027593 1.27642857398892
0.875061288259368A A A LNCV6_145736_PI430048170 mRNA
TGCTCTCTTCCATTCACCCCTTCAGCTCAGCAACAATAAAGCTGCTTTACTTGGAAAAAA NM_001128600 RefSeq
chr1 + 152842853 152843983 LCE6A NA late cornified envelope 6A NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132643_PI430048170 0.0222711263659731 0.6183081115065331 0.1424930223468
10.022176735763 10.1256923817834 P P P 10.5685425064687 10.9898623122975
10.7850100555909 P P P LNCV6_132643_PI430048170 mRNA
CCTAGGGTTATGTCCAGTTGGGGTTTTTAAGGCAGCACAGACTGCCAAGTACTGTTTTTT NM_003362RefSeq chr12
+ 109098117 109110993 UNG 7374 "uracil-DNA glycosylase, transcript variant 1"
GO:0004844|GO:0005515|GO:0043066|GO:0005634|GO:0016446|GO:0005739|GO:0006281|GO:0006284|GO:0006
285|GO:0016447|GO:0045008|GO:0016032|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139346_PI430048170 0.1334859591025750.7576974635511721 3.7049834246037
13.2001159114995 13.1268959806946 P P P 13.8881009252856 13.7787951489583
13.6250615395736 P P P LNCV6_139346_PI430048170 mRNA
CCCCGCCTCCTTTCTGTTTTATTTTTGAGGAAATAAAATAACCAAGTGCTAAATCTTGTA NM_001130517 RefSeq
chr22 + 37019641 37029822 MPST 4357 "mercaptopyruvate sulfurtransferase, transcript variant 3"
GO:0043005|GO:0070814|GO:0030054|GO:0016784|GO:0009440|GO:0005743|GO:0045202|GO:0009636|GO:0004
792|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139939_PI430048170 0.346981704454 0.8052295561055050.570812471012584
0.6172397016954890.519275515641771A A A 0.7675201969145380.497506261789265
1.27226650509667 A A A LNCV6_139939_PI430048170 mRNA
CGCACAAACTTGTCGGTATGAGCTATATAATAACAAACACAAATAAATAAAAGGGAGCCT NM_013236RefSeq chr22
+ 45671797 45845307 ATXN1025814 "ataxin 10, transcript variant 1"
GO:0005515|GO:0048471|GO:0005737|GO:0016020|GO:0005886|GO:0043025|GO:0005615|GO:0031175|GO:0030
425|GO:0042802|GO:0007399|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130262_PI430048170 0.0299485195548631 0.6806093346943975.16410737502763
5.15434948609762 5.16204087663543 P P P 5.57598646969703 5.65164840806373

5.89818795208249 P P P LNCV6_130262_PI430048170 mRNA
GGCCTTAGCTTCTGGCTTTTAATTTTGCCAGCTAAGGACATAAAACAAAAATAAACAAAC NM_016142 RefSeq chr11
+ 43680592 43856619 HSD17B12 51144 hydroxysteroid (17-beta) dehydrogenase 12
GO:0005515|GO:0004303|GO:0006703|GO:0005518|GO:0010811|GO:0044281|GO:0035338|GO:0031012|GO:0030
198|GO:0005789|GO:0019432|GO:0006633|GO:0016021|GO:0001968|GO:0008201|GO:0044255|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138676_PI430048170 0.886448251966944 1.03362071306923 0.476697758270281
2.13037965283538 2.00836933682481 A A A 1.59354747195827 2.00795552729265
1.28367715501923 A A A LNCV6_138676_PI430048170 mRNA
CTACCACCTGTGCAATTGTCACTTTTCTTTCACTCCCTGAATAAAGTATCTATGCATAAA NM_001017418 RefSeq
chr1 - 153070227 153071608 SPRR2B NA small proline-rich protein 2B NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_41224_PI430048170 0.69793850994283 2.97282387258964 12.0513415104754 15.4376300656465
11.6398595031704 P M P 12.4727220160771 12.5629153897521 12.4754484604218 P P P
LNCV6_41224_PI430048170 mRNA
CATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAAGGAATCATACATCTCAAA NM_014045 RefSeq chr14
+ 22871750 22878082 LRP10 26020 low density lipoprotein receptor-related protein 10
GO:0005905|GO:0016020|GO:0016021|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130259_PI430048170 0.380914043325037 1.11493511795294 0.47598913815748
0.872180500809591 0.486535901945433 A A A 0.489687300679347 0.506608542807833
0.401655039152477 A A A LNCV6_130259_PI430048170 mRNA
ATGTACGTGCTGTTCTACTTTATATGATGTGAGAAGCCAACATCAGTGTCCCTTGGCAGC NM_020167 RefSeq chr5
- 152391540 152405279 NMUR2 56923 neuromedin U receptor 2
GO:0043006|GO:0007631|GO:0006821|GO:0019722|GO:0005886|GO:0004930|GO:0048016|GO:0007267|GO:0007
200|GO:0002023|GO:0006940|GO:0007417|GO:0005525|GO:0007204|GO:0042924|GO:0007218|GO:0001607|GO:0
005229|GO:0048265|GO:0006816|GO:0016021|GO:0007625|GO:0050482 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132680_PI430048170 0.31588017267607 0.650466184720469 0.274232831920812
0.499261336368064 0.498896148359399 A A A 1.64047979798113 0.902070362595806
0.284866373942999 A A A LNCV6_132680_PI430048170 mRNA
CTTGACCAGCATATCTGTTTTCTGATTGCGCTCTTCACAATTAAAGGCCTCCTGCAAACC NM_001252597 RefSeq
chr6 - 35794981 35797344 CLPS 1208 "colipase, pancreatic, transcript variant 2"
GO:0016042|GO:0006629|GO:0007603|GO:0044241|GO:0005576|GO:0044281|GO:0043085|GO:0008047|GO:0001
523|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56736_PI430048170 0.0606770838203822 1.23630104493313 6.99498659387746
7.28312030963887 7.0258392335236 P P P 6.73293726824708 6.93208036981567
6.72903280625612 P P P LNCV6_56736_PI430048170 mRNA
TTAACTCAAGAGAATTCCTGTTCTCCTTGTGCTATGATTTGGACACAAGATTCTGGATAC NM_031484 RefSeq chr10
+ 97713707 97718152 MARVELD1 83742 MARVEL domain containing 1
GO:0007049|GO:0005737|GO:0005886|GO:0005634|GO:0016021|GO:0005856 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140911_PI430048170 0.446110121438425 1.16132922062225 3.81640924593106
3.55433229517868 3.52539044778063 P P P 3.88893786770925 2.94400953542494
3.27082804011291 P P P LNCV6_140911_PI430048170 mRNA
AAGGGCTGAACTTTAAAAATGTAAACTTACAAGACAAAAGGCTCTTTTCAGAGCCACCCA NM_003514 RefSeq chr6
- 27892698 27893185 HIST1H2AM 8336 "histone cluster 1, H2am"
GO:0005515|GO:0008150|GO:0046982|GO:0005634|GO:0019899|GO:0000786|GO:0003677|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116447_PI430048170 0.732007835763023 1.05973104515046 2.97916460730686

2.43020747062789 2.74848688784399 A A A 2.54677364905005 3.05275583346253
2.24089297062035 A P A LNCV6_116447_PI430048170 mRNA
AAATATCAGCCTCCAGTGGCAGCAGAGTGGAAGATGGTGAACACCAAGTTAAAATGAAGG NM_020183 RefSeq
chr12 + 27332853 27425813 ARNTL2 56938 "aryl hydrocarbon receptor nuclear translocator-like 2,
transcript variant 1"
GO:0005667|GO:0006355|GO:0003700|GO:0006357|GO:0006366|GO:0000982|GO:0005730|GO:0070888|GO:0005
634|GO:0007165|GO:0005737|GO:0009649|GO:0045944|GO:0046983|GO:0042753|GO:0007623|GO:0004871|GO:0
045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132449_PI430048170 0.5111226152320481.04505101403105 0.287302631062124
0.2979354967859710.517453677618376 A A A 0.3206284878570190.277923151334731
0.324846713539053 A A A LNCV6_132449_PI430048170 mRNA
CTGTGAAATGTCCGTCATATCTCAGAGCATATAGAGGGAATTAAATAAACACAAAGCATT NM_153447 RefSeq chr19
+ 55999725 56061808 NLRP5 126206 "NLR family, pyrin domain containing 5"
GO:0043487|GO:0007566|GO:0005730|GO:0001701|GO:0005524|GO:0043623|GO:0005829|GO:0005739|GO:0009
566|GO:0043234|GO:0031647|GO:0045179|GO:0070997|GO:0009887|GO:0034613 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145245_PI430048170 0.1729629474918891.10031785946747 8.51409180909242
8.62936445287233 8.44261892205097 P P P 8.51585868366511 8.31847585143311
8.33576631461167 P P P LNCV6_145245_PI430048170 mRNA
GTGGCCTCCTGTTCTCACCCCATTGTTATTTTGGCTTTTTTAATATAAAATGTACATTGA NM_002712 RefSeq chr2 +
241149657 241183650 PPP1R7 5510 "protein phosphatase 1, regulatory subunit 7, transcript variant 1"
GO:0008599|GO:0008150|GO:0050790|GO:0005737|GO:0007059|GO:0005694|GO:0035307|GO:0030234|GO:0005
634|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128394_PI430048170 0.1329827957789410.4257538666641030.384058282373313
1.18618242394971 1.23815768292102 A A A 2.68471129802001 2.42673287243141
1.10045876711791 A A A LNCV6_128394_PI430048170 mRNA
GTTGGCAGAACAATAAAGTGCATTTGCTCAGGCCCCTGATGCCTAACTTGCACCAAAAAA NM_002280 RefSeq chr17
- 41476688 41481140 KRT35 3886 "keratin 35, type I"
GO:0005882|GO:0005198|GO:0009653|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_119185_PI430048170 0.6099388244282431.12383812147902 0.27788979401899
0.3112641384117020.960797601311165 A A A 0.4918035095146240.334326280747159
0.319396888988399 A A A LNCV6_119185_PI430048170 mRNA
CCTTTAAAGCACAACCACAGATATTGGTAAAAATGGAACAGAATTACCTCAATACCTCTT NM_178498 RefSeq chr11
- 26667018 26722027 SLC5A12 159963 "solute carrier family 5 (sodium/monocarboxylate
cotransporter), member 12" GO:0016324|GO:0016021|GO:0006814|GO:0055085|GO:0070062|GO:0015293 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139510_PI430048170 0.0130890278149783 1.09323905766645 0.361307783639091
0.4353962152126460.373636333815771 A A A 0.2438113735574820.29354590039105
0.247721755272502 A A A LNCV6_139510_PI430048170 mRNA
CCATGGGCTTCATTTATCAGTTTTTTCCCTTTTTAATTGGTGGAGAGAGACAAAAGTTTT NM_001080531 RefSeq
chr4 + 145680203 145732796 C4orf51 NA chromosome 4 open reading frame 51 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139897_PI430048170 0.0222632250813473 0.5375354234350021 0.2285320666483
10.2309157459246 10.3050851467493 P P P 10.8530001876237 11.2914872016422
11.2674144603908 P P P LNCV6_139897_PI430048170 mRNA
AAAGCAATTCTTGTTTTAGTTTCTTTGCGAAGCCTGCTCCTCCTTCCCTTCATAAGGACT NM_033260 RefSeq chr6 +
1312439 1314758 FOXQ1 94234 forkhead box Q1
GO:0043565|GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0031069 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_136677_PI430048170 0.2966657875604691.56007279859258 3.10478885705894
3.55564183932667 3.45638471035923 P P P 1.32751808185858 3.21545793073359 3.0512473470033
A P P LNCV6_136677_PI430048170 mRNA
TGCCTTCTCCAGACTGTTCTGACAAGGTAATGAAAATAAAATGCACTTGGATTTTTCCAG NM_018397RefSeq chr3
- 53816296 53846393 CHDH 55349 choline dehydrogenase
GO:0050660|GO:0019285|GO:0005743|GO:0008812|GO:0055114 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132525_PI430048170 0.21344281951131 0.8947466407539416.01658252631273
5.76412606097648 6.06591785127568 P P P 6.07244366919821 6.13242593715667
6.13995542095073 P P P LNCV6_132525_PI430048170 mRNA
CCAGGGGGAGATTTATAGATCCATTGAACATCTAGATAAAATGGGTATGAGTATTATAGA NM_015955RefSeq chr2
- 31867809 32010664 MEMO1 51072 "mediator of cell motility 1, transcript variant 1"
GO:0005515|GO:0032886|GO:0005634|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139226_PI430048170 0.3631610050386040.7244329223033096.0697954178589
6.22016876495119 6.23316772129542 P P P 5.91236663874369 7.03238722997652
6.75944979469667 P P P LNCV6_139226_PI430048170 mRNA
TTAGATTTCGAGCTTATTCTCTTCTAGCAGTTTCTTGCCACCATGTCGGAAACCGCTCCT NM_005322RefSeq chr6
- 27866791 27867581 HIST1H1B 3009 "histone cluster 1, H1b"
GO:0000790|GO:0042826|GO:0030307|GO:0006325|GO:0006334|GO:0050821|GO:0000122|GO:0031490|GO:0051
574|GO:0005720|GO:0071169|GO:0000786|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138510_PI430048170 0.00956821748729547 1.79117735986506 3.88727927676471
3.61617479973109 3.47020156384675 P P P 2.59660968455061 2.79630134957753
3.05299988541135 A P P LNCV6_138510_PI430048170 mRNA
GAGCTTCATAATACGTTATATTGTTCCGAAGCAGCTCGTTGAGAAACATTTGTTTTCAAT NM_001136239 RefSeq
chr5 + 123089145 123188051 PRDM6 93166 PR domain containing 6
GO:0051151|GO:0034968|GO:0005634|GO:0003676|GO:0045892|GO:0046872|GO:0042803|GO:0006351|GO:0022
008|GO:0018024 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128758_PI430048170 0.436642665906907 1.07382722463233 7.9617777484269
8.18475081626116 7.92414077171678 P P P 8.09585551771284 7.84118733706669
7.82287319961386 P P P LNCV6_128758_PI430048170 mRNA
ATGTATAGGGCTAAATATATGCTTGTTTCCTTGCACCTGTGTACTTCCCCTCTCTCCCTC NM_001286790 RefSeq chr4
- 77713386 77819390 CNOT6L 246175 "CCR4-NOT transcription complex, subunit 6-like, transcript
variant 1"
GO:0005515|GO:0010467|GO:0006355|GO:0008284|GO:0005634|GO:0031047|GO:0046872|GO:0030014|GO:0006
351|GO:0006417|GO:0005829|GO:0061157|GO:0004535|GO:0005737|GO:0010606|GO:0000289|GO:0000288 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145112_PI430048170 0.2405562894043350.3867371228458770.422320923447871
0.3901878078655680.244962823987542A A A 1.2357108255987 0.405802891433412
2.64115929336988 A A P LNCV6_145112_PI430048170 mRNA
GTCTATGGTGCAAAGACCACACAGATTCGCATTCATGTGGTAAAAATGTTCTGTTCATAA NM_012375RefSeq chr11
- 5151430 5152369 OR52A123538 "olfactory receptor, family 52, subfamily A, member 1"
GO:0050911|GO:0007608|GO:0007165|GO:0004984|GO:0007186|GO:0005886|GO:0005887|GO:0004930|GO:0004
888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141183_PI430048170 0.6258363049540780.9853713833244170.483598771013115
0.4031728122469070.443458219515785A A A 0.4006606991651430.496380024390407
0.49599867646035 A A A LNCV6_141183_PI430048170 mRNA
CTTATGTCTGGATCCTGATGATTTCACAGCTAAATGGCAAAAATAAAACATGTTTCCCAT NM_144575RefSeq chr2
- 30722770 30807445 CAPN13 92291 calpain 13 GO:0005737|GO:0004198|GO:0005509|GO:0006508

. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100176_PI430048170 0.6422194378927661.04565997618682 5.66905100870727
5.88517723507621 5.56220965151704 P P P 5.75546272891093 5.6855191141321
5.48803966649957 P P P LNCV6_100176_PI430048170 mRNA
TTTATTTCCAGTGGGACTCCCTGCTGCTAGAGACTGGCTTCCTGGCCGTGCTGGTGGCCC NM_033200RefSeq chr22
- 50502946 50507706 LMF2 91289 lipase maturation factor 2 GO:0016020|GO:0005789|GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141307_PI430048170 0.1976623180006250.76703883406081 5.06520765702509
4.95099121082534 5.66580039494859 P P P 5.5879910831308 5.72091921665999 5.6239194737783
P P P LNCV6_141307_PI430048170 mRNA
GTGAAATCCCCTTCAGTCTTTTCAGATTGCATTGACTGTCCTCTTGATTTTTCATATTAC NM_203437RefSeq chr2 +
64524304 64593004 AFTPH 54812 "aftiphilin, transcript variant 1"
GO:0005737|GO:0005794|GO:0030276|GO:0030121|GO:0005654|GO:0005634|GO:0015031|GO:0043231|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128721_PI430048170 0.4328441245582021.05110332317718 0.288543447639146
0.2909934267672830.500478642409391 A A A 0.3068048158182290.267398603182261
0.300210000523112 A A A LNCV6_128721_PI430048170 mRNA
CATAGCTCTTTGGAGAACTAGGTGTTGTAATTCAGTTATGAAGCTATTTTCTCTGTAACA NM_178438RefSeq chr1
+ 152510843 152512177 LCE5A 254910 late cornified envelope 5A GO:0031424 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_63644_PI430048170 0.0189229349679647 1.14244140119026 9.89745675309558
9.84537734906023 9.95227223441142 P P P 9.74766893874405 9.7406985522976
9.62933023722073 P P P LNCV6_63644_PI430048170 mRNA
AAGCCTTCCCCCTGCTTTGCATGGCTCCCGGGGCGCTGACTGCGTGTTAACATCAGGTGA NM_001038618 RefSeq
chr17 + 82458183 82488267 NARF 26502 "nuclear prelamin A recognition factor, transcript variant 3"
GO:0005730|GO:0005652|GO:0005634|GO:0031981|GO:0005638|GO:0005521 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_99056_PI430048170 0.0553040711248477 1.2517857646267 7.40743447548238
7.18391686355131 7.13578246629013 P P P 6.96284020463031 6.90917579707089
6.89710121250378 P P P LNCV6_99056_PI430048170 mRNA
TGAAGCCCCGGAGCATCCACGAGTTGTCTGTGGAGCAGCAGCTCTACTACAAGGAGATCA NM_005641RefSeq chr7
- 100107069 100119372 TAF6 6878 "TAF6 RNA polymerase II, TATA box binding protein (TBP)-
associated factor, 80kDa, transcript variant 1"
GO:0005515|GO:0010467|GO:0006352|GO:0006355|GO:0006368|GO:0003700|GO:0005669|GO:0006367|GO:0008
285|GO:0046982|GO:0006366|GO:0005634|GO:0045786|GO:0003677|GO:0033276|GO:0051090|GO:0005737|GO:0
071339|GO:0016032|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142777_PI430048170 0.0610128210134792 2.07192648300018 4.13803446350427
4.53123796371121 4.41878892216041 P P P 2.61403654711311 3.55316667681229
3.59934824630432 A P P LNCV6_142777_PI430048170 mRNA
TGTTTGTGTTTGTGTAGCTAGGTATCTGGCACTTCTGACGATGCATTGTTGCTTTTTTCC NM_005189RefSeq chr17 +
79778177 79787650 CBX2 84733 "chromobox homolog 2, transcript variant 1"
GO:0035102|GO:0000792|GO:0005515|GO:0031519|GO:0000791|GO:0045137|GO:0005634|GO:0000122|GO:0035
064|GO:0003677|GO:0006351|GO:0030154|GO:0003682|GO:0005654|GO:0016568 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_142270_PI430048170 0.8956675534835670.9949041080942320.275827739299345
0.4724843055245480.319096780171947 A A A 0.4175643295652910.331788057792749
0.34617892406302 A A A LNCV6_142270_PI430048170 mRNA
AATGTTATCCCGTCGTTCAACAACGACAAGAAGCTGTCCAAATATGAGACCCTGCAGATG NM_005172RefSeq chr4
+ 93828926 93829991 ATOH1 474 atonal homolog 1 (Drosophila)

GO:0043066|GO:0042668|GO:0003700|GO:0021987|GO:0042472|GO:0006366|GO:0005634|GO:0000978|GO:0007417|GO:0042667|GO:0031490|GO:0001077|GO:0045666|GO:0007411|GO:0045944|GO:0045609|GO:0046983|GO:0001764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135013_PI430048170 0.5118530191397620.78312869030458 2.2220135095591 2.56718833967252 0.363164160391745A A A 2.65824374543262 2.49759720840624 1.68147760168128 A P A LNCV6_135013_PI430048170 mRNA
ACAGCCTGTGCCCCAGGCTTGTCTGTGGGGACAAGGACCAGGGTTAAAATGTTCATAAAA NM_001646RefSeq chr19 + 44942237 44945496 APOC4 346 apolipoprotein C-IV
GO:0034361|GO:0006629|GO:0034364|GO:0010890|GO:0006869|GO:0070328|GO:0005319 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126857_PI430048170 0.0142255422922357 0.1910859527006460.693550890007893 0.76522990947215 0.657584826592696A A A 2.46988871062168 3.41679077320235 3.23168440748401 A P P LNCV6_126857_PI430048170 mRNA
GTCTATTCTGTTTCCTACCCTGAACACATTAAAATGGTAGGAACTAATGCTTGTCTTATT NM_000465RefSeq chr2 - 214725645 214809711 BARD1 580 "BRCA1 associated RING domain 1, transcript variant 1"
GO:0005515|GO:0004842|GO:0045732|GO:0016567|GO:0003723|GO:0016874|GO:0000151|GO:0005634|GO:0042803|GO:0043231|GO:0070531|GO:0046826|GO:0005737|GO:0001894|GO:0007050|GO:0019900|GO:0085020|GO:0043066|GO:0043065|GO:0046982|GO:0005730|GO:0031436|GO:0006974|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132405_PI430048170 0.1266629720123920.4962134604111191.14757382773466 0.3856992108861640.358796642420242A A A 2.25163649184813 1.62600622429996 0.874236694139282A A A LNCV6_132405_PI430048170 mRNA
CTCTCTCCTGAGGCTGTTGAATCTGATGAATTAGCAGATAGGAAAGAACTTAGAAAATTA NM_001879RefSeq chr3 - 187216084 187292022 MASP1 5648 "mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor), transcript variant 1"
GO:0005515|GO:0004252|GO:0005509|GO:0005576|GO:0005615|GO:0006898|GO:0042803|GO:0001867|GO:0045916|GO:0006956|GO:0045087|GO:0006508|GO:0008233|GO:0048306 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119105_PI430048170 0.3473917617458690.83644646921575 0.254256165327931 0.2638466348704970.394885605937518A A A 0.3710670079467280.918549832385598 0.32169347436105 A A A LNCV6_119105_PI430048170 mRNA
CTTCCGCAGGGCCGTGTCTGAGCTGGACGCCAAGCAGGCAGAGGCCATCATGGTAAGAGG NM_199292RefSeq chr11 - 2163928 2171805 TH 7054 "tyrosine hydroxylase, transcript variant 1"
GO:0005515|GO:0033162|GO:0046684|GO:0009651|GO:0018963|GO:0007605|GO:0008016|GO:0009653|GO:0010043|GO:0048596|GO:0007507|GO:0034641|GO:0042745|GO:0051602|GO:0009414|GO:0032496|GO:0009887|GO:0031667|GO:0007613|GO:0009416|GO:0007612|GO:0032355|GO:0051412|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133719_PI430048170 0.5807396837483911.05229564128229 8.14856538675212 7.84990368942652 7.96298389430188 P P P 7.79604436912051 8.08121071832278 7.86384668955805 P P P LNCV6_133719_PI430048170 mRNA
TGAGGATGTGACCCCATCTGGGCATCATTTAACCAATAAAATTTCTCGAATGGACCATAA NM_032193RefSeq chr11 - 65717672 65720938 RNASEH2C 84153 "ribonuclease H2, subunit C"
GO:0032299|GO:0005634|GO:0006401 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139659_PI430048170 0.0370645927877096 0.4883538469616334.09228835622269 3.93413903035397 4.65704361754375 P P P 5.29677992807195 5.2366797994274 5.35322888471709 P P P LNCV6_139659_PI430048170 mRNA
GTACCTCCAAATCTTTAATGTCGAAATAAAGGGCTTTTTGCCATTTCTGTTTTCAGTTCANM_001172574 RefSeq chr8 + 6406591 6447419 MCPH1 79648 "microcephalin 1, transcript variant 2"
GO:0005515|GO:0005737|GO:0021987|GO:0005815|GO:0005654|GO:0000278|GO:0042802 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_128917_PI430048170 0.2329680681022080.9272901729553841 3.3761861787571
13.4452353557503 13.3558563641853 P P P 13.4526686780574 13.4186932268042
13.6255302071844 P P P LNCV6_128917_PI430048170 mRNA
GCTGAATCTGGGATCTCAAATTGCCTCTGACCTTTTATAAGACAGTTTATCTTCAAATAA NM_178167RefSeq chr16
- 1997651 2009821 ZNF598 90850 zinc finger protein 598 GO:0008270 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_110059_PI430048170 0.0855707225364639 1.25904459706095 5.85855074715011
6.14579451659049 6.0591186237418 P P P 5.91686314257465 5.56862241240615
5.56697985736557 P P P LNCV6_110059_PI430048170 mRNA
GAAACAAACATGAATGAAATCGTGGCTCAGATTGAGGCTCAAAACAGGCTGGAGAAATCC NM_005829RefSeq
chr15 - 89830598 89894385 AP3S2 10239 "adaptor-related protein complex 3, sigma 2 subunit,
transcript variant 1" GO:0048490|GO:0005794|GO:0030123|GO:0008565|GO:0008089|GO:0006886|GO:0030659
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129877_PI430048170 0.1051018049267611.50061391727143 9.34134583772371
9.64566866872298 9.33107502825016 P P P 9.29238751513824 8.62847731614042
8.54099565543921 P P P LNCV6_129877_PI430048170 mRNA
TCACATTTGCTCAGGAAGTGGGTATCAAATTGAGGTGGGGGTGTCAGAGGAGGCAAAGGG NM_024108RefSeq
chr19 - 45162927 45178243 TRAPPC6A 79090 "trafficking protein particle complex 6A, transcript
variant 1" GO:0005515|GO:0005794|GO:0005783|GO:0016192 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135119_PI430048170 0.6718143183651610.9564715671647524.06746820699804
3.59522777797658 3.54879852723564 P P P 3.90412510557597 3.77151235875979
3.78372047823992 P P P LNCV6_135119_PI430048170 mRNA
ATAAGAAAAACAAAAGAAAAAGACAGTGGAAAAAAGAGACCAAGGCGCCTGCCCCACTGC NM_014654RefSeq
chr1 - 30869465 30908633 SDC3 9672 syndecan 3
GO:0005886|GO:0007603|GO:0005796|GO:0005975|GO:0006027|GO:0044281|GO:0001523|GO:0006024|GO:0016
020|GO:0030198|GO:0009405|GO:0016021|GO:0030204|GO:0030203|GO:0043202 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136789_PI430048170 0.2482109842327090.4933539246862530.304252813280982
0.3251391126950360.330829866941167A A A 2.16203866043814 0.733855111129377
0.538998626869444A A A LNCV6_136789_PI430048170 mRNA
TGCTCCCGATGATGAGACTCTAGAGTTTACAACTGAAACACACTGTCATTTATGATATTA NM_145304RefSeq chr7
+ 148590564 148615860 C7orf33 202865 chromosome 7 open reading frame 33 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_128508_PI430048170 0.5272400057561761.08090462519954 11.1958989461384
10.7597167802038 11.0798904014465 P P P 10.9919900318737 10.9406783240598
10.7933795048592 P P P LNCV6_128508_PI430048170 mRNA
GATGCTGTTGGGAAGTTATCAATAAAAAGACACCATTACTAAAAAGGGAAAAGTACACCT NM_001171948 RefSeq
chr19 + 18557761 18569387 KXD1 79036 "KxDL motif containing 1, transcript variant 1"
GO:0005515|GO:0031083|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121332_PI430048170 0.8510485879169331.07201494668627 0.434197812232674
1.33857949200541 0.333143850456871A A A 1.19216922570056 0.322857545053976
0.332145581095614A A A LNCV6_121332_PI430048170 mRNA
GACTTTATGTTCATCGTAAATTACACACAGGAGTGAAACCTCATATTTGTGAGAAATGTG NM_013362RefSeq chr19
+ 44113394 44133102 ZNF225 7768 zinc finger protein 225
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139437_PI430048170 0.0706578584992038 0.6252016469324277.44453428146465

7.4725421964315 6.93900196206285 P P P 7.60919142247283 8.3246372152294
7.92541350134032 P P P LNCV6_139437_PI430048170 mRNA
TTATGAGGAAACTCGCGGAGTGCTGAAAGTTTTCCTGGAAAATGTAATCCGCGATGCTGT NM_003539RefSeq chr6
- 26188709 26189076 HIST1H4D 8360 "histone cluster 1, H4d"
GO:0005515|GO:0010467|GO:0006325|GO:0005634|GO:0045653|GO:0000723|GO:0000183|GO:0000786|GO:0070
062|GO:0035574|GO:0035575|GO:0046982|GO:0006334|GO:0006335|GO:0005576|GO:0006336|GO:0000228|GO:0
003677|GO:0032776|GO:0034080|GO:0043234|GO:0016020|GO:0045814|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140612_PI430048170 0.0904098602971191 1.52801987290729 5.10154201837971
4.81702653026585 4.44037431792703 P P P 4.35890644633345 4.38475693175826
3.77780315578093 P P P LNCV6_140612_PI430048170 mRNA
TTCTGGGATATATGGAGGATTCTTTCCCCAGAGGCTCCCAATCAGCTTTTGTTCTAGACT NM_002739RefSeq chr19
+ 53882212 53907647 PRKCG 5582 "protein kinase C, gamma"
GO:0048471|GO:0005886|GO:0007635|GO:0007268|GO:0005634|GO:0007202|GO:0032095|GO:0030425|GO:0005
829|GO:0035556|GO:0043524|GO:0046777|GO:0007173|GO:0005911|GO:0007611|GO:0031397|GO:0048011|GO:0
042177|GO:0030168|GO:0043278|GO:0005524|GO:0032425|GO:0060384|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132994_PI430048170 0.00640062262964127 0.6025460567252745.68066346848213
5.53781125290892 5.44393667883545 P P P 6.15086653479712 6.20726264089599
6.48424365960329 P P P LNCV6_132994_PI430048170 mRNA
AAAGCCATAACCAAAAGTCATTTTAGAGTACTGCTAGGTTACTCAACCTATCATCACATT NM_001290117 RefSeq
chr10 + 49942032 49974850 TIMM23B 100652748 "translocase of inner mitochondrial membrane 23
homolog B (yeast), transcript variant 1"
GO:0005744|GO:0015450|GO:0008150|GO:0003674|GO:0016021|GO:0005575|GO:0071806|GO:0006886 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_38412_PI430048170 0.0249433895131659 1.80527817025135 4.01885683354128
3.46041170622848 3.6912382257558 P P P 3.02156974498227 3.07520746046449
2.50680633574236 P P P LNCV6_38412_PI430048170 mRNA
TATCGTCAGCCTCTGGTGAGAAGCAGCAGCATCCTTCCAGAGAGTCACTTCTGATCCCCA NM_001282328 RefSeq
chr22 - 30576624 30607013 PES1 23481 "pescadillo ribosomal biogenesis factor 1, transcript variant
4"
GO:0005515|GO:0000463|GO:0000793|GO:0033365|GO:0008283|GO:0006364|GO:0005730|GO:0005634|GO:0070
545|GO:0007000|GO:0005737|GO:0016020|GO:0051726|GO:0043021|GO:0042273|GO:0005654|GO:0030687|GO:0
000466 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134877_PI430048170 0.0804421796800379 1.28376910783927 5.21323560788961
5.15084680605089 5.53996985343316 P P P 4.94396710335018 4.80668614662116 5.0893672142209
P P P LNCV6_134877_PI430048170 mRNA
GTTCTTTGCCATTTATGCAGGAAACTACCCTTTTCTCAATATAACCAAACAAAGGCTAAT NM_001012398 RefSeq
chr16 - 53491039 53503304 AKTIP 64400 "AKT interacting protein, transcript variant 1"
GO:0005515|GO:0030897|GO:0005794|GO:0016567|GO:0005886|GO:0008333|GO:0005730|GO:0006915|GO:0045
022|GO:0015031|GO:0032092|GO:0005737|GO:0019787|GO:0001934|GO:0007032|GO:0007040|GO:0031625|GO:0
070695 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134482_PI430048170 0.00412360279472966 0.7755039014906821 3.9811162205519
14.0251423025196 13.913382029475 P P P 14.4216391635696 14.3334023021618
14.2627727850364 P P P LNCV6_134482_PI430048170 mRNA
ATCTGGGAACTGCCTCTGCCTGGGCCAAAGCTATTCCATTAAAACTTTATTGCTGTGCTT NM_001001795 RefSeq
chr8 - 144526218 144529074 C8orf82 NA chromosome 8 open reading frame 82 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127388_PI430048170 0.00329456541127926 2.23475167658736 12.7600127011225

13.0458965994459 12.9238794719118 P P P 12.0024773864009 11.6512505564528
11.5727200401209 P P P LNCV6_127388_PI430048170 mRNA
AAGTCTCTGGCCTCATAAAAGGTGGCTGTGGGTCGTCAGGAATCTGCGCCATCTTCCTGG NM_016535 RefSeq chr19
+ 55643619 55645623 ZNF581 51545 zinc finger protein 581
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130804_PI430048170 0.8993379795601451.02164288922633 0.381381025715255
1.93240000357812 1.8951777374866 A A A 1.0133533910329 1.51823280436549
1.91414842902404 A A A LNCV6_130804_PI430048170 mRNA
AAGATCACAGAACTCTCCAAAGAAGTCTTCAATCTTAAGGAAGCCTTGAAGGAGCAGCCG NM_133475 RefSeq chr19
+ 4183353 4224814 ANKRD24 170961 ankyrin repeat domain 24 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132861_PI430048170 0.00734921046195376 0.2084157146847244.10098255198284
3.3731041809606 4.03765149408918 P P P 6.01917930239576 6.19109531642292
6.18840148510606 P P P LNCV6_132861_PI430048170 mRNA
ACGCTAGAGGGGGCCTCTGATTTAAAGAAATAAAAAGGACTTTTCTAAAATGGATGTGTA NM_153223 RefSeq chr5
- 123344884 123423592 CEP120 153241 "centrosomal protein 120kDa, transcript variant 1"
GO:0032880|GO:0005813|GO:0005737|GO:0021987|GO:0022027|GO:0032886|GO:0030953|GO:0008022|GO:0022
008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138762_PI430048170 0.0508058520332477 0.6018706353204327.49761449442753
7.44809289713968 7.71010385265538 P P P 7.96604654278198 8.19563730261192
8.62601688948295 P P P LNCV6_138762_PI430048170 mRNA
CAAAAATCATCTGATGGTATAGATGGATCCTAGTCCTTTTCATTACCTGATGGTAGAAAT NM_024996 RefSeq chr3
+ 158644527 158692571 GFM1 85476 "G elongation factor, mitochondrial 1"
GO:0005515|GO:0070125|GO:0032543|GO:0006996|GO:0005759|GO:0003924|GO:0005525|GO:0003746 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49965_PI430048170 0.2633026782184821.12815260636549 0.6476637230617590.947679994634121
0.605132706075862 A A A 0.5865127250071240.5632427530107720.55332642223221 A A A
LNCV6_49965_PI430048170 mRNA
CAAACAATAGATTTTGAAGGTTTCAAACTATTCATGAAGACATTCCTGGAAGCCGAGCTT NM_004080 RefSeq chr7
- 14145048 14841450 DGKB 1607 "diacylglycerol kinase, beta 90kDa, transcript variant 1"
GO:0035556|GO:0016310|GO:0005737|GO:0003951|GO:0005886|GO:0007596|GO:0005509|GO:0004143|GO:0030
168|GO:0005524|GO:0007205 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73931_PI430048170 0.54039566645954 1.0755094396849 7.10104578038789 7.3811299106949
7.52590560695272 P P P 7.22198515674172 7.12760439252224 7.36525305803269 P P P
LNCV6_73931_PI430048170 mRNA
GTACGTTGCTTCTTGTTCTTCACAATTCATGACTTAAGTACCAAAATGCATACCAGTTAT NM_001291504 RefSeq
chr3 - 195514421 195543401 PPP1R2 5504 "protein phosphatase 1, regulatory (inhibitor) subunit 2,
transcript variant 1" GO:0005515|GO:0005977|GO:0004865|GO:0043666|GO:0009966|GO:0006091|GO:0043086
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127661_PI430048170 0.0136858739156904 0.6849630654134827.14471499791617
7.34962579768909 7.46060210384179 P P P 7.68277927492546 7.93913624971394
7.97136248723504 P P P LNCV6_127661_PI430048170 mRNA
TCGGCCTGAGTTTGTGCAGCTTGTTAAGACAACTCTTGTGTACGCTATGTTGAAGCTCAA NM_006459 RefSeq chr10
- 100150089 100185977 ERLIN1 10613 ER lipid raft associated 1
GO:0005515|GO:0043234|GO:0005783|GO:0005789|GO:0016021|GO:0030433 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128299_PI430048170 0.9400091799727620.9900026748589630.500726602721672
0.2521459762974090.301066855784892 A A A 0.2636425339052080.247547442323987

0.574365231087263 A A A LNCV6_128299_PI430048170 mRNA
CCAAGGGAGAAATGAGAATTAGCTTAATTGCTGCCTTTAATGTGTTTTTGAGGAACTTAA NM_018713 RefSeq chr1
- 219914263 219928651 SLC30A10 55532 "solute carrier family 30, member 10, transcript variant 1"
GO:0005886|GO:0008324|GO:0006829|GO:0016021|GO:0006828 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_126805_PI430048170 0.1707370560628010 0.7236319301420778 2.2258359631136
8.21528998203185 8.42849578106051 P P P 8.35323645804774 8.73024135974976
9.10023564286922 P P P LNCV6_126805_PI430048170 mRNA
CTGCCTTCAACCACAGATCAAATACTTCAAGAGCCATTTAATAAATATGGCAGAACTATA NM_000946 RefSeq chr12
- 56731579 56752362 PRIM1 5557 "primase, DNA, polypeptide 1 (49kDa)"
GO:0006271|GO:0000082|GO:0016020|GO:0000723|GO:0006270|GO:0003896|GO:0000722|GO:0006269|GO:0005
654|GO:0000278|GO:0046872|GO:0032201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133697_PI430048170 0.00459028986542414 0.2306304320168717 .92717508387276
7.91174190756576 7.74038006140211 P P P 9.62608331687518 9.95397458078934
10.2815031037432 P P P LNCV6_133697_PI430048170 mRNA
CCTCCCGATTTGTTCACCTATTTTGTGCTTTAAATCTCAATAAAATACTTACTGAGGGAA NM_006275 RefSeq chr20
+ 43457863 43463604 SRSF6 6431 "serine/arginine-rich splicing factor 6, transcript variant 1"
GO:0008380|GO:0006369|GO:0010467|GO:0048025|GO:0006366|GO:0003723|GO:0010837|GO:0006376|GO:0031
124|GO:0045617|GO:0061041|GO:0006406|GO:0016607|GO:0000166|GO:0000381|GO:0000398|GO:0060501|GO:0
000380|GO:0060548|GO:0005654|GO:0036002 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138355_PI430048170 0.957996873059111 1.00196453454376 8.33371688554874
8.19801130826976 8.39701847994941 P P P 8.2026817702903 8.22771741380886
8.48030397098623 P P P LNCV6_138355_PI430048170 mRNA
TCTAGTGCCTAGTGTTGCTTTTCTGATGTAATAAAAGGTGGTCTGGCAGAACCTAAAAAA NM_021627 RefSeq chr3
+ 185586242 185631097 SENP2 59343 SUMO1/sentrin/SMT3 specific peptidase 2
GO:0005515|GO:0032091|GO:0060711|GO:0030111|GO:0060712|GO:0032875|GO:0015031|GO:2000045|GO:0009
950|GO:0035562|GO:0007507|GO:0005643|GO:0045944|GO:0006508|GO:0016055|GO:0031965|GO:0016926|GO:0
016925|GO:0060707|GO:0019904|GO:0016929|GO:0031410|GO:0016605|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142741_PI430048170 0.4004010680200390 .79927110995684 4.06097716676803 2.8352506257342
3.96404076371488 P A P 4.07021842710681 3.92092668278795 4.12037101911783 P P P
LNCV6_142741_PI430048170 mRNA
CATTTAGCCAAGAAATCCACAAGTAAAGTACTCTTATGAAAACTTGTAAGTCAGGATGCT NM_018341 RefSeq
chr6_KI270797v1_alt + 26823 56786 ERMARD 55780 "ER membrane-associated RNA degradation,
transcript variant 1" GO:0005789|GO:0007275|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_139460_PI430048170 0.2182473519866280 .6032040008288230 .309681197597743
0.3066331624317250 .496400137396815 A A A 0.3046624681681341 .52867024552017
1.21629798907546 A A A LNCV6_139460_PI430048170 mRNA
GCGCAGTCCAGAGCATGTATGAATAATCTCATAAAACAGTATCACAGACATTAAGCTAAA NM_031439 RefSeq chr8
- 10723767 10730574 SOX7 83595 SRY (sex determining region Y)-box 7
GO:0001706|GO:0003700|GO:0008285|GO:0006357|GO:0006366|GO:0044212|GO:0003705|GO:0005634|GO:0060
828|GO:0043280|GO:0043565|GO:0005737|GO:0045893|GO:0045892 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127926_PI430048170 0.7321489573240890 .9826915130701612 .6702617405273
12.7669226904465 12.6056024382208 P P P 12.6915759291567 12.6283964393678
12.7978603217471 P P P LNCV6_127926_PI430048170 mRNA
CCCCCAGACTAGCATGTGGTTCTATATTTGTAAAGTTATTGGGATAAGAAACAATTAAAC NM_052951 RefSeq chr20
+ 45791936 45811427 DNTTIP1 116092 "deoxynucleotidyltransferase, terminal, interacting protein 1"

GO:0006355|GO:0005730|GO:0005654|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126629_PI430048170 0.3715745038583420.7548986009346830.24435840020569 0.2723304434145320.326358016367023A A A 1.21862268473706 0.329626494806039 0.317393066546785A A A LNCV6_126629_PI430048170 mRNA GGACTGTATTCATCAAGGTATTATACCACAGCACTCTATGGAAATCTCAAGATTAGAAAA NM_152628RefSeq chr8 - 100572883 100649665 SNX31 169166 sorting nexin 31GO:0043234|GO:0035091|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_37505_PI430048170 0.5090990138786281.21146244813016 2.02513436376724 1.25438441578372 1.90760362368678 A A A 0.5641131013401492.23933240284666 1.15429479675091 A A A LNCV6_37505_PI430048170 mRNA AGAGACATGGGAGTGAAATTCACACCCACTCTGGCTTTCATACCATGGGTCTGAACATTA NM_001199743 RefSeq chr16 + 23641365 23673747 DCTN5 84516 "dynactin 5 (p25), transcript variant 4"
GO:0019886|GO:0005813|GO:0000777|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131689_PI430048170 0.0958595782956044 1.5168439483587 3.1988527659858 3.88182153894409 3.35673976156026 P P P 3.21185811360151 2.61019742478996 2.83884929936766 P P P LNCV6_131689_PI430048170 mRNA CCCTGGAAAACAGACGGGTCTGAGACTGAAATTGTTTTACCAGCTCCCAGGGTGGACTTC NM_021978RefSeq chr11 + 130159786 130210362 ST14 6768 suppression of tumorigenicity 14 (colon carcinoma)
GO:0016323|GO:0005886|GO:0004252|GO:0030216|GO:0005887|GO:0006508|GO:0008236|GO:0005615|GO:0019897|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142128_PI430048170 0.00431703735884078 0.4734280098584286.67950803825595 6.35403123084419 6.58293677267011 P P P 7.40352252368946 7.56095309157497 7.8681654002646 P P P LNCV6_142128_PI430048170 mRNA ACTCAATACCTAGAACTGCACCTAGCTCATGATGGTACCTAATAAATACTTCAATGAAAT NM_001130031 RefSeq chr19 - 9648661 9675100 ZNF562 54811 "zinc finger protein 562, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129304_PI430048170 0.000569193779056063 8.5368618661221 8.1594724386721 8.14013521877111 8.30857612236511 P P P 4.93923088825128 5.370424298005 4.98325525089982 P P P LNCV6_129304_PI430048170 mRNA AAGATGAAAACCTTTATGAAGGCCTGAACCTGGACGACTGCTCCATGTATGAGGACATCT NM_001783RefSeq chr19 + 41877119 41881372 CD79A 973 "CD79a molecule, immunoglobulin-associated alpha, transcript variant 1"
GO:0050853|GO:0042113|GO:0019815|GO:0005886|GO:0042100|GO:0005771|GO:0030183|GO:0045121|GO:0016021|GO:0009897|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145276_PI430048170 0.0532405277286399 1.22282037517165 12.847954215498 12.8562799094593 12.641454057478 P P P 12.4945923244497 12.5096158092857 12.4807926409209 P P P LNCV6_145276_PI430048170 mRNA ACCATTCCTTCCTCTTAGCCCCAGGAGCAAATTAAAAGGTACAGTTAAAATCCTAAAAAA NM_199184RefSeq chr6 - 43225628 43229473 DNPH1 10591 "2'-deoxynucleoside 5'-phosphate N-hydrolase 1, transcript variant 2"
GO:0009159|GO:0008283|GO:0030307|GO:0050144|GO:0005634|GO:0042803|GO:0005737|GO:0030855|GO:0009116|GO:0005654|GO:0009117|GO:0070694|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134885_PI430048170 0.2282927216720441.02524100303151 0.332383797997616 0.3274201247153940.267156202984302A A A 0.27052116825178 0.280962943484393 0.268465145589997A A A LNCV6_134885_PI430048170 mRNA ATAAATGGCTTTTGCTGAGTCAGTAGCGACCTAGAGCACTCTACTTATAGTCATTGAGTC NM_001080537 RefSeq chr3 + 63652667 63665215 SNTN 132203 "sentan, cilia apical structure protein" GO:0005929 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144650_PI430048170 0.0326067109831875 0.7158256856176285.85411200092768
5.79639342872676 6.14948957884061 P P P 6.26966219294787 6.3646469287632
6.61556446135666 P P P LNCV6_144650_PI430048170 mRNA
TGTGGTTTTTTCCCCTTTTTAATCTAACTGCCTGTTGACATTGACACTCATCACGGTTGT NM_002582RefSeq
chr16_KI270853v1_alt - 8556 203127 PARN 5073 "poly(A)-specific ribonuclease, transcript variant 1"
GO:0005515|GO:0010467|GO:0090305|GO:0019901|GO:0005730|GO:0005634|GO:0007292|GO:0046872|GO:0005
829|GO:0004535|GO:0004518|GO:0005737|GO:0000166|GO:0000184|GO:0009451|GO:0003730|GO:0000289|GO:0
000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137334_PI430048170 0.00829419915135755 0.4296192370853124.4165236111748
3.78622239753829 4.27446195953175 P P P 5.17004201529458 5.3182961709948
5.67142019724021 P P P LNCV6_137334_PI430048170 mRNA
GAGGAATTTGCTGTTGACAGCCAAAGTATAGTGTACAAGATTGATGTAACTTGATATGTA NM_001286792 RefSeq
chr13 + 23979625 24307074 SPATA13 221178 "spermatogenesis associated 13, transcript variant 3"
GO:0005515|GO:0030334|GO:0030032|GO:0032587|GO:0030175|GO:0032855|GO:0030027|GO:0005085|GO:0043
547|GO:0005737|GO:0016477|GO:0046847|GO:0005654|GO:0030676 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141718_PI430048170 0.00511013574242699 0.5551550798766138.22569468105035
7.86621584095164 8.14886311334646 P P P 8.82042316788624 8.93491578617036
9.04788060581723 P P P LNCV6_141718_PI430048170 mRNA
GATGTGGGATGAACCTGGAATGAACGAATTAAATAAAGACATGCATCCATCTGTCAGCGA NM_001040445 RefSeq
chr2 + 238426984 238452250 ASB1 51665 ankyrin repeat and SOCS box containing 1
GO:0042036|GO:0035556|GO:0005622|GO:0030539|GO:0003674|GO:0016567 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133207_PI430048170 0.35622834472884 0.9456393821957697.07513913791474
7.04359786717414 7.09827567075512 P P P 7.0594569514972 7.27714230956234
7.11385691737256 P P P LNCV6_133207_PI430048170 mRNA
AAAGACGCCAGAGTTCTCGCTGAAGAATGTGAGAATTCCTGTGCATTGTTTTTTCTGATG NM_014285RefSeq chr9
+ 130693759 130704894 EXOSC223404 "exosome component 2, transcript variant 1"
GO:0034475|GO:0005515|GO:0010467|GO:0034427|GO:0030307|GO:0006364|GO:0071038|GO:0008312|GO:0071
035|GO:0005730|GO:0043928|GO:0004532|GO:0005634|GO:0071034|GO:0000178|GO:0005829|GO:0071051|GO:0
005737|GO:0000175|GO:0000177|GO:0000176|GO:0071049|GO:0000467|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129582_PI430048170 0.3795856228557841.17553875939631 0.505516999743241
0.5106991729928351.06911151906506 A A A 0.40304298258337 0.5541988415658220.4995979454111
A A A LNCV6_129582_PI430048170 mRNA
GTAGAGGTTTCCGGGCAGTAATTCTATCCAACTTAAAAAGGCTCTTTTAAGAGCCGCCTA NM_003534 RefSeq
chr6 - 26270917 26271384 HIST1H3G 8355 "histone cluster 1, H3g"
GO:0005515|GO:0010467|GO:0046982|GO:0006325|GO:0006335|GO:0005576|GO:0005634|GO:0000228|GO:0003
677|GO:0032776|GO:0043234|GO:0060968|GO:0016020|GO:0000183|GO:0007596|GO:0045814|GO:0040029|GO:0
005654|GO:0000786|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126806_PI430048170 0.0343121404375171 0.74717257462719 5.83241646250228
5.87632977287978 6.06255388421321 P P P 6.17222493370601 6.3230671938191
6.52600574978021 P P P LNCV6_126806_PI430048170 mRNA
TGCATTCTGTAGGAAATGAAACGTGAATTTAACTCGGGTTGCAAGAAATAAAAATGTCAG NM_004782 RefSeq
chr22 + 20859003 20891213 SNAP29 9342 "synaptosomal-associated protein, 29kDa"
GO:0000046|GO:0019905|GO:0043005|GO:0005813|GO:0016082|GO:0030054|GO:0005886|GO:0045202|GO:0031
201|GO:0006887|GO:0015031|GO:0006903|GO:0005484|GO:0005737|GO:0061025|GO:0031629 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_107146_PI430048170 0.351092586564609 1.03587155466321 0.413083308284637 0.280494874482047 0.301492234386733 A A A 0.267526649485505 0.309624199504234 0.268532905503205 A A A LNCV6_107146_PI430048170 mRNA TTCAAGCCAGCGAATTTATTCCTTAAAACCAGAAACTGAACCTCGGCACGGGAAAGGAGT NM_002998 RefSeq chr8 + 96493653 96611809 SDC2 6383 syndecan 2 GO:0005515|GO:0007603|GO:0005886|GO:0045202|GO:0044281|GO:0031000|GO:0007411|GO:0030198|GO:0043025|GO:0030204|GO:0030203|GO:0043202|GO:0001666|GO:0048013|GO:0005975|GO:0005796|GO:0006027|GO:0030165|GO:0001523|GO:0006024|GO:0048814|GO:0008150|GO:0048813|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130022_PI430048170 0.213348689244566 0.66842164307708 2.25276578377311 1.84018141502125 2.75460160648699 A A A 2.42682602163627 3.3894210206133 2.75002159102461 A P P LNCV6_130022_PI430048170 mRNA CCTAAAAATTGTCAAAAACAGTCAATAGGGCTACTGCTGGCCCAAAGACCATTTAGGTCC NM_020886 RefSeq chr11 - 113797874 113875570 USP28 57646 "ubiquitin specific peptidase 28, transcript variant 1" GO:0005515|GO:0016579|GO:0004843|GO:0008283|GO:0005730|GO:0005634|GO:0006974|GO:0004197|GO:0043234|GO:0042771|GO:0034644|GO:0006281|GO:0061136|GO:0010212|GO:0043161|GO:0005654|GO:0000077 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129139_PI430048170 0.500190161449324 1.04363729656014 0.296454960049337 0.306388710643992 0.513977794020791 A A A 0.323680750706298 0.282626359756113 0.335736698092831 A A A LNCV6_129139_PI430048170 mRNA GCAGCTAATTTTACTGTAAAGAAGGGCCATGGTATAGTAGATAAATAAAATCCAAGGCAA NM_003126 RefSeq chr1 - 158610705 158686716 SPTA1 6708 "spectrin, alpha, erythrocytic 1" GO:0030097|GO:0005515|GO:0007009|GO:0008091|GO:0046982|GO:0008360|GO:0005509|GO:0031235|GO:0032437|GO:0014731|GO:0015629|GO:0051693|GO:0032092|GO:0005829|GO:0051015|GO:0006779|GO:0007411|GO:0042102|GO:0005200|GO:0007015|GO:0002260 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132164_PI430048170 0.635968000095023 0.774235207965608 1.04299726428551 0.324139013208905 0.398069758210075 A A A 0.363465848438999 0.452599475859789 1.73348059802337 A A A LNCV6_132164_PI430048170 mRNA CTGTCTAACAAGCACTCTTTGAAAGCAAAGATGTTTTAGTGTTCAGCTTTTAAATTGAGC NM_001080521 RefSeq chr11 + 13009422 13012106 RASSF10 644943 Ras association (RalGDS/AF-6) domain family (N-terminal) member 10 GO:0007165|GO:0000922|GO:0005815|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129110_PI430048170 0.169290211872917 0.844171635264583 6.35389559724088 6.52193719937335 6.78003352973604 P P P 6.74062040191171 6.81823473851655 6.85985973146706 P P P LNCV6_129110_PI430048170 mRNA CAATTAAACTTTTTTCTACAATGTATTTGTTTGCGAGTAGGACTTGGGAGTCATTGGGAA NM_032390 RefSeq chr2 - 121726944 121736927 NIFK 84365 nucleolar protein interacting with the FHA domain of MKI67 GO:0005515|GO:0016072|GO:0005737|GO:0000794|GO:0006461|GO:0000166|GO:0010923|GO:0009303|GO:0003723|GO:0005730|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131670_PI430048170 0.497191568458314 0.882159561676667 0.624006193938004 0.509686722146622 0.559313147794678 A A A 1.09804387720754 0.526802162205393 0.536032669202384 A A A LNCV6_131670_PI430048170 mRNA CTTCAGAAATCATGTCTGTAAATTAGATGAGCCAAAATAAAGGACAATTGGGTTGATGCT NM_000138 RefSeq chr15 - 48408305 48645788 FBN1 2200 fibrillin 1 GO:0001656|GO:0005515|GO:0035583|GO:0035582|GO:0005509|GO:0005578|GO:0071560|GO:0001527|GO:0005576|GO:0005615|GO:0005604|GO:0031012|GO:0007507|GO:0001501|GO:0022617|GO:0030198|GO:0070062|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139631_PI430048170 0.193655517434889 0.791946989209171 0.372307661621985 0.363122098497028 0.271492689533998 A A A 0.945324904241611 0.366896613109381 0.648512535015509 A A A LNCV6_139631_PI430048170 mRNA TGCAACTGTCACTGGCAACATGGAATCTAAAGAAGAGAGAAGATGTGAGGACCCTTCCAA NM_001277372 RefSeq chr2 + 202073254 202197163 KIAA2012 100652824 KIAA2012 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116823_PI430048170 0.107797477215644 0.931269541690601 0.272078844752711 0.278198508129983 0.301001006945658 A A A 0.457161216990215 0.370658674660961 0.328824307711352 A A A LNCV6_116823_PI430048170 mRNA ACAGACATTAGCATGTCAGACTTCGAGAACTCCAGGGAATTTGGAGCCAATGACAACATG NM_002644 RefSeq chr1 - 206928521 206946466 PIGR 5284 polymeric immunoglobulin receptor GO:0043235|GO:0007173|GO:0005886|GO:0002415|GO:0005887|GO:0001895|GO:0001792|GO:0038093|GO:0043113|GO:0005615|GO:0001580|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140044_PI430048170 0.134617078930642 2.33710288871862 3.58535179551721 3.48001741228644 4.28857930570283 P P P 1.30525993905737 2.22710613800166 3.47496906483122 A A P LNCV6_140044_PI430048170 mRNA GGGTAGAGTTCTGAAGGAGAACTACTGGTCTTATTGTACACTTGCTGTACCTATTTTTAT NM_205855 RefSeq chr7 - 135729597 135748846 FAM180A 389558 "family with sequence similarity 180, member A" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143974_PI430048170 0.400256585290139 0.815645639135357 8.56605689310568 7.89570785781755 7.84865934637413 P P P 8.73179707792369 8.494108148861 7.986059889849 P P P LNCV6_143974_PI430048170 mRNA GAAGATTCCTAAAATTTGAGAGACAAAATAAATGGAAGACATGAGAACCTTCCAGAGTCC NM_002116 RefSeq chr6_GL000256v2_alt + 1240283 1243714 HLA-A 3105 "major histocompatibility complex, class I, A, transcript variant 1 (A*03:01:0:01 allele)" GO:0005515|GO:0002474|GO:0005886|GO:0005783|GO:0019221|GO:0042608|GO:0006955|GO:0060337|GO:0042605|GO:0030670|GO:0071556|GO:0016032|GO:0070062|GO:0060333|GO:0042270|GO:0032729|GO:0012507|GO:0030881|GO:0002480|GO:0005794|GO:0002486|GO:0009986|GO:2000568|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134906_PI430048170 0.254596197869659 0.383725065206968 0.494148125900643 0.665976341093468 0.628827554330434 A A A 1.82822258411963 2.79521717567944 0.425232086574661 A P A LNCV6_134906_PI430048170 mRNA GGAATGAATACTTCAGATGCTTTCAGGAGTGACACAAGAACACAATGATTTTTGCTTATA NM_182680 RefSeq chrX + 11293412 11300761 AMELX 265 "amelogenin, X-linked, transcript variant 3" GO:0005515|GO:0030345|GO:0034505|GO:0009986|GO:0008283|GO:0070172|GO:0070166|GO:0005578|GO:0050801|GO:0001837|GO:0031214|GO:0001649|GO:0042802|GO:0007165|GO:0032967|GO:0046848|GO:0002062|GO:0042475|GO:0007155|GO:0008083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134553_PI430048170 0.218473807870303 1.28645879359989 9.58880559744741 9.63720164356538 9.69660046140007 P P P 9.68316119188245 8.93144180972346 9.10921667105178 P P P LNCV6_134553_PI430048170 mRNA TGTAACGTTCGCGTTAGGAAAGATGGTGTTTATTCCAGTTTGCATTTTTATGGTGAAATA NM_005088 RefSeq chrY + 1591592 1602518 AKAP17A 8227 "A kinase (PRKA) anchor protein 17A, transcript variant 1" GO:0005515|GO:0006397|GO:0008380|GO:0006355|GO:0005634|GO:0007165|GO:0042113|GO:0005737|GO:0000166|GO:0016607|GO:0005654|GO:0005681|GO:0043484|GO:0051018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139400_PI430048170 0.0731827148394339 0.923885923533791 0.403620216851559 0.416365609910393 0.337471260413727 A A A 0.427896112834293 0.517133558696804 0.553428663126342 A A A LNCV6_139400_PI430048170 mRNA

GGGTGGGTAGACTTAGGAATTTTCTACTTGGTAAAAGCATTATACAGTCATAGGAGAAAG NM_001098535 RefSeq chr22 + 32357866 32361161 RFPL3 10738 "ret finger protein-like 3, transcript variant 1" GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137844_PI430048170 0.0458964468731549 0.578237991996038 5.57326650812509 5.56145027661998 6.1885479007735 P P P 6.53939319123033 6.49872416089567 6.73739761663882 P P P LNCV6_137844_PI430048170 mRNA
CTAGTGAAACTAGTGGATTTCTCTTCTTCCTCTTTATTTTCTGCATGTTAAATGTGAACC NM_024616 RefSeq chr3 + 112086334 112118197 C3orf52 79669 "chromosome 3 open reading frame 52, transcript variant 2" GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127648_PI430048170 0.00552965515093555 0.501506338327304 3.61905483578028 3.35719037065728 3.23272946222661 P P P 4.65085367188239 4.18586337454952 4.34740368936164 P P P LNCV6_127648_PI430048170 mRNA
TTGTGTTGCCCCTTTGGCCCCATTAAGCAGTAATAAACATTTGTTCTGAAGTCCAAAAAA NM_001243765 RefSeq chr1 + 174799896 174995308 RABGAP1L 9910 "RAB GTPase activating protein 1-like, transcript variant 4" GO:0032880|GO:0017137|GO:0005794|GO:0032851|GO:0005634|GO:0005769|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137008_PI430048170 0.827750056113499 0.993310843441546 0.392742199578163 0.364168421120203 0.249976486798792 A A A 0.328677770533786 0.361708666910844 0.349277380740795 A A A LNCV6_137008_PI430048170 mRNA
ACCTAAAAGGACCTGGGAGTACTTCAGTCCCTTATCCTAATCAGCCTTTCTAGACCCATA NM_020365 RefSeq chr1 - 44850521 44986722 EIF2B3 8891 "eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa, transcript variant 1" GO:0005515|GO:0005851|GO:0010467|GO:0051716|GO:0009408|GO:0016779|GO:0043434|GO:0003743|GO:0006412|GO:0006413|GO:0005829|GO:0009749|GO:0043547|GO:0005085|GO:0032057|GO:0005737|GO:0014003|GO:0044267|GO:0008135 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122789_PI430048170 0.0116934571895529 0.404924850852589 3.70568011933227 3.01094053696153 3.11636156807491 P P P 4.6937095939313 4.37689392713955 4.74895948860062 P P P LNCV6_122789_PI430048170 mRNA
GTGGCTCCTATTATGTACAATTTTAGTGCTAAGTACTGTGTTAATGATGGCTATCAAACA NM_152395 RefSeq chr3 + 131381764 131388830 NUDT16 131870 "nudix (nucleoside diphosphate linked moiety X)-type motif 16, transcript variant 2" GO:0008284|GO:0005634|GO:0044281|GO:0003729|GO:0035870|GO:0006382|GO:0042803|GO:0035863|GO:0005737|GO:0030515|GO:0006508|GO:0000287|GO:0030145|GO:0005730|GO:0055086|GO:0006402|GO:0005525|GO:0046709|GO:0050072|GO:0016077|GO:0090068|GO:0034656|GO:2000233|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129271_PI430048170 0.589133336891388 1.06710252293001 9.25644907835101 9.11974989687791 9.16759422751535 P P P 8.74294005270878 9.10616115445435 9.35280758315778 P P P LNCV6_129271_PI430048170 mRNA
ACCCTGGTGTACCTCTCAGTGGCAGAATAAACATCAACACAGGTTCAAGAACTGAAAAAA NM_002490 RefSeq chr22_KI270928v1_alt - 7870 13229 NDUFA6 4700 "NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa" GO:0022904|GO:0031966|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0008137|GO:0006979|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136105_PI430048170 0.0563220454041341 1.81193570014387 4.23393253031817 4.85242988276111 4.48535469061477 P P P 3.85622481352857 3.94957197260839 3.13050387211734 P P P LNCV6_136105_PI430048170 mRNA
AGATCTCCGTGATGACAGCCACCATAGTCTTCATTATGATCCCCTTCTCTCTGATTGTCA NM_206899 RefSeq chr12 + 55636891 55637833 OR10P1 121130 "olfactory receptor, family 10, subfamily P, member 1" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA

NA NA NA NA NA NA NA
LNCV6_52277_PI430048170 0.0473962904744439 0.448390606545585 0.323785532308739
0.309130910906739 1.18997464405842 A A A 1.79131621207722 1.73671576989072
1.94432486225277 A A A LNCV6_52277_PI430048170 mRNA
ACCGGATCCCCCAGATCCTCAACATGGCCTCAGAACTGGAGTTCAACTTAGAGACGATGC NM_005424 RefSeq
chr1 + 43300894 43323110 TIE1 7075 "tyrosine kinase with immunoglobulin-like and EGF-like
domains 1, transcript variant 1"
GO:0005515|GO:0030336|GO:0018108|GO:0001525|GO:0001701|GO:0005524|GO:0007165|GO:0005887|GO:0045
026|GO:0016525|GO:0007498|GO:0032526|GO:0004714|GO:0001570 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_82782_PI430048170 0.710099371034576 0.883094222878996 3.01869182263484
0.859883434376778 2.68841052973622 P A A 2.35889836073801 1.88478128235625
3.2793157505698 A A P LNCV6_82782_PI430048170 mRNA
TGACAAGCTTTCCACTCACAGGGGAGAGGCTACTGCAGAACCTGACGGTTCAGGCTGAGT NM_024742 RefSeq
chr16 + 31458995 31467167 ARMC5 79798 "armadillo repeat containing 5, transcript variant 2"
GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130918_PI430048170 0.00634791292778689 0.837928755496285 11.7474501318228
11.6932984045674 11.8177005274504 P P P 11.9449717618129 12.0498133890015
12.0295370883947 P P P LNCV6_130918_PI430048170 mRNA
CAGCACTCGATTGTTGTAAACTGTTGTTTTGTATGAGCGAAATTGTCTTTACTAAACAGA NM_004759 RefSeq chr1
+ 206685019 206734285 MAPKAPK2 9261 "mitogen-activated protein kinase-activated protein
kinase 2, transcript variant 1"
GO:0019369|GO:0005515|GO:0010467|GO:0006691|GO:0051403|GO:0034605|GO:0002756|GO:0018105|GO:0000
165|GO:0002755|GO:0032496|GO:0070062|GO:0005813|GO:0048839|GO:0038124|GO:0038123|GO:0032680|GO:0
034134|GO:0006950|GO:0002224|GO:0045087|GO:0005654|GO:0032675|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144058_PI430048170 0.00774547815699949 1.34420289347947 14.1987427584315
14.2461272237781 14.1184678540716 P P P 13.8007632592852 13.8408810023349
13.6362717197335 P P P LNCV6_144058_PI430048170 mRNA
TGGGACATGTTTGCAATAAAGGAAAGGTTTGTGGCGCCTGTCATGGCAGGCATCTCATGG NM_025072 RefSeq
chr9 - 128120692 128128462 PTGES2 80142 "prostaglandin E synthase 2, transcript variant 1"
GO:0048471|GO:0015035|GO:0009055|GO:0005634|GO:0003677|GO:0046903|GO:0016829|GO:0005829|GO:0005
739|GO:0050220|GO:0043295|GO:0000139|GO:0001516|GO:0045454|GO:0016021|GO:0045893|GO:0055114|GO:0
020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140129_PI430048170 0.0707795358707238 1.25779737172902 10.6553452687244
10.6315898233206 10.6350393832037 P P P 10.1891008477107 10.2279560416419
10.4930034540399 P P P LNCV6_140129_PI430048170 mRNA
AGTGGATTGACTCCTTTGCTGAAGTCAGTTATTCATCAAGAATGCAATTAGACTAATTGT NM_014018 RefSeq
chr8 - 79918859 80030271 MRPS28 28957 mitochondrial ribosomal protein S28
GO:0070124|GO:0005739|GO:0070125|GO:0008150|GO:0070126|GO:0032543|GO:0006996|GO:0005743|GO:0005
763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134088_PI430048170 0.0362849360888698 0.491235437887021 3.87203284201046
3.95251296012232 4.64178626559029 P P P 4.79115012243858 5.20291342405443
5.57355150953152 P P P LNCV6_134088_PI430048170 mRNA
GTAAGGATATACTTAGCTACATTTTCAGTCAGTATGAACTTCCTGATACAAATGTAGGGA NM_024420 RefSeq
chr1 + 186828899 186988981 PLA2G4A 5321 "phospholipase A2, group IVA (cytosolic, calcium-
dependent)"
GO:0046456|GO:0019369|GO:0005743|GO:0035965|GO:0044281|GO:0006690|GO:0005829|GO:0005544|GO:0005
737|GO:0004622|GO:0042127|GO:0047498|GO:0004623|GO:0006654|GO:0071236|GO:0050482|GO:0005794|GO:0

006663|GO:0036149|GO:0005509|GO:0036148|GO:0030168|GO:0036150|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136269_PI430048170 0.223921420484611 0.946785240706408 0.251900514930584 0.350822806817365 0.287987459801462 A A A 0.459781233088367 0.354119706231682 0.311142881123283 A A A LNCV6_136269_PI430048170 mRNA
CAATGGGATCTTTTAAGTACTCTTCAGTTTGTTCCAAGAAATGTGCCTACTGAAATCAAA NM_198465 RefSeq chrX + 105822542 105958610 NRK 203447 Nik related kinase
GO:0035556|GO:0060721|GO:0005737|GO:0005083|GO:0008285|GO:0007567|GO:0004702|GO:0007256|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139838_PI430048170 0.0263010053059081 0.460541796919481 4.35357442340657 3.50809101224368 3.69119243351867 P P P 4.63746949757702 5.15498629555435 5.19467898946239 P P P LNCV6_139838_PI430048170 mRNA
CAGCCAATGGGGAGGAATAGGATAATGCAAACACATGTTTTGTTTTCTCATTTTCAAATA NM_181352 RefSeq chr12 + 14385063 14502935 ATF7IP 55729 "activating transcription factor 7 interacting protein, transcript variant 1"
GO:0005515|GO:0005667|GO:0045898|GO:0006200|GO:0003714|GO:0006325|GO:0005634|GO:0000122|GO:0006351|GO:0006306|GO:0005737|GO:0016032|GO:0005654|GO:0045893|GO:0045892|GO:0016887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133971_PI430048170 0.426396270182679 1.22094960494059 5.14019172592611 4.50123827915144 4.32294447611215 P P P 4.25541915436843 4.55720297816404 4.40483751471387 P P P LNCV6_133971_PI430048170 mRNA
CTAAAAGGGGCCAGCCTCCTGGCTCCTGCTTGTAGATGGATGAAATAGCACCAGATATGT NM_080608 RefSeq chr20 - 45886490 45887599 SPATA25 128497 spermatogenesis associated 25
GO:0003674|GO:0016021|GO:0007283|GO:0005575|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94928_PI430048170 0.123775850604067 0.821351796987901 11.807847476995 11.7317418060165 12.0513415104754 P P P 11.9301194529073 12.2470851022226 12.2614592185658 P P P LNCV6_94928_PI430048170 mRNA
CTTAGTGTTCCTTGCATTTTGGGACAGAATGGAATCTCAGACCTTGTGAAGGTGACTCTG NM_001165414 RefSeq chr11 + 18396265 18408218 LDHA 3939 "lactate dehydrogenase A, transcript variant 3"
GO:0005515|GO:0044262|GO:0005634|GO:0044281|GO:0006096|GO:0005829|GO:0005739|GO:0004459|GO:0016020|GO:0006090|GO:0021762|GO:0035686|GO:0031668|GO:0044237|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133329_PI430048170 3.84441434437751e-05 0.344909312486321 6.67699022983844 6.85026136193928 6.84229011985405 P P P 8.2468886205139 8.31354547501177 8.41763166439964 P P P LNCV6_133329_PI430048170 mRNA
AACATGATTTTAAATTATGTGCCTTTACTGCAGCTTTCTTGCTCTCTTTGTGTGTGTGCA NM_001304944 RefSeq chr12 + 49346916 49353684 DNAJC22 79962 "DnaJ (Hsp40) homolog, subfamily C, member 22, transcript variant 1" GO:0042026|GO:0051087|GO:0051082|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73389_PI430048170 0.00268755700525528 2.09600703418302 4.21291609388015 4.22445322979719 4.57755914308429 P P P 3.44818332256252 3.1190820832178 3.25623863524691 P P P LNCV6_73389_PI430048170 mRNA
ATTGGAAAAGCTCAACTTGAAGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTAT NM_212543 RefSeq chr3 - 119211741 119240905 B4GALT4 8702 "UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4, transcript variant 1"
GO:0005975|GO:0044281|GO:0008378|GO:0046872|GO:0042339|GO:0000139|GO:0003945|GO:0018146|GO:0032580|GO:0009405|GO:0016021|GO:0044267|GO:0030203|GO:0006643|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137147_PI430048170 0.7569381537500740.9339775487062083.88578014685591
3.63153077886888 3.81150185701761 P P P 2.85628617654161 2.86374868787556
4.88796808416024 P P P LNCV6_137147_PI430048170 mRNA
CAGCTGTTTCTAAACCCAGACACTGTTTGTAATAGACTGGAAATAAAATGTTCTTTCCTT NM_173660RefSeq chr4
+ 3463305 3494482 DOK7 285489 "docking protein 7, transcript variant 1"
GO:0031594|GO:0030054|GO:0019901|GO:0005886|GO:0007528|GO:0061098|GO:0005158|GO:0043113|GO:0035
091 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141437_PI430048170 0.3560184837591620.3080281997786750.257664210187592
0.2661230132203370.397193451882719A A A 0.6433442692328363.20857820317577
0.327034555060806A P A LNCV6_141437_PI430048170 mRNA
GTGGTCTTCTGTGATTATTTATGCTGCCTCCCAAGGATAGAATTGAAATAAAATGTTTTC NM_001190457 RefSeq
chr15 + 68631987 68727805 CORO2B 10391 "coronin, actin binding protein, 2B, transcript variant 3"
GO:0005737|GO:0051015|GO:0030036|GO:0016020|GO:0003779|GO:0015629 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140159_PI430048170 0.30673381185474 1.04819897337508 0.49264181046549
0.3311793805222810.420163295010534A A A 0.2900485031525760.356151343027373
0.39657199410182 A A A LNCV6_140159_PI430048170 mRNA
ATTCAAGAATCTGAAAAGTAGACAAGAGGACTCCAGTTGCCTCAGGTTGGTTCTGCTGTG NM_001122853 RefSeq
chr5 + 150660840 150679368 MYOZ3 91977 "myozenin 3, transcript variant 1"
GO:0005515|GO:0030018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137057_PI430048170 0.5570582752978220.9834747349792080.280610065054588
0.2932390699504820.385791964925616A A A 0.3716224234280870.312639037541928
0.349188912255939A A A LNCV6_137057_PI430048170 mRNA
TTCCAGAACCGACGCTACAAATGCAAGAGACAGCGCCAGGACAAGTCGCTGGAACTGGCT NM_001136271
RefSeq chr8 - 23702450 23706598 NKX2-6 NA NK2 homeobox 6 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136706_PI430048170 0.52909771974379 0.9182898745023640.467466783859421
0.6864440508699960.411734277044301A A A 0.9143424257567840.498626515132085
0.494975852721186A A A LNCV6_136706_PI430048170 mRNA
GGCAGACAATTGCAATACTTGTACTAAACACTGGAATACAAATGCATGACTCATATCTAT NM_014978RefSeq chr10
+ 104641100 105265242 SORCS3 22986 sortilin-related VPS10 domain containing receptor 3
GO:1900452|GO:0016020|GO:0007218|GO:0007613|GO:0016021|GO:0007612|GO:0008188 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_113691_PI430048170 0.4489560141526960.9592541298138459.54441644581402 9.3946271767633
9.45167098344949 P P P 9.63156351158291 9.45381468058748 9.48299039083265 P P P
LNCV6_113691_PI430048170 mRNA
AGAGGATGAGACCATTGATGCCGAGGTCATGAACTCTCTAGCAGTTACTATGGATGACTT NM_007126RefSeq chr9
- 35056067 35072742 VCP7415 valosin containing protein
GO:0005515|GO:0048471|GO:0045732|GO:0016567|GO:0006200|GO:0005783|GO:0032436|GO:0005634|GO:0034
214|GO:0032403|GO:0019985|GO:0045184|GO:0043231|GO:0042802|GO:0030968|GO:0005829|GO:0006302|GO:0
008289|GO:0034605|GO:0005737|GO:0031334|GO:0035800|GO:0051260|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_102152_PI430048170 0.0054988068992353 0.6277142905345863.06845155250565
3.0835143877195 2.87404752706242 P P P 3.65623290115372 3.72815525902465
3.66532852601924 P P P LNCV6_102152_PI430048170 mRNA
CCCTTGCCAGCACATGAAAACAAACTGGAATTTGTATATATAAGCATTGTGTATGTATTC NM_005751RefSeq chr7
+ 91940874 92110673 AKAP9 10142 "A kinase (PRKA) anchor protein 9, transcript variant 2"
GO:0005515|GO:0060306|GO:0007268|GO:0015459|GO:0007283|GO:0060307|GO:0086091|GO:0036064|GO:0005
829|GO:0043231|GO:0033138|GO:0060009|GO:0000086|GO:0008076|GO:0006810|GO:0005856|GO:0000242|GO:0

005813|GO:0006996|GO:0005794|GO:0005102|GO:0044325|GO:0007165|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134506_PI430048170 0.2650468655023841.19428559319246 3.41351632244464 3.93110671480593 3.69581810382444 P P P 3.66496650205938 3.36014368795066 3.26184527043742 P P P LNCV6_134506_PI430048170 mRNA ATGTGAACATGGACTCGAAGACATGGCCCTTTCTCTGTAGTTGATTTTTTAAATGTGCCA NM_006039RefSeq chr17 + 62627400 62693601 MRC2 9902 "mannose receptor, C type 2"
GO:0005515|GO:0016020|GO:0030574|GO:0005518|GO:0030246|GO:0016021|GO:0005925|GO:0001649|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145235_PI430048170 0.2448781875342710.8098857886873898.87839583045702 8.78842720894396 9.23985812735662 P P P 8.94269859360131 9.3517243492306 9.50810590242374 P P P LNCV6_145235_PI430048170 mRNA CTATACTTGTGTTTTGTTTGGGGGCTGGGAAATGTATTTTTACATTGTAGCCAATCATTTNM_017801RefSeq chr3 - 32481311 32502911 CMTM6 54918 CKLF-like MARVEL transmembrane domain containing 6
GO:0016020|GO:0006935|GO:0016021|GO:0005615|GO:0005125|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137448_PI430048170 0.00105499509256559 0.4750348037174775.3532782944686 5.05132148758738 5.12797204218927 P P P 6.13007559446965 6.33923993451046 6.29397368832403 P P P LNCV6_137448_PI430048170 mRNA GTTCTTCTCTGTATGCTGTTGACCTAATGATTTATGCAATCTCTGTAATTTCTTATGCAG NM_032813RefSeq chr13 - 100603835 100674935 TMTC4 84899 "transmembrane and tetratricopeptide repeat containing 4, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126833_PI430048170 0.2964774030310581.20352756954954 3.63324174489194 3.8111204185148 4.06694967006014 P P P 3.67139943799818 3.18434102705769 3.8142713250381 P P P LNCV6_126833_PI430048170 mRNA GGGGATACAGTTAAATGTAGCAACTCTTGAGTTCATTTTTTCCCACTGTAGCAAAATTAA NM_001130415 RefSeq chr12 + 12725916 12791465 APOLD1 81575 "apolipoprotein L domain containing 1, transcript variant 1"
GO:0001666|GO:0005886|GO:0006869|GO:0042157|GO:0042118|GO:0005576|GO:0016021|GO:0001525|GO:0030154|GO:0045601|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129814_PI430048170 0.0791909086960661.05220038148896 0.437944291264225 0.4954025011817320.483769868204465A A A 0.3554854116148840.399576358988196 0.44119112184308 A A A LNCV6_129814_PI430048170 mRNA CGGGACCCTGAGTATTGAGCTCTGGTGAATAAAAAGGTTTTCTAGTCGTCTTTGAAAAAA NM_001029861 RefSeq chr19 - 45913214 45914778 NANOS2 NA nanos homolog 2 (Drosophila) NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133768_PI430048170 0.1701212844148190.9591391396027860.27558228197219 0.3404195590629550.3124070838494 A A A 0.4270622439489220.335783833696388 0.345099251437997A A A LNCV6_133768_PI430048170 mRNA TATGTGAGGTCAAAACCAAACTCTTATTCTCAGTGGAAAACTCCAGTTGTAATGCATATT NM_006922RefSeq chr2 - 165087519 165204067 SCN3A 6328 "sodium channel, voltage gated, type III alpha subunit, transcript variant 1"
GO:0005737|GO:0086010|GO:0005886|GO:0005248|GO:0035725|GO:0034765|GO:0001518|GO:0006814|GO:0019228 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138911_PI430048170 0.0526578204333106 1.79447108433624 2.9827212959114 3.59510318782851 3.39963300136004 P P P 2.91608174419014 2.40115108128042 2.06705841330425 P P A LNCV6_138911_PI430048170 mRNA CCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTAATCATAACA NM_001184830 RefSeq chrX - 66021737 66040125 VSIG4 11326 "V-set and immunoglobulin domain containing 4, transcript

variant 4" GO:0032703|GO:0006957|GO:0005515|GO:0016021|GO:0070062|GO:0042130 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140703_PI430048170 0.0104499841212638 0.2622639293884220.336394742483087 0.3381472309650830.397752589846973A A A 2.44674719208392 1.85891111745523 2.47987668833407 A A P LNCV6_140703_PI430048170 mRNA
GTATTACTATGATGCACACCTATGACCCAAGGCCCTCATAAAGATACCATGTGTGACAAA NM_001080446 RefSeq chr11 - 45906534 45907282 C11orf94 NA chromosome 11 open reading frame 94 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132792_PI430048170 0.0326641443216466 1.87312793635117 4.31701879623134 3.60212415156834 3.81523418293338 P P P 2.90558154160954 2.78614456033719 3.35728987947827 P P P LNCV6_132792_PI430048170 mRNA
GAACCCTGCAACATGTTAGACATTACCGTAAAATTAAAACGCACAAATTTGCAGATCAAA NM_001146288 RefSeq chr22 + 20967158 20981360 AIFM3 150209 "apoptosis-inducing factor, mitochondrion-associated, 3, transcript variant 3"
GO:0005739|GO:0051537|GO:0005783|GO:0050660|GO:0016491|GO:0005743|GO:0097194|GO:0045454|GO:0005634|GO:0046872|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132072_PI430048170 0.0878692796679162 0.8872237551873888.57773640653154 8.50952496829415 8.36689582649784 P P P 8.610042618678 8.64498249483676 8.72266285603428 P P P LNCV6_132072_PI430048170 mRNA
TCATGTCACTGAGTTCCAGCCGCTTTTAGAGTAAAGTCGTTTATCATCAAAGCCAAAAAA NM_014698RefSeq chr1 - 225845531 225882720 TMEM63A 9725 transmembrane protein 63A
GO:0000166|GO:0016021|GO:0005765|GO:0070062|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143185_PI430048170 0.209319435351935 1.21855281946387 4.53785545341165 4.2561253880802 4.15448950838294 P P P 3.84770115715536 4.33247689300765 3.88893786770925 P P P LNCV6_143185_PI430048170 mRNA
CTCCTCGGCACCTGGTTATTAAGAACTGAATATTTTTCCACTTGAATTTAGTGCTATTAG NM_001079843 RefSeq chr1 - 10636605 10796676 CASZ1 54897 "castor zinc finger 1, transcript variant 1"
GO:0006355|GO:0005737|GO:0007275|GO:0005654|GO:0003677|GO:0046872|GO:0006351|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132406_PI430048170 0.446981115082518 1.16666005251512 0.343036985432894 0.3738601343746130.972027084215662A A A 0.3734341226119510.383942383739854 0.354985545053607A A A LNCV6_132406_PI430048170 mRNA
ACACCATCTGCTGTTCGTGGATTTCAACCTATTGAGATACAGCAGGTTATAGTCTCCGAA NM_005193RefSeq chrX + 73447253 73454585 CDX4 1046 caudal type homeobox 4
GO:0060711|GO:0001077|GO:0001568|GO:0045944|GO:0005634|GO:0000122|GO:0009952|GO:0000978|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126711_PI430048170 0.732128422379795 0.814474417648527 14.1868504917354 13.764698843919 13.4336007190675 P P P 13.0871602037833 14.6371772117456 14.242784713781 P P P LNCV6_126711_PI430048170 mRNA
GCCCCTTGCCTCGATATTGCCAGTTTCTTGTGCAATAAACAATCAGCAGCTGTGAAAAAA NM_007014RefSeq chr16 + 69762283 69941741 WWP2 11060 "WW domain containing E3 ubiquitin protein ligase 2, transcript variant 1"
GO:0005515|GO:0004842|GO:0016567|GO:0016874|GO:0032410|GO:0000151|GO:0005634|GO:0046718|GO:0043433|GO:0005737|GO:0070534|GO:0042787|GO:0001085|GO:0042391|GO:0034765|GO:0070062|GO:0000122|GO:0051224|GO:0051865|GO:0016020|GO:0010629|GO:0043161|GO:0045892|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141755_PI430048170 0.290162133132789 0.637354464666861 4.61697956637696 4.53227342012622 3.02532923605506 P P P 5.02829523219088 5.17708122495929

4.23014830655497 P P P LNCV6_141755_PI430048170 mRNA
CATTCTCTACATCTATGCTCTCCCTAGATCTAGCTATTCTTTTGATATGGACAAAATAGTNM_001013358 RefSeq
chr11_JH159137v1_alt + 18233 19151 OR9G9 NA "olfactory receptor, family 9, subfamily G, member 9"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101844_PI430048170 0.2228381270263171.18134661539115 4.38376925548273
4.74939472889165 4.80265275501589 P P P 4.38489205426305 4.43593445653228
4.42811480294707 P P P LNCV6_101844_PI430048170 mRNA
AGTGTATCACGGAGTGAATTTGGACCAAACTGTAAAGGAATTTATCGTATTTCTAAAGCA NM_001017927 RefSeq
chr2 - 119302443 119366682 C2orf76130355 chromosome 2 open reading frame 76 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138508_PI430048170 0.0710172257415181 1.12836511495377 8.56574624308636
8.61408509306287 8.72395656280291 P P P 8.47359556490454 8.36116469811575
8.54498780155579 P P P LNCV6_138508_PI430048170 mRNA
CTTCCATTCTAACCTCAGAGATCTGTTTCTCTAGAAAAAATGTCCATCTCTGGCTTTAAT NM_001243780 RefSeq
chr10 + 80408485 80432997 FAM213A 84293 "family with sequence similarity 213, member A,
transcript variant 4" GO:0005739|GO:0005737|GO:0016209|GO:0045670|GO:0070062|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137019_PI430048170 0.00482753402953801 0.5762399573062167.71256597617984
7.36076750519382 7.56095309157497 P P P 8.32749209078515 8.18002649076547
8.51444363441469 P P P LNCV6_137019_PI430048170 mRNA
CTCCTCCCTATCAAACTAGTATAATGATTTTGAATCGGTACAGTGTGTTTAACTGTAACT NM_001251905 RefSeq
chr12 - 105173296 105233405 APPL2 55198 "adaptor protein, phosphotyrosine interaction, PH domain
and leucine zipper containing 2, transcript variant 3"
GO:0005515|GO:0007165|GO:0007049|GO:0005737|GO:0016581|GO:0008283|GO:0031901|GO:0005634|GO:0010
008|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104670_PI430048170 0.5028796770021461.21406480334089 1.18190569780202
0.4137809058186210.301180122808794A A A 0.3928552874539140.433547230263022
0.397664982152424A A A LNCV6_104670_PI430048170 mRNA
AAAGGTCAAGGAGTTCATCGTGGACATCTTGCAATTCTTGGACATTGGTCCTGATGTCAC NM_002380RefSeq chr8
+ 97869082 98036718 MATN2 4147 "matrilin 2, transcript variant 1"
GO:0031012|GO:0005515|GO:0008150|GO:0003674|GO:0031104|GO:0008347|GO:0007411|GO:0005509|GO:0005
578|GO:0001764|GO:0048678|GO:0005604 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127401_PI430048170 0.0616495093180479 0.49854743976816 4.51022910143328
4.65338261871604 3.71645138284603 P P P 5.40406969738121 5.42977846744894
5.21357714838449 P P P LNCV6_127401_PI430048170 mRNA
GCATTTCTCTGCCCCCCAACTTTTTTCTTTTTAAAAATAAGATGGGGAGTGTTCATAAAA NM_152372RefSeq chr1
- 24056040 24112175 MYOM3127294 myomesin 3 GO:0031430|GO:0042803 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_134646_PI430048170 0.000440268376171204 0.4858957317061288.66378353364659
8.46249504717523 8.6734948853084 P P P 9.65386143108646 9.55325870182779
9.72123843738494 P P P LNCV6_134646_PI430048170 mRNA
GGTGGTTGGAACATGTTTGAATTTTATTCTAAGTACTGTCTACAAGTTCTGCAATAAACC NM_006505RefSeq chr19
+ 44643797 44666160 PVR5817 "poliovirus receptor, transcript variant 1"
GO:0005515|GO:0005886|GO:0009986|GO:0034329|GO:0009615|GO:0005615|GO:0045216|GO:0060370|GO:0005
737|GO:0016337|GO:0016477|GO:0001618|GO:0050776|GO:0045954|GO:0042271|GO:0002860|GO:0016032|GO:0
004872|GO:0016021|GO:0050839|GO:0005925|GO:0070062|GO:0034332 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142377_PI430048170 0.2245895427993840.9853193799756610.343334941852339
0.3748069127445980.336051719102536A A A 0.3753525490986590.386073503164381

0.356921697755181 A A A LNCV6_142377_PI430048170 mRNA
GGGGTTTGTCCTTTTCCTACCCTGATGTCAAACTTATGCATGGATTTCATTAAAAAAGAA NM_005649 RefSeq chr5
- 178711520 178730702 ZNF354A 6940 zinc finger protein 354A
GO:0006355|GO:0003700|GO:0006357|GO:0007605|GO:0005634|GO:0003677|GO:0046872|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145143_PI430048170 0.803429914639726 0.992434754419611 0.467335134891379
0.482585700720367 0.383095986217983 A A A 0.510701366962107 0.422175758288985
0.433363839526291 A A A LNCV6_145143_PI430048170 mRNA
AGTACAAAGCCAAGAAGTTTGAGGAGGTGAATGAGACTACGCTGAAAATCGCGGCTTTGA NM_002559 RefSeq
chr11 + 57338366 57370076 P2RX3 5024 "purinergic receptor P2X, ligand gated ion channel, 3"
GO:0009408|GO:0010524|GO:0009409|GO:0019228|GO:0050850|GO:0005639|GO:0009743|GO:0050909|GO:0043
197|GO:0048167|GO:0043195|GO:0006810|GO:0043025|GO:0001614|GO:0033198|GO:0051260|GO:0014832|GO:0
005791|GO:0035590|GO:0001666|GO:0005794|GO:0004931|GO:0007274|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_70234_PI430048170 0.793894213377985 1.04569411629734 5.23170676630451 4.6307724864571
5.07029772529821 P P P 4.41291653179672 4.93012157745465 5.32068997186389 P P P
LNCV6_70234_PI430048170 mRNA
GATCTTAACCGACTTGCCAAGAAGTTTCAAAGACAAGCAGCAAACTTACAAGATTGTTAC NM_000251 RefSeq chr2
+ 47403066 47483228 MSH2 4436 "mutS homolog 2, transcript variant 1"
GO:0005515|GO:0019724|GO:0032405|GO:0016446|GO:0007281|GO:0042803|GO:0006119|GO:0043524|GO:0003
690|GO:0003697|GO:0006298|GO:0032357|GO:0008094|GO:0000400|GO:0000287|GO:0000404|GO:0019901|GO:0
045190|GO:0000403|GO:0000406|GO:0001701|GO:0042771|GO:0006281|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136698_PI430048170 0.488483492176419 1.1268674865503 0.291311866054524
0.856911346093287 0.362702347083296 A A A 0.383074045533643 0.321486678097899
0.356773565058864 A A A LNCV6_136698_PI430048170 mRNA
CCCTATGTGTGGTTCATGTGTATGTTTTGCCTATGAAAGTTGAAACTGTTTTCTAAATGTNM_001333 RefSeq chr9 -
97029676 97039310 CTSV 1515 "cathepsin V, transcript variant 1"
GO:0010839|GO:0043005|GO:0030984|GO:0048102|GO:0016540|GO:0010259|GO:0021675|GO:0007283|GO:0005
615|GO:0032403|GO:0031069|GO:2000249|GO:0046697|GO:0042393|GO:0019886|GO:0060008|GO:0022617|GO:0
030198|GO:0006508|GO:0043204|GO:0030141|GO:0070062|GO:0043202|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139575_PI430048170 0.326923923808718 1.06250875342401 12.6641999621898
12.8574013262225 12.8290990178084 P P P 12.6157824190793 12.7821790572899
12.6929494040943 P P P LNCV6_139575_PI430048170 mRNA
TTCCCTCTGGTCGGTTGTGGGGCTCAATAAATGGCTCTGTGAACTTCCCCTGCACTGCCA NM_058190 RefSeq chr21
+ 44940039 44976973 FAM207A 85395 "family with sequence similarity 207, member A" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_127625_PI430048170 0.956380337414152 0.792994905995562 1.32031560755132
2.14908845000077 0.304772036973281 A A A 0.312903066978436 0.311997104530069
2.96651223493574 A A P LNCV6_127625_PI430048170 mRNA
AAATGTTACACTTTCCCTTCAGGCATCCATTAATAAAAGAAATTGCCATGCTTACTGCCA NM_001130918 RefSeq
chr17 - 48762230 48817107 TTLL6 284076 "tubulin tyrosine ligase-like family member 6, transcript
variant 1"
GO:0005515|GO:0051013|GO:0018095|GO:0005737|GO:0003353|GO:0015631|GO:0016874|GO:0001578|GO:0036
064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137263_PI430048170 0.167703916612582 0.493105107086341 0.449515242848903
1.15872221151501 0.877734828236338 A A A 2.57253101107544 1.04948230885752
1.58738043401204 A A A LNCV6_137263_PI430048170 mRNA

ACCAGGAAAAGAAAAAATACATCATGCTGGAAATAAAGCTGCGGAACTCTGAACGGGCGC NM_001256024 RefSeq chr10 - 48446024 48605131 ARHGAP22 58504 "Rho GTPase activating protein 22, transcript variant 1"
GO:0043547|GO:0005515|GO:0051056|GO:0006355|GO:0007264|GO:0005634|GO:0001525|GO:0005925|GO:0030154|GO:0006351|GO:0005829|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142695_PI430048170 0.7801205280833070.85998588281549 1.67965747206195 1.38816638770896 0.453692456705045A A A 0.481569679824863 1.55672458694008 2.0083042517285 A A A LNCV6_142695_PI430048170 mRNA
TAGGATCTTCACTTTTGCTATTTCCTCAATATCAGAAAATTCACACTGAAGAGAGCACCA NM_001286769 RefSeq chr8 - 144772223 144787345 ZNF34 80778 "zinc finger protein 34, transcript variant 2"
GO:0006355|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132603_PI430048170 0.0138667708479449 0.6622019787799216.32963789836388 6.21088134918587 5.98450607173694 P P P 6.64012266956704 6.96570866622429 6.70314641542359 P P P LNCV6_132603_PI430048170 mRNA
AAGCCATCCAATGAGGCAACCCCTTCAAAATAATTTTAATACAAAGGATGCAAACATCTA NM_001144995 RefSeq chr14 - 99511265 99604390 CCDC85C 317762 coiled-coil domain containing 85C
GO:0043296|GO:0021987|GO:0005923 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127286_PI430048170 0.7649713799177330.9297515540485470.2737255401798791.6259637672774 1.31738752844179 A A A 1.66261545852218 1.31747918423837 0.71562281241071 A A A LNCV6_127286_PI430048170 mRNA
AGTTAGAAGCAAAGGCCCTCTTAATGGATGTCATATCTGAAGTGGCTCAGTTACGGGGTT NM_005294RefSeq chr9 + 123033642 123035665 GPR21 2844 G protein-coupled receptor 21
GO:0007186|GO:0005887|GO:0004930|GO:0046627|GO:0042593|GO:0040018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127095_PI430048170 0.4457321922875321.27180004322322 2.24795338048067 2.40753055019438 3.21606742997732 A A P 2.31419843198702 2.2959775549988 2.41389880872108 A A P LNCV6_127095_PI430048170 mRNA
CATTACAATTGGGTGAAACACATTTTACAGCTCTCAATAAATGTTTGCTGTCGCTCTTAA NM_152435RefSeq chr12 + 95943292 95968592 AMDHD1 144193 amidohydrolase domain containing 1
GO:0034641|GO:0003674|GO:0050480|GO:0019557|GO:0019556|GO:0006548|GO:0044281|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128360_PI430048170 0.6863581664922650.8134802122011790.570204323788741 2.14915149540406 0.736172471001518A A A 1.77459205202406 0.443279179114511 2.18410543574428 A A A LNCV6_128360_PI430048170 mRNA
TGTGCCCACATCCGAAGCACAAGGACATCAAATCATCAGCACAAGAACATCAACAGGAATNM_172006RefSeq chr20 - 45684650 45705019 WFDC10B 280664 "WAP four-disulfide core domain 10B, transcript variant 1"
GO:0010466|GO:0005576|GO:0030414 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139498_PI430048170 0.8254605623984571.16618689718298 1.67015401650668 0.5172347007681170.32260563694973 A A A 0.6301729253430391.04008911264141 0.510445831490209A A A LNCV6_139498_PI430048170 mRNA
TCAGGGTGTTTGCCCAATAATAAAGCCCCAGAGAACTGGGCTGGGCCCTATGGGATTGGT NM_004062RefSeq chr16 - 66908121 66918984 CDH16 1014 "cadherin 16, KSP-cadherin, transcript variant 1"
GO:0016339|GO:0016323|GO:0005509|GO:0016021|GO:0007155|GO:0007156|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134597_PI430048170 0.91726663306262 1.00399776981581 8.70545620079004 8.65548349715134 8.47236625557215 P P P 8.29189244197404 8.84524717683668 8.63606084437453 P P P LNCV6_134597_PI430048170 mRNA
TGAGCCTCGCTTGTCTAGATTGTCCTCTTTGTGCCAAAGAAATAAACCCTTAGGACTTGG NM_207351RefSeq chr3

- 9945541 9952394 PRRT3 285368 proline-rich transmembrane protein 3 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134192_PI430048170 0.0865182022574852 0.0818915931005638 0.360302465499993 0.3841413772524140.294632873605115A A A 1.55349665586327 4.81187703108193 3.96042645069859 A P P LNCV6_134192_PI430048170 mRNA GGCATTTGTTATCTAGGGGGCTTTGAATATGGTAGAAAGGTAAATATCGTTACTCAAGAG NM_001292009 RefSeq chr6 - 63719979 65707225 EYS 346007 "eyes shut homolog (Drosophila), transcript variant 4" GO:0003674|GO:0050908|GO:0005509|GO:0043403|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142946_PI430048170 0.6210369507747441.13279920700882 3.20685177877207 3.86397924033212 3.23096008609577 P P P 2.43086183427765 3.75197334482866 3.3823519370917 P P P LNCV6_142946_PI430048170 mRNA CGGGCTCGAAGAAAATAATTCTCTATTATTTTTATTACCAAGCGCTTCTTTCTGACTCTA NM_000820RefSeq chr13 - 113820548 113864103 GAS6 2621 growth arrest-specific 6 GO:0006909|GO:0005515|GO:0032715|GO:0005615|GO:0030296|GO:0018105|GO:0045860|GO:0006508|GO:0033159|GO:0032689|GO:0048018|GO:0043027|GO:0005796|GO:0005509|GO:0019064|GO:0031589|GO:0043277|GO:0030168|GO:0032720|GO:0032825|GO:0010804|GO:0010934|GO:0043491|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132910_PI430048170 0.00130579075916241 1.42171428426771 10.825156229364 10.9742802570751 10.949237866972 P P P 10.3422191525631 10.4322426127777 10.4532987604586 P P P LNCV6_132910_PI430048170 mRNA TTGAAGCAGATGAGGCCCTGGATTCCAGTTGGGTTTCTCGGGGTCCAGACAAACTGCTGC NM_013342RefSeq chr19_KI270938v1_alt - 81432 90168 TFPT 29844 TCF3 (E2A) fusion partner (in childhood Leukemia) GO:0005515|GO:0031965|GO:0006355|GO:0043065|GO:0046982|GO:0019901|GO:0005884|GO:0005730|GO:0005634|GO:0006310|GO:0097190|GO:0003677|GO:0006351|GO:0031011|GO:0005737|GO:0006281|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132524_PI430048170 0.4986116545546220.9678135723159219.79618552083117 9.68044260136623 9.81717836860978 P P P 9.90067053679572 9.79054344970746 9.74336716497663 P P P LNCV6_132524_PI430048170 mRNA CCAACTGAGAAGGAAAAACTTCTGTATGGAGGAAAAGACAGTAAACATGACAGACTGATA NM_015679RefSeq chr9 - 128309116 128322418 TRUB2 26995 TruB pseudouridine (psi) synthase family member 2 GO:0009982|GO:0005737|GO:0001522|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128214_PI430048170 0.7044799490064680.9382186992017360.284540112576203 0.3001581340221090.956289274429744A A A 0.3153739934197190.812077026967691 0.747255764286131A A A LNCV6_128214_PI430048170 mRNA AACTGGAAGTCGGGTTTTGGAGGAAATGGTTCTAACAGCAACCCCTGCTCAGAAACTTAT NM_080385RefSeq chr7 + 130344789 130368730 CPA5 93979 "carboxypeptidase A5, transcript variant 1" GO:0006508|GO:0008270|GO:0005576|GO:0004181 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64496_PI430048170 0.0291516310650511 0.4586027838535971 0.1181451437539 9.38041384031485 9.25866295618671 P P P 10.9991043776251 10.8222008821425 10.4041860884315 P P P LNCV6_64496_PI430048170 mRNA ACCCTCTCTCCCAGTCAAGTGGTCACCAGCAGGACTGAAGGGGACAGCCCCTTTGCAGTG NM_002248RefSeq chr19 + 17951301 17999121 KCNN1 3780 "potassium channel, calcium activated intermediate/small conductance subfamily N alpha, member 1" GO:0005516|GO:0005737|GO:0046982|GO:0005886|GO:0008076|GO:0043025|GO:0007268|GO:0015269|GO:0006813|GO:0071805|GO:0016286 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126639_PI430048170 0.2076660829774731.05409514164912 0.449784441378472 0.3105914068949740.345090203131131A A A 0.2709591850647120.32978845131679 0.279669366601979A A A LNCV6_126639_PI430048170 mRNA

TTAAAGAAGCCTTCCATGACATATCCCATTGTCTGAAAGCCCAGATGGAAAAGATCGGAC NM_182541 RefSeq chrX
+ 103710908 103714032 TMEM31 203562 transmembrane protein 31 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134463_PI430048170 0.9228448061971750.9967579191001615.75874826461 5.73362048245171
5.71642371601024 P P P 5.67744058792154 5.79776492069658 5.74543796144882 P P P
LNCV6_134463_PI430048170 mRNA
ATTTTAGTGTCGATGTGAAATGCCCCGTGATCAATAATAAACCAGTGGATGTGAATTAGT NM_014620 RefSeq chr12
+ 54016851 54056030 HOXC4 3221 "homeobox C4, transcript variant 1"
GO:0043565|GO:0005515|GO:0006355|GO:0003700|GO:0051216|GO:0071837|GO:0005634|GO:0009952|GO:0006
351|GO:0048562 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109713_PI430048170 0.5349028567455379 2.4224709959459 2.27423521781878
10.2342085971047 0.494272400552264 A P A 2.38060612530991 2.12428787574859
1.82073114932848 A A A LNCV6_109713_PI430048170 mRNA
CACAGATCTTGGATTAAAAGATGCTCAAGAATATGCCAGAAAACTGAAGAGGTTGGAAAA NM_175605 RefSeq chr13
+ 20567068 20691437 IFT88 8100 "intraflagellar transport 88, transcript variant 1"
GO:0060426|GO:0021513|GO:0007368|GO:0060122|GO:0045598|GO:0007288|GO:0001654|GO:0070613|GO:0034
405|GO:0050680|GO:0031122|GO:0009952|GO:0021537|GO:0036064|GO:0007224|GO:0060091|GO:0060914|GO:0
008104|GO:0007219|GO:0090102|GO:0060021|GO:0055007|GO:0002080|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145131_PI430048170 0.1670494421985980.5075993054374020.332188899658059
0.3617827675856170.340131019632173 A A A 1.90524517766445 1.23266321243932
0.495500232146881 A A A LNCV6_145131_PI430048170 mRNA
GGGGAGGGAAATGTTATCAACGGTTTCATTGAAATTAAATCCAAAAAGTTATTTCCTCAG NM_001187 RefSeq chr21
+ 10413519 10454661 BAGE 574 - GO:0005576 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131214_PI430048170 0.4674979940763940.85172153704127 0.306697879906512
0.2715198207256590.320973503700005 A A A 0.2827975529710660.268195321975506
0.937509620866977 A A A LNCV6_131214_PI430048170 mRNA
TCCTTCCGTGGTCACAGCTGAAAGAAACAATAAATTGAGTGTGGATCAATTTGCAAAAAA NM_145004 RefSeq
chr8_KI270822v1_alt + 13213 190632 ADAM32 203102 ADAM metallopeptidase domain 32
GO:0006508|GO:0008270|GO:0016021|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144708_PI430048170 0.00197051623013967 0.3541219801783167.90397209919987
7.64366982962926 8.11891088652226 P P P 9.19233979377513 9.2722060501448
9.68431647759863 P P P LNCV6_144708_PI430048170 mRNA
ACTGTGATTGGAGCCTTACCTTTGTATAGTGAAATTTGCATTTCTATGTCAACATCCAGA NM_174938 RefSeq chr9
- 83244623 83538433 FRMD3 257019 "FERM domain containing 3, transcript variant 1"
GO:0008092|GO:0005737|GO:0016021|GO:0005856|GO:0019898 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129323_PI430048170 0.9153365479632160.99108849606671 0.949065225866204
0.5918281144015940.415458254027116 A A A 0.2899056442443870.3141011521659781.2318042989267
A A A LNCV6_129323_PI430048170 mRNA
ACTTGGCAGTGGTTTTTTCTCACCCTTCCTTTTTAACAATAAAATCCCATTTGGGTCTTG NM_153209 RefSeq chr17 +
74326211 74355820 KIF19 124602 kinesin family member 19
GO:0008017|GO:0005929|GO:0005871|GO:0005737|GO:0060404|GO:0008574|GO:0008152|GO:0005874|GO:0016
887|GO:0005524|GO:0070462|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142394_PI430048170 0.0353519048989574 0.5328904994846766.77877585129833
6.46641242895782 6.84695370642538 P P P 7.19120664409645 7.61829335772438
7.93890903309901 P P P LNCV6_142394_PI430048170 mRNA
GAATGCTGAAAAGCTACTAGACTGGAAAACAAACACTGCATTATGTATGTTAAGTGACTA NM_001204517 RefSeq

chr1 - 169921328 170068915 KIFAP3 22920 "kinesin-associated protein 3, transcript variant 4"
GO:0005515|GO:0008285|GO:0016939|GO:0005783|GO:0072383|GO:0036064|GO:0005829|GO:0019886|GO:0008
104|GO:0015630|GO:0061024|GO:0005876|GO:0007017|GO:0070062|GO:0007018|GO:0005813|GO:0000794|GO:0
043066|GO:0006996|GO:0005794|GO:0005930|GO:0072372|GO:0046587|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140315_PI430048170 0.0919838244120645 1.05858785544222 0.470568273898466
0.5625828906068950.510096886651394A A A 0.38353491416527 0.441235041263198
0.472136456277125A A A LNCV6_140315_PI430048170 mRNA
TGATCCCTTGCATTTGCATCAAAAGCTTTAGTTTCACTGGAAATGCTGACTTCAACAATT NM_145119RefSeq chrX
- 69160737 69165522 PJA1 64219 "praja ring finger 1, E3 ubiquitin protein ligase, transcript variant 1"
GO:0005515|GO:0030163|GO:0005737|GO:0004842|GO:0016567|GO:0016874|GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144995_PI430048170 0.5691046088280420.9360915474243051 2.4198319618431
12.5318120520943 12.5272304268431 P P P 12.3403789961139 12.7620923839681
12.6332574642856 P P P LNCV6_144995_PI430048170 mRNA
TAGCAAATTCCCAGTAGGATGTCATGTAAGTTCCTTCCCCCTCTTAGAGATTGAAGGCTG NM_024096RefSeq chr16
- 30423697 30430052 DCTPP1 79077 dCTP pyrophosphatase 1
GO:0032556|GO:0000287|GO:0051289|GO:0047429|GO:0009143|GO:0047840|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135219_PI430048170 0.0541541828196330.4569576947358192.82941086786762 2.1501429461368
1.81320765831596 A A A 3.43932313217186 3.38173812359015 3.54692963961586 P P P
LNCV6_135219_PI430048170 mRNA
GTTCTGAAACCCTGCCTTGTTACTTACCTTTATTAAAAGAACCGAAATAATGCCTAACTC NM_004279RefSeq chr7
+ 103297425 103314686 PMPCB 9512 peptidase (mitochondrial processing) beta
GO:0005759|GO:0006626|GO:0006508|GO:0005743|GO:0004222|GO:0044267|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_103883_PI430048170 0.5569399330776071.03896634799352 0.278441459023483
0.2903257337555490.504016071099741A A A 0.3254814973727660.281499290341326
0.311356435953753A A A LNCV6_103883_PI430048170 mRNA
GAAAGTATGGGATACAAATACATTACAAGTCACAGACAAGAAATATTAGCAGTTTCCTGG NM_001007233 RefSeq
chr5 - 60873831 60945078 ERCC8 1161 "excision repair cross-complementation group 8, transcript
variant 2"
GO:0000209|GO:0005515|GO:0004842|GO:0010165|GO:0005634|GO:0045739|GO:0032403|GO:0016363|GO:0003
678|GO:0006974|GO:0051865|GO:0043234|GO:0000109|GO:0006281|GO:0006283|GO:0043161|GO:0005654|GO:0
031464|GO:0006289|GO:0009411|GO:0006979|GO:0008094 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_76256_PI430048170 0.00129971550872222 0.2459152522736967.22445724942246
6.77227907114373 7.09003317955873 P P P 9.1280325258888 8.94652243046201
9.11313179951928 P P P LNCV6_76256_PI430048170 mRNA
ACTTCCACTGATGCCCTTACTGTGCCAAAACAAAAATCTTAAGAAAAGCAAGTAGACACC NM_004060RefSeq chr5
+ 163437570 163445016 CCNG1 900 "cyclin G1, transcript variant 1"
GO:0005515|GO:0007095|GO:0048471|GO:0043066|GO:0019904|GO:0010243|GO:0005634|GO:0000079|GO:0030
425|GO:0007067|GO:0006949|GO:0007420|GO:0043025|GO:0016049|GO:0051301 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139215_PI430048170 0.00456950084213274 0.4553200134316160.325311533811897
0.7409790662378640.267281993252717A A A 1.40832627574733 1.80408440664149
1.54562692381514 A A A LNCV6_139215_PI430048170 mRNA
ATGGCCATCTTATGGCGGATATTTTGGGAGTTTATTGCAAACATGGTCATTCATTTTCTA NM_020337RefSeq chr4
- 124664048 124712732 ANKRD50 57182 "ankyrin repeat domain 50, transcript variant 1" GO:0005515

. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95625_PI430048170 0.297902347676548 1.05116996393662 0.49925767899164 0.330848286639857
0.426026030433196 A A A 0.289081628453413 0.358327051447095 0.395644879923218 A A A
LNCV6_95625_PI430048170 mRNA
TTAGCACATGTCCTCCAGATCATATTATCCGCCTACAAATATAGCCTGTTAGCGCACAGG NM_024512 RefSeq chr3
- 46515387 46566550 LRRC2 79442 leucine rich repeat containing 2 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139394_PI430048170 0.496797598302602 0.894013379813704 8.0818199167357
8.04115781698478 7.87221027048727 P P P 8.47236625557215 8.05146337307906
7.90269738590735 P P P LNCV6_139394_PI430048170 mRNA
GGAGGTCTTAAACAAGGTATTTTTCAACTTAAAAGTACTGCCAGCGTTTCATTTTGCAAA NM_001919 RefSeq chr16
- 2239871 2251601 ECI1 1632 "enoyl-CoA delta isomerase 1, transcript variant 1"
GO:0005739|GO:0016860|GO:0006635|GO:0004165|GO:0005759|GO:0005743|GO:0044281|GO:0044255|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130479_PI430048170 0.245368183643752 1.2186446204021 5.08630687854585
5.34542440859693 4.90250720724477 P P P 4.91047548306698 5.05505245375128
4.48949776508526 P P P LNCV6_130479_PI430048170 mRNA
TTAATTTATCTGTCTCTGTATATGAGGCTTCCCCCTGGGGTCCTGCATTATGGTACTTTC NM_001281956 RefSeq chr1
- 33513998 34165274 CSMD2 114784 "CUB and Sushi multiple domains 2, transcript variant 1"
GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141602_PI430048170 0.862369752186527 1.120222428896 1.16581559530347
0.403807790990159 2.20217738299172 A A A 1.94474008999602 0.274639351873639
1.15854815884095 A A A LNCV6_141602_PI430048170 mRNA
CTTAGACCCTCATGCTGCCAATATCCTAATAAAAAGGTGACCATCTGTGCCGGGAAAAAA NM_003019 RefSeq chr10
- 79937739 79949105 SFTPD 6441 surfactant protein D
GO:0005515|GO:0005581|GO:0048286|GO:0007585|GO:0072593|GO:0005578|GO:0005576|GO:0030139|GO:0001
817|GO:0005615|GO:0005764|GO:0006898|GO:0042130|GO:0045085|GO:0050766|GO:0045087|GO:0030246|GO:0
043129|GO:0048246|GO:0042742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60892_PI430048170 0.14431422557339 1.09676667472337 0.512889118235951 0.668695088997901
0.612827892439281 A A A 0.357457623470967 0.481319438143831 0.553396058243468 A A A
LNCV6_60892_PI430048170 mRNA
GCCAGTGAAAAAGGCAGGACCAGTCCAAGTCCTCATTGTCAAAGATGACCATTCCTTTGA NM_001127713 RefSeq
chr14 + 50533081 50633066 ATL1 51062 "atlastin GTPase 1, transcript variant 3"
GO:0005515|GO:0030424|GO:0005794|GO:0005783|GO:0003924|GO:0007409|GO:0005525|GO:0042802|GO:0000
137|GO:0000139|GO:0008152|GO:0005789|GO:0051260|GO:0016021|GO:0007029 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140720_PI430048170 0.445786551906769 0.926538357396194 11.5487204603809
11.3222281555205 11.5367184029225 P P P 11.4481830857388 11.5041519303676
11.7750348985901 P P P LNCV6_140720_PI430048170 mRNA
CACCTTCAACACCTTACAAGTAAAGACAATGAAGAACAGTTGAAACATGCAAAATATGGA NM_018838 RefSeq chr12
- 94971327 95003713 NDUFA12 55967 "NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12,
transcript variant 1"
GO:0022904|GO:0005739|GO:0005737|GO:0005747|GO:0007585|GO:0005743|GO:0009055|GO:0044281|GO:0008
137|GO:0006979|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129636_PI430048170 0.00543538961980079 0.300060456304925 5.07282218113956
4.42412753643084 5.0697159130633 P P P 6.43468081972277 6.58837956666304
6.81899061165173 P P P LNCV6_129636_PI430048170 mRNA
CCATGTCTTTGGCAAAGATCTAACACAATGTCTTAAGTATAATAGGTAGTCTCTGTTTGT NM_006391 RefSeq chr11
+ 9384621 9448127 IPO7 10527 importin 7

GO:0005515|GO:0005215|GO:0006606|GO:0007165|GO:0042393|GO:0050790|GO:0005083|GO:0005737|GO:0016020|GO:0005643|GO:0045087|GO:0008536|GO:0016032|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137918_PI430048170 0.00201494910654513 0.681630464689958 15.2327509948507 15.1961429512607 15.319866896558 P P P 15.6914495604631 15.8515397473029 15.8611827673751 P P P LNCV6_137918_PI430048170 mRNA CACTCCTTTGTCTTGGAACTGTCTTATTTTTGTTCTGTAAATGTCTATTGCCGTAAATTG NM_001303115 RefSeq chr12 + 49227925 49273338 TUBA1C 84790 "tubulin, alpha 1c, transcript variant 2" GO:0005515|GO:0005881|GO:0051258|GO:0005874|GO:0003924|GO:0005634|GO:0005525|GO:0031982|GO:0006184|GO:0030705|GO:0005198|GO:0006457|GO:0005200|GO:0051084|GO:0007017|GO:0044267|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131299_PI430048170 0.624811557640174 1.12664239783622 1.21185211885896 1.42925164049589 0.646558537355132 A A A 0.657989471566171 0.367333786225256 1.56946208870084 A A A LNCV6_131299_PI430048170 mRNA CAGGTTTCCACTTAAGTCATGGGAATAAAAGTGGACAAGGACTGAAGCTTTATGAGCTCA NM_004483 RefSeq chr16 - 81081946 81096375 GCSH 2653 "glycine cleavage system protein H (aminomethyl carrier), transcript variant 1" GO:0005739|GO:0005960|GO:0019464|GO:0006546|GO:0004047|GO:0019899|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140556_PI430048170 0.439154367213893 0.883751787122196 0.356341359508554 0.33180414404228 0.261286925511677 A A A 0.806952010385614 0.320573711264625 0.299331494364037 A A A LNCV6_140556_PI430048170 mRNA GCTGTTATGAGTGGCTTTAATGAATAAACATTTGTAGCATCCTCTTTAATGGGTAAACAG NM_001145873 RefSeq chr2 - 86784604 86808396 CD8A 925 "CD8a molecule, transcript variant 3" GO:0005515|GO:0042288|GO:0005886|GO:0019901|GO:0005576|GO:0015026|GO:0042803|GO:0050850|GO:0051607|GO:0045065|GO:0006955|GO:0042110|GO:0005887|GO:0019882|GO:0042101|GO:0050776|GO:0007169|GO:0002456|GO:0009897. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131967_PI430048170 0.013706097962466 1.34397335540057 5.25607996088524 5.03723870683218 5.07835286875973 P P P 4.71928357851866 4.81433490885249 4.55633294642758 P P P LNCV6_131967_PI430048170 mRNA GCAACCCAATAGCATAAATGTCCTTTTTCCCCCCAAATATGGTCTAGATGAGTTATTATA NM_001745 RefSeq chr5 + 134738479 134752160 CAMLG 819 calcium modulating ligand GO:0005515|GO:0007165|GO:0016020|GO:0007173|GO:0001881|GO:0005783|GO:0016032|GO:0006952|GO:0016021|GO:0050839 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127847_PI430048170 0.639580285992837 1.20690755499403 2.94344750607465 2.81519076137152 1.8262067081572 A A A 2.37596561072784 2.34121719599392 2.28842505950112 A A A LNCV6_127847_PI430048170 mRNA TAAAGGAACTGCGAGATGCTTTCCGAGAGTTTGACACCAATGGTGATGGGGAAATAAGCA NM_001033677 RefSeq chr12 + 120640618 120667324 CABP1 9478 "calcium binding protein 1, transcript variant 3" GO:0005515|GO:0048471|GO:0030054|GO:0005886|GO:0005634|GO:0005615|GO:0030425|GO:0042803|GO:0005829|GO:0045211|GO:0043025|GO:0005856|GO:0005938|GO:0004857|GO:0005509|GO:0019904|GO:0014069|GO:0043086|GO:0044325|GO:0031800|GO:0043234|GO:0000139|GO:0042308|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74134_PI430048170 0.0740390138183204 0.610705138460552 6.84844108471683 6.29833077634889 6.083217978624 P P P 7.10354677078774 7.2708568752883 7.09405850240811 P P P LNCV6_74134_PI430048170 mRNA GTGGCTCTTATTTCTGAATTCAAAGCTTGTGAAAAAATAAAGAAAATGAACTGCCCACTG NM_001288661 RefSeq chr4 - 5820763 5890226 CRMP1 1400 "collapsin response mediator protein 1, transcript variant 3" GO:0005515|GO:0006139|GO:0005737|GO:0005815|GO:0007411|GO:0016812|GO:0043025|GO:0005819|GO:0030425|GO:0007399|GO:0006208|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_97194_PI430048170 0.3509737869662670.9765392574553580.4706331716958490.383578781184943
0.427133062864077 A A A 0.4211053199923320.4878503215281670.475581437469079 A A A
LNCV6_97194_PI430048170 mRNA
ATCGTCACGGGCATTCTTATTAGTCAGGCTTGAAAAGACTCAGAGGATATGATGATGTCA NM_000340 RefSeq chr3
- 170996347 171026979 SLC2A2 6514 "solute carrier family 2 (facilitated glucose transporter), member 2,
transcript variant 1"
GO:0005886|GO:0005975|GO:0044281|GO:0055085|GO:0015149|GO:0070837|GO:0035428|GO:0055056|GO:0008
645|GO:0005903|GO:0005737|GO:0006112|GO:0050796|GO:0015758|GO:0016020|GO:0005887|GO:0031018|GO:0
009405|GO:0033300|GO:0005355 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137033_PI430048170 0.3881038726261830.9695110199154740.408028298187947
0.4331107932571970.29888865921239 A A A 0.4033526270348330.456423482095042
0.417237914019744 A A A LNCV6_137033_PI430048170 mRNA
GCACTAACATCTGTAGTACTAATCTTTTTTCCAGTGGCTTTAAACTGCAAATAAGGAATG NM_020855 RefSeq chr19
+ 22634323 22667670 ZNF492 57615 zinc finger protein 492
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129401_PI430048170 0.3899971272422021.15538654338671 9.57531308713388
9.08163318122414 9.07326232868354 P P P 9.07694765994111 9.22915239535163
8.83054378066485 P P P LNCV6_129401_PI430048170 mRNA
AATAAAGAGGCCAGAGAGCACCAAGTGAGCTCATGTTTCACCAGAGGTGGATAAAACCAA NM_023078 RefSeq
chr8_KI270816v1_alt - 93952 99654 PYCRL 65263 pyrroline-5-carboxylate reductase-like
GO:0055129|GO:0055114|GO:0004735 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132883_PI430048170 0.4611006108699791.20015629249437 0.351520839041671
0.3686440457116141.09055402323076 A A A 0.4223840809841340.346444810734305
0.380464690040601 A A A LNCV6_132883_PI430048170 mRNA
TCCTAACAGGAGGGGTGTAATGTGACATTGTTCATACTTGCTAATAAATACATTATTGCC NM_001135691 RefSeq
chr8 - 20144854 20183206 SLC18A1 6570 "solute carrier family 18 (vesicular monoamine
transporter), member 1, transcript variant 1"
GO:0070083|GO:0006855|GO:0006836|GO:0005789|GO:0008504|GO:0016021|GO:0015844|GO:0055085|GO:0015
238 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72060_PI430048170 0.1653854562493211.33020694656307 5.25824471875837 4.80538799572461
4.61858215547682 P P P 4.29574004197276 4.49444878645479 4.70485122003419 P P P
LNCV6_72060_PI430048170 mRNA
AGTGACAAAATTCATTCAGACCGCACATGTTAGAGGCAGGGAATGAAGAAGGTACTGTGG NM_005137 RefSeq
chr22 - 19036281 19122454 DGCR2 9993 "DiGeorge syndrome critical region gene 2, transcript
variant 1" GO:0050890|GO:0030246|GO:0009887|GO:0016021|GO:0007155 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138207_PI430048170 0.0199457760985113 0.33546842572673 6.63861563930668
6.48195861032562 6.67028304733711 P P P 7.65770359327686 8.2742716022739
8.47381930750235 P P P LNCV6_138207_PI430048170 mRNA
GAGCCGGTGGCAGGAGGAAGGCTGTTTTCACAAATGACTTGTAATGTCGTGATTAAAAAA NM_020770 RefSeq chr1
+ 151511385 151538691 CGN 57530 cingulin
GO:0003382|GO:0005515|GO:0008017|GO:0030054|GO:0000226|GO:0003779|GO:0016459|GO:0008150|GO:0003
774|GO:0070830|GO:0008152|GO:0007179|GO:0005923 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136629_PI430048170 0.00754042143323652 0.4834392374098496.19509406754293
6.5054943775112 6.15398262268009 P P P 7.03859859862256 7.57805549632814
7.35958324920787 P P P LNCV6_136629_PI430048170 mRNA
GTCGAAAGTTAATCCTCATGGACCCTAGTTTAAAGGGTATGTGTTTTATAGGAATAAATC NM_017955 RefSeq chr14
- 105009572 105021088 CDCA4 55038 "cell division cycle associated 4, transcript variant 1"

GO:0005515|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144888_PI430048170 0.0181350401702053 1.19602122663249 10.9432193086246
10.9065660779627 10.7844150986257 P P P 10.6656191278513 10.6671933161369
10.5269647388359 P P P LNCV6_144888_PI430048170 mRNA
CACCTTCTAGATGACCCCTTAATAAAGTGATGGCCCCACAGAAGAAATGCCTTCAAAAAA NM_001282311 RefSeq
chrX - 154506158 154516242 FAM3A 60343 "family with sequence similarity 3, member A, transcript
variant 5" GO:0008150|GO:0003674|GO:0005576|GO:0005575 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_134895_PI430048170 0.0846958045401463 0.514810084249563 7.51402689287716
6.47741146535615 6.39515599341859 P P P 8.12828343267421 7.86998056630155
7.47479267085249 P P P LNCV6_134895_PI430048170 mRNA
CTCCCACCCATTAACCTCCTCCCAAAAAACAAGTAAAGTTATTCTCAATCCATCAAAAAA NM_001080547 RefSeq
chr11 - 47354857 47378576 SPI1 6688 "Spi-1 proto-oncogene, transcript variant 1"
GO:0005515|GO:0000790|GO:0090241|GO:0003700|GO:0006366|GO:0051525|GO:0000981|GO:0003705|GO:0003
723|GO:0044027|GO:0045944|GO:0045347|GO:0001085|GO:0030098|GO:0030225|GO:0030851|GO:0043011|GO:0
035019|GO:0002320|GO:0060033|GO:0006357|GO:0001205|GO:0001047|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145259_PI430048170 0.632103777697066 1.01328726470217 0.492122716180442
0.536032669202384 0.424798500101846 A A A 0.482600328123853 0.453941392306793
0.461298394410338 A A A LNCV6_145259_PI430048170 mRNA
GAGAAGTCCAGAATGCATTCAAGAAAGTGTTGAGAAGGCAAAAATTTCTATAAGTTTGGA NM_001005566 RefSeq
chr11 - 58422264 58423313 OR5B2 NA "olfactory receptor, family 5, subfamily B, member 2" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126687_PI430048170 0.0453893998269624 1.13791753979585 11.4253336748692
11.2955247344623 11.3340873023673 P P P 11.0733576710807 11.2469563929078
11.1732960104574 P P P LNCV6_126687_PI430048170 mRNA
CCTGGGAATCTGTCATTCGTGGGTGCTTCAGAGTAAAATCAATGAGTTTCTGAGCAGAAA NM_032630 RefSeq
chr14 - 102348281 102362916 CINP 51550 cyclin-dependent kinase 2 interacting protein
GO:0006260|GO:0005515|GO:0007049|GO:0006281|GO:0005634|GO:0051301 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_135960_PI430048170 0.0333962288856776 0.46855365578489 4.89113018141766
4.62533975811789 5.38951174601563 P P P 6.01635230914888 6.11203374007324
6.1613283953245 P P P LNCV6_135960_PI430048170 mRNA
TCTCGAAATAGACTTTATTCTTACCTAGGCTTCAGACAACAGTTTTATAGAGCAGTTACT NM_173824 RefSeq chr3
+ 88149742 88157965 C3orf38 285237 chromosome 3 open reading frame 38 GO:0006915 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79718_PI430048170 0.150092387889867 0.925774533753916 9.92887691949896
9.81172741622054 9.98809210400445 P P P 10.0157534303928 9.97577907898715
10.0747887904741 P P P LNCV6_79718_PI430048170 mRNA
CCTGGGAAACCTGCCTTTGTATGTGGAAGTATACCTGGCTTTTTAAAATATATGTATTTA NM_001009552 RefSeq
chr8 - 30785609 30812836 PPP2CB 5516 "protein phosphatase 2, catalytic subunit, beta isozyme"
GO:0005515|GO:0010468|GO:0042542|GO:0034976|GO:0000159|GO:0005634|GO:0008022|GO:0046872|GO:0005
829|GO:0046580|GO:0000922|GO:0006470|GO:0008637|GO:0008543|GO:0043161|GO:0004722|GO:0046677|GO:0
000775|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130694_PI430048170 0.0744571087693386 1.23806632543559 10.1984990238398
10.3646661723292 10.4971674088258 P P P 9.8843603978487 10.0347633417357
10.2135291261629 P P P LNCV6_130694_PI430048170 mRNA
GGCAAGCAAGTGCTGTGAAATAACATCATCTTAGTCCCTTGGTGTGTGGGGTTTTTGTTT NM_001009999 RefSeq
chr1 + 23019447 23083691 KDM1A 23028 "lysine (K)-specific demethylase 1A, transcript variant 1"

GO:0005515|GO:0032454|GO:0000790|GO:0032453|GO:0003700|GO:0032452|GO:0044212|GO:0006325|GO:0050681|GO:0045654|GO:0034648|GO:0046886|GO:2000179|GO:0000122|GO:0001701|GO:0043392|GO:0045648|GO:0006482|GO:0016491|GO:0005654|GO:0019899|GO:0045892|GO:0008134|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137355_PI430048170 0.579615567545078 0.989732713541505 0.36214498277355 0.373939365554513 0.30142361485041 A A A 0.355756165354233 0.377955153552803 0.349352160409341 A A A LNCV6_137355_PI430048170 mRNA CTAGAAGAATGCCACACACAAATATGACTCATTTGATTATCCTACAGAAATCTGTTGTCA NM_181534 RefSeq chr17 - 40748020 40755332 KRT25 147183 "keratin 25, type I"
GO:0005882|GO:0003674|GO:0005737|GO:0045109|GO:0042633|GO:0005198|GO:0007568|GO:0070062|GO:0031069 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129935_PI430048170 0.328039344329305 1.15198648731438 11.6378510393527 12.1136253004135 11.8441805769981 P P P 11.6757724220096 11.8570431847591 11.4633415556064 P P P LNCV6_129935_PI430048170 mRNA ACATGGGGTCTATTCACAGATTCCTCTGCGGGCTCTGCTCCCCACTACGAGGTGTTTGTG NM_001142623 RefSeq chr17 - 42189086 42194532 GHDC 84514 "GH3 domain containing, transcript variant 3"
GO:0008150|GO:0003674|GO:0016020|GO:0005783|GO:0005635 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136660_PI430048170 0.5142915270116740.9139731922106576.57377378063772 6.70130010773224 6.69748179879965 P P P 6.58776556725157 6.67190566601024 7.06055651846465 P P P LNCV6_136660_PI430048170 mRNA GCCCTCCTTCTTTCTCAATAGCTACTTTCTTACTGCTTTTTGAAAATAATATGCAACCAA NM_014435 RefSeq chr4 - 75913655 75941013 NAAA 27163 "N-acylethanolamine acid amidase, transcript variant 1"
GO:0006629|GO:0008150|GO:0005737|GO:0016810|GO:0005764|GO:0070062|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134873_PI430048170 0.6188180747933450.9505807718083971 2.0005369775666 2.2711702182518 2.2642057970035 P P P 2.1941476015673 2.1144835051715 2.4422072779111 P P P LNCV6_134873_PI430048170 mRNA GATTTGTAGTTGTGTGTGCAGCACTTCGCCCTGATATGTGTGCTCTACAATAAAAACCAA NM_017758 RefSeq chr17 + 18183552 18209953 ALKBH5 54890 "AlkB family member 5, RNA demethylase"
GO:0006397|GO:0001666|GO:0006406|GO:0016607|GO:0016706|GO:0005634|GO:0007283|GO:0035515|GO:0046872|GO:0035553|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129662_PI430048170 0.4170202250493110.7522166703752033.16427869310393 1.78779239682398 3.7839107646558 P A P 3.16669611250914 3.76511655171705 3.61398798234622 P P P LNCV6_129662_PI430048170 mRNA ATACACAGTTCTATCCAACAGAAACTGTATCTTTCTGTTTGTCAGAAGTTCTCCGTTAGT NM_001017922 RefSeq chr1 + 42817104 42844989 ERMAP 114625 "erythroblast membrane-associated protein (Scianna blood group), transcript variant 1" GO:0005886|GO:0031410|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141425_PI430048170 0.0250142842342646 2.02931593704933 3.4523645208861 4.09601750316685 4.03264380925394 P P P 2.53937762911541 2.72658228344461 3.24088086391239 P P P LNCV6_141425_PI430048170 mRNA AGGGCCTTAGAAATGTCAATGGGGCAGGAAGAAAACACAATTTCTAACTGCCTGTTTTTG NM_003462 RefSeq chr1 + 37556918 37566857 DNALI1 7802 "dynein, axonemal, light intermediate chain 1"
GO:0007338|GO:0005515|GO:0045504|GO:0005737|GO:0005930|GO:0008152|GO:0006928|GO:0005858|GO:0030175|GO:0003777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127716_PI430048170 0.37002182593641 1.75653517044206 0.381102447386032 2.32076245551451 1.21198301138095 A A A 1.30530372218869 0.290238245267032 0.275317610812871 A A A LNCV6_127716_PI430048170 mRNA

CTTTAGGAAGAATAAAGTGCCTTCTGAGCAAGCAGCTCAGGGTCTGCATCAGTGAAAAAA NM_152393 RefSeq chr3 + 42685518 42692446 KLHL40 131377 kelch-like family member 40 GO:0031672 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136026_PI430048170 0.5036775016350430.957365376856923 0.272388068095882 0.44131295952479 0.297703563110887 A A A 0.5090902642575880.404925096562364 0.282919931511768 A A A LNCV6_136026_PI430048170 mRNA
GACCCATACCTGATGGTTCAGTCTGTCCTTAAGTTAAAAGAATTTTGCTTTTCTAATGTT NM_001267616 RefSeq chr3 + 35639173 35685887 ARPP21 10777 "cAMP-regulated phosphoprotein, 21kDa, transcript variant 5" GO:0034605|GO:0008150|GO:0005516|GO:0003674|GO:0005737|GO:0005575|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145158_PI430048170 0.00103916347273767 1.36006372854013 9.04740842315579 9.07097302361112 9.03123555092503 P P P 8.6569876488826 8.59386285518364 8.56652299643965 P P P LNCV6_145158_PI430048170 mRNA
CCTTCCAGTGGGAATTTGGAGACTTTTTGGTTTGTAAATATATCCCTTTTTCTAACATCT NM_152260 RefSeq chr15 + 40569292 40574694 RPUSD227079 "RNA pseudouridylate synthase domain containing 2, transcript variant 1" GO:0009982|GO:0008150|GO:0005575|GO:0001522 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130951_PI430048170 0.00672788718891726 0.7225682572683467.84202258286734 7.69837766513394 7.68223536020337 P P P 8.2407525418234 8.18292076241274 8.21018679284766 P P P LNCV6_130951_PI430048170 mRNA
GTCCCCTAAATTTCTGTTCTAGTTTTAAATTTCTCTAGAACTTGCAATAGTTGGGGGTTT NM_032740 RefSeq chr2 + 127701022 127703833 SFT2D3 84826 SFT2 domain containing 3 GO:0016021|GO:0016192|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131059_PI430048170 0.0336460825666866 0.85105250389392 11.0352075995292 11.0208466327226 11.1914207685792 P P P 11.2766238325861 11.2587013660771 11.4115770129263 P P P LNCV6_131059_PI430048170 mRNA
GTGGCTTGTACAGTTTTGAAACTCCCGTTCTATTTTATGATGGTTGATAATAGTCAGTAA NM_025106 RefSeq chr1 + 9292881 9369531 SPSB1 80176 splA/ryanodine receptor domain and SOCS box containing 1 GO:0035556|GO:0005515|GO:0005737|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133617_PI430048170 0.9485013614529270.95039405897257 2.37775266779469 2.83512501619724 2.4344404816016 A A A 2.03695468044463 2.58245343715822 3.09952789099167 A P P LNCV6_133617_PI430048170 mRNA
TGAGCTTCATGGATTTTCTCTCCAAAACAAGCCAGCACAACTAACTGTAGCAGAATTGTA NM_014838 RefSeq chr22 + 49853848 49890078 ZBED4 9889 "zinc finger, BED-type containing 4" GO:0005737|GO:0046983|GO:0005654|GO:0005634|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96345_PI430048170 0.8090587208189440.982794273624343 0.39437237149905 0.411376708730499 0.452825411233485 A A A 0.5895886914157810.339830586334782 0.392728280457706 A A A LNCV6_96345_PI430048170 mRNA
TCTTCCTTAAGAACAGGATCTATAGCTTTAAAATGTCTTCTTCTATGGGAAATTTCCTGC NM_130847 RefSeq chr11 + 94768341 94876753 AMOTL1 154810 "angiomotin like 1, transcript variant 1" GO:0005515|GO:0003365|GO:0030054|GO:0031410|GO:0035329|GO:0030027|GO:0005829|GO:0042802|GO:0043536|GO:0005737|GO:0016324|GO:0008180|GO:0005923|GO:0016055 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133135_PI430048170 0.3151322836192951.01197252377123 0.325927496530116 0.2991035079105050.281693977638295 A A A 0.29034035233952 0.288402349366364 0.276779201732111 A A A LNCV6_133135_PI430048170 mRNA
CCATTCCTCAGGTATAAGTTCTATAAACAGGCTTGGAATCTGGGTAATTAAAAACAGAAA NM_005272 RefSeq chr1 - 109603266 109613083 GNAT2 NA "guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 2" NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_143232_PI430048170 0.3463556886386991.14458946404411 0.505148055350537
0.9493736907745740.511613600250001A A A 0.4531013698159830.478867771971537
0.495694480498593A A A LNCV6_143232_PI430048170 mRNA
TAAAAGGCTCTGAGGAGGCTTAAAGTACCTAGTTTGAGTGGAGTTATCAAGTGAGGTCCA NM_020768RefSeq chr5
+ 144170872 144477381 KCTD1657528 potassium channel tetramerization domain containing 16
GO:0043235|GO:0042734|GO:0030054|GO:0008277|GO:0045211|GO:0051260 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143991_PI430048170 0.000182328934882017 2.77305803155126 8.94077958946859
9.14037976886791 9.19661437944138 P P P 7.4745767851441 7.64612088523109
7.74234570653666 P P P LNCV6_143991_PI430048170 mRNA
CAATCTCTAGTTGTCACTTTCCTCTTCCACTTTGATACCATTGGGTCATTGAATATAACT NM_001733RefSeq chr12 -
7080210 7092447 C1R715 "complement component 1, r subcomponent"
GO:0005515|GO:0006956|GO:0006955|GO:0004252|GO:0045087|GO:0006958|GO:0005509|GO:0006508|GO:0008
236|GO:0072562|GO:0005576|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_46853_PI430048170 0.00308144229425845 0.4047261727071372.29500512230836
1.93831157759237 2.38446763036651 A A A 3.62867511847675 3.37759549853183
3.55261682400553 P P P LNCV6_46853_PI430048170 mRNA
TATGGCATTGGGCTTTCAGTAGCCAGTCAGCTCATTAATACTTTCAACAAAGATAGTTTT NM_018036RefSeq chr14
- 96281257 96363341 ATG2B 55102 autophagy related 2B
GO:0006995|GO:0005811|GO:0034045|GO:0000422|GO:0000407|GO:0000045|GO:0019898 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142815_PI430048170 0.00490720358902116 0.5771159085744347.97058191581726
8.00120155751524 8.23424486889452 P P P 9.00077542800731 8.6530019583557
8.92348249375748 P P P LNCV6_142815_PI430048170 mRNA
CAAGTGTATTTTTAACTGTCTGGTTTGTACTTTTATGACTTTTGTACTACCAAAGCGGAG NM_001085400 RefSeq
chr4 - 37610633 37686377 RELL1 768211 "RELT-like 1, transcript variant 1"
GO:0005886|GO:0015630|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142367_PI430048170 0.0529187378653876 2.50840592672437 4.0885732889643
5.03318745224877 3.92758914528351 P P P 3.35736399630226 2.89254341568435
3.04058694312878 P P P LNCV6_142367_PI430048170 mRNA
GGGGAGGACAGGTTGGTAAAACATGAAAAGGTAAATAAAATTACTTGTTTGAAACCACTG NM_001267822 RefSeq
chr17 + 4740014 4746119 ZMYND15 84225 "zinc finger, MYND-type containing 15, transcript
variant 3" GO:0005737|GO:0042826|GO:0007286|GO:0005634|GO:0045892|GO:0046872|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142462_PI430048170 0.1698705135391161.08561280477987 4.89282951589357
4.84132926232134 4.85778082803355 P P P 4.6699403531719 4.70018306206037
4.85949428475207 P P P LNCV6_142462_PI430048170 mRNA
CCTACAGGTGCATACTGTTCTGCTTTTCCAATAAATACGAGCGGCGATTTCAACCACAAA NM_001282658 RefSeq
chr10 - 12896624 13099773 CCDC3 83643 "coiled-coil domain containing 3, transcript variant 2"
GO:0005783|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128912_PI430048170 0.4261357115997131.02495714684116 0.370884053224144
0.2583898552687210.275995799257591A A A 0.2601913606017530.283349043992665
0.257454083190506A A A LNCV6_128912_PI430048170 mRNA
GGCAGGAAGATGAGAAGAAATCTTCAGGGTGATTTCTGGAGCCTGAAAAGAATAAAAAAC NM_017589RefSeq
chr11 - 111467530 111512354 BTG4 54766 B-cell translocation gene 4
GO:0008285|GO:0045930|GO:0030182|GO:0007050|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143326_PI430048170 0.2798237240153091.10192120189013 11.839115585704
11.6584071320239 11.8142014485141 P P P 11.7613510058317 11.441126286925

11.6769772583451 P P P LNCV6_143326_PI430048170 mRNA
GGGTTGATTAATTTCTGCACAGGGAGTGAGATTATTAAAGTAACACACACACAAAGTAAA NM_012248 RefSeq chr16
- 30443624 30445975 SEPHS2 22928 selenophosphate synthetase 2
GO:0016310|GO:0004756|GO:0016260|GO:0005575|GO:0005524 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143931_PI430048170 0.0780447361812956 1.19465909271385 12.3196537296665
12.339029348035 12.3485871784837 P P P 11.9231579104984 12.1171744090874
12.1846920507419 P P P LNCV6_143931_PI430048170 mRNA
GACCTTTTCAAAGACAATAGGGGGTCTTGACATGTTTGTTGTATGTAAAGATGATAAGAT NM_022371 RefSeq chr1
+ 179081976 179095994 TOR3A 64222 "torsin family 3, member A"
GO:0006200|GO:0005783|GO:0051085|GO:0005788|GO:0016887|GO:0005524|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136852_PI430048170 0.8461771834737541.01413350814765 9.77068789634378
9.62933023722073 9.8358451168275 P P P 9.52473468177236 9.82853593426551
9.80988437015145 P P P LNCV6_136852_PI430048170 mRNA
AGGTCTTCACACCCTGATTCCTCAAGTTTTCTGCTTAGTGGCACTGACATTAAGTAGTGG NM_006268 RefSeq chr11
+ 65333753 65352980 DPF2 5977 "D4, zinc and double PHD fingers family 2"
GO:0006355|GO:0005813|GO:0005737|GO:0000790|GO:0006915|GO:0008270|GO:0005654|GO:0000978|GO:0097
190|GO:0006351|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129292_PI430048170 0.404075655815237 1.12612046534572 4.49320058521691
4.66003298473046 4.65496409993152 P P P 4.0636583917998 4.4973276090809
4.67319268934443 P P P LNCV6_129292_PI430048170 mRNA
ACAACTTTGTACAAATGGTTACTGTAGTCACATAGTGGCACAACCAGGCCTAGCACCCAA NM_001287390 RefSeq
chr9 - 128832941 128882075 CCBL1 883 "cysteine conjugate-beta lyase, cytoplasmic, transcript variant
4"
GO:0006559|GO:0070189|GO:0006569|GO:0047312|GO:0047804|GO:0008483|GO:0008652|GO:0044281|GO:0042
803|GO:0005829|GO:0097053|GO:0034641|GO:0005737|GO:0030170|GO:0006575|GO:0047316|GO:0005654|GO:0
016212|GO:0036141|GO:0047945 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132066_PI430048170 0.161961750826551 0.621510229456029 2.6324753359595
2.92185105870976 3.85972460709332 A P P 3.59915863613482 4.07562589847248
4.04867460739816 P P P LNCV6_132066_PI430048170 mRNA
TTCCTGTTACACTGTGTTCAGCTATCTTCAGCCACCTTAAATTCCCATGGATGAGTTTTC NM_001282437 RefSeq chr10
- 100273277 100286712 BLOC1S2 282991 "biogenesis of lysosomal organelles complex-1, subunit 2,
transcript variant 4"
GO:0005515|GO:0008625|GO:0048490|GO:0005813|GO:0008284|GO:0043015|GO:0032438|GO:0005634|GO:0008
022|GO:0031175|GO:0005739|GO:0031083|GO:0045944|GO:0007020|GO:0000930|GO:0060155|GO:0008089|GO:0
055037|GO:0045893. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138759_PI430048170 0.0314533664956331 0.340857417340166 1.38196505328928
2.25416558484987 2.44674719208392 A A A 3.76937681265737 3.69011384813012
3.47156653540017 P P P LNCV6_138759_PI430048170 mRNA
GGCACACAGGAATTTAGGTTGGGCGAATTCACACTAACAAATTATAACTAAAAATTGGTA NM_001278940 RefSeq
chr14 - 81175452 81220952 GTF2A1 2957 "general transcription factor IIA, 1, 19/37kDa, transcript
variant 3"
GO:0005515|GO:0010467|GO:0006355|GO:0006368|GO:0006367|GO:0046982|GO:0006366|GO:0003713|GO:0003
677|GO:0005737|GO:0017025|GO:0016032|GO:0005654|GO:0005672|GO:0008134 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138992_PI430048170 0.0622295230383909 0.396712478465602 2.0542942089765
2.23760710660641 2.46984795529044 A A A 2.79363578567254 3.96327512314628
3.78559501409924 A P P LNCV6_138992_PI430048170 mRNA

TGCTTAGTCCTTTAGTTGGGAAACAGAATCAGGGCATAGAGCAGAAGAGAGCTTGACACT NM_152574RefSeq chr9 - 15170843 15307360 TTC39B 158219 "tetratricopeptide repeat domain 39B, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132658_PI430048170 0.1350164262885191.2138316081722 6.50740466349007 6.57892882848576 6.2321927002734 P P P 6.36991886896206 6.07927274629794 6.02942568223301 P P P LNCV6_132658_PI430048170 mRNA
AGACATGTCAGGAATAGATTAGGCACCCCTCTTCCTTAATGAAATGTGGCAGTCCTCTCA NM_001478RefSeq chr12 - 57625894 57633239 B4GALNT1 2583 "beta-1,4-N-acetyl-galactosaminyl transferase 1, transcript variant 1"
GO:0030173|GO:0016020|GO:0006687|GO:0005886|GO:0019915|GO:0005975|GO:0003947|GO:0001574|GO:0006486|GO:0007283|GO:0030259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131403_PI430048170 0.3317243200294241.04209086691127 0.304648646158981 0.2721205203996920.422935515405427A A A 0.2871182663710260.2522689436653760.2860057852477 A A A LNCV6_131403_PI430048170 mRNA
CCCTCTTTATAAAGCATTATATTACTTGGAATGGCTTGGTCAACTGTGTTCAGTTCATAA NM_021949RefSeq chrX + 153536121 153582929 ATP2B3 492 "ATPase, Ca++ transporting, plasma membrane 3, transcript variant 1"
GO:0005516|GO:0005794|GO:0005886|GO:0005524|GO:0031982|GO:0055085|GO:0046872|GO:0005388|GO:0034220|GO:0007596|GO:0008152|GO:0070588|GO:0006810|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106566_PI430048170 0.0637824829443453 1.30534709589097 8.51731172076089 8.39636117204625 8.5964654075821 P P P 7.92068731146951 8.07883155645299 8.33391444805272 P P P LNCV6_106566_PI430048170 mRNA
GGCGGCTGCACATGACATCAAATTGTTTCCTGAATTTATTAAGGAGTGTAAATAAAGCCT NM_018361RefSeq chr8 + 6708356 6761500 AGPAT5 55326 1-acylglycerol-3-phosphate O-acyltransferase 5
GO:0005741|GO:0044281|GO:0005635|GO:0008654|GO:0003841|GO:0005739|GO:0002244|GO:0005789|GO:0016024|GO:0019432|GO:0016021|GO:0006644|GO:0006654|GO:0044255|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145218_PI430048170 0.1400348530221470.5244139420303280.3463925942924541.6979926828573 1.57888116511415 A A A 1.76025835312973 2.73478045729676 2.09211038674941 A P A LNCV6_145218_PI430048170 mRNA
GCTTACTGGCAAACATGAAAAATCGGCTTACCATTAAAGTTCTCAATGCAACCATAAAAA NM_001278736 RefSeq chr17_KI270857v1_alt - 106023 114905 CCL5 6352 "chemokine (C-C motif) ligand 5, transcript variant 2"
GO:0005515|GO:0006887|GO:0043621|GO:0005615|GO:0042803|GO:0043623|GO:0031726|GO:0030298|GO:0006935|GO:0000165|GO:0031729|GO:0031663|GO:0045070|GO:0045071|GO:0050679|GO:0031584|GO:0008009|GO:0045744|GO:0030335|GO:0042531|GO:0009636|GO:0014068|GO:0042056|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101635_PI430048170 0.0981574361464481 0.4575195248605671.57363846313788 0.406148416359107 0.494720758689736A A A 2.29804308413798 2.39008386836803 1.21547317782491 A A A LNCV6_101635_PI430048170 mRNA
GTTTCCTTCCTTCGCAGCTTTTAGACCAAAATATGAAAGACTTACAGGCCTCGCTACAAG NM_001136020 RefSeq chr7 - 8113184 8262281 ICA1 3382 "islet cell autoantigen 1, 69kDa, transcript variant 3"
GO:0003674|GO:0005737|GO:0030054|GO:0000139|GO:0019904|GO:0006836|GO:0030672|GO:0030667|GO:0030658|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132788_PI430048170 0.9406647556781920.9943339919699450.282515362883145 0.2935507754831710.501402796004715A A A 0.3155239361481210.275486872454034 0.510629470539937A A A LNCV6_132788_PI430048170 mRNA
CAGATCACATGGCCTAGAGGCAATGTTGCATATACCTTAATCTTTGATATGAATAATATC NM_007332RefSeq chr8 - 72021250 72075584 TRPA1 8989 "transient receptor potential cation channel, subfamily A, member

1"
GO:0042542|GO:0005262|GO:0005886|GO:0042493|GO:0009409|GO:0032421|GO:0055085|GO:0034220|GO:0005887|GO:0070588|GO:0050968|GO:0050955|GO:0048265|GO:0050966|GO:0006811|GO:0015267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139769_PI430048170 0.3889638807404180.5924165593474710.38687696504066
0.3772146494758810.267437018266546A A A 1.92797746481576 0.335755693507167
0.447984839643117A A A LNCV6_139769_PI430048170 mRNA
TCCTCTGAGCATAATTATATCTGAGAGCACAGGGAGCTCCTCATTCCATGTATTTTTCAA NM_001040710 RefSeq
chr2 + 24175042 24191698 FAM228A NA "family with sequence similarity 228, member A" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132809_PI430048170 0.5985205162301691.09446937065043 9.0797924459597
9.08351850782642 9.00333116248584 P P P 9.58299827865059 8.35828789926547
8.50724725026646 P P P LNCV6_132809_PI430048170 mRNA
CCCACCTCTGTTTATTCTGTAAACTGCAACCTATAAATAACCTTTAGCATTCCTATTGTANM_170744RefSeq chr10 +
71212534 71302878 UNC5B 219699 "unc-5 homolog B (C. elegans), transcript variant 1"
GO:0005515|GO:0043524|GO:0043065|GO:0007411|GO:2001240|GO:0014068|GO:0016021|GO:0097190|GO:0033564. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126907_PI430048170 0.0619381891560489 1.3368835427229 10.3302214988143
10.0445377441585 9.90128117117149 P P P 9.76446882361086 9.73741507017008
9.54088519823709 P P P LNCV6_126907_PI430048170 mRNA
GGGGAAATGTCTGTACTTTGGGAAGTCACAGAAATACATTTTTGTGCAAAATGGAAAAAA NM_006336RefSeq chr9
- 128729787 128771934 ZER1 10444 "zyg-11 related, cell cycle regulator"
GO:0004842|GO:0016567|GO:0051438|GO:0031462 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110790_PI430048170 0.0304828782824272 1.43505323995589 6.54118409101156
6.95648128791427 6.77799599893625 P P P 6.41550398917387 6.22564836579491
6.08149526188644 P P P LNCV6_110790_PI430048170 mRNA
TTAGAGGCAGACATTAAATACACTCAGTCGGCCTCCACCCTCTCTGCCGTGGGCGGCTTT NM_001257096 RefSeq
chr20 + 21705658 21718486 PAX1 5075 "paired box 1, transcript variant 2"
GO:0006366|GO:0008283|GO:0001756|GO:0043367|GO:0005634|GO:0048538|GO:0003677|GO:0001501|GO:0060017|GO:0043374|GO:0045944|GO:0060349|GO:0061056 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121907_PI430048170 0.4827331350586540.3338722273261530.473672114750548
0.5064607833106140.910923473840717A A A 0.5435207942399983.49059881720206
0.430704369878903A P A LNCV6_121907_PI430048170 mRNA
TGACTTTGGCAGCTAACAGGCCACTAGTATCCTACTAAAGCTTTTGTCTGGATAGGAGCA NM_033066RefSeq chr2
- 201644873 201698694 MPP4 58538 "membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)" GO:0042734|GO:0005737|GO:0035418|GO:0005654|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134282_PI430048170 0.1451204743341020.7319735880812535.76104360702227
5.09106183290357 5.1865752338794 P P P 5.84422820745281 5.87452957049006 5.762576179011
P P P LNCV6_134282_PI430048170 mRNA
AGATTTGCTCAGAAACTCTGCCCAAGATTGGGCAGAAGTTACTTTAAAAAGACTTGGTTC NM_153603RefSeq chr16
- 23388492 23453191 COG7 91949 component of oligomeric golgi complex 7
GO:0005515|GO:0005794|GO:0033365|GO:0000139|GO:0034067|GO:0006890|GO:0050821|GO:0005730|GO:0017119|GO:0006486|GO:0006886|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144448_PI430048170 0.0488335386810137 0.5455713407297687.17536641092608
6.752547013849 6.92544926641492 P P P 7.34562582949519 7.92186364323013
8.13043954315854 P P P LNCV6_144448_PI430048170 mRNA
AAGGGCCCCATTAAAGGGTGAACTTGTAATAAATTGGAATTTCAAATAAACCTCATGTAC NM_032408RefSeq chr7
- 73440397 73522285 BAZ1B 9031 "bromodomain adjacent to zinc finger domain, 1B"

GO:0005515|GO:0000793|GO:0006355|GO:0016572|GO:0018108|GO:2000273|GO:0005524|GO:0006351|GO:0006974|GO:0006302|GO:0006333|GO:0035173|GO:0003007|GO:0005721|GO:0071884|GO:0003682|GO:0070577|GO:0008270|GO:0004713|GO:0048096|GO:0043596|GO:0004715 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67678_PI430048170 0.0607161536279335 0.7587911155152474.10401131776921 4.51449367213135 4.31321682342629 P P P 4.54865640316081 4.70549323688975 4.88206634514388 P P P LNCV6_67678_PI430048170 mRNA ATTATGTTGTTAGACAAGAATATTCCCATTCCACACATCAAGCTGATTGACTTTGGTCTG NM_014326RefSeq chr15 - 63907035 64046322 DAPK2 23604 death-associated protein kinase 2 GO:0005515|GO:0005516|GO:0034423|GO:0043276|GO:0006915|GO:0042981|GO:0031410|GO:0005524|GO:0042802|GO:0035556|GO:0005737|GO:0046777|GO:0004674|GO:0010506|GO:2001242|GO:0006468|GO:0004683 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127177_PI430048170 0.3282608402731890.7633758165836650.39307566887874 0.2858436110836580.328846916838865A A A 1.18931442659577 0.304209932979092 0.53346899270726 A A A LNCV6_127177_PI430048170 mRNA ATTCCTCCAGCTGTTGAAATGAAGTCTGCCAAATCTTGCTCTAACAAATAAAATGTTATC NM_022159RefSeq chr1 - 78889763 79006810 ADGRL4 NA adhesion G protein-coupled receptor L4 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124315_PI430048170 0.4199624456644440.7179466510047780.297264082732184 0.2648588820901910.381487532173341A A A 0.3602790515343841.43572957028207 0.275850618450146A A A LNCV6_124315_PI430048170 mRNA ATAAATGGATTGTTATATCCAGAACTCACAGCCCAACCTGAACAACCTGACTGCTGTGGG NM_001470RefSeq chr6_GL000251v2_alt - 1088707 1119666 GABBR1 2550 "gamma-aminobutyric acid (GABA) B receptor, 1, transcript variant 1" GO:0005515|GO:0030054|GO:0005886|GO:0004965|GO:0007268|GO:0005576|GO:0007214|GO:0007194|GO:0007193|GO:0030425|GO:0038039|GO:0042734|GO:0005737|GO:0005887|GO:0045211 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55939_PI430048170 0.320382444321245 1.10653479119183 9.44753628807536 9.33869597912001 9.20290007392105 P P P 8.9621822392592 9.3039197226273 9.27124042016126 P P P LNCV6_55939_PI430048170 mRNA ATTCTTGCCTCTAGCAATGACAACCTGTGATGTCTCACAGTAGAGCACTTAGCGCAGAAT NM_024701RefSeq chr10 - 5638856 5666595 ASB13 79754 "ankyrin repeat and SOCS box containing 13, transcript variant 1" GO:0035556|GO:0005515|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136819_PI430048170 0.2848797017435991.1658290925948 0.84347727137597 0.4004769052074220.426307162602796A A A 0.32010260447818 0.335635562829807 0.393552756691039A A A LNCV6_136819_PI430048170 mRNA TGGCAAGGAAATCATCTAAACCCATAACCATAGTTTCAATGTACATAAACCCAGGCTGAA NM_182497RefSeq chr17_JH159146v1_alt - 127110 136530 KRT40 125115 "keratin 40, type I" GO:0005882|GO:0005198 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136910_PI430048170 0.0345077740805765 1.25576416349501 10.6887344779432 10.6033036495972 10.871251873757 P P P 10.2667927470807 10.4426088664911 10.4728444748688 P P P LNCV6_136910_PI430048170 mRNA GCCTCCAGCATTTCCTGATTTCCTCTGTGGTAATAAAAGCTTTCTGTGCTTAGGAAAAAA NM_003314RefSeq chr5 + 160009099 160065545 TTC1 7265 "tetratricopeptide repeat domain 1, transcript variant 1" GO:0005515|GO:0005737|GO:0006457|GO:0051082|GO:0005778 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141810_PI430048170 0.6736970130003930.9424110246985797.43083917000638 7.40166658583953 7.59989276330199 P P P 7.5363336128849 7.30898786942665 7.80838537245634 P P P LNCV6_141810_PI430048170 mRNA

CACAGACCAACAAGTAAGCCAACAAAAAATTAACCAGCACATTTAGCTTCTCTTTTTTCT NM_001135752 RefSeq chr10 - 73134523 73168095 ECD 11319 "ecdysoneless homolog (Drosophila), transcript variant 2" GO:0005515|GO:0006110|GO:0006355|GO:0005737|GO:0006366|GO:0008283|GO:0003713|GO:0005654|GO:2000045. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139090_PI430048170 0.54660313859669 0.94058078636725811.0571643494244 11.1925372504219 11.4198982213655 P P P 11.1622441353014 11.3125127824195 11.4673438510831 P P P LNCV6_139090_PI430048170 mRNA
CCCCCTCAGAAGAATCATGAATTTGCAACAGACCTAATTTTTGGTTACTTTTTGTCTTAT NM_138610RefSeq chr5 - 135334380 135399238 H2AFY 9555 "H2A histone family, member Y, transcript variant 3" GO:0005515|GO:0000793|GO:0000790|GO:0044212|GO:0071901|GO:0005634|GO:0001739|GO:0001558|GO:0000182|GO:0010385|GO:0007549|GO:0000786|GO:0061187|GO:0070062|GO:0001740|GO:0046982|GO:0019901|GO:0005730|GO:0006334|GO:0000122|GO:0003677|GO:0031490|GO:0030291|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141342_PI430048170 0.1056527968760861.12749852553006 13.066844714028 13.0858340281807 12.9653126266298 P P P 12.8135690794165 12.9984215119514 12.7797780984981 P P P LNCV6_141342_PI430048170 mRNA
CCTTTATGCTGGATCATGTGCTACTGGTATAAAGTTCTGGCCTTCTACCTTAAATGAAAA NM_003172RefSeq chr9 - 133351804 133356485 SURF1 6834 "surfeit 1, transcript variant 1" GO:0009060|GO:0005515|GO:0006754|GO:0005746|GO:0008535|GO:0004129|GO:0016021|GO:0055114|GO:0006119. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132001_PI430048170 0.4913514721011040.6783568706378160.536058372521366 0.9857097759108570.459075709963337A A A 2.01939140214561 0.716349017476593 0.471008272346134A A A LNCV6_132001_PI430048170 mRNA
GGGCAAATTGAATGAAGTATTATTATCTGTCTCTTGTAGTACAATGTATCCAACAGACAC NM_015967RefSeq chr1 - 113813810 113871759 PTPN22 26191 "protein tyrosine phosphatase, non-receptor type 22 (lymphoid), transcript variant 1" GO:0005515|GO:0050855|GO:0048471|GO:0017124|GO:0050868|GO:0005634|GO:0050860|GO:0032817|GO:0035335|GO:0005737|GO:0006470|GO:0030217|GO:0045088|GO:0009898|GO:0019900|GO:0004725|GO:0035644 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62485_PI430048170 0.0451722263730679 1.30132862548735 4.82377058624442 4.94473626434935 5.15315199042212 P P P 4.55024440921909 4.46635630383251 4.76754295502452 P P P LNCV6_62485_PI430048170 mRNA
TTCTACCAATCGTTTGCTAACTTTACCCGAGAGGCTTCACATGTGCCTTTCTCTGCAGTA NM_144598RefSeq chr15 + 99251361 99386309 LRRC28 123355 "leucine rich repeat containing 28, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106754_PI430048170 0.3361620581653631.23144239292324 3.88711726178584 3.92881182910986 3.86433292469991 P P P 3.43857410976725 4.0707842974628 3.09801787357297 P P P LNCV6_106754_PI430048170 mRNA
GCCATGAAATGCATTGAGGAGAAATTCCAGTTCACCCTCTCACACTCTTACCATATTACC NM_001082619 RefSeq chr11 - 112064009 112074171 PIH1D2 120379 "PIH1 domain containing 2, transcript variant 2" GO:0017160 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140928_PI430048170 0.2084346594226870.4604739303379970.345232518095883 0.3840492540383330.301815114072652A A A 0.2658400821709871.68725512543798 1.94376320576163 A A A LNCV6_140928_PI430048170 mRNA
TTTGAGCATCATCTCGGCTTACATTTTCTCTGTGGAAAACATCAGCCATTACATTACTTG NM_153244RefSeq chr10 - 15095384 15097319 C10orf111 221060 chromosome 10 open reading frame 111 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138378_PI430048170 0.6832369059701071.18123393381584 2.1098175911927 1.35888176754806 2.55814119878891 A A A 2.0856821359831 1.72667371785924

1.70351596113418 A A A LNCV6_138378_PI430048170 mRNA
AAGAGCCAGGACTTTTGATAGTGAATTGAAAAGGTTATAAAAAAGTGGGGGAGGTTTGGGNM_024697RefSeq chr3
- 21420997 21751324 ZNF385D 79750 zinc finger protein 385D GO:0008270|GO:0005634|GO:0003676
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145613_PI430048170 0.2903278774046160.7523421144861855.09344172134936
3.95522785629001 4.20412754106548 P P P 4.79697336372341 5.11987219270991 4.8034618686455
P P P LNCV6_145613_PI430048170 mRNA
TGTGCCTGTGTGTTTATGTGAGCATGAGGTTCATTTTAAGTAAACTTAAAATTTCCCAGA NM_152445RefSeq chr14
- 73932991 73950414 FAM161B 145483 "family with sequence similarity 161, member B" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_142405_PI430048170 0.7737984324240520.9851378493178210.540751411685275
0.4661221645440720.305454384384437A A A 0.3991596069131040.506399508610501
0.479354402739201A A A LNCV6_142405_PI430048170 mRNA
CAAACAATTGCTGGAGGGAATATGGAGTTATCTGATGCACTTCCTCTTTGACCACTCCAA NM_001005169 RefSeq
chr11 + 4594038 4595013 OR52I1 NA "olfactory receptor, family 52, subfamily I, member 1"NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142789_PI430048170 0.0305902381365718 1.12467650506466 0.748804261665688
0.8376510413344470.732130966266288A A A 0.6116615383722090.611131766780537
0.589396295941304A A A LNCV6_142789_PI430048170 mRNA
TTCGTGAAAGGAAGAGCAGTTGTTATTTATTGTGAGGTCTCTTGCTTGTAAAGTAAAAGC NM_006350RefSeq chr5
+ 53480433 53486474 FST 10468 "follistatin, transcript variant FST317"
GO:0005515|GO:0007389|GO:0007276|GO:0043395|GO:0032926|GO:0005576|GO:0005634|GO:0000122|GO:0030
509|GO:0043616|GO:0031069|GO:0008585|GO:0051798|GO:0001501|GO:0005737|GO:0048185|GO:0002244|GO:0
042475|GO:0045596|GO:0004871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103469_PI430048170 0.7238257803503671.01208068569278 0.426141997380621
0.4134796298393720.303902664757401A A A 0.3334048984169830.377510082325463
0.383227254602679A A A LNCV6_103469_PI430048170 mRNA
GCGCTGCTTGAATACAGCTCAAATTTGTTTATTTGCCAACACAAGTTTACATATATGCAT NM_144980RefSeq chr6
- 165279663 165309622 C6orf118 168090 chromosome 6 open reading frame 118 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142257_PI430048170 0.8701664742247890.99133181600042 5.60413944273522
5.71704935985389 6.04407742032513 P P P 5.80897506880724 5.78022351549288
5.84981344965671 P P P LNCV6_142257_PI430048170 mRNA
CTGTAGACAAATGTAAATAAAGCCTGTGAGTCAAGCATCAAGTGGTGTTTGTTAGAAATA NM_005455RefSeq chr1
- 71063290 71081289 ZRANB2 9406 "zinc finger, RAN-binding domain containing 2, transcript
variant 2"
GO:0008380|GO:0006397|GO:0005515|GO:0006355|GO:0003700|GO:0003723|GO:0008270|GO:0005654|GO:0005
634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133328_PI430048170 0.00363656873014352 0.1921415862357390.292392679449946
0.5331775812852880.36427891438048 A A A 2.34902650457708 2.99338573349614
2.91580676633632 A P P LNCV6_133328_PI430048170 mRNA
GACTGAAGGCTCCTGCAAACATAAATTGCTGATATGGATATAGTAACATAAGAAATACCA NM_001102398 RefSeq
chr1 - 23304689 23344364 HNRNPR 10236 "heterogeneous nuclear ribonucleoprotein R, transcript
variant 1"
GO:0005515|GO:0006397|GO:0008380|GO:0010467|GO:0003723|GO:0005730|GO:0071013|GO:0005737|GO:0000
166|GO:0000398|GO:0030529|GO:0005654|GO:0005681 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73092_PI430048170 0.1020010547993050.7894165458534664.43329544038615 4.04593901576279
4.39536390097079 P P P 4.53359169103816 4.52904640904247 4.84309762722057 P P P
LNCV6_73092_PI430048170 mRNA

GTTTCATCTGTCCCAGCTGAAAATAAATCTGTCTTAAATGAACATCAGGAGACATCTAAA NM_001141947 RefSeq chr3 + 56557155 56621820 CCDC66 285331 "coiled-coil domain containing 66, transcript variant 1" GO:0046548|GO:0060060 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140459_PI430048170 0.4050890847826290.7714038816907473.37491907427289 0.3319956177728391.11472515536351 P A A 2.78220406378962 2.30578398455158 2.60027800108241 P A P LNCV6_140459_PI430048170 mRNA
GGTAGGCATTCTCCTGGGAAATTTTCATTTCCATTTTATCGCCAAACAAAATAAAAAGCA NM_021115 RefSeq chr22 + 26169473 26383597 SEZ6L 23544 "seizure related 6 homolog (mouse)-like, transcript variant 1" GO:0008344|GO:0090036|GO:0021680|GO:0043025|GO:0005789|GO:0016021|GO:0060074 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141002_PI430048170 0.00374020075893946 0.78277380701519 5.92378685592123 5.98815923805153 6.00798183101201 P P P 6.26874094243561 6.40596769074076 6.30299350371346 P P P LNCV6_141002_PI430048170 mRNA
TTGGGGTGGGGACTGTCCTACTGTAACCCCTGTGAAAAACCTTGAAATATAACACTCCAT NM_001193511 RefSeq chr12 - 53480491 53499660 MAP3K12 7786 "mitogen-activated protein kinase kinase kinase 12, transcript variant 1"
GO:0005515|GO:0030424|GO:0019901|GO:0005886|GO:0016572|GO:0007254|GO:0005524|GO:0042803|GO:0030426|GO:0005829|GO:0035556|GO:0000186|GO:0005737|GO:0046777|GO:0004672|GO:0018105|GO:0016020|GO:0004674|GO:0018107|GO:0006468|GO:0004709 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136191_PI430048170 0.0472890132649986 0.3100802234219430.371252541987871 0.3596459812012820.269346973319639A A A 1.34060879151224 2.59578044489477 1.85543708976743 A P A LNCV6_136191_PI430048170 mRNA
GTATGTGAAAACATACTTTCTCTTTATTACAGAAACAGTCACTTGCCACCAAAAATGCTG NM_001288726 RefSeq chr11 + 31509728 31784525 ELP4 26610 "elongator acetyltransferase complex subunit 4, transcript variant 3"
GO:0045859|GO:0005515|GO:0006368|GO:0006357|GO:0000993|GO:0006325|GO:0008023|GO:0005737|GO:0033588|GO:0043966|GO:0043967|GO:0000123|GO:0005654|GO:0008607|GO:0004402 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55409_PI430048170 0.0777399148416022 0.5024756157470832.27874198821995 2.03981207930958 2.85579330604649 A A P 3.98273261146866 2.98375122588999 3.09208123059514 P P P LNCV6_55409_PI430048170 mRNA
ATTGTAAAACATTGCCCATCTGTCTTGCTCACTCTTAAACTCTCCCAAGAACAAGGCCGG NM_152491 RefSeq chr1 - 205828021 205850148 PM20D1 148811 peptidase M20 domain containing 1
GO:0050792|GO:0003674|GO:0006508|GO:0008233|GO:0050691|GO:0046872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132048_PI430048170 0.5546667867356610.8530158562569910.4288418561081121.9897312871268 0.38945906448369 A A A 1.82807956671519 0.9986624827833761.15115807593971 A A A LNCV6_132048_PI430048170 mRNA
AGTGGGGATGTGGCATGGTAGCGTCTGTTCATCCATGGAATAAAACATTATTTTACCACT NM_130797 RefSeq chr7 + 154052417 154894290 DPP6 1804 "dipeptidyl-peptidase 6, transcript variant 1"
GO:0006508|GO:0008236|GO:0016021|GO:0008239|GO:0019228|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137259_PI430048170 0.2748654209521950.8427344445346151 0.0944256240437 10.0532812749485 10.3425393751016 P P P 10.1905273309607 10.3045833473904 10.7017706780116 P P P LNCV6_137259_PI430048170 mRNA
GGAATTCAGAGGAAAACCCAGATTCAGTGATTAACAATGCCAAAAAATGCAAGTAACTAG NM_012325 RefSeq chr20 + 32819892 32850405 MAPRE1 22919 "microtubule-associated protein, RP/EB family, member 1"
GO:0005515|GO:0031253|GO:0031115|GO:0005881|GO:0005813|GO:0005794|GO:0006996|GO:0030981|GO:0008283|GO:0005874|GO:0005819|GO:0035372|GO:0035371|GO:0008022|GO:0005829|GO:0005737|GO:0007067|GO:0

051010|GO:0000086|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137781_PI430048170 0.00106561556901109 0.7852464763674297.23089083534304
7.21095831213 7.19103798738259 P P P 7.56059574381508 7.55890471939863 7.56000897174546 P
P P LNCV6_137781_PI430048170 mRNA
GAACGGAATGCCGTTGTTTTATAACTTTGAACAAATGTATTTACTGCCCTTCTCATTTCA NM_001288794 RefSeq
chr5 + 178130960 178148570 RMND5B 64777 "required for meiotic nuclear division 5 homolog B (S.
cerevisiae), transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143479_PI430048170 0.0380804161564183 1.28962991191815 5.60664219375779
5.85900009814035 5.65323164708421 P P P 5.51858544149906 5.26503657115456
5.22951492739494 P P P LNCV6_143479_PI430048170 mRNA
TTAACTGTTCAACTGGAAAATTTTTAGTTTTTCTAGCCAGGTGTGGTGGCACACACTTGT NM_001278716 RefSeq
chr6 - 98873724 98948006 FBXL4 26235 "F-box and leucine-rich repeat protein 4, transcript variant
2" GO:0006511|GO:0005758|GO:0000151|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132897_PI430048170 0.00367987252801774 1.19493801236889 11.3752585891914
11.3122093702477 11.2883712521691 P P P 11.0787448017571 11.0826755378351
11.0447129752824 P P P LNCV6_132897_PI430048170 mRNA
ACTCAGGCTAGTGTCAGCGTCTTGGTTTGGGGAGAAAAAATTAAATGTTTCGGTTTTTGT NM_001035254 RefSeq
chr9 - 127940581 127980533 FAM102A 399665 "family with sequence similarity 102, member A,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136084_PI430048170 0.000386675905833513 0.5110661497094417.5191708726055
7.32987256251843 7.3220280281139 P P P 8.29466929736648 8.30857612236511 8.4747901701698
P P P LNCV6_136084_PI430048170 mRNA
CGGCAGCTGTGTTTAGCCCCTCCAGATGGAAGTTTCACTTGAATGTAAAATAATAAAGTT NM_016612RefSeq chr8
+ 23528849 23572550 SLC25A37 51312 "solute carrier family 25 (mitochondrial iron transporter),
member 37" GO:0048250|GO:0005743|GO:0005381|GO:0044281|GO:0016021|GO:0055072|GO:0034755 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138274_PI430048170 0.1036427387118050.3709916534917 2.4124421924602
0.28229937387758 1.53409473022454 A A A 2.46418728848894 3.10298792051368
3.50134544655749 A P P LNCV6_138274_PI430048170 mRNA
GAAGACCTGTAACACTAAGTACTTGAGAGTTACAGTCTGAATAATGAAGTCGTACCAGCT NM_198402RefSeq chr3
- 123494515 123585077 HACD2 NA 3-hydroxyacyl-CoA dehydratase 2 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_89037_PI430048170 0.00780855656198073 0.4584848831967263.47539687093631
2.96268637625222 3.39052982419799 P A P 4.0890558565663 4.47248094788898
4.63904670056187 P P P LNCV6_89037_PI430048170 mRNA
CCTTTTCCCAATGGGGTGGGGGAGGGAAGAAGGATATTAAAATAAGTTTTAAGAAGCAAA NM_001284333 RefSeq
chr17 + 62479024 62615480 TLK2 11011 "tousled-like kinase 2, transcript variant C"
GO:0005515|GO:0005882|GO:0048471|GO:0005634|GO:0071480|GO:0032435|GO:0005524|GO:0006974|GO:0035
556|GO:0007049|GO:0007059|GO:0018105|GO:0004674|GO:0010507|GO:0006468|GO:0001672|GO:0016568 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144916_PI430048170 0.7135442019390530.8908962327740344.40675263653471
4.42823721383212 4.14793346734297 P P P 4.78636756855802 4.66788682814981
3.89316996806498 P P P LNCV6_144916_PI430048170 mRNA
TGCAAGACGCATCCCCTGCAAAACACACTGGCTCATTTTAAAGCTCTCACCTTCCAAGGC NM_152769RefSeq chr19
- 1229947 1237991 C19orf26 255057 chromosome 19 open reading frame 26 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129838_PI430048170 0.0326902191860814 3.54690954532897 3.69887150743737
3.83235721541402 4.25757868070827 P P P 2.84837977105666 1.56616325759798
1.53950021887673 P A A LNCV6_129838_PI430048170 mRNA

CCTGTCCATTATGAATGGCCTACTGTTCTATTATTTGTTTTGACTTGAATTTATCCACCA NM_177949 RefSeq chrX - 101655280 101659891 ARMCX2 9823 "armadillo repeat containing, X-linked 2, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131303_PI430048170 0.00035972690643775 2.80055625396687 9.36802144384111 9.34685730187836 9.12406408551459 P P P 7.84701212736223 7.92489779622337 7.60314759244853 P P P LNCV6_131303_PI430048170 mRNA
GTGTCATCTTACCCTTTACAGAGAAATTAAATGGCCTTGGTGGGACCAAATGGGAAAAAA NM_001303439 RefSeq chr17 + 45160173 45170040 HEXIM2 124790 "hexamethylene bis-acetamide inducible 2, transcript variant 1"
GO:0005515|GO:0005737|GO:0045736|GO:0004861|GO:0017069|GO:0005654|GO:0005634|GO:0000122|GO:0045892|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135889_PI430048170 0.210361200794495 0.83951037432196 7.01848915261851 6.82699946555048 6.88452712349514 P P P 6.88954651100682 7.34635933511216 7.2203275361962 P P P LNCV6_135889_PI430048170 mRNA
TCATCCGATTCCCCTGTAGCAGTCACTGACAGTAAATAAACCTTTGCAAACGTTAAAAAA NM_021014 RefSeq chrX - 48346427 48356753 SSX3 10214 "synovial sarcoma, X breakpoint 3"
GO:0006355|GO:0005634|GO:0003676|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139475_PI430048170 0.0234491797874074 0.750741253138321 8.31593901603239 8.20465338367332 8.01068763503435 P P P 8.60183639209598 8.70762417706108 8.46917094838582 P P P LNCV6_139475_PI430048170 mRNA
TCCCACATCAACCATTAAAGTTATTTAACAGCAGCCTTCACCTGGCTCCTGAGGAAAAAA NM_033046 RefSeq chr2 - 74425860 74440583 RTKN 6242 "rhotekin, transcript variant 2"
GO:0005515|GO:0007165|GO:0006915|GO:0017049|GO:0007266|GO:0005575|GO:0005525|GO:0005095|GO:0043086 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133416_PI430048170 0.244859072269601 1.32681302361776 0.469007939447871 1.26253448550864 0.970785689044634 A A A 0.819782477471301 0.342903373615243 0.373115482692786 A A A LNCV6_133416_PI430048170 mRNA
GACCCTAAATGGACCCTTGTGAAATATATCATTCCTTAGTTTCCCCATCTTTTCTGTCTT NM_001005283 RefSeq chr11 + 58190433 58191518 OR9Q2 NA "olfactory receptor, family 9, subfamily Q, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145489_PI430048170 0.982040225517211 0.999653251140773 0.487973511098042 0.50906272427901 0.400862590513928 A A A 0.508687418557414 0.442748912361427 0.449310097101101 A A A LNCV6_145489_PI430048170 mRNA
AAGGTGCCATCTTGTGGTATTGACTTGTATTTATAACAAATAAACTGCTCAAGAGACTGC NM_001080427 RefSeq chr2 + 136990891 137677717 THSD7B 80731 "thrombospondin, type I, domain containing 7B"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139162_PI430048170 0.0029205220501424 0.409734347422933 8.88624909720569 8.64418190152238 8.83110790268097 P P P 9.86707761338423 10.0157534303928 10.3148566148416 P P P LNCV6_139162_PI430048170 mRNA
GCCCACCTTTAACAGAGCACCCCTTTGAAAGTTTTATAGGTATGAAATATATGTAGATAT NM_032558 RefSeq chr9 + 94374550 94460920 HIATL1 84641 hippocampus abundant transcript-like 1
GO:0005215|GO:0005886|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51834_PI430048170 0.0888175977749149 0.6241932137373 2.35562590622474 2.71903153141202 2.92466256635473 A A P 2.90127384408512 3.38047073930265 3.70349960841127 P P P LNCV6_51834_PI430048170 mRNA
GACCATCACACACATGAAAATGGCTATAATCCTCACTGTATTTTCTTGTTCTTCTTGAAA NM_001040616 RefSeq chr15 - 100569222 100602240 LINS 55180 lines homolog (Drosophila) NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69260_PI430048170 0.575665946580246 1.25252542693119 3.11486538500496 2.44473393524972

1.68626571762844 P A A 2.08385379970105 0.7643334148671842.98084125573419 A A P
LNCV6_69260_PI430048170 mRNA
GGGTGGGGTGAGAGTGTGTGGAGTAAGGACATTCAGAATAAATATCTGCTGCTCTGCTCA NM_000023 RefSeq chr17
+ 50166004 50175932 SGCA 6442 "sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein),
transcript variant 1"
GO:0042383|GO:0005737|GO:0007517|GO:0006936|GO:0016010|GO:0005911|GO:0016012|GO:0005509|GO:0045
121|GO:0016021|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135175_PI430048170 0.0920527294502475 1.04241814407443 0.401828309378627
0.4290099273280650.354672845385581 A A A 0.3123332496952640.340226389134419
0.353817976394679 A A A LNCV6_135175_PI430048170 mRNA
CATTCATGTGCATTTTTCTGCCACTGACCACAAGACGATTTCCTGAGTTTTGTAATCCTC NM_005199 RefSeq chr2
+ 232539726 232546328 CHRNG 1146 "cholinergic receptor, nicotinic, gamma (muscle)"
GO:0030054|GO:0005886|GO:0007268|GO:0055085|GO:0005892|GO:0007165|GO:0006936|GO:0005887|GO:0015
464|GO:0045211|GO:0042391|GO:0006810|GO:0004889|GO:0015267 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133945_PI430048170 0.8322800531181520.9721870069299690.837700956394259
0.4065760340367970.310532253854854 A A A 0.5539599042015020.799697420467005
0.343221439644345 A A A LNCV6_133945_PI430048170 mRNA
GGCTTTAGAGAGCAATCTTTGTATGACACCAGAAAACTCTTCATGCTATTGAATGATAAA NM_001165032 RefSeq
chr6 + 13924866 13980009 RNF182 221687 "ring finger protein 182, transcript variant 1"
GO:0005515|GO:0005737|GO:0004842|GO:0016567|GO:0016874|GO:0008270|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143278_PI430048170 0.3194149755803791.38625774781194 1.29735020701654
0.2911300076092160.49756944815542 A A A 0.30890683597373 0.269562416671893
0.298487850488515 A A A LNCV6_143278_PI430048170 mRNA
CTTTCATCTACAGCCTGAGGAACAAAGATATGAAAAGGGGTTTGAAGAAATTAAGACACA NM_001005235 RefSeq
chr9 + 122723989 122724925 OR1L4 254973 "olfactory receptor, family 1, subfamily L, member 4"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_76666_PI430048170 0.6454758181978181.10849296878917 4.6919978669703 4.01445438558224
4.08040340715265 P P P 4.36678601714531 4.06147351663811 3.9846734975244 P P P
LNCV6_76666_PI430048170 mRNA
TTGAATGTCATTAAGATGAAATCCAGTGACTTCCTGGAGAGTGCAGAACTGGACAGCGGA NM_003804 RefSeq chr6
+ 3076823 3115187 RIPK1 8737 receptor (TNFRSF)-interacting serine-threonine kinase 1
GO:0005515|GO:0031264|GO:0070231|GO:0046330|GO:0032403|GO:0032757|GO:0042802|GO:0002756|GO:0043
068|GO:0046777|GO:0071356|GO:0070926|GO:0051260|GO:0043123|GO:0044257|GO:0031625|GO:0043124|GO:0
060545|GO:0032760|GO:0005123|GO:0002224|GO:0045651|GO:0033209|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131825_PI430048170 0.3574832254139430.4526252108468180.246213434436719
0.3074734666286790.287493887115959 A A A 0.45800027997203 0.355236449227802
2.43250608937168 A A P LNCV6_131825_PI430048170 mRNA
TCTTGCAAACGGGATTGCAAAAAATCCACTTCCAGCCAACTGGATTGTGTTGACACAACC NM_001146182 RefSeq
chr17_GL383564v2_alt + 131007 132561 KRTAP16-1 NA keratin associated protein 16-1 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128230_PI430048170 0.6840881891960541.04401644044679 13.3951355408085
13.0684033390069 13.1670495058365 P P P 13.2492771098927 13.2592363878197
12.9319661597586 P P P LNCV6_128230_PI430048170 mRNA
CTACGAACACCCCTGAGGCCCCGGACGCCCCCGGACACAATAAAGGTGTGAAGCTTCGAA NM_005205 RefSeq
chr16 - 31427730 31428428 COX6A2 1339 cytochrome c oxidase subunit VIa polypeptide 2

GO:0004129|GO:0006091|GO:0005751 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140628_PI430048170 0.0138580073084362 0.5678013015995440.280054000994063
0.5174638402937990.348554977948565A A A 0.9262642679916731.39094818232576
1.25043784484121 A A A LNCV6_140628_PI430048170 mRNA
TGCCCTGGTGGACACTTGCCCACCATCCTGTGAGTAAAAGTGAAATAAAAGCTTTGACTA NM_001767RefSeq chr1
+ 116754463 116769229 CD2 914 CD2 molecule
GO:0005515|GO:0005886|GO:0050900|GO:0042803|GO:0016337|GO:0030101|GO:0005911|GO:0045580|GO:0004
872|GO:0034113|GO:0046658|GO:2000484|GO:0009986|GO:0032760|GO:0005102|GO:0006915|GO:0005576|GO:0
030887|GO:0042110|GO:0007596|GO:0005887|GO:0009898|GO:0001766|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132773_PI430048170 0.0685887768506583 1.01315833433152 0.321353345363726
0.3055971127183660.312200927423377A A A 0.3027415361542040.296931463432472
0.282870542584575A A A LNCV6_132773_PI430048170 mRNA
ATTGGGAAATATCAGCTGCTCACTATTATCTGCAGTATTGATAAGACTACAGCTATATCT NM_001100396 RefSeq
chr2 + 54330933 54361577 C2orf73 129852 chromosome 2 open reading frame 73 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_124809_PI430048170 0.1341865304864450.6981655840793622.57819161815341
2.49746555535995 2.87187761319767 A A P 3.56950575539511 2.98199189403455
2.87851459388233 P P P LNCV6_124809_PI430048170 mRNA
TCTCTCCTCACCTGCAGCATCATCTGTTACCTCACCTTCGGAGACAAGATCAAGGACGAC NM_000500RefSeq
chr6_GL000256v2_alt + 3306770 3342857 CYP21A2 1589 "cytochrome P450, family 21, subfamily
A, polypeptide 2, transcript variant 1"
GO:0006705|GO:0006805|GO:0005506|GO:0004509|GO:0008395|GO:0006704|GO:0044281|GO:0005789|GO:0016
125|GO:0005496|GO:0008202|GO:0020037|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130475_PI430048170 0.0390348524373725 1.29747972098194 10.1292471638102
10.198019045876 10.1247224603203 P P P 9.92109029251848 9.76514161476067
9.62452900321685 P P P LNCV6_130475_PI430048170 mRNA
GGGGACAGTGCTACACTCGTCTCCACTGTTTGTTTTACTTCCCCAAAATGGACCTTTTTT NM_001114123 RefSeq
chrX - 47635519 47650604 ELK1 2002 "ELK1, member of ETS oncogene family, transcript variant
1"
GO:0005515|GO:0003700|GO:0034142|GO:0006366|GO:0000981|GO:0005634|GO:0071480|GO:0051403|GO:0030
154|GO:0030425|GO:0005739|GO:0002756|GO:0003690|GO:0071394|GO:0045944|GO:0002755|GO:0043025|GO:0
043679|GO:0009416|GO:0034138|GO:0048011|GO:0038124|GO:0038123|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139484_PI430048170 0.6230710745660841.51717290856492 2.10084351681095
2.41759421279205 0.306357200900021A A A 1.49842074657005 0.744472856273781
1.41319968825083 A A A LNCV6_139484_PI430048170 mRNA
GTGGGTGAGCAGCAGATGTAGTTTCCATTTCCCTGGGGGTTTAATTTTCCAAACTTTGTC NM_175900RefSeq chr16
- 29742464 29746019 C16orf54 283897 chromosome 16 open reading frame 54 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56072_PI430048170 0.41546290004468 0.9592907899454860.2662836207388230.415432202711506
0.298149411908881A A A 0.4767978012158380.3681827726079780.314300152974957A A A
LNCV6_56072_PI430048170 mRNA
TGCAGCATGGAACAATTACAGGATTTTTTATCAAGCAGAAATGCATCGAACAACGAGAAT NM_001204062 RefSeq
chr10 + 22316382 22331485 COMMD3-BMI1 NA COMMD3-BMI1 readthrough NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138725_PI430048170 0.0598501766115493 0.7597346089443355.71385506697709
5.48239661742605 5.39358397655152 P P P 5.93608466242623 6.11624115797139
5.71871940119753 P P P LNCV6_138725_PI430048170 mRNA

AAACAAAGGCTAAACCAGGATTTATAAGAGAGGGCTTATAAATCCCTCTGCCGACGCAGG NM_024907 RefSeq chr19 - 38941400 38975813 FBXO17 115290 "F-box protein 17, transcript variant 2" GO:0005515|GO:0001948|GO:0019005 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_136020_PI430048170 0.602437986306294 1.0915618476888 11.6623029829733 11.4767872906342 11.6561741873904 P P P 12.0592078918498 11.0822103723348 11.0370970997471 P P P LNCV6_136020_PI430048170 mRNA
CCCCTTGGTTTTGTGTTACAAGAGTTGTTGGAGACAGTTTCAGATGATTATTTAATTTGT NM_172230 RefSeq chr11 - 65127278 65134532 SYVN1 84447 "synovial apoptosis inhibitor 1, synoviolin, transcript variant 2" GO:0005515|GO:0016567|GO:0016881|GO:0005783|GO:0030433|GO:0001701|GO:0030968|GO:0016020|GO:0005789|GO:0005654|GO:0008270|GO:0016021|GO:0006987|GO:0044267|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_142381_PI430048170 0.0229712055503312 0.437843195181818 6.07361885733364 5.89458194219897 6.0267020324087 P P P 6.75969274887147 7.3400395296909 7.39416069028143 P P P LNCV6_142381_PI430048170 mRNA
TCAGTGTTGTACATAGCATAAAAACTCTGCAGAGAAGTATTCCCAATAAGGAAATAGCAT NM_003246 RefSeq chr15 + 39581078 39598921 THBS1 7057 thrombospondin 1 GO:0005515|GO:0006986|GO:0034976|GO:0003417|GO:0005615|GO:0032914|GO:0034605|GO:0001948|GO:0010763|GO:0006493|GO:0030198|GO:0032026|GO:0030335|GO:0009986|GO:0017134|GO:0005509|GO:0030169|GO:0030168|GO:0010748|GO:0010595|GO:0010751|GO:0010596|GO:0005178|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_130300_PI430048170 0.186224790380368 1.46525495018516 6.97528655920394 7.51007743064035 6.61728430210873 P P P 6.63388842243232 6.46041540334969 6.490422649911 P P P LNCV6_130300_PI430048170 mRNA
TGGGCAGCATGGGAGCCTGATCCTTCTGACATAAATAAACACAATGCATGCAGGAAAAAA NM_000287 RefSeq chr6 - 42963872 42979243 PEX6 5190 peroxisomal biogenesis factor 6 GO:0005515|GO:0042623|GO:0006625|GO:0016561|GO:0050821|GO:0008022|GO:0005524|GO:0032403|GO:0005829|GO:0005737|GO:0008152|GO:0007031|GO:0016887|GO:0005778|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_134231_PI430048170 0.637505975808491 0.697278513276313 1.24918256764951 0.441280198950249 0.360601756160984 A A A 0.479606020129663 2.16074855145972 0.413507431456214 A A A LNCV6_134231_PI430048170 mRNA
GTTGTGAGGCTATAGAGACTTATTCTACCAGTAAAACAGGTCAATCCTTTTACATGTTTA NM_000489 RefSeq chrX - 77504877 77786269 ATRX 546 "alpha thalassemia/mental retardation syndrome X-linked, transcript variant 1" GO:0005515|GO:0070087|GO:0005634|GO:0035064|GO:0007283|GO:0042393|GO:0060009|GO:0045944|GO:0010571|GO:0031933|GO:0006338|GO:0032508|GO:0070603|GO:0006355|GO:0072711|GO:0030330|GO:0006334|GO:0004386|GO:0015616|GO:0006310|GO:0006336|GO:0005524|GO:0003677|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_136324_PI430048170 0.369101289970286 0.908987829407781 4.49383954815931 4.47012976853259 4.60322861566787 P P P 4.48683727357306 4.60417612090032 4.86619238612885 P P P LNCV6_136324_PI430048170 mRNA
GAACAAAGGTGTGCTCTGAGCTTCTTCATATTTCACCTTCACCCTCACCTGTGTTCTCTT NM_002154 RefSeq chr5 + 133051969 133105017 HSPA4 3308 heat shock 70kDa protein 4 GO:0006986|GO:0005739|GO:0051131|GO:0045040|GO:0005524|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_132829_PI430048170 0.392607957244096 0.960177858946512 0.380421559452369 0.423501261050779 0.353150213842089 A A A 0.519959338421642 0.464499594245137 0.343784304731424 A A A LNCV6_132829_PI430048170 mRNA
GAGTCTTAAAATAGAGGAAGAGTAAGCAAAGCATGTCAAGTTTTTGTTTTCTGCATTCAG NM_002363 RefSeq chrX

+ 30243730 30252038 MAGEB1 4112 "melanoma antigen family B1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143920_PI430048170 0.3347639900517490.81612345242801 0.352904632409865 0.3748184097602940.33218389555195 A A A 0.4256030657977131.03078382707447 0.389551944218139A A A LNCV6_143920_PI430048170 mRNA TTTCATGATAAATTTGTGTTGTGTCCCTGGTAGCAGAAATCCTTACCTATATGTTTCTGANM_031963RefSeq chr17_JH159148v1_alt - 68108 69140 KRTAP9-8 83901 keratin associated protein 9-8 GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129105_PI430048170 0.19244087943332 0.8230227431469641 0.994998497909 10.6913937060807 10.4578673389399 P P P 11.1672151088083 10.9459542738017 10.9110120381093 P P P LNCV6_129105_PI430048170 mRNA AAGGGACCTTTCCGAAAAACATCTTTTGGGGAAATAAAAATGTGGACTGTGCGAGGAAAA NM_005689RefSeq chr2 - 219209765 219218990 ABCB6 10058 "ATP-binding cassette, sub-family B (MDR/TAP), member 6 (Langereis blood group)" GO:0015886|GO:0015439|GO:0005794|GO:0015562|GO:0005886|GO:0015232|GO:0005783|GO:0005741|GO:0005740|GO:0055085|GO:0005524|GO:0005739|GO:0006879|GO:0006779|GO:0007420|GO:0006810|GO:0043588|GO:0031307|GO:0043190|GO:0070062|GO:0020037|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135223_PI430048170 0.5562990218555180.8321120154508140.464519982392819 0.9690540707529430.530209276925512A A A 0.3299904075195021.35975860147571 0.9432526010245 A A A LNCV6_135223_PI430048170 mRNA CAGGAGCCTTCATTAAAACAGAAATTTTAGGGAAAACCACAAAAACCTTCGTAAAGTGAA NM_033160RefSeq chr9 + 66900728 66921439 ZNF658 26149 zinc finger protein 658 GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130448_PI430048170 0.1031502369794281.36403313521756 4.60071467843864 4.18618173710231 4.05068089858544 P P P 3.74533289899384 4.0048586509742 3.78849657502418 P P P LNCV6_130448_PI430048170 mRNA CTTTGTGGATGTGGGCACAGTGAAGAGCAATAAAGAGTGTGAGGTTCCTGCTGGAAAAAA NM_002334RefSeq chr11 - 46856716 46918622 LRP4 4038 low density lipoprotein receptor-related protein 4 GO:0005515|GO:0031594|GO:0051290|GO:0009954|GO:0009953|GO:0016600|GO:0030425|GO:0042803|GO:0030279|GO:0030198|GO:0097110|GO:0043025|GO:0042475|GO:0016055|GO:0090090|GO:0001942|GO:0030971|GO:0009986|GO:0001822|GO:0005509|GO:0014069|GO:0006897|GO:0097104|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134420_PI430048170 0.1038500731689690.8718907783300981 5.4722053857075 15.2258568123915 15.2791307031093 P P P 15.5362196892575 15.6142012151984 15.4257232711243 P P P LNCV6_134420_PI430048170 mRNA GTCAGCGGGTGACGTGTGTTCTTTTGAGTCCTTGTATGAATAAAAGGCTGGAAACCTACA NM_002081RefSeq chr2 + 240435697 240468078 GPC1 2817 glypican 1 GO:0007603|GO:0005886|GO:0044281|GO:0031225|GO:0005615|GO:0014037|GO:0007411|GO:0030200|GO:0030204|GO:2001016|GO:0030203|GO:0070062|GO:0043202|GO:0005975|GO:0005796|GO:0005507|GO:0017134|GO:0005578|GO:0006027|GO:0043395|GO:0001523|GO:0006024|GO:0032288|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136219_PI430048170 0.00882831710056359 1.45135562999264 7.98490649044251 7.98507903244372 7.74370591988043 P P P 7.50621725071772 7.36199083961423 7.23356120089191 P P P LNCV6_136219_PI430048170 mRNA GTAGACCTACTTGCTCACATGCAGATTTGAGAGGACCTCAACGGCTTTTCTCACAAAAAA NM_199069RefSeq chr3 + 49021640 49023493 NDUFAF3 25915 "NADH dehydrogenase (ubiquinone) complex I, assembly factor 3, transcript variant 1" GO:0005515|GO:0032981|GO:0005743|GO:0005634 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_136655_PI430048170 0.4596898154378641.16525976515618 4.13576700984983 3.9846734975244
3.63834742115359 P P P 3.91070468383551 3.94516334685618 3.15621559415415 P P P
LNCV6_136655_PI430048170 mRNA
TAAAACTTTGGAAAGCACTTTCTAGAACTGAAGAAGGTAAAACCTCCTCACCCCCATCCT NM_024897RefSeq chr1
- 156243320 156248117 PAQR6 79957 "progestin and adipoQ receptor family member VI, transcript
variant 1" GO:0004872|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137593_PI430048170 0.3969687203140911.1029393878404 0.721083654011544
0.4144803310809710.314050633695116A A A 0.32473177617269 0.361411758230283
0.370770810475809A A A LNCV6_137593_PI430048170 mRNA
CAAAAAGCCAACTGCTGTCAGGGACTGGCGGGTATAGCACCTGGGTCAAACACCTGGATG NM_001164375
RefSeq chr10 - 71711700 71719821 C10orf105 NA "chromosome 10 open reading frame 105,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140220_PI430048170 0.9831457097645170.9354176425244021.98864009506781
0.50540486960052 1.87940157907957 A A A 2.44166508872567 1.53434602841124
0.447992419023948A A A LNCV6_140220_PI430048170 mRNA
AGAAATTGCATGAATGCCCAGTGAGGGGAGGTCTTTCATGCATATAAAAAGGTAATGTTT NM_024855RefSeq chr20
+ 38748453 38772446 ACTR5 79913 ARP5 actin-related protein 5 homolog (yeast)
GO:0005515|GO:0031011|GO:0006355|GO:0005737|GO:0070914|GO:0006310|GO:0005634|GO:0006351|GO:0006
302 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134358_PI430048170 0.2942879689541331.05316665088103 0.502921206629514
0.3278317414114230.425891618804896A A A 0.2874890407652210.358837555608575
0.38954827319589 A A A LNCV6_134358_PI430048170 mRNA
TTGTGCTTTCCTGAAAGCAGTAACCAAGAGTTAAGATATCCCTAATGTTTTGCTTAAACT NM_001049RefSeq chr14
+ 38207998 38213063 SSTR1 6751 somatostatin receptor 1
GO:0043005|GO:0008285|GO:0005886|GO:0007584|GO:0007586|GO:0007267|GO:0007268|GO:0021549|GO:0007
215|GO:0007283|GO:0004994|GO:0005737|GO:0042594|GO:0042923|GO:0005887|GO:0007187|GO:0007218|GO:0
071392|GO:0030900|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141217_PI430048170 0.8695249495220940.9802609024820275.36929942752854
4.96000934831268 4.94982717755622 P P P 4.8852680764014 5.206702084907
5.28410141911603 P P P LNCV6_141217_PI430048170 mRNA
CCCAGTGAAGCCATATCAAAAGTGGAAATTTGAAAAATATTATGAAGCCTGAAGTGTAAC NM_014568RefSeq chr2
+ 157257827 157311401 GALNT5 11227 polypeptide N-acetylgalactosaminyltransferase 5
GO:0004653|GO:0006493|GO:0000139|GO:0030246|GO:0016266|GO:0016021|GO:0005575|GO:0044267|GO:0046
872|GO:0006024|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130802_PI430048170 0.1195289825507640.3329435994653460.397149449133523
0.3792997113308420.407752824843379A A A 0.8303710813303751.88506526415411
2.67235891989432 A A P LNCV6_130802_PI430048170 mRNA
CCTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAAAGC NM_006691RefSeq chr11
- 10557865 10568818 LYVE1 10894 lymphatic vessel endothelial hyaluronan receptor 1
GO:0005886|GO:0005975|GO:0009611|GO:0006928|GO:0044281|GO:0009653|GO:0007165|GO:0016020|GO:0005
540|GO:0007160|GO:0005887|GO:0006810|GO:0009405|GO:0030212|GO:0004872|GO:0030214|GO:0030203|GO:0
070062|GO:0004888. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131068_PI430048170 0.1499502053023720.5218133306014780.649515060855433
0.5618518717270630.339417010662124A A A 1.20186216527601 2.0787822487653
0.794838786944547A A A LNCV6_131068_PI430048170 mRNA
TGCTGTAAAAATATGACACGTTTTCAACCCCCGCAAGCCAAAGATCCATGGGTTCATTAA NM_001033018 RefSeq
chr8 - 11973936 11974599 DEFB136 NA "defensin, beta 136" NA . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_54799_PI430048170 0.2879757721140970.8899475514740938.07084251413178 7.90538008487934
8.04365081245066 P P P 7.96428589318023 8.35149052592439 8.18814562589059 P P P
LNCV6_54799_PI430048170 mRNA
TACAAATATGTGTCTAAGTACAGCCTGGTCAAGAACAAGATCAGCAAGAGCAGCTTCCGC NM_080388RefSeq chr1
- 153606890 153613038 S100A16 140576 S100 calcium binding protein A16
GO:0051592|GO:0005737|GO:0005886|GO:0005509|GO:0005730|GO:0042803|GO:0070062|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139594_PI430048170 0.5026409768434671.49165829687469 1.9785700471143
2.15935491423086 0.458601086767482A A A 1.53389329478812 1.21231895947467 0.4279260509201
A A A LNCV6_139594_PI430048170 mRNA
TACCTCCTTGACTAAGCTGGTTCCTTGTGTCAAAGCACCTCATGCCTTCCATTAAAGAGA NM_002215RefSeq chr3
+ 52777585 52792068 ITIH1 3697 "inter-alpha-trypsin inhibitor heavy chain 1, transcript variant 1"
GO:0010951|GO:0004867|GO:0005509|GO:0030212|GO:0072562|GO:0005576|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138365_PI430048170 0.3164851807979341.04038335031448 0.309410232858063
0.27004963884683 0.412217702975444A A A 0.2853460883017350.253039456654326
0.28546418683221 A A A LNCV6_138365_PI430048170 mRNA
AACTCGCTCAGAAGAGGGAACTAAGCATTTTTGGCAACCAATGGCAGATATCTATGGCAG NM_021080RefSeq chr1
- 56997905 58250539 DAB1 1600 "Dab, reelin signal transducer, homolog 1 (Drosophila)"
GO:0043005|GO:0048471|GO:0007264|GO:0021942|GO:0021517|GO:0005829|GO:0021799|GO:0045860|GO:0007
628|GO:0043025|GO:0051645|GO:0042493|GO:0014069|GO:0045177|GO:0021813|GO:0016358|GO:0046426|GO:0
021589|GO:0005903|GO:0048712|GO:0007162|GO:0016020|GO:0045666|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136396_PI430048170 0.57044652219962 0.96605417027312 0.492236738077205
0.4894936118919470.266838481777696A A A 0.4056507906826220.527267720602037
0.473940998625335A A A LNCV6_136396_PI430048170 mRNA
TGAGTAGCTGGTGTGGAAGTGCTGATAGAATATGATAGGAGGATGACCATCACCTTGTCT NM_013939RefSeq chr19
+ 15728023 15729052 OR10H2 26538 "olfactory receptor, family 10, subfamily H, member 2"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_92779_PI430048170 0.213977435319972 0.804153976443853 4.11187903623303
4.11683077350791 4.33681465889895 P P P 4.62813802406099 4.68555980748965
4.14913984061447 P P P LNCV6_92779_PI430048170 mRNA
ACGTCCGCATTCACACAGGTGAGAAGCCATGCCAGTGTGTGATGTGCGGTAAGGCCTTCA NM_001287603 RefSeq
chr1 - 15941868 15976132 ZBTB17 7709 "zinc finger and BTB domain containing 17, transcript
variant 3"
GO:0005515|GO:0003700|GO:0007398|GO:0045786|GO:0003677|GO:0001702|GO:0006351|GO:0046872|GO:0030
968|GO:0005654|GO:0006987|GO:0045893|GO:0044267 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128098_PI430048170 0.31005233691417 1.03019233120866 0.30035969209791
0.256230184798595 0.364664313636639 A A A 0.275138990434135 0.246537361524169
0.272728155152592 A A A LNCV6_128098_PI430048170 mRNA
GCCAAATAAAGCGGTGTGTGTGTACTGCAGCTGTAGGTGAACTTAAAAATAATAATAAAA NM_001037160 RefSeq
chr2 - 10056798 10080411 CYS1 NA cystin 1 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137952_PI430048170 0.46829112584122 0.844723546195178 5.68311664011339
4.67715208171001 4.85737725848089 P P P 5.62802513181046 5.4333595438085
5.03388070010132 P P P LNCV6_137952_PI430048170 mRNA
CCCTGGCCTCCTTCTGCGATGAAGCCTTTATACTTGAAAATAAAATGTGAAAGCACTCAA NM_001145028 RefSeq

chr19 - 14053366 14059159 PALM3 342979 paralemmin 3
GO:0005515|GO:0008063|GO:0005737|GO:0005886|GO:0001960|GO:0032496|GO:0005524 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_41252_PI430048170 0.610590395962428 1.48076120757558 3.66891012782312
2.6461762927894 1.32858948494226 P A A 2.9677898596019 2.27201268492848
0.895208506974188 P A A LNCV6_41252_PI430048170 mRNA
ATGAATCTCCTTCTTCATGGAGATTGGGACTGAGAAAAACTGGCAGCCACAACATGCTGA NM_002481 RefSeq
chr1 + 202348701 202588569 PPP1R12B 4660 "protein phosphatase 1, regulatory subunit 12B,
transcript variant 1"
GO:0007165|GO:0006937|GO:0005737|GO:0000086|GO:0005654|GO:0043085|GO:0008047|GO:0000278 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_136205_PI430048170 0.510381398291061 0.774534806314748 0.439050023383725
0.443315784736865 0.466056106112443 A A A 0.321405917917565 1.42575710515175
0.436398092826599 A A A LNCV6_136205_PI430048170 mRNA
TCTAAGTTGGTTTAATAGTTAAAAGCTGCTGTAGATTTATTCTGCCCACAACTTGGGGGT NM_001652 RefSeq
chr12 + 49972836 49977139 AQP6 363 "aquaporin 6, kidney specific"
GO:0007588|GO:0009992|GO:0015112|GO:0055085|GO:0005253|GO:0016324|GO:0034220|GO:0005887|GO:0015
250|GO:0015793|GO:0042476|GO:0006810|GO:0006833|GO:0015254|GO:0015706|GO:0030658 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136301_PI430048170 0.407872386433137 0.760367843370965 0.371674087759278
0.742791967330933 0.433669893190932 A A A 1.41146448206201 0.309753596285893
0.831205312978421 A A A LNCV6_136301_PI430048170 mRNA
TGCCCCTCAGAGAGGCATGTGATGTGCAAGGAAAATAATAGGATATAAAACACATCAAGT NM_002062 RefSeq
chr6 + 39048780 39087744 GLP1R 2740 glucagon-like peptide 1 receptor
GO:0005886|GO:0008016|GO:0006950|GO:0044281|GO:0007204|GO:0004967|GO:0007190|GO:0006112|GO:0050
796|GO:0007186|GO:0071377|GO:0019933|GO:0007611|GO:0016021|GO:0004888 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_73088_PI430048170 0.595652670650016 0.986497461802947 0.423309057936504
0.434313658027855 0.358886642403328 A A A 0.47275964836826 0.39113218572248
0.411342718858823 A A A LNCV6_73088_PI430048170 mRNA
GGTTGGAAAAGAAATCAATTTTTTAAACCACTAATGCTTGCCAAGAAATCGCCTTATGAG NM_015576 RefSeq
chr3 - 55508307 56468363 ERC2 26059 ELKS/RAB6-interacting/CAST family member 2
GO:0005515|GO:0048786|GO:0042734|GO:0005737|GO:0030054|GO:0005856|GO:0030426 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136506_PI430048170 0.133884977273146 0.944209766086146 0.242575983874618
0.276597824445706 0.31127568803894 A A A 0.428688056465287 0.337740640198907
0.310633458171248 A A A LNCV6_136506_PI430048170 mRNA
GGGGTATAATCATGTTGTAGGTACTTAAATGCATTCCGCAAATCAAAATATCTTGATGGA NM_012090 RefSeq
chr1 + 39084166 39487138 MACF1 23499 microtubule-actin crosslinking factor 1
GO:0005515|GO:0008017|GO:0005886|GO:0043001|GO:0045773|GO:0006928|GO:0030177|GO:0015629|GO:0051
893|GO:0005737|GO:0051015|GO:0007050|GO:0005856|GO:0016055|GO:0016887|GO:0005794|GO:0001707|GO:0
005874|GO:0005509|GO:0032886|GO:0003779|GO:0032587|GO:0007163|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137433_PI430048170 0.493231028971247 1.05424373827104 10.7149965826731
10.7581442197351 10.7531026497233 P P P 10.460719018251 10.7634707781097
10.7537832119932 P P P LNCV6_137433_PI430048170 mRNA
CCAGAACTTTGAATGTTTGCATACTTGTGGATGTACCTTTCAAATATGTTTGTCTTGTGT NM_133644 RefSeq
chr19 + 17337516 17342731 GTPBP3 84705 "GTP binding protein 3 (mitochondrial), transcript
variant IV" GO:0006184|GO:0005739|GO:0003924|GO:0005634|GO:0005525|GO:0006400 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_136436_PI430048170 0.110020484956538 0.925528333384399 0.31297640744122
0.320492976980312 0.288540947482885 A A A 0.492008514303715 0.413056762586451
0.348505292855059 A A A LNCV6_136436_PI430048170 mRNA
GGCCTTCTTCATGCTTTAATCCATGAAGCTTTTTCATTCAGATTAACCTTCTGTAATTCC NM_001005479 RefSeq
chr3 + 98264284 98265262 OR5H6 NA "olfactory receptor, family 5, subfamily H, member 6
(gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129031_PI430048170 0.41663907479124 14.8210108687525 5.68043398024682
0.334449075834454 0.269487414118407 P A A 0.270156315153818 0.282229736478458
0.268564264220816 A A A LNCV6_129031_PI430048170 mRNA
CTTTAAATTCTGGGTGTGGGAGTCAGTGATTTATCTGTGTGCAGCAGTTCACCCCATCAT NM_177437 RefSeq
chr7 + 143443452 143444409 TAS2R60 338398 "taste receptor, type 2, member 60"
GO:0050913|GO:0033038|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0001580 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145464_PI430048170 0.527507343659941 0.5797872730978 0.716349017476593
0.53248969000585 2.11587545725788 A A A 2.19845344957734 2.80801782550645
0.276865674426462 A P A LNCV6_145464_PI430048170 mRNA
TAAAACCCTGGAGGTTTCCCGTGGGCTCGTTCAAGAACTTTCCAGCTGTTGTTTAAAAGA NM_014692 RefSeq chr16
+ 4958316 5019155 SEC14L5 9717 SEC14-like 5 (S. cerevisiae)
GO:0005622|GO:0005215|GO:0006810|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144791_PI430048170 0.00632258535002678 0.5410345742584416.31405907371013
5.95726567318461 6.34728863564595 P P P 6.93920279124654 7.030908576666
7.31194898435545 P P P LNCV6_144791_PI430048170 mRNA
GTGAGAAACCAGGAGATATTTTCATCTTGTTCGGAAATACTTGTATGTATTTTGGTGTCA NM_001080479 RefSeq
chr5 + 73626157 73941993 ARHGEF28 64283 "Rho guanine nucleotide exchange factor (GEF) 28,
transcript variant 1"
GO:0035556|GO:0060052|GO:0048013|GO:0005886|GO:0032321|GO:0007411|GO:0003723|GO:0021955|GO:0005
089|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129390_PI430048170 0.925664313628776 0.9888363453417530.344310472699555
0.3946591907269170.317099150974591 A A A 0.2519477448049840.28331934852445
0.551327337282248 A A A LNCV6_129390_PI430048170 mRNA
GTTTTTCTAGAGTTTCAGTCTAAGGGAAAATGTGATTTAGGGCTTTGGAAATTGGCTAAA NM_144670 RefSeq chr12
+ 8822553 8876785 A2ML1 144568 "alpha-2-macroglobulin-like 1, transcript variant 1"
GO:0010951|GO:0004867|GO:0030414|GO:0005615|GO:0052548|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_110693_PI430048170 0.431860505626915 0.8870443569834783.63893500616946
3.76533653898079 4.31913787116166 P P P 4.14778127715322 4.10034415769208 4.0873262030732
P P P LNCV6_110693_PI430048170 mRNA
GCCTCTTCCTCTCGGTCCCATATTGAACTCGAGTTGGAAGAGGCGAGTCCGGTCTCAAAA NM_194247 RefSeq chr2
+ 177212693 177223957 HNRNPA3 220988 heterogeneous nuclear ribonucleoprotein A3
GO:0008380|GO:0005515|GO:0010467|GO:0000166|GO:0000398|GO:0030529|GO:0003723|GO:0005654|GO:0005
634|GO:0071013 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49528_PI430048170 0.165733241061 1.03361984103488 0.3383842308049660.34925474978431
0.27660861284399 A A A 0.2691526078329290.2844816189378970.268498631701238 A A A
LNCV6_49528_PI430048170 mRNA
GCAACAAAAACAGTGTATCAGCAACAAATCAAAATCCTGAGTGCTAACCTGGAAAGAGAA NM_001164399
RefSeq chr14 - 59505066 59576831 CCDC175 NA coiled-coil domain containing 175 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_139656_PI430048170 0.90311905468739 0.8514979736739021.82174844152555

0.3143421543021630.274239691366835A A A 0.24730081235774 0.2723467585302552.2133267494315
A A A LNCV6_139656_PI430048170 mRNA
TTAAGTGTCTCTACAACTTTGAATAAAGGGAAATGCCCAAGATGTCCTGATCTGAAAAAA NM_002232RefSeq chr1
- 110672451 110675033 KCNA3 3738 "potassium channel, voltage gated shaker related subfamily A,
member 3, transcript variant 1"
GO:0005251|GO:0015271|GO:0005244|GO:0005886|GO:0008076|GO:0007268|GO:0051260|GO:0045121|GO:0034
765|GO:0016021|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104951_PI430048170 0.1618067031633391.21054388648218 11.3158977992717
11.0730545711321 11.5046414944447 P P P 10.9829490243819 11.0314648115575
11.0826755378351 P P P LNCV6_104951_PI430048170 mRNA
ACGCCTTTCAAGGGTGTACGCAAAGCACTCATTGATACCCTTTTGGATGGCTATGAAACA NM_001098616 RefSeq
chr1 - 154206700 154220797 C1orf43 25912 "chromosome 1 open reading frame 43, transcript variant
3" GO:0050662|GO:0016021|GO:0055114|GO:0016616 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49691_PI430048170 0.574586246852135 1.05489183933858 7.70617837722182 7.6805089722974
7.47595603190356 P P P 7.69280273479813 7.59936044700524 7.32526032565354 P P P
LNCV6_49691_PI430048170 mRNA
CTGCCCGCGGCCGCCGTCGTCTACCTGGGATTCCTGTGCCACTCGAGGGTCCACCCCGCT NM_001146685 RefSeq
chr1 + 1426127 1427787 TMEM88B NA transmembrane protein 88B NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_143945_PI430048170 0.2874000577872330.6042636250895360.287162485305673
0.3139933244213511.27665239087977 A A A 1.2600144115304 0.5675181899900672.0735318939267
A A A LNCV6_143945_PI430048170 mRNA
GCATGCTTGTCTAATTCACTGATTATGCATACATTCACCTCAAAATGCTACTAAAACAAC NM_153840RefSeq chr6
- 46997702 47042363 ADGRF1 NA "adhesion G protein-coupled receptor F1, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128223_PI430048170 0.0313586704810822 4.10536662545067 4.69266041196142
4.50276275986215 4.32505775056203 P P P 1.80714001319028 2.01870716155323
3.19407391562875 A A P LNCV6_128223_PI430048170 mRNA
CTTCCAAGCTGCCTAAAGCGCTGTTTTAGGTTCATTTATTTTATTATGTTCAGAAGCATCNM_019043RefSeq chr10 +
26438336 26567803 APBB1IP 54518 "amyloid beta (A4) precursor protein-binding, family B, member 1
interacting protein"
GO:0005515|GO:0007165|GO:0005886|GO:0007596|GO:0030168|GO:0005856|GO:0005925|GO:0030027|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139209_PI430048170 0.00186829111583392 0.3907163602105072.8143651956411
2.38927929951421 2.60944747432819 A A A 3.704004316401 4.16994984764295
3.99986068303361 P P P LNCV6_139209_PI430048170 mRNA
CCATCAGTGTTAACTCCCTGTGACAGGGATGAAGGAAAATACTTTAATAGTTCAAAAAAT NM_001197104 RefSeq
chr11 + 118436489 118526824 KMT2A 4297 "lysine (K)-specific methyltransferase 2A, transcript variant
1"
GO:0005515|GO:0003700|GO:0008285|GO:0006366|GO:0044212|GO:0071440|GO:2001040|GO:0080182|GO:0006
325|GO:0032411|GO:0005634|GO:0009952|GO:0042800|GO:0042803|GO:0042802|GO:0045322|GO:0005737|GO:0
071339|GO:0045944|GO:2000615|GO:0070577|GO:0001046|GO:0035162|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135021_PI430048170 0.2989113272974450.9048471639137588.69232449252497 8.7067955195859
8.90815260200868 P P P 8.76904764293327 8.87367741650479 9.08891298427215 P P P
LNCV6_135021_PI430048170 mRNA
CAGCTAGAAAGATGCTGACTTTGTCAAACTTGCATTTATATGAAAACCTTCTGTCTCTAA NM_181578RefSeq chr12
+ 118016700 118032237 RFC5 5985 "replication factor C (activator 1) 5, 36.5kDa, transcript variant 2"
GO:0005515|GO:0003689|GO:0005634|GO:0005524|GO:0006260|GO:0006261|GO:0006271|GO:0006281|GO:0000

723|GO:0006283|GO:0000722|GO:0006297|GO:0005654|GO:0005663|GO:0006289|GO:0019899|GO:0000278|GO:0
032201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139683_PI430048170 0.0369505608125451.4924092980839 6.16204185041801
6.17315219126932 6.08335043195256 P P P 5.71998184123368 5.62831862356717
5.30721252980429 P P P LNCV6_139683_PI430048170 mRNA
TTGTTTCTGGCCCGTTGGCATCGCTGCCTTCTGTCTAGCCCAGAAGACCAACAAGGCTTG NM_001098821 RefSeq
chr19 + 41376532 41384082 TMEM91 NA "transmembrane protein 91, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80670_PI430048170 0.3892351377254410.8976896280085776.37128139010896 6.39129406317666
5.93216021302877 P P P 6.45890685218345 6.26148819067266 6.47670200786075 P P P
LNCV6_80670_PI430048170 mRNA
TTTCTACCATGCCCTCTATCCCCGAGCCTGGACTGTCTATCAGCTTCCTGGCCAGAATGT NM_020944RefSeq chr9
- 35736865 35749228 GBA2 57704 "glucosidase, beta (bile acid) 2"
GO:0006665|GO:0005886|GO:0006687|GO:0021954|GO:0004348|GO:0016139|GO:0044281|GO:0005790|GO:0006
680|GO:0000139|GO:0005789|GO:0008206|GO:0016021|GO:0008422 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142412_PI430048170 0.3872859172044151.14724503107453 11.1210865450429
11.0144610714842 10.998025510394 P P P 10.4192209144088 11.0979562824387
10.9411162171131 P P P LNCV6_142412_PI430048170 mRNA
GGCCACCAGCCTGGGTTCCTCACCTTGTGAAATAAAATCTTCTCCCCTAGACACAAAAAA NM_003550RefSeq chr7
- 1815791 2232948 MAD1L1 8379 "MAD1 mitotic arrest deficient-like 1 (yeast), transcript variant
1"
GO:0005515|GO:0072686|GO:0007094|GO:0005813|GO:0007093|GO:0005819|GO:0005634|GO:0090235|GO:0015
629|GO:0005829|GO:0005737|GO:0007067|GO:0005643|GO:0000777|GO:0000776|GO:0000278|GO:0051301 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126699_PI430048170 0.000134856598848101 0.365102618522538 6.88515368984503
6.75441302683525 7.00143403599644 P P P 8.35162693052553 8.20255615932392 8.4477477187658
P P P LNCV6_126699_PI430048170 mRNA
GAGGGGGTAATTTTTGGATGTATCTGGACTTTTAAAAAATGTGCCTATATTTATAGCACC NM_021021RefSeq chr8
- 120535744 120812069 SNTB1 6641 "syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic
component 1)"
GO:0042383|GO:0005515|GO:0043234|GO:0005516|GO:0005737|GO:0006936|GO:0016010|GO:0045202|GO:0003
779|GO:0030165|GO:0005856|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134408_PI430048170 0.0890797768135434 0.7728260753545042.8352506257342
2.61331759012642 2.38049872258178 A A A 2.88961988136705 3.18554277455795
2.88390137820147 P P P LNCV6_134408_PI430048170 mRNA
ACGAGAAAGTATCTATTTTTGGCTAAATAAATGAGCTGCTGCCACTTTGACTATAACCCG NM_024336RefSeq chr16
- 54283299 54286466 IRX3 79191 iroquois homeobox 3
GO:0043565|GO:0001656|GO:0030424|GO:0006355|GO:0005737|GO:0045665|GO:0045666|GO:0007498|GO:0005
634|GO:0072086|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141109_PI430048170 0.0204098683449156 0.3567449886627466.71665454634663
6.67117210475243 6.84917078928918 P P P 7.85725946721011 8.08910959669454
8.64197218301284 P P P LNCV6_141109_PI430048170 mRNA
ATAGTAGAATTTTCCAGGTCACAGACCCAAGCTTCCATGGGTTGTTACTGTGCTGTACCA NM_139283RefSeq chr12
- 110534431 110583259 PPTC7 160760 PTC7 protein phosphatase homolog (S. cerevisiae)
GO:0005739|GO:0016311|GO:0004721|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131741_PI430048170 0.0763790544847925 0.7097179596609093.74010958547539
3.94713997114971 4.2985052165804 P P P 4.42279857340576 4.32131902880816
4.74670572725655 P P P LNCV6_131741_PI430048170 mRNA

CAAACTTTACTGTAGGACTATTGTGGTGTTCTTAACAGATTTGTAATTTCAAGATGCGTG NM_003796RefSeq chr19 + 29942238 30016612 URI1 8725 "URI1, prefoldin-like chaperone, transcript variant 1" GO:0005515|GO:0006357|GO:0001106|GO:0004864|GO:0005634|GO:2001243|GO:0019212|GO:0000122|GO:0009615|GO:0001558|GO:0030425|GO:0006351|GO:0005739|GO:0005737|GO:0071363|GO:0071383|GO:0010923|GO:0003682|GO:0005665. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93341_PI430048170 0.2495645862801460.7895910222687693.01660111888694 3.3066860262696 3.51623063138014 P P P 3.69738741105628 3.89304761846303 3.23911779583978 P P P LNCV6_93341_PI430048170 mRNA
ATCAGCCAACCGCCTGCCATGGAGACTTTCTTTAGGAGACATTTCCGGGGGAAGGTGCCA NM_001105540 RefSeq chr11 + 46361594 46380554 DGKZ 8525 "diacylglycerol kinase, zeta, transcript variant 4" GO:0004857|GO:0005515|GO:0005886|GO:0030168|GO:0005634|GO:0001727|GO:0008022|GO:0043086|GO:0005524|GO:0046872|GO:0030027|GO:0007205|GO:0035556|GO:0046580|GO:0016310|GO:0005737|GO:0003951|GO:0016477|GO:0045930|GO:0007596|GO:0004143|GO:0046834|GO:0005654|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140067_PI430048170 0.0921547040027136 0.5115755914305462.8776038338843 2.96605922459548 1.8227111157996 A A A 3.68521245206768 3.33881357379159 3.762765510403 P P P LNCV6_140067_PI430048170 mRNA
GCAATATCTGTTACTAGAGAACATTCCCATGTGTTTAAACTCTTCACTTCTTAGATGCAT NM_001193460 RefSeq chr12 + 65278642 65466907 MSRB3 253827 "methionine sulfoxide reductase B3, transcript variant 3" GO:0005739|GO:0005783|GO:0030091|GO:0033743|GO:0008270|GO:0006979|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72744_PI430048170 0.5090844557241031.04178450844323 0.2975708213970470.307343729149349 0.510911466252818A A A 0.3257110324951350.2845562211063380.338056403357306A A A LNCV6_72744_PI430048170 mRNA
TCTAACAAGTCTGGAGGAAAGAATGGGAAGAACTATTTGTAAACAACAATTACTTGGCAA NM_014744RefSeq chr3 - 17157161 17740907 TBC1D5 9779 "TBC1 domain family, member 5, transcript variant 2" GO:0005515|GO:0005776|GO:0030122|GO:0035612|GO:0006914|GO:0032851|GO:0015031|GO:0070969|GO:0042594|GO:0042147|GO:0002092|GO:0005097|GO:0010008|GO:0010508|GO:0030904. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130637_PI430048170 0.00734152937127532 0.5666376234816774.882223221081 4.95809368656358 4.61087090162841 P P P 5.55535941335713 5.71637825893299 5.65600590244778 P P P LNCV6_130637_PI430048170 mRNA
GTGAGACCATAGGACATTTGAACAATCTTTTCTTCTACCCATCTAGAAAAGCATCTTTTT NM_007110RefSeq chr14 - 20365666 20413420 TEP1 7011 telomerase-associated protein 1 GO:0005737|GO:0005697|GO:0000781|GO:0003720|GO:0030529|GO:0003723|GO:0000722|GO:0006278|GO:0005524|GO:0016363 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132323_PI430048170 0.3976039444093191.15119148452887 3.90139034889904 3.55459132779041 4.11946007279757 P P P 3.69689614293056 3.44287015422285 3.85231484995898 P P P LNCV6_132323_PI430048170 mRNA
CCTTTACTAAGAGCTCACAACTTTTTCAGCATGCACGAATTCATACAGGTGAGAAACCCT NM_152604RefSeq chr19 + 37226463 37243672 ZNF383 163087 zinc finger protein 383 GO:0006355|GO:0005737|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133527_PI430048170 0.2636181651331191.93437291834363 2.38855739815757 1.04105135792005 0.688458648398599A A A 0.2821500111723410.4226214352977151.0338735512834 A A A LNCV6_133527_PI430048170 mRNA
GCTGTTTGTAGTAAGAAATCTTTGTGGAACCCCAGTGTGTGAAGTAAATTGTATGTTATT NM_001010887 RefSeq chr9 + 19408926 19452502 ACER2 NA alkaline ceramidase 2 NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_131677_PI430048170 0.0701794235771906 1.30509601283224 7.41287535955235
7.47588539224395 7.47907693032569 P P P 6.94355222735798 6.95407854365856
7.29096711873114 P P P LNCV6_131677_PI430048170 mRNA
GGATGTGCCACTTTTGGCACCAAACGTGTATGTCATTTTTATTTCCATTTTATAAACATG NM_021931RefSeq chr20
+ 38962337 39039723 DHX35 60625 "DEAH (Asp-Glu-Ala-His) box polypeptide 35, transcript variant 1"
GO:0004004|GO:0006396|GO:0005737|GO:0000398|GO:0071013|GO:0005524 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144891_PI430048170 0.1691240471049760.6881276090492587.50382322089477
6.62231189610856 6.63694376641531 P P P 7.50594569649293 7.68533995159543
7.35713526360958 P P P LNCV6_144891_PI430048170 mRNA
TCCCCTTCCCCTGCTGACCTTGGAGGAATGACAATAAATCCCATGAACAGCATGAAAAAA NM_005954RefSeq chr16
+ 56589354 56591088 MT3 4504 metallothionein 3
GO:0005515|GO:0006707|GO:0030308|GO:0071732|GO:0051354|GO:0006882|GO:0060049|GO:0005622|GO:0043
524|GO:0019430|GO:0060547|GO:0070374|GO:0070371|GO:0010942|GO:0043027|GO:0010940|GO:0000060|GO:0
036091|GO:0016209|GO:0005507|GO:0097214|GO:0043085|GO:0010507|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137463_PI430048170 0.0479615834793233 1.1091173273606 0.722298720436615
0.8120667556407310.691868968291247A A A 0.6060920537375550.596739749298856
0.577745430864866A A A LNCV6_137463_PI430048170 mRNA
CTGCTGGCCTTGACCAGGAGTTCATATATAACTGTTATTACAGAGGAATTGTTATAACTA NM_002747RefSeq chr18
+ 50560113 50731826 MAPK4 5596 "mitogen-activated protein kinase 4, transcript variant 1"
GO:0005515|GO:0007049|GO:0005737|GO:0046982|GO:0019901|GO:0000165|GO:0006468|GO:0005634|GO:0005
524|GO:0042803|GO:0004707 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129052_PI430048170 0.7930256676734671.0416810857742 7.43172226135867
7.22358392375258 7.73601445450114 P P P 7.37740316612809 7.13578246629013
7.69333245772891 P P P LNCV6_129052_PI430048170 mRNA
CCAGAGATCTGATCTTCAAGCAAGAAAATAAGCAGTGTTGTACTTGTGAATTTTGTGATA NM_005484RefSeq chr14
+ 20343613 20357904 PARP2 10038 "poly (ADP-ribose) polymerase 2, transcript variant 1"
GO:0006471|GO:0005515|GO:0006281|GO:0006284|GO:0005730|GO:0005654|GO:0005634|GO:0097191|GO:0003
677|GO:0003950 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141456_PI430048170 0.0298651696100462 0.4624641010238541.71926924743 2.4943120449866
2.31698079589746 A A A 3.17553058902034 3.42963631576549 3.36011118568715 P P P
LNCV6_141456_PI430048170 mRNA
CCTACCTCTGCCTATTTTAAATCCAGGTTCTGCATAAGACTTTTGGAGAAAAAATTCTAA NM_005421RefSeq chr9
+ 105662456 105663104 TAL2 6887 T-cell acute lymphocytic leukemia 2
GO:0021794|GO:0006355|GO:0035264|GO:0046983|GO:0030901|GO:0009791|GO:0003677|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135022_PI430048170 0.1779221112300311.2577010411529 7.00719819299692
7.51007743064035 7.37912128739354 P P P 7.2336078539612 6.82204211234732
6.85718107261883 P P P LNCV6_135022_PI430048170 mRNA
TCAACTATAATAATGAGCTGCCGATGTATAGGAAAGGGACTGTGTTGATATGGCAGAAGG NM_017872RefSeq chr5
+ 157731314 157739764 THG1L 54974 tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)
GO:0005739|GO:0005737|GO:0000287|GO:0000049|GO:0051289|GO:0008193|GO:0005525|GO:0005524|GO:0008
033|GO:0006400|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106361_PI430048170 0.2994991947935171.04961449651312 6.67323311930524 6.7027542415315
6.59962080322236 P P P 6.48997768345728 6.64403776556361 6.62901494749504 P P P
LNCV6_106361_PI430048170 mRNA
AATCCCAGAGCAGCTGAACTCTTCCACCAGCTTTCTCAGGCCTTGGAGGTGCTGACCGAT NM_018163RefSeq chr15
- 40767868 40807478 DNAJC17 55192 "DnaJ (Hsp40) homolog, subfamily C, member 17"

GO:0005737|GO:0000166|GO:0003723|GO:0005634|GO:0000122 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78658_PI430048170 0.5099759263322380.86304316612076 1.36409556379158 2.65006394680009 1.14377945722504 A A A 2.05320797640861 2.03531686451697 2.19109304568336 A A A LNCV6_78658_PI430048170 mRNA TATCACACACATCTCCGCGGAGCAGAAGCGGCGCTTCAACATCAAGCTGGGGTTTGACAC NM_032951 RefSeq chr7 - 73593193 73624540 MLXIPL 51085 "MLX interacting protein-like, transcript variant 1"
GO:0071157|GO:0008284|GO:0003700|GO:0070328|GO:0090324|GO:0005634|GO:0044281|GO:0009653|GO:0010255|GO:0042803|GO:0005829|GO:0035538|GO:0035556|GO:0046889|GO:0005737|GO:0033137|GO:0045944|GO:0045821|GO:0005667|GO:0006355|GO:0046982|GO:0006357|GO:0045723|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134497_PI430048170 0.2643930769655970.7962062005525290.556961023884846 0.5307043631430520.28998734144758 A A A 1.16143605083207 0.6045160860757870.5264885347887 A A A LNCV6_134497_PI430048170 mRNA GCTCATCTAAACATGGGCATCTTGATTCATAGAAATGAAATAGAATATAGGAACTACGAC NM_001220473 RefSeq chr12 - 81257974 81758695 PPFIA2 8499 "protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2, transcript variant 2"
GO:0005515|GO:0048786|GO:0005737|GO:0009986|GO:0007160|GO:0007268|GO:0032403|GO:0014047|GO:0007269|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93432_PI430048170 0.3514574555501131.01767052518928 0.3097795130467950.329310507695887 0.378586900377176 A A A 0.3288190621899780.3161947583283330.297554309746928 A A A LNCV6_93432_PI430048170 mRNA CCTAAAGGAGTATTTAAAAAAGAGGATGATATTGATCTGCTTGGTGAAGAGTTCAGGAAA NM_018365 RefSeq chr15 - 56428730 56465137 MNS1 55329 meiosis-specific nuclear structural 1
GO:0005882|GO:0051321|GO:0005930|GO:0036126|GO:0070986|GO:0005635|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103356_PI430048170 0.2451457947544250.815192958430068 3.82272012211376 3.90183713165145 3.98859683495054 P P P 3.94645763910045 4.07917697605076 4.51392978276339 P P P LNCV6_103356_PI430048170 mRNA GCTTCAGAAATCTCTGCGTTTGATATTCAAACATCATATGCCGGAAATTTTCACAGTTTT NM_001193466 RefSeq chr17_KI270908v1_alt - 732027 894904 KANSL1 284058 "KAT8 regulatory NSL complex subunit 1, transcript variant 1"
GO:0005515|GO:0006325|GO:0005634|GO:0043981|GO:0043982|GO:0043984|GO:0043996|GO:0071339|GO:0000123|GO:0043995|GO:0000777|GO:0005654|GO:0046972 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53450_PI430048170 0.0456765030282215 1.30505997483274 7.52242499378342 7.47798918708411 7.80761713810654 P P P 7.24617956008724 7.315768029524 7.10874223850413 P P P LNCV6_53450_PI430048170 mRNA TTTCGGGAAACCAACAAGGAGGAGTGTATCTGCAGCCATCCTGAACCCCAGTTGCCAGGC NM_021933 RefSeq chr1 + 12019241 12032049 MIIP 60672 migration and invasion inhibitory protein NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124586_PI430048170 0.0091063101444194 2.33435166766082 7.53052091576571 7.4275409472345 7.56785799162798 P P P 6.41727470247581 5.98253507076298 6.4184592753634 P P P LNCV6_124586_PI430048170 mRNA CTCTTATGATGAGATTTCTGGTCAAGGAGCGAGCTCTCAGGATACGAAGACATTTGACGT NM_007028 RefSeq chr6_GL000256v2_alt - 1401828 1412013 TRIM31 11074 tripartite motif containing 31
GO:0005739|GO:0051091|GO:0016567|GO:0046597|GO:0045087|GO:0016874|GO:0019221|GO:0032897|GO:0008270|GO:0060333|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131412_PI430048170 0.6798665624669610.8257464869308430.412939738992248 0.4340795545109910.933882671078997 A A A 0.3958196044630791.5427445625508

0.41455988817131 A A A LNCV6_131412_PI430048170 mRNA
GTGTATGCTGGTATTTTAGAAGCCACCAATTTCTGGACTATCTGATTATTAACAAAGATG NM_001195296 RefSeq
chr14 + 37197912 37551259 MIPOL1 145282 "mirror-image polydactyly 1, transcript variant 1"
GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133626_PI430048170 0.00734045115073988 0.3478803837631251 2.6449467029331
12.5777175584566 12.6586293068361 P P P 13.8852004887932 14.1475481178929 14.377968288615
P P P LNCV6_133626_PI430048170 mRNA
CCACAGGGGTGGTGTCAAATGCTATTGAAATTGTGTTGAATTGTATGCTTTTTCACTTTT NM_000602 RefSeq chr7
+ 101127088 101139266 SERPINE1 5054 "serpin peptidase inhibitor, clade E (nexin, plasminogen
activator inhibitor type 1), member 1"
GO:0033629|GO:0005515|GO:0010467|GO:0035491|GO:0006367|GO:0010469|GO:0005886|GO:0004867|GO:2000
098|GO:0002020|GO:0005615|GO:0032757|GO:0014912|GO:0061044|GO:0061045|GO:0030198|GO:0045944|GO:0
042127|GO:0031093|GO:0007179|GO:0070062|GO:0030336|GO:0005102|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_100752_PI430048170 0.1065735098941870 .7293279928908049.23164696496251
9.40626553284307 9.26968665725275 P P P 9.74357084258793 9.45313839805553
10.0261979579654 P P P LNCV6_100752_PI430048170 mRNA
TCAGAAAACTGAAACCCGATTAGCTCGTGTCAATGAGCAGAGAATGAAGGCTGCAGAGAA NM_014706 RefSeq
chr12 - 108522213 108561389 SART3 9733 squamous cell carcinoma antigen recognized by T cells 3
GO:0000244|GO:0005515|GO:0010468|GO:0015030|GO:0030624|GO:0005691|GO:0006334|GO:0030621|GO:0005
634|GO:0000387|GO:0071001|GO:0071002|GO:0048872|GO:0042393|GO:0000902|GO:0071425|GO:0005737|GO:0
016607|GO:0000166|GO:0000398|GO:0005654|GO:0046540|GO:0017070 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_137766_PI430048170 0.0278547520797932.38267048510657 3.97440617645007
3.45293873893261 4.15426994954799 P P P 2.14664170086274 3.13760655800619
2.44292819546157 A P P LNCV6_137766_PI430048170 mRNA
ATGTCCTTCCATTACATCTCAATGGGAGACTGCATAGGATGGCTTGAGGACTTCTTGATG NM_130900 RefSeq chr6
- 150020129 150025532 RAET1L NA retinoic acid early transcript 1L NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141432_PI430048170 0.5788921273464620.6804803780860066.79547997047395
6.44770208817109 6.86926756655496 P P P 8.08870583449805 6.25928880986565
6.83901494438708 P P P LNCV6_141432_PI430048170 mRNA
CATGTATTTACTCTGCCAGGTGCCTATATTCCAATAAAATGTTCATCCTTGAAGAGCTGA NM_052966 RefSeq chr1
- 184791024 184974586 FAM129A 116496 "family with sequence similarity 129, member A"
GO:0005515|GO:0003674|GO:0034976|GO:0005737|GO:0016020|GO:0005886|GO:0001934|GO:0001933|GO:0045
727|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97230_PI430048170 0.0217001086436122 0.6717669804423425.71290332452496
5.29949799384656 5.43364446908491 P P P 6.07322205623331 5.91577985035353 6.1965466223689
P P P LNCV6_97230_PI430048170 mRNA
ACAAGCCTGGTGGAGGAGATGTCAAGATTGAAAGTCAGAAGTTGAACTTCAAGGAGAAGG NM_002375 RefSeq
chr3 - 47850689 48089279 MAP4 4134 "microtubule-associated protein 4, transcript variant 1"
GO:0005515|GO:0008017|GO:0072686|GO:0005886|GO:0005875|GO:0005874|GO:0051294|GO:0005737|GO:0005
198|GO:0051012|GO:0015630|GO:0007052|GO:0051301|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128863_PI430048170 0.00807055010103522 0.4675953035852013.68928741762149
4.11097426024151 4.06069607577694 P P P 4.98272302975255 5.053495352204
5.14573097791712 P P P LNCV6_128863_PI430048170 mRNA
CTCCTAAGGTAAAGCAGGGTACTTTCCCTGGAATTTCCTTTTTAAATAAATATCTGTTTC NM_015434 RefSeq chr1
- 211940398 212035660 INTS7 25896 "integrator complex subunit 7, transcript variant 1"

GO:0005515|GO:0005694|GO:0032039|GO:0000077|GO:0071479|GO:0016180 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131609_PI430048170 0.8324403977946730.9547026211988770.599644228018806 0.7254221216927861.86357627794364 A A A 1.64770915297987 0.553162723406052 1.33923156569162 A A A LNCV6_131609_PI430048170 mRNA TGTGCTTATTGCTGTGGCCCAGTGTCTGTACACAGTAGGTGGCTAATAAAGTTTTAGGCA NM_001144872 RefSeq chr12 + 113149857 113159276 CCDC42B 387885 coiled-coil domain containing 42B NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144926_PI430048170 0.0230940834544252 1.11243374207981 10.6240967810985 10.6978994726803 10.6550448236975 P P P 10.4388637430111 10.5373564175873 10.5383688938809 P P P LNCV6_144926_PI430048170 mRNA GTGGCAGTCTTGGTCAGTAGTTTAAAGAGTTTCCCTACTTTTTAACCCTTTTTGAAATAA NM_001199054 RefSeq chr16_KI270855v1_alt - 212998 216989 CDIP1 29965 "cell death-inducing p53 target 1, transcript variant 1" GO:0042771|GO:0003674|GO:0006915|GO:0005634|GO:0033209 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137035_PI430048170 0.9516330701788491.17709994847408 8.07883155645299 9.62311538440504 8.03365764983451 P P P 8.63211877538553 8.37611757329993 8.61927965932548 P P P LNCV6_137035_PI430048170 mRNA GCACTGTGACTTGTTATTCAAGTTGTATGTCTACTGTTCCATCTATCACGTTTTATACCT NM_022903 RefSeq chr3 - 49162534 49166352 CCDC71 64925 coiled-coil domain containing 71 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129112_PI430048170 0.46944299188074 1.1978974747455 0.678011490992871 1.37670370034364 0.610315481160732A A A 0.8332645600434360.411751086720174 0.736172471001518A A A LNCV6_129112_PI430048170 mRNA CAGAAGCCTTCAAGGAAACAACATAAATATAAATATCTCTGTGGCCAGTCTCTACAAAAA NM_001301106 RefSeq chr15 + 92471676 92501117 C15orf32 145858 "chromosome 15 open reading frame 32, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133645_PI430048170 0.7087880949310870.9033898809191530.53495304798796 2.38805017554612 2.18583309342311 A A A 2.1045384552516 2.48144426301775 1.35017312290872 A P A LNCV6_133645_PI430048170 mRNA TGATGCACATCTTCCAGAATCTGGGGAGCTGCAGGGCCCTTTGTGCAGTGGCTCATACCT NM_005299 RefSeq chr6 - 167156871 167157831 GPR31 2853 G protein-coupled receptor 31 GO:0007186|GO:0005886|GO:0005887|GO:0004930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144263_PI430048170 0.00407643720047085 1.45789228396704 4.66268271042974 4.49272966796223 4.65066797418963 P P P 4.17125340568574 3.93296619493778 4.06651490211866 P P P LNCV6_144263_PI430048170 mRNA AGCAGGACATCGGTGCTTTGCTGTCCATCTTCCCATGCTGCAATTTCTTCCTGAGATTTC NM_001267 RefSeq chr17 - 50464491 50468866 CHAD 1101 chondroadherinGO:0060348|GO:0001502|GO:1900155|GO:0005578 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136734_PI430048170 0.43427256830295 1.24397843007961 3.61922823049872 3.84665895479124 3.53687966335713 P P P 2.15415359412559 4.42610951683746 2.2704886260907 A P A LNCV6_136734_PI430048170 mRNA GGTAGAACCATAATCCTTAGGAAAAATCCCTTCCTCTTAGGAATAAAGAAATCACTGATT NM_001017961 RefSeq chr1 - 166070018 166166721 FAM78B 149297 "family with sequence similarity 78, member B" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135347_PI430048170 0.0383634539939657 0.7219180340947071 0.4541680089105 10.1834592618621 10.2543379691163 P P P 10.9538856563624 10.5440784902713 10.7889579464217 P P P LNCV6_135347_PI430048170 mRNA GTTTGTGTTGCAGGTGTTGATAGTTGTTTTAAGGATTGTTAGGTATAGGAAATCCAGTAA NM_025130 RefSeq chr10

+ 69220302 69267559 HKDC1 80201 hexokinase domain containing 1
GO:0004340|GO:0008865|GO:0001678|GO:0046835|GO:0019318|GO:0019158|GO:0051156|GO:0005524|GO:0006
096|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134459_PI430048170 0.0154274965402826 0.6183000262510077.01832260097051
7.18076566386973 7.39099377279823 P P P 8.05228265333194 7.63520249066063
7.97459020739921 P P P LNCV6_134459_PI430048170 mRNA
AGTGGTACTTCTAAATCATAAAAGTTGGGGAAAGAGACCTTTAAAATCTTGTGGTGTTGA NM_032312RefSeq chr2
+ 32277888 32306589 YIPF4 84272 "Yip1 domain family, member 4"
GO:0005794|GO:0005886|GO:0005783|GO:0016021|GO:0043231 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138522_PI430048170 0.0769198911590498 0.4748621216359310.339334007623013
0.3318426395050521.26542289311746 A A A 1.08908487613097 1.86483160111626
2.20402111340562 A A A LNCV6_138522_PI430048170 mRNA
GCCTTACATGTGGATATTAACAGTGTAAACAATACCACATATAACCATCAAGATACCTTG NM_005470RefSeq chr10
- 26746595 26861087 ABI1 10006 "abl-interactor 1, transcript variant 1"
GO:0008092|GO:0005515|GO:0031209|GO:0008285|GO:0030054|GO:0005783|GO:0061098|GO:0001756|GO:0006
928|GO:0005634|GO:0030175|GO:0032403|GO:0005829|GO:0030426|GO:0005622|GO:0030296|GO:0045211|GO:0
005856|GO:0070062|GO:0072673|GO:0048010|GO:0014069|GO:0018108|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137129_PI430048170 0.0006800084180474 0.3988574053189496.55382975348751
6.30105412756936 6.54024241615586 P P P 7.71453173828821 7.66007221593361
7.99027352139293 P P P LNCV6_137129_PI430048170 mRNA
TAAGCAGGTTCAAAGTTATCCCATGATAGTGGCATTCTTATTTGTATATATGTGCTTTCC NM_178812RefSeq chr8
+ 97644178 97730260 MTDH 92140 metadherin
GO:0005515|GO:0003725|GO:0051897|GO:0048471|GO:0005783|GO:0005634|GO:0005737|GO:0016324|GO:0046
581|GO:0051092|GO:0070830|GO:0001085|GO:0043123|GO:0031663|GO:0031965|GO:0043066|GO:0051059|GO:0
003713|GO:0005730|GO:0000122|GO:0045766|GO:0016604|GO:0005789|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140137_PI430048170 0.13666948865014 0.6641284480996271 4.0835832042834 13.197780788403
13.332591862276 P P P 14.2433225206435 14.2726849395025 14.0219445083675 P P P
LNCV6_140137_PI430048170 mRNA
ACCCCGCCACGCCCTGCCGTCCAGCATGATTAAAGAATGCTGTCTCCTCTTGGCAAAAAA NM_031910RefSeq chr22
- 37180165 37188290 C1QTNF6 114904 "C1q and tumor necrosis factor related protein 6, transcript
variant 1" GO:0070208|GO:0005581|GO:0005615|GO:0042802 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_70899_PI430048170 0.00713576609478586 1.34433334926054 6.12533342473484
5.98737680793733 6.16225358215203 P P P 5.65540988828635 5.71088801195253
5.63269538583426 P P P LNCV6_70899_PI430048170 mRNA
CAAAGATAGGTGATCTTCAGCTTTGCAAACTGGATGAACTAGATTGCTTGATCAAAGGAA NM_153638RefSeq chr20
+ 3889094 3923855 PANK2 80025 "pantothenate kinase 2, transcript variant 1"
GO:0004594|GO:0015939|GO:0051881|GO:0007286|GO:0006767|GO:0015937|GO:0044281|GO:0005524|GO:0005
829|GO:0009060|GO:0005758|GO:0016310|GO:0070584|GO:0006766|GO:0009108 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138185_PI430048170 0.6930330053311930.9818763119944699.26133656549408
9.35370688246559 9.36345806432746 P P P 9.42116146711063 9.25583194218819
9.37780350441894 P P P LNCV6_138185_PI430048170 mRNA
TCGGAGACTGAGTTCCACAACTTTTTTAGTAGCTCATAGTGTTATTTTTCTACTCTCTTC NM_001173991 RefSeq chr11
+ 61392359 61398863 TMEM216 51259 "transmembrane protein 216, transcript variant 3"
GO:0042384|GO:0005929|GO:0006996|GO:0060271|GO:0036038|GO:0016021|GO:0005856|GO:0005829 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135893_PI430048170 0.3269123603056931.19192143174143 4.60001209222574
5.10138415413019 4.54402483649243 P P P 4.68915479061117 4.52847838664772
4.31070002231239 P P P LNCV6_135893_PI430048170 mRNA
TAAATAAACTGTGTCTGTCTTTGAGAAAGCACCTACCTGTCTTCTGTGCAGCTAGGGCTG NM_015705 RefSeq chr22
+ 40370561 40410289 SGSM3 27352 "small G protein signaling modulator 3, transcript variant 1"
GO:0005515|GO:0017137|GO:0032486|GO:0033126|GO:0032483|GO:0032851|GO:0048227|GO:0007050|GO:0005
097|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93425_PI430048170 0.5816001332943170.9540469597063728.13133928053592 7.84349367396689
8.19191930951214 P P P 8.16681200296358 8.19469768465801 8.02675700281011 P P P
LNCV6_93425_PI430048170 mRNA
TACATGCACAACAAGCATGAGCTCGCCCACGCCTTCGACCGCTACGAGACCGCTCACTCG NM_080875 RefSeq chr1
+ 1615414 1630610 MIB2 142678 "mindbomb E3 ubiquitin protein ligase 2, transcript variant 1"
GO:0005515|GO:0005737|GO:0004842|GO:0016567|GO:0007219|GO:0016874|GO:0000151|GO:0008270|GO:0003
779|GO:0004871|GO:0043123|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135981_PI430048170 0.000801326116589436 0.5490751727683997.33797134715324
7.16447790826971 7.36840183867897 P P P 8.13606685917242 8.28266296930731
8.04515552294327 P P P LNCV6_135981_PI430048170 mRNA
GCTGAAGCTGTTATTTTCAGTCAGGAAGACTACCTGTCATGAAGGTATAAAATAATTTAG NM_001242397 RefSeq
chr12 - 43793722 43806375 TWF1 5756 "twinfilin actin-binding protein 1, transcript variant 1"
GO:0048471|GO:0042989|GO:0005546|GO:0032587|GO:0030175|GO:0015629|GO:0030016|GO:0005524|GO:0003
785|GO:0005737|GO:0005911|GO:0030837|GO:0004713|GO:0005925|GO:0043538 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_73073_PI430048170 0.0211425154919269 1.71336344054661 4.29723715744342
4.47028066690693 4.83553741789172 P P P 3.60846311201888 3.95230218958595
3.74413938320554 P P P LNCV6_73073_PI430048170 mRNA
TTTTCCCTGTATCCTGATTTTCAGAAAGGGCTTTAGTCTCTGAGCTGTGGCTAGTAGCTG NM_198563 RefSeq chr3
- 52836755 52897581 TMEM110 375346 transmembrane protein 110
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103503_PI430048170 0.2877616557087010.8936596737304860.389417211581879
0.3615868416204970.251387570403922 A A A 0.3246759455992050.449060713288143
0.694139530658942 A A A LNCV6_103503_PI430048170 mRNA
CAAGATCCCCGATGGAGAGAGAGTGGACTTTGAGACATCCACCGGAAGCGCATGGAGAAG NM_001276347
RefSeq chr1 - 201359007 201377700 TNNT2 7139 "troponin T type 2 (cardiac), transcript variant 7"
GO:0005861|GO:0030049|GO:0055010|GO:0008016|GO:0045214|GO:0032780|GO:0003779|GO:0032781|GO:0030
017|GO:0005829|GO:0051592|GO:0030172|GO:0006937|GO:0031013|GO:0008152|GO:0005200|GO:0005865|GO:0
005523|GO:0016887|GO:0055009 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130936_PI430048170 0.4492724068565071.23783273382224 3.66274764295017
3.59915863613482 2.79568685354613 P P A 3.09632913339697 3.26935153187558
2.89464136385986 P P P LNCV6_130936_PI430048170 mRNA
CAATTCAGGGGCCTCTCATACCCTCTACTGTGAGATGTTACTAAAGAACCTTAGTAACTT NM_001012729 RefSeq
chr19 - 57151725 57167488 DUXA NA double homeobox A NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_38414_PI430048170 0.8189636229769290.9921685413183870.2624946367394880.279571295262323
0.410393933713528 A A A 0.3654025134684510.3149606330849940.310055354149724 A A A
LNCV6_38414_PI430048170 mRNA
AGTGAAGAACAATATGTAGGAAAATGGGACCAACTTATGTGTGTTCTGAGCCTCAAAACC NM_014653 RefSeq chr12
+ 108129470 108250536 WSCD2 9671 "WSC domain containing 2, transcript variant 1" GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_144015_PI430048170 0.176896103356907 1.14022050222632 9.49826030991469
9.39291838474707 9.18576291394081 P P P 9.21168075535756 9.18196512296149
9.13152908097745 P P P LNCV6_144015_PI430048170 mRNA
ATTGGAGCTCTGGGAGATGCTGGAATAAAAGACAAGAGTTACATCTGGACTTGGAAAAAA NM_018125 RefSeq chr1
+ 17539834 17697875 ARHGEF10L 55160 "Rho guanine nucleotide exchange factor (GEF) 10-like,
transcript variant 1" GO:0005737|GO:0032321|GO:0005089 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_141057_PI430048170 0.541370321662959 0.826997333238223 0.435029524576413
1.46271425310105 2.17548686324955 A A A 1.98242651262561 2.0574156701942
1.21165477152181 A A A LNCV6_141057_PI430048170 mRNA
ATGAAGCACATTCGAATGAAGGGATCACGGGGGTCAGAACAAAAACCATTCTAGAACCGT NM_001004330
RefSeq chr12 + 92736488 92772092 PLEKHG7 NA "pleckstrin homology domain containing, family G
(with RhoGef domain) member 7" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136029_PI430048170 0.0397851610043965 0.348472982033325 0.418295570769474
0.316496967775133 1.44353177436714 A A A 2.50490263305699 2.20164149279715
2.30375488900639 P A P LNCV6_136029_PI430048170 mRNA
GTATTGAGGACAGCACTCACATACTGTGGGAAAGAATAATACTTGATTAGGACTTATTAT NM_152943 RefSeq chr12
+ 133181408 133207111 ZNF268 10795 "zinc finger protein 268, transcript variant 3"
GO:0005515|GO:0046022|GO:0043497|GO:0071157|GO:0008284|GO:0045732|GO:0008285|GO:0003700|GO:0045
597|GO:0005634|GO:0015629|GO:0030154|GO:0046872|GO:0005737|GO:0045944|GO:0071356|GO:0006355|GO:0
043066|GO:0090073|GO:0030335|GO:0043065|GO:0000122|GO:0003677|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129899_PI430048170 0.270675328743109 1.24033542291826 5.14221014460666
4.99231404319378 5.3592904013525 P P P 5.14471452213433 4.39914966975335
4.94269793880282 P P P LNCV6_129899_PI430048170 mRNA
GGCAGTGGGGGTGACTTTTCTTATATTAATAATATTTACATCCAATACACTGAATCTTCC NM_001204173 RefSeq
chr8 + 66667551 66862022 C8orf44-SGK3 NA C8orf44-SGK3 readthrough NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_139992_PI430048170 0.136401903226322 0.570745324763543 7.792575148086
6.56234218809533 6.64625743173421 P P P 8.14210237598361 8.01026663013953 7.5639783384672
P P P LNCV6_139992_PI430048170 mRNA
CTCCTCCCTCTTTTGCTGTATAATGAGATTGAAGATATAAAGACATTTTGTACCCTGTAA NM_020644 RefSeq chr11
- 8947200 8964773 TMEM9B 56674 "TMEM9 domain family, member B, transcript variant 1"
GO:0007165|GO:0016021|GO:0004871|GO:0043123 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129274_PI430048170 0.0131941784964897 0.375101909132005 9.70954102443612
9.43184623954823 9.68838751893653 P P P 10.5756851476708 11.1376688444309
11.2841172281677 P P P LNCV6_129274_PI430048170 mRNA
GTTCGCTTATCAACTAATGATTTAGTGATCAAATTGTGCAGTACTTTGTGCATTCTGGAT NM_001130823 RefSeq
chr19 - 10133345 10195079 DNMT1 1786 "DNA (cytosine-5-)-methyltransferase 1, transcript variant 1"
GO:0005515|GO:0010467|GO:0008327|GO:0003886|GO:0005657|GO:0003723|GO:0005634|GO:0016458|GO:0010
216|GO:0071230|GO:0009008|GO:0042127|GO:0090116|GO:0000122|GO:0003677|GO:0006351|GO:0006306|GO:0
010628|GO:0032776|GO:0005721|GO:0051571|GO:0051573|GO:0003682|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_92413_PI430048170 0.168764667659478 2.20752458385675 0.341837467361065 1.6741427294679
1.84599678698075 A A A 0.284052862993422 0.272364835343561 0.290292770123825 A A A
LNCV6_92413_PI430048170 mRNA
CTAAGGACAAGTATGTGCGCAGCCTGTGGAAGCTCTTTGCTCACCACAACCGCTATGTGC NM_002005 RefSeq chr15
+ 90884457 90895776 FES 2242 "FES proto-oncogene, tyrosine kinase, transcript variant 1"
GO:0005515|GO:0008283|GO:0008360|GO:2000145|GO:2000251|GO:0030155|GO:0005829|GO:0005737|GO:0046

777|GO:0045639|GO:0007173|GO:0006935|GO:0007411|GO:0042127|GO:0015630|GO:0060627|GO:0038083|GO:0
034987|GO:0043304|GO:0031116|GO:0005794|GO:0007275|GO:0018108|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_109413_PI430048170 0.2682897628227621.32726916289469 2.90481739661641
3.41963971934001 3.74495220762112 A P P 2.90983325517591 3.05732861276987
2.99397473345815 P P P LNCV6_109413_PI430048170 mRNA
TGTTATCCATGCCCAATCCAGGGACCTGCCACGCATCTTTAGGGTGACAACCTCCCAGCT NM_017525RefSeq chr11
- 64824189 64844569 CDC42BPG 55561 CDC42 binding protein kinase gamma (DMPK-like)
GO:0035556|GO:0005515|GO:0050790|GO:0005737|GO:0005083|GO:0000287|GO:0031532|GO:0004674|GO:0006
468|GO:0031252|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133155_PI430048170 0.9336393684158131.12761780816114 0.484910284234932
2.26416647716101 2.15837300791194 A A A 1.48780977039852 1.03607154490987
2.20314977603433 A A A LNCV6_133155_PI430048170 mRNA
GAATTAAGCTTGCCCTTGTAACAAAATATGTTTTGGTATAGTTACCAGGACACTTACTGA NM_130810RefSeq chr15
- 55430307 55508234 DYX1C1161582 "dyslexia susceptibility 1 candidate 1, transcript variant 1"
GO:0005515|GO:0036159|GO:0007368|GO:0005737|GO:0005886|GO:0061136|GO:0030331|GO:0033146|GO:0036
158|GO:0005634|GO:0003341|GO:0001764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128591_PI430048170 0.0331017135031849 0.5553030887550945.49804599241356
4.81017366592773 5.3602682809826 P P P 5.82350523959406 6.26651240259319
6.17520258015787 P P P LNCV6_128591_PI430048170 mRNA
GCATTAAAAGCTGTTACCAAGTTGTCAGAACATAAGAGCGAAAACAAGGTCATATGTAAT NM_020791RefSeq chr17
+ 29390924 29551903 TAOK1 57551 "TAO kinase 1, transcript variant 1"
GO:0005515|GO:0031577|GO:0031572|GO:0046330|GO:0097194|GO:0032874|GO:0005524|GO:0006974|GO:0005
829|GO:0000186|GO:0004672|GO:0006281|GO:0051493|GO:0000165|GO:0004674|GO:0016301|GO:0006468|GO:0
000278|GO:0004709|GO:0016740|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143528_PI430048170 0.00128970442506907 1.30565993131293 9.17754665068288
9.12725696999439 9.24730814479407 P P P 8.79919531630785 8.84427354491123
8.75546296258775 P P P LNCV6_143528_PI430048170 mRNA
TCTGCTAGAAGAGACCTTGAACAAGTTCAATTTTGCCAGGAACAGTACCCTCAACTCAGC NM_013392RefSeq chr2
+ 27428605 27442257 NRBP1 29959 nuclear receptor binding protein 1
GO:0005515|GO:0010467|GO:0048471|GO:0006367|GO:0005524|GO:0030027|GO:0042803|GO:0012505|GO:0006
888|GO:0004672|GO:0016020|GO:0005654|GO:0006468|GO:0005938 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134074_PI430048170 0.000878638037270525 0.45048466169911312.322612038818
12.1284650432264 12.3050491115185 P P P 13.3709603607156 13.389540417392
13.4535465582078 P P P LNCV6_134074_PI430048170 mRNA
AGCCCCTAAAGGCAAGAAGAAAAAGTAAAAGACCTTGGCTCATAGAAAGTCACTTTAATA NM_004990RefSeq chr12
+ 57487952 57516655 MARS 4141 methionyl-tRNA synthetase
GO:0005739|GO:0010467|GO:0005737|GO:0000049|GO:0016020|GO:0006431|GO:0004825|GO:0005524|GO:0070
062|GO:0006418|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107652_PI430048170 0.6364909032105340.9054444415393794.86843177580571
4.86429833614655 4.586505759453 P P P 5.20626056943269 4.97313642122749
4.50062181112379 P P P LNCV6_107652_PI430048170 mRNA
ACCACCTCTAATGCCTCTGGTCGCCGCACTTCTGATGTCCGTAGGCCTTAAATCTGCCTG NM_153490RefSeq chr17
- 41500980 41505613 KRT13 3860 "keratin 13, type I, transcript variant 1"
GO:0009314|GO:0071300|GO:0005198|GO:0007010|GO:0005634|GO:0045111|GO:0045095|GO:0043587|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139704_PI430048170 0.0608181454970794 1.10654542096 0.624543268878596
0.7142097567058350.697764035523582A A A 0.6213543922453630.481539887324228

0.492781422986431 A A A LNCV6_139704_PI430048170 mRNA
GTGTGTCACATGGGGTCAGTAAGTTCTCAATAAAAATTGTTAAGAAATGCCATTCAAACC NM_001099685 RefSeq
chrX + 120158560 120164039 RHOXF2B 727940 "Rhox homeobox family, member 2B"
GO:0043565|GO:0006355|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93162_PI430048170 0.00804559803236693 1.36269131476125 6.65829839893876
6.81537650664443 6.87890862942327 P P P 6.32332370798622 6.45373707801626
6.23667976754173 P P P LNCV6_93162_PI430048170 mRNA
TGAATGTTTTAGCTGGTGCCTTGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGT NM_080652 RefSeq chr3
- 185489600 185499057 TMEM41A 90407 transmembrane protein 41A GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133767_PI430048170 0.8465736091131440.9618659086969921 1.2258326300122
11.4400712265793 11.6177112610742 P P P 11.4129869120256 11.2020247218922
11.7989181358656 P P P LNCV6_133767_PI430048170 mRNA
GTAGGGTTTAATCCCCAGTAAAATTGCCATATTGCACATGTCTTAATGAAGTTTGAATGT NM_001967 RefSeq chr3
+ 186783571 186789896 EIF4A2 1974 eukaryotic translation initiation factor 4A2
GO:0005515|GO:0010467|GO:0048471|GO:0016281|GO:0019221|GO:0004386|GO:0003743|GO:1900260|GO:0005
524|GO:0006412|GO:0006413|GO:0005829|GO:0006446|GO:0016032|GO:0044267|GO:0016887|GO:0000289|GO:0
000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137607_PI430048170 0.0146012380945295 0.6265512352564413 0.0967132056412
13.4167395688686 13.2788714167506 P P P 13.904104112329 13.9724498931048
13.9561292733617 P P P LNCV6_137607_PI430048170 mRNA
TACCTTTCGTGCGGTGGATTCTTTTTAACTCCGTCTACCTGGCGTTTTGTTAGAAATGTC NM_004907 RefSeq chr19 +
13150467 13154904 IER2 9592 immediate early response 2 GO:0005737 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_64298_PI430048170 0.0122318058286898 0.6074742749782236.63624345221324
6.31816521178293 6.48518536486497 P P P 6.99190345315829 7.16724902697057
7.42251825353723 P P P LNCV6_64298_PI430048170 mRNA
TCTCGACCTGACTTAGTGATAGAGGTATATTAAAGTCTTCCACTAGCATGGTAGATTAAC NM_024341 RefSeq chr19
+ 7069459 7087967 ZNF557 79230 "zinc finger protein 557, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_10279_PI430048170 0.0353645308351565 1.42703869232837 5.94338502053892
5.57223444719977 5.79109597374339 P P P 5.48760457535226 5.20207104651681
5.06980511850434 P P P LNCV6_10279_PI430048170 mRNA
CAAGTTCGAGCATCTTAAAATGATTCAACAGGAGGAGATAAGGAAGCTCGAGGAAGAGAA NM_207366 RefSeq
chr7 - 55793543 55862789 SEPT14 NA septin 14 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142244_PI430048170 0.1101456153243651.01238997750136 0.322570278243462
0.3023243937122640.302865567729539 A A A 0.299120431773684 0.294318450863826
0.28105773430016 A A A LNCV6_142244_PI430048170 mRNA
GTATATGACTTCCTTACAGTGCTACATTAACAGGATATTTCATTACATGCATCTGGTATC NM_003391 RefSeq chr7
- 117276630 117323289 WNT2 7472 "wingless-type MMTV integration site family member 2, transcript
variant 1"
GO:0005515|GO:0060045|GO:0008284|GO:0005886|GO:0071300|GO:0030324|GO:0090263|GO:0007267|GO:0071
560|GO:0061072|GO:0048146|GO:0005615|GO:0005109|GO:0060317|GO:0005737|GO:0051091|GO:0002088|GO:0
060501|GO:0030182|GO:0045944|GO:0060716|GO:0060492|GO:0016055|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_20197_PI430048170 0.2799756264649181.0830992981001 8.54264782404188 8.39536554342972
8.6596259277644 P P P 8.38408075508169 8.42869222655425 8.45067721589036 P P P

LNCV6_20197_PI430048170 mRNA
GGTCCAGACAAATTCAGAATATGATCCTTCTCGGTGTTTTGCCTTTGTTCACGACCTGTG NM_181725 RefSeq chr17
+ 62423884 62450093 METTL2A 339175 methyltransferase like 2A GO:0016427|GO:0030488 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137550_PI430048170 0.00302695209687765 0.5253564634617388.25636722291838
8.21137916611626 8.41083785578181 P P P 9.34710155040939 9.28443551287149
9.02017723098188 P P P LNCV6_137550_PI430048170 mRNA
AATGACCAGCAGGTATTTCTATAATGGTACATCCATGGCCTGTGAGACTTTCCAGTACGG NM_001633 RefSeq chr9
- 114060127 114078472 AMBP 259 alpha-1-microglobulin/bikunin precursor
GO:0005515|GO:0005886|GO:0004867|GO:0072562|GO:0005615|GO:0042803|GO:0043231|GO:0018298|GO:0030
163|GO:0019862|GO:0046329|GO:0016032|GO:0042167|GO:0007155|GO:0070062|GO:0007565|GO:0009986|GO:0
036094|GO:0005576|GO:0006898|GO:0046904|GO:0010951|GO:0050777|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139567_PI430048170 0.8417264684151291.01909307781456 4.77527630717199
4.66729958295944 5.04672852131561 P P P 4.2966459610422 5.14916179490719
4.86298385201837 P P P LNCV6_139567_PI430048170 mRNA
TAAAGACTTTGGAGCTAGAGAAGCCTTTTCCAGCAATGATTATTGACTTCACCACACCCC NM_020348 RefSeq chr10
+ 99329098 99394331 CNNM1 26507 cyclin and CBS domain divalent metal cation transport mediator 1
GO:0005886|GO:0016021|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129282_PI430048170 0.4303055043176091.20957886160589 7.47184087774733
7.10361548156214 7.11319918694041 P P P 7.58978670292477 6.41862441736156
6.59596022386885 P P P LNCV6_129282_PI430048170 mRNA
GAAACCTAGTCACTTCCTAAAGCAAAAGGAGAAACATTCTTTACCTCCAAATGTTTTAGT NM_007076 RefSeq chr12
+ 108515273 108519603 FICD 11153 FIC domain containing
GO:0034259|GO:0018117|GO:0016021|GO:0005524|GO:0070733 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_58567_PI430048170 0.2017015531222351.0460483501275 0.3494489227939160.339738838652205
0.449870348975577 A A A 0.3088864937976350.29305548200227 0.344384676948069 A A A
LNCV6_58567_PI430048170 mRNA
AGAAGAAGCCTTTGGGACCAAGGAAACTTTCCCCTGATCATCAAGAATCTTAAGATAGAA NM_001195014 RefSeq
chr12 + 6789471 6820810 CD4 920 "CD4 molecule, transcript variant 2"
GO:0005515|GO:0050852|GO:0042289|GO:0005886|GO:0030260|GO:0031295|GO:0050731|GO:0001816|GO:0042
803|GO:0050850|GO:0006955|GO:0001948|GO:0042101|GO:0045860|GO:0016032|GO:0004872|GO:0032507|GO:0
050863|GO:0019901|GO:0015026|GO:0045234|GO:0050690|GO:0045058|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_109973_PI430048170 0.2945035001102340.2682601076191311.85653273125389
0.3427537944580960.25707049786211 A A A 0.3181476130444243.88541476106493
2.73478045729676 A P P LNCV6_109973_PI430048170 mRNA
AGAAAAAGCAGAACGAAAAAGAAAAGCTGAAGCTGCTAGGCTACATCGCCAGAAGATCAT NM_174916 RefSeq
chr15 - 42942899 43106088 UBR1 197131 ubiquitin protein ligase E3 component n-recognin 1
GO:0071233|GO:0006511|GO:0032007|GO:0004842|GO:0000502|GO:0016567|GO:0016874|GO:0070728|GO:0000
151|GO:0008270|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97222_PI430048170 0.4324071685939620.8872452418936055.1099683108471 4.65835345981211
4.92606213962523 P P P 4.79983583810693 5.29420098915991 5.11089883662308 P P P
LNCV6_97222_PI430048170 mRNA
AATCGTCAGTGAGAAGTCCAGATACTCTCTCCATCAGAACATGGACAAGATCAAGGTTCC NM_020676 RefSeq chr3
+ 58237531 58294734 ABHD6 57406 abhydrolase domain containing 6
GO:0005739|GO:0030336|GO:0032281|GO:0008152|GO:0047372|GO:0060292|GO:2000124|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_140524_PI430048170 0.00186509272528451 0.4815036215060595.9280225971397
6.16365477428397 6.08614167549322 P P P 7.14619256293835 6.9161919189486
7.26678373024728 P P P LNCV6_140524_PI430048170 mRNA
CTGTGCTGTATAGAACTGTCACTAACATTAAAGAAAGAGGACACATTTTTCAAGATCTGT NM_006024RefSeq chr7
+ 27740094 27829767 TAX1BP1 8887 "Tax1 (human T-cell leukemia virus type I) binding protein 1,
transcript variant 1"
GO:0005515|GO:0043066|GO:0045087|GO:0006915|GO:0032088|GO:0019900|GO:0032480|GO:0070062|GO:0005
829. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128775_PI430048170 0.1102677749579862.11562837204693 2.59358260785168
1.39419875231145 1.52711947574556 A A A 0.4355686805185990.382099468889173
1.48647068584892 A A A LNCV6_128775_PI430048170 mRNA
ATGTGAACATGGAAACAACTTCTAGTATTGGATCTGAAAATAAAGTGTCATCCAAGCCAT NM_001076RefSeq
chr4_GL000257v2_alt - 222963 247131 UGT2B15 7366 "UDP glucuronosyltransferase 2 family,
polypeptide B15"
GO:0052696|GO:0006805|GO:0052695|GO:0009813|GO:0001972|GO:0005789|GO:0015020|GO:0016021|GO:0032
870|GO:0008202|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130525_PI430048170 0.30196447141407 1.3032922952439 4.24895121053852
4.95228774360957 4.1668321839399 P P P 4.27502989992627 4.10372548192255
3.96086937408324 P P P LNCV6_130525_PI430048170 mRNA
TGTCCCGGAACCTGCTCTGGTACATCCCCCACTACTTCTACCACTTCAGCTTCCTCATGG NM_001039165 RefSeq
chr11 - 3227810 3232386 MRGPRE 116534 "MAS-related GPR, member E"
GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106729_PI430048170 0.3917062389206290.8702587689905854.73626111650834
4.72827409833967 4.43719821521711 P P P 5.08845329322096 4.52253748800927
4.85657036150474 P P P LNCV6_106729_PI430048170 mRNA
TACATTAACAGGAAGCGGAAAAACAATTGCCATGGCAACCACATTGAGATGCAGGCCATG NM_017602RefSeq
chrX - 48922025 48957631 OTUD5 55593 "OTU deubiquitinase 5, transcript variant 1"
GO:0071108|GO:0004843|GO:0070536|GO:0045087|GO:0032496|GO:0006508|GO:0032480|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140425_PI430048170 0.0838767232498991.37403725330953 9.66270450919129
9.72003563537354 9.94836513860452 P P P 9.53886998464286 8.98887670200467 9.3897542203137
P P P LNCV6_140425_PI430048170 mRNA
GCAGTATTGATCTGACTGTGGAAACATCCTCTCACTTGCATTCTTTTAACTTAAAACTAT NM_001802RefSeq chr16
- 22345935 22374617 CDR2 1039 "cerebellar degeneration-related protein 2, 62kDa"
GO:0005515|GO:0003674|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140870_PI430048170 0.0361764268379613 1.3023946352332 8.45854879081639
8.35986110685936 8.2819705068267 P P P 8.11787214837721 8.0274802189459
7.79847655337392 P P P LNCV6_140870_PI430048170 mRNA
TCACGCAGTCAGGGAACAGGTGAGGAAAGAAATAAATAAGTGATTCTAATGCTGCCTAAANM_006368RefSeq chr9
+ 35732319 35737008 CREB3 10488 cAMP responsive element binding protein 3
GO:0005515|GO:0034976|GO:0003700|GO:0006366|GO:0051928|GO:0035497|GO:0005783|GO:0000982|GO:0042
994|GO:0030176|GO:0005634|GO:0001558|GO:0042803|GO:0005829|GO:0031726|GO:0005737|GO:0008140|GO:0
006935|GO:0045944|GO:0042127|GO:0046983|GO:0043025|GO:0016032|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141026_PI430048170 0.0447201716325801 0.6236006797351537.25379675542468
6.74451010839173 7.32969395218904 P P P 7.65520046650543 7.81355771647782
7.95478441837805 P P P LNCV6_141026_PI430048170 mRNA
CCTAACATGACAGATGAGTAGTAAATGTTGATATATCCTATACATGACAGTGTGAGACTT NM_003211RefSeq chr12
+ 103965814 103988878 TDG 6996 thymine-DNA glycosylase

GO:0005515|GO:0032091|GO:0010467|GO:0030983|GO:0005886|GO:0006366|GO:0035511|GO:0005634|GO:0009790|GO:0042803|GO:0035562|GO:0003690|GO:0005080|GO:0080111|GO:0006298|GO:0008263|GO:0032183|GO:0001104|GO:0019904|GO:0000122|GO:0003684|GO:0019104|GO:0006281|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127011_PI430048170 0.0666694021448189 0.1980434875594882.44036955573834 0.4494062462939350.260815799493872A A A 3.98789473700522 4.32725968923893 2.14130057052453 P P A LNCV6_127011_PI430048170 mRNA TAAGCCCTTGCTCAGTAAATTTAATTGAATTAAAGTGAATAAAAGGTTTGGTTTCTTTGG NM_001005850 RefSeq chr19 - 56662651 56671755 ZNF835 90485 zinc finger protein 835
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135629_PI430048170 0.1045022352659690.6008184371282843.56967615628013 3.30019878669835 2.59832407109396 P P A 4.09663560863479 3.88139641363071 3.84709594275833 P P P LNCV6_135629_PI430048170 mRNA TGGGCAGAATATGTGCTGGTCAATAAATGTGTCAGAAAATGAGTAATTTTCTGACTGCAC NM_001164415 RefSeq chrX + 149774071 149776870 HSFX2 NA "heat shock transcription factor family, X linked 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135912_PI430048170 0.4328997503850291.10521857453155 6.24934135760925 6.26252339215683 6.07673099208314 P P P 5.83652936392946 6.35739916468188 5.91243518497194 P P P LNCV6_135912_PI430048170 mRNA CCGGCACAGGCTTTGAGCTCATTATAACCACACTCCTTGTCTCGTGTCTGCCTCAAAAAA NM_201574RefSeq chr2 + 219627569 219641980 SLC4A3 6508 "solute carrier family 4 (anion exchanger), member 3, transcript variant 2"
GO:0016020|GO:0005886|GO:0005452|GO:0005887|GO:0006810|GO:0051453|GO:0015701|GO:0055085|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132684_PI430048170 0.3268946194864580.6778252432439321 3.6013078804374 15.3821157405139 15.3937606927222 M P P 15.5105331661868 15.5852330491591 15.5807816577061 P P P LNCV6_132684_PI430048170 mRNA CCGCCCCTCCACCCCCGCGGGAGCCCCTGCCCCACGCTAATAAAATGTGTTGCGAGGCTG NM_033513RefSeq chr19 + 507496 519654 TPGS1 91978 tubulin polyglutamylase complex subunit 1
GO:0008017|GO:0030424|GO:0005813|GO:0031514|GO:0007288|GO:0005874|GO:0007268|GO:0007275|GO:0030425|GO:0018095|GO:0005737|GO:0070740|GO:0051648|GO:0030534 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75757_PI430048170 0.0187214122757979 1.40627825373913 4.22310084250314 4.36513311850158 4.40048829054812 P P P 3.65417816929447 3.86027951550725 3.98546308733632 P P P LNCV6_75757_PI430048170 mRNA TGCTCAGAATTGTCTACTAGGCTGACTATGTATCACCTCTTCAGCTTGGATCCAATTGTG NM_020801RefSeq chr5 - 91368723 91383332 ARRDC3 57561 arrestin domain containing 3
GO:0005515|GO:0001659|GO:0044252|GO:0005886|GO:0090327|GO:0031699|GO:0060613|GO:0051443|GO:0043588|GO:0031651|GO:0071879|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128583_PI430048170 0.5571894318309931.073666784742 5.06533340791528 5.25975110866696 5.08993148465449 P P P 4.79974908044349 5.34692203268941 4.90875303433279 P P P LNCV6_128583_PI430048170 mRNA TTCGACCAATTCAACCCTTTGCCCCACCTTTATTAAAATCTTAAACAACGGGTCAAAAAA NM_001174104 RefSeq chr5 - 140631727 140633701 CD14 929 "CD14 molecule, transcript variant 3"
GO:0006909|GO:0005515|GO:0034142|GO:0070891|GO:0005886|GO:0009408|GO:0045471|GO:0007249|GO:0050715|GO:0031225|GO:0005615|GO:0045807|GO:0002756|GO:0006954|GO:0002755|GO:0051602|GO:0032026|GO:0034138|GO:0070062|GO:0038124|GO:0016019|GO:0038123|GO:0009986|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_69807_PI430048170 0.2237593334071243.26995752612858 2.96987554732783 0.343339916905565
1.51105877064082 A A A 0.2823333609275770.2818109910129770.291241227922587 A A A
LNCV6_69807_PI430048170 mRNA
CACTGATGACACAACAGAAAAGAAACTGTAGACCTTGGGACAATCAACATTTAAATAAAC NM_052942 RefSeq chr1
- 89258950 89272861 GBP5 115362 "guanylate binding protein 5, transcript variant 1"
GO:0071346|GO:0016020|GO:0008152|GO:0003924|GO:0031410|GO:0005525|GO:0042802 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138062_PI430048170 0.0341794254964577 0.2652879174004582.27548384300412
0.7045878229138131.3638473542228 A A A 2.57338349478442 3.83443093418213
3.79469761927249 A P P LNCV6_138062_PI430048170 mRNA
CGTCGGAAAGCCAAGCCATTTCTGTCTCCAGAGTTGTTCTCTTAAACTGATATGAGTTCT NM_002716 RefSeq chr11
- 111737880 111766445 PPP2R1B 5519 "protein phosphatase 2, regulatory subunit A, beta, transcript
variant 1" GO:0005515|GO:0060561|GO:0045121|GO:2001241|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139029_PI430048170 0.9068177343776150.9858556565345150.326135450592758
1.25837912073797 0.362818749189336 A A A 0.7374519889324440.259489018183013
1.09648462809917 A A A LNCV6_139029_PI430048170 mRNA
TAAAGCTGAGACCAAGAATAACCCTGGAAAAGTTTCCTCCATGATAGCAACCACCAGCCA NM_020646 RefSeq chr11
- 8937571 8943033 ASCL3 56676 achaete-scute family bHLH transcription factor 3
GO:0005667|GO:0006357|GO:0046983|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143571_PI430048170 0.1905319904042540.5211028573102290.364524528422498
0.7522002345518080.336283654501115 A A A 0.4554307727723311.88692109693533
1.61166389877284 A A A LNCV6_143571_PI430048170 mRNA
ACTGGGCTTGGCCTTGAGAGAAAGCCTTCTGTTTAATAAAGTACATTTTCTTCAGTAATC NM_005330 RefSeq chr11
- 5268349 5270143 HBE1 3046 "hemoglobin, epsilon 1"
GO:0019825|GO:0005833|GO:0005506|GO:0007596|GO:0005344|GO:0072562|GO:0000122|GO:0051291|GO:0031
721|GO:0020037|GO:0015671|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91696_PI430048170 0.59567738929463 0.9347260105771371 2.0949470445285 12.3212660972853
12.4076537061361 P P P 12.1372113112696 12.3819479538558 12.5806947181423 P P P
LNCV6_91696_PI430048170 mRNA
CATGACTTCCCTCAGTTTTATCCTTTAGGGATTGTGCAACATGATTGATCTTGATGGATT NM_002947 RefSeq chr7
- 7636943 7718607 RPA3 6119 "replication protein A3, 14kDa"
GO:0005515|GO:0006302|GO:0034605|GO:0000082|GO:0006271|GO:0003697|GO:0000723|GO:0000724|GO:0042
127|GO:0000722|GO:0006297|GO:0006298|GO:0005662|GO:0006260|GO:0003684|GO:0007346|GO:0006281|GO:0
006283|GO:0000730|GO:0006284|GO:0005654|GO:0006289|GO:0000718|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137687_PI430048170 0.1062095075068391.64730425524744 3.38734535266196
2.67756356612514 2.52927719994222 P A A 2.35473264167609 1.91148943063761
2.28194349977152 A A A LNCV6_137687_PI430048170 mRNA
CCCGGCTCGTCGGTCAGCGACGTGGACCAGGAGGAGCCGCGGTTCGGGGCCGTGGCCACC NM_024888 RefSeq
chr19 - 812487 821952 LPPR3 79948 "lipid phosphate phosphatase-related protein type 3, transcript
variant 1" GO:0016311|GO:0016021|GO:0008195 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145740_PI430048170 0.158531609835847 0.367959400257363 0.358701723855147
0.432551654727542 0.369075197569612 A A A 1.43185229300404 2.65156474957901
0.749505234703695 A P A LNCV6_145740_PI430048170 mRNA
CTGGTGGCTGACAAAGATGTAGTTTCCATCAGTCAATAAAACCTGAGAGGAGAGATGAGG NM_004979 RefSeq
chrX - 48961377 48971844 KCND1 3750 "potassium channel, voltage gated Shal related subfamily

D, member 1"
GO:0005251|GO:0005886|GO:0008076|GO:0043025|GO:0007268|GO:0051260|GO:0034765|GO:0016021|GO:0005575|GO:0071805|GO:0046872|GO:0030425 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132109_PI430048170 0.041851280456137 0.788039142538538 14.1240864344274 14.2740781672976 14.3513835114254 P P P 14.4399762886809 14.5835083695087 14.7495600183783 P P P LNCV6_132109_PI430048170 mRNA CACTTTGCTGTTCCTTACTTTACTGCCTGAATAAAGAGCCCTAAGTTTGTACTATATACT NM_001469 RefSeq chr22 + 41621162 41664048 XRCC6 2547 "X-ray repair complementing defective repair in Chinese hamster cells 6, transcript variant 1"
GO:0005515|GO:0044212|GO:0071481|GO:0005634|GO:0006303|GO:0005829|GO:0006302|GO:0003691|GO:0004003|GO:0003690|GO:0000723|GO:0050769|GO:0045944|GO:0016032|GO:0032481|GO:0032508|GO:0000783|GO:0005667|GO:0071475|GO:0033151|GO:0005730|GO:0008022|GO:0005524|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138779_PI430048170 0.925695141766344 1.01010083205838 8.67405629170343 8.72063542332783 8.4039970671064 P P P 8.50990106147268 8.75485733438231 8.49523098961398 P P P LNCV6_138779_PI430048170 mRNA GCTGTCTTCCTCTTTTCACATCATGGCGACAGTAATAAAGCCCACCTCCAGTGGAAAAAA NM_001137601 RefSeq chr14 + 104801180 104804711 ZBTB42 NA zinc finger and BTB domain containing 42 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138971_PI430048170 0.565545274300949 2.16247936387256 0.459370062335676 2.41315829272886 3.80299621432297 A A P 0.56391825400554 2.15958091220505 1.85092040924996 A A A LNCV6_138971_PI430048170 mRNA GTGTACATGTTTACTGTCACTTTTGATATGGTCTTATCCAGTGTGAACAGCAATTTATTC NM_007052 RefSeq chrX - 100843323 100874345 NOX1 27035 "NADPH oxidase 1, transcript variant 1"
GO:0050661|GO:0005515|GO:0045730|GO:0008284|GO:0030054|GO:0006801|GO:0046330|GO:0046872|GO:0003081|GO:0006954|GO:0016175|GO:0030198|GO:0071438|GO:0034765|GO:0042743|GO:0042554|GO:0072592|GO:0071455|GO:0006739|GO:0001525|GO:0045726|GO:0048661|GO:0010575|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136223_PI430048170 0.0256460709674901 0.734987906144718 12.3329460604721 12.3394668289 12.5714242002595 P P P 12.7481684200262 12.7715525722729 13.0498254400584 P P P LNCV6_136223_PI430048170 mRNA GGTTTGATTTCTCGTTCATTGTACACTGCCTCTGAACATCTAATTGTTTTTAGTTGTCTA NM_007178 RefSeq chr12 + 15882353 15903476 STRAP 11171 serine/threonine kinase receptor associated protein
GO:0005515|GO:0005886|GO:0050680|GO:0005102|GO:0005634|GO:0000122|GO:0010719|GO:0060394|GO:0000387|GO:0005829|GO:0005737|GO:0030277|GO:0032797|GO:0005654|GO:0007179|GO:0034719|GO:0030512|GO:0010633 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_3373_PI430048170 0.0127775322297312 1.4187100378528 8.79160035287457 9.07135567605122 8.85485799664948 P P P 8.3696277337907 8.55609209061373 8.27957057656456 P P P LNCV6_3373_PI430048170 mRNA ATCCTCCGCACTGAGTGAGGGTGCTGGAGGCAGACTCGAGGGCCGAATTGTTTCTAGTTA NM_006221 RefSeq chr19 + 9835206 9849689 PIN1 5300 "peptidylprolyl cis/trans isomerase, NIMA-interacting 1, transcript variant 1"
GO:0005515|GO:0000413|GO:0019221|GO:2000146|GO:0005634|GO:0050815|GO:0060393|GO:0050816|GO:0005737|GO:0051443|GO:0070373|GO:0032480|GO:0030512|GO:0007088|GO:0032465|GO:0003755|GO:0030496|GO:0031434|GO:0032794|GO:0007049|GO:0016607|GO:0032321|GO:0045087|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141760_PI430048170 0.639984197976435 1.09985670630253 3.99952097578514 3.38615323934641 3.61355294744247 P P P 4.03505390327702 3.06470531974989

3.38085548490346 P P P LNCV6_141760_PI430048170 mRNA
ACAGGATGGCTGGGTGGGGGTGGGAAGAAAAGATTAGGCCTTTGATTTATATTCATTTTG NM_022756 RefSeq
chr1 - 37489960 37514819 MEAF6 64769 "MYST/Esa1-associated factor 6, transcript variant 1"
GO:0005515|GO:0070776|GO:0005813|GO:0006355|GO:0005730|GO:0006325|GO:0006351|GO:0043981|GO:0005
737|GO:0043983|GO:0043982|GO:0043984|GO:0043968|GO:0035267|GO:0044154|GO:0005654 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_70206_PI430048170 0.0162561774226195 0.429922274279724 4.87770515598228
4.64739500884018 4.66721365689971 P P P 5.58765077107959 6.26618776046473
5.92402987173195 P P P LNCV6_70206_PI430048170 mRNA
AGCAGCTTGGTGAAGCGGGAAGTCTCCAAGGGCCGGTTCTTCAGCACCAGAGCCCGAAGA NM_003250 RefSeq
chr17 + 40062814 40093867 THRA 7067 "thyroid hormone receptor, alpha, transcript variant 2"
GO:0005515|GO:0010467|GO:0003700|GO:0006367|GO:0044212|GO:0006366|GO:0008016|GO:0009409|GO:0003
707|GO:0010831|GO:2000143|GO:0042994|GO:0005634|GO:0030878|GO:0050994|GO:0070324|GO:0032403|GO:0
060509|GO:0005829|GO:0045944|GO:0008050|GO:0043401|GO:0007611|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141906_PI430048170 0.0387245824403921 1.94064722597646 2.73427856254482
2.79265666451592 3.19818043551232 A A P 1.86370703256374 1.51889354416991
2.3850426767686 A A P LNCV6_141906_PI430048170 mRNA
GGAACAAAACTCTAACTTTAGGAATGGCTTTGGTTTCAGCCTTCAGTTAAAGTAATTGAT NM_019120 RefSeq
chr5 + 141177789 141180500 PCDHB8 56128 protocadherin beta 8
GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134058_PI430048170 0.182161717699515 0.342436521588109 0.507791596267487
0.367482338997979 0.389193608404494 A A A 0.441615561226582 2.54300991278405
2.18840377327424 A A A LNCV6_134058_PI430048170 mRNA
CCCTTATCCACTGCTCCTCTAGGTGGCCCATTTATGGTTTGTTGTAAGAGAAAAATTAAA NM_002066 RefSeq
chr8 + 142834800 142846846 GML 2765 glycosylphosphatidylinositol anchored molecule like
GO:0008285|GO:0005886|GO:0006915|GO:0031225|GO:0019898|GO:0006977 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_133311_PI430048170 0.546464490737641 0.962140243597303 0.268166510923291
0.449784441378472 0.302044398458615 A A A 0.502385344664999 0.397046192599665
0.286036924229767 A A A LNCV6_133311_PI430048170 mRNA
CTCAGTGTGATAATTGTGTCTACAGCTAAAATGGAAATAGTTTTATCTGTACAGTTGTGC NM_213594 RefSeq
chr12 + 106582906 106762804 RFX4 5992 "regulatory factor X, 4 (influences HLA class II
expression), transcript variant 3"
GO:0005515|GO:0003700|GO:0006357|GO:0021696|GO:0070613|GO:0005634|GO:0000978|GO:0021537|GO:0006
351|GO:0021516|GO:0042384|GO:0001077|GO:0045944|GO:0003682|GO:0030901|GO:0021914 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139089_PI430048170 0.060824717017399 0.588280325801702 4.84102366951378
4.68186188680176 4.89862629616143 P P P 5.13679983340078 5.67659003376403
5.82593484067392 P P P LNCV6_139089_PI430048170 mRNA
GGAAATTTTACCTTTAAAAGATTATTTAAGACAGGAACCAGGAGGCTTGGGAACAGGGAA NM_182488 RefSeq
chr13 - 27066149 27171896 USP12 219333 ubiquitin specific peptidase 12
GO:0005515|GO:0004197|GO:0006511|GO:0016579|GO:0004843|GO:0005575 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_132045_PI430048170 0.387673840888832 0.761706746719139 2.24717797790471
3.56733221982908 1.72759166410209 A P A 3.1554995076211 2.89900160053572
3.28891065286917 P P P LNCV6_132045_PI430048170 mRNA
GCATTCAAGTCTTGCTAAACATAAGATAATTCACACTGGAGAGAAACCCTACAAATGTAA NM_001159524 RefSeq

chr7 + 64207202 64220290 ZNF735 NA zinc finger protein 735 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136113_PI430048170 0.273581606625603 0.672796625979915 0.320036963919483 0.326883196845226 0.290536602563085 A A A 1.44700112115959 0.619712396468351 0.350205623484915 A A A LNCV6_136113_PI430048170 mRNA AGAACCCTGAAATGAAGACGGGCTTCATCCAATGTGCTGCATAAATAATCAGGGATTCTG NM_000765 RefSeq
chr7 - 99705036 99735200 CYP3A7 1551 "cytochrome P450, family 3, subfamily A, subpolypeptide 7"
GO:0004497|GO:0006805|GO:0070330|GO:0019825|GO:0005506|GO:0005789|GO:0044281|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138440_PI430048170 0.205434441518238 0.550415394717142 2.77562711786434 1.33423063484164 0.709052814095918 A A A 2.77350789157417 2.40217228557234 2.97604820648553 P A P LNCV6_138440_PI430048170 mRNA GTTGTGCTTAGTAAATGTGTGTCATTAATGCTGTATTCTCCTAGCTATTATGGAAACTTG NM_000259RefSeq chr15 - 52307283 52529050 MYO5A 4644 "myosin VA (heavy chain 12, myoxin), transcript variant 1"
GO:0005516|GO:0042641|GO:0035371|GO:0015031|GO:0006887|GO:0005764|GO:0032402|GO:0051643|GO:0042438|GO:0006810|GO:0043025|GO:0070062|GO:0042470|GO:0017137|GO:0032869|GO:0005794|GO:0031585|GO:0005509|GO:0006892|GO:0050808|GO:0044267|GO:0030073|GO:0001750|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141445_PI430048170 0.5718649588803390.96084824058135 0.406892719610069 0.4139529063687670.318016015891816A A A 0.58949633200637 0.350536453910731 0.36078639389746 A A A LNCV6_141445_PI430048170 mRNA AGATATGATGCCACGTATTCTAGAAGATGAAGGATTCTATATTCAGAGAAAGCCAGAAAT NM_001130446 RefSeq
chr10 + 95907964 95938658 C10orf131 NA chromosome 10 open reading frame 131 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143024_PI430048170 0.2373417343486941.04248385237014 0.461657247299599 0.3698788758844640.423685371923924A A A 0.3010717543187980.355065669192832 0.418100153467517A A A LNCV6_143024_PI430048170 mRNA CTGGATTCTGTTCAACTGTAATCAATGAAAAAGATGTACGTTGTAGACAAAGTTGCAGAA NM_018027RefSeq chr10 - 13643705 14330867 FRMD4A 55691 FERM domain containing 4A
GO:0090162|GO:0005737|GO:0005923|GO:0030674|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144525_PI430048170 0.9423645320683311.00383586651144 10.9352130649573 10.9790821661339 11.1071972378532 P P P 10.9023122998549 11.0007852379102 11.100595546022 P P P LNCV6_144525_PI430048170 mRNA ACGTTAGGCCTGAGTAGCTCCCCTCCATCCTTGTAGACGCTCCAGTCCCTACTACTGTGA NM_199141RefSeq chr19 + 10871576 10922772 CARM1 NA coactivator-associated arginine methyltransferase 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143277_PI430048170 0.2295278899689821.12441508484307 4.95338266470699 5.11354527942902 4.79009987450903 P P P 4.92188726121895 4.7149945170294 4.72096808667037 P P P LNCV6_143277_PI430048170 mRNA ACGGTGGGCAGAGAGCCTACTAGGAAATGTGCAGAATAAACTATTTTTTGAAGGAAAAAA NM_001093RefSeq chr12 + 109139396 109268225 ACACB 32 acetyl-CoA carboxylase beta
GO:0005515|GO:0014070|GO:0006768|GO:0006767|GO:0060421|GO:0005741|GO:0005634|GO:0044281|GO:0046872|GO:0005829|GO:0005739|GO:0051289|GO:0006633|GO:0003989|GO:0044255|GO:0006853|GO:0042493|GO:0046322|GO:0010884|GO:2001295|GO:0006084|GO:0005524|GO:0012505|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132124_PI430048170 0.4279105263858840.9103664178718091 4.9048717431395 14.7047094404898 14.6282263205683 P P P 14.6452500275211 15.0500057685567 14.933810966719 P P P LNCV6_132124_PI430048170 mRNA

TACAGGGGGCACTGGGACCTGGATTTGTTTTTCTAAATAAAGTTGGAAAAGCAGAAAAAA NM_014501 RefSeq chr19 - 55401281 55407957 UBE2S 27338 ubiquitin-conjugating enzyme E2S GO:0010994|GO:0035519|GO:0085020|GO:0010458|GO:0004842|GO:0016874|GO:0005524|GO:0031145|GO:0044314|GO:0051488|GO:0070534|GO:0005737|GO:0070979|GO:0019787|GO:0005680|GO:0006464|GO:0031625|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110145_PI430048170 0.62111853411549 0.96866851199496 5.93096925382904 6.02416133638055 5.74032374829267 P P P 6.01229467844661 5.91243518497194 5.92069775080825 P P P LNCV6_110145_PI430048170 mRNA
AAGCAGCATGAGCTGATGACACTGGATGGCTTCATGATGTACCTGTTGTCGCCGGAGGGG NM_133373 RefSeq chr17 - 45111639 45132533 PLCD3 113026 "phospholipase C, delta 3" GO:0005886|GO:0043647|GO:0001525|GO:0044281|GO:0032154|GO:0046872|GO:0005829|GO:0016042|GO:0035556|GO:0004435|GO:0042127|GO:0060716|GO:0004871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129028_PI430048170 0.385286235025607 1.29337321259229 0.355200527885614 1.23496834788184 0.416349214261445 A A A 0.363898456936148 0.327415219018473 0.37745473954835 A A A LNCV6_129028_PI430048170 mRNA
AAGGCATACCTTTAAGAGAAGCCCTTTGAATAATCAAGTGCTAAAACAAAATCAGGTGCT NM_078628 RefSeq chrX + 11758158 11767977 MSL3 10943 "male-specific lethal 3 homolog (Drosophila), transcript variant 4" GO:0006355|GO:0003700|GO:0006366|GO:0043984|GO:0006325|GO:0072487|GO:0007275|GO:0005654|GO:0005634|GO:0035064|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139905_PI430048170 0.0269106033758602 1.4234838509596 11.4133960990619 11.6558598311665 11.7786408973273 P P P 11.0456564943069 10.9665054519057 11.3084566899409 P P P LNCV6_139905_PI430048170 mRNA
CCCTGGAATTCATTAATTGTTTGCTTTGGACATGTGGAAAGAGCCTTACTAATAAAATTG NM_015514 RefSeq chr14 + 23469688 23478193 NGDN 25983 "neuroguidin, EIF4E binding protein, transcript variant 2" GO:0000462|GO:0030424|GO:0005737|GO:0032040|GO:0005730|GO:0030175|GO:0030425|GO:0006417|GO:0000775 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135482_PI430048170 0.191479392959692 1.87165066428258 0.292054879676609 1.32433192937695 1.65621016760727 A A A 0.30671578410824 0.26729869520178 0.305312906748072 A A A LNCV6_135482_PI430048170 mRNA
AGATCTATGTGTCACTGATCATTGTAAATAAAGTGGACCTGCTTTTACAGCCCTGTCACT NM_207334 RefSeq chr1 + 20552438 20555020 FAM43B 163933 "family with sequence similarity 43, member B" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133453_PI430048170 0.996554292742383 1.2593593562777 0.828785509686797 3.24242573383711 0.839095861231056 A A A 2.04732136328083 0.626948993536979 2.22281372981494 A A A LNCV6_133453_PI430048170 mRNA
TTTGACAAAGAGGGCAAGGGCTACATTGACTGGAACACACTCAAGTACGTGCTAATGAAC NM_138705 RefSeq chr1 + 1914826 1917294 CALML6 163688 calmodulin-like 6 GO:0005737|GO:0005509|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137411_PI430048170 0.116839246211946 1.09754641138851 0.691211048424545 0.83152935845316 0.666437573334145 A A A 0.579504090461103 0.619188078198492 0.592909060727134 A A A LNCV6_137411_PI430048170 mRNA
AATGCTGCACTGTTTACACCCTGACTGTGCTTAAAAACACTTTCACTAATAAATGGTTAT NM_001040113 RefSeq chr16_KI270853v1_alt - 1361145 1515023 MYH11 4629 "myosin, heavy chain 11, smooth muscle, transcript variant SM2B" GO:0005515|GO:0042470|GO:0005516|GO:0001725|GO:0048013|GO:0005524|GO:0030485|GO:0005829|GO:0006939|GO:0048739|GO:0032982|GO:0003774|GO:0051015|GO:0006936|GO:0007411|GO:0008152|GO:0005859|GO:0008307|GO:0030241|GO:0070062|GO:0048251 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138868_PI430048170 0.00378461631188754 1.9743173348317 5.71042487821096 5.7040305619227 5.84809796680848 P P P 4.66183879655309 4.67087167549311

4.96880792659697 P P P LNCV6_138868_PI430048170 mRNA
AAAGGAAAACAAGCTCATCAATTCCACGCAGCCCAGCGGGGAGGACTCAGAGGCAAAGGC NM_024014 RefSeq
chr7 - 27145582 27147774 HOXA6 3203 homeobox A6
GO:0043565|GO:0006355|GO:0003700|GO:0048704|GO:0005634|GO:0009952|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143138_PI430048170 0.2276249953799110.8016651627406971 0.8875985053551
10.8368045211482 11.1956495432237 P P P 10.9742802570751 11.2819872894174
11.5832989047735 P P P LNCV6_143138_PI430048170 mRNA
AAGCTGAAAGCTGGATACCTAATGTCAGTGGAGTCTTCTGAGTGTTTCCTGGAAGAAGTC NM_003366 RefSeq chr16
+ 21953287 21983347 UQCRC2 7385 ubiquinol-cytochrome c reductase core protein II
GO:0005515|GO:0005743|GO:0005750|GO:0044281|GO:0032403|GO:0046872|GO:0006119|GO:0005739|GO:0009
060|GO:0022904|GO:0006508|GO:0004222|GO:0044237|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143142_PI430048170 0.00856682092020627 0.60107305046789 7.4136502109456
7.72112425901929 7.51962210099683 P P P 8.22880690843827 8.3157634263414
8.32804640662599 P P P LNCV6_143142_PI430048170 mRNA
TGGGAAGGAAACAGGCCCCATTTTGTATATAGTTGCAACTTAAACTTTTTGGCTTGCAAA NM_001040022 RefSeq
chr20 + 1894166 1939894 SIRPA 140885 "signal-regulatory protein alpha, transcript variant 1"
GO:0017124|GO:0016020|GO:0005886|GO:0007596|GO:0016021|GO:0050900|GO:0007155|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141025_PI430048170 0.2269826946192341.3574564267476 4.16549192896812
3.57148112082065 3.7109524174104 P P P 3.80564706594716 3.35241160197729 2.8927884490348
P P P LNCV6_141025_PI430048170 mRNA
GAAAACAATTTCAAATACTTTTAAACCGTCTTCTCCTGGTAAAAAGCCTGGTGGAATGAA NM_001114357 RefSeq
chr4 + 185429390 185449667 C4orf47 441054 chromosome 4 open reading frame 47 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145171_PI430048170 0.1726275009630910.5156130118064361.76146655639258
0.2514350796628212.02550825435503 A A A 2.79923685356304 2.4273867574001
2.15070648390503 P P A LNCV6_145171_PI430048170 mRNA
GTCCCTCTCTGTGGAAGAATACTGAATAGAAGAGAGAAATCACTCAATATGTGGAATGAC NM_198682 RefSeq chr4
- 143870865 143905563 GYPE 2996 "glycophorin E (MNS blood group), transcript variant 2"
GO:0005886|GO:0005887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143228_PI430048170 0.0219758584544898 1.37845676339403 10.4821163525824
10.7666539588342 10.5989711888234 P P P 10.1072138056533 10.1619532922778
10.2020920017256 P P P LNCV6_143228_PI430048170 mRNA
TTTTGGTACGATTCCTGTCATCCCTATTGCAGAGTCGTGTCCCCAATAAACAGGTGTCTT NM_016423 RefSeq chr14
- 21090045 21098649 ZNF219 51222 "zinc finger protein 219, transcript variant 1"
GO:0005515|GO:0006355|GO:0003700|GO:0005634|GO:0000122|GO:0000978|GO:0004969|GO:0003677|GO:0046
872|GO:0006351|GO:0001078|GO:0007186|GO:0001505|GO:0016021|GO:0045892 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_70643_PI430048170 0.2789696395032471.1347485670314 7.31806793387769 7.30993269928647
7.47084945853314 P P P 6.95140473054414 7.16375616570381 7.40636205961673 P P P
LNCV6_70643_PI430048170 mRNA
CAGATTGTACCAGAGCCCATGGATTTCAGAAAATTATCTACATTCAGAGAAAGTTTTAAG NM_001080391 RefSeq
chr2 + 230416155 230545602 SP100 6672 "SP100 nuclear antigen, transcript variant 1"
GO:0005515|GO:0030870|GO:0070087|GO:0019221|GO:0005634|GO:0043433|GO:0042803|GO:0042802|GO:0046
826|GO:0051091|GO:0005737|GO:0060337|GO:0000723|GO:0016032|GO:0034340|GO:0006338|GO:0034341|GO:0
032526|GO:0006978|GO:0019900|GO:0034097|GO:0060333|GO:0003714|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_103347_PI430048170 0.73167389197882 1.01521709757547 0.406849193067831
0.5352683251561110.439665243249551A A A 0.5313619956994790.390080657408182
0.393531340551439A A A LNCV6_103347_PI430048170 mRNA
ATTTGAAACTGGGATACGCTTGGTAGCTTTTTTGTTTTAACACAAAGTAAACCTGTGAAG NM_024120RefSeq chr20
+ 13785025 13818421 NDUFAF5 79133 "NADH dehydrogenase (ubiquinone) complex I, assembly factor
5, transcript variant 1" GO:0032981|GO:0003674|GO:0031314|GO:0008168|GO:0032259 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_145678_PI430048170 0.0292470877172690.5467641487426732.04339268724028
2.23581215897832 2.73628657424577 A A A 3.06687523790095 3.49256456493006
3.12202222757872 P P P LNCV6_145678_PI430048170 mRNA
GGATTGCTTCAGATGGTTTGCTGTATCATTTTTCTTCTTTTTCTTTTCCTGGGGACTTGT NM_002397RefSeq chr5 -
88718240 88883466 MEF2C 4208 "myocyte enhancer factor 2C, transcript variant 1"
GO:0005515|GO:0003700|GO:0000983|GO:0006366|GO:0000981|GO:0003139|GO:0003185|GO:0003138|GO:0001
947|GO:0007507|GO:0002756|GO:0014033|GO:0002062|GO:0000165|GO:0002755|GO:0007611|GO:0002467|GO:0
014902|GO:0030501|GO:0000977|GO:0034134|GO:0001205|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128786_PI430048170 0.3773424092903871.3340515810078 0.374099670136876
0.3801496315786931.30091218236587 A A A 0.3253115338118970.317931666277362
0.372388556960767A A A LNCV6_128786_PI430048170 mRNA
GAAGATTCAGTTCAGCCTAAATCAAAACTTCCACCTTGTGTTCACTTCAAAGATGGCCCA NM_004256RefSeq chr3
+ 38265806 38278315 SLC22A13 9390 "solute carrier family 22 (organic anion/urate transporter),
member 13"
GO:0090416|GO:0016324|GO:0015695|GO:0005887|GO:0015747|GO:0055085|GO:0015101|GO:2001142|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54958_PI430048170 0.6738549721138611.02882720538699 12.5017373950442 12.5751506311557
12.544814788068 P P P 12.3059947381642 12.5647691805305 12.6105760761248 P P P
LNCV6_54958_PI430048170 mRNA
TGTGTCCTCCGTTCATTCCATGGCTGGGAGTCACTGATGCTGCCTCTGCCTTCTGATGCT NM_001277224 RefSeq
chr1 - 159918106 159923717 TAGLN2 8407 "transgelin 2, transcript variant 1"
GO:0005515|GO:0051015|GO:0030855|GO:0031982|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_114727_PI430048170 0.6730363041393341.06537322162812 0.281247910617199
0.7779772920223020.377377922476457A A A 0.5094350608421140.40145371378384
0.292926266663955A A A LNCV6_114727_PI430048170 mRNA
TATTCTTGTTAGGCAGTGTAAGTCATCATTGCCAAGAGCTTCCAAACCACCTAAGCTGCC NM_152543RefSeq chr4
- 158893531 159035181 C4orf45 152940 chromosome 4 open reading frame 45 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_110884_PI430048170 0.3689579056889291.57635359266168 0.34565031506063
1.73539985352231 0.470537212154947A A A 0.3416345253793290.311616089218105
0.366392161400608A A A LNCV6_110884_PI430048170 mRNA
AAAGCTGCTTCTGAACTCTACATAGAGACTGAGAAAAAGAAGCGCGAGAAAGCGTACCTG NM_003024RefSeq
chr21 + 33642477 33889305 ITSN1 6453 "intersectin 1 (SH3 domain protein), transcript variant 1"
GO:0005515|GO:0051897|GO:0043005|GO:0030054|GO:0005886|GO:0007264|GO:0045202|GO:0030139|GO:0005
829|GO:0005085|GO:0043524|GO:0007411|GO:0005089|GO:0070064|GO:0051056|GO:0048011|GO:0043065|GO:0
048013|GO:0005509|GO:0048488|GO:0097190|GO:0030027|GO:0043547|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137794_PI430048170 0.0546174023019543 0.86626637098201 6.23614724228247
6.11501492606467 6.02871843070201 P P P 6.39462471895776 6.30070209027593
6.31161806172397 P P P LNCV6_137794_PI430048170 mRNA

TACAGTCTTGCTGTTTCTGTTTCATCTGCAAGAATTATGACCCACACACTCCAGCTGCAG NM_144628RefSeq chr20 - 435476 462553 TBC1D20 128637 "TBC1 domain family, member 20, transcript variant 1"
GO:0005515|GO:0001675|GO:0017137|GO:0031965|GO:0046726|GO:0005783|GO:0090110|GO:0032851|GO:0019068|GO:0034389|GO:0006888|GO:0030173|GO:0072520|GO:0033126|GO:0005789|GO:0007030|GO:0070309|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127782_PI430048170 0.0262618383044228 1.22975040574019 10.0870429444018 10.2543379691163 10.2562413247591 P P P 9.9147446896748 9.92338926789523 9.87028467039421 P P P LNCV6_127782_PI430048170 mRNA
GAGTATCTATATAAATATATATTTCCCTGGTTCCTGTCCCTTTTCCCTGCCCCAACTTCT NM_001165967 RefSeq chr17 - 8120589 8124092 HES7 84667 "hes family bHLH transcription factor 7, transcript variant 1"
GO:0001501|GO:0007219|GO:0001756|GO:0046983|GO:0007498|GO:0005634|GO:0048511|GO:0014807|GO:0000122|GO:0003677|GO:0006351|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136528_PI430048170 0.59422634186448 0.9844036669344470.382687724207281 0.3814666745086570.271889507066293A A A 0.35498108940423 0.391461994560648 0.360145491008678A A A LNCV6_136528_PI430048170 mRNA
TCTCTTCCTTTGGTTATTAAGGTCACTAAATAAAGGAAGTGCCTTGGAAAACCCGTGAAA NM_017433RefSeq chr10 + 25934072 26212536 MYO3A 53904 myosin IIIA
GO:0005516|GO:0048839|GO:0007605|GO:0051491|GO:0016459|GO:0030175|GO:0032433|GO:0030898|GO:0005524|GO:0032426|GO:0001917|GO:0000146|GO:0005737|GO:0051015|GO:0046777|GO:0031941|GO:0004672|GO:0043531|GO:0018105|GO:0004674|GO:0018107|GO:0060002|GO:0007601|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140689_PI430048170 0.5150672081408780.7035805623421341.48531389751364 2.32560866430384 0.426347511578881A A A 1.81043055861636 2.86491438353591 1.1515857696187 A P A LNCV6_140689_PI430048170 mRNA
AGTTGGTATGGGCCCTGAAGTCAGGGAGGATTAGGATGAGCAAAAAACAAGGTGTATGTT NM_001001412 RefSeq chr10 - 103453386 103458891 CALHM1 255022 calcium homeostasis modulator 1
GO:0005262|GO:0005244|GO:0050916|GO:0050917|GO:0042802|GO:0050913|GO:0005887|GO:0070588|GO:0005789|GO:0015867|GO:0034765|GO:0051260|GO:0005227|GO:0006812 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135919_PI430048170 0.2562488734777690.4079140184850690.778838093400129 0.8739018961188060.776227822858148A A A 0.6115469756193322.05919541159528 2.84837977105666 A A P LNCV6_135919_PI430048170 mRNA
GTGTTTACTTCCCATGCACTTAATACCCTTATGCGCTAATTTTGTGAATTAAGTTTACTG NM_005862RefSeq chr3 - 136337156 136752403 STAG1 10274 stromal antigen 1
GO:0005515|GO:0007067|GO:0007059|GO:0005694|GO:0003682|GO:0005654|GO:0005634|GO:0000278|GO:0000785|GO:0000775|GO:0051301|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132920_PI430048170 0.3904719805678981.05048355665995 0.294506142281574 0.2846657977679190.47789229124147 A A A 0.2978904137159360.25977369944965 0.294257116963566A A A LNCV6_132920_PI430048170 mRNA
GCAGATGCATGTGTTGCTTTACAGAGTTTAGCAAAAGCTCTTAATTTTATGTCATACTGT NM_001127644 RefSeq chr5 + 161847933 161899959 GABRA1 2554 "gamma-aminobutyric acid (GABA) A receptor, alpha 1, transcript variant 3"
GO:0005230|GO:0030054|GO:0005886|GO:0004890|GO:0034707|GO:0007268|GO:0016917|GO:0007214|GO:0055085|GO:0005254|GO:0034220|GO:0005887|GO:0045211|GO:0008144|GO:0006810|GO:0051932|GO:0071420 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131304_PI430048170 0.2890460888131161.2683442913139 5.96714185654537 6.41387884870345 6.58303062639574 P P P 6.3994995088682 5.84567508039907 5.64989956345772 P P P LNCV6_131304_PI430048170 mRNA
TGTCCGTACCTATCAGAATGTTTTCTTGACACTTCCATGTTGGCTCTTCTCAGCTTTTTT NM_207299RefSeq chr9 +

101028748 101325135 LPPR1 54886 "lipid phosphate phosphatase-related protein type 1, transcript variant 1" GO:0008152|GO:0016021|GO:0003824|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143734_PI430048170 0.5595745491302731.04704273922394 10.3338005045164
10.5371617660416 10.4241396886643 P P P 10.1960480137544 10.5069772778581
10.3834780437381 P P P LNCV6_143734_PI430048170 mRNA
TGTATAAAAATGACCCTGTAGGGGCAATTCACAATGCTGAGTCTCTGAGGAGGTGATCAG NM_004328RefSeq chr2
+ 218659655 218663443 BCS1L 617 "BC1 (ubiquinol-cytochrome c reductase) synthesis-like, transcript variant 1"
GO:0033617|GO:0005739|GO:0005515|GO:0032981|GO:0034551|GO:0005750|GO:0007005|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115747_PI430048170 0.00406690694445248 1.44850532089427 7.14920787073148
7.01882850237423 7.04937374299674 P P P 6.53375719474151 6.64859431438513
6.42601855288486 P P P LNCV6_115747_PI430048170 mRNA
TGGGAAAACACCCTCAGACACCCACAATAAGGACTGCTCCATCGCAGCCACTGGCAAAAG NM_019104RefSeq
chr19 + 35748360 35754519 LIN37 55957 lin-37 DREAM MuvB core complex component
GO:0005515|GO:0017053|GO:0000086|GO:0051726|GO:0005654|GO:0000278 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145733_PI430048170 0.0450740946112693 0.6281577630845774.75199128101598
4.51778611115252 4.15403333952465 P P P 5.04191799225476 5.18934891813025
5.25834071247557 P P P LNCV6_145733_PI430048170 mRNA
TGCCAGCCTCTCTGATCCCTCAATTTGGTCTGTTTTCAAAATATAGAACGCCAAACTGCT NM_001271718 RefSeq
chr4 - 56809859 56821742 SPINK2 6691 "serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor), transcript variant 1" GO:0010951|GO:0004866|GO:0004867|GO:0005576 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_135046_PI430048170 0.0870169181129647 0.5535131263455594.34054066879089
4.20272030838264 4.35198537832069 P P P 4.62087780346576 5.52403279369653
5.17563703696942 P P P LNCV6_135046_PI430048170 mRNA
GCAGCAAGCCATGATCTAGGTCTTCGAGTAGAATTCTCAGTTTTGGTTCATTTAAAAATG NM_015341RefSeq chr2
+ 96335740 96377095 NCAPH 23397 "non-SMC condensin I complex, subunit H, transcript variant 1"
GO:0005515|GO:0000796|GO:0007076|GO:0005737|GO:0016020|GO:0005634|GO:0000278|GO:0051301|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136239_PI430048170 0.0495907981015028 0.4314919423469891.76744406321893
2.12786298118684 1.95513012987266 A A A 3.44732644932611 2.50666841240808
3.38051744706363 P P P LNCV6_136239_PI430048170 mRNA
GGACTGAAAGGTATACATCTGTGAGTTTTGTTCTCACTTCCACCTCTAATTTGAAGAACA NM_198833RefSeq chr18
+ 63970028 63989374 SERPINB8 5271 "serpin peptidase inhibitor, clade B (ovalbumin), member 8, transcript variant 2" GO:0010951|GO:0005515|GO:0004867|GO:0005615|GO:0070062|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_83372_PI430048170 0.0706478041839798 0.92254950854803 7.49728302761874
7.55657259976103 7.47921223417122 P P P 7.55294685200416 7.65183503175186
7.67542630104366 P P P LNCV6_83372_PI430048170 mRNA
TCTCTTCAGGACCTGCAAACATGAGAAGCTGACCTTGGACCTGACGGTGCTCCTGGGTGT NM_014520RefSeq chr17
- 4538895 4555386 MYBBP1A 10514 "MYB binding protein (P160) 1a, transcript variant 2"
GO:0005515|GO:0006355|GO:0042564|GO:0003714|GO:0003887|GO:0005730|GO:0001047|GO:0005634|GO:0071
158|GO:0032922|GO:0001649|GO:0006351|GO:0043231|GO:0006913|GO:0043565|GO:0022904|GO:0005737|GO:0
072332|GO:0071897|GO:0016020|GO:0042149|GO:0045892|GO:0008134 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_111000_PI430048170 0.3925611532808371.22553978063845 5.41445297668008
5.28128899577721 5.48297920148803 P P P 5.64581485697851 4.45137796017036

4.95793773046262 P P P LNCV6_111000_PI430048170 mRNA
AACACAGTTTCATTTGACAAAGATTCCACCGTCCAAGTCTTTGAGGCCACGATAAGGGTC NM_014674 RefSeq chr3
+ 5187673 5219965 EDEM1 9695 "ER degradation enhancer, mannosidase alpha-like 1"
GO:0005515|GO:0004571|GO:0005509|GO:0030176|GO:0030433|GO:0030968|GO:0051787|GO:0006457|GO:0005
789|GO:0006987|GO:0044267|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142349_PI430048170 0.8977622455974561.00521347478709 2.3618120980513
2.23566043703197 2.45030095413121 A A A 2.60989097656604 1.98428522529278
2.37143800570446 A A A LNCV6_142349_PI430048170 mRNA
CCAAATTTTTGTTGGTGGGCTGAACAAAGATAAAACTAATAAAGTATGTGTGGATACCAC NM_020133 RefSeq chr6
- 161130024 161274075 AGPAT4 56895 1-acylglycerol-3-phosphate O-acyltransferase 4
GO:0019432|GO:0016024|GO:0005789|GO:0044281|GO:0016021|GO:0008654|GO:0006644|GO:0006654|GO:0003
841|GO:0044255|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129291_PI430048170 0.2930618892437930.8567411647081397.61106526107651
7.72947833623691 8.16857250898908 P P P 8.11693278989782 7.93450175846954
8.17744487006318 P P P LNCV6_129291_PI430048170 mRNA
GTTTTTCCAAAGCAGTTAACCCAACTCCTAACAACATTTTCGGGGGATCTGACCTTTTTT NM_001008661 RefSeq
chr1 - 88935772 88992960 CCBL2 56267 "cysteine conjugate-beta lyase 2, transcript variant 1"
GO:0006520|GO:0006569|GO:0070189|GO:0009058|GO:0047804|GO:0044281|GO:0042803|GO:0005739|GO:0034
641|GO:0097052|GO:0006103|GO:0030170|GO:0016212|GO:0047315 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133380_PI430048170 0.0700174449173782 0.5783365089477985.15463680742062
4.71857424700385 5.5717125027835 P P P 5.85664235753994 6.00616182029618
6.06897793101428 P P P LNCV6_133380_PI430048170 mRNA
GTGGTGGAGACCTTTATTTAAGGTGATTTTTACAGAAATGTGATTTTGCTGTAGGTGATT NM_022482 RefSeq chr20
+ 23364383 23373046 GZF1 64412 GDNF-inducible zinc finger protein 1
GO:0001658|GO:0005794|GO:0001206|GO:0005730|GO:0005634|GO:0000122|GO:0000978|GO:0046872|GO:0006
351|GO:0043565|GO:0001078|GO:0005737|GO:0000980|GO:0005654|GO:0045892 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128133_PI430048170 0.0217085996376673 1.48822904075568 7.45368698661779
7.57751933983293 7.84445438879332 P P P 7.11917648612353 6.84863270440612
7.19280223015607 P P P LNCV6_128133_PI430048170 mRNA
GGACAGATGTACATAGAAGGTGCCTACTCATTGTATTTTGATGATTTCATTAACAGGTAA NM_001198862 RefSeq
chr1 - 212364473 212414901 TMEM206 55248 "transmembrane protein 206, transcript variant 1"
GO:0009986|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126875_PI430048170 0.3961722308172120.6891680707229690.418621927020063
0.38972410467001 0.244301502370611 A A A 0.3518227481786240.407197006002263
1.56415880045262 A A A LNCV6_126875_PI430048170 mRNA
CTTCGCAACCAGGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTTGC NM_001004724 RefSeq
chr14 + 20143735 20144662 OR4N5 NA "olfactory receptor, family 4, subfamily N, member 5" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82248_PI430048170 0.9266704599348580.9850760572256117.99035351763896 7.78423513204023
7.56052123215048 P P P 8.17608079039264 7.94347422336356 7.11024351497352 P P P
LNCV6_82248_PI430048170 mRNA
AAGAATTTCCCGCGTGTCTCCTATATCACAGCCTTGGATTTCTATATCGCCATCTGCTTC NM_004961 RefSeq chrX
- 151953123 151974679 GABRE 2564 "gamma-aminobutyric acid (GABA) A receptor, epsilon"
GO:0005230|GO:0030054|GO:0005887|GO:0004890|GO:0045211|GO:0034707|GO:0006810|GO:0007214|GO:0005
254 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128723_PI430048170 0.3059694384814180.8391410226355770.403277358455471
0.3980225888485150.420343070950191 A A A 0.9280841245823580.33661039976706 0.6558744628056

A A A LNCV6_128723_PI430048170 mRNA
CTGATGAACAAGCATTTAGATCGTAACATGGTAAAGCCTATTACCAGCCAATGTTGTTAG NM_152309RefSeq chr10
- 96593311 96720522 PIK3AP1 118788 phosphoinositide-3-kinase adaptor protein 1
GO:0034154|GO:0034142|GO:0034123|GO:0016020|GO:0005886|GO:0034122|GO:0034134|GO:0050727|GO:0014
068|GO:0034162|GO:0042802|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108793_PI430048170 0.9236086061639180.96072412764015 3.33982309607435
3.47643947630552 3.98154825513672 P P P 3.2070485343466 3.56227629535148
4.13087254050877 P P P LNCV6_108793_PI430048170 mRNA
AATTGGGAATTACACCTGAAAGCTTTGTTAGGAACTCTGCAGGAAAGTCATCATCCTACC NM_152562RefSeq chr8
+ 25458996 25507909 CDCA2 157313 cell division cycle associated 2
GO:0007067|GO:0005737|GO:0007059|GO:0005694|GO:0035307|GO:0005654|GO:0051301 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135186_PI430048170 0.4152983227484150.7761341762567290.645267416873531
0.8046128460442360.624908484167717A A A 0.8042142626084260.603002985857414
1.57893026213534 A A A LNCV6_135186_PI430048170 mRNA
TGAATTGTGAATTCAGTTCTGAATTGTGTTCCCACCAGCACCACCAAATGCTGGCCTCTA NM_001001668 RefSeq
chr19 + 56567520 56582894 ZNF470 NA zinc finger protein 470 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135172_PI430048170 0.7253974955124571.03488842463993 5.88504570232228 5.9314981388495
5.82246452486564 P P P 5.94040729708482 6.0101199069426 5.48869859041823 P P P
LNCV6_135172_PI430048170 mRNA
TCCTGCCACCCTTATACCTGTTCAGCCTCCTAAAGAGGGACAAACTCTGTCTCTGCGTGC NM_080863RefSeq chr17
+ 44170705 44179083 ASB16 92591 ankyrin repeat and SOCS box containing 16
GO:0035556|GO:0005515|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_43750_PI430048170 0.3936048853579391.47060058515071 3.35716174388223 2.87600856996209
3.13218502456073 P A P 0.4102035951476343.00891004517538 3.09482747047361 A P P
LNCV6_43750_PI430048170 mRNA
AGGTCACCAAACGTGATGAAGACTCTTCTTTGATGCAGCTGAAAGAAGAATTTAGAACCT NM_001300850 RefSeq
chr1 - 173931083 173993072 RC3H1 149041 "ring finger and CCCH-type domains 1, transcript variant 1"
GO:0043488|GO:0001782|GO:0016567|GO:0033962|GO:0050856|GO:0010494|GO:0046007|GO:0000956|GO:0030
889|GO:0048536|GO:0048535|GO:0010608|GO:0042098|GO:0000932|GO:0002635|GO:0008270|GO:0045623|GO:0
003730|GO:0043029|GO:0002634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133876_PI430048170 0.8498452006494310.8156966671447090.327132509636284
1.62979388956376 1.90153828358073 A A A 0.2542699545124291.58615079192608
2.51524806998898 A A P LNCV6_133876_PI430048170 mRNA
CGCCTTGAGTACTGGGACAACCTTTGATTACTCATTATATCCTCAATAAATATTTGTTGA NM_181785RefSeq chr13
- 28700080 28719013 SLC46A3 283537 "solute carrier family 46, member 3, transcript variant 1"
GO:0008150|GO:0003674|GO:0016021|GO:0055085|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_91246_PI430048170 0.0546785545317772 0.7585118684495528.60619667467444
8.62601688948295 8.8845260347454 P P P 8.89840891446216 9.11638589842972
9.28888879268583 P P P LNCV6_91246_PI430048170 mRNA
AGAAGATAGCTATTTTGGGATTTGCATTCAAAAAGGACACTGGTGATACAAAGAATCTTC NM_003359RefSeq chr4
- 39498755 39527598 UGDH 7358 "UDP-glucose 6-dehydrogenase, transcript variant 1"
GO:0006805|GO:0052695|GO:0009055|GO:0006065|GO:0044281|GO:0001702|GO:0006024|GO:0005829|GO:0003
979|GO:0051287|GO:0005654|GO:0006011|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134128_PI430048170 0.1857418208206761.13613098454985 8.20510427233976
8.29564788221641 8.42494013857692 P P P 8.05595526508552 7.99928166714212 8.3075652134647

P P P LNCV6_134128_PI430048170 mRNA
GGGCATAGGAACGGTGTCATGGAGTCCAAATAAAGTGGATATTCCTGCTCGGACAAAAAANM_001037537 RefSeq
chr10 - 13277795 13299746 PHYH 5264 "phytanoyl-CoA 2-hydroxylase, transcript variant 2"
GO:0005515|GO:0048037|GO:0031418|GO:0005782|GO:0097089|GO:0009055|GO:0044281|GO:0046872|GO:0005
739|GO:0001561|GO:0048244|GO:0006720|GO:0044255|GO:0005777 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_110957_PI430048170 0.00132379716927884 0.4065250224510297.54046323972152
7.49286062722001 7.16474321087643 P P P 8.55323325832962 8.84785387186386
8.70593419869236 P P P LNCV6_110957_PI430048170 mRNA
GGCCTGGGTTTACAACGCTGTTAGGAAAATTAACCAATGAATAAAGCAACGTTCAGTGCG NM_012429RefSeq chr22
+ 30396940 30425303 SEC14L2 23541 "SEC14-like 2 (S. cerevisiae), transcript variant 1"
GO:0005215|GO:0005737|GO:0005543|GO:0045540|GO:0006810|GO:0005634|GO:0016021|GO:0045893|GO:0008
431|GO:0006351|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139642_PI430048170 0.0654096767866653 0.82395816304689 12.1860389037135
12.3995786994319 12.3535601531943 P P P 12.4339184761024 12.6088326853556
12.7280766459175 P P P LNCV6_139642_PI430048170 mRNA
CCGGTATAAAGGATGCCCAAGGTCTTTGTACGTGTGTAGGAGTTAGCGTGTTTGATATTG NM_006291RefSeq chr14
+ 103126326 103137439 TNFAIP2 7127 "tumor necrosis factor, alpha-induced protein 2"
GO:0000145|GO:0051601|GO:0000149|GO:0001525|GO:0006887|GO:0005615|GO:0030154 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139547_PI430048170 0.0265484561417829 1.29284741507833 11.5520270898659
11.3312079826611 11.5944360367705 P P P 10.9937407507228 11.159050970121
11.2175910218006 P P P LNCV6_139547_PI430048170 mRNA
GGATGATTCTGGAGCTCTATTAGGAGAAAAGTAATCATTTTAGGTCTTAAAGACTTCAAG NM_181527RefSeq chr20
+ 20017794 20033629 NAA20 51126 "N(alpha)-acetyltransferase 20, NatB catalytic subunit, transcript
variant 2" GO:0005622|GO:0031416|GO:0005737|GO:0017196|GO:0004596|GO:0005634 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_134629_PI430048170 0.60719162988016 0.9888634582866820.418365921715715
0.4246779467174720.36246184648028 A A A 0.4579414634152740.386230809429974
0.409683835730286A A A LNCV6_134629_PI430048170 mRNA
TCAGGCGCAAACCTGGCGCCAGTGTCTAAATGTCCATCATTCTCAGACCAACAGAAAAAA NM_001242659 RefSeq
chr1 - 1598007 1600096 C1orf233 643988 chromosome 1 open reading frame 233 GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131509_PI430048170 0.5796023692402151.23423502349167 1.36821518668051
0.3351765734359461.42692372569319 A A A 1.05998891354939 0.889809937456445
0.437561026186874A A A LNCV6_131509_PI430048170 mRNA
AAATCACTGGAATTCAATTTTGTGGTCTTTCCCCTTTCAGCAAGGACGGAAGGCTGTGGA NM_001136505 RefSeq
chr16 - 66754975 66801620 CCDC79 283847 coiled-coil domain containing 79
GO:0007129|GO:0045141|GO:0000781|GO:0003682|GO:0003677 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137819_PI430048170 0.00467256503156614 0.7817433578411016.91197829501121
6.84384977819571 6.76556544308622 P P P 7.16328755227014 7.2850052689876
7.13820284273643 P P P LNCV6_137819_PI430048170 mRNA
TACAGGGCATCCCTCCTTCCCATCTACGGGTGTTCTCAATAAACAATGTACAGTTGTTTG NM_005418RefSeq chr11
- 8693351 8910951 ST5 6764 "suppression of tumorigenicity 5, transcript variant 1"
GO:0017112|GO:0032851|GO:0070374 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111008_PI430048170 0.9449769408818280.9303113857967441.73940665975481
0.3434218654087810.290450945435069A A A 0.2456363760220510.361517971159841
1.92491566151856 A A A LNCV6_111008_PI430048170 mRNA

CCATCAACTACACCGTGATTCTCAGCAGCTAAACACTAAAAATAAAAATGATTTTAGGAC NM_173472RefSeq chr3 - 10081319 10108231 FANCD2OS 115795 "FANCD2 opposite strand, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136260_PI430048170 0.00629998676641759 0.5957629637791699.89336731787262 9.77706072319953 9.72478730261088 P P P 10.3668350813116 10.6981190498523 10.5579901365757 P P P LNCV6_136260_PI430048170 mRNA
GGATGTTATTTGTACGAAGGGCAGTTCGTAAACAGCACTTGTTCTTTTAATAAAAGAATG NM_005937RefSeq chr17_KI270857v1_alt + 2740938 2765122 MLLT6 4302 "myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6" GO:0005515|GO:0006355|GO:0008270|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134907_PI430048170 0.9418504009326260.97884880476254 6.22624952918644 5.99582755157619 6.19882178736621 P P P 5.82669050420018 6.23825555758201 6.40044513963182 P P P LNCV6_134907_PI430048170 mRNA
ATCCTAACACAGGCAGGCACCAGAAATAAATGTCTCAGCACTTTACAGATGACTAAAAAT NM_014629RefSeq chr8_KI270821v1_alt + 7351 142017 ARHGEF10 9639 Rho guanine nucleotide exchange factor (GEF) 10
GO:0005515|GO:0051298|GO:0005813|GO:0032321|GO:0022011|GO:0051496|GO:0033126|GO:0090307|GO:0019894|GO:0005089|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131519_PI430048170 0.3445159992517070.8115905728425457.8079754480185 7.1466615007724 7.18125961622273 P P P 7.94260227639194 7.81293980127046 7.30976084783668 P P P LNCV6_131519_PI430048170 mRNA
TCTGTGAGGGGGACGATTGCCAGCCGCCCGCGTACACCTACAACAACATCACCTGTGCCA NM_001146006 RefSeq chr16 - 1790412 1793733 IGFALS 3483 "insulin-like growth factor binding protein, acid labile subunit, transcript variant 1"
GO:0007165|GO:0005654|GO:0005576|GO:0007155|GO:0044267|GO:0005615|GO:0070062|GO:0005520 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136846_PI430048170 0.0256146593035052 0.6444822152653536.71331101278018 7.1368048907555 7.14341314758169 P P P 7.55963788021291 7.5350779485083 7.82281394162318 P P P LNCV6_136846_PI430048170 mRNA
CCTCAAAGAGAAATAATAACAGTAATAGTGGTGCTGGGAACAATATGGCAGATTATTGAA NM_001270374 RefSeq chr10 + 80079244 80092551 TMEM254 80195 "transmembrane protein 254, transcript variant 9"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142877_PI430048170 0.000429705278866497 2.06330397060495 11.6584071320239 11.8548294980022 11.6375399098432 P P P 10.6693220983556 10.7923430762755 10.5545453655334 P P P LNCV6_142877_PI430048170 mRNA
CCCCACCTAAAAAGACCAAGCATTGATGCCCAAGTTTTGGAAATATTCTGTTTTAAAAAG NM_003730RefSeq chr6 - 166929515 166956589 RNASET2 8635 ribonuclease T2
GO:0003723|GO:0033897|GO:0005788|GO:0005576|GO:0004540|GO:0005764|GO:0005615|GO:0070062|GO:0043202|GO:0006401 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115481_PI430048170 0.000467544089782646 1.8359265578852 6.8460861580904 6.91584407269904 7.05346870685373 P P P 5.95658923732441 6.14722850318703 6.08335043195256 P P P LNCV6_115481_PI430048170 mRNA
TTTCCTGGTGACTTTTGGCTTCATTTGGGGTATGATGCTTCTGCACTTTACCATCCAGCA NM_002410RefSeq chr2 + 134254258 134454621 MGAT5 4249 "mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase"
GO:0030144|GO:0000139|GO:0016021|GO:0044267|GO:0070062|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145166_PI430048170 0.5784417746204330.8398148714331871.10902149458753 2.52936999742656 1.35767445256164 A A A 1.40456901529287 2.10284795895544

2.47284021390044 A A P LNCV6_145166_PI430048170 mRNA
AGAGGCAATAGGTAAATGGGGCCCATTAGGTCCCTCACTCCACAGAGTGAGCCAGTGAGG NM_002447RefSeq
chr3 - 49887002 49903873 MST1R 4486 "macrophage stimulating 1 receptor, transcript variant 1"
GO:0038145|GO:0005515|GO:0051897|GO:0001725|GO:0008284|GO:0009986|GO:0006928|GO:0018108|GO:0006
952|GO:0007275|GO:0009615|GO:0005524|GO:0007338|GO:0007165|GO:0043406|GO:0005887|GO:0045087|GO:0
005011|GO:0019899|GO:0007169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143480_PI430048170 0.0224459574708652 0.46258359610084 3.8521200557028
4.0866322038822 4.63953838503252 P P P 5.12987007436853 5.31865939553865
5.55171974418442 P P P LNCV6_143480_PI430048170 mRNA
TATCTGTTAAACTGAGGTTTCATTGACGTGTCCCTATTAATAAACGTTATTTGCCCCACA NM_018696RefSeq chr18
+ 50968016 50988120 ELAC1 55520 elaC ribonuclease Z 1
GO:0016891|GO:0042779|GO:0005634|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140657_PI430048170 0.3341535490416451.03537232530807 0.351083804953818
0.3534572777131690.468570110704515A A A 0.3422742573867390.314243801207245
0.368782128880354A A A LNCV6_140657_PI430048170 mRNA
GTCCTACACTTTAAGCTGCTCCTTTGGTATGACTCTATACTTATGGAAATGTAGAAACAA NM_003269RefSeq chr6
+ 108166057 108188809 NR2E1 7101 "nuclear receptor subfamily 2, group E, member 1, transcript variant
2"
GO:0010467|GO:0021960|GO:0006367|GO:0060041|GO:0008347|GO:0042826|GO:0003707|GO:0060291|GO:0021
772|GO:0030198|GO:0045944|GO:0002118|GO:0043401|GO:0001662|GO:0035019|GO:0060164|GO:0021895|GO:0
021542|GO:2000179|GO:0043066|GO:2000178|GO:2000648|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127979_PI430048170 0.000114575314882756 0.335114565103781 0.441372103759269
0.3244944237072140.564641723939102A A A 2.04590608727087 1.93150222038493
2.09030147709388 A A A LNCV6_127979_PI430048170 mRNA
TATAAATAAACTCTTTGCTATTCAGAAAACCTCAAGGGGCCCCCACATTCACTAAGCATG NM_014728RefSeq chrX
+ 12138465 12724523 FRMPD4 9758 FERM and PDZ domain containing 4
GO:0005515|GO:0043197|GO:0051835|GO:0005546|GO:0005856 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140321_PI430048170 0.0240697581620041 0.3102888789136522.75058028027431
2.74673444046213 3.72458351917003 A A P 4.70353855194988 4.75827083731512
5.03582578494246 P P P LNCV6_140321_PI430048170 mRNA
TCTATGAGCTGAGTGTTCAATTAGCTTTGCCTACTGAGTTCAATTTTATGTCAATACAAC NM_002294RefSeq chrX
- 120426147 120469349 LAMP2 3920 "lysosomal-associated membrane protein 2, transcript variant A"
GO:0031088|GO:0005886|GO:0005770|GO:0019904|GO:0050821|GO:0030168|GO:0005765|GO:0005764|GO:0016
020|GO:0007596|GO:0031902|GO:0002576|GO:0030670|GO:0016021|GO:0019899|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136164_PI430048170 0.2806174190548671.13217799348982 8.40602064336681
8.55510367915534 8.80797120977205 P P P 8.43299802055893 8.33953686548932
8.48443960126222 P P P LNCV6_136164_PI430048170 mRNA
ACTGAAGTGGCAGTCTACGACAAGGATGAAGTCTTTCATTTTTTCAATGTTTTAGCAAGC NM_018453RefSeq chr14
- 34515928 34539737 EAPP 55837 E2F-associated phosphoprotein
GO:0008284|GO:0005737|GO:0005794|GO:0032968|GO:0005654|GO:0005634|GO:0034244 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131816_PI430048170 0.2737553690691552.16443288473122 1.93354374630402
2.39100896930224 0.371246593370827A A A 0.5618518717270630.465620166474361
0.947679994634121A A A LNCV6_131816_PI430048170 mRNA
CGGCTCGAGGGGGTGGATACTGTGAGTTTAATTATAAAGAATGACCTGGTACAAAAGCCA NM_001195076 RefSeq

chr19 + 50649444 50659310 C19orf81 NA chromosome 19 open reading frame 81 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97977_PI430048170 0.0722867641507781 0.72219449349104 4.75645464646765 4.48969802472977 4.82440823754459 P P P 4.94175706758257 5.06931857400499 5.44155042931322 P P P LNCV6_97977_PI430048170 mRNA
ACAGCTTAGTCTAATATCAGCAATGATTAAGAACCTTAAGGAACAAGGAGTTACGTTCCC NM_003473 RefSeq chr10 + 17644124 17716822 STAM 8027 "signal transducing adaptor molecule (SH3 domain and ITAM motif) 1, transcript variant 1"
GO:0005515|GO:0007165|GO:0007173|GO:0031901|GO:0005070|GO:0016197|GO:0042059|GO:0061024|GO:0009967|GO:0006886|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136987_PI430048170 0.358022649650903 0.96740074394436 0.414338344147523 0.4402390878034690.306979889009219 A A A 0.4123459869583170.466866701060568 0.428676087628935 A A A LNCV6_136987_PI430048170 mRNA
ATTGACACATCATCATATTAAAAAATCTCCACGAGTGATTGATTTTACTCTGCAGCCAGG NM_001039615 RefSeq chr8 + 12089337 12115516 ZNF705D NA zinc finger protein 705D NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67295_PI430048170 0.969562971375826 1.03297524798099 3.49055344437503 2.55519232449366 3.26025243341163 P A P 2.78471555570813 3.13253903380397 3.34848134671052 P P P LNCV6_67295_PI430048170 mRNA
ATTGAATGGGCTACCTATACCTGCACTTTGGGATTCCATGTTTTTGGAGTGTGGCCAGAA NM_001008707 RefSeq chr14 + 99793407 99942058 EML1 2009 "echinoderm microtubule associated protein like 1, transcript variant 1"
GO:0005515|GO:0008017|GO:0048471|GO:0005875|GO:0005509|GO:0005874|GO:0000226|GO:0005829|GO:0007405|GO:0015631|GO:0002244|GO:0007420|GO:0007052 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141321_PI430048170 0.00507207759170671 0.328126097467358 10.8304141910199 10.5317818827886 10.7422601663227 P P P 11.9769450329205 12.2829111411346 12.6135463862479 P P P LNCV6_141321_PI430048170 mRNA
AAGATTTCTGGCAGTGTGGGATGGATGAATGAAGTGGAATGTGAACTTTGGGCAAGTTAA NM_005415 RefSeq chr2 + 112645856 112663823 SLC20A1 6574 "solute carrier family 20 (phosphate transporter), member 1"
GO:0005886|GO:0035435|GO:0006796|GO:0055085|GO:0007165|GO:0005436|GO:0016020|GO:0005887|GO:0006810|GO:0035725|GO:0004872|GO:0005315|GO:0004871|GO:0005316|GO:0043123|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138300_PI430048170 0.62616084275104 0.980240622773127 0.478583066036079 0.4885724208397640.371053621802498 A A A 0.3970206283907270.524571238562214 0.502712485966061 A A A LNCV6_138300_PI430048170 mRNA
GTTCTGCAAGTAAACCTGTGTTAATACTTGTCAACAACTGCAGAGTTTATGATACGAATA NM_001145204 RefSeq chr16 + 12901619 13240416 SHISA9 729993 "shisa family member 9, transcript variant 1"
GO:0030054|GO:0008328|GO:0032591|GO:0032281|GO:0045202|GO:0048172 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61224_PI430048170 0.04031968440644 0.618689999858075 8.26579661227379 7.7009416840551 7.73872832424605 P P P 8.80548050925457 8.51474192822316 8.51513427770727 P P P LNCV6_61224_PI430048170 mRNA
TTGGATATTGCGTTTGGAACACACCACACGAAAATGATGCTGCTGCTCTATGAAGAAGGC NM_018319 RefSeq chr14 + 89955901 90044764 TDP1 55775 "tyrosyl-DNA phosphodiesterase 1, transcript variant 1"
GO:0005515|GO:0000012|GO:0005737|GO:0004527|GO:0006281|GO:0003690|GO:0090305|GO:0003697|GO:0005634|GO:0017005|GO:0006302 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136565_PI430048170 0.0582635394986751 0.74426646165972 7.01824655206473 6.97451789798607 7.33235915068472 P P P 7.42683724564237 7.40895622340924 7.76593558662935 P P P LNCV6_136565_PI430048170 mRNA

TATTATGCCTGAATGACTCCACTGTTTTTCTCTAATGCTTGATTTAGGTAGCCTTGTGTT NM_006209 RefSeq chr8 - 119557076 119638866 ENPP2 5168 "ectonucleotide pyrophosphatase/phosphodiesterase 2, transcript variant 1"
GO:0005886|GO:0090305|GO:0004551|GO:0006928|GO:0006796|GO:0005615|GO:0006955|GO:0004528|GO:0006935|GO:0004622|GO:0047391|GO:0005044|GO:0030334|GO:0005509|GO:0045765|GO:0003676|GO:0006898|GO:0007186|GO:0016787|GO:0005887|GO:0008270|GO:0030247|GO:0034638|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130527_PI430048170 0.1787122483745420.9358289759317750.417862054077711 0.4402630115000380.325410593703652A A A 0.4195299027316330.474005571771132 0.575251168158256A A A LNCV6_130527_PI430048170 mRNA
GCTTTTGAATTGCACTGAACAGAATTAAGAAATACTCATGTGCAATAGGTGAGAGAATGT NM_002425 RefSeq chr11 - 102770501 102780628 MMP10 4319 matrix metallopeptidase 10
GO:0030334|GO:0022617|GO:0030198|GO:0030574|GO:0005509|GO:0006508|GO:0005578|GO:0008270|GO:0005576|GO:0004222|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140288_PI430048170 0.4243334112772250.8477622042834470.578614160751578 0.3929216709441090.544860560157202A A A 1.04694685793269 0.775496734902336 0.325806247291239A A A LNCV6_140288_PI430048170 mRNA
GGAAGAAGCAGATGAGAAACTCTTGAGATCTTGGTCCTGTGTTTTTTCTGCCACCAAAGG NM_004778 RefSeq chr11 - 60850924 60855971 PTGDR2 11251 prostaglandin D2 receptor 2
GO:0043005|GO:0045745|GO:0019722|GO:0005886|GO:0004930|GO:0007268|GO:0004956|GO:0007193|GO:0004958|GO:0006955|GO:0042923|GO:0006935|GO:0007186|GO:0005887|GO:0007187|GO:0007218|GO:0001785 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128562_PI430048170 0.1460819099096380.9268259679962750.275506916326274 0.3097356327487930.279536411079867A A A 0.48290454449717 0.388211400181747 0.318038235687611A A A LNCV6_128562_PI430048170 mRNA
CTACGTAACTTGCGAATCTGTTTACCCTCACTTGCAAATAAAATAAGTGCAAATAAAGCA NM_152418 RefSeq chr8 - 87870742 87874068 DCAF4L2 138009 DDB1 and CUL4 associated factor 4-like 2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129607_PI430048170 0.0222366206821358 0.3816395532499240.505630814781942 1.21122738723566 1.16456736913496 A A A 1.93622477049957 2.88407033407208 2.15425547315421 A P A LNCV6_129607_PI430048170 mRNA
CCGTGAAATAGGTGAGATAAATTAAAAGATACTTAATTCCCGCCTTATGCCTCAGTCTAT NM_002362 RefSeq chrX + 151916236 151925170 MAGEA4 4103 "melanoma antigen family A4, transcript variant 2"
GO:0005515|GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128531_PI430048170 0.4444501367856681.44765012120538 2.12736314803195 0.6061525545306691.74391366292025 A A A 0.4236306968534331.68967108187135 0.860908120698879A A A LNCV6_128531_PI430048170 mRNA
GCTCTACTACAGTAAATGACTGTAAAATTGTCAGTGGCTTACAACAACGTATCTTTTTCG NM_001993 RefSeq chr1 - 94529175 94541857 F3 2152 "coagulation factor III (thromboplastin, tissue factor), transcript variant 1"
GO:0005515|GO:0051897|GO:0030335|GO:0004896|GO:0005886|GO:0009986|GO:0006919|GO:0019221|GO:0002543|GO:0002020|GO:0005615|GO:0045766|GO:0031233|GO:0050927|GO:0031012|GO:0005543|GO:0001938|GO:0007596|GO:0002541|GO:0007598|GO:0010641|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128628_PI430048170 0.33298660155658 1.28525527729469 0.421420987087023 1.23051814570177 0.555556381139688A A A 0.3966585722979940.446427666581735 0.413749319018862A A A LNCV6_128628_PI430048170 mRNA
ATTATCTCAGAGAGAAGCGACTACTATAATCAGCTGAAGCAGAAAGGCGTCAAAGTGCCC NM_152492 RefSeq chr1 + 3752400 3771645 CCDC27 148870 coiled-coil domain containing 27 NA . NA - . NA

NA NA NA NA NA NA NA NA
LNCV6_128330_PI430048170 0.000961739241463527 2.40697131103681 8.98565449777949
9.14791324914993 9.0865446432407 P P P 7.92269321393937 7.85438958665179
7.63002765721964 P P P LNCV6_128330_PI430048170 mRNA
AAGTCCTGACCTTTGTTCTCTTGACGGAATAAAAGCTTGCTTATCCTTATACTTACCAAA NM_018381 RefSeq chr19
+ 10086118 10093252 C19orf66 55337 chromosome 19 open reading frame 66 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128667_PI430048170 0.00190984927953206 6.02021268348906 4.04174485302478
4.89615436465944 4.64939693073498 P P P 1.5537835826844 2.40900471741546
1.84948792255889 A P A LNCV6_128667_PI430048170 mRNA
CTGTCTTGGCTTTCATGTTATTAAACGTATGCATGTGAAGAAAGGGTGTTTTTCTGTTTT NM_004233 RefSeq chr6 +
14117633 14136917 CD83 9308 "CD83 molecule, transcript variant 1"
GO:0014070|GO:0007165|GO:0032733|GO:0005886|GO:0032743|GO:0005887|GO:0043372|GO:0006959|GO:0032
713|GO:0006952|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130490_PI430048170 0.221630922872385 2.91189946240505 0.37591354397194
2.78016298704876 1.47309773353858 A A A 0.307527266273723 0.307738559586681
0.359210164722672 A A A LNCV6_130490_PI430048170 mRNA
ATTTTAGAGCCAAGATGCAAGGAGTTTATGGGCATTATGACACTCGGCTGCTTGCCAACA NM_198491 RefSeq chr16
- 85098351 85112508 FAM92B 339145 "family with sequence similarity 92, member B" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_101203_PI430048170 0.397458257004555 0.8461759168936 3.99704380664105
4.23597897344202 3.7037631489064 P P P 4.57791488150438 4.10456297183764
3.94968230760418 P P P LNCV6_101203_PI430048170 mRNA
GGGCAATTAGCCATCCCCCTCTGACTTTGGTCATTGTGCTGGTTCTGATATATATTTTTT NM_001280544 RefSeq chr14
- 72661042 72892649 DPF3 8110 "D4, zinc and double PHD fingers, family 3, transcript variant 4"
GO:0008150|GO:0071565|GO:0006355|GO:0008270|GO:0006351|GO:0016568|GO:0007399 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134820_PI430048170 0.625876919111872 1.04912411537482 12.6524302505851
12.4826835260548 12.5971988858049 P P P 12.226696418664 12.6203948814384
12.6458130200368 P P P LNCV6_134820_PI430048170 mRNA
GTCTAGAGTCAGCTTACATCCCTGAGCAGGAAAGTTTACCCATGAAGATTGGTGGGATTT NM_001769 RefSeq chr12
+ 6200315 6238271 CD9 928 CD9 molecule
GO:0005515|GO:0008285|GO:0005886|GO:0006928|GO:0005615|GO:0007338|GO:0016324|GO:0009414|GO:0031
092|GO:0007155|GO:0070062|GO:0032504|GO:0030913|GO:0030168|GO:0031982|GO:0030666|GO:0005178|GO:0
007596|GO:0007420|GO:0007342|GO:0005887|GO:0014003|GO:0002576|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140974_PI430048170 0.470808857440331 2.22521507283526 0.284030469013647
2.93505825183286 2.90174405393656 A P P 0.832438810344621 1.41370572809947 1.5348844245902
A A A LNCV6_140974_PI430048170 mRNA
TGACCTAAGGGAATGTCTGGTTACCTCCTAGTTATACAAGCAAAATCTGCATAGTATGTA NM_152701 RefSeq chr7
+ 48171459 48647495 ABCA13 154664 "ATP-binding cassette, sub-family A (ABC1), member 13"
GO:0005215|GO:0008152|GO:0006810|GO:0016021|GO:0016887|GO:0005524 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135065_PI430048170 0.166737778341591 0.693822053018232 4.49691873880253
5.22577633557774 5.12394300645622 P P P 5.64971130026158 5.73896333484797
5.04989123081588 P P P LNCV6_135065_PI430048170 mRNA
CTAGTAACCATCTTGCATCGTCTTAGTCTCCCCATTAAATAAACTTTTCCTACAAACTAA NM_018343 RefSeq chr5
- 97160866 97183301 RIOK2 55781 "RIO kinase 2, transcript variant 1"
GO:0004674|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139582_PI430048170 0.1073688998073821.05697943386135 0.416623771771586
0.3311995350168570.318172955159861A A A 0.2599435695994060.314326703679862
0.253095889869534A A A LNCV6_139582_PI430048170 mRNA
GTAGGTGTTTAACAGTGTTATTTTGCCACTGGTAATGTGTAAACTGTGAGTGATTTACAA NM_001037582 RefSeq
chr4 - 82629536 82798857 SCD5 79966 "stearoyl-CoA desaturase 5, transcript variant 1"
GO:0005506|GO:0004768|GO:0005789|GO:0006633|GO:0016021|GO:0055114 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_89802_PI430048170 0.0857575603538502 0.71847978059805 4.77542758817307
4.64232544797984 5.21376706694712 P P P 5.1913449772461 5.35520701061679
5.55633514362222 P P P LNCV6_89802_PI430048170 mRNA
CCGTACAAGATTTATTAGGCAGCTTATTGTTCCGAATGTAAAGAGTGGAGCTTTAAGTAA NM_001271769 RefSeq
chr5 - 78002325 78294755 AP3B1 8546 "adaptor-related protein complex 3, beta 1 subunit,
transcript variant 2"
GO:0048490|GO:0005794|GO:0019903|GO:0032438|GO:0030123|GO:0005765|GO:0006886|GO:0030665|GO:0030
742|GO:0016020|GO:0051138|GO:0007596|GO:0006622|GO:0048007|GO:0008089 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139831_PI430048170 0.4998404595398591.0726555232373 0.347725157977447
0.3552824821259620.689733022172269A A A 0.39777576849285 0.339049394945947
0.378819735213985A A A LNCV6_139831_PI430048170 mRNA
ACTGGAGAACCTTGAGATCTACACTTTCCTGTCGAAAAAGTGCCTGAAGAAGCTCTCTAG NM_001142306 RefSeq
chr5 - 179641543 179645046 C5orf60 NA chromosome 5 open reading frame 60 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131221_PI430048170 0.2166610850566320.6355998192451291.66566442574117
0.2790719313098160.322487444341163A A A 1.65667376956773 1.30803607788538
1.69557741973444 A A A LNCV6_131221_PI430048170 mRNA
GATTGCCTTAGAGACTGAAAAATATACGCTTTTATAGGCCGGGGTTTTAGTTCATTTGAC NM_014505 RefSeq chr12
+ 70366281 70434292 KCNMB4 27345 potassium channel subfamily M regulatory beta subunit 4
GO:0005515|GO:0005513|GO:0005886|GO:0046928|GO:0007268|GO:0015459|GO:0019228|GO:0019229|GO:0005
887|GO:0007596|GO:0008076|GO:0001508|GO:0006813|GO:0015269|GO:0071805 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138665_PI430048170 0.0615229929045031.26438091597063 7.14685442875978
7.15673182706696 7.26865755162714 P P P 6.70840793749806 7.04330020747437
6.78681586396153 P P P LNCV6_138665_PI430048170 mRNA
AAGTGTCTGACACCTCCAGAATCCATTCCCAAGAAGTGCCTCTGGTCCCACTAGCACCTG NM_000512 RefSeq chr16
- 88813733 88856966 GALNS 2588 galactosamine (N-acetyl)-6-sulfatase
GO:0043890|GO:0003943|GO:0005975|GO:0042340|GO:0009405|GO:0044281|GO:0008484|GO:0030203|GO:0046
872|GO:0070062|GO:0043202|GO:0042339 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135467_PI430048170 0.0931715416398460.9244105826025820.302533467416817
0.3029436692079670.291888238264227A A A 0.47987621420261 0.403208086075429
0.351595653272963A A A LNCV6_135467_PI430048170 mRNA
TGACTTCTCTGATCTGTCTTGGTCGTTTGTGTTATAAAACCAAAGTTCTCTACAGACTTT NM_001190468 RefSeq chr5
- 37812676 37835827 GDNF 2668 "glial cell derived neurotrophic factor, transcript variant 3"
GO:0001656|GO:0008344|GO:0001658|GO:0001755|GO:0001759|GO:0060676|GO:0031175|GO:0042803|GO:0051
584|GO:0043524|GO:0007411|GO:0045944|GO:2001240|GO:0001941|GO:0048255|GO:0090190|GO:0043066|GO:0
005102|GO:0072107|GO:0005576|GO:0060688|GO:0030432|GO:0072108|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126798_PI430048170 0.4520755478074611.36126509962421 4.28063642159754
3.08188579026287 3.24175869288581 P P P 3.21679569618433 2.61252959059408
3.58902583442983 P P P LNCV6_126798_PI430048170 mRNA

TTAGAGATGAGAGAAGTAGGGAGCTTATCATTATTTAGTCTGATCAGACAATATCTTCAC NM_001286588 RefSeq
chr6 + 143060841 143190602 AIG1 51390 "androgen-induced 1, transcript variant 3"
GO:0005515|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129363_PI430048170 0.1135365819128370.6930926869598157.42397685703317
7.20623604768818 7.51466382683394 P P P 7.57507201278884 7.82182637502695
8.26551081552278 P P P LNCV6_129363_PI430048170 mRNA
TTCAGTTATCTCCAGAGCCATTTCACCCTTTAGAGTGAGTCACATGCAGGGAGTGTGAAT NM_001297742 RefSeq
chr11 - 13387995 13440279 BTBD10 84280 "BTB (POZ) domain containing 10, transcript variant 1"
GO:0005737|GO:0044342|GO:0005730|GO:0005654|GO:0005634|GO:0042327 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_79191_PI430048170 0.0841711498197751.20024256259973 11.4994601703284 11.3113798377676
11.3901022129893 P P P 10.9465403165372 11.2330754680064 11.2198249667811 P P P
LNCV6_79191_PI430048170 mRNA
TCACTGCCATACAGGTTTTCCAATACACAAGTGCTAGAAAATACACACAATTCCCCAATG NM_001243749 RefSeq
chr7 - 135165779 135170826 C7orf49 78996 "chromosome 7 open reading frame 49, transcript variant
2" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141653_PI430048170 0.00547247297267362 1.4849601897615 9.61907224027922
9.77022658627119 9.77294474580298 P P P 9.13395163311876 9.17658258197329
9.14540938719878 P P P LNCV6_141653_PI430048170 mRNA
CAGCTGACTTGCAAACTCTTCTAAGGCCACTTAGATTTTCTTTTTCAAGTTTGGGTTGTG NM_138358RefSeq chr19
+ 10928747 10930240 C19orf52 90580 chromosome 19 open reading frame 52 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128409_PI430048170 0.8856840444979141.00260467830767 0.439859445390559
0.4544251840923490.389384719676194A A A 0.4455949975707980.403762899012185
0.423553789722587A A A LNCV6_128409_PI430048170 mRNA
GGTTTTAATGTTATATCTGATGCTGCTATATCCACTGTCCAACGGAGTTAGACGAAAAAA NM_033131RefSeq chr1
+ 228007021 228061271 WNT3A 89780 "wingless-type MMTV integration site family, member 3A"
GO:0005515|GO:0071300|GO:0045599|GO:0090263|GO:0048843|GO:0030879|GO:0005110|GO:0005615|GO:0001
947|GO:0005109|GO:0007411|GO:0030198|GO:0061184|GO:0048018|GO:0048337|GO:0042472|GO:0010387|GO:0
009986|GO:0005796|GO:0019904|GO:0003713|GO:0021874|GO:0001701|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144339_PI430048170 0.6923679890777811.27820867179624 0.380518347494984
1.76968810846196 0.394119894126049A A A 0.3046002486157110.941115953927933
0.640738911420159A A A LNCV6_144339_PI430048170 mRNA
TCGCTCAGGCTTTAGTGACTATATGACACAACCACGGAGAAATAAACCTTGTTAAGACAA NM_174952RefSeq chr4
- 97558873 98143240 STPG2 285555 sperm-tail PG-rich repeat containing 2 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_133270_PI430048170 0.000183737527401871 0.3522377214568079.48406604433936
9.4281897543209 9.21241333512443 P P P 10.7768162745186 11.0197365425252
10.8473425412686 P P P LNCV6_133270_PI430048170 mRNA
CCAGAGAAGCTGGAAGCCTGCCGAAAACAGGAGCAAATGGCGTTTTATAAATTATTTTTT NM_213647RefSeq chr5
+ 177086871 177098142 FGFR4 2264 "fibroblast growth factor receptor 4, transcript variant 3"
GO:0030133|GO:0005515|GO:0008286|GO:2000188|GO:0008284|GO:0005886|GO:0005783|GO:2000573|GO:0001
759|GO:0010715|GO:0061144|GO:0005737|GO:0046777|GO:0007173|GO:0070857|GO:0005911|GO:0070374|GO:0
008201|GO:0005007|GO:0048011|GO:0005794|GO:0017134|GO:0048015|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135379_PI430048170 0.8613563218187850.9749771006729977.31815803972021
7.17876277003878 7.55024810379997 P P P 7.18245742337537 7.32526032565354
7.63590575218559 P P P LNCV6_135379_PI430048170 mRNA

CATGTTACCTCTTCATACACTCCTATAACTGTGGCATTGCAAAAAATAAAAATAACCACC NM_144609 RefSeq chr17 - 44677436 44689797 CCDC43 124808 "coiled-coil domain containing 43, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141729_PI430048170 0.298532754265678 1.02873681790654 0.298397042903227 0.276483246082277 0.372670587091478 A A A 0.287361000586205 0.263111087044812 0.276125695942772 A A A LNCV6_141729_PI430048170 mRNA
CTTATTCCAACCCCAGGATCAGAGAAGATTCTTTACCTGCAGTAACTGACACATTTCCAA NM_001161630 RefSeq chr11 + 95025257 95027596 KDM4E NA lysine (K)-specific demethylase 4E NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138578_PI430048170 0.00378741835159404 1.92853074391305 6.74249558479335 6.61966192445084 6.9171091975853 P P P 5.57533507433728 5.89998937457814 5.94916701443501 P P P LNCV6_138578_PI430048170 mRNA
GGAAGAGAAGACAAAACGAGTCTTTCATTCGGTGTGAACTTTTCTCTTTAATTTTAACTG NM_001134 RefSeq chr4 + 73436218 73455785 AFP 174 alpha-fetoprotein GO:0005737|GO:0042448|GO:0006810|GO:0001542|GO:0060395|GO:0005615|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135154_PI430048170 0.347431785217237 0.342719303454451 0.502054393981726 0.529349214307625 0.426651747676889 A A A 3.17235597720194 0.441598210708578 0.920061281454207 P A A LNCV6_135154_PI430048170 mRNA
CGGTGACTGTATTACATGTTGTTATAGAAAACTGATTTTAGAGTTCTGATCGTTCAAGAG NM_001253849 RefSeq chr1 - 117143586 117203836 VTCN1 79679 "V-set domain containing T cell activation inhibitor 1, transcript variant 2" GO:0072643|GO:0050868|GO:0042102|GO:0001562|GO:0005102|GO:0072602|GO:0016021|GO:1900042|GO:0009897|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132927_PI430048170 0.00362534751790739 0.4185606227446 6.11798390595156 5.59389468020649 5.8651395768605 P P P 6.91905786874483 7.22271699120791 7.23076229390793 P P P LNCV6_132927_PI430048170 mRNA
GTGCTTGTGTGTGTGTAATTGAAAAAACTGGGAAATCCTGCTTTGTTGGTAATAAATCAA NM_015110 RefSeq chr9 + 70258961 70354873 SMC5 23137 structural maintenance of chromosomes 5 GO:0005515|GO:0000781|GO:0030054|GO:0030915|GO:0045842|GO:0005634|GO:0006303|GO:0005524|GO:0007067|GO:0000724|GO:0016605|GO:0000722|GO:0005654|GO:0034184|GO:0090398|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129988_PI430048170 0.0193888885855572 0.644855114963148 9.72790139997456 9.67439623820865 9.70877337851815 P P P 10.1512713248441 10.3727437424198 10.4683537031706 P P P LNCV6_129988_PI430048170 mRNA
TGGTCACATGGTTCTATTTAAATAGCCTAATAAACACATCTGGAGCCTGTCTTGAAAAAA NM_018346 RefSeq chr17 + 50478799 50485980 RSAD1 55316 "radical S-adenosyl methionine domain containing 1, transcript variant 1" GO:0005739|GO:0051539|GO:0006779|GO:0046872|GO:0004109|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64463_PI430048170 0.30145358688034 1.14323360048854 9.59816279230845 9.61155282790352 9.90035085667872 P P P 9.30727056997679 9.44887452791706 9.75781719831958 P P P LNCV6_64463_PI430048170 mRNA
TATTGTGGGAAGTCATAACCCACAGATAGATCAACCTAAGAATCCTGGCCCTTCTCCACT NM_003290 RefSeq chr19 + 16076324 16103003 TPM4 7171 "tropomyosin 4, transcript variant Tpm4.2" GO:0001725|GO:0005862|GO:0030049|GO:0005509|GO:0002102|GO:0006928|GO:0003779|GO:0001649|GO:0005829|GO:0031941|GO:0006936|GO:0016020|GO:0030863|GO:0005856|GO:0008307|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135142_PI430048170 0.0274022486850409 0.463434509208144 6.83243602110299 6.15692179564622 6.66020687783869 P P P 7.22076638021975 7.64975615328789

8.06681448274568 P P P LNCV6_135142_PI430048170 mRNA
GTGTCAAGATCATAGAGAATGGTGCTTTTTACTACAGTTAGCACATGCATTTTTAGAAAC NM_002357 RefSeq
chr2 + 69915040 69942944 MXD1 4084 "MAX dimerization protein 1, transcript variant 1"
GO:0003712|GO:0001078|GO:0003700|GO:0008283|GO:0003714|GO:0046983|GO:0007275|GO:0005634|GO:0000
122|GO:0000978|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59626_PI430048170 0.00573245564339265 0.557281252759609 7.49966387816196
7.3188420879824 7.66181288826994 P P P 8.25862036456585 8.35870027879268
8.40982438673285 P P P LNCV6_59626_PI430048170 mRNA
GTCGTGAGAGATCTGAGCTTCACACCCAGTGGCAGTTTGATTTTGGTCTCCGCGTCACGG NM_018639 RefSeq
chr12 - 118032690 118061211 WSB2 55884 "WD repeat and SOCS box containing 2, transcript
variant 2" GO:0035556|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65286_PI430048170 0.0494643139613318 0.711733470463434 6.73557337563493
6.25720647289638 6.45168215042772 P P P 6.98289817119197 6.85841579022396
7.10483616939736 P P P LNCV6_65286_PI430048170 mRNA
CACATATGGATGTATGTTGAAAGTGGATGATGGAGAAATAAAATGTGGTTTTCTTTGGGG NM_024620 RefSeq
chr19 - 58126327 58150781 ZNF329 79673 zinc finger protein 329
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_137706_PI430048170 0.0622034552724721 1.41009796351015 4.71218176697845
4.81867172937035 4.35587269239774 P P P 4.20344054133245 4.05256921003134
4.17843831723799 P P P LNCV6_137706_PI430048170 mRNA
AAAGAGCAATGAACAATGGAAACTTCAGAGAGCTGAAGAAAGGGGGAGGCCTGTGTTCTT NM_030652 RefSeq
chr6_GL000256v2_alt + 3480810 3484492 EGFL8 80864 "EGF-like-domain, multiple 8, transcript variant 1"
GO:0005509|GO:0005576|GO:0001701 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_132471_PI430048170 0.0142239278326873 0.544034265063788 4.240315601551
3.78589958800958 3.93019184842307 P P P 4.61561051124741 5.15430033329761
4.80671071796523 P P P LNCV6_132471_PI430048170 mRNA
GGCTCTAATTCCCCAAACCTGAAACTTCATACCCTGGGATTCTAATACCTATGTCCTGAG NM_019601 RefSeq
chr22 + 24181475 24189106 SUSD2 56241 sushi domain containing 2
GO:0005515|GO:0006955|GO:0005886|GO:0030247|GO:0016021|GO:0006898|GO:0070062|GO:0005044 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_138177_PI430048170 0.331661089656394 2.08596078381021 1.68521409699315
2.53980342248652 0.33153271710137 A A A 0.423402114694062 0.79424713481474
0.893283116027788 A A A LNCV6_138177_PI430048170 mRNA
AGATAATGCATGTAGGGGAAAAGTTTCTCAAGAAGGTGGAAGAGGCAGCAGGACTTGGAT NM_152722 RefSeq
chr11 - 124919249 124936412 HEPACAM 220296 hepatic and glial cell adhesion molecule
GO:0030424|GO:0005737|GO:0005911|GO:0007050|GO:0034613|GO:0016021|GO:0007155|GO:0040008 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_132758_PI430048170 0.0306984864582983 0.807220956839112 9.22766278913149
9.04093433699856 8.99487737946489 P P P 9.46943153606554 9.37525896936199
9.35370688246559 P P P LNCV6_132758_PI430048170 mRNA
CCTTTGTGTCTAATAGCTAAACAAACATGTGAAACGAATAAAAAGTCCCTCATGTCTGGT NM_001003676 RefSeq
chr11 + 46936688 47162247 C11orf49 79096 "chromosome 11 open reading frame 49, transcript
variant 1" GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128273_PI430048170 0.195891931159959 1.11074727487766 7.13079482160639
7.08704500030861 7.33311508849187 P P P 7.01608100095204 6.94392574024989
7.14150874678008 P P P LNCV6_128273_PI430048170 mRNA
GGGCATCACTCAGGATGTGTATAAGATCTTAATATTGACTAGTTTCACATCCAGGTTTCT NM_022761 RefSeq

chr11 + 111879223 111884073 C11orf1 64776 chromosome 11 open reading frame 1
GO:0008150|GO:0003674|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142033_PI430048170 0.0327156081314608 0.582608891941439 6.16033682508164
6.59444561352818 6.71714736073376 P P P 7.376992988841 7.29096711873114
7.19362424722482 P P P LNCV6_142033_PI430048170 mRNA
AAAGCGAGTGTTAGGTTGGTTAGAGGGTTTAATATTTTCTGCAATGGTTTGTAGGAATTT NM_014033 RefSeq
chr12 + 50924750 50932517 METTL7A 25840 methyltransferase like 7A
GO:0005811|GO:0005737|GO:0016020|GO:0005783|GO:0008757|GO:0032259|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137890_PI430048170 0.036337674910306 0.663013662204354 6.62552959685476
6.19285472311759 6.65539247540023 P P P 6.89661734210196 7.09079010654579
7.2838498702882 P P P LNCV6_137890_PI430048170 mRNA
CCCATTCTGTCTTTGACTGCCTCATTCAATAAATAGTTAAAAATGTGGCAACAGGAAAAA NM_001293163 RefSeq
chr7 + 129611701 129757082 NRF1 4899 "nuclear respiratory factor 1, transcript variant 3"
GO:0001666|GO:0006996|GO:0006357|GO:0031100|GO:0044281|GO:0006091|GO:0000978|GO:0006351|GO:0051
593|GO:0001077|GO:0005737|GO:0045944|GO:0051602|GO:0032496|GO:0005654|GO:0007005|GO:0032355|GO:0
044255|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127613_PI430048170 0.0198699259944604 2.24308004510947 4.92801533056757
4.44833274506463 4.40161829390774 P P P 3.28970390864547 3.87124289323589
3.05557404014225 P P P LNCV6_127613_PI430048170 mRNA
AAACTGTGCTCGTGGCGGGATAAGAATTCGGCGGCATGTGTGGTGTACGAGGACATGTCG NM_006137 RefSeq
chr17 - 82314869 82317604 CD7 924 CD7 molecule
GO:0042110|GO:0006955|GO:0048873|GO:0016020|GO:0005886|GO:0004872|GO:0016021|GO:0007169|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114927_PI430048170 0.680845417417215 0.668214894248831 1.56569660141066
0.332399514766428 0.320575424869679 A A A 2.46327944035255 0.431694802978684
0.400207274081135 A A A LNCV6_114927_PI430048170 mRNA
GTAGAAACATTAAACATAGAGAGACCTGAACCATCTCTAAAGATAGTCGAACTGGATGAT NM_001199201 RefSeq
chr3 - 167240288 167380297 ZBBX 79740 "zinc finger, B-box domain containing, transcript variant
1" GO:0005622|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137469_PI430048170 0.0163578593932896 1.66718119270634 6.05866655490799
5.86330465499157 6.0123738354359 P P P 5.48541265777436 5.05513374708724
5.15266673829572 P P P LNCV6_137469_PI430048170 mRNA
GGCGCCTGAGGACTGCAGATCTCCACTGACCTCTTTCCCTAGATTAAGATGGGACCCAGT NM_001171690 RefSeq
chr22 + 37807904 37817176 GCAT 23464 "glycine C-acetyltransferase, transcript variant 1"
GO:0005739|GO:0019518|GO:0006520|GO:0009058|GO:0008890|GO:0030170|GO:0005654 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138211_PI430048170 0.93243434000001 0.996624404475808 0.591396498430655
0.490096513309392 0.373034163944217 A A A 0.419042986614744 0.539880660575808
0.515683524438046 A A A LNCV6_138211_PI430048170 mRNA
AGACAGGAAATGATTTGGCCTGTGGGAGTATGGCAACCCACAGGATTCTGCAATATTAGA NM_002043 RefSeq
chr6 - 89257120 89315299 GABRR2 2570 "gamma-aminobutyric acid (GABA) A receptor, rho 2"
GO:0005230|GO:0030054|GO:0005886|GO:0004890|GO:0019904|GO:0034707|GO:0007268|GO:0007214|GO:0055
085|GO:0005254|GO:0007165|GO:0034220|GO:0005887|GO:0045211|GO:0006810|GO:0007601 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_106664_PI430048170 0.122163510358496 0.369188234230243 0.262207344254181
0.273648526011389 0.303578069985548 A A A 1.11801268870304 2.51217449672441
0.993226178202197 A P A LNCV6_106664_PI430048170 mRNA

GAGTCATTTAAGGCTGCAAGCAGTATTTACAACAGAGGGTACAAGTTCTATCTGAAAAAA NM_001024630 RefSeq chr6 + 45328316 45551082 RUNX2 860 "runt-related transcription factor 2, transcript variant 1" GO:0071773|GO:0005515|GO:0010467|GO:0000790|GO:0008284|GO:0003700|GO:0006367|GO:0045879|GO:0048701|GO:0005737|GO:0002063|GO:0070491|GO:0042475|GO:0048469|GO:0032332|GO:0005667|GO:0019904|GO:0002051|GO:0043425|GO:0030509|GO:0000978|GO:0000979|GO:0005524|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135383_PI430048170 0.80403235588446 1.16344145240015 1.55437486674021 0.415194383834097 0.244557575698329 A A A 0.3683753834712541.02704361527187 0.44378432540169 A A A LNCV6_135383_PI430048170 mRNA
CCTCACTCTATCCCTGAAAACAGTGAATGTTATATGAAGTTTGTTCTCAAGTTCTCTCTA NM_144681 RefSeq chr17 - 8729927 8744836 CCDC42 146849 "coiled-coil domain containing 42, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127699_PI430048170 0.0436699540248177 0.54248581827753 3.53449131225755 3.99415653798223 4.21005280434192 P P P 4.85062975882546 4.78464670984891 4.82962972317678 P P P LNCV6_127699_PI430048170 mRNA
GTGGAAAACATACGGAAAACTAGTCTAGACTTTAAAGAATTGTGATCAGGTCACATTGTT NM_016570 RefSeq chr12 - 29340645 29381210 ERGIC2 51290 ERGIC and golgi 2 GO:0005794|GO:0016020|GO:0033116|GO:0005789|GO:0005730|GO:0016021|GO:0016192|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141009_PI430048170 0.0040291578004418 0.2320207296399633.50348220584931 3.38057010980891 4.12717555586385 P P P 5.57946458723023 5.94113339253275 5.90262027643529 P P P LNCV6_141009_PI430048170 mRNA
CAGCAGACATAACAACAGAGTGTTAGAGACTGGAATAAATATGAATTTGGCTGAAATGTG NM_001008397 RefSeq chr5 + 55160117 55167301 GPX8 493869 glutathione peroxidase 8 (putative) GO:0004602|GO:0004601|GO:0005788|GO:0016021|GO:0000302|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126889_PI430048170 0.0564293825070485 0.7216288187998947.43587496674889 7.39019246340924 7.83688952585551 P P P 7.95648351435563 7.95408344998948 8.1940754755929 P P P LNCV6_126889_PI430048170 mRNA
GCTGGTCTTTACTTTTTGCCAAAATCAACATATAATGAAGAGATGCCTTTGTTTCATGAG NM_003022 RefSeq chrX + 81201803 81298547 SH3BGRL 6451 SH3 domain binding glutamate-rich protein like GO:0017124|GO:0005737|GO:0005070|GO:0009967|GO:0005634|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106913_PI430048170 0.1897025476864833.75494385221199 0.5180402239703153.1924768100637 2.36842134362704 A P A 0.4100092502088770.49806326241777 0.536197991583242 A A A LNCV6_106913_PI430048170 mRNA
TTCTCGTTCACTCCCAAACCCAAGTGTCCAAGGCTCCAGTCCTAGGAGAACAGTCCCTGG NM_001711 RefSeq chrX + 153494888 153509546 BGN 633 biglycan GO:0030133|GO:0019800|GO:0009986|GO:0005796|GO:0005975|GO:0050840|GO:0005578|GO:0005576|GO:0044281|GO:0005539|GO:0042383|GO:0031012|GO:0030208|GO:0030207|GO:0008150|GO:0030206|GO:0001974|GO:0030198|GO:0009405|GO:0030204|GO:0030203|GO:0070062|GO:0043202|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132347_PI430048170 0.83370047496321 0.8744695155935160.351945532617028 0.3812669424858981.36789744146429 A A A 1.72303366428821 0.393323203047059 0.362522068900891 A A A LNCV6_132347_PI430048170 mRNA
GAAGTTCGCATATATTATGATTACACTGATGTGTAGGCCTTTTATTGTTTGTTGGAATCG NM_023915 RefSeq chr3 - 151294085 151316848 GPR87 53836 G protein-coupled receptor 87 GO:0008150|GO:0007186|GO:0045028|GO:0005887|GO:0035589|GO:0007194 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137724_PI430048170 0.1963304156749331.22024476357028 6.61090996749546
6.68963384001018 6.78718825942511 P P P 6.7175868429733 6.21219986356569
6.24449941591744 P P P LNCV6_137724_PI430048170 mRNA
TTTTCTTTGGGGGTGGAAAAGGAAAACAATTCAAGCTGAGAAAAGTATTCTCAAAGATGC NM_004360RefSeq chr16
+ 68737291 68835541 CDH1 999 "cadherin 1, type 1, E-cadherin (epithelial)"
GO:0060576|GO:0005515|GO:0005802|GO:0030054|GO:0008013|GO:0007605|GO:0050680|GO:0016342|GO:0042
993|GO:2000008|GO:0031175|GO:0016339|GO:0016337|GO:0001948|GO:0070830|GO:0030198|GO:0051260|GO:0
050839|GO:0070062|GO:0071285|GO:0022408|GO:0045295|GO:0009986|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135041_PI430048170 0.1629055151340491.93559088004367 2.90592183733345 4.2152115992796
3.04819993760085 A P P 2.52635698793526 2.96360041591671 2.06346963568451 A P A
LNCV6_135041_PI430048170 mRNA
ATCAATTTGTGGAAGCTCGTGTGTCTTCTCAACTGATAAACCATACGTTCCCTAAGCAAA NM_001076680 RefSeq
chr17 - 27878313 27893383 LYRM9 201229 LYR motif containing 9 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_88924_PI430048170 0.00681007726776307 0.4348927001087175.06763441493956
5.65019878959986 5.52663350622759 P P P 6.377518301426 6.80686679207238
6.69326814377445 P P P LNCV6_88924_PI430048170 mRNA
AGAATCCTCACTGAGCTCCCAGTCCAGAGAGAAGCCAGACAATTAAAACAGTAATGACAANM_001040715 RefSeq
chr16 - 67175601 67183980 KIAA0895L 653319 KIAA0895-like NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136051_PI430048170 0.00241473007019812 0.4904008141037365.12802003742019
5.06332201884477 5.30356706739176 P P P 6.02379951361315 6.15029896333303
6.39113252377389 P P P LNCV6_136051_PI430048170 mRNA
GTTGGTACTAGCCATTAACTTAAAGGTGGTGGGAAAAAAGCACATACTTTAAACATGTAT NM_019030RefSeq chr5
- 55256244 55307693 DHX29 54505 DEAH (Asp-Glu-Ala-His) box polypeptide 29
GO:0005739|GO:0004004|GO:0006396|GO:0016282|GO:0003743|GO:0005634|GO:0043024|GO:0005524|GO:0006
413 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145331_PI430048170 0.1625429895472920.4329458631661772.30806899789375
0.4257903991200752.60384774398053 A A A 2.66374336448799 3.23096008609577 3.6844335187122
A P P LNCV6_145331_PI430048170 mRNA
CTCTTGTACCTGGTGTGTCTTTATTTCAGTAGGTATTCTTTTATGTGCTTTAGTAAGTCT NM_001193552 RefSeq chr19
- 36743477 36772814 ZNF850 342892 "zinc finger protein 850, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137366_PI430048170 0.00808503722410515 2.94937429904884 2.27118764763446
1.70020997840866 2.26811800203412 A A A 0.2698039741912570.242892814331879
0.987424197762461 A A A LNCV6_137366_PI430048170 mRNA
GCAGGGAGCACTTATACTTTTTCCTAATGTCTGTATAACAAATTTCTATGCAAGTACATG NM_001146037 RefSeq
chr18 + 45726952 45752520 SLC14A1 6563 "solute carrier family 14 (urea transporter), member 1
(Kidd blood group), transcript variant 4"
GO:0016323|GO:0005886|GO:0005887|GO:0005372|GO:0015265|GO:0015204|GO:0006833|GO:0071918|GO:0055
085|GO:0015840 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134809_PI430048170 0.35624346929684 0.7172048303154150.44378432540169
0.4369483717257230.377799347978069 A A A 1.48571336260375 0.491353901610734
0.474442446562873 A A A LNCV6_134809_PI430048170 mRNA
TACAACCTACACAACTGTAGAACAATAAACAGAAACCAGCAGACAGCGGAGCATAAAAAA NM_001145132
RefSeq chr5 + 157671552 157680154 C5orf52 100190949 chromosome 5 open reading frame 52 NA .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_144241_PI430048170 0.9521724427601310.9469286123282491.40759666971823 1.0263313581033
2.01841133199215 A A A 1.98255714951341 0.6947944826559521.87203409007965 A A A
LNCV6_144241_PI430048170 mRNA
CGTCATCTAGCCACCCAGCGGCAAATCCAAATAAAGGGGACTTCCACCCAGAGTGGGTGA NM_001008269
RefSeq chr3 - 48620841 48621756 TMEM89 440955 transmembrane protein 89
GO:0005634|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140099_PI430048170 0.0434737583301947 0.50845720287261 4.37998246840853
3.94249104669257 4.66942670256318 P P P 4.80479229310851 5.45967969713592
5.62285833147242 P P P LNCV6_140099_PI430048170 mRNA
CCCCAGGGTTTTATCTAGAATACTATGATTAGGTAGTTGAGCACTTTATCTTATACTGTT NM_145018RefSeq chr11
+ 82901694 82934657 DDIAS 220042 DNA damage-induced apoptosis suppressor
GO:0071850|GO:0030097|GO:0034644|GO:0005737|GO:0071345|GO:2000270|GO:0007286|GO:0071447|GO:0006
915|GO:0005634|GO:0071480|GO:0006974 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133869_PI430048170 0.000350575860433113 1.81429051030483 9.59314679329283
9.4018251301393 9.47416979937568 P P P 8.58744775548879 8.72956846119532 8.5752520028062
P P P LNCV6_133869_PI430048170 mRNA
CTGGGGCAGAGGATAGGGAATCTCTTATTAAAACTAACATGAAATATGTGTTGTTTTCAT NM_138961RefSeq chr11
- 124753122 124762327 ESAM 90952 endothelial cell adhesion molecule
GO:0016337|GO:0005912|GO:0005886|GO:0007596|GO:0016021|GO:0005923|GO:0050900|GO:0007156|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75488_PI430048170 0.9109980188950450.9560509839917485.46692207784909 5.5460258554871
5.67642266492463 P P P 5.13515046377806 5.72177830345639 5.92378685592123 P P P
LNCV6_75488_PI430048170 mRNA
AGGCTAGAACCCTTGGAACACAGAAGGAGAACGATATGTGGTACCCCAAATTATCTCTCT NM_006622RefSeq chr5
- 58453982 58460139 PLK2 10769 "polo-like kinase 2, transcript variant 1"
GO:0005515|GO:0007093|GO:0032436|GO:0007265|GO:0060291|GO:0060292|GO:0046599|GO:0032403|GO:0030
425|GO:0032092|GO:0005622|GO:0000082|GO:0048167|GO:0007613|GO:0004871|GO:0061000|GO:0007052|GO:0
043123|GO:0005813|GO:0043066|GO:0032486|GO:0005814|GO:0005524|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_64831_PI430048170 0.00012527098373162 1.31641503522414 13.6647826225386
13.7304016733539 13.7109203054174 P P P 13.2744803186862 13.3214880339691
13.3205788589555 P P P LNCV6_64831_PI430048170 mRNA
TAAAAGGTGCCAGGAGGAGCATGGGTGTGGAAGTCCTGTCAGCCAAGAAATAAAAGTTTA NM_053046RefSeq
chr19 + 40799428 40808441 EGLN2 112398 "egl-9 family hypoxia-inducible factor 2, transcript variant
1"
GO:0005515|GO:0031545|GO:0001666|GO:0045732|GO:0031418|GO:0071456|GO:0061418|GO:0005634|GO:0001
558|GO:0008198|GO:0005829|GO:0043523|GO:0018401|GO:0019826|GO:0016706|GO:0045454|GO:0005654|GO:0
055114|GO:0030520. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62040_PI430048170 0.3330186248118251.21649174996868 3.06723316001305 3.63280840752517
3.42631076363821 P P P 3.27371798215313 2.67274745132646 3.30399503030587 P P P
LNCV6_62040_PI430048170 mRNA
TATGCATTTCATGGTAGCCGCCTAGAAAACTTCCATTCCATTATCCACAATGGCCTGCAC NM_017851RefSeq chr15
- 65258098 65286680 PARP16 54956 "poly (ADP-ribose) polymerase family, member 16"
GO:0005515|GO:0071902|GO:0071782|GO:0005783|GO:0005635|GO:0003950|GO:0030968|GO:0070213|GO:0006
471|GO:0016020|GO:0005789|GO:0060548|GO:0016021|GO:0006987|GO:0019900|GO:0043539 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138818_PI430048170 0.2853571832656540.8575236101908838.33506671698517
8.37339467640761 8.65070892067061 P P P 8.50159976741165 8.55646466999751 8.9455977058887
P P P LNCV6_138818_PI430048170 mRNA

CTTCTAATTTCCAATAGTCCGTGAAAGTTGGGGCTGAAGTACCTAAGTGTGAATGTCTCT NM_007362 RefSeq chr3 - 196935401 196942593 NCBP2 22916 "nuclear cap binding protein subunit 2, 20kDa, transcript variant 1" GO:0005515|GO:0000339|GO:0008380|GO:0006369|GO:0010467|GO:0006368|GO:0006366|GO:0003723|GO:0031124|GO:0005634|GO:0031047|GO:0005829|GO:0005737|GO:0006406|GO:0000184|GO:0000166|GO:0006408|GO:0016032|GO:0000340|GO:0008334|GO:0045292|GO:0006370|GO:0034660|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132185_PI430048170 0.178894610267821 0.913230944858601 0.443955967687662 0.467402960826966 0.311082587826057 A A A 0.659274438259396 0.496307410694775 0.456483236718593 A A A LNCV6_132185_PI430048170 mRNA
GCTCACATAGATATGACTTGGGAAGTGACACCAGTTCTTTTAAAATAAATTTGTATGCTC NM_175611 RefSeq chr21 - 29536932 29939964 GRIK1 2897 "glutamate receptor, ionotropic, kainate 1, transcript variant 2" GO:0030054|GO:0005886|GO:0005234|GO:0007268|GO:0014054|GO:0030425|GO:0034220|GO:0045211|GO:0015277|GO:0006810|GO:0030534|GO:0051966|GO:0051967|GO:0035249|GO:0060079|GO:0007215|GO:0007417|GO:0032230|GO:0007399|GO:0042734|GO:0035235|GO:0032983|GO:0060080|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101112_PI430048170 0.581659808130275 1.47309947737954 2.33604549021727 1.88653245900085 0.358876498935968 A A A 1.21972003448375 0.466385410856093 1.63108968844392 A A A LNCV6_101112_PI430048170 mRNA
CCCCTCTTAGAACTTGACCAAAATAGAAGTAAATTAAAGTTGTACATTGGACACCTGACA NM_178040 RefSeq chr12 + 991207 1495933 ERC1 23085 "ELKS/RAB6-interacting/CAST family member 1, transcript variant epsilon" GO:0005515|GO:0006355|GO:0017137|GO:0007252|GO:0008385|GO:0045202|GO:0007275|GO:0015031|GO:0030165|GO:0043522|GO:0042734|GO:0005737|GO:0051092|GO:0000139|GO:0042147 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132759_PI430048170 0.238163562104553 1.72536599247 1.80445053468219 1.05299255547217 0.395567197469591 A A A 0.501550734737699 0.381655674544349 0.345819583344802 A A A LNCV6_132759_PI430048170 mRNA
TTTCCTTACTGGTGCTGAAAGGAAGGATGGATAACGAGGAGAAAATAAAACTGTGAGGCT NM_018667 RefSeq chr16 - 68358326 68448506 SMPD3 55512 "sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)" GO:0006665|GO:0007049|GO:0006685|GO:0000137|GO:0006687|GO:0005886|GO:0000139|GO:0002244|GO:0004767|GO:0044281|GO:0030072|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127853_PI430048170 0.409078016267197 1.16864804695327 3.7870503560639 3.96518923299894 3.31586412854868 P P P 3.54382375202532 3.53753711744114 3.38173812359015 P P P LNCV6_127853_PI430048170 mRNA
TTTATAAACATTTGGAAGTTTTCTCCCCCATCTTCTTAAGAAGCAGGGGGGCAGGTGGAG NM_182527 RefSeq chr22 + 29720354 29731831 CABP7 164633 calcium binding protein 7 GO:0048471|GO:0005886|GO:0005509|GO:0016021|GO:0032588 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104359_PI430048170 0.0614194959592118 1.21885627785367 13.2410658354115 13.3470469119297 13.3636730209095 P P P 12.9053225035242 12.9822435204721 13.1948759713488 P P P LNCV6_104359_PI430048170 mRNA
CTCTGGGACAGAGCCTCACAGATGATGTCCATGTTTTGTGTGAATGAAACTCAAACACTC NM_017971 RefSeq chr1 - 1401895 1407313 MRPL2055052 mitochondrial ribosomal protein L20 GO:0070124|GO:0005515|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005761|GO:0005743|GO:0019843 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113990_PI430048170 0.400903393480656 0.799584332574508 5.66669406427822 5.16545186421325 4.95663225221681 P P P 5.65085022616348 5.97018655270206 5.1008071092983 P P P LNCV6_113990_PI430048170 mRNA

AGGTGCACGCAAAGTTAATTTACACCCCCCGCGAGATTTCCTCTACATGACAAAGAAAGA NM_182529 RefSeq chr7 - 108562143 108569453 THAP5 168451 "THAP domain containing 5, transcript variant 2" GO:0007049|GO:0005654|GO:0005634|GO:0045786|GO:0002020|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126867_PI430048170 0.0297314628851172 0.9557052790482650.406812557210304 0.3799358588104350.35707245285258 A A A 0.4414427549210390.45938527677958 0.439425800610755 A A A LNCV6_126867_PI430048170 mRNA
CAATGCTGAACCCATTGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAA NM_001001967 RefSeq chr11 + 55773437 55774382 OR5D13 NA "olfactory receptor, family 5, subfamily D, member 13 (gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135538_PI430048170 0.0161824308533285 0.5119595666322945.82110220455418 5.59269437720833 6.14116088388998 P P P 6.96516725633254 6.4586861702629 7.01848915261851 P P P LNCV6_135538_PI430048170 mRNA
TGAGGTCTATGTACCTTAATCTCGTTTCTCCTTACCACAATCTTAAATAGATTTCAGCTGNM_001278624 RefSeq chr4 - 47847232 47914557 NFXL1 152518 "nuclear transcription factor, X-box binding-like 1, transcript variant 3" GO:0001078|GO:0000977|GO:0016020|GO:0006366|GO:0008270|GO:0005634|GO:0016021|GO:0000122 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145467_PI430048170 0.268343081892911 1.02248047964902 0.30669418628676 0.3084569118641520.370998216717974 A A A 0.3099083721843050.29521398562801 0.285637805290009 A A A LNCV6_145467_PI430048170 mRNA
GGTCTTTTTGTGTGCATATGTATATGTTTTGGGGAATGGGGTATTCACTTTTGTTACTCANM_153839 RefSeq chr6 + 47656589 47697797 ADGRF2 NA adhesion G protein-coupled receptor F2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139407_PI430048170 0.55906881471944 0.9745021581477240.421501598612244 0.4094818174050980.250535329566935 A A A 0.3692924470466940.433080339236222 0.396453990978607 A A A LNCV6_139407_PI430048170 mRNA
CTGTATTAAGGTTTATGGCTGCAATAAAAAGCATACTTTCAGACAAACGGGGAATTTCCT NM_021073 RefSeq chr6 - 55755439 55875577 BMP5 653 bone morphogenetic protein 5 GO:0007389|GO:0071676|GO:0008285|GO:0051216|GO:0010719|GO:0010894|GO:0005615|GO:0060395|GO:0030539|GO:0045944|GO:0043408|GO:1900006|GO:0050679|GO:0031988|GO:0010862|GO:0003323|GO:0042981|GO:0005575|GO:0030509|GO:0005160|GO:0005125|GO:0001501|GO:0001503|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142644_PI430048170 0.00193426166875047 1.96454484321157 10.4816443924697 10.7224942018334 10.4209640986678 P P P 9.48033958719859 9.67465031437623 9.55880483867717 P P P LNCV6_142644_PI430048170 mRNA
GACATCACAGCATTTCAGTGTCAGTCACATTTTAAACTGATCAGCCTTTGTATAATGTTT NM_006690 RefSeq chr20 + 35226735 35277001 MMP24 10893 matrix metallopeptidase 24 (membrane-inserted) GO:0097150|GO:0045296|GO:0005509|GO:0005578|GO:0043085|GO:0032588|GO:0005887|GO:0044331|GO:0006508|GO:0010001|GO:0008270|GO:0004222|GO:0008047|GO:0050965|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128804_PI430048170 0.5714121750876470.9903525734304280.325067059743422 0.3343759416436050.375734909217673 A A A 0.3807560417154250.32668069014317 0.369641057567812 A A A LNCV6_128804_PI430048170 mRNA
TAAGTTCACTAAAACCCTGGATTGAAAGTGAAAATTATGTTCCTAGAACAAAATGTACAA NM_001190986 RefSeq chr6 - 49727380 49744437 CRISP3 10321 "cysteine-rich secretory protein 3, transcript variant 2" GO:0003674|GO:0045087|GO:0042581|GO:0005578|GO:0006952|GO:0005576|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129619_PI430048170 0.00123677002296079 1.46447242009568 11.7213395466342 11.7509202068794 11.5902793606736 P P P 11.0630072767891 11.2193622586537

11.1297650155433 P P P LNCV6_129619_PI430048170 mRNA
GTTTAATCTCCTTTTGTGAGTTTGGTGGGGAAGGGAAGGGTATATAGATTGTATTAAAAA NM_001164093 RefSeq
chr12 + 6724282 6731875 COPS7A 50813 "COP9 signalosome subunit 7A, transcript variant 1"
GO:0005737|GO:0008180|GO:0010388|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128874_PI430048170 0.0258835648907789 0.703990870099698 2.58050583171497
2.54431317907037 2.87800692084666 A A A 3.25715638944067 2.97288080469946
3.29469249591571 P P P LNCV6_128874_PI430048170 mRNA
CCTCCTAGGCTTATCCCTAAAAATGCTCGCTCAGAGAATTAATTATAAACTTGTTTTGTT NM_001126328 RefSeq
chr4 - 53460269 53591586 LNX1 84708 "ligand of numb-protein X 1, E3 ubiquitin protein ligase, transcript variant 1"
GO:0005515|GO:0005737|GO:0004842|GO:0042787|GO:0016874|GO:0051260|GO:0008270|GO:0030165 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58125_PI430048170 0.00406727505207267 0.392154293436848 6.79736329482909
6.71318231775091 6.9241904670336 P P P 7.92048525767677 8.13864776504271
8.39567564901506 P P P LNCV6_58125_PI430048170 mRNA
GGAAGTATTGTTATCCCTAGCATGAGTGTAATGGTGATATGAAAAACTTTGTCTTGTCAT NM_015423 RefSeq chr11
+ 106077564 106098692 AASDHPPT 60496 aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase
GO:0005515|GO:0000287|GO:0015939|GO:0009059|GO:0006766|GO:0006767|GO:0044281|GO:0008897|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131011_PI430048170 0.991391903971539 1.00932521439334 4.27823075292713
4.30457200460891 4.84086023510137 P P P 4.3532016498092 4.74548170533446
4.31705776061372 P P P LNCV6_131011_PI430048170 mRNA
CTTGATTCATTTGCATATGCATTAATTAAACTGAAACCAAGACAGCGGCTCCCTACTAAA NM_173811 RefSeq chr11
- 46603305 46617227 HARBI1 283254 harbinger transposase derived 1
GO:0005813|GO:0005737|GO:0004518|GO:0090305|GO:0005634|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135839_PI430048170 0.757539786892668 1.20116006839017 0.255456620751278
1.60075651751615 0.402969516365214 A A A 0.367939643847584 0.409124414629804
1.00092447125981 A A A LNCV6_135839_PI430048170 mRNA
GAGGAAACTAAGGGCAAACAGTTCGTTACACTTACGGGAATCTTATTTCCCTCTCTAGGG NM_024583 RefSeq chr2
+ 174395728 174429575 SCRN3 79634 "secernin 3, transcript variant 1"
GO:0006508|GO:0006887|GO:0016805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137339_PI430048170 0.101579681417478 0.506782371234452 6.15727383022429
5.14795130319921 4.81271546892342 P P P 6.75853668640829 6.35622992555975
6.24893066024721 P P P LNCV6_137339_PI430048170 mRNA
AACAATTAAAAGAAGAGCTGGGAGATGCTGCTGCTATCATGCGAATCACTGCTGACATGA NM_006576 RefSeq chr12
- 57797375 57816069 AVIL 10677 advillin
GO:0043005|GO:0030424|GO:0005737|GO:0060271|GO:0010976|GO:0007010|GO:0003779|GO:0042995|GO:0015629|GO:0051693|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142225_PI430048170 0.00199958964508465 2.2800331038832 9.83668161962296
10.099142789353 9.95950769539897 P P P 8.76818460052137 8.82613065959361
8.74459617118875 P P P LNCV6_142225_PI430048170 mRNA
TGCACTCACAGGATCCTGAGCTGCACTTACCTGTGAGAGTCTTCAAACTTTTAAACCTTG NM_002872 RefSeq chr22
- 37225260 37244299 RAC2 5880 "ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)"
GO:0008284|GO:0005886|GO:0007264|GO:0005884|GO:0010810|GO:0045453|GO:0003924|GO:0060263|GO:0005635|GO:0005829|GO:0010592|GO:0007411|GO:0010310|GO:0007015|GO:0070062|GO:0051056|GO:0030168|GO:0005525|GO:0030027|GO:0071593|GO:0006184|GO:0007165|GO:0007186|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_142074_PI430048170 0.11240824570546 0.7669357965059180.261018053397341
0.2862942043173740.343838595519019A A A 0.3922062164750950.837789749806138
0.77203568421655 A A A LNCV6_142074_PI430048170 mRNA
GTGGGAGGCAGATTTCCAAAGAGTTAATCCAAAATAAAATTAATCTGTCATTGATTGCCT NM_001099334 RefSeq
chr2 - 208165346 208190049 C2orf80 389073 chromosome 2 open reading frame 80 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142347_PI430048170 0.00823481700529244 0.6028765781439421 0.9189969933466
11.0309936366321 11.1991429937496 P P P 11.7333017272736 11.6052724668978 11.987981805235
P P P LNCV6_142347_PI430048170 mRNA
ACAGCTTCAGTGTATAAATGCATGAGTATTCTTTCTGTTCTGTTTTGTGCTCTCTTGTAC NM_152284 RefSeq chr8 +
81732452 81759513 CHMP4C 92421 charged multivesicular body protein 4C
GO:0005515|GO:0032466|GO:0006997|GO:0019058|GO:0030496|GO:0010824|GO:0015031|GO:0042803|GO:0005
829|GO:0009838|GO:0050792|GO:0000920|GO:0007034|GO:0031902|GO:0016197|GO:0061024|GO:0016032|GO:0
007080|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131577_PI430048170 0.4403427794377750.9871148925762730.367209825215951
0.3726046580837070.356243433519238A A A 0.4159693595954230.349459566826191
0.386038911883856A A A LNCV6_131577_PI430048170 mRNA
TTATTAACTCTGGGATCTTAAAGGTCGACGTGGACTGCTGCGAGAAGGATTTGTGCAATG NM_001130478 RefSeq
chr8 - 143157913 143160636 LY6H 4062 "lymphocyte antigen 6 complex, locus H, transcript variant
2" GO:0005886|GO:0009887|GO:0031225|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142888_PI430048170 0.2785170169618510.7749822400639164.63437642197731 5.1941711884826
4.79216272373335 P P P 5.54195425720789 4.79428233506209 5.34700190643334 P P P
LNCV6_142888_PI430048170 mRNA
GTGGTGATTAAATCTTGGTTACAACATCCTGGGAAGTTTCCTGAACAACTGTAAAATAAT NM_001256487 RefSeq
chr3 - 121663198 121749767 GOLGB1 2804 "golgin B1, transcript variant 3"
GO:0005515|GO:0005801|GO:0005793|GO:0005794|GO:0016020|GO:0005795|GO:0000139|GO:0007030|GO:0016
021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142290_PI430048170 0.15045592608084 0.7673700851296236.66047559347817
6.47072071511029 6.31722747863576 P P P 6.51307076693372 7.00929597661024
7.03513523132319 P P P LNCV6_142290_PI430048170 mRNA
TGGGGAACCCTAAACCCAACTCTGTTGATGTGAAAAATGCAGTGAAAAATATTGACGAAA NM_014849 RefSeq chr1
- 149903319 149917882 SV2A 9900 "synaptic vesicle glycoprotein 2A, transcript variant 1"
GO:0048786|GO:0043005|GO:0031594|GO:0005886|GO:0019901|GO:0005783|GO:0022857|GO:0006874|GO:0055
085|GO:0008021|GO:0005737|GO:0005911|GO:0006836|GO:0009405|GO:0004872|GO:0030672|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137767_PI430048170 0.1659706911862970.8329902808600098.55034001628221
8.44946886474274 8.78217220290133 P P P 8.65426104615069 8.8496739098086
9.06071772504354 P P P LNCV6_137767_PI430048170 mRNA
GTTTGCTTTTTTACAATCATGTGGACACAAGCATAAGTAAAGAAAATTTGTCAACCAGGC NM_002887 RefSeq chr5
+ 168486457 168519304 RARS 5917 arginyl-tRNA synthetase
GO:0005515|GO:0010467|GO:0000049|GO:0004814|GO:0005524|GO:0017101|GO:0005829|GO:0006418|GO:0005
739|GO:0005737|GO:0034618|GO:0016020|GO:0006420|GO:0005654|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141400_PI430048170 0.0348530454018821 1.52018856431676 7.64195526928627
7.78049427415381 7.73247589137683 P P P 7.34330358440773 6.88184162162964
7.08317276084806 P P P LNCV6_141400_PI430048170 mRNA
ATCTTCTGTACTTCACTCCAAGGTACATTTGCTTACTGACAGCATTTTTGTTAAAACTGT NM_001297665 RefSeq chr1
- 51287257 51322268 TTC39A 22996 "tetratricopeptide repeat domain 39A, transcript variant 6"

GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133829_PI430048170 0.1064533201008260.7136575534077526.22853586248678
5.73116201199914 6.10394003890968 P P P 6.43573998083171 6.23741725408712
6.83121148325833 P P P LNCV6_133829_PI430048170 mRNA
CGGTTGTTGCTAGTATAAAGTAATTTGTGTGGCAGTTTGTACTGTGCTGAGTTTTTAAAA NM_014804RefSeq chr17
- 6578324 6640927 KIAA0753 9851 KIAA0753 GO:0005813|GO:0005737 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_98757_PI430048170 0.5881176684682190.9646347552267170.5195449238184740.504319873786636
0.271321693517158 A A A 0.4075396593697660.5568433414830880.495907117495121 A A A
LNCV6_98757_PI430048170 mRNA
CTGTCATTTTTGACCACATTTCCAGAAGGAAGACTTAAGTACCAACATGTTAATTTCCTA NM_001206997 RefSeq
chr4 + 80335719 80963756 C4orf22 255119 "chromosome 4 open reading frame 22, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129637_PI430048170 0.2157576633216691.58910397397597 2.20014554970956
3.33285675385999 2.7149583168583 A P A 2.65037220605149 1.59200343646665 2.0254507299464
P A A LNCV6_129637_PI430048170 mRNA
TACTCTGCTAAGTTCTGGGGATGAGGAAATTAATAAAGGTACAGTCTTGCCTTCAAAAAA NM_018404RefSeq chr17
+ 30921735 30959193 ADAP2 55803 ArfGAP with dual PH domains 2
GO:0005515|GO:0005886|GO:0043325|GO:0005547|GO:0005546|GO:0005740|GO:0043547|GO:0007507|GO:0008
060|GO:0005737|GO:0043533|GO:0032312|GO:0008270|GO:0030674 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128250_PI430048170 0.1012890205214290.8215774513662921 3.7519106486843
13.4567498612912 13.4127519583595 P P P 13.9515550431602 13.8484966143257
13.6834619870774 P P P LNCV6_128250_PI430048170 mRNA
TTGGCCTATAATGTTAAAAGAAAGCAGGAAGGTGGGTAAATAAAAATCTTGGTGCCTGGA NM_001161766 RefSeq
chr20 - 34280264 34311802 AHCY 191 "adenosylhomocysteinase, transcript variant 2"
GO:0043005|GO:0042470|GO:0001666|GO:0002439|GO:0006805|GO:0007584|GO:0005634|GO:0019510|GO:0044
281|GO:0032259|GO:0042802|GO:0005829|GO:0004013|GO:0034641|GO:0005737|GO:0042745|GO:0000096|GO:0
071268|GO:0030554|GO:0006730|GO:0033353|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131583_PI430048170 0.0779210460500077 0.6833120769959874.7787857492509
4.26072186188647 4.82615235910207 P P P 5.08851308033358 5.26638427872923
5.21828139375486 P P P LNCV6_131583_PI430048170 mRNA
GCTCCATGGTGAGAGCACAGCAACTCATTTATATATATATATATAGGCTTTGTTGATGAA NM_032832RefSeq chr6
- 149818757 149864344 LRP11 84918 low density lipoprotein receptor-related protein 11 GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101895_PI430048170 0.4066551986451331.55761062233021 1.79242379779133
0.4146151786670660.402163870257455 A A A 0.3906269681914080.370873268583452
0.404866436835023 A A A LNCV6_101895_PI430048170 mRNA
TGTGGCAATACAGTAGTTATTAAGCCAGCAGAGCAAACACCACTCAGTGCACTCTACATG NM_001206897 RefSeq
chr15 - 57953423 58065923 ALDH1A2 8854 "aldehyde dehydrogenase 1 family, member A2,
transcript variant 4"
GO:0048471|GO:0008284|GO:0008285|GO:0001758|GO:0071300|GO:0030324|GO:0033189|GO:0021983|GO:0016
918|GO:0009954|GO:0009952|GO:0005829|GO:0031076|GO:0005737|GO:0014032|GO:0042574|GO:0042573|GO:0
006776|GO:0030182|GO:0042572|GO:0034097|GO:0032355|GO:0035799|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130313_PI430048170 0.0035964532240233 0.5973792608966178.99694098834714
8.75497393882555 8.88127408124928 P P P 9.44586868793332 9.65955710256283
9.75098397159513 P P P LNCV6_130313_PI430048170 mRNA

CTCGTGGCAACAAGGCTATGTTCTGTTAGGAGTTACCTTAAACTGTGTAAAAATATTTTT NM_001201338 RefSeq chr19 + 5623034 5668478 SAFB 6294 "scaffold attachment factor B, transcript variant 1" GO:0005515|GO:0006325|GO:0001047|GO:0005634|GO:0006351|GO:0003690|GO:0000166|GO:0003682|GO:0045944|GO:0005654|GO:0042445|GO:0040007|GO:0030520 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_132128_PI430048170 0.74498795939152 0.9321139223955491 0.818082020419 10.9231644115473 11.1029966169371 P P P 10.6478243005264 11.0958123642229 11.336938299519 P P P LNCV6_132128_PI430048170 mRNA
ACTTGTCCTGGTTCATCTTAGTTAATGTGTTCTTTGCCAAGGTGATCTAAGTTGCCTACC NM_014176 RefSeq chr1 - 202331656 202341966 UBE2T 29089 ubiquitin-conjugating enzyme E2T GO:0035519|GO:0085020|GO:0004842|GO:0006513|GO:0016874|GO:0005634|GO:0044314|GO:0005524|GO:0006974|GO:0051865|GO:0070534|GO:0005737|GO:0006281|GO:0070979|GO:0019787|GO:0003682|GO:0005654|GO:0070936|GO:0031625. NA - . NA NA NA NA NA NA NA NA NA LNCV6_132019_PI430048170 0.0175422520548241 0.7087620776998791 3.009800047712 13.0811138679839 13.202781311662 P P P 13.4558613886766 13.5420483953296 13.7733514733736 P P P LNCV6_132019_PI430048170 mRNA
TGCCCAGATTTTGATGTAGTCTAATTGACATCCTTCTCTTCCCAACTTTTGTGTGATCTT NM_181716 RefSeq chr17 - 16342533 16353498 CENPV 201161 centromere protein V GO:0016846|GO:0031508|GO:0032467|GO:0001667|GO:0005634|GO:0051233|GO:0034508|GO:0003674|GO:0005737|GO:0007067|GO:0015630|GO:0000777|GO:0000776|GO:0005654|GO:0051301|GO:0033044 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_139679_PI430048170 0.6757487605835131 .06283368344409 6.52677083799731 6.10017067025776 6.35120904853454 P P P 5.91962190330107 6.19890129476416 6.55644441151112 P P P LNCV6_139679_PI430048170 mRNA
CAGGGCTATTTTGGGACCTACAAATAAATGTGATTCCCAGCAGCTTCAATTTTTGATATT NM_001164440 RefSeq chr5 + 10564322 10657816 ANKRD33B 651746 ankyrin repeat domain 33B NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_129717_PI430048170 0.38303401761579 1.3796724867967 1.30916046795538 0.2857282163099651 .37973896399166 A A A 0.2918506455429120.281322106418818 1.08828522586706 A A A LNCV6_129717_PI430048170 mRNA
TGGGGATGGAAGTGCCCTCAATAAGCTGGGGAGAGAGGACATTTATAAACAATTATATCT NM_001286947 RefSeq chr9 - 110322460 110337884 TXNDC8 NA "thioredoxin domain containing 8 (spermatozoa), transcript variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_133923_PI430048170 0.35361413665908 1.41630126018772 1.77463998065365 0.5575688967490391 .05619020163494 A A A 0.4894691206531710.909390638476426 0.714600001533879A A A LNCV6_133923_PI430048170 mRNA
TTTATTGTCTGAGTCTTTGTTCAGTCCTTGCTTTCCAATAATAAACTCAGGGGGACATGC NM_002457 RefSeq chr11_KI270927v1_alt + 149267 178809 MUC2 4583 "mucin 2, oligomeric mucus/gel-forming" GO:0005515|GO:0030277|GO:0006493|GO:0005796|GO:0070703|GO:0070702|GO:0016266|GO:0044267|GO:0043687. NA - . NA NA NA NA NA NA NA NA NA LNCV6_140096_PI430048170 0.1573721075563730 .9436017751066970 .244551101354191 0.30703817723369 0.296655979025415A A A 0.4419319060229870 .344113106429483 0.310990282453297A A A LNCV6_140096_PI430048170 mRNA
ATTTTCCTGAACATTTGCTTGAAATATTTTGTTAGGGCCTCAAAGACGATACCTGTCTTT NM_175747 RefSeq chr6 - 137492198 137494394 OLIG3 167826 oligodendrocyte transcription factor 3 GO:0021520|GO:0001106|GO:0046983|GO:0005634|GO:0000122|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_140047_PI430048170 0.4187446887991910 .93508823734204 7.6601910918533 7.62500034847144 7.62232568581876 P P P 7.59244981131627 7.69026995026966 7.89846635671934 P P P LNCV6_140047_PI430048170 mRNA

CAGCTATTGGTCTTTCCAGCTGTTATAATCTAAAGTATTCTTATGATCTGTGTAAGCTCT NM_005443 RefSeq chr4 - 107613665 107720263 PAPSS1 9061 3'-phosphoadenosine 5'-phosphosulfate synthase 1
GO:0006805|GO:0050427|GO:0050428|GO:0005975|GO:0016779|GO:0044281|GO:0005524|GO:0005829|GO:0016310|GO:0001501|GO:0004020|GO:0000103|GO:0004781|GO:0009405|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134399_PI430048170 0.00169416315977728 0.35744144672009 8.32804640662599 7.84055743819251 8.1904969187562 P P P 9.65043335908071 9.35734764500124 9.81066366118342 P P P LNCV6_134399_PI430048170 mRNA
GCCACTCTAATTTATGGGGGCTTTTGGTTTTTTCCTATTGTACTTTGTATGTAGAATTGT NM_001244710 RefSeq chr2 - 69319768 69387254 GFPT1 2673 "glutamine--fructose-6-phosphate transaminase 1, transcript variant 1"
GO:0004360|GO:0032869|GO:0006042|GO:0006048|GO:0045719|GO:0032922|GO:0030968|GO:0005829|GO:0016051|GO:0006112|GO:0051289|GO:0009744|GO:0030246|GO:0006488|GO:0006987|GO:0044267|GO:0006002|GO:0016597|GO:0070062|GO:0043687|GO:0006541|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140569_PI430048170 0.2168603144971 2.59191471330535 0.343137679011719 2.50322744530084 1.34531944095979 A A A 0.28679665305105 0.27475679968223 0.295587602694611 A A A LNCV6_140569_PI430048170 mRNA
AACACAAGGTGCAAGTGGCATGAAGAAAATGATATTCTCTTCTGTGCTTTAGCTGTTTGC NM_032858 RefSeq chr1 + 166989088 167022212 MAEL 84944 "maelstrom spermatogenic transposon silencer, transcript variant 1"
GO:0010467|GO:0048471|GO:0005634|GO:0007283|GO:0031047|GO:0030154|GO:0005737|GO:0034587|GO:0000785|GO:0043046|GO:0001741|GO:0046620|GO:0043066|GO:0008630|GO:0007275|GO:0000122|GO:0003677|GO:0009566|GO:0007129|GO:0000902|GO:0033391|GO:0030849|GO:0043186|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_41245_PI430048170 0.211508209908299 1.08755449303167 0.631851635341388 0.837700956394259 0.643879734365669 A A A 0.542672099548773 0.617200512934664 0.598644855229327 A A A LNCV6_41245_PI430048170 mRNA
AAACTCTTGGCATTTGGCTTTGCCTTTCTGGACACAGAAGTATTTGGCAAAGCCCAACAC NM_002838 RefSeq chr1_GL383520v2_alt + 280372 363885 PTPRC 5788 "protein tyrosine phosphatase, receptor type, C, transcript variant 1"
GO:0050853|GO:0005515|GO:0050852|GO:0050857|GO:0005886|GO:0030890|GO:0048539|GO:0048864|GO:0035335|GO:0002378|GO:0051607|GO:0006470|GO:0001960|GO:0005001|GO:0002244|GO:0007411|GO:0042100|GO:0006933|GO:0045860|GO:0042102|GO:0051726|GO:0004725|GO:0070062|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132171_PI430048170 0.00267706185842624 1.42410365585291 5.91274817268884 5.83005359748326 5.7270762310048 P P P 5.26704682686418 5.29770438959056 5.37863045573955 P P P LNCV6_132171_PI430048170 mRNA
GAAGGTCAGTAATTCCGACTTTCTCAGCAGTGGTGTCTCTGAATTACTGCAAAGGGTAAA NM_183040 RefSeq chr6 - 15523570 15663058 DTNBP1 84062 "dystrobrevin binding protein 1, transcript variant 2"
GO:0005515|GO:0030424|GO:0033162|GO:0043005|GO:0048490|GO:0030054|GO:0032438|GO:0005634|GO:0014059|GO:0031175|GO:0005829|GO:0030426|GO:0005737|GO:0043197|GO:0045211|GO:0061024|GO:0030672|GO:0031532|GO:0006892|GO:0014069|GO:0010628|GO:0042383|GO:0016528|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133664_PI430048170 0.167337050409999 0.546572511679931 1.89186255624324 0.320968470165073 0.418801265587627 A A A 1.77561135173869 1.71508212976891 2.2672757998971 A A A LNCV6_133664_PI430048170 mRNA
AATGCAGGAAACCAACATGTCATTGACACCTCTCTTCTTTACTTTTCCCCATATCTAATC NM_138333 RefSeq chr9 + 68780047 68783693 FAM122A 116224 family with sequence similarity 122A NA . NA - . NA

NA NA NA NA NA NA NA NA
LNCV6_140814_PI430048170 0.0063555091303096 0.5614129380938057.51944689488243
7.22716569776371 7.52115545834992 P P P 8.44091739502748 8.03259091761777
8.28320760779742 P P P LNCV6_140814_PI430048170 mRNA
CAATGTCCTTCCATAGCATGGGAAGAAGAAAATAAACATCTCCTTTCCAACAGCAAAAAA NM_019008RefSeq chr22
+ 39502229 39518134 MIEF1 54471 "mitochondrial elongation factor 1, transcript variant 1"
GO:0005739|GO:0005515|GO:0008053|GO:0043531|GO:0000266|GO:0090314|GO:0005741|GO:0016021|GO:0090
141|GO:0019003|GO:0042802|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140486_PI430048170 0.26277738048667 1.72623938691978 3.73791529619554
2.37123437074477 2.58087943164803 P A A 2.28159014900147 2.25475900229308
2.18822250218304 A A A LNCV6_140486_PI430048170 mRNA
CTGGCCCCTGCAGGAGTCAGGCCTGGTCTCACGCTCAATAAACTCCGGACTGAAGATGCA NM_148961RefSeq chr2
- 240139028 240140656 OTOS 150677 otospiralin GO:0007605|GO:0005576 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_145317_PI430048170 0.1306550896431110.7242236934378973.67554384800176
3.07471481517886 3.42600430796415 P P P 4.17362450716075 3.57929517770907
3.81948817596645 P P P LNCV6_145317_PI430048170 mRNA
CTTGAAGCTATTCTCCCCTAATTAATATCTCGAGACTGAGCAAAATATCTCATGTAAGAT NM_052883RefSeq chr3
- 126607051 126655124 TXNRD3 114112 "thioredoxin reductase 3, transcript variant 1"
GO:0005783|GO:0050660|GO:0015035|GO:0009055|GO:0004791|GO:0045454|GO:0007275|GO:0005634|GO:0007
283|GO:0030154|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107114_PI430048170 0.7125170847908970.9432210840136493.62912481817035
3.58231999027272 3.24093915830414 P P P 3.25478776998203 3.74671495208546
3.68606176912516 P P P LNCV6_107114_PI430048170 mRNA
AATAAGGAAACAGGGGAGCTGATCACCTTCTATTACTATTGGAAGAAGACCCCCGAAGCA NM_012102RefSeq chr1
- 8352403 8817640 RERE 473 "arginine-glutamic acid dipeptide (RE) repeats, transcript variant 1"
GO:0005515|GO:0006355|GO:0003700|GO:0005634|GO:0007275|GO:0006607|GO:0006351|GO:0008267|GO:0043
565|GO:0000118|GO:0003682|GO:0006338|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127992_PI430048170 0.0107644677496158 0.6386875501498194.43293614140459
4.55761176090988 4.62925295604499 P P P 5.37022735637439 5.15792820834703
5.01681081286485 P P P LNCV6_127992_PI430048170 mRNA
CATAATTGGAAAGGACCTTTGTCTGTTTTTCCTCTTGGGTGCCTTCCAGAACGCATCTCA NM_001261RefSeq chr9
+ 127786025 127790773 CDK9 1025 cyclin-dependent kinase 9
GO:0005515|GO:0071157|GO:0010467|GO:0006368|GO:0006367|GO:0044212|GO:0006366|GO:0008283|GO:0043
231|GO:0005737|GO:0045944|GO:0016032|GO:0007179|GO:0008024|GO:0031056|GO:0005524|GO:0003677|GO:0
008023|GO:0008353|GO:0006351|GO:0050434|GO:0006281|GO:0004672|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129477_PI430048170 0.0216948573967922 0.5157485611523897.01790242702992
6.93871404311131 7.40743447548238 P P P 7.78554750035058 7.9584920097997
8.44681429767217 P P P LNCV6_129477_PI430048170 mRNA
CCAGTGACTCCTAATCTTTTTCAAGTTAAGACACCTTACCATTGCTTATTTGGTTTTATG NM_001184717 RefSeq chr3
+ 156674925 156706768 TIPARP 25976 "TCDD-inducible poly(ADP-ribose) polymerase, transcript variant 1"
GO:0030097|GO:0006807|GO:0045732|GO:0001822|GO:0008209|GO:0048705|GO:0005634|GO:0009791|GO:0046
872|GO:0035326|GO:0003950|GO:0006471|GO:0008210|GO:0008585|GO:0071407|GO:0060325|GO:0048745|GO:0
010629|GO:0060021|GO:0044236|GO:0048008|GO:0001570 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_129127_PI430048170 0.0486019049825873 0.5169025932638047.0313725878178
7.09462825980603 7.54564100817824 P P P 7.69344072546821 8.16418481200333 8.5890697072089
P P P LNCV6_129127_PI430048170 mRNA

ACTGCTTGGGATGTGTTCTTTGGCAGCTTGTGAGATTACTTTACCTAGTGTTTATAAAGT NM_013296RefSeq chr1 + 108876980 108930422 GPSM2 29899 G-protein signaling modulator 2 GO:0005515|GO:0050790|GO:0005737|GO:0007186|GO:0060487|GO:0000132|GO:0045177|GO:0005938|GO:0042802|GO:0030695 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_134837_PI430048170 0.55830675653825 0.8719829330670384.0843714569389 3.65886288151102 3.87490251709376 P P P 4.4926108999304 3.89529017868129 3.74118201475164 P P P LNCV6_134837_PI430048170 mRNA

AGACTGTCTGCTGCAAGCCTGTGTGCTGTATGCCCGTCTGCTGTGGGCCTTCTTCTTCAT NM_198699RefSeq chr21 + 44697171 44698044 KRTAP10-12NA keratin associated protein 10-12 NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_132236_PI430048170 0.000483768632092069 0.34118577670330711.6597527478086 11.8241067766916 12.0155778400701 P P P 13.3040995839297 13.2504359095888 13.5964871803724 P P P LNCV6_132236_PI430048170 mRNA

GTCCTACATGCAAGTACATGTTTTTAATGTTGTCTGTCTTCTGTGCTGTTCCTGTAAGTT NM_002107RefSeq chr1 + 226062706 226072002 H3F3A 3020 "H3 histone, family 3A" GO:0005515|GO:0010467|GO:0046982|GO:0030307|GO:0031492|GO:0005576|GO:0005634|GO:0006336|GO:0000228|GO:0000979|GO:0032776|GO:0043234|GO:0000183|GO:0007596|GO:0045814|GO:0040029|GO:0000788|GO:0000980|GO:0005654|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_139395_PI430048170 0.454062100446857 0.59257095048043 0.375887787835741 0.3481387486845920.402629413592234A A A 0.3059980812047652.01846237211405 0.357261709863388A A A LNCV6_139395_PI430048170 mRNA

TGCAATTGAATGAAGAAGCATTAACGAAAACCAATATTTAAGTACAGTGGACAGCTTAGG NM_174981RefSeq chr21 + 13610176 13641585 POTED 317754 "POTE ankyrin domain family, member D" GO:0005886 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_132704_PI430048170 0.0718887408244640.655135445561906 9.87608921617178 9.92416433265808 10.1448520547871 P P P 10.2806758437046 10.5080530668844 10.92579832991 P P P LNCV6_132704_PI430048170 mRNA

CTCCTTGGGGTTGATAGGAATTTTCTCTTGCTTTCTCAATAAAGTCTCTATTCATCTCAT NM_016548RefSeq chr9 - 86026142 86099595 GOLM1 51280 "golgi membrane protein 1, transcript variant 1" GO:0005515|GO:0006997|GO:0005794|GO:0005887|GO:0005615|GO:0070062|GO:0019216 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_103887_PI430048170 0.70632737402566 1.03167920407207 9.91449409013783 9.84785395014283 10.1032709112939 P P P 9.77863813241826 10.0631531062073 9.886763105519 P P P LNCV6_103887_PI430048170 mRNA

TCTGGAATCTTTGAGACCAAGTTCCAGGTGGACAAAGTCAACTTCCACATGTTTGACGTG NM_080425RefSeq chr20 + 58852980 58911195 GNAS 2778 "GNAS complex locus, transcript variant 2" GO:0005515|GO:0007608|GO:0009306|GO:0051216|GO:0005159|GO:0007606|GO:0031224|GO:0031698|GO:0048701|GO:0048589|GO:0001894|GO:0006833|GO:0070062|GO:0071107|GO:0007565|GO:0031683|GO:0006184|GO:0060348|GO:0001958|GO:0032320|GO:0071870|GO:0007189|GO:0030133|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_132314_PI430048170 0.5108525457589690.860468345940746 5.87974852215087 5.55981375279709 5.76039484018531 P P P 5.49741373390271 6.28489071129955 5.9795655469876 P P P LNCV6_132314_PI430048170 mRNA

ACACATACTAGTTGAGAAGGGAAATCAGGGCTAATGAAACAGCTCAACTGTCTGGCAGAG NM_003724RefSeq chr8 - 142657459 142669994 JRK 8629 "Jrk homolog (mouse), transcript variant 1" GO:0005515|GO:0008150|GO:0003674|GO:0005737|GO:0030529|GO:0005634|GO:0005575|GO:0003729|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_145076_PI430048170 0.5834011401186340.75222214289856 2.87222325860977 0.3456722646733131.54091759903213 A A A 0.9733514262018252.64839894406783

2.81930153706598 A P P LNCV6_145076_PI430048170 mRNA
GACATTAGAGTCAAATCAGCCTTGACCTGAGTTTGTTGATTTAACATTGATTTCAAGCAT NM_001277120 RefSeq
chr19 - 52838531 52857649 ZNF468 90333 "zinc finger protein 468, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139961_PI430048170 0.0159926823750871 0.784692575587741 6.54098517172903
6.41282645363938 6.63616991871481 P P P 6.82301167116349 6.82231616337277
6.99571624352192 P P P LNCV6_139961_PI430048170 mRNA
GCTGAGAAGGGGACAAGGTTTACGTCATGTACTAAAATAATAGACAATGTATCGCTTTAA NM_032772 RefSeq chr10
- 75397829 75401894 ZNF503 84858 "zinc finger protein 503, transcript variant 1"
GO:0061351|GO:0006355|GO:0008285|GO:0010629|GO:0070315|GO:0005634|GO:0003676|GO:0046872|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70798_PI430048170 0.0761607956444061.30143167763391 8.83110790268097 8.93034640687791
9.09157660748702 P P P 8.72266285603428 8.30659050470907 8.66157153417638 P P P
LNCV6_70798_PI430048170 mRNA
ATAGAAGGCATGGTCAAAGATTTGATTAACCGGATGGACTATGTGGAGATCAACATCGAC NM_005336 RefSeq chr2
- 241227266 241315700 HDLBP 3069 "high density lipoprotein binding protein, transcript variant 1"
GO:0005515|GO:0005737|GO:0005886|GO:0034364|GO:0006869|GO:0005634|GO:0008289|GO:0008203 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140470_PI430048170 0.0397827347207411.29396537923699 4.69238637248609
4.93307686270801 4.84681513261197 P P P 4.39589201938894 4.31439587244964
4.63700861147385 P P P LNCV6_140470_PI430048170 mRNA
AGGGATCTTTCAAATGGATAGTGAGTTGCCTTTTCCTATAGGTGACAATCAGAGATTTAA NM_001166012 RefSeq
chr18 - 35251057 35290245 ZSCAN30 100101467 "zinc finger and SCAN domain containing 30,
transcript variant 1" GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132238_PI430048170 0.7126974084359350.9065717182264445.35169375155937
5.16801029033491 5.46878704365585 P P P 4.94707161215822 5.65300602015489
5.71106184959948 P P P LNCV6_132238_PI430048170 mRNA
CACGTTTGAAGTTAGCAACTGCTTAAAGTTATGCCCCATTAAAATTGCTTTCTCAAAAGT NM_005324 RefSeq chr17
- 75776433 75779935 H3F3B NA "H3 histone, family 3B (H3.3B)" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137509_PI430048170 0.7061560627238341.02343340769706 0.275750042808217
0.2831718993981320.48578178952869 A A A 0.337561763323051 0.289137318694822
0.327297803083777 A A A LNCV6_137509_PI430048170 mRNA
GTTCACAAATGTAGCAACAGCTCACATGACTGAGTAGGTAGAAAATGTGAAATAAATCTC NM_001288985 RefSeq
chr17 - 68867286 68955392 ABCA8 10351 "ATP-binding cassette, sub-family A (ABC1), member 8,
transcript variant 1"
GO:0005886|GO:0008152|GO:0006810|GO:0005743|GO:0042626|GO:0016021|GO:0055085|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136768_PI430048170 0.2108061574575920.77632526243418 8.33031764693991
7.78869093019541 7.77195620653093 P P P 8.63808578716545 8.30073638894461
8.06199503293115 P P P LNCV6_136768_PI430048170 mRNA
GGCTTCCCCTCCCTCGTTTTCAAAGATAAATGAAATAAACGTGCGCGGACTGTCAAAAAA NM_005029 RefSeq chr10
- 102230188 102241474 PITX3 5309 paired-like homeodomain 3
GO:0006355|GO:0070306|GO:0005634|GO:0000978|GO:0006351|GO:0001077|GO:0002089|GO:0002088|GO:0048
666|GO:0071542|GO:0045944|GO:0009887|GO:0007626|GO:0030901|GO:0045893 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134383_PI430048170 0.8565351860543230.9950512338009990.277341548655545

0.3106835730061980.400710059064042A A A 0.3672493447694430.329615263361471
0.315687425522753A A A LNCV6_134383_PI430048170 mRNA
CCATAAAAGTGAAAGAGTTGTATTGGAGCTCAGTGCTGTAAAACACCCGCGACAACAAGC NM_020877RefSeq chr17
+ 7717353 7833744 DNAH2 146754 "dynein, axonemal, heavy chain 2, transcript variant 1"
GO:0001539|GO:0008152|GO:0005874|GO:0005858|GO:0003777|GO:0016887|GO:0005524|GO:0007018 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143925_PI430048170 0.0147836209771443 0.3840022630060452.94719980014715
2.8079643319836 3.18201800840067 A A P 3.9751865740337 4.25545113178559
4.76178700849579 P P P LNCV6_143925_PI430048170 mRNA
GGTCTAGACCATCAGATAGATTTATTCAAATATTTTCTGGGAACCTTTATGGGTAGAACA NM_001039697 RefSeq
chr9 + 15422783 15461629 SNAPC36619 "small nuclear RNA activating complex, polypeptide 3,
50kDa"
GO:0010467|GO:0006355|GO:0009301|GO:0006366|GO:0005730|GO:0005654|GO:0005634|GO:0006383|GO:0003
677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132091_PI430048170 0.5452248370303664.223834874313 0.358854636802636
4.46400895022682 0.590156060707004A P A 1.71911742042822 0.379266066437944
0.369695026039227A A A LNCV6_132091_PI430048170 mRNA
ACAGAAGCATAAGCCGCCATGTCACTGTGTGAATATAGTCTGAGCACAAACTTGAAAAAA NM_001304388 RefSeq
chr15 - 23439385 23447243 GOLGA6L2 283685 golgin A6 family-like 2 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_133976_PI430048170 0.00310116848738173 0.5092438917301245.01811299306484
4.95517545938305 5.25796599923417 P P P 6.00807019155773 6.01811236234023
6.14000066658155 P P P LNCV6_133976_PI430048170 mRNA
AGTTATAAAAGCATAATTGCTTTATATTTTGGATCATTTTTTACTGGGGGCGGACTTGGG NM_172373RefSeq chr13
- 40931918 41019372 ELF1 1997 "E74-like factor 1 (ets domain transcription factor), transcript variant
1"
GO:0005515|GO:0003700|GO:0006366|GO:0000981|GO:0005634|GO:0000978|GO:0001817|GO:0030154|GO:0050
860|GO:0001077|GO:0045944|GO:0005654|GO:0045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128386_PI430048170 0.00654369845818638 0.4497713209677926.11577325165035
5.93854688225704 6.49980143651255 P P P 7.0938793289671 7.33943464878661
7.59389341070396 P P P LNCV6_128386_PI430048170 mRNA
AAATGTGATCTGGCTGTGTTTGTCTTCTGTACAAAGCCTGAAGTGCTTATGGTTTTTTGG NM_001024948 RefSeq
chr1 + 93448130 93554661 FNBP1L 54874 "formin binding protein 1-like, transcript variant 1"
GO:0072583|GO:0005515|GO:0005886|GO:0097320|GO:0006914|GO:0051491|GO:0006900|GO:0008289|GO:0016
050|GO:0042384|GO:0005737|GO:0030050|GO:0016023|GO:0005856|GO:0005938|GO:0010324|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140642_PI430048170 0.3176714471243251.21951675365683 6.10599595785242
6.35366148610238 6.02893309506411 P P P 6.32667114451841 5.62074264508295
5.57329918212162 P P P LNCV6_140642_PI430048170 mRNA
CTCCTGTCTAGGTGCCCCTGATGACGGGATGCTCTTTAAATAATAAAGATGGTTTTGATT NM_182983RefSeq chr19
+ 35040505 35066573 HPN 3249 "hepsin, transcript variant 1"
GO:0005515|GO:0097066|GO:0005886|GO:0004252|GO:0030307|GO:0008360|GO:0050680|GO:0010719|GO:0010
693|GO:0005911|GO:0006508|GO:0043025|GO:0090103|GO:2000611|GO:0071805|GO:0070008|GO:0034769|GO:0
070062|GO:0042632|GO:0031965|GO:0043066|GO:0009986|GO:0097195|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130063_PI430048170 0.1075984150189460.5318061558469632.3989926261913
2.44102898030807 2.21605472499899 A A A 3.79772100472882 2.75033937787479
3.04087791013164 P P P LNCV6_130063_PI430048170 mRNA
GAAAATCTGGATCTCCCTTGAGCAGTTTTCTATAAAGTCTGCAATAATCTCAGATACTCT NM_001195528 RefSeq

chr11 + 75240904 75243704 TPBGL NA trophoblast glycoprotein-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143806_PI430048170 0.576603973035415 0.961816967690188 0.439195983408292 0.29307552857582 0.346506121507204 A A A 0.56222548835766 0.326789069176862 0.350219430820934 A A A LNCV6_143806_PI430048170 mRNA TCTGCTAGAATGATAAATGTCATGGTGGTCTATAACTCCAAATAAACAATGCAACGTTCC NM_002944 RefSeq chr6 - 117288366 117425855 ROS1 6098 "ROS proto-oncogene 1, receptor tyrosine kinase" GO:0005515|GO:0032006|GO:0005886|GO:0008283|GO:0019903|GO:0018108|GO:0007283|GO:0005524|GO:0030154|GO:0002066|GO:0016020|GO:0010629|GO:0016049|GO:0006468|GO:0016021|GO:0004713|GO:0004714|GO:0070372|GO:0007169|GO:0010966 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135016_PI430048170 0.222196289696987 1.02939022464633 0.406548642728447 0.342972854063008 0.375088192456477 A A A 0.301076594288155 0.322092168073228 0.375740283407462 A A A LNCV6_135016_PI430048170 mRNA CATTTAGCCTTGCGAGAGTCAGATACATTTGGAACACTATCTCCTAGGTCATATCAAGAA NM_001287252 RefSeq chr5 + 132747444 132754403 CCNI2 NA "cyclin I family, member 2, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144624_PI430048170 0.234222773788031 0.554550098128136 2.59627190665173 2.45730281682955 0.588497737871438 A A A 2.87585131157511 3.10012021128895 2.92681987621047 P P P LNCV6_144624_PI430048170 mRNA GCTGCACATTCTTCCAAAATGATCCTTAGCACAATCTATTGTATGATGGAATGAATAGAA NM_031418 RefSeq chr11 + 26332130 26663289 ANO3 63982 anoctamin 3 GO:0034220|GO:0005886|GO:0017128|GO:0006869|GO:0005229|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128540_PI430048170 0.0101194681027193 0.496969095324317 11.7192290117954 11.6104652293775 11.4272119113217 P P P 12.272615740888 12.7318060351951 12.7454744376554 P P P LNCV6_128540_PI430048170 mRNA TTGGCCATACCACAGAGCTAGATTGCCCAGGTCTGGGCTGAATAAAACAAGGTTTTTCTA NM_005576 RefSeq chr15 + 73926447 73952137 LOXL1 4016 lysyl oxidase-like 1 GO:0031012|GO:0016641|GO:0001669|GO:0030198|GO:0005507|GO:0032496|GO:0005576|GO:0018277|GO:0005615|GO:0055114|GO:0035904|GO:0005604 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126733_PI430048170 0.0852465055977432 0.537338440420952 11.8951342021463 11.139107369724 10.7570750713103 P P P 12.4326788211697 12.3204019385046 11.9155560679072 P P P LNCV6_126733_PI430048170 mRNA AGCCCTTCTCCCTGCACTCATGAAACCCCAATAAATATCCTCATTGACAACCAGAAAAAA NM_001178126 RefSeq chr22 + 22887779 22895833 IGLL5 100423062 "immunoglobulin lambda-like polypeptide 5, transcript variant 1" GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132613_PI430048170 0.244415706151228 1.06713430650707 0.59523963556471 0.759339373281201 0.584431170517412 A A A 0.53268084999055 0.567478113814029 0.564113101340149 A A A LNCV6_132613_PI430048170 mRNA GCTATGTGGTTCAGTTAATCAGTGTGCCAAGATTCTAATAAAGTTGACCTTGGGTTCTGT NM_001080451 RefSeq chr14 - 94442463 94452785 SERPINA11 256394 "serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 11" GO:0010951|GO:0004867|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140786_PI430048170 0.886212293909183 1.01898850899614 8.7495539325234 8.69364759648175 9.11568103571671 P P P 8.66859056645479 8.68181923878908 9.11775005510365 P P P LNCV6_140786_PI430048170 mRNA CTTTTCCCAGTAATAATGACTGCTGTGTTGGATTCCTTCTGCAAATAAAAGTGTATACAT NM_006430 RefSeq chr2 - 61868126 61888671 CCT4 10575 "chaperonin containing TCP1, subunit 4 (delta), transcript variant 1"

GO:0005515|GO:0042470|GO:0005813|GO:0005832|GO:0005874|GO:0007339|GO:0005524|GO:0044297|GO:0005829|GO:0005737|GO:0006457|GO:0051084|GO:0002199|GO:0005654|GO:0051082|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70617_PI430048170 0.0527772107936803 0.738794526788393 6.27933855961362 6.34888513097307 6.67268003059898 P P P 6.81346583705062 6.96534142473538 6.85936703680233 P P P LNCV6_70617_PI430048170 mRNA TGAGTGGATATGACCAAGTTCTGCAGGAAAACTCCAGTGACTATCAGTCAAACCTTGCTT NM_019597 RefSeq chrX + 101408132 101414140 HNRNPH2 3188 "heterogeneous nuclear ribonucleoprotein H2 (H'), transcript variant 1"
GO:0008380|GO:0010467|GO:0016020|GO:0000166|GO:0000398|GO:0030529|GO:0003723|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137443_PI430048170 0.00411676940971792 0.250818650602571 3.52861962667624 3.68359727730861 3.46720714823083 P P P 5.17807812701666 5.67629910041289 5.75466943390517 P P P LNCV6_137443_PI430048170 mRNA GCCAAATGCAGCATGATACCTCTATCAGGAAAATTAAATTTTAACACAGCCACCAAATAT NM_138786 RefSeq chr3 - 149318497 149333761 TM4SF18 116441 "transmembrane 4 L six family member 18, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142255_PI430048170 0.442276776527144 0.964381515664789 13.8299905732438 13.8216180469042 13.7930283179911 P P P 13.764698843919 13.9440897600381 13.8872974200501 P P P LNCV6_142255_PI430048170 mRNA TCTCCACCCTTCGCTGTGTCCCGTATCTCAATAAAGAGAATCTGCTCTCTTCAGAAAAAA NM_001004333 RefSeq chr17 + 7012416 7014533 RNASEK 440400 "ribonuclease, RNase K, transcript variant 1"
GO:0009303|GO:0016021|GO:0005575|GO:0004521 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131955_PI430048170 0.00131615617710043 1.60194769755888 7.15299004384407 7.2336078539612 7.1342758818983 P P P 6.43052977211604 6.44596449032446 6.60063462883531 P P P LNCV6_131955_PI430048170 mRNA CAGTCACTCTTGCACTATTCCTTCTCCAAGCCAGAAACCACATTTAATTTCATAAATAAA NM_032995 RefSeq chr2 + 130917396 131047253 ARHGEF4 50649 "Rho guanine nucleotide exchange factor (GEF) 4, transcript variant 2"
GO:0005515|GO:0051056|GO:0048011|GO:0043065|GO:0007264|GO:0019904|GO:0030032|GO:0032587|GO:0097190|GO:0032855|GO:0005829|GO:0005085|GO:0043547|GO:0046847|GO:0030676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140888_PI430048170 0.410536217712283 0.851206683482173 4.10072596684784 4.49551449468571 4.99513307355186 P P P 4.71991665149795 4.68120851493742 5.00514416966285 P P P LNCV6_140888_PI430048170 mRNA GCCATAACAAATTGTTTGGTCCAAAATGAAAGCTATATTCAGAAGGTTTGCACCTCAAAA NM_001093755 RefSeq chr5 + 65624730 65666127 TRAPPC13 80006 "trafficking protein particle complex 13, transcript variant 1" GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125449_PI430048170 0.543586142294318 1.03771706319919 12.7147612462018 12.9208336736301 12.8359724503163 P P P 12.6807493399114 12.8628136804818 12.7694195446549 P P P LNCV6_125449_PI430048170 mRNA CGTGTGCAGGATCAATTGTAGGAGGAAATTTCTTTTTTATTAAAAGCGAATGTGTATCCC NM_032302 RefSeq chr7 - 1567333 1569993 PSMG3 84262 "proteasome (prosome, macropain) assembly chaperone 3, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139794_PI430048170 0.00104549087852697 2.08333728650057 3.90198785140623 3.71608842495551 3.75316788952534 P P P 2.74047277533848 2.57317959270209 2.87219452366866 P P P LNCV6_139794_PI430048170 mRNA TGGCTCTGTCACACTCGAAGCCAGGCTTGATCAATAAACACAATGGTATTCCACGTCAAA NM_032206 RefSeq

chr16 + 57017073 57083524 NLRC5 84166 "NLR family, CARD domain containing 5"
GO:0005515|GO:0005634|GO:0032088|GO:0000979|GO:0005524|GO:0005829|GO:0060335|GO:0005737|GO:0051607|GO:0060339|GO:0045345|GO:0045087|GO:0045944|GO:0060340|GO:0032480|GO:0043549 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140193_PI430048170 0.00244181692904605 0.254213913095189 5.64730937624559 5.41617356868655 5.75354668684261 P P P 7.21358025881821 7.6347891524959 7.84660122989693 P P P LNCV6_140193_PI430048170 mRNA
TGCATATATCACTAGTGCCAAGACATAAAGCGGGGGAAAATATATTTTTACCCAAACATT NM_018243 RefSeq
chr4 + 76949713 77038615 SEPT11 NA septin 11 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_25194_PI430048170 0.00345622375820582 0.67677854295698 10.4200444203542 10.2580985053213 10.2620360241941 P P P 10.9029137004908 10.899469086214 10.8324267060096 P P P LNCV6_25194_PI430048170 mRNA
CCCCATGTTTCTCTCCCTCTGCGTCTTAGCACCTTTCTTCTGTTCAAAGTTTTCTGTAAA NM_003075 RefSeq chr12 - 56161851 56189567 SMARCC2 6601 "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2, transcript variant 1"
GO:0005515|GO:0071565|GO:0000790|GO:0006357|GO:0043044|GO:0003713|GO:0031492|GO:0006325|GO:0000122|GO:0006337|GO:0000978|GO:0071564|GO:0006351|GO:0043234|GO:0016514|GO:0017053|GO:0000980|GO:0005654|GO:0006338|GO:0045893|GO:0045892|GO:0021882 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141786_PI430048170 0.00324165172833724 0.349484261766122 3.00950086400989 2.41867872597457 2.53559970674512 P A A 4.00114033026063 4.06378061136946 4.47223213618083 P P P LNCV6_141786_PI430048170 mRNA
GTCCTCCATATGTGGGCTTAACATATGTACCACTCCATTTTAGAAAAATCTCATTAAATG NM_018061 RefSeq chr1 + 108692309 108701800 PRPF38B 55119 "pre-mRNA processing factor 38B, transcript variant 1"
GO:0008380|GO:0006397|GO:0071011 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95746_PI430048170 0.231027183069159 1.30434351300524 5.2410326355149 5.45183004635997 4.77796898360325 P P P 4.87667082582928 5.02737916008345 4.43251762560467 P P P LNCV6_95746_PI430048170 mRNA
TAAAAATTGCAGATATGCCTTTGCATTCGCCTCTCTCCAGATACCAAAGCACTGTGATTT NM_207408 RefSeq
chr5 + 126631721 126636282 TEX43 NA testis expressed 43 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61129_PI430048170 0.921850971235964 1.022530667631 4.21936628845463 3.71194838492019 3.63530092921328 P P P 3.57369060653322 4.11511427848042 3.8021106517448 P P P LNCV6_61129_PI430048170 mRNA
CCTTGTGGCGTTTTTCTTTCATGTGGAAGTTGGAAGACAAGGTGAAAGGGGCCAAAAGTT NM_001039479 RefSeq
chr14 - 74661251 74713104 AREL1 9870 apoptosis resistant E3 ubiquitin protein ligase 1
GO:0043066|GO:0005737|GO:0004842|GO:0042787|GO:0016874|GO:0006915|GO:0005634|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134666_PI430048170 0.556154303967762 1.0523985698163 7.75308044177159 7.64409469563888 7.89022789247241 P P P 7.59431664077371 7.87528614047777 7.58830375248973 P P P LNCV6_134666_PI430048170 mRNA
TGTCACTTCCGCCATCGTGGTCATCACTTCAGGCATCGCAGCCATCGTGTTGTCACGCTA NM_033504 RefSeq
chr1 - 32894594 32901352 TMEM54 113452 transmembrane protein 54
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106594_PI430048170 0.629454682081546 0.818370551286202 0.441653094286292 0.753402293796677 0.347184838454394 A A A 0.339681818774017 0.389366637705535

1.43221007995342 A A A LNCV6_106594_PI430048170 mRNA
ATAAAGACTGGCGCTTGCAGAGTGGAGTATAAAAAGGAGTTGCTGCCAGTCTTCAGATCA NM_001291006 RefSeq
chr22 + 21045959 21064168 LRRC74B 400891 "leucine rich repeat containing 74B, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138450_PI430048170 0.146618283127276 0.435851893260236 0.468382255341163
2.24590789667064 0.356499837704291 A A A 1.6499551517177 2.47500742682826
3.0525703692576 A P P LNCV6_138450_PI430048170 mRNA
CTTGCTCTTTGATAGCCACCTCCTAGGAATGGAGACAATAAAACTCTGTATTTGCATGTG NM_015313 RefSeq
chr11 + 120336908 120489936 ARHGEF12 23365 "Rho guanine nucleotide exchange factor (GEF)
12, transcript variant 1"
GO:0005515|GO:0051056|GO:0048011|GO:0001664|GO:0043065|GO:0007264|GO:0038032|GO:0097190|GO:0005
829|GO:0005737|GO:0007186|GO:0016020|GO:0007411|GO:0032321|GO:0005089|GO:0070062|GO:0005096 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133966_PI430048170 0.0540955345725777 0.797166049756356 7.66654322479869
7.99027352139293 7.84090881430654 P P P 8.11947039625167 8.12828343267421
8.24576350971733 P P P LNCV6_133966_PI430048170 mRNA
TCAAGTATGTGGTTCATTCTTAGAACCAAGGGAAATACTGCTCCCCCCATTTGCTGACGT NM_001497 RefSeq
chr9 - 33110640 33167358 B4GALT1 2683 "UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase,
polypeptide 1"
GO:0008092|GO:0030057|GO:0060046|GO:0030112|GO:0030879|GO:0031526|GO:0050900|GO:0005615|GO:0042
803|GO:0007219|GO:0003945|GO:0030198|GO:0002064|GO:0030203|GO:0070062|GO:0018279|GO:0032504|GO:0
002526|GO:0005794|GO:0005975|GO:0048487|GO:0004461|GO:0008378|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136021_PI430048170 0.0925079305497925 0.622760662073077 4.74277946641715
4.45004362294092 5.12141719914063 P P P 5.01426913937039 5.50762906426673
5.81181440896818 P P P LNCV6_136021_PI430048170 mRNA
CTCCCATAAAACAGCCTTGGTAATAAAGAAGTTATCACACCAAGACATACCTTTTAGATT NM_194313 RefSeq
chr9 - 34252379 34329200 KIF24 347240 kinesin family member 24
GO:0005515|GO:0008017|GO:0005871|GO:0006996|GO:0005814|GO:0005874|GO:0003777|GO:0005524|GO:0005
829|GO:0043234|GO:0042384|GO:0008152|GO:0016887|GO:0007019|GO:0007018 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_126686_PI430048170 0.436725523220503 1.22283982055364 3.11586020211432
3.87906349990163 3.88982962944355 P P P 3.51330231124648 3.5135061578346
3.07126449775506 P P P LNCV6_126686_PI430048170 mRNA
CAGTAGGAAAACAGGGCTGGCCCTTTTCTTTGGTGATGAACACAAACTGCACCCTTTTTT NM_006961 RefSeq
chr16 - 71474072 71489351 ZNF19 7567 zinc finger protein 19
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_137241_PI430048170 0.037843786830041 0.513919151316881 6.58345309320473
6.12226215763154 6.93548499081876 P P P 7.13503373295084 7.55405861498195
7.85695623487262 P P P LNCV6_137241_PI430048170 mRNA
TTTACCAGGTGTGGACTTAAGTTGCTAGGCTTGCAGTAAGAATTGCCAGCCACTCATTGT NM_015483 RefSeq
chr7 - 32868165 32891856 KBTBD2 25948 kelch repeat and BTB (POZ) domain containing 2 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136800_PI430048170 0.389038683144846 1.49393361389568 0.37695878091952
0.386169912781787 1.62418186112886 A A A 0.331107800643774 0.322917175258838
0.377058763904675 A A A LNCV6_136800_PI430048170 mRNA
CTGTACAATAATATGTATGAACTCAGTTACTAGGGGACTGTATTGTGACATTATCAACCT NM_153456 RefSeq
chr13 + 96090838 96839562 HS6ST3 266722 heparan sulfate 6-O-sulfotransferase 3

GO:0016021|GO:0017095|GO:0015015 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_129265_PI430048170 0.342670848365705 1.27236064545254 6.46455936381103
7.0993983104214 7.27351759920272 P P P 6.9421949462317 6.34008422886105
6.56681375899919 P P P LNCV6_129265_PI430048170 mRNA
TTTTACAATCTGTATCTTTGACAATTCTGGGTGCGAGTGTGAGAGTGTGAGCAGGGCTTG NM_006732 RefSeq
chr19 + 45467994 45475179 FOSB 2354 "FBJ murine osteosarcoma viral oncogene homolog B,
transcript variant 1"
GO:0051412|GO:0007565|GO:0003700|GO:0006366|GO:0042493|GO:0005634|GO:0043278|GO:0000122|GO:0051
591|GO:0003677|GO:0032870|GO:0009612|GO:0043565|GO:0003690|GO:0071277|GO:0032570|GO:0008134 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_3684_PI430048170 0.22949634009211 1.15483218038301 12.0758645075124
12.1144835051715 12.1661412139524 P P P 11.6468236599133 12.0687622143688
11.9855912694919 P P P LNCV6_3684_PI430048170 mRNA
GTTTTATCCCCTGCCTAATGCTGCGAGAAGCACAGAATAAACTTTTTGTCACTCTCTGCG NM_021210 RefSeq
chr17 - 7930344 7931949 TRAPPC1 58485 "trafficking protein particle complex 1, transcript variant 1"
GO:0006888|GO:0017112|GO:0005801|GO:0005794|GO:0030008|GO:0005783|GO:0032851 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_68917_PI430048170 0.611149968163421 0.949249135429189 5.29280929020958
5.76927409639855 5.6906174404114 P P P 5.7388758997972 5.65293018208835
5.62768698562784 P P P LNCV6_68917_PI430048170 mRNA
ATTTTCTTATTCGATGAGGCTACTAAAGCTGATCCACTTTGGGGTGGTCCATCACTTGCA NM_001199691 RefSeq
chr1 + 95117922 95244953 TMEM56-RWDD3 NA TMEM56-RWDD3 readthrough NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_138141_PI430048170 0.0124677007662038 0.51102910828543 10.1691061983239
10.2583196947639 10.6921750710626 P P P 11.1215106377938 11.2642822918714
11.6436728356291 P P P LNCV6_138141_PI430048170 mRNA
CAAACAGTTAAGTCCATTCTCTGGTACTAGCTACAAATTCGGTTTCATATTCTACTTAAC NM_016131 RefSeq chr2
+ 26033859 26137454 RAB10 10890 "RAB10, member RAS oncogene family"
GO:0005802|GO:0009306|GO:0005886|GO:0043001|GO:0003924|GO:0007409|GO:0006886|GO:0006904|GO:0097
051|GO:0000145|GO:0030859|GO:0019882|GO:0016197|GO:0017157|GO:0030670|GO:0061024|GO:0032482|GO:0
016192|GO:0030659|GO:0070062|GO:0032869|GO:0005794|GO:0071782|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129452_PI430048170 0.0193903981532611 1.45041323597112 9.51965869240764
9.85735214050652 9.58387057985679 P P P 9.30980009966298 9.02639687263779
9.01852397209476 P P P LNCV6_129452_PI430048170 mRNA
TAAAATGGGACCTCCGAACCAACCCTGCCCCTCAGAAATGCCCTGCCTATTAAATGAGCT NM_152559 RefSeq
chr7 - 73834590 73842525 WBSCR27 155368 Williams Beuren syndrome chromosome region 27 NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139692_PI430048170 0.632079196775242 0.933752910912945 6.55593031789767
7.08911604254984 7.07628989720109 P P P 6.94911151693158 6.86095508211641
7.24127358067147 P P P LNCV6_139692_PI430048170 mRNA
TCACAGGCTTGGGAAATCCTGTTAGCATGCAGAATAATGTGGTAACTTTGTCAATTTCCC NM_001007794 RefSeq
chr1 + 111139626 111185102 CEPT1 10390 "choline/ethanolamine phosphotransferase 1, transcript
variant 2"
GO:0006629|GO:0006646|GO:0031965|GO:0004307|GO:0044281|GO:0046872|GO:0005789|GO:0004142|GO:0016
021|GO:0006644|GO:0006657|GO:0006656|GO:0046474 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138173_PI430048170 0.171074734980031 1.45536759904104 1.21129509600464

0.412131150013187 1.01522647958901 A A A 0.369259126414626 0.359369921281311
0.40002360456942 A A A LNCV6_138173_PI430048170 mRNA
AGAGACATGAAGGGAGCCCTGAGCAGAGTCATTCATCAGAAGAAAACTTTCTTCTCTCTC NM_003553 RefSeq
chr17 - 3397465 3398410 OR1E1 8387 "olfactory receptor, family 1, subfamily E, member 1"
GO:0050911|GO:0007608|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144032_PI430048170 0.976408769916548 1.06098633264992 0.469488182046677
0.522896573866659 1.59338205884102 A A A 1.11225296698191 0.979567246519421
0.453838522858051 A A A LNCV6_144032_PI430048170 mRNA
ATTGGGAGGCCTTTTGGCAAACAGTGTCTATTTTACAGAGAGGCAAACCAAGCCTCCTTA NM_004210 RefSeq
chr10 + 103493977 103592552 NEURL1 9148 neuralized E3 ubiquitin protein ligase 1
GO:0090129|GO:0004842|GO:0048471|GO:0030054|GO:0008285|GO:0006513|GO:0005886|GO:0016874|GO:0007288|GO:0051491|GO:0045183|GO:0071230|GO:0007219|GO:0043197|GO:0045211|GO:0043204|GO:0060999|GO:0045746|GO:0043065|GO:0045741|GO:0014069|GO:0030317|GO:0006417|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143163_PI430048170 0.63516324619466 1.02095972028798 0.30117362444158
0.292293780618974 0.447186666629343 A A A 0.346510433209334 0.303593558222382
0.305667148720989 A A A LNCV6_143163_PI430048170 mRNA
ATACACACCAGGCCGTCACTTTGGGTTCTGGCATAAGTTCAGAACAATTCAAGTCCATGT NM_001010898 RefSeq
chr1 + 110150509 110202201 SLC6A17 388662 "solute carrier family 6 (neutral amino acid transporter), member 17"
GO:0015804|GO:0015816|GO:0030054|GO:0015820|GO:0005887|GO:0005328|GO:0015824|GO:0006836|GO:0030672|GO:0032328|GO:0055085|GO:0008021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131052_PI430048170 0.0257495951882312 0.614111405441476 5.11817489165443
5.30834479483994 5.63380922404285 P P P 5.81651685243562 6.07605867825899 6.2874764507663
P P P LNCV6_131052_PI430048170 mRNA
CTTCTTTATTTGAACTGTATTATACTCTCAGACCCTCATCCTGCCTAGAAATGAATAAGT NM_177965 RefSeq chr8
- 95244912 95269234 C8orf37 157657 chromosome 8 open reading frame 37
GO:0005737|GO:0030054|GO:0005886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130890_PI430048170 0.0320843578631676 0.637695415102539 7.28553954579636
7.56434234464876 7.83146475448629 P P P 7.99140128577506 8.3090260808743
8.35323645804774 P P P LNCV6_130890_PI430048170 mRNA
CCAGTGACCCTTTTATCCTTTCTAGGCACATTTCTTGTTGTTGTTGTTGTTGCAGTTCCC NM_024665 RefSeq chr3 -
177020753 177197260 TBL1XR1 79718 transducin (beta)-like 1 X-linked receptor 1
GO:0005515|GO:0016575|GO:0044212|GO:0008013|GO:0003714|GO:0006325|GO:0005634|GO:0044281|GO:0000122|GO:0006351|GO:0042393|GO:0047485|GO:0000118|GO:0007219|GO:0045944|GO:0017053|GO:0043161|GO:0005654|GO:0005876|GO:0045893|GO:0060070|GO:0044255 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_144126_PI430048170 0.000777525556576091 0.151640701263467 6.15994320070651
6.27007905786938 5.71684620623075 P P P 8.84013567385949 8.89611626100187
8.61686283316557 P P P LNCV6_144126_PI430048170 mRNA
CCTACAAAGAAAAACACTCCCACTCTTGTCATACCTAATTGTTCCTGCTGTGGTTTGGGG NM_005144 RefSeq chr8
- 22114418 22131052 HR 55806 "hair growth associated, transcript variant 1"
GO:0016604|GO:0006355|GO:0003700|GO:0003714|GO:0016491|GO:0005634|GO:0045892|GO:0003677|GO:0046872|GO:0006351|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136701_PI430048170 0.0328772470419942 1.50612223397618 10.2039662674156
10.6749135824695 10.4752575197748 P P P 10.0713075595096 9.86707761338423
9.65104559021685 P P P LNCV6_136701_PI430048170 mRNA
AAGGAAAAAACAAAACAAAACTCTAAAGGTAAACGCGGTCCTTCTCCCTCTCTCATGTGG NM_000298 RefSeq

chr1_GL383519v1_alt - 94315 106457 PKLR 5313 "pyruvate kinase, liver and RBC, transcript variant 1"
GO:0009408|GO:0044281|GO:0051591|GO:0006096|GO:0005829|GO:0006754|GO:0006006|GO:0033198|GO:0042
866|GO:0004743|GO:0070062|GO:0001666|GO:0032869|GO:0000287|GO:0007584|GO:0005975|GO:0030955|GO:0
005524|GO:0009749|GO:0016310|GO:0006112|GO:0010226|GO:0031325|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145043_PI430048170 0.1442391268899711.19025242875385 9.67977699436026
9.76267890821449 9.95259983381979 P P P 9.32219534441714 9.629912885496
9.67770111607292 P P P LNCV6_145043_PI430048170 mRNA
TTGTCTTCTCTGTGCTGGTCCTTTCTTATGTCCTCATAAAAGCTCAGATGATGGTATCTG NM_001291866 RefSeq chr1
+ 230057788 230282130 GALNT2 2590 "polypeptide N-acetylgalactosaminyltransferase 2, transcript
variant 2"
GO:0048471|GO:0005794|GO:0030145|GO:0005795|GO:0016266|GO:0002378|GO:0004653|GO:0030173|GO:0000
139|GO:0006493|GO:0016020|GO:0018242|GO:0032580|GO:0030246|GO:0018243|GO:0044267|GO:0070062|GO:0
043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138240_PI430048170 0.3757503996581611.20841791053602 5.35765773973352
4.94431795847981 4.85949428475207 P P P 5.1843251299547 4.75931147806338
4.32112898123345 P P P LNCV6_138240_PI430048170 mRNA
TGCTGGCCCTCTTAATTTTGGTGTATGTGCTTCCAAGTATCTAAACCTCCAGTCTGATCT NM_001005353 RefSeq
chr1 + 65147829 65232145 AK4205 "adenylate kinase 4, transcript variant 1"
GO:0046033|GO:0046034|GO:0042493|GO:0004550|GO:0004017|GO:0009142|GO:0005525|GO:0046899|GO:0005
524|GO:0001889|GO:0005739|GO:0006165|GO:0007420|GO:0005759|GO:0046039|GO:0006172|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144610_PI430048170 0.0333469911079455 0.2413099641318170.450016978609609
0.4616044290580550.375259121430187A A A 1.7115377830564 2.46803502346879
2.98819249613731 A A P LNCV6_144610_PI430048170 mRNA
GTGAGTTCTGACAAGAATGAAATTCCACATACAACATAACTGTAAATTGTTGGTAGGTAG NM_206907RefSeq chr5
- 40759378 40798195 PRKAA15562 "protein kinase, AMP-activated, alpha 1 catalytic subunit, transcript
variant 2"
GO:0005515|GO:0006695|GO:0070301|GO:0004679|GO:0047322|GO:0050321|GO:0005622|GO:0031669|GO:0016
055|GO:0045821|GO:0009411|GO:0010332|GO:0008610|GO:0019395|GO:0031588|GO:0009631|GO:0035174|GO:0
046318|GO:0005654|GO:0048511|GO:0004691|GO:0045542|GO:0010508|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137090_PI430048170 0.0593589021712778 0.6357193716930445.25968684136544
5.07945982311998 5.25205378932142 P P P 5.47528850437816 5.98040912216855
6.03944130027527 P P P LNCV6_137090_PI430048170 mRNA
CTGGGCAAATTAACAAATGTTTGTAAACATGAATGTTCAGGAACTACTGATGTACCTCAA NM_152444RefSeq chr14
+ 73851917 73885466 PTGR2 145482 "prostaglandin reductase 2, transcript variant 1"
GO:0036132|GO:0005737|GO:0006693|GO:0047522|GO:0008270|GO:0070062|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126957_PI430048170 0.2845755489080621.04686668648123 0.452262791106271
0.2999305418488550.346826967718102A A A 0.2751564362020040.330683026672607
0.298653428377915A A A LNCV6_126957_PI430048170 mRNA
GCATGTTCTCATTTCCTTATCATACAATTCTTTGAGAGGTATCATTAGCTGCGTCTTATT NM_001290330 RefSeq chr16
+ 88940038 88951524 LOC100129697 NA uncharacterized LOC100129697 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_140988_PI430048170 0.7727137587968231.02494488491739 15.8897203767856
16.0358080620334 16.146172071012 P P P 15.7903407747963 16.0605580974083
16.1058510952792 P P P LNCV6_140988_PI430048170 mRNA
GGCCCCGCTCCCTCTGCTGGCCATGGCCCCCCCGCCCGCGTGCCGGTCCCCGATGTCACC NM_001141936 RefSeq

chr4 + 2042049 2043970 C4orf48 401115 "chromosome 4 open reading frame 48, transcript variant 2" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143350_PI430048170 0.4667845598542961.13041704572854 10.8448703692189
11.3837536952944 11.281153331252 P P P 10.7407833982615 11.1569062902342
11.1018962483355 P P P LNCV6_143350_PI430048170 mRNA
TTATATTGTCCTCCCCTATTTTAAGACGTGAATGTCTCAGCGAGGTGTAAAGTTGTTCGC NM_001124RefSeq chr11
+ 10304979 10307402 ADM 133 adrenomedullin
GO:0005515|GO:0008284|GO:0031700|GO:0008285|GO:2001214|GO:0006701|GO:0060712|GO:0031102|GO:0008
015|GO:0060670|GO:0031100|GO:0030819|GO:0009409|GO:0007267|GO:0005615|GO:0007204|GO:0031623|GO:0
007507|GO:0005737|GO:0048589|GO:0042594|GO:0045906|GO:0045909|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138520_PI430048170 0.0250913106957876 1.68155451707398 5.98919900485176
6.52109409250291 6.18187561832589 P P P 5.64372225336812 5.45041226969281
5.38703333332295 P P P LNCV6_138520_PI430048170 mRNA
TGCAAACTTTTGACGTCCTGATTGCTCCAGGGCCCTCTTCCAACTCAGTTTCTTGTTTTT NM_001301191 RefSeq chr15
- 77613023 77819524 LINGO1 84894 "leucine rich repeat and Ig domain containing 1, transcript variant 5"
GO:0048011|GO:0005154|GO:0005886|GO:0048715|GO:0043491|GO:0021954|GO:0050771|GO:0016021|GO:0050
770|GO:0031175 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74469_PI430048170 0.0635772954526670.64595579120701 3.62487336233449 3.73573950387335
3.21706942527549 P P P 4.33234954229613 3.78038237198462 4.33856038161129 P P P
LNCV6_74469_PI430048170 mRNA
TAAGACCTTACTATGTAGGACCTATTAGGATATTAAAACCCCCATTTCCTCCTATTCCTT NM_001302807 RefSeq
chr4 + 70397881 70410197 PROL1 58503 "proline rich, lacrimal 1, transcript variant 2"
GO:0010951|GO:0004866|GO:0001895|GO:0005576|GO:0030414|GO:0005615|GO:0051930 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138134_PI430048170 0.0141174230851664 0.5901956342743625.2983024239999
5.4249070880446 5.76115666455928 P P P 6.11158606166682 6.1786962190132
6.48815905249929 P P P LNCV6_138134_PI430048170 mRNA
CAGCCACTGTTACCAATTTCATGTGTATTCCTTTAACTCTGTTTTAAAGTAAGTCTCTGA NM_001282931 RefSeq chr19
- 29698885 29715545 C19orf12 83636 "chromosome 19 open reading frame 12, transcript variant 7"
GO:0005739|GO:0031966|GO:0005783|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_58173_PI430048170 0.0274822286792387 1.32512555324375 4.21451431670198
4.49059644270478 4.23014830655497 P P P 4.02844339710239 3.92789882346249
3.76540620640958 P P P LNCV6_58173_PI430048170 mRNA
ATGTACACTACGTTGATAGCCATGACTGGATGGTATATGGACAAGACTTCCATTGCTGTG NM_001077691 RefSeq
chr11 - 111782194 111871281 ALG9 79796 "ALG9, alpha-1,2-mannosyltransferase, transcript variant 3"
GO:0000030|GO:0052926|GO:0016020|GO:0005783|GO:0005789|GO:0016021|GO:0006488|GO:0044267|GO:0052
918|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139481_PI430048170 0.0278102416392294 1.49315307813376 11.3956198163651
11.6673699352505 11.6985549931402 P P P 10.8495540544533 10.8890835914412
11.2685227993263 P P P LNCV6_139481_PI430048170 mRNA
TTCTCAAGCTCTCCAATAAATATGACCACCAAGATGCAGAACTCTTTCAGGACTTCTTTT NM_014463RefSeq chr3
+ 14178727 14198369 LSM3 27258 "LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)"
GO:0006397|GO:0005515|GO:0010467|GO:0000398|GO:0043928|GO:0005634|GO:0071013|GO:0005829|GO:0000
288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128099_PI430048170 0.0365502942904102 1.48426237967099 6.12944692527014
6.40755981491535 6.48964959462767 P P P 5.55965735469664 6.04260125872015

5.69548968160375 P P P LNCV6_128099_PI430048170 mRNA
GCTTCATTCAACATTTTCTATCTAGCTCTTCATGGTGCTGCTCCTGCTATGGTTCCACAGNM_153034RefSeq chr10 -
47365495 47384273 ZNF488 118738 zinc finger protein 488
GO:0005515|GO:0006366|GO:0006357|GO:0048714|GO:0014003|GO:0000981|GO:0005634|GO:0045892|GO:0003
677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111578_PI430048170 0.4586783247842650.85553616911033 0.367300420324512
0.3467850129248740.257791031869997A A A 0.3059074825377120.941293147892929
0.304875816469149A A A LNCV6_111578_PI430048170 mRNA
CAATTTGCCAAGCTCCTGAAGCAGAAGAGGATCACCCTGGGATATACACAGGCCGATGTG NM_001285986 RefSeq
chr6_GL000256v2_alt - 2467752 2470601 POU5F15460 "POU class 5 homeobox 1, transcript
variant 4"
GO:0005515|GO:0010468|GO:0090081|GO:0003700|GO:0044212|GO:0006366|GO:0000981|GO:0005634|GO:0035
413|GO:0060913|GO:0001714|GO:0009653|GO:0005829|GO:0005737|GO:0045944|GO:0090308|GO:0042789|GO:0
035019|GO:0031625|GO:0005667|GO:0006355|GO:0009786|GO:0001824|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136059_PI430048170 0.0148286572114723 0.3401674120012993.73862590176704
3.93854848966518 4.00743637906686 P P P 4.97251046779315 5.5204818095432
5.76278937989545 P P P LNCV6_136059_PI430048170 mRNA
CCTCTACTCAAAGTTAAAACTGACCAAAGTTACTGGCTTTTTACTTTGCTAGAACAACAA NM_001198RefSeq chr6
+ 106086319 106109939 PRDM1 639 "PR domain containing 1, with ZNF domain, transcript variant 1"
GO:0060576|GO:0005515|GO:0003700|GO:0042826|GO:0060707|GO:0045579|GO:0008168|GO:0001893|GO:0030
889|GO:0005634|GO:0000122|GO:0000978|GO:0009791|GO:0032259|GO:0007281|GO:0046872|GO:0006351|GO:0
010628|GO:0001078|GO:0005737|GO:0045165|GO:0031665|GO:0042462 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_137382_PI430048170 0.73437913142172 1.11900044142433 5.62349593965801
6.51180617083189 5.72126801745179 P P P 5.62240275932936 5.82855343528255
6.05875994502415 P P P LNCV6_137382_PI430048170 mRNA
TAATGTATATTTTTTCAATGTTGTCGTGAGTGCAGCCCATGTTCCTGCGTGCAGCTCACG NM_014718RefSeq chr12
+ 7130370 7158934 CLSTN3 9746 calsyntenin 3
GO:0000139|GO:0045211|GO:0005509|GO:0035249|GO:0005789|GO:0016021|GO:0051932|GO:0007416|GO:0007
156|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91144_PI430048170 0.9594635108138391.00154230170275 9.16647121810378 8.74981424311649
8.77372902474755 P P P 8.99421340377964 8.93219004234325 8.78829821266452 P P P
LNCV6_91144_PI430048170 mRNA
CCTTATTGGAAAGATCCAAATAATGACTTCAGAAAAAACTTGAAAGTAACAGCAGTGCCT NM_032731RefSeq chr17
+ 6640901 6644541 TXNDC17 84817 thioredoxin domain containing 17
GO:0005515|GO:0004601|GO:0009055|GO:0047134|GO:0033209|GO:0070062|GO:0055114|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143297_PI430048170 0.3855969008747550.8146045775774912.94933786017662
3.44830111275534 3.59255801740345 A P P 3.19130612421288 3.93870028365057
3.72482395943214 P P P LNCV6_143297_PI430048170 mRNA
TGAATAGTGGAGGACAGGTCTACAAGTATCTACATATCTAAAGAATATGGAAAGTCTTCA NM_144976RefSeq chr19
- 12525369 12551542 ZNF564 163050 zinc finger protein 564
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132444_PI430048170 0.3084848153083491.44743115218305 1.5142707522544
0.4897182953219050.536046930455276A A A 0.3496172553811210.394734178698124
0.43987468972817 A A A LNCV6_132444_PI430048170 mRNA
ATCTCGGACCAGGAGGCTGTGGCCGCCATTGAGAAGTTCGTGGATGATGAGAAGATCCTG NM_006843RefSeq chr12

- 113392445 113403887 SDS10993 serine dehydratase
GO:0005739|GO:0003941|GO:0005737|GO:0030170|GO:0006094|GO:0042866|GO:0004794|GO:0006565|GO:0042
803|GO:0006567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129934_PI430048170 0.00921187633588372 0.4878070087982935.97138697568165
5.84176237515429 5.43899024068754 P P P 6.66394744295534 6.97421835463767
6.75473547684306 P P P LNCV6_129934_PI430048170 mRNA
ATGCCCAAGCAACGGGATCCCAAATCTAACTAAACACCATCTGGAATCCTGATGTGGAAA NM_001126106 RefSeq
chr14 - 22773222 22819811 SLC7A7 9056 "solute carrier family 7 (amino acid transporter light chain,
y+L system), member 7, transcript variant 3"
GO:0006520|GO:0005886|GO:0006865|GO:0050900|GO:0003333|GO:0055085|GO:0016323|GO:0006461|GO:0015
171|GO:0005887|GO:0007596|GO:0006810|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138316_PI430048170 0.00291549015884002 0.3402882048165424.73825703954501
4.25778319382488 4.1996079619068 P P P 5.64791617864751 6.22972028547659
5.98779910767677 P P P LNCV6_138316_PI430048170 mRNA
CTCCCTTCACCAGCCGAACCAATGTCAAAATTAATAAAGAAATGGACTAATGGCAAAAAA NM_001142446 RefSeq
chr8 - 41653224 41896762 ANK1 286 "ankyrin 1, erythrocytic, transcript variant 9"
GO:0005515|GO:0030018|GO:0005886|GO:0072661|GO:0005634|GO:0006887|GO:0055072|GO:0005829|GO:0016
323|GO:0007411|GO:0048821|GO:0045211|GO:0007010|GO:0051117|GO:0030673|GO:0005856|GO:0008093|GO:0
030507|GO:0014731|GO:0045199|GO:0031430|GO:0015672|GO:0042383|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145576_PI430048170 0.3994960751768310.7786297054575642.61485226151024
1.66508876638317 0.949035583859145A A A 2.04619237405829 2.30015174822081
2.42340215951764 A A P LNCV6_145576_PI430048170 mRNA
TAAGCTTACTCACTGACAGCCTTTCACTCTCCACAAATACATTAAAGATATGGCCATCAC NM_001127701 RefSeq
chr14_KI270847v1_alt - 1493318 1507264 SERPINA1 5265 "serpin peptidase inhibitor, clade A
(alpha-1 antiproteinase, antitrypsin), member 1, transcript variant 5"
GO:0005515|GO:0005783|GO:0004867|GO:0002020|GO:0005615|GO:0042802|GO:0001948|GO:0034014|GO:0032
496|GO:1900004|GO:0031093|GO:0034097|GO:0032355|GO:0070062|GO:0001666|GO:0010288|GO:0033986|GO:0
005794|GO:0005578|GO:0030168|GO:0005576|GO:0006953|GO:0010951|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142981_PI430048170 0.8729848171292590.9932475336493050.5232789928123
0.4563001098811570.318932462336272A A A 0.3870207610477860.483045962619768
0.46345592877808 A A A LNCV6_142981_PI430048170 mRNA
CCTCCACAGATGCACTTTAAAAAGCCACTCATGCTTTGGCTTAAACTGTAATTAATTTAT NM_023940RefSeq chr4
+ 52862327 52866835 RASL11B 65997 "RAS-like, family 11, member B"
GO:0006184|GO:0016020|GO:0007264|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133982_PI430048170 0.00276271737745982 1.34588045703383 10.1102287657675
10.055636173316 9.99852019713356 P P P 9.68838751893653 9.65529657553089
9.53258489396105 P P P LNCV6_133982_PI430048170 mRNA
GGCTTGGGGGAAGAATAGATTTAGTAAAGCAGGAAGATCTGTTGTTACTTAACAGAAAAA NM_001519RefSeq chr14
- 105209285 105300992 BRF1 2972 "BRF1, RNA polymerase III transcription initiation factor 90 kDa
subunit, transcript variant 1"
GO:0043488|GO:0010467|GO:0009304|GO:0006355|GO:0000126|GO:0009303|GO:0017025|GO:0008270|GO:0005
654|GO:0006384|GO:0006383 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88669_PI430048170 0.0990003467011908 0.7435984849463414.93981457086089 4.7732448136273
5.33287546269224 P P P 5.52880872726755 5.29247029712869 5.55131933833106 P P P
LNCV6_88669_PI430048170 mRNA
CAGGATTCAAAGTTGTACATACATGTGATTACTTCTGTTTTTTACACCCACATACAGTAC NM_001297642 RefSeq
chr12 - 7094549 7109278 C1RL 51279 "complement component 1, r subcomponent-like,

transcript variant 3" GO:0004252|GO:0045087|GO:0006958|GO:0006508|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141726_PI430048170 0.2282035656301571.17283818445554 8.55519809540579 8.65106700328384 8.57803171332686 P P P 8.06858429365591 8.45685473644542 8.52940400362775 P P P LNCV6_141726_PI430048170 mRNA CTGGTTCCATCTCTGCTATATGGGAATGAAAATAAAGAAACATATTTCTTGGCTTGTCTA NM_001168531 RefSeq chrX - 15243986 15270467 ASB9 140462 "ankyrin repeat and SOCS box containing 9, transcript variant 4" GO:0035556|GO:0005739|GO:0005515|GO:0045732|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128248_PI430048170 0.6004953035730450.8704369938211174.99819083861231 4.67835365397417 5.07482958103479 P P P 4.58482964643588 5.22765958056924 5.43915584809044 P P P LNCV6_128248_PI430048170 mRNA TAGGTGTATTCTTAAATTCAGACAGGGGAAGATTCTTTCACATATCACTCAGTTACCTCC NM_001123168 RefSeq chr1 - 206186255 206202419 FAM72A NA "family with sequence similarity 72, member A" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112353_PI430048170 0.0572231037115414 0.79829842650996 6.87847209979503 6.7555595346397 6.59156089272303 P P P 6.8869431810341 7.14803569839561 7.16351500142233 P P P LNCV6_112353_PI430048170 mRNA CGCTTGAATCAGGCCATCGAAAGAAATGCCTTCCTGGAAAGTGAACTTGATGAAAAAGAG NM_001143979 RefSeq chr16 + 15643266 15726351 NDE1 54820 "nudE neurodevelopment protein 1, transcript variant 1" GO:0005515|GO:0008017|GO:0021987|GO:0007100|GO:0000132|GO:0032154|GO:0005829|GO:0007405|GO:0042802|GO:0051642|GO:0007059|GO:0047496|GO:0000086|GO:0005871|GO:0005813|GO:0006996|GO:0005874|GO:0019904|GO:0051303|GO:0051298|GO:0016020|GO:0016477|GO:0007020|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134033_PI430048170 0.3899014753865560.9557274960101310.26554201371752 0.2834592655386960.386242583711927A A A 0.4836381509583370.329252078952447 0.315177111957455A A A LNCV6_134033_PI430048170 mRNA GCTCTCCAACATAGGGTGGTCTCATTCTTCTGGAGACTTTTTTAGATAAAGTAAAATAAT NM_021191 RefSeq chr12 + 55019944 55030017 NEUROD4 58158 neuronal differentiation 4 GO:0006355|GO:0045597|GO:0005634|GO:0003677|GO:0006351|GO:0035881|GO:0007405|GO:0045165|GO:0007219|GO:0048666|GO:0046983|GO:0010001|GO:0001764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61003_PI430048170 0.0502971382656398 0.4951397126207221.90955122752422 2.37221988829935 2.91164189351306 A A P 3.20889177502615 3.58380918625488 3.58548922869436 P P P LNCV6_61003_PI430048170 mRNA AAATGGCCTTGTGAAAAAGGGTAAAGAACAAAACACACAGCGAAGCTTTTTTCTCAGAAT NM_001530 RefSeq chr14 + 61695400 61748259 HIF1A 3091 "hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor), transcript variant 1" GO:0042541|GO:0005515|GO:0010468|GO:0003700|GO:0003705|GO:0001755|GO:0000989|GO:0001947|GO:0006879|GO:0007219|GO:0042789|GO:0031625|GO:0035035|GO:0006089|GO:0019901|GO:0014850|GO:0001892|GO:0032722|GO:0030502|GO:0008542|GO:0032963|GO:0019896|GO:0005654|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129590_PI430048170 0.9001451233796331.00145149576666 0.365646256754001 0.3631832280467140.386056207627792A A A 0.3833544555467840.340680338268822 0.384254312286542A A A LNCV6_129590_PI430048170 mRNA TGTCACTGCCAGCTCTGGACACTTACTTTTGGAATAAAGCAAAGAGTGAACACTAAAAAA NM_001001938 RefSeq chr9 + 88990862 88996142 C9orf47 286223 "chromosome 9 open reading frame 47, transcript variant 1" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60756_PI430048170 0.0957136633494623 0.5984443396536663.77725855953952 3.64289925024821 4.4000435123403 P P P 4.18492835643243 4.95455740433949 4.9005354128518

P P P LNCV6_60756_PI430048170 mRNA
GCGGGAGTGTTTTTCTTTAGGTGTACAATATGCAATAATAGTGACATCTTTCAGAAAGAG NM_017769 RefSeq chr14
+ 30559122 30620061 G2E3 55632 G2/M-phase specific E3 ubiquitin protein ligase
GO:0000209|GO:0005737|GO:0004842|GO:0016874|GO:0001824|GO:0005730|GO:0006915|GO:0008270|GO:2001
243 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108154_PI430048170 0.82069643074723 0.7808461262187811.18452945125455
1.31380269619804 0.260634952989289 A A A 2.25698199541587 0.343490145955644
0.659919079803213 A A A LNCV6_108154_PI430048170 mRNA
ACAATGTCTTTATCACGGGACCTACTGGCTCTGTCAAAATCGGGGACCTGGGCCTGGCCA NM_032387 RefSeq chr17
+ 42780630 42797066 WNK4 65266 WNK lysine deficient protein kinase 4
GO:0005515|GO:0006821|GO:0090188|GO:0050801|GO:0070294|GO:0005524|GO:0019869|GO:0035556|GO:0005
737|GO:0008104|GO:0004674|GO:0050794|GO:0072156|GO:0006468|GO:0005923|GO:0006811 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_51468_PI430048170 0.5092271791323970.6177503249855572.67695597732356 1.16862513556243
1.70222688672913 A A A 1.19394643294086 3.39987788681133 2.68161335364196 A P P
LNCV6_51468_PI430048170 mRNA
CTTCAGTGTTGTTAACAGCAAGAGAAAATTGGGTTTGTTTAAAAATCTACTTCTCTGAGG NM_201274 RefSeq chr17
+ 17042759 17192648 MPRIP 23164 "myosin phosphatase Rho interacting protein, transcript variant 2"
GO:0005515|GO:0005737|GO:0003779|GO:0015629|GO:0005925 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141921_PI430048170 0.3068545267143520.8487380160865870.477378915253185
0.4225093113311280.427901296189141 A A A 0.9823914023254840.499988884817256
0.500331443615177 A A A LNCV6_141921_PI430048170 mRNA
GTGCTGTGGAAATGGAAGAAACCATCTTCACAGACTGTAGGAGAATTCAACATATAATTT NM_173848 RefSeq chr8
+ 84183350 84921843 RALYL 138046 "RALY RNA binding protein-like, transcript variant 3" GO:0000166
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136392_PI430048170 0.2090073373597030.7974075824208423.74808798757161
3.27513017308794 3.43406264704696 P P P 4.10812671993282 3.76490378292833
3.54912496714266 P P P LNCV6_136392_PI430048170 mRNA
CCGTGTCTTCCCAGGTTTACAATCAGAGAATCACAGCTGCTTTAATAAATGTTATTTATA NM_001195129 RefSeq
chr2 + 232520462 232525715 PRSS56 646960 "protease, serine, 56"
GO:0004252|GO:0005783|GO:0006508|GO:0043010 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128834_PI430048170 0.1554931448367240.7984690214445415.49081104083038
5.23251219503773 5.09865592244377 P P P 5.86400632287293 5.52618423100274
5.39194444935324 P P P LNCV6_128834_PI430048170 mRNA
AGCCAGCACTCTGGAGGCTGCTGCTGAAGTGGACCTTGACTTCCTCTTCCTTCTGATTCT NM_178352 RefSeq chr1
+ 152796750 152798181 LCE1D 353134 late cornified envelope 1D
GO:0048471|GO:0005737|GO:0050890|GO:0071277|GO:0031424|GO:0001533 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141969_PI430048170 0.5014567068814331.02842367466275 0.285502281706569
0.3108307474018790.439195983408292 A A A 0.3264998038331190.297492878488731
0.294768835928015 A A A LNCV6_141969_PI430048170 mRNA
AGCCTACTACCACAATTACCAAATATTCTGAAAATTTCTAGTATGGTGAAGATGGAGAGA NM_001170330 RefSeq
chr4 - 119296418 119304445 C4orf3 401152 "chromosome 4 open reading frame 3, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134963_PI430048170 0.6267515198179551.10921075924335 0.938380839111252
0.2787536425995870.354332937248213 A A A 0.3864197382605270.318577674373941
0.505561713864995 A A A LNCV6_134963_PI430048170 mRNA
ATATAGTCTCACCATTCCTAGGAGCTAAATGGGTGTGTCTAGTAGGGGCATCAGTTCATC NM_213600 RefSeq chr15

- 42141133 42156641 PLA2G4F 255189 "phospholipase A2, group IVF, transcript variant 1"
GO:0036149|GO:0036148|GO:0032587|GO:0044281|GO:0005765|GO:0031982|GO:0046872|GO:0005829|GO:0036150|GO:0071407|GO:0001516|GO:0004622|GO:0047498|GO:0006644|GO:0009395|GO:0071236|GO:0036151|GO:0050482|GO:0046474|GO:0036152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140891_PI430048170 0.460648195953115 1.15733295994176 5.11415786621146
4.53101873958554 4.64997273570412 P P P 4.46041592214733 4.26714410987784
4.92249227342415 P P P LNCV6_140891_PI430048170 mRNA
GGCGACTCTGCTCTCTATTTAAAAGCGTGCACAATCAAAAGTACTATGCAATTTTAGGAC NM_005110 RefSeq chr5
- 180300699 180353315 GFPT2 9945 glutamine-fructose-6-phosphate transaminase 2
GO:0016051|GO:0004360|GO:0006112|GO:0030246|GO:0006488|GO:0006048|GO:0044267|GO:0006002|GO:0043687|GO:0018279|GO:0006541|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139337_PI430048170 0.425274153692973 1.49853744285434 3.36943188740418
1.81358803241209 3.06249051471778 P A P 1.54691149438948 2.19850903102757
2.86892080899085 A A P LNCV6_139337_PI430048170 mRNA
GCATGAGGAGTATGGGAAAAACAGAATAAAGGAATCTGCCTTTAAGGAGCTTACAATCAT NM_032898 RefSeq chr3
- 196706276 196712294 CEP19 84984 centrosomal protein 19kDa GO:0000922|GO:0005814|GO:0036064
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126998_PI430048170 0.0161144669458879 1.48121929072116 10.2364310498016
10.2848528767405 10.1002717204631 P P P 9.83302997937747 9.59113757658822
9.48049840191232 P P P LNCV6_126998_PI430048170 mRNA
AGAACAGAAACCCTGCCCCCACTTAATAATAAAAAGAAAGTTTATTGATGGGTGGTTGC NM_024310 RefSeq chr19
+ 29665419 29675476 PLEKHF1 79156 "pleckstrin homology domain containing, family F (with FYVE domain) member 1"
GO:0048471|GO:0070273|GO:0006915|GO:2001244|GO:0005634|GO:0032266|GO:0005765|GO:0072659|GO:0005764|GO:0046872|GO:0016050|GO:0007032|GO:0010314|GO:0010008|GO:0005768|GO:0010508 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129704_PI430048170 0.284680133099617 0.430086691018454 0.999303611371893
0.301779983365926 0.463600225158035 A A A 2.60784799301213 1.76235569066675
0.30087613180571 P A A LNCV6_129704_PI430048170 mRNA
GCTATTAAAATGACATAGGATTGCAGACTGCTGCTGTTAATACGAGCATTTTAAGCAAAA NM_020780 RefSeq chr1
+ 11479237 11537583 PTCHD2 57540 patched domain containing 2
GO:0042632|GO:0003674|GO:0031965|GO:0005783|GO:0032368|GO:0008158|GO:0016021|GO:0007224 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137939_PI430048170 0.0185084157572714 1.70265729032256 10.0587084260988
10.4683537031706 10.2752599836627 P P P 9.5606569423979 9.507712759647
9.45773535268834 P P P LNCV6_137939_PI430048170 mRNA
TCCAGAAACTTGGAGAAATGGGGGTTGGGAACTTATGCAGACATGGATTTATTTTTCAAC NM_173587 RefSeq chr11
- 63911220 63916844 RCOR2 283248 REST corepressor 2
GO:0005667|GO:0003700|GO:0003714|GO:0003682|GO:0005634|GO:0045892|GO:0003677|GO:0000785|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_5659_PI430048170 0.410561036278241 0.765890527418393 3.27345628591982 1.97058404391565
1.1452793142417 P A A 3.023472095181 2.63391032409937 2.65358439916386 P P P
LNCV6_5659_PI430048170 mRNA
TAACGGCAGCCATCTTGTTTGTTTGAGTGAATCGGAAAGGAGGCGCCGGCTGTGGCGGCG NM_006265 RefSeq chr8
- 116845933 116874866 RAD21 5885 RAD21 homolog (S. pombe)
GO:0005515|GO:0006357|GO:0005694|GO:0006915|GO:0006310|GO:0005829|GO:0006302|GO:0008278|GO:0007067|GO:0007059|GO:0016020|GO:0034991|GO:0005654|GO:0071168|GO:0000278|GO:0000785|GO:0000775|GO:0051301|GO:0007131. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145138_PI430048170 0.282583190403769 1.24182091216144 1.1312818390079

0.58949633200637 0.506150913138293 A A A 0.425607183275034 0.462290042784346
0.483877674807436 A A A LNCV6_145138_PI430048170 mRNA
CATTCTTTATCTCCTTGAAGCCATAATGGTGCTGAGTGACTTCCAACACGATTTGCTGGC NM_031415 RefSeq chr8
- 129748195 129786888 GSDMC 56169 gasdermin C
GO:0005739|GO:0008150|GO:0003674|GO:0005737|GO:0005815 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139585_PI430048170 0.0010316348844274 0.563789236311297 4.47778891411399
4.69804368813325 4.59206359382612 P P P 5.48180610369452 5.27339858203996
5.49108190332921 P P P LNCV6_139585_PI430048170 mRNA
CCCAGTAACGGTTAACTCTTCTCTTGTGTATATGCAAATAAACCTATTATTCACTTCTCANM_003861 RefSeq chr14 -
69050919 69153197 DCAF5 8816 "DDB1 and CUL4 associated factor 5, transcript variant 1"
GO:0005739|GO:0016567|GO:0080008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143322_PI430048170 0.0492586447545109 0.542212724220322 6.16740529951609
5.84809796680848 5.73951344178666 P P P 6.34287364197571 7.16606263040816
6.81439158923849 P P P LNCV6_143322_PI430048170 mRNA
GACCATTATATTCTACTGTGAGAAGTGCAGTCTGCACTATATTGTTTTAAAAACGAAGAG NM_032829 RefSeq chr12
+ 109714381 109770507 FAM222A 84915 "family with sequence similarity 222, member A" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_88606_PI430048170 0.216440390383571 0.956435467880514 0.40412472132389 0.391374004023835
0.364369973893352 A A A 0.501799699549956 0.468314823028363 0.38009734609237 A A A
LNCV6_88606_PI430048170 mRNA
AGTCCTCGAGCATAGTGGAGTTCTTCAGCTTAGTGACCCGGAGCTCAAACATCCCTGCGG NM_173588 RefSeq chr11
- 18704304 18726230 IGSF22 283284 "immunoglobulin superfamily, member 22" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132843_PI430048170 0.241161656629247 0.485443017679008 0.413710691935207
0.415452034205584 0.430658701542338 A A A 0.320910039452415 2.12689341996893
1.40663698236682 A A A LNCV6_132843_PI430048170 mRNA
AGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGCAGAGTTGTGGGCAGAAATATTTCT NM_001004469 RefSeq
chr1 - 159535077 159536007 OR10J5 127385 "olfactory receptor, family 10, subfamily J, member 5"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143362_PI430048170 0.00609424408719557 0.77479491800333 13.4972369891592
13.5663397018887 13.3982707087753 P P P 13.8736156915077 13.8930059958907
13.8029454344239 P P P LNCV6_143362_PI430048170 mRNA
GAGTATATAGGTTTTGTACCTTTTTTACAGGAAGGTGACTTTCTGTAACAATGCGATGTA NM_002167 RefSeq chr1
- 23557929 23559794 ID3 3399 "inhibitor of DNA binding 3, dominant negative helix-loop-helix
protein"
GO:0005515|GO:0001656|GO:0003700|GO:0005634|GO:0045662|GO:0043433|GO:0007507|GO:0005737|GO:0030
182|GO:0015630|GO:0030855|GO:0051726|GO:0046983|GO:0042476|GO:0006275|GO:0043065|GO:0003714|GO:0
019904|GO:0009611|GO:0007275|GO:0000122|GO:0007417|GO:0006351|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_52116_PI430048170 0.232165065489706 1.27460204619637 6.82274531400525 6.85590780859037
6.84863270440612 P P P 6.01981264726595 6.57776249765056 6.77748544848243 P P P
LNCV6_52116_PI430048170 mRNA
TCCAGAGGCAGCCTTTGGTACTTAAAATATCTGTAGCTGATTAAATTTTTCCCAACAACC NM_001144002 RefSeq
chrX - 16587998 16712217 CTPS2 56474 "CTP synthase 2, transcript variant 3"
GO:0005739|GO:0015949|GO:0055086|GO:0044281|GO:0006220|GO:0044210|GO:0005524|GO:0003883|GO:0006
541|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136903_PI430048170 0.197274051486358 1.4330691705562 3.82239178013713

3.12483376173622 3.22018544594486 P P P 3.30091474412694 2.88079358459014
2.38970212690765 P P A LNCV6_136903_PI430048170 mRNA
CGAGGCTGGGGGCCGAGGGTGCGTAGTCGGGGGAGACAGCCGGTCCTAGGGGGCCCTTTG NM_207401 RefSeq
chr1 - 247110159 247112417 C1orf229 388759 chromosome 1 open reading frame 229 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_53211_PI430048170 0.3316935516003580.7777331755224134.99870828498369 4.09927289878694
4.06770596880401 P P P 5.05814220992766 4.89983743910372 4.4288051269926 P P P
LNCV6_53211_PI430048170 mRNA
TACTGATATTTATGAGACTGTGGCTGCTGCAACATCAGAATCCACTACTGTAGAGCCTGG NM_016449 RefSeq chr22
- 23608451 23632321 DRICH1 51233 aspartate-rich 1 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136376_PI430048170 0.0429950109788213 0.4088176372469473.27288896940122
2.19728569177074 3.06000929763267 P A P 4.30727404654391 3.97466130875877
4.30318443275144 P P P LNCV6_136376_PI430048170 mRNA
CATTTATCTTTATAGCTTTTCTGTACCTAATATTGTGTCTTGTGCGTAGGATGTGCTCAA NM_177532 RefSeq chr4 -
73571549 73620570 RASSF6 166824 "Ras association (RalGDS/AF-6) domain family member 6, transcript
variant 1" GO:0005515|GO:0007165|GO:0043065|GO:0006915 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128368_PI430048170 0.3297679193056710.5016776854888441.14017146201598
0.3214478668242361.64850371497184 A A A 3.05178074942568 1.04812304918312
1.47156458456565 P A A LNCV6_128368_PI430048170 mRNA
GAGGCCGTCATGAAGCTCTGTGTTGTCTGTTTTATTTTATAACCTTCCTCTCAACTATTA NM_004561 RefSeq chr11 +
65787033 65797219 OVOL1 5017 ovo-like zinc finger 1
GO:0006366|GO:0051729|GO:0001822|GO:0000981|GO:0005634|GO:0000122|GO:0007283|GO:0000978|GO:0046
872|GO:0009913|GO:0001078|GO:0007010|GO:0007498 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133918_PI430048170 0.2384470847293630.8225179759466874.60045243811076
4.24985980985118 4.20249425578391 P P P 4.39122697452663 4.91561777827951
4.57542992813286 P P P LNCV6_133918_PI430048170 mRNA
AGACAGGACATTAAAAGAGAGCGAGAGAGAGAAACAGTTCAGATTACTGCACATGTGGAT NM_000684 RefSeq
chr10 + 114044046 114046908 ADRB1 153 adrenoceptor beta 1
GO:0005515|GO:0009409|GO:0002024|GO:0002025|GO:2001259|GO:0031694|GO:0061051|GO:0042596|GO:0003
084|GO:0051924|GO:0007613|GO:0086004|GO:0005088|GO:0046982|GO:0007568|GO:0035240|GO:0030165|GO:0
004939|GO:0001996|GO:0046878|GO:0060080|GO:0032320|GO:0005887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131034_PI430048170 0.000961092558640425 0.2471549825347794.76832805769149
4.29265624402175 4.28001969286454 P P P 6.71162223814082 6.5312796104497
6.14695235911126 P P P LNCV6_131034_PI430048170 mRNA
CACAGTGGAAGGGTAGAGAGCCACAGTCCCCAAATCCTATGCAATAAAGTGCCTCTTAGG NM_138345 RefSeq chr3
+ 184230528 184242329 VWA5B2 90113 von Willebrand factor A domain containing 5B2 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_142514_PI430048170 0.0826914089845819 1.1223504412363 6.73550033452609
6.57749252677703 6.63471416556109 P P P 6.41180830931992 6.59072269304858
6.44368167939083 P P P LNCV6_142514_PI430048170 mRNA
ATCTCTGTTTTTAAGCAGAAATTCATTGTGCAGAAAAGTCCTCCAGAGCTCTGTGGCCCC NM_017891 RefSeq chr1
- 1081817 1116356 C1orf159 54991 chromosome 1 open reading frame 159 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142635_PI430048170 0.0118033422898628 1.49419620515706 7.70281739537633
8.03144868316738 7.95610748746075 P P P 7.46129048619963 7.31446844339934
7.18322844190775 P P P LNCV6_142635_PI430048170 mRNA

TGAAAAACTCAGCAGAGAAATTCGAGACCATTTTGCAAGACTGTGCCCTTCTCCTCAGGA NM_032950 RefSeq chr17_KI270857v1_alt - 388 30239 MMP28 79148 "matrix metallopeptidase 28, transcript variant 2" GO:0010760|GO:0005737|GO:0005509|GO:0006508|GO:0005578|GO:0008270|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145625_PI430048170 0.167504917423987 1.24434549921756 7.51543637128125 7.69344072546821 8.00578948602708 P P P 7.22391208600542 7.45705290058888 7.60542556260406 P P P LNCV6_145625_PI430048170 mRNA
TTCTAAGCCAGTAATTCCATTCTTAAATACCTCACTGTCTTGGCCATGGGGAAGCACTAT NM_001003684 RefSeq chr22 + 29767368 29770413 UQCR10 29796 "ubiquinol-cytochrome c reductase, complex III subunit X, transcript variant 2" GO:0022904|GO:0008121|GO:0006122|GO:0005743|GO:0005750|GO:0044281|GO:0044237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106078_PI430048170 0.411482471797153 0.949140146516909 7.62260633269601 7.70369828328596 7.56298825994575 P P P 7.59186401508392 7.69490247363163 7.82262829330788 P P P LNCV6_106078_PI430048170 mRNA
TATTAGGTCAGCCCCACCATGAGTTAGATTCCAAGACGATTGACCCCAAAGTTGCATTTC NM_170721 RefSeq chr17 + 57257012 57633183 MSI2 124540 "musashi RNA-binding protein 2, transcript variant 2" GO:0008266|GO:0005737|GO:0000166|GO:0048864|GO:0005844 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133006_PI430048170 0.0837056934058301 1.18237374637222 0.361798859653382 0.600769439619803 0.559784809212041 A A A 0.265374461930244 0.277696992661502 0.265329730153626 A A A LNCV6_133006_PI430048170 mRNA
CACCTACAAGGAATTTTCAAATCCACTTTTAAAACAGAAACCGGTAAATGCGCCGTATTG NM_005477 RefSeq chr15 - 73319858 73369264 HCN4 10021 hyperpolarization activated cyclic nucleotide gated potassium channel 4
GO:0005261|GO:0005886|GO:0008015|GO:0005222|GO:0005248|GO:0031226|GO:0007268|GO:0001701|GO:0042802|GO:0006936|GO:0030552|GO:0002027|GO:0005887|GO:0043195|GO:0005249|GO:0042391|GO:0035725|GO:0034765|GO:0071320|GO:0071805|GO:0006812|GO:0071321 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70794_PI430048170 0.0525529516673072 1.29411597387016 5.48896824357551 5.2483192025918 5.13206425490663 P P P 5.0759364607996 4.84580163942286 4.84232444381938 P P P LNCV6_70794_PI430048170 mRNA
TGATGTCCTTGGAGTTCTACAAGTGGAACTTAAGTGTCAAAAAGAATATGTGGTTTTTAG NM_001001891 RefSeq chr2 + 241188508 241225376 ANO7 50636 "anoctamin 7, transcript variant NGEP-L" GO:0006821|GO:0030054|GO:0005886|GO:0005783|GO:0017128|GO:0005634|GO:0055085|GO:0005829|GO:0005622|GO:0034220|GO:0006869|GO:0005229|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127420_PI430048170 0.363332240080597 0.487490791888517 1.25684843165576 1.03270319249693 0.283166989107647 A A A 0.291079818109024 2.38805017554612 2.36090786552471 A P P LNCV6_127420_PI430048170 mRNA
TTTGACCACAATCTTCAGCTGTGTGTGGGCAATCCCAGGAAGACAAAATCTGCATTTAAG NM_001836 RefSeq chr14 - 24505354 24508265 CMA1 1215 "chymase 1, mast cell" GO:0042277|GO:0002003|GO:0004252|GO:0050727|GO:0005576|GO:0005615|GO:0045766|GO:0050720|GO:0005622|GO:0031012|GO:0022617|GO:0016485|GO:0030198|GO:0006508|GO:0008236|GO:0030901|GO:0071333|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142075_PI430048170 0.306367174215261 1.81196959818807 0.326966123791776 1.88773210718946 2.0104367253134 A A A 0.27185720486618 1.34566953991196 0.274133932978503 A A A LNCV6_142075_PI430048170 mRNA
TCATTCCTGCAGAAGGTTTGTGACGTAGCTGTGCCTGTACCTGGGGCAGAGAGGATGCCA NM_138814 RefSeq chr22 - 43879677 43892013 PNPLA5 150379 "patatin-like phospholipase domain containing 5, transcript variant

1" GO:0016042|GO:0016787 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129186_PI430048170 0.3050271049608290.6648740842120760.371035959338803
2.03026938676499 0.314734736027973A A A 1.20528135570715 2.13457264280847
1.70606648743985 A A A LNCV6_129186_PI430048170 mRNA
AGACTGGAGAAAGGCCTTAGACTGTCGCTGAATCAATATGACCTGACTTAAAGCAGAAAC NM_198542RefSeq chr19
+ 57499853 57508229 ZNF773 374928 "zinc finger protein 773, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_89551_PI430048170 0.21354577839845 0.7918625758902281 4.9003120302304 14.268948377213
14.2997554850128 P P P 14.9313507251627 14.7914705411337 14.8442128345867 P P P
LNCV6_89551_PI430048170 mRNA
AAACATTCTCCTCCGCATAAGCCTACATCAGACCAAAATATTAAACTGACAATTAACAGC NM_001190702 RefSeq
chr11 - 10507886 10509176 MTRNR2L8 NA MT-RNR2-like 8 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129695_PI430048170 0.0430708639926968 0.9554605741191740.417932786117139
0.3672942689848220.369196578345548A A A 0.4450817423141670.46390298267315
0.443115945638432A A A LNCV6_129695_PI430048170 mRNA
GGAACTCTTTTCATCTTGCAAAGAGAAAAAGCCAGTCTTTCCAGAATAAATATTCATCTG NM_001258428 RefSeq
chr5 + 140360201 140375137 SLC4A9 83697 "solute carrier family 4, sodium bicarbonate cotransporter,
member 9, transcript variant 1"
GO:0005886|GO:0005452|GO:0005887|GO:0051453|GO:0045177|GO:0015701|GO:0035725|GO:0055085|GO:0008
510|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114374_PI430048170 0.8162024999516091.02460900990906 0.309217639621865
1.86705800798927 1.36070044478743 A A A 2.23506227659403 0.370724134769347
0.350641264235858A A A LNCV6_114374_PI430048170 mRNA
TTGGCCATTCCAACAGCTCAAGTCTTCCCTGATCAAGTCACCGGAGCTTTCAAAGAAGGA NM_001159740 RefSeq
chr6_GL000256v2_alt + 2871378 2873603 LTA 4049 "lymphotoxin alpha, transcript variant 1"
GO:0032729|GO:0001666|GO:0002876|GO:0005164|GO:0043065|GO:0050830|GO:0007584|GO:0042493|GO:0048
147|GO:0005102|GO:0007267|GO:0006915|GO:0060252|GO:0005125|GO:0005615|GO:0048535|GO:0007165|GO:0
002925|GO:0016020|GO:0006959|GO:0032496|GO:0044130 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_127293_PI430048170 0.6484443880299381.44905340468286 0.2556925358935991.8820280204668
2.43945966718059 A A A 0.4832848967809191.80765098765887 1.14558692392063 A A A
LNCV6_127293_PI430048170 mRNA
ATTATCAGCAGACTCTTTTATACTTTATGGGGCATCTACATACTACTTCCGCCACTCTTCNM_001288770 RefSeq chr17
+ 73232232 73248956 C17orf80 55028 "chromosome 17 open reading frame 80, transcript variant 4"
GO:0008150|GO:0003674|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138248_PI430048170 0.000173397289712697 2.59650837472473 8.738173064047
8.82628142628953 8.63396266546093 P P P 7.37767891442169 7.46754822151391
7.21899341765293 P P P LNCV6_138248_PI430048170 mRNA
GCTCTCTGAACAAGTTGAAAGTCCAAATAAAACTTACCTGTTCCATCTGTGCTCAAAAAA NM_014726RefSeq chr17
+ 47695263 47712063 TBKBP1 9755 TBK1 binding protein 1 GO:0005515|GO:0045087 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_51926_PI430048170 0.1770775329128241.01932532027183 0.3171057324054160.281066599594506
0.273633985943328A A A 0.2629998809268660.2637720755750140.262566175318515A A A
LNCV6_51926_PI430048170 mRNA
TTCTAGACGTTTTGGCTTGAACCATCTGAAAAACTGCCTCAAGCTTTTGCATGGTTCCCA NM_001302819 RefSeq
chr22 - 31933520 31938454 C22orf24 25775 "chromosome 22 open reading frame 24, transcript
variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_98028_PI430048170 0.178279348398961 1.08899001043971 12.1809144804667 12.1543755303263
12.026900550322 P P P 11.9605445908946 12.1111720849981 11.9189917153708 P P P
LNCV6_98028_PI430048170 mRNA
TGGACAGACCTTCACGTTCCCAGATCTGTTTCCCGAGAAAGACGAGAGCCCTGAAGGCAG NM_021134 RefSeq
chr11_KI270721v1_random + 2584 11804 MRPL236150 mitochondrial ribosomal protein L23
GO:0070124|GO:0070125|GO:0070126|GO:0003735|GO:0006996|GO:0032543|GO:0003723|GO:0005730|GO:0005
743|GO:0006412|GO:0005762|GO:0005739|GO:0000166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109790_PI430048170 0.186005531783067 0.880501828588441 7.46673668283828
7.15999878602529 7.20124438548426 P P P 7.47832309338739 7.46415430792144
7.45580242304938 P P P LNCV6_109790_PI430048170 mRNA
CCAATGTGAAGTTCATCTTGCAGCATTTACTATGCACAACAGAGTAACTATCGAAATGAC NM_005561 RefSeq chr13
+ 113297153 113323426 LAMP1 3916 lysosomal-associated membrane protein 1
GO:0005515|GO:0048102|GO:0005886|GO:0097208|GO:0090160|GO:0005764|GO:0030425|GO:0005737|GO:0044
194|GO:0043025|GO:0016032|GO:0070062|GO:0043323|GO:0042470|GO:0005770|GO:0072594|GO:0005771|GO:0
019904|GO:0006914|GO:0050821|GO:0042383|GO:0016020|GO:0005887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133112_PI430048170 0.438142079330315 0.915334910624209 6.23460526152402
6.20161719951386 6.66307278371142 P P P 6.51550893791715 6.46493689602837
6.54787467083414 P P P LNCV6_133112_PI430048170 mRNA
GGTGAGAACTAATTATTGTCCATACTTGTAGCATTCTTCATTAAAGTCTTGCTTCTCTCA NM_005652 RefSeq chr16 -
69355560 69385988 TERF2 7014 telomeric repeat binding factor 2
GO:0005515|GO:0030870|GO:0005634|GO:0042803|GO:0005737|GO:0003691|GO:0000723|GO:0032214|GO:0031
627|GO:0070198|GO:0000784|GO:0000783|GO:0000781|GO:0016233|GO:0005794|GO:0042162|GO:0008022|GO:0
001701|GO:0031848|GO:0001309|GO:0007049|GO:0003682|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139576_PI430048170 0.103465632256442 1.19374098065688 4.16543779438653
4.17125340568574 4.25005429988609 P P P 3.91463866539891 4.10965015596318
3.77820349400865 P P P LNCV6_139576_PI430048170 mRNA
TAAAAAGCTTCTTTTACCTAACCCACCTCCCAAGGGCTCCATTTGTAAAAGTACAGACCA NM_152519 RefSeq chr2
- 210021420 210171370 KANSL1L 151050 KAT8 regulatory NSL complex subunit 1-like GO:0000123 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68537_PI430048170 0.0248470791476845 1.42696794987993 5.49601956200255
5.27464887536089 5.61047275323054 P P P 4.86000001804246 5.16055976512544
4.81682938632609 P P P LNCV6_68537_PI430048170 mRNA
CCAAGAGTGCTGATACCTTTTTAAATTTAGAGGGGCAGGCTTAAATAAAGGACTAAATAT NM_001085411 RefSeq
chr5 - 36192588 36241798 NADK2 133686 "NAD kinase 2, mitochondrial, transcript variant 1"
GO:0005739|GO:0016310|GO:0006741|GO:0003951|GO:0019674|GO:0005524|GO:0042803 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144612_PI430048170 0.0396498431785922 0.607154762898277 11.2277974219929
11.3210492485205 11.441126286925 P P P 11.6982262209032 12.2149285651199
12.1881347126567 P P P LNCV6_144612_PI430048170 mRNA
CTGTTGATGTAATGATGTGGAACTCCTCTAAAAATTACAGTATTGTCTGTGAAGGTATCT NM_001069 RefSeq chr6
- 3153665 3157549 TUBB2A 7280 "tubulin, beta 2A class IIa"
GO:0051258|GO:0005874|GO:0003924|GO:0005634|GO:0005525|GO:0055085|GO:0031982|GO:0006184|GO:0005
737|GO:0006457|GO:0005200|GO:0051084|GO:0007017|GO:0044267|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133928_PI430048170 0.0905837270514968 1.559673945607 2.6805234920333
3.22796002505436 2.99096940825477 A P P 2.270168248452 2.73011302695818
1.90923412856225 A P A LNCV6_133928_PI430048170 mRNA

TAAAAGAAGGCTGGGAAGAAGAGTTCCAGCAGCTACGCCTGCTCCCAGAGGCAACCTCCT NM_001007530 RefSeq chr17 - 14235855 14236833 CDRT15 146822 CMT1A duplicated region transcript 15 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129786_PI430048170 0.766841506774146 0.950937901577767 4.34528873228279 4.31800356050504 3.62434406321872 P P P 3.93924632765551 4.13862868756926 4.48312688041042 P P P LNCV6_129786_PI430048170 mRNA
TAAGAAGCTGCTCTGTATGCTAAAGCTTTCTCTCCTCAATAAAAATATAAAGGGTGTGTA NM_001024455 RefSeq chrX - 72127110 72131901 RGAG4 340526 retrotransposon gag domain containing 4 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141147_PI430048170 0.707227939585765 0.953620656862193 7.0275545847528 7.09816335872624 7.14093693599032 P P P 7.05165903868658 6.98326933308591 7.40342665889682 P P P LNCV6_141147_PI430048170 mRNA
GATGTATTTCTCTATGAGACCTGTTGCTGAGATTGCTTTTCTAAACATATATGTCCTGTT NM_032230 RefSeq chr12 + 82358496 82479237 METTL25 84190 methyltransferase like 25 GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129395_PI430048170 0.0853990140937154 0.639623039400737 6.55428639118959 6.70112402676301 6.78460213101334 P P P 6.96023334342298 7.25562063802819 7.67690370401199 P P P LNCV6_129395_PI430048170 mRNA
GCCCCAATTTGCTTGAATGGGAAAACTCTCTCATTTGACCCTTATAGGTAGAAATAATGA NM_032587 RefSeq chr5 + 40841307 40855354 CARD6 84674 "caspase recruitment domain family, member 6" GO:0006915|GO:0042981 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135534_PI430048170 0.0046140245123041 0.555752169036459 5.33045992245568 5.22594467421785 5.18235554993174 P P P 5.93596483837713 6.25755485876442 6.07361885733364 P P P LNCV6_135534_PI430048170 mRNA
CTTCTTCTGAACTATTATTAAATAAGTGAATACAAAGGCCCTATGATGGGAAATCCAGAC NM_032876 RefSeq chr14 - 22971173 22982642 AJUBA 84962 "ajuba LIM protein, transcript variant 1" GO:0005515|GO:0035313|GO:0005886|GO:0030032|GO:2000637|GO:0005634|GO:0005829|GO:0016339|GO:0051015|GO:0031334|GO:0043406|GO:0000932|GO:0005911|GO:0048041|GO:0000086|GO:0043123|GO:0030334|GO:0033673|GO:0005667|GO:0001666|GO:0005815|GO:0045294|GO:0003714|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91393_PI430048170 0.658367902866862 0.958823098718823 6.08176242536396 6.35885110597141 6.12842659198911 P P P 6.24742745069786 6.41012279091417 6.09138700475841 P P P LNCV6_91393_PI430048170 mRNA
TGTGATCACCACATTACCGTCTGTGGTCCGGCTCCTGGTGACAGCTGGTGCCAGCCCCAT NM_005178 RefSeq chr19 + 44748720 44760044 BCL3 602 B-cell CLL/lymphoma 3 GO:0042345|GO:0005515|GO:0048471|GO:0003700|GO:0007249|GO:0005634|GO:0042088|GO:0048536|GO:0005737|GO:0032996|GO:0030198|GO:0045944|GO:0002467|GO:0030674|GO:0033257|GO:0042742|GO:0000060|GO:0032729|GO:0043066|GO:0045415|GO:0030330|GO:0002268|GO:0042536|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144653_PI430048170 0.0269825613425465 0.328908994391293 2.07982141961478 2.90259137690577 1.94122872193384 A A A 3.86219893480173 3.99501846969368 4.06838763176257 P P P LNCV6_144653_PI430048170 mRNA
CTCACATTACAATACAATTACTGGAAGCAAGTACTGCATTTCCTATGCAACAAAAAAGGA NM_001134673 RefSeq chr1 + 61082307 61462788 NFIA 4774 "nuclear factor I/A, transcript variant 1" GO:0014070|GO:0006355|GO:0003700|GO:0030054|GO:0005634|GO:0000122|GO:0000978|GO:0019079|GO:0006351|GO:0006260|GO:0001077|GO:0045944|GO:0005654|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129089_PI430048170 0.383612230491251 1.02776129452792 0.348945223084687 0.350018211668168 0.452444673891446 A A A 0.348073332468374 0.316529367049802

0.370253760204302 A A A LNCV6_129089_PI430048170 mRNA
CAACTCTGACTTTTCTGGTGCAACAGTGGAGAATCTTACCATTGGATTTCTTTAACTTGT NM_002007 RefSeq
chr11 - 69773028 69775403 FGF4 2249 fibroblast growth factor 4
GO:0008286|GO:0008284|GO:0060591|GO:0010463|GO:0007267|GO:0005634|GO:0005829|GO:0007173|GO:0045
944|GO:0042475|GO:0051781|GO:0070374|GO:0008201|GO:0043066|GO:0048011|GO:0048015|GO:2000544|GO:0
060561|GO:0005576|GO:0005104|GO:0007165|GO:0060363|GO:0001502|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_68506_PI430048170 0.173394826321198 1.17039442739535 13.223685522278
13.3079917545187 13.3959055833983 P P P 12.8826293266279 13.0520703404547
13.2881211573614 P P P LNCV6_68506_PI430048170 mRNA
TCTTGGACCTTGGTCAGTTGTGCTATTCATTATTAAACACTAAAACTTTGGCGGTTCTTG NM_001537 RefSeq
chr16 + 83807902 83813002 HSBP1 3281 heat shock factor binding protein 1
GO:0034605|GO:0006936|GO:0003714|GO:0005654|GO:0005634|GO:0000122|GO:0035987|GO:0005856|GO:1900
034 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130879_PI430048170 0.70668778703635 0.909212979380587 11.0687665241372
10.8684120612145 11.0778638416998 P P P 10.6448696275685 11.407335665635
11.2754016163066 P P P LNCV6_130879_PI430048170 mRNA
AGTCAGCTGAATCCCGATAGTACTAGGTCCCCTTCCCTCCGCATCCCGTCAGCTGGAAAA NM_006617 RefSeq
chr1 - 156668762 156677397 NES 10763 nestin
GO:0005882|GO:0032091|GO:2000179|GO:0072089|GO:0048858|GO:0007417|GO:0043086|GO:0019215|GO:0003
674|GO:0030844|GO:0005737|GO:0031076|GO:0043524|GO:0005198|GO:0007420|GO:0000086|GO:0045111 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49655_PI430048170 0.637867107988549 0.9691598534648650.551236105586797
0.4868404907241280.271654512964317A A A 0.4118770626804140.547164684019978
0.497653919405633A A A LNCV6_49655_PI430048170 mRNA
GGGTCTGATTTTACTTGTCGTTATCTCCATCTTGGTTACCATAGTGACTATCATTACTTT NM_001257308 RefSeq chr5
+ 129748190 129765063 KIAA1024L 100127206 KIAA1024-like GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_135004_PI430048170 0.3691164674023971.26878868803252 0.324239440384494
1.06582296353867 0.26880140867203 A A A 0.2534896301827530.2634370418968
0.255576788616211A A A LNCV6_135004_PI430048170 mRNA
ATTATTATCTCTTTCCAGCCTCATTCAGCTATTCTTACTGACATACCAGTCTTTAGCTGG NM_001184866 RefSeq chr1
+ 161706971 161714352 FCRLA 84824 "Fc receptor-like A, transcript variant 1"
GO:0005737|GO:0005576|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136494_PI430048170 0.0980422408162370.5687979242132541.7524670172135
1.92139418176104 2.80399702613825 A A A 3.26111725359922 2.74619038658117
3.09835989903933 P P P LNCV6_136494_PI430048170 mRNA
ATGTCACTAAGTTGTCATCCCACATAAATTGATGTGCAGCATAGGGTATTAAATCTACAT NM_003112RefSeq chr7
+ 21428070 21514533 SP4 6671 Sp4 transcription factor
GO:0005737|GO:0006366|GO:0006357|GO:0000981|GO:0015630|GO:0008016|GO:0003713|GO:0005654|GO:0003
677|GO:0046872|GO:0045171 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135599_PI430048170 0.139597463367355 1.2037370921259 6.35112510710702
6.64272958225366 6.73606599627167 P P P 6.32498936942456 6.21111011607424
6.41161089277331 P P P LNCV6_135599_PI430048170 mRNA
TTAGCTGTTATACTGAGATGAAGAAGAAAACAGGTGGATTGCCTTGGTATTTAGGAAATA NM_198276RefSeq chr2
- 62500220 62506469 TMEM17 200728 transmembrane protein 17
GO:0042384|GO:0060170|GO:0035869|GO:0036038|GO:0016021|GO:0007224 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130477_PI430048170 0.30039958124713 1.0373990032776 0.355705929040802

0.3582822035148590.469818961446576A A A 0.3415211644677580.315691530873056
0.370134793821859A A A LNCV6_130477_PI430048170 mRNA
TTAACACAACTCTTTGTTCAAATGTACTATGGTCTCTTTTAGAGTCAGACTCCTAGACTC NM_001816RefSeq chr19
- 42580242 42594930 CEACAM8 1088 carcinoembryonic antigen-related cell adhesion molecule 8
GO:0006955|GO:0005886|GO:0007596|GO:0005887|GO:0031225|GO:0050900|GO:0005615|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135731_PI430048170 0.00816153430594237 1.89152995137839 12.762417648835
12.8432051842033 12.8272723674972 P P P 11.7874436881846 12.0829999006188
11.7842060898739 P P P LNCV6_135731_PI430048170 mRNA
AAAGCTAAGTGTCTGTGTGGCTGTGGAGCTCGAGGGTCTGTGAATAAAGGCGGCGGCACTNM_207368RefSeq chr17
- 81822360 81833294 FAM195B 348262 "family with sequence similarity 195, member B, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133886_PI430048170 0.0281151936006149 0.53438718184076 6.97441307922941
7.11011559648868 7.06497246410518 P P P 7.61606909089123 8.01535687877612
8.17730441679714 P P P LNCV6_133886_PI430048170 mRNA
CACTTCGAAAGGAAGCCTTTCCCCAGCTTGGCAGCTGAATAAACCAATAGCTTTGTACAT NM_017741RefSeq chr4
- 17800654 17810758 DCAF1654876 DDB1 and CUL4 associated factor 16
GO:0005515|GO:0016567|GO:0080008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141484_PI430048170 0.21692063034189 0.9159705467481160.418601419484671
0.3866320007317850.248123909084278A A A 0.34334708095207 0.537009736407115
0.549401879832168A A A LNCV6_141484_PI430048170 mRNA
TTTTTTAATCTTGTTTTCTGCTGTGCCCAAATTATTAATAAATCAGATTGCATTAAAAAA NM_053280RefSeq chr11 +
196760 200258 ODF3 113746 "outer dense fiber of sperm tails 3, transcript variant 1"
GO:0007275|GO:0007283|GO:0030154|GO:0001520 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144522_PI430048170 0.411105451313315 1.03066694761305 0.498778142163579
0.3714127736308260.381760684371413A A A 0.38988339902723 0.346633935311261
0.387788227481486A A A LNCV6_144522_PI430048170 mRNA
CTTTGTAGTACTACTTAAAAGCATGTCGGAATATAAGAATAAAAAGGATTATGGGAGGGG NM_020638RefSeq chr12
- 4368226 4379728 FGF23 8074 fibroblast growth factor 23
GO:0008286|GO:0048011|GO:0048015|GO:0042369|GO:0055062|GO:0005576|GO:0005105|GO:0006796|GO:0030
502|GO:0005615|GO:0030154|GO:0046888|GO:0010980|GO:0045668|GO:0007173|GO:0008543|GO:0030643|GO:0
045087|GO:0070374|GO:0045893|GO:0008083|GO:0090080|GO:0038095|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135990_PI430048170 0.0182229701463887 1.76230531993133 7.85328688801703
7.67747664714166 8.11059736369455 P P P 7.04122947296762 7.04024624314112
7.13840509715835 P P P LNCV6_135990_PI430048170 mRNA
CCTAAAAGCAGTATCTGTTATTTAGCTGTAAACCAAGTTGGAAGCTATTCGGATAATTTC NM_014888RefSeq chr7
- 121348850 121396368 FAM3C 10447 "family with sequence similarity 3, member C, transcript variant 1"
GO:0008150|GO:0005794|GO:0016023|GO:0007275|GO:0005576|GO:0005125|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_80757_PI430048170 0.0114528928287503 1.14498624915215 7.14836539928074
7.05739611594819 7.06168080666222 P P P 6.95307924370378 6.84146494641799
6.88655539037489 P P P LNCV6_80757_PI430048170 mRNA
TTCAATTTCGAACGTGGAACAGAGCAGGACATTTGCTTTTCGGCGAACTTCAACGTGGTT NM_001201380 RefSeq
chr9 - 41891889 42129504 CNTNAP3B 728577 contactin associated protein-like 3B
GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129812_PI430048170 0.0314794984129206 0.4934008935615223.5981493765181
3.29183215325708 3.25044358031094 P P P 3.92637016884955 4.52516005760956
4.66969143921506 P P P LNCV6_129812_PI430048170 mRNA

ATTTGTTTGATGGGTCCCAGGAAACACTAATAAAAACCACAGAGACCAGCCTGGAAAAAA NM_001206616 RefSeq chr11 + 34632463 34663287 EHF 26298 "ets homologous factor, transcript variant 1" GO:0003700|GO:0005794|GO:0006357|GO:0006366|GO:0008283|GO:0000981|GO:0005634|GO:0007275|GO:0000978|GO:0003677|GO:0001077|GO:0045944|GO:0030855|GO:0005654|GO:0045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130506_PI430048170 0.6131138045535130.9849601044488420.279113078483377 0.2884737467777280.391779082600851 A A A 0.3689007413600140.310657982669687 0.347525990614133 A A A LNCV6_130506_PI430048170 mRNA
TCTTGGATTTCCAGATTACACCAAAGACTGTTTCCAACTTGACTGAGAGCAGCTCCGAGT NM_000078 RefSeq chr16 + 56961922 56983844 CETP 1071 "cholesteryl ester transfer protein, plasma, transcript variant 1" GO:0017127|GO:0070328|GO:0044281|GO:0030301|GO:0005615|GO:0010874|GO:0008289|GO:0015914|GO:0015485|GO:0034364|GO:0034197|GO:0070062|GO:0008203|GO:0042632|GO:0010745|GO:0043691|GO:0055088|GO:0031210|GO:0005576|GO:0005548|GO:0055085|GO:0031982|GO:0006898|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140437_PI430048170 0.0797858850035443 0.9156641737600751 0.7459991808916 10.6944598967525 10.6580893186864 P P P 10.761616606545 10.9077680934091 10.8079587363796 P P P LNCV6_140437_PI430048170 mRNA
GCTGGAAATTTATATCAGTGTCTGGGCTCCCAAGAACATAAATGTAATTGCCAAAGCAAA NM_013393 RefSeq chr7 - 2234290 2242198 FTSJ2 29960 FtsJ RNA methyltransferase homolog 2 (E. coli) GO:0005739|GO:0031167|GO:0008283|GO:0006364|GO:0008650|GO:0005730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140339_PI430048170 0.7605479640288521.04297812363506 7.10235211404126 6.95696018408991 7.37028374441681 P P P 7.13025530614603 6.68963384001018 7.37664071604376 P P P LNCV6_140339_PI430048170 mRNA
ATGGGATTTACTCTGCTTTACCAGTTAGTTTCATAATAAACAAATAGTCTGTATCGCCTG NM_018370 RefSeq chr12 + 101877326 101923623 DRAM1 55332 DNA-damage regulated autophagy modulator 1 GO:0005737|GO:0006914|GO:0010506|GO:0006915|GO:0016021|GO:0005765|GO:0005764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138170_PI430048170 0.5006289611538690.8538547629091752.23015750564399 3.02317531865809 3.35071526143464 A A P 3.28333892330045 2.8352506257342 3.33496879389667 P P P LNCV6_138170_PI430048170 mRNA
AGGGCACCTGTAACTGGGAATCTGAGTTTGACCTAAAAGTCATTAAAATAACATGAATCA NM_174898 RefSeq chr2 - 99284237 99301176 LYG1 129530 lysozyme G-like 1 GO:0009253|GO:0016998|GO:0003796|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63321_PI430048170 0.2398589423367031.21502496501014 5.44848610567282 4.94668540486258 5.25498934183269 P P P 5.21751534893659 4.76876534473833 4.82176947586631 P P P LNCV6_63321_PI430048170 mRNA
ATGCAAATATCCTTGAAAAACAAGCAAAGGAGGAATCTGTGCCAGAAGTGGGATCCAGGC NM_001085423 RefSeq chr17 + 64449114 64468643 MILR1 284021 "mast cell immunoglobulin-like receptor 1, transcript variant L" GO:0043303|GO:0005887|GO:0033004|GO:0042629 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73343_PI430048170 0.0487293916238793 0.6672697066588619.73174600556805 9.69763150562249 10.1737701902552 P P P 10.2869700470352 10.3393215116174 10.735417106704 P P P LNCV6_73343_PI430048170 mRNA
GAGGGGGAGAACTTGGAGTTCATATGTATCTTCTTATTTTCTTGAAATTTGTACAAGCTG NM_001278712 RefSeq chr3 - 112532506 112561963 ATG3 64422 "autophagy related 3, transcript variant 2" GO:0005515|GO:0016567|GO:0000422|GO:0043653|GO:0000153|GO:0005829|GO:0019787|GO:0006612|GO:0019776|GO:0019777|GO:0000045|GO:0019899|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131997_PI430048170 0.4882392801922341.85796121158327 2.6792243233633

1.70906509588825 0.243280390449553 A A A 1.26285205368668 0.758196559606753
0.809925985471771 A A A LNCV6_131997_PI430048170 mRNA
AATAAGGATATGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTTCTTCCCTTTGA NM_001004459 RefSeq
chr11 - 58203203 58204181 OR1S2 219958 "olfactory receptor, family 1, subfamily S, member 2"
GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131582_PI430048170 0.00814528429501952 1.25989598395032 10.6432459209415
10.6197382357366 10.6545427992543 P P P 10.3338005045164 10.349426652226
10.2317984632802 P P P LNCV6_131582_PI430048170 mRNA
CTTGAGTATCTTCCCCACCCTATTAAATTACATCCGGTGCTTCGGCTTGTACAGAAAAAA NM_031288 RefSeq chr2
+ 74455022 74457960 INO80B 83444 INO80 complex subunit B
GO:0005515|GO:0006355|GO:0005886|GO:0005730|GO:0005634|GO:0006310|GO:0006351|GO:0046872|GO:0031
011|GO:0005737|GO:0006281|GO:0005654|GO:0006338 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127370_PI430048170 0.492548908433824 1.08668436135918 9.55838808962335
9.81477961808678 9.93465549719704 P P P 9.45797985965166 9.63089082305558
9.85653695578398 P P P LNCV6_127370_PI430048170 mRNA
TAGGAGACGTGGAATTGAGACTAATAACTTGGATGTTAACACTGTTTACTGTTTTTTCAC NM_003864 RefSeq chr4
+ 173370941 173377532 SAP30 8819 "Sin3A-associated protein, 30kDa"
GO:0005515|GO:0010467|GO:0006355|GO:0003714|GO:0006325|GO:0000122|GO:0035914|GO:0003677|GO:0046
872|GO:0006351|GO:0000118|GO:0045814|GO:0040029|GO:0005654 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_75820_PI430048170 0.392146747528204 1.18239648503741 0.36778200744741 0.369582806572849
0.96102600174465 A A A 0.351406047246092 0.326724326480622 0.378982919124966 A A A
LNCV6_75820_PI430048170 mRNA
AAACTGACTTGTAACTGGATCATCATTGTATTCTCCAAGATTTGTTTCTGTGCCCAACTT NM_173488 RefSeq chr5
- 102371781 102499016 SLCO6A1 133482 "solute carrier organic anion transporter family, member 6A1,
transcript variant 1" GO:0005215|GO:0005886|GO:0006810|GO:0016021 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129789_PI430048170 0.705504546398737 0.84330934335719 7.33893466988674
7.24803950779046 6.90254083148299 P P P 7.90808563385238 7.44620769804743
6.63676813377133 P P P LNCV6_129789_PI430048170 mRNA
TATTACGTTCCTGCCTGGGCCACTGACTTGGATAAATACAAATAAACCAAATACCATTCA NM_004734 RefSeq chr13
- 35768651 36131377 DCLK1 9201 "doublecortin-like kinase 1, transcript variant 1"
GO:0048675|GO:0021952|GO:0007417|GO:0009615|GO:0005524|GO:0007399|GO:0035556|GO:0048813|GO:0004
672|GO:0004674|GO:0005887|GO:0016197|GO:0006468|GO:0005057|GO:0030900|GO:0001764 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_67147_PI430048170 0.318957485525525 1.33526907143665 2.63405012279368 3.1359270648943
3.47733737785895 A P P 3.19501941087463 2.18535421834537 2.55258684426292 P A P
LNCV6_67147_PI430048170 mRNA
TTCGCTTTAACCACCCGGCTGAAGCCAAGTGGATGAAAAGCATGATTCCAGCAGGGGGCC NM_015157 RefSeq chr11
+ 118606497 118658038 PHLDB123187 "pleckstrin homology-like domain, family B, member 1, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122104_PI430048170 0.079885988190657 0.766521945800262 12.2853970168275
12.3838480868719 12.6898537602056 P P P 12.7791430784347 12.6831552032711
13.0530651934257 P P P LNCV6_122104_PI430048170 mRNA
CGAGCCCACTCGAGCCGCAGCCATGTCTGGGGACGAATGATTTTTGATCCTACTATGAGC NM_003908 RefSeq chr20
- 34088308 34112279 EIF2S2 8894 "eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa"
GO:0005515|GO:0005850|GO:0010467|GO:0002176|GO:0003723|GO:0003743|GO:0001701|GO:0006412|GO:0046
872|GO:0006413|GO:0005829|GO:0044267|GO:0008135|GO:0008584 . NA - . NA NA NA NA NA NA

NA NA NA
LNCV6_135918_PI430048170 0.0125510554102925 0.6948467916036755.63715075787992
5.41846523485874 5.3484910489128 P P P 5.91266239821601 6.06327128285492
6.01573219670198 P P P LNCV6_135918_PI430048170 mRNA
AAAGACTCCCTTTAGTCCCTTTTTCAATTAAAACCTATGGTGAAAAAGGCGTTTGCACTC NM_012118RefSeq chr4
+ 139015758 139045939 CCRN4L25819 CCR4 carbon catabolite repression 4-like (S. cerevisiae)
GO:0006397|GO:0048471|GO:0006355|GO:0033962|GO:0003700|GO:0006366|GO:0009991|GO:0000290|GO:0005
634|GO:0003729|GO:0046872|GO:0032922|GO:0045995|GO:0004535|GO:0005737|GO:0045668|GO:0000932|GO:0
010629|GO:0045600|GO:0032496|GO:0042752|GO:0007623|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140852_PI430048170 0.4148729869439821.18019122503921 5.88458432748934
5.59867089595958 5.65667612419085 P P P 4.88912020771774 5.62361162533766
5.77944437982382 P P P LNCV6_140852_PI430048170 mRNA
TCTTTGTGACTGAGCCAGTAGACTCACACTATATGCTTTTTTGGGTTTGCCCGTTCCTTCNM_001281773 RefSeq chr20
- 47209213 47356889 ZMYND8 23613 "zinc finger, MYND-type containing 8, transcript variant 7"
GO:0005515|GO:0001106|GO:0070491|GO:0008270|GO:0005634|GO:0000122 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145353_PI430048170 0.4761392260440930.8367136874482533.88837179334642
4.34543765616703 4.21321493140077 P P P 4.80320602281544 4.37917640451263
3.94796812810615 P P P LNCV6_145353_PI430048170 mRNA
AAGGCTGCTGTACTGGTTGAATTGTGTCCCCCTCAAATTCACATCCTTCTTGGAATCTCA NM_012275RefSeq chr2
+ 113059107 113064743 IL36RN 26525 "interleukin 36 receptor antagonist, transcript variant 1"
GO:0005149|GO:0001960|GO:0032715|GO:0045087|GO:0019221|GO:0005152|GO:0005615|GO:0005125|GO:0032
700|GO:0019732 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130595_PI430048170 0.8929452080683310.9901858493469059.77549626521443
10.0452986623674 10.0010752570306 P P P 9.83937324756164 9.94925002806 10.0800989762628 P
P P LNCV6_130595_PI430048170 mRNA
GTGTACCTCAGCTTTTTCCCTCACTTGCATCAATAAAGCTTCTGTGTTTGGAACAGCTAA NM_000608RefSeq chr9
+ 114329788 114333256 ORM2 5005 orosomucoid 2
GO:0006810|GO:0002682|GO:0072562|GO:0006953|GO:0005615|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_77030_PI430048170 0.00658585942839277 1.56703379026495 5.331147750586
5.25988082700835 5.22344127859 P P P 4.58458284163743 4.50808336169843 4.7673509387604 P
P P LNCV6_77030_PI430048170 mRNA
CCTTCAAGGTTTTCAGGGATCTAGGGGACACAAATCTAACAAATCCTAATGTATATTATT NM_001242894 RefSeq
chr6 + 28349913 28369177 ZKSCAN3 80317 "zinc finger with KRAB and SCAN domains 3, transcript
variant 1"
GO:0003700|GO:0006914|GO:0005634|GO:0000122|GO:0000978|GO:0003677|GO:0046872|GO:0006351|GO:0043
565|GO:0001078|GO:0005737|GO:0003682|GO:0010507|GO:0045893|GO:2000773|GO:0045892|GO:0007040 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137014_PI430048170 0.0463107198900236 0.7582847787291558.08205028523217
8.17182922040665 7.94811147613143 P P P 8.28940084471285 8.66054201586322
8.43390058117672 P P P LNCV6_137014_PI430048170 mRNA
CAGCCTTGTTTCTCATGTAATGCAGTGACGCTGTCATTAAACACGTGGATTCATGTGTGG NM_016263RefSeq chr19
+ 3506296 3536757 FZR1 51343 "fizzy/cell division cycle 20 related 1 (Drosophila), transcript variant
2"
GO:0005515|GO:0008284|GO:0031965|GO:0045732|GO:0070306|GO:0031572|GO:0090344|GO:0051437|GO:0051
436|GO:0031145|GO:0051439|GO:0005829|GO:0051488|GO:0040020|GO:0007067|GO:0006281|GO:0070979|GO:0
005680|GO:0005654|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_127337_PI430048170 0.19937468803178 1.14617042763311 5.84971534476459 5.6609295673506
5.80704084407683 P P P 5.3514286868863 5.6963612583657 5.661784319752 P P P
LNCV6_127337_PI430048170 mRNA
GTAGGTGATGGTATGATATCAAACTATTTTGCAGTTGTAAATAGGGGACAGATGGAAAAT NM_198516RefSeq chr11
- 11270873 11622014 GALNT18 374378 polypeptide N-acetylgalactosaminyltransferase 18
GO:0004653|GO:0000139|GO:0030246|GO:0006486|GO:0016021|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_50329_PI430048170 0.3248433284600050.5413617712758350.3800772073607060.404525509414068
1.77644766659524 A A A 0.5987313912075971.90011726502492 2.56811214414769 A A P
LNCV6_50329_PI430048170 mRNA
CTGTTTCATAGAGCAGAGGAAACAGGCGAAGAATCATTTTCAGTACAAAACGGTTCGATT NM_001277813 RefSeq
chr8 + 63168552 63212788 YTHDF3253943 "YTH N(6)-methyladenosine RNA binding protein 3,
transcript variant 2" GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130877_PI430048170 0.1496969303870760.3003720884075710.446772507616827
0.4441143342167630.254865686729298A A A 0.5648723969944782.44316294568588
2.61397476569116 A A P LNCV6_130877_PI430048170 mRNA
TCACCACCTGTCATGAAGCTTATCTGTTTTCTGATTTGAATAAACTTTGTGTTGTGCAAA NM_020122RefSeq chr2
+ 84971107 85059472 KCMF1 56888 potassium channel modulatory factor 1
GO:0016874|GO:0008152|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128088_PI430048170 0.00162687877489988 0.5655732378236354.01891571905619
4.10642077072876 3.92182570689387 P P P 4.78310292196343 4.73542261851667
4.98846519867375 P P P LNCV6_128088_PI430048170 mRNA
CAAGCTTTGGGTCTCTGGAGTATAACTTTTTGTAACATTAGCCATTATTTGGTAACAGAA NM_001195304 RefSeq
chr10 - 110898729 110919366 BBIP1 92482 "BBSome interacting protein 1, transcript variant 1"
GO:0005515|GO:0042384|GO:0005929|GO:0034464|GO:0005737|GO:0006996|GO:0015031|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144482_PI430048170 0.00342884162472381 2.12353069546727 7.50816174088128
7.46320037760994 7.52506724479146 P P P 6.51734808864427 6.44977916550826 6.2582658278723
P P P LNCV6_144482_PI430048170 mRNA
TAAAAGGCTCTAATACAACCTATAAGGACTGCAAAGTATGGCCAGGGGGTAGTCGGACTT NM_024684RefSeq chr11
+ 77821161 77872352 AAMDC 28971 "adipogenesis associated, Mth938 domain containing"
GO:0043066|GO:0005737|GO:0045944|GO:0045600 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129970_PI430048170 0.0682781982555215 0.6942235021789934.93613379094423
5.2661625494606 5.53203902361047 P P P 5.57294679922534 5.8533502726221
5.92523602778028 P P P LNCV6_129970_PI430048170 mRNA
AGCCTATCAACATAGTATAGTCAGCCAGAACATTAAAGTTTCTTTGTTTCAACTCTCACA NM_001080821 RefSeq
chr19 - 12390013 12401274 ZNF799 90576 zinc finger protein 799
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139876_PI430048170 0.1050160654984781.3345832838252 2.60944747432819
3.07610611537595 2.86917765372786 A P P 2.64217129262563 2.50869764317215
2.14821610242527 A A A LNCV6_139876_PI430048170 mRNA
TTATACTGCAGTATTATATGCTCCATGAGACTGTGGCACTTTCTGACATCATGGGGGCAG NM_054028RefSeq chr8
+ 11330985 11332186 SLC35G5 83650 "solute carrier family 35, member G5" GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144531_PI430048170 0.2004808165573481.06785374785371 0.514885434420382
0.3728440309926960.504402594686537A A A 0.2954701340768050.375240583475037
0.43804457309969 A A A LNCV6_144531_PI430048170 mRNA
CCCAGCTTCTTTCTCAATGAGAAAGAAAGCATGTGTATGTCTGTTTATGGCGACTTCAGG NM_017417RefSeq chr12

+ 4720585 4772726 GALNT8 26290 polypeptide N-acetylgalactosaminyltransferase 8
GO:0004653|GO:0006493|GO:0000139|GO:0030246|GO:0016266|GO:0016021|GO:0044267|GO:0046872|GO:0043
687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141580_PI430048170 0.0286304201429349 0.478104749359485 2.82982375613723
3.12874409031016 2.77730440051432 A P A 3.5036921083062 4.25884601910573
4.08897574597478 P P P LNCV6_141580_PI430048170 mRNA
GTAAGTTCCTGCATATTCATTATAAGATGGCAAATCAAACTTTTCTAGGATGAAGACAGC NM_003774 RefSeq chr12
- 89519412 89524806 GALNT4 8693 polypeptide N-acetylgalactosaminyltransferase 4
GO:0048471|GO:0005794|GO:0005975|GO:0016266|GO:0046872|GO:0004653|GO:0000139|GO:0006493|GO:0030
246|GO:0016021|GO:0044267|GO:0043687|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128111_PI430048170 0.565414514693293 1.12294745547889 2.3280262523291
2.22400532837757 1.99332763856971 A A A 2.04414962741035 2.48388953819994
1.29812375472013 A A A LNCV6_128111_PI430048170 mRNA
ACTGGATGGTCATTTGCATCTCCGTAAATGTGCTCTGCTCCTCAGCTGAGAGAGAAAAAA NM_000733 RefSeq chr11
+ 118304579 118316175 CD3E 916 "CD3e molecule, epsilon (CD3-TCR complex)"
GO:0005515|GO:0050852|GO:0017124|GO:0032753|GO:0005886|GO:0031295|GO:0050731|GO:0030159|GO:0045
879|GO:0050850|GO:0035556|GO:0042608|GO:0042105|GO:0007172|GO:0005911|GO:0042101|GO:0042102|GO:0
046641|GO:0001772|GO:0032729|GO:0046982|GO:0019901|GO:0007584|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_110733_PI430048170 0.176010766396924 1.12537429913082 0.652172261031469
0.393070358878768 0.627121811866363 A A A 0.286043708060703 0.410697482619188
0.472108721785459 A A A LNCV6_110733_PI430048170 mRNA
ACAGTCTGGCAGATCCAGTTTCCATCAAAGGGACCTCTCTTGTCACCAAAATTTAAAAAA NM_139073 RefSeq chr2
+ 230996123 231007284 SPATA3 130560 spermatogenesis associated 3 GO:0003674|GO:0005575 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139025_PI430048170 0.0222792513570012 1.49149005003956 11.1709528059258
11.4945514500511 11.5591156640129 P P P 10.819191958708 10.7191372258486 10.973753561686
P P P LNCV6_139025_PI430048170 mRNA
GATGGCCCATAAGGAATTCCAGACCAATATTTCTTCCTGCGGTTTATTCTATGTTTTATA NM_013242 RefSeq chr16
- 58113592 58129392 CFAP20 29105 cilia and flagella associated protein 20
GO:2000253|GO:0060296|GO:0018095|GO:0005929|GO:0005814|GO:0060271|GO:0005874|GO:0007275|GO:0005
634|GO:2000147|GO:0036064|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129530_PI430048170 0.364738443495564 0.872366472688544 8.30260297971038
8.08143204075122 8.18462371693399 P P P 8.09083499801336 8.39991468495255
8.62767638384782 P P P LNCV6_129530_PI430048170 mRNA
GGACATCTTTCCTCTGACACGTGGGAATGGGTGATATTTGTGTAATAAAATTTTTAAAAG NM_012308 RefSeq chr11
+ 67119268 67258079 KDM2A 22992 "lysine (K)-specific demethylase 2A, transcript variant 1"
GO:0000790|GO:0006355|GO:0005730|GO:0006325|GO:0005634|GO:0006303|GO:0006351|GO:0051864|GO:0045
322|GO:0070544|GO:0005654|GO:0008270|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131158_PI430048170 0.23522566239552 1.48861257499454 0.275451889369623
1.32730939754205 0.885772566772834 A A A 0.337702473034248 0.289259652571072
0.326863815866093 A A A LNCV6_131158_PI430048170 mRNA
CAACTTTTTAGGAGTGCTTCCTCACAGTTACCAAGAATAAAGAAAGCTGGCCACCATAAA NM_004271 RefSeq chr6
+ 6588700 6654983 LY86 9450 lymphocyte antigen 86
GO:0006954|GO:0005886|GO:0008283|GO:0045087|GO:0006959|GO:0031666|GO:0006915|GO:0005615 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144742_PI430048170 0.175324125412456 0.905178362860135 12.4949661818727
12.7214591053376 12.5228865964714 P P P 12.6308410168986 12.7585994575123
12.7870288986486 P P P LNCV6_144742_PI430048170 mRNA

TGTTTGTAATCCTTGGTTCGCCCGGTTTTCTGTTTTCAGTAAAGTCTCGTTACGCCAGCT NM_005354 RefSeq chr19 - 18279693 18281656 JUND 3727 "jun D proto-oncogene, transcript variant 1" GO:0005515|GO:0016922|GO:0014070|GO:0003700|GO:0044212|GO:0006357|GO:0006366|GO:0007568|GO:0043434|GO:0005634|GO:0009612|GO:0045669|GO:0043565|GO:0043234|GO:0003690|GO:0002076|GO:0045944|GO:0071277|GO:0032496|GO:0007623|GO:0005654|GO:0009416|GO:0019899|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133017_PI430048170 0.8985256919158830.9955682920497111.12766728335014 2.73231949574301 2.52582291473536 A A A 2.64719748492394 2.460250137693 1.52938703186391 P P A LNCV6_133017_PI430048170 mRNA
TCTGAATGGATTGATTCCAATAAAAGCATATATCATTGTGGTAGGGTAGGTGGGGCGGGG NM_174924 RefSeq chr16 - 20359169 20404711 PDILT 204474 "protein disulfide isomerase-like, testis expressed" GO:0031545|GO:0034976|GO:0016477|GO:0006457|GO:0005783|GO:0007286|GO:0003756|GO:0045454|GO:0007275 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144649_PI430048170 0.0189299099055464 0.2931314047091881.36159909946925 0.3166637544848310.499683488401997 A A A 2.57648436695238 2.34081707992102 2.76719811969334 P P P LNCV6_144649_PI430048170 mRNA
TTTTTACTTTTTTGCGTGTGGAGCTGTATTCCCGAGACCAACGAAGCGTTGGGATACTTC NM_003247 RefSeq chr6 - 169215779 169254114 THBS2 7058 thrombospondin 2 GO:0051965|GO:0005515|GO:0016525|GO:0005509|GO:0031091|GO:0005576|GO:0007155|GO:0008201|GO:0005604 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69475_PI430048170 0.0756953860640462 1.32331412813443 7.07216726953034 7.31660812847677 7.05251352984838 P P P 6.9688855133719 6.74337482339358 6.4927167983376 P P P LNCV6_69475_PI430048170 mRNA
TTTGATGCCATGTTCAACGGGGGAATGGCCACAACATCCACGGAGATTGAGCTGCCCGAC NM_017797 RefSeq chr19 - 1985447 2015703 BTBD2 55643 BTB (POZ) domain containing 2 GO:0005515|GO:0000932 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91564_PI430048170 0.0222872433341766 0.5163026835004041.93538468799309 2.28191398301584 2.51330368000571 A A A 3.34103893475929 2.80216529354177 3.42990389427358 P P P LNCV6_91564_PI430048170 mRNA
GAAGGAAAGTTAGACGTAACTTCTAATTTCTAGTTCCAGTAAGCATCTCTTCTTGGAAAA NM_001134456 RefSeq chr3 + 101779441 101828231 NXPE3 91775 "neurexophilin and PC-esterase domain family, member 3, transcript variant 1" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116597_PI430048170 0.0860260792381398 1.21623301540612 4.39797347906893 4.518410293041 4.1905184666306 P P P 4.16439557577304 4.03288767338275 4.07811407926757 P P P LNCV6_116597_PI430048170 mRNA
ATTAGGCCTCAGACCCAACTCTGGTCCTGGCTCCACAACAGTGGCTGCCACTCACTTTGT NM_000525 RefSeq chr11 - 17385248 17388659 KCNJ11 3767 "potassium channel, inwardly rectifying subfamily J, member 11, transcript variant 1" GO:0005886|GO:0008282|GO:0005783|GO:0007268|GO:0044281|GO:0005635|GO:2001259|GO:0005829|GO:0070852|GO:0005739|GO:0015272|GO:0014704|GO:0015467|GO:0043209|GO:0005249|GO:0008076|GO:0031072|GO:0071356|GO:0042391|GO:0043025|GO:0033198|GO:0006006|GO:0034765|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64380_PI430048170 0.7203494135040270.9545617831937380.4108553823917170.348216288466126 0.32311481004351 A A A 0.2559704565901480.3126965942314160.678750563536577 A A A LNCV6_64380_PI430048170 mRNA
AACTTGAAAAGATAATTCACCAAGTGGAAGAACGACTTGCAAATCCTGTGTCTGGTGGGG NM_001290083 RefSeq chr19 + 11597419 11619159 ZNF627 199692 "zinc finger protein 627, transcript variant 2" GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_127969_PI430048170 0.0198322471353055 0.187562110761172 0.277265878044384
0.287399252277767 0.500062843601203 A A A 1.98121340387109 2.91657161077367 3.1714805366071
A P P LNCV6_127969_PI430048170 mRNA
AACCAACCTGTGTATTAGGTGTTAGCCCCAATAGCCATGCATGAAATCTTTAAATAAAAG NM_015480 RefSeq chr3
+ 111071758 111137560 PVRL3 25945 "poliovirus receptor-related 3, transcript variant 1"
GO:0005515|GO:0005886|GO:0034329|GO:0060042|GO:0045216|GO:0042803|GO:0009566|GO:0043296|GO:0016
337|GO:0005913|GO:0002089|GO:0045211|GO:0016021|GO:0050839|GO:0007156|GO:0034332 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128339_PI430048170 0.241540130997482 0.807995300132543 0.462597001349243
0.49859222240976 0.417174710860019 A A A 1.02983260709564 0.426404857073301
0.783247935666682 A A A LNCV6_128339_PI430048170 mRNA
GCTAACTGGTAGAGAAATGGAGATTAACACTTTGTTAATGGAAACCTCCAAATAAAGGAA NM_019110 RefSeq chr6
- 28241704 28252296 ZKSCAN4 387032 "zinc finger with KRAB and SCAN domains 4, transcript variant
1" GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_54102_PI430048170 0.0806890356352998 1.20482308957242 7.0603416083871
6.82140141566153 7.11256999940142 P P P 6.76050919049794 6.6538654307699
6.78646650478115 P P P LNCV6_54102_PI430048170 mRNA
GACCTTCAGATGGAAGTAGTTACATTATAGATTACTATGGAACCAGACTTACAAGACTGA NM_032027 RefSeq chr1
- 61681046 61725423 TM2D1 83941 TM2 domain containing 1
GO:0001540|GO:0007186|GO:0005887|GO:0004930|GO:0005654|GO:0097190 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134533_PI430048170 0.792177790082219 1.01833683109382 13.0884298112167
13.1779690092024 13.3336238938136 P P P 13.089625593406 13.2121670852511
13.2264459616535 P P P LNCV6_134533_PI430048170 mRNA
GATACTTTTATACTTGTTTCTGCTTTTGCTGCTCTTGATCCCACCTTTGCTCCTGACAAC NM_003915 RefSeq chr20 -
35626030 35653909 CPNE1 8904 "copine I, transcript variant 3"
GO:0006629|GO:0005544|GO:0005215|GO:0001786|GO:0016192|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131540_PI430048170 0.128022133725987 0.289502951134778 2.3714746216305
1.98395605387672 2.54413880764569 A A A 2.58039938123296 4.44428772651226
4.58099062878018 P P P LNCV6_131540_PI430048170 mRNA
CCAGGGAGGACTGGGAACCTTATCTCTTGAGATATTTGCATAATTTATTTAATTTAAGCC NM_052934 RefSeq chr1
- 205913047 205943460 SLC26A9 115019 "solute carrier family 26 (anion exchanger), member 9,
transcript variant 1"
GO:0006820|GO:0006821|GO:0005886|GO:0009986|GO:0055085|GO:0005254|GO:0006885|GO:0010628|GO:0016
324|GO:0015301|GO:0015106|GO:0051117|GO:0008271|GO:0015701|GO:0016021|GO:0070062|GO:0006811 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141725_PI430048170 0.0798977249440176 0.799827838995423 7.89834098856119
8.23878415325781 8.18741220486242 P P P 8.40280196154545 8.29821840245213
8.59695780851814 P P P LNCV6_141725_PI430048170 mRNA
CAGCTAATTGGAAAACAGATGTCTTCTTCTGTCCTATTGATGCTGGTGTTTAAAAAACAT NM_024095 RefSeq chr12
- 48147788 48157594 ASB8 140461 ankyrin repeat and SOCS box containing 8
GO:0035556|GO:0005737|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76336_PI430048170 0.31440192778626 1.28877336699125 3.25656549220876 3.4368562956865
3.70656738840236 P P P 3.58715911414736 3.05284678914539 2.49355212457355 P P P
LNCV6_76336_PI430048170 mRNA
TCAACTTGATGAAGTTCGACAGCTATGCGCGCTTCGTCAAGTCCCCGCTGTACCGCGAGT NM_006480 RefSeq chr5
+ 177357842 177372598 RGS14 10636 regulator of G-protein signaling 14

GO:0008017|GO:0030054|GO:0005886|GO:0038032|GO:0030159|GO:0060291|GO:0005634|GO:0043620|GO:0030425|GO:0035556|GO:0001965|GO:0031914|GO:0005737|GO:0007059|GO:0043197|GO:0050769|GO:0045211|GO:0043407|GO:0070373|GO:0007051|GO:0007612|GO:0006979|GO:0005813|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134791_PI430048170 0.147158931188743 1.16466338656434 0.720890440931777 0.394463472050526 0.640168029005271 A A A 0.279907871413168 0.418947490066357 0.412379953201508 A A A LNCV6_134791_PI430048170 mRNA CAACCAATGATTGTTCAGTTAATGAATAAAAGGCCTTTGACACAGTTCACCTATTCATGT NM_001143763 RefSeq chr10 - 133553899 133565634 SYCE1 93426 "synaptonemal complex central element protein 1, transcript variant 3" GO:0000801|GO:0007130|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140991_PI430048170 0.853821708440136 0.988416681123973 8.73400333958783 9.05404992354249 9.48948198984479 P P P 9.23043932904114 9.00424921691634 9.18391616074142 P P P LNCV6_140991_PI430048170 mRNA GCTTTGATTGACTTGGATCTTTATATAGGATTTAATGGTTGCTCACTGAAAACTGAAGCT NM_032026 RefSeq chr8 - 124488494 124539088 TATDN1 83940 "TatD DNase domain containing 1, transcript variant 1" GO:0006308|GO:0004536|GO:0043229|GO:0005634|GO:0016888|GO:0000737|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144673_PI430048170 0.0330565267163504 1.19584062122982 0.687254229474586 0.828389216725002 0.883087819917074 A A A 0.651987727642268 0.473541377182104 0.499623625847712 A A A LNCV6_144673_PI430048170 mRNA GGAACTTCTCTCAATCTGCTTGGCTTGGCCTAGAGAAGTGGCCATTTTATCAACAGGAAA NM_199355 RefSeq chr16 - 77282127 77435114 ADAMTS18 170692 "ADAM metallopeptidase with thrombospondin type 1 motif, 18" GO:0001654|GO:0090331|GO:0006508|GO:0005578|GO:0008270|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139199_PI430048170 0.201193396462812 0.841733370061604 9.49262596676281 9.23799567888653 9.0114777481634 P P P 9.57164723381275 9.59816279230845 9.34501286015223 P P P LNCV6_139199_PI430048170 mRNA GCTGGAGGTGTGACACCTTCAGTTCTGTTCCTATTAAAGGACCTTCTGAAGGGCAAAAAA NM_203374 RefSeq chr19 - 55620740 55624575 ZNF784 147808 zinc finger protein 784 GO:0006355|GO:0002244|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135948_PI430048170 0.00358596414321287 1.91341563969799 8.22447043371474 8.06233266889726 8.18221133555795 P P P 7.40607387758192 7.0834403230677 7.15570707521353 P P P LNCV6_135948_PI430048170 mRNA CCCCATCTTTGTCTTGAAACAAAAACTGTTTTAAGACGTCTACGTTGAATTATTCAGAGA NM_006855 RefSeq chr22 + 38468061 38483447 KDELR3 11015 "KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3, transcript variant 1" GO:0046923|GO:0005789|GO:0016021|GO:0006621|GO:0016192|GO:0015031|GO:0006987|GO:0044267|GO:0030968 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132934_PI430048170 0.779821280567168 0.964082825049862 0.375673382583888 0.376196831126235 0.316823167063895 A A A 0.652950377289971 0.295483691650357 0.244112767370173 A A A LNCV6_132934_PI430048170 mRNA AATGGGGATTGGTGGAAAACTCCTGACTGGTATTACTGGGTTTGGTATAATTTAATTTAA NM_016519 RefSeq chr4 + 70592257 70607287 AMBN 258 ameloblastin (enamel matrix protein) GO:0030345|GO:0008283|GO:0005578|GO:0042475|GO:0007155|GO:0031214|GO:0008083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136843_PI430048170 0.583424037709509 1.06110482603261 6.80517910636597 6.79220066944231 7.14520581924569 P P P 6.77617197479134 6.80341334667754 6.930043711489

P P P LNCV6_136843_PI430048170 mRNA
GTGGGGCAGAGGCTTTTTAAAAACATGTGATTAGGGAGCTATCTTTATCTGAATAATAAC NM_001098621 RefSeq
chr14_KI270847v1_alt + 299591 301642 TMEM251 26175 "transmembrane protein 251, transcript variant
1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142688_PI430048170 0.0394343023823807 1.67809996629151 4.80063419529109
4.81407978750133 4.34791234361948 P P P 4.2769332046666 3.75722668915543
3.65518669164605 P P P LNCV6_142688_PI430048170 mRNA
ATGTTTTGGAATGGCCAGAGTGAGGCAAAGGGGATCCCTGAAATAACATTAGAACATACA NM_001012361 RefSeq
chr9 - 113315650 113340340 WDR31 114987 "WD repeat domain 31, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_139904_PI430048170 0.000282574897987559 0.69757781127026610.7395471723925
10.6355492973004 10.6940535570462 P P P 11.2697729607349 11.1928880602513
11.1650419112076 P P P LNCV6_139904_PI430048170 mRNA
GAGGACCAGGGCTGGCAGATGTTGTCTACCTGCTGAAGAATAAAGATTTCTTTTGGTAAA NM_022362RefSeq chr10
- 97458323 97498609 MMS19 64210 "MMS19 nucleotide excision repair homolog (S. cerevisiae),
transcript variant 1"
GO:0005515|GO:0016226|GO:0030331|GO:0003713|GO:0005819|GO:0030159|GO:0005634|GO:0044281|GO:0006
259|GO:0006351|GO:0006974|GO:0000160|GO:0005737|GO:0007059|GO:0006281|GO:0016020|GO:0005654|GO:0
009725|GO:0006289|GO:0045893|GO:0030674|GO:0005675|GO:0071817 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_145172_PI430048170 0.188921281055151 0.8552738291576099.61925348899071 9.7057038868229
9.88061614755856 P P P 9.75023220589976 9.98163075813703 10.1367737305051 P P P
LNCV6_145172_PI430048170 mRNA
GTCTGTGTCTTTTTTCCATGAGAAATCACTGTTGCAAATTGCCTATAAATTGACTCTACTNM_001184705 RefSeq chr4
+ 107989713 108035175 HADH 3033 "hydroxyacyl-CoA dehydrogenase, transcript variant 1"
GO:0014823|GO:0032868|GO:0006635|GO:0042493|GO:0005743|GO:0070403|GO:0003857|GO:0044281|GO:0005
739|GO:0005737|GO:0005759|GO:0005654|GO:0046676|GO:0044255 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_131021_PI430048170 0.481389681612195 0.90358264188068 5.33426237844675
5.00736984642665 4.69492804974633 P P P 5.02613273233051 5.32569306030913
5.17869280009955 P P P LNCV6_131021_PI430048170 mRNA
TCACCTGGAGAGAGAGAGGGAAAGCTGTGCCAGAAATAAATGGTTATTGAGGTCAAAAAA NM_001164458
RefSeq chr7 - 150247211 150323669 ACTR3C 653857 "ARP3 actin-related protein 3 homolog C (yeast),
transcript variant 1" GO:0034314|GO:0008150|GO:0003674|GO:0005885|GO:0003779|GO:0005524|GO:0070062
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138231_PI430048170 0.429411863793617 1.30671183456576 2.7373736388158
2.01530142394552 1.6356874585795 A A A 1.68909739279539 1.64903826560066
2.07528206308183 A A A LNCV6_138231_PI430048170 mRNA
GGAGGGGTGGGAACATTTTTATGGCTTTATGAATTGGAATTTCATAGGCTTATTTACCTA NM_004746RefSeq chr18
- 3496031 4455266 DLGAP1 9229 "discs, large (Drosophila) homolog-associated protein 1,
transcript variant 1" GO:0005515|GO:0030054|GO:0045211|GO:0007268|GO:0005575 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_126913_PI430048170 0.6660674185618381.13660016194787 1.21962277845925
0.4014114792193070.420100130029468A A A 0.43442202148006 0.778838093400129
0.401767521563974A A A LNCV6_126913_PI430048170 mRNA
CATCTGAAGAAGGAGATAAAGATACACCAGTGGCAATATTTTATGCAATAGTAATCCCAT NM_001005517 RefSeq
chr3 + 98353853 98354819 OR5K4 NA "olfactory receptor, family 5, subfamily K, member 4" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129694_PI430048170 0.484393813340996 0.974623271772836 0.494476884165153

0.5174267167854590.405286627553312A A A 0.5153106102555750.448001055944261
0.56515422647896 A A A LNCV6_129694_PI430048170 mRNA
AAGTGGGTACATAACATTTTCAGGGAAAGGTGACTTGAAACGTAGTTTTAAATTAGAACG NM_005454RefSeq chr9
- 14719733 14722717 CER1 9350 "cerberus 1, DAN family BMP antagonist"
GO:0071773|GO:0003419|GO:0001657|GO:0007369|GO:0008285|GO:2000381|GO:0035582|GO:0023019|GO:0030
178|GO:0032926|GO:0005576|GO:0030509|GO:0030282|GO:0009952|GO:0005125|GO:0005615|GO:0042803|GO:0
007399|GO:0030514|GO:0016015|GO:0042074|GO:0009948|GO:0036122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128754_PI430048170 0.2271295057542780.7287484681954234.02917088629456
2.98604643804713 3.57994736160975 P P P 4.14198693836457 4.14890970699692
3.83702756303973 P P P LNCV6_128754_PI430048170 mRNA
GTCTTCCGTGTCCGGGTGGGCTGAAAGTTTTTAATAAAATTTTAGCTAAACATTTGTTTA NM_001080435 RefSeq
chr15 + 82809627 82834861 WHAMM 123720 "WAS protein homolog associated with actin, golgi
membranes and microtubules"
GO:0008017|GO:0097320|GO:0005874|GO:0030032|GO:0071933|GO:0003779|GO:0006888|GO:0005737|GO:0000
139|GO:0033116|GO:0048041|GO:0051127|GO:0007015|GO:0017049|GO:0030659 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140296_PI430048170 0.0564582224352798 0.6500478892361238.63396266546093
8.05373106609388 8.12083030195451 P P P 8.82860630197943 9.06483090430386
8.83899965435734 P P P LNCV6_140296_PI430048170 mRNA
CCCCCTTTCCCCACTTCCTTGACTGCTGTGATGTGAATTAAAGATAAATACGTGATACTG NM_004947RefSeq chr3
+ 50675240 51384198 DOCK3 1795 dedicator of cytokinesis 3
GO:0043547|GO:0005515|GO:0005085|GO:0017124|GO:0005737|GO:0007264 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141569_PI430048170 0.000559828039809161 1.37749830823754 11.3017232891643
11.3105229417499 11.3833623857913 P P P 10.8604551361481 10.9316911816506 10.816355839703
P P P LNCV6_141569_PI430048170 mRNA
TGTACAGGGCTAGGTTTTTTCAATGAAGTTTCTGTATTAAAGGAGTGGCTCTGGAAAAAA NM_001304563 RefSeq
chr16 + 29996208 30005790 INO80E 283899 "INO80 complex subunit E, transcript variant 3"
GO:0006260|GO:0005515|GO:0031011|GO:0006355|GO:0006281|GO:0005730|GO:0006310|GO:0005654|GO:0005
634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145567_PI430048170 0.5129937403644680.7319023104898580.718613845091893
0.5009534516242420.351226953050838A A A 0.4957792321196040.38465347507198
1.68221257849562 A A A LNCV6_145567_PI430048170 mRNA
CAACATCCACACTAGGCAGGAATATGAGGTGTAAACTCACAAACACTTGGCTCCTAGAGA NM_012351RefSeq chr1
+ 159439721 159440810 OR10J1 26476 "olfactory receptor, family 10, subfamily J, member 1"
GO:0007338|GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0005887|GO:0004930|GO:0007606 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127040_PI430048170 0.1127398282244061.47042188498481 5.64457951997784
5.99953935358884 6.37600608971091 P P P 5.28928665091156 5.5826915754558
5.55417424750155 P P P LNCV6_127040_PI430048170 mRNA
GGTCCTGAAGGAAATTCTTATAACTCAACATTTGTCTGGTCTTATAAGTAAAGACAGCTT NM_006952RefSeq chr3
+ 119173577 119205153 UPK1B 7348 uroplakin 1B
GO:0016324|GO:0005198|GO:0030855|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145490_PI430048170 0.4158822924916030.5697148680275990.418317881926959
0.4143590927923230.311646234722431A A A 2.083914883677 0.408603541629258
0.374587339248774A A A LNCV6_145490_PI430048170 mRNA
TAACAGCTCTCTTCAATGACATAGAAAGTTCATGGAACTCATGTTTTTAAAGGGCTATGT NM_031409RefSeq chr6

+ 167122752 167139141 CCR6 1235 "chemokine (C-C motif) receptor 6, transcript variant 2"
GO:0070098|GO:0005886|GO:0002407|GO:0006928|GO:0007204|GO:0007165|GO:0006955|GO:0006968|GO:0006
935|GO:0007186|GO:0005887|GO:0045087|GO:0006959|GO:0004950|GO:0016493|GO:0004872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128113_PI430048170 0.00043811927379171 0.56821123229384 7.7225412767242
7.62419644709634 7.7197941333562 P P P 8.539453525152 8.40359729380587
8.56689745731385 P P P LNCV6_128113_PI430048170 mRNA
CCTGCCTTTGTACTTTAAACTCATGGAAGGATAACTACCTTCACGTTTTGAAATAAATGT NM_001001417 RefSeq
chr17 - 36165680 36176624 TBC1D3B NA "TBC1 domain family, member 3B" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140483_PI430048170 0.4363620247953981.09536376373511 0.368866108268776
0.3676442012362090.74258762846537 A A A 0.4022168176917420.332687446986908
0.382321222641376A A A LNCV6_140483_PI430048170 mRNA
AACAATGAGCCCTAAGAACCAATGAGAAGTCCGAAGGTGAGAACTATCCAATGAGAGTGG NM_001040025
RefSeq chr17 - 81681193 81683924 ARL16 339231 ADP-ribosylation factor-like 16
GO:0005622|GO:0007264|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104024_PI430048170 0.000154153222389498 0.7279149013762851 2.4381104912284
12.3599843176974 12.4241346135793 P P P 12.8876998790253 12.884551943205
12.8247826345617 P P P LNCV6_104024_PI430048170 mRNA
GAGACTGTAACTAGTGATGTTTGTACAACCAAAGACTCTATTTTGTGGTTTAAGGAGAAT NM_182706RefSeq
chr8_KI270816v1_alt - 267966 292426 SCRIB 23513 "scribbled planar cell polarity protein, transcript
variant 1"
GO:0005515|GO:0016080|GO:0005886|GO:0008283|GO:0060088|GO:0035089|GO:0034750|GO:0016323|GO:0016
337|GO:0005913|GO:0008105|GO:0005911|GO:0045211|GO:0001921|GO:0016032|GO:0060603|GO:0021747|GO:0
031252|GO:0070062|GO:0035748|GO:0043065|GO:0001843|GO:0060561|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131229_PI430048170 0.4018636711797210.9462473242515347.16828433911819
7.29652501299755 7.03414471915278 P P P 7.32271144592193 7.22530513996589
7.19902134950526 P P P LNCV6_131229_PI430048170 mRNA
AAATCCTCCCCTACTTCATTGTATAATAAAGAATTTGGCCTTTGTCTTCAGTTCCTGAAA NM_014311RefSeq chr12
- 54180357 54188994 SMUG1 23583 "single-strand-selective monofunctional uracil-DNA glycosylase 1,
transcript variant 1"
GO:0004844|GO:0005515|GO:0005730|GO:0000703|GO:0003677|GO:0043231|GO:0019104|GO:0006281|GO:0017
065|GO:0006284|GO:0045008|GO:0006285|GO:0005654|GO:0000737 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145155_PI430048170 0.40240299050518 0.98164303954169 0.375188490545911
0.3896334385066420.343556490402315A A A 0.4401478196878140.358409522236248
0.389210315586969A A A LNCV6_145155_PI430048170 mRNA
ACACTCAAGACTGTCACAGTGCAGGGCAAGACTGAGACACTGGAAGTGGAGCTGCAGGTG NM_001039213
RefSeq chr19 + 44699150 44710714 CEACAM16 NA carcinoembryonic antigen-related cell adhesion
molecule 16 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112152_PI430048170 0.0112675127535824 0.5506781455101788.07736807907322
8.0809625446965 8.38940820524771 P P P 8.7509303647734 9.13085444078518
9.22811857310133 P P P LNCV6_112152_PI430048170 mRNA
ACTTGTCCTATAGTACATGACAGGGCTGAGAGTGGACTGTAGTTCTTAGCTGAACCCTTT NM_032012RefSeq chr9
- 109015134 109119945 TMEM245 23731 transmembrane protein 245
GO:0008150|GO:0003674|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129095_PI430048170 0.4291062753399520.8921649721613958.78217220290133
8.58502661907591 8.68067703972788 P P P 8.54841934873051 9.06371329303297

8.88970812162152 P P P LNCV6_129095_PI430048170 mRNA
GCTAGCATTACTAACCAACTGTTGGAAGCTCTGAAAATAAAAGATCTTGAACCCATAAAA NM_001789 RefSeq chr3
- 48157177 48188311 CDC25A 993 "cell division cycle 25A, transcript variant 1"
GO:0005515|GO:0009314|GO:0019901|GO:0008283|GO:0000079|GO:0035335|GO:0005829|GO:0006260|GO:0034
644|GO:0000082|GO:0007067|GO:0000086|GO:0051726|GO:0005654|GO:0000278|GO:0004725|GO:0051301 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113737_PI430048170 0.292961810511851 0.649398070470693 1.42825809859373
0.290581739090794 1.27537751024844 A A A 0.926789014700098 1.75117053905886
2.16600404343383 A A A LNCV6_113737_PI430048170 mRNA
TTTCAGTCCTGTCCAGCTGCATCAGCTTCGAGCTCAGATTTTAGCTTATAAAATGCTGGC NM_003070 RefSeq chr9
+ 2015218 2193623 SMARCA2 6595 "SWI/SNF related, matrix associated, actin dependent regulator
of chromatin, subfamily a, member 2, transcript variant 1"
GO:0005515|GO:0071565|GO:0000790|GO:0030308|GO:0008285|GO:0044212|GO:0006325|GO:0005634|GO:0035
887|GO:0071564|GO:0043231|GO:0042393|GO:0016514|GO:0045944|GO:0006338|GO:0045111|GO:0008094|GO:0
006355|GO:0001105|GO:0006357|GO:0003713|GO:0004386|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133763_PI430048170 0.152651548647661 0.738673211735854 6.08487643818648
5.68106708230104 5.36101202105556 P P P 6.21521227891715 6.11109671085525
6.20101940883632 P P P LNCV6_133763_PI430048170 mRNA
ATTATGAGGGTGGTGATGGTCCCTGTTAAGGACTATTGTGTGCTTGCAAGTTGGCATGTA NM_001164692 RefSeq
chr14 + 24310150 24312053 LTB4R2 56413 "leukotriene B4 receptor 2, transcript variant 2"
GO:0051546|GO:0016020|GO:0007186|GO:0006935|GO:0005886|GO:0005887|GO:0001632|GO:0007194|GO:0004
974 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143103_PI430048170 0.264639833462048 0.872545547162244 0.260453581979555
0.282967797037915 0.34811655321745 A A A 0.389672623873553 0.726529280071928
0.334947281319795 A A A LNCV6_143103_PI430048170 mRNA
CAATGGGAATTGATTCTGTTTATTGTCTGTACCATTTTGCTACCAGTTACATTGAACTGC NM_198503 RefSeq chr1
- 196225780 196608431 KCNT2 NA "potassium channel, sodium activated subfamily T, member 2,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116029_PI430048170 0.602812985448137 1.096419093714 5.17495583401275
5.06053079579327 5.13432924736715 P P P 4.28162592809769 5.03238418087181
5.43442390086468 P P P LNCV6_116029_PI430048170 mRNA
AGAATCAAGCAGTGAAAGGAAAAGTTGCTGGAGCACTCCTGAGAGCCATCTTCAAAGGTT NM_001113378 RefSeq
chr15 + 89243962 89317131 FANCI 55215 "Fanconi anemia, complementation group I, transcript
variant 1"
GO:0005515|GO:0007049|GO:0005737|GO:0006281|GO:0016020|GO:0005886|GO:0070182|GO:0031398|GO:0005
654|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134500_PI430048170 0.000355003771690321 5.19932748358601 5.38179660096091
5.76499509341135 5.47948964822976 P P P 2.86758783258458 3.3824198893364
3.22229668503909 P P P LNCV6_134500_PI430048170 mRNA
ATGAGATCCGTGCTTTTATCTTGTCTCAGACTCCCAATGATAGGCACATACTCTCCTCTG NM_001294306 RefSeq
chr19 + 36773117 36777078 LOC728485 728485 uncharacterized LOC728485 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_145302_PI430048170 0.00364935910082595 1.65607400951662 6.06275551553035
6.32371733939886 6.24418843333822 P P P 5.6239194737783 5.50059844281287
5.31890229762009 P P P LNCV6_145302_PI430048170 mRNA
TACTTCAATGAGGCCTTCACCTTCCTGGTGCCCTTCAGCCAGGTCCAGAATGTGGACCTG NM_001290332 RefSeq
chr11 + 1834309 1837521 SYT8 90019 "synaptotagmin VIII, transcript variant 1"
GO:0005215|GO:0005886|GO:0001669|GO:0016021|GO:0007340|GO:0048306|GO:0008021 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_134068_PI430048170 0.1813657230102111.18574003418611 4.51537026702169
4.78685281821374 4.70253426637042 P P P 4.57477454819224 4.16499847877308
4.50826531533244 P P P LNCV6_134068_PI430048170 mRNA
GCGTACTGCCTGTGAAAATCTGACTTTGGCAAATCAAATCCTCTTTTCCTTTTGAAAAAA NM_000434RefSeq
chr6_GL000252v2_alt - 3106829 3110710 NEU1 4758 sialidase 1 (lysosomal sialidase)
GO:0006665|GO:0009313|GO:0030054|GO:0005886|GO:0006687|GO:0004308|GO:0044281|GO:0005765|GO:0005
764|GO:0043231|GO:0052794|GO:0016042|GO:0052796|GO:0052795|GO:0016023|GO:0006488|GO:0044267|GO:0
070062|GO:0043687|GO:0018279|GO:0043202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134905_PI430048170 0.0358954565350995 2.29830282474782 2.20660144689734
3.01017557621891 2.90044136551717 A P P 1.6791695887361 1.49992248870225
1.44988302343391 A A A LNCV6_134905_PI430048170 mRNA
CCTTCACTTCAAAGAAGTCAAATTTCATGAAGAAAACCTCTGGCACATTGACAAATACTA NM_176813RefSeq chr7
- 16859405 16881989 AGR3 155465 anterior gradient 3
GO:0005515|GO:0008150|GO:0002162|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135278_PI430048170 0.3575782329706990.7191470015640250.620218691393531
2.57525818826365 0.515870533959398A A A 2.18828459906512 2.19987803689388
1.70527904794961 A A A LNCV6_135278_PI430048170 mRNA
GAAAACCAGTATCTGCCAGGTGCTCAGTGACTGGCCATCACATTAATGAATGACGAGATT NM_004070RefSeq chr1
+ 16021990 16034050 CLCNKA 1187 "chloride channel, voltage-sensitive Ka, transcript variant 1"
GO:0007588|GO:0044070|GO:0034220|GO:0005886|GO:0005887|GO:0005247|GO:0034707|GO:0006810|GO:0034
765|GO:0055085|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135410_PI430048170 0.0535858917700899 0.9521154523029530.418894793407615
0.3546728453855810.369454943905486A A A 0.4728613507789040.46520830536329
0.417492859337826A A A LNCV6_135410_PI430048170 mRNA
AAGAAAGAAATGGAAGAGGTCTGGAAAATCGTCCGGAAGCTGCTGATTGAGGGCTTAAGA NM_001145011
RefSeq chr16 + 4556489 4600317 C16orf96 NA chromosome 16 open reading frame 96 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105370_PI430048170 0.6936813813568521.07052899668039 8.13864776504271
8.19200885098973 8.67168653776156 P P P 8.14551035372015 8.14953772726549
8.45216194666138 P P P LNCV6_105370_PI430048170 mRNA
ATGAAGCTCCCCTTTATGAAATATTCTCCCAGGAAAATCTAGAAGATAATGATGTCTCAG NM_016104RefSeq chr6
+ 116571366 116593601 RWDD1 51389 "RWD domain containing 1, transcript variant 2" GO:0005515 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126894_PI430048170 0.0177011396401188 0.7467474733636556.14313950422817
6.18434516662398 6.40488215192815 P P P 6.52931302535166 6.71122749688146
6.75962131819917 P P P LNCV6_126894_PI430048170 mRNA
CTGGTACTTCCTTTCAGTAGGGCGCTAATGTATACACATTAATGATAAGTTGATAACATT NM_003272RefSeq chr1
+ 236142531 236208909 GPR137B 7107 G protein-coupled receptor 137B
GO:0016020|GO:0005887|GO:0005765 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91840_PI430048170 0.3002668500642030.8595280945697465.74547439983926 5.58418173135831
6.15994320070651 P P P 6.18630754359843 6.00880623192521 6.00464052394948 P P P
LNCV6_91840_PI430048170 mRNA
AAGCCGTCTACCCACTATATACCATTGTATTTATCTATTACGCATTCTGCTTGGTATTAANM_001284201 RefSeq chr14
+ 59484442 59505406 JKAMP 51528 "JNK1/MAPK8-associated membrane protein, transcript variant 3"
GO:0006986|GO:0005789|GO:0016021|GO:0030433|GO:0031625 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143952_PI430048170 0.000105106392773383 2.33640759179057 7.65217980597095
7.84488901191531 7.70137000268326 P P P 6.59824008175753 6.4940698832852

6.43553733937139 P P P LNCV6_143952_PI430048170 mRNA
GCTCATGCACAGTTTAGGCCATGTACAGCTGGCATCTAATAAATGTTTTCATGAAAAAGA NM_181304RefSeq chr14
+ 22829882 22835037 MRPL52122704 "mitochondrial ribosomal protein L52, transcript variant 4"
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0006412|GO:0005
762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130075_PI430048170 0.0218768645189892 1.54069308834102 7.42788380229189
7.74462924502521 7.86351551744527 P P P 6.94690446195085 6.97362369204096
7.25805874416988 P P P LNCV6_130075_PI430048170 mRNA
AGTCAGTGATAACCACTGACCAGATGCTATCAATACACTATGTGTCCTTTTTAGAATAAA NM_033028RefSeq chr15
+ 72686178 72738476 BBS4 585 "Bardet-Biedl syndrome 4, transcript variant 1"
GO:0005515|GO:0007608|GO:0034452|GO:0034451|GO:0007286|GO:0015031|GO:0045494|GO:0032402|GO:0001
947|GO:0001895|GO:0071539|GO:0045444|GO:0030534|GO:0000242|GO:0003085|GO:0001103|GO:0005813|GO:0
006996|GO:0032465|GO:0000281|GO:0005814|GO:0046548|GO:0048487|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127999_PI430048170 0.8050114924473251.01084402484705 0.430250833464322
0.5178503047876920.47718667602477 A A A 0.5271392481684020.505782384857859
0.339825969641131 A A A LNCV6_127999_PI430048170 mRNA
ACAGGGCCTGGACCTCTAAAATTTTGCAAAAACAAAAGGTTCTAAGATGATTTCAGGAAA NM_001289987 RefSeq
chr6 - 75308083 75493829 FILIP1 27145 "filamin A interacting protein 1, transcript variant 1"
GO:0005737|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128028_PI430048170 0.3205467092466121.25674323905991 0.348164239993427
1.03048934554094 0.369093442571515 A A A 0.2884496395952210.2783185017212
0.300854895320492 A A A LNCV6_128028_PI430048170 mRNA
CCAGGTCCCAAAAGAAAAGGCCACAGATTCGAGGCAACAATAAAGATTTATCTTGTTGTC NM_182575RefSeq chr19
- 48740887 48746909 IZUMO1 284359 izumo sperm-egg fusion 1
GO:0007338|GO:0035036|GO:0005886|GO:0007342|GO:0005102|GO:0016021|GO:0007155|GO:0002080|GO:0042
803|GO:0032504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126796_PI430048170 0.0997693568718011 1.17476196200171 5.31920092919601
5.24588947008657 5.04318918455046 P P P 4.93476266971382 5.10422579730263 4.8763319423181
P P P LNCV6_126796_PI430048170 mRNA
GGCACTCATGTGAAGCCCACCCCTCTGTGGTCAGTAAATTCTCCAGAAAGCGCCAAAAAA NM_001114748 RefSeq
chr1 - 1534777 1540360 TMEM240 339453 transmembrane protein 240 GO:0097060|GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139818_PI430048170 0.0974223079457322 0.7870077386929517.9458577592617
8.0315701700801 8.14719398382724 P P P 8.26309334285507 8.24386183740005
8.62806696909464 P P P LNCV6_139818_PI430048170 mRNA
CAGAAATTGGACTTTGGTTTTCAGACATGGGACTCTCATGTTAACAAAGAATAAATAAGC NM_004569RefSeq chr14
- 67589305 67600300 PIGH 5283 "phosphatidylinositol glycan anchor biosynthesis, class H"
GO:0017176|GO:0006501|GO:0005783|GO:0016254|GO:0005789|GO:0003824|GO:0044267|GO:0006506|GO:0006
464|GO:0000506|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101370_PI430048170 0.5352992055406460.7721215039582342.62072832713003
2.82750684717804 3.33462459706843 A A P 3.82740308919318 2.50579927673762
3.37149906270861 P A P LNCV6_101370_PI430048170 mRNA
TCAACAGACGAGGATTCACTTCCAAAGAGACATATTATGCAAGGAAGCAACTTGGAAGAGNM_032423RefSeq chr19
+ 52397867 52418404 ZNF528 84436 zinc finger protein 528
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_107770_PI430048170 0.0899572482731709 0.6000079558360383.29166435660173
3.88058366132274 4.15484983112062 P P P 4.49955126026773 4.55421472564917

4.61128364744515 P P P LNCV6_107770_PI430048170 mRNA
CAATGGAATTTTCTCTGATCATTGTTACAGTGTCTGTTCTATGAGACAGCCAGATTTAAA NM_016331 RefSeq chr3
+ 179323762 179335535 ZNF639 51193 "zinc finger protein 639, transcript variant 1"
GO:0005515|GO:0003700|GO:0044212|GO:0030307|GO:0005634|GO:0046718|GO:0000978|GO:0043621|GO:0046
872|GO:0006351|GO:0043923|GO:0043922|GO:0001077|GO:0045944|GO:0005654|GO:0045892 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141482_PI430048170 0.755826685421577 1.07874649358664 0.381968466880911
1.49451340823715 1.13841803364938 A A A 0.250563807688929 1.70065751165988
0.506432177489966 A A A LNCV6_141482_PI430048170 mRNA
CCATGGCCCCTGTTGTTGAAGTACGTAGGAAACTGAATACATAACTGCAATCTGAAAAAA NM_024410 RefSeq chr8
+ 102551619 102561017 ODF1 4956 outer dense fiber of sperm tails 1
GO:0019904|GO:0007275|GO:0005634|GO:0007283|GO:0030154|GO:0001520 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_52015_PI430048170 0.87505434530978 1.0069244346882 0.512674334967451 0.45527188990212
0.356300694780529 A A A 0.378658104852019 0.463507720196616 0.455026165711372 A A A
LNCV6_52015_PI430048170 mRNA
TGGAAGTTTTGCACTGCATCTTAACTGAAAGCCCAGAAGCCTTAAATCTGATAGCGGAGG NM_001036 RefSeq chr15
+ 33310961 33866103 RYR3 6263 "ryanodine receptor 3, transcript variant 1"
GO:0005516|GO:0048471|GO:0048763|GO:0030314|GO:0071286|GO:0051481|GO:0005509|GO:0006941|GO:0071
313|GO:0033017|GO:0055085|GO:0071318|GO:0034220|GO:0051289|GO:0071277|GO:0070588|GO:0015278|GO:0
006816|GO:0016021|GO:0005219 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116061_PI430048170 0.42683975437203 0.780477427401215 0.34066322091628
0.322713515064027 0.28415051169091 A A A 0.310891341979605 0.314447268286418
1.20235805864545 A A A LNCV6_116061_PI430048170 mRNA
GAGCCATTTTATATAGAAACAAAACCCATAAGAGCACACAGTAACAAAGCAAACAGATAC NM_001252127 RefSeq
chr15 + 50908671 51005900 AP4E1 23431 "adaptor-related protein complex 4, epsilon 1 subunit,
transcript variant 2" GO:0005905|GO:0005794|GO:0016192|GO:0006886|GO:0030117 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_88260_PI430048170 0.100452641709098 1.52763037327424 8.33002492431326 8.8917230581311
8.3490530190658 P P P 7.67152290391321 7.68197919160873 8.34785312597816 P P P
LNCV6_88260_PI430048170 mRNA
AGTAAAGATGGGACAATTGTCCTTGGGACTCGAATCAGGTCAAGGTCAAGGTCAACATGA NM_014727 RefSeq chr19
+ 35718018 35738880 KMT2B 9757 lysine (K)-specific methyltransferase 2B
GO:0005515|GO:0003700|GO:0080182|GO:0009994|GO:0006325|GO:0005634|GO:0016458|GO:0042800|GO:0003
677|GO:0006351|GO:0001541|GO:0035097|GO:0005654|GO:0008270|GO:0051569|GO:0048096|GO:0051568|GO:0
030728 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71681_PI430048170 0.18698071679841 0.240364080966687 0.49889334082588 0.472402333659046
0.253416934096487 A A A 0.400571082043398 3.13969772906538 2.69534853775554 A P P
LNCV6_71681_PI430048170 mRNA
GACTCCACTTTAGAGATACACCAAAGCCACCGTTGTTACACAAGTTATTAAACTATTATA NM_021219 RefSeq chr21
+ 25639281 25717562 JAM2 58494 "junctional adhesion molecule 2, transcript variant 1"
GO:0005515|GO:0016337|GO:0007162|GO:0046982|GO:0005886|GO:0030198|GO:0007596|GO:0005887|GO:0005
923|GO:0050900 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145117_PI430048170 0.00557166444964139 1.33170879865143 11.5761808796778
11.514566539329 11.4767872906342 P P P 11.0909436048923 11.2064249772898 11.02627571019
P P P LNCV6_145117_PI430048170 mRNA
TCACCGAGGAAGACTTCCAGAAGTTCCAGCAGGAATACTTCGGCAGCTAGGCTCCCTGGA NM_194326 RefSeq chr22
- 39529092 39532855 RPS19BP1 91582 "ribosomal protein S19 binding protein 1, transcript variant 1"
GO:0005515|GO:0005737|GO:0005730|GO:0005654|GO:0019899 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_132052_PI430048170 0.5181370058468771.04449480574619 0.284678786126898
0.2952946577997080.516038014715851 A A A 0.32073699520489 0.277636991097043
0.32081496297619 A A A LNCV6_132052_PI430048170 mRNA
CCAAGTACAATGCTGGACTTCGTTTGAATCAGATTCAAATAAACCACTTGTAAAAAGACA NM_001001665 RefSeq
chr2 - 127183835 127205767 CYP27C1 NA "cytochrome P450, family 27, subfamily C, polypeptide 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131842_PI430048170 0.1644478187988170.5504591372586392.43911693095105
3.87280331929564 3.26680979850021 A P P 3.46005496865828 4.51561490335456
4.32717763684722 P P P LNCV6_131842_PI430048170 mRNA
GGTATTCTAGCTCTTACCTCTATGTTCTTTCTCACGTCTCCTAAAGACAAAATTGTTTAA NM_139240RefSeq chr1 +
172420687 172468829 C1orf105 92346 "chromosome 1 open reading frame 105, transcript variant 1"NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142697_PI430048170 0.9754858362416451.00555859131813 9.64214034643247 9.9544891341872
9.82234879337445 P P P 9.87502641516554 9.7793099590145 9.75476173397159 P P P
LNCV6_142697_PI430048170 mRNA
ATTCTTCTATATTGTACAGAGTGGGGCAAAACACGCCCCCATCTGCTGCCTTTTCTATTG NM_002931 RefSeq
chr6_GL000255v2_alt + 4402916 4407130 RING1 6015 ring finger protein 1
GO:0035102|GO:0005515|GO:0031519|GO:0035518|GO:0004842|GO:0016874|GO:0005634|GO:0048593|GO:0009
952|GO:0001739|GO:0006351|GO:0005737|GO:0016607|GO:0003682|GO:0005654|GO:0008270|GO:0045892 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134970_PI430048170 0.0606117596353178 1.41459621614915 7.5031421174949
7.9216834714556 7.6068499519769 P P P 7.43282150419764 7.16006687764414
6.92662154550371 P P P LNCV6_134970_PI430048170 mRNA
TTCTTGTACTTCTCCAAGGACCAGGGGAAGGACGAGGACACCGAAGAGCAGAAGGAGGCA NM_019112 RefSeq
chr19 + 1040102 1065571 ABCA7 10347 "ATP-binding cassette, sub-family A (ABC1), member 7"
GO:0006909|GO:0005215|GO:0017121|GO:0034504|GO:0005886|GO:1900223|GO:0010875|GO:0050766|GO:0005
737|GO:0016324|GO:0034380|GO:0007613|GO:0070374|GO:0043190|GO:0016887|GO:0033344|GO:0005794|GO:0
009986|GO:0001891|GO:0032587|GO:0032780|GO:0005548|GO:0032781|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135224_PI430048170 0.00987428665087595 1.3007662070813 13.1362869965007
13.1551322933968 12.9835808567941 P P P 12.7672511450441 12.7777355170759
12.5904189440066 P P P LNCV6_135224_PI430048170 mRNA
CAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTTCACCTGGAAAAAA NM_001243725 RefSeq
chr3 + 51671273 51704323 TEX264 51368 "testis expressed 264, transcript variant 5" GO:0070062
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139198_PI430048170 0.000910380924981876 0.397962004953961 0.940588375626169
0.601099984148709 0.852193847527539 A A A 2.343856575162 2.03559523148329
1.99789784512397 A A A LNCV6_139198_PI430048170 mRNA
GTATTTTTTGATAAAGATATATTCTTGGGCCACAGTAGCTGGAGATATAATGCCGGAGGA NM_152458 RefSeq
chr16 - 30580672 30585771 ZNF785 146540 zinc finger protein 785
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142936_PI430048170 0.00711729564722505 2.81449773824229 6.84469093206041
7.60536333229362 7.25747647613586 P P P 6.05552666056771 5.73385088213221
5.48097972115165 P P P LNCV6_142936_PI430048170 mRNA
ATGTTCTGTGAGGCCCAAGAGAACACATGGAGTCTTAGCAAATGCACTAATGTATTCCGG NM_007021 RefSeq
chr10 - 44976260 44978882 C10orf10 11067 chromosome 10 open reading frame 10
GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_143596_PI430048170 0.874866257458533 0.961812284342019 4.86485949285284 4.62046989541579 4.56897514387805 P P P 4.41486222372665 4.67618784568376 5.07256611143988 P P P LNCV6_143596_PI430048170 mRNA GCTGACTACTAACAGGTCATTGCCAGGTGTATTTCTATACTCTTTGAAGAATAACATTTT NM_007223 RefSeq chr15 - 39799021 39920892 GPR176 11245 "G protein-coupled receptor 176, transcript variant 1" GO:0007186|GO:0005887|GO:0004930|GO:0007268 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138831_PI430048170 0.0300640244714441 0.315910000370507 1.82919488906294 0.67776184264282 1.7122605432479 A A A 3.40497614946895 2.97608246306263 3.039686262417 P P P LNCV6_138831_PI430048170 mRNA TTCTCTAATGTGGGGTTTTTTGTTTGTTTGTTTGTTTTGAGGGTAGAGGGAATCCCCTCC NM_194314 RefSeq chr1 - 197153683 197200542 ZBTB41 360023 zinc finger and BTB domain containing 41 GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136361_PI430048170 0.0037763793977325 0.545186743471526 5.68157271747094 5.80088066385819 6.03736468609351 P P P 6.6318136173822 6.67655907669368 6.85059575689975 P P P LNCV6_136361_PI430048170 mRNA GAGGTAGCATACCTGAAAATGTACGTGTGTGTTTGTTGTATTTTTTCACATTTTGTGAAC NM_152556 RefSeq chr7 - 112819146 112939877 C7orf60 154743 chromosome 7 open reading frame 60 GO:0031167|GO:0016433 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138469_PI430048170 0.439544735324807 1.16508706647424 0.925830967748713 0.275213878577748 0.391106149796296 A A A 0.369720334695965 0.309357279557659 0.337549965536415 A A A LNCV6_138469_PI430048170 mRNA ATGTAGAAAAGTAGGCATAGTGTCGCATGCTGCAGTAAAGAGCTACATAGACCACCTGAA NM_004211 RefSeq chr11 + 20599399 20655064 SLC6A5 9152 "solute carrier family 6 (neurotransmitter transporter), member 5" GO:0015375|GO:0005886|GO:0036233|GO:0005328|GO:0006836|GO:0006810|GO:0007268|GO:0016021|GO:0060012|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145057_PI430048170 0.140187897632904 1.0668246309234 10.3263721826765 10.3637556879905 10.2932823234054 P P P 10.1819836069227 10.2018562840109 10.3167619540592 P P P LNCV6_145057_PI430048170 mRNA ATTGCTTTGTAATGGTTTGTGATACTTGAAACATCACGGTGCATAATAAAGTAGGTCTGC NM_003192 RefSeq chr6 - 42744495 42746146 TBCC 6903 tubulin folding cofactor C GO:0000902|GO:0005737|GO:0006457|GO:0005874|GO:0051087|GO:0003924|GO:0051084|GO:0032391|GO:0007023|GO:0005856|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142989_PI430048170 0.000714894835195412 0.54982363175958 9.30540461596382 9.46768800684989 9.24124155762804 P P P 10.2897168902986 10.2098049593907 10.1074564367287 P P P LNCV6_142989_PI430048170 mRNA TCTGCCTCCCCTTAAAGGGGAGACCTCAGAAGTAAAGGAATTTGATGTTGTGTTTTTGTT NM_004861 RefSeq chr22 - 30554636 30564889 GAL3ST1 9514 galactose-3-O-sulfotransferase 1 GO:0006682|GO:0001733|GO:0016020|GO:0000139|GO:0005887|GO:0042552|GO:0008146|GO:0007283|GO:0006487 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133538_PI430048170 0.783198414056497 0.924532953026931 5.58986468577665 5.14874738515161 4.66285898972406 P P P 5.54509379958836 5.50015352294739 4.69565202310651 P P P LNCV6_133538_PI430048170 mRNA TGACAAACCTGCCTCTTTCCCTGAAACCATTCAATAAAACCTCTGATCAAAGTGTCAAAA NM_145272 RefSeq chr17 + 35760896 35765079 C17orf50 146853 chromosome 17 open reading frame 50 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119808_PI430048170 0.65743864276836 0.929016073883898 4.21686210967653

3.69416275177021 3.67857751117306 P P P 4.22982232882374 3.99981153565094
3.69716274616644 P P P LNCV6_119808_PI430048170 mRNA
ATGATAGGATAAAGGAGGGACATTAAGAAATAAATTCCCCCTCACGACCCTCGCTGAGCT NM_001204218 RefSeq
chr12 - 117208141 117361802 NOS1 4842 "nitric oxide synthase 1 (neuronal), transcript variant 2"
GO:0005515|GO:0005516|GO:0009408|GO:0010523|GO:0010181|GO:0006941|GO:0043267|GO:0045202|GO:0006
809|GO:0051926|GO:0005856|GO:0051701|GO:0005506|GO:0051346|GO:0007520|GO:0018119|GO:0033555|GO:0
044325|GO:0004517|GO:0043234|GO:0003958|GO:0042738|GO:0051612|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_33426_PI430048170 0.00719876866880657 2.84647741204644 4.31583416280805
4.64943927857327 4.99207448043093 P P P 3.52062467262235 3.13660965032674
2.74903401091151 P P P LNCV6_33426_PI430048170 mRNA
TCTCTAAGGGATCTCTGTTGCTTGGAGAATAAACCCTCGGATTCCTTCCTTGGCTCTCGG NM_001278655 RefSeq
chr20 + 50267485 50279795 LINC01272 NA long intergenic non-protein coding RNA 1272 NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145495_PI430048170 0.733312100436067 1.21799102351472 1.74130122425217
0.332970797606011 0.45956329133933 A A A 0.345374516209896 0.350557857861396
1.24039157633343 A A A LNCV6_145495_PI430048170 mRNA
GTTGTTTATCAGTATATAGACCTACCATTAGTAGAAATGATGTATGGCAGGCTTTCTTGA NM_015617 RefSeq
chr15 - 55538886 55588852 PYGO1 26108 pygopus family PHD finger 1
GO:0005515|GO:0034504|GO:0007289|GO:0002244|GO:0001822|GO:0045944|GO:0008270|GO:0005654|GO:0016
055|GO:0009791 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129684_PI430048170 0.802364729947051 1.09932005148116 0.321285067459768
1.39920136046939 0.48956913819907 A A A 0.306511126420051 1.21427880897412
0.328877508472752 A A A LNCV6_129684_PI430048170 mRNA
TGTGACTTTTTTCTGGGGTCAAAGAGAAACCCCGAGACACTGTACACTGTTCCTTTTCAC NM_017509 RefSeq chr19
- 50825288 50831523 KLK15 55554 "kallikrein-related peptidase 15, transcript variant 4"
GO:0004252|GO:0006508|GO:0008236|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127144_PI430048170 0.123420602100292 0.707184546496266 5.5929173803783
4.99825659220056 4.91561777827951 P P P 5.91698169833524 5.71923839402986
5.42697809725912 P P P LNCV6_127144_PI430048170 mRNA
CTCCTCCTGTGATGTCCTGCTCCCAACCATTTGTACTCTTCATTACAAAAGAAATAAAAA NM_001937 RefSeq chr1
- 168695456 168729204 DPT1805 dermatopontin
GO:0031012|GO:0008285|GO:0030199|GO:0005578|GO:0007155|GO:0005615|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144784_PI430048170 0.00323866974944851 0.29562980395002 3.22003756795317
3.66134106716068 3.93556802444825 P P P 5.05978312485594 5.38074041364596
5.67404524820542 P P P LNCV6_144784_PI430048170 mRNA
AGTCAGGTACGAAGCGCTTGATACGTGGAATTTTTCTCTATATCAAGTTTAAATTTCTGG NM_144721 RefSeq chr4
+ 75514443 75530026 THAP6 152815 THAP domain containing 6 GO:0015630|GO:0003677|GO:0046872
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130708_PI430048170 0.851896031586748 1.19373957895643 0.307495655096628
0.254481775304063 1.83874064015454 A A A 0.265434035461253 0.492603017317551
1.27707819224381 A A A LNCV6_130708_PI430048170 mRNA
CATTAGTTGTGGCACCCATGTGATTAGATAGTTCCTGACAAAATAAATGTATGTCCTTCC NM_173528 RefSeq chr15
+ 81134302 81149175 C15orf26 161502 chromosome 15 open reading frame 26 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_100642_PI430048170 0.215600308281211 0.803714028082535 9.6333396887869
9.89195694277365 10.1179302699743 P P P 10.1127276260435 9.96696844354034
10.4967233132525 P P P LNCV6_100642_PI430048170 mRNA

TTGTAGTAGAGTGTAAACCTTTTCCCATGCCCAGTCTTCAAATTTCTAATGTTTTGCAGTNM_006330RefSeq chr8 - 54046366 54102017 LYPLA1 10434 "lysophospholipase I, transcript variant 1" GO:0005739|GO:0002084|GO:0008474|GO:0004622|GO:0050999|GO:0006631|GO:0042997|GO:0046209|GO:0044281|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139554_PI430048170 0.8288933253245960.95414120473692 1.57778465899841 0.7568387006348181.80730051081859 A A A 0.5906189447866840.5699983116540352.4795542860733 A A A LNCV6_139554_PI430048170 mRNA
CAGGTTTATTCATCTCATCTTTCTGTTACAGGATGATTAATTGTACAGTTACATCACACG NM_001164537 RefSeq chr1 + 231626814 232041273 DISC1 27185 "disrupted in schizophrenia 1, transcript variant a" GO:0031929|GO:0005515|GO:0021846|GO:0005813|GO:0090128|GO:0030054|GO:0005874|GO:0000226|GO:0002052|GO:0014069|GO:0030177|GO:0036064|GO:0005739|GO:2000060|GO:0051560|GO:0045211|GO:0010975|GO:0021799|GO:0034613|GO:0001764|GO:0060070 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135753_PI430048170 0.3806237306347970.7500152997895540.256893930243912 0.2716442650837981.44589317213792 A A A 0.60228995131851 1.51847513034882 1.29399202570219 A A A LNCV6_135753_PI430048170 mRNA
GGAATTATTTGAACACGGGAAAGTGAAACTAGGTCTGCATGAAGTATAGGAAATTTAAGT NM_017780RefSeq chr8 + 60678764 60868027 CHD7 55636 chromodomain helicase DNA binding protein 7 GO:0060123|GO:0005515|GO:0060429|GO:0021553|GO:0060041|GO:0006364|GO:0007605|GO:0008015|GO:0048844|GO:0005634|GO:0048752|GO:0007512|GO:0050767|GO:0021772|GO:0042048|GO:0007628|GO:0060021|GO:0048806|GO:0040018|GO:0006355|GO:0042472|GO:0021545|GO:0005730|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131644_PI430048170 0.0486236229969440.40413743862591 3.25816486571489 2.81777338548174 2.09513029736552 P A A 3.94516334685618 4.13878949014452 4.22295457642838 P P P LNCV6_131644_PI430048170 mRNA
CAGCATGTCAAATGTGAAGATTATTGTGTGGGATCCTTTGGTTTCATTGTTATGATGTAT NM_001609RefSeq chr10 + 123008912 123058290 ACADSB 36 "acyl-CoA dehydrogenase, short/branched chain" GO:0005739|GO:0034641|GO:0005759|GO:0050660|GO:0006631|GO:0009083|GO:0003995|GO:0044281|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137769_PI430048170 0.0391565283210265 1.24130664148241 9.79403085260408 9.87381922085203 9.61396165079071 P P P 9.52024808916487 9.43815334300017 9.39724029747364 P P P LNCV6_137769_PI430048170 mRNA
CAGTCCTGTTCAGAAAGGGGCTCTTCTGAGCAGAAATGGCTAATAAACTTTGTGCTGATC NM_005419RefSeq chr12 - 56341597 56360253 STAT2 6773 "signal transducer and activator of transcription 2, 113kDa, transcript variant 1" GO:0005515|GO:0003700|GO:0005886|GO:0006357|GO:0019221|GO:0003677|GO:0007259|GO:0006351|GO:0042802|GO:0005829|GO:0051607|GO:0005737|GO:0060337|GO:0060338|GO:0016032|GO:0005654|GO:0004871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144424_PI430048170 0.1449755548476731.04166051251502 0.355804511573903 0.3832785972031260.295924928951244A A A 0.2808285831590830.299113259675768 0.279706267906635A A A LNCV6_144424_PI430048170 mRNA
CGGGGTGGTAACTGAGTTTGTGTTATATGTTGTTTTAATAAATGCACAATGCTCTCTTCC NM_032588RefSeq chr1 - 26051304 26067634 TRIM63 84676 "tripartite motif containing 63, E3 ubiquitin protein ligase" GO:0005515|GO:0010468|GO:0030018|GO:0004842|GO:0016567|GO:0016874|GO:0005874|GO:0005634|GO:0014732|GO:0031430|GO:0031432|GO:0007165|GO:0005737|GO:0006936|GO:0014878|GO:0043161|GO:0008270|GO:0004871|GO:0070555|GO:0071549 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134437_PI430048170 0.9776958042194610.9996151325376030.309133453263682 0.3161507347434610.408618757554367A A A 0.36282033855069 0.313324186743658 0.361032322375809A A A LNCV6_134437_PI430048170 mRNA
GTAATGGATTGCCGTTTGTACCTGTATCAGTATTGCTGTGTAAAAATTCTGTATCAGAAT NM_001126128 RefSeq

chr3 - 71771654 71785206 PROK2 60675 "prokineticin 2, transcript variant 1"
GO:0043066|GO:0001664|GO:0008283|GO:0005576|GO:0001525|GO:0007283|GO:0007204|GO:0019233|GO:0000
187|GO:0006954|GO:0006935|GO:0007186|GO:0045987|GO:0007218|GO:0007623 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141897_PI430048170 0.8715549851377280.9850538396516597.63843434518698
7.40132000278703 7.45799503953163 P P P 6.67196054014415 7.97927646407537
7.62983816668553 P P P LNCV6_141897_PI430048170 mRNA
CATATGATAATACCATTCTGCATAGTATTACTGACTCAGTAAAGAGCTATTTCCAGGAGT NM_016240RefSeq chr8
+ 27634059 27673020 SCARA351435 "scavenger receptor class A, member 3, transcript variant 1"
GO:0009650|GO:0005581|GO:0000139|GO:0005789|GO:0016021|GO:0006979|GO:0006898|GO:0005044 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132574_PI430048170 0.10571094147012 1.06743093164062 0.476223021274728
0.5836273100005550.530783088501691A A A 0.3742698814882670.447150511827039
0.486542938242808A A A LNCV6_132574_PI430048170 mRNA
GGTCTTTAATGACCATTGTGTCTACATCAAGTTCATAACTTTTCACCTTTACAATCTGCT NM_032567RefSeq chr5 +
80319970 80321841 SPZ1 84654 spermatogenic leucine zipper 1
GO:0006355|GO:0005737|GO:0003700|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131035_PI430048170 0.9927808756982030.9999816595427820.401331375786891
0.2599109586524310.301190933841346A A A 0.2758036284127040.303583914622755
0.384586986307307A A A LNCV6_131035_PI430048170 mRNA
AGAGTCGAAAATGGGAATCTGAATGTCTAGAGTGGAATTCAGGCTTGAGAATACATGAGGNM_001009611 RefSeq
chr1 - 12879211 12886201 PRAMEF4 NA PRAME family member 4 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_144853_PI430048170 0.7523065982199121.10774762726802 0.269935336898627
0.2782144496908681.08780259835485 A A A 0.3444990629531210.660427892023671
0.323898585696777A A A LNCV6_144853_PI430048170 mRNA
GATATGAAGACAGCTATGAAGAAGCTGAGGATAAAACCATGTGGCATTCCATTGCCTTGT NM_172194RefSeq chr14
+ 19747427 19748369 OR4Q3 NA "olfactory receptor, family 4, subfamily Q, member 3" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130143_PI430048170 0.8854544318027970.9026221622823430.568507896710746
1.74617694745909 1.35569590411731 A A A 2.03502594707735 1.4463070542141
0.455734635751157A A A LNCV6_130143_PI430048170 mRNA
TTTCTGTGACACTTCCCCAATTTTAGCTCTGTCCTGCACTGATACATACAACACCGAAAT NM_001005200 RefSeq
chr11 + 56105042 56105981 OR8H2 NA "olfactory receptor, family 8, subfamily H, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132977_PI430048170 0.92480679779226 1.00904181597119 7.67197230703732
7.67840882335063 7.33083503346575 P P P 7.77590400211278 7.57684810824882 7.2721750175062
P P P LNCV6_132977_PI430048170 mRNA
CTCATGGTTGGCCCAGCCCTCCATTGTCTGTGTTTTTCAAAATCCAATTGTGGCTTTTTT NM_001037984 RefSeq chr17
- 81244810 81295339 SLC38A10 124565 "solute carrier family 38, member 10, transcript variant 1"
GO:0060348|GO:0005794|GO:0015171|GO:0016021|GO:0006814|GO:0003333 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133159_PI430048170 0.0156197755523861.68442425281717 10.87440776621
10.9670028472014 10.703670313124 P P P 10.2456099652974 10.2052296412876
9.81110622716808 P P P LNCV6_133159_PI430048170 mRNA
TGAGTGGCTGGAGTGGTCAATAAAGCCACATGTGCCTGTGGCCCAGATGTCTCTGTGCCT NM_138431RefSeq chr8
+ 144509035 144511228 MFSD3 113655 "major facilitator superfamily domain containing 3, transcript
variant 1" GO:0015295|GO:0005887|GO:0006810|GO:0005789|GO:0055085|GO:0015992 . NA - . NA

NA NA NA NA NA NA NA NA
LNCV6_144709_PI430048170 0.2702121618264751.70641201420537 2.82828731650352
3.53917136611992 2.13365925289925 A P A 3.04358653790839 1.45709063080363
1.35357774017696 P A A LNCV6_144709_PI430048170 mRNA
TGTGTGCCCCAGGCACGTGTAATAAAGAACCCGAGCAGATGCCTCCTGCTTGAACCAGGA NM_024919RefSeq chr6
- 168055783 168079159 FRMD1 79981 "FERM domain containing 1, transcript variant 1" GO:0005856 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143729_PI430048170 0.472306181205 0.922065679966891 0.48212167693168
0.5237506231410950.422609595418352A A A 0.4686354459671370.825684018001809
0.455777764028217A A A LNCV6_143729_PI430048170 mRNA
GAAGCGTGTTTATTTTGAAGACAAACATAACAAATATAAGGAGCATAGGAGGGTTGTAGT NM_178558RefSeq chr7
- 64519876 64563127 ZNF680 340252 "zinc finger protein 680, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_70343_PI430048170 0.8050899904069481.02663517061004 10.4084854316103 10.4967233132525
10.7410445935773 P P P 10.4384737593848 10.3453457338578 10.7395471723925 P P P
LNCV6_70343_PI430048170 mRNA
TCAGCTGTGGTTATTTAAAGCAGACTTACATGTAAACCGGAATCCTCTCTATACAAGTTT NM_016467RefSeq chr2
- 189770266 189784371 ORMDL1 94101 "ORMDL sphingolipid biosynthesis regulator 1, transcript
variant 1" GO:0006672|GO:0005789|GO:0016021|GO:0090155 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139600_PI430048170 0.60361919658778 0.92107223936104 5.88363274909673
5.40864070941355 5.18652445974241 P P P 5.73734154757194 5.77485130970304
5.38042250612259 P P P LNCV6_139600_PI430048170 mRNA
TTTTTTCCCCTGAATTCTCGCTCCTTTCCCTTATACATTAAGGGATTTAGGCAGGTGCGG NM_001136509 RefSeq
chr16 - 31435563 31443027 ZNF843 283933 zinc finger protein 843
GO:0005515|GO:0003676|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129575_PI430048170 0.7686312881394991.01633588984046 0.269179743162727
0.2848922679882640.460335773891868A A A 0.3443012679248510.298578144063758
0.30890683597373 A A A LNCV6_129575_PI430048170 mRNA
CCGGTGACCCTATCATTTTCCAAATAATTGTTGCTAGTACTTAGTTAATTAGACCCATTT NM_198485RefSeq chr3
+ 189171973 189323482 TPRG1 285386 tumor protein p63 regulated 1 GO:0005737 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135718_PI430048170 0.0497926557147774 0.6669508482110727.38273439482768
7.67058189972817 7.96572186270625 P P P 8.28642515231846 8.08651036585781
8.43665422180161 P P P LNCV6_135718_PI430048170 mRNA
TTAATGAAATCTGTATGGATATGGAAATGCTTGCCCTAATAAAAGCCTACATATACCTCC NM_015469RefSeq chr9
+ 104747687 104760122 NIPSNAP3A 25934 nipsnap homolog 3A (C. elegans)
GO:0005515|GO:0005634|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130907_PI430048170 0.9932306079477741.00102516075369 0.266775998365348
0.2734295939659610.437662399851096A A A 0.3528620820485530.299149393397673
0.327497080652479A A A LNCV6_130907_PI430048170 mRNA
GAGGTGAAGAAAGCTGTGTTGAAACTTAGAGACAAAGTAGCACATCCTCAGAGGAAATAA NM_001004462
RefSeq chr11 + 124015574 124016510 OR10G4 NA "olfactory receptor, family 10, subfamily G, member
4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136804_PI430048170 0.7844232733467460.811873231903122 0.374279249486408
1.30657791019055 0.469818961446576A A A 1.90153828358073 0.395411637205825
0.37592781156171 A A A LNCV6_136804_PI430048170 mRNA
GTGATAACTGTGATGTATGTGGCAGTGACCCCAGCATTAAATCCTTTCATCTATAGTCTG NM_012352RefSeq chr17

+ 3197516 3198448 OR1A2 26189 "olfactory receptor, family 1, subfamily A, member 2"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0032467|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_96615_PI430048170 0.22482839139978 0.8720453990201591 1.9552889464717 11.8150737610241
12.0508228901586 P P P 11.9145956032677 12.2183653035808 12.2659380833726 P P P
LNCV6_96615_PI430048170 mRNA
ACTACTGGCATTGTGATGGACTCTGGTGACGGGGTCACCCACACTGTGCCCATCTATGAG NM_001145442 RefSeq
chr14 + 18967433 19003752 POTEM 641455 "POTE ankyrin domain family, member M" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_144867_PI430048170 0.1804965560657966 .25461657572828 0.309965591805211
3.47872883386664 3.39159978979013 A P P 0.2954341431948740.262726127077556
0.300431154291152 A A A LNCV6_144867_PI430048170 mRNA
GCTGAAGTGTTCATAAGATAACAATAGGCTTGAATCTCCAATTCAAATGAATGTCAAAGC NM_002163 RefSeq chr16
+ 85899167 85922605 IRF8 3394 interferon regulatory factor 8
GO:0005515|GO:0006909|GO:0032729|GO:0000975|GO:0006366|GO:0003705|GO:0019221|GO:0042832|GO:0032
735|GO:0060261|GO:0000122|GO:0005829|GO:0006955|GO:0071222|GO:0060337|GO:0030099|GO:0005654|GO:0
044130|GO:0042742|GO:0060333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134973_PI430048170 0.455904743150395 1.54351700214747 1.81729641425264
0.361336234676957 0.341261619070882 A A A 0.409994772815611 0.396493082865615
0.368793301586452 A A A LNCV6_134973_PI430048170 mRNA
AAGACCAAAATCGAAGAGGCCACGGTCACAGCTGAGGATATCTTGTATTAATAGCCTTCC NM_001079827 RefSeq
chr4 + 17515164 17527104 CLRN2 NA clarin 2 NA . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_90835_PI430048170 0.7607603053873365 0.9645828086022841.78999989213011 0.395570670421544
0.262311935685649 A A A 0.619820992609557 1.48250911954022 0.896309183347066 A A A
LNCV6_90835_PI430048170 mRNA
TATTGTCGGCTTTCGCCAAATCACAAAGTCCTGCATTACGGAGACTTAGAAGAGAGTCCT NM_001206482 RefSeq
chr7 - 36852905 37353668 ELMO1 9844 "engulfment and cell motility 1, transcript variant 5"
GO:0005515|GO:0048010|GO:0017124|GO:0030036|GO:0005886|GO:0006915|GO:0006928|GO:0006911|GO:0050
690|GO:0005829|GO:0005737|GO:0016601|GO:0016020|GO:0045087|GO:0016032|GO:0005856|GO:0038096 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135303_PI430048170 0.31155714754217 0.6944532793640760.43205129231349
0.4839997427345660.473765095718831 A A A 0.8052694768700910.393243930824551
1.53389329478812 A A A LNCV6_135303_PI430048170 mRNA
GCCCCAACGTGTTACCACTCTTACTAGTTTTTTGTTAATCTTTCCGGCATTTTTAAATAA NM_001012509 RefSeq chr5
- 33945866 33984675 SLC45A2 51151 "solute carrier family 45, member 2, transcript variant 2"
GO:0033162|GO:0042438|GO:0016021|GO:0007601|GO:0050896 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137626_PI430048170 0.0288678989065192 0.7681659748691746.94541441641436
7.13934499473345 7.03071476554556 P P P 7.24209798889067 7.48971512204051
7.51623096236864 P P P LNCV6_137626_PI430048170 mRNA
GGGAATTTTAAGCCCTTCTCATCACCCAATTGGATGTTTTTGCTTATAGCAAATTCCTGC NM_014967 RefSeq
chr15_KI270905v1_alt + 3189604 3228836 FAN1 22909 "FANCD2/FANCI-associated nuclease 1,
transcript variant 1"
GO:0005515|GO:0043130|GO:0000287|GO:0008409|GO:0070336|GO:0005634|GO:0045171|GO:0005737|GO:0004
528|GO:0006281|GO:0000724|GO:0005654|GO:0006289|GO:0017108|GO:0000737|GO:0033683 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_104514_PI430048170 0.2638068707868680.6061020237977253.48430813314759 3.518786791364
1.7172259486072 P P A 3.99457414288788 3.99519248302166 3.44805494739649 P P P

LNCV6_104514_PI430048170 mRNA
ACTCTACCACTTTCCTGCCAATTGTGATGCCTGTGCCAAACCTCTCTGGCATGTTTTTAA NM_005406RefSeq chr18
- 20949741 21111851 ROCK1 6093 "Rho-associated, coiled-coil containing protein kinase 1"
GO:0005515|GO:0030036|GO:0005886|GO:2000145|GO:0051492|GO:0007266|GO:0051894|GO:0050900|GO:0051
893|GO:0050901|GO:0030155|GO:0046872|GO:0006921|GO:0005829|GO:0006939|GO:0045616|GO:0043524|GO:0
007411|GO:0032956|GO:0007159|GO:0022614|GO:0005856|GO:0048010|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127642_PI430048170 0.0343748444049889 0.654272709713 4.50576128031413
4.36087516983256 4.26356780382047 P P P 5.21163661597564 4.71782372350559 5.0050589617656
P P P LNCV6_127642_PI430048170 mRNA
GTAACAGCAACAACCATCCTGTACATGGAGATTTGAGTGATTAAAATGGATTTTCATATC NM_001256829 RefSeq
chr16 + 30740190 30745196 TMEM265 100862671 transmembrane protein 265 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138162_PI430048170 0.0579863698312146 1.33908587317459 9.43844742172822
9.65955710256283 9.40582484364274 P P P 8.92149702898087 8.96892204988474
9.32796222899344 P P P LNCV6_138162_PI430048170 mRNA
TCCTTACTGAAAAGTCTTGAGCAAACAGTTGCCGCTCTCCACCCCCTGCTTTTTAAAAAA NM_181809RefSeq chr1
+ 39491645 39529869 BMP8A 353500 bone morphogenetic protein 8a
GO:0051216|GO:0002024|GO:0010862|GO:0042981|GO:0030509|GO:0060395|GO:0005125|GO:0005160|GO:0005
615|GO:0001503|GO:0070700|GO:0043408|GO:0048468|GO:2000505|GO:0008083|GO:0040007|GO:0046676 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138544_PI430048170 0.0946180387010229 0.4855944031777853.29601557401834
2.05668791189949 3.17243556304523 P A P 3.89957009369087 3.84445964061709
4.17565473317956 P P P LNCV6_138544_PI430048170 mRNA
CTACTTTTTACAAAAGGGCAAACTGGGCTGATGTAAATGTTTTACTTTCAACTGTGTTCT NM_003274RefSeq chr21
+ 44012324 44106551 TRAPPC10 7109 trafficking protein particle complex 10
GO:0005515|GO:0034498|GO:0006891|GO:0035725|GO:0016021|GO:0015081|GO:0006814 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139434_PI430048170 0.3979391288999990.9009590201546661 0.0390830659519
10.1278277159643 10.0539950514225 P P P 10.1346090200747 10.4666803052547
10.0366130409136 P P P LNCV6_139434_PI430048170 mRNA
TACGGTTTCGGTGGTTGAGCGTCCCTTTCTATCAACAAAAGGCCCTTTTTAGGGCCCCCA NM_003541RefSeq chr6
- 27831173 27831527 HIST1H4K 8362 "histone cluster 1, H4k"
GO:0005515|GO:0010467|GO:0006325|GO:0005634|GO:0045653|GO:0000723|GO:0000183|GO:0000786|GO:0070
062|GO:0035574|GO:0035575|GO:0046982|GO:0006334|GO:0006335|GO:0005576|GO:0006336|GO:0000228|GO:0
003677|GO:0032776|GO:0034080|GO:0043234|GO:0016020|GO:0045814|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140130_PI430048170 0.000497518047545017 1.50753354204535 10.94366863945
10.8551791679913 10.9273684738364 P P P 10.395089226971 10.2826061776535
10.2701686908395 P P P LNCV6_140130_PI430048170 mRNA
CCTACTTAATTCTGATAAACCTGTCTAAGCAATACTTAGGAGGCTTACTTCTTTGGATTA NM_014015RefSeq chr16
- 10928890 10942400 DEXI 28955 Dexi homolog (mouse) NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_133623_PI430048170 0.3689512610266830.75505728932625 3.43921832835409
1.86425410451612 2.3637438820344 P A A 2.87506817100723 2.97747745996338
3.43187983193856 P P P LNCV6_133623_PI430048170 mRNA
TTTCCTTCCCCATCTCTTGTACACATTTTAATAAAATAAGGGTTGGCTTCTGAACTACAA NM_015430RefSeq chr11
- 35431828 35526031 PAMR1 25891 "peptidase domain containing associated with muscle regeneration
1, transcript variant 1" GO:0008152|GO:0005576|GO:0003824 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_135513_PI430048170 0.9839967578036680.9982233093934513.7527985842475
13.5947749869925 13.5286882122629 P P P 13.71970557011 13.6777581746478
13.4850857829388 P P P LNCV6_135513_PI430048170 mRNA
AAGGGGGCAATAAATGTTGAGCCAAGAGCTTCAAATTACTCTAGAGAAACCGACAAAAAA NM_000713RefSeq
chr19 - 40447783 40465818 BLVRB 645 biliverdin reductase B
GO:0005737|GO:0042602|GO:0006778|GO:0005886|GO:0004074|GO:0005654|GO:0044281|GO:0042167|GO:0070
062|GO:0055114|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141245_PI430048170 0.02007520781823 0.3140404398327524.50244432892854
4.42283803412323 4.40906999980511 P P P 5.65960122836784 6.07037007751664
6.49790704275903 P P P LNCV6_141245_PI430048170 mRNA
CAGGTTCACATAATAACCCCATTTGAATCCAAATTTGTGTATATTTTCTTATGCCAGCAG NM_001303131 RefSeq
chr12 + 100593617 100628288 GAS2L3 283431 "growth arrest-specific 2 like 3, transcript variant 3"
GO:0008017|GO:0005515|GO:0005737|GO:0030036|GO:0015630|GO:0005874|GO:0000226|GO:0007050|GO:0003
779|GO:0015629 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133342_PI430048170 0.0103287295328289 1.67576838580797 9.35885131104813
9.5549560974389 9.78390186190609 P P P 8.81630130069253 8.67845847398572
8.98367883462733 P P P LNCV6_133342_PI430048170 mRNA
CTTAAGGAGTGGGATTCCTACTTTATGTAATGGGGTCGAAATCTTTGAACACATTATTTA NM_016213RefSeq chr15
+ 64387803 64455303 TRIP4 9325 thyroid hormone receptor interactor 4
GO:0005515|GO:0035035|GO:0016922|GO:0005815|GO:0006366|GO:0003713|GO:0030331|GO:0005634|GO:0002
020|GO:0005737|GO:0044389|GO:0005654|GO:0008270|GO:0045893|GO:0030520 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133203_PI430048170 0.5760863635209660.8584291139232650.495258536357581
0.3195855271446960.405227165471368A A A 0.2825603359310991.0970973350443
0.359445079282722A A A LNCV6_133203_PI430048170 mRNA
ACTTGCTGGAACTTGTGACTGTCAAAGCTCCATTAATAAATTACATGCACCTGGAAAAAA NM_001168247 RefSeq
chr1 - 41015596 41021755 SLFNL1 200172 "schlafen-like 1, transcript variant 2" GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67143_PI430048170 0.0517526806061741 1.27914236930303 10.3367555417606
10.5653291778233 10.6730317887852 P P P 10.1749569655142 10.0381541948121
10.3043576157323 P P P LNCV6_67143_PI430048170 mRNA
CCAGATTGATTACTCAAGCAGACAGCACACGAAATACTATTTTTCTCCTAATATGCTGTT NM_015523RefSeq chr11
+ 114439385 114450278 REXO2 25996 RNA exonuclease 2
GO:0005739|GO:0005758|GO:0008408|GO:0006139|GO:0090305|GO:0000175|GO:0005759|GO:0005730|GO:0005
634|GO:0003676|GO:0005925|GO:0009117 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139122_PI430048170 0.17202589391408 0.5276042878282880.262144389267472
0.2697272190910480.395946065510567A A A 0.3684903043968111.33128749858774
1.69808020406118 A A A LNCV6_139122_PI430048170 mRNA
CAGGGACTTAGGGAACTTATTCTAATTGAGAATCAGAGGCTTAATAAACCTGAAGGTTTA NM_001270396 RefSeq
chr12 + 75391069 75432397 GLIPR1L2 144321 "GLI pathogenesis-related 1 like 2, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91166_PI430048170 0.00172090837799883 3.47949706322632 4.31552722563187
4.08409573833462 4.38376925548273 P P P 2.41157163783446 2.74290044772383
2.19594649693708 A P A LNCV6_91166_PI430048170 mRNA
AGCAATAATTACCTGACCAAGGAGGAGTGCCTCAAGAAATGTGCCACTGTCACAGAGAAT NM_021102RefSeq chr19
+ 38264457 38292614 SPINT2 10653 "serine peptidase inhibitor, Kunitz type, 2, transcript variant a"
GO:0010951|GO:0005737|GO:0004866|GO:0004867|GO:0006928|GO:0005576|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_144125_PI430048170 0.3418525557660631.72166912543861 0.940928968781612
2.10587460265734 0.392608130888062A A A 0.33373882131493 0.317322767698924
0.904198003260758A A A LNCV6_144125_PI430048170 mRNA
TGTATGTGAAGGTGACTTCCATCCAGGACTGGGTTCAGAAGACCATAGCTGAGAACTAAT NM_005143RefSeq chr16
+ 72054608 72061056 HP 3240 "haptoglobin, transcript variant 1"
GO:0005515|GO:2000296|GO:0042542|GO:0016209|GO:0051354|GO:0072562|GO:0005576|GO:0006952|GO:0006
953|GO:0003824|GO:0005615|GO:0006898|GO:0030492|GO:0031838|GO:0071682|GO:0008152|GO:0010942|GO:0
042742|GO:0070062|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127885_PI430048170 0.0960880220224492 1.5355074130782 1.90996289132474
1.70616914283201 2.00045978576982 A A A 0.819135554978861 1.63618562648105
1.20504034648127 A A A LNCV6_127885_PI430048170 mRNA
CATCAGAAGACTGTTGACTGCTTTGCATTTTGGGCTCTTCTATATATTTTGTAAAGTAAG NM_014591RefSeq chr10
- 101825973 101843920 KCNIP2 30819 "Kv channel interacting protein 2, transcript variant 1"
GO:0005515|GO:0005250|GO:0005513|GO:0046923|GO:0005509|GO:0008016|GO:0007268|GO:0015459|GO:2001
257|GO:0044325|GO:0042802|GO:0071435|GO:0007165|GO:0005737|GO:0086009|GO:0047485|GO:0006936|GO:0
045163|GO:0008076|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140132_PI430048170 0.8364745590188061.11167790477023 0.355961057278832
1.45215575950449 0.286201285110457A A A 0.389842292489783 1.14570408096011
0.246946511831689A A A LNCV6_140132_PI430048170 mRNA
GGCAGCTTATCCCATGTAACTTTATCCGTTTAGTGGAATTCCAGTAAAAATCCAATTTTA NM_207419RefSeq chr16
- 1088225 1096244 C1QTNF8 NA C1q and tumor necrosis factor related protein 8 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_121988_PI430048170 0.0193526104937688 0.7920257052967986.84707747997935
6.90717650141911 7.04078177011564 P P P 7.33513380313756 7.13467136931326
7.33223128226052 P P P LNCV6_121988_PI430048170 mRNA
TGGACACGGTGATGTGTCCCAACATGCCCAACAAAAGCGTCCTGCTCTACACGCTCTCCT NM_020311RefSeq chr2
+ 236569736 236582351 ACKR3 57007 atypical chemokine receptor 3
GO:0005515|GO:0048471|GO:0070098|GO:0005886|GO:0009986|GO:0001525|GO:0015026|GO:0019958|GO:0031
623|GO:0005905|GO:0006935|GO:0007186|GO:0016494|GO:0016032|GO:0070374|GO:0016021|GO:0055037|GO:0
007155|GO:0001570|GO:0005769|GO:0005044|GO:0005768 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_138435_PI430048170 0.1511217012902020.9165706245291541 0.0532812749485
9.89953242755524 9.98451966702557 P P P 10.047682541463 10.2120886887289
10.0525730092108 P P P LNCV6_138435_PI430048170 mRNA
ATGGATGACATGGACATGGACTTAGACAAGGAATTTCTCCAGGACTTGAAGGAGCTCAAG NM_198897RefSeq chr11
- 65883739 65888539 FIBP 9158 "fibroblast growth factor (acidic) intracellular binding protein,
transcript variant 1"
GO:0070527|GO:0005739|GO:0016020|GO:0017134|GO:0008543|GO:0005654|GO:0005634|GO:0070062|GO:0012
505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133599_PI430048170 0.3288862484692041.05248477122806 0.327239848559913
0.326578927607175 0.495348345483868A A A 0.312092202222754 0.283766770542817
0.338037305055227A A A LNCV6_133599_PI430048170 mRNA
TGATGAGGATTAAGGTGTTGACTTGCCTCTTTCAGAGATAAATGACAAGCCTTCAAAAAA NM_001841RefSeq chr1
- 23873969 23913327 CNR2 1269 cannabinoid receptor 2 (macrophage)
GO:0005886|GO:0045759|GO:0033004|GO:0019233|GO:0030425|GO:0004949|GO:0031234|GO:0001975|GO:0006
955|GO:0006954|GO:0051001|GO:0005887|GO:0007187|GO:0050728|GO:0032496|GO:0043204|GO:0032229 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133051_PI430048170 0.0447030886866472 1.26924973081634 11.2662026697391
11.0456564943069 11.0074389393909 P P P 10.5895467556537 10.8206968725014

10.8752164002206 P P P LNCV6_133051_PI430048170 mRNA
CCAGCCCGCCTGTCCCTAGATTCAGCCACATCAGAAATAAACTGTGACTACACTTGGCAA NM_018174RefSeq chr19
+ 17719451 17734515 MAP1S 55201 microtubule-associated protein 1S
GO:0005515|GO:0008017|GO:0048471|GO:0030054|GO:0001578|GO:0045202|GO:0005634|GO:0042995|GO:0030
425|GO:0005829|GO:0042802|GO:0005737|GO:0051015|GO:0015631|GO:0047497|GO:0043025|GO:0005874|GO:0
005819|GO:0005730|GO:0048487|GO:0097194|GO:0003677|GO:0007399|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132581_PI430048170 0.0578235951022331 1.54457312825036 8.52394603554949
9.07839635195121 9.04429884733569 P P P 8.4666038742591 8.34241836934023
7.97613008018717 P P P LNCV6_132581_PI430048170 mRNA
GTTCAAGGCAGAAAATCCAAAAAATAAATAAACTGTACACACAGCCGCCGCGCCCACTAANM_000524RefSeq chr5
- 63960047 63962292 HTR1A 3350 "5-hydroxytryptamine (serotonin) receptor 1A, G protein-coupled"
GO:0005515|GO:0014062|GO:0008284|GO:0005886|GO:0008283|GO:0046883|GO:0007198|GO:0007210|GO:0042
053|GO:0042428|GO:0004993|GO:0007186|GO:0050795|GO:0005887|GO:0042310|GO:0001662|GO:0035640 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139505_PI430048170 0.890936244645982 1.0033734529651 0.355780573539378
0.332284738310211 0.2635163257399 A A A 0.312896350207071 0.32382155282903
0.301789473227504 A A A LNCV6_139505_PI430048170 mRNA
ACACTGCTGTTTTGGAATGTTCAGAAATAAAGACTCTATTTCAGCAATATCAGGTCATGC NM_001242868 RefSeq
chr13 + 77697853 77764242 SLAIN1 122060 "SLAIN motif family, member 1, transcript variant 3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51997_PI430048170 0.0735604100657260.7999838950114467.81270100985034 7.72806947998582
8.04638401166727 P P P 8.00147622231116 8.24031520398322 8.31232815203652 P P P
LNCV6_51997_PI430048170 mRNA
ATCAGGCCTTGCTTGTTCCTGCATTAGCCTCAGGGATTTAGAGATACTGTTGTTACTTCT NM_058216RefSeq chr17
+ 58692572 58734342 RAD51C 5889 "RAD51 paralog C, transcript variant 1"
GO:0005515|GO:0048471|GO:0005657|GO:0048476|GO:0008821|GO:0005634|GO:0007283|GO:0005739|GO:0005
737|GO:0000724|GO:0007131|GO:0008094|GO:0000400|GO:0006310|GO:0005524|GO:0003677|GO:0010971|GO:0
006281|GO:0007596|GO:0033065|GO:0007062|GO:0005654|GO:0000737|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138041_PI430048170 0.3132227029531444.30497171227432 0.2972998812387024.1347851181822
3.18622508709916 A P P 0.291736584724403 1.00654925420381 1.69919409775011 A A A
LNCV6_138041_PI430048170 mRNA
ATGTGAGAAAGCCCACACCCTAATGGAGGTGACTGAAACGGAACCACTAAAAGCACAAAA NM_001025357
RefSeq chr8 + 116938224 116944000 AARD 441376 alanine and arginine rich domain containing
protein GO:0030324 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108914_PI430048170 0.0973247171075653 1.3598284351696 5.1218842110584
4.88278723015289 5.40590644190578 P P P 4.80625582252275 4.42639291401083
4.85802684556895 P P P LNCV6_108914_PI430048170 mRNA
CCACCCACCCTTTTCAAGTTTAGATAGTGTTTCAGCTGCTGTCCCAAAGTAACAAAACAA NM_024052RefSeq chr17
+ 18039296 18068404 GID4 79018 GID complex subunit 4 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140565_PI430048170 0.02177762253868 1.40776835195219 12.6898537602056
12.4333389727352 12.4605383617051 P P P 12.0771426153887 12.0159673408848 12.023616221225
P P P LNCV6_140565_PI430048170 mRNA
GTCAGGTCTTTTGTGATTTCCTCTGATGCAGGAGAGGAAAAATTGTAATTGATGAAAATA NM_001286789 RefSeq
chr21 + 36069923 36073177 CBR1 873 "carbonyl reductase 1, transcript variant 2"
GO:0019369|GO:0019371|GO:0004090|GO:0017144|GO:0044281|GO:0031982|GO:0005829|GO:0047021|GO:0016
655|GO:0050221|GO:0030855|GO:0042373|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA

NA NA NA
LNCV6_140271_PI430048170 0.4301962259792520.7619311386142211.87908412352983
3.39339922156627 3.43168375040149 A P P 2.9915162529053 3.75260106794017
3.50450954849129 P P P LNCV6_140271_PI430048170 mRNA
TTTGGTACTGTAAAACACCTTTTCAGAATGAGTAAATGCTGCATATGCATTTTGGAGTTG NM_018293RefSeq chr3
+ 88139111 88144664 ZNF654 55279 zinc finger protein 654
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131746_PI430048170 0.1694044720854 0.8622129341769930.304778217429908
0.3060350931494920.290621792644798A A A 0.4826911867908170.68902983232351
0.351166012227491A A A LNCV6_131746_PI430048170 mRNA
CTTAGGAACAAGGAAGTCCAAGGTACTCTAAAGAGGATGCTTGAAAAGAAGAGAACTTCA NM_001004488
RefSeq chr7 + 144074219 144075152 OR2A25392138 "olfactory receptor, family 2, subfamily A, member
25" GO:0050912|GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0008527|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139458_PI430048170 0.3761514197147330.7519650967577670.516533785028131
0.4606770448159560.565323070251818A A A 1.44028542852975 0.402931145145225
0.734963042684102A A A LNCV6_139458_PI430048170 mRNA
CAGAGTGAATGCAAAAAAGAGAGATGTACTTGGAGTCGGATATACAATTTATCCCTAATT NM_014625RefSeq chr1
- 179550538 179575952 NPHS2 7827 "nephrosis 2, idiopathic, steroid-resistant (podocin), transcript
variant 1"
GO:0005515|GO:0007588|GO:0005886|GO:0031532|GO:0072249|GO:0005783|GO:0031235|GO:0043234|GO:0005
887|GO:0005911|GO:0036057|GO:0045121|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138861_PI430048170 0.1113083189749370.8717467839964881 1.0558347527006
11.0789839092631 11.0165058377684 P P P 11.1367378281074 11.2120813910983
11.3858287948723 P P P LNCV6_138861_PI430048170 mRNA
CCCTGAAGCCTGAGTGAGACACATGAAGAAAACTGTGTTTCATTTAAAGATGTTAATTAA NM_020888RefSeq chr1
+ 32741910 32774970 KIAA1522 57648 "KIAA1522, transcript variant 1" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_126877_PI430048170 0.9224440673905641.0243512111666 7.89393672295695
7.63504428213895 7.25665153461512 P P P 7.80722384983545 7.56298825994575 7.3439957961346
P P P LNCV6_126877_PI430048170 mRNA
CATCTTTTTGCTCTAGCCCTTCCTCTCCAAAATAAAATCAAATAAAGGAAAATCTCCACC NM_005297RefSeq chr22
+ 40679177 40682814 MCHR1 2847 melanin-concentrating hormone receptor 1
GO:0007631|GO:0060170|GO:0005886|GO:0051928|GO:0004930|GO:0030273|GO:0042562|GO:0031513|GO:0006
091|GO:0008022|GO:0007193|GO:0007204|GO:0008188|GO:0007186|GO:0005887|GO:0007218 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141552_PI430048170 0.0722918947000951 1.48094423558956 4.16677890287381
4.58803267298745 4.71943117132081 P P P 4.02656608185046 3.92546384517602
3.87436632223234 P P P LNCV6_141552_PI430048170 mRNA
GAAAGTGTGGGCTGAAGATGGTTGGTTTCATGTTTTTGTATTATGTATCTTTTTGTATGG NM_006472RefSeq chr1
- 145992441 145996631 TXNIP 10628 thioredoxin interacting protein
GO:0005515|GO:0042542|GO:0005634|GO:0006606|GO:0035872|GO:0005829|GO:0005758|GO:0005737|GO:0042
127|GO:0051782|GO:0032355|GO:0031625|GO:0004857|GO:0043065|GO:0042493|GO:0000122|GO:0043086|GO:0
006351|GO:0009749|GO:0009612|GO:0051592|GO:0007049|GO:0030216|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142770_PI430048170 0.000880332982336373 1.97247291046246 5.56500989529651
5.47327080586122 5.32163850490766 P P P 4.58985634850269 4.31638629211893
4.51051280000043 P P P LNCV6_142770_PI430048170 mRNA

TGAAACCATGACTGGGCCCACTGTCAGACAGAAATTAGAATAGGAGGCACATTTTTTACC NM_012135 RefSeq chr6 + 3849397 3851317 FAM50B 26240 "family with sequence similarity 50, member B" GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142598_PI430048170 0.0102435041773882 1.95638083027703 4.95845921996311 4.5384093458217 4.83167063260338 P P P 3.97785169754871 3.47844761687694 3.94707777005645 P P P LNCV6_142598_PI430048170 mRNA
CCTTTGGAGATTTTTTAATCCTTTTTTATTCCATAAGAAGTCGTTTTTAGGGAGAACGGG NM_006892 RefSeq chr20 + 32762384 32809356 DNMT3B 1789 "DNA (cytosine-5-)-methyltransferase 3 beta, transcript variant 1"
GO:0005515|GO:0010467|GO:0003886|GO:0006346|GO:0031503|GO:0010424|GO:0005634|GO:0046872|GO:0043231|GO:0045322|GO:0005737|GO:0071230|GO:0009008|GO:0010212|GO:0051718|GO:0090116|GO:0003714|GO:0042493|GO:0000122|GO:0006306|GO:0010628|GO:0032776|GO:0005720|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142003_PI430048170 0.0207437279633085 1.21885906075885 12.8813820506171 12.9576773478364 12.9866433301914 P P P 12.5530809800155 12.7525470695989 12.6586293068361 P P P LNCV6_142003_PI430048170 mRNA
TGTACTCCCATGACAACATCATCTGTGGCATCACCTCTGTTGCCTTCTCGCGCAGCGGAC NM_005273 RefSeq chr7 + 100673739 100679169 GNB2 2783 "guanine nucleotide binding protein (G protein), beta polypeptide 2"
GO:0005515|GO:0048471|GO:0005886|GO:0005246|GO:0003924|GO:0007268|GO:0044281|GO:0005765|GO:0032403|GO:0005615|GO:0031982|GO:0044297|GO:0043234|GO:0051020|GO:0006112|GO:0007186|GO:0016020|GO:0071377|GO:0004871|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138015_PI430048170 0.000287456881429856 0.227817599348772 6.9705745153786 7.21118680718283 6.76219500502629 P P P 8.92018108160025 9.34427974224235 9.08472522453309 P P P LNCV6_138015_PI430048170 mRNA
GCAGTCAGCGTCAGTGCTCATCTACGTTAATAAAGTGGTCCTATTTATGGCGGCAAAAAA NM_001145320 RefSeq chr9 + 133532163 133575519 ADAMTSL2 9719 "ADAMTS-like 2, transcript variant 2"
GO:0005515|GO:0006508|GO:0005578|GO:0008270|GO:0004222|GO:0030512 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131289_PI430048170 0.00375934938052364 0.538387074258264 9.60998578737021 9.91958266660081 9.94130789416146 P P P 10.543115781632 10.7158534838427 10.8936759357187 P P P LNCV6_131289_PI430048170 mRNA
TGGGTTTTTCTACCGTTTTTGTAGATGTCATGATGTCACGACCCCTGCACCCTGAAAAAA NM_001007563 RefSeq chr9 - 38406527 38424447 IGFBPL1 347252 insulin-like growth factor binding protein-like 1
GO:0005576|GO:0001558|GO:0005520 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141710_PI430048170 0.700000288196420 0.913387125041447 3.4682138859127 3.18858966327551 3.15020689342515 P P P 3.8102684548511 3.16995350774603 3.13579086467586 P P P LNCV6_141710_PI430048170 mRNA
TACTGCATCCTGTAGACATGGAGGGTTTCCCCCCTTATTCTGGGTCTGATTATTTTTAAA NM_032299 RefSeq chr11 - 103050683 103092215 DCUN1D5 84259 "DCN1, defective in cullin neddylation 1, domain containing 5"
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143358_PI430048170 0.0687412368766930 0.868127102859529 10.1617267512808 10.1559260908948 10.1116541515716 P P P 10.2267122212839 10.4177215625728 10.3901644768867 P P P LNCV6_143358_PI430048170 mRNA
AAATTTATTTTTGTTTGGGTGGACCCACTGGCCTGTCAGTCTCAATAAAGGGACCGGAGT NM_022095 RefSeq chr20 - 45948652 45972194 ZNF335 63925 zinc finger protein 335
GO:0005515|GO:0006355|GO:0044212|GO:0080182|GO:0050671|GO:0002052|GO:0005634|GO:0000979|GO:0001701|GO:0006351|GO:0046872|GO:0048854|GO:0035097|GO:0050769|GO:0007420|GO:0048812|GO:0040029|GO:0051569|GO:0021895. NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133915_PI430048170 0.4690045876130930.9849304584829050.390361176595692
0.3983240994838760.350756814545811A A A 0.4427415707433650.366017578157458
0.395811197699932A A A LNCV6_133915_PI430048170 mRNA
AGGATGAATCAATGTTTCTGGAGACATGAGATGTGCCAAATGGAGAAACCAATGTTTCTG NM_198185RefSeq chr11
- 7689923 7706394 OVCH2 NA ovochymase 2 (gene/pseudogene) NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_142988_PI430048170 0.2727758289714211.42366584205892 0.364878307243979
0.84603176694068 1.41180458718054 A A A 0.3538619473153210.569823534585723
0.349087583033404A A A LNCV6_142988_PI430048170 mRNA
ACCTCAGGAACGTCTACGCCAAGAACAACATGTGGTTCGACTTCGGCTTCGACCCCAACG NM_022134RefSeq
chr2_KI270776v1_alt + 11160 16385 GAL3ST2 64090 galactose-3-O-sulfotransferase 2
GO:0008150|GO:0001733|GO:0016020|GO:0009058|GO:0032580|GO:0008146|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144858_PI430048170 0.2231777875960550.7979833475728095.17282530758392
5.70422455179756 5.72609324526304 P P P 6.11914203271914 5.85089349654738
5.63365991926027 P P P LNCV6_144858_PI430048170 mRNA
CAAAAAGTCAGTTGATATGACACAGTCACAGACAGAACAGTCAGCAGCCCAAGAAAGGTC NM_002198RefSeq
chr5 - 132481608 132490773 IRF1 3659 interferon regulatory factor 1
GO:0005515|GO:0000790|GO:0008285|GO:0006366|GO:0035458|GO:0019221|GO:0005634|GO:0005829|GO:0051
607|GO:0005737|GO:0060337|GO:0045944|GO:0051726|GO:0007050|GO:0032481|GO:0060333|GO:0032728|GO:2
000564|GO:0006915|GO:0000978|GO:0003677|GO:0002819|GO:0001077|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132746_PI430048170 0.3285206416625881.04720860309928 0.310193923985662
0.28660791647009 0.449157847772824A A A 0.2934090968233550.260827599587672
0.297203490341583A A A LNCV6_132746_PI430048170 mRNA
CTGGCAAAACCTCTAAAACTGTCAAGAAAATGCTTGAAAGTTGATTTGTCATAGTGCAAA NM_032270RefSeq chr1
+ 89633084 89719535 LRRC8C 84230 "leucine rich repeat containing 8 family, member C"
GO:0005515|GO:0016020|GO:0005886|GO:0005789|GO:0045444|GO:0016021|GO:0006811 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_81359_PI430048170 0.000230093861653666 2.10277354707136 11.7433647524266
11.8605813570693 11.9403305447363 P P P 10.6607126036283 10.7914084731841
10.8740727834334 P P P LNCV6_81359_PI430048170 mRNA
TTCTCCTAGACCCGTGACCTGAGATGTGTGATTTTTAGTCATTAAATGGAAGTGTCTGCC NM_004878RefSeq chr9
- 129738335 129753065 PTGES 9536 prostaglandin E synthase
GO:0019369|GO:0019371|GO:0014070|GO:0048471|GO:0002526|GO:0006693|GO:0008285|GO:0044281|GO:0002
544|GO:0051592|GO:0007165|GO:0050220|GO:0043295|GO:0001516|GO:0016020|GO:0005641|GO:0032496|GO:0
005789|GO:0032526|GO:0016021|GO:0034097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129073_PI430048170 0.0250220770410244 0.5230439448976432.88649275702922
3.44960620640786 3.28934556737229 A P P 4.15495700605662 4.22854974707395
4.10072596684784 P P P LNCV6_129073_PI430048170 mRNA
CCATCTTAAAGCTAAGTTTACCCAAGTACTTTCAGCAAGCAGAAAAATGAAACTCTTTGT NM_031217RefSeq chr11
- 28020615 28108199 KIF18A 81930 kinesin family member 18A
GO:0005828|GO:0005515|GO:0008017|GO:0043130|GO:0005634|GO:0015031|GO:0070463|GO:0005829|GO:0019
886|GO:0005737|GO:0051010|GO:0008574|GO:0015630|GO:0007019|GO:0007018|GO:0005871|GO:0005815|GO:0
003779|GO:0005524|GO:0001726|GO:0007596|GO:0005901|GO:0008152|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_90936_PI430048170 0.3773867321364131.30196006738557 0.426351537468017 0.447743512492461
1.2932096852826 A A A 0.3959572125568260.390214777703075 0.417564329565291A A A
LNCV6_90936_PI430048170 mRNA

TGACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTG NM_001300780 RefSeq chr5 - 116443554 116574926 SEMA6A 57556 "sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A, transcript variant 1" GO:0005515|GO:0030424|GO:0005886|GO:0007411|GO:0007010|GO:0009887|GO:0006915|GO:0004872|GO:0016021|GO:0007166|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_7630_PI430048170 0.2733269270103221.7375131154172 8.59146206939429 9.17361068336503 9.31885756231003 P P P 9.53736101253511 6.1826158972702 6.73076952548618 P P P LNCV6_7630_PI430048170 mRNA
GGCGGTTCATCCTCTTCTGCTTCAAATAAAAAGTCATTAATTTATTAAAACTTGTGTGGC NM_002155 RefSeq chr1 + 161524539 161526897 HSPA6 3310 heat shock 70kDa protein 6 (HSP70B') GO:0006986|GO:0006200|GO:0042623|GO:0005814|GO:0072562|GO:0005524|GO:0005829|GO:0034605|GO:0042026|GO:0005737|GO:0008180|GO:0031072|GO:0051082|GO:0019899|GO:0070370|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141565_PI430048170 0.00798125358365138 0.5705277573101834.57048630783962 4.57132812664774 4.22516552546125 P P P 5.15060753545657 5.3357724619443 5.32881067936691 P P P LNCV6_141565_PI430048170 mRNA
AGTTTAGCAGTGACCTCAGCAACCCCTCCTTTTTATTTTTTCCTTTAAAAACATTTCAGT NM_004405 RefSeq chr2 - 172099437 172102750 DLX2 1746 distal-less homeobox 2 GO:0045746|GO:0003727|GO:0003700|GO:0051216|GO:0021544|GO:0005634|GO:0009954|GO:0000122|GO:0048701|GO:0043565|GO:0021766|GO:0021772|GO:0007420|GO:0045944|GO:0003682|GO:0048715|GO:0042475|GO:0048755|GO:0021893|GO:0021882 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67926_PI430048170 0.752913457257586 1.01107965099596 8.12934810850279 8.04019719193785 8.14246364404018 P P P 8.02559242174959 8.14677782060248 8.09153182724155 P P P LNCV6_67926_PI430048170 mRNA
AAGATTTGGTTTCAGAACCGGCGCATGAAGTGGAAAAAGGAGAACAAGACCGCGGGCCCG NM_004502 RefSeq chr17 - 48607232 48611021 HOXB7 3217 homeobox B7 GO:0005515|GO:0006355|GO:0003700|GO:0005634|GO:0007275|GO:0048704|GO:0009952|GO:0006351|GO:0043565|GO:0005737|GO:0030099|GO:0005654|GO:0090190 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119131_PI430048170 0.29929132525596 1.23926413397511 0.445948422113511 1.05731775188653 0.452435184921778 A A A 0.3140590664572020.365827824335526 0.433833664876739 A A A LNCV6_119131_PI430048170 mRNA
CGAAGACAGCGATGGCTGCTGGCTAAGAAGCGCGTGGTGCGAATGTTGCTGGTGATCGTT NM_176875 RefSeq chr11 + 6259673 6272127 CCKBR 887 cholecystokinin B receptor GO:0015054|GO:0005515|GO:0007631|GO:0008284|GO:0005886|GO:0008283|GO:0007586|GO:0007200|GO:0048565|GO:0001696|GO:0007204|GO:0046935|GO:0043551|GO:0004435|GO:0005887|GO:0048732|GO:0008152|GO:0004951|GO:0031741|GO:0007166|GO:0007600 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138213_PI430048170 0.8505117029089721.01089853401338 0.503253909414189 0.3843333431289870.300316549478357 A A A 0.4572389804034990.351835654507191 0.336116120770926 A A A LNCV6_138213_PI430048170 mRNA
CTATATAGATCAACCTCCACCAAACTTACCCAAACAGCATTTGTTTTATTTGAAACTCAC NM_001256704 RefSeq chr6 - 89177503 89217777 GABRR12569 "gamma-aminobutyric acid (GABA) A receptor, rho 1, transcript variant 3" GO:0005230|GO:0030054|GO:0005886|GO:0004890|GO:0034707|GO:0007268|GO:0007214|GO:0005254|GO:0055085|GO:0034220|GO:0005887|GO:0045211|GO:0006810 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145551_PI430048170 0.18404662521818 0.7055939223382327.95797445824956 8.83442211656244 8.01089776515415 P P P 8.86314115394261 8.55240301004385 9.03293265887283 P P P LNCV6_145551_PI430048170 mRNA
TTTTATTTTGTTTCTCTAGTGTTATGGCAGTGGAGGTGGGAATTTAGTCCCCAGGTGGGA NM_004381 RefSeq chr6_GL000254v2_alt - 3457287 3470260 ATF6B 1388 "activating transcription factor 6 beta,

transcript variant 1"
GO:0005515|GO:0003700|GO:0044212|GO:0035497|GO:0005634|GO:0030176|GO:0006351|GO:0030968|GO:0005
622|GO:0043565|GO:0007165|GO:0032993|GO:0005789 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79431_PI430048170 0.123567338372778 1.06922947005577 0.599130818462917 0.657989471566171
0.608422895555685 A A A 0.605553595494403 0.481240033742254 0.486268325563581 A A A
LNCV6_79431_PI430048170 mRNA
TCAGGTTTTTGAGGAAACAAAGATTTGTGGTAACTGAAGGTGTTGGGTCAGTGGCCAGGT NM_003382 RefSeq chr7
- 159028174 159144957 VIPR2 7434 "vasoactive intestinal peptide receptor 2, transcript variant 1"
GO:0007190|GO:0007165|GO:0007186|GO:0005886|GO:0004999|GO:0005887|GO:0004930|GO:0007267|GO:0048
662 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127898_PI430048170 0.417049184798835 0.908770123477101 5.6567683995116
5.80447008460061 6.14447769923728 P P P 6.09427601510832 6.06717432056092
5.89440849713997 P P P LNCV6_127898_PI430048170 mRNA
CTCCAGCTGTCAGTAGCCTGATGATTTTATGGTTGTTATAGTAAATTGCTATCATTTTACNM_152653 RefSeq chr3 +
23203292 23590805 UBE2E2 7325 ubiquitin-conjugating enzyme E2E 2
GO:0005515|GO:0070534|GO:0004842|GO:1900087|GO:0070979|GO:0032020|GO:0016874|GO:0070936|GO:0005
524|GO:0006974|GO:0042296 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132280_PI430048170 0.788577465527884 0.973143460133878 2.65551929365034
1.37427730168982 2.04768931594472 A A A 2.29011451948508 2.28671927896699 1.8546630302451
A A A LNCV6_132280_PI430048170 mRNA
TTTACAGTTTTTTCAACCCAACACTTAACCCCCTGATTTACAGCCTGAGGAACGGAGAGG NM_001005287 RefSeq
chr7 + 144318124 144319057 OR2A1 NA "olfactory receptor, family 2, subfamily A, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136531_PI430048170 0.00726259534664286 0.848381080655048 11.1911204053889
11.3108701529148 11.2691445081311 P P P 11.4743239029667 11.4680463062334
11.5417972173804 P P P LNCV6_136531_PI430048170 mRNA
GCCCTTGGTGATAGGCACATTTTTTACCAGTCTATCATTTGGTCATTAAATTTGTTTACA NM_052848 RefSeq chr19 +
41310188 41324883 CCDC97 90324 coiled-coil domain containing 97 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_127838_PI430048170 0.480914051565757 1.14654346924046 0.944848453080008
0.364969608991511 0.342076707184524 A A A 0.421009241495656 0.344325150973935 0.3777823230713
A A A LNCV6_127838_PI430048170 mRNA
TGGGACTGTTTCAGACTTGGAAAGGTCACAGAAGGAAAATAATATAATAAAGTGACAACT NM_033440 RefSeq chr1
+ 15456727 15472091 CELA2A 63036 "chymotrypsin-like elastase family, member 2A"
GO:0004252|GO:0006508|GO:0005576|GO:0017171 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139902_PI430048170 0.14425796776041 0.701796622121079 0.594738348597925
0.562106443169122 1.08249913545771 A A A 0.859148608011497 1.59832272110901
1.28175442386609 A A A LNCV6_139902_PI430048170 mRNA
GGGTCTAGTGCCCTGCATTCCTTTGAGGCAAAAAATAAATGGGCTATGACTGGTTAAATG NM_170736 RefSeq chr21
+ 38256803 38301824 KCNJ15 3772 "potassium channel, inwardly rectifying subfamily J, member 15,
transcript variant 1"
GO:0005515|GO:0005242|GO:0005886|GO:0005887|GO:0010107|GO:0007268|GO:0034765|GO:0006813 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129836_PI430048170 0.528958209882947 0.85975296341021 0.415637715878827
0.433628947364469 0.361463134447502 A A A 0.321638949827866 1.05195034004962
0.371441397828038 A A A LNCV6_129836_PI430048170 mRNA
CTGCTCCAAGAGAACATTGAAAAGAATAAAGGTGAAATCAACCACATTTTCCAGCAAATT NM_001631 RefSeq chr2
+ 232456111 232460745 ALPI 248 "alkaline phosphatase, intestinal"
GO:0000287|GO:0005886|GO:0004035|GO:0016311|GO:0008270|GO:0031225|GO:0016021|GO:0002020 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144714_PI430048170 0.0561476503433865 3.00142433024872 10.2306659203387
10.2609896482707 10.4270149148343 P P P 9.43792871450689 7.99791522775394 8.3156948296343
P P P LNCV6_144714_PI430048170 mRNA
TTGGCTGTGGCTGGAATAAATCATTTATTACTTGGGAGTCCCATTTTGGACACTAATAAT NM_017983 RefSeq chr17
- 68421280 68457512 WIPI1 55062 "WD repeat domain, phosphoinositide interacting 1"
GO:0005802|GO:0030136|GO:0050681|GO:0034497|GO:0005829|GO:0030968|GO:0005737|GO:0006497|GO:0005
856|GO:0000045|GO:0006995|GO:0000422|GO:0000421|GO:0030331|GO:0080025|GO:0006914|GO:0005102|GO:0
000407|GO:0032266|GO:0034045|GO:0048203|GO:0000139|GO:0006987|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93770_PI430048170 0.00161384392357235 0.4729669656304934.15152467055263
3.85659899436404 4.16499847877308 P P P 5.23444058108664 5.01355285344635
5.17723773200892 P P P LNCV6_93770_PI430048170 mRNA
GAAGAAGCTTTTCAGAATCAGAAAGTGATCATAGATACACTAATCACCAAACTGATGGAA NM_015905 RefSeq chr7
+ 138460333 138585587 TRIM24 8805 "tripartite motif containing 24, transcript variant 1"
GO:0005515|GO:0004842|GO:0008285|GO:0016567|GO:0006366|GO:0016874|GO:0043434|GO:0005634|GO:0035
064|GO:0055074|GO:0005829|GO:0034056|GO:0002039|GO:0030163|GO:0046777|GO:0031647|GO:0070577|GO:0
016922|GO:0005719|GO:0003713|GO:0005102|GO:0071391|GO:0042981|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139235_PI430048170 0.577349177304597 1.12333206337142 9.67349727034926
9.22061335618297 8.96111814032112 P P P 9.16419097291783 9.14812122444879
9.13092542299735 P P P LNCV6_139235_PI430048170 mRNA
GAAGGTGGCGTTTCCACCTTTTCCATAATAAAATAGAAATGTGTGTAGAACTGGAAAAAA NM_005782 RefSeq chr17
- 81887834 81891586 ALYREF 10189 Aly/REF export factor
GO:0005515|GO:0008380|GO:0006369|GO:0010467|GO:0006366|GO:0031124|GO:0005634|GO:0071013|GO:0046
784|GO:0005829|GO:0043231|GO:0006406|GO:0032786|GO:0003697|GO:0000166|GO:0035145|GO:0070062|GO:0
000346|GO:0001649|GO:0016020|GO:0016607|GO:0000398|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132450_PI430048170 0.928883956030885 0.967391686631944 0.40143150438249
0.876192633197739 0.446196226646197 A A A 1.0573845334707 0.345774969285859
0.399569432334773 A A A LNCV6_132450_PI430048170 mRNA
TCGGTCTCACAAGGACCTCTTAACCCCTCAATAAAGTGTTACATTTCTAAACATTGGAAA NM_134444 RefSeq chr19
+ 55836577 55881854 NLRP4 147945 "NLR family, pyrin domain containing 4"
GO:0032479|GO:0006954|GO:0045087|GO:0032481|GO:0005524|GO:0070062|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_120086_PI430048170 0.179151372389741 1.24273749541049 3.997242720978
4.27024336515136 4.21884612117379 P P P 3.73565701749092 3.60502325550157
4.15961559725761 P P P LNCV6_120086_PI430048170 mRNA
TGTGGAGTTTGGAGCTCGTATGGTCAACATTGATGGAAAACAAATCAAACTGCAAATCTG NM_032846 RefSeq chr14
- 21459019 21476973 RAB2B 84932 "RAB2B, member RAS oncogene family, transcript variant 1"
GO:0006184|GO:0045921|GO:0005886|GO:0000139|GO:0005789|GO:0003924|GO:0032482|GO:0019003|GO:0016
192|GO:0005525|GO:0006886|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127886_PI430048170 0.604171116022767 0.855395197769065 3.29025049535123
0.824838849232784 3.16852354422863 P A P 2.41347944930764 3.49262534059453
2.89433820775629 A P P LNCV6_127886_PI430048170 mRNA
CATCACCATTTTAATTCTGTGGTTGAAAGTCATGGAACGAATAAAGTGTCAGATTTAGGG NM_138378 RefSeq chr11
- 111874055 111879457 FDXACB1 91893 "ferredoxin-fold anticodon binding domain containing 1,
transcript variant 1" GO:0000287|GO:0000049|GO:0006432|GO:0004826|GO:0005524|GO:0008033 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_141647_PI430048170 0.00264046538473535 0.3122170532231944.02044234343873
3.94217071980697 3.85732699098817 P P P 5.38711199374569 5.83411523614384
5.60686867613217 P P P LNCV6_141647_PI430048170 mRNA
CTTAAGGTGCACAGTAAATGTACAGATAGTTATAGGCCACTGTTTTGTAATGTAGTACAT NM_020841RefSeq chr12
- 76351797 76559809 OSBPL8 114882 "oxysterol binding protein-like 8, transcript variant 1"
GO:0051897|GO:0031965|GO:0030336|GO:0090204|GO:0016020|GO:0015485|GO:0010891|GO:0006869|GO:0046
628|GO:0045444 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_50575_PI430048170 0.2483978443257321.29215675381959 1.03668208439044 0.440414696225472
0.378262089417116A A A 0.2690579294683850.2983732671665830.273760406038007A A A
LNCV6_50575_PI430048170 mRNA
TCTATTGAAGTCAGCTTGAACAAAGGCAAAACATTCTTCAAGAGCAATGTCAGCATCACC NM_001278688 RefSeq
chr10 + 46286996 46330207 ANTXRLNA anthrax toxin receptor-like NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137628_PI430048170 0.0934341417154737 0.7706576689319095.10806585777743
5.26596228283705 5.58803547226166 P P P 5.56439183731427 5.74685824282437
5.80936432120333 P P P LNCV6_137628_PI430048170 mRNA
TCTTTAAATCTCAGGACTTCTGAAGAGTTTTATTCTTCTTCACTATCTGTGGCATGACCA NM_022786RefSeq chr1 +
230979076 231000733 ARV1 64801 ARV1 homolog (S. cerevisiae)
GO:0006665|GO:0090181|GO:0005789|GO:0008206|GO:0030301|GO:0016021|GO:0055085 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144776_PI430048170 0.1326088013060990.9464854718281420.242915043296873
0.2730911944550810.317272477703287A A A 0.4228035060544750.335000962082856
0.312106611591022A A A LNCV6_144776_PI430048170 mRNA
GAAAAAAGATACGGAGGATTTATGAGATTTTAATATCTTTTCCCACTAGTGGCCCCAGGC NM_001135690 RefSeq
chr8 - 56440953 56446723 PENK 5179 "proenkephalin, transcript variant 1"
GO:0005515|GO:0001964|GO:0007165|GO:0007218|GO:0001515|GO:0002118|GO:0007626|GO:0005576|GO:0001
662|GO:0005184|GO:0019233 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141672_PI430048170 0.1711985383522980.7768336124481590.281726950420095
0.2903795671636640.398878787413246A A A 0.3660270931787080.694906929756828
0.947734721360053A A A LNCV6_141672_PI430048170 mRNA
CTCATAAAAGAGAAGAGTGTTCCATTTCAGTCTCAATAAACACTTCCCTCATTCTTTCAA NM_004170RefSeq chr9
+ 4490426 4587469 SLC1A1 6505 "solute carrier family 1 (neuronal/epithelial high affinity glutamate
transporter, system Xag), member 1"
GO:0015501|GO:0005886|GO:0051938|GO:0070779|GO:0005313|GO:0007268|GO:0055085|GO:0016324|GO:0016
020|GO:0042883|GO:0005887|GO:0051260|GO:0016595|GO:0017153|GO:0070062|GO:0006811|GO:0033229 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145405_PI430048170 0.00192211184180485 0.3036603248434695.67247029583718
5.42583025913406 5.69769548058483 P P P 7.02718889291154 7.33424825304594
7.55941686208828 P P P LNCV6_145405_PI430048170 mRNA
GAAAACACTGTTCTTACCCTCGAACCCTGATGTGGTTCCATTATGTAAATATTTCAAATA NM_021239RefSeq chr14
+ 73058512 73121368 RBM25 58517 RNA binding motif protein 25
GO:0008380|GO:0006397|GO:0005515|GO:0005737|GO:0016607|GO:0000166|GO:0000381|GO:0042981|GO:0005
681|GO:0005654|GO:0003729 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104643_PI430048170 0.0702791650784336 0.63237730409797410.2957067644403
9.82234879337445 9.53762765623322 P P P 10.7809332630766 10.5496117394995
10.3840220967195 P P P LNCV6_104643_PI430048170 mRNA
AAATGAAAGTCGCCTCTCCCGAAATGACATCCAGTCTGAAAAGTGGTCCATCAGCAAACA NM_001007471 RefSeq
chr9 - 70535048 71121598 TRPM3 80036 "transient receptor potential cation channel, subfamily M,
member 3, transcript variant 9"

GO:0005262|GO:0034220|GO:0005261|GO:0005886|GO:0070588|GO:0016048|GO:0016021|GO:0005227|GO:0050951|GO:0055085|GO:0006812 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100478_PI430048170 0.0436410542647999 2.65541676456397 2.02250180728049 3.24567330133053 2.3805701559832 A P A 1.5591713418706 0.678563840353434 1.33096419056748 A A A LNCV6_100478_PI430048170 mRNA CAGGGACCCCAGACAGCAATGATGTGGACAGCAACGACCTGGAGAGACAAGGCCTACTTT NM_182538RefSeq chr17 + 4433923 4488204 SPNS3 201305 spinster homolog 3 (Drosophila)
GO:0040011|GO:0046624|GO:0006869|GO:0003376|GO:0016021|GO:0005765|GO:0055085|GO:0031982 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142654_PI430048170 0.0282693812775315 0.6213263496614845.19956726308501 5.09089851396672 5.60180619001383 P P P 6.24703213196391 5.82980234006231 5.8905879881575 P P P LNCV6_142654_PI430048170 mRNA ACATTGCATCAGGTTCTAAAATCCCAAACCCCAAACAGCCTGGAACATGTTACTCTGATT NM_144597RefSeq chr15 - 83004392 83011641 C15orf40 123207 "chromosome 15 open reading frame 40, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131933_PI430048170 0.00578070214334387 0.62056423001486911.2519342422845 11.3024865170335 11.2448424735651 P P P 11.9035767341738 11.871591618846 12.080897564102 P P P LNCV6_131933_PI430048170 mRNA CAACTCAGTTGTCCACCACAGGGGAATTTTGAATGTCTTTTGTTTTTGTTTTGTTTTGAA NM_031206RefSeq chrX - 65512581 65534806 LAS1L 81887 "LAS1-like (S. cerevisiae), transcript variant 1"
GO:0005737|GO:0016020|GO:0005815|GO:0071339|GO:0006364|GO:0005730|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127405_PI430048170 0.00686623288151917 0.326435978350245 0.295635500344806 0.329001610431414 0.402819299036792 A A A 1.74555129840575 1.84115072949366 2.23940435576229 A A A LNCV6_127405_PI430048170 mRNA TTAACGGTTCACGTCTAGCCAAATAACTGTTTTGGAATAAAAACCTTGGTGGTGAAAAAA NM_016322 RefSeq chr9 - 121178136 121202087 RAB14 51552 "RAB14, member RAS oncogene family"
GO:0005515|GO:0048471|GO:0005886|GO:0042175|GO:0032456|GO:0003924|GO:0009790|GO:0005765|GO:0005764|GO:0006886|GO:0043231|GO:0005829|GO:0090387|GO:0032880|GO:0005622|GO:0030670|GO:0061024|GO:0032482|GO:0016192|GO:0030140|GO:0030659|GO:0070062|GO:0005791|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141255_PI430048170 0.9165727575901 1.00538081408956 0.352908548486248 0.519328361186881 0.40110105364096 A A A 0.505480753188131 0.378524015580986 0.367096852974762 A A A LNCV6_141255_PI430048170 mRNA CTGTGAATGAGAAAGTATTTGTCTCTCCAACTTGAAAATGCACTGTATTTCCTGTGATAT NM_024581 RefSeq chr6 - 118959828 119078647 FAM184A 79632 "family with sequence similarity 184, member A, transcript variant 1" GO:0008150|GO:0003674|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133613_PI430048170 0.699130859541626 0.945076251867122 3.49213105017006 4.39291132447692 3.94812719077339 P P P 4.13035653215091 3.86312802803125 4.20185077183419 P P P LNCV6_133613_PI430048170 mRNA CTCAGATCTTTGGACCTTTCCAATGCGTCTCTTTCTCCTGTTATTGCTGCAATGTATTTT NM_024508 RefSeq chr3 - 111592899 111595335 ZBED2 79413 "zinc finger, BED-type containing 2" GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127284_PI430048170 0.102000524422885 1.06675503972572 0.473612548374063 0.577050908259004 0.528869661691736 A A A 0.372607815316145 0.443593744954895 0.483327209289744 A A A LNCV6_127284_PI430048170 mRNA GGGCTATAGCATAATTAGATTTTCTGGCTTTCAAAAATTTGGATTGCAATCACAGCAAAC NM_199286 RefSeq chr12 + 7711453 7717556 DPPA3 359787 developmental pluripotency associated 3

GO:2000653|GO:0005737|GO:0001939|GO:0040016|GO:0005634|GO:0035064|GO:0001940|GO:0016568 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_141947_PI430048170 0.0686669108206964 0.83293064578921 7.64513253035989
7.74426998891755 7.45282918274509 P P P 7.94083174853405 7.91653367037043
7.78637996318581 P P P LNCV6_141947_PI430048170 mRNA
TCATGATTGTGATAAACCATCGCGGTTAATGACAGCAGAAGGTTCTTTGTCGCTCCCCAT NM_173804 RefSeq
chr19 - 55226633 55229264 TMEM86B 255043 transmembrane protein 86B
GO:0005737|GO:0016020|GO:0047409|GO:0047408|GO:0046485|GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_125351_PI430048170 0.393284811807698 0.925207192843857 15.4847049615393
15.1391448843491 15.1739612104822 P P P 15.3090060133565 15.4267084842471
15.4211852134286 P P P LNCV6_125351_PI430048170 mRNA
CGGCGCCTCCCCTCACCCCCGGCCGCCTTCCCTCCATCCGTTCCAGGGACCTCACCCTCG NM_001722 RefSeq
chr8 + 22245105 22251167 POLR3D 661 "polymerase (RNA) III (DNA directed) polypeptide D,
44kDa"
GO:0032728|GO:0010467|GO:0000790|GO:0006386|GO:0006385|GO:0003677|GO:0006383|GO:0005829|GO:0051
607|GO:0005737|GO:0045089|GO:0001056|GO:0045087|GO:0003682|GO:0005666|GO:0005654|GO:0032481 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134214_PI430048170 0.0989880505036015 0.482246747589577 2.2090661515091
0.778070048591068 1.60058011526328 A A A 2.81092823944511 2.78858893614477
2.46089359552813 P P P LNCV6_134214_PI430048170 mRNA
GGTGTTCATCTCTTTCAGAAGTTTGTAGAAGAAAGAGATGTTTTTAAGACCAGAATACTC NM_033418 RefSeq
chr1 - 169792531 169794920 METTL18 92342 methyltransferase like 18
GO:0005737|GO:0006479|GO:0008276 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_128999_PI430048170 0.162650837684506 0.937761964841233 9.68289986348914
9.56305120080838 9.58604361588616 P P P 9.6239486557476 9.74718087474941
9.73855796321537 P P P LNCV6_128999_PI430048170 mRNA
CGCGGACCCCATTACAATAAATTTTAAATAAAATCCTGTTTCTGGCTCTGGATTGAAAAA NM_001042539 RefSeq
chr16 + 29806536 29811183 MAZ 4150 "MYC-associated zinc finger protein (purine-binding
transcription factor), transcript variant 2"
GO:0005515|GO:0006369|GO:0005737|GO:0006367|GO:0045944|GO:0003682|GO:0000981|GO:0005654|GO:0005
634|GO:0000979|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143462_PI430048170 0.111995761886892 0.963686829938272 0.377234087706823
0.398100777839372 0.326980385366006 A A A 0.423206849956746 0.434430562095774
0.405545508695633 A A A LNCV6_143462_PI430048170 mRNA
GTTTAAAATAGTACCCGGTTCAATGAAAGAGCCTAAACCATCTTAACTCAGCTTTAAAAC NM_130773 RefSeq
chr2 + 124025286 124915377 CNTNAP5 129684 contactin associated protein-like 5
GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143447_PI430048170 0.0641063314146922 0.562096966682058 4.53108509271775
3.97907644828954 4.86770540953358 P P P 5.32457271430433 5.16322410835998
5.49895326559183 P P P LNCV6_143447_PI430048170 mRNA
AATGTAATTATTAATAGGTTTCTAATTTACATGTTTCCTGTTTAGATAAGATTATTTTAT NM_152608 RefSeq chr1
- 225982701 225999365 SDE2 163859 SDE2 telomere maintenance homolog (S. pombe) NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142970_PI430048170 0.596925138949224 0.969622495780247 0.49902826641009
0.507514233360004 0.300991658274637 A A A 0.402992429498064 0.547125025790829
0.496557963628988 A A A LNCV6_142970_PI430048170 mRNA
CTTGCTTCATGCTGCTTAAGTTACCAGATGAATGCTGAGAAATAAGTAATCACAGACATT NM_024893 RefSeq

chr20 + 24469198 24666617 SYNDIG1 79953 synapse differentiation inducing 1
GO:0051965|GO:0030054|GO:0014069|GO:0060076|GO:0006886|GO:0042803|GO:0044297|GO:0009607|GO:0043197|GO:0005887|GO:0043198|GO:0031901|GO:0045211|GO:0035254|GO:0097091 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127917_PI430048170 0.958385207140302 1.00771605473255 2.99572965068153 3.18877233858342 3.51000294664799 A P P 3.09844381359633 3.03830427391901 3.52215736298639 P P P LNCV6_127917_PI430048170 mRNA
AGTTTTCAGACATTAAGTGACTGTATCATGTTCGGTTTAATAAAGAATTTATGCAGCACC NM_152384 RefSeq
chr2 + 169479495 169506655 BBS5 129880 Bardet-Biedl syndrome 5
GO:0001103|GO:0005515|GO:0060170|GO:0034464|GO:0006996|GO:0032266|GO:0015031|GO:0032402|GO:0036064|GO:0005829|GO:0044458|GO:0001947|GO:0005622|GO:0042384|GO:0007601|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141871_PI430048170 0.473569316951393 1.05674512201289 7.62906100732687 7.60957916436563 7.64006076088939 P P P 7.34501441305107 7.65833967693723 7.61699279472849 P P P LNCV6_141871_PI430048170 mRNA
GGGAATTATGCTGTTCATTTATAATAGTGGACATTATGGAGAGCTCTGATTCCTACATAA NM_018332 RefSeq
chr16 + 70346920 70373378 DDX19A 55308 DEAD (Asp-Glu-Ala-Asp) box polypeptide 19A
GO:0031965|GO:0043065|GO:0003723|GO:0004386|GO:0015031|GO:0005524|GO:0010043|GO:0003674|GO:0008150|GO:0005737|GO:0016020|GO:0005643|GO:0008152|GO:0051028 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137387_PI430048170 0.16870300990109 1.50751482219681 5.22057857389705 5.28279845721105 5.38916937346626 P P P 4.02485627518757 4.89153049561282 5.01777941256123 P P P LNCV6_137387_PI430048170 mRNA
CCTCTAGTCGAAGACAATATTTGATTCCTAGTTCTGTTTGGGGCAAATTTTCATTTATCT NM_005100 RefSeq chr6 + 151239998 151358561 AKAP12 9590 "A kinase (PRKA) anchor protein 12, transcript variant 1"
GO:0005515|GO:0005886|GO:0008179|GO:0030819|GO:0006605|GO:0010739|GO:0005737|GO:0007186|GO:0090036|GO:0005856|GO:0051018|GO:0005925|GO:0005938 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88680_PI430048170 0.155090755445938 0.603260851626884 1.5065468512497 2.52042920529622 2.71383655871361 A A A 2.93415431985797 2.96371735788333 3.27077485233793 P P P LNCV6_88680_PI430048170 mRNA
AGAATCATTTTTGAACCTAAGGAAAGATGATGCGTCGGAAAGTACTTCTTTGTCAGCATT NM_015633 RefSeq
chr12 + 26938371 26966648 FGFR1OP2 26127 "FGFR1 oncogene partner 2, transcript variant 1"
GO:0042060|GO:0042803|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136956_PI430048170 0.910197352098799 0.992460346018229 3.598075493745 3.23435753439719 3.28059908384437 P P P 3.87312547448515 2.89324201353213 3.23160810076039 P P P LNCV6_136956_PI430048170 mRNA
TTCCTTTTCTTGGTTTTAATTTCTGAGCAGATGATTGTGCTGTGGGAACAGCACACAGTG NM_199330 RefSeq
chr15 - 82848976 82952724 HOMER2 9455 "homer scaffolding protein 2, transcript variant 2"
GO:0048875|GO:0035584|GO:0030054|GO:0046982|GO:0005886|GO:0019904|GO:0005730|GO:0007216|GO:0048148|GO:0045177|GO:0003779|GO:0005634|GO:2001256|GO:0042803|GO:0030425|GO:0005737|GO:0030160|GO:0008277|GO:0035256|GO:0045211|GO:0043025|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139153_PI430048170 0.360673760326348 1.02977371103268 0.296209364868456 0.287554169630282 0.397518683694865 A A A 0.29942598474501 0.275716377001623 0.281663773355003 A A A LNCV6_139153_PI430048170 mRNA
GATCACTCTTTATATGTGGATTAAGTTCCCTTAGATACATTGGATTAGTCCTTACCAGTA NM_019851 RefSeq chr8 - 16992824 17002165 FGF20 26281 fibroblast growth factor 20

GO:0008286|GO:0008284|GO:0048011|GO:0060113|GO:0060043|GO:0048015|GO:0007267|GO:0005104|GO:0005576|GO:0007165|GO:0007173|GO:0008543|GO:0045087|GO:0070374|GO:0008083|GO:0038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145174_PI430048170 0.782842116244635 0.955475210144578 6.3415708297499 6.08241579992807 6.13960888852179 P P P 5.92712588642705 6.36506182675978 6.43143497816403 P P P LNCV6_145174_PI430048170 mRNA
GATTGATACTGGAGTCTCATTCTGCCTGATTAAAAATGGAATTAGTATGCAACACTGAAA NM_152383 RefSeq chr2 + 231961582 232337198 DIS3L2 129563 "DIS3 like 3'-5' exoribonuclease 2, transcript variant 1"
GO:0005515|GO:0034427|GO:0000287|GO:0008285|GO:0000291|GO:0004540|GO:0010587|GO:0008266|GO:0051306|GO:0005737|GO:0007067|GO:0000175|GO:0000932|GO:0019827|GO:0005844|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132158_PI430048170 0.551182881020688 0.822736555489336 0.48803471620038 0.318872696117228 0.394237905354332 A A A 0.279182311676093 0.349138135275097 1.22090392598955 A A A LNCV6_132158_PI430048170 mRNA
GATGTTGAACTGGGAACATTCCAGAAGGATTCCACGTGAAGCAGTGTTTGCATTTGTATG NM_001278522 RefSeq chr10 + 28846407 28881897 C10orf126 283080 chromosome 10 open reading frame 126 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139486_PI430048170 0.6996630319720120.9638530872532080.335755693507167 0.3231800800861060.455297056291202A A A 0.3038503854469160.620302222367038 0.331388442240837A A A LNCV6_139486_PI430048170 mRNA
CTTCATTTAAATATGCACGGTTAAAATGAATAGCGGCCTAAAGAATAACACTGATCTCTC NM_018972RefSeq chr8 + 74350382 74367100 GDAP1 54332 "ganglioside induced differentiation associated protein 1, transcript variant 1"
GO:0005739|GO:0005737|GO:0016020|GO:0000266|GO:0006626|GO:0005634|GO:0032526|GO:0031307 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144298_PI430048170 0.0125719390819291 0.2650186427192971.3077665716949 2.18676137282385 2.06593259571559 A A A 3.67720508848029 3.77865996136794 3.98211423218795 P P P LNCV6_144298_PI430048170 mRNA
TTGTCAGCCTGGGAAACAGATGCGTTCTTATTTTTTGAAGTTGTGTGACCCTGGACTGTC NM_152715RefSeq chr11 + 121024103 121089645 TBCEL 219899 "tubulin folding cofactor E-like, transcript variant 1"
GO:0005737|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142017_PI430048170 0.5148818401495840.9662465660792370.507128542649331 0.3244883559425360.309056384865341A A A 0.4820405951443810.430064703109359 0.384040962660521A A A LNCV6_142017_PI430048170 mRNA
ATTGCTACTGGATTCTTAACTAGAGAAAACTTACAGAACAGGTGTTAAGCCTTTTCCAAT NM_001100159 RefSeq chr7 + 48035510 48061297 C7orf57 136288 "chromosome 7 open reading frame 57, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130099_PI430048170 0.1758290817663132.13520299054033 1.76128052111349 2.5121119889595 0.794619371642661A A A 0.3430003988640751.33904262772639 0.348793937264917A A A LNCV6_130099_PI430048170 mRNA
GGTGCCAAAAATAGTTGAACATCGACATCAAAAAGATTCTTTCTGTCTGCTTATTCACAT NM_001078170 RefSeq chr2 - 87757200 87825767 RGPD2 729857 RANBP2-like and GRIP domain containing 2 GO:0000042 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131209_PI430048170 0.3537209684030681.02118726198428 0.336092596685247 0.2535368484029280.273083901731978A A A 0.2551099792830380.262715314532751 0.255428662058787A A A LNCV6_131209_PI430048170 mRNA
TTCCAGTAATACTATTTCTGATAGGGGGCCATTGATTGAGGGTAGCTTGTTGCAATGCTT NM_005593RefSeq chr12 + 80716928 80719668 MYF5 4617 myogenic factor 5
GO:0005515|GO:0006366|GO:0003705|GO:0001756|GO:0048704|GO:0035914|GO:0042693|GO:0042692|GO:0048

743|GO:0030198|GO:0045944|GO:0043010|GO:0060415|GO:0006357|GO:0046982|GO:0070888|GO:0001228|GO:0
000978|GO:0007517|GO:0051149|GO:0001503|GO:0007519|GO:0001502|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129383_PI430048170 0.0116151097708052 1.28580605401834 11.6769772583451
11.7818796594665 11.5691176994396 P P P 11.2401055909928 11.3746968230214
11.3297537405355 P P P LNCV6_129383_PI430048170 mRNA
CATTGAGGAGCTCCCTAGCTGAACGGGTTACCCTGGTCATTAATAAAGCTGTGACTGGTC NM_014205 RefSeq chr11
- 65116402 65117738 ZNHIT2 741 "zinc finger, HIT-type containing 2" GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_99281_PI430048170 0.02402541488438 1.31906246445778 10.3584634808338 10.4671935352564
10.5379470072882 P P P 9.96755302612338 9.96212315662959 10.2250774840814 P P P
LNCV6_99281_PI430048170 mRNA
GGAAATGACTGCAGTGGCCTAATTGTCTTCACTTGAATTGAAAATAAATAATTTGAGAGC NM_018352 RefSeq chr4
+ 163494520 163520539 TMA16 55319 translation machinery associated 16 homolog (S. cerevisiae)
GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133215_PI430048170 0.0105288756177145 1.67201013468634 11.0421490919885
11.0633568785776 10.9670028472014 P P P 10.3303849169349 10.4087261885706
10.0918662571445 P P P LNCV6_133215_PI430048170 mRNA
AGTGCAATCTATGTGATGTCTTCCAACGTTAATAAATCACACAGCCTCCCAGGAGGGAGA NM_001029885 RefSeq
chr1 + 1324762 1328896 CPTP 80772 ceramide-1-phosphate transfer protein
GO:0005640|GO:0051861|GO:0005794|GO:0005543|GO:0005886|GO:0046836|GO:0005548|GO:0010008|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143956_PI430048170 0.8586365652255090.9475271702828056.56478573636376
6.20260722121535 5.97427167082829 P P P 6.62624116627514 6.47419535767451
5.81496850006114 P P P LNCV6_143956_PI430048170 mRNA
AGAAAGATCCACCCTCAAATGTCAGAGCTATGTTCCCTCCAGCAGTGGTATTAATACTGC NM_001178065 RefSeq
chr3 + 122184333 122286497 CASR 846 "calcium-sensing receptor, transcript variant 1"
GO:0005515|GO:0005513|GO:0005886|GO:0004930|GO:0007635|GO:0006874|GO:0009653|GO:0070509|GO:0001
503|GO:0007186|GO:0004435|GO:0005887|GO:0008152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138525_PI430048170 0.5484142877063571.24046762874381 0.475390169200767
0.56570050031247 1.50698557406617 A A A 0.4658223098182770.877103040537291
0.472358139706157 A A A LNCV6_138525_PI430048170 mRNA
CTAGGTGATGCCATACCATTTTAAAAGTAGTAAGAGTTTGCTGCCCAAATAGTTTTTCTT NM_178127 RefSeq chr11
- 101890673 101916522 ANGPTL5 253935 angiopoietin-like 5 GO:0005576 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_22630_PI430048170 0.0248845139237538 0.6419970867941366.00776907098831
6.45783784482161 6.39905069327376 P P P 6.86714383472267 6.83503904081201
7.10531053463091 P P P LNCV6_22630_PI430048170 mRNA
CGGCAAGATTTTCCTCAGCATCTGGTGTCAAGACACTCGTCACTATTAATTCGGAAAGAA NM_182543 RefSeq chr10
- 18545206 18651637 NSUN6 221078 "NOP2/Sun domain family, member 6"
GO:0003723|GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139991_PI430048170 0.9169282757410680.9861756025227468.35555680346379
8.36732759716526 8.67627663620694 P P P 8.37937800603642 8.34987750063197
8.72302326481795 P P P LNCV6_139991_PI430048170 mRNA
GCCCTCATCATAGTTCCTGATTGTCTCTTAAAGTAAGTGGTTTATAGACATTACTATTTCNM_001284527 RefSeq chr16
- 3382080 3401065 ZSCAN32 54925 "zinc finger and SCAN domain containing 32, transcript variant
1" GO:0005515|GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0003677|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141515_PI430048170 0.7944110079574371.07148858938685 1.05334446641136

0.35698915462973 0.358094355997787 A A A 0.8338490622167580.359661722333877
0.336657621077462 A A A LNCV6_141515_PI430048170 mRNA
ATCCAGGTACATAGCCATAAAGGGATGAGCTAGAGAGGTCTCCATATTATCATTCAATGT NM_003608 RefSeq chr14
+ 88005123 88014811 GPR65 8477 G protein-coupled receptor 65
GO:0006955|GO:0031532|GO:0007186|GO:0005886|GO:0005887|GO:0004930|GO:0051496|GO:0030819|GO:0010
447|GO:0006915|GO:0007275|GO:0032862 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127448_PI430048170 0.2231228856370260.820147396296984 0.335684816664733
0.3187661401362450.44384495935552 A A A 0.8411807940764410.74129223443717
0.327483360721355 A A A LNCV6_127448_PI430048170 mRNA
AAATGAAATGGAAAACTGGACCATGGGACTCTGGCAAACCTGTGTCATCCAAGAGGAAGT NM_001185149
RefSeq chr4 - 183321763 183322426 CLDN24 NA claudin 24 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127630_PI430048170 0.0367269144538904 3.0717429147176 3.17997170493744
4.21889234864403 4.09200258499322 P P P 2.61035958246314 2.56020776209945
1.35606190490062 A A A LNCV6_127630_PI430048170 mRNA
GAGTCTGTTTGACTAGTGCTAAAGGAAACAATTCATGCGGATGTATAAAACTCGCTCTTT NM_012263 RefSeq chr22
- 43039515 43089428 TTLL1 25809 "tubulin tyrosine ligase-like family member 1, transcript variant 1"
GO:0018095|GO:0005737|GO:0035082|GO:0003351|GO:0005874|GO:0070740 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_65225_PI430048170 0.00143486212037701 2.31390518335303 12.363377032094
12.5017373950442 12.1111720849981 P P P 11.1160132515672 10.9546091597441
11.2828123697117 P P P LNCV6_65225_PI430048170 mRNA
GGGTTTAAGGGACTTGGGGAGCCACTGGAAGAATAATAAAAGTGTTGCTCTTTATCATCT NM_012267 RefSeq chr19
- 55262222 55280383 HSPBP1 23640 "HSPA (heat shock 70kDa) binding protein, cytoplasmic
cochaperone 1, transcript variant 1"
GO:0005515|GO:0004857|GO:0006457|GO:0032436|GO:0031398|GO:0043086 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143279_PI430048170 0.0354226590362988 0.6948926707526782.74689137678174
2.55040568939135 3.00642549972187 A A P 3.3860655914021 3.37412485526207
3.14258356673639 P P P LNCV6_143279_PI430048170 mRNA
TTTCTCATTGATCACAGATGTGCCCAGAGTAGCCCAGGTCACTGTTAACTAGTGTTTCTG NM_001433 RefSeq chr17
- 64043029 64130142 ERN1 2081 endoplasmic reticulum to nucleus signaling 1
GO:0005515|GO:0008380|GO:0035924|GO:0005783|GO:0005637|GO:0030176|GO:0033120|GO:0042803|GO:0030
968|GO:0042802|GO:0005739|GO:0005737|GO:1900103|GO:0007050|GO:0006379|GO:0006355|GO:0000287|GO:0
004521|GO:0005524|GO:0006351|GO:0043531|GO:0070059|GO:0004674|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131415_PI430048170 0.10510594646684 0.6217708571946721.54496241391605
2.16265519612409 2.49796208683244 A A A 2.6507518474167 2.68318380418678
3.04901621370883 P P P LNCV6_131415_PI430048170 mRNA
CTGGTGTAGATTGGATTATATTTTTCCTTTGGGGACTAGAATACTAGAAGAACTTCAGTA NM_145052 RefSeq chrX
+ 75274058 75304897 UPRT 139596 "uracil phosphoribosyltransferase (FUR1) homolog (S. cerevisiae),
transcript variant 1" GO:0032868|GO:0007565|GO:0005737|GO:0007595|GO:0006222|GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_81210_PI430048170 0.36214286102918 0.8901463842840456.30144525391599 5.94179462033422
5.82990599327796 P P P 6.29857932438243 6.28224539999608 6.02276919633048 P P P
LNCV6_81210_PI430048170 mRNA
AGCTTTATAAAGACTTCAGCCACCCCTGCACCTGGCAGGTGTTGGATGGGGCTGAGGACA NM_031219 RefSeq chr9
- 113373415 113376061 HDHD3 81932 "haloacid dehalogenase-like hydrolase domain containing 3,
transcript variant 1" GO:0005739|GO:0005515|GO:0016787|GO:0008152 . NA - . NA NA NA NA NA

NA NA NA NA
LNCV6_95995_PI430048170 0.2893703583463881.57320757312086 0.3336353134823861.58212569940917
0.571557571374333 A A A 0.28631012568169 0.2687818801322370.292258240570385 A A A
LNCV6_95995_PI430048170 mRNA
TGAGGTTCACGTGAATACTAGTCAAAGAGGATTTCAACAGAAACTGCTTTATCCAAATTC NM_001161529 RefSeq
chrY + 1268799 1309935 CSF2RA 1438 "colony stimulating factor 2 receptor, alpha, low-affinity
(granulocyte-macrophage), transcript variant 7"
GO:0004896|GO:0005886|GO:0005887|GO:0045471|GO:0019221|GO:0005576|GO:0004872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143861_PI430048170 0.0714733517421464 1.13873847830385 10.2577290869307
10.3701739092301 10.4666803052547 P P P 10.1984990238398 10.1154916529682
10.2236397286678 P P P LNCV6_143861_PI430048170 mRNA
TCAGGAAGAGCCTCCCTTTCTTTGCGTCTCCCTTTCTTTAATTAACATTTTCAAAAGTAA NM_001136494 RefSeq chr1
- 230837118 230869589 C1orf198 84886 "chromosome 1 open reading frame 198, transcript variant 2"
GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144285_PI430048170 0.00834795511849628 0.3339253723567277.01691783179968
7.03629763319632 6.97034195738522 P P P 8.28377588152945 8.64984205982283
8.79160035287457 P P P LNCV6_144285_PI430048170 mRNA
GAGATATTAATGCCCAGACAAAAAGCTAATACCAGTCACTCGATAATAAAGTATTCGCAT NM_005585 RefSeq chr15
+ 66702335 66781999 SMAD6 4091 "SMAD family member 6, transcript variant 1"
GO:0005515|GO:0001657|GO:0043627|GO:0003700|GO:0008285|GO:0010991|GO:0030617|GO:0044212|GO:0005
634|GO:0060394|GO:0046872|GO:0005829|GO:0042802|GO:0030514|GO:0035556|GO:0070698|GO:0006955|GO:0
005737|GO:0045444|GO:0007179|GO:0030512|GO:0031625|GO:0005667|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131995_PI430048170 0.0914228174592774 0.4466085694679921.54795901770011
1.03345894732333 1.32170407504549 A A A 2.52799379189617 1.65818527593455 2.9641117898772
A A P LNCV6_131995_PI430048170 mRNA
GGAAGCAATTATCTGTGGAAAAAAGGACTGTCTTGAAAACGCATCACAGTTGTATTTTTT NM_001304533 RefSeq
chr8 + 62248941 62966472 NKAIN3 286183 "Na+/K+ transporting ATPase interacting 3, transcript
variant 1" GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129715_PI430048170 0.0543609655995952 1.04237422880121 0.410332420193422
0.4423391398552530.454708819662706 A A A 0.3524193897123270.365733871096621
0.409353278476849 A A A LNCV6_129715_PI430048170 mRNA
CTCCTCACTTTGTTTCAAACCTTTCTGGCAGTGGGATGATTCGAATTCACTTTTAAAATT NM_000209 RefSeq chr13 +
27920030 27926314 PDX1 3651 pancreatic and duodenal homeobox 1
GO:0008284|GO:0003700|GO:0008285|GO:0006366|GO:0007263|GO:0003705|GO:0031100|GO:0010040|GO:0060
290|GO:0005634|GO:0006091|GO:0032403|GO:2000675|GO:0005829|GO:0007224|GO:0003309|GO:0010260|GO:0
045944|GO:0010157|GO:0006006|GO:0009887|GO:0032024|GO:0001046|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_69163_PI430048170 0.8340110536299430.9698456766683918.42797805569634 8.26240590763701
8.256857814222 P P P 8.57793846507947 8.36072083826877 8.10994850220057 P P P
LNCV6_69163_PI430048170 mRNA
TTACCAGAGCCTCTGCCTCTTCCTCTGTCTCCTGTGGGCAGCGCTCAGGACCACCCTCTT NM_001099652 RefSeq
chr14 + 52553147 52637713 GPR137C 283554 G protein-coupled receptor 137C GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139455_PI430048170 0.0220596739697052 1.26613647367382 14.0620946372355
14.2138236659102 14.2359186121814 P P P 13.8333290900562 13.7015089882626
13.9510527478742 P P P LNCV6_139455_PI430048170 mRNA
ATCTAAGCCACAATGGTGCGCATGAATGTCCTGGCAGATGCTCTCAAGAGTATCAACAAT NM_001019 RefSeq chr16

- 18782954 18790334 RPS15A 6210 "ribosomal protein S15a, transcript variant 2"
GO:0010467|GO:0008284|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0006415|GO:0009
615|GO:0045787|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0000184|GO:0
022627|GO:0016032|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141567_PI430048170 0.9327752287446910.9252643968647593.3225123161622 3.0999351565989
3.0177092580754 P P P 3.84087676396099 3.35510539591836 2.09411826183427 P P A
LNCV6_141567_PI430048170 mRNA
CCGCCGACCTTCAGCTTTGTGGGACTATCAGGAAAAAACAAAACAAAAACAAAATGTAGA NM_178120RefSeq chr2
+ 172085479 172089673 DLX1 1745 "distal-less homeobox 1, transcript variant 1"
GO:0045746|GO:0021544|GO:0048706|GO:0005634|GO:0009954|GO:0000122|GO:0043565|GO:0021766|GO:0043
524|GO:0003682|GO:0048715|GO:0042475|GO:0021893|GO:0021882 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138307_PI430048170 0.7947252108293260.8844567133414590.378586900377176
1.25912481983151 0.954563483842007A A A 1.70784133040465 0.536325494100224
0.722701645419249A A A LNCV6_138307_PI430048170 mRNA
ATTTCAGTCATTTCCTGCTGCAACTAAGTCAGCAACACAGTTTCTCTGATGTCGAAAAAA NM_024070RefSeq chr7
+ 100219247 100221488 PVRIG 79037 poliovirus receptor related immunoglobulin domain containing
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144533_PI430048170 0.5472597372104780.9013072663581254.56014438618739
3.95880989337576 3.5893629956564 P P P 4.28761031776863 4.13314892697632
4.30041687189813 P P P LNCV6_144533_PI430048170 mRNA
CAGGTGACCCTTTGGGATAAAATTGCCTTAGGGTATGAAATAAACTATAACTAAAATGGT NM_021823RefSeq chr15
+ 75023554 75050726 PPCDC 60490 "phosphopantothenoylcysteine decarboxylase, transcript variant 1"
GO:0015939|GO:0006766|GO:0006767|GO:0015937|GO:0009108|GO:0044281|GO:0005829|GO:0004633 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90553_PI430048170 0.0847085473460176 1.73403157269942 5.35697316840539
5.98249529317419 5.19574365509179 P P P 4.77773995739272 4.68486379769775
4.81156307989433 P P P LNCV6_90553_PI430048170 mRNA
CCTTCCAGCGTGCAGGCCAGTCCTCCTGGCATTCTTCTAATTACACCGAGCTGTGAGTTA NM_001291905 RefSeq
chr17 + 19219381 19223730 LOC388436 NA uncharacterized protein ENSP00000382042 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_137811_PI430048170 0.3965760530255631.97938654937458 0.755102216202343
2.87229993705125 2.78346643294272 A A A 1.74344323004901 1.06094236113649
1.37612124391923 A A A LNCV6_137811_PI430048170 mRNA
GCTCCAGGGCGAAATGGTGAACATGTCACACAACAAGGAATAAAGAGATGGTTTTTGCTG NM_173637RefSeq chr19
- 6426036 6433779 SLC25A41 284427 "solute carrier family 25, member 41"
GO:0005743|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74230_PI430048170 0.0731949586766399 2.79114233805063 4.2844003694517
4.61827360645667 4.80129793395274 P P P 3.7494573933947 2.01506694220877
3.04953391689002 P A P LNCV6_74230_PI430048170 mRNA
GCTTTCCCCATCCAACATGGTTCTTCTGTTCCACAGACATTAAAGGGGCTTTCTGCAATT NM_173463RefSeq chr4
- 24806116 24980204 CCDC149 91050 "coiled-coil domain containing 149, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134650_PI430048170 0.1088514335534690.9256563094016171 4.06471498149
14.0511031314665 13.9798697910593 P P P 14.1218085561262 14.2257051481644
14.0800348286668 P P P LNCV6_134650_PI430048170 mRNA
ATACAGTGGGAAAACCAGTCGGGACCTTTAATAAAAGACCTTGGCTTTCTAGTCAAAAAA NM_014595RefSeq chr17
- 75130224 75131795 NT5C 30833 "5', 3'-nucleotidase, cytosolic, transcript variant 1"
GO:0009223|GO:0055086|GO:0005634|GO:0044281|GO:0046872|GO:0005829|GO:0005739|GO:0046135|GO:0005

737|GO:0006195|GO:0019103|GO:0006144|GO:0016311|GO:0008253|GO:0008252|GO:0006206|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132594_PI430048170 0.1448530237957370.7821817660127149.23111911622882
8.89146399694838 8.65471627546198 P P P 9.42262715338648 9.25979119582927
9.20803129356392 P P P LNCV6_132594_PI430048170 mRNA
GCCTGCTACCTCTCCTGTCTTCATAGAACCATTGCCTTAGAATTATTGTATGACACATTT NM_018247RefSeq chr6
- 75252921 75284916 TMEM30A 55754 "transmembrane protein 30A, transcript variant 1"
GO:0005515|GO:0070863|GO:0016324|GO:0005794|GO:0016020|GO:0005783|GO:0006855|GO:0010976|GO:0036
010|GO:0016021|GO:0045332|GO:0030658 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137460_PI430048170 0.3221319394773430.8392240614283860.311804933828595
0.4455529763069520.332521786526001A A A 0.4760767839450010.363426598917352
0.944711046057272A A A LNCV6_137460_PI430048170 mRNA
CTTGGACCTGTGAGTTTTAGGAAACTGGACCTTTTCTGAAGACCTTAGAATAGGGAGTTG NM_016277RefSeq chr6
- 57186993 57222314 RAB23 51715 "RAB23, member RAS oncogene family, transcript variant 1"
GO:0005515|GO:0021513|GO:0005776|GO:0005886|GO:0003924|GO:0042992|GO:0005525|GO:0015031|GO:0045
861|GO:0045335|GO:0006184|GO:0042384|GO:0005737|GO:0006968|GO:0008589|GO:0030670|GO:0032482|GO:0
000045|GO:0019003|GO:0097094|GO:0042733|GO:0010008|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_137325_PI430048170 0.2223820358734750.8611088959087821 0.3828801227384
10.0366130409136 10.0560618316623 P P P 10.1913379153047 10.5356790932689
10.4019182223614 P P P LNCV6_137325_PI430048170 mRNA
ATGCCCCTTATTTATGGGAACCATTTCATTCTAACAGAATAAACCGAGAAGGAAACCAGA NM_017870RefSeq chr11
+ 60924440 60937159 TMEM132A 54972 "transmembrane protein 132A, transcript variant 1"
GO:0008150|GO:0003674|GO:0000139|GO:0005789|GO:0016021|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142052_PI430048170 0.0103965202009249 0.69333595412416 5.96236952315799
5.72411789325492 6.00886982318827 P P P 6.3181094314815 6.41254783045464
6.55571583662852 P P P LNCV6_142052_PI430048170 mRNA
GGAGAATTCACACTTATTGAGTAACTGATGTCATACAACCTGGAATTTCTGAATTCCAAA NM_018195RefSeq chr11
+ 112074243 112085150 C11orf57 55216 "chromosome 11 open reading frame 57, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118664_PI430048170 0.9056440238178110.9766332050458 0.380178267702712
0.4638611426308470.421470090634692A A A 0.2883706510513040.730723997473793
0.305063521309472A A A LNCV6_118664_PI430048170 mRNA
GCTGGAGTTCAACAGATGTAAAGACTTCAGTGAAGCAATAAACACAAAACTCTGGGAGAANM_001005388 RefSeq
chr1 + 204828653 205022822 NFASC 23114 "neurofascin, transcript variant 1"
GO:0005515|GO:0002175|GO:0005886|GO:0030913|GO:0042552|GO:0033270|GO:0019226|GO:0086080|GO:0005
622|GO:0043194|GO:0033010|GO:0033268|GO:0050808|GO:0045162|GO:0007411|GO:0007422|GO:0071205|GO:0
034113|GO:0016021|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107277_PI430048170 0.767809276764062 1.05253078895844 11.544376065354
11.8784407914335 12.119037995135 P P P 11.5851229477903 11.6742203742318
12.0703579631563 P P P LNCV6_107277_PI430048170 mRNA
CAGCATGCCAGCCTTTAAGATTGAATTAGATTGTGTTGTTGTGGTTTTATTTCTGAAAGT NM_020189RefSeq chr8
+ 109334322 109345960 ENY2 56943 "enhancer of yellow 2 homolog (Drosophila), transcript variant 1"
GO:0016578|GO:0070390|GO:0006368|GO:0030374|GO:0006406|GO:0005643|GO:0000124|GO:0003713|GO:0006
325|GO:0071819|GO:0045893|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141171_PI430048170 0.2555152471991940.8498238649249627.9691473235431
7.55850005293631 7.43775720374601 P P P 7.95161868207022 7.978892702826
7.78700434905795 P P P LNCV6_141171_PI430048170 mRNA

GCAGCTCCTGCCACCCCTGCCTTAAGATTTCCCATTAAATGCATCTGTTTAGAAGCCCTG NM_001025200 RefSeq chr16 - 75204095 75207174 CTRB2 440387 chymotrypsinogen B2 GO:0009235|GO:0022617|GO:0004252|GO:0030198|GO:0006766|GO:0007586|GO:0006508|GO:0006767|GO:0005576|GO:0044281|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_142806_PI430048170 0.0575567233782912 3.34271725178313 1.32690842431726 2.68479932947228 2.81962908443248 A A P 0.3798722936410390.471890987503561 1.06893479339949 A A A LNCV6_142806_PI430048170 mRNA
CTCACTGCCCATGATTCAGAGCTTTCAAGGATAGGCTTTATTCTGCAAGCAATACAAATA NM_000559RefSeq chr11 - 5248271 5249857 HBG1 3047 "hemoglobin, gamma A" GO:0019825|GO:0005833|GO:0005506|GO:0007596|GO:0005344|GO:0020037|GO:0015671|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_134807_PI430048170 0.0315066172558395 1.2346980544063 10.0857363205492 10.2327305796861 10.3053129309195 P P P 9.86241360108967 9.91633188000486 9.940065197273 P P P LNCV6_134807_PI430048170 mRNA
CCTCCCCTAGAGCTATTCTCCTTTGGGTTTCTTGCTGCTTCAATTTTATACAACCATTAT NM_000520RefSeq chr15 - 72343436 72376179 HEXA 3073 hexosaminidase A (alpha polypeptide) GO:0004563|GO:0006665|GO:0046982|GO:0006687|GO:0005975|GO:0044281|GO:0042339|GO:0030207|GO:0016020|GO:0009405|GO:0042340|GO:0030212|GO:0030214|GO:0030204|GO:0030203|GO:0070062|GO:0043202 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135884_PI430048170 0.5820605547886580.9026213951296160.357864643808062 0.3616469134410330.481283095239937A A A 0.8988545661023370.308778178526646 0.363610501741687A A A LNCV6_135884_PI430048170 mRNA
GATCATTGGTCGTGGCTGAAACATCTGTCAATAAAATGGCTACACTCACTTGCTGCGAAA NM_145053RefSeq chr11 - 5514392 5516726 UBQLNL 143630 ubiquilin-like NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_136478_PI430048170 0.1919399135980881.16405609545655 0.59564941848878 0.4321293517211270.819782477471301A A A 0.2933891235551560.410531967743013 0.504801215797545A A A LNCV6_136478_PI430048170 mRNA
GATGAAGGCAGCAATAAAGAGAGTATGCAAACAGCTAGTGATTTACAAGAAGATCTCATANM_001005504 RefSeq chr8 - 166085 167024 OR4F21 NA "olfactory receptor, family 4, subfamily F, member 21" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_104033_PI430048170 0.000587627517505786 1.89733631177328 8.87188830090508 8.93294752973771 9.06657660086866 P P P 8.15408881536281 8.02694120569225 7.91548823498747 P P P LNCV6_104033_PI430048170 mRNA
ATGGCAAGAATTCCTCTTTGACTCTGACTGGAGAGACTTCCTCTGCTAAATTACCTCGCT NM_001255995 RefSeq chr14 + 75985752 76059291 IFT43 112752 "intraflagellar transport 43, transcript variant 3" GO:0005737|GO:0006996|GO:0005815|GO:0060271|GO:0015630|GO:0030991|GO:0072372|GO:0035721 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135672_PI430048170 0.4928126691739210.8831112397741916.69942404094447 7.0905201991227 7.3246970635085 P P P 6.90748536428396 7.31318114193202 7.4466996966964 P P P LNCV6_135672_PI430048170 mRNA
CTGTTGTATGGGACATTCCTATGTTTTAGAGTTGCAGTAAAACTTTGATGATAACCTCAA NM_001100816 RefSeq chr5 - 157138439 157142775 MED7 9443 "mediator complex subunit 7, transcript variant 1" GO:0005515|GO:0005667|GO:0010467|GO:0031965|GO:0001104|GO:0006367|GO:0006357|GO:0003713|GO:0005634|GO:0005739|GO:0016592|GO:0019827|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_144347_PI430048170 0.0384814940819719 2.23403447369683 2.69347911442091 3.02233117550765 3.06611988149448 A P P 1.15734364739562 2.11381305254342 1.89625537737977 A A A LNCV6_144347_PI430048170 mRNA
AATGACAAGGATATGACCATGTCCTTCCATTACATCTCAATGGGAGACTGCACAGGATGG NM_001001788 RefSeq

chr6 - 149916877 149923152 RAET1G NA "retinoic acid early transcript 1G, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95765_PI430048170 0.4918594947661360.819027545162334 2.89786842602797 2.76227077829704
1.25098177920462 A A A 2.5562457099868 2.97681388063535 2.70831935743544 A P P
LNCV6_95765_PI430048170 mRNA
TCAACAACATTATGTGGGCAAGAAACACAGAAAACAGGAGACCAAGCTCAAACTAATGGC NM_012279 RefSeq
chr5 + 177022679 177067982 ZNF346 23567 zinc finger protein 346
GO:0005515|GO:0003725|GO:0005737|GO:0043065|GO:0005730|GO:0008270|GO:0005654|GO:0005634|GO:0019
899 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130919_PI430048170 0.0626131595119059 0.9613796118078330.370378203982387
0.3887299528082330.329771787758861 A A A 0.4276644514787970.429721110857732
0.402429679518128 A A A LNCV6_130919_PI430048170 mRNA
AGATATGTTAAATTACTGGCATTCTCTGGGTACCAAATAAAAAGGCTGCAACTTTCTAAC NM_014496 RefSeq chrX
- 84058345 84187935 RPS6KA6 27330 "ribosomal protein S6 kinase, 90kDa, polypeptide 6"
GO:0000287|GO:2000381|GO:0005730|GO:0007268|GO:0005634|GO:0007417|GO:0005524|GO:0045992|GO:0005
829|GO:0005739|GO:0007165|GO:0004672|GO:0007411|GO:0004674|GO:0070373|GO:0005654|GO:0006468|GO:0
006978 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138155_PI430048170 0.5852789925849391.26756580495576 2.72658228344461
3.08146893694946 1.6999793879984 A P A 2.85925156588213 1.64498259094137
2.02821344394655 P A A LNCV6_138155_PI430048170 mRNA
CAAGTCTTGGGAAGAAACAGTTTAATCACTCCCAAGTCCTGGGCAACAGATGACCTTCAA NM_001114974 RefSeq
chr17 + 4584538 4608319 SMTNL2 342527 "smoothelin-like 2, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_137501_PI430048170 0.2749452952149570.73042645116169 0.254913000988315
0.2825419910505070.292032314983337 A A A 0.4585141226521190.360376825734946
1.21240695518978 A A A LNCV6_137501_PI430048170 mRNA
TTTCAGTTTGTATCAAAAAACAAAGAAAAACTTGCCGAGCTTTGGGGGAAAAGAAAAGGC NM_152323 RefSeq chr12
+ 101476878 101486997 SPIC 121599 Spi-C transcription factor (Spi-1/PU.1 related)
GO:0043565|GO:0006366|GO:0006357|GO:0045944|GO:0000981|GO:0001824|GO:0005634|GO:0030154 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138620_PI430048170 0.2182114202601461.43858053102558 0.498295126519801
1.34946804047659 1.2857594697671 A A A 0.4755814374690790.535277450574448
0.685551042863474 A A A LNCV6_138620_PI430048170 mRNA
ACATCACGGAGATTGCAGATCTGACTCAGAAGATCTTTGACCTTCGAGGCAAGTTTAAGC NM_000363 RefSeq chr19
- 55151767 55157732 TNNI3 7137 troponin I type 3 (cardiac)
GO:0005515|GO:0060047|GO:0030049|GO:0005861|GO:0055010|GO:0019901|GO:0019904|GO:0006874|GO:0001
980|GO:0032780|GO:0003779|GO:0006940|GO:0060048|GO:0030017|GO:0046872|GO:0005829|GO:0007507|GO:0
030172|GO:0031014|GO:0019855|GO:0001570|GO:0048306 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_127008_PI430048170 0.4018751320872140.9093139029143576.36900639275391
6.43643138644575 6.82464840842328 P P P 6.62764574523826 6.69411435855214
6.75981831537575 P P P LNCV6_127008_PI430048170 mRNA
GTGGTATTTGGAATGTATGTATCTTCTGAACCCTACATCAAGTTGAAAAGGTTTGTTTTC NM_052857 RefSeq chr17
+ 34961529 34963186 ZNF830 91603 zinc finger protein 830
GO:0005515|GO:0051276|GO:0007067|GO:0005737|GO:0016607|GO:0033260|GO:0001832|GO:0060729|GO:0005
654|GO:0046872|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140342_PI430048170 0.0106246490524925 1.23417224748402 7.04799381217755
7.18953632046237 7.1204471588008 P P P 6.91244911738304 6.79171055277676
6.74125389224722 P P P LNCV6_140342_PI430048170 mRNA

TGTCTATTTTTTCAATTTCCCCTCTTCTCCTTTATTGATCTCTGCTTTTAATACACCACT NM_058164RefSeq chr19 - 9853717 9936552 OLFM2 93145 "olfactomedin 2, transcript variant 2"
GO:0030054|GO:0009306|GO:0032281|GO:0045202|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143883_PI430048170 0.0645060693446134 0.4276389272725151.48033268755187 2.61284471627257 2.74337881360908 A A A 3.95607834225212 3.48301585651666 3.29075247744664 P P P LNCV6_143883_PI430048170 mRNA
CTGTAATGGGGGTTTATGCCTGGACAATTAAGTGTTTTATTTGTTTTCTGAAATGATGTG NM_017420RefSeq chr14 - 60709537 60724134 SIX4 51804 SIX homeobox 4
GO:0034504|GO:0003700|GO:0046661|GO:0048699|GO:0005634|GO:0048538|GO:0009653|GO:0048701|GO:0072075|GO:0032880|GO:0005737|GO:0043524|GO:0030238|GO:0045944|GO:0090190|GO:0050678|GO:0030910|GO:0043066|GO:0042472|GO:0045214|GO:0072107|GO:0006351|GO:0060037|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125873_PI430048170 0.6684057300981850.9450615739072725.68106708230104 5.30794946505706 5.01887522625242 P P P 5.53976316855625 5.25091067924429 5.52086609447044 P P P LNCV6_125873_PI430048170 mRNA
AAGCAGGGCTTCCAGTTTTTCTGCAAAACAGAAGATATGAAGAGGAAGTGGATGGAGCAG NM_001134398 RefSeq chr9 - 133761893 133992324 VAV2 7410 "vav 2 guanine nucleotide exchange factor, transcript variant 1"
GO:0010468|GO:0005515|GO:0005154|GO:0005886|GO:0007264|GO:0030032|GO:0046872|GO:0005829|GO:0005085|GO:0043552|GO:0007411|GO:0005089|GO:0051056|GO:0048010|GO:0048011|GO:0043065|GO:0048013|GO:0030168|GO:0001525|GO:0097190|GO:0007165|GO:0016477|GO:0030193|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140398_PI430048170 0.0706668113034717 1.16988951954448 11.1352137688537 11.100595546022 11.0917952438229 P P P 10.7771215891122 10.8565366704833 11.0057859311495 P P P LNCV6_140398_PI430048170 mRNA
ATTGATTTCTGCTTTTAGGGCCCCGTTTCCATCCAGAAATAAAGGGAAATGCTGGCTTCA NM_053052RefSeq chr1 + 227734995 227781231 SNAP47116841 "synaptosomal-associated protein, 47kDa"
GO:0005515|GO:0019905|GO:0048471|GO:0016082|GO:0005886|GO:0031201|GO:0060291|GO:0030425|GO:0012505|GO:0005484|GO:0031083|GO:0043025|GO:0031629 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143347_PI430048170 0.0727999428148289 0.6547379002109366.15101254620388 6.07053520017131 6.06935180316165 P P P 6.36390021443557 6.74496039004526 6.95563882696802 P P P LNCV6_143347_PI430048170 mRNA
GTGCCTGTATGATATCAGGCACAATTAATGCAAATTAGGCAGACCTATTTATTCTAGATG NM_001031701 RefSeq chr12 - 103772302 103841197 NT5DC3 51559 5'-nucleotidase domain containing 3
GO:0043235|GO:0005739|GO:0016311|GO:0008253|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144778_PI430048170 0.3234687986425741.04884993642382 0.312397189168911 0.2925882580896090.456720478456739A A A 0.2953023975450180.263832616495053 0.301488898112855A A A LNCV6_144778_PI430048170 mRNA
GTCACAGAACGCATGGTATTTCACTTGTTTTTCTCATTAAAAGTGATTACCTTTGCTGTA NM_001136116 RefSeq chr5 + 179023774 179034387 ZNF879 345462 zinc finger protein 879
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_5406_PI430048170 0.4809333691827970.9638081382069181 3.7442169941539 13.6777581746478 13.5542612744348 P P P 13.6472286772654 13.7883580896906 13.7030811196479 P P P LNCV6_5406_PI430048170 mRNA
GTTCACTTTGTCGCCCTTGGAGAAAGCTGTTTTTCTTTAACTAAAAATAACCAAAATGCT NM_001281729 RefSeq chr20 + 34516383 34540958 DYNLRB1 83658 "dynein, light chain, roadblock-type 1, transcript variant

5"
GO:0005813|GO:0005737|GO:0006996|GO:0016020|GO:0007632|GO:0008152|GO:0005874|GO:0006810|GO:0072
372|GO:0005868|GO:0003777|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134491_PI430048170 0.9152398412272990.9927039421782870.398244919130815
0.5012844001204770.415139386018273A A A 0.5321694818440130.488479018254839
0.319186544738637A A A LNCV6_134491_PI430048170 mRNA
GTCTTAATTCAGAAGCACTCCAAATCTAATCATCAGCTATTTCTGATTAGAGATAAAGCC NM_001004753 RefSeq
chr11 + 4821385 4822414 OR51F2 NA "olfactory receptor, family 51, subfamily F, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137167_PI430048170 0.38858108997053 0.7917496128543033.05656217100405
1.93920287745855 1.91843890330389 P A A 2.68450746626687 3.04130215862092
2.45030095413121 A P P LNCV6_137167_PI430048170 mRNA
GAAAAACTTCAAGCAGTTCTCCAGCCAGCCCAGGTGTGGCAGACATAAGCCCTGGTGCTA NM_001105572 RefSeq
chr1 - 20163990 20175194 PLA2G2C NA "phospholipase A2, group IIC" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_133468_PI430048170 0.0270497706155645 0.5094067221981515.45479465383222
5.20253395793784 5.75403610544337 P P P 6.04561249989313 6.4462426907728
6.79535119198218 P P P LNCV6_133468_PI430048170 mRNA
GTTGGCAATTGGTATCATCAATGATACTCATTTTTTAATAACCAAAGGCAGGGGAAAATC NM_001007538 RefSeq
chr13 - 26044596 26051060 SHISA2 387914 shisa family member 2
GO:0005789|GO:0007275|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139552_PI430048170 0.00982758975773712 1.16498531739202 11.7447442267641
11.7685845812759 11.8264465973279 P P P 11.5347425310069 11.512878784393
11.6297520015633 P P P LNCV6_139552_PI430048170 mRNA
GAAACTAGGGCTCCCACTAACTTATGAGGTTTTTAAACACATTGAAAATGACATGACATT NM_006191 RefSeq chr12
+ 56104318 56113910 PA2G4 5036 "proliferation-associated 2G4, 38kDa"
GO:0005515|GO:0043066|GO:0003700|GO:0008283|GO:0006364|GO:0045597|GO:0005730|GO:0005634|GO:0003
677|GO:0006351|GO:0006417|GO:0005737|GO:0016020|GO:0030529|GO:0005654|GO:0007050|GO:0045892|GO:0
031625|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140960_PI430048170 0.00262427492322814 0.3231681012461433.07791496053516
2.75813269193563 2.93392105865184 A A P 4.26238492165835 4.53359169103816
4.82565581637643 P P P LNCV6_140960_PI430048170 mRNA
AGGGAGAGGTTTTCTAGTCTGCAAACTGAAACAGTGTAAGAAGAATAAAGTCTATGACTT NM_004664 RefSeq chr12
- 80797391 80937915 LIN7A 8825 lin-7 homolog A (C. elegans)
GO:0005515|GO:0043005|GO:0048839|GO:0097025|GO:0045202|GO:0014069|GO:0048489|GO:0006887|GO:0015
031|GO:0030165|GO:0045199|GO:0007269|GO:0016323|GO:0006461|GO:0008105|GO:0005911|GO:0045211|GO:0
005923|GO:0097016|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132582_PI430048170 0.4011596676753871.05404059573338 0.29727718319059
0.2978444881683070.503626730389403A A A 0.3050816988096810.267051262812627
0.308420175584947A A A LNCV6_132582_PI430048170 mRNA
ATTGGGCATTTTTGTGGCTGACTTTGAACGTCAGAAAAAAGTCTACAGTCAATTTTATTG NM_000866 RefSeq chr3
+ 87982575 87993769 HTR1F 3355 "5-hydroxytryptamine (serotonin) receptor 1F, G protein-coupled"
GO:0004993|GO:0005886|GO:0007187|GO:0005887|GO:0007268|GO:0051378|GO:0007193|GO:0007210 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131881_PI430048170 0.44347368950715 1.02389793850547 0.418930764031653
0.3051593106558020.345327995741372A A A 0.2911619990654210.320049175446723
0.357538530018061A A A LNCV6_131881_PI430048170 mRNA
TAGGCTCAAGATCAATCTTTACAGATTGATATTTTCAGTTTTTAATCGACTGGACTGCAG NM_005797 RefSeq chr11
- 118253415 118264536 MPZL2 10205 "myelin protein zero-like 2, transcript variant 1"

GO:0005515|GO:0033077|GO:0005886|GO:0016021|GO:0005856|GO:0009653|GO:0007156 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127858_PI430048170 0.0270950716516663 0.27140750854411 2.36253950862006
1.76357212467508 3.11898233943894 A A P 4.23125382701828 4.28289369570755
4.65654642353774 P P P LNCV6_127858_PI430048170 mRNA
TTCAGTTTTTAACCACTTTTAGGTTTTCCCCTTACAGAAACCACAGAAATATTCCCTTAGNM_005095RefSeq chr1 +
35268966 35421944 ZMYM4 9202 "zinc finger, MYM-type 4"
GO:0005737|GO:0022604|GO:0007010|GO:0005730|GO:0008270|GO:0007275|GO:0005654|GO:0005634|GO:0003
677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138017_PI430048170 0.529593055269947 0.800883120366962 1.46647834056141
1.48515320441458 1.9394048815593 A A A 1.31075667744423 2.46309407810198
1.90317687533101 A P A LNCV6_138017_PI430048170 mRNA
CGGGAAAGTCACAGAGCTGCCTGGGCTTGTACCTGGCCACATAAAGCCCCAGTTTAAAGC NM_032152RefSeq chr19
- 8490055 8502654 PRAM1 84106 PML-RARA regulated adaptor molecule 1
GO:0005515|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129043_PI430048170 0.504076266171337 0.920170485149776 5.58518705275407 5.533328901604
5.62957762208868 P P P 5.42799439232696 5.78284274101021 5.86287672280246 P P P
LNCV6_129043_PI430048170 mRNA
TCTGTCCAAGTCCAGTCAATAAAGGAGCTCTTCTGCTTCCCCACTTGTGATTTGAAAAAA NM_018094RefSeq chrX
+ 51743384 51746230 GSPT2 23708 G1 to S phase transition 2
GO:0005515|GO:0010467|GO:0007049|GO:0000184|GO:0003924|GO:0006415|GO:0005525|GO:0044267|GO:0006
412|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136169_PI430048170 0.0182075671903856 2.40793349669917 3.75671945181076
3.64145150326294 2.98796493186947 P P P 2.22082568002522 2.57137412369307
1.80137190529517 A A A LNCV6_136169_PI430048170 mRNA
TATGGTGCGATTCAATGACTGACTCATTTAATCAAGTGGGGACCTGTCTGTCTGTGCCTT NM_024825RefSeq chr19
- 13931186 13938476 PODNL1 79883 "podocan-like 1, transcript variant 1" GO:0005578 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_138646_PI430048170 0.347050262171333 0.754704394955112 0.474472385989421
0.455666434340154 0.406350357684044 A A A 1.36202188471384 0.511545291308856
0.504078973001325 A A A LNCV6_138646_PI430048170 mRNA
GGCCTGGTCTAAGAAAACACATTGCAATCTATTTTGGCAGACTTCTTTCAAATAAAATAC NM_005602RefSeq chr3
+ 170418864 170434691 CLDN11 5010 "claudin 11, transcript variant 1"
GO:0016338|GO:0005886|GO:0005198|GO:0045178|GO:0016021|GO:0007283|GO:0005923|GO:0008366|GO:0070
062|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140313_PI430048170 0.00738598637155701 0.122130316842082 0.592070273391459
1.2484894982084 0.590198466652893 A A A 2.95458063658599 4.17475008567785
4.19463014117042 P P P LNCV6_140313_PI430048170 mRNA
CATTGTAATTACAGATGCACCTTTCAGGAGCATCTCCATTAAATGGTTCATAGATGATTT NM_032873RefSeq chr11
+ 122655689 122814479 UBASH3B 84959 ubiquitin associated and SH3 domain containing B
GO:0005515|GO:0005737|GO:0051279|GO:0090331|GO:0005634|GO:0006469|GO:0035335|GO:0004725 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137461_PI430048170 0.177267883746817 0.89494187440613 9.38079065745965
9.66370678368342 9.56667142901137 P P P 9.64490801184004 9.74576946423626
9.71323802742505 P P P LNCV6_137461_PI430048170 mRNA
CTTGTATCTTGATGCTTTATAATCCTGACTCTCGACGTGTTCATTTATACAAAATCAGGA NM_017817RefSeq chr13
- 110523065 110561737 RAB20 55647 "RAB20, member RAS oncogene family"
GO:0005794|GO:0005886|GO:0003924|GO:0005525|GO:0006886|GO:0043231|GO:0006184|GO:0045335|GO:0030
100|GO:0030670|GO:0032482|GO:0090383|GO:0019003|GO:0090385|GO:0005769 . NA - . NA NA NA

NA NA NA NA NA NA
LNCV6_132743_PI430048170 0.0379515989127228 0.686639341966029 4.26104946050985
4.70066174661897 4.48995903766167 P P P 4.85371892117461 4.95773603008801
5.26790803427777 P P P LNCV6_132743_PI430048170 mRNA
TATGCTGCACTGCCTCATTCAGAGATAGATGCCTGCATGGGTCCTGGCGATTATTTTAAT NM_006778 RefSeq
chr6_GL000256v2_alt - 1450870 1459861 TRIM10 10107 "tripartite motif containing 10, transcript
variant 1" GO:0008150|GO:0003674|GO:0005737|GO:0046597|GO:0045087|GO:0030218|GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136756_PI430048170 0.37759394840547 1.25334181594559 1.35372470543997
0.85256594590179 0.55046861209267 A A A 0.329588743794452 1.05151201373178
0.399447116739155 A A A LNCV6_136756_PI430048170 mRNA
TGGAAGTCAAGATGATCAGAGCATCCTGAGTATCTGTTCTGTGATCAATCCATCCACTGC NM_001277397 RefSeq
chr19 + 55771804 55773179 RFPL4AL1 NA ret finger protein-like 4A-like 1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_105650_PI430048170 0.574588869378978 0.889972861719819 3.11761509387453
2.95594296133263 1.988425054036 P A A 2.97392420814082 2.71757564335703
3.08669537798622 P P P LNCV6_105650_PI430048170 mRNA
CTCCCAAGAGTGATGCAGAGGAGCCCCCGTTGACCAGGAAGAGGAGCAAGAAGGAGAGGG NM_001300895
RefSeq chr11 + 67455346 67461774 CABP4 57010 "calcium binding protein 4, transcript variant 2"
GO:0007165|GO:0046549|GO:0060040|GO:0043195|GO:0005509|GO:0045202|GO:0005576|GO:0007602|GO:0008
594|GO:0007601|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145004_PI430048170 0.128814459512589 0.693852631416534 5.73513004022084
4.97878030921096 5.61211114466464 P P P 6.10425512147545 5.84902750593526
6.05027349211752 P P P LNCV6_145004_PI430048170 mRNA
CATTGGCCCTGACAAAAAGGTGCTACGGTAGTGATGAAATTATAAGTAGATTTGTAGTTT NM_002758 RefSeq chr17
+ 69414696 69542329 MAP2K6 5608 mitogen-activated protein kinase kinase 6
GO:0005515|GO:0034142|GO:0070423|GO:0060048|GO:0051403|GO:0035872|GO:0005829|GO:0042692|GO:0002
756|GO:0000187|GO:0004702|GO:0002755|GO:0022602|GO:0007050|GO:0005856|GO:0072709|GO:0034138|GO:0
004708|GO:0006355|GO:0043065|GO:0038124|GO:0038123|GO:0019901|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135155_PI430048170 0.468057569623606 1.27617251377662 0.447860919932406
1.35815926313811 0.382494616969595 A A A 0.52144243993528 0.40718739603094
0.41968576028058 A A A LNCV6_135155_PI430048170 mRNA
GGCTGTGGCTTTTTATATTCAACAGCCAATAAAAAATGCACAACATGCTAAGATCAAAGC NM_031422 RefSeq chr18
- 26915630 27185338 CHST9 83539 "carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9,
transcript variant 1"
GO:0006790|GO:0005975|GO:0001537|GO:0005576|GO:0044281|GO:0030166|GO:0016051|GO:0030206|GO:0000
139|GO:0009405|GO:0042446|GO:0016021|GO:0030204|GO:0030203 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130542_PI430048170 0.930292867538294 1.27271937256532 0.35940103454486
0.319802420904329 2.26449869925134 A A A 0.610555659432053 1.27092616454345
0.867079627875995 A A A LNCV6_130542_PI430048170 mRNA
GATACCGTGTTTTCTTTGTATTGTGTTCTACCTTCCCTTTCACTGAAAATGATCACTTCA NM_004538 RefSeq chrX -
93670925 93673683 NAP1L3 4675 nucleosome assembly protein 1-like 3 GO:0006334|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132489_PI430048170 0.220077088024962 0.622671907440799 4.40149132790195 2.8756423387394
3.00279617701782 P A P 4.32753659658256 4.2737985824901 4.26142863953126 P P P
LNCV6_132489_PI430048170 mRNA
ACCCTCCCTCTTGGTGAATTATTACACTGTAAGAAATGTATATGCTACTGTGTTACATGT NM_000910 RefSeq chr4

+ 155208628 155217078 NPY2R 4887 neuropeptide Y receptor Y2
GO:0005515|GO:0005886|GO:0007263|GO:0030818|GO:0051048|GO:2000252|GO:0003214|GO:0007204|GO:0007193|GO:0007218|GO:0045987|GO:0004872|GO:0001662|GO:0007626|GO:0031645|GO:0046010|GO:0005246|GO:0051967|GO:0002793|GO:0031513|GO:0003151|GO:0046903|GO:0045785|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82464_PI430048170 0.0605489679994777 0.6525605254138246.24796089119932 6.3238793422729 6.49092760455432 P P P 7.27051695101848 6.66460540639988 6.92135730033627 P P P LNCV6_82464_PI430048170 mRNA
AGTTAGATTCTATGGAAAGTTCTGAGACATCTTGTAGAGACCTTTCCAGCTCACCCCCAG NM_005399RefSeq chr1 - 147155105 147172589 PRKAB2 5565 "protein kinase, AMP-activated, beta 2 non-catalytic subunit, transcript variant 1"
GO:0045859|GO:0005515|GO:0008286|GO:0006996|GO:0031588|GO:0004679|GO:0006853|GO:0044281|GO:0042802|GO:0005829|GO:0007165|GO:0006112|GO:0042304|GO:0061024|GO:0005654|GO:0006468|GO:0006633|GO:0007050|GO:0007005|GO:0044255 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58268_PI430048170 0.860497552694781 1.05552399350285 1.25474197316315 2.86989952957573 1.60351304138105 A A A 0.5724943885744582.73889264883722 1.96444576624878 A P A LNCV6_58268_PI430048170 mRNA
AGTTGGAGCCACAAATAGATGGTCAGACCTGGGCTGAGCGGGCACTTCGGGAGAATGAAC NM_032780RefSeq chr11 + 118531087 118535835 TMEM25 84866 "transmembrane protein 25, transcript variant 1"
GO:0005886|GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142647_PI430048170 0.0718024880337708 0.7986189990527398.94862381768166 8.99713360194118 9.25051595075766 P P P 9.3918364084712 9.22426807371835 9.55325870182779 P P P LNCV6_142647_PI430048170 mRNA
ATGAAAGACAGCAAGACAATTGTGGCAATTAATAAAGACCCAGAAGCTCCAATTTTCCAA NM_000126RefSeq chr15 - 76216287 76311469 ETFA 2108 "electron-transfer-flavoprotein, alpha polypeptide, transcript variant 1"
GO:0022904|GO:0005739|GO:0005759|GO:0050660|GO:0016491|GO:0009055|GO:0044281|GO:0044237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54711_PI430048170 0.9849697692730520.9892523984029126.49587378313291 6.44251120297081 6.56501301895128 P P P 6.58251006505016 6.69960204138967 6.23043895276032 P P P LNCV6_54711_PI430048170 mRNA
TTTACTGGTTGGGAATCCAAAGTTAATGCCAAGAAGCAGCCGCCAGTTGGGATCAAATGT NM_001170755 RefSeq chr1 - 144421385 144459464 NBPF15 284565 "neuroblastoma breakpoint family, member 15, transcript variant 1" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133566_PI430048170 0.9628133200272 1.03918462817237 0.382376932453051 1.66372746536931 0.407131729466023A A A 0.5364848149575281.53699333032375 0.295051765454284A A A LNCV6_133566_PI430048170 mRNA
TGAGTGAACTGTTTCTGGAAGGTAGAGTTCATTAAGATGAACTCCCTATTTCAAGTGTTT NM_024857RefSeq chr17 + 30831969 30895865 ATAD5 79915 "ATPase family, AAA domain containing 5"
GO:0005634|GO:0005524|GO:0006974 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141421_PI430048170 0.00641947273378811 2.29806404782855 1.81320765831596 1.89812255588633 1.3643271065925 A A A 0.8080002806735780.305946111175239 0.361138376040837A A A LNCV6_141421_PI430048170 mRNA
CCCTTGTGTAATTGCTTTGTGTGCGACAGGGAGGAAGTTTCAATAAAGCAGCAACAAGCT NM_006762RefSeq chr1 - 30732467 30757836 LAPTM5 7805 lysosomal protein transmembrane 5
GO:0005887|GO:0006810|GO:0005765|GO:0005764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136685_PI430048170 0.6673394855211830.9244127315697770.620677582769751 0.78616056035555 0.604325987486568A A A 1.12382696512116 0.589632951528394 0.574615020968537A A A LNCV6_136685_PI430048170 mRNA

ATTGTAGAGACACAATGAAACAGTTGCTCTGTGTTGGGAAGTGATCCAGTGTCATCGCTG NM_007225 RefSeq chr17 + 49575935 49583809 NXPH3 11248 neurexophilin 3 GO:0003674|GO:0007218|GO:0005102|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127498_PI430048170 0.769929798796019 0.92627969692308 1.12681177714632 0.352927300320074 0.362466709253503 A A A 0.356464360985815 0.613507607800202 1.21040954251049 A A A LNCV6_127498_PI430048170 mRNA
AGGTAAGCTTTTTCTATTCACCCTGCTGTGTAAATGAGCTTTGGACAATTTCTGCTCAGA NM_020233 RefSeq chr17 + 10697609 10711558 ADPRM 56985 "ADP-ribose/CDP-alcohol diphosphatase, manganese-dependent" GO:0047631|GO:0008152|GO:0046872|GO:0047734 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128169_PI430048170 0.27334884786861 1.0890649774398 12.2458498700351 12.4914147526828 12.2898000830561 P P P 12.3253836036397 12.2067872283715 12.1309991142788 P P P LNCV6_128169_PI430048170 mRNA
CCCAGCAAGGATAACATTCAAAGGAGCTCACATTTATGGAATGGATGAATCAATAAATTA NM_020158 RefSeq chr19 - 41386370 41397351 EXOSC5 56915 exosome component 5 GO:0005515|GO:0010467|GO:0003723|GO:0006364|GO:0005730|GO:0043928|GO:0004532|GO:0035327|GO:0005634|GO:0000178|GO:0005829|GO:0045006|GO:0051607|GO:0005737|GO:0000175|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108749_PI430048170 0.983755067446422 0.97083711136069 2.9877343307398 2.84438525124951 1.82065770452083 A A A 2.90453274890051 3.08062020281035 1.70455617440301 P P A LNCV6_108749_PI430048170 mRNA
AGTGCCCTCTGGTGGCAGTCATCAAAATCGCTTCTAGACTTGTTTTTATTTTTAAATAAA NM_001130699 RefSeq chr6 - 154154482 154330081 IPCEF1 26034 "interaction protein for cytohesin exchange factors 1, transcript variant 1" GO:0005737|GO:0004601|GO:0005886|GO:0005344|GO:0006979|GO:0055114|GO:0015671 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140622_PI430048170 0.0325544612048617 0.782858147032337 10.488335079941 10.4654344408119 10.7208165477761 P P P 10.8304141910199 10.8478427040201 11.0585832508011 P P P LNCV6_140622_PI430048170 mRNA
GTCTGTATGAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCCTATAGAAAATGCC NM_020154 RefSeq chr15 - 34084022 34101852 EMC7 56851 ER membrane protein complex subunit 7 GO:0072546|GO:0008150|GO:0030246|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136356_PI430048170 0.144171399501054 0.463811453279801 0.339582669880891 0.338821116825152 0.267543608276199 A A A 1.83764707227309 0.466922545384106 1.62946394871217 A A A LNCV6_136356_PI430048170 mRNA
GATGCTTGTTCTGAAAGTAAGATCAGTGAACTGCTTTTCAGTCTCAATCTTTGAGAATTG NM_024743 RefSeq chr4_GL000257v2_alt - 504477 527810 UGT2A3 79799 "UDP glucuronosyltransferase 2 family, polypeptide A3, transcript variant 1" GO:0052696|GO:0052695|GO:0009813|GO:0015020|GO:0016021|GO:0032870|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130421_PI430048170 0.363694357394197 0.774073695753948 0.385715038386294 0.410254981797822 0.306810822344924 A A A 0.395142703227852 0.430554515238725 1.2263837785619 A A A LNCV6_130421_PI430048170 mRNA
CCTCTCTGTATATTGCAGTTTCATGAACCAAGTATTACTGCCTCAACAATTAAAAACAAC NM_003862 RefSeq chr5 + 171419662 171457626 FGF18 8817 fibroblast growth factor 18 GO:0008286|GO:0030949|GO:0008284|GO:0030324|GO:0007267|GO:0005111|GO:0005615|GO:0009653|GO:0007173|GO:0002063|GO:0043406|GO:0032332|GO:0070374|GO:0048011|GO:0048015|GO:0005730|GO:0005576|GO:2000546|GO:0005105|GO:0001525|GO:0007399|GO:0007165|GO:0001958|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_3734_PI430048170 0.927657730547571 0.995854690291658 0.615991094832815 0.50217917784112 0.389159826257599 A A A 0.425668048960285 0.570107637794573 0.534550056649326 A A A

LNCV6_3734_PI430048170 mRNA
ATGCATTCCAGAAACTGTTGATTGTTGTTCTAGAAAGTGGTAAAATAGCTGTGGAGTACA NM_145654RefSeq
chr17_KI270857v1_alt - 152612 165308 RDM1 201299 "RAD52 motif containing 1, transcript variant 1"
GO:0005737|GO:0015030|GO:0006281|GO:0000166|GO:0016605|GO:0003723|GO:0005730|GO:0006310|GO:0003
677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140685_PI430048170 0.0262408045467347 0.5523992522042438.12417715700797
7.86511131926709 7.86299258974275 P P P 8.43466999291462 8.93454220339232
9.00367194127162 P P P LNCV6_140685_PI430048170 mRNA
TTACCACATCAACTGATTAAAGCAGTGACCAGCAGGAACTGCCCAGAGAACTGGAAAAAA NM_001271023
RefSeq chr3 + 48447092 48465655 ATRIP 84126 "ATR interacting protein, transcript variant 4"
GO:0006260|GO:0005515|GO:0006281|GO:0005654|GO:0005634|GO:0000077|GO:0070530 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142299_PI430048170 0.0159847153484924 0.9394253338097640.372955997082346
0.3377769798809150.325766113188662A A A 0.4647689733597050.435799253981124
0.406203213654999A A A LNCV6_142299_PI430048170 mRNA
TGGCCGCATGTAACACATTCCTCTGTCTCATTCTAATAAATGGACATTAGCTCTAAAAAA NM_000440RefSeq chr5
- 149857955 149944793 PDE6A 5145 "phosphodiesterase 6A, cGMP-specific, rod, alpha"
GO:0060041|GO:0007603|GO:0005886|GO:0051480|GO:0047555|GO:0046037|GO:0022400|GO:0007601|GO:0046
872|GO:0016056 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142708_PI430048170 0.3282997634733570.7251642474194021.05556785116974
0.2496935664352350.295002868504714A A A 0.7509563106122270.608440874818968
1.58025139075729 A A A LNCV6_142708_PI430048170 mRNA
GAGTAGTCTTTAAATAATCATTTCAGGGATTGTGTGAGAGTAGTCTCACAATTTACACTC NM_152517RefSeq chr2
- 177550152 177552796 TTC30B 150737 tetratricopeptide repeat domain 30B
GO:0005515|GO:0042384|GO:0005929|GO:0042073|GO:0006996|GO:0030992|GO:0072372 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144341_PI430048170 0.0376118707823669 0.7790007460280114.10786345347219
4.02837996286929 4.09410176118698 P P P 4.45157940547288 4.28588106481707
4.56176623083279 P P P LNCV6_144341_PI430048170 mRNA
CTACAGTTGTTGCTCTGAGGATCTTAATTTTGTTACTTTCTAGGCTACATGAAGCTATCTNM_001278503 RefSeq chr11
+ 125592794 125622759 STT3A 3703 "STT3A, subunit of the oligosaccharyltransferase complex
(catalytic), transcript variant 1"
GO:0005515|GO:0016020|GO:0043686|GO:0005789|GO:0004579|GO:0016021|GO:0008250|GO:0044267|GO:0043
687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140901_PI430048170 0.2796867595330781.10768478204393 5.30276703581556
5.24827504718905 5.48827044730768 P P P 5.02356401402065 5.21895045369831
5.34703339390557 P P P LNCV6_140901_PI430048170 mRNA
CTCCGACTTACCTCTTTTTGAAAAGAGAGTTTTTATTAAGTGAACCATCACGATATTGGC NM_183050RefSeq chr6
+ 80106626 80346270 BCKDHB 594 "branched chain keto acid dehydrogenase E1, beta polypeptide,
transcript variant 1"
GO:0003863|GO:0005515|GO:0007584|GO:0009083|GO:0051384|GO:0044281|GO:0051591|GO:0032403|GO:0003
826|GO:0005739|GO:0034641|GO:0005759|GO:0016831|GO:0005947|GO:0055114 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132682_PI430048170 0.1297903158920960.9255449240349520.277445524791315
0.3010267691493890.282758852945242A A A 0.4794834074042190.387413276925413
0.325122587282814A A A LNCV6_132682_PI430048170 mRNA
TAGTCTAAGGAATAGGGCTATACAGACAGCTCTGAGGAATGCTTTCAGAGGGAGATTGCT NM_001004478 RefSeq
chr1 + 158606438 158607380 OR10Z1 NA "olfactory receptor, family 10, subfamily Z, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_142239_PI430048170 0.1069763427106610.8107208255656023.42099175362303
3.41284993319977 3.09138491712083 P P P 3.472470225065 3.80124282809779
3.56326435539087 P P P LNCV6_142239_PI430048170 mRNA
AACTGCCTGACGTTGCACGATTTCAGCTTCATTCCTCTGATAGAACAAAGCGAAATGCAG NM_021258RefSeq chr1
- 24119770 24143285 IL22RA1 58985 "interleukin 22 receptor, alpha 1"
GO:0050829|GO:0008150|GO:0042015|GO:0004896|GO:0005886|GO:0019221|GO:0016021|GO:0004904 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143516_PI430048170 0.0030683740975639 1.20702840101012 10.2878877621338
10.3106167954512 10.2298721744549 P P P 9.96038182071167 10.0657619675216
9.98695824203311 P P P LNCV6_143516_PI430048170 mRNA
TCTCCACGCTGAATGTGATTTTTGAAAACAGCTTATGTAATTAAAGGTTGAATGGCACAT NM_000191RefSeq chr1
- 23801876 23825459 HMGCL 3155 "3-hydroxymethyl-3-methylglutaryl-CoA lyase, transcript variant
1"
GO:0031406|GO:0006637|GO:0051262|GO:0030145|GO:0000287|GO:0007584|GO:0005102|GO:0005743|GO:0044
281|GO:0046872|GO:0042803|GO:0001889|GO:0005739|GO:0070542|GO:0042594|GO:0046951|GO:0005759|GO:0
046950|GO:0007005|GO:0000062|GO:0006552|GO:0044255|GO:0004419|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137010_PI430048170 0.0372705932179483 0.559233594361784 0.341337650439105
0.962318765597244 0.29704403791117 A A A 1.46647834056141 1.07666671748987
1.62009706227393 A A A LNCV6_137010_PI430048170 mRNA
CTTCTACATTAAGTTTCCAGATAAGGCTTCTGAGAACTATAAATAAAGCATCCTAAGCTG NM_207308 RefSeq
chr1 - 153992691 154155116 NUP210L 91181 "nucleoporin 210kDa-like, transcript variant 1"
GO:0060009|GO:0007286|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_145277_PI430048170 0.628977673025564 0.909800706176612 0.562087551374259
0.351310349025257 0.527690264153306 A A A 0.979628702683728 0.382713359232346
0.415507560938781 A A A LNCV6_145277_PI430048170 mRNA
TCTTTAATGTCACAGGCAGGTCCAGGGTTTGAGTTCATACCCTGTTACCATTTTGGGGTA NM_001286402 RefSeq
chr16 + 10877197 10924983 CIITA 4261 "class II, major histocompatibility complex, transactivator,
transcript variant 1"
GO:0005515|GO:0016746|GO:0044212|GO:0019221|GO:0032403|GO:0045348|GO:0006955|GO:0016301|GO:0045
345|GO:0045944|GO:0034341|GO:0033613|GO:0046677|GO:0060333|GO:0003713|GO:0000122|GO:0008022|GO:0
005525|GO:0005524|GO:0003677|GO:0006351|GO:0016310|GO:0032966|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131626_PI430048170 0.000651892099798172 1.49012061790223 7.96952399655386
7.89871403766306 7.86104564122452 P P P 7.36409422687192 7.31348002277786
7.32705526829764 P P P LNCV6_131626_PI430048170 mRNA
CAGGTAGCAGAATTTTTAAAGAAATTGAAGGTTTTGGGACATATATGTGACAGCAATAGG NM_001080471 RefSeq
chr1 + 156893730 156916434 PEAR1 375033 platelet endothelial aggregation receptor 1
GO:0043654|GO:0001891|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131685_PI430048170 0.00894234939249634 1.40091970950036 9.25769053330309
9.3462611840269 9.0897943740333 P P P 8.79387605445717 8.83169966893395
8.61120005012646 P P P LNCV6_131685_PI430048170 mRNA
ACCCTATAAGAGCACTGACATGTTTCAGTGTCCTCTTCCTCCCTAAATATTCTACAATGG NM_016323 RefSeq chr4
+ 88457116 88506168 HERC5 51191 HECT and RLD domain containing E3 ubiquitin protein ligase 5
GO:0050688|GO:0005515|GO:0048471|GO:0004842|GO:0032020|GO:0016874|GO:0019221|GO:0005634|GO:0000
079|GO:0005829|GO:0051607|GO:0005737|GO:0042787|GO:0045087|GO:0032480|GO:0042296 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_136665_PI430048170 0.533860101271247 0.950112136405353 9.3039197226273
9.27926110398326 9.40068389801569 P P P 9.26027384097023 9.36476942521527
9.56625697822566 P P P LNCV6_136665_PI430048170 mRNA
GAATTCTACATCGGTCTAATCTACTTTAGGACTGGATCCCATAAAAGTTATAAGTTCCTT NM_014519 RefSeq
chr17 - 5105735 5123102 ZNF232 7775 zinc finger protein 232
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_136040_PI430048170 0.795336737639886 0.97988133672902 0.650283274195552
0.549808300106426 0.343581333253179 A A A 0.416218042361552 0.651019535229611
0.571337835908705 A A A LNCV6_136040_PI430048170 mRNA
TATCTCTGTGATGATTTCTGTGCTCTTCGCTGTTTGCAATTGCTAAATAAAGCAGATTTA NM_005554 RefSeq
chr12 - 52487173 52493397 KRT6A 3853 "keratin 6A, type II"
GO:0005515|GO:0008284|GO:0016020|GO:0042060|GO:0005200|GO:0005634|GO:0045095|GO:0002009|GO:0030
154|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138001_PI430048170 0.266344524126318 0.94704747015731 10.2830845513748
10.1863785649407 10.2424635312356 P P P 10.2462951149432 10.4119607449875
10.2855364634048 P P P LNCV6_138001_PI430048170 mRNA
CCGGGGATGGATCTTTTCTAAATGTTATTACTTGTAAATAAAGTCTATTTTTCTCCCGTG NM_001286561 RefSeq
chr11 - 72002863 72080693 NUMA1 4926 "nuclear mitotic apparatus protein 1, transcript variant 2"
GO:0005515|GO:0008017|GO:0000132|GO:0005634|GO:0016363|GO:0030425|GO:0005829|GO:0005737|GO:0000
086|GO:0043025|GO:0005876|GO:0070062|GO:0006997|GO:0051321|GO:0005694|GO:0005819|GO:0045177|GO:0
000922|GO:0007067|GO:0000139|GO:0005198|GO:0060487|GO:0005654|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134178_PI430048170 1.37358535767002e-05 0.373713714484354 11.003308719045
11.1139538456172 11.0722051949851 P P P 12.4188503940934 12.4750132545621
12.5545161875144 P P P LNCV6_134178_PI430048170 mRNA
GGTGCCAGACCCAAAAGCTTTTCCTACAGTGATACCCTTTATTTTTACTTCCCCTTGACT NM_007040 RefSeq
chr19 + 41264321 41307692 HNRNPUL1 11100 "heterogeneous nuclear ribonucleoprotein U-like
1, transcript variant 1"
GO:0005515|GO:0008380|GO:0006396|GO:0010467|GO:0006355|GO:0003723|GO:0005634|GO:0009615|GO:0006
351|GO:0000398|GO:0030529|GO:0005654|GO:0019899 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_136876_PI430048170 0.137953834434315 0.854810183019505 9.57416708880805
9.34552988308838 9.22455206913444 P P P 9.71057844806298 9.5586788700782
9.57106168433793 P P P LNCV6_136876_PI430048170 mRNA
GGGCAGAAAGGAGGGAGGATTCGTCCCATTACAATAATGAAATAATGATATTCTAATTTT NM_014940 RefSeq
chr16 + 77190918 77199646 MON1B 22879 "MON1 secretory trafficking family member B,
transcript variant 1" GO:0005515|GO:0016192|GO:0012505 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_65349_PI430048170 0.322251101947953 1.00878905420005 0.333917638640296
0.325723292016386 0.305660456538765 A A A 0.316384298363492 0.316604376880902
0.29447358771739 A A A LNCV6_65349_PI430048170 mRNA
ACAAAATTCCATCAAGAAAGGTTCCAGTTGGTCTCACAGACGTATGGATATCCGAGGAGC NM_001303052 RefSeq
chr2 - 1789112 2331313 MYT1L 23040 "myelin transcription factor 1-like, transcript variant 1"
GO:0006355|GO:0003700|GO:0008270|GO:0005634|GO:0003677|GO:0030154|GO:0006351|GO:0007399 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_91413_PI430048170 0.977182107040802 0.999033157623254 6.87818982995793
6.63987976884563 6.53363446376907 P P P 6.62586311187567 6.94506259847295
6.46479354995759 P P P LNCV6_91413_PI430048170 mRNA

TCAGCAGGGAGGAGAGGCTGCATAAGTGCCGGCTCTGCTACAAGCAGCTTAAGAGCATCA NM_005886 RefSeq chr16 + 57735747 57757250 KATNB1 10300 katanin p80 (WD repeat containing) subunit B 1 GO:0008017|GO:0030424|GO:0005886|GO:0005634|GO:0006605|GO:0007079|GO:0030426|GO:0051013|GO:0005737|GO:0015630|GO:0043025|GO:0010942|GO:0005813|GO:0031117|GO:0046982|GO:0005874|GO:0030496|GO:0008352|GO:0008568|GO:0000922|GO:0045502|GO:0016020|GO:0008152|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137582_PI430048170 0.0956893243398488 1.13517050513112 9.0427384877691 9.0413965955758 9.19027142045116 P P P 8.84134660359013 8.84002543875215 9.04011351788008 P P P LNCV6_137582_PI430048170 mRNA
GGTGATTCTGACTTGAGTATTTACATGGACCATGGTGATATCCAAAAGAAAAATGCTTTT NM_022157 RefSeq chr1 - 38838196 38859823 RRAGC 64121 "Ras-related GTP binding C, transcript variant 1" GO:0005515|GO:0008380|GO:0032008|GO:0000287|GO:0046982|GO:0007264|GO:0003924|GO:0006915|GO:0005634|GO:0005525|GO:0005764|GO:0006351|GO:0043231|GO:0005737|GO:0071230|GO:0016049|GO:0010506|GO:0005654|GO:0034613|GO:0019003|GO:0034448|GO:0009267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131674_PI430048170 0.50312152655227 1.21930263528671 3.15694723073222 2.30213794101487 2.34974001066989 P A A 2.17333246714129 2.81966079290095 1.98911150989592 A P A LNCV6_131674_PI430048170 mRNA
TGATTAGAACCCTGCCATTTTATAGCCTTTAGCTCGATCTCCGACCGTTCATTTAAAAAA NM_002065 RefSeq chr1 - 182378092 182392206 GLUL 2752 "glutamate-ammonia ligase, transcript variant 1" GO:0008283|GO:0007268|GO:0005634|GO:0044281|GO:0005829|GO:0042802|GO:0005739|GO:0034641|GO:0005737|GO:0004351|GO:0004356|GO:0043204|GO:0051260|GO:0032024|GO:0043679|GO:0070062|GO:0009267|GO:0050679|GO:0005791|GO:0000287|GO:0030145|GO:0006538|GO:0051968|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127067_PI430048170 0.0214532855590278 0.177256266183329 2.95265577577068 1.61969917346927 2.88162400012967 A A P 4.90792047248765 5.07993371835672 5.27594003878612 P P P LNCV6_127067_PI430048170 mRNA
CTTCAATGTTTTCATGAATGTTACCCAAAAAGCTGTGTTTTCTTTGGTCAGAGGTCAAAA NM_001289864 RefSeq chr1 + 7784428 7845180 PER3 8863 "period circadian clock 3, transcript variant 5" GO:0005515|GO:0007165|GO:0005737|GO:0045187|GO:0005634|GO:0004871|GO:0000122|GO:0019900|GO:0032922|GO:0031625|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131667_PI430048170 0.00064219431660164 1.72252554150534 9.75943982977275 9.88383184041135 9.76772505442461 P P P 9.0427384877691 9.03202969689685 8.98539307615301 P P P LNCV6_131667_PI430048170 mRNA
GCTGTCAGCATACACAAACACCCAAATTATGCCATGATCTCAAATAAAAGGAACATTTTT NM_214462 RefSeq chr6 - 168306903 168319754 DACT2 168002 "dishevelled-binding antagonist of beta-catenin 2, transcript variant 1" GO:1900108|GO:0005739|GO:0003382|GO:0007162|GO:0070097|GO:0008013|GO:0072061|GO:0002244|GO:0005080|GO:0043588|GO:0051018|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131282_PI430048170 0.242657967378113 0.777110989031534 4.9189881064661 4.09663560863479 4.37870905550746 P P P 4.61100757833795 4.94982717755622 5.0166311428257 P P P LNCV6_131282_PI430048170 mRNA
GAACGGGCAGTTGAATTAAAATTTATGAGACACAAGATATATGAAGAATGTTGCAGTCCT NM_145243 RefSeq chr1 - 58480718 58546799 OMA1 115209 OMA1 zinc metallopeptidase GO:0006629|GO:0031966|GO:0034982|GO:0002024|GO:0005743|GO:0006950|GO:0046872|GO:0097009|GO:0010637|GO:0006006|GO:0006515|GO:0016021|GO:0004222|GO:0042407 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136038_PI430048170 0.440551379782413 1.18832989412963 3.08101348992218

3.21791084605635 2.94547785977863 P P P 3.42938879716356 2.52371265754594
2.29553256251093 P P A LNCV6_136038_PI430048170 mRNA
GTGTGTTCTGTATGGGTCCAGCTGCGTTTCCATCACTCGCTAATAAATCAACAGAAACAC NM_016233 RefSeq
chr1 + 17249097 17284232 PADI3 51702 "peptidyl arginine deiminase, type III"
GO:0018101|GO:0005737|GO:0005509|GO:0004668 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_3722_PI430048170 0.0665659453780657 0.327696448364756 1.8808945849952
0.484981927607093 0.369620586240179 A A A 2.72705708355177 2.67500159843667
2.68826407500127 A P P LNCV6_3722_PI430048170 mRNA
ATAAAAATTCTCAAAGACCCCTACCTGCAGAGGAAGCTGCTAAAGCACACAAAATGTCCA NM_032946 RefSeq
chrX - 101832111 101857577 NXF5 55998 "nuclear RNA export factor 5, transcript variant 1"
GO:0005515|GO:0005737|GO:0006406|GO:0000166|GO:0003723|GO:0050658|GO:0007275|GO:0005634 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_141651_PI430048170 0.391454776392849 2.20517484387984 0.277892273037474
2.48717207617775 0.465036037663574 A A A 0.332849938439374 0.29603269571449
0.299901840050478 A A A LNCV6_141651_PI430048170 mRNA
GAGTGGAAAACTAAGGTCATTGCCTCTCATGGATAAAATGTTATTTCACTGGTAAAGAAA NM_001159747 RefSeq
chr10 + 96000090 96032684 CC2D2B 387707 "coiled-coil and C2 domain containing 2B, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139469_PI430048170 0.24138372619306 0.678673327759499 6.41539545175336
6.42339056697251 6.69720299656418 P P P 6.39573407821108 7.3459086051289
7.30604467175614 P P P LNCV6_139469_PI430048170 mRNA
GATGGGTCTTTCAGATTTTGGTTCTCTTTAGCTTCTGGTTCTTGAAAGAAATTAATCTGT NM_022836 RefSeq chr1
+ 113905292 113914086 DCLRE1B 64858 DNA cross-link repair 1B
GO:0005515|GO:0000781|GO:0005813|GO:0008409|GO:0031860|GO:0090305|GO:0005634|GO:0031848|GO:0005
737|GO:0006281|GO:0000723|GO:0000075|GO:0031627 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_137987_PI430048170 0.0809694631419128 1.19455175834782 8.23442116435317
8.12798331914921 8.01932644170786 P P P 8.020872369181 7.86716504962523
7.71622363012408 P P P LNCV6_137987_PI430048170 mRNA
TGCTGTGTGCCTGTCTGCTCTGGGGCTTCCTCTCTGTGCTGCCAGAAGTCTAGCTGCCAG NM_198695 RefSeq
chr21 + 44612078 44612954 KRTAP10-8 NA keratin associated protein 10-8 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_138673_PI430048170 0.00287575655391377 0.670194300495955 12.5401023624513
12.4771804657135 12.3190317217629 P P P 13.1011680312621 13.0353272408692
12.9359889790009 P P P LNCV6_138673_PI430048170 mRNA
GCTTATTTCTGCCAGTATATTTTGGACACTTTATAATCATTAAAGCACTTTCTTGGCAGG NM_002939 RefSeq
chr11_KI270832v1_alt - 24152 36462 RNH1 6050 "ribonuclease/angiogenin inhibitor 1, transcript
variant 1"
GO:0005515|GO:0005737|GO:0032311|GO:0008428|GO:0045765|GO:0006402|GO:0043086|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_121377_PI430048170 0.188595665786583 2.30756740101928 1.71793694821016
0.485665882541548 2.2694971586865 A A A 0.524476794583668 0.418533598629236
0.429606859461843 A A A LNCV6_121377_PI430048170 mRNA
CTACCCAGAGCAAGACCACAGCTGGTGAACAGTCCAGAGCAGACAAGATGGAGACAAATT NM_001193306
RefSeq chr19 - 51745769 51751897 FPR1 2357 "formyl peptide receptor 1, transcript variant 1"
GO:0005515|GO:0005886|GO:0007263|GO:0006928|GO:0007200|GO:0004982|GO:0000187|GO:0007165|GO:0050
786|GO:0006935|GO:0007186|GO:0004872|GO:0007188|GO:0016021|GO:0005768 . NA - . NA NA
NA NA NA NA NA NA NA

LNCV6_141082_PI430048170 0.195965722190839 1.01638515023089 0.3086804742821
0.273436914782034 0.312898721405144 A A A 0.282642390833774 0.269941518847637
0.27238362861857 A A A LNCV6_141082_PI430048170 mRNA
CAGCTTTTTCCTCTCATAGCATTTTCTATAGCGAATGTAATATGCCTCTTATCTTCATGA NM_025208 RefSeq chr11
- 103907185 104164299 PDGFD 80310 "platelet derived growth factor D, transcript variant 1"
GO:0071230|GO:0000139|GO:0050730|GO:0005788|GO:0051781|GO:0007275|GO:0005576|GO:0048008|GO:0005
161|GO:0008083|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144904_PI430048170 0.0410225960419999 0.550069741330424 2.47154152116645
1.92280062179545 2.7019676106554 A A A 3.21218638504101 3.04070856150051
3.49935387341201 P P P LNCV6_144904_PI430048170 mRNA
AAGGGCTGATGTGAAGGAGCACTGTAAATTTTTATAACTTAGTAATGAGTATTCTTAGGC NM_148893 RefSeq chr11
- 22822051 22829836 SVIP 258010 small VCP/p97-interacting protein
GO:0000836|GO:0031333|GO:0005886|GO:0000139|GO:0030868|GO:0005789|GO:0043621|GO:0070062|GO:0010
508 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137712_PI430048170 0.1869593701612852.55716988650047 0.2944241319978981.7673537286969
2.22554548695154 A A A 0.2931858042802710.2557733339527230.287438566827635 A A A
LNCV6_137712_PI430048170 mRNA
CTATCACAATTACATCTCTTCTAGGAAAATGTGTCTCCTTATTTCAGGCCTATTTTTGAC NM_003265 RefSeq chr4 +
186069154 186085098 TLR3 7098 toll-like receptor 3
GO:0005515|GO:0032755|GO:0034123|GO:0046330|GO:0007249|GO:0005765|GO:0032757|GO:0042802|GO:0002
756|GO:0051607|GO:0045078|GO:0009597|GO:0042742|GO:0032728|GO:0009986|GO:0032760|GO:0032722|GO:0
002224|GO:0045359|GO:0071346|GO:0005887|GO:0045087|GO:0045356|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141007_PI430048170 0.4573981804387730.7092564213347680.405434772798576
0.3789924414687750.40334444585773 A A A 1.58324089978106 0.33115082545048
0.390929203061824 A A A LNCV6_141007_PI430048170 mRNA
GGGTTTCATAGTAACTGTGTTACTTGCCAATCATTCTAGGCTGATGTAAATAAATTTCCA NM_000831 RefSeq chr1
- 36795526 37034243 GRIK3 2899 "glutamate receptor, ionotropic, kainate 3"
GO:0030424|GO:0030054|GO:0005886|GO:0001640|GO:0005234|GO:0007268|GO:0007196|GO:0032839|GO:0030
425|GO:0034220|GO:0043195|GO:0045211|GO:0004970|GO:0042391|GO:0015277|GO:0043204|GO:0051967|GO:0
007216|GO:0035249|GO:0007215|GO:0042734|GO:0035235|GO:0032983|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_81198_PI430048170 0.1006480347923730.8275364650564125.2072620551307 5.21464292173151
5.50211484546959 P P P 5.42922020087753 5.59971967668286 5.71973247115606 P P P
LNCV6_81198_PI430048170 mRNA
AAATCATCCTGGAGCTAGCATGCTCATGCACATTCATCTGGATACTTCATCACTCAAGAC NM_021218 RefSeq chr9
- 112686510 112718107 INIP58493 INTS3 and NABP interacting protein
GO:0005515|GO:0006281|GO:0010212|GO:0070876|GO:0005654|GO:0005634|GO:0006974 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141773_PI430048170 0.00993391621613554 0.2996294856388185.00406986750552
4.72194422827737 5.11170623502811 P P P 6.17041293055758 6.78791370052279
7.00054596051277 P P P LNCV6_141773_PI430048170 mRNA
GTTTCAAACATATCTGAATGTATAAAATAAGAGTAAATGCCCTACATGGTGTGATGCTGC NM_001102653 RefSeq
chr4 - 145133649 145179680 OTUD4 54726 "OTU deubiquitinase 4, transcript variant 3"
GO:0071108|GO:0004843|GO:0006508|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134448_PI430048170 0.0329388079138843 1.0492552978407 14.855558114037
14.8634115556116 14.8105612589739 P P P 14.7759794629081 14.7495600183783
14.7960789111859 P P P LNCV6_134448_PI430048170 mRNA
CACGTGAGCGACAGAAATGAGGGACTGGGATCTGCACAGCCATTAAATTATAAATCTGGA NM_001039182 RefSeq

chr16 - 30192934 30194306 BOLA2B654483 bolA family member 2B GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144606_PI430048170 0.00133617513261593 0.6387118447376927.30505182939695 7.33748974180318 7.30017193565357 P P P 7.9068555296779 7.94619327734557 8.02759899967645 P P P LNCV6_144606_PI430048170 mRNA GGTTTTTCTGTGCTTTGTCATTTTACTCTGATAGGAATTTTTGTTACCTAACTCTGTGCA NM_005093RefSeq chr20 + 33562364 33650031 CBFA2T2 9139 "core-binding factor, runt domain, alpha subunit 2; translocated to, 2, transcript variant 2"
GO:0005515|GO:0003700|GO:0045944|GO:0003714|GO:0030855|GO:0010976|GO:0010977|GO:0005634|GO:0045892|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145463_PI430048170 0.35806724196301 1.05225315778917 0.322223297796398 0.3243763089290690.503390632933612A A A 0.3143769804422140.283547057425584 0.338686657644893A A A LNCV6_145463_PI430048170 mRNA CTTTCCTCAGACTATTTTCCAGCCTTCTGTCAGTCAGCAGTGAAACTTATAAAATTTTTT NM_020535RefSeq chr19_GL000209v2_alt - 46834 56299 KIR2DL5A 57292 "killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 5A" GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128241_PI430048170 0.0150201293471152 0.4815273897857696.79355096491539 6.4112956763689 6.85284432432478 P P P 7.41646779136792 7.67897354252113 8.08434654519963 P P P LNCV6_128241_PI430048170 mRNA TATGGGAGAAGGGGGAGTAATGACTTGTACAAACAGTATTTCTGGTGTATATTTTAATGT NM_001432RefSeq chr4 + 74365142 74388760 EREG 2069 epiregulin
GO:0005515|GO:0005154|GO:0008284|GO:0008285|GO:0042700|GO:0019221|GO:0050680|GO:0007267|GO:0043434|GO:0048146|GO:0001819|GO:0001556|GO:0005615|GO:0009653|GO:0000187|GO:0007173|GO:0045860|GO:0009887|GO:0048160|GO:0042108|GO:0045410|GO:0048011|GO:0051151|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138958_PI430048170 0.4113878494833810.9785500837497830.373334723420338 0.4002610221445190.337573513442073A A A 0.4547775926691540.361388081507037 0.387923571722135A A A LNCV6_138958_PI430048170 mRNA TGTAAGATGCACACTTCTATTACAAGTGAAACCTACGCCAAATGTTAAAGACAAATAGCA NM_139166RefSeq chr8 - 106759482 106770244 ABRA 137735 actin-binding Rho activating protein
GO:0051091|GO:0005886|GO:0045944|GO:0035025|GO:0003713|GO:0003779|GO:0015629|GO:0030017|GO:0006351|GO:0000060 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132029_PI430048170 0.1441858054264291.06827657467331 11.6448909522899 11.6491097446243 11.5196528778095 P P P 11.4961200960834 11.4756357451826 11.5584593791461 P P P LNCV6_132029_PI430048170 mRNA TCCTAGAAAACCCATTGTGTCTCTGGATTTCTAGCACATTACTAAAAGAGCCTCTGCTTT NM_001143819 RefSeq chr12 + 113221437 113298584 TPCN1 53373 "two pore segment channel 1, transcript variant 1"
GO:0005515|GO:0086010|GO:0005245|GO:0005886|GO:0005765|GO:0055085|GO:0042802|GO:0034220|GO:0072345|GO:0070588|GO:0006816|GO:0034765|GO:0016021|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130609_PI430048170 0.4583464965217731.04183010593396 0.313926148013983 0.3208268406593970.502304714791948A A A 0.3282872319824390.291538680477427 0.347333439173415A A A LNCV6_130609_PI430048170 mRNA AAATTCCTGGCAAATTTTTACATCAATGGAGGCAAACACTGGACCCATGGTCACCTGAGG NM_001256699 RefSeq chr9 + 137251260 137253483 C9orf173 NA "chromosome 9 open reading frame 173, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141259_PI430048170 0.67806127704946 0.9617801546781630.494152393751622 0.6160974614080030.537082815784701A A A 0.3973889831367390.7137968292828

0.686663967335934 A A A LNCV6_141259_PI430048170 mRNA
CATGCCCACAACCTCACCAGAGGGAGAATTATGTTTCTAAATATGTTTACTTTGGGACAG NM_002003 RefSeq chr9
- 134909584 134917960 FCN1 2219 ficolin (collagen/fibrinogen domain containing) 1
GO:0005515|GO:0005581|GO:0001664|GO:0043654|GO:0005576|GO:0031232|GO:0046872|GO:0001867|GO:0006
956|GO:0007186|GO:0046597|GO:0002752|GO:0045087|GO:0034394|GO:0030246|GO:0033691|GO:2000484|GO:0
008329 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140316_PI430048170 0.186552582994347 1.26382291539502 7.86931550707718 8.3520549790836
7.83578473160728 P P P 7.81380491534042 7.63172516355934 7.65104654723222 P P P
LNCV6_140316_PI430048170 mRNA
GGGAGGCAATAAAGATATTTGGCCTTCTTTGGCTTTCTTTGCTTAGCAGCGCCTAAAAAA NM_022453 RefSeq chr2
- 218663863 218672058 RNF25 64320 ring finger protein 25
GO:0004842|GO:0051092|GO:0016567|GO:0051059|GO:0016874|GO:0008270|GO:0005634|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70253_PI430048170 0.0614065710315992 1.14293264670235 5.50404976888809
5.32565468819926 5.34078389012344 P P P 5.22869596001753 5.14832411027909
5.22076202790359 P P P LNCV6_70253_PI430048170 mRNA
GAGAGAGATCTGCTATTTCTTTGTGGAGACATCAATGTATTTCTTACCAAAAGACACTTT NM_001080394 RefSeq
chr8 + 47260877 47736001 SPIDR 23514 "scaffolding protein involved in DNA repair, transcript
variant 1"
GO:0005515|GO:0072711|GO:0031334|GO:0000724|GO:0070202|GO:0005654|GO:0000228|GO:2000781|GO:0071
479|GO:0010569|GO:0006974 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145343_PI430048170 0.0036414048271702 0.303687861853628 3.99770188098798
3.27145062721021 3.59332701652841 P P P 5.10391759530289 5.34143348581933
5.62081232701629 P P P LNCV6_145343_PI430048170 mRNA
CTAGGGGTTAGCCAACAAGATATACCAAGCATGAAAACCTGTAAAACTTAATAAAATGCT NM_032796 RefSeq chrX
+ 16719583 16762684 SYAP1 94056 "synapse associated protein 1, transcript variant 1"
GO:0005737|GO:0005794|GO:0005654|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129080_PI430048170 0.889539192280917 1.01965112136173 1.67553071295148
0.726573310426601 1.83459627827411 A A A 0.459865935617533 1.51187432514108
2.00948297844048 A A A LNCV6_129080_PI430048170 mRNA
AACAAATGGCTGCCTTCTGGTGTTTTTATTCTATTTCATCTCATTAACACTACAACCTTG NM_002010 RefSeq chr13 +
21671075 21704501 FGF9 2254 fibroblast growth factor 9
GO:0060045|GO:0008286|GO:0030949|GO:0008284|GO:0090263|GO:0048706|GO:0007267|GO:0030178|GO:0030
326|GO:0006606|GO:0005615|GO:0045880|GO:0005737|GO:0007173|GO:0002062|GO:0030238|GO:0051781|GO:0
008201|GO:0070062|GO:0050679|GO:0048505|GO:0048011|GO:0042472|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131518_PI430048170 0.00709375257559212 0.684797231442314 8.01139052794829
7.81648141826959 8.08635812020751 P P P 8.42523933597399 8.61275468633497
8.52217184315876 P P P LNCV6_131518_PI430048170 mRNA
ACTCACCACCTACATGTTAGTTTTGGGTCTGACCAAATTTGCAGTGGGAATTGTGTTGAT NM_152386 RefSeq chr2
+ 222424602 222558898 SGPP2 130367 sphingosine-1-phosphate phosphatase 2
GO:0042392|GO:0006665|GO:0005783|GO:0030148|GO:0016311|GO:0006670|GO:0005789|GO:0044281|GO:0016
021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127714_PI430048170 0.909434251017611 1.48185351908817 0.399306012544765
3.39296703886889 1.55213537196684 A P A 2.26162428401102 1.32610715034688
1.40888102589694 A A A LNCV6_127714_PI430048170 mRNA
AAATTGTCTCCCCAAGACAGCTCAAAATATCCACACCTCGGCAACAGTCTAAGATGAGAG NM_000682 RefSeq chr2
- 96112874 96116245 ADRA2B 151 adrenoceptor alpha 2B
GO:0005515|GO:0007565|GO:0032811|GO:0005886|GO:0035625|GO:0007267|GO:0030168|GO:0051379|GO:0001

525|GO:0045777|GO:0010700|GO:0004938|GO:0070474|GO:0007186|GO:0045666|GO:0000165|GO:0005887|GO:0
007596|GO:0003056|GO:0032148|GO:0071883 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142011_PI430048170 0.3365522391865341.59911741959128 2.11803429096825
0.5955451934815251.10888849967931 A A A 0.2805157991105170.2772756594977681.3683581538562
A A A LNCV6_142011_PI430048170 mRNA
TAAAGACTTCCACAAAGACCTCCCCTAAATCTGAAGGTCTTCCTGATCCAGTTGGGAATG NM_181788RefSeq chr12
+ 48328979 48330279 H1FNT 341567 "H1 histone family, member N, testis-specific"
GO:0000790|GO:0030261|GO:0007290|GO:0007275|GO:0005634|GO:0035092|GO:0005524|GO:0003677 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59324_PI430048170 0.5073493400672680.9102863152589250.2692766280876380.28493028915686
0.456127125673123 A A A 0.7556511803121620.2957758930066320.325995056355518 A A A
LNCV6_59324_PI430048170 mRNA
CCCTGATTCTGCGTGAGAAAGGCTATCTCTACAGAAACTAAAACGGTATCAACGGTTTCT NM_013244RefSeq chr12
- 85979258 86838904 MGAT4C 25834 "MGAT4 family, member C"
GO:0000139|GO:0016021|GO:0044267|GO:0046872|GO:0043687|GO:0018279|GO:0008454 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133079_PI430048170 0.1755859408620892.03225748930825 0.407389917168803
1.80371618833797 1.62946394871217 A A A 0.3511581894485210.401828309378627
0.374255319231771 A A A LNCV6_133079_PI430048170 mRNA
TTTTTCTTACCCTCTATCCATATAAAATCCAAAGCAACCAGCCTCCTAGGGAGCACAGGA NM_001282394 RefSeq
chr9 + 93184929 93319373 WNK2 65268 "WNK lysine deficient protein kinase 2, transcript variant 1"
GO:0035556|GO:0005737|GO:0046777|GO:0008285|GO:2000651|GO:0005886|GO:0004674|GO:0070373|GO:0006
468|GO:0005524|GO:2000021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145026_PI430048170 0.0264204812572257 0.1593197667153535.22707466880952
4.62889157958349 5.30213221240241 P P P 6.5489561941959 7.93470834493991
8.22751430543784 P P P LNCV6_145026_PI430048170 mRNA
CTGTTAACCAAATTTTGAGCAAGGAGTCTCAAAGGTAATTCTGAACCAGAATTACATGTT NM_181672RefSeq chrX
+ 71533061 71575897 OGT 8473 "O-linked N-acetylglucosamine (GlcNAc) transferase, transcript
variant 1"
GO:0005515|GO:0035020|GO:0005886|GO:0071300|GO:0016262|GO:0080182|GO:0006325|GO:0005634|GO:0005
829|GO:0005739|GO:0005737|GO:0006493|GO:0045944|GO:0043996|GO:0030854|GO:0043995|GO:0000123|GO:0
031397|GO:0008375|GO:0032868|GO:0061087|GO:0005815|GO:0007584|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130240_PI430048170 0.3065914310077790.9181405793057497.54890973875428
7.79604436912051 7.48459172237057 P P P 7.6805089722974 7.7922266602668
7.74333891544604 P P P LNCV6_130240_PI430048170 mRNA
GTTGAGCAGGCCTGTCTCTCCTATTAAGTAAAAATAAATAGTAGTAGTATGTTTGTAAGC NM_006763RefSeq chr1
+ 203305535 203309601 BTG2 7832 "BTG family, member 2"
GO:0005515|GO:0008306|GO:0017148|GO:0014070|GO:0021542|GO:2000178|GO:0008285|GO:0021954|GO:0060
213|GO:0043434|GO:0035914|GO:0009952|GO:0031175|GO:0006351|GO:0006974|GO:0009612|GO:0043524|GO:0
001077|GO:0006281|GO:0045944|GO:0051602|GO:0006479|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_134439_PI430048170 0.5332137375498180.9837678406091980.409900304257707
0.4239867646659270.351985434838637 A A A 0.4697984744271360.381853691965183
0.40460525405257 A A A LNCV6_134439_PI430048170 mRNA
CCATGTATGAGACACTTTTTTACAAAAAGTGCCGTATATACATATGTAACAGGTGAGTGT NM_032859RefSeq chr13
+ 108218414 108234255 ABHD13 84945 abhydrolase domain containing 13
GO:0016787|GO:0016020|GO:0008152|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143937_PI430048170 0.00109636303501139 1.86544261538025 7.29116394446893

7.29696116138207 7.47108406245313 P P P 6.46024413532236 6.50088069606073
6.40527894528097 P P P LNCV6_143937_PI430048170 mRNA
CAAAAATTATGGGTAGTTTTGGTGGTCTTGATGCAGTTGTAAGCTTGGGGTATGAAGGTT NM_001301838 RefSeq
chr12 + 6943816 6946003 C12orf57 113246 "chromosome 12 open reading frame 57, transcript
variant 5" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128853_PI430048170 0.9793431617202620.9988905484087230.43707234426161
0.4939021056308620.480038271881806A A A 0.3578756762325080.432224692528078
0.614144746598591A A A LNCV6_128853_PI430048170 mRNA
TATCTATTTAGCATTTTTCCCAGTATGAAAGGATATGAGAAACCGGGCCCACTTCACAAA NM_001190478 RefSeq
chr10 + 55598989 55600727 MTRNR2L5 NA MT-RNR2-like 5 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_97219_PI430048170 0.4507207980196180.9089415104078781 6.0997119589088 15.64038320482
15.5580804487265 P P P 15.8549441707971 15.9674393910154 15.9474551819301 P P P
LNCV6_97219_PI430048170 mRNA
TAATACCCATAGTAGGCCTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACACC NM_001190470 RefSeq
chr5 - 80649999 80651035 MTRNR2L2 100462981 MT-RNR2-like 2 GO:0005737|GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137872_PI430048170 0.000465785440685718 0.1625351839555930.368254492423647
0.31486401355298 0.390214777703075A A A 2.81112542051638 3.06016368257528
3.05295587624477 P P P LNCV6_137872_PI430048170 mRNA
CACGTCCAAACTGTCTCCTAGCAGCTTTTGGACTATATATCACTTGATGTTAAAGTATCT NM_052885RefSeq chr12
- 39755020 40105859 SLC2A13 114134 "solute carrier family 2 (facilitated glucose transporter), member
13" GO:0005886|GO:0022891|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132488_PI430048170 0.1928743845363290.8283662508503813.6255302071844
13.2483491029949 13.137802293176 P P P 13.4940880008748 13.7905723306433
13.5718197844502 P P P LNCV6_132488_PI430048170 mRNA
ACCCAGCCGCACACAGGCCTAGAGGTAACCAATAAAGTATTAGGGAAAGGTGTGAAAAAA NM_005809RefSeq
chr19 - 12796819 12801910 PRDX2 7001 peroxiredoxin 2
GO:0043066|GO:0016209|GO:0042981|GO:0008379|GO:0005829|GO:0005737|GO:0043524|GO:0019430|GO:0034
599|GO:0042744|GO:0000302|GO:0006979|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134672_PI430048170 0.0935711919055032 0.7776807509104676.95648128791427
7.0643037378971 7.38235671598924 P P P 7.41640867575325 7.37676991683636
7.70948157612935 P P P LNCV6_134672_PI430048170 mRNA
CTAACTGGTTTTTTGGCCAGGGAGAGTTTTGGGTTATTATCCCTTTTCTTTAATTTTCAT NM_001289166 RefSeq chr19
+ 44212527 44237268 ZNF227 7770 "zinc finger protein 227, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133428_PI430048170 0.00541950866182166 0.39640783234875 3.23444680205058
3.27226603224319 2.98969771637314 P P P 4.19323043412805 4.76311549768589
4.50496005307695 P P P LNCV6_133428_PI430048170 mRNA
CTGGTTCTATTTTAATGTAGCACTGGAAGTGTGTGGCAGAAGAATTAGTCAAAGAAATAA NM_031218RefSeq chr19
+ 19900912 19935573 ZNF93 81931 zinc finger protein 93
GO:0006355|GO:0003700|GO:0070895|GO:0008270|GO:0005634|GO:0045892|GO:0003677|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82909_PI430048170 0.3685045905693150.8215190864834452.84723063870703 3.10854213142654
3.52103207474075 A P P 3.13068145087126 3.38278903983684 3.81179313480858 P P P
LNCV6_82909_PI430048170 mRNA
AGTGTATCTGAGGAGCTCCATAAAGAGGTTCAAGAAGCCTTTCTCACACTGCACAAGCAT NM_001080432 RefSeq

chr16 + 53703962 54114467 FTO79068 fat mass and obesity associated
GO:0001659|GO:0070989|GO:0043734|GO:0005634|GO:0010883|GO:0042245|GO:0035515|GO:0008198|GO:0035553|GO:0035516|GO:0035552|GO:0006307|GO:0016607|GO:0040014|GO:0080111|GO:0070350|GO:0044065|GO:0060612 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94682_PI430048170 0.0380281357590925 0.5370490921987129.16168529292556
8.58914787867095 8.509266838151 P P P 9.75690416745442 9.70954102443612
9.56892765071966 P P P LNCV6_94682_PI430048170 mRNA
CCCGCTCTCCTCATCCTATTCCTAAATTAGGCTAATAAAGTGAAATTGGTATACTTTCCA NM_001145354 RefSeq
chr7 + 131110095 131496639 MKLN1 4289 "muskelin 1, intracellular mediator containing kelch motifs, transcript variant 1" GO:0007165|GO:0031532|GO:0007160|GO:0008360|GO:0005938|GO:0001726|GO:0005829
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143499_PI430048170 0.9298711994759910.995193225205315 0.399045279856516
0.39757298834716 0.423591974894404 A A A 0.5091725431478450.334154571317988
0.392345452010129 A A A LNCV6_143499_PI430048170 mRNA
TTCCAAGTTGATTCCAACACGCTAGAGCAGGGTTGTCCAATAGAAATACAACATAATTTA NM_175911 RefSeq chr1
+ 247937028 248100922 OR2L13 284521 "olfactory receptor, family 2, subfamily L, member 13, transcript variant 1"
GO:0005515|GO:0050911|GO:0008150|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127879_PI430048170 0.1570850894703881.47701682636075 1.52025561129293
0.7783531190683160.815505068439844 A A A 0.6254534841410190.451859931363736
0.469167574888091 A A A LNCV6_127879_PI430048170 mRNA
AATAACTCTTAAGAGAGACACACCTCCAGTAAGACCTTAAGACAGTTCTGTCATAAAAAA NM_145233 RefSeq chr19
- 12144893 12156731 ZNF625 90589 "zinc finger protein 625, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144946_PI430048170 0.2156556663234630.6574385518054572.24200691246897
1.34197180395473 2.68497100152944 A A A 2.89240375266201 2.48294751333079
2.96665576314107 P P P LNCV6_144946_PI430048170 mRNA
CTGAGTCTGCAGGAGAAACAAACTAAACATTATAGTTTTATAGCTGCTATCTTGTTAACC NM_017752 RefSeq chrX
+ 106802688 106876147 TBC1D8B 54885 "TBC1 domain family, member 8B (with GRAM domain), transcript variant 1" GO:0005509|GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136670_PI430048170 0.7066023520188180.983711013026752 0.325011568456492
0.4658701863066410.349461605036178 A A A 0.4838776748074360.367848716205944
0.360302465499993 A A A LNCV6_136670_PI430048170 mRNA
CATCTATATCTTTTTCTTGTTTGAGCTGTTACTACATTGTACATGGCATGTGGGATCAAT NM_005048 RefSeq chr2 +
208406829 208494506 PTH2R 5746 "parathyroid hormone 2 receptor, transcript variant 1"
GO:0007186|GO:0005886|GO:0004991|GO:0005887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141213_PI430048170 0.00331411415481758 2.61595129245612 9.80736933283453
10.3214766184993 10.1364890283494 P P P 8.85172239398883 8.72868560587952
8.55359115430181 P P P LNCV6_141213_PI430048170 mRNA
TTGATGTCCTTCCAAGAATAAAGTCTTTCCCTGGTGATGGTCTCTCGCTCTGTCTTTCCA NM_145637 RefSeq chr22
- 36226208 36239954 APOL2 23780 "apolipoprotein L, 2, transcript variant beta"
GO:0006629|GO:0008035|GO:0060135|GO:0005102|GO:0005576|GO:0007275|GO:0006953|GO:0008289|GO:0016020|GO:0006869|GO:0005789|GO:0042157|GO:0008203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144389_PI430048170 0.00267750704012693 0.2486203717901835.41488290847719
5.13302285217618 5.67273086865567 P P P 7.19280223015607 7.16071669667475
7.83622470963377 P P P LNCV6_144389_PI430048170 mRNA

CACGTCAGTTACACATTAAAGCCAGACCCCATGATAAAATTCCACAAAATGGAAATAAAA NM_002959 RefSeq chr1 - 109309565 109397941 SORT1 6272 "sortilin 1, transcript variant 1" GO:0005515|GO:0008625|GO:0010468|GO:0048471|GO:0005886|GO:0010465|GO:0030136|GO:0048227|GO:0005765|GO:0016050|GO:0030379|GO:0046323|GO:0007218|GO:0032580|GO:0032509|GO:0030140|GO:0032868|GO:0048011|GO:0031965|GO:0014902|GO:0005794|GO:0048406|GO:0009986|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60163_PI430048170 0.0459792249120699 1.2424297908861 6.5498481618147 6.60324117930049 6.78832777623705 P P P 6.32849981884605 6.31930848888085 6.36471021709922 P P P LNCV6_60163_PI430048170 mRNA
TGGGTCAAGGCTGAAAAACTGTGATCTTTATTTTTCCAGAAAACCATGTTCTGCTTGTTT NM_030911 RefSeq chr13 + 49247910 49293486 CDADC1 81602 "cytidine and dCMP deaminase domain containing 1, transcript variant 1" GO:0016787|GO:0008152|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102050_PI430048170 0.438042648768382 0.942012597927585 5.44311036345205 5.29865452799634 5.55965735469664 P P P 5.3882548726297 5.56914907161131 5.60513777431166 P P P LNCV6_102050_PI430048170 mRNA
ATCACATCTACATGCATGTTGCTATCAGGATGTTGATTCATTAGTCATGCCTGAAGAGGG NM_014743 RefSeq chr4 + 6782731 6884172 KIAA0232 9778 "KIAA0232, transcript variant 1" GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130173_PI430048170 0.462071131101933 0.906292249303099 0.656308880474679 0.546090070779617 0.351991303273418 A A A 0.418483765358675 0.648695059466747 0.890731117796811 A A A LNCV6_130173_PI430048170 mRNA
CATACTCCCATGGCTAGAATTGGTATTAGCTCCAATACAAGGTTAAATGTTACAATCTTA NM_021032 RefSeq chr3 - 192139392 192409049 FGF12 2257 "fibroblast growth factor 12, transcript variant 1" GO:0008344|GO:0007254|GO:0007267|GO:0007268|GO:0005104|GO:0005634|GO:2000649|GO:2001258|GO:0005615|GO:0044325|GO:0007399|GO:0050905|GO:0007507|GO:0007165|GO:0010765|GO:0008543|GO:0086002|GO:0003254|GO:0008083|GO:0008201|GO:0017080 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144159_PI430048170 0.344927003997614 0.947535561819683 0.330425501523664 0.406334029247257 0.308240946601381 A A A 0.520636635728778 0.439325082762965 0.312546202455737 A A A LNCV6_144159_PI430048170 mRNA
CTTCCTTCTGTGTACTTTTCCTTGAATGTGCACTTTTATAACATGAAAAATAAAGGTGGG NM_005046 RefSeq chr19 - 50976478 50984064 KLK7 5650 "kallikrein-related peptidase 7, transcript variant 1" GO:0097209|GO:0022617|GO:0008544|GO:0004252|GO:0030198|GO:0006508|GO:0008236|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132014_PI430048170 0.168361088740096 1.37733034738099 6.04054537371059 6.20879357171513 6.73804097039331 P P P 5.97878915461614 5.78189966131437 5.92859314573438 P P P LNCV6_132014_PI430048170 mRNA
TTTTATAAAGAAAAGAAGTCTGATATCTTGGGCAGCTTGCTGCTTACTGGGGAGACCAGC NM_001135216 RefSeq chr6 - 28324737 28336134 ZSCAN31 64288 "zinc finger and SCAN domain containing 31, transcript variant 4" GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141801_PI430048170 0.197696908921374 1.04618758551756 0.351067442112441 0.342150210779813 0.45096944429509 A A A 0.30985646523627 0.294704473008533 0.346263331084064 A A A LNCV6_141801_PI430048170 mRNA
TTGGTAGAAAAGTCACAAGATGAGCTTGTGACTATGAAGAGAGCAAAAGCTAACTTTTTT NM_001009992 RefSeq chr1 - 182054569 182061712 ZNF648 NA zinc finger protein 648 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134979_PI430048170 0.107242351518286 0.837933900878562 6.23540192545574 6.24967565834408 6.20942252931756 P P P 6.30184425937723 6.55275974176383 6.58886621677047 P P P LNCV6_134979_PI430048170 mRNA

CTCCCTGAGCCTGTACCAACTAGATTCTTCATATGTATTTGTAACAGATTAAATTGGAAA NM_144964 RefSeq chr9 + 37753802 37778972 TRMT10B 158234 "tRNA methyltransferase 10 homolog B (S. cerevisiae), transcript variant 1" GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145664_PI430048170 0.2327097386734171.08033167235384 0.615501440753377
0.8134462932125460.6199205058149 A A A 0.5363457210321860.599644228018806
0.586667399681659 A A A LNCV6_145664_PI430048170 mRNA
AGTTATCCCACCTTTGACTTGAGGAGACCTTCATCTAAGGAGAATCTAAGGAGGCCTTCT NM_005538 RefSeq chr12 + 57434684 57452062 INHBC 3626 "inhibin, beta C"
GO:0010862|GO:0005576|GO:0042981|GO:0005125|GO:0005160|GO:0005615|GO:0060395|GO:0005179|GO:0043408|GO:0048468|GO:0008083|GO:0040007|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139263_PI430048170 0.0174571184576211 0.6403445323413589.79482232524103
9.44769820406347 9.58711179194266 P P P 10.4603458213391 10.0309427069765
10.2570310144271 P P P LNCV6_139263_PI430048170 mRNA
CTGGAGAGCAGTATTGCTGTAGTAGGAATGTTTTAACAGTGTCATATGAAAAAGAACAAA NM_001859 RefSeq chr9 + 113221527 113264492 SLC31A1 1317 "solute carrier family 31 (copper transporter), member 1"
GO:0005886|GO:0005770|GO:0015088|GO:0035434|GO:0055085|GO:0006878|GO:0005375|GO:0005887|GO:0006855|GO:0043025|GO:0072719|GO:0055037|GO:0006825 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121246_PI430048170 0.9506409101584680.9960743524939450.293965823772779
0.2947429127280630.410560549810283 A A A 0.4496203577356270.278944023776616
0.28426756293612 A A A LNCV6_121246_PI430048170 mRNA
AGCTTTTAAGTGGTCCTCAAAGCTTACTGAACATAAGATAACTCATACTGGAGAGAAACC NM_001256648 RefSeq chr19_GL383575v2_alt - 166138 170222 ZNF43 7594 "zinc finger protein 43, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135639_PI430048170 0.4061179112082940.9784304131851680.476825618487872
0.3748938798305190.438021854993685 A A A 0.4416272461517350.488807014608709
0.455102816506392 A A A LNCV6_135639_PI430048170 mRNA
CTCTTTCTCTGCTGTTGCAAATACATGGATAACACCGTTAATTCCATGTGTTTTCATAAT NM_207007 RefSeq chr17_KI270909v1_alt + 165044 167015 CCL4L1 NA "chemokine (C-C motif) ligand 4-like 1, transcript variant CCL4L" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135390_PI430048170 0.5706713037702290.89742107584291 5.37674433802358
5.08697266599608 5.3516106627642 P P P 5.57301493902171 5.02257769139388
5.63115139139242 P P P LNCV6_135390_PI430048170 mRNA
GAGAATCCCACGGGTGATCATTTGCAATAAATGTGGATGTAATGAAGGCTGTTGAAAAAA NM_001135153 RefSeq chr8 + 22367536 22422736 SLC39A14 23516 "solute carrier family 39 (zinc transporter), member 14, transcript variant 3"
GO:0071577|GO:0071578|GO:0005794|GO:0005886|GO:0005783|GO:0006882|GO:0015093|GO:0015684|GO:0055085|GO:0030027|GO:0005385|GO:0005887|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58566_PI430048170 0.0114018951190776 0.5581689871830235.19799326188193
5.04942507899595 4.87107282272947 P P P 5.86564502614121 5.8931705344742
5.90159766879705 P P P LNCV6_58566_PI430048170 mRNA
AGCTGAGGCAGCCAGCAGATCTCAGCAGCCCAGTCCAAATAAACTCCCTGTCAGCAGCAA NM_002286 RefSeq chr12 + 6772503 6778455 LAG3 3902 lymphocyte-activation gene 3
GO:0045085|GO:0042289|GO:0050868|GO:0045954|GO:0016021|GO:0003823|GO:0009897|GO:0007166|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51686_PI430048170 0.3486801002805061.03421679055743 0.5326136975428730.582410843088591
0.519062016709335 A A A 0.5749832489536610.45378936763061 0.457140023981848 A A A
LNCV6_51686_PI430048170 mRNA
TGAGAACAAATCCCAGGCACTGGGGTGTAGCCTGATTGTTAAACATCAATAAAGGCTCCT NM_001195520 RefSeq

chr12 - 132603149 132610451 LRCOL1 100507055 leucine rich colipase-like 1
GO:0016042|GO:0007586|GO:0005576|GO:0043085|GO:0008047 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135232_PI430048170 0.477419251294092 1.16349831988056 7.1707427977389
6.86223826520881 6.42544878619466 P P P 6.52706470388501 6.75290004592318
6.60920959904769 P P P LNCV6_135232_PI430048170 mRNA
CTCTGCAGGAATGCAGGGAGGGCCGGGCTCCGCCCCAGGGTTATTTCTAAGTTGAAAAAA NM_000265 RefSeq chr7
+ 74773961 74789376 NCF1 653361 neutrophil cytosolic factor 1
GO:0045730|GO:0005515|GO:0002474|GO:0017124|GO:0008283|GO:0006801|GO:0050665|GO:0006691|GO:0001
878|GO:0030425|GO:0005829|GO:0002679|GO:0006954|GO:0045986|GO:0016175|GO:0006612|GO:0043025|GO:0
032010|GO:0090382|GO:0070947|GO:0070946|GO:0005791|GO:0042554|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_26800_PI430048170 0.000969750151395371 0.3708541541340227.20623604768818
7.08806613643699 7.45844229565768 P P P 8.48933760961338 8.64763944154602
8.90356767146155 P P P LNCV6_26800_PI430048170 mRNA
TGAGTGCGTTTTGTCCTTCACGTAACCTTCGCTGGTAAAAATAAGCCCATGTGATGTCCA NM_021249 RefSeq chr14
- 34561411 34630109 SNX6 58533 "sorting nexin 6, transcript variant 1"
GO:0005515|GO:0034452|GO:0005634|GO:0006886|GO:0042803|GO:0006897|GO:0005622|GO:0016050|GO:0005
737|GO:0007175|GO:0031901|GO:0042147|GO:0016023|GO:0035091|GO:0045892|GO:0030512|GO:0019898|GO:0
030904 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127567_PI430048170 0.45531913462998 0.7571067775840840.491576585343317
0.5858539710703850.494648573395171 A A A 1.52489280319536 0.463594906937352
0.529941186922732 A A A LNCV6_127567_PI430048170 mRNA
TTGGATAAAAGTGCACACCTTAAAACAAATTGAGGAAGCACAGTATTTCAGTACAGTGGA NM_001099771 RefSeq
chr2 - 130073534 130129222 POTEF 728378 "POTE ankyrin domain family, member F"
GO:0001895|GO:0072562|GO:0005938|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145246_PI430048170 0.00254750685429188 0.6291606707421087.05566276510982
7.21398520593502 7.27916667802574 P P P 7.77893865523108 7.89122119560999
7.89034991391105 P P P LNCV6_145246_PI430048170 mRNA
GAAAGACTCTTTTTACCAGAGGTTTCCTCTTAGGTGTTAGGAGTTAATACATATTAGGTT NM_003844 RefSeq chr8
- 23191456 23225167 TNFRSF10A 8797 "tumor necrosis factor receptor superfamily, member 10a"
GO:0005515|GO:0008625|GO:2001239|GO:0005886|GO:0007250|GO:0045569|GO:0006919|GO:0006915|GO:0097
191|GO:0002020|GO:0097190|GO:0007165|GO:0004872|GO:0016021|GO:0071260|GO:0005035|GO:0008134 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129213_PI430048170 0.00088694840924407 0.2756309610085132.35727634142616
1.90193551145313 2.29701313560405 A A A 3.87007779614234 4.14874555511438
4.13901810471558 P P P LNCV6_129213_PI430048170 mRNA
CCAACGATTGGAAATGGTTAAGTAAATTTTGGTGTATTGCTAGTGCTATCACAGAATGTT NM_001821 RefSeq chr1
- 241628864 241635930 CHML 1122 choroideremia-like (Rab escort protein 2)
GO:0043547|GO:0017137|GO:0005737|GO:0018344|GO:0005968|GO:0004663|GO:0005654|GO:0006886|GO:0005
829|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_87546_PI430048170 0.212082205496676 0.6196408848140793.03630466010295 1.42989077533693
2.00898615471216 P A A 2.85956900896008 3.17313052572835 2.96449172816191 P P P
LNCV6_87546_PI430048170 mRNA
TTTTAAGCTGTCAGCCCCCACAATCCCAGAGAAATGACTAGACAGAACCAATAAAGCCTC NM_152343 RefSeq chr17
- 45254392 45262112 SPATA32 124783 spermatogenesis associated 32
GO:0048471|GO:0003779|GO:0007283 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138656_PI430048170 0.0494046716817167 0.6310350438426844.07524694470123

4.6741739974245 4.49934268933279 P P P 5.19493981397311 5.11653388192102 4.9860061349999
P P P LNCV6_138656_PI430048170 mRNA
GCTGAGATATCTGTTTTGCAACAAGATGGGCTATATCTAAATAAAGACATGATCAAAGGT NM_182487 RefSeq chr9
+ 124777157 124814891 OLFML2A 169611 "olfactomedin-like 2A, transcript variant 1"
GO:0031012|GO:0030198|GO:0050840|GO:0005576|GO:0042803 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139030_PI430048170 0.0527370339658386 1.36072135740248 9.69380209154252
9.93644046273809 10.1083548473779 P P P 9.43692244887406 9.30167871141489
9.67207028215081 P P P LNCV6_139030_PI430048170 mRNA
AGACAATTGACAAGGAACTTATTGATCATTCTCCGAAAGCAACTCCTGACAATTAAGCAT NM_002492 RefSeq chr3
+ 179604786 179624500 NDUFB5 4711 "NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5,
16kDa, transcript variant 1"
GO:0022904|GO:0005739|GO:0005747|GO:0006120|GO:0005743|GO:0005654|GO:0044281|GO:0016021|GO:0008
137|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59545_PI430048170 0.610477100683466 1.31684888246698 0.342724377326524 1.82909148926825
1.73824145427821 A A A 0.759294484976955 1.53735032764103 0.677611221119292 A A A
LNCV6_59545_PI430048170 mRNA
CACGTGGCGCAAGGATGCGGAGCTTTATCTGTTGTCCGTTATTACTCAGAGCACCTACTG NM_001164372 RefSeq
chr12 - 110452485 110468721 GPN3 51184 "GPN-loop GTPase 3, transcript variant 2"
GO:0005515|GO:0043234|GO:0016787|GO:0008152|GO:0005525 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135959_PI430048170 0.348548634914009 1.03199568457247 0.296234018301492
0.268823411641089 0.390080657408182 A A A 0.286750451829895 0.257542285145008
0.277202247376787 A A A LNCV6_135959_PI430048170 mRNA
GGAAACAAAGTTCTAGCATTTACAAAACTCAGATCTCAAAGCTCTGCTTGTATTTGTGAT NM_001097579 RefSeq
chrX + 41688972 41697277 GPR34 2857 "G protein-coupled receptor 34, transcript variant 4"
GO:0007186|GO:0045028|GO:0005887|GO:0004930|GO:0035589 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128575_PI430048170 0.387948165798825 1.05263562774536 0.313050024818665
0.316065802799239 0.509319180541885 A A A 0.312982310905677 0.278822516475382
0.332985171747105 A A A LNCV6_128575_PI430048170 mRNA
CTCATTGCTGCTATCCAGCACACAGATTTGTGCTTGTGTCTGATTTGTTTAATAAAGGGA NM_018192 RefSeq chr3
- 189956727 190121119 P3H2 55214 "prolyl 3-hydroxylase 2, transcript variant 1"
GO:0031418|GO:0008285|GO:0005794|GO:0005506|GO:0030198|GO:0019797|GO:0005783|GO:0032963|GO:0005
788|GO:0019511|GO:0055114|GO:0005604 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133082_PI430048170 0.130037770857287 0.818923063376166 13.9172780538237
13.7448776249275 13.5582168033812 P P P 13.8143210989469 14.179965314642
14.0883915755341 P P P LNCV6_133082_PI430048170 mRNA
GGGTCCACGCCTCTGCTGTAGCTTATGAAATTAACTAATTGAAAATTCACTGGTTGGTGG NM_003258 RefSeq chr17
- 78174078 78187204 TK1 7083 "thymidine kinase 1, soluble"
GO:0046104|GO:0043097|GO:0044281|GO:0019206|GO:0009165|GO:0005829|GO:0042802|GO:0051289|GO:0014
856|GO:0031667|GO:0009157|GO:0009636|GO:0048565|GO:0055086|GO:0060138|GO:0005524|GO:0051414|GO:0
001889|GO:0016310|GO:0006139|GO:0071897|GO:0008270|GO:0046688|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132724_PI430048170 0.667212848863422 0.854823175413649 1.47221047009174
0.303513582583155 1.5196548701719 A A A 1.67699564399249 1.71659397982088
0.640962821977454 A A A LNCV6_132724_PI430048170 mRNA
TGGGAGCCAGCCTGGATGTTTTTAAACAGAGTCTAAACATGATTTTCTTAAGCTTCAGTG NM_001193341 RefSeq
chr6 + 43645029 43671011 RSPH9 221421 "radial spoke head 9 homolog (Chlamydomonas), transcript

variant 2" GO:0035082|GO:0031514|GO:0005930|GO:0003341|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62234_PI430048170 3.80075203365077e-05 1.70743172566044 6.75585144803555 6.84216281230201 6.8013982444897 P P P 6.07737539659336 6.02681706032774 5.97936212219332 P P P LNCV6_62234_PI430048170 mRNA
ACATGATTGCCAAGGCCCCTGACTTCCTCACACTTTCCACATCCGGATCTGAGGACACTG NM_001301224 RefSeq
chr15 - 78104605 78131535 CIB2 10518 "calcium and integrin binding family member 2, transcript variant 4"
GO:0042383|GO:0005515|GO:0001917|GO:0031594|GO:0005178|GO:0005509|GO:0072562|GO:0045494|GO:0055074|GO:0005927 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133248_PI430048170 0.130457230285511 1.05155562972932 0.608920239204323 0.66450953983657 0.562547887008541 A A A 0.586317196331301 0.516523195581429 0.516233720603187 A A A LNCV6_133248_PI430048170 mRNA
GCCCATTTGACTGTATTACAAGTTAGTTAATTACTCATATAGTTGGCCACATATTATGGG NM_001271754 RefSeq
chr13 + 101452592 101720857 ITGBL1 9358 "integrin, beta-like 1 (with EGF-like repeat domains), transcript variant 4" GO:0005576|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137184_PI430048170 0.681579417385833 1.03669523527042 8.95447856816431 8.7191927402846 8.67761106844167 P P P 8.63841449364159 8.8833741454181 8.67703013054892 P P P LNCV6_137184_PI430048170 mRNA
ATCTGAGAGCCTCCTTCCAGCCCCATAACGCTGTTAACAAGTAGGAAAAATTAAAGCTCC NM_017621 RefSeq chr7 - 102456219 102464874 ALKBH4 54784 "alkB, alkylation repair homolog 4 (E. coli)"
GO:0006355|GO:0036090|GO:0030496|GO:0031032|GO:0003779|GO:0005634|GO:0006351|GO:0046872|GO:0005737|GO:0032451|GO:0006482|GO:0016706|GO:0070938|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143766_PI430048170 0.156503533430702 0.869356146459659 10.5199285950028 10.2667927470807 10.4163790114696 P P P 10.6502951545947 10.722780071328 10.4314371860029 P P P LNCV6_143766_PI430048170 mRNA
AGCCTGAAGATCATCACCAAGGCCAAGTCCCTGCGCATTGCCGAGTATGCCTTCAAGCTG NM_174869 RefSeq chrX - 153785765 153794523 IDH3G 3421 "isocitrate dehydrogenase 3 (NAD+) gamma, transcript variant 2"
GO:0000287|GO:0006099|GO:0005975|GO:0005730|GO:0044281|GO:0005524|GO:0005739|GO:0006102|GO:0051287|GO:0004449|GO:0005759|GO:0005654|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101521_PI430048170 0.12944176438733 1.11022002696548 8.11827734954659 7.9987192276587 8.21390932749925 P P P 7.93780987342039 8.00147622231116 7.94628248218752 P P P LNCV6_101521_PI430048170 mRNA
TTTAAAAAAGGAAACAGGTACATTCGCTGCCAGAAAGAGGTGGGAAAGAGCTTTGAGCGG NM_015327 RefSeq
chr1 - 156249223 156282829 SMG5 23381 SMG5 nonsense mediated mRNA decay factor
GO:0005515|GO:0010467|GO:0035303|GO:0005737|GO:0006406|GO:0000184|GO:0005634|GO:0051721|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130950_PI430048170 0.194118101519975 0.609689819900567 0.467047447915751 0.420521566922384 0.451256310072946 A A A 0.484014011972929 1.14204043474585 1.63196917432723 A A A LNCV6_130950_PI430048170 mRNA
TTGCAACACATAAAGTTGCGTAAGAAACTTTACCAAGAGGAGTATTATAGCCAAGTTTTC NM_001253699 RefSeq
chr5 + 65926553 66081023 ERBB2IP 55914 "erbb2 interacting protein, transcript variant 8"
GO:0005515|GO:0030056|GO:0031965|GO:0030054|GO:0005886|GO:0045104|GO:0005634|GO:0045175|GO:0006605|GO:0045197|GO:0005604|GO:0005176|GO:0007165|GO:0005737|GO:0007049|GO:0009925|GO:0005178|GO:0007173|GO:0007229|GO:0005200|GO:0016049|GO:0005654|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144007_PI430048170 0.48487158221932 1.04514095946398 0.281812138155947 0.293999409618052 0.499764264900176 A A A 0.316743921474288 0.276787239921973 0.3012286352199

A A A LNCV6_144007_PI430048170 mRNA
ACCCCAATCCCAAATTTTGTTTTGGTTCTAACTACCTCCAGAATGTGTTCAATAAAATGC NM_000424RefSeq chr12
- 52514574 52520459 KRT5 3852 "keratin 5, type II"
GO:0005515|GO:0005882|GO:0005886|GO:0034329|GO:0005634|GO:0005829|GO:0005739|GO:0005737|GO:0008
544|GO:0016020|GO:0097110|GO:0005200|GO:0031581|GO:0045095|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135802_PI430048170 0.3460336988601791.07795057250977 12.2373661346977
12.4959407384768 12.4843817796216 P P P 12.2347750775188 12.361022473419
12.3087267686927 P P P LNCV6_135802_PI430048170 mRNA
TATTTATTCTCCCCTAACCCAGGGCAATGTCAGCTATTGGCAGTAAAGTGGCGCTACAAA NM_032339RefSeq chr17
- 39729155 39730535 MIEN1 84299 migration and invasion enhancer 1
GO:0043066|GO:0008430|GO:0005737|GO:0030335|GO:0031235|GO:0051491|GO:0006915|GO:0045454|GO:0005
654|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127339_PI430048170 0.3281900525189011.12586285211126 0.724886118179053
0.3319394563072360.372236514555607A A A 0.3301628236443670.319490488582524
0.299370651178531A A A LNCV6_127339_PI430048170 mRNA
GTGGAGAAGGGTAATAAGTTTTCTGAATACCTTTGCATTGTCTTGTTCACATATATTGCT NM_001013659 RefSeq
chr19 + 37506938 37543337 ZNF793 NA zinc finger protein 793 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133905_PI430048170 0.8377165750543620.9501066304782843.68736943087052
4.84665419147805 3.20567018629286 P P P 4.8049161672143 3.80777478826158
3.53567134400956 P P P LNCV6_133905_PI430048170 mRNA
GGGGACGGGTTCATCTGAGTAAACATAAACCCCAACTTGTGCCATTCTTTATAAAATGAT NM_005060RefSeq chr1
- 151806070 151831872 RORC 6097 "RAR-related orphan receptor C, transcript variant 1"
GO:0005515|GO:0010467|GO:0060850|GO:0006805|GO:0006367|GO:0003700|GO:0045598|GO:0003707|GO:0005
634|GO:0010906|GO:0048535|GO:0042093|GO:0048541|GO:0008142|GO:0043401|GO:0004879|GO:0033077|GO:0
045586|GO:0072539|GO:0070244|GO:0001223|GO:0003677|GO:0019218|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138900_PI430048170 0.1703243494838641.17407854334237 3.2993129755952
3.42389078826156 3.67674882815553 P P P 3.28282286653514 3.32176397899219
3.11879722505115 P P P LNCV6_138900_PI430048170 mRNA
GCTAGTTAAAGGTAGTTCAGTCTCTTTCAAATTAAAAGTTTCACTTGCTTCAACAGAGAC NM_014476RefSeq chr4
- 185500660 185535558 PDLIM3 27295 "PDZ and LIM domain 3, transcript variant 1"
GO:0008092|GO:0007507|GO:0005515|GO:0030018|GO:0005737|GO:0008270|GO:0007015|GO:0015629|GO:0008
307 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72679_PI430048170 0.4474431721452570.4253637992959050.3457461150991470.29984798967816
0.391318640560547A A A 2.70267157875826 0.2797108631720990.311562151216983P A A
LNCV6_72679_PI430048170 mRNA
ACTGTTGACTTCTACCCAGAGGACAAGAACATTTTTAGTTCCCAAGGAATGTACATCAGC NM_016362RefSeq chr3
- 10285749 10292947 GHRL 51738 "ghrelin/obestatin prepropeptide, transcript variant 1"
GO:0008343|GO:0060124|GO:0030424|GO:0043627|GO:0051216|GO:0061098|GO:0032691|GO:0032100|GO:0060
399|GO:0045409|GO:0032095|GO:0007204|GO:0005615|GO:0001696|GO:0046697|GO:0000187|GO:0030296|GO:0
042127|GO:0040013|GO:0006006|GO:0051461|GO:0030252|GO:0032024|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133585_PI430048170 0.1781701767293470.91938201581423 10.4227134124905 10.268998440386
10.3496673335426 P P P 10.3996206195753 10.4205990695301 10.5820521045106 P P P
LNCV6_133585_PI430048170 mRNA
AAATGTCAGCATCATGCAAAGTGCAACGGAATAGTGAATTTTGCTCTAAAAGAGCATGAA NM_018983RefSeq chr4
+ 109815509 109824737 GAR1 54433 "GAR1 ribonucleoprotein, transcript variant 1"

GO:0015030|GO:0005261|GO:0031429|GO:0006364|GO:0005730|GO:0005634|GO:0001522|GO:0006812 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136166_PI430048170 0.460604219660357 1.26943773233954 1.20375985095814 0.3034731157532880.272420000077258 A A A 0.275589015822221 0.272541450614948 0.400229502336608 A A A LNCV6_136166_PI430048170 mRNA TATAAGAGTGACTTGACCAAGGACGTCACAACATCAGTGCTGATAGTGAACAACAAGGCC NM_018960 RefSeq chr6 + 42960761 42963880 GNMT 27232 glycine N-methyltransferase
GO:0005515|GO:0005977|GO:0032259|GO:0006111|GO:0005542|GO:0005737|GO:0051289|GO:0016594|GO:0046500|GO:0006555|GO:0006730|GO:0006464|GO:0017174 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129697_PI430048170 0.7059689956649830.803345015951512 0.412738356728342 0.436627556660154 1.21122738723566 A A A 1.80279423190568 0.468489306353737 0.43440494009695 A A A LNCV6_129697_PI430048170 mRNA GTGCTTTGTAAATGTCTTATTTGTGTAATAAAGTTAATGCAAGTAGAAGTGCTGGCACTG NM_001242335 RefSeq chr9 - 122202576 122221740 LHX6 26468 "LIM homeobox 6, transcript variant 5"
GO:0043565|GO:0006355|GO:0003700|GO:0021800|GO:0021799|GO:0021877|GO:0048469|GO:0008270|GO:0005634|GO:0006351|GO:0021853 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139963_PI430048170 0.2299698172020151.0434603525115 0.336558245080024 0.3144771226646870.432216851652761 A A A 0.299012182067924 0.278930726053313 0.323569351870617 A A A LNCV6_139963_PI430048170 mRNA TAATTTCCCACCATTGAACCTTCCTGTTGGTGTGAGATGCCAAATCTGTGAAAACCAGAC NM_001258280 RefSeq chr3 + 44729605 44737083 ZNF501 115560 "zinc finger protein 501, transcript variant 2"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141623_PI430048170 0.6199760233117480.80820383873287 0.505493625900766 0.5334209819905660.751646099654917 A A A 1.53891472162199 0.443988667558115 0.448361292848614 A A A LNCV6_141623_PI430048170 mRNA CCACATGGGCTAAAACAGGTGTAATAGTCAATAAAATGGTCCCAGAAAACCATCGACCAG NM_018961 RefSeq chr21 + 42403861 42447680 UBASH3A 53347 "ubiquitin associated and SH3 domain containing A, transcript variant 1" GO:0005634|GO:0001817|GO:0050860|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130512_PI430048170 0.0360104370508387 0.559124632792262 6.25198987228579 6.54594706202205 6.35321250265809 P P P 6.85733889442235 7.21728145527498 7.53052091576571 P P P LNCV6_130512_PI430048170 mRNA GGCACATATGGTCCACTGGAGACAATGTATGATTGAGTTTTTCTTTGGTCTAAAAATTAT NM_006460 RefSeq chr17 + 45147316 45152101 HEXIM1 10614 hexamethylene bis-acetamide inducible 1
GO:0007507|GO:0005515|GO:0005737|GO:0045736|GO:0004861|GO:0017069|GO:0005654|GO:0005634|GO:0000122|GO:0045892|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131396_PI430048170 0.11770994295258 0.962867772525086 0.287780265717848 0.3177421751038130.350851107149546 A A A 0.411667940175267 0.366154233960542 0.342146436105753 A A A LNCV6_131396_PI430048170 mRNA CGCCTGCTTACCTGTGAAGACATAAGAAAATCTTAGTAACTACCAGATTATCTTTAGAAT NM_145203 RefSeq chr13 - 37103259 37105664 CSNK1A1L 122011 "casein kinase 1, alpha 1-like"
GO:0006909|GO:0000902|GO:0005737|GO:0018105|GO:0004674|GO:0030529|GO:0008360|GO:0005634|GO:0016055|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142669_PI430048170 0.0227765938022337 0.5009141907717464.97318625612172 4.30676738137509 4.78492732423617 P P P 5.57649704472483 5.6819468980246 5.8628265639294 P P P LNCV6_142669_PI430048170 mRNA GGAGGGAAGTGAACCTTGAAACTGTTTTGCCAATAACCTAACAAACAAAATGATATTTAC NM_022802 RefSeq chr10 - 124987848 125027884 CTBP2 1488 "C-terminal binding protein 2, transcript variant 2"

GO:0005515|GO:0008285|GO:0030054|GO:0003714|GO:0003713|GO:0045202|GO:0005634|GO:0042974|GO:0019079|GO:0035563|GO:0006351|GO:0016616|GO:0048386|GO:0051287|GO:0050872|GO:0045944|GO:0003682|GO:0017053|GO:0045892|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136659_PI430048170 0.0808185927426789 0.58673308412838 1.06487423124934 1.22423367050004 1.93862862257119 A A A 2.0457205556732 2.3483760110595 2.28082792013337 A A A LNCV6_136659_PI430048170 mRNA
AATATCACTACTCTTTAACGAGTGCCAAATCTTTTCCCACTTTTGCTCTTCCCCAAGGAA NM_017521 RefSeq chr2 - 218981086 218985657 FEV 54738 FEV (ETS oncogene family)
GO:0043565|GO:0003700|GO:0003690|GO:0006366|GO:0006357|GO:0042551|GO:0003714|GO:0000981|GO:0048665|GO:0005634|GO:0045893|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142589_PI430048170 0.0391855693025288 0.7141299692748559.91152968399194 9.54197468148395 9.64949858261949 P P P 9.98355205947439 10.3882094524453 10.1855557940443 P P P LNCV6_142589_PI430048170 mRNA
GAACCATGAGAATATCAGTGATACTGATGAGAATAAACTAAACGCCTTTGTAACAGCAAA NM_052876 RefSeq chr19 + 13118287 13141147 NACC1 112939 "nucleus accumbens associated 1, BEN and BTB (POZ) domain containing"
GO:0016604|GO:0008284|GO:0005737|GO:0030054|GO:0051260|GO:0005654|GO:0005634|GO:0045892|GO:0006351|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139005_PI430048170 0.0348716913444507 1.70074129976785 5.759855568294 6.33850963325396 5.98347180870223 P P P 5.60561547192765 5.02201308839585 5.14813473523666 P P P LNCV6_139005_PI430048170 mRNA
AACAACGTCTTCTTCTCTTGGTCCTATTTTTCTGGGTGGCTGGCCTTACCCTTCTCAATT NM_152353 RefSeq chr19 - 51367097 51369003 CLDND2 125875 claudin domain containing 2 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140531_PI430048170 0.2224108121733180.6506955775132962.21977036345075 3.5827370711537 2.36393956200988 A P A 3.76871171650027 3.35441978844165 3.26686925283952 P P P LNCV6_140531_PI430048170 mRNA
GGATACCTTATTTCCCTAGCTATCATCTCCTGACTTAATGTTTTTTAAACCCACCAATAT NM_033380 RefSeq chrX + 108439843 108697545 COL4A51287 "collagen, type IV, alpha 5, transcript variant 2"
GO:0031594|GO:0022617|GO:0030198|GO:0007528|GO:0007411|GO:0030574|GO:0005605|GO:0005587|GO:0005788|GO:0005576|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128090_PI430048170 0.9588056138538230.9993890534138365.53769318848653 4.64329583439113 4.71693366088087 P P P 5.52648917120926 5.00837655337986 4.28703031218169 P P P LNCV6_128090_PI430048170 mRNA
TAAAAGACAAGTTATTTTAAAAAGACATAAAATGCCATCCGTGGGGGGTGTGGCCGGCGT NM_001128636 RefSeq chr7 + 1709161 1747954 ELFN1 392617 extracellular leucine-rich repeat and fibronectin type III domain containing 1
GO:0050808|GO:0019902|GO:0010923|GO:0004864|GO:0016021|GO:0060076|GO:0030425|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133516_PI430048170 0.498335174099669 0.891340635419522 7.89034991391105 7.34050900961956 7.2372418343613 P P P 7.8717040367014 7.7279552739054 7.41842961807474 P P P LNCV6_133516_PI430048170 mRNA
TGACATGGAAGCTGGGCTCCCTCTCCACTCTGAGATCATCAGCTGGGTAAAGGTCAGTGG NM_182500 RefSeq chr2 + 11133052 11146790 C2orf50 130813 chromosome 2 open reading frame 50 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58249_PI430048170 0.946731764144964 0.96065316826162 6.47269888013855 6.61728430210873 6.32968641868162 P P P 6.91368363742704 6.52102091607789 6.04369475282087 P P P LNCV6_58249_PI430048170 mRNA
TACCTTGTTAGAGCAACACCAGTGGGGGCTGTACCCATCCGATCATCTCCTGCCAGGTCA NM_001077263 RefSeq

chr11 - 117900640 117929453 TMPRSS13 84000 "transmembrane protease, serine 13, transcript variant 1" GO:0004252|GO:0006508|GO:0072562|GO:0016021|GO:0006898|GO:0005044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109659_PI430048170 0.853996384317725 2.29446419740117 4.00171968905773 0.366944531509944 0.4425095386735 P A A 1.40315035655112 1.96115290955891 0.675765959023183 A A A LNCV6_109659_PI430048170 mRNA CCCCATGCTTGCCCAGGAGTCCTATCCAAAGAAGAGAAATTACACTATGGAAATTGTACC NM_152788 RefSeq
chr12 - 98734790 99984654 ANKS1B 56899 "ankyrin repeat and sterile alpha motif domain containing 1B, transcript variant 1"
GO:0005737|GO:0030054|GO:0015030|GO:0046875|GO:0043197|GO:0045211|GO:0014069 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136535_PI430048170 0.492396456103127 1.42936983066639 1.72061023964358 0.447046980625068 0.334805644875597 A A A 0.476860346130614 0.363746357979296 0.54928390780457 A A A LNCV6_136535_PI430048170 mRNA AAACAAAGAGGTGAAGATTCTCTGGCTGCGATATCAGTGGGATAAATCTCTCTGGACCAT NM_001040705 RefSeq
chr8 + 7495845 7509311 DEFB107B NA "defensin, beta 107B" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133430_PI430048170 0.166681106194816 0.42150503484179 0.40675832717877 0.3636501200127072.52791195409621 A A A 1.69621903109805 2.81355930261851 3.26451503811999 A P P LNCV6_133430_PI430048170 mRNA CAGTTGCATATTTTGTGTCTGAAATTTCTTTAGATGCTGAAAAAGGATGATCGACAAGTG NM_001144878 RefSeq
chr8 - 81656915 81686354 IMPA1 3612 "inositol(myo)-1(or 4)-monophosphatase 1, transcript variant 2"
GO:0052833|GO:0052832|GO:0052834|GO:0000287|GO:0006021|GO:0030145|GO:0006661|GO:0043647|GO:0044281|GO:0006796|GO:0031403|GO:0042803|GO:0005829|GO:0042802|GO:0046854|GO:0007165|GO:0005737|GO:0046855|GO:0008934|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117084_PI430048170 0.165271366771108 0.521957979410606 11.3761474619434 9.70536239671014 9.73497036548349 P P P 11.5584593791461 11.5898712163996 11.1202038511143 P P P LNCV6_117084_PI430048170 mRNA GGAGCCCCCGGCCGCCCCGAGTGGAGCGGATCCACGGGCAGATGCAGATGCCTCGAGCCA NM_018836 RefSeq
chr1 + 4655044 4783791 AJAP1 55966 "adherens junctions associated protein 1, transcript variant 1" GO:0016323|GO:0016324|GO:0005912|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105097_PI430048170 0.482907659208981 0.882401174047243 1.22498313205376 1.49663209850157 0.600799088671727 A A A 1.32027439602885 1.30639038284814 1.37588371128283 A A A LNCV6_105097_PI430048170 mRNA CATCAATCACGGGAACCCCTTCAACATGGAGGTGCTGGTGGATTCCTGGCCTGAATATCA NM_001220494 RefSeq
chr11 + 58927628 58957074 GLYATL1 92292 "glycine-N-acyltransferase-like 1, transcript variant 2"
GO:0005739|GO:0047961|GO:0008152|GO:0047946 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128430_PI430048170 0.0504985041042124 1.48924753476455 8.41726076202335 8.95714930816072 8.68703846108814 P P P 8.37563637499577 8.02575315406262 7.95007905091612 P P P LNCV6_128430_PI430048170 mRNA TTTGCAGTCAAGTACTGATGCATCCAAGCCAGGCCCATGCCTGGTGTCTCCCTGACTGCA NM_015666 RefSeq chr20 + 62183024 62202754 MTG2 26164 mitochondrial ribosome-associated GTPase 2
GO:0006184|GO:0000287|GO:0070129|GO:0042254|GO:0005759|GO:0005761|GO:0005743|GO:0003924|GO:0044065|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135496_PI430048170 0.0158299212824198 0.580805852790238 7.11294820493143 6.59631195133999 6.83090511240301 P P P 7.41985865909227 7.66833852354831 7.82191340918463 P P P LNCV6_135496_PI430048170 mRNA

GTACAGGTCTCTGTAAAAAGTCCTTGCTGTCTCAGCAGCCAATCAACTTATAGTTTATTT NM_006015 RefSeq chr1 + 26696030 26782110 ARID1A 8289 "AT rich interactive domain 1A (SWI-like), transcript variant 1" GO:0005515|GO:0071565|GO:0000790|GO:0060674|GO:0005634|GO:0071564|GO:0016514|GO:0042766|GO:0006338|GO:0016922|GO:0003408|GO:0006357|GO:0043044|GO:0003713|GO:0001843|GO:0031491|GO:0006337|GO:0003205|GO:0000122|GO:0003677|GO:0006351|GO:0042921|GO:0005654|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135388_PI430048170 0.7493862733055530.9797295119527690.559517591410295 0.4698578512594510.254821051114513 A A A 0.4006532312842820.517160777027943 0.469395967026861 A A A LNCV6_135388_PI430048170 mRNA
CGGAACATCTTGCCTACCTAGCAAAGAAGTGTGACCATTCTTTCGGAATTAAATACAATA NM_001044369 RefSeq chr18 - 74435727 74457268 FAM69C 125704 "family with sequence similarity 69, member C" GO:0008152|GO:0005789|GO:0016021|GO:0016772 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128550_PI430048170 0.4641277628010932.18704840035905 0.263450523261954 2.58840658793039 0.310025078408351 A A A 0.4255302024072730.334222586183078 0.335609125116569 A A A LNCV6_128550_PI430048170 mRNA
GCCTTGCTTTTAAATTAAACAGCTACAGCCATTTAAGCCTTGAGGATAATAAAGCTTGAG NM_001944 RefSeq chr18 + 31447768 31478702 DSG3 1830 desmoglein 3 GO:0030057|GO:0005886|GO:0005509|GO:0006915|GO:0016021|GO:0007156|GO:0006921|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131268_PI430048170 0.7450699359910250.8852880258358342.77826798645019 0.3335970757152430.298708926295486 A A A 0.43982133384179 1.34282209715063 2.73750657550011 A A P LNCV6_131268_PI430048170 mRNA
GAGGGAAAAATCACTATCAAGATCACCCATATCTGTCTTGGAGGCGATTTATTTTAAAAA NM_001013403 RefSeq chrX - 139955724 139965518 CXorf66 NA chromosome X open reading frame 66 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142779_PI430048170 0.3080954261560860.7542872180050860.27941413149734 0.5045952244643690.338043791658289 A A A 0.5196715584740450.417564329565291 1.26090666575342 A A A LNCV6_142779_PI430048170 mRNA
AGGGGTGCAGCAAGTGCTTTCTATGCGTTTCTTCATTAAAACATTAGGCTAATACAGGCA NM_001164586 RefSeq chr1 + 201190824 201228952 IGFN1 91156 immunoglobulin-like and fibronectin type III domain containing 1 GO:0008150|GO:0030018|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142430_PI430048170 0.4712789370921125.63005893553546 0.394174235379113 4.42789005811604 0.271566751303379 A P A 0.7913344125189640.344440166656017 0.345497935806172 A A A LNCV6_142430_PI430048170 mRNA
CCACTGACAAACTTATATTCATATTCTACAGGGTGATGACTCCCATGATGAATCCTTTAA NM_001004482 RefSeq chr9 - 104598456 104599413 OR13C5 NA "olfactory receptor, family 13, subfamily C, member 5" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130174_PI430048170 0.0892961882639244 0.6785419870187642.5650518380511 2.84068508467671 3.22966331107146 A A P 3.51797532513415 3.47257985405883 3.39874079657102 P P P LNCV6_130174_PI430048170 mRNA
GAAACTTCTGTCAGGATAACATCAGCAAATTCTCAAACAGTTATGGACTCTCAGGAGCAT NM_001001436 RefSeq chr16 - 46802046 46831162 C16orf87 388272 chromosome 16 open reading frame 87 GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136126_PI430048170 0.6201734537028081.07019080282036 5.52011686147215 5.46760052373559 5.68102157534686 P P P 5.05324249117644 5.44688936567975 5.79040163083191 P P P LNCV6_136126_PI430048170 mRNA
TGTCTGCCTTTTATGAATTTGTATATGTGAATAGAGTTTGGGGGTTGCCAAAAATTGCAT NM_015650 RefSeq chr2 + 238320543 238400900 TRAF3IP1 26146 "TNF receptor-associated factor 3 interacting protein 1, transcript variant 1"

GO:0005515|GO:0008017|GO:0050687|GO:0005813|GO:0006996|GO:0035050|GO:0005930|GO:0021532|GO:0072372|GO:0036064|GO:0042384|GO:0005929|GO:0031076|GO:0042073|GO:0030992|GO:0042733|GO:0032688 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136946_PI430048170 0.1000366664536720.941959867222233 0.26974996583143 0.2772709771064510.320383642502855 A A A 0.436794900993901 0.359641858495317 0.328096587028116 A A A LNCV6_136946_PI430048170 mRNA GATGTCATCATATGTGTAGGCAGAAATAAGCTTTGTTCTATATCTCTTCTAAGACAGTTG NM_031291 RefSeq chr4 + 127730399 127774292 SLC25A31 83447 "solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31"
GO:0005739|GO:0005215|GO:0031514|GO:0005743|GO:0005634|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132907_PI430048170 0.638001250785686 1.10386215212984 2.89729713173522 3.0844918210008 2.53755881827999 A P A 1.8123487112533 2.76851211020474 3.22762936839719 A P P LNCV6_132907_PI430048170 mRNA GCTCAAAATGTGGCCTAAGTAGCCATTGGCATGTCTAGATGAACAAATAAAAATAAAGAT NM_018945 RefSeq chr6 + 135851695 136195571 PDE7B 27115 phosphodiesterase 7B
GO:0007165|GO:0004115|GO:0007268|GO:0046872|GO:0006198|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127594_PI430048170 0.0381607044846642 0.7106705404954158.78884228985587 8.43758966030852 8.38226937899366 P P P 8.91737595848621 9.17618736401021 9.01603409360209 P P P LNCV6_127594_PI430048170 mRNA TTAATCAGGGGACAGGGCTCTCTAATAAAGCTGCTGGCAGTGCCCAGGACGGTGAAAAAA NM_001283009 RefSeq chr20 + 63657809 63696253 RTEL1 51750 "regulator of telomere elongation helicase 1, transcript variant 3"
GO:0005515|GO:0051539|GO:0006281|GO:0004003|GO:0000723|GO:0005634|GO:0044281|GO:0032508|GO:0005524|GO:0003677|GO:0046872|GO:0010569 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129679_PI430048170 0.971352951589025 1.11765279230128 3.77331049529008 0.3971414152916890.280809414666039 P A A 0.3257374891408663.57989574548593 0.365293319544521 A P A LNCV6_129679_PI430048170 mRNA AACAGATGCATTGTTGCTTTTCTGTGCTGTCTCTGCAGATTAAAACATAATGATTACACT NM_005459 RefSeq chr3 - 108907794 108953830 GUCA1C 9626 guanylate cyclase activator 1C
GO:0007165|GO:0007603|GO:0005509|GO:0031284|GO:0022400|GO:0007601|GO:0016056|GO:0008048 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129325_PI430048170 0.0281470570957480.279833369860322 3.95256824928405 3.52408359462982 3.89475181002713 P P P 4.85172955553326 5.75223884008518 6.06214380761271 P P P LNCV6_129325_PI430048170 mRNA GATCTTGGCTAAGAGAGTATTTTTCCCCTTGTAATTATGACTCTGAGATAAAATTGCCAT NM_001042517 RefSeq chr13 - 59665588 60163985 DIAPH3 81624 "diaphanous-related formin 3, transcript variant 1"
GO:0030036|GO:0017048|GO:0005634|GO:0003779|GO:0007283|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141742_PI430048170 0.0251933509682931 0.4640442515943014.2190172070609 4.10760041792159 4.21641515620869 P P P 4.89496929894601 5.39812225169942 5.50521456082135 P P P LNCV6_141742_PI430048170 mRNA GCAAAGGTAGCCTTTTGGGCTTTTTAATGAATATGACCCCTATAGAAAAGTCAAGAAAAA NM_021145 RefSeq chr7 + 87152553 87196332 DMTF1 9988 "cyclin D binding myb-like transcription factor 1, transcript variant 1"
GO:0007049|GO:0006355|GO:0005737|GO:0003700|GO:0003682|GO:0005654|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106904_PI430048170 0.2760435357959921.14272673809905 6.91969808956349

7.20130565645596 7.25602213666627 P P P 6.959043119387 6.72397253061387
7.11238476934595 P P P LNCV6_106904_PI430048170 mRNA
AACACAAGATGGGGACTCCTGCTTCTGGAAGGAAAAGAACACCTGTGAAAGACCGATTTT NM_006309 RefSeq chr3
- 37052625 37174605 LRRFIP2 9209 "leucine rich repeat (in FLII) interacting protein 2, transcript variant
1" GO:0005515|GO:0008150|GO:0030275|GO:0005575|GO:0016055 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_91038_PI430048170 0.4788618672081310.8807926587743552.55024369082726 2.54751440265646
1.83711330223681 A A A 2.31553918074091 2.58918002014871 2.66644003516711 A P P
LNCV6_91038_PI430048170 mRNA
CCATTTCTATATGATGCTCCTCCCAATATTCTGAAACATGTGGTTGGACAGTTCAGTAAG NM_001253854 RefSeq
chr10 + 22345444 22417610 SPAG6 9576 "sperm associated antigen 6, transcript variant 3"
GO:0031514|GO:0005930|GO:0030030|GO:0015630|GO:0005874|GO:0007286|GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132205_PI430048170 0.0115724605633022 0.3464537093702154.64739500884018
5.05652962859647 5.16865146149932 P P P 5.95539255310982 6.68069471262682 6.7491707324417
P P P LNCV6_132205_PI430048170 mRNA
GCTGTTCTGCTCATATATGAATTTTTAATGCAGCAATGTTGACTTTGTTTCATACTGCCA NM_002849 RefSeq chr12 -
70638072 70920804 PTPRR 5801 "protein tyrosine phosphatase, receptor type, R, transcript variant 1"
GO:0005515|GO:0048471|GO:0005886|GO:0019901|GO:0001701|GO:0005615|GO:0035335|GO:0006470|GO:0005
001|GO:0070373|GO:0016021|GO:0038128|GO:0004725|GO:0010633 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133722_PI430048170 0.9595113346447391.00889314696579 0.71151267408266
0.5596006332560690.321930826387387 A A A 0.3925387106460540.628463796539078
0.550230698136221 A A A LNCV6_133722_PI430048170 mRNA
AGACTCCGCCTTTCTAATCACAAATGTAGCCTACAAGCAAGCGGCTTTGGATTGCTTATG NM_020737 RefSeq chr6
- 40391633 40587464 LRFN2 57497 leucine rich repeat and fibronectin type III domain containing 2
GO:0030054|GO:0045211|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69818_PI430048170 0.0615758555386573 0.7236761103262356.04896800089659
5.54866354360125 5.86084426461961 P P P 6.45935196764986 6.15936253732817
6.26690366903748 P P P LNCV6_69818_PI430048170 mRNA
CTGTGGAAGAGATGAATGGAAAAGAAATAAGTGGTAAAATCATATTTGTAGGCCGTGCAC NM_001135653 RefSeq
chr1 - 39560812 39576849 PABPC4 8761 "poly(A) binding protein, cytoplasmic 4 (inducible form),
transcript variant 1"
GO:0005515|GO:0006396|GO:0010494|GO:0017130|GO:0005634|GO:0006412|GO:0006401|GO:0008266|GO:0005
737|GO:0000166|GO:0007596|GO:0030529|GO:0008143 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_9160_PI430048170 0.0254348797225239 0.86659569985268 13.5964871803724
13.5542612744348 13.6805569537952 P P P 13.7700342452853 13.7733514733736
13.9062755658641 P P P LNCV6_9160_PI430048170 mRNA
TTTTTTGTGTATGTACTTAGCTGTACTATAAGTAGTTGGTTTGTATGAGATGGTTAAAAA NM_001099285 RefSeq
chr2 + 231708524 231713540 PTMA 5757 "prothymosin, alpha, transcript variant 1"
GO:0005515|GO:0005737|GO:0005654|GO:0005634|GO:0006351|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133102_PI430048170 0.0495020236502127 0.6483562067386856.29833077634889
6.21317062827103 6.14056003357154 P P P 6.59948286987125 7.12339754204407
6.75792831504803 P P P LNCV6_133102_PI430048170 mRNA
CAAGACCAAGGAGAATGTTGTACAGAGCGTGACCTCAGTGGCCGAGAAGACCAAGGAGCA NM_003087 RefSeq
chr10 + 86958530 86963260 SNCG 6623 "synuclein, gamma (breast cancer-specific protein 1)"
GO:0071464|GO:0008344|GO:0048471|GO:0009306|GO:0005815|GO:0005886|GO:0043014|GO:0042493|GO:0048
487|GO:0005819|GO:0046928|GO:0007268|GO:0042220|GO:0014059|GO:0005737|GO:0050808|GO:0002118|GO:0

043025|GO:0043679|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138449_PI430048170 0.000517423708183144 1.40668530644799 11.4454635053119
11.3889360827592 11.3227892282133 P P P 10.859668334317 10.8687770358711
10.9526227161607 P P P LNCV6_138449_PI430048170 mRNA
CCAGGGCTGGGACATTATGTAGGAGCCACTTCATAAACATTCTCTTTACTCATCAAAAAA NM_033112RefSeq chr6
+ 43021646 43029599 RRP36 88745 ribosomal RNA processing 36 homolog (S. cerevisiae)
GO:0000462|GO:0006364|GO:0005730|GO:0005634|GO:0042274|GO:0030686 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140721_PI430048170 0.0112175318702073 1.1688929962297 12.7593538683494
12.8852621777877 12.7864102685825 P P P 12.5438776568125 12.6429973051937
12.5699502425416 P P P LNCV6_140721_PI430048170 mRNA
ACAAATCGAGGACTTCGAGGCTCGCATCGCGCTGTTGCCACTGTTACAGGCAGAAACCGA NM_015965RefSeq chr19
+ 19516209 19528204 NDUFA13 51079 "NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13"
GO:0005515|GO:0030308|GO:0045732|GO:0035458|GO:0071300|GO:0005743|GO:0044281|GO:0005739|GO:0005
737|GO:0045039|GO:0044237|GO:0070062|GO:0031966|GO:0072593|GO:2001243|GO:0097190|GO:0005524|GO:0
022904|GO:0003954|GO:0043280|GO:0010952|GO:0005746|GO:0005747|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137425_PI430048170 0.0505083648792661.34991508911333 8.83075471197218
9.00404813802086 9.23466704776349 P P P 8.4327801028703 8.56777061033779
8.77780718776168 P P P LNCV6_137425_PI430048170 mRNA
GAAATCATATTTTTCCAGTGGACCATCCTCCAGTGGCTGTGGTTGTTGAGCATGCTTTCA NM_012434RefSeq chr6
- 73593378 73654014 SLC17A5 26503 "solute carrier family 17 (acidic sugar transporter), member 5"
GO:0006820|GO:0030054|GO:0005886|GO:0006865|GO:0005765|GO:0055085|GO:0005737|GO:0015739|GO:0016
020|GO:0005887|GO:0015136|GO:0030672|GO:0005351|GO:0006488|GO:0044267|GO:0043687|GO:0018279|GO:0
006811|GO:0015992. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143975_PI430048170 0.145568050509414 1.04466965595819 0.421254722812237
0.427466723399244 0.439585019765231 A A A 0.322439814616589 0.357346587754435
0.417821197095735 A A A LNCV6_143975_PI430048170 mRNA
GAAGGGCATGCTGAGCACTCAAACAATTTGTTCTTACTTAAAATAAAATGACAACAAACC NM_001261828 RefSeq
chr11 + 60396013 60417755 MS4A14 84689 "membrane-spanning 4-domains, subfamily A, member
14, transcript variant 4" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131333_PI430048170 0.0759865485715435 0.338279501618918 1.15324825098979
2.13841060627452 2.98476283395913 A A P 3.69496560078827 3.76236671189755
4.04174485302478 P P P LNCV6_131333_PI430048170 mRNA
AAAGCAACTGAGTGTAGATTTGCAACTATAGTGTGTATCTTCATTTGTGTGATGAAAGAG NM_001134415 RefSeq
chr3 - 186546066 186570543 TBCCD155171 "TBCC domain containing 1, transcript variant 1"
GO:0030334|GO:0000902|GO:0005737|GO:0051661|GO:0008360|GO:0007010|GO:0031616|GO:0003779|GO:0051
684 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131231_PI430048170 0.961281362635592 0.99703543552951 5.20350919077452
4.96576504859997 4.7390627396324 P P P 5.18921711569336 4.87781998127239
4.86782803317004 P P P LNCV6_131231_PI430048170 mRNA
AATGCACCCACTCTCTTCCTTGTTTTGGGGTATAATAAAATCCAGTAACTTGTTTCTGAA NM_172000RefSeq chr1
- 182398116 182400616 TEDDM1 127670 transmembrane epididymal protein 1 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128836_PI430048170 0.566494469606955 1.01844385249169 0.416546129900525
0.431462681074016 0.355804511573903 A A A 0.322696019785289 0.3577852754109
0.442688763064436 A A A LNCV6_128836_PI430048170 mRNA
AAGATTTCAAACTCTGTCCTGGAAGATTCCTCCGACCTAGAATCCAGAAATCTGCCCTCT NM_178354RefSeq chr1
+ 152776371 152776969 LCE1F 353137 late cornified envelope 1F GO:0031424 . NA - . NA

NA NA NA NA NA NA NA NA
LNCV6_140702_PI430048170 0.2960894699069640.9245878879831550.530131186284332
0.4913217447447980.261138260533784A A A 0.5968532681140770.54703155312065
0.490478226304626A A A LNCV6_140702_PI430048170 mRNA
ATGGGAGATGCTGATTGTAGGGTCTGAGTTAGATACTGTTAACTAAAATGCTTGTTGATA NM_021167RefSeq chr7
+ 92447447 92460067 GATAD1 57798 "GATA zinc finger domain containing 1, transcript variant 1"
GO:0043565|GO:0006355|GO:0003700|GO:0008270|GO:0005654|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_52468_PI430048170 0.3875560798174120.7791636854462311.95452092678641 1.6320864710157
3.087917275186 A A P 2.43155445569959 2.76887012574027 2.93632893755833 A P P
LNCV6_52468_PI430048170 mRNA
CACAGCTATTGACTCTATTTTCTGAAGGCAAAAATGCATGTTTGTTAGAATGGAAACAGA NM_012093RefSeq chr1
+ 77282601 77559969 AK526289 "adenylate kinase 5, transcript variant 2"
GO:0046034|GO:0015949|GO:0005815|GO:0004550|GO:0009220|GO:0055086|GO:0044281|GO:0004017|GO:0009
142|GO:0019206|GO:0005524|GO:0005829|GO:0006165|GO:0005737|GO:0006172|GO:0006173 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143194_PI430048170 0.3651297116214190.8615810019147458.2232943068214
8.05146337307906 8.30820317375247 P P P 8.29485765610877 8.16402906205109
8.72042047239695 P P P LNCV6_143194_PI430048170 mRNA
GTTAAGTGTGTGTGTGTTTTCTGTACCCAACCAGACTTTAAATAAAACAAACATGAAACC NM_014521RefSeq chr2
+ 234951983 235055714 SH3BP4 23677 SH3-domain binding protein 4
GO:0043090|GO:0005515|GO:0030308|GO:0032007|GO:0008285|GO:0030136|GO:0005634|GO:0042802|GO:0006
897|GO:0050790|GO:0005737|GO:0005905|GO:0071230|GO:0005092|GO:0017016|GO:0034260|GO:0070062|GO:0
010508 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138908_PI430048170 0.00173211708897024 0.4706213441387197.91069928800296
8.06031890855491 8.10149066536811 P P P 9.01833753205315 9.00090069874042
9.30203651378626 P P P LNCV6_138908_PI430048170 mRNA
TGTGTTCACTCTAAAAATGCAAATAAAGACTGCTTCCTTAGAGGGTGCTCATACAAAAAA NM_033121RefSeq chr12
+ 109999429 110039430 ANKRD13A 88455 ankyrin repeat domain 13A GO:0005886|GO:0005770 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129050_PI430048170 0.8890613633616611.15083469909084 2.33471299554662
0.4215111137066510.358039088830281A A A 1.29608683556009 0.910689687368028
1.21739845208627 A A A LNCV6_129050_PI430048170 mRNA
TGACTGTTTCCAGAGTGCTTATAATATACATAACTCCCTGGAAATAACTGAGCACTTTGA NM_006186RefSeq chr2
- 156324431 156332775 NR4A2 4929 "nuclear receptor subfamily 4, group A, member 2"
GO:0005515|GO:0008344|GO:0010467|GO:0021986|GO:0006367|GO:0003707|GO:0016265|GO:0005634|GO:0009
791|GO:0042053|GO:0042416|GO:0043576|GO:0043524|GO:0005737|GO:0010035|GO:0045944|GO:0031668|GO:0
043401|GO:0004879|GO:0001666|GO:0046982|GO:0042551|GO:0021952|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145499_PI430048170 0.89015280848191 1.00837277826289 5.47299316774521
5.25019929732483 5.26227322099967 P P P 5.61529803952839 5.09385289108041
5.19695260905175 P P P LNCV6_145499_PI430048170 mRNA
GTTTCCCTCAGTCATTTGGTTTATGTTTGGTTATGGCAAGATGTTACAGCATTTATAGTT NM_031271RefSeq chr8 -
30831543 30849017 TEX15 56154 testis expressed 15
GO:0034502|GO:0032880|GO:0009566|GO:0030539|GO:0048873|GO:0007283|GO:0007130|GO:0010569|GO:0007
140 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141372_PI430048170 0.00636228086496063 0.4053110265105043.25356430929268
2.94040717962109 3.57226268726685 P A P 4.33995793380958 4.45193145509057
4.89140703471403 P P P LNCV6_141372_PI430048170 mRNA

GTGACTAGGTTTTTAAGGATACAGCTTATAAGTTGCTATCAATTTTCACTACCTAAGCAG NM_016002RefSeq chr1
+ 246724075 246768138 SCCPDH 51097 saccharopine dehydrogenase (putative)
GO:0005811|GO:0005739|GO:0016020|GO:0016491|GO:0030496|GO:0005634|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139609_PI430048170 0.0022128851324594 1.14029339616186 14.7885384773236
14.8081710040674 14.7742617534001 P P P 14.596624708638 14.6333891097927
14.5722864264299 P P P LNCV6_139609_PI430048170 mRNA
AATGACATTTCCCTGCAGGATTACATTGCAGTGAAGGAGAAGTATGCCAAGTACCTGCCT NM_001009RefSeq chr19
+ 58387268 58394804 RPS5 6193 ribosomal protein S5
GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0003729|GO:0006415|GO:0006
412|GO:0006413|GO:0005829|GO:0006414|GO:0016020|GO:0000184|GO:0022627|GO:0030529|GO:0016032|GO:0
006450|GO:0044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131805_PI430048170 0.0738538898353334 0.6638241751391994.77446282302297
4.13072828540948 4.36272445953125 P P P 4.94091656904369 5.06237640375235
5.10771374107873 P P P LNCV6_131805_PI430048170 mRNA
GGCTGAAGGTGTGAAAATCCTAAGAGGATTTCATATTGAATATGTGTACACAATCTTAAC NM_016133RefSeq chr2
+ 118088473 118110021 INSIG2 51141 insulin induced gene 2
GO:0005515|GO:0006695|GO:0032868|GO:0042472|GO:0045717|GO:0044281|GO:0010894|GO:0070542|GO:0060
363|GO:0032933|GO:0032937|GO:0005789|GO:0060021|GO:0006641|GO:0042474|GO:0008134 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138533_PI430048170 0.2692333526536280.9719431180402410.330128013084943
0.3738556809707050.326936028340495A A A 0.4351910968979090.346089603289513
0.371822380130771A A A LNCV6_138533_PI430048170 mRNA
CTTTTACATGTTGGGCGAATTTGTGTCCGTGCTGAAGTTTATTAAAGGAAAATAGATGGA NM_203314RefSeq chr3
- 197509782 197555987 BDH1 622 "3-hydroxybutyrate dehydrogenase, type 1, transcript variant 3"
GO:0045471|GO:0005743|GO:0044281|GO:0005739|GO:0005737|GO:0005543|GO:0042594|GO:0005759|GO:0032
355|GO:0044255|GO:0032868|GO:0051412|GO:0060416|GO:0007584|GO:0042493|GO:0009636|GO:0003858|GO:0
001889|GO:0007420|GO:0046952|GO:0046951|GO:0046950|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140393_PI430048170 0.0616620168897633 0.80345890729348 5.22178990595356
5.30529478324066 5.0430100714335 P P P 5.49204127560958 5.66959545181017
5.35005617938275 P P P LNCV6_140393_PI430048170 mRNA
CTGTGGAGGACACACTCTCAGTTTGTTTTTGACTTTGGTTTATTTAAAAAACAAGCCAAA NM_018688RefSeq chr8
- 22620430 22669148 BIN3 55909 bridging integrator 3
GO:0010591|GO:0005515|GO:0014839|GO:0000910|GO:0005737|GO:0008104|GO:0005884|GO:0048741|GO:0007
015|GO:0000917|GO:0009826|GO:0008093 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145233_PI430048170 0.0170574983427661 0.6047335347999227.76007686940334
7.56175940947783 8.02461832569883 P P P 8.30450845600554 8.48182707464856
8.74094537583783 P P P LNCV6_145233_PI430048170 mRNA
CCCCCTTTCATTTGAAGGACCAGTTTTTCATGGTACTTGTCTTGATCTTTTTCATAGTGT NM_181521RefSeq chr16 -
66614749 66696707 CMTM4 146223 "CKLF-like MARVEL transmembrane domain containing 4, transcript
variant 2" GO:0006935|GO:0016021|GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_119272_PI430048170 0.0365819168756688 1.42687607638745 5.40729195769067
5.6583613628865 5.41985076757026 P P P 5.20444815944362 4.96935720183541
4.75170257946832 P P P LNCV6_119272_PI430048170 mRNA
TGAGGCAAGAGAAGGCCAGAAACCATGCCCATGGGGTCTCTGCAACCGCTGGCCACCTTG NM_014207RefSeq
chr11 + 61102457 61127851 CD5 921 CD5 molecule
GO:0005515|GO:0008037|GO:0005886|GO:0008283|GO:0005887|GO:0031295|GO:0004872|GO:0097190|GO:0009

897|GO:0006898|GO:0005044|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122861_PI430048170 0.00598961042028835 1.77665494375581 9.57370846602063
9.56278352420839 9.82627687067504 P P P 8.83934563563579 8.77478623614486
8.87505596434944 P P P LNCV6_122861_PI430048170 mRNA
TTCCTTGGAAGCTCTTACGTGATGTGGGAAATGACAACACAGGTGTCACACTACTACTTG NM_206963 RefSeq chr3
- 158697107 158732486 RARRES1 5918 "retinoic acid receptor responder (tazarotene induced) 1,
transcript variant 1" GO:0008285|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_104053_PI430048170 0.0957389772098685 1.06596504755636 0.465715583054909
0.5571760963590150.525716276789459 A A A 0.36394554083213 0.431945424176774
0.475542182849212 A A A LNCV6_104053_PI430048170 mRNA
CTGTTGACTTCAAAGATAAATTGGAAGAAACGAAAGGTCAGATCAACAACTCAATTAAGG NM_002639 RefSeq chr18
+ 63476910 63505085 SERPINB5 5268 "serpin peptidase inhibitor, clade B (ovalbumin), member 5"
GO:0010951|GO:0005515|GO:0050678|GO:0005737|GO:0030198|GO:0004867|GO:0060512|GO:0006928|GO:0005
615|GO:0002009|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132291_PI430048170 0.2636234842977770.6103561714948722.31798082420425
1.54779799833302 3.00930856012043 A A P 2.29424166542917 3.56326435539087
3.23661981485129 A P P LNCV6_132291_PI430048170 mRNA
GGGCATCTTTTAGAGTTAACTTTTCTCATTGCCATCCAAAAATAGCTTGCTTGTTTAACTNM_033397 RefSeq chr10 -
104309695 104333905 ITPRIP 85450 "inositol 1,4,5-trisphosphate receptor interacting protein, transcript
variant 1" GO:0016020|GO:0005886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132002_PI430048170 0.00388982519343839 0.7434149789923211 1.5731381942976
11.500848766111 11.4493267353266 P P P 11.9530909600785 11.9150064286547
11.9409226676497 P P P LNCV6_132002_PI430048170 mRNA
ACCCGACATTTTTCAGCTCTTTGCTATTGAAATAATAAACCACCCTGTTCTGTGGCCCGT NM_015466 RefSeq chr3
+ 47380981 47413441 PTPN23 25930 "protein tyrosine phosphatase, non-receptor type 23, transcript
variant 1"
GO:0005515|GO:0019901|GO:2000643|GO:0005634|GO:0015031|GO:0035335|GO:0036064|GO:0005737|GO:0060
271|GO:0016023|GO:0005654|GO:0043162|GO:0004725|GO:0005769|GO:0070062|GO:0005768|GO:0010633 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136718_PI430048170 0.1563460959056190.486333541692341 2.01633097932951
0.3660451902028062.06806540516663 A A A 2.22770863228952 2.71411804191261
3.06088395609156 A P P LNCV6_136718_PI430048170 mRNA
GTTGTGGACCCAGGAAATTTTCCATAAGTCTTGCTTGATAACAATGTGATTGTACAAAAT NM_152731 RefSeq chr6
+ 56954974 57027344 BEND6 221336 BEN domain containing 6
GO:0045746|GO:0045666|GO:0001106|GO:0003682|GO:0005634|GO:0000122 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145650_PI430048170 0.00867483482205127 2.38218244502354 8.09112874247242
8.2888641521088 8.27561890807572 P P P 7.26908895502575 6.73031442980446 6.8507955275703
P P P LNCV6_145650_PI430048170 mRNA
TGACTACCTTGACTTGAAATGCTCTTTTGCACAAGGAAATAAAGCGTCCTCTCAGTAATG NM_003561 RefSeq
chr16_KI270853v1_alt - 245406 267531 PLA2G10 8399 "phospholipase A2, group X"
GO:0019369|GO:0051977|GO:0043030|GO:0044281|GO:0043433|GO:0007411|GO:0004623|GO:0006654|GO:0042
632|GO:0010744|GO:0036149|GO:0005509|GO:0036148|GO:0090238|GO:0010884|GO:0005576|GO:0004620|GO:0
016042|GO:0032270|GO:0036150|GO:0090370|GO:0032308|GO:0006644|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131910_PI430048170 0.8192632329629310.936613166409915 2.08481558620586
2.99494888864673 2.84125692580374 A A P 3.21893395210082 2.2860242439021
2.70137638894896 P A P LNCV6_131910_PI430048170 mRNA

GTGTGCACATCTGACAGTGGTAATCTTTGGGTCAGGGAATTATAGATAAATTTTCTTTAA NM_015044 RefSeq chr16 - 23463541 23510494 GGA2 23062 "golgi-associated, gamma adaptin ear containing, ARF binding protein 2"
GO:0005802|GO:0005515|GO:0030131|GO:0005794|GO:0030306|GO:0030136|GO:0016192|GO:0006886|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143412_PI430048170 0.86415464221445 1.0324767001513 7.39969989960762 7.94170476592371 7.83410935645021 P P P 7.90670714126297 7.64222574475878 7.51530573688062 P P P LNCV6_143412_PI430048170 mRNA
TCAACATCATTGACATCCTGGCGCTCCTGCCGTTCTACGTGTCGCTGCTGCTGGGGCTGG NM_012283 RefSeq chr18 + 79863667 79899816 KCNG2 26251 "potassium channel, voltage gated modifier subfamily G, member 2"
GO:0005251|GO:0005886|GO:0008016|GO:0007268|GO:0044281|GO:0006112|GO:0050796|GO:0008076|GO:0034765|GO:0051260|GO:0016021|GO:0006813|GO:0071805|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142237_PI430048170 0.00705572817164935 0.1342057541938610.405879661737024 0.6364139571883740.356160885772558 A A A 2.7796394154779 3.3328170445141 3.81249137978925 P P P LNCV6_142237_PI430048170 mRNA
CCACTAGGGATTCTGAAAAGTTCGTGAGCTGAAACAAATAAATTGAGTTGGAAGATTAAA NM_005504 RefSeq chr12 - 24810023 24949459 BCAT1 586 "branched chain amino-acid transaminase 1, cytosolic, transcript variant 1"
GO:0008283|GO:0004084|GO:0052656|GO:0052654|GO:0052655|GO:0009083|GO:0044281|GO:0005829|GO:0042802|GO:0005739|GO:0034641|GO:0000082|GO:0009082 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130413_PI430048170 0.0495343940237791.10782604021921 12.6196391323648 12.498650909576 12.5677682419714 P P P 12.4908017918575 12.3593283468049 12.3920131169288 P P P LNCV6_130413_PI430048170 mRNA
GGGTAGCCAAGTGATCTTCCCATTCACAGAGTTAGTAAACCTCTGTACTACATGCTGAAA NM_005015 RefSeq chr14 + 22766521 22771789 OXA1L 5018 oxidase (cytochrome c) assembly 1-like
GO:0005515|GO:0051262|GO:0031966|GO:0051354|GO:0051205|GO:0032780|GO:0042803|GO:0005739|GO:0009060|GO:0032981|GO:0043234|GO:0005746|GO:0033615|GO:0006461|GO:0097031|GO:0032592|GO:0097177|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49537_PI430048170 0.9144436398869770.93756637962891 1.08341365772751 0.966200705609814 1.5880087389712 A A A 1.88538420502373 0.8136274323415421.06924823165751 A A A LNCV6_49537_PI430048170 mRNA
AATAAGACCTGGGCTGAGGCCGACCTCTACTGTTCTGAGTTCTCTGTGGGCAGGAAGTCC NM_001256720 RefSeq chr16 + 19285782 19310947 CLEC19A NA "C-type lectin domain family 19, member A" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134272_PI430048170 0.2437198451885591.6456596810514 3.17641320422982 2.8097857034956 2.44800215758854 P A A 2.79305494953522 2.08395288261713 0.92561135733518 P A A LNCV6_134272_PI430048170 mRNA
AATATTTAGGGCAATAAGCAGCATTGGCCTGGAGTGCCAGAGCGTCACCTCCAGGGGGGA NM_020415 RefSeq chr19 + 7669085 7670454 RETN 56729 "resistin, transcript variant 1"
GO:0032868|GO:0007568|GO:2000252|GO:0005634|GO:0010714|GO:0005615|GO:0048661|GO:0009612|GO:0014911|GO:2000872|GO:0008150|GO:0005179|GO:0050806|GO:0045444|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134584_PI430048170 0.6886176032656621.06180147580747 7.3197901205982 6.93383354057525 7.17518524441666 P P P 6.60766547329388 7.06131160234057 7.41484926038031 P P P LNCV6_134584_PI430048170 mRNA
GAGCCAGCTGGTATATTGTCAGGAAGCACTATTTAAAATGTGAACTGTTATAGAGTAAAT NM_020853 RefSeq chr12 + 13044380 13083449 KIAA1467 57613 KIAA1467 GO:0016021 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_133543_PI430048170 0.37704314805254 1.00857541511146 0.412185359156707
0.418825367567312 0.394497679004962 A A A 0.404575463860548 0.376361886481092
0.407518993695082 A A A LNCV6_133543_PI430048170 mRNA
CGTGAAAACACATTTGCTTTTTGTGATATGCACAATGTAGATAAGTGTTCTGTCTGACTT NM_021111 RefSeq chr9
+ 36036912 36124455 RECK 8434 reversion-inducing-cysteine-rich protein with kazal motifs
GO:0010951|GO:0005515|GO:0016020|GO:0005886|GO:0004866|GO:0030198|GO:0007566|GO:0004867|GO:0008
191|GO:0031225|GO:0001955 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133729_PI430048170 0.0660164087081778 1.3927842882698 13.6890949128143
13.809387646424 13.8726827349222 P P P 13.0253203493455 13.3414598448147
13.5318401905955 P P P LNCV6_133729_PI430048170 mRNA
GCAGGGGGTGATTTTTGCTCTTGTCCTGAGAAATAACAGTGCTGTTTTAAAAAACATTTG NM_001134493 RefSeq
chr6 + 41787442 41789896 TOMM6 100188893 translocase of outer mitochondrial membrane 6
homolog (yeast) GO:0005739|GO:0006626|GO:0005742|GO:0044267 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_127515_PI430048170 0.0352479632938443 1.37371086613424 9.24360002347666
9.04429884733569 9.29831384291436 P P P 8.51679254835378 8.77041596259811
8.90983759443213 P P P LNCV6_127515_PI430048170 mRNA
TTGGGAGGCGGTTTGGGAGAACACATTTCTAATTTGAATGAAATGAAATCTATTTTCAGT NM_001278352 RefSeq
chr9 + 32384602 32450834 ACO1 48 "aconitase 1, soluble, transcript variant 1"
GO:0005515|GO:0051539|GO:0005794|GO:0006099|GO:0005783|GO:0003723|GO:0003994|GO:0010040|GO:0009
791|GO:0046872|GO:0006417|GO:0005829|GO:0005739|GO:0006879|GO:0006101|GO:0050892|GO:0005737|GO:0
030350|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130852_PI430048170 0.0405268557766742 0.95702241372718 0.379776755836591
0.38613532381281 0.334733358127614 A A A 0.436603927923909 0.440111399439683
0.414464816035141 A A A LNCV6_130852_PI430048170 mRNA
CACCAAGGTTGTGGATCTTAAGGTATGTATGGAAAGGAACTCATTTATCAAATTGTAAGT NM_018092 RefSeq chr16
- 47081519 47144025 NETO2 81831 "neuropilin (NRP) and tolloid (TLL)-like 2, transcript variant 1"
GO:0032983|GO:0035255|GO:0014069|GO:2000312 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129790_PI430048170 0.399380038339099 0.559842423083857 0.428326267925487
0.440023579439659 0.361219057720527 A A A 0.476967806475691 2.13664267751959
0.413718273033195 A A A LNCV6_129790_PI430048170 mRNA
ATACATGATACATATTAATCCATTAAAGACTAGTGGGAATGTATCAGCCAGAGTAGCAAG NM_006646 RefSeq chr13
+ 26557702 26688946 WASF3 10810 "WAS protein family, member 3, transcript variant 1"
GO:0005737|GO:0006461|GO:0014003|GO:0008360|GO:0030032|GO:0007010|GO:0030041|GO:0003779|GO:0005
856|GO:0030027|GO:0070062|GO:0031643 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134409_PI430048170 0.592347819755019 0.833907223481033 0.661713729576575
0.403067167425792 0.574797290232021 A A A 1.35732678586246 0.398293267098049
0.473857205033768 A A A LNCV6_134409_PI430048170 mRNA
CTGCCACACAAACGTATGTAAATGTATATACCCACACACATACACACATATGTCATATAT NM_006564 RefSeq chr3
+ 45943480 45948353 CXCR6 10663 chemokine (C-X-C motif) receptor 6
GO:0070098|GO:0006954|GO:0007186|GO:0006935|GO:0005886|GO:0016494|GO:0005887|GO:0004930|GO:0015
026|GO:0019079 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142388_PI430048170 0.506134864028496 0.949090040709683 5.93313274434498
6.03700766134969 6.10042924652922 P P P 5.96403564075995 6.25042283018306
6.07259076298349 P P P LNCV6_142388_PI430048170 mRNA
AACACAAAATTACTCTGCCATTGTTTCCAGCTTCCCTCCTACAATAGAATGAAGTTTTTT NM_006930 RefSeq chr5
- 134156390 134177033 SKP1 6500 "S-phase kinase-associated protein 1, transcript variant 1"
GO:0031519|GO:0005515|GO:0035518|GO:0004842|GO:0016567|GO:0051437|GO:0031146|GO:0031145|GO:0051

439|GO:0005829|GO:0000082|GO:0007219|GO:0000086|GO:0007623|GO:0016032|GO:0005654|GO:0031467|GO:0000278|GO:0019005|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130901_PI430048170 7.87573258264011e-05 3.63439787533408 7.68098066004209 7.93061011068967 7.73792568123231 P P P 5.75791118568895 5.98702796880264 6.01773532518489 P P P LNCV6_130901_PI430048170 mRNA
TACTTTTCTCCTAAGTCTACCCTGGACACTTTTTAGGGCACCTGGAGAGAACTTTCCTCT NM_178570RefSeq chr11 + 57460536 57477539 RTN4RL2 349667 reticulon 4 receptor-like 2
GO:0031103|GO:0009986|GO:0045121|GO:0004872|GO:0046658|GO:0009897|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_41212_PI430048170 0.0357309051905941.14643205352779 6.918298806577 6.78797756452772 6.8318751938263 P P P 6.6154246597925 6.7440636789643 6.5852972122246 P P P LNCV6_41212_PI430048170 mRNA
CACCTTTGAGATGGCCAAGGTTCTCTTTCTCTCTCTTCACTGCTGTCCATAAGCACTATA NM_001283021 RefSeq chr14 + 24232421 24239241 GMPR2 51292 "guanosine monophosphate reductase 2, transcript variant 5"
GO:0006144|GO:0043101|GO:0046037|GO:0055086|GO:0044281|GO:0003920|GO:0046872|GO:0055114|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132219_PI430048170 0.885606867134833 1.01980058594585 2.22121568137885 1.69309058706007 2.22403101030736 A A A 1.51937357195013 2.30561366875807 2.17435773127833 A A A LNCV6_132219_PI430048170 mRNA
GGGAGGCTCCCTCGGAATAAATGTATGCAACACAAATAAGGCATTTTATTTTTTAAAAGA NM_001109754 RefSeq chr12 - 70516850 70637440 PTPRB 5787 "protein tyrosine phosphatase, receptor type, B, transcript variant 1"
GO:0043235|GO:0005515|GO:0006470|GO:0005887|GO:0005001|GO:0016311|GO:0006796|GO:0001525|GO:0035335 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137126_PI430048170 0.00820846047079106 0.468926116967927 2.69312572277225 2.59097077946086 2.49228088281597 A A A 3.49286435958487 3.57859355178847 3.94803776886602 P P P LNCV6_137126_PI430048170 mRNA
TTTGGACAGCCGCTCTGGTTTAAAGATATGTACAAACCTCTCAGTGCCACAAGAATAAAT NM_001006607 RefSeq chr17 + 46512709 46555648 LRRC37A2 474170 "leucine rich repeat containing 37, member A2"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140399_PI430048170 0.382808109244262 1.02503949872847 0.298594663549889 0.314855111898146 0.400166551757473 A A A 0.318668059267578 0.299608461057556 0.290232071027867 A A A LNCV6_140399_PI430048170 mRNA
CTCTGCATCATACTTAACCCTGCGACATGCGTACAGTATGCATATTTTGTTTTGAAAAAA NM_001080396 RefSeq chr13 - 107168530 107867112 FAM155A 728215 "family with sequence similarity 155, member A"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129004_PI430048170 0.635986593815508 0.924165861263299 0.529384366341756 0.696609647127906 0.568318344698068 A A A 1.03034420123327 0.509560390281089 0.539796227721636 A A A LNCV6_129004_PI430048170 mRNA
TTTGTCTGTCTACAAAAATCAACACAAACAGAACTCCTCTGCACGTGAATTTTCATCTAT NM_005092RefSeq chr1 - 173041219 173050963 TNFSF18 8995 "tumor necrosis factor (ligand) superfamily, member 18"
GO:0005164|GO:0043066|GO:0005886|GO:0009986|GO:0005102|GO:0007267|GO:0032813|GO:0005125|GO:0005615|GO:0033209|GO:0007165|GO:0051092|GO:0002309|GO:0042129|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145419_PI430048170 0.0854308217531423 0.728431102213485 7.48928869903895 7.46465111529604 7.83473796864491 P P P 7.84834094579277 7.9430841401158 8.3487679826855 P P P LNCV6_145419_PI430048170 mRNA
GGGACAGAACCCTACTTTTTGTAGAGGAACTTAATCTGAATAAAGTCTGAGTTTTTCAGT NM_018180RefSeq chr10

- 125836339 125881315 DHX32 55760 DEAH (Asp-Glu-Ala-His) box polypeptide 32
GO:0005739|GO:0004004|GO:0005737|GO:0000398|GO:0005681|GO:0005524 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137070_PI430048170 0.1095963018635331.82878271210231 13.0090673634427
12.9428059655383 12.9853308327035 P P P 12.710277664254 11.6045222653175
11.7447442267641 P P P LNCV6_137070_PI430048170 mRNA
GTTGGACAGGTTTGAGTCAAATTGTACTTTGCTCCATTGTTAATTGAGAAACTGTTTCAA NM_006389RefSeq chr11
- 119044184 119057246 HYOU1 10525 "hypoxia up-regulated 1, transcript variant 1"
GO:0005783|GO:0006950|GO:0005576|GO:0005524|GO:0006898|GO:0030968|GO:0016020|GO:0071682|GO:0002
931|GO:0005788|GO:0006987|GO:0005925|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_52381_PI430048170 0.6188268927891191.0139714232964 0.3000820688945880.320826840659397
0.397975600426977 A A A 0.3604568008533620.306152190898851 0.293192848922721 A A A
LNCV6_52381_PI430048170 mRNA
GGCATTTATGTAATCTACTCAAAGAAACCTGTGCTAGATCTGCAGAAAAGACAAAGAAAT NM_001282541 RefSeq
chr1 + 114854802 114995369 SYCP1 6847 "synaptonemal complex protein 1, transcript variant 2"
GO:0000802|GO:0000801|GO:0007283|GO:0003677|GO:0051878|GO:0032880|GO:0000711|GO:0051026|GO:0001
673|GO:0007130|GO:0035092|GO:0007131|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137749_PI430048170 0.6137169658477631.01552946783926 0.291024379673925
0.3255495385916360.410272622919425 A A A 0.3418665516020530.317910901203509
0.302725921805586 A A A LNCV6_137749_PI430048170 mRNA
CCTTGATCTATAGTTTACGAAACAAAGATGTAAAATATGCCCTACGAAGGACATGGAATA NM_001005202 RefSeq
chr11_JH159136v1_alt + 129055 129994 OR8K3 219473 "olfactory receptor, family 8, subfamily K, member 3
(gene/pseudogene)" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134590_PI430048170 0.0533585452414819 1.30368267546498 6.02994170769513
5.69222440714275 5.86171315824762 P P P 5.34091026121006 5.67758782602115
5.41527569336199 P P P LNCV6_134590_PI430048170 mRNA
ATTAAAAACCAACTTTCGACTTCTGAAAAGAAGGCTACGGGAGAGTCTCCAGTGAGGGGT NM_014508RefSeq chr22
+ 39014259 39018820 APOBEC3C 27350 "apolipoprotein B mRNA editing enzyme, catalytic polypeptide-
like 3C"
GO:0016814|GO:0005515|GO:0051607|GO:0005737|GO:0009972|GO:0045087|GO:0080111|GO:0016032|GO:0008
270|GO:0005634|GO:0010529|GO:0045071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143235_PI430048170 0.4898168721369631.09050586954705 7.16782522111779
7.17536641092608 7.30823632358743 P P P 6.79395259155391 7.04743678028694
7.37934847308052 P P P LNCV6_143235_PI430048170 mRNA
CACCAACTTGGGAACTGCTTGTCTCACGTTGCTTTGTTTTTTACAATAATAAAAGCATTA NM_001265597 RefSeq
chr19 + 57633166 57642779 ZNF211 10520 "zinc finger protein 211, transcript variant 3"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137957_PI430048170 0.0647906222120318 0.45010294411598711.2360378179314
10.2006915423996 10.1940208553172 P P P 11.866419920976 11.8351334499288
11.6386670675908 P P P LNCV6_137957_PI430048170 mRNA
CCCCTCCTCCACTTCTCTAATACCAGTGACAAGTATTATTAATAAAGAGCGTACATCTTC NM_031923RefSeq chr10
+ 7818503 8015053 TAF3 83860 "TAF3 RNA polymerase II, TATA box binding protein (TBP)-
associated factor, 140kDa"
GO:0005515|GO:0010467|GO:0006368|GO:0005669|GO:0006367|GO:0006366|GO:0005634|GO:0000122|GO:0043
433|GO:0002039|GO:0051457|GO:0016032|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA
NA NA NA

LNCV6_140987_PI430048170 0.5100168449498830.9641892913439981 2.3076913502227
12.3440442466593 12.24244605425 P P P 12.4628693326538 12.2555304840994
12.3277190777024 P P P LNCV6_140987_PI430048170 mRNA
TGAAGCACCCACCATGTTCTTGAACAATCAGGTTTCTAAATAAACAACTGGACCATCAAA NM_006812RefSeq chr12
+ 57693954 57721557 OS910956 "osteosarcoma amplified 9, endoplasmic reticulum lectin, transcript variant 1"
GO:0005515|GO:0000836|GO:0034976|GO:0016567|GO:0044322|GO:0006605|GO:0002020|GO:0030433|GO:0001948|GO:0042787|GO:0005788|GO:0030246|GO:0006621 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128691_PI430048170 0.0150742955731056 0.3101350016730690.4588437536668
0.8437449825619020.452306023294928A A A 1.67797264127339 2.45630405304836 2.5710531656158
A P P LNCV6_128691_PI430048170 mRNA
CAAGGGGTGGACTGTGGGATGCATGCCCTGGCAACATTGAAGTTCGATCATGGTAAAAAANM_003775RefSeq chr19
+ 3178737 3180332 S1PR4 8698 sphingosine-1-phosphate receptor 4
GO:0006955|GO:0007186|GO:0005886|GO:0005887|GO:0004930|GO:0003376|GO:0007202|GO:0007189|GO:0038036|GO:0007204|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142791_PI430048170 0.2088385622429310.9696963691096910.308442873745268
0.3527315707565910.328465328376627A A A 0.4204976729190210.337253257538099
0.364160201503159A A A LNCV6_142791_PI430048170 mRNA
TTGTTAGAAAATTCTGGCTGAAATTCTCATGAGATGGGTCAGGGAACCTTGGAGTGGCAG NM_173642RefSeq chr1
+ 42380796 42424229 RIMKLA 284716 ribosomal modification protein rimK-like family member A
GO:0005737|GO:0072590|GO:0005524|GO:0046872|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144626_PI430048170 0.1442503202098471.68093486726451 5.41105953673381
5.51534787236697 5.21610229693462 P P P 4.96448334915552 4.86819551224241
3.82868438206057 P P P LNCV6_144626_PI430048170 mRNA
GACGGAGGCAAGGACAAGACGAGTCCGAGCTCAATAAATGCGCTGTGCACCCTCAAAAAA NM_139284RefSeq chr19 - 35124512 35135274 LGI4 163175 "leucine-rich repeat LGI family, member 4"
GO:0008344|GO:0042551|GO:0022011|GO:0005615|GO:0014009 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141993_PI430048170 0.3609836312291241.12972592241114 9.01807083593825
8.88970812162152 9.35485296861656 P P P 8.88140751848255 8.91861447016454
8.97397057487068 P P P LNCV6_141993_PI430048170 mRNA
CTATGCATAGCCTAAGAGTTATAGGCTTAAAGATGTCGAGTAACTAAAAACTGTATTGCT NM_198486RefSeq chr6
+ 42879932 42886993 RPL7L1 285855 ribosomal protein L7-like 1 GO:0005840 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132146_PI430048170 0.0142213357813023 0.48271424518532 4.6688132376478
4.55293279268834 4.45215127771248 P P P 5.27521773563907 5.80461549601463
5.70177548832726 P P P LNCV6_132146_PI430048170 mRNA
GGGGATTGGATGAAAGTCAAAGGTTGTCTACTTTAAGAAAATAAAATACCCTGAATGGAG NM_002073RefSeq chr22
+ 23070482 23125034 GNAZ 2781 "guanine nucleotide binding protein (G protein), alpha z polypeptide"
GO:0005886|GO:0005783|GO:0005834|GO:0003924|GO:0005635|GO:0031683|GO:0005525|GO:0007193|GO:0046872|GO:0005829|GO:0035556|GO:0006184|GO:0007186|GO:0031821|GO:0007188|GO:0004871|GO:0005057|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61423_PI430048170 0.0758587920322386 1.05042690959756 0.432679034108799
0.4851672904687370.477305857000772A A A 0.3534933365840230.392981550810065
0.435147437697022A A A LNCV6_61423_PI430048170 mRNA
TCTTTTCTCTTTGGGTGATAGTCAGAGAGTGGTGTTTTTGTTCAGGTGGGAAGGATTGGA NM_153046RefSeq chr14
+ 103928479 104052667 TDRD9 122402 tudor domain containing 9

GO:0006396|GO:0010467|GO:0005634|GO:0007275|GO:0007283|GO:0031047|GO:0005524|GO:0030154|GO:0004
004|GO:0009566|GO:0034587|GO:0043186|GO:0071547|GO:0007140|GO:0043046 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137055_PI430048170 0.1258064347114351.24671630201689 0.61366098677398 1.0607239423935
0.80957606093278 A A A 0.6274868419985090.4566218368888380.474218659957439A A A
LNCV6_137055_PI430048170 mRNA
TCATACACATAGCAACATTATTGCAGAGGAATTATTGCCATTTAGGTAATAGAGCAATGG NM_033176RefSeq chr20
- 21395366 21397409 NKX2-4 NA NK2 homeobox 4 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_76035_PI430048170 0.0867737439278152 1.41468211930385 5.09555160530647 5.1840758055482
4.78290152382462 P P P 4.3691706322012 4.28706319771459 4.86485949285284 P P P
LNCV6_76035_PI430048170 mRNA
AATCATGATAACCCTGATCACTGAGCAGCTACAGAAGCAGACTCTGGATGAGCTGAAATG NM_001135647 RefSeq
chr5 + 138337534 138349729 FAM53C 51307 "family with sequence similarity 53, member C,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136770_PI430048170 0.3225920340176431.06185674457043 8.68956515621052 8.6106921888594
8.67521409477183 P P P 8.46210318424598 8.6971435938126 8.54780344423503 P P P
LNCV6_136770_PI430048170 mRNA
AAATGGGCATTTTACAAGAAGTACGAATCTTATTTTTCCTGTCCTGCCCGTGAGGGTGGG NM_004383RefSeq chr15
+ 74782083 74803198 CSK1445 "c-src tyrosine kinase, transcript variant 1"
GO:0005515|GO:0050852|GO:0008285|GO:0005886|GO:0048709|GO:0032715|GO:0031295|GO:0042997|GO:0001
817|GO:0045779|GO:0030154|GO:0042802|GO:0005829|GO:0050765|GO:0005737|GO:0007173|GO:0043406|GO:0
005911|GO:0042127|GO:0071375|GO:0070373|GO:0010989|GO:0070064|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128498_PI430048170 0.00266635194203495 0.60713905624808 5.92693093740246
6.15343343620362 6.14695235911126 P P P 6.80662254699433 6.869632232349
6.71807936189088 P P P LNCV6_128498_PI430048170 mRNA
ACACATGCCTTGATCATAGCACTTGCCTGCGCTTCTTCAGAGTCATTAATTTGCTTCTCG NM_001278251 RefSeq
chr11 - 65375191 65383701 SLC25A45 283130 "solute carrier family 25, member 45, transcript variant
4" GO:0005743|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129909_PI430048170 0.00445482726605012 2.28770630368719 9.70172416206693
9.88129460497424 9.56022263740263 P P P 8.21640919007296 8.62112554873894
8.69725893278822 P P P LNCV6_129909_PI430048170 mRNA
CTGGGTATGTGCCTACCGATGACAATGTGTAAATAAATGCGTGTTCACACCCACAAAAAA NM_006876RefSeq chr11
- 66345371 66347690 B4GAT1 11041 "beta-1,4-glucuronyltransferase 1"
GO:0005794|GO:0005975|GO:0030311|GO:0015020|GO:0044281|GO:0046872|GO:0035269|GO:0042339|GO:0030
173|GO:0008532|GO:0000139|GO:0018146|GO:0007411|GO:0009405|GO:0030203|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_94232_PI430048170 0.000255307657807211 3.63202822491446 6.61702951501677
6.89229271771254 6.60153439234017 P P P 4.83836623590296 4.95089333692686
4.75123535850356 P P P LNCV6_94232_PI430048170 mRNA
CGTTATCACCAGAGCTATCTGCTTCACTTCAAATGCTTATTAAATTTCAATCTGAGACTC NM_001007255 RefSeq
chr1 + 161098390 161100348 KLHDC9 126823 "kelch domain containing 9, transcript variant 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137905_PI430048170 0.489032660032271 1.1014298727351 8.89693610020922
8.51815879795918 8.42338151811106 P P P 8.5264654617454 8.59087094536256
8.33558337110264 P P P LNCV6_137905_PI430048170 mRNA
CCACCAAAGCAATCTCTAAGCTTATAAAGGAGAAACATATATATATGGGGTTTTTTGGAG NM_021259RefSeq chr16
- 370775 381950 TMEM8A 58986 transmembrane protein 8A

GO:0008150|GO:0003674|GO:0005887|GO:0007155|GO:0005765|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131530_PI430048170 0.396239503253149 1.04405840150818 0.294218291727595 0.27937117022385 0.45428224853489 A A A 0.302258777746952 0.256620393894612 0.288604896968291 A A A LNCV6_131530_PI430048170 mRNA TCCAGGCTTGATTTGGAGGGTGAATGACGCCTAGCAAGATGTATTGTACTTGTGTTTTTT NM_198999 RefSeq chr7 - 103374207 103446177 SLC26A5 NA "solute carrier family 26 (anion exchanger), member 5, transcript variant a" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131192_PI430048170 0.340925401498895 1.39095888342153 0.330942207196505 1.36946210972589 0.490143419810618 A A A 0.333021383257874 0.300738889406141 0.356359221574116 A A A LNCV6_131192_PI430048170 mRNA GCCTCTGCCGGGAACAGAGTGTTCATATGCTGTTAGAATTTTTTATTGTAAAATAAAATG NM_012194 RefSeq chr11 + 33542330 33674100 KIAA1549L 25758 KIAA1549-like GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132118_PI430048170 0.139796109054917 0.88208219862198 5.18002622546381 5.29873339288797 5.01626616327243 P P P 5.40046580441373 5.38633749885222 5.26108971539217 P P P LNCV6_132118_PI430048170 mRNA TGGGAGCACTGGACACTTAAATCCTCATCTGTCCTCCTTTCCTGTAAATAAAAGCCCTTC NM_013353 RefSeq chr1 - 151169986 151176071 TMOD4 29765 tropomodulin 4 (muscle) GO:0051015|GO:0006936|GO:0030239|GO:0005865|GO:0007015|GO:0005523|GO:0051694 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135996_PI430048170 0.000227788227856 5.12368599774137 4.23358209909716 4.67806842986649 4.37878684194403 P P P 2.29660340708463 2.0865615826015 1.83510645012608 A A A LNCV6_135996_PI430048170 mRNA AAGTGACTTTTTACAGAAGCCACTGAACCTGGTTATTTTGGCAAATCGTCCGTCTCGAGG NM_001284260 RefSeq chr7 - 151381120 151410038 WDR86 349136 "WD repeat domain 86, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142171_PI430048170 0.00728468811070953 1.18462663236235 10.8005505054529 10.6814873328083 10.744140347708 P P P 10.4709480957651 10.4874550293568 10.5361356494347 P P P LNCV6_142171_PI430048170 mRNA CGAGAGGTGTCATGAAGAAAGTTCTGTTCAATAAGGTTTTGGAATGTTTCCTTTCAAAAA NM_014306 RefSeq chr22 - 32387574 32412287 RTCB 51493 "RNA 2',3'-cyclic phosphate and 5'-OH ligase" GO:0006388|GO:0005737|GO:0017166|GO:0005634|GO:0003972|GO:0001890|GO:0005524|GO:0001701|GO:0072669|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73074_PI430048170 0.481706581714663 1.16377123385755 4.15730556572101 4.73980283779228 4.86821518862932 P P P 4.2184878726278 4.52204915604966 4.44596832394259 P P P LNCV6_73074_PI430048170 mRNA CTGGGAAGATTATCTAGAAGAAACAGGGTCCACAGCAGTTCCCTATGGGTCTTTTAAACA NM_016329 RefSeq chr3 - 52903566 53046073 SFMBT1 51460 Scm-like with four mbt domains 1 GO:0005515|GO:0048635|GO:0042393|GO:0003714|GO:0005654|GO:0005634|GO:0007283|GO:0045892|GO:0030154|GO:0006351|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133783_PI430048170 0.616671803460868 0.894420632219694 1.9150884417225 0.3960156874541 0.304356931942891 A A A 1.42820493678768 1.46370545214882 0.695197587926926 A A A LNCV6_133783_PI430048170 mRNA TCCAGAAGTGCAGCCACTATCTATTCTCTGAAGAAATCACTTCTGGCTGTCAGTTGCAAA NM_000206 RefSeq chrX - 71107405 71111631 IL2RG 3561 "interleukin 2 receptor, gamma" GO:0005515|GO:0004911|GO:0004913|GO:0005886|GO:0004917|GO:0019982|GO:0019976|GO:0007165|GO:0006955|GO:0016020|GO:0005887|GO:0038111|GO:0016032|GO:0038110|GO:0035771|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_142513_PI430048170 0.3653244909707871.01301951355848 0.328206755840966
0.3024491630609520.273106625457062A A A 0.286392046456351 0.286713237483774
0.275168040103897A A A LNCV6_142513_PI430048170 mRNA
GCACTACACATGATCCTTCTGTGCTTGCTTGCATCTTTAATAAAGACATGTTCCCGGCGT NM_014351RefSeq chr22
- 43824506 43862498 SULT4A1 25830 "sulfotransferase family 4A, member 1"
GO:0005515|GO:0008150|GO:0006805|GO:0050427|GO:0008146|GO:0044281|GO:0008202|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132237_PI430048170 0.5771885342725160.95662126319690412.465963754412
12.2962226941315 12.5438776568125 P P P 12.3880952497802 12.465963754412
12.6429973051937 P P P LNCV6_132237_PI430048170 mRNA
GGGTAGCTATTAAGGTACTAGAATTGATAAATGTGTACAACAGGGTCCTTTTGCAATAAA NM_001013699 RefSeq
chr12 - 31791184 31792241 H3F3C 440093 "H3 histone, family 3C"
GO:0046982|GO:0030307|GO:0005719|GO:0031492|GO:0000786 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140226_PI430048170 0.4673390890872940.8426032464944175.40327283585236
4.64674244182306 4.4042869985017 P P P 5.26579717474848 5.31958626411466
4.73749839125203 P P P LNCV6_140226_PI430048170 mRNA
CCCGCCTTCCTGCCAAGCCGAGGGCGACGGTGATCCCCAGCTTAGTAAGAAAAGTAAATA NM_024886RefSeq chr10
- 102449836 102451543 C10orf95 79946 chromosome 10 open reading frame 95 GO:0005515 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141162_PI430048170 0.0195748602841404 0.2079445400191980.621360800796745
1.0209622543261 2.00847009638895 A A A 3.30156599138325 3.73274386830706
3.73892182411999 P P P LNCV6_141162_PI430048170 mRNA
GGCAGGGAAAAACTAGTTTTGAGTGTCTTTAGATAGAAACATGAGACTAAGGTTTGATTT NM_014155RefSeq chr11
- 130226678 130314712 ZBTB44 29068 "zinc finger and BTB domain containing 44, transcript variant 3"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_64157_PI430048170 0.3280133263885361.06144664824548 9.06187531647382 8.96911666536228
8.93731452207383 P P P 9.02834081238841 8.87188830090508 8.80362033940976 P P P
LNCV6_64157_PI430048170 mRNA
GTATAGCAGCCTGGCCCTGGTCACCTCCTGGCTCTTCATCCAGCATTCCATGATCTACTT NM_001033026 RefSeq
chr19 - 1009650 1021142 TMEM259 91304 "transmembrane protein 259, transcript variant 1"
GO:0005737|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128487_PI430048170 0.00254936819981135 0.2599098171808776.88730038043577
6.70440410524571 6.9306387894539 P P P 8.4747901701698 8.80223183695747
9.03313034888382 P P P LNCV6_128487_PI430048170 mRNA
CAGATTTGTACAAGTATTGGATGATTCCTTGAGTTTACAGCTGTACAAATAGTGTGGAAA NM_002508RefSeq chr1
- 235975831 236065181 NID1 4811 nidogen 1
GO:0005509|GO:0005518|GO:0010811|GO:0005605|GO:0043394|GO:0005576|GO:0032836|GO:0071944|GO:0005
604|GO:0031012|GO:0007160|GO:0022617|GO:0030198|GO:0043237|GO:0043236|GO:0071711|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128402_PI430048170 0.00150634298834677 2.15770978749395 12.7928953345072
13.1318246806962 12.9385195756477 P P P 11.9660483939029 11.8229775854584
11.7579130408239 P P P LNCV6_128402_PI430048170 mRNA
CAACCCTGACCGTGACCGTTTGCTATATTCCTTTTTCTATGAAATAATGTGAATGATAAT NM_005953RefSeq chr16
+ 56608565 56609497 MT2A 4502 metallothionein 2A
GO:0071294|GO:0005515|GO:0048471|GO:0019221|GO:0005634|GO:0035690|GO:0036016|GO:0005829|GO:0036
018|GO:0005737|GO:0006878|GO:0008144|GO:0008270|GO:0045926|GO:0060333 . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_132608_PI430048170 0.6815861354075631.05260726153015 4.82304592595482
4.71152895458548 4.44765126338291 P P P 4.76458227097045 4.66875916537464
4.31439587244964 P P P LNCV6_132608_PI430048170 mRNA
TGGTTGTCCAGGCTCTGCAGAGCGCAGCAGGGCTTTTCATTAAAGGTATTTATATTTGTA NM_198443RefSeq chr16
+ 67884877 67886368 NRN1L 123904 neuritin 1-like GO:0005886|GO:0031225|GO:0007399 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134691_PI430048170 0.0647823666930328 1.18824918816833 0.852313851081167
0.6403637987908020.613640558138859A A A 0.34674265984564 0.468690179348337
0.549246443916948A A A LNCV6_134691_PI430048170 mRNA
ACTGGAGGTCACAGTTATTTATTGATCACAATTGTGGACATTAAAACAGAAACTGTTCAC NM_145270RefSeq chr16
+ 560421 565529 PRR35 146325 proline rich 35 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134029_PI430048170 0.1175372364277011.04741422312373 0.377763354867906
0.3861842632808320.462265783467283A A A 0.3282274594371360.321968470547586
0.376414307519166A A A LNCV6_134029_PI430048170 mRNA
CCAGATGCAACTACAATGGATTTTACTAGTTTGGTGTGTCAGTATTTCTTTGACTCATTA NM_002077RefSeq chr9
- 124878293 124941107 GOLGA1 2800 golgin A1
GO:0005802|GO:0048471|GO:0005794|GO:0032580|GO:0043231|GO:0000042 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142851_PI430048170 0.9066231594325231.01425822731515 4.06886037762411
4.43753725738141 3.59226825362805 P P P 4.47116187584771 4.12467511768165
3.34736652825091 P P P LNCV6_142851_PI430048170 mRNA
TCTCAAATGTTACCTACTAAGGGATGCCTGGGTAAGCCACTCAGCTACCTAATTCCTCAA NM_020056RefSeq chr6
+ 32741385 32746887 HLA-DQA2 3118 "major histocompatibility complex, class II, DQ alpha 2"
GO:0050852|GO:0012507|GO:0005886|GO:0019221|GO:0031295|GO:0042613|GO:0005765|GO:0032588|GO:0030
666|GO:0019886|GO:0006955|GO:0000139|GO:0005887|GO:0071556|GO:0032395|GO:0030669|GO:0010008|GO:0
060333|GO:0030658. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130530_PI430048170 0.0416515229482387 1.71162895249907 5.06012572933985
4.94781403402946 5.05814220992766 P P P 4.03215992543383 4.06085081946965
4.58118511273593 P P P LNCV6_130530_PI430048170 mRNA
CCTGGGTTTGTTTTCCTTGGGGTGGTGTAGATTGTATGAGTAAGAAGTATTAATTTTTTA NM_130439RefSeq chr10
+ 110207604 110287365 MXI1 4601 "MAX interactor 1, dimerization protein, transcript variant 2"
GO:0005737|GO:0008285|GO:0003714|GO:0046983|GO:0005730|GO:0042994|GO:0005634|GO:0000122|GO:0003
677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116377_PI430048170 0.0883350873314437 0.631192891062722 4.12628156443201
3.49836617212979 4.24182658515938 P P P 4.37525749936862 4.52266658008302
4.99129689282457 P P P LNCV6_116377_PI430048170 mRNA
GAAGATTTGTCATTTAAAAGAGTATTCTCTGGCTGTATTTCCAGCAGTTATGAACTTGAG NM_013320RefSeq chr12
+ 104064457 104106526 HCFC2 29915 host cell factor C2
GO:0005737|GO:0006357|GO:0005886|GO:0003713|GO:0016032|GO:0005654|GO:0005634|GO:0000122 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137253_PI430048170 0.00385024777464495 0.309731711393685 2.09865210498467
1.6328185839859 2.35525406182495 A A A 3.39650239900015 3.97913987697432
3.81355461687172 P P P LNCV6_137253_PI430048170 mRNA
TCACTTAGCACAGATTTGTAATTATGCATGTAATAAAGCACAGCCTTATCCACCCTGAAA NM_001127899 RefSeq
chrX + 49922614 50099235 CLCN5 1184 "chloride channel, voltage-sensitive 5, transcript variant 1"
GO:0007588|GO:0005247|GO:0045177|GO:0005765|GO:0055085|GO:0005254|GO:0005524|GO:0006897|GO:0044
070|GO:0015297|GO:0034220|GO:0000139|GO:0016020|GO:0005887|GO:0006810|GO:0010008 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140547_PI430048170 0.1465781233531890.7827860815970851 2.0745004189693

11.9706859804657 11.5277784320189 P P P 12.103992862598 12.2435566774042
12.3325233804524 P P P LNCV6_140547_PI430048170 mRNA
GCTTGACCTGCGGGTGCTTTGCCTTAAAAAGAAATAAAAGATGTGAACTTGGGCAAGTTA NM_004819RefSeq chr19
- 45815441 45863290 SYMPK 8189 symplekin
GO:0005515|GO:0006378|GO:0005737|GO:0005886|GO:0035307|GO:0005654|GO:0005923|GO:0007155|GO:0005
856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137420_PI430048170 0.9168031149021391.00950974352493 0.289252559181807
0.5758644512480520.403669112072958A A A 0.53121292309594 0.399750243548368
0.302181731239582A A A LNCV6_137420_PI430048170 mRNA
GGGACTTTCCAGTTGAAAAGAAAACATGCTATGTCATTTTTATCCATTATCCCTGGAACT NM_139319RefSeq chr12
+ 100357078 100422059 SLC17A8 246213 "solute carrier family 17 (vesicular glutamate transporter),
member 8, transcript variant 1"
GO:0043005|GO:0030054|GO:0007605|GO:0005313|GO:0006836|GO:0030672|GO:0016021|GO:0006814|GO:0055
085|GO:0015293|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130549_PI430048170 0.3765592948445181.06656603323619 0.516523195581429
0.2823634226858210.27918809747079 A A A 0.2726446984239660.271313017172699
0.268259371096101A A A LNCV6_130549_PI430048170 mRNA
GGATACAGAGATGCCAATTGAAAGCAGAAAGTTCTACTCTCGTATCTGTTTTTTATCTTA NM_031891RefSeq chr18
+ 61490541 61555132 CDH20 28316 "cadherin 20, type 2"
GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130532_PI430048170 0.0234385693450358 0.74846928562438410.8458500263966
10.7368220219594 10.9112195682424 P P P 11.0744301736165 11.297204029085
11.3657524011342 P P P LNCV6_130532_PI430048170 mRNA
CGGCCTAACCTTAGAACACATTTGTAACTGAATACAGTGTTTTCAATTTGTACAGAATAG NM_005969RefSeq
chr11_KI270831v1_alt - 175477 223447 NAP1L44676 nucleosome assembly protein 1-like 4
GO:0005515|GO:0005737|GO:0006334|GO:0005634|GO:0051082 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137474_PI430048170 0.0102458767043590.9552036409901650.322646551217248
0.3548056349204650.345363595958001A A A 0.4052468653944180.389482927436843
0.426396447736243A A A LNCV6_137474_PI430048170 mRNA
GAAGCTTTCAGATAAGTTTAGGCTATTCAACTTTTCTAAAGAGATGGTTGGTTCACCTAA NM_031913RefSeq chr3
+ 138434572 138478414 ESYT3 83850 extended synaptotagmin-like protein 3
GO:0005515|GO:0005543|GO:0005887|GO:0006869|GO:0044232|GO:0031227|GO:0046872|GO:0031234 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143638_PI430048170 0.0401730792753209 0.78088875964020310.6287099644256
10.5418832667296 10.6718111229096 P P P 10.9822583779929 10.8079587363796
11.1098239086301 P P P LNCV6_143638_PI430048170 mRNA
GAAAACACGCTGTATACCTAGATGATGACTAAATGCAAAATCCTTGGGCTTTGGTTTTTT NM_024334RefSeq chr3
+ 14124939 14143680 TMEM43 79188 transmembrane protein 43
GO:0005515|GO:0005794|GO:0005788|GO:0043621|GO:0071763|GO:0005639 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144418_PI430048170 0.00627469712935242 0.5392937303771135.04704914821076
4.72026104259697 5.13575353662299 P P P 5.65684989811478 5.89226079697337
6.03400524825649 P P P LNCV6_144418_PI430048170 mRNA
GGTTTTCACTGCTTCTATTTTTCTACTGTTACTGATAAGCATGTAACACTGACTTTATCC NM_001002860 RefSeq
chr14_KI270847v1_alt - 352111 447654 BTBD7 55727 "BTB (POZ) domain containing 7, transcript variant
1" GO:0060693|GO:0007275|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126821_PI430048170 0.0107181995950967 0.5497806897167068.78862204106865
8.65158931190706 8.87505596434944 P P P 9.37458098417089 9.68737644167602

9.81628409847424 P P P LNCV6_126821_PI430048170 mRNA
CCATGGTATTACTTGCTAAATGCACTGATTTCATAAGTATGTGGAATCCTTTTCCTTTTG NM_001256798 RefSeq chr20
- 32443058 32585073 NOL4L 140688 "nucleolar protein 4-like, transcript variant 1"
GO:0005737|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126941_PI430048170 0.49591988625891 1.0451991393898 0.281549814238981
0.2931811732430970.505088757965589A A A 0.3179974991338990.276859105303391
0.30447648291159 A A A LNCV6_126941_PI430048170 mRNA
CTGTGTTGGTGCTCAATGCAGTGTAGACATGTTTTCAAATAAAACAAATGATTGTGTACA NM_006474RefSeq chr1
+ 13583756 13617957 PDPN 10630 "podoplanin, transcript variant 1"
GO:0006693|GO:0005886|GO:0030324|GO:0008283|GO:0008360|GO:0015884|GO:0031527|GO:0006865|GO:0031
528|GO:0006928|GO:0030175|GO:2000045|GO:0001946|GO:0016324|GO:0016337|GO:0006954|GO:0015171|GO:0
010572|GO:0015250|GO:0005372|GO:0006833|GO:0030335|GO:0048286|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_73980_PI430048170 0.0567398867370291 0.80274466599522 8.54024759613176
8.71405629465787 8.48506926231515 P P P 8.71636998138348 9.02418663508379
8.94245297445203 P P P LNCV6_73980_PI430048170 mRNA
GTTGGTTTCTAAAATAAAGCCAAACAAGCCAGCACATGCAGAGGCTTGGACCCTGATAGA NM_005929RefSeq chr3
- 197001740 197029816 MFI2 4241 "antigen p97 (melanoma associated) identified by monoclonal
antibodies 133.2 and 96.5, transcript variant 1"
GO:0005515|GO:0005506|GO:0009986|GO:0001558|GO:0008199|GO:0006879|GO:0097286|GO:0005887|GO:0010
756|GO:0042127|GO:1900025|GO:0090091|GO:0046658|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144370_PI430048170 0.0320981859566674 1.49354738636866 8.01508986340842
7.91733378613232 7.87776530954433 P P P 7.25782435691225 7.59476823131327
7.1916896336479 P P P LNCV6_144370_PI430048170 mRNA
TGAAGGGCTTTCTCACCCCAGCTCTGGCTATGCCCAGTTCTCTGAGAAAGGAGCTCAGTG NM_002461 RefSeq
chr16 - 88651939 88663149 MVD 4597 mevalonate (diphospho) decarboxylase
GO:0006695|GO:0008284|GO:0019287|GO:0044281|GO:0008299|GO:0005524|GO:0042803|GO:0005829|GO:0004
163|GO:0030544|GO:0006488|GO:0044267|GO:0006489|GO:0043687|GO:0005777|GO:0018279 . NA - .
NA NA NA NA NA NA NA NA
LNCV6_134593_PI430048170 0.00492717994052389 1.92590683722698 7.09561908051477
7.2964106016202 7.01384804353633 P P P 6.19592763752175 6.23486576757545
6.15211057585724 P P P LNCV6_134593_PI430048170 mRNA
GTTGGGCTAGATTACAGAGGGCTCATTTTCTACGTCATGTATTTTATGATACTTGAATTT NM_001282669 RefSeq
chr1 + 3857266 3885429 DFFB 1677 "DNA fragmentation factor, 40kDa, beta polypeptide (caspase-
activated DNase), transcript variant 1"
GO:0004536|GO:0000790|GO:0006309|GO:0030263|GO:0005730|GO:0006915|GO:0005654|GO:0005634|GO:0019
899|GO:0006921|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141912_PI430048170 0.0260813772329982 1.2608433522528 6.64251862442366
6.5387456706206 6.38729682024161 P P P 6.28549645336447 6.14000066658155
6.14651484466834 P P P LNCV6_141912_PI430048170 mRNA
GCCGTTACTATTTTCTAAGAAATGACTTTTCTGTGAACCAACAGTAACAAAAACCTCAGT NM_012166 RefSeq
chr9 - 37510891 37576253 FBXO10 26267 F-box protein 10
GO:0005515|GO:0005737|GO:0004842|GO:0016567|GO:0042787|GO:0006915|GO:0000151|GO:0042981 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_138873_PI430048170 0.534543069851202 0.91073111272707 4.98585559558996
4.82176947586631 4.29622623949371 P P P 4.91398903681778 4.96605987079955
4.70131219229151 P P P LNCV6_138873_PI430048170 mRNA
TGGTCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGG NM_001001923 RefSeq

chr9 + 122788932 122789895 OR5C1 NA "olfactory receptor, family 5, subfamily C, member 1" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131441_PI430048170 0.171784033406137 0.974482956054962 0.299929457851194
0.336787452673226 0.359395973999494 A A A 0.393861150457015 0.368881749122609
0.345460758691988 A A A LNCV6_131441_PI430048170 mRNA
TTTTTTACAGTGACATCTCATCAGCTCCCTATTGTCAAGAAGTAGCTCCAAAGTCTTTGA NM_080740 RefSeq
chr22_KI270875v1_alt - 149393 155938 ZNF280A 129025 zinc finger protein 280A
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_109052_PI430048170 0.114950051700019 0.56013002603388 2.43930140950178
1.54628091917245 1.21563148954223 A A A 2.77767395112736 2.24805724892205
2.89445579138177 P A P LNCV6_109052_PI430048170 mRNA
ATGGAAAAGACTGTTATGAAGCCAGATGAACCTTTCTCCAGTCTTCCTTCACTATTTTTT NM_001085384 RefSeq
chr19 - 57696274 57709211 ZNF154 7710 "zinc finger protein 154, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145017_PI430048170 0.1804880976055830.9645688034532970.391029689466075
0.4126402742897080.3235826767617 A A A 0.4212391008859170.44751960094906
0.415915472678936A A A LNCV6_145017_PI430048170 mRNA
GCAATAAGTAAATATGTACTGGTTGAATGCCTCTGGAGACCTAGAGTTTAAAGTTTTAAG NM_178470RefSeq chrX
- 126549382 126552859 DCAF12L1 139170 DDB1 and CUL4 associated factor 12-like 1
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132378_PI430048170 0.921109197785635 1.3661559413766 0.408049862631064
3.81148027854533 2.2347970233233 A P A 2.12530052340439 2.00187020319665
2.66120590289321 A A P LNCV6_132378_PI430048170 mRNA
TTGTCTGCGCCTGAAAAGGGCGGAAGAGTTACAATAAAGTTTACAAGCGAGAACCCGAAA NM_024016RefSeq
chr17 - 48612345 48614939 HOXB8 3218 homeobox B8
GO:0043565|GO:0008344|GO:0006355|GO:0003700|GO:0045638|GO:0048704|GO:0005634|GO:0007625|GO:0009
952|GO:0021516|GO:0019233|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98753_PI430048170 0.547725922009885 1.26735553801975 1.37192058291696 0.410035309150657
0.244927336334241 A A A 0.368035968724746 0.499914242108435 0.401523980621273 A A A
LNCV6_98753_PI430048170 mRNA
TGCTGCTGGCAACCATGATTCTAGTGGACATTTTCCAGTGAAGGCTGAAGTGTTAGACAT NM_001130016 RefSeq
chr4 + 76074694 76112802 ART3 419 "ADP-ribosyltransferase 3, transcript variant 1"
GO:0006471|GO:0005887|GO:0003956|GO:0031225|GO:0070062|GO:0003950 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136914_PI430048170 0.976233230969872 0.984944577153548 2.22489939770832
0.570395409375039 1.13458271836866 A A A 2.18446502373923 1.36336949830179
0.44841785808534 A A A LNCV6_136914_PI430048170 mRNA
AGCTTAAGAAACAAAGATGTAAAAGACGCCTTCAGAAAGGTCGCTAGGAGACTCCAGGTG NM_001005211
RefSeq chr11 - 58118499 58119444 OR9I1 NA "olfactory receptor, family 9, subfamily I, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145484_PI430048170 0.841118494019017 1.12979037540282 1.35539766131724
2.26680372802435 0.284907109487604 A A A 2.14026124288403 0.995870271391794
0.263147332375844 A A A LNCV6_145484_PI430048170 mRNA
TTCCTGCTTCTCTAGGCAAGGTCCCGTCATAGCAATTATATTTATTATCCCTTGAAAAAA NM_002529RefSeq chr1
+ 156860878 156881850 NTRK1 4914 "neurotrophic tyrosine kinase, receptor, type 1, transcript variant 2"
GO:0005515|GO:0021553|GO:0010465|GO:0046579|GO:0048678|GO:0042803|GO:0043068|GO:0043524|GO:0060
009|GO:0046777|GO:0007411|GO:0051602|GO:0007611|GO:0043025|GO:0031667|GO:0070374|GO:0005166|GO:0

048406|GO:0009986|GO:0051968|GO:0007568|GO:0018108|GO:0071316|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131855_PI430048170 0.0171845017450007 1.56782463262967 6.69986141446842 6.98821359454825 6.60947692587375 P P P 6.30792148320725 6.14465447040882 5.89696618255921 P P P LNCV6_131855_PI430048170 mRNA AATAATAAAAAAGTTTTGGCTTTTTTCTTTAGAAACCGGCCACCTGCTTCCCCCGCGGGG NM_021025RefSeq chr5 + 171309283 171312134 TLX3 30012 T-cell leukemia homeobox 3
GO:0043565|GO:0005515|GO:0006355|GO:0002087|GO:0045665|GO:0007585|GO:0048665|GO:0005634|GO:0007417|GO:0001764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100286_PI430048170 0.00727248679088634 0.32572466924624 3.8428256734536 3.08616584133688 3.54531482929314 P P P 4.66065057404748 5.43984351399932 5.21979026226569 P P P LNCV6_100286_PI430048170 mRNA CATCCTCAGAGGTGTGCCTCTTTTCTTTATTATTAGAGGCAAAACGAACAATTTTATAGG NM_005414RefSeq chr3 + 170357684 170396849 SKIL 6498 "SKI-like proto-oncogene, transcript variant 1"
GO:0005515|GO:0010467|GO:0006367|GO:0070306|GO:0046332|GO:0005634|GO:0007283|GO:0032403|GO:0070208|GO:0070207|GO:0005737|GO:0007050|GO:0007179|GO:0034097|GO:0046677|GO:0002260|GO:0030512|GO:0001669|GO:0003714|GO:0019904|GO:0001825|GO:0042981|GO:0000122|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141074_PI430048170 0.000102272562151624 0.658076269853221 9.16597397549795 9.14695088307942 9.20363765499165 P P P 9.76046201322104 9.74177299293461 9.82461104147081 P P P LNCV6_141074_PI430048170 mRNA CCAGTGTATCATTGTTTTACTGCCCTTGTAGTACTGGAATTTAGTTGGAAGAATAAAACA NM_018064RefSeq chr6 - 87674859 87702267 AKIRIN255122 akirin 2
GO:0032755|GO:0008284|GO:0045944|GO:0045087|GO:0017053|GO:0010950|GO:0032496|GO:0005634|GO:0009790|GO:0000122|GO:0019899|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76381_PI430048170 0.139562608451273 0.868554737125204 11.1050457319613 10.8461908423238 10.8130325321556 P P P 11.0897394546446 11.2246306052031 11.0730545711321 P P P LNCV6_76381_PI430048170 mRNA AAGCTCTTCAACACGTCTGTGGAGGTGCTGCCCTTCGACAACCCTCAGTCAGACAAGGAG NM_054013RefSeq chr5 - 179797597 179802875 MGAT4B 11282 "mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B, transcript variant 2"
GO:0000139|GO:0006491|GO:0016021|GO:0044267|GO:0046872|GO:0043687|GO:0018279|GO:0008454 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144243_PI430048170 0.0337261604648183 1.72770878357695 10.4442065101475 10.4098715776108 10.2534686047128 P P P 9.24974595024404 9.85843000553573 9.57611400439067 P P P LNCV6_144243_PI430048170 mRNA TAGTAGCTTCAAACTGGAAATAGCGAAATAAAATAACTCAGTCTGCAGCCCCAGAAAAAA NM_003088RefSeq chr7 + 5592804 5606656 FSCN1 6624 fascin actin-bundling protein 1
GO:0005515|GO:0001725|GO:0030036|GO:0030054|GO:0008283|GO:0003779|GO:0030175|GO:0015629|GO:0005829|GO:0005737|GO:0051015|GO:0016477|GO:0048870|GO:0008144|GO:0071437|GO:0030674|GO:0051017|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141078_PI430048170 0.158569366622247 0.754772248364258 3.83561270275532 3.34967102048289 3.15304396498428 P P P 3.74665763180474 3.78631406785314 4.08633469365156 P P P LNCV6_141078_PI430048170 mRNA ACTGGAGACGCAAGAACAAAAAGAACCAAGTAGAGAGAGTGGAGCTGCTTTATTGCCCTT NM_002566RefSeq chr19 + 10111520 10115388 P2RY11 NA "purinergic receptor P2Y, G-protein coupled, 11" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143772_PI430048170 0.563902669968898 0.899036674917733 6.16535119493171 6.329851728277 6.2255524533063 P P P 5.99992444438284 6.62099362598161 6.49371091904197 P P P

LNCV6_143772_PI430048170 mRNA
TTTTGACAGATGGCGGGACGGAAATGCAATAGACCAGCCTGCAAGAAAGACATGTGTTTT NM_207380 RefSeq chr15
- 40331451 40340967 C15orf52 388115 chromosome 15 open reading frame 52 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_135711_PI430048170 0.904116106585086 0.780264099763237 2.53080081359776
1.44785880456756 2.13913465008296 A A A 0.752625721641912 2.44657817526184
3.23451363420512 A A P LNCV6_135711_PI430048170 mRNA
GTAATCCTACATTCATGTATTCATTGGCAGTACGGAGTAATAAATGCAGCAATGTCATAA NM_001172435 RefSeq
chr2 + 135052264 135170709 RAB3GAP1 22930 "RAB3 GTPase activating protein subunit 1 (catalytic),
transcript variant 1"
GO:0017112|GO:0017137|GO:0071782|GO:0060079|GO:0032851|GO:0021854|GO:0034389|GO:0043087|GO:0043
234|GO:0005737|GO:0097051|GO:0060325|GO:0007420|GO:0033126|GO:0043010|GO:0048172|GO:0005097|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142113_PI430048170 0.139374854943560 0.631129456991845 11.4841421601701
10.9687175457957 10.7247453308276 P P P 12.1186180951701 11.8120618237729
11.2002342035716 P P P LNCV6_142113_PI430048170 mRNA
TGATCTCCCTCCCTACTTATGTATCTTAGTTCTGCAGTTCAGAGTGAAGGTTGGGGGTTA NM_001093730 RefSeq
chr2 - 206651620 206718396 DYTN NA dystrotelin NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139160_PI430048170 0.219940578207038 0.794226417640933 0.48153575421196
0.437233244016423 0.314258740248205 A A A 0.365042048802926 0.870145314608673
0.935483635368554 A A A LNCV6_139160_PI430048170 mRNA
AAGCCAACTGTTACTTGATTCTGCTTTTAGTTCTTAAGAGGATCAGGCTTTTAAATACTC NM_018298 RefSeq chr1
- 85018081 85048540 MCOLN3 55283 "mucolipin 3, transcript variant 1"
GO:0005737|GO:0034220|GO:0042491|GO:0005886|GO:0070588|GO:0007626|GO:0016021|GO:0055085 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134773_PI430048170 0.259974368525721 0.522594536954702 0.424808889075091
1.20568819554768 2.00483321887435 A A A 1.78172074431348 3.08956772462134
1.43895646286778 A P A LNCV6_134773_PI430048170 mRNA
CTGATAATTTGTCTCTCAGCTCCTGGGTATCATCTTCTTCCAGTTTTCCTGGGTTTCAGC NM_001077653 RefSeq chr7
- 35202429 35254100 TBX20 57057 "T-box 20, transcript variant 1"
GO:0060045|GO:0035922|GO:0060577|GO:0010991|GO:0003700|GO:0003180|GO:0008283|GO:0008015|GO:0003
215|GO:0005634|GO:0009953|GO:0003143|GO:0001947|GO:0005737|GO:0006936|GO:0045944|GO:0001085|GO:0
048370|GO:0055008|GO:0021524|GO:0001102|GO:0003279|GO:0001706|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_57967_PI430048170 0.376586295993135 0.482533903469412 1.93531521961196 0.632529583343399
0.582393339411714 A A A 2.97423805202511 0.502506365890007 2.31233834249494 P A A
LNCV6_57967_PI430048170 mRNA
ATCCAAAAGCGTTTCTTCCCCTTTCTACGTGTGCACTAAATTCTAAAACAAAAATTGGAA NM_001286059 RefSeq
chr11 - 82973132 83034569 RAB30 27314 "RAB30, member RAS oncogene family, transcript variant 1"
GO:0005802|GO:0005801|GO:0005795|GO:0003924|GO:0031985|GO:0005525|GO:0034389|GO:0006886|GO:0005
737|GO:0016020|GO:0008152|GO:0007030|GO:0032482|GO:0019003 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143515_PI430048170 0.00179254613751221 1.67156076460193 5.26202034336386
5.2576359397611 5.03723870683218 P P P 4.4961570154259 4.5219315215072
4.31804575311483 P P P LNCV6_143515_PI430048170 mRNA
AATTACTGGCTGATTCAGTATCAACGGCTTTTGAACCAGAAGCCCTTGTCCTTGAAGCTG NM_138361 RefSeq chr9
+ 127451485 127503501 LRSAM1 90678 "leucine rich repeat and sterile alpha motif containing 1,
transcript variant 1"

GO:0000209|GO:0005515|GO:0070086|GO:0004842|GO:0016874|GO:0005576|GO:0046755|GO:0051865|GO:0030163|GO:0005737|GO:0005179|GO:0016020|GO:0045806|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139324_PI430048170 0.151120906594225 1.16757130630422 7.01860079451794 7.03051559473644 6.91996093703164 P P P 6.92839705250706 6.78460213101334 6.56510626835963 P P P LNCV6_139324_PI430048170 mRNA
GACGTGATTTTTCCATGCAGCATCTGGTGTGAATAAAACAGCAGTTGACTGATGTTTAAA NM_138430 RefSeq chr13 - 113421939 113453524 ADPRHL1 113622 "ADP-ribosylhydrolase like 1, transcript variant 1"
GO:0003875|GO:0000287|GO:0051725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130248_PI430048170 0.225366868209862 0.880755278669502 0.348575259399153 0.325778755935122 0.303473115753288 A A A 0.703545196240113 0.428180633595302 0.373935840137837 A A A LNCV6_130248_PI430048170 mRNA
GGCTTCGTTGTGTTAACAAGTTGACACCATGACTAGTAAATGTAAACGTGTATGTATAAA NM_018215 RefSeq chr19 - 46466490 46471563 PNMAL1 55228 "paraneoplastic Ma antigen family-like 1, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75443_PI430048170 0.905430449710399 1.11573847806483 1.81148788242477 1.50592623468718 0.288471354780479 A A A 1.61944799171348 0.953158313560815 0.829742419019498 A A A LNCV6_75443_PI430048170 mRNA
TCTTTCAAGACTTTAATCTGATCTTGTGTCTTAGAGAAGCCCCCATACCTGGTAGAGCAT NM_198449 RefSeq chr5 - 50396196 50441400 EMB 133418 embigin
GO:0030054|GO:0035879|GO:0005887|GO:0045202|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59336_PI430048170 0.0394302710015495 0.540821734699222 4.43557270298137 4.62851426777492 5.21634071517677 P P P 5.4054485244808 5.80205587859214 5.81536292821037 P P P LNCV6_59336_PI430048170 mRNA
CATGCTTCAGAAATATTGTTGCTTAGGGTGATTTGGGCAGCTAAATAGTAAGTACTTTTT NM_172240 RefSeq chr12 - 89419720 89526262 POC1B 282809 "POC1 centriolar protein B, transcript variant 1"
GO:0005515|GO:0042384|GO:0005813|GO:0000922|GO:0008283|GO:0005814|GO:0001895|GO:0036064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138595_PI430048170 0.285631861964657 0.938954521144531 15.1252748880393 15.043342411377 15.0592755863794 P P P 15.2726288130715 15.1620262682438 15.0592755863794 P P P LNCV6_138595_PI430048170 mRNA
TGTTACCTCCTTCAGTTGATAATAAACCTTTCTGAGATGCAGAGGGTCCAGGTCAAAAAA NM_001085365 RefSeq chr2 - 131483959 131492491 MZT2A NA mitotic spindle organizing protein 2A NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135428_PI430048170 0.800564365755949 0.991203153256746 0.269009500429874 0.273875857129076 0.41416846467175 A A A 0.360358844770027 0.30362285878416 0.335514869535459 A A A LNCV6_135428_PI430048170 mRNA
TTACATCTGTGGAGTCCTGATCCATGCTCTGATCAACCACTACTCAATCAGGACAAATCG NM_001278392 RefSeq chr19 + 51478642 51490605 CEACAM18 NA carcinoembryonic antigen-related cell adhesion molecule 18 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_41273_PI430048170 0.501096599293376 0.937335986462427 6.01156749747828 5.60355251469276 5.6600398799889 P P P 5.824984402351 5.85064909289642 5.91291990587569 P P P LNCV6_41273_PI430048170 mRNA
TAGACAGAGAATCCTCTCATGATGAATGTCAGGATGCTCTAAACATTCTCCCAGTCCCTG NM_015383 RefSeq chr1 - 148531384 148595717 NBPF14 25832 "neuroblastoma breakpoint family, member 14" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138899_PI430048170 0.526515369719782 1.06120106705995 5.76834301250376 5.54340205158035 5.47988489940425 P P P 5.51856430311595 5.65896091812075

5.35745300653742 P P P LNCV6_138899_PI430048170 mRNA
GCCTGCGCAGAGATTGGCTGTGGGCCTCAGTTTCCCCATTTTATAAAGTTTTAAAATCTG NM_176871 RefSeq chr8
+ 22580473 22598025 PDLIM2 64236 "PDZ and LIM domain 2 (mystique), transcript variant 1"
GO:0051371|GO:0001725|GO:0031005|GO:0008270|GO:0005634|GO:0030864|GO:0015629|GO:0005925|GO:0070
062|GO:0032036 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134003_PI430048170 0.327781237616226 0.697369258833426 0.280748107424716
0.285547260377147 0.458177765401908 A A A 1.4512345025383 0.545491015001099
0.340131874395803 A A A LNCV6_134003_PI430048170 mRNA
GGCTATGCCTGCTACTGCCCATGGTGTTATGAAAGATCTTGGTTTTCTGGCTGCTTCTGA NM_181620 RefSeq chr21
+ 30601120 30601267 KRTAP22-1 NA keratin associated protein 22-1 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_101975_PI430048170 0.15924212645899 1.6583424830071 3.09703840844329
3.52552057941226 3.26707969651862 P P P 2.79324525757151 2.93971601410381
1.72442370062163 P P A LNCV6_101975_PI430048170 mRNA
ACCTATGGTGGTTGTTACGGCAACAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAG NM_181642 RefSeq chr15
+ 40844047 40857655 SPINT1 6692 "serine peptidase inhibitor, Kunitz type 1, transcript variant 1"
GO:0010951|GO:0060674|GO:0016020|GO:0030198|GO:0004867|GO:0060670|GO:0005576|GO:0005615|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136134_PI430048170 0.0340233278063649 2.0071115594343 5.7957833088985
5.92543156202254 5.55427275428675 P P P 4.87680987600454 5.0425747397008
4.25024118276086 P P P LNCV6_136134_PI430048170 mRNA
TGGGTCTTGCAGTTTTTCAGGAGGCCTTGATTAAAATGCAAATACTTGTCTGAGAAAAAA NM_153006 RefSeq chr17
+ 44004663 44009068 NAGS 162417 N-acetylglutamate synthase
GO:0034641|GO:0006536|GO:0005759|GO:0006526|GO:0000050|GO:0044281|GO:0004042 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130687_PI430048170 0.0954394221724256 0.7078273651814545.99302101622092
5.80722692013181 5.85537187801439 P P P 6.11392218788048 6.28948591929095 6.6921285818749
P P P LNCV6_130687_PI430048170 mRNA
CCTATGGACTCAATTGCTATTATTTTAAACCTGCATGATTGTACCATGCAATACTATTCG NM_018082 RefSeq chr12
+ 106357657 106510198 POLR3B 55703 "polymerase (RNA) III (DNA directed) polypeptide B, transcript
variant 1"
GO:0010467|GO:0032728|GO:0006386|GO:0006385|GO:0032549|GO:0003677|GO:0006383|GO:0046872|GO:0005
829|GO:0051607|GO:0045089|GO:0001056|GO:0045087|GO:0005666|GO:0005654|GO:0032481 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_70906_PI430048170 0.0474812391096518 0.7618363239377998.921989710428
8.65211788657453 8.81359416307076 P P P 9.24310244211834 9.33385043510047
8.97747613385725 P P P LNCV6_70906_PI430048170 mRNA
TTACTTCCGCGGCTCCTATTCATACACGCAGGTGGGCTCCAGCGGGGCGGATGTGGAGAA NM_001270691 RefSeq
chr20 + 4148778 4187747 SMOX 54498 "spermine oxidase, transcript variant 6"
GO:0052901|GO:0006805|GO:0005634|GO:0044281|GO:0005829|GO:0046592|GO:0034641|GO:0005737|GO:0006
598|GO:0006596|GO:0006595|GO:0052895|GO:0046208|GO:0052894|GO:0055114 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139371_PI430048170 0.79098128025056 0.912265593368921 5.88789499519931
5.40082582507983 5.6729092237104 P P P 6.21111011607424 5.7932995771339
5.23277528534787 P P P LNCV6_139371_PI430048170 mRNA
CCTCTACCCTCACCCTGAGCTGTCTTGTTGAAAACAGTAATAAAAACATTACTTTACATT NM_006439 RefSeq chr4
+ 150581924 150584693 MAB21L2 10586 mab-21-like 2 (C. elegans)
GO:0010172|GO:0008284|GO:0001654|GO:0043010|GO:0005634|GO:0007399 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_140214_PI430048170 0.0353112741759598 0.5660458600650777.72055870360023
7.70484372891955 7.96041671968351 P P P 8.22313008428273 8.74286024447657
8.82652862626433 P P P LNCV6_140214_PI430048170 mRNA
TTTGTACAGTGGTAACTCCCAATGAGGCTTCTGTTATCATTTGGTGTGCTTTCTCTGTCANM_001018072 RefSeq chr12
+ 107318419 107659642 BTBD11 121551 "BTB (POZ) domain containing 11, transcript variant a"
GO:0046982|GO:0016021|GO:0060395 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131478_PI430048170 0.3629361138581390.6342354496606750.518347467316508
2.05815570609133 1.09563787737138 A A A 2.76861073476225 1.40081387326634
1.45368745297509 P A A LNCV6_131478_PI430048170 mRNA
GCTCTTTAACTTTTCTTTTCCTTTTTCATCGGGCTCTTTCCTAAAAAGCTGAGCTGTAAA NM_014080RefSeq chr15 -
45092653 45114161 DUOX2 50506 dual oxidase 2
GO:0048839|GO:0042335|GO:0005509|GO:0019221|GO:0030282|GO:0030878|GO:0048855|GO:0009615|GO:0051
591|GO:0009566|GO:0016324|GO:0004601|GO:0035264|GO:0042446|GO:0006590|GO:0016174|GO:0016021|GO:0
042744|GO:0006979|GO:0070062|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_10786_PI430048170 0.15243745621415 0.6959995968861783.57633083411378 3.85359883484509
3.49979304574908 P P P 4.4570093560781 4.27007687694912 3.68982041235793 P P P
LNCV6_10786_PI430048170 mRNA
ATTGTCTCTGTCTGCTTTTTACTGCCTGATGTGGTCGCTCTCGTACATCTTCTTTCCAGA NM_001242750 RefSeq chr1
+ 42787989 42798230 LOC100129924 NA uncharacterized LOC100129924 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_64205_PI430048170 0.3035135307407660.8592035964599251 1.6512505564528 11.4740086465785
11.1758903806023 P P P 11.878688945704 11.4439998244241 11.6416967685626 P P P
LNCV6_64205_PI430048170 mRNA
AAGGACGTTCCCATGGTAGAAAAGAAGAGCAAGAAACCCAAGAAGAAAGAGAAAAAACAC NM_001261826
RefSeq chr19 - 2100987 2151557 AP3D1 8943 "adaptor-related protein complex 3, delta 1
subunit, transcript variant 3"
GO:0005215|GO:0048490|GO:0005794|GO:0006726|GO:0033365|GO:0061088|GO:0032438|GO:0048499|GO:0072
657|GO:0005765|GO:0006886|GO:0030117|GO:0000139|GO:0016020|GO:0051138|GO:0043195|GO:0048007|GO:0
035646|GO:0005654|GO:0008089|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131190_PI430048170 0.3312685738238951.04473006258266 11.3090547956563
11.2308012337275 11.297204029085 P P P 11.1436957002912 11.1894881378521
11.3105229417499 P P P LNCV6_131190_PI430048170 mRNA
CATCTCAACTGTGCTTGTCTTATGCAGAAATATAAAGCGATGGCCAGGTTGGACTTCAAA NM_001282766 RefSeq
chr9 + 37485934 37503697 POLR1E 64425 "polymerase (RNA) I polypeptide E, 53kDa, transcript
variant 2"
GO:0010467|GO:0009303|GO:0006363|GO:0005730|GO:0006362|GO:0006361|GO:0005634|GO:0006360|GO:0003
677|GO:0001189|GO:0001179|GO:0005736|GO:0045814|GO:0001054|GO:0040029|GO:0005654 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_77476_PI430048170 0.2502058799722180.6968063912115013.26935153187558 2.5175026005846
3.86035848691054 A A P 3.97436365001174 3.7037631489064 3.82276226411976 P P P
LNCV6_77476_PI430048170 mRNA
GTTTAGTCCCAAGAGAATAGCGTTTTAAAAAAGAAAAACAAGATTTGGAGTCATTGTGGG NM_015525RefSeq chr6
- 82169986 82247754 IBTK 25998 "inhibitor of Bruton agammaglobulinemia tyrosine kinase,
transcript variant 1"
GO:0005737|GO:0051209|GO:0019901|GO:0016020|GO:0061099|GO:0030292|GO:0001933|GO:0005654 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128968_PI430048170 0.0160930161390774 1.24114606999211 13.7636850943339
13.9402178425799 13.7612930658288 P P P 13.424119628849 13.5457207883392

13.5637726470714 P P P LNCV6_128968_PI430048170 mRNA
CCTGTGCGGACAGCCCTTCCTCCCATTTCCCATTAAAGAGCCAGTTTATTTTCTAAAAAA NM_018973RefSeq chr1
- 155139890 155140407 DPM3 54344 "dolichyl-phosphate mannosyltransferase polypeptide 3, transcript variant 1"
GO:0005515|GO:0006501|GO:0004582|GO:0033185|GO:0005783|GO:0005975|GO:0018406|GO:0031501|GO:0030176|GO:0035269|GO:0035268|GO:0031647|GO:0016020|GO:0005789|GO:0006488|GO:0044267|GO:0006506|GO:0043687|GO:0018279. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144556_PI430048170 0.723046214549304 0.87688942984279 2.52175067632162
2.58109454433732 2.60801881559755 A A A 2.1335271948821 2.75789535806925
3.19750517050482 A P P LNCV6_144556_PI430048170 mRNA
GCCTTTATTTCAAGTGGTTCTTGAATTCCCTCCAGTCTCATTGTGAAAGGGGCAGGGAAA NM_002945RefSeq chr17
+ 1829978 1899554 RPA1 6117 "replication protein A1, 70kDa"
GO:0005515|GO:0008284|GO:0005634|GO:0046872|GO:0006302|GO:0034605|GO:0000082|GO:0006271|GO:0048873|GO:0003697|GO:0000723|GO:0000724|GO:0000722|GO:0006297|GO:0006298|GO:0005662|GO:0030097|GO:0006310|GO:0000800|GO:0001701|GO:0003684|GO:0006260|GO:0006261|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138893_PI430048170 0.325674424642705 1.56258591603667 1.61181094411788
0.432209723547312 0.365595682474948 A A A 0.269646450805358 0.297837446643328
0.274038924755035 A A A LNCV6_138893_PI430048170 mRNA
GCTTGCTCTACTTAAAATTCCTCACAATGTTGAATTTTGACCTGTATTCAGAAGAATTCC NM_152679RefSeq chr4
+ 48483342 48489524 SLC10A4 201780 "solute carrier family 10, member 4"
GO:0005887|GO:0015721|GO:0008508|GO:0006814|GO:0055085 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129364_PI430048170 0.41075777975463 1.72677816583219 1.97670413512703
0.387847034414103 0.286932399998729 A A A 0.304938938937117 0.326441798067459
0.326931475629978 A A A LNCV6_129364_PI430048170 mRNA
AATGAGTGTATGAAAAGGTGAAGGTGGGAGCACCTTGACCCAGGGATGTGATGGTTTATT NM_201648RefSeq chr11
- 58708756 58731974 GLYAT 10249 "glycine-N-acyltransferase, transcript variant 1"
GO:0005739|GO:0006637|GO:0032787|GO:0016746|GO:0006805|GO:0047961|GO:0005759|GO:0006544|GO:0009636|GO:0044281|GO:0047962|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132949_PI430048170 0.210273623395854 1.02181936473726 0.324969108790746
0.308316466273199 0.267352495739844 A A A 0.267816399683235 0.274315560629254
0.26567932526174 A A A LNCV6_132949_PI430048170 mRNA
TTTTGAAAACCTTCCATCTTATTGGCATTTTCTGGGGTTGTGAGGGAAACGGGGATGGCA NM_182704RefSeq chr19
+ 39515112 39520686 SELV 348303 selenoprotein V GO:0008430|GO:0045454 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_129736_PI430048170 0.0865847527663377 0.568153084611052 8.20821053680489
7.9852660719958 8.42407710636823 P P P 8.53033018472221 8.94245297445203
9.47042691261697 P P P LNCV6_129736_PI430048170 mRNA
GGCCATATATATTGCCTCCTTATCCTTGAGATTTCACTACCTTTATGTTAAAAGTTGTGT NM_001690RefSeq chr3 +
113747018 113812058 ATP6V1A 523 "ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A"
GO:0008286|GO:0046034|GO:0051701|GO:0005886|GO:0016469|GO:0033180|GO:0005765|GO:0055085|GO:0005524|GO:0005829|GO:0005739|GO:0006879|GO:0033572|GO:0005902|GO:0016324|GO:0046961|GO:0005887|GO:0006810|GO:0015991|GO:0090382|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106360_PI430048170 0.270045008753587 0.818045598076505 7.0831284283193
6.41862441736156 6.46707583977095 P P P 7.01702402594868 6.95258269245197
6.96680788868067 P P P LNCV6_106360_PI430048170 mRNA
ACGTCATTTCATCTTCACCCCCACCTCCAAATGAGGCTTGAAATGAGATGAGATGTTCCT NM_014383RefSeq chr19
+ 35712927 35717038 ZBTB32 27033 zinc finger and BTB domain containing 32

GO:0005515|GO:0030097|GO:0006366|GO:0003714|GO:0005634|GO:0000122|GO:0000228|GO:0001817|GO:0003677|GO:0006281|GO:0042098|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113767_PI430048170 0.173323445446311 0.503914893140059 0.308781206806012 1.23783911748298 2.07401754803881 A A A 1.60765833297821 2.30954312175356 2.90481739661641 A P P LNCV6_113767_PI430048170 mRNA CTGAGCATAATCTGAAATATCACCCAGGAGAAGAGAATTTTAAGTTGACTATGGTGAAAC NM_001017926 RefSeq chr8 - 123248449 123274487 ZHX1 11244 "zinc fingers and homeoboxes 1, transcript variant 1"
GO:0005515|GO:0003700|GO:0046982|GO:0003714|GO:0005654|GO:0005634|GO:0000122|GO:0045892|GO:0003677|GO:0046872|GO:0030154|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129816_PI430048170 0.0712819828398698 1.22308034054101 12.09279760055 12.1091220256162 12.1696054107648 P P P 11.6591398742669 11.8656668429833 11.9600946927354 P P P LNCV6_129816_PI430048170 mRNA CCCTCTGCTTCTCGGGGTCCAGTGCATTTTGTTTCTGTATATGATTCTCTGTGGTTTTTT NM_007313 RefSeq chr9 + 130713880 130887675 ABL1 25 "ABL proto-oncogene 1, non-receptor tyrosine kinase, transcript variant b"
GO:0005515|GO:0002333|GO:0046632|GO:0050731|GO:0048538|GO:0048536|GO:0030155|GO:0030154|GO:0042692|GO:0007173|GO:0007411|GO:0030100|GO:0042127|GO:0034446|GO:0006298|GO:0043123|GO:0033690|GO:0038083|GO:0006979|GO:0043124|GO:0019905|GO:0031965|GO:0022408|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137023_PI430048170 0.00416686069719528 0.391888001662477 8.06709953060447 7.70244491857512 8.06154832880344 P P P 9.23985812735662 9.29407389140774 9.37764229802518 P P P LNCV6_137023_PI430048170 mRNA GCCTTATTTCAGGGAAGCCTTTGAAGCTATGATGGACATAAGTCTAAATTAAATGTATGT NM_024814 RefSeq chr7 + 107743696 107761667 CBLL1 79872 "Cbl proto-oncogene-like 1, E3 ubiquitin protein ligase, transcript variant 1"
GO:0045807|GO:0005515|GO:0016337|GO:0007162|GO:0004842|GO:0030335|GO:0016567|GO:0016874|GO:0000151|GO:0008270|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132565_PI430048170 0.378394984124003 0.775114212314934 5.68778913260817 5.59871570198484 5.97346192451671 P P P 5.52018424183735 6.25198987228579 6.45906297388888 P P P LNCV6_132565_PI430048170 mRNA CCACTCCATAGTCTGGTATTCTGAGCACTAGCTTAATATTTCTTCACTTGAATATTCTTA NM_017669 RefSeq chrX - 72204656 72239008 ERCC6L 54821 excision repair cross-complementation group 6-like
GO:0005515|GO:0005813|GO:0005886|GO:0004386|GO:0003677|GO:0005524|GO:0005829|GO:0005737|GO:0007067|GO:0016020|GO:0008152|GO:0000777|GO:0005654|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132174_PI430048170 0.0261536090080916 0.358245502254286 6.01260353374272 5.49698108835993 5.55451118962026 P P P 6.50431262170907 7.47739980763548 7.39640755656941 P P P LNCV6_132174_PI430048170 mRNA TCCCAGTGACCAGCCACAGGAGATGTCCAATAAAGTATGTGATGAAATGGTCTTAAAAAA NM_002417 RefSeq chr10 - 128096660 128126204 MKI67 4288 "marker of proliferation Ki-67, transcript variant 1"
GO:0005515|GO:0000793|GO:0005737|GO:0007126|GO:0016020|GO:0008283|GO:0005730|GO:0005634|GO:0008022|GO:0005524|GO:0000775 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137989_PI430048170 0.281058607351704 1.05123923954746 0.338942997654598 0.336852164191232 0.483756800190002 A A A 0.31326429416967 0.290334414479295 0.344144361045059 A A A LNCV6_137989_PI430048170 mRNA GTCCTGGGTGGACATTTGAAGAATTATATTCATTCCAACTTGAAGAATTATTCAACACCT NM_006865 RefSeq chr19_GL949747v2_alt - 270615 275031 LILRA3 11026 "leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3, transcript variant 1"
GO:0007165|GO:0005886|GO:0006952|GO:0005576|GO:0004872|GO:0003823|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_144234_PI430048170 0.4863531851812070.8634625624438130.271720181328003
0.2959540331359070.442244996051482A A A 0.9424851037748560.305833742926459
0.305181962874891A A A LNCV6_144234_PI430048170 mRNA
TTACCAGGGCTTGGGGACCCAATGCAAAGATGATGACTATTTAATAAAATGGAAAATTTA NM_022054RefSeq chr14
+ 90061764 90185857 KCNK1356659 "potassium channel, two pore domain subfamily K, member 13"
GO:0005244|GO:0005886|GO:0007268|GO:0005267|GO:0034765|GO:0016021|GO:0071805 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143799_PI430048170 0.2811607321163041.03725433520099 0.528796665071245
0.6189897266599460.50143906023201 A A A 0.4970647315697970.4942257988124
0.502253363945055A A A LNCV6_143799_PI430048170 mRNA
GTTTAGGCCTTTTGTCTTCGGCACTTAGGATCCTAATGACAATAAATTATTTATGAAGAG NM_001037225 RefSeq
chr11 - 64938229 64972091 C11orf85 283129 "chromosome 11 open reading frame 85, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134765_PI430048170 0.00051421089825259 1.39108877228752 14.9271704624221
14.9132959255005 14.8182477932248 P P P 14.4346522245774 14.4426917104661 14.353467227964
P P P LNCV6_134765_PI430048170 mRNA
TCCTTCAGCCCCATCATGTGCTTTGGGATGAGTGTAAATAAAACGGGGCTGTGGCTTGGG NM_016068RefSeq chr7
- 101239611 101245090 FIS1 51024 fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)
GO:0005515|GO:0035584|GO:0006626|GO:0001836|GO:0090141|GO:0007204|GO:0005739|GO:0008053|GO:0051
561|GO:0051260|GO:0005779|GO:0005777|GO:0016559|GO:0010821|GO:0000422|GO:0000266|GO:0005102|GO:0
090314|GO:2001244|GO:0043653|GO:0043280|GO:0043234|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138769_PI430048170 0.00459192354324741 0.6975214024181749.34735782844384
9.23985812735662 9.15515334905189 P P P 9.80124037027588 9.86196474374062
9.63524560794104 P P P LNCV6_138769_PI430048170 mRNA
ACACCCGTCTTTCCATGATGGCAGAGACATCCAGTCAGGACCTGACCCGTCTCTGTCTGA NM_031454RefSeq chr22
+ 50200978 50217616 SELO 83642 selenoprotein O NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_98877_PI430048170 0.3327649708934150.9038514816220390.3540820545917770.383265047358581
0.325155753075653A A A 0.7088949800820580.3964426650938160.370090237037817A A A
LNCV6_98877_PI430048170 mRNA
TGCACAGCAGTTCCACAGGCACAAGCAGCTGATCCGATTCCTGAAACGGCTCGACAGGAA NM_000589RefSeq
chr5 + 132673985 132682678 IL4 3565 "interleukin 4, transcript variant 1"
GO:0005515|GO:0071677|GO:0014070|GO:0060041|GO:0048295|GO:0043031|GO:0005615|GO:0045348|GO:0006
935|GO:0035745|GO:0007565|GO:0071288|GO:0045191|GO:2000320|GO:0042832|GO:2000424|GO:0002674|GO:0
005125|GO:0002227|GO:0042113|GO:0002230|GO:0050776|GO:0045893|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142907_PI430048170 0.6985308739503340.9459778430404655.41103139404177
5.39110493508052 6.00969267205515 P P P 5.47679479916451 5.74691412235522
5.88789499519931 P P P LNCV6_142907_PI430048170 mRNA
CCTAAGTTACTCAAAGCACTGCTTCTTGGTCCTTGTTTTCTTTTGCCTTGTACTATCTTG NM_014774RefSeq chr1 -
46675158 46719064 EFCAB14 9813 EF-hand calcium binding domain 14 GO:0005509 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134039_PI430048170 0.1640039335543661.34276926139829 2.08065095576404
1.85885569957604 1.97373481610686 A A A 1.09010965251078 1.66478431847302
1.79787826612688 A A A LNCV6_134039_PI430048170 mRNA
AGAAAACCTCTTTGTTTTAAAAGGGAGGTGGGGGTAGAAGTAAAAGGATGATCATGGGAG NM_005232RefSeq
chr7 - 143391111 143408892 EPHA1 2041 EPH receptor A1
GO:0030336|GO:0008284|GO:0030335|GO:0048013|GO:0005886|GO:0019901|GO:0018108|GO:0032862|GO:0001

525|GO:0005524|GO:0045766|GO:0005005|GO:0046777|GO:0032314|GO:0004672|GO:0005887|GO:0007411|GO:0051496|GO:0034446|GO:0006469|GO:0035019|GO:0001954|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88101_PI430048170 0.2904211980394460.9119849608370668.26432014188946 8.37747980833102 8.59844386730146 P P P 8.55519809540579 8.5408032052485 8.56313893197494 P P P LNCV6_88101_PI430048170 mRNA TGATCTGGTTCAGAAGCCAAGTTATTATGTTAGACTGGGATCCCTGTCTACCAAGCTTCA NM_001122RefSeq chr9 - 19115760 19127606 PLIN2 123 "perilipin 2, transcript variant 1"
GO:0005811|GO:0014070|GO:0005886|GO:0019915|GO:0005783|GO:0042493|GO:0005634|GO:0005576|GO:0044281|GO:0015909|GO:0044255|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129690_PI430048170 0.6099145456798170.854069860036 0.52568796672334 0.5148869489215410.499367481300229A A A 1.24698768388133 0.374232316132221 0.426694680860564A A A LNCV6_129690_PI430048170 mRNA TCTTAAATATTTCCATCAGCCCATCTCAACAATATATGTCCTATAAATGGACCATCCTTG NM_015596RefSeq chr19 - 51056205 51065110 KLK13 26085 kallikrein-related peptidase 13
GO:0005515|GO:0005737|GO:0016787|GO:0004252|GO:0016485|GO:0006508|GO:0005576|GO:0030141|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67370_PI430048170 0.0737438001636272 1.76810191519501 9.39689172195514 10.1801406903091 10.1346090200747 P P P 9.19213850772369 8.90767720095447 9.24802938436511 P P P LNCV6_67370_PI430048170 mRNA TGTACGTTCTCACCTCTTATGCTTAGTTGGAACTAAGCAGTTTGTAAACTTTCATCCTTT NM_001267774 RefSeq chr17 - 28328324 28335489 IFT20 90410 "intraflagellar transport 20, transcript variant 1"
GO:0005515|GO:0002046|GO:0036064|GO:0007224|GO:0061351|GO:0035845|GO:0051642|GO:0042073|GO:0015630|GO:0055007|GO:0070062|GO:0005813|GO:0006996|GO:0005794|GO:0005814|GO:0001822|GO:0031514|GO:0044292|GO:0072372|GO:0060828|GO:0005929|GO:0042384|GO:0000139|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143793_PI430048170 0.0172526562017546 0.7006233379804835.34091026121006 5.55424609415314 5.62176940440096 P P P 6.05945266114845 5.96562850365929 6.04462110737959 P P P LNCV6_143793_PI430048170 mRNA CATCCTAAAACTGCCTTTTCCTATGGTTTTGTCAATAAAACACTATGATGTTGGTCTGTTNM_017520RefSeq chr13 + 19633647 19673459 MPHOSPH8 54737 M-phase phosphoprotein 8
GO:0005515|GO:0005886|GO:0005730|GO:0005634|GO:0035064|GO:0006351|GO:0005720|GO:0005737|GO:0044030|GO:0000788|GO:0005654|GO:0045892|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133834_PI430048170 0.0676580298055354 0.7161244607990875.80114834986025 5.76594455675263 6.051158647408 P P P 6.2480573817899 6.14562274178267 6.63866436183726 P P P LNCV6_133834_PI430048170 mRNA CGTGAACACTTTGTGCCTGTTTTCTATGGTTGTGGAGAATTAATGAACAAATCAATATGT NM_001077195 RefSeq chr1 - 23359447 23369864 ZNF436 80818 "zinc finger protein 436, transcript variant 1"
GO:0005515|GO:0006355|GO:0005737|GO:0003700|GO:0005654|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140823_PI430048170 0.0546084913969489 0.6372044405896272.81808730093777 2.63178999143139 2.16600404343383 A A A 3.00277235844937 3.44195595654272 3.16257625043471 P P P LNCV6_140823_PI430048170 mRNA TCATGCAGATTGAGATCAAAAGTCCCTCTGCTTGGGATCAAATTAATGTTTGACAGAGCT NM_001277126 RefSeq chr19 - 53793600 53824403 NLRP12 91662 "NLR family, pyrin domain containing 12, transcript variant 3"
GO:0005515|GO:0045751|GO:0045409|GO:0005634|GO:0050710|GO:0050711|GO:0031953|GO:0005737|GO:0045345|GO:0050718|GO:0070373|GO:0009968|GO:0043122|GO:0043124|GO:0045381|GO:0006919|GO:0032088|GO:0008656|GO:0005524|GO:0007165|GO:0008588|GO:0043281|GO:0071345|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_76017_PI430048170 0.815394283333563 1.01476109491409 12.9428059655383 13.0341950772722
13.1519945520734 P P P 13.0037248205913 12.9313835231621 13.1309908854449 P P P
LNCV6_76017_PI430048170 mRNA
TGGTATGTAGAGCTTAGATTTCCCTATTGTGACAGAGCCATGGTGTGTTTGTAATAATAA NM_000358 RefSeq chr5
+ 136028894 136063818 TGFBI 7045 "transforming growth factor, beta-induced, 68kDa"
GO:0005515|GO:0005802|GO:0005886|GO:0008283|GO:0005518|GO:0050840|GO:0005578|GO:0005576|GO:0001
525|GO:0005615|GO:0005604|GO:0031012|GO:0007162|GO:0005178|GO:0030198|GO:0002062|GO:0007155|GO:0
007601|GO:0050896|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140748_PI430048170 0.00349446504595512 1.35575307887448 12.1473129533966
12.101319044979 11.9798708923316 P P P 11.6283752871679 11.6951474385581
11.5909023905812 P P P LNCV6_140748_PI430048170 mRNA
GAGGTCCAGGGAGGGATTTAGGAAATAAAGTTTCTACCTATTTGATGAGCCTCTAAAAAA NM_148179 RefSeq chr9
- 34610484 34612113 RPP25L 138716 "ribonuclease P/MRP 25kDa subunit-like, transcript variant 2"
GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143009_PI430048170 0.0803232741552941 3.1177125365 34 5.66875302066991
5.67397677192129 5.78744687432983 P P P 5.20844800285066 5.56571770002958
5.14842953387593 P P P LNCV6_143009_PI430048170 mRNA
AATGTTCGATTTGATACTTAAACTTGAGGAGAGGCAGAGAGAGGTCTGGGAACTGCACCA NM_001257994 RefSeq
chr22 - 20111865 20117295 TRMT2A 27037 "tRNA methyltransferase 2 homolog A (S. cerevisiae),
transcript variant 3" GO:0006396|GO:0001510|GO:0000166|GO:0008173 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_128837_PI430048170 0.0754003380409413 0.583919127715923 9.53018658330927
9.40037572116032 9.02185838701229 P P P 9.68374802832897 10.5338595317766
9.97840470595138 P P P LNCV6_128837_PI430048170 mRNA
ACCAGCTCTAAGTAATTCTAACGTCTTCATACCCAATCCCAAAGGCTCTTTTAAGAGCCA NM_003522 RefSeq chr6
+ 26199558 26199988 HIST1H2BF 8343 "histone cluster 1, H2bf"
GO:0046982|GO:0050830|GO:0019731|GO:0006334|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0005
615|GO:0003677|GO:0070062|GO:0002227 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134728_PI430048170 0.560221632450898 0.953540480809252 9.31108182742108
9.16016409177475 8.93824584390837 P P P 9.22968697164689 9.25443314833309
9.15351517221558 P P P LNCV6_134728_PI430048170 mRNA
AACTTGAGAGGCACTCTGCCCTCTTCCCTATAAAATCACACAGCGTGATTTTACAAGGTC NM_006253 RefSeq chr12
+ 119667955 119681624 PRKAB1 5564 "protein kinase, AMP-activated, beta 1 non-catalytic subunit"
GO:0045859|GO:0005515|GO:0008286|GO:0006996|GO:0031588|GO:0019901|GO:0004679|GO:0005634|GO:0051
291|GO:0005829|GO:0010628|GO:0007165|GO:0004672|GO:0061024|GO:0006468|GO:0006633|GO:0007050|GO:0
007005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133802_PI430048170 0.419586651324759 1.04028998924169 0.327181355059465
0.331836029439081 0.492221866166934 A A A 0.332305612644555 0.298954487265593
0.354672845385581 A A A LNCV6_133802_PI430048170 mRNA
CCCTCTATTTATTTTTATGTCAGGTGAACTGGCATGCTGAACATATATATATATAGGCTC NM_145172 RefSeq chr1
+ 85062297 85133138 WDR63 126820 "WD repeat domain 63, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141829_PI430048170 0.106211136777447 1.25875588417012 10.8355043742593
10.9634072908507 11.2600971277392 P P P 10.6831020797635 10.5678654685339 10.833157858116
P P P LNCV6_141829_PI430048170 mRNA
AACCCCAGGCCTGAAGAAATAAAGTAAAATTAATCTGGTAATTTGTCACGGATTAGTTGT NM_001003703 RefSeq
chr21 - 25724479 25735654 ATP5J 522 "ATP synthase, H+ transporting, mitochondrial Fo complex,
subunit F6, transcript variant 1"

GO:0005215|GO:0015078|GO:0022857|GO:0005743|GO:0044281|GO:0005753|GO:0005739|GO:0022904|GO:0021762|GO:0042776|GO:0000276|GO:0016887|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136132_PI430048170 0.0280096706958289 0.66077160259782 7.20773199024355 7.48003645098906 7.02188442921845 P P P 8.00635656393179 7.89150323629041 7.61463402702652 P P P LNCV6_136132_PI430048170 mRNA
TCACGTATGTGACCGTGTGGACTATTTCAAGGTGCTGATGCAACACTAATAAACCTGGAG NM_001100913 RefSeq chr14 + 105314414 105398147 PACS2 23241 "phosphofurin acidic cluster sorting protein 2, transcript variant 1"
GO:0005739|GO:0005783|GO:0072661|GO:0016032|GO:0006915|GO:0005788|GO:0000045|GO:0034497 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144233_PI430048170 0.8252164537014440.9173942455260475.11030101368313 4.75494921613134 3.9329147150024 P P P 5.28596808823425 4.81379461356179 4.05250385714468 P P P LNCV6_144233_PI430048170 mRNA
GCTTCTCTCAGTCACTGCTGGCGCTTTCTTAATCTTTATCCAATAAAATGAAACAAAAAA NM_022055RefSeq chr2 - 47520775 47570331 KCNK1256660 "potassium channel, two pore domain subfamily K, member 12"
GO:0005244|GO:0005267|GO:0034765|GO:0016021|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134741_PI430048170 0.6581769520197330.9452902762395363.77852610260629 4.13064139597736 3.65758497902272 P P P 4.09964671672064 3.72384084775807 4.00366084872326 P P P LNCV6_134741_PI430048170 mRNA
ATCTGTAATAATCCTTAAAAATCAGCACACAAATCCATTCCAGGTAGCTTTGCCACCCCA NM_153215RefSeq chr3 + 50279026 50288114 LSMEM2 132228 "leucine-rich single-pass membrane protein 2, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131219_PI430048170 0.5134880187096411.04495524398743 0.28313903866502 0.2936215654574520.514160815706786A A A 0.3197427003473010.277007528433569 0.31545756522614 A A A LNCV6_131219_PI430048170 mRNA
AACTTTCTGATCGATAGAAACTTCCAGGTGTCCATGCTGGCAGTGGACGAGATGTATGAT NM_017682RefSeq chr19 + 12752592 12758457 BEST2 54831 bestrophin 2
GO:0008150|GO:0007608|GO:0005929|GO:0003674|GO:0051899|GO:0005886|GO:0034707|GO:0005254 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139912_PI430048170 0.3129431190415 1.3344399842897 3.57941683595422 4.04022147112177 3.16543082642154 P P P 2.67013059461051 3.43338438311897 3.43861731056726 A P P LNCV6_139912_PI430048170 mRNA
TATGCATCTACTTGGCAAGGTCATAGACAATTCCTCCAGAGACACTGAGCCAGTCTTTGA NM_153281RefSeq chr3 - 50299888 50312381 HYAL1 3373 "hyaluronoglucosaminidase 1, transcript variant 8"
GO:0030308|GO:0051216|GO:0030307|GO:0036117|GO:0044281|GO:0005764|GO:0005615|GO:0071467|GO:0030207|GO:1900106|GO:0005737|GO:0006954|GO:0036120|GO:0001618|GO:0071356|GO:0030204|GO:0030203|GO:0046677|GO:0070062|GO:0045927|GO:0043202|GO:0050679|GO:0005975|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139797_PI430048170 0.2047828791674760.8473879307546026.78751498160374 6.64156185182798 6.73535694928727 P P P 6.96114350764754 7.16428061753386 6.72640006029685 P P P LNCV6_139797_PI430048170 mRNA
TGTTCTTTTGCCCCATTTCTCAACATAGCACACTTGTGCACTGAGAGGAGGGAGCATTAT NM_033198RefSeq chr17 - 28553387 28571869 PIGS 94005 "phosphatidylinositol glycan anchor biosynthesis, class S"
GO:0006501|GO:0005515|GO:0016020|GO:0016255|GO:0005789|GO:0042765|GO:0003923|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104765_PI430048170 0.0130105399856913 0.6535660276871876.68524151837216 6.38966770281888 6.55252232320269 P P P 7.18314191109661 6.95164230357533 7.32430447952776 P P P LNCV6_104765_PI430048170 mRNA

CAGATTTCAAAACCCAGCCCTGTCTGTTAAGAGTGAGGCAGAATATTACTGAAGAATGAT NM_001031806 RefSeq chr17 + 19648750 19677591 ALDH3A2 224 "aldehyde dehydrogenase 3 family, member A2, transcript variant 1"
GO:0006714|GO:0052814|GO:0046577|GO:0004029|GO:0005743|GO:0006081|GO:0004028|GO:0007417|GO:0050061|GO:0043231|GO:0008544|GO:0007422|GO:0005789|GO:0016021|GO:0033306|GO:0070062|GO:0055114|GO:0004030|GO:0005777. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136963_PI430048170 0.00969769426042101 0.6549550914247634.58103684118568 4.89462062192844 4.71104183661464 P P P 5.39393193674094 5.46849491067251 5.15489025887362 P P P LNCV6_136963_PI430048170 mRNA
GGCTTCTGGCCTCGGCGTCTGTCAAGCAGAAGGGATGTTTGTCACTTGTTCTGCAACTTG NM_017708RefSeq chr19 - 48600599 48613437 FAM83E 54854 "family with sequence similarity 83, member E" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136530_PI430048170 0.000164814801582589 2.54756314724876 5.01165373802974 5.23983385987594 5.1713552987443 P P P 3.92721760175948 3.68661500446131 3.7604310358341 P P P LNCV6_136530_PI430048170 mRNA
TACTGTTCCTCTTTCATATGTAGGAGGGTTTAAAAGTTCAGCGAATGGGCAAGGTACAAA NM_153376RefSeq chr4 - 7040849 7043001 CCDC96 257236 coiled-coil domain containing 96 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142501_PI430048170 0.0675321365526522 0.600828654252561 3.75680412233657 3.32532433406822 3.50618229676444 P P P 3.89934032554019 4.66620544148727 4.15224697846008 P P P LNCV6_142501_PI430048170 mRNA
CCCTTTCCAACTCACAACCAATAAAGGGGCTTGGGCTGTGCTTTGACTAAGGTGAAAAAA NM_003466RefSeq chr2 - 113215996 113278921 PAX8 7849 "paired box 8, transcript variant PAX8A"
GO:0005515|GO:0001658|GO:0003700|GO:0044212|GO:0001655|GO:0048793|GO:0005634|GO:0030878|GO:0009653|GO:0072305|GO:0072278|GO:0071371|GO:0045944|GO:0072307|GO:0004996|GO:2000612|GO:2000611|GO:0090190|GO:0042472|GO:0001822|GO:0071599|GO:0001823|GO:1900215|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143148_PI430048170 0.7845586075261790.95566775162799 0.307917074043718 1.62067117118274 1.05534225367649 A A A 1.30427388297142 0.689202828534652 1.38173171054294 A A A LNCV6_143148_PI430048170 mRNA
CTCTAGTGCTTACCACTCGGTTTATTATTCATAATCTGCAATTCAATAAAGGCTTTGTGTNM_001040284 RefSeq chr16 + 50152917 50235308 PAPD5 64282 "PAP associated domain containing 5, transcript variant 1"
GO:0006397|GO:0003887|GO:0006364|GO:0005730|GO:0005575|GO:0003677|GO:0046872|GO:0004652|GO:0005737|GO:0007067|GO:0071897|GO:0071044|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88675_PI430048170 0.61893549202915 0.9158015146735558.07774467841012 7.85353340271594 8.03191049951093 P P P 7.84214487308384 8.00390791877806 8.43958400863277 P P P LNCV6_88675_PI430048170 mRNA
AAGGTCATGCTGGTGGGTTAGCTAAACCAAGAAGGAGACCTTTTCACAATGGAAAACCTG NM_001423RefSeq chr12 + 13196667 13216774 EMP1 2012 epithelial membrane protein 1
GO:0005515|GO:0008219|GO:0016020|GO:0008544|GO:0005886|GO:0008283|GO:0032060|GO:0016049|GO:0007275|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145594_PI430048170 0.00683415712396912 4.03083984616075 4.10426606109168 4.60925715753878 4.67349367217498 P P P 2.97942109470854 2.23840907058846 2.01704949652983 P A A LNCV6_145594_PI430048170 mRNA
GTATTGTCAGAGTTGAATATCACCTCTCAAAAGCATCACCTCTATCTGCCTCATCTCACA NM_000928RefSeq chr12 - 120322110 120327789 PLA2G1B 5319 "phospholipase A2, group IB (pancreas)"
GO:0032052|GO:0050830|GO:0010524|GO:0044240|GO:0050714|GO:0048146|GO:0044281|GO:0005615|GO:0032431|GO:0035556|GO:0000187|GO:0051092|GO:0015758|GO:0045944|GO:0047498|GO:0004623|GO:0007015|GO:0006633|GO:0030141|GO:0006654|GO:0050482|GO:0019370|GO:0032869|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_144642_PI430048170 0.0262022032340145 0.6303975749688281 1.8047292632357
11.8212845649708 12.2609762644429 P P P 12.5971988858049 12.4545245150457
12.8517654030568 P P P LNCV6_144642_PI430048170 mRNA
GGAGAGAAGCTCTTCAATAGCTAAGCATCTCCTTACAGTCACTAATATAGTAGATTTTAA NM_000689 RefSeq chr9
- 72900661 72953317 ALDH1A1 216 "aldehyde dehydrogenase 1 family, member A1"
GO:0006805|GO:0001758|GO:0006069|GO:0004029|GO:0006081|GO:0004028|GO:0044281|GO:0005829|GO:0005
099|GO:0005737|GO:0032320|GO:0042572|GO:0018479|GO:0005497|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135301_PI430048170 0.0586594021591871 1.19510383463375 10.7782058380439
11.019341570923 10.8030756443362 P P P 10.6182131088684 10.523883390337
10.6944598967525 P P P LNCV6_135301_PI430048170 mRNA
GGAAGATGCGGAAAAGGCTGTGATTGACTTGAATAACCGTTGGTTTAATGGACAGCCGAT NM_001025204 RefSeq
chr21 - 43092955 43107578 U2AF1 7307 "U2 small nuclear RNA auxiliary factor 1, transcript variant c"
GO:0005515|GO:0006397|GO:0008380|GO:0006369|GO:0010467|GO:0015030|GO:0006366|GO:0031124|GO:0050
733|GO:0071013|GO:0046872|GO:0006406|GO:0000166|GO:0016607|GO:0000398|GO:0005654|GO:0005681 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135463_PI430048170 0.523269932840907 0.807775156065971 6.36118676687055 6.1311010407118
6.14477752787902 P P P 5.82784408529943 6.69342574039648 6.85590780859037 P P P
LNCV6_135463_PI430048170 mRNA
CTCGTCTGTTTCAAATACAGTGCAGTCAGTTTTATATGATGTGCAATAAACCAAAAAGGC NM_032444 RefSeq chr16
- 3581182 3611584 SLX4 84464 SLX4 structure-specific endonuclease subunit
GO:0005515|GO:0000790|GO:0030054|GO:0048476|GO:0008821|GO:0010792|GO:0043085|GO:0033557|GO:0006
260|GO:0005737|GO:0006281|GO:0070522|GO:0000724|GO:0048257|GO:0005654|GO:0017108|GO:0006289|GO:0
072429|GO:0008047|GO:0000737|GO:0000784 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134152_PI430048170 0.5028506645141 0.885321491932739 7.39661334314482
7.13674594413509 6.99305714478474 P P P 6.97936141713058 7.58252125488011
7.45377339730731 P P P LNCV6_134152_PI430048170 mRNA
GGGCTTCTGTACAACTCAACTTGTATACACTGTGTACACACAACCAGCCAAACGAAAACC NM_020719 RefSeq chr19
+ 49591654 49626439 PRR12 57479 proline rich 12 GO:0003677 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137717_PI430048170 0.445111160932431 1.4536667163758 2.57181003167129
1.15474553713524 2.46944498412482 A A A 1.79048659784739 2.08362396012134
0.793697684728256 A A A LNCV6_137717_PI430048170 mRNA
CAAAACCCTCTTTGAGAACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGT NM_017442 RefSeq chr3
- 52221079 52226163 TLR9 54106 toll-like receptor 9
GO:0032755|GO:0032717|GO:0034123|GO:0032715|GO:0034122|GO:0046330|GO:0005764|GO:0032757|GO:0002
755|GO:0045078|GO:0043123|GO:0042742|GO:0032728|GO:0032760|GO:0032722|GO:0002224|GO:0045359|GO:0
045087|GO:0045356|GO:0005789|GO:0050707|GO:0010008|GO:0034162|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_57026_PI430048170 0.0346741649074422 1.31609044817779 5.41644862128398
5.55283383581369 5.64006158056993 P P P 5.29605017706506 5.15742219272792
4.95571437455521 P P P LNCV6_57026_PI430048170 mRNA
TTTGCTTTTCAAGAGGGAACTGAGTCCAGGCCAGACTGGGTTGCTCCCCTTTCTCTCGGC NM_021932 RefSeq chr11
+ 207510 215175 RIC8A 60626 "RIC8 guanine nucleotide exchange factor A, transcript variant 1"
GO:0005515|GO:0005886|GO:0001701|GO:0007193|GO:0005085|GO:0043547|GO:0001965|GO:0005737|GO:0042
074|GO:0007186|GO:0008542|GO:0071711|GO:0070586|GO:0001944|GO:0005096 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143684_PI430048170 0.0558414739662952 0.767216368055945 9.59050945541028

9.19542294179895 9.3802410183747 P P P 9.66692345893054 9.77987967303934
9.88513390240002 P P P LNCV6_143684_PI430048170 mRNA
GCCAGACTTCTAAAATAAATGTTTTGGAATTCAATGGGTAAATAAATGCTGCTTTGGGGA NM_003405 RefSeq chr22
+ 31944492 31957603 YWHAH 7533 "tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
activation protein, eta"
GO:0005515|GO:0086010|GO:0005886|GO:0005159|GO:0035259|GO:0006886|GO:0005829|GO:0005737|GO:1900
740|GO:0014704|GO:0048167|GO:0061024|GO:0030659|GO:0070062|GO:0006713|GO:0046982|GO:0019904|GO:0
006915|GO:0003779|GO:2000649|GO:0097193|GO:0044325|GO:0021762|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_68597_PI430048170 0.3993792766185371.77334057635874 0.3901516638233521.48582875067192
2.41517707327227 A A A 0.7345870830263460.5262484694465361.15192125424767 A A A
LNCV6_68597_PI430048170 mRNA
TGGGGCTACGATGTGGCGGTCAAGATCGTAAACTCGAAGGCGATATCCAGGGAGGTCAAG NM_006871 RefSeq
chr14 - 24336020 24340036 RIPK3 11035 receptor-interacting serine-threonine kinase 3
GO:0005515|GO:0051351|GO:0051353|GO:0034142|GO:0005886|GO:2000452|GO:0046006|GO:0007249|GO:0048
538|GO:0070235|GO:0048536|GO:0051291|GO:0032403|GO:0048535|GO:0042802|GO:0005829|GO:0005739|GO:0
032147|GO:0002756|GO:0032649|GO:0004704|GO:0051092|GO:0046777|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_94768_PI430048170 0.0147094301872141 0.55323084670119 5.44554066101977
4.95768395632827 5.02176323413813 P P P 5.84463455099703 6.06908695125262
6.10971008084404 P P P LNCV6_94768_PI430048170 mRNA
AGACCCCAAACACAGTCTTTACCTCGCCTGTGCACTCATGGTTAGAGGAAATGTACAAAT NM_016262 RefSeq chr6
- 112070656 112087548 TUBE1 51175 "tubulin, epsilon 1"
GO:0006184|GO:0051258|GO:0007098|GO:0005874|GO:0005200|GO:0003924|GO:0005525|GO:0000242 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145677_PI430048170 0.1021187136500680.3147807092691142.80401844139262
0.3856949779206531.90919552657443 A A A 3.88248328445491 3.76076988242056
3.31692595301604 P P P LNCV6_145677_PI430048170 mRNA
CCCTCCTCTGTATGCTGTCACACCTATATTATTAAACTTATCACATTGCATTGTAATTAC NM_176894 RefSeq chr3 -
151326307 151329549 P2RY13 53829 "purinergic receptor P2Y, G-protein coupled, 13"
GO:0008150|GO:0007186|GO:0005886|GO:0045028|GO:0005887|GO:0005783|GO:0035589|GO:0007194 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134062_PI430048170 0.0800807014267447 1.2075173601314 12.5287000740222
12.6208749542026 12.7555161787162 P P P 12.3871697671375 12.1875160065046
12.5055990781119 P P P LNCV6_134062_PI430048170 mRNA
AGGGTTCAAGTCTGCTTTCCACAGAATCAGGCATGCTGTTAATAAATACTGGTTTAATCA NM_003776 RefSeq chr22
+ 19432512 19436073 MRPL40 64976 mitochondrial ribosomal protein L40
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0005761|GO:0005743|GO:0005
730|GO:0005634|GO:0009653 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143053_PI430048170 0.5359955089397870.9444729137203940.449815601077666
0.4837698682044650.417529855073914 A A A 0.7279452795925790.414238746498482
0.435162554066822 A A A LNCV6_143053_PI430048170 mRNA
GCACCATTATGTGACTCTTCATATAACCCTTTTTTCTACGGCAGCATTAAAATTGTCTTT NM_020856 RefSeq chr19 -
31274944 31349284 TSHZ3 57616 teashirt zinc finger homeobox 3
GO:0001656|GO:0005515|GO:0001657|GO:0030324|GO:0005634|GO:0072105|GO:0001701|GO:0003677|GO:0046
872|GO:0006351|GO:0072193|GO:0030426|GO:0005739|GO:0002087|GO:0050881|GO:0072195|GO:0003682|GO:0
060993|GO:0051152|GO:0050975|GO:0005654|GO:0045892 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_130994_PI430048170 0.2137592900204061.18707674445904 0.591655962180712

0.2766162053666320.721310239781555 A A A 0.3348115454801760.272415381530156
0.274706275836412 A A A LNCV6_130994_PI430048170 mRNA
TCAATGAGAACAACAACACAGGAATCATCAAGGGTCATTACAACCGGCGGACTTTGTTGT NM_001115 RefSeq chr8
- 130780300 131040589 ADCY8 114 adenylate cyclase 8 (brain)
GO:0005886|GO:0007268|GO:0007202|GO:0044281|GO:0007193|GO:0046872|GO:0035556|GO:0007173|GO:0071
377|GO:0007611|GO:0006171|GO:0006833|GO:0034199|GO:0048011|GO:0007616|GO:0008294|GO:0055085|GO:0
005524|GO:0003091|GO:0007165|GO:0006112|GO:0004016|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_64533_PI430048170 0.379464118456761 1.00993234931166 0.3312478511413120.310157658568461
0.28846277111984 A A A 0.3017820217895560.3015105057147410.284045497110749 A A A
LNCV6_64533_PI430048170 mRNA
CTATGAATTGAATTGTCTGTTCTAGGACTGGGCACAGATTTTCCCATTAAAATTTTTGAC NM_025245 RefSeq chr19
- 19561706 19618916 PBX4 80714 "pre-B-cell leukemia homeobox 4, transcript variant 1"
GO:0043565|GO:0001741|GO:0003700|GO:0006366|GO:0005634|GO:0045893 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_80047_PI430048170 0.0234873152535198 0.9448687266622070.3988787874132460.3448097342667
0.347119993315928 A A A 0.4642287704905990.4520439741822280.420272546827595 A A A
LNCV6_80047_PI430048170 mRNA
GTGCTGTTCTGTATGGGTGTCTATACCCTTATTCCAAGGTGAATAAATAAAGTTGTGTTT NM_001198625 RefSeq
chr8 - 91954966 92095654 RUNX1T1 862 "runt-related transcription factor 1; translocated to, 1 (cyclin
D-related), transcript variant 5"
GO:0005515|GO:0003700|GO:0003714|GO:0006091|GO:0003677|GO:0006351|GO:0016363|GO:0046872|GO:0042
802|GO:0005739|GO:0005737|GO:0005654|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99867_PI430048170 0.0729427834227138 0.74149218576426 8.95105954953435
8.73577848923122 9.03856435174635 P P P 9.07060493779583 9.38202074225999
9.54441644581402 P P P LNCV6_99867_PI430048170 mRNA
ACATTGTTTTGTTACTGCTCCTACCCACCAAGGGGATAAAGAAGGCGAGTTCTGAGTGTT NM_001100619 RefSeq
chr18 + 23135762 23260470 CABLES1 91768 "Cdk5 and Abl enzyme substrate 1, transcript variant 2"
GO:0005515|GO:0007049|GO:0007596|GO:0005634|GO:0051301|GO:0007399|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144330_PI430048170 0.7814212667569691.02043316222868 6.46103886348986 6.5673805046032
6.34160421492165 P P P 7.00100363882845 6.13050308960229 5.92120978107964 P P P
LNCV6_144330_PI430048170 mRNA
GCTATCTTTTCTAGATGTGCACAAAATTGATGTTAATAAAACTGGTTCCTGCCCTCTAAA NM_153225 RefSeq chr8
- 73064542 73093272 SBSPON 157869 "somatomedin B and thrombospondin, type 1 domain
containing" GO:0031012|GO:0006955|GO:0005578|GO:0030247|GO:0006898|GO:0005044 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_127102_PI430048170 0.6529163356423531.14204967624764 1.18358179111782
1.56740712595201 0.551746830370029 A A A 0.6478135135900851.571965239254
0.408834480368616 A A A LNCV6_127102_PI430048170 mRNA
ATGTGTGAAGAGATAGGGTTATTGAGAAGAGAAAACAGAACGCTGGTCATCCGTGGCACT NM_001048212
RefSeq chr16 - 2530034 2531408 CEMP1 NA cementum protein 1 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_110354_PI430048170 0.3138659959213071.41710359088269 1.49964998608536
0.9429404480152290.374249197474965 A A A 0.6030667823416950.467527647881437
0.448916628698362 A A A LNCV6_110354_PI430048170 mRNA
ACAAGGAAGGAGATCATGAGATTTTAACAACGACGACTACATTTGTGCGTGGGACCTGGA NM_054113 RefSeq chr19
- 16161367 16173525 CIB3 117286 "calcium and integrin binding family member 3, transcript variant
1" GO:0005509 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_127527_PI430048170 0.0492535313775480.7557535773471725.2646618419353
5.03047454337369 4.96265698195058 P P P 5.44971620016661 5.69211990822301
5.32075777499036 P P P LNCV6_127527_PI430048170 mRNA
ATCTCACTCTTCCTCATCCTCTGCAATATCACACTGTGGATGATGCCTGCATTTGGCATA NM_001272005 RefSeq
chr17 + 74935801 74949992 OTOP3 347741 "otopetrin 3, transcript variant 2"
GO:0016021|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141333_PI430048170 0.000429888814831686 0.28938247842393 7.33872583619324
7.22198515674172 7.36293037419447 P P P 8.94625577005929 9.08073995124637
9.25116215753183 P P P LNCV6_141333_PI430048170 mRNA
GCAGCTTCATTTTCCAGATACCTTGACGCAGAATAAATTTTTTCATCATTTAGGTGCAAA NM_006547RefSeq chr7
- 23310208 23470376 IGF2BP3 10643 insulin-like growth factor 2 mRNA binding protein 3
GO:0005515|GO:0017148|GO:0048027|GO:0010467|GO:0003723|GO:0005634|GO:0006412|GO:0009653|GO:0045
182|GO:0005829|GO:0042035|GO:0005737|GO:0000166|GO:0051028|GO:0003730 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_142646_PI430048170 0.3262054720228591.04605723958555 0.487550490569527
0.3226185381433580.406743817125659A A A 0.2881339745376660.351968818466853
0.384962303757593A A A LNCV6_142646_PI430048170 mRNA
ATTTTACTATGACTACAACACGGTGCAGACTGTGGGCATGACTCTGGCAACCATCTTGTT NM_022006RefSeq chr19
+ 35143249 35154302 FXYD7 53822 FXYD domain containing ion transport regulator 7
GO:0034220|GO:0005886|GO:0051117|GO:0016021|GO:0055085|GO:0005216|GO:0043269 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140097_PI430048170 0.00422562659726155 0.4920302668840467.73001832202774
7.70533828948772 8.07160510543159 P P P 8.63590641707467 8.86086505518509
9.07603753420299 P P P LNCV6_140097_PI430048170 mRNA
AACGTTAACTGTGAAGTTACACACAGTAGCTGACTTCAAAGTGCCTGTTCTGTAAATTTT NM_031216RefSeq chr18
+ 12947983 12987536 SEH1L 81929 "SEH1-like (S. cerevisiae), transcript variant 2"
GO:0007077|GO:0010467|GO:0050830|GO:0019221|GO:0019058|GO:0002534|GO:0005635|GO:0044281|GO:0015
031|GO:0008645|GO:0005829|GO:0051315|GO:0015758|GO:0016032|GO:0006999|GO:0005975|GO:0019083|GO:0
055085|GO:0010827|GO:0031080|GO:0009405|GO:0000777|GO:0000776|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132316_PI430048170 0.2234670897998040.7663660547367415.05014620389299
4.81997016082011 5.33445457743525 P P P 5.15563139104249 5.32365685005964 5.8340493990665
P P P LNCV6_132316_PI430048170 mRNA
CTGAATCACTCCTTCTGTATTAGGGCATATACTTTCACTCTAAAACATTGTGGTAAATGA NM_153810RefSeq chr10
- 118680981 118755246 CACUL1 143384 "CDK2-associated, cullin domain 1"
GO:0005515|GO:0031461|GO:0006511|GO:0008284|GO:0000082|GO:0019901|GO:0045860|GO:0031625 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138538_PI430048170 0.0853291430731336 0.7448115454176444.31727524215476
4.11828413366367 3.80683081942228 P P P 4.54546823872605 4.59206359382612
4.41973741696114 P P P LNCV6_138538_PI430048170 mRNA
GGCAATGTGTTATACTTGGAAAGAGGTCATATTAATTTTATCACATTTTTGGGACTCAGC NM_001195643 RefSeq
chr3 - 94057921 94063223 DHFRL1 200895 "dihydrofolate reductase-like 1, transcript variant 1"
GO:0050661|GO:0005743|GO:0046105|GO:0003729|GO:0009165|GO:0005739|GO:0005759|GO:0046653|GO:0046
654|GO:0006545|GO:0006730|GO:0004146|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133716_PI430048170 0.4729749081310611.02281153971098 0.371537489193776
0.2530334641525240.278918765924753A A A 0.2630786678401570.283488582775526
0.261907601792489A A A LNCV6_133716_PI430048170 mRNA
GGGCAATGCTCTAGGTTTTTGGTGGCAGTCAATTTGGTATTATATATGATCATTTTCAAT NM_003413RefSeq chrX
+ 137566186 137572100 ZIC3 7547 Zic family member 3

GO:0005515|GO:0035469|GO:0007368|GO:0003700|GO:0071910|GO:0030324|GO:0005634|GO:0000978|GO:0009952|GO:0046872|GO:0006351|GO:0043565|GO:0001947|GO:0035545|GO:0001077|GO:0005737|GO:0045944|GO:0005654|GO:0045893|GO:0035019|GO:0071907 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142058_PI430048170 0.5529936085531111.3840526885174 2.86612517708722
3.34341746392211 1.73384477355885 A P A 1.96553570420455 2.37839370585947
2.56059484715058 A A P LNCV6_142058_PI430048170 mRNA
GTTAATCTTGGTGCTCTATGGTGCATTAGCAGAGATATGAACAATTAAATGAAGACAAAG NM_001142310 RefSeq
chr2 + 216081865 216102783 TMEM169 92691 "transmembrane protein 169, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132852_PI430048170 0.34408392508666 0.920433669538511 0.506072101885905
0.5383313873543090.441109477755282A A A 0.768823028150653 0.612139833998212
0.447192310224046A A A LNCV6_132852_PI430048170 mRNA
CCACTACATATGCACAAAATCTGCTGGATAAGTTTTAAGAGGGATATATTCTGAAAGCAT NM_001297705 RefSeq
chr1 + 81800396 81992738 ADGRL2 NA "adhesion G protein-coupled receptor L2, transcript variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144970_PI430048170 0.1479673929030470.805142536133007 12.8751800438304
12.5995565011557 12.3757913632712 P P P 13.107928356193 12.9251134975012
12.7803135853553 P P P LNCV6_144970_PI430048170 mRNA
CCGAAAACCCTGCCTTACCTCTCCCTTCCCCCTAACATTAAACTATTTGGCATGAAAAAA NM_005995 RefSeq chr11
- 67631302 67639560 TBX10 347853 T-box 10
GO:0003700|GO:0006357|GO:0005634|GO:0009653|GO:0003677|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138330_PI430048170 0.1651459415295350.713866010507162 2.98524408021136
2.88109669514821 3.11016343062771 P A P 3.20404480526298 3.25281598204189
3.88369428499574 P P P LNCV6_138330_PI430048170 mRNA
AATTGGAAGAATCAATACAGCTTAGATGGAGGTCTCCTCATCCAGTGGTAATAAAACATC NM_001195386 RefSeq
chr17 + 40819184 40836274 TMEM99 147184 "transmembrane protein 99, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127770_PI430048170 0.1861519752175480.764159981619596 5.32542341466916
5.45068455572221 6.00841689370594 P P P 5.78237636779469 6.00738434930862
6.22068797203775 P P P LNCV6_127770_PI430048170 mRNA
TATGTAAAAATGTGTGTACAGACTCACTGATGCAGCACTGTAGCCCATCACCTTGGAGCA NM_015316 RefSeq chr14
- 103733750 103847590 PPP1R13B 23368 "protein phosphatase 1, regulatory subunit 13B"
GO:0005515|GO:0005737|GO:0072332|GO:0005886|GO:0005654|GO:0005634|GO:0045786|GO:0008134 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133471_PI430048170 0.0330544177419341 1.67892280111939 7.98475139382774
7.98931019232935 7.65254003330334 P P P 6.87879977500682 7.47630242681811
6.98088867036748 P P P LNCV6_133471_PI430048170 mRNA
GGTGGTGAAAACAAACCCCGTGTATCTCTCAATAAAGGTGGCCGAAGGGCCTCGATGTGG NM_002531 RefSeq chr20
+ 62708836 62762771 NTSR1 4923 neurotensin receptor 1 (high affinity)
GO:0005515|GO:0008344|GO:0043066|GO:0005794|GO:0005886|GO:0004930|GO:0005783|GO:0007268|GO:0007186|GO:0005887|GO:0007218|GO:0045121|GO:0016492 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132178_PI430048170 0.0201808057374149 1.55112924803014 6.40063239273242
6.47455991306525 6.1923088607674 P P P 5.57665077148578 5.97688862528421 5.5919917117704
P P P LNCV6_132178_PI430048170 mRNA
ACATGGTCCGGAGATACACCCAGCTACCAATTCGGGACCAGGACCAACAGGACCGGACCC NM_001195259
RefSeq chr19 + 7916146 7919095 TGFBR3L 100507588 "transforming growth factor, beta receptor III-like" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133488_PI430048170 0.0872032028117032 0.761362867251229 2.89440013762044

3.03316045854626 2.57941800260069 A P A 3.02805185800962 3.26033634909793 3.4099154160231 P P P LNCV6_133488_PI430048170 mRNA GTGAACTTGTTGCACTGCAGAAACATATTCAGAGTTTATCTATGTAACTTATTCACTCTG NM_023037 RefSeq chr13 + 32031299 32296639 FRY 10129 furry homolog (Drosophila) GO:0005737|GO:0000922|GO:0005815 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101346_PI430048170 0.101958314417735 0.336348582783592 2.45339681182845 0.278687480942905 1.72730658880862 A A A 3.18622508709916 3.47872883386664 3.24554319917302 P P P LNCV6_101346_PI430048170 mRNA GTGGTTAATTATGATATTGAGTGGTGCATGAGGTAGGTGTTTAGAGTAATATTCTTTTGC NM_001297560 RefSeq chr19 - 21291159 21329439 ZNF708 7562 "zinc finger protein 708, transcript variant 2" GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144354_PI430048170 0.558826501770927 1.63243820948204 2.1933279347313 0.391514419704205 0.284771260652313 A A A 0.48212167693168 0.788155024164305 0.296139201124738 A A A LNCV6_144354_PI430048170 mRNA TTCATCACGTATGTGCTGCTACCTGTACAGCAGACATGCCGCTCCAGTGACATTTATAAT NM_001142644 RefSeq chr2 - 227979953 228181645 SPHKAP 80309 "SPHK1 interactor, AKAP domain containing, transcript variant 1" GO:0005739|GO:0005515|GO:0030018|GO:0006928|GO:0010738|GO:0051018|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132215_PI430048170 0.00266704397664933 0.70682819629959 9.86368408095577 9.81244428905145 9.73884882852502 P P P 10.1995319328613 10.3331234764634 10.380691935544 P P P LNCV6_132215_PI430048170 mRNA TGCTGTAGAGTTCACTGTTGTACACAGTCTGTTTTCTATTTGTTAAGAAAAACTACAGCA NM_002840 RefSeq chr1 + 43530875 43623672 PTPRF 5792 "protein tyrosine phosphatase, receptor type, F, transcript variant 1" GO:0016477|GO:0005887|GO:0005001|GO:0007185|GO:0007155|GO:1900121|GO:0032403|GO:0008201|GO:0035335|GO:0004725|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136836_PI430048170 0.229386294312085 1.19151964114013 3.86895207777315 3.64802313282789 3.73113218143151 P P P 3.79158540931506 3.39096924718264 3.26159359643529 P P P LNCV6_136836_PI430048170 mRNA TCTTCATCTGTGACTCCTGGTCTGAAAATGTTGTTATGCTATTAAAGTGATTTCATTCTG NM_000729 RefSeq chr3 - 42257825 42266170 CCK 885 "cholecystokinin, transcript variant 1" GO:0005515|GO:0030424|GO:0008284|GO:0032099|GO:0050731|GO:0001836|GO:0007409|GO:0005615|GO:0007205|GO:0030425|GO:0043194|GO:0051901|GO:0043195|GO:0043203|GO:0043204|GO:0001662|GO:0005184|GO:0032461|GO:0006919|GO:0005576|GO:0007165|GO:0005179|GO:0042755|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120954_PI430048170 0.632103736057207 0.941881259149127 9.93367415778272 9.83434829190322 9.84426004740927 P P P 9.729724028211 10.1859107205649 9.92128965780522 P P P LNCV6_120954_PI430048170 mRNA ACTGCTCCACCAAGGGTGCCCTGGACATGCTGACCAAGATCCGAGTGAATGCAGTAAACC NM_016286 RefSeq chr17 - 82035880 82037697 DCXR 51181 "dicarbonyl/L-xylulose reductase, transcript variant 1" GO:0005881|GO:0005997|GO:0005634|GO:0006739|GO:0005903|GO:0005902|GO:0016655|GO:0016020|GO:0051289|GO:0006006|GO:0050038|GO:0070062|GO:0042732|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90406_PI430048170 0.699753524431294 1.05185907900201 8.62847731614042 8.31019460455956 8.17354830808533 P P P 8.24305438877865 8.37165868331724 8.3142323931631 P P P LNCV6_90406_PI430048170 mRNA CCTTGCATGGATACATGGGAGGGAGACGTTATAGATTAAGAAATGATAGCAAGATAAACA NM_001170569 RefSeq

chrX - 119538148 119565409 CXorf56 63932 "chromosome X open reading frame 56, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145136_PI430048170 0.429447501000966 0.659201905778093 0.538073247915342
0.42744830792196 0.246774232962638 A A A 0.378068203833421 1.76922255035961
0.416313899923146 A A A LNCV6_145136_PI430048170 mRNA
GATACAGAGAACCTCTCAATAAATGATTTGTCGCCTGTCTGACTGATTTACCCTAGGAAA NM_001974 RefSeq chr19
+ 6887548 6940453 ADGRE1 NA "adhesion G protein-coupled receptor E1, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145206_PI430048170 0.177859483290954 0.381136203591334 0.392361573151428
0.431381554397096 0.364382114727494 A A A 0.481153045596322 2.45030095413121
1.80668590606048 A P A LNCV6_145206_PI430048170 mRNA
GTTCTACCCCTGGGATGTTTTGAGGGTCTTTGCAAGAATCATTAATACAAAGAATTTTTT NM_002982 RefSeq chr17
+ 34255276 34257201 CCL2 6347 chemokine (C-C motif) ligand 2
GO:0009408|GO:0035684|GO:0008360|GO:0019221|GO:0045202|GO:0005615|GO:0030968|GO:0043524|GO:0006935|GO:0000165|GO:0044299|GO:0031727|GO:0009887|GO:0007179|GO:0031663|GO:0010332|GO:0046677|GO:0005791|GO:0008009|GO:0032869|GO:0036006|GO:0032760|GO:0002523|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133553_PI430048170 0.00350725616451076 0.25772110664911 6.07009718119257
5.68303038734791 6.16740529951609 P P P 7.51339796859709 7.91548823498747
8.29821840245213 P P P LNCV6_133553_PI430048170 mRNA
GTAGGCTGAATCAATTATTTCAAGTGCACCTTATTAACAAAAGTATCAGTGGATCCAACA NM_032521 RefSeq chr20
+ 50731543 50753741 PARD6B 84612 par-6 family cell polarity regulator beta
GO:0005515|GO:0030334|GO:0005886|GO:0034329|GO:0045177|GO:0005634|GO:0007409|GO:0045216|GO:0005829|GO:0043234|GO:0005737|GO:0007049|GO:0006461|GO:0007163|GO:0070830|GO:0007043|GO:0005923|GO:0005938|GO:0070062|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128062_PI430048170 0.00136514238103893 0.455659418490477 4.75637858488985
4.78591824041825 5.08801986858086 P P P 5.87811567157108 5.97556006885209
6.18517310558741 P P P LNCV6_128062_PI430048170 mRNA
TACTCCATCTGCCACAGAATCCAGGATTCTATAGTTTTTTAGTTTCACTTCCCTATGTTC NM_175921 RefSeq chr5 +
41904367 41921636 C5orf51 285636 chromosome 5 open reading frame 51 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_134200_PI430048170 0.00420094849197822 0.444958564092028 5.14993221962735
5.05216922136866 4.89113018141766 P P P 6.41924737361988 5.95188486783801
6.20092717265061 P P P LNCV6_134200_PI430048170 mRNA
GGGCTGGAACATTATGAGTGCTCAATAAATATAAACTAATGAGAATGGTGGTGATGGAAA NM_001130858 RefSeq
chr15 - 43533461 43590253 PPIP5K1 9677 "diphosphoinositol pentakisphosphate kinase 1, transcript variant 5"
GO:0000827|GO:0006020|GO:0033857|GO:0005886|GO:0043647|GO:0003993|GO:0052724|GO:0052723|GO:0044281|GO:0000832|GO:0005524|GO:0005829|GO:0016310|GO:0005737|GO:0016311|GO:0005654 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_41218_PI430048170 0.0103073700505532 1.47380789023776 5.56825398620758
5.32163850490766 5.45104155085122 P P P 4.85181565783085 4.93048448901367
4.88944149851009 P P P LNCV6_41218_PI430048170 mRNA
ACACATAAACGGCAGTGTTAAAACATGAATGACTGTGTCTGCCTGTCCCCAAACAGGACA NM_022970 RefSeq chr10
- 121478329 121598458 FGFR2 2263 "fibroblast growth factor receptor 2, transcript variant 2"
GO:0005515|GO:0001657|GO:0033688|GO:0007409|GO:0009791|GO:0021860|GO:0042803|GO:0043231|GO:0031069|GO:0009880|GO:0007173|GO:0009887|GO:0005938|GO:0042472|GO:0005794|GO:0009986|GO:0017134|GO:0010453|GO:0030916|GO:0010518|GO:0018108|GO:0000122|GO:0001701|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_136925_PI430048170 0.0945555071338363 1.13979727496128 11.7188589796177
11.9292994077212 11.7569089613751 P P P 11.6685239699483 11.670992175032
11.5015973791076 P P P LNCV6_136925_PI430048170 mRNA
GGTGACGGCGACTGAGAGTGTGCGACGCGCCCCAGCCTCCCACATAAAGTTATAATTCTC NM_001007125 RefSeq
chr20 - 64083379 64084359 LKAAEAR1 198437 LKAAEAR motif containing 1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_135199_PI430048170 0.265580837748482 1.05000585862466 0.338125166564208
0.331303074413444 0.471409116248456 A A A 0.308503918180606 0.286447564606385
0.338587915710688 A A A LNCV6_135199_PI430048170 mRNA
CCTGATCCATCAGAATACTCGAAAGAGAAATACCGACTGAGTGTATTCATTAAAGAATTA NM_144659 RefSeq chr21
- 32574840 32585535 TCP10L 140290 t-complex 10-like
GO:0005515|GO:0001106|GO:0070491|GO:0005634|GO:0000122|GO:0043621|GO:0006351|GO:0042802 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137115_PI430048170 0.598818291839552 1.07707619257685 4.6943350407413 4.656253612781
4.31906655865961 P P P 4.56697392289308 4.63450885708777 4.12429821641753 P P P
LNCV6_137115_PI430048170 mRNA
ATCAACATCAAAGGGAACATGTCTGGGAACCGCCGCACAGCCAACATCAAGAGCCTAGGT NM_001037329
RefSeq chr11 + 6239091 6244477 CNGA4 1262 cyclic nucleotide gated channel alpha 4
GO:0005223|GO:0007608|GO:0060170|GO:0006996|GO:0007603|GO:0005222|GO:0030552|GO:0000139|GO:0030
553|GO:0005887|GO:0005249|GO:0030660|GO:0042391|GO:0071805 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_115397_PI430048170 0.0701471018168894 1.15478892040712 14.9672244572676
15.1336753896646 15.1472797983206 P P P 14.859161139127 14.7764171817672
14.9886198989383 P P P LNCV6_115397_PI430048170 mRNA
ATGTAAAAGGCCCCGTGCGCGAGGGCGACGTGCTCACCCTTTTGGAGTCAGAGCGAGAAG NM_001031 RefSeq
chr19 + 8321499 8322396 RPS28 6234 ribosomal protein S28
GO:0010467|GO:0003735|GO:0019083|GO:0006364|GO:0006614|GO:0019058|GO:0015935|GO:0006415|GO:0006
412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0000184|GO:0022627|GO:0016032|GO:0042274|GO:0
044267|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126494_PI430048170 0.574786112318496 1.07303714769501 4.91045493556214
4.75248002321289 5.06831152512173 P P P 4.57225547063801 5.10130115290903 4.7168888598928
P P P LNCV6_126494_PI430048170 mRNA
ATGTGATTACTGTGGGAAAGGCTTTAGTGACTTCTCAGGATTGCGCCACCACGAGAAAAT NM_144680 RefSeq chr17
- 11977438 11997372 ZNF18 7566 "zinc finger protein 18, transcript variant 1"
GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0003677|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138674_PI430048170 0.274135067384612 0.668133707623462 0.271950664183094
0.299930541848855 0.40460525405257 A A A 0.367061244378678 0.630184266137743
1.48207364814289 A A A LNCV6_138674_PI430048170 mRNA
CAGAGTTGCCATGTCAACACATGGGGAATGATATGATAGAAACAATCTTTATGACTAAAA NM_153217 RefSeq chr5
+ 73173195 73175143 TMEM174 134288 transmembrane protein 174 GO:0005789|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137274_PI430048170 0.424799089974127 0.804237174766948 0.680574012261668
0.491803509514624 0.357820269344038 A A A 1.3116653756283 0.525697403473772
0.498679611932683 A A A LNCV6_137274_PI430048170 mRNA
CCAGTGTTCTTTTGGTTCTGATTTCATCAGTCTCAATAAAGTTCCGATCTCTCTTTAAAA NM_001098814 RefSeq chr16
- 4189373 4242080 SRL NA sarcalumenin NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128822_PI430048170 0.417593903378408 1.06922698759645 8.93968538022665
9.15184292286252 9.16168529292556 P P P 8.83257908409837 9.03033492873209

9.09829238519636 P P P LNCV6_128822_PI430048170 mRNA
TGATTTTACTTTAGAACACTACAGAGTTCCTGGACCGGGTGAAGGCATTAGCTGGGTGTT NM_005539RefSeq chr10
+ 132537848 132783480 INPP5A 3632 "inositol polyphosphate-5-phosphatase, 40kDa"
GO:0005515|GO:0052658|GO:0043647|GO:0016020|GO:0005886|GO:0052659|GO:0046856|GO:0044281|GO:0004
445|GO:0042731|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137973_PI430048170 0.27146645702036 1.13833741192511 6.44540715589782
6.85642208399895 6.63746635786584 P P P 6.47247891705722 6.50793982720154
6.42628832412041 P P P LNCV6_137973_PI430048170 mRNA
GTTTGTTTCATTTGTTGACTTAGTTTCCAGCCAAGAAGGAAACGACTGTCTCCCCCATGT NM_139069RefSeq chr5
- 180233594 180292071 MAPK9 5601 "mitogen-activated protein kinase 9, transcript variant JNK2-b1"
GO:0005515|GO:0014075|GO:0051403|GO:0010770|GO:0031175|GO:0046328|GO:0002756|GO:0004705|GO:0034
644|GO:0002755|GO:0071356|GO:0031396|GO:0038124|GO:0038123|GO:0010744|GO:0034134|GO:0031394|GO:0
006950|GO:0009636|GO:0031435|GO:0032722|GO:0007417|GO:0002224|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135972_PI430048170 0.4689805399827340.9129440827429831 2.5331561587721
12.5702548252712 12.7300552708726 P P P 12.4671579497256 12.871768711498 12.860793554036
P P P LNCV6_135972_PI430048170 mRNA
AGAGGATCTGGCTCTAGGTTGGGATCAATCCTGAATTTCGTTATGTGTTAATTTACTTTT NM_002629RefSeq chr10
+ 97426269 97433441 PGAM1 5223 phosphoglycerate mutase 1 (brain)
GO:0045730|GO:0005515|GO:0019901|GO:0004082|GO:0004083|GO:0005975|GO:0006094|GO:0044281|GO:0043
456|GO:0006096|GO:0005829|GO:0006110|GO:0005737|GO:0016020|GO:0016311|GO:0009405|GO:0006006|GO:0
004619|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137765_PI430048170 0.4021409580406971.06076742476047 10.7410445935773
10.8296688311874 10.8142167392173 P P P 10.5406280668217 10.816355839703
10.7597167802038 P P P LNCV6_137765_PI430048170 mRNA
TATTCCTTACAGCTTCCTTGTAACCACAGCCCTAAATCCATGATAAAGCTACTCTTGTAC NM_012151RefSeq chrX
- 155456913 155458615 F8A1 8263 coagulation factor VIII-associated 1
GO:0008150|GO:0003674|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127099_PI430048170 0.0309390498941318 0.5089294235688484.1776571270586
4.48002896267817 4.32348440399768 P P P 4.86140573222232 5.44791602850064
5.52448686611659 P P P LNCV6_127099_PI430048170 mRNA
TTGTTGTTGTTGTTTTTTCATGCCCCATACTACTGAATAAACTAGTTCTGTGCGGGTACANM_001408RefSeq chr1 +
109250018 109275756 CELSR2 1952 "cadherin, EGF LAG seven-pass G-type receptor 2"
GO:0022407|GO:0006355|GO:0005886|GO:0004930|GO:0005509|GO:0003341|GO:0021999|GO:0032880|GO:0048
813|GO:0042384|GO:0005737|GO:0007186|GO:0021591|GO:0033326|GO:0016021|GO:0001764|GO:0016055|GO:0
007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135975_PI430048170 0.7305347325665270.9570477612539715.22051801928171
5.23892783640393 4.82667847228332 P P P 4.96945958725882 5.37315922675593
5.14127752881638 P P P LNCV6_135975_PI430048170 mRNA
GAAGTTACCATGGGAAGTCCCAAGAGGAATACTGCTTCTTTCATAAACATGGTCCTCTCC NM_001013672 RefSeq
chr17 + 410326 414666 C17orf97 400566 chromosome 17 open reading frame 97 GO:0016598 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134340_PI430048170 0.0687713209373693 0.5582859349644883.9133456585363
3.27707481887464 3.90906966283654 P P P 4.023764996774 4.71597232867483
4.84365595199766 P P P LNCV6_134340_PI430048170 mRNA
GCACACATAAAACAATGCCCTTTTGTGTACATTCAGGCATACCCATTTTAATCAATTTGA NM_002203RefSeq chr5
+ 52989325 53094779 ITGA2 3673 "integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor),
transcript variant 1"
GO:0005515|GO:0014070|GO:0005518|GO:0030879|GO:0033591|GO:0014075|GO:0051971|GO:0060100|GO:0007

411|GO:0001618|GO:0030198|GO:0009887|GO:0033343|GO:0008305|GO:0038065|GO:0046982|GO:0009986|GO:0
014850|GO:0031589|GO:0038064|GO:0045785|GO:0005178|GO:0031346|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131770_PI430048170 0.1485626744190040.6601782061528151 0.2415687472143
9.43382642654979 9.27450034323507 P P P 10.4785864485969 10.340752518121
10.0979000712022 P P P LNCV6_131770_PI430048170 mRNA
TGCTCCTCTCTCCCAGTCTGTGCAATAAAGGTCGTGAAGATCTCTCAGCCAGGGAAAAAA NM_014262RefSeq chr12
+ 6828372 6839854 P3H3 NA prolyl 3-hydroxylase 3 NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139761_PI430048170 0.9331196665731730.9905196695044820.331172117572339
0.8330415988587860.472781132950088A A A 0.5740213965183690.784340789326155
0.331883388173557A A A LNCV6_139761_PI430048170 mRNA
GTAGGAAATGGAGGGTCATAGGACTTCGCTAAAATTCTGATACTGTTTACAAAGAAAACC NM_147191RefSeq chr10
- 125766455 125775821 MMP21 118856 matrix metallopeptidase 21
GO:0031012|GO:0002244|GO:0005509|GO:0006508|GO:0008270|GO:0005576|GO:0004222 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_88946_PI430048170 0.0439551780417399 1.27062451722157 6.19705355530264
6.05122482271055 6.29847845619126 P P P 5.77087621029172 5.71595567737837
6.01596470508185 P P P LNCV6_88946_PI430048170 mRNA
CTTCCAGTTATTTATTTGGGGTCTGAAGGATATCAACAGCTCATCTGTGACCAACAGGGC NM_001145548 RefSeq
chr16 - 84974460 85011535 ZDHHC7 55625 "zinc finger, DHHC-type containing 7, transcript variant
1"
GO:0018345|GO:0005794|GO:0018230|GO:0016409|GO:0005730|GO:0008270|GO:0005654|GO:0005634|GO:0016
021|GO:0019706|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101875_PI430048170 0.541567664963265 1.09500440721026 7.23133895999104
6.97826237719429 7.07356141308933 P P P 6.60605354338485 7.33611137312704
6.86278105171305 P P P LNCV6_101875_PI430048170 mRNA
TTTCTTCAAGAGTTTGGTCATCGAGCTGGACAAAGATCTTTATGGCCCTGACAACCACCT NM_003078RefSeq chr7
- 151238972 151277145 SMARCD3 6604 "SWI/SNF related, matrix associated, actin dependent regulator
of chromatin, subfamily d, member 3, transcript variant 2"
GO:0005515|GO:0071565|GO:0000790|GO:0003139|GO:0035257|GO:0005634|GO:0044281|GO:0071564|GO:0003
219|GO:0042692|GO:0005737|GO:0030374|GO:0016514|GO:0006338|GO:0044255|GO:0016922|GO:0003407|GO:0
006357|GO:0003713|GO:0005102|GO:0043393|GO:0002052|GO:0006337|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144968_PI430048170 0.1663208960614540.8548247733397999.36067234110299
9.35538571334852 9.43739338227975 P P P 9.39873036921136 9.66484154953636
9.74766893874405 P P P LNCV6_144968_PI430048170 mRNA
CGAGGCATTAACCCCATGGTTAATGGACTGGTCACCAGTTTTTATTTTATTTTTATGAAT NM_014754RefSeq chr8
+ 96261885 96334551 PTDSS1 9791 "phosphatidylserine synthase 1, transcript variant 1"
GO:0016020|GO:0005789|GO:0044281|GO:0016021|GO:0006644|GO:0016740|GO:0006659|GO:0046474 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142042_PI430048170 0.198851172289625 0.7690742334887364.80115822487202
4.15539696077289 4.44387304367979 P P P 4.52113503826398 5.03077077853107
5.00312620670368 P P P LNCV6_142042_PI430048170 mRNA
TGATTTTGTTCTCTCTCCTTTGTCTGTTTGTTGTCAAAGATGCTGCTGGGCAGACAGGCA NM_004978RefSeq chr1
+ 110210713 110234052 KCNC4 3749 "potassium channel, voltage gated Shaw related subfamily C,
member 4, transcript variant 1"
GO:0005251|GO:0031594|GO:0005886|GO:0005267|GO:0007268|GO:0046928|GO:0005249|GO:0008076|GO:0034
765|GO:0043679|GO:0051260|GO:0016021|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA

NA NA NA
LNCV6_129920_PI430048170 0.3409572237084981.82603748004876 2.84641832931006
1.38196505328928 1.05556785116974 A A A 1.46701770191497 0.42666945776997
1.26036535709344 A A A LNCV6_129920_PI430048170 mRNA
ACCACATTTAAGTGATCTAAAACCCATAGCATTGTAGTCATGGCAACCCGCTAAACTTTC NM_002037RefSeq chr6
- 111660331 111873452 FYN2534 "FYN proto-oncogene, Src family tyrosine kinase, transcript variant 1"
GO:0005515|GO:0008360|GO:0050900|GO:0030154|GO:0043524|GO:0042608|GO:0001948|GO:0042609|GO:0007
173|GO:0007411|GO:0042127|GO:0007612|GO:0043123|GO:0038083|GO:0014069|GO:0030168|GO:0014068|GO:0
007417|GO:0044325|GO:0031234|GO:0042110|GO:0046875|GO:0008543|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131949_PI430048170 0.0628767398765881 0.6483191575296439.52925751146782
9.31885756231003 9.72221695819694 P P P 9.83412584692815 10.083495770859
10.4816443924697 P P P LNCV6_131949_PI430048170 mRNA
CATTTGTAAATCATGGGAATGTATTTGATGGTAATTGCCTGTGGTGGTTGTATCATGATT NM_001025100 RefSeq
chr18 - 77012782 77132818 MBP 4155 "myelin basic protein, transcript variant 8"
GO:0005515|GO:0005886|GO:0042552|GO:0007568|GO:0007268|GO:0009636|GO:0005634|GO:0002020|GO:0007
417|GO:0008366|GO:0033269|GO:0006955|GO:0070542|GO:0021762|GO:0043218|GO:0043025|GO:0032570|GO:0
061024|GO:0050771|GO:0034612|GO:0019911|GO:0046689 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_135835_PI430048170 0.39032413210694 1.14162577382951 0.436764879925457
0.4866673549060850.938405744840989A A A 0.5259971760728530.401042784503582
0.412835710050164A A A LNCV6_135835_PI430048170 mRNA
CGTCATAGGCTTCTGCACGTTGGATCAACTAATGTTGTTTACAATATAGATGACATTTTA NM_003914RefSeq chr13
+ 36432271 36442882 CCNA1 8900 "cyclin A1, transcript variant 1"
GO:0005515|GO:0019901|GO:0010389|GO:0000079|GO:0007283|GO:0005829|GO:0000082|GO:0007067|GO:0000
083|GO:0000086|GO:0015630|GO:0005654|GO:0000278|GO:0007141|GO:0051301 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_93773_PI430048170 0.0092605629951541 3.58161201219658 3.68478022029743
3.36487555316489 3.91952108338646 P P P 2.2858471415192 1.74866502790876
1.29559197133965 A A A LNCV6_93773_PI430048170 mRNA
TCGTGGTAGCAACTCTTCCACAATTAAAGTTCCTCTTTAGAGAGCAAAGACCACCTACAG NM_012472RefSeq chr8
- 132571952 132675617 LRRC6 23639 "leucine rich repeat containing 6, transcript variant 1"
GO:0060287|GO:0044458|GO:0005515|GO:0036159|GO:0005929|GO:0003674|GO:0005737|GO:0036158|GO:0003
341|GO:0030317|GO:0008584 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134186_PI430048170 0.1866885237792490.4359426213390420.316277587393728
0.2957758930066320.315995458561065A A A 0.2971766617659461.86324190450318
1.87207409340977 A A A LNCV6_134186_PI430048170 mRNA
CTCCTACAGGGAAATGTATCTGACTCTGTTTACATAATTTGTTGCATTACTTAGTACAGA NM_014974RefSeq chr10
- 274189 689668 DIP2C 22982 DIP2 disco-interacting protein 2 homolog C (Drosophila)
GO:0008150|GO:0003674|GO:0008152|GO:0005634|GO:0005575|GO:0003824|GO:0008134 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139655_PI430048170 0.0589676449800485 0.7680651292157298.22928885231033
8.15511235508456 8.19182770669445 P P P 8.38546404105364 8.58200074810809
8.73111992537082 P P P LNCV6_139655_PI430048170 mRNA
CCTTTATCACATAACTGTAATATTTGGTTGCTCAGCATAAGTGATGGAAGCAAACACTAA NM_021137RefSeq chr17
+ 28335521 28347009 TNFAIP1 7126 "tumor necrosis factor, alpha-induced protein 1 (endothelial)"
GO:0005515|GO:0004842|GO:0016567|GO:0035024|GO:0045740|GO:0043149|GO:0019904|GO:0005730|GO:0006
915|GO:0009790|GO:0006260|GO:0005737|GO:0006955|GO:0016477|GO:0031463|GO:0051260|GO:0043161|GO:0
017049|GO:0005768. NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133630_PI430048170 0.0858432672048212 0.3770130481258170.57600494849788
2.37783672804681 1.57383757533412 A A A 2.80814489042269 3.19474065150368
3.24433450359126 P P P LNCV6_133630_PI430048170 mRNA
CCTTGTATGCCAGCACCTGGTAACAGTAGAGATTTTTATACATTAATCTTGATCTGTTTT NM_015904RefSeq chr2
+ 99337370 99400265 EIF5B 9669 eukaryotic translation initiation factor 5B
GO:0005515|GO:0010467|GO:0006446|GO:0003924|GO:0003743|GO:0005525|GO:0044267|GO:0006412|GO:0006
413|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145560_PI430048170 0.489040193275019102.941069961561 7.19949502312042
16.0908765464567 7.4647333327378 P M P 7.35814757983387 8.05483862100531
7.97261358694224 P P P LNCV6_145560_PI430048170 mRNA
AGGATGATGTGCTGTATGCGCTGAAAGACGAGTAAAGGGGCTTCACAAGTTAAAAGACTG NM_004153RefSeq
chr1 - 52372828 52404471 ORC1 4998 "origin recognition complex, subunit 1, transcript variant 1"
GO:0005515|GO:0000808|GO:0005886|GO:0005730|GO:0005634|GO:0003677|GO:0005524|GO:0005829|GO:0006
260|GO:0000082|GO:0005737|GO:0000083|GO:0006270|GO:0003682|GO:0005654|GO:0005664|GO:0000278 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134287_PI430048170 0.8696079338828591.04076092053153 1.00565041642793
1.60602941773696 0.420830177204308A A A 1.7034348970599 0.516573452740717
0.539113471506281A A A LNCV6_134287_PI430048170 mRNA
AAAGTTGGCAGATGGCAACACAGCTAGGGAGCAATAATTTTGTTGTGGGGAGGATTTGGT NM_006441RefSeq chr15
- 79843546 79897049 MTHFS 10588 "5,10-methenyltetrahydrofolate synthetase (5-
formyltetrahydrofolate cyclo-ligase), transcript variant 1"
GO:0005737|GO:0005542|GO:0030272|GO:0046653|GO:0015942|GO:0005524|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130282_PI430048170 0.2458830505088131.09668664261266 10.4956653526405
10.7280270648802 10.4775786771671 P P P 10.447997022542 10.4813379644911
10.3845702614718 P P P LNCV6_130282_PI430048170 mRNA
AGTACAGGGCAGGAGCTGCTGTGGTGTTCCCTTGGCAAATGAAAGTTTTATTTTCGTTTG NM_005125RefSeq chr11
+ 66593218 66606019 CCS9973 copper chaperone for superoxide dismutase
GO:0005515|GO:0051353|GO:0005507|GO:0006801|GO:0015035|GO:0005634|GO:0035434|GO:0005829|GO:0015
680|GO:0005737|GO:0005375|GO:0019430|GO:0008270|GO:0000302|GO:0055114|GO:0004784 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137848_PI430048170 0.00245217509282885 1.33496052080318 14.8155711761944
14.6911003669162 14.8367459345292 P P P 14.4317719139703 14.3667193788746
14.2955708180533 P P P LNCV6_137848_PI430048170 mRNA
TCACAGGCAAGAGCAAGAAGAGAAACTGACCCTGAATGTTCAATAAAGTTGATTCTTTGT NM_173852RefSeq chr1
- 155169407 155173328 KRTCAP2 200185 keratinocyte associated protein 2
GO:0008150|GO:0003674|GO:0016021|GO:0005575|GO:0008250 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134760_PI430048170 0.2190896740427390.8557342366303089.38574350099378
9.46843859496794 9.24159969051869 P P P 9.34861316183811 9.7722799840204
9.62666231978581 P P P LNCV6_134760_PI430048170 mRNA
TCACTTTTACTGCTTTGTAGTGACTCGTGCTCTCCAACCTGTCTTCCTGAAAAACCAAGG NM_000302RefSeq chr1
+ 11934666 11975542 PLOD1 5351 "procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1"
GO:0001666|GO:0031418|GO:0005506|GO:0008475|GO:0042803|GO:0008544|GO:0030198|GO:0030867|GO:0005
789|GO:0046947|GO:0006464|GO:0055114|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131782_PI430048170 0.1206289893024111.12752048531482 10.2324225061847
10.0288982681354 10.0430957017275 P P P 9.92855378216706 9.92161043449502
9.94378004695836 P P P LNCV6_131782_PI430048170 mRNA
TCCCTGTGAGATTGAATACTTGTGCCACACATGTCACAAAAGAGTATGGAAATAAAAGAA NM_022750RefSeq chr7

- 140023743 140063721 PARP12 64761 "poly (ADP-ribose) polymerase family, member 12, transcript variant 1" GO:0008152|GO:0005634|GO:0046872|GO:0003950 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100806_PI430048170 0.2345475597437821.28683909310511 7.15354122306562
7.46513972298778 7.30155548677745 P P P 7.37634740321271 6.77191140984795
6.57151977132913 P P P LNCV6_100806_PI430048170 mRNA
CTCGAAGCACAGCACACACTAACATCACCGTGGATGGACTTGAACCCGGGTGTTTGTATG NM_002842RefSeq chr19
- 55181246 55209506 PTPRH 5794 "protein tyrosine phosphatase, receptor type, H, transcript variant 1" GO:0005515|GO:0005737|GO:0006470|GO:0005887|GO:0005001|GO:0006915|GO:0035335 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131382_PI430048170 0.4315622131621550.9340914279436771 1.8066574240366
11.9027772517624 11.7616784460556 P P P 12.1027314438431 11.8142014485141
11.8345609851796 P P P LNCV6_131382_PI430048170 mRNA
GACTACAGCTGCCTTGTCTAAAACCTGGGATCTTAAAAGTGTTATTTTGGCTTTTATTTTNM_017877RefSeq chr2 +
26764273 26781231 SLC35F6 54978 "solute carrier family 35, member F6"
GO:0005739|GO:0005515|GO:0008284|GO:0006810|GO:0016021|GO:0005765|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132736_PI430048170 0.8745132730595481.03535010637099 3.17684735650329
2.81649577550495 2.29170683550456 P A A 2.83380612987447 3.14347023738324 2.1048969094293
P P A LNCV6_132736_PI430048170 mRNA
AACTTTTGAAAGCCCCTGCGTTCTGAGTGGACCGATTTCTAAATCCATACCTACACACCA NM_016102RefSeq chr1
- 228407934 228416882 TRIM17 51127 "tripartite motif containing 17, transcript variant 1"
GO:0005622|GO:0005515|GO:0004842|GO:0016874|GO:0008270|GO:0005575|GO:0051865 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144575_PI430048170 0.0263318507507252 1.14116957574425 0.700291593846384
0.7691105993514680.771473904596911 A A A 0.6392516151861080.506182825814999
0.521316965810093 A A A LNCV6_144575_PI430048170 mRNA
ATCCTTTCTTCTATTTCTTTCTTTTGTGGCCAGAAAGTCAGGACCTCAAAGAGGTATAAG NM_214711RefSeq chr4
+ 70154186 70166609 PRR27 NA proline rich 27 NA . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_139054_PI430048170 0.0115732180545537 0.2973848798245870.691883109008969
0.2856407444523021.02307824307151 A A A 1.7985719065695 2.66558802802697
2.70951375089098 A P P LNCV6_139054_PI430048170 mRNA
AAACAGACACTGTCATATTTATTTGTGAAAACCTGATTCAATATTGCATCAGCTGCTCTG NM_001297574 RefSeq -
- 0 0 --- NA "transcriptional regulating factor 1, transcript variant 1" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133406_PI430048170 0.0133863410839226 0.3069468285056164.76028216654384
4.73210545318735 4.77711395977523 P P P 6.10857191857344 6.39842796009493
6.79243385417643 P P P LNCV6_133406_PI430048170 mRNA
GCTGGAACTACTCGTATAAGGACTAGACTGTATTTTTGACATGCTCCTATTTTTGTAACT NM_018698RefSeq chrX
+ 109535780 109544698 NXT2 55916 "nuclear transport factor 2-like export factor 2, transcript variant 1"
GO:0005737|GO:0005634|GO:0051028|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137787_PI430048170 0.000926535332933732 0.4217184093107443.86084215451562
4.01323206532996 4.20775583594707 P P P 5.2031892121307 5.41439056475949
5.21219149625769 P P P LNCV6_137787_PI430048170 mRNA
GCTTGAGATATGGTTAACTTTTTTCTTTTGTTGGTTTTGACTTAGATGGACACCATGAGA NM_015885RefSeq chr11
+ 83157094 83185793 PCF11 51585 PCF11 cleavage and polyadenylation factor subunit
GO:0008380|GO:0006379|GO:0010467|GO:0006369|GO:0006366|GO:0000398|GO:0031124|GO:0005849|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141151_PI430048170 0.3418936204788510.8831713080914596.50352105738509

6.72985912255803 6.83419904551557 P P P 6.90191939007555 6.6263243833631 7.0632278807729
P P P LNCV6_141151_PI430048170 mRNA
GTGCATCGTGTCAACTACTGTACATGTTGGTCATGTGAAAGGAATTATATATGTATAGTA NM_145291 RefSeq chr4
+ 4290196 4321786 ZBTB49 166793 zinc finger and BTB domain containing 49
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130770_PI430048170 0.0127727249798522 0.5250967117933236.66404947373553
7.11745159504399 7.16238041828195 P P P 7.88389131660856 7.79315046226136
8.08937420628241 P P P LNCV6_130770_PI430048170 mRNA
ATTACGGCATCAGAAAGGGCAACTTACTCTTCCTGGCATGTTATTGTATTGGAGGGTGAC NM_006398 RefSeq
chr6_GL000253v2_alt - 820770 825085 UBD 10537 ubiquitin D
GO:0005515|GO:0006511|GO:0016567|GO:0043065|GO:0016235|GO:0010243|GO:0032446|GO:0005634|GO:0005
737|GO:0070842|GO:0070628|GO:0006508|GO:0034612|GO:0034341|GO:0043011|GO:0043123 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132611_PI430048170 0.0651343876620443 0.7833478878433335 12.8618179577047
12.6564342488098 12.5092090214238 P P P 13.0042670569831 13.205020184511
12.8778508865453 P P P LNCV6_132611_PI430048170 mRNA
ACGGATGCGTGGGCAGAGGAATGTGGGCTATGTAGTCATAATAAATTAGGACACAAAAAA NM_001640 RefSeq
chr3 + 49674001 49683501 APEH 327 acylaminoacyl-peptide hydrolase
GO:0031965|GO:0005737|GO:0004252|GO:0006508|GO:0008242|GO:0050435|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128886_PI430048170 0.0497840239001975 0.662335164228868 8.46824504388554
7.93176223294068 8.04715109306889 P P P 8.65235030964713 8.87285250677274
8.75337505245225 P P P LNCV6_128886_PI430048170 mRNA
ACTTTGGGAGGGTAAAGGACAGGGGCCTTATTTAAAATAAAGACTGAAGGATAATAAGTG NM_019020 RefSeq chr17
- 79932342 80035858 TBC1D16 125058 "TBC1 domain family, member 16, transcript variant 1"
GO:0005515|GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95802_PI430048170 0.1484175838784540.6749920147450324.9318112331499 4.9342324636813
5.77500957320995 P P P 5.70299043105603 5.67222617973316 6.09917507996421 P P P
LNCV6_95802_PI430048170 mRNA
ATTTGGTTCAACGACTCTTCTTTGCTGGACAGATCAATGGCACCACTGGTTATGAGGAAG NM_001123226 RefSeq
chr6 + 73461730 73501456 MTO1 25821 "mitochondrial tRNA translation optimization 1, transcript
variant 3" GO:0005739|GO:0050660|GO:0070899|GO:0055114 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137634_PI430048170 0.6345437295922920.9854889496069390.425058381080644
0.4491552940033570.360997125438302 A A A 0.4937168371402030.393644275073019
0.41054625884743 A A A LNCV6_137634_PI430048170 mRNA
GTAAAAAGGGATATCTATGGATTTCCCTAGGTAGGAGATAACAAGTATGTACCATTACTG NM_001442 RefSeq chr8
- 81478496 81483238 FABP4 2167 "fatty acid binding protein 4, adipocyte"
GO:0071285|GO:0005811|GO:0042632|GO:0005215|GO:0005504|GO:0005634|GO:0044281|GO:0001816|GO:0005
737|GO:0050872|GO:0050873|GO:0050729|GO:0006810|GO:0006469|GO:0019433|GO:0045892|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133042_PI430048170 0.7742066898198171.05527504557965 3.47264240881903
3.41375184598829 3.99583708433123 P P P 2.95485421544632 3.74655086671061
3.86405189965975 P P P LNCV6_133042_PI430048170 mRNA
TGCTGCCAGATAATCTAAGTCTTCCAATGCCTGCATCAAACTTTCTGGTGCTAGGAAAGG NM_078469 RefSeq chr10
+ 125823534 125842807 BCCIP 56647 "BRCA2 and CDKN1A interacting protein, transcript variant C"
GO:0005515|GO:0007049|GO:0019908|GO:0006281|GO:0061101|GO:0005634|GO:0000079|GO:0019207 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_130797_PI430048170 0.0160354526880266 0.61849873540603312.6698856840471
12.5659030754572 12.9739042023332 P P P 13.4068479794916 13.2305330259162
13.6522491408862 P P P LNCV6_130797_PI430048170 mRNA
CTACGAGAGTGATACTTTGCTGAAAAGTCTTTCCCCTATTGTTTATCTATTGTCAGTATT NM_058179RefSeq chr9 +
78297074 78330093 PSAT1 29968 "phosphoserine aminotransferase 1, transcript variant 1"
GO:0034641|GO:0005737|GO:0030170|GO:0008652|GO:0004648|GO:0006564|GO:0044281|GO:0008615|GO:0070
062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136809_PI430048170 0.0263606830756252 0.78791271726737915.8029138054361
15.7788558801574 16.0228830827664 P P P 16.2540137565447 16.1047189663179
16.2840224807028 P P P LNCV6_136809_PI430048170 mRNA
GGGTGTCTAAGTTTCCCCTTTTAAGGTTTCAACAAATTTCATTGCACTTTCCTTTCAATA NM_021009RefSeq chr12 -
124911644 124915041 UBC 7316 ubiquitin C
GO:0005515|GO:0002474|GO:0010467|GO:0006367|GO:0007220|GO:0019221|GO:0007249|GO:0019058|GO:0002
020|GO:0002756|GO:0034220|GO:0007173|GO:0007219|GO:0002755|GO:0007179|GO:0006977|GO:0000209|GO:0
038124|GO:0038123|GO:0005975|GO:0005978|GO:0034134|GO:0042059|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_70445_PI430048170 0.5222017004756550.9447708829862044.29998542915218 4.0629196776491
4.05839298699755 P P P 4.06001105635903 4.25994106958677 4.34598247538186 P P P
LNCV6_70445_PI430048170 mRNA
GCACAGATTTATGTAATGTCAACTTTACTGAGAATTTTCCACCTCCTGACACAACACCAC NM_001204RefSeq chr2
+ 202376326 202567751 BMPR2 659 "bone morphogenetic protein receptor, type II (serine/threonine
kinase)"
GO:0005515|GO:0030308|GO:0006366|GO:0044214|GO:0048842|GO:0005615|GO:0001946|GO:0009925|GO:0002
063|GO:0004702|GO:0042127|GO:0043025|GO:0007178|GO:0003085|GO:0023014|GO:0001707|GO:0030501|GO:0
009986|GO:0048286|GO:0030509|GO:0032924|GO:0030166|GO:0010595|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132966_PI430048170 0.1941199776655673.01714070451614 0.341440018847542
2.67631341337392 1.70734035621463 A A A 0.2719616964836640.267466563025508
0.27473662613223 A A A LNCV6_132966_PI430048170 mRNA
GAGGTAAAGAAAGCTCTGTTGAAGCTGAAAAATGGGTCAGTATTTGCTCAGGGTGAATAG NM_001004463 RefSeq
chr11 - 124038065 124039001 OR10G7 NA "olfactory receptor, family 10, subfamily G, member 7"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128327_PI430048170 0.2331154420390150.8514973166411257.13972119160476
7.06311460489693 7.51543637128125 P P P 7.53261320406886 7.3048944500983
7.60178650880856 P P P LNCV6_128327_PI430048170 mRNA
TTCTTATTGCCTTTGGCTGTTGATTAGTACAGTACAAGTGCGATTTCAAAAAGATCTTGA NM_022735RefSeq chr1
- 226144678 226186722 ACBD3 64746 acyl-CoA binding domain containing 3
GO:0005739|GO:0005515|GO:0006694|GO:0005794|GO:0016020|GO:0000139|GO:0006810|GO:0016021|GO:0000
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128635_PI430048170 0.1747687170101660.4230352038580591.79674247310555
0.4057306546514360.267024926666556 A A A 2.29837409815083 2.86659175035314
0.982972529060579 A P A LNCV6_128635_PI430048170 mRNA
GAAGGATCTTGCCTGCATGAAACATGTTCTCAATAAAACTCTGTGTTGAATTTATGCCAA NM_001763RefSeq chr1
+ 158254136 158258268 CD1A 909 CD1a molecule
GO:0071723|GO:0005515|GO:0030881|GO:0006955|GO:0005886|GO:0005887|GO:0030884|GO:0030883|GO:0048
007|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140854_PI430048170 0.4311070829377680.6271508729772420.564366542404336
0.4081493448379540.555289360705382 A A A 1.99659428873001 0.517587802373717
0.479961727757175 A A A LNCV6_140854_PI430048170 mRNA

TTGTAGCTGTAGAGTACTAATATTTGTACTCTCTTGCAAAGAATGTGATCTAGTTGTGGA NM_017658 RefSeq chr14 - 44924309 44961976 KLHL28 54813 kelch-like family member 28 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136568_PI430048170 0.385970523094288 0.974845852415756 0.452444673891446 0.453232567763099 0.375679683624815 A A A 0.409666277912313 0.499997386019761 0.481749799412279 A A A LNCV6_136568_PI430048170 mRNA
CTGGCACAGACTACTTAAATGGGTCTGTTTTCACTTTGCTCATTTTTCTTCAATAAATCT NM_033122 RefSeq chr4 + 70334953 70337116 CABS1 85438 "calcium-binding protein, spermatid-specific 1" GO:0031514|GO:0005509|GO:0005743|GO:0007283 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133395_PI430048170 0.938943686447328 1.00257966819892 5.18328131745484 5.30638832905062 5.11670153199544 P P P 4.97017615855369 5.36331104025679 5.24064004394321 P P P LNCV6_133395_PI430048170 mRNA
TGGGATAAGTCTGGGACACTGTTTCAGTTCAATAAAGAGGCTTTTTTCTTCCTTAAAAAA NM_001040177 RefSeq chr10 + 4826176 4848059 AKR1E2 83592 "aldo-keto reductase family 1, member E2, transcript variant 1" GO:0005737|GO:0050571|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140371_PI430048170 0.528084111863699 0.880385670339161 0.44012726141259 0.497956680953608 0.47635403456708 A A A 1.03194363140112 0.404403794975923 0.440488583592069 A A A LNCV6_140371_PI430048170 mRNA
TTCAACCCAGACTTTGCTGGGATCTCTTCCTTTTTCATTAAAGACAATTTGAAATGCTGT NM_001243079 RefSeq chr19 + 1524073 1535456 PLK5 126520 polo-like kinase 5 GO:0002357|GO:0031572|GO:0005730|GO:0006927|GO:0005524|GO:2000045|GO:0005737|GO:0007067|GO:0004672|GO:0071363|GO:0010976|GO:0006468|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128855_PI430048170 0.0236902142633433 0.361636255456198 7.10884118765818 6.28034460961104 6.79292322647949 P P P 8.18667098349315 8.27461281721331 8.23934696048921 P P P LNCV6_128855_PI430048170 mRNA
GGATGCTATCTCAATCTAAAAAATCATCACCACCCTACCCAAGAACAGGGTTTGTTAAGA NM_001190489 RefSeq chr10 - 37601437 37602931 MTRNR2L7 NA MT-RNR2-like 7 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130881_PI430048170 0.102743539662458 1.1078515429554 0.63090523338705 0.54179375336324 0.735075580345493 A A A 0.42690619758056 0.500324984201702 0.541421167796372 A A A LNCV6_130881_PI430048170 mRNA
GTAAACATTTCCATTGTTTTATGATTTAGCCAGTGATTCCCCAAAGCAGCCTCTTAGTGT NM_001178016 RefSeq chr2 + 161624334 161985276 SLC4A10 57282 "solute carrier family 4, sodium bicarbonate transporter, member 10, transcript variant 3" GO:0006821|GO:0005886|GO:0055085|GO:0007399|GO:0016323|GO:0005452|GO:0005887|GO:0015701|GO:0051453|GO:0035725|GO:0016021|GO:0008510|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96889_PI430048170 0.333860827437432 1.0731291417327 4.43810152209184 4.57316676453207 4.38181955296954 P P P 4.5066732357165 4.26484690479432 4.31127906958177 P P P LNCV6_96889_PI430048170 mRNA
GGAAGATGGGTTGATCAACAAATAGGAGAAAATCTGATTGTGCCAGGAGGAGTGAAGACC NM_001197293 RefSeq chr8 + 26514192 26658177 DPYSL2 1808 "dihydropyrimidinase-like 2, transcript variant 1" GO:0005515|GO:0021510|GO:0042220|GO:0030425|GO:0005829|GO:0030426|GO:0005739|GO:0014049|GO:0021772|GO:0007411|GO:0043195|GO:0007010|GO:0043025|GO:0070062|GO:0019901|GO:0042493|GO:0005874|GO:0048489|GO:0007399|GO:0006897|GO:0007165|GO:0006139|GO:0001975|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135776_PI430048170 0.378412495650133 1.23560398061989 6.3677225224813 6.9192699364843 6.11316660516796 P P P 6.10627579483877 6.30792148320725 6.18373934770154 P P P LNCV6_135776_PI430048170 mRNA

GTGTATAAGACTTAGCTGGAATCCAACTAAAGATTTGGGCTGGTCTCTCCATCTTAACGT NM_173825 RefSeq chr3 - 120686680 120742537 RABL3 285282 "RAB, member of RAS oncogene family-like 3" GO:0006184|GO:0003924|GO:0032482|GO:0019003|GO:0005525|GO:0006886|GO:0012505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132130_PI430048170 0.9729750481117 0.964717046890491 1.84835887073271 0.4984968281924341.11023961667297 A A A 1.99119141879228 1.03786280599735 0.491539644797979 A A A LNCV6_132130_PI430048170 mRNA
AGCATTGTGTATATAGCAGACATGGAGGTCCTGCAGCAGGAGGTGCTCAATAAACACAAA NM_033199 RefSeq chr3 - 48561717 48563768 UCN2 90226 urocortin 2 GO:0035902|GO:0001664|GO:0008283|GO:0051431|GO:0042562|GO:0007586|GO:0033685|GO:0005102|GO:0006950|GO:0071456|GO:0046882|GO:0005576|GO:0005615|GO:0071385|GO:0005179|GO:0010629|GO:0031669|GO:0006171|GO:0007189. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142110_PI430048170 0.7066791369147310.9046141604704490.311262026137659 1.28604406302772 0.287013250822622 A A A 0.9660520240162321.17822946567667 0.262592873593403 A A A LNCV6_142110_PI430048170 mRNA
TGACAGCGTCATCAATAGCATATTCACATATTTCCATAGTACTATGTTTGCTTTTCTTCC NM_001040071 RefSeq chr4 + 8949750 8950401 LOC650293 650293 seven transmembrane helix receptor NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116684_PI430048170 0.0890042305258392 0.4238373391049560.298415128624715 1.79031191434271 1.24827139070685 A A A 2.48161290368861 2.45839976648561 2.48183911902148 A P P LNCV6_116684_PI430048170 mRNA
TCAGGCTATTTGTATGCTGGAAAGACGAGAGAAACCTTCACCAAGCATGTTTGGTGAGCT NM_152586 RefSeq chr10 - 73497537 73575675 USP54 159195 ubiquitin specific peptidase 54 GO:0005515|GO:0006511 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128541_PI430048170 0.4810589006553840.918366696688461 0.639155896776491 0.56107370893686 0.331685403427372 A A A 0.4080777690789820.656496980733664 0.823381847392272 A A A LNCV6_128541_PI430048170 mRNA
GCTGCTTACTTTCTCATGAAAAGTAAAGATGTTTACAGTGTATGCCAAGTTTTCAGTTTC NM_001163278 RefSeq chrX - 124375905 124963817 TENM1 10178 "teneurin transmembrane protein 1, transcript variant 1" GO:0048471|GO:0008285|GO:0005886|GO:0005783|GO:0051491|GO:0005634|GO:0016363|GO:0042803|GO:0006955|GO:0005737|GO:0033138|GO:0030838|GO:0007218|GO:0043406|GO:0005856|GO:0008201|GO:0005794|GO:0046982|GO:0006359|GO:0005576|GO:0090316|GO:0006351|GO:0007399|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145031_PI430048170 0.00424490003795815 0.4400911832257161 0.5665023522895 10.588375624874 10.972047714589 P P P 11.6667463118177 11.8295578462304 12.1729864342729 P P P LNCV6_145031_PI430048170 mRNA
TTCTCCTCTTTAATATTGCTGTGAACAGTGGTGCCCATTGTAGCATATGTTTGATTTTTT NM_015161 RefSeq chr16 - 18791668 18801535 ARL6IP1 23204 ADP-ribosylation factor-like 6 interacting protein 1 GO:0005515|GO:0005784|GO:0016020|GO:0006613|GO:0016021|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145688_PI430048170 0.0343158284071657 0.6436896120475416.27186064024551 6.20319482525771 6.57408136957347 P P P 6.75862586924863 6.90044031487673 7.27410912019017 P P P LNCV6_145688_PI430048170 mRNA
GGCCATATTTATAGAATGCTGAACTCAATGTGCAAGTTGTACTGTATGCAGTTTTGTAAA NM_006996 RefSeq chr1 - 169463910 169485970 SLC19A2 10560 "solute carrier family 19 (thiamine transporter), member 2" GO:0005515|GO:0015403|GO:0015234|GO:0015888|GO:0005886|GO:0015884|GO:0006767|GO:0071934|GO:0008517|GO:0044281|GO:0042723|GO:0006766|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130823_PI430048170 0.00107593774078641 6.19623590054189 5.08741432627785 5.21839048183367 5.20844800285066 P P P 2.78948728671168 2.42212981917639

2.37552363210079 P P P LNCV6_130823_PI430048170 mRNA
CCAGTCTATTCACAGAAGTGTTAACTTTTCTAACAGAAAGCATGATTTTGATTGCTTACC NM_006207 RefSeq chr8
+ 17576432 17643133 PDGFRL 5157 platelet-derived growth factor receptor-like
GO:0008150|GO:0005019|GO:0004992|GO:0007186|GO:0035791|GO:0005576|GO:0005575 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127166_PI430048170 0.3221761303823720.8985615269454871 2.2416064431413
11.9485819892794 11.8670767637128 P P P 12.3345260048664 12.0781345144863
12.1217099582552 P P P LNCV6_127166_PI430048170 mRNA
CCCAAGTCTCTGGGGGTGGAAAGGAGGAAGAGATACTAGTTAAAGATTTTAAAAATGTAA NM_001302545 RefSeq
chr2 - 218264128 218270209 AAMP 14 "angio-associated, migratory cell protein, transcript variant 1"
GO:0010595|GO:0005737|GO:0009986|GO:0005886|GO:0014909|GO:0001525|GO:0008201|GO:0030154 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136918_PI430048170 0.2614350372430981.77564429533588 3.18469061323442
2.38882568005584 1.6538376548289 A A A 1.88155421075336 0.725658569027178
2.17121334045832 A A A LNCV6_136918_PI430048170 mRNA
TTACCAGAAAAAGAAGCTATGCTTCAAAGAAAATGATGGCTGAAGACCTAGGGAACAAGG NM_001277710
RefSeq chrY + 2691186 2741309 CD99 4267 "CD99 molecule, transcript variant 3"
GO:0005737|GO:0005886|GO:0005887|GO:0007155|GO:0005925 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_73313_PI430048170 0.0126534295753346 0.5754664282424096.91584407269904
6.47882337664121 6.55074101459154 P P P 7.37110417359968 7.39274301228582
7.60085474836454 P P P LNCV6_73313_PI430048170 mRNA
CTGGCAGAGATGTGCCTGGCATCAGAAGGGATGAAAATGGAAGAATCAAAGCTAATAAAA NM_001142568
RefSeq chr3 + 107522935 107811329 BBX 56987 "bobby sox homolog (Drosophila), transcript variant 1"
GO:0060348|GO:0006355|GO:0005737|GO:0005654|GO:0003677|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130198_PI430048170 0.0109691221481119 0.1818759029146270.297579155404609
0.3189723147445260.283809571496696 A A A 2.21160426245963 2.89097094847806
3.04623897689242 A P P LNCV6_130198_PI430048170 mRNA
TGAAAGGTTGAAAGTCTGTACTTACAGAACTTTTGAGTTCACAGTGCTTTCTGGAAATAA NM_001253 RefSeq chr6
+ 44387513 44450424 CDC5L 988 cell division cycle 5-like
GO:0008380|GO:0000974|GO:0005515|GO:0010467|GO:0006355|GO:0005730|GO:0005634|GO:0071013|GO:0003
677|GO:0006351|GO:0005737|GO:0006281|GO:0016607|GO:0016020|GO:0072422|GO:0071987|GO:0000398|GO:0
003682|GO:0005654|GO:0005662 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126697_PI430048170 0.6971589793450290.6820535118318062.15210254580647
2.93323244440235 1.15690989343554 A A A 3.55909596610387 2.84718131959571
1.00150202516523 P P A LNCV6_126697_PI430048170 mRNA
GGTGGCAGGACAAGAGAAGGCATTGAGCTTTTTCTTTCATTTTCCTATTAAAAAATACAA NM_001252 RefSeq chr19
- 6585838 6591152 CD70 970 CD70 molecule
GO:0005515|GO:0005164|GO:0005886|GO:0008283|GO:0005102|GO:0007267|GO:0097191|GO:0002020|GO:0005
125|GO:0005615|GO:0007165|GO:0006955|GO:0005887|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_126692_PI430048170 0.8705951010803230.9195912724293851.53050561659367
0.3802715620997360.384728432414603 A A A 0.4861246479784091.7018907093618
0.403484064920024 A A A LNCV6_126692_PI430048170 mRNA
TAATCCTGTCATCTTGCTCCAATTAGAGCCGCTTCCATTAAGAAGATCGTGACAAATTCC NM_198989 RefSeq chr13
- 50711025 50843939 DLEU7 220107 "deleted in lymphocytic leukemia, 7" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_144934_PI430048170 0.8308166937496331.12693382221836 1.45781550739556

0.3938906137109970.327142275019915A A A 0.4209118993720950.500878009206419
0.972932041879798A A A LNCV6_144934_PI430048170 mRNA
TCGCTACAGTAAGGACCTGAAGTGACTTTGAGAAATTCACCCTCACAAACCTTCCTTCAG NM_022135RefSeq chr3
- 119642051 119660590 POPDC2 64091 popeye domain containing 2
GO:0008150|GO:0003674|GO:0030552|GO:0002027|GO:0042391|GO:0016021|GO:0060931 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128536_PI430048170 0.0343117459914986 1.71585647467164 3.51965518465174
3.96880792659697 4.14856782710599 P P P 2.91067919934078 3.13833067765535
3.29585222957779 P P P LNCV6_128536_PI430048170 mRNA
CCCTCTTCTGAGCTGTGTATTCATGTAGAGGGATGTATTCAGCCTTTTTAGTGAACATTT NM_203376RefSeq chr1
- 205083128 205084460 TMEM81 388730 transmembrane protein 81 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129526_PI430048170 0.1516918673615571.09657403273149 5.99456018947373
6.17177253813259 6.18181709369864 P P P 6.02400637560637 6.01156749747828
5.91887623339453 P P P LNCV6_129526_PI430048170 mRNA
CTCTGATGCCTGCTGTCTCAGTGTTTGGTTATTATGCAAACAAGTAATGTTTGAAATATA NM_025163RefSeq chr3
- 196946342 196968871 PIGZ 80235 "phosphatidylinositol glycan anchor biosynthesis, class Z"
GO:0000030|GO:0005783|GO:0005789|GO:0000026|GO:0016021|GO:0006506 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132403_PI430048170 0.4430456068604050.7600043924256372.91451965383239
0.9040706748299871.81593134536616 A A A 2.40098879240536 1.99402709816601
2.95429515488027 A A P LNCV6_132403_PI430048170 mRNA
GTGAAATAATCATAACTCCTTGCTCCCAGAGAAGCTATCACCTCCATTTCTAAAACCATT NM_178155RefSeq chr14
+ 65410591 65744121 FUT8 2530 "fucosyltransferase 8 (alpha (1,6) fucosyltransferase), transcript
variant 1"
GO:0017124|GO:0005737|GO:0006491|GO:0032580|GO:0007179|GO:0046368|GO:0018279|GO:0070062|GO:0036
071|GO:0042355|GO:0009312|GO:0005794|GO:0007585|GO:0033578|GO:0001701|GO:0016020|GO:0000139|GO:0
016477|GO:0007229|GO:0043112|GO:0016021|GO:0008424|GO:0006487|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135736_PI430048170 0.7882826378220451.18217877052661 3.18930277546696
1.85347075392134 3.29951754326379 P A P 2.93357641494467 2.09030147709388 2.8485960682888
P A P LNCV6_135736_PI430048170 mRNA
GCTTGTTCTTCCTGCCAAATGATCAGAGAGGAACATTCCATTTATTTGTAGTGGATTTCC NM_001178106 RefSeq
chrX + 152914441 152973481 ZNF185 7739 "zinc finger protein 185 (LIM domain), transcript variant 1"
GO:0005737|GO:0005886|GO:0008270|GO:0015629|GO:0005925 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136633_PI430048170 0.3994046049628490.8371863619700570.381386471210164
0.4532176395487170.40250135412467 A A A 0.2911760294925751.02268821851136
0.599111611654602A A A LNCV6_136633_PI430048170 mRNA
GCTGCCTATGAATGGAGATTCAGTAGTCATTGTATGCATCTTTAAGTCAAATGTGTATTA NM_003812RefSeq chr2
+ 206443643 206621131 ADAM23 8745 ADAM metallopeptidase domain 23
GO:0005515|GO:0005178|GO:0005887|GO:0006508|GO:0008270|GO:0005576|GO:0007417|GO:0007155|GO:0004
222|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134624_PI430048170 0.0571950517874322 1.03635184234772 11.6982262209032
11.701133154848 11.6654097231254 P P P 11.6156533138913 11.6283752871679
11.6659947810437 P P P LNCV6_134624_PI430048170 mRNA
CTCTTCCTGTTCCTGTTGACATGTCGTTGTTTAAATAAATCTCACTTGCCACCAGTAAAA NM_016309RefSeq chr16
+ 25111725 25178230 LCMT1 51451 "leucine carboxyl methyltransferase 1, transcript variant 1"
GO:0005515|GO:0031333|GO:0006481|GO:0090266|GO:0006479|GO:0003880|GO:0042981|GO:0008757|GO:0010

906|GO:0006464|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142334_PI430048170 0.1946297692876140.69100506867806 3.76233215952565
2.73691657776952 3.52553655272059 P A P 3.93885300238959 3.92113621419986 3.9509938538727
P P P LNCV6_142334_PI430048170 mRNA
AGATAATTTTGTTAAAGTTGGCTTGCTTGGGCGGGTGCTTGGTCCAGAGGGAGAAAAGAA NM_001162536 RefSeq
chr1 - 88979455 88992960 RBMXL1 494115 "RNA binding motif protein, X-linked-like 1, transcript
variant 1" GO:0003727|GO:0000166|GO:0006376|GO:0005681|GO:0045893 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_108135_PI430048170 0.00109338240666095 2.43393740818556 9.4810764233201
9.48660252953241 9.56810581774196 P P P 8.11671078371632 8.19597065302807
8.36375550550773 P P P LNCV6_108135_PI430048170 mRNA
GGGTTCCTGATTTCTGTATACATGTAGCTTTGCCAGATATGTACTTAGTAATATAAACTG NM_005552RefSeq chr14
+ 103629187 103686231 KLC1 3831 "kinesin light chain 1, transcript variant 1"
GO:0005515|GO:0030424|GO:0005871|GO:0005874|GO:0035418|GO:0003777|GO:0035617|GO:0006886|GO:0030
426|GO:0005829|GO:0019886|GO:0003774|GO:0015631|GO:0016020|GO:0007596|GO:0035253|GO:0008152|GO:0
043025|GO:0016032|GO:0016023|GO:0008088|GO:0007018 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_105622_PI430048170 0.4727808598763040.7863770111384380.48901552941951
0.4557386681243811.18329880103293 A A A 0.3926567597012671.25201986884646
1.44473084364795 A A A LNCV6_105622_PI430048170 mRNA
CCAATGATAGGAATCTGTGATTAATAAAACATTTGGGAAGGGTACATGTTACACTTCACA NM_007131RefSeq chrX
- 135285786 135344087 ZNF75D7626 "zinc finger protein 75D, transcript variant 1"
GO:0006355|GO:0003700|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138749_PI430048170 0.00146917592908412 1.41461882572923 13.9782808514066
14.1287444551992 14.1058644600975 P P P 13.5286882122629 13.6576887533345
13.5258118798324 P P P LNCV6_138749_PI430048170 mRNA
CCCTCAACCCATCTTCCTAGTGTTTGTGAAATAAACTTGGTATTTGTCTGGGTCAGTGCA NM_001294333 RefSeq
chr1 + 43974647 43978300 ATP6V0B 533 "ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b,
transcript variant 3"
GO:0008286|GO:0005215|GO:0005774|GO:0051701|GO:0015078|GO:0055085|GO:0006879|GO:0033572|GO:0015
991|GO:0030670|GO:0016021|GO:0090382|GO:0010008|GO:0033179|GO:0015992 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_96169_PI430048170 0.0880778164647226 1.20056097844376 7.13891427724476
7.00455303919369 6.93069431228643 P P P 6.79589776659672 6.8991757714946
6.57726448236587 P P P LNCV6_96169_PI430048170 mRNA
GTTTCCGGACCCCCATCCAAGAGGAGCAGGCCGACGCCCACTCCACCCTGGCCAAGATCT NM_003327RefSeq chr1
- 1211325 1214168 TNFRSF4 7293 "tumor necrosis factor receptor superfamily, member 4"
GO:0045859|GO:0009986|GO:0030890|GO:0042981|GO:0050710|GO:0033209|GO:0043433|GO:0006955|GO:0006
968|GO:0005031|GO:0006954|GO:0042098|GO:0005887|GO:0051024|GO:0045892|GO:0009897 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_55545_PI430048170 0.9635355743776340.9981335109150160.2926565531975510.528814831242099
0.379263293472212 A A A 0.5004369999321380.3866592210424440.326227683867769 A A A
LNCV6_55545_PI430048170 mRNA
AGCAACAGATGAACAGCCTCACATTGGAAATTACCGTTTACAAAAAACAATAGGGAAGGG NM_001286124
RefSeq chr1 + 220528182 220664457 MARK1 4139 "MAP/microtubule affinity-regulating kinase 1,
transcript variant 1"
GO:0070300|GO:0000287|GO:0005886|GO:0050321|GO:0005546|GO:0005524|GO:0035556|GO:0005737|GO:0004
674|GO:0007010|GO:0015630|GO:0001786|GO:0006468|GO:0001764|GO:0005856|GO:0016055 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_132009_PI430048170 0.0426645817350177 0.7240211907489975.75321295994019
6.18533392474977 5.99329401551521 P P P 6.35769914027983 6.40635709877992
6.58743747894002 P P P LNCV6_132009_PI430048170 mRNA
CACCTGGAGCCTTTATAAAGTTTTTCTCTATGCAGACAACCATTGATTTACTCTGCTGTA NM_024762RefSeq chr19
- 57807081 57814913 ZNF552 79818 zinc finger protein 552
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139290_PI430048170 0.0203724113137339 0.78868611481310410.7343042991944
10.9400280890385 10.7877690005577 P P P 11.1374228309859 11.2900579289965
11.0604895764177 P P P LNCV6_139290_PI430048170 mRNA
TAAAGTCTGATGAAGGCAGGGGTGGTGATTCATGCTGTGTGACTGACTGTGGGTAATAAA NM_000017RefSeq chr12
+ 120725737 120740008 ACADS 35 "acyl-CoA dehydrogenase, C-2 to C-3 short chain, transcript variant 1"
GO:0006635|GO:0031966|GO:0050660|GO:0004085|GO:0051384|GO:0005634|GO:0044281|GO:0033539|GO:0005
739|GO:0042594|GO:0051289|GO:0005759|GO:0003995|GO:0000062|GO:0046359|GO:0044255 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130670_PI430048170 0.0918830106708341 1.04313689150239 0.462795730477413
0.5300887258461950.472833283708939A A A 0.3959394868854750.431053256801221
0.456222295843517A A A LNCV6_130670_PI430048170 mRNA
CATGACTCAGATTCGAAGAGACAGATTTTATCTTCCTTTCATTTCTTTCTCTTGTGCATT NM_205856RefSeq chrX +
48127220 48132613 SPACA5389852 sperm acrosome associated 5 GO:0008152|GO:0003796|GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141577_PI430048170 0.43305178262127416.584890159599 5.94421939648949
0.2761162442510780.351168604102734M A A 0.44028215017166 0.319726055209586
0.330607942226553A A A LNCV6_141577_PI430048170 mRNA
AGCCCAGTTGTAACTTGGTAAAGGCAAGCTTCTGTACCTTTGTTATAATTAATTGTATAC NM_020911RefSeq chr7
- 132123331 132576564 PLXNA491584 "plexin A4, transcript variant 1"
GO:0021960|GO:0005886|GO:0021644|GO:0048485|GO:0002116|GO:0005622|GO:0021784|GO:0021793|GO:0050
923|GO:0021615|GO:0048841|GO:0017154|GO:0007411|GO:0021637|GO:0071526|GO:0016021|GO:0021612 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135111_PI430048170 0.3246395900989890.615736257522557 2.04593351317586
3.07905050548607 1.42438404443505 A P A 3.4321054487039 2.02782940456559 3.3100914330432
P A P LNCV6_135111_PI430048170 mRNA
TATACCATCCTCACACCCTTATTAAACCCTCTCATCTACAGTCTGAGGAACAGGGATGTG NM_001005471 RefSeq
chr1_KI270892v1_alt + 35922 36849 OR2T6 NA "olfactory receptor, family 2, subfamily T, member 6"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132998_PI430048170 0.2279412741177761.04978508551456 0.354316103376428
0.3554486131465110.477793014809195A A A 0.32007117134385 0.302981792576682
0.357211760588239A A A LNCV6_132998_PI430048170 mRNA
GAGCCAGATGAAGGGAACAATCAGGACTATTCCTAGACACTAGCAAAATCTAGAAAATAA NM_080866RefSeq
chr11 + 63369788 63410240 SLC22A9 114571 "solute carrier family 22 (organic anion transporter),
member 9"
GO:0016323|GO:0015347|GO:0015301|GO:0015913|GO:0043252|GO:0015636|GO:0016021|GO:0055085|GO:0009
914 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129317_PI430048170 0.0198231887203013 0.5123263083438726.63643966823405
6.23357570824084 6.44723649924829 P P P 7.03802768069518 7.43013916705597
7.69696914854105 P P P LNCV6_129317_PI430048170 mRNA
GCTTTGTACATGAACAGATGCTGAGTATCTGTTATCATTGTATTGTTTAGTGTCAGTGTA NM_003594RefSeq chr1
+ 117060326 117102869 TTF2 8458 "transcription termination factor, RNA polymerase II"

GO:0008380|GO:0005515|GO:0006353|GO:0006397|GO:0008026|GO:0006369|GO:0006355|GO:0003677|GO:0005524|GO:0008023|GO:0005737|GO:0005681|GO:0008270|GO:0008094 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139031_PI430048170 0.553083164107643 0.979411190335796 0.257219854177143 0.272154857599839 0.388761173903515 A A A 0.377195581242487 0.321621441513152 0.312126734110454 A A A LNCV6_139031_PI430048170 mRNA
TTACCTTGATTCAATGTTAAAAACTATTAACACCCTAACAACACAGAAGCAGACGCAGCC NM_001168331 RefSeq chr3 + 120596280 120602411 NDUFB4 4710 "NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa, transcript variant 2"
GO:0031965|GO:0005743|GO:0044281|GO:0005739|GO:0022904|GO:0005747|GO:0006120|GO:0005654|GO:0016021|GO:0008137|GO:0006979|GO:0044237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83107_PI430048170 0.00262200315199012 1.46882724488388 7.33859808517762 7.13195828001814 7.18612744870615 P P P 6.58148296592211 6.755992588417 6.65793405867686 P P P LNCV6_83107_PI430048170 mRNA
AGCACTTTCTGAACCTACAGAAGTTGGGTATTGTCTGAAATCCCAGAGGACCCATAAGTG NM_030581 RefSeq chr16 - 74873572 74985119 WDR59 79726 WD repeat domain 59 GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144051_PI430048170 0.361044877613276 1.24250337728148 3.66608658658483 4.23858281996008 4.4632620214137 P P P 3.86075427214971 3.64359407636627 4.0123155390629 P P P LNCV6_144051_PI430048170 mRNA
CAGCTGTTTGAAGTTTGTATATTTTCCGTACTGCAGAGCTTACACAAAATTGAAGAATGT NM_030802 RefSeq chr17 - 49710324 49764156 FAM117A 81558 "family with sequence similarity 117, member A" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134450_PI430048170 0.46286290068219 0.92130532973638 0.488730420253104 0.451814927828144 0.430935365290676 A A A 0.387465297947054 0.794050926662082 0.514889052392735 A A A LNCV6_134450_PI430048170 mRNA
GTACACCAGTATTTTGCATTCAGTATTGTCAAGGCCATGACTGTTGTTTTAGTAAACTTG NM_001102654 RefSeq chr12 + 5432113 5495299 NTF3 4908 "neurotrophin 3, transcript variant 1"
GO:0008284|GO:0032856|GO:0050732|GO:0007267|GO:2000251|GO:0050731|GO:0021675|GO:0000187|GO:0043524|GO:0033138|GO:0007411|GO:0045944|GO:0032148|GO:0005166|GO:0030335|GO:0042490|GO:0048406|GO:0042552|GO:0005102|GO:0050804|GO:0005576|GO:0045687|GO:0007274|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133587_PI430048170 0.316869684108961 0.738646201290696 0.334064178681537 0.292167364022714 0.462751939140449 A A A 0.65189269751097 0.296102228178348 1.281589159933 A A A LNCV6_133587_PI430048170 mRNA
GGGGTTTCCATTTTAATGGGAACAATGTAGAATATATCTGTCTTCCCTTTATAGATTCCA NM_152441 RefSeq chr12 - 1565992 1594165 FBXL14 144699 F-box and leucine-rich repeat protein 14
GO:0005515|GO:0005737|GO:0004842|GO:0005794|GO:0042787|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133872_PI430048170 0.406777001175612 1.05363245018036 0.299829863311775 0.302065870975437 0.508245071219476 A A A 0.307376490081204 0.269650240503765 0.316652701612476 A A A LNCV6_133872_PI430048170 mRNA
GGGAACAAGCCCTTAATCTGCATAATGAGTGTTCAATAAACAGTTGTCAAACTTTGAAAA NM_012114 RefSeq chr19 + 15049479 15058292 CASP14 23581 "caspase 14, apoptosis-related cysteine peptidase"
GO:0004197|GO:0005737|GO:0008630|GO:0008544|GO:0031424|GO:0006508|GO:0005634|GO:0045095|GO:0070268|GO:0097192|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134521_PI430048170 0.00166040462503334 0.448922200701112 4.40792747107894 4.23992905032823 4.60476274593824 P P P 5.47032042290985 5.56768406025766 5.69531070896922 P P P LNCV6_134521_PI430048170 mRNA

GAAGTCATCGTGACCAATGTTACAGTAATTTCTGTTAGCTGATTGTGGTAAACAATGTTT NM_007106RefSeq chr13 - 29764407 29850683 UBL3 5412 ubiquitin-like 3 GO:0005622|GO:0005886|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145344_PI430048170 0.1439774868316831.17788969337043 10.774160410696 11.0110801125971 10.6666123684212 P P P 10.6687428936667 10.6456123530859 10.4398686213711 P P P LNCV6_145344_PI430048170 mRNA
TGTTCCCTGGAAGTAGGGCCTGCTCTCCATCCCAGTGAAATAAACATGTATTAGACACCT NM_024578RefSeq chr19 + 17226203 17229219 OCEL1 79629 occludin/ELL domain containing 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122093_PI430048170 0.0230129861327923 0.69263107257375412.3699449379296 12.215322566094 12.2380963820611 P P P 12.5899476986209 12.8834390628935 12.9220662166419 P P P LNCV6_122093_PI430048170 mRNA
TTTGAAATAGTCTGTGTGAAGGTGAAAGTGCAGTTCAGTAATAAACTGTGTTTACTCAGT NM_138578RefSeq chr20 - 31664457 31722853 BCL2L1 598 "BCL2-like 1, transcript variant 1" GO:0005515|GO:0019050|GO:0030054|GO:0097284|GO:0007283|GO:2000811|GO:0051402|GO:0007281|GO:0042803|GO:0042802|GO:0000910|GO:0043524|GO:0008637|GO:0005759|GO:0097136|GO:0030672|GO:0005813|GO:0031965|GO:0019901|GO:0046982|GO:0071312|GO:2001244|GO:2001243|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143992_PI430048170 0.9831327838451771.0711625167066 4.2202729373716 2.83896201667066 3.74851436699917 P A P 3.40001718117969 3.47539687093631 3.90204044680338 P P P LNCV6_143992_PI430048170 mRNA
GTAAAGCTTCCATGCTTCACCCTTGACATGATTACCCTTGAGTAAAACATGGGAATTTGT NM_024102RefSeq chr1 - 111439889 111449208 WDR77 79084 WD repeat domain 77 GO:0060770|GO:0005515|GO:0010467|GO:0008284|GO:0005794|GO:0006357|GO:0006325|GO:0005634|GO:0034660|GO:0000387|GO:0034709|GO:0005829|GO:0005737|GO:0030374|GO:0005654|GO:0060528 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138966_PI430048170 0.8148718821314990.9904873351196690.302660392331217 0.2901813980093830.369392776593111A A A 0.2990335629568110.280614993952773 0.421138003181272A A A LNCV6_138966_PI430048170 mRNA
TAGTGACCAGACTTACTTGCACTGTATTTATTGAAATTCAGGCTTGGAGTGGCCTGGGAG NM_001145975 RefSeq chr17 + 28473645 28497780 SLC13A2 9058 "solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2, transcript variant 1" GO:0016020|GO:0005886|GO:0005887|GO:0006810|GO:0006835|GO:0006814|GO:0055085|GO:0015361|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131926_PI430048170 0.0756737167815704 0.9440696738841960.28929231516175 0.3058356978236640.324172297650534A A A 0.4394844903394330.378748723646708 0.348900535663457A A A LNCV6_131926_PI430048170 mRNA
GGATCTGAAATGTCAGTTCTAGTATTTAGAGAGACTTCTCTAATAATACCGGGTGATATT NM_001287746 RefSeq chr6 - 55434372 55579214 HMGCLL1 54511 "3-hydroxymethyl-3-methylglutaryl-CoA lyase-like 1, transcript variant 4" GO:0048471|GO:0016020|GO:0005783|GO:0046951|GO:0005789|GO:0046872|GO:0004419|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127876_PI430048170 0.2483152630815460.9668994864537690.393884574707965 0.4185636416826830.316037033926904A A A 0.4146031827036120.447677929402902 0.413603108250817A A A LNCV6_127876_PI430048170 mRNA
CTCCAGAAATAACACTCTTGAGTACAACAATAAAAGCCCTCTTCAAACACACTCAAAAAA NM_001076675 RefSeq chr19 - 20619938 20661596 ZNF626 199777 "zinc finger protein 626, transcript variant 1" GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_50149_PI430048170 0.18092861570256 0.5104762032183710.3866472662395241.91290900304242
1.85843144363673 A A A 2.14569620195855 3.13111048186353 1.94677439606528 A P A
LNCV6_50149_PI430048170 mRNA
TAATGCAGTGGTTTCTCTGGTCACTCACGGTCCAGCACTAGCACGCAGCAGTCGGGGAAA NM_001129895 RefSeq
chr6 - 167975923 167976939 HGC6.3 100128124 uncharacterized LOC100128124 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135748_PI430048170 0.9052665942579320.9942081625435310.61261922915429
0.5010414627925070.382209704320196A A A 0.4249294315187130.568998929758585
0.53241488137729 A A A LNCV6_135748_PI430048170 mRNA
GTTTGGAAAGAATACACAGAGCAAGATGATTTACAATAAACCTTTTGACCTAACGCACAA NM_178549RefSeq chr1
+ 227563518 227662463 ZNF678 339500 "zinc finger protein 678, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145399_PI430048170 0.2297876042047510.8710970128134590.3427988907137
0.33677404927751 0.299150399813425A A A 0.3241680339045880.513977794020791
0.712170649161358A A A LNCV6_145399_PI430048170 mRNA
CAGATGTTCTGTTTTTACTTGCCTGGTACTCATGGTAGAGCCATACATTTCTTTTTTCTT NM_021148RefSeq chr7 +
64903241 64931577 ZNF273 10793 "zinc finger protein 273, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136541_PI430048170 0.5615393602494 0.9190200081066010.370552853601986
0.3497005840664690.413098747904837A A A 0.30760478552774 0.78699412846664
0.355123757351225A A A LNCV6_136541_PI430048170 mRNA
TTCGGCTACGTGCACTTCAGGCAGGAGCTGAACAAGAGCCTTCAGGAGTGTCTGTCCACA NM_021819RefSeq chr15
+ 74812852 74825758 LMAN1L 79748 "lectin, mannose-binding, 1 like"
GO:0033116|GO:0030246|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142384_PI430048170 0.425928199290894 1.02296753373759 0.370370391684304
0.369884644073408 0.273260568273634 A A A 0.298673133413093 0.316203526190521
0.302450391397525 A A A LNCV6_142384_PI430048170 mRNA
CTTCGATAATTAAACCAAGGAAGCAATCTGTAACTGCTTTTCGGAACACTAAAACCATAT NM_003248 RefSeq
chr5 + 80035298 80083284 THBS4 7060 thrombospondin 4
GO:0005515|GO:0006986|GO:0034976|GO:0048771|GO:0005783|GO:0005509|GO:0071603|GO:0050731|GO:0005
576|GO:0005615|GO:0005604|GO:0031012|GO:0005178|GO:0016529|GO:0034103|GO:0001938|GO:0016525|GO:0
090023|GO:0051781|GO:0048266|GO:0008083|GO:0008201|GO:0070062|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130868_PI430048170 0.0106116874931755 0.64706863710191 9.05557175904624
9.02096285973767 9.24957843058064 P P P 9.6881366669208 9.57895565887573
9.93092973334466 P P P LNCV6_130868_PI430048170 mRNA
AAACTGTGTCCAATATCGTTCAGTTTCCTGGGTCTTTTTCTTATTAGCACATTTGAGAAA NM_024638 RefSeq chr3
+ 114056734 114088421 QTRTD1 79691 "queuine tRNA-ribosyltransferase domain containing 1,
transcript variant 1" GO:0005739|GO:0005737|GO:0008270|GO:0008479|GO:0008616 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_39327_PI430048170 0.434166368263049 0.762544076704742 3.78599964577143
2.59701649537579 2.61196827941376 P A A 3.69718350874558 3.81418021753801
2.80822796924006 P P P LNCV6_39327_PI430048170 mRNA
TTTCATTCAAAGAAGAGCAGACTCAGCCACCCACACCACTACAGCTCAGATCGAGAAAAT NM_015570 RefSeq
chr7 + 69598918 70793068 AUTS2 26053 "autism susceptibility candidate 2, transcript variant 1"
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA
NA

LNCV6_132675_PI430048170 0.201196181097136 0.897145782904983 8.07333584465542 8.19469768465801 8.2318235781482 P P P 8.22045950975901 8.25521879153373 8.4841835235956 P P P LNCV6_132675_PI430048170 mRNA TGCTTAAACAATAAATACACCTGAGTTAGTTTTCCAAACCTTTCCTCCTGATTAAATGCC NM_017887 RefSeq chr1 - 53214099 53220639 C1orf123 54987 "chromosome 1 open reading frame 123, transcript variant 1" GO:0008150|GO:0003674|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139757_PI430048170 0.726546449533239 0.98352050789299 0.471850765473565 0.423775088328554 0.262514220502513 A A A 0.367533033557676 0.445198395229631 0.424444872161557 A A A LNCV6_139757_PI430048170 mRNA TCTACACTGCCTCGGGTATAAAGTGAAGAAGCAAGATAATGAGGGATAAAGCTGAAAAGG NM_017676 RefSeq chr5 - 103085999 103120138 GIN1 54826 gypsy retrotransposon integrase 1 GO:0015074|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136204_PI430048170 0.00802683484945391 0.52008252686242 6.0306972955221 6.02082008110374 6.04724663142536 P P P 6.79986706527255 7.07949936181765 7.03378106117512 P P P LNCV6_136204_PI430048170 mRNA GTCTCTACTCTGCCCCTTGTTGTAAATAGTTTGAGTAAAACAAAACTAGTTACCTTTGAA NM_145697 RefSeq chr1 + 163321932 163355763 NUF2 83540 "NUF2, NDC80 kinetochore complex component, transcript variant 1" GO:0005515|GO:0003674|GO:0007067|GO:0007059|GO:0016020|GO:0000777|GO:0005634|GO:0000278|GO:0031262|GO:0000775|GO:0051301|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141092_PI430048170 0.188542324978019 0.745858157873832 2.89595372321694 3.34499618635026 3.71517147646654 A P P 3.53842855023413 3.837735398124 3.93493978100006 P P P LNCV6_141092_PI430048170 mRNA CTACTTGTCCAGTTCAAATAAGAAATAAGGACAAGCCTAACTTCATAGAAACCTCTCTAT NM_001142556 RefSeq chr5 + 163460510 163491946 HMMR 3161 "hyaluronan-mediated motility receptor (RHAMM), transcript variant 1" GO:0005737|GO:0016020|GO:0009986|GO:0005886|GO:0005540|GO:0005975|GO:0009405|GO:0030212|GO:0044281|GO:0030214|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126997_PI430048170 0.00101162981890469 0.42629809925357 6.51213186802907 6.53226237924746 6.83731228216711 P P P 7.67135848479938 7.9260394599065 7.97961801815666 P P P LNCV6_126997_PI430048170 mRNA TCAGGAACCAAGGGGAAATGTTGTGAGATAACATTTACATTGTCAACCTTTATTGACTTT NM_024613 RefSeq chr8 + 95133720 95156685 PLEKHF2 79666 "pleckstrin homology domain containing, family F (with FYVE domain) member 2" GO:0030133|GO:0005515|GO:0005783|GO:0031901|GO:0015031|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132451_PI430048170 0.941817311201091 0.994952516831049 0.280348690560403 0.542534261241582 0.367379546582821 A A A 0.519532679083616 0.416690421552872 0.278302125127158 A A A LNCV6_132451_PI430048170 mRNA GCCTCAGTTAGAGGATGTTCCTCTTGGTGACCTCATGTAATTAGCTCATTCAATAAAGCA NM_004895 RefSeq chr1 + 247418048 247449104 NLRP3 114548 "NLR family, pyrin domain containing 3, transcript variant 1" GO:0005515|GO:0042347|GO:0050713|GO:0051259|GO:0035872|GO:0005829|GO:0051607|GO:0005737|GO:0006954|GO:0051092|GO:0050718|GO:0009595|GO:0032621|GO:0072559|GO:0050701|GO:0006919|GO:0042834|GO:0006915|GO:0032088|GO:0006952|GO:0002674|GO:0005524|GO:0043280|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137888_PI430048170 0.20971628213973 2.7794537072006 0.36481388842412 2.61907587281506 1.3922377288516 A A A 0.265682285366711 0.279294298347408

0.265700965889059 A A A LNCV6_137888_PI430048170 mRNA
AAGATTTCAGACAAGGTCATCAGCCAGAAGGAGGGAGACTTCTTCTTTGATTCCTTGAGG NM_001080527 RefSeq
chr2 + 127535801 127637728 MYO7B 4648 myosin VIIB
GO:0005515|GO:0016324|GO:0003774|GO:0008152|GO:0003779|GO:0016459|GO:0005524|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_120278_PI430048170 0.317751282355638 1.06873146407735 13.0244089725752
12.838371327394 13.0684033390069 P P P 12.9113331539995 12.8399033098253
12.9014011173751 P P P LNCV6_120278_PI430048170 mRNA
TAAGGATGACCCGTCCAAGCCGGTCCACCTCACAGCCTTCCTGGGATACAAGGCTGGCAT NM_000967 RefSeq chr22
- 39312881 39319665 RPL3 6122 "ribosomal protein L3, transcript variant 1"
GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0003723|GO:0019058|GO:0005730|GO:0005634|GO:0006
415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0000184|GO:0016032|GO:0071353|GO:0
005654|GO:0022625|GO:0044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_73366_PI430048170 0.0019062082407066 0.432905952279735 3.48375815428252
3.25665523281406 3.28100516970316 P P P 4.55386630005999 4.51464399840089
4.58657371220128 P P P LNCV6_73366_PI430048170 mRNA
GTGACAGTATCCTTACCTGCCATTTAATATTAGCCTCGTATTTTTCTCACGTATATTTAC NM_001164343 RefSeq chr3
- 114314499 115071414 ZBTB20 26137 "zinc finger and BTB domain containing 20, transcript variant 3"
GO:0001078|GO:0005654|GO:0005634|GO:0000122|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136284_PI430048170 0.212081555360531 0.903588393093251 14.4161809920298
14.1678655210087 14.1567160657883 P P P 14.4275568523441 14.3602444640218
14.4061222766594 P P P LNCV6_136284_PI430048170 mRNA
ATCCCTTTGCTTGTGGCAGGAGATGGCTTAAATAAATAACTTAAATTTAGATTGGTCATG NM_004373 RefSeq chr12
+ 120438089 120440742 COX6A1 1337 cytochrome c oxidase subunit VIa polypeptide 1
GO:0022904|GO:0004129|GO:0005743|GO:0044281|GO:0006091|GO:0055085|GO:0005751|GO:0044237 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128137_PI430048170 0.0146273174846052 1.26360220755361 6.46516647594511
6.53236293904918 6.36860502411363 P P P 5.9915773986855 6.17410672482495
6.18446415754511 P P P LNCV6_128137_PI430048170 mRNA
CCTCCTTTACCCTTTCAGATACAATCACGCCAGCCACGTTGTTTTGAAAATTTCTTTTTT NM_001039503 RefSeq chr16
- 31083423 31088809 PRSS53 339105 "protease, serine, 53" GO:0004252|GO:0006508|GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132645_PI430048170 0.189145807420088 0.592049897691376 4.99058657833965 5.0132325865103
5.30170951211975 P P P 5.14069877646507 5.83611618506727 6.36564859530497 P P P
LNCV6_132645_PI430048170 mRNA
GACGGAAGGGTTTTCCTATGTATCAAAACTTGTCTATAATTATGTCATCTATGTACCTAG NM_015278 RefSeq chr6
+ 148342592 148552048 SASH1 23328 SAM and SH3 domain containing 1
GO:0000209|GO:0019901|GO:0031435|GO:0008022|GO:0045766|GO:0010595|GO:0043234|GO:0032947|GO:0016
020|GO:1900745|GO:0031666|GO:0043507|GO:1900044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137434_PI430048170 0.875155759928071 0.978122752149956 10.8942669234746
11.1015431695557 11.0694772918263 P P P 11.2919664759567 10.900543573878
10.9443345637942 P P P LNCV6_137434_PI430048170 mRNA
ATATTTCCTACTCTTTAGGCATGGACTCTCCTTTCCCTTTGTTAGTGTCCTGGGTTCCCA NM_019096 RefSeq chr6 -
43620480 43629246 GTPBP2 54676 "GTP binding protein 2, transcript variant 1"
GO:0005515|GO:0008150|GO:0008152|GO:0003924|GO:0005525|GO:0043231 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134651_PI430048170 0.356451626014607 0.565623160892633 0.267979534575516

0.3335321226142350.275049195040978A A A 0.4869930183466331.94979238519798
0.300092419455759A A A LNCV6_134651_PI430048170 mRNA
TGAGCTCTTGAGGATCAGAGTTAAGTATCCATTGATAATATGTGTTCATTTTGCTCTATG NM_018227RefSeq chr4
- 67615760 67701171 UBA6 55236 ubiquitin-like modifier activating enzyme 6
GO:0005515|GO:0006511|GO:0005737|GO:0016567|GO:0019780|GO:0005524|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143785_PI430048170 0.5594672799787150.9668310587582230.475087650706398
0.46523077354683 0.255360938542049A A A 0.3980397415220660.501590646722724
0.450679354616754A A A LNCV6_143785_PI430048170 mRNA
CCTGTCTTGAATCCTATCATTTACAGTTTCAGGAATAAGGATGTCACAAGGGCTTTGAAA NM_001004693 RefSeq
chr1 - 248592829 248593768 OR2T10 NA "olfactory receptor, family 2, subfamily T, member 10" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132935_PI430048170 0.0276976478400284 1.69541016071441 5.11476221262112
5.26444291300598 5.60705615098176 P P P 4.79268289870907 4.23119890398349 4.6644677648054
P P P LNCV6_132935_PI430048170 mRNA
TGTGGATCTGCTATTGGGTTGGTATTTTAAACTTTCACTTGGGTGAAACTTGTTCATCAT NM_001081461 RefSeq
chr17 - 76712831 76726799 JMJD6 23210 "jumonji domain containing 6, transcript variant 1"
GO:0005515|GO:0008380|GO:0048024|GO:0003727|GO:0070815|GO:0060041|GO:0005886|GO:0030324|GO:0003
723|GO:0005634|GO:0002040|GO:0042802|GO:0007507|GO:0033746|GO:0048821|GO:0033749|GO:0004872|GO:0
006397|GO:0006355|GO:0033077|GO:0070079|GO:0005506|GO:0070078|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135131_PI430048170 0.000771135132238381 0.1735999203265533.48504706071488
2.80937331689377 3.09002217384039 P A P 5.27515787924369 5.81181440896818
5.88339859546428 P P P LNCV6_135131_PI430048170 mRNA
GTGCCTTACTAAATATGGGAATGTCTAACTTAAATAGCTTTGAGATTTCAGCTATGCTAG NM_002546RefSeq chr8
- 118923556 118952144 TNFRSF11B 4982 "tumor necrosis factor receptor superfamily, member 11b"
GO:0046685|GO:0043627|GO:0007584|GO:0042493|GO:0005578|GO:0006915|GO:0005576|GO:0005125|GO:0005
615|GO:0045779|GO:0007165|GO:0001501|GO:0030198|GO:0032026|GO:0004872|GO:0042489 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139444_PI430048170 0.32947067753236 0.75451509978062 0.296016567934197
0.2964908275837730.298381225043115A A A 1.19734823861688 0.395294087596275
0.352110786196786A A A LNCV6_139444_PI430048170 mRNA
GTAAATAAATAAGTAAATAACCAACCAACCCTGAGGAACATCTTGTTTCTGTAAAAAAAA NM_006955RefSeq chr10
- 42589083 42638837 ZNF33B 7582 zinc finger protein 33B
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138946_PI430048170 0.4820211329443081.06785468785726 6.76177542002828 6.5453865572872
6.50685626623856 P P P 6.53515907489894 6.65866602672445 6.33049499988698 P P P
LNCV6_138946_PI430048170 mRNA
CCCCTACTCACTCTTCCCTTTTCTTCTCTCAGTGTTGTCTGAATAAAGTGTGAAATCTTT NM_024909RefSeq
chr6_GL000254v2_alt + 1970883 1988721 ATAT1 79969 "alpha tubulin acetyltransferase 1,
transcript variant 2"
GO:0072686|GO:0021542|GO:0030424|GO:0050662|GO:0006996|GO:0045598|GO:1900227|GO:0007283|GO:0005
829|GO:0070507|GO:0005905|GO:0019799|GO:0071929|GO:0048666|GO:0005925 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135865_PI430048170 0.8039756739636850.9544709657854917.21728145527498
6.81899061165173 6.8557149521564 P P P 7.36232814886459 6.79854869958513
6.90299439068603 P P P LNCV6_135865_PI430048170 mRNA
AGGAAGTAGGTAAGAGCAATAAATGTGACATGTTATGTCATCATAGTAGGAGCTCATGGG NM_021203RefSeq chr3

+ 133784032 133821492 SRPRB 58477 "signal recognition particle receptor, B subunit"
GO:0005881|GO:0010467|GO:0007264|GO:0006614|GO:0005525|GO:0006412|GO:0030968|GO:0005737|GO:0016
020|GO:0005789|GO:0016021|GO:0006987|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107778_PI430048170 0.1541554149277830.2240669887953530.327230074254037
0.3339131269852440.336141568256809A A A 1.39250189275051 3.58055165767617 1.1824845641342
A P A LNCV6_107778_PI430048170 mRNA
ACACCATGGAAAACTTTCAAGTCTGATTATGTGGTATTTATCCCTTTGCAAGGAGAGATA NM_001012967 RefSeq
chr4 - 168356734 168480514 DDX60L 91351 "DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like,
transcript variant 1" GO:0003723|GO:0008152|GO:0004386|GO:0005524 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144246_PI430048170 0.7126703386513351.05034059040371 7.53624877010619
7.25832403339746 7.17344695291439 P P P 6.89372892600184 7.45774598726104
7.36823535778584 P P P LNCV6_144246_PI430048170 mRNA
CCCATCCTTACCTGAGACCTCACCTCCAAGAAATTAATGGTCTTTTCAATGGAGAAAAAA NM_207395RefSeq chr19
+ 58451603 58457832 ZNF324B NA zinc finger protein 324B NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132148_PI430048170 0.5690306040686761.05429949619154 3.2006484933386
3.02388410963706 2.9590023988747 P P P 2.91877223730921 3.18779463635951
2.83512501619724 P P P LNCV6_132148_PI430048170 mRNA
GCCGTGGGTGCCAGGTTCCCGGTTGGAACCTGCAATAAACTCGCTGTTCCTCGCAAAAAA NM_032037RefSeq chr19
- 19514218 19515660 TSSK6 83983 testis-specific serine kinase 6
GO:0005515|GO:0000287|GO:0004674|GO:0007275|GO:0006468|GO:0005634|GO:0009966|GO:0035092|GO:0005
524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101534_PI430048170 0.18700844286034 4.8120889671674 0.407633376302021
3.45806756159709 2.68037349616584 A P A 0.355991642958095 0.363489023845618
0.406122468569042 A A A LNCV6_101534_PI430048170 mRNA
CAAGGAGCGGCAGTGCTACCTCAGGTTAGGCCAAAGACTCTGATTCCAGACAGCCTCCCC NM_138415RefSeq chr22
- 44881162 45009700 PHF21B 112885 "PHD finger protein 21B, transcript variant 1" GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128292_PI430048170 0.405453188276687 1.13285706575614 7.3800243303046
7.36199083961423 7.65622343206486 P P P 6.91788342200123 7.40681625824496
7.48946359186976 P P P LNCV6_128292_PI430048170 mRNA
GGCGGGGCGTTAAAGTTCATATCCCAGTGTCCTTTGAATCGACTTCCTTTTTTCTTTTTT NM_000978RefSeq chr17 -
38850067 38853800 RPL23 9349 ribosomal protein L23
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0005730|GO:0006415|GO:0006
412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0000184|GO:0006610|GO:0016032|GO:0
005840|GO:0022625|GO:0044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_135374_PI430048170 0.9649682034893650.9917688556370681 1.5616019589329
11.6389709424001 11.6678463811071 P P P 11.4732761913717 11.8222358759788
11.5885943279115 P P P LNCV6_135374_PI430048170 mRNA
AAGAACTATCTTTCTTGTAGCAAAGCTGCACCTGATGATGCTGCCTCTCCTCTCTGTGTT NM_015140RefSeq chr22
- 43166621 43187131 TTLL12 23170 tubulin tyrosine ligase-like family member 12 GO:0006464 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_28178_PI430048170 0.6177977051999120.9640455441330730.5588326810038520.51625187753558
0.277981534696922A A A 0.4108369345126480.5926565190474990.517861892085266A A A
LNCV6_28178_PI430048170 mRNA
GGATTCCATAGCTGGAATCTCCTCTCTTAGCTCAGTGAAAAATAAAAATCCCAAATGGTG NM_001030005 RefSeq
chr15 + 74826609 74831795 CPLX3 594855 complexin 3

GO:0019905|GO:0030054|GO:0005886|GO:0005326|GO:0046928|GO:0045202|GO:0030073|GO:0016079|GO:0005829. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131327_PI430048170 0.1724005711508710.7118568669563296.4802403174406 6.12751669568217 6.56078527904944 P P P 6.46349982408721 6.84126008389185 7.26055216991765 P P P LNCV6_131327_PI430048170 mRNA
GAAAGTCTTACTCCTTTGTTAGTTTTGTTTCTGCACAACTACTGTACTTTTCCATATGGA NM_033394RefSeq chr2 + 158968633 159232659 TANC1 85461 "tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1, transcript variant 1"
GO:0097062|GO:0030054|GO:0045211|GO:0008542|GO:0043025|GO:0014069|GO:0043679|GO:0007520|GO:0030425. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132409_PI430048170 0.1082709413891110.7356397665656678.2411052729554 8.28985905077308 8.58431408151318 P P P 8.61047067387035 8.66092285455919 9.13668174083662 P P P LNCV6_132409_PI430048170 mRNA
GTCTTGATCACTAAGCAAAGCTGCTAGTGGGATTCTATATTTCGTGTCATCTTTTTTATT NM_000276RefSeq chrX + 129540274 129592553 OCRL 4952 "oculocerebrorenal syndrome of Lowe, transcript variant a"
GO:0005802|GO:0005515|GO:0006629|GO:0005886|GO:0043647|GO:0007264|GO:0030136|GO:0005634|GO:0044281|GO:0032855|GO:0005829|GO:0005737|GO:0032314|GO:0030670|GO:0030675|GO:0070062|GO:0051056|GO:0005795|GO:0006661|GO:0052745|GO:0005798|GO:0001701|GO:0048365|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127944_PI430048170 0.0545854174306821 0.6142196284780754.57403488335434 4.24279124554866 4.96524634767316 P P P 5.0160217766867 5.45095244777453 5.47124730041906 P P P LNCV6_127944_PI430048170 mRNA
ACAGTAGCAACATAAAGGAACCTGCTTAGAAGAGGTTTTTATGGTGTGATTGTGTTTTTT NM_022098RefSeq chr22 + 40857080 40932819 XPNPEP3 63929 "X-prolyl aminopeptidase 3, mitochondrial, transcript variant 1"
GO:0005739|GO:0030145|GO:0016485|GO:0003094|GO:0004177|GO:0006508|GO:0008237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132024_PI430048170 0.6666689522795641.02061759156615 0.275680902918223 0.3023573858130660.450294354776749A A A 0.3408703908442760.302676329045794 0.302318075989869A A A LNCV6_132024_PI430048170 mRNA
CCTGTCATTTGTTTGTTTTTAGGGTTAAATGTGGGTAACCTGTAGTATTCTGCTATACTA NM_022843RefSeq chr13 - 61409685 61415522 PCDH20 64881 protocadherin 20
GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140158_PI430048170 0.991429336625767 1.03846647086998 0.343239597565087 0.3697004227753331.35249423269364 A A A 0.9964843203217060.373923779436689 0.708209459460985A A A LNCV6_140158_PI430048170 mRNA
GCATCTGTGATAAACTATCAATGAGGCTCCCATCATGCCATTTTTTGTTCATTTTAATCT NM_016599RefSeq chr4 + 119135783 119187789 MYOZ2 51778 myozenin 2
GO:0005515|GO:0030346|GO:0008150|GO:0030018|GO:0031433|GO:0003779|GO:0015629|GO:0030017 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126884_PI430048170 0.2136170731748182.00423940966478 2.12714712734422 0.5078352253344761.11092243823827 A A A 0.4966833941949720.384495444130192 0.322346069649151A A A LNCV6_126884_PI430048170 mRNA
TGATTATTGTTGTACTTCTCTCATTTGGCCATACCCCACAGTATAATCTGTCCCCATCCT NM_001525RefSeq chr1 + 31617699 31627318 HCRTR1 3061 hypocretin (orexin) receptor 1
GO:0016499|GO:0042277|GO:0007631|GO:0005886|GO:0007218|GO:0005887|GO:0004930|GO:0045187|GO:0007268|GO:0017046|GO:0008188|GO:0032870 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140571_PI430048170 0.00031556458124213 3 0.2166377941709818.36375550550773 8.46480050526568 8.74618840431853 P P P 10.5967938591602 10.5794001709098 11.0048163153789 P P P LNCV6_140571_PI430048170 mRNA

GTAGTCCATAGCGCTTTTATATGCATTATTCTGTAATTTGTTTGTACTGCGGCAACTTTT NM_001304499 RefSeq chr16_KI270853v1_alt - 1523717 1546650 FOPNL 123811 "FGFR1OP N-terminal like, transcript variant 4" GO:0042384|GO:0005813|GO:0034453|GO:0031514|GO:0034451|GO:0005634|GO:0036064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141314_PI430048170 0.0782951048606611 0.7196679656766468.66859056645479 8.64259309851505 8.29506198987621 P P P 9.17571046484415 9.13936627140295 8.69680163573714 P P P LNCV6_141314_PI430048170 mRNA
GCCCAGGCTGCTCTGTTACATCTCCCATTTATTGTTTACTTTTATAAATTTGCTTCTAAG NM_053023 RefSeq chr11 + 58579113 58621550 ZFP91 80829 "ZFP91 zinc finger protein, transcript variant 1" GO:0070534|GO:0004842|GO:0007250|GO:0016874|GO:0005634|GO:0003676|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126748_PI430048170 0.1657315152848190.7684834307254613.281747167773 13.3558563641853 13.3444687204087 P P P 13.3558563641853 13.9172780538237 13.7916799583624 P P P LNCV6_126748_PI430048170 mRNA
AAGAAGTGGCGGTTCGGCCGGAGGTTCCATCGTATCCAAAAGGCTCTTTTCAGAGCCACC NM_021059 RefSeq chr1 + 149852618 149853125 HIST2H3C NA "histone cluster 2, H3c" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135484_PI430048170 0.00622401816510519 1.67035484299364 9.52731907639435 9.6369651965317 9.79602213626434 P P P 8.87856100407187 8.74342784208833 9.10695332037669 P P P LNCV6_135484_PI430048170 mRNA
AGTGGTTCTCACTCATCTTTGCCTTCCTTACCTCGTGATCTCACCATTCCAGATTGAAATNM_001206427 RefSeq chr10 - 103389050 103396513 USMG5 84833 "up-regulated during skeletal muscle growth 5 homolog (mouse), transcript variant 3" GO:0016021|GO:0070062|GO:0005753 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131385_PI430048170 0.1238081051770130.9641615396474340.417306155918111 0.4201498176506430.352716177497345 A A A 0.42718617476918 0.472531441570599 0.449060713288143 A A A LNCV6_131385_PI430048170 mRNA
CTCAGTGGGTGAGATCCAGACCCACTGGTGCAATGTCTTAAATACACATGACTGTTTTTC NM_000723 RefSeq chr17 - 39173455 39197703 CACNB1 782 "calcium channel, voltage-dependent, beta 1 subunit, transcript variant 1" GO:0016529|GO:0005245|GO:0007528|GO:0007411|GO:0006612|GO:0070588|GO:0006810|GO:0030315|GO:0008331|GO:0007268|GO:0005891 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83005_PI430048170 0.0463601881995587 0.5346814353655113.85749868955398 3.58420807455519 3.89741825017835 P P P 4.38560164247616 5.10795953456437 4.46093615497135 P P P LNCV6_83005_PI430048170 mRNA
TCTTGAGATGGTGGAGAAGTGCATCTTTGTGATGATCTGGAGGTATTTGCTGCTCATGCT NM_025082 RefSeq chr16 - 67828156 67847458 CENPT 80152 centromere protein T GO:0005515|GO:0051276|GO:0046982|GO:0006334|GO:0005634|GO:0003677|GO:0005829|GO:0034080|GO:0007067|GO:0051382|GO:0007059|GO:0000777|GO:0000776|GO:0005654|GO:0000278|GO:0000775|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133085_PI430048170 0.0037245822265422 1.33101264066292 6.29142782077551 6.31827941755718 6.42344301003016 P P P 5.82936667840686 5.97977301987632 5.98450607173694 P P P LNCV6_133085_PI430048170 mRNA
AAGTATGTTCACTATGAAATTGATGCTTGCATGGATTCTGAGGCCCCTGGCAGCAAAGAC NM_019852 RefSeq chr14 - 21498130 21511375 METTL3 56339 methyltransferase like 3 GO:0061157|GO:0006397|GO:0010467|GO:0001510|GO:0016607|GO:0019827|GO:0003723|GO:0007623|GO:0080009|GO:0005654|GO:0005634|GO:0016422 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129166_PI430048170 0.0657515014328603 1.04952696205468 0.337682266479461 0.3644504750555580.29260594563532 A A A 0.2528226817390130.277824852133353

0.255655196478083 A A A LNCV6_129166_PI430048170 mRNA
GGGACTTTCCTGGAAGCAAAGGCAGTCACATCTGGCATAATCATAATAAAGAAAACAACT NM_001257378 RefSeq
chr22 - 30459228 30472047 SEC14L3 266629 "SEC14-like 3 (S. cerevisiae), transcript variant 2"
GO:0005622|GO:0005215|GO:0006810|GO:0016021|GO:0070062|GO:0008289 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128727_PI430048170 0.506301459666808 1.29926545276102 0.405507568993015
1.40606367604534 0.285878855882418 A A A 0.390381722619899 0.445686274838794 0.4057932721712
A A A LNCV6_128727_PI430048170 mRNA
AGTTTTTCTAGCCAAGTGTTTGGGGCTTTAATAAAACTTGTTTCTTTTTCCTCTCCTGGA NM_025248 RefSeq
chr17_KI270857v1_alt - 2565324 2641249 SRCIN1 80725 SRC kinase signaling inhibitor 1
GO:0005515|GO:0030334|GO:0030424|GO:0019901|GO:0061098|GO:0061099|GO:0014069|GO:0045202|GO:0006
887|GO:0015629|GO:0030425|GO:0005737|GO:0045211|GO:0034446|GO:0061001|GO:0005925 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_82301_PI430048170 0.272925883544453 0.865425126287327 3.78839808246168 3.35983659663787
3.31787085067559 P P P 3.67190135050852 3.74969318777492 3.71745379907383 P P P
LNCV6_82301_PI430048170 mRNA
ATTTAGAGAGAAGAGAGCAGCTCCTAGCAGCATCAACATCTATTTGTCGCTTATTTGCCC NM_001018025 RefSeq
chrX - 155064033 155071272 MTCP1 4515 mature T-cell proliferation 1 GO:0005739|GO:0008283 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141976_PI430048170 0.0096127889043554 0.504750660613942 4.70591663651183
5.16480363874805 5.20703007337748 P P P 5.82541854816244 6.19724530095295
6.04164998990148 P P P LNCV6_141976_PI430048170 mRNA
GACAGTGAGATATCGGGAAACCCCATGAAAATAGATGCATAATAAAGGTGAAAATCATTT NM_001271818 RefSeq
chr7 + 102433529 102456821 ORAI2 80228 "ORAI calcium release-activated calcium modulator 2,
transcript variant 3" GO:0005515|GO:0016021|GO:0030426 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_141322_PI430048170 0.267078087246038 0.619888696639663 1.90638460182475
2.33034982039227 1.94486693957152 A A A 2.13774922548736 2.39635803782591
3.42033332355385 A A P LNCV6_141322_PI430048170 mRNA
TAGCTTTTCTTGTTCCTGGACTAGGCAATGAATAAGCAACAATGTATCTTTTCTGTGTTC NM_001178020 RefSeq
chr16 + 66427296 66482842 BEAN1 146227 "brain expressed, associated with NEDD4, 1, transcript
variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143697_PI430048170 0.000878140323840321 0.203944480121497 2.10038649246899
1.96369414901661 2.46506983092715 A A A 4.70358155473091 4.08993310844061
4.59336542484926 P P P LNCV6_143697_PI430048170 mRNA
ATGTGCCAAAGCTTTTACCCGGTCTTCAAGACTTACTCAACATAAGAAAATTCATAGGAT NM_001001415 RefSeq
chr19 + 21505634 21538277 ZNF429 353088 zinc finger protein 429
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106364_PI430048170 0.426156454358772 0.866493358142966 5.55726701448876
5.67329734312566 4.90670872442046 P P P 5.45443019623174 5.71211448085975
5.68884106941946 P P P LNCV6_106364_PI430048170 mRNA
AGGAACCAGGACATGAGCCGGCAGTACGAGCAGATGCATAAGGAGCTGACAGACAAGCTC NM_207311 RefSeq
chr12 + 119989843 120094495 CCDC64 NA coiled-coil domain containing 64 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134634_PI430048170 0.168671295376791 0.564936687489045 2.48708638852026
1.54887569616089 3.14674723389267 A A P 2.97055484076354 3.48564012416865
3.55338903335124 P P P LNCV6_134634_PI430048170 mRNA
GCAGTTATGTGATGCAACACTTGATGGTACAGTAAATTTACTGGCATTTTTCTCCTTAAA NM_001142550 RefSeq

chr1 - 108970215 109042228 WDR47 22911 "WD repeat domain 47, transcript variant 1"
GO:0005737|GO:0005874|GO:0007275 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142173_PI430048170 0.0347240807224706 0.6462457323207983.19872806186205
2.68727886826518 2.88441704368586 P A P 3.45787833360207 3.67536243070993
3.56512741116448 P P P LNCV6_142173_PI430048170 mRNA
GAGCTGAATTAGAGGTACTGAATTAAGGACAGTACAAATGAAGTAAAAAGGTTTTCTCCA NM_001282337 RefSeq
chrX + 115560849 115650859 PLS3 5358 "plastin 3, transcript variant 4"
GO:0060348|GO:0005737|GO:0005509|GO:0003779 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143388_PI430048170 0.9156576747442120.9652991489545335.34305338273906
4.88796808416024 4.9432938193079 P P P 4.73341490360812 5.50283100864541
5.02903016044904 P P P LNCV6_143388_PI430048170 mRNA
CATGCTGAACAAAGCTTGAAGTTTAAAACTTTCCTCCCTTCCTCTGTTTATATGAAGTAA NM_001015508 RefSeq
chr8 - 30995801 31033715 PURG 29942 "purine-rich element binding protein G, transcript variant B" GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68839_PI430048170 0.000626601334434602 2.1240434726012 4.82044415560628
4.74132109154463 5.01733298418687 P P P 3.88199882779563 3.7883655401549
3.65335028536182 P P P LNCV6_68839_PI430048170 mRNA
AAGCACGGTCACGGGAAGTTGTTATTTAAAGATGGCAGTTATTACGAAGGGGCGTTTGTG NM_024848 RefSeq chr1
- 2321252 2391751 MORN1 79906 "MORN repeat containing 1, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_102176_PI430048170 0.0878540534327108 0.7485642559895725.06200309465198
5.06390634293349 5.43996100110472 P P P 5.84532666170636 5.37609435670597
5.59328897574425 P P P LNCV6_102176_PI430048170 mRNA
AAATCTGACTGCTGATGTGGGCTTCATTGACTCCTTCAGGCCTCTGTACACACATGAATA NM_003262 RefSeq chr3
+ 169966791 169998373 SEC62 7095 SEC62 homolog (S. cerevisiae)
GO:0005791|GO:0016235|GO:0016020|GO:0005783|GO:0008565|GO:0006613|GO:0005789|GO:0006620|GO:0004
872|GO:0045111|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115457_PI430048170 0.00409784069917651 1.56971317172179 6.39781114600825
6.66672715076041 6.467246026983 P P P 5.80479104571099 6.00665322998252
5.77110082488198 P P P LNCV6_115457_PI430048170 mRNA
AACCGTGTTATGGTGACAAAGATAAACGGCGGCATTGTTTTGCTACCTGGAAGAATATTT NM_001278579 RefSeq
chr2 + 147844516 147930827 ACVR2A 92 "activin A receptor, type IIA, transcript variant 1"
GO:0071773|GO:0005515|GO:0007368|GO:0005886|GO:0050999|GO:0048706|GO:0034673|GO:0007283|GO:0043
621|GO:0009952|GO:0046872|GO:0005737|GO:0004702|GO:0019838|GO:0048185|GO:0007178|GO:0005024|GO:0
030510|GO:0023014|GO:0030501|GO:0009986|GO:0010862|GO:0043084|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130362_PI430048170 0.00139405326711916 0.3053095981704284.09766753702119
3.79656885694545 4.28658511364536 P P P 5.8454532931155 5.6170806377043
5.88099980527234 P P P LNCV6_130362_PI430048170 mRNA
CGGATAGATTGAGATGTTCTTTCACATCAGATGATCTGTAACACTGTAAGATACTGATCT NM_001206 RefSeq chr9
- 70384596 70414657 KLF9 687 Kruppel-like factor 9
GO:0010839|GO:0050847|GO:0097067|GO:0003700|GO:0005886|GO:0006357|GO:0007566|GO:0005634|GO:0003
677|GO:0006351|GO:0046872|GO:0071387|GO:0005737|GO:0007623|GO:0005654 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145444_PI430048170 0.2000218877616662.07688882875397 1.45178574509772
2.03021982225059 0.383538784838307 A A A 0.3616222113129620.320705056079041
0.462715648897845 A A A LNCV6_145444_PI430048170 mRNA
GTATAAATGTGACAAAGACACTAATAACATGTTAGCCTCCACCCAAAATAAAATGGGCTT NM_001059 RefSeq chr4
- 103589467 103719816 TACR3 6870 tachykinin receptor 3

GO:0005515|GO:0060259|GO:0005886|GO:0007568|GO:0007217|GO:0043278|GO:0042538|GO:0005634|GO:0045777|GO:0042220|GO:0042053|GO:0032809|GO:0004995|GO:0005737|GO:0032590|GO:0070474|GO:0005887|GO:0010460|GO:0032355. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72040_PI430048170 0.0153415785366451 1.45449281452366 8.53102236672628 8.4312172561162 8.34394369936786 P P P 7.88992167861911 8.06068017182419 7.72002554271025 P P P
LNCV6_72040_PI430048170 mRNA
AACCCACAGAGCTGATGCTGCAGATGAACCTGCTGGAACTCATCCGGAAGCTGCAGCAGA NM_005675 RefSeq
chr22_KI270734v1_random + 131493 137393 DGCR6 8214 DiGeorge syndrome critical region gene 6
GO:0003674|GO:0005578|GO:0009887|GO:0005634|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143089_PI430048170 0.0232196883200586 1.89229892954518 8.15585487387233 8.42052050865547 8.17795673181617 P P P 7.68678168525034 7.12803385810033 7.11803071138448 P P P LNCV6_143089_PI430048170 mRNA
TCTCTTCTCCTGCCTGGATTATTTAAAAAGCCATGTGTGGAAACCCACTATTTAATAAAA NM_006875 RefSeq chrX - 48913181 48919136 PIM2 11040 "Pim-2 proto-oncogene, serine/threonine kinase"
GO:0043066|GO:0008285|GO:0008283|GO:0050821|GO:0009615|GO:0005524|GO:0007346|GO:0000082|GO:0005737|GO:0046777|GO:0008637|GO:0004674|GO:0006468|GO:0045893|GO:0043123|GO:0007140|GO:0010508 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133095_PI430048170 0.598155662357518 0.975990086334603 0.427062243948922 0.395421600146123 0.257289854283796 A A A 0.34274544244272 0.459881144832959 0.385477147475174 A A A LNCV6_133095_PI430048170 mRNA
AATCCTCCATGAAAAAGCTCATGGCCTGTGTGAGTCAGGATAACTTCTCCTTGTCATCAG NM_021247 RefSeq chr16 - 11273198 11273595 PRM3 58531 protamine 3
GO:0008150|GO:0003674|GO:0005737|GO:0030261|GO:0007275|GO:0005634|GO:0030317|GO:0007283|GO:0005575|GO:0000786|GO:0003677|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128346_PI430048170 0.00204812935433621 3.55412321711931 5.3226517855834 5.95911367698399 5.73873856834548 P P P 3.79649514075618 3.57312240040647 4.16927043047026 P P P LNCV6_128346_PI430048170 mRNA
CAAGTTTGTAGAATAAACACTGGTTTCCTAGCCATCCTCTGAAAACAGTATGAAACATGA NM_022147 RefSeq chr3 + 187368379 187371581 RTP4 64108 receptor (chemosensory) transporter protein 4
GO:0005515|GO:0005737|GO:0006612|GO:0016021|GO:0001580 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129351_PI430048170 0.674050224489609 1.14581927150307 3.68237440745319 3.13605332378635 2.68344191125665 P P A 3.19474065150368 2.93163676276058 2.9443410438174 P P P LNCV6_129351_PI430048170 mRNA
GCTGGGTGTCTGTGGAAATGAGATTAAAAACTGTACAATCTCAGATTTTACTAAAATGCA NM_024871 RefSeq chr3 - 183815875 183825605 MAP6D1 79929 MAP6 domain containing 1
GO:0032418|GO:0008017|GO:0048813|GO:0018009|GO:0005801|GO:0005516|GO:0005874|GO:0005798|GO:0007026|GO:0000226 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140181_PI430048170 0.964779292880393 0.998141640455842 0.480411107822169 0.508532772986043 0.409181271854607 A A A 0.544292156682558 0.425896809366538 0.434756135367253 A A A LNCV6_140181_PI430048170 mRNA
TTGATAACTGCCCTGACTGTGGCAACAGGTCATTTTATGACCTGGAGGCAGATCAATACT NM_001300891 RefSeq
chr1_KI270766v1_alt + 118730 122582 LOC101929983 NA PRAME family member 9/15-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133131_PI430048170 0.370770962050642 0.913276652091161 11.02627571019 11.046763647911 11.1998697409207 P P P 11.0206215348656 11.2434991087125 11.3846269190718 P P P
LNCV6_133131_PI430048170 mRNA
CTATGTTGGTGTTAGGGGTGGTGTGGAGATTGTTAATCTTGTATAAAGCAATTCAATAAA NM_001079514 RefSeq

chr16 + 4847630 4882401 UBN1 29855 "ubinuclein 1, transcript variant 2"
GO:0005515|GO:0003700|GO:0006357|GO:0016605|GO:0010923|GO:0016032|GO:0006336|GO:0005654|GO:0005
634|GO:0005923|GO:0003677|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132493_PI430048170 0.0123987993406648 0.76452655723577813.2744803186862
13.2338628015125 13.3227944848908 P P P 13.5598657935896 13.661703697614
13.7656877124374 P P P LNCV6_132493_PI430048170 mRNA
GCTTGCTTATGTGTAGGTGAACAGTCACGCCTGAAACTTTGAGGATAACTTTTTAAAAAA NM_004044RefSeq chr2
+ 215311955 215349773 ATIC 471 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP
cyclohydrolase
GO:0021987|GO:0009168|GO:0003360|GO:0003937|GO:0031100|GO:0055086|GO:0021549|GO:0044281|GO:0042
803|GO:0005829|GO:0005739|GO:0004643|GO:0046452|GO:0006139|GO:0010035|GO:0016020|GO:0006144|GO:0
046654|GO:0009116|GO:0070062|GO:0006189 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61856_PI430048170 0.5859452533039940.76903336021412 1.18501811803285 0.275445651524402
1.33509045735161 A A A 1.34474736678651 1.96011910427562 0.464911657700123A A A
LNCV6_61856_PI430048170 mRNA
AGCCATATCTCCTTTCCCTACAAAAGAAAAGCATACTGTTAAAATGTGCTTACCAATACT NM_016132RefSeq chr15
- 48139427 48178361 MYEF2 50804 "myelin expression factor 2, transcript variant 1"
GO:0014902|GO:0005737|GO:0000166|GO:0030182|GO:0005654|GO:0005634|GO:0003677|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129675_PI430048170 0.0947787668132878 0.8256153116946667.8349580814494
7.8309607019929 7.87323348622309 P P P 8.02779709938614 8.02331792170395
8.30003202752218 P P P LNCV6_129675_PI430048170 mRNA
TGTGTGTCTGACAACTTCTCATTAGCCCAACTTATGATGTTTCTAGGGATATAAAACATT NM_001077351 RefSeq
chr14 - 22900644 22919187 RBM23 55147 "RNA binding motif protein 23, transcript variant 1"
GO:0006397|GO:0005515|GO:0016020|GO:0000166|GO:0003723|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106393_PI430048170 0.3498064844604251.05296027899625 0.317336777569691
0.3144612384334670.494698830442006A A A 0.3069458945560110.27570453916259
0.327508625605164A A A LNCV6_106393_PI430048170 mRNA
TGATGGTTTGCTACCGCACGGACGACGAGGAGGACCTGGGCATTTATGTCGGAGAGGTAA NM_001303513
RefSeq chrX - 153802165 153830567 PDZD4 57595 "PDZ domain containing 4, transcript variant 3"
GO:0005938 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134980_PI430048170 0.2091063008625140.8625376503662769.7032072560631
9.49826030991469 9.82178152753816 P P P 10.0819758143866 9.72234699038877
9.85415820830602 P P P LNCV6_134980_PI430048170 mRNA
CATGGGGTATGTAGACTAGTAACACATAAGAAAATTGCAGTAAGATGGTAACAAAACCTC NM_005875RefSeq chr3
+ 40309681 40312426 EIF1B 10289 eukaryotic translation initiation factor 1B
GO:0006446|GO:0003743|GO:0005575|GO:0006413 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128964_PI430048170 0.0152240901324597 0.3115882693913473.14755733034565
2.06541508625943 2.75387077423135 P A A 4.05739062800287 4.37014253763196
4.71104183661464 P P P LNCV6_128964_PI430048170 mRNA
TGGTGGTTTCTAAATAAATACCTGGCCAGAGGACCATCACCTGTCACCTTATTAAAACAG NM_001284280 RefSeq
chr14 - 91457480 91510480 SMEK1 55671 "SMEK homolog 1, suppressor of mek1 (Dictyostelium),
transcript variant 3" GO:0030289|GO:0005737|GO:0006470|GO:0005815|GO:0045722|GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_83112_PI430048170 0.5501996706116960.7681438889519370.9972672332767272.00340890498986
1.64351421128577 A A A 1.08560628479323 2.10197917156989 2.45166368984139 A A P
LNCV6_83112_PI430048170 mRNA
CAATTGAGGAAAGAGGCGATCTCTTTGGAAAAGCACTTAATCTGAACACAGACTTTGTTT NM_153688RefSeq chr16

+ 75148522 75172234 ZFP1 162239 ZFP1 zinc finger protein
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_109108_PI430048170 0.8202113690171711.02847615936292 9.10072965444376
9.51178407650894 9.32979308738905 P P P 9.54991212123261 9.21368102028317
9.03893480582424 P P P LNCV6_109108_PI430048170 mRNA
AGCAAGTTCACCAACAGCTGCCACCTCTACCTGTGGCTGTTCCTCCTGCTGCTGCCCCTG NM_014801 RefSeq chr1
- 232984135 233295713 PCNXL2 80003 pecanex-like 2 (Drosophila) GO:0016021 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_94625_PI430048170 0.4487142157308180.9541450083148910.3746963883714420.369493564464569
0.329935640908309 A A A 0.3618142030857160.5598766437070520.346015505600865 A A A
LNCV6_94625_PI430048170 mRNA
CAAGGAACTCACCATGCTTTTTCAGAAAGTTGCTGGTGAATAAAAGCATTCGGCAGCGTC NM_001037340 RefSeq
chr1 + 65992615 66374579 PDE4B 5142 "phosphodiesterase 4B, cAMP-specific, transcript variant c"
GO:0032729|GO:0050852|GO:0001780|GO:0048471|GO:0030018|GO:0004115|GO:0004114|GO:0032743|GO:0030
593|GO:0005634|GO:0050900|GO:0005891|GO:0035690|GO:0046872|GO:0044325|GO:0005829|GO:0071222|GO:0
030552|GO:0071872|GO:0086004|GO:0006198 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107697_PI430048170 0.754598148432807 1.19604494691168 0.304100175410371
0.307677337055983 1.52839911864887 A A A 0.484391493819183 0.852733318921197
0.34939745665769 A A A LNCV6_107697_PI430048170 mRNA
AACTTCTCAGGTGCTGCCGTGAAGAACACACAGCCTGAGGACGGGGTGGAAATGGACACT NM_001278428
RefSeq chr19_KI270938v1_alt + 645384 652924 LILRB4 11006 "leukocyte immunoglobulin-like receptor,
subfamily B (with TM and ITIM domains), member 4, transcript variant 3"
GO:0005515|GO:0007165|GO:0005886|GO:0045671|GO:0004872|GO:0016021|GO:0003823|GO:0070062|GO:0002
376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101073_PI430048170 0.542545486877626 1.03499705937804 0.283349043992665
0.29651046428957 0.482149133531696 A A A 0.3145133763413460.312196037483007
0.295028306884093 A A A LNCV6_101073_PI430048170 mRNA
AGAAGATGTACCTGTACAACATCCAGGAAAAGGACACCTTCTTTGATAATGCCACCCGCA NM_001278597 RefSeq
chr12 - 5562650 5946232 ANO2 57101 "anoctamin 2, calcium activated chloride channel,
transcript variant 2"
GO:0034220|GO:0046982|GO:0005886|GO:0034707|GO:0005229|GO:0031513|GO:0005654|GO:0055085|GO:0042
803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127932_PI430048170 0.4213977916380510.8849753266378326.42015878572455
6.13439910899023 5.85982766464014 P P P 6.44097173716027 6.45204480359618
6.07333646954745 P P P LNCV6_127932_PI430048170 mRNA
ATCCATGATAGTCAAAGTCTCTGGTCCCTGCCATGGAAACCAGACAGAGTCTCATTAATG NM_001031850 RefSeq
chr19 - 42902081 42917924 PSG6 5675 "pregnancy specific beta-1-glycoprotein 6, transcript
variant 2" GO:0003674|GO:0007565|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129196_PI430048170 0.0188417213984814 0.6878960172767320.452673620295009
0.4299999176878050.326094232361198 A A A 0.7670232072875271.09719523162036
0.948034995763562 A A A LNCV6_129196_PI430048170 mRNA
CCCTGTGAATTAAGGCAGAGTTTTACTGTAATATTTGCAAGTATCCAAAATGGTTACTGA NM_001083335 RefSeq
chr19 - 44326552 44356704 ZNF112 7771 "zinc finger protein 112, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_92084_PI430048170 0.2283148874065471.19175795198815 3.44838389277698 3.16717139628031
3.39322090811001 P P P 3.33487950555043 2.79915132079147 3.08111254079005 P P P
LNCV6_92084_PI430048170 mRNA

ATCATATGACAAGGACAAGAGTGTTCTGGCTTTCAGAGGAATCCCTTTGTGAGTACAGAG NM_032213 RefSeq chr2 + 85354719 85391752 ELMOD3 84173 "ELMO/CED-12 domain containing 3, transcript variant 1" GO:0006909|GO:0060091|GO:0005737|GO:0032420|GO:0005856|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132642_PI430048170 0.0378011536581420.7578080980563498.4938000214734 8.49710175984452 8.71967984062308 P P P 8.8845260347454 8.84980066054245 9.16694201972726 P P P LNCV6_132642_PI430048170 mRNA
AATGATTAACTGTACAACCTGTATCTGCTGGGTGTTCTTGTTATCATATTGTAAAACAGC NM_024745 RefSeq chr16 - 46580555 46621399 SHCBP1 79801 SHC SH2-domain binding protein 1 GO:2000177|GO:0008543|GO:0042169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135536_PI430048170 0.0576058878093115 2.05157529858621 1.92371612967973 2.91732229992007 2.68376568703767 A A A 1.40788277507369 1.87497194065736 1.22776160935427 A A A LNCV6_135536_PI430048170 mRNA
ATCGATATCTACATGATGGATATTGTATTAATAGGGGCATAAATAAAGGTCGAAGAGTCG NM_153038 RefSeq chr2 + 222298146 222305217 CCDC140 151278 coiled-coil domain containing 140 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143716_PI430048170 0.2942986279485431.7297875678384 2.76004319832739 4.0823812734942 4.23727893435214 A P P 2.9247133916038 3.07067835319463 3.10731057698849 P P P LNCV6_143716_PI430048170 mRNA
ACAGATATTTATCCAAGGGTTCACTGATTCCCGAATAAATGCCAGGAACATTCATGTAAA NM_001010917 RefSeq chr10 + 97850237 97871578 GOLGA7B NA "golgin A7 family, member B" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145038_PI430048170 0.3786561123257570.7786803931195171.30803607788538 2.47071528751883 2.45833169095164 A A A 2.33486604152262 2.40182489695689 2.81282263266029 A A P LNCV6_145038_PI430048170 mRNA
TTCTTGTCCTTGCTTTATAATGCATATGTGCTTAGAAATAAACAGGTTTCACGTGGACTC NM_030615 RefSeq chr6 + 168017872 168045089 KIF25 3834 "kinesin family member 25, transcript variant 1" GO:0008017|GO:0005871|GO:0005737|GO:0000070|GO:0006996|GO:0008152|GO:0005874|GO:0010507|GO:0003777|GO:0016887|GO:0005524|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139916_PI430048170 0.6858805485069731.04243902223548 9.38926155758088 9.5406018184384 9.68415847895321 P P P 9.26968665725275 9.45713271281434 9.69131809110583 P P P LNCV6_139916_PI430048170 mRNA
CTGCTTTACACATGTTATACCATTGTTTTTTCCCTCAAGTATTTTTTCCCTGTGAAGAAG NM_080651 RefSeq chr8 + 117520712 117540262 MED30 90390 "mediator complex subunit 30, transcript variant 1" GO:0003712|GO:0005515|GO:0010467|GO:0001104|GO:0006367|GO:0006357|GO:0005634|GO:0046966|GO:0030374|GO:0030518|GO:0042809|GO:0016592|GO:0019827|GO:0004872|GO:0005654|GO:0045893|GO:0030521 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143400_PI430048170 0.0102397398604638 0.5521380210342493.03986064292312 3.41280498305305 3.29448501277683 P P P 4.04340560753983 3.88952805629353 4.36771352527583 P P P LNCV6_143400_PI430048170 mRNA
GAGAGACACGGACCACCAAAGGCTTGATTTTTCTTCATCCTACATTATATTCAAAACAAA NM_021925 RefSeq chr2 - 20684013 20823130 LDAH NA "chromosome 2 open reading frame 43, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135873_PI430048170 0.3741925747918560.7404360058979314.3987251113313 2.36804113878532 2.3050641635591 P A A 3.64958821428626 3.75579860583147 4.00683941922908 P P P LNCV6_135873_PI430048170 mRNA
GCCAGCTAATAAATTGTCACACAATGGAAAATCATATGCCACAACATTCATTGTAAGGTT NM_020177 RefSeq chr5 - 115520910 115544894 FEM1C 56929 fem-1 homolog c (C. elegans) GO:0005737|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_130707_PI430048170 0.57528148842611 1.04123092263989 7.22358392375258
7.28435449740206 7.08720857920517 P P P 7.22397368853792 7.20994977526572
6.98066498481395 P P P LNCV6_130707_PI430048170 mRNA
TACTGTGACCCTCCCGGTCTTCATTGGCAATATTGCTGTGAACCATGCCCCAGTGAGCCC NM_152285 RefSeq chr9
+ 137605643 137615360 ARRDC1 92714 arrestin domain containing 1
GO:0005886|GO:0031410|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115192_PI430048170 0.563546202164599 1.02009308426286 0.411119052763538
0.2767148747525460.319844281614588 A A A 0.2844953591348990.311730952616184
0.328291694235888 A A A LNCV6_115192_PI430048170 mRNA
CTCTAATGACACCATTCTTCTGGAAAATGCTGGAGAAGCAATAAAGGTTGTACCAGTCAG NM_002854 RefSeq
chr22_KI270877v1_alt - 21487 40260 PVALB 5816 parvalbumin
GO:0043234|GO:0030424|GO:0005737|GO:0046982|GO:0051480|GO:0005509|GO:0043025|GO:0005634|GO:0042
803|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93690_PI430048170 0.0256821986349637 1.54665673171924 4.68432345065107
5.04388602637152 4.63866054903884 P P P 4.33758681902811 4.23255139943116
3.91087622082244 P P P LNCV6_93690_PI430048170 mRNA
TCTTGACCTTAGCTCTGTATCAAAATTGCCTGAGAAACTGCTTAAGAAAACAGATGTCAT NM_001300958 RefSeq
chr1 - 32364632 32394461 BSDC1 55108 "BSD domain containing 1, transcript variant 5" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126812_PI430048170 0.719545691823854 0.992029318978406 0.43350895159748
0.4424616768636080.3702878949547 A A A 0.4650724437753890.398460921648211
0.417610954329294 A A A LNCV6_126812_PI430048170 mRNA
TTTCTTAGTCGTGTGTATAGTCCTAAATTTCCCCAAACTATGTGTTCATTTGGATTGTGT NM_001009909 RefSeq chr11
+ 24496969 25082640 LUZP2 338645 "leucine zipper protein 2, transcript variant 1" GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132011_PI430048170 0.0166237449896155 0.594615703372832 5.54565186992868
5.14534955122254 5.60669770743299 P P P 6.01162425880144 6.30782029485181
6.25334193720512 P P P LNCV6_132011_PI430048170 mRNA
ACTTAGGGCCAGATGCACTGTAAACATTGCAGGTTTAAACATAAAGGAGTCTTTAAAAAA NM_198467 RefSeq chr7
+ 77696425 77779803 RSBN1L 222194 round spermatid basic protein 1-like GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135771_PI430048170 0.656975695241955 1.31255792362865 1.8517646299328
0.4751523455280210.435316376352913 A A A 0.3874132769254130.898402375977452
0.737357809628548 A A A LNCV6_135771_PI430048170 mRNA
CAAGAGAACAATAGAGTGGGTCTCTTGGGGAAACATAATAAAAATGAACTTTTCTCACCT NM_001146210 RefSeq
chr7 - 102345751 102356444 SPDYE6 NA speedy/RINGO cell cycle regulator family member E6 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135478_PI430048170 0.126108527694515 0.710142380247144 4.33285875838933
4.32858888658838 4.72066754636457 P P P 4.5457472542058 5.08170036974087
5.19297114089193 P P P LNCV6_135478_PI430048170 mRNA
GGGAGAGAAATGTCCAAAAGAGATCTGCTGATCTGCTGAGAGTTTCAAACAAACAAAAAA NM_001160167
RefSeq chr11 + 36296174 36465204 PRR5L 79899 "proline rich 5 like, transcript variant 1"
GO:0005739|GO:0010762|GO:0001934|GO:0001933|GO:0014068|GO:0031932|GO:0009968|GO:0031625 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141713_PI430048170 0.651374520040281 1.25776569081402 1.67925863468387
0.5049749001539920.388651621615766 A A A 0.3873395619475790.545194277451397
0.962164129521266 A A A LNCV6_141713_PI430048170 mRNA
CAGGCTACTGGAATTGGTTATTAAAAGAAAAAGGAAAAAGAAGAATCTTGCTGCTTTCAG NM_020640 RefSeq chr3
- 182938157 182980601 DCUN1D1 54165 "DCN1, defective in cullin neddylation 1, domain containing 1"

GO:0005515|GO:0008150|GO:0000151 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138581_PI430048170 0.4150348136726810.7260296861917761.34922758839284
0.5157746777905260.40592593973371 A A A 1.49646209392124 1.64035809114308
0.44829873369568 A A A LNCV6_138581_PI430048170 mRNA
TGCAATACAAAAATCGTATCTCAAGGGAAAATACTCAAAGAAAGAAAAGTGGCAGCACTT NM_001882RefSeq chr5
+ 76952854 76969474 CRHBP 1393 corticotropin releasing hormone binding protein
GO:0005515|GO:0005783|GO:0051424|GO:2000310|GO:0031045|GO:0005634|GO:0005615|GO:0030425|GO:0005
622|GO:0045055|GO:0006954|GO:0035865|GO:0071392|GO:0071356|GO:0001963|GO:0043196|GO:0071277|GO:0
007611|GO:0043204|GO:0043679|GO:0051460|GO:0030141|GO:0042277|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93252_PI430048170 0.0376520720886471 2.07894257880391 4.15802862244977
4.07656508069605 3.97775845248409 P P P 3.44610052513283 2.74041117660075
2.74413798355428 P P P LNCV6_93252_PI430048170 mRNA
TGTTAAGATTCCAGTGAGAAACCATGGGATCCTGATGGAGACCCACAAAGAACTGAAACC NM_152449RefSeq chr15
- 99727400 99733444 LYSMD4 145748 "LysM, putative peptidoglycan-binding, domain containing 4,
transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138975_PI430048170 0.5718921219857941.09316167002047 0.399201360469385
0.8010076861313130.25433547149763 A A A 0.3540326441415330.40106518198171
0.370438282861152 A A A LNCV6_138975_PI430048170 mRNA
CACCAAGATGTAATGATGATTCTATTCCATTTTGAAAAGGGTCTGAGAAAGTGTACAGGT NM_030806RefSeq chr1
+ 184387015 184629021 C1orf21 81563 chromosome 1 open reading frame 21 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_127632_PI430048170 0.1526406083092671.08915519794624 10.5321607602274
10.4756468058756 10.3665039969407 P P P 10.3475613934294 10.4147285688536
10.2420507756803 P P P LNCV6_127632_PI430048170 mRNA
GATAGTGAGCATAGTCCCCACCTCCACCCCTCACAATTTATTTGAATACTTCAATTGTGC NM_006633RefSeq chr5
+ 76403254 76708132 IQGAP2 10788 "IQ motif containing GTPase activating protein 2, transcript variant
1"
GO:0034314|GO:0005516|GO:0009986|GO:0007264|GO:0005874|GO:0005547|GO:0071933|GO:0003779|GO:0030
175|GO:0015629|GO:0043086|GO:0030027|GO:0005099|GO:0048365|GO:0005902|GO:0007165|GO:0005737|GO:0
051015|GO:0031941|GO:0032320|GO:0070493|GO:0017048|GO:0005095|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_95177_PI430048170 0.45691407442822 0.8553906150653360.5064426719989170.45007066280378
0.33279718943128 A A A 0.3771872503817991.04591039625862 0.45064117594943 A A A
LNCV6_95177_PI430048170 mRNA
ATGTACCGGAACATGCTTATCGACTGTGAGAACCAGTGTGTCATCATTAGTGGAGAGAGT NM_012335RefSeq chr19
- 8520789 8577447 MYO1F 4542 myosin IF
GO:0005516|GO:0030335|GO:0050830|GO:0043312|GO:0003779|GO:0005524|GO:0008150|GO:0003774|GO:0007
162|GO:0016461|GO:0031941|GO:0032956|GO:0045088|GO:0008152|GO:0030864 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_38534_PI430048170 0.13110607292963 0.9623951063172240.4022988732780390.414382006166373
0.33764495400879 A A A 0.4284552715802790.4599232752706330.432815843071132 A A A
LNCV6_38534_PI430048170 mRNA
TTAATTATTATATCCAGTTGATATCTTTGTTTATGTAGATAACAAAAGCAGCAGAAAGAC NM_001159293 RefSeq
chr19 - 20537991 20565820 ZNF737 100129842 zinc finger protein 737
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141032_PI430048170 0.0333616979659857 0.7233023031715545.917934168479
5.654059694582 5.52977530209991 P P P 6.32130438520962 6.16496081309384

6.03037816372015 P P P LNCV6_141032_PI430048170 mRNA
GCACCCAGACTTTTGCCCCCATTCCTGCTACTTGTGAACAAATAAAGATTCATATACTCA NM_001001343 RefSeq
chr5 - 157341598 157345721 FNDC9 408263 fibronectin type III domain containing 9 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142424_PI430048170 2.89039335591148e-05 0.5167740534937765.03507744414778
4.97205241175707 5.08455309055874 P P P 5.98383526237674 5.93159083728493
6.03382935847166 P P P LNCV6_142424_PI430048170 mRNA
TTAGAAGCTGCCTGCCTTTTAGTTGTTTCTTGCCTTTAATAAAATGTTATCAGTTCCCCC NM_031940RefSeq chr8 -
38988807 38996522 TM2D2 83877 "TM2 domain containing 2, transcript variant 2" GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118885_PI430048170 0.0139773252475849 1.1798602429854 8.32070158345063
8.4327801028703 8.31990306913166 P P P 8.095682632313 8.20132232171012
8.05969749706822 P P P LNCV6_118885_PI430048170 mRNA
TGTGCAGGAGCCAGGCCTCCCCCTGGGTCCCCATGATGAGAGAATGGGTTCTGCTCATGT NM_002900RefSeq chr10
+ 47348370 47357875 RBP3 NA "retinol binding protein 3, interstitial" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_82038_PI430048170 0.0924165828547758 1.20389446113326 8.2044378721959 7.9111095135612
8.062486571571 P P P 7.62340136508828 7.91666075146933 7.83410935645021 P P P
LNCV6_82038_PI430048170 mRNA
GCTACTCATGGCAAGAAACAGACAAAGCCCCATGAAAAATAAAACAAAACAAAAGTCATT NM_032227RefSeq
chrX + 110003113 110177788 TMEM164 84187 "transmembrane protein 164, transcript variant 2"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130329_PI430048170 0.177959299696589 1.44490789138998 0.335778784887677
0.8622742961288441.1608997563088 A A A 0.2949139286420280.275850618450146
0.312152104740714A A A LNCV6_130329_PI430048170 mRNA
CCCTCAAGTCATTCATTTATCCTAATACTGGGGAACAATAAATTAAGACATGCATCTCTA NM_023919RefSeq
chr12_KI270904v1_alt - 237 1333 TAS2R7 50837 "taste receptor, type 2, member 7"
GO:0033038|GO:0007186|GO:0005886|GO:0008527|GO:0016021|GO:0001580 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143950_PI430048170 0.0364347368613738 0.5924918064612092.11930880583791
1.77553718894318 1.58978984828143 A A A 2.71801084282159 2.80031090134753
2.21610414699453 A P A LNCV6_143950_PI430048170 mRNA
GTCAATCATTACTCAAAGAATGATGAAGGTATTTGGTGTATGCCAAAGAATAAAGGCGTT NM_138969RefSeq chr8
- 56300010 56320682 SDR16C5 195814 "short chain dehydrogenase/reductase family 16C, member 5"
GO:0050908|GO:0042574|GO:0042572|GO:0005789|GO:0016021|GO:0004745|GO:0043616|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145320_PI430048170 0.5430638205117620.8801219688111637.72035451576994
7.36796493091487 7.57309133359516 P P P 7.29607894090447 7.97877785002617
7.87188511882606 P P P LNCV6_145320_PI430048170 mRNA
TGTTCCAATCAATGCAGTTGACAATAAAGGAATGAGTATCGTCACGGAGTTGACTGCCTT NM_002254RefSeq chr2
- 25926585 25982574 KIF3C 3797 kinesin family member 3C
GO:0008017|GO:0005871|GO:0006996|GO:0005874|GO:0072384|GO:0072372|GO:0003777|GO:0005524|GO:0005
829|GO:0030705|GO:0019886|GO:0003774|GO:0007596|GO:0008152|GO:0016887|GO:0007018 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132469_PI430048170 0.5990019361741620.832506460494151 1.02720006410542
0.3565063545079690.295168111973218A A A 0.5069955569480550.428332700513936 1.4292945856619
A A A LNCV6_132469_PI430048170 mRNA
AGGAGCTTCGGCACCATGTCTGGTTTGGATTCATCTAAATAAATATGTGGTTCCCCAGTG NM_001010985 RefSeq
chr1 - 109292364 109307041 MYBPHL NA "myosin binding protein H-like, transcript variant 1" NA .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99881_PI430048170 0.206205349299511 0.8072996503903426.57519293325148 6.7725311131523
6.81827733134666 P P P 7.00448521238674 6.73938260727846 7.30453111966297 P P P
LNCV6_99881_PI430048170 mRNA
AAGAGTTGGGAAGTTAATTTTGGTTATATTGAGCATGGTGAGAAGAGAAATGCACTTGTT NM_145246 RefSeq chr10
- 93667882 93702572 FRA10AC1 118924 "fragile site, folic acid type, rare, fra(10)(q23.3) or fra(10)(q24.2)
candidate 1" GO:0005515|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136366_PI430048170 0.7187570670564551.26732930299244 2.38268712482175
0.3612559339231761.56743690071485 A A A 0.8149437016354810.511807209006419
2.09832803325009 A A A LNCV6_136366_PI430048170 mRNA
TATGCTCCAGAAATAACTGCCCCTGAAGAGAATGAGGAATTACCTTGCACTGAACCATAG NM_001010860 RefSeq
chr14 + 77377418 77391244 SAMD15 161394 sterile alpha motif domain containing 15 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_101725_PI430048170 0.00697783777814525 0.5554622697540317.45487050010174
7.16496305831758 7.58648942129361 P P P 8.09978796031873 8.2824484542313
8.38601334738259 P P P LNCV6_101725_PI430048170 mRNA
ATCTCTCTAACCATTTGAAGTTGATTTCTCAATGCTAACTAATCAAGAGAAGTAGGAAGC NM_001199189 RefSeq
chr5 - 87394261 87412904 CCNH 902 "cyclin H, transcript variant 2"
GO:0005515|GO:0010467|GO:0006368|GO:0006367|GO:0006366|GO:0006363|GO:0006362|GO:0006361|GO:0006
360|GO:0005634|GO:0000079|GO:0070985|GO:0000082|GO:0045944|GO:0000086|GO:0016032|GO:0016538|GO:0
008094|GO:0019907|GO:0019901|GO:0006370|GO:0008353|GO:0050434|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140344_PI430048170 0.296581800286825 1.34175342201724 3.58239868889513
4.10147219324457 3.56497715492425 P P P 3.7261860006711 3.47616822722695
2.62744594609501 P P P LNCV6_140344_PI430048170 mRNA
GGGAAGCTCTTTTCTCCTGCAGAAAGGGCCACCCATGATACTCCACTCCCAGCAGCTCAA NM_033553 RefSeq chr1
- 42162690 42164724 GUCA2A 2980 guanylate cyclase activator 2A (guanylin)
GO:0030250|GO:0005179|GO:0031284|GO:0005576|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138802_PI430048170 0.178799953445417 0.650224170520521 5.15055419334901
5.16763417428474 5.58339943597064 P P P 5.31907986979117 5.99970459297666
6.31718713170395 P P P LNCV6_138802_PI430048170 mRNA
ACAAAGTTGTATCCTTTCTGGAGAAGACTGGGTTTGTAGATGAAACTGAAGCTGCCAAAG NM_018186 RefSeq chr1
+ 169795408 169853088 C1orf112 55732 chromosome 1 open reading frame 112 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127744_PI430048170 0.0160472629342572 0.7579629139245029.7184829873544
9.61854123516875 9.82735064419598 P P P 10.1030079421485 9.99833634919929
10.2580985053213 P P P LNCV6_127744_PI430048170 mRNA
GTGATTCCATCTGGGCAAAAGTCTGAAGATCTGAAATAACTTTATATCAAACCATTGATC NM_017453 RefSeq chr20
- 49113338 49188367 STAU1 6780 "staufen double-stranded RNA binding protein 1, transcript variant
T3"
GO:0003725|GO:0005515|GO:0005791|GO:0046726|GO:0008298|GO:0005783|GO:0010494|GO:0005875|GO:0030
425|GO:0044297|GO:0005737|GO:0016020|GO:0043025|GO:0008157|GO:0045070|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136297_PI430048170 0.217445580863801 0.9138984211875067.30735732983559
7.07547950603911 7.13815812105328 P P P 7.23288663982558 7.41442267312631
7.26692362143824 P P P LNCV6_136297_PI430048170 mRNA
CCAATGACATTTTGCCACTTGAAACAATAAATAAAGTTTTTTGGGAATTGGTGCTGTCCA NM_033396 RefSeq chr11
- 57299628 57324939 TNKS1BP1 85456 "tankyrase 1 binding protein 1, 182kDa"

GO:0010467|GO:0005886|GO:0030506|GO:0005634|GO:0030014|GO:0005829|GO:0005737|GO:0005724|GO:0005654|GO:0005856|GO:0007004|GO:0019899|GO:0000289|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128941_PI430048170 0.0712877211574263 0.78319052225917813.0180122649373 12.902541999675 13.114233153271 P P P 13.4433701566224 13.1350256874729 13.4961484815745 P P P LNCV6_128941_PI430048170 mRNA
AGGAAAGGCTGTAGAAGGAAATATACCTTAACAGGCTGATTTGGAGTGAGCCAGAAAAAA NM_006835RefSeq chr4 - 77048020 77075972 CCNI 10983 cyclin I GO:0051726|GO:0007283 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49906_PI430048170 0.2428268548613931.10719452798083 5.82784408529943 6.07640278472537 5.80094475431547 P P P 5.71891060437524 5.75688558634511 5.80370113945314 P P P LNCV6_49906_PI430048170 mRNA
AATTAATAAAATGCACATATCCCAGTCCATTGAGGCACCCTTGACAGCGACAGACACAGC NM_018198RefSeq chr1 - 6634167 6701906 DNAJC11 55735 "DnaJ (Hsp40) homolog, subfamily C, member 11" GO:0005515|GO:0005743|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140908_PI430048170 0.00992126534565434 0.8365681404894747.40607387758192 7.3013878173066 7.32845428057663 P P P 7.58620553813101 7.61653120052156 7.6074040496118 P P P LNCV6_140908_PI430048170 mRNA
TCTCAGCCTATTTTGTGTCCTAATGATTCGCTCAATAAACATGTTTGAATCCACACGTTA NM_001282717 RefSeq chr7 + 100177742 100214387 STAG3 10734 "stromal antigen 3, transcript variant 3" GO:0007059|GO:0000795|GO:0030893|GO:0005730|GO:0005634|GO:0007130|GO:0005615|GO:0000775 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144530_PI430048170 0.178651965564071 1.15668117311048 8.52512559616305 8.84810069045341 8.67722527095402 P P P 8.47754370103015 8.31957789490749 8.62530410120553 P P P LNCV6_144530_PI430048170 mRNA
CTTTGATGATGTAACTTGACCTTCCAGAGTTATGGAAATTTTGTCCCCATGTAATGAATA NM_001114735 RefSeq chr15 - 79960889 79971301 BCL2A1 597 "BCL2-related protein A1, transcript variant 2" GO:0005515|GO:0051400|GO:0043066|GO:0046982|GO:0008630|GO:0005741|GO:2001243|GO:0042803|GO:0097192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133832_PI430048170 0.0324209095881466 0.6512517060928726.50013211276504 6.02627056834254 6.15016337517945 P P P 6.96275107322111 6.75645460198837 6.84882755285978 P P P LNCV6_133832_PI430048170 mRNA
TTTGTGCACATTGAGGGCATGGGCAGAATCTGCTCCCAAAAGCATTGAAAGCCAATATGA NM_178582RefSeq chr20 + 31514409 31539923 HM13 81502 "histocompatibility (minor) 13, transcript variant 4" GO:0005515|GO:0005791|GO:0005886|GO:0009986|GO:0005783|GO:0031293|GO:0071458|GO:0042500|GO:0042803|GO:0016020|GO:0033619|GO:0071556|GO:0008233|GO:0006509|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137937_PI430048170 0.874583132238601 0.985576035040179 5.29550153475114 5.0063945295194 4.68389347819074 P P P 4.87061131304455 5.22382744659143 4.99618511863303 P P P LNCV6_137937_PI430048170 mRNA
CTGTTGTTCTGGGACCAGAGTATTTTTGTTAATAAAACTCAAAAGCCATCCATGCTCAGG NM_004608RefSeq chr16 - 30085793 30091884 TBX6 6911 T-box 6 GO:0001191|GO:0001102|GO:0001707|GO:0003700|GO:0001708|GO:0023019|GO:0014043|GO:0005634|GO:0000122|GO:0003677|GO:0009653|GO:0006351|GO:0032525|GO:0045944|GO:0001085|GO:0010977|GO:0007498 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137557_PI430048170 0.88900770088428 0.98330629550243 0.490220795085635 0.4353560296127920.445952481932419 A A A 0.3261872546198910.677174149304194 0.418295570769474 A A A LNCV6_137557_PI430048170 mRNA
AGACCTTCTGACTCATCAAAGACTACATGAGCAGAGAGAAACATTATAAATGTAGTAAGT NM_001304449 RefSeq

chr2 + 132307143 132318747 ZNF806 NA zinc finger protein 806 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132819_PI430048170 0.6731686786809641.01240491386744 10.7973058063438 10.7885034211819 10.8290341198674 P P P 10.7943928501983 10.8461908423238 10.7183589145176 P P P LNCV6_132819_PI430048170 mRNA
TGGTGACCCCAAAAATGAAACCATCAATAAAGACTGAGTTGCCAGCAGTGTGTAGAGTGG NM_022752 RefSeq chr19 + 42076137 42081567 ZNF574 64763 zinc finger protein 574
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129144_PI430048170 0.1833811332947080.9219233232677067.80690583480532 7.7622620998367 7.60452506057717 P P P 7.90602161112519 7.7994253981056 7.82568367036035 P P P LNCV6_129144_PI430048170 mRNA
TCTTTTCGGTGCTCCCTAATCCAAGCAGCTTGACTTTAGAGAAGTTGCAGAAGCAGTGAA NM_001029859 RefSeq chr11 - 78171243 78188629 KCTD21 283219 potassium channel tetramerization domain containing 21
GO:0051260 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93797_PI430048170 0.0314002951792491 1.25778275586243 9.20911218802534 9.05899909210953 9.19377761500902 P P P 8.97696482434167 8.7608709998453 8.72285374219959 P P P LNCV6_93797_PI430048170 mRNA
TTTGACGAAAAGAAGGAGATCAACAAACGGAAGCAGCTGATCCTGGAGGGGAAGGACCCT NM_019070 RefSeq chr19 + 18919674 18928633 DDX49 54555 "DEAD (Asp-Glu-Ala-Asp) box polypeptide 49, transcript variant 1" GO:0008152|GO:0004386|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142587_PI430048170 0.3197053151659821.07089236284793 0.269918565735801 0.5028258436989040.470280536735404 A A A 0.3428333400042260.293709074602674 0.320471411131426 A A A LNCV6_142587_PI430048170 mRNA
GTACTATGTGCATGCATACTACCTATTTCTAAACTTTGCCATATTGAGGCCTTTATAAAC NM_018557 RefSeq chr2 - 140231426 142131701 LRP1B 53353 low density lipoprotein receptor-related protein 1B
GO:0043235|GO:0005041|GO:0005509|GO:0016021|GO:0015031|GO:0006898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127869_PI430048170 0.8044679693802020.97997417223811 9.83359336743766 9.45246818188601 9.66484154953636 P P P 9.64786581335313 9.81317240578029 9.59335448689911 P P P LNCV6_127869_PI430048170 mRNA
TTGTCCAGACTCTACCCGCAGTCCAGCTGGTGCACACGTTTTGAGGAGAGGCAGTGATTC NM_033113 RefSeq chr19 + 55476331 55484487 ZNF628 89887 zinc finger protein 628
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129561_PI430048170 0.0114647950963478 0.4177570235834065.11824488225886 4.53490906964435 4.55357451589906 P P P 6.00455674691728 5.87970931911047 6.16517841600095 P P P LNCV6_129561_PI430048170 mRNA
CCAAGCAAAAAACATTTGTAAGATACACGGTATCTATTTGGAGCAACGGTTTTTGTAACT NM_017782 RefSeq chr10 + 5684837 5763740 FAM208B 54906 "family with sequence similarity 208, member B"
GO:0005737|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57626_PI430048170 0.5028961883071780.7360565215662440.4261879878631312.1522489798597 0.368945427991218 A A A 2.39129398297006 0.8263822521285781.37835014334886 P A A LNCV6_57626_PI430048170 mRNA
CTAGGGGCGGAGTTTCTCGTAAGGGGCAAGGCCAAGGCATCTTGTATTGGGGCTGACAGG NM_000327 RefSeq chr11 + 62612740 62615121 ROM1 6094 retinal outer segment membrane protein 1
GO:0010468|GO:0042622|GO:0005887|GO:0061298|GO:0007155|GO:0007601|GO:0060219 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133137_PI430048170 0.9274017476159390.9853884717096640.580159637883898

0.6236705570895640.5553238863498 A A A 0.8297424190194980.482094822322115
0.483334089255184 A A A LNCV6_133137_PI430048170 mRNA
CTGCAAGCTTTCAAAACTGCTCTAGAAAACTTCTCCAGAGCACTCAAACAAATAGAGTAG NM_001080478 RefSeq
chr5 + 191510 195353 LRRC14B NA leucine rich repeat containing 14B NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_137372_PI430048170 0.0336970400323378 1.29358727897699 8.87120697059254
9.04533479770655 8.7367595445671 P P P 8.59522552482486 8.57275750372201
8.37811231254949 P P P LNCV6_137372_PI430048170 mRNA
AAGAGTGGGACCCCAGGGGCTCCCCTCCCATCTTGAGCTCTTCCTGAATAAAGCCTCATA NM_001807 RefSeq
chr9 + 133061977 133071863 CEL 1056 carboxyl ester lipase
GO:0052689|GO:0005515|GO:0006629|GO:0006707|GO:0004806|GO:0044241|GO:0005576|GO:0044281|GO:0030
157|GO:0003824|GO:0005615|GO:0018350|GO:0009062|GO:0030299|GO:0005737|GO:0016787|GO:0047372|GO:0
006641|GO:0044258|GO:0008201|GO:0070062|GO:0004771 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_141169_PI430048170 0.549015445110114 1.02127408391196 0.40094098995746
0.262889668208668 0.306747840044668 A A A 0.27980767725901 0.304359911102046
0.298653428377915 A A A LNCV6_141169_PI430048170 mRNA
CCTGCATTCATGTGACATGTCTGGGGAACAGAAGATAAATAAAGGATCTTGCTGAAAACC NM_020437 RefSeq
chr22 + 26429313 26445012 ASPHD2 57168 aspartate beta-hydroxylase domain containing 2
GO:0016020|GO:0018193|GO:0051213|GO:0016021|GO:0046872|GO:0055114 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_140291_PI430048170 0.0691367763586249 2.24288776017224 4.53673449552675
4.55146136439262 4.6920337734717 P P P 4.04356338335366 2.90687475793603
3.05970206425218 P P P LNCV6_140291_PI430048170 mRNA
GGTTTATGGCGATTGTTTTCTTGGACGGATAGTGTAAAATAAACTTCTCTGTTCTCTAAA NM_020689 RefSeq
chr20 + 19212645 19722897 SLC24A3 57419 "solute carrier family 24 (sodium/potassium/calcium
exchanger), member 3"
GO:0005886|GO:0035725|GO:0006816|GO:0016021|GO:0055085|GO:0006813|GO:0015293|GO:0008273|GO:0006
811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145023_PI430048170 0.126844785335533 1.55314879886275 9.22084359134973
9.28938789480009 9.63156351158291 P P P 9.20604809079592 8.21112514304933
8.68237407969297 P P P LNCV6_145023_PI430048170 mRNA
CTACAGAAAATAGTTGCGTGTATGGGAGAACAGTCATTGTAATTGGGTAGTTTTGTTAAT NM_014570 RefSeq
chr22 - 42796525 42857402 ARFGAP3 26286 "ADP-ribosylation factor GTPase activating protein 3,
transcript variant 1"
GO:0005515|GO:0005794|GO:0009306|GO:0006886|GO:0005829|GO:0043547|GO:0008060|GO:0005737|GO:0000
139|GO:0016020|GO:0032312|GO:0008565|GO:0008270|GO:0016192 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_104401_PI430048170 0.994350966435248 1.00117708488986 10.1327092747008
10.3812337948745 10.3260007722161 P P P 10.1782663225179 10.2593157068152
10.4001130677985 P P P LNCV6_104401_PI430048170 mRNA
TGATGGCAAGCTCTTCCCCAGCGATGGTTTTCGTGACTGCAAGAAGGGGGATCCCAAGCA NM_001114309 RefSeq
chr1 + 202010561 202017187 ELF3 1999 "E74-like factor 3 (ets domain transcription factor,
epithelial-specific), transcript variant 2"
GO:0005515|GO:0003700|GO:0006357|GO:0006366|GO:0060056|GO:0000981|GO:0001824|GO:0003713|GO:0005
634|GO:0007275|GO:0000978|GO:0001077|GO:0005737|GO:0006954|GO:0008544|GO:0030198|GO:0045944|GO:0
030855|GO:0045893|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142172_PI430048170 0.0515171985589741 1.34167374892273 10.3673344779421
10.3760953554325 10.3172805114234 P P P 9.71205252967732 10.0496037695745

10.0049071867727 P P P LNCV6_142172_PI430048170 mRNA
GGGGCCAGATGTATAGTATTCAGTATATATTTTGTAAATAAAATGTTTTGTGGCTAGGGG NM_178508 RefSeq
chr6 - 34246379 34249108 C6orf1 221491 "chromosome 6 open reading frame 1, transcript variant
1" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136229_PI430048170 0.00668293231175005 3.11399610376354 4.32717763684722
3.80813582698955 3.93960350388416 P P P 2.54309964466692 2.65990405159453
1.89662739201792 A A A LNCV6_136229_PI430048170 mRNA
ACACCAGTGACGCCGCTGTGTGTCTTAGCATGGAAATAAATAAACCTGAATGTACGTGCT NM_172367 RefSeq
chr17_KI270862v1_alt + 240267 243012 TUSC5 286753 tumor suppressor candidate 5
GO:0009607|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145653_PI430048170 0.12994621750815 0.93233671153015 0.260685379954256
0.277128831520011 0.296610503576492 A A A 0.456336999979766 0.362549934946647
0.315408205307465 A A A LNCV6_145653_PI430048170 mRNA
GTATATTATATGGCAGGAGCTACTGAGAACATAAAATCTTGGCGAGTCATTAAACTTATG NM_014621 RefSeq
chr2 + 176151384 176153221 HOXD4 3233 homeobox D4
GO:0043565|GO:0006355|GO:0003700|GO:0007275|GO:0005634|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_137432_PI430048170 0.144505082959179 0.939303506177925 0.244012654919165
0.284685694780842 0.29894370832298 A A A 0.442619588272532 0.346406324695362
0.306785746388142 A A A LNCV6_137432_PI430048170 mRNA
ATTCAAGATGAGGGAATGCATTTCTTAAATTACTGACAAGTATGAGTCATAGGCTTAAGG NM_001004757 RefSeq
chr11 + 5422110 5423206 OR51Q1 390061 "olfactory receptor, family 51, subfamily Q, member 1
(gene/pseudogene)" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_143286_PI430048170 0.74286297592862 1.04389397214434 4.49429495405889
4.8272761338748 4.8957064644757 P P P 4.94754226483173 4.53072510594428
4.54416449062342 P P P LNCV6_143286_PI430048170 mRNA
ATTCTCAGGGATCATACCTTAATGTTTTCAGTATGTCTGCGTTCTCCTACTAGATTGTAT NM_198141 RefSeq chr15
+ 42274167 42353666 GANC NA "glucosidase, alpha; neutral C, transcript variant 1" NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_127089_PI430048170 0.386770687029295 0.503905177561944 0.44451353161012
0.486880125436604 0.391173347196458 A A A 2.3899920779693 0.5925302316281
0.416706092811091 A A A LNCV6_127089_PI430048170 mRNA
CCTCTTTCTCTTGCCCTGGGGAATTTGGGACACAGAATAAAGGTGTTTGCCCACAAAAAA NM_001195831 RefSeq
chr1 + 43172329 43254358 CFAP57 149465 "cilia and flagella associated protein 57, transcript
variant 5" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133370_PI430048170 0.906588009728998 0.763947847998239 2.4540425869197
1.50326544490142 1.88567978072596 A A A 0.699982866368872 2.2022343364062
3.24702278658331 A A P LNCV6_133370_PI430048170 mRNA
CCCTCCATCCTGAGACCACTCTTTCTTAATGTTCTAATTTTAACTAAATGCATGTAAATG NM_145250 RefSeq
chr14 - 20582892 20590258 RNASE11 122651 "ribonuclease, RNase A family, 11 (non-active)"
GO:0004519|GO:0090305|GO:0005576|GO:0003676 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140511_PI430048170 0.013502205672118 0.629267914881841 5.3690419417366
5.56691904054624 5.61190165984392 P P P 6.0876782039862 6.03468332229069
6.41204568177308 P P P LNCV6_140511_PI430048170 mRNA
TTAAATGTCCAAATGCAAACCTTTGTGACTTCCTTTGGAGGACTTGGCAGCACAGCATGC NM_001283018 RefSeq
chr20 - 23374518 23421519 NAPB 63908 "N-ethylmaleimide-sensitive factor attachment protein,
beta, transcript variant 1"

GO:0035494|GO:0019905|GO:0005483|GO:0005774|GO:0031201|GO:0061025|GO:0006886|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_143348_PI430048170 0.00021898945939409 0.197143632182233 8.2473890915789
8.38226937899366 8.12417715700797 P P P 10.3736400557002 10.7771215891122
10.6144120121664 P P P LNCV6_143348_PI430048170 mRNA
CTGAAACCCTCCTTCTGTGGCAACTTGTACTGAAAATCTGGTGCTCAATAAAGAAGCCCA NM_000022 RefSeq
chr20 - 44619521 44651735 ADA 100 adenosine deaminase
GO:0005515|GO:0046638|GO:0033089|GO:0042542|GO:0046061|GO:0030054|GO:0060407|GO:0060205|GO:0005
764|GO:0005615|GO:0048541|GO:0006157|GO:0002906|GO:0032261|GO:0006154|GO:0043025|GO:0033197|GO:0
009986|GO:0048286|GO:0070244|GO:0007568|GO:0043278|GO:0001890|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131150_PI430048170 0.170025563943369 0.7964894283579760.826977952444558
0.36555929029169 0.426138955156929A A A 0.92467659493571 1.07195140154849
0.614676867851686A A A LNCV6_131150_PI430048170 mRNA
GTCCTGCAAATTGCACCCCCTATGAAAGAGGAATAATATACCAAGGTCTAATAAATTTTA NM_030966RefSeq
chr17_JH159146v1_alt - 183279 184250 KRTAP1-3 81850 keratin associated protein 1-3
GO:0008150|GO:0045095|GO:0030280 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127855_PI430048170 0.7954045769945750.9769499276722897.72524922413582
7.12893707216012 7.19692370041528 P P P 7.51692941534599 7.36840183867897
7.33679335945688 P P P LNCV6_127855_PI430048170 mRNA
AAACAGTGAAGTCTCCTTCCCTCCTTTAGAACTCATTTTCTCTTCCCAAAAAGTGTTATC NM_001289088 RefSeq
chr1 + 35059785 35115858 ZMYM1 79830 "zinc finger, MYM-type 1, transcript variant 1"
GO:0046983|GO:0008270|GO:0005634|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129896_PI430048170 0.0195334262718357 2.92506426267778 6.64177822303463
7.43931603354958 7.34330358440773 P P P 5.66289368297732 5.48654040689587
5.74124989165521 P P P LNCV6_129896_PI430048170 mRNA
AAGCTAAGCGACTGTACGTGCTACTAAAAATGTCTGACACTGAAATAATTTTACTCAACT NM_138448RefSeq chr2
+ 54115272 54305298 ACYP2 98 "acylphosphatase 2, muscle type"
GO:0005739|GO:0003998|GO:0006796 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144814_PI430048170 0.6636971119636291.06253815995648 0.33685857997352
0.3602876679179170.740365047786389A A A 0.2524934315053 0.66372458150085
0.255360938542049A A A LNCV6_144814_PI430048170 mRNA
AGGAAATCCAGGACATGCTGAAGAAGTTCTTCTGCAAGGAAAAGCCCCCGAAAGAAGATA NM_054021RefSeq
chrX - 137030147 137031674 GPR101 83550 G protein-coupled receptor 101
GO:0043235|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_126688_PI430048170 0.5777457858464341.05980330111946 8.20458630469371
8.35335850818478 8.4407695248002 P P P 8.0664402214858 8.15290818514678
8.50036302579978 P P P LNCV6_126688_PI430048170 mRNA
GTTCTGAACCGTATGTGGCGTATTGTTATTAGGTTCTAGCTTCCTTTAAACTAATAAAGA NM_020200RefSeq chr10
- 24848606 24952644 PRTFDC1 56952 "phosphoribosyl transferase domain containing 1, transcript
variant 1"
GO:0006178|GO:0006166|GO:0006168|GO:0000287|GO:0000166|GO:0046100|GO:0032264|GO:0032263|GO:0004
422|GO:0046038|GO:0042803|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133771_PI430048170 0.6203918685220790.9782151962036741 1.3621415460681
11.4001421609437 11.5296818813556 P P P 11.4227113103803 11.4392173398248
11.5285013207305 P P P LNCV6_133771_PI430048170 mRNA
CTTCCCAATTCTGAAGGTGGAAAAGGCAAGATTGAAGTTTTGGACAGTCCAGCAAGTAAA NM_152318RefSeq chr12
+ 104986319 104994727 C12orf45 121053 chromosome 12 open reading frame 45 NA . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_59101_PI430048170 0.4948270984804381.10822170676829 3.24728066141788 3.73913719869338
3.6983838933265 P P P 3.52164359038151 3.46440862822958 3.29409559809442 P P P
LNCV6_59101_PI430048170 mRNA
AGACTCAAGTCAATCCCCTCAAGGATCTGCATTCAGGCCTGCTCCACAAATGATTCATTT NM_000456RefSeq chr12
+ 55997258 56005525 SUOX 6821 "sulfite oxidase, transcript variant 1"
GO:0043546|GO:0034641|GO:0005758|GO:0000096|GO:0000098|GO:0005759|GO:0009055|GO:0008482|GO:0044
281|GO:0070221|GO:0030151|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2281_PI430048170 0.00550883762072387 0.3396507615204870.855344857174541
0.3333274363424230.987041517601457A A A 2.64153963250879 2.26486026292493
1.93574781801363 P A A LNCV6_2281_PI430048170 mRNA
TAGTAATTGATACTTGGGAGATAGTTGCCCACTTGGGCAAAAACGCATGCAGAAGGTGGA NM_014518RefSeq chr19
- 44426250 44448477 ZNF229 7772 "zinc finger protein 229, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137998_PI430048170 0.4244720921389821.31357615090548 1.47666890176201
0.4949048745633281.47139905748693 A A A 1.31618388533271 0.418250947419358
0.561781013718226A A A LNCV6_137998_PI430048170 mRNA
CAGTCTCCTATTTTGTCAGCTGCTTGTGTTGATTAAAACTTCAATAAAGATCCTGTGATA NM_001271829 RefSeq
chr9 - 16203934 16253107 C9orf92 100129385 "chromosome 9 open reading frame 92, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143514_PI430048170 0.000547321597019438 4.77989748188402 8.02483686916771
8.38011476228887 7.81774102590343 P P P 5.69482096124635 6.11297294032288
5.65479458500666 P P P LNCV6_143514_PI430048170 mRNA
AAGGAGGCCTCTGTCATTTTAAAGACTCGTGTTTACAGTTTTGTATCCAAGGCCAAAAAA NM_025268RefSeq chr14
+ 105526615 105530202 TMEM121 80757 transmembrane protein 121
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139548_PI430048170 0.2937676362792591.15550381654037 5.76885671984134
5.88721931546804 5.83005359748326 P P P 5.33459175311546 5.89039241629763
5.58410800193173 P P P LNCV6_139548_PI430048170 mRNA
GTGGGAAGGGATAATTTATCATACTGAGACTTGTTCTTGGTTCCTGTTTGAAACTAAAAT NM_003394RefSeq chr12
- 48965339 48971858 WNT10B 7480 "wingless-type MMTV integration site family, member 10B"
GO:0071464|GO:0006629|GO:0008284|GO:0071300|GO:0045599|GO:0045899|GO:0090263|GO:0050680|GO:0032
434|GO:0005615|GO:0007224|GO:0005109|GO:0051091|GO:0030858|GO:0050909|GO:0002062|GO:0071374|GO:0
000086|GO:0030182|GO:0007050|GO:0016055|GO:0060070|GO:0014835|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_52357_PI430048170 0.0276846150447891 1.41677472102995 6.54024241615586 6.7230988635484
6.84620904477622 P P P 6.42601855288486 6.08582416921444 6.07814393901296 P P P
LNCV6_52357_PI430048170 mRNA
CCATTTGGACACTTGGAGACCAGAAAGCTTCTTTGACAAAGTGAAGAAGAACAGACAAAA NM_001077394 RefSeq
chr1 - 100989624 101025806 DPH5 51611 "diphthamide biosynthesis 5, transcript variant 1"
GO:0004164|GO:0005575|GO:0044267|GO:0032259|GO:0017183|GO:0043687|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141354_PI430048170 0.7066888707437781.07228313963744 3.13646632323507
3.68717493451046 3.6723970535561 P P P 3.54879852723564 3.18141168171831
3.50194831921458 P P P LNCV6_141354_PI430048170 mRNA
CCAACAGCTATTCTATTTGTCCATAAACTTTTTTGAGTGCCTAATATGTACAGTTGACTG NM_001261430 RefSeq
chr17 - 42968087 42980528 PTGES3L NA "prostaglandin E synthase 3 (cytosolic)-like, transcript
variant 5" NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_132224_PI430048170 0.00252424329559986 0.4134995292658325.3250880411704
5.03717888022094 5.22159736750476 P P P 6.22500323554543 6.47537195545577
6.68387631217495 P P P LNCV6_132224_PI430048170 mRNA
GCTCAGCCTTACATAGAAACTCCTAGATTTTCACTAACGCATTTCACAAAAGTAAATAAG NM_001242336 RefSeq
chr5 + 154038958 154057454 MFAP3 4238 "microfibrillar-associated protein 3, transcript variant 3"
GO:0005886|GO:0030198|GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131752_PI430048170 0.7238973267951381.43164446420485 0.29707298253705
2.47284021390044 1.10875125570104 A A A 0.973773014821165 1.40277092063523
0.708521581680581 A A A LNCV6_131752_PI430048170 mRNA
CAGGGGTCCATGACCCATCTAGGAGACTTTATAGCAGTTGGGTGGGAGGGGAATGCTCTT NM_001174164 RefSeq
chr7 - 128350324 128361685 PRRT4 NA "proline-rich transmembrane protein 4, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145102_PI430048170 0.00620789626411069 2.93449020923417 8.72310707982085
8.80699586744315 8.57715329229303 P P P 7.2719755838197 7.34034298787685
6.78368036650128 P P P LNCV6_145102_PI430048170 mRNA
TTCAGTCTGGCTTGAAATTTGGGGATGTTAATGAGGGTCCTCTGGTTTTTGGTAACCAGG NM_152911 RefSeq chr10
+ 133379236 133391696 PAOX 196743 "polyamine oxidase (exo-N4-amino), transcript variant 1"
GO:0052901|GO:0006805|GO:0052902|GO:0005782|GO:0052903|GO:0052904|GO:0005102|GO:0044281|GO:0046
592|GO:0034641|GO:0006598|GO:0006596|GO:0052899|GO:0006595|GO:0009446|GO:0046208|GO:0046203|GO:0
009447|GO:0055114. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143127_PI430048170 0.1181703896138030.9652750185732850.445123865613166
0.3740004095614260.398336870101587 A A A 0.4349249419799290.477017905830046
0.459081307241181 A A A LNCV6_143127_PI430048170 mRNA
CTGTGTAGCATTTCCTTCTGGTTAAGAACATGCAGATAATCCAAATAAACAGATTTGACT NM_001101339 RefSeq
chr12 - 24993430 24997439 C12orf77 NA chromosome 12 open reading frame 77 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_90203_PI430048170 0.0055866063863902 0.5779981360668512.65470082782663
2.36142719936219 2.53394747588059 A A A 3.36535342388932 3.31728742401132
3.25277441093656 P P P LNCV6_90203_PI430048170 mRNA
CAGTTAACCTATTTTGTGTCTGTAGGCTGACCTCAACCCTGTAACGTAACCCATTAAAAT NM_017489 RefSeq chr8
+ 73008861 73047752 TERF1 7013 "telomeric repeat binding factor (NIMA-interacting) 1, transcript
variant 1"
GO:0051974|GO:0005515|GO:0008017|GO:0007094|GO:0005634|GO:0042803|GO:0003691|GO:0005737|GO:0032
211|GO:0000723|GO:0000086|GO:0032214|GO:0051260|GO:0031627|GO:0000784|GO:0000783|GO:0000781|GO:0
031116|GO:0043065|GO:0046982|GO:0008301|GO:0042493|GO:0042162|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131439_PI430048170 0.9005116901053731.31827968106809 2.9220905622035
0.3337780187941382.30015174822081 A A A 2.31865316581545 1.48531389751364 1.4076652785496
A A A LNCV6_131439_PI430048170 mRNA
GGACAATATCCATTAGCCATTATCTTGCTGCGTATGAATAACCCTCTCTCACAAAAATAA NM_001302627 RefSeq
chr7 + 47795290 47819846 C7orf69 80099 "chromosome 7 open reading frame 69, transcript variant
2" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141241_PI430048170 0.0147499127315227 0.75523782629422 10.4718511379551
10.3351483963825 10.2103081893944 P P P 10.6383113094771 10.7761780296002
10.8233347286162 P P P LNCV6_141241_PI430048170 mRNA
AATGAGCCATTCTCAATAAACATTATTCTCACTGCAAAATGGTGGTAGCCCCTGAAAAAA NM_031444 RefSeq chr22
- 24540422 24555307 GUCD1 83606 "guanylyl cyclase domain containing 1, transcript variant 4" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128730_PI430048170 0.2951382140463480.74873429009139 2.59477572428469

2.73198602426558 3.35819776519911 A A P 3.10368041985201 3.015366075195
3.80277224712483 P P P LNCV6_128730_PI430048170 mRNA
TTAAACATATAAAGTAAAACAGGTCTGAGGGCTTTGTAGATGATTAAAGTCTCCACCTTC NM_001167575 RefSeq
chr9 - 26840684 26892828 CAAP1 79886 "caspase activity and apoptosis inhibitor 1, transcript
variant 2" GO:0006915 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140903_PI430048170 0.6635561026875622.35340463899885 0.460991508756654
0.47901510679927 3.53409585107677 A A P 1.50651266165066 0.543502152412901
0.848600841885726A A A LNCV6_140903_PI430048170 mRNA
CCCTCCACATAGAGGGAATCAATCGACTTTTGTATACTGATTTTTGTATTTGCTTCTTTA NM_001278713 RefSeq chr11
- 71814044 71821547 ZNF705E NA zinc finger protein 705E NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_141275_PI430048170 0.2178924123078030.8386236157835217.54270791884522
7.48075856712786 7.53880132490434 P P P 7.49229438664825 7.93713985067396
7.85753412575991 P P P LNCV6_141275_PI430048170 mRNA
GGCTTCTGTCGGGGGGAGAGTATATAATGGAGGAAATATTATGTATTGAGATTATATTTA NM_001172659 RefSeq
chr4 - 2269596 2364877 ZFYVE28 57732 "zinc finger, FYVE domain containing 28, transcript
variant 1" GO:0005515|GO:0031901|GO:0007175|GO:0042059|GO:0032266|GO:0046872|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142847_PI430048170 0.0149380877105669 0.6954508800852429.8857009230576
9.86538987475219 10.162290676495 P P P 10.4879351387179 10.3570547096149
10.6453194823367 P P P LNCV6_142847_PI430048170 mRNA
CTGACTTACTTTGGTTGGTTCCTAGTGCTACTTGTTTTACAAACTACACTTTGTAGAATT NM_006224RefSeq chr17 -
1517988 1562816 PITPNA 5306 "phosphatidylinositol transfer protein, alpha"
GO:0006629|GO:0005737|GO:0015914|GO:0008526|GO:0008525|GO:0007411|GO:0007601|GO:0070062|GO:0008
289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137542_PI430048170 0.8857829481639250.9426091125678040.809198469726099
2.40308239639485 1.62329074545847 A A A 2.34816885841504 1.95036899603407
0.833592595845321A A A LNCV6_137542_PI430048170 mRNA
GAAGGGTCCTCTGGGGTTCTTCCAACAACCTATTCTAATAGACAAATCCACATGAAAAAA NM_000804RefSeq chr11
+ 72135724 72139890 FOLR3 2352 folate receptor 3 (gamma)
GO:0005542|GO:0016020|GO:0015884|GO:0005576|GO:0019898 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144572_PI430048170 0.2437678859690420.61696524956812 1.37580069533598
1.47285312129336 1.43996313915954 A A A 2.06108924211125 2.66176901648277
1.37944592809671 A P A LNCV6_144572_PI430048170 mRNA
GTAAAGATTCAACAGATCTCCCACGTTTCCATTTTCTTTGCACAGATTTATTTATCTGCANM_001039152 RefSeq chr1
+ 192316991 192367284 RGS21 NA regulator of G-protein signaling 21 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133104_PI430048170 0.0535627266469246 0.6154437668113063.24005696215226
2.69188883968142 2.65857143548963 P A A 3.49295814075929 3.65857101659356
3.61161220511519 P P P LNCV6_133104_PI430048170 mRNA
GGCCAAAGACATGACATCAAATAAGTAATAGACATCACCAGCAATGAATTTTGAAAAGCA NM_014028RefSeq chr6
- 108041408 108074737 OSTM1 28962 osteopetrosis associated transmembrane protein 1
GO:0005737|GO:0034220|GO:0030316|GO:0005634|GO:0016021|GO:0005765|GO:0055085|GO:0043231|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144093_PI430048170 0.0551342318248339 0.4232394493092933.27005746038235
2.9379290736705 3.07875228127569 A A P 3.79068655773333 4.15438459421522
4.86862232258262 P P P LNCV6_144093_PI430048170 mRNA
GCTCTGACTGGTTTTAATAGTCACCTTCATGATTATAGCAACTAATGTTTGAACAAAGCT NM_000110RefSeq chr1

- 97077743 97921059 DPYD 1806 "dihydropyrimidine dehydrogenase, transcript variant 1"
GO:0050661|GO:0017113|GO:0006214|GO:0051539|GO:0006210|GO:0050660|GO:0006212|GO:0006222|GO:0055
086|GO:0044281|GO:0046872|GO:0042803|GO:0005829|GO:0019483|GO:0046135|GO:0005737|GO:0006145|GO:0
004152|GO:0006206|GO:0055114|GO:0006208 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142201_PI430048170 0.0561082775510321 1.04762005320496 0.345629661305465
0.3412427529536450.28487397247245 A A A 0.2455999111623240.276946873065407
0.248436204078437A A A LNCV6_142201_PI430048170 mRNA
GGCCCAAACTTAGCTACATTGTTTATTGGCTCCCAAAGTCGGGATTGAAGAGTGAAAAGA NM_001278322 RefSeq
chr3 + 39467572 39516003 MOBP 4336 "myelin-associated oligodendrocyte basic protein,
transcript variant 1" GO:0005739|GO:0048471|GO:0019911|GO:0007399 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_126559_PI430048170 0.00297056021712615 0.6116249434842845.4181364138344
5.28486782950856 5.56526839929017 P P P 6.02700940457723 6.09906883608847
6.27253106720269 P P P LNCV6_126559_PI430048170 mRNA
GAGGTCTTACAACTAAAGTCCAAGAATCTCTAAAGAAACAGGAGGGACTTCTTAAAAATA NM_001162429 RefSeq
chr3 + 33798570 33869707 PDCD6IP 10015 "programmed cell death 6 interacting protein,
transcript variant 2"
GO:0001772|GO:0005515|GO:0042470|GO:0017124|GO:0006997|GO:0005815|GO:0031871|GO:0019058|GO:0006
915|GO:0010824|GO:0015031|GO:0070971|GO:0031982|GO:0042803|GO:0005829|GO:0000920|GO:0005737|GO:0
016020|GO:0016032|GO:0007080|GO:0005925|GO:0070062|GO:0048306 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_134954_PI430048170 0.6508845519773590.92032900939185 4.46940847110379
4.34357885088228 3.70479175103747 P P P 4.50861996385951 4.42577583310347
4.00384026772067 P P P LNCV6_134954_PI430048170 mRNA
TTGTGTATAGGTACCGAGCTGTGGATACAGGAGAGAATGAATAAAATTCTAACACAAAAA NM_001130448 RefSeq
chr15 + 40769960 40772449 C15orf62 643338 chromosome 15 open reading frame 62
GO:0005739|GO:0005737|GO:0030838|GO:0005886|GO:0032321|GO:0008360|GO:0031274|GO:0017049|GO:0007
266|GO:0005856|GO:0005100 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133889_PI430048170 0.2638383630489791.02218727376943 0.307162578468221
0.3091700937577780.370008747584939A A A 0.3103231145502150.295962219806138
0.285861184283448A A A LNCV6_133889_PI430048170 mRNA
CCAGTTTGCCTTGCCAAATAAACTCTGTTTATGTGAATTTATTAAACGACCATGCCATAA NM_024730RefSeq chr12
- 18080868 18090193 RERGL 79785 "RERG/RAS-like, transcript variant 1"
GO:0006184|GO:0016020|GO:0007264|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130891_PI430048170 0.0843112383244858 0.5604956736428153.9959275104953
3.09143784062216 3.849323275533 P P P 4.57828321444505 4.44768619356525 4.5654203820783
P P P LNCV6_130891_PI430048170 mRNA
TAGCCAAGAACAGCTCATTTTGTGAATTTCAGTTTTTAAGTGGCTGCTTTTTGATTTGGTNM_002035RefSeq chr18 -
63327737 63367273 KDSR 2531 3-ketodihydrosphingosine reductase
GO:0006665|GO:0047560|GO:0006666|GO:0016020|GO:0005783|GO:0030148|GO:0005789|GO:0044281|GO:0016
021|GO:0005615|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76125_PI430048170 0.4233852991487051.12659716423806 6.11010303027876 6.14520279565869
6.01620839547624 P P P 6.12540110570291 6.05325085541573 5.50362276606896 P P P
LNCV6_76125_PI430048170 mRNA
GGTCAGCCTCTCACTCTTCCTTCAGGTTACTAACAAAATTTCGTAGCTAAAGAATGCCAT NM_015071RefSeq chr5
+ 142770726 143229007 ARHGAP26 23092 "Rho GTPase activating protein 26, transcript variant 1"
GO:0005515|GO:0007009|GO:0051056|GO:0030036|GO:0007264|GO:0005575|GO:0005100|GO:0005829|GO:0007
399|GO:0005543|GO:0032321|GO:0005856|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142304_PI430048170 0.6980461973389790.9868075523737620.403886484892622

0.4556985192101760.36286222226589 A A A 0.4972345799806740.38287195429681
0.398637950271941 A A A LNCV6_142304_PI430048170 mRNA
AACTCAGCCATGAGCATCATCAATAAGTACACAGAACGGTGCAAAGACCTCAACACCTTC NM_138331 RefSeq chr14
+ 21057821 21058455 RNASE8 122665 "ribonuclease, RNase A family, 8"
GO:0005576|GO:0004522|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130982_PI430048170 0.5004068206466750.9362167731664428.15748075533375
8.23055793266999 8.54264782404188 P P P 8.3550865413692 8.34311463403353
8.53891135993188 P P P LNCV6_130982_PI430048170 mRNA
CAGTACCATAACTACAGAACCTGTCATCTGTATTTTTTGTTCTCACCCCGTTTTTGTTAT NM_004275 RefSeq chr6 -
41905352 41921147 MED20 9477 mediator complex subunit 20
GO:0005515|GO:0010467|GO:0006367|GO:0001104|GO:0006366|GO:0006357|GO:0003899|GO:0016592|GO:0005
654|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139169_PI430048170 0.4029294075578972.38319422434214 0.423242354602074
2.79738370628434 0.554557419000713 A A A 0.5499125972766290.397445757089016
0.394819404196467 A A A LNCV6_139169_PI430048170 mRNA
CGTCATCCATGGGTATTAAAAGGACACTGTCAAGTACTTTTTTAAACTAGTTTTTAGGGT NM_020814 RefSeq chr2
- 216257861 216372027 MARCH4 NA "membrane-associated ring finger (C3HC4) 4, E3 ubiquitin protein
ligase" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128476_PI430048170 0.0228678517741201 0.7468953510962261 0.620134428388
10.5998674473957 10.3688125379323 P P P 10.8492887162469 11.1179839319165
10.8827409832276 P P P LNCV6_128476_PI430048170 mRNA
GGTAGGCATTTCACTGGTTTATGAAGCTCGAGTTTCATTAAATATGTTAAGAATCAAAGC NM_001161454 RefSeq
chr11 - 61348747 61362283 CYB561A3 220002 "cytochrome b561 family, member A3, transcript
variant 1" GO:0031902|GO:0016491|GO:0016021|GO:0005765|GO:0046872|GO:0055114 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_129191_PI430048170 0.1559359710488440.7132396536294794.52369660131082
3.68802570920857 3.95406335913736 P P P 4.64632704435153 4.3916251065712 4.7014276259243
P P P LNCV6_129191_PI430048170 mRNA
GGTCCACCTCCCTTTATAAACCCCACCAGAACCACATCATTAAAAGGTTTGACTGCGCAC NM_004790 RefSeq chr11
- 62976596 62985023 SLC22A6 9356 "solute carrier family 22 (organic anion transporter), member 6,
transcript variant 1"
GO:0005515|GO:0031404|GO:0005886|GO:0097254|GO:0015347|GO:0031427|GO:0043252|GO:0015742|GO:0055
085|GO:0042803|GO:0043234|GO:0016323|GO:0034220|GO:0005452|GO:0005887|GO:0005901|GO:0015711|GO:0
051260|GO:0008514|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127868_PI430048170 0.7313784783477121.20036838127889 1.66737057219346
0.53804816006155 0.433715466309499 A A A 0.8538675349577370.448448871105579
0.855283321199984 A A A LNCV6_127868_PI430048170 mRNA
GACAACTGAGCAGCCTCTGGAGAGGGGCCATTAATAAAGCTCAACATCATTGGCAAAAAA NM_006770 RefSeq
chr2 + 118942168 118994660 MARCO 8685 macrophage receptor with collagenous structure
GO:0030666|GO:0005581|GO:0002221|GO:0005886|GO:0005887|GO:0045087|GO:0043277|GO:0007166|GO:0006
898|GO:0008329|GO:0005044|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133191_PI430048170 0.0757143026854923 0.9265712285515450.322713515064027
0.3099655918052110.297241980942348 A A A 0.4801784198547750.412477330710653
0.365133900240924 A A A LNCV6_133191_PI430048170 mRNA
CTTTTCCTAAGAGTCTGAAACCATTCCATTTCATTTTGGTGAAATGTGTCTGTTTCTAAG NM_173625 RefSeq
chr17_KI270857v1_alt + 1612049 1628727 C17orf78 284099 chromosome 17 open reading frame
78 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129693_PI430048170 0.0145110265717253 0.4759919040567686.01726115228793
6.16339796016457 6.44611887503317 P P P 6.92325236228799 7.27946587871806

7.59324594332604 P P P LNCV6_129693_PI430048170 mRNA
GAGTTGCTCTGTTTTCTTCAACTGTATTTATTGCTGCATTTCTCAGCATAAACTTATCCC NM_001839 RefSeq chr1 -
94896948 94927223 CNN3 1266 "calponin 3, acidic, transcript variant 1"
GO:0005516|GO:0005737|GO:0030855|GO:0031032|GO:0003779|GO:0015629|GO:0005925 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143695_PI430048170 0.206748673385635 0.871925629884802 0.257355415321253
0.26867010234551 0.321467301454698 A A A 0.430689741897212 0.671087711497363
0.316734346072967 A A A LNCV6_143695_PI430048170 mRNA
CACTTTAAAGACATGAATGAACTCACTCTGGAGAGAAGAAGCTGCATGAAAATTACTTAA NM_001300883 RefSeq
chr19 - 9528004 9538645 ZNF426 79088 "zinc finger protein 426, transcript variant 2"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_2304_PI430048170 0.231525702434789 0.396126809358297 0.623574891750087 0.539537357713356
1.12729771231382 A A A 0.604364894893755 2.1662384306273 2.82058323488357 A A P
LNCV6_2304_PI430048170 mRNA
AGCAACTGCAAATAAAACCGCGACTCTTCTGGAAAGAATCAACGTTATCGTCCACCTGCT NM_001202438 RefSeq
chr10 + 125719514 125764143 EDRF1 26098 "erythroid differentiation regulatory factor 1, transcript
variant 1" GO:0006355|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91410_PI430048170 0.298320860690745 1.51562645785797 0.508491869418069 1.47599294143826
0.301392835479459 A A A 0.263094076069674 0.246583814738359 0.263777182498999 A A A
LNCV6_91410_PI430048170 mRNA
CTCAGCTATTCTTGGGCCAGATGGGGCCTGACCGATAGAATAAAAGACTTTTCTACAACA NM_020707 RefSeq chr3
- 42692662 42702827 HHATL 57467 "hedgehog acyltransferase-like, transcript variant 1"
GO:0048471|GO:0005783|GO:0060262|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132531_PI430048170 0.269129092708351 1.0999051994126 11.1451589147144
11.4313980085487 11.357957339114 P P P 11.2804341213415 11.0915924080588 11.159050970121
P P P LNCV6_132531_PI430048170 mRNA
CTTGCTGATTTTATGCAAAGGGCTGGCATTCTGATTGTTCTTTTTTCAGGTTTAATCCTT NM_020216 RefSeq chr1 +
201982637 202006147 RNPEP 6051 arginyl aminopeptidase (aminopeptidase B)
GO:0019370|GO:0005886|GO:0004177|GO:0008235|GO:0006508|GO:0008270|GO:0005576|GO:0005615|GO:0070
062|GO:0004301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130029_PI430048170 0.161303701378051 1.06695750705202 0.60598004948978
0.502477426955396 0.624543268878596 A A A 0.454008622129821 0.561684738984965
0.436564308948836 A A A LNCV6_130029_PI430048170 mRNA
GCTAATCCACACCAGTGGACTTGAAACACGCTTTGGGTTGCTGTATGGTAGTATGCTAAA NM_001024601 RefSeq
chr1 - 212830142 212847649 SPATA45 NA spermatogenesis associated 45 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_137481_PI430048170 0.0181166927217619 0.479583414438948 5.50832802167711
5.00616866632118 5.65043653652112 P P P 6.32715610480795 6.44942802095094
6.62893387764746 P P P LNCV6_137481_PI430048170 mRNA
CCTCCTCTCATTGTAACGAAATTAATTCCAGCTGCAGTGAGAAAACTTAAAAATCATGAT NM_004507 RefSeq chr7
- 47963287 47979625 HUS1 3364 "HUS1 checkpoint homolog (S. pombe), transcript variant 1"
GO:0005515|GO:0007093|GO:0030896|GO:0005730|GO:0005634|GO:0009790|GO:0071479|GO:0006974|GO:0006
260|GO:0005737|GO:0006281|GO:0000724|GO:0001932|GO:0005654|GO:0006468|GO:0008156|GO:0000077|GO:0
009411 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134654_PI430048170 0.339155204831757 0.968058703480037 0.250351431039738
0.264191874481765 0.366763290897147 A A A 0.383078839325096 0.317664677752566
0.322969652413716 A A A LNCV6_134654_PI430048170 mRNA

CCACCTTTCCTCAGACTATTTTTCAGCCTTCTGGCATCAGCAAACCTTATAAAATTTTTT NM_002255 RefSeq chr19_KI270890v1_alt - 81937 92852 KIR2DL4 3805 "killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4, transcript variant 1" GO:0005515|GO:0007165|GO:0006968|GO:0016020|GO:0005886|GO:0005887|GO:0050776|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134806_PI430048170 0.1060028936152 0.87613836953161612.13905853928 12.36953782343 12.3432315740591 P P P 12.4791530318775 12.5166524924093 12.4381104912284 P P P
LNCV6_134806_PI430048170 mRNA
ATTGCCACCTTCACTCCTGTGTCTCCAGCTGATTAGCCTCAGACTCTTCTTTTATTGTTT NM_006337 RefSeq chr12 - 49558293 49568145 MCRS1 10445 "microspherule protein 1, transcript variant 1" GO:0005515|GO:0006355|GO:0030054|GO:0005730|GO:0006325|GO:0006310|GO:0015629|GO:0006351|GO:0043981|GO:0031011|GO:0005737|GO:0043982|GO:0006281|GO:0043984|GO:0071339|GO:0043996|GO:0043995|GO:0000123|GO:0046972|GO:0005654|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139684_PI430048170 0.203696341091012 1.1835859180892 8.94818931743086 9.26968665725275 9.36891538540299 P P P 8.95511287707751 9.01641831740687 8.91671319279465 P P P LNCV6_139684_PI430048170 mRNA
CTGTTGGAAGCTTGTTTTCCAGTCTCTTGTACAGCGTTTTAAAAGAAATGGATTCTATTT NM_001800 RefSeq chr19 - 10566461 10568955 CDKN2D 1032 "cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4), transcript variant 1" GO:0005515|GO:0048102|GO:0030308|GO:0008285|GO:0019901|GO:0071901|GO:0007605|GO:0033280|GO:0005634|GO:0000079|GO:0005829|GO:0042326|GO:0000082|GO:0005737|GO:0000731|GO:0004861|GO:0007050|GO:0032526|GO:0043154|GO:0000278|GO:0009411 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130016_PI430048170 0.00295347182924382 0.2692664131812873.02263425049889 2.59633397370525 2.66159642312395 A A A 4.22710374991078 4.79373733687341 4.89107694365769 P P P LNCV6_130016_PI430048170 mRNA
AAGTTTGACCTGGTTGTGTTATTTTACCAGACCTTGGTAAAAGAACTATTTTGGAAACAG NM_005813 RefSeq chr2 - 37250502 37317079 PRKD3 23683 protein kinase D3 GO:0035556|GO:0005515|GO:0005737|GO:0016020|GO:0006468|GO:0005654|GO:0004697|GO:0005524|GO:0046872|GO:0007205 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62424_PI430048170 0.00127794362698127 0.3761162302157443.47001146879199 3.20268014125381 3.03298335675698 P P P 4.4292712606134 4.83757032933418 4.67605607814021 P P P LNCV6_62424_PI430048170 mRNA
ATCGACATCCTCACCGAGCCCAAGACATCGGGAAACGGCTCGAGGTGCGGAAGACCGTGA NM_001289824 RefSeq chr15 + 90872877 90883458 FURIN 5045 "furin (paired basic amino acid cleaving enzyme), transcript variant 3" GO:0005802|GO:0032455|GO:0019058|GO:0002020|GO:0032911|GO:0005615|GO:0052548|GO:0016486|GO:0007219|GO:0016485|GO:0030198|GO:0030574|GO:0006508|GO:0007179|GO:0070062|GO:0009986|GO:0048406|GO:0005796|GO:0043043|GO:0019068|GO:0004175|GO:0008233|GO:0045121|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134365_PI430048170 0.0144602590868586 0.5087581376634554.00884570140671 4.00884570140671 4.02014909245377 P P P 4.78518555987309 4.95737673705623 5.19121098777478 P P P LNCV6_134365_PI430048170 mRNA
CCATAGGTTAAAATGCCACCAAAACTGGCCTTTGCCTAATATCCCTCATTGACTATTTAG NM_001301875 RefSeq chr5 - 43379194 43397264 CCL28 56477 "chemokine (C-C motif) ligand 28, transcript variant 4" GO:0008009|GO:0006955|GO:0006935|GO:0060326|GO:0007584|GO:0005576|GO:0007204|GO:0005615|GO:0001954|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134101_PI430048170 0.0406398426937338 0.73389456018137 10.5369398992125 10.2998895117252 10.1495065867821 P P P 10.7437157921434 10.8786704282024 10.7247453308276 P P P LNCV6_134101_PI430048170 mRNA

ACCTGCTGTGGGTCCAGCAGGTTTTTACTTGAGTACAATAAAAAGTCTGAGTCAAGGGTG NM_024044 RefSeq chr16 + 30193842 30197566 SLX1B NA "SLX1 structure-specific endonuclease subunit homolog B (S. cerevisiae), transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126630_PI430048170 0.3990930263025910.8428907647501545.57113635535337 5.57822493571924 5.97309557982717 P P P 5.5717125027835 5.97997992960048 6.26551956683763 P P P LNCV6_126630_PI430048170 mRNA
GTTGACTTTTTGATGCTGGCACGAGGTTTTTGTCCACTTTTTTCATATATCTGTGTATAA NM_001012994 RefSeq chr9 + 112750853 112874987 SNX30 NA sorting nexin family member 30 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66456_PI430048170 0.8117567160626040.9527017762377 13.7378175399942 13.8736156915077 13.9217248908926 P P P 13.5582168033812 13.9510527478742 14.1739939271355 P P P LNCV6_66456_PI430048170 mRNA
TGCTCACCATACGGCTCTAACAGATTAGGGGCTAAAACGATTACTGACTTTCCTTGAGTA NM_001178017 RefSeq chr2 + 119367252 119372546 DBI 1622 "diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein), transcript variant 4"
GO:0018345|GO:0005794|GO:0005783|GO:0060291|GO:0030156|GO:0097038|GO:0008289|GO:0005739|GO:0036042|GO:0021670|GO:0046983|GO:0006810|GO:0007611|GO:0006641|GO:0001662|GO:0001942|GO:0036151|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142109_PI430048170 0.0815586501429909 1.29368788704119 11.8226301122037 11.7989181358656 11.627336967176 P P P 11.1098239086301 11.4868456616092 11.5114860764092 P P P LNCV6_142109_PI430048170 mRNA
CCCCACAAAAGGAGGGAAGCTGTAGCTGTTTGGATGTGAGGAGAATGAAACTACAAAAAA NM_025150 RefSeq chr1 + 150487363 150507609 TARS2 80222 "threonyl-tRNA synthetase 2, mitochondrial (putative), transcript variant 1"
GO:0010467|GO:0003674|GO:0005759|GO:0004829|GO:0070159|GO:0005575|GO:0005524|GO:0006418 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110344_PI430048170 0.0127112128591724 2.24834066825299 5.74833335453408 6.30729572555954 5.82164011066398 P P P 5.18561220165138 4.64489965028292 4.5157010996562 P P P LNCV6_110344_PI430048170 mRNA
ACCTGCTGCACCAGCAGCTGCAGGAGCTGCACGCCCACGTGGTGCTTCCCGACCCGGCGG NM_002741 RefSeq chr19 + 14433353 14471867 PKN1 5585 "protein kinase N1, transcript variant 2"
GO:0005515|GO:0042826|GO:0005886|GO:2000145|GO:0005634|GO:0050681|GO:0032154|GO:0042393|GO:0005737|GO:0030374|GO:0005080|GO:0006357|GO:0030496|GO:0007257|GO:0035407|GO:0006972|GO:0005524|GO:0006351|GO:0035402|GO:0048365|GO:0007165|GO:0004672|GO:0004674|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78176_PI430048170 0.00204599229918993 1.76618823889796 7.2090048907145 7.38381011502552 7.47199826063188 P P P 6.50764021600356 6.40206307030236 6.69059702540993 P P P LNCV6_78176_PI430048170 mRNA
ACATCCAGAGAAATCTAAACTGCTGTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTC NM_014399 RefSeq chr7 + 16753725 16784536 TSPAN13 27075 tetraspanin 13 GO:0016020|GO:0005887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52084_PI430048170 0.3107094978963851.46025883750791 8.23862359516711 8.72156593785944 8.98393035699116 P P P 8.79486398534177 8.05020709173681 7.06029152415504 P P P LNCV6_52084_PI430048170 mRNA
GCAGGGTTCTTTTCTCTACGTGTCATGTTAAAATTGCCAAATAAAGTACCTCTGCCTGTG NM_032454 RefSeq chr6_GL000256v2_alt + 3314929 3315373 STK19 8859 "serine/threonine kinase 19, transcript variant 2" GO:0004674|GO:0006468|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132836_PI430048170 0.5528231919804330.780626292926188 1.73062459606861

2.49491046251369 3.00162440134811 A A P 3.38375955729023 2.84256225000818
2.04309487580646 P P A LNCV6_132836_PI430048170 mRNA
GTAGCATTTGTACACATGGCCCTGTATTGTCCTTGAAGAACATCAATAAAATATATGGTT NM_174976RefSeq chr14
- 77131269 77141791 ZDHHC22 283576 "zinc finger, DHHC-type containing 22"
GO:0018345|GO:0005794|GO:0005783|GO:0008270|GO:0016021|GO:0072659|GO:0019706 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_79625_PI430048170 0.667508970394916 0.960144318763953 7.50718744433393 7.19513840418766
7.30835829628523 P P P 7.30087920233552 7.57324827702641 7.31332144373745 P P P
LNCV6_79625_PI430048170 mRNA
ATGGCAGCAGAGATCGTTACAGACATTTTTATCTCCTGATCAAGATGGCCTTCGTGCTGT NM_025232RefSeq chr8
- 22138019 22141935 REEP4 80346 receptor accessory protein 4
GO:0008017|GO:0007067|GO:0005783|GO:0007084|GO:0005874|GO:0005789|GO:0006998|GO:0016021|GO:0051
301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137877_PI430048170 0.0744348385772851 1.34552048510225 4.53718153335174
4.41785082752229 4.50861996385951 P P P 3.95069749145545 3.87680635694821
4.31517843096713 P P P LNCV6_137877_PI430048170 mRNA
AGATAAGCCACTGGGATAACTGCTTCTCATGCTTTGCAAATTGCAGAAGAATGAGAAAGG NM_014167RefSeq chr12
- 82352303 82358420 CCDC59 29080 "coiled-coil domain containing 59, transcript variant 1"
GO:0005515|GO:0006355|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135171_PI430048170 0.0103677836657141 .25745770669526 0.870673645197614
0.9170702884282811.00031807918957 A A A 0.7045445919073430.522010873547649
0.566645510696343 A A A LNCV6_135171_PI430048170 mRNA
AACCCTGAAACATGACGAGAGTGTTGTAAAGTGTGGAAATGCCTTCTTAAAGTTTATAAA NM_018661RefSeq
chr8_KI270813v1_alt - 111964 113419 DEFB103B 55894 "defensin, beta 103B"
GO:0006965|GO:0005796|GO:0045087|GO:0005576|GO:0042742 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144170_PI430048170 0.1942149243857240.7412849313839340.494368330530638
0.9048959899489390.265607740873915 A A A 1.38005826930611 0.829927745980466
0.737744583410676 A A A LNCV6_144170_PI430048170 mRNA
ATAAATCTTTTCTTTTTGCCTTTTGGCCCTAGGATCGTGTTTAGGAGGATTATCCCACCCNM_013444RefSeq chrX +
56563592 56567010 UBQLN2 29978 ubiquilin 2 GO:0005515|GO:0005737|GO:0005886|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142974_PI430048170 0.0337311550009923 1.51219874908997 8.47034040897227
8.50538913500743 8.44901434533735 P P P 7.63492283202289 7.9617777484269
8.01052978425104 P P P LNCV6_142974_PI430048170 mRNA
GCGCATTGTGCACTGGTTTACTTTAAAATGTACAGATTCTTCTCGTTAAATTCTTGATAG NM_020820RefSeq chr20
- 48624254 48827883 PREX1 57580 "phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1"
GO:0005515|GO:0048471|GO:0005886|GO:0030593|GO:0006801|GO:0032855|GO:0005100|GO:0043231|GO:0005
829|GO:0030426|GO:0035556|GO:0005737|GO:0030833|GO:0005543|GO:1900026|GO:0007186|GO:0030217|GO:0
043198|GO:0050773|GO:0030041|GO:0042119|GO:0005089|GO:0019899 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_54025_PI430048170 0.0711293423716791.07201715427454 0.4232990167715180.316380175674018
0.399943150687827 A A A 0.2636651664826290.3165906688117580.259859349920882 A A A
LNCV6_54025_PI430048170 mRNA
GCACCTGCAGGTCTTGGACATTGAAGGCAACTTAGAGTTTGGTGACATTTCCAAGGACCG NM_001199080 RefSeq
chr1 + 53062051 53085502 PODN 127435 "podocan, transcript variant 2"
GO:0030336|GO:0005737|GO:0008285|GO:0005518|GO:0005578|GO:0005615 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_103554_PI430048170 0.4216243480478231.44313503203376 2.12495371868929 1.2564159121273
2.72537220250277 A A A 1.28506323202035 2.05911301973449 1.40942669190112 A A A
LNCV6_103554_PI430048170 mRNA
ATTATTGGTTCTTCTTCAGCACTGTGGCCTCGGCCACAGCTGGCATGCTCTGCCTGATCG NM_024786RefSeq chr5
- 795604 850986 ZDHHC11 79844 "zinc finger, DHHC-type containing 11"
GO:0005783|GO:0008152|GO:0008270|GO:0016021|GO:0019706 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128312_PI430048170 0.1088272530481011.25636416172265 7.97695461252718
7.97669461638011 7.99131019748736 P P P 7.44343799016906 7.61707608156323
7.86535314098996 P P P LNCV6_128312_PI430048170 mRNA
TGACCCATCTGGCATTGCCAACGAAGCCTTCATTAAAATGTTTTCTTTGCTTGCAAAAAA NM_001195RefSeq chr20
- 17493904 17531369 BFSP1 631 "beaded filament structural protein 1, filensin, transcript variant 1"
GO:0005882|GO:0005739|GO:0008150|GO:0005737|GO:0005212|GO:0005886|GO:0070307|GO:0005200|GO:0048
469|GO:0015629 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130407_PI430048170 0.3134539565077991.19780281127932 1.29116964311058
0.8536678274926770.917752276245356A A A 0.6604278920236710.473515401419974
1.11100025403619 A A A LNCV6_130407_PI430048170 mRNA
GGTCAAAAATGGATAAACAATGGCATTTGGAGCAAAACTTTCAGCTTCTTCGTTTTAGTT NM_001258000 RefSeq
chr10 + 44292749 44294649 C10orf142 NA uncharacterized LOC100130539 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_129503_PI430048170 0.6909821180568141.0976005033587 1.12563842898673
1.20132500773896 0.421802819636951A A A 1.4353621642126 0.357373089956111
0.398214906087018A A A LNCV6_129503_PI430048170 mRNA
TTCTGTACCATTTATTTGCTCCCAATGTTTATGATAATAAAGGCACCGCTGATGGGGACC NM_000250RefSeq chr17
- 58269855 58280935 MPO 4353 myeloperoxidase
GO:0050832|GO:0042582|GO:0005634|GO:0005764|GO:0005615|GO:0001878|GO:0032094|GO:0046872|GO:0005
739|GO:0002679|GO:0004601|GO:0019430|GO:0032496|GO:0030141|GO:0042744|GO:0044130|GO:0008201|GO:0
006979|GO:0070062|GO:0043066|GO:0007568|GO:0006952|GO:0009612|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135659_PI430048170 0.7380269567370640.9904498763263850.287038810762024
0.2984954558165150.399491414046797A A A 0.3658718598946640.310506874111148
0.35227905336544 A A A LNCV6_135659_PI430048170 mRNA
TTCTTTTCTCTTCCAAAAAGAATTCCCTGGCAGAGAATCTATCATTCCAAAAGGTAACCT NM_172159RefSeq chr3
+ 156290986 156539138 KCNAB1 7881 "potassium channel, voltage gated subfamily A regulatory beta
subunit 1, transcript variant 3"
GO:0005886|GO:0007268|GO:0015459|GO:0034705|GO:0070402|GO:0005829|GO:0031234|GO:0004033|GO:0005
249|GO:0007611|GO:0006813|GO:0071805|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103945_PI430048170 0.4224667019679210.9697657199809350.41320736231742
0.4366191178702060.29256381711743 A A A 0.40065068126733 0.45940783583211
0.418680569766978A A A LNCV6_103945_PI430048170 mRNA
CCTGTAAACTGCTGTTTGTGGTTTACTCGTTATTAGATTTGTCAAAGGTTTATCTAGCTT NM_001193628 RefSeq chr19
+ 56643158 56657246 SMIM17NA small integral membrane protein 17 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133568_PI430048170 0.4281759988011511.01887645833054 0.303036208237105
0.3276396567384920.39207741164032 A A A 0.33085297038666 0.31453238257156
0.297711788763195A A A LNCV6_133568_PI430048170 mRNA
GTAAGTTGCTTCCTAACATCCTTGGACTGAGAAATTATACTTACTTCTGGCATAACTAAA NM_002426RefSeq chr11
- 102862732 102875034 MMP12 4321 matrix metallopeptidase 12
GO:0060054|GO:0035313|GO:0022617|GO:0004175|GO:0030198|GO:0030574|GO:0005509|GO:0006508|GO:0005

578|GO:0008270|GO:0005576|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135517_PI430048170 0.0949983720484242 0.89717750885787 10.7761780296002
10.8403814032961 10.7350284905782 P P P 10.8752164002206 11.0527543755605
10.8883098426512 P P P LNCV6_135517_PI430048170 mRNA
CAGGAACCTCAACTTCCCCTAAGTTTGTAAAAATGCACTTTTGTAGCTTTTCAGAATTAA NM_176880RefSeq chr19
- 19201410 19203429 NR2C2AP 126382 "nuclear receptor 2C2-associated protein, transcript variant 2"
GO:0005515|GO:0010467|GO:0006367|GO:0005654|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137255_PI430048170 0.3176655298151940.9311070542613951 2.1164313651137
12.1737417750877 12.144763488609 P P P 12.3593283468049 12.2711702182518
12.1022331626893 P P P LNCV6_137255_PI430048170 mRNA
TTGGGTCTGAACGCGAAATAAAGAAATCCTCTCAGCCCGCCTTTGCCAGCGTCGTCCCTC NM_001287RefSeq chr16
- 1444932 1475084 CLCN7 1186 "chloride channel, voltage-sensitive 7, transcript variant 1"
GO:0005247|GO:0031410|GO:0005765|GO:0005254|GO:0005524|GO:0055085|GO:0044070|GO:0015297|GO:0034
220|GO:0016020|GO:0006810|GO:0016021|GO:0009268 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131702_PI430048170 0.0781860495766821 1.06172020105218 0.414784103710338
0.3549833172306380.314845649601134A A A 0.2599958981869090.313042466799014
0.253376187185323A A A LNCV6_131702_PI430048170 mRNA
ACAATTCCAAACATACAAGAGGCTGCCTCTTAACACAGCACTTAGACACGTGCTGTTCCA NM_012314RefSeq
chr19_GL949748v2_alt + 812554 828448 KIR2DS4 3809 "killer cell immunoglobulin-like receptor, two
domains, short cytoplasmic tail, 4, transcript variant 1" GO:0005886|GO:0005887|GO:0045087 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127810_PI430048170 0.7312553281349790.9523472166842454.69013564383476
4.16046147674674 3.78160311499063 P P P 4.37903577658424 4.48791397507235
4.09406754849273 P P P LNCV6_127810_PI430048170 mRNA
CTTCACTGAGATGTGTTTCTTTGTTGAACTTTGTGTGTGTGTGTTTAGAATATAACAGAC NM_001099772 RefSeq
chr1 + 46798997 46819349 CYP4B1 1580 "cytochrome P450, family 4, subfamily B, polypeptide 1,
transcript variant 1"
GO:0006805|GO:0005506|GO:0070330|GO:0018879|GO:0044281|GO:0019825|GO:0042738|GO:0008144|GO:0018
585|GO:0018917|GO:0005789|GO:0020037|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105287_PI430048170 0.3041389488714291.08122066142598 6.43677052557718
6.17222493370601 6.25871639609717 P P P 6.19119170437566 6.25048672193505
6.09662253796013 P P P LNCV6_105287_PI430048170 mRNA
TTGTATTTGGGCAGAACTTGAGGGACAGAGTTAAGCTGATAAATGAGAGCGTGGACGAAG NM_007322RefSeq
chr19 - 5916140 5978309 RANBP3 8498 "RAN binding protein 3, transcript variant RANBP3-d"
GO:0005515|GO:0005737|GO:0008536|GO:0070412|GO:0046907|GO:0005654|GO:0005634|GO:0015031 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121382_PI430048170 0.0021171038077872 1.20287950610205 6.75473547684306
6.8180013398707 6.83689749758356 P P P 6.54433195468915 6.55676348155969 6.5099331313971
P P P LNCV6_121382_PI430048170 mRNA
GCTCAGAGGACTCTATACAGAGACGTGATGCTGGAGAATTATAGGAACCTGGTCTCCCTG NM_207333RefSeq chr19
- 52876171 52891346 ZNF320 162967 zinc finger protein 320
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139128_PI430048170 0.2611173885832680.9111537178139665.41394463844843
5.24005019272991 5.55417424750155 P P P 5.51873948532533 5.59344575429964
5.51438899203478 P P P LNCV6_139128_PI430048170 mRNA
AGGTAGGAACGGAATTTTGAGGGCAAAGAAACCTGTGTTTCCATGGAATTGCTGAGACGT NM_018425RefSeq chr10
+ 97640685 97676432 PI4K2A 55361 phosphatidylinositol 4-kinase type 2 alpha

GO:0005515|GO:0004430|GO:0043005|GO:0030054|GO:0031224|GO:0044281|GO:0005765|GO:0030425|GO:0005
829|GO:0005739|GO:0002561|GO:0043025|GO:0043204|GO:0030672|GO:0005794|GO:0000287|GO:0035651|GO:0
006661|GO:0031410|GO:0005524|GO:0046854|GO:0042734|GO:0035838|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_64158_PI430048170 0.6690242424813660.9509792128618284.52422638364063 4.79660441587315
4.12742183953007 P P P 4.53973515347353 4.65605735531211 4.54400494369707 P P P
LNCV6_64158_PI430048170 mRNA
TTTAAGAAGTTCGAGCGGACGTCATCCAGTGGTACCATGTCGTCCACGGAGGAGCTGGTG NM_012292RefSeq chr19
+ 1067165 1087831 HMHA1 NA "histocompatibility (minor) HA-1, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_127406_PI430048170 0.0218299462140666 7.19154402109647 5.76039484018531
6.13678349939081 5.9642726643006 P P P 3.79082763197545 2.08123144399456
2.98757063249058 P A P LNCV6_127406_PI430048170 mRNA
GTGTGCTGGGGGACTTTTGCCTTGTTTGTAATGTTAAAGTTTTTGTTTACATTGAGAATA NM_153274RefSeq chr1
- 44783584 44787754 BEST4 266675 bestrophin 4
GO:0008150|GO:0003674|GO:0005886|GO:0034707|GO:0005254 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143200_PI430048170 0.0169573150039156 0.5685185896420625.50920224560369
5.35668477813287 5.78311449320535 P P P 6.32265229628156 6.36583587118796
6.43517256857459 P P P LNCV6_143200_PI430048170 mRNA
CGTGCTATGATGTGTCTCACATTGGATGATATTCCACTTTGGGAATTTTAGTATTTGTATNM_015325RefSeq chr5 +
5422672 5490234 ICE1 23379 interactor of little elongation complex ELL subunit 1
GO:0042796|GO:0005515|GO:0031334|GO:0015030|GO:0035363|GO:0045945|GO:0042795|GO:0035327|GO:0090
316|GO:0008023|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141570_PI430048170 0.00107857012861916 0.6633757127326727.04879345384563
6.87645467400106 6.95865171426278 P P P 7.52052478938272 7.65057561897616
7.48913212052285 P P P LNCV6_141570_PI430048170 mRNA
TGATCTCTTCCCCCAACTTCCTAACACTTATTAATTTATGAAACTGTTTTTCTCAGCGCA NM_015001RefSeq chr1 +
15847863 15940455 SPEN 23013 spen family transcriptional repressor
GO:0001191|GO:0005515|GO:0003700|GO:0003714|GO:0000122|GO:0006351|GO:0000166|GO:0003697|GO:0007
219|GO:0050769|GO:0017053|GO:0001085|GO:0016032|GO:0005654|GO:0045893|GO:0045892|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144328_PI430048170 0.000385561082948171 0.3361286887608656.84097964556162
6.72962987436202 6.59801179386919 P P P 8.12914406498127 8.47236625557215
8.27542157957086 P P P LNCV6_144328_PI430048170 mRNA
GTCGGAATCCACGGGCTGCAGATTTTCCAAAACAATCGTTGTATCTTTATTGACTTTTTT NM_001005291 RefSeq
chr17 - 17811348 17837011 SREBF1 6720 "sterol regulatory element binding transcription factor 1,
transcript variant 1"
GO:0005515|GO:0006629|GO:0008286|GO:0003700|GO:0032810|GO:0030324|GO:0005783|GO:0005634|GO:0044
281|GO:0005635|GO:0051591|GO:0032403|GO:0032094|GO:0005829|GO:0071398|GO:0005737|GO:0045944|GO:0
033762|GO:0046983|GO:0032526|GO:0046676|GO:0044255|GO:0003062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130847_PI430048170 0.0173106902592589 0.4046048634820171 0.3580115705349
9.69217353055456 9.71205252967732 P P P 11.4173531624846 11.514566539329
10.7317212322792 P P P LNCV6_130847_PI430048170 mRNA
CCTCTCCCCACCTTTGCCATTCTTAAGTATTGAATGTACTTTGTATAATTTTAGTGGAAT NM_152727RefSeq chr16 +
57092542 57147966 CPNE2 221184 copine II GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_93259_PI430048170 0.6646008206026390.9673916716820871 2.1047110024901 12.358262364343

12.3394668289 P P P 12.4049998642518 12.1865127831714 12.3589071475956 P P P
LNCV6_93259_PI430048170 mRNA
GACTTTGAATTCTAACGACGAGCCGTGTTGAAACTTCTTTTGTATGTGTGTGTGTTTTTTT NM_001258446 RefSeq chr8
- 143309325 143359977 TOP1MT 116447 "topoisomerase (DNA) I, mitochondrial, transcript variant 2"
GO:0042645|GO:0006260|GO:0005739|GO:0003917|GO:0007059|GO:0003918|GO:0005730|GO:0006338|GO:0005
634|GO:0031298|GO:0006265|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138412_PI430048170 0.7125011864920320.97086154892439 0.612318052965169
0.5472492626594240.310160063362314 A A A 0.40987605271054 0.639463562546993
0.556291740743648 A A A LNCV6_138412_PI430048170 mRNA
CCTACATGTCTGTATGTCATCAAAGTTGGCCTAATAAATGCATAACCTCTCAATGAAAAA NM_001080489 RefSeq
chrX + 48761749 48773648 GLOD5 392465 glyoxalase domain containing 5 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_134610_PI430048170 0.00280884860290909 3.20194503555041 9.91923372485658
10.4346289225764 10.2472007626271 P P P 8.61973169527667 8.58288048760345 8.3982997722846
P P P LNCV6_134610_PI430048170 mRNA
ACAGACATGGTTTGTCACTGTTGAGCTTCTGTTCCTAGAGAATCCTAGAGGCTTGATTGG NM_024827 RefSeq chr3
+ 13480214 13506424 HDAC11 79885 "histone deacetylase 11, transcript variant 1"
GO:0032041|GO:0070932|GO:0070933|GO:0006355|GO:0016575|GO:0005886|GO:0005634|GO:0046970|GO:0006
351|GO:0000118|GO:0014003|GO:0004407|GO:0046969|GO:0070062|GO:0008134|GO:0016568 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_99083_PI430048170 0.4471933560833721.54615764857986 0.4531013698159830.383017256330549
1.88184398260111 A A A 0.3046667510173360.3554486131465110.676212185152257 A A A
LNCV6_99083_PI430048170 mRNA
TGAAGACAATACTTCGTGGGGTTGTCCTGAAGGAATACCTCACAATGAAAGCCTTTGTGG NM_000083 RefSeq chr7
+ 143316125 143352004 CLCN1 1180 "chloride channel, voltage-sensitive 1, transcript variant 1"
GO:0005886|GO:0005247|GO:0034707|GO:0005254|GO:0019227|GO:0055085|GO:0042383|GO:0044070|GO:0006
936|GO:0034220|GO:0005887|GO:0006810|GO:0034765 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143209_PI430048170 0.00845363929028267 0.3688009935853263.68802570920857
3.90683272634683 4.30515217824687 P P P 5.37334619736947 5.34708337073377
5.55661395579576 P P P LNCV6_143209_PI430048170 mRNA
GTAAAGATTTAGAATTCACCTAAGTCCAAAGGAAAACACGTGGTTTTTAAAGCCATTAGG NM_019028 RefSeq chr11
+ 19117144 19176420 ZDHHC13 54503 "zinc finger, DHHC-type containing 13, transcript variant 1"
GO:0015693|GO:0005794|GO:0005783|GO:0015095|GO:0043231|GO:0007165|GO:0000139|GO:0016020|GO:0030
660|GO:0008152|GO:0016409|GO:0008270|GO:0004871|GO:0016021|GO:0043123|GO:0019706 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132023_PI430048170 0.2769574350193551.0204657596245 0.303377857381757
0.2639714725091070.3320246336735 A A A 0.2794443928208140.261210899634286
0.271785448377663 A A A LNCV6_132023_PI430048170 mRNA
CCCCACTGGGTAGTTTATATACTACCCTATAGGTCATGCCAAAAATGAATAAAAGTTTAA NM_173814 RefSeq chr15
- 55611540 55743119 PRTG 283659 protogenin GO:0007275|GO:0016021|GO:0005615 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136943_PI430048170 0.4336358988508991.3997440047538 0.505959506913618
1.62998858608987 0.438218496745247 A A A 0.5565165590374190.442875394613438
0.447497736857315 A A A LNCV6_136943_PI430048170 mRNA
TCCAAAGTGGTTTTGTAGTGTTGGGTGCTATGAGTAGGTATGGATCTCTGTTGATTGACT NM_213599 RefSeq chr11
+ 22193175 22283367 ANO5 203859 "anoctamin 5, transcript variant 1"
GO:0005622|GO:0006821|GO:0034220|GO:0005886|GO:0005789|GO:0005229|GO:0016021|GO:0055085|GO:0031
982 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99528_PI430048170 0.2249820886239190.4666135905522051.1803349240052 0.469687006054317

0.325427442035929 A A A 2.02101587021852 0.5077024738792392.33043922218805 A A A
LNCV6_99528_PI430048170 mRNA
TGGGCTGATGTCTGATGAAATTTTAAGCCCCAGCTATAGCTACTACAAAGAAAAGTGGCT NM_001288615 RefSeq
chr15 - 99136322 99249619 TTC23 64927 "tetratricopeptide repeat domain 23, transcript variant 8"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127140_PI430048170 0.3119159077869530.8937331119054381 0.4836055368307
10.2632930298824 10.1321142311422 P P P 10.4816443924697 10.2772895895531
10.6091530304789 P P P LNCV6_127140_PI430048170 mRNA
GGTGAACCAGTAGGGAAGCTAGAAACAAACCCAATATTTACCAAAATTTAGGGTATAATA NM_015698RefSeq chrX
- 49113384 49123801 GPKOW 27238 G patch domain and KOW motifs
GO:0005515|GO:0008150|GO:0003674|GO:0005654|GO:0003676 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_23909_PI430048170 0.6554623203616151.00962519443205 0.4633662920980080.492945454707822
0.407197006002263 A A A 0.4564522206979870.42569812282161 0.441046072000826 A A A
LNCV6_23909_PI430048170 mRNA
TGATCTTTGGTGGCATTGACTCTTCTTACTACACTGGAAGTCTGAACTGGGTGCCTGTTA NM_014224RefSeq chr11
+ 61241156 61251457 PGA5 NA "pepsinogen 5, group I (pepsinogen A)" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_135868_PI430048170 0.9371119359814590.9897643064895919.75977777205817
9.62492111134926 9.80372174230965 P P P 9.61257022349997 9.66793835561994
9.93710622363411 P P P LNCV6_135868_PI430048170 mRNA
GTTCTTGAACAGTTTATGCAGTGCTGCTTTGCCAAATAAAGTTAAAAGTAAAAGAGGCAA NM_005389RefSeq chr6
+ 149749694 149811421 PCMT1 5110 "protein-L-isoaspartate (D-aspartate) O-methyltransferase,
transcript variant 1" GO:0004719|GO:0005737|GO:0005783|GO:0030091|GO:0006479|GO:0031982|GO:0070062
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143558_PI430048170 0.0565440773804887 0.4076198096226452.81143766867758
1.48038896099095 1.92126290244658 A A A 3.6277169230778 3.59046028178689 3.1621825853097
P P P LNCV6_143558_PI430048170 mRNA
AAACAGGACATGTGTGAGGCAAAAGCTGCAGGAATTTCTATCAGGCAGATCTGACCTCAT NM_014256RefSeq chr19
+ 17795109 17813576 B3GNT310331 "UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3"
GO:0005975|GO:0030311|GO:0016266|GO:0044281|GO:0008378|GO:0042339|GO:0008532|GO:0000139|GO:0006
493|GO:0018146|GO:0005887|GO:0009405|GO:0047223|GO:0044267|GO:0030203|GO:0043687 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_53993_PI430048170 0.4720917607940271.04600318149966 0.3014938439897920.310177051953092
0.514836296409075 A A A 0.3220082295623140.2826335549843960.336921099040784 A A A
LNCV6_53993_PI430048170 mRNA
TGTTAAAACCTCAAGGAATCAAGACATGTTACTCTGTATTTAAGGGTAAGCCCCACAGCG NM_001135181 RefSeq
chr1 + 48222684 48248644 SLC5A9 200010 "solute carrier family 5 (sodium/sugar cotransporter),
member 9, transcript variant 1" GO:0005215|GO:0005886|GO:0016021|GO:0006814|GO:0055085|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137309_PI430048170 0.3610940605565110.9394804631372080.516573452740717
0.4689137827348450.255861286317006 A A A 0.5369157717676270.51670152494335
0.470252245845851 A A A LNCV6_137309_PI430048170 mRNA
CAACATTTAGTGAAGATTCTTCTGTAGAAAGGACACAAACCTAAACTCAGAAGCCTAAAT NM_001197184 RefSeq
chr14 - 31482943 31487945 GPR33 NA "G protein-coupled receptor 33 (gene/pseudogene), transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140358_PI430048170 0.0298748393795888 0.2640604871502440.43374466083207
0.3650000416233821.71293724755519 A A A 3.22191893357368 2.65335842609727
2.76251164565194 P P P LNCV6_140358_PI430048170 mRNA

ACCTGATTTTGTATCCCCCTGTAGCAGCATTACTGAAATACATAGGCTTATATACAATGC NM_001190839 RefSeq chr12 - 14881180 14885919 MGP 4256 "matrix Gla protein, transcript variant 1" GO:0031012|GO:0005515|GO:0030500|GO:0001503|GO:0001502|GO:0005509|GO:0005578|GO:0008147|GO:0030154|GO:0070062|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139714_PI430048170 0.819107468901896 1.02371617783183 0.653856452360535 0.3395323897815960.384586986307307 A A A 0.3469460378137040.617042179502511 0.313362114196121 A A A LNCV6_139714_PI430048170 mRNA
TGGGGTAAATAGCAAATGTTCAAACTTTGCAGGCATTTTGACATTCATCATAACAACACA NM_014379 RefSeq chr8 - 109967003 109974730 KCNV1 27012 "potassium channel, voltage gated modifier subfamily V, member 1" GO:0005251|GO:0005886|GO:0005887|GO:0008076|GO:0015459|GO:0007268|GO:0051260|GO:0034765|GO:0016021|GO:0008200|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143488_PI430048170 0.00742326411318047 1.24751579668535 9.9417884300651 10.0371800564565 9.96979588643924 P P P 9.72337183610064 9.69380209154252 9.57164723381275 P P P LNCV6_143488_PI430048170 mRNA
TTAGTTCATCTGTTCACTCGTAATAAAAAGAATTCTCTCAGGTCAGAGCCTGTGAAAAAA NM_001172223 RefSeq chr11 - 1469447 1486779 MOB2 81532 "MOB kinase activator 2, transcript variant 1" GO:0044306|GO:0048471|GO:0005737|GO:0030036|GO:0010976|GO:0005730|GO:0001934|GO:0005634|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134869_PI430048170 0.0740497401871471 0.602993201689083 2.70718590623873 2.35403500512102 3.20713281647527 A A P 3.31250186409194 3.63404584265231 3.61753078208507 P P P LNCV6_134869_PI430048170 mRNA
CTGCCCCTTTTTTAAATTACTGGCATTGAATATTGAGTTCATATGGTAATAGCAGGGTTT NM_006020 RefSeq chr14 - 77672405 77708013 ALKBH1 8846 "alkB, alkylation repair homolog 1 (E. coli)" GO:0003906|GO:0005719|GO:0070989|GO:0001890|GO:0042245|GO:0001701|GO:0042056|GO:0008198|GO:0031175|GO:0050918|GO:0005739|GO:0043524|GO:0048589|GO:0006281|GO:0006307|GO:0080111|GO:0070579|GO:0001764|GO:0000737. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113359_PI430048170 0.0923945093632528 0.843360051989627 8.59314975077076 8.53072390965241 8.45067721589036 P P P 8.79953559553162 8.89894515475408 8.60119539052077 P P P LNCV6_113359_PI430048170 mRNA
TCCATCCTGGGCTTCATGGCTGCAGAGCAGGGCGTGCACATCTCCAAGGTGGCAGAGTCA NM_005629 RefSeq chrX + 153688296 153696593 SLC6A8 6535 "solute carrier family 6 (neurotransmitter transporter), member 8, transcript variant 1" GO:0015881|GO:0005886|GO:0005328|GO:0044281|GO:0005575|GO:0034641|GO:0003674|GO:0008150|GO:0006936|GO:0005887|GO:0006600|GO:0006810|GO:0006836|GO:0016021|GO:0005308|GO:0006814|GO:0005309 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116518_PI430048170 0.0615832024770987 0.879482608938543 3.57028138857422 3.75192372913898 3.66915889308506 P P P 3.94720715778896 3.80676381125864 3.79386381074532 P P P LNCV6_116518_PI430048170 mRNA
CAGATTCAGGCCTTGACAGTAGAGAATTAAATTTTGGGAGTTCTGTGGAAGTACAAGGGC NM_024678 RefSeq chr11 - 78435960 78574864 NARS2 79731 "asparaginyl-tRNA synthetase 2, mitochondrial (putative), transcript variant 1" GO:0005739|GO:0010467|GO:0006421|GO:0005759|GO:0004816|GO:0003676|GO:0005524|GO:0006418 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137111_PI430048170 0.00819692723090037 0.492529454606948 4.53400348162974 4.28771201021947 4.63193571742256 P P P 5.27161080708954 5.42487960599242 5.79298333469265 P P P LNCV6_137111_PI430048170 mRNA
CAGTACTGTAATTGGAAATGGCTTTACTCTGAAAATTAGGTTAGTGGGTTGGTGTAAATT NM_001282656 RefSeq chr11 + 9460964 9528524 ZNF143 7702 "zinc finger protein 143, transcript variant 2"

GO:0005515|GO:0010467|GO:0006366|GO:0006357|GO:0006359|GO:0005654|GO:0006383|GO:0003677|GO:0046
872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141752_PI430048170 0.18386695245315 0.78114916360374 3.84860341227753
3.55513498742495 3.88164553333704 P P P 4.43857896659524 4.0232501765708 3.8494900910367
P P P LNCV6_141752_PI430048170 mRNA
CATTTGCCTAAGGAGGTAGCAGCAATCCCTAATATATATATATAGTGAGAACTAAAATGG NM_004836RefSeq chr2
- 88556740 88627576 EIF2AK3 9451 eukaryotic translation initiation factor 2-alpha kinase 3
GO:0017148|GO:0005515|GO:0034976|GO:0006983|GO:0019722|GO:0010998|GO:0006412|GO:0030968|GO:0042
802|GO:0046777|GO:0002063|GO:0018105|GO:0045444|GO:0051260|GO:0019903|GO:0019217|GO:0032057|GO:0
001501|GO:0001503|GO:0070059|GO:0005789|GO:0006987|GO:0019899|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137850_PI430048170 0.931096946000509 1.00318927472107 0.305498891224438
0.312492976893506 0.419746157295253 A A A 0.358173951256295 0.309684941777617
0.358419612720956 A A A LNCV6_137850_PI430048170 mRNA
CGATAAAGTGTTTTTAGTATGCTTTTAGTCTCTTGTAACTGGGGAGAAGCAGTGTTTTTT NM_018248 RefSeq chr4
+ 177309836 177362938 NEIL3 55247 nei endonuclease VIII-like 3 (E. coli)
GO:0003906|GO:0003684|GO:0019104|GO:0003690|GO:0003697|GO:0000405|GO:0006284|GO:0008270|GO:0005
634|GO:0006289|GO:0000737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128848_PI430048170 0.0301295945299272 1.41147708421802 10.1318068340146
10.4395715425579 10.2554129814808 P P P 9.62982718008406 10.0059006183079
9.68705765471941 P P P LNCV6_128848_PI430048170 mRNA
GGCAGGGGTTGGAAACTTAGCACTTTATATTTATACAGAACATTCAGGATATGTCAATAA NM_004418 RefSeq
chr2 - 96143168 96145440 DUSP2 1844 dual specificity phosphatase 2
GO:0005515|GO:0000188|GO:0001706|GO:0006470|GO:0008330|GO:0005634|GO:0008138|GO:0035335|GO:0017
017|GO:0004725|GO:0051019 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136561_PI430048170 0.0816171852248021 1.0376246989482 0.392687621205189
0.407539659369766 0.450408035437225 A A A 0.351458402936235 0.346185714636844
0.393298122006604 A A A LNCV6_136561_PI430048170 mRNA
GACTGGAAGGTGAAATTGGTCCATTTTAGAGCATTACTATTATGCTATCTGTCCATTTAA NM_001290072 RefSeq
chr6 - 46159181 46171010 ENPP5 59084 "ectonucleotide pyrophosphatase/phosphodiesterase 5
(putative), transcript variant 1"
GO:0007154|GO:0016787|GO:0005886|GO:0008152|GO:0005576|GO:0016021|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141977_PI430048170 0.0484107439389381 1.42726283535065 8.52148200955571
8.93077000477542 8.54337962383452 P P P 8.26723785877033 8.12271714671509
8.09783786769109 P P P LNCV6_141977_PI430048170 mRNA
TTCTACCCAAGGCATTGGTCTAGCTTTTCCTACAATGAACCTATCTTTGGAGGTTCAAGC NM_152288 RefSeq
chr16 + 30949083 30954938 ORAI3 93129 ORAI calcium release-activated calcium modulator 3
GO:0005515|GO:0002115|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_103181_PI430048170 0.105148508711341 0.644941776725163 4.55524252068448
4.72717396167464 4.66170770678563 P P P 4.87824362715163 5.23002101230304
5.63882704793638 P P P LNCV6_103181_PI430048170 mRNA
TACTAACTACTGGATCTTACCCACGGCTGCCAACCTGCATTAGGGACAAAATTATTCCTC NM_004229 RefSeq
chrX - 40649542 40735552 MED14 9282 mediator complex subunit 14
GO:0003712|GO:0005515|GO:0010467|GO:0001104|GO:0006367|GO:0006357|GO:0003713|GO:0005634|GO:0046
966|GO:0030374|GO:0030518|GO:0016020|GO:0042809|GO:0045944|GO:0016592|GO:0019827|GO:0004872|GO:0
005654|GO:0045893|GO:0030521 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141326_PI430048170 0.0104231313796064 1.44782287490892 10.47959469538

10.3347142586832 10.5417174538405 P P P 10.0318498405669 9.97365044746402
9.74043366813571 P P P LNCV6_141326_PI430048170 mRNA
ATGGATCTGGTTCAAGAGGAGTTTCTGCAGAGATTAGATTTCTACCAACACAGCTGGCTG NM_021640 RefSeq
chr12 + 53299685 53307181 C12orf10 60314 chromosome 12 open reading frame 10
GO:0005739|GO:0003674|GO:0043473|GO:0005654|GO:0005634|GO:0070062|GO:0035641 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133759_PI430048170 0.457835406860193 1.15085886350426 3.36123981239978
3.11202510490727 2.91793054947112 P P P 3.38005965502585 2.7147171789359
2.59285613267312 P P P LNCV6_133759_PI430048170 mRNA
GCAGATACTGTGTTTCCTTGCTCTTCGTCCATATCAATAAAATTAAGTTTCTCGTCTTAA NM_198481 RefSeq
chr19_GL949746v1_alt - 15192 38320 VSTM1 NA "V-set and transmembrane domain containing 1,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64268_PI430048170 0.0288475570554396 1.12534919115336 11.3852437134009
11.3673833523568 11.2832145543736 P P P 11.175168087318 11.241623721767
11.1068285550791 P P P LNCV6_64268_PI430048170 mRNA
GTGTGTCAGCAGACAGGCCTGCAGATACCCCAGCTCCCAGCCCCTCCAAAGATTTACTTT NM_205767 RefSeq
chr19 - 5678413 5680896 C19orf70 125988 chromosome 19 open reading frame 70 GO:0005739 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145257_PI430048170 0.881257089557017 0.988349203563004 0.29549048998104
0.53220356760877 0.364809593733855 A A A 0.531177815587888 0.438047945288059
0.272580147015786 A A A LNCV6_145257_PI430048170 mRNA
CACAGAGAGAGTACATCTGTGAACAAGTAAACTCTACTTGGAAAACTACGTTTACTTTAT NM_001008496 RefSeq
chr22 - 24719033 24774720 PIWIL3 440822 "piwi-like RNA-mediated gene silencing 3, transcript
variant 1"
GO:0051321|GO:0005737|GO:0003723|GO:0007275|GO:0031047|GO:0007283|GO:0030154|GO:0006417 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_60077_PI430048170 0.0464093872898425 0.75123600480962 7.90509602966967
7.71247185943258 8.04473935941676 P P P 8.16751850373522 8.21829852610245
8.50952496829415 P P P LNCV6_60077_PI430048170 mRNA
CCTGCTTGCAGCATATTAGAACAGACGATCCATGCTAATATTGTATTTTCTCTTAAAACA NM_014059 RefSeq
chr13 + 41457405 41470877 RGCC 28984 regulator of cell cycle
GO:0005515|GO:0008285|GO:2000573|GO:0010718|GO:0005634|GO:2000048|GO:0050715|GO:0050710|GO:0071
158|GO:0003331|GO:0006956|GO:0005737|GO:0051091|GO:0045944|GO:0001100|GO:0005813|GO:0072537|GO:0
019901|GO:0071456|GO:0090272|GO:0045840|GO:0070412|GO:0030295|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144676_PI430048170 0.127074749442945 1.1993646070435 6.81073431701377
6.54272558572544 6.49775259421083 P P P 6.47684223192499 6.42088750107499
6.16859206367549 P P P LNCV6_144676_PI430048170 mRNA
GCAGCGCTGGCAGAACAGTCTGCGCCACAACCTCTCCTTCAACGACTGCTTCATCAAGAT NM_012182 RefSeq
chr15 + 60004221 60005943 FOXB1 27023 forkhead box B1
GO:0033504|GO:0006357|GO:0006366|GO:0021510|GO:0061379|GO:0000981|GO:0001756|GO:0001655|GO:0005
634|GO:0061377|GO:0021855|GO:0061374|GO:0043565|GO:0021767|GO:0021794|GO:0022029|GO:0043524|GO:0
007412|GO:0061381|GO:0007595|GO:0008542|GO:0030901|GO:0061030 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138594_PI430048170 0.00510178238308108 1.58083773816277 8.24576350971733
8.42108356820142 8.47381930750235 P P P 7.85328688801703 7.54873535700119
7.74989791238357 P P P LNCV6_138594_PI430048170 mRNA
CAGACTGAATAGATCTTAACTGTCTCCTACATGTGTGTTTTCAAATGTGTATAGATGCTA NM_003528 RefSeq chr1
- 149884459 149886682 HIST2H2BE 8349 "histone cluster 2, H2be"

GO:0046982|GO:0050830|GO:0019731|GO:0006334|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0005615|GO:0003677|GO:0070062|GO:0002227 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143226_PI430048170 0.412013684574316 1.42148575908293 1.42484829484527 0.260364714708159 0.271976671601446 A A A 0.253376187185323 0.257601700252021 0.255018948671439 A A A LNCV6_143226_PI430048170 mRNA
TATGCACAGAAATGTCACTGCTTCCTGGCTGACATCATCATGGATTCCATCAGGCAAAAG NM_001100915 RefSeq chr16 - 67289489 67326758 KCTD19 146212 potassium channel tetramerization domain containing 19 GO:0051260 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136605_PI430048170 0.0998064889647181 1.67787324619147 3.45008157541206 3.6636985125862 4.0354784599721 P P P 3.30554484613604 2.35166832489404 3.14546790958014 P A P LNCV6_136605_PI430048170 mRNA
GAGTCTTCATGTACTTCATTAAAAAATAACATGGATTCCATACTGAGAGCCTATCTACAC NM_001272071 RefSeq chrX - 15825805 15855014 AP1S2 8905 "adaptor-related protein complex 1, sigma 2 subunit, transcript variant 1"
GO:0006892|GO:0005765|GO:0030119|GO:0006886|GO:0032588|GO:0005829|GO:0050690|GO:0019886|GO:0005905|GO:0000139|GO:0008565|GO:0061024|GO:0016032|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132362_PI430048170 0.057586176419446 0.828236216805404 9.78330358253 9.72653019851998 9.53258489396105 P P P 10.0270754478564 10.0185777296758 9.81433836464651 P P P LNCV6_132362_PI430048170 mRNA
GGGGCAGTGGGTTGGGGTTGTTTTTACTACAAAATAAGTTACTTAGTTTTATAAAGACAA NM_001127266 RefSeq chr4 - 1715951 1721357 TMEM129 92305 "transmembrane protein 129, E3 ubiquitin protein ligase, transcript variant 1"
GO:0006986|GO:0008150|GO:0003674|GO:0016567|GO:0016874|GO:0005789|GO:0016021|GO:0005575|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62808_PI430048170 0.698934611859784 1.00849147092519 0.341132322381469 0.340836084503881 0.412647499742907 A A A 0.363803537109429 0.322476695582294 0.372439358029303 A A A LNCV6_62808_PI430048170 mRNA
AAGATACCCCTTCAGCGACTAGAGAGCTACAGGAGAATCACCAGTGGCAAATGTCCCCAG NM_002986 RefSeq chr17 + 34285667 34288180 CCL11 6356 chemokine (C-C motif) ligand 11
GO:0005515|GO:0008360|GO:0005615|GO:0032855|GO:0006955|GO:0006954|GO:0006935|GO:0030838|GO:0007010|GO:0070670|GO:0007015|GO:0070371|GO:0007155|GO:0009314|GO:0008009|GO:0030335|GO:0006874|GO:0060763|GO:0005576|GO:0002544|GO:0009615|GO:0045766|GO:0007165|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136062_PI430048170 0.00139653103943596 0.406907742517258 7.33529432071326 7.27899576680628 7.55590662736022 P P P 8.57734013607254 8.5507128014998 8.91894008953987 P P P LNCV6_136062_PI430048170 mRNA
CTTGCCACTACAAGTAAATCCCCCATTTAATATTTTCTTCTTTAGCATAGCACTGTCATT NM_015252 RefSeq chr2 + 62705865 63046486 EHBP1 23301 "EH domain binding protein 1, transcript variant 1"
GO:0005737|GO:0005886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63495_PI430048170 0.30338992482805 1.16241744138316 4.21653945317566 4.08360966484124 4.16410724090499 P P P 4.03088824059272 4.14540478451949 3.58001282919044 P P P LNCV6_63495_PI430048170 mRNA
ACTATGTGATGCTGAGATCGGCCATTCTGGGCGTGCCTGTCCCTGAGGGCCTAGATAAAG NM_006456 RefSeq chr17 - 76565378 76586063 ST6GALNAC2 10610 "ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2"
GO:0030173|GO:0008373|GO:0006493|GO:0000139|GO:0016266|GO:0006488|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_135843_PI430048170 0.0973398120473737 1.98518736373121 2.11294990029203
2.52667715338151 1.51909599409544 A A A 1.61617527033699 0.36547642466492
1.118729489614 A A A LNCV6_135843_PI430048170 mRNA
ACTAAGCAGATTCAGAGTGGCATACTTCGTTTATTCTCTCTGCCTCACTCTAGAGCATGA NM_001004750 RefSeq
chr11 + 5351507 5352446 OR51B6 NA "olfactory receptor, family 51, subfamily B, member 6" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129115_PI430048170 0.000225517805411585 0.5308401583597277.38389865446146
7.35985656904518 7.37901093127725 P P P 8.33328895185109 8.27198515166591
8.25742697408626 P P P LNCV6_129115_PI430048170 mRNA
TATAAAGACAACCCTGGCTTTTCTATTGCCTTGTTGCTTGCTGAATATAAGGAATGGGGT NM_005016RefSeq chr12
+ 53452101 53481162 PCBP2 5094 "poly(rC) binding protein 2, transcript variant 1"
GO:0005515|GO:0008380|GO:0050687|GO:0010467|GO:0016071|GO:0003723|GO:0005634|GO:0003677|GO:0005
829|GO:0051607|GO:0005737|GO:0016020|GO:0000398|GO:0045087|GO:0030529|GO:0043161|GO:0005654|GO:0
019899|GO:0032480|GO:0005925|GO:0031625|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_128383_PI430048170 0.756963181386825 1.02742119402156 8.02631649845658
7.86855435829895 7.73428645793647 P P P 7.8580626626215 7.96442732100093
7.69139248463955 P P P LNCV6_128383_PI430048170 mRNA
TTGACCTGAAAATCCATAGGGCAGGGCCCACTACTTTCCAAAGAAATAAAAGAACAATTA NM_001303124 RefSeq
chr12 + 56118219 56122496 ZC3H10 84872 "zinc finger CCCH-type containing 10, transcript variant 2"
GO:0005515|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106871_PI430048170 0.48574933021635 0.9760158408743130.397376751799843
0.4099212073163880.278899433311757A A A 0.3776487075882630.426727595436151
0.390027446175856A A A LNCV6_106871_PI430048170 mRNA
ACGAGAACTTCTCGTCGCCAAAATGCCCAGTTGGGTATCTGGGTGATAGGCTGGTTGGCC NM_014079RefSeq chr3
- 126342634 126357393 KLF15 28999 Kruppel-like factor 15
GO:0005515|GO:0072112|GO:0001077|GO:2000757|GO:0044212|GO:0015758|GO:0045944|GO:0014898|GO:0010
001|GO:0005634|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134204_PI430048170 0.630958681410983 1.18382544788975 3.26089041138791
2.17548686324955 2.64145323738397 P A A 2.54772093623054 2.63097747333052 2.3624234112921
P P P LNCV6_134204_PI430048170 mRNA
AAATATAACCAAGAGTTGTACACCACCCACGGTCTCATCAAGGGTCCTCTGTCGAAAGTT NM_173482RefSeq chr19
+ 15010726 15023271 CCDC105 126402 coiled-coil domain containing 105 GO:0070062 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_141095_PI430048170 0.00319895476485103 0.55369998742688 5.82579847227707
5.57297468187351 5.50111357315409 P P P 6.30547051158437 6.56137270299784
6.59500262944547 P P P LNCV6_141095_PI430048170 mRNA
CTTCTAAGAAAAAACAAAAAGACCGTGAGTTATTGCCCAGCAATAATCATGTTGTTACTG NM_145725RefSeq chr14
+ 102777478 102911500 TRAF3 7187 "TNF receptor-associated factor 3, transcript variant 1"
GO:0050688|GO:0005515|GO:0035631|GO:0004842|GO:0034142|GO:0016567|GO:0016874|GO:0031996|GO:0001
817|GO:0005829|GO:0005739|GO:0030162|GO:0002756|GO:0032648|GO:0004871|GO:0034138|GO:0032480|GO:0
031625|GO:0005164|GO:0019901|GO:0006915|GO:0042981|GO:0032088|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145766_PI430048170 0.481781065669303 1.08738012688906 4.17188706771586 4.0579596745434
4.11137649933021 P P P 3.66608658658483 4.19329615378104 4.07044557472658 P P P
LNCV6_145766_PI430048170 mRNA
CCTGTGGCTGTTCCCACATCCCCTTGAATATCCCAGGAAAAATAAAACGGCAGAACTGCA NM_001080418 RefSeq
chr1 - 34865435 34929585 DLGAP3 58512 "discs, large (Drosophila) homolog-associated protein
3" GO:0005515|GO:0030054|GO:0001540|GO:0045211|GO:0007267|GO:0014069 . NA - . NA NA NA

NA NA NA NA NA NA
LNCV6_144928_PI430048170 0.0865925220255863 1.22820645654248 7.35279177000387
7.61050247914094 7.69145995317466 P P P 7.17650795183628 7.26485197039211
7.34034298787685 P P P LNCV6_144928_PI430048170 mRNA
CCATAGTGCTCCTTGGGTATTGCCAATATCCTATTATTTCTGTGTAAAATGAAGATACTG NM_014280RefSeq chr1
- 28200278 28233031 DNAJC8 22826 "DnaJ (Hsp40) homolog, subfamily C, member 8"
GO:0008380|GO:0010467|GO:0000398|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130303_PI430048170 0.136876380251944 1.04783668517682 0.486009626935023
0.579326599025541 0.496934563386006 A A A 0.424751390543027 0.457845006073576
0.478735347563233 A A A LNCV6_130303_PI430048170 mRNA
CAGTGATCTAGCTTGATAAGGACATTCATAAGTAACTGGATGATTCTTTAACATTGCAGA NM_000318RefSeq chr8
- 76980257 77000288 PEX2 5828 "peroxisomal biogenesis factor 2, transcript variant 1"
GO:0042632|GO:0005515|GO:0000038|GO:0006635|GO:0006699|GO:0045540|GO:0050680|GO:0048147|GO:0000
122|GO:0031648|GO:0016020|GO:0007031|GO:0016593|GO:0008270|GO:0001764|GO:0016558|GO:0005779|GO:0
005778 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140279_PI430048170 0.603220359412066 1.0312080587722 0.463787396602155
0.626025232176712 0.422076161876389 A A A 0.545676506752414 0.413928361899274
0.423645665480356 A A A LNCV6_140279_PI430048170 mRNA
TGTGTTTCATTCTCCAAAGGACAGGAACTGAGACTTATGGGCCAGAAGATACTGGAAGAT NM_182761RefSeq chr5
+ 119629558 119635822 FAM170A 340069 "family with sequence similarity 170, member A, transcript
variant 1" GO:0006366|GO:0005634|GO:0045893|GO:0003677|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144215_PI430048170 0.0165612451941671 0.0845225732397259 0.512127921742062
0.354725515141368 2.0462284106104 A A A 4.52933496999307 4.7923620523063
4.91000889464035 P P P LNCV6_144215_PI430048170 mRNA
TGGGTTGACATTAATAAGAATGCTTTAGAACAGAAGACAAACTGTATTGCATTGTGGTCA NM_017998RefSeq chr9
- 74946582 74952886 C9orf40 55071 chromosome 9 open reading frame 40 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_129180_PI430048170 0.103659982418307 0.541934153530384 4.42013067958327
4.09370678749743 4.33377434616243 P P P 4.68757164568239 5.70111739442202
4.92719262858009 P P P LNCV6_129180_PI430048170 mRNA
GTGAATCTCTTCTCCCTTTGAAGAAACTATACATTTATTGTTACGGTATGAAGTCTTCTG NM_057749RefSeq chr8
- 94880224 94895254 CCNE2 9134 cyclin E2
GO:0005515|GO:0000082|GO:0006270|GO:0000075|GO:0016538|GO:0005654|GO:0000079|GO:0000278|GO:0051
301|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137345_PI430048170 0.052883865335876 0.416456680447596 0.311540257702929
0.324591389268759 0.370604742226441 A A A 1.05882166791947 1.50201721139771
2.06209925599126 A A A LNCV6_137345_PI430048170 mRNA
TTACCATCTCTAGCTGCCATTTGTGGGGGGAACAAAACAAGGGAATCCTGATTGTGTACA NM_003966RefSeq chr5
- 9035025 9546121 SEMA5A 9037 "sema domain, seven thrombospondin repeats (type 1 and type
1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A"
GO:0051897|GO:0021536|GO:0005886|GO:0007267|GO:0035373|GO:0048842|GO:0002043|GO:0048843|GO:0035
413|GO:0007413|GO:0007411|GO:0030836|GO:0007155|GO:0070062|GO:0001569|GO:0043395|GO:0045766|GO:0
007399|GO:0050918|GO:0007162|GO:0016020|GO:0001938|GO:0060326|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133902_PI430048170 0.0872265697402489 1.12964650349663 0.565053300794095
0.728758897596467 0.737401510743885 A A A 0.609318589656451 0.44061987051191
0.453941392306793 A A A LNCV6_133902_PI430048170 mRNA
GATTGATTTGTCCTCAGTGCAAAAAGCATCTTTTGAAGAACTATTTCCAAATGTCAGCAA NM_001303622 RefSeq

chr5 - 131806990 131945698 MEIKIN NA meiotic kinetochore factor NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137851_PI430048170 0.9664768369095451.01166510399884 5.04737668432105 5.25132598985477 4.73952383782798 P P P 5.03993082483569 5.15183264248244 4.82242254412646 P P P LNCV6_137851_PI430048170 mRNA GCAAGGAAAAAGAAAGCCTATGGGAAATGGCTGTGCTCCCAACATAGCTTTGCAGATGAT NM_145043 RefSeq chr8 + 11769662 11787345 NEIL2 252969 "nei endonuclease VIII-like 2 (E. coli), transcript variant 1" GO:0008017|GO:0003906|GO:0003684|GO:0005737|GO:0006284|GO:0008270|GO:0005876|GO:0005634|GO:0006289|GO:0000737|GO:0016799 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145578_PI430048170 0.5912493613876980.9639641673560930.527554156252623 0.5053738713618140.268922166412615 A A A 0.4084310832612930.562582890606895 0.499500321566397 A A A LNCV6_145578_PI430048170 mRNA CCGCAATTAGTCCTTTGATGCTAATTTATGCTGATAACCAAATATTCAAGACTCTGCAAA NM_173858 RefSeq chr1 + 247256071 247257145 VN1R5 317705 vomeronasal 1 receptor 5 (gene/pseudogene) GO:0016503|GO:0007186|GO:0005886|GO:0016021|GO:0019236 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104366_PI430048170 0.0210641949747817 1.25966775095287 6.29709094053609 6.44097173716027 6.35516465734308 P P P 6.16347719635632 5.98963844346894 5.93461769427198 P P P LNCV6_104366_PI430048170 mRNA TACTTCTTGCCTGCTCTCAGTTTGTTCCCGAAATGAGACTTGGTGCACTCTATACCTACT NM_006045 RefSeq chr20 - 51596774 51768411 ATP9A 10079 "ATPase, class II, type 9A" GO:0005802|GO:0048471|GO:0000287|GO:0005886|GO:0006890|GO:0005524|GO:0045332|GO:0006897|GO:0031901|GO:0004012|GO:0008152|GO:0016021|GO:0055037|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142852_PI430048170 0.2433464983547070.7487597612900670.282587121409992 0.35081546296956 0.278018023098533 A A A 0.5005095760429830.404050038163433 1.14349889027869 A A A LNCV6_142852_PI430048170 mRNA GTGTTCAGTTACTGAGTTTCAAAAATGTTTTGGTGGCATGAGGACAAAATTTCATTGAAG NM_015000 RefSeq chr12 + 27244144 27325957 STK38L 23012 serine/threonine kinase 38 like GO:0035556|GO:0005515|GO:0005737|GO:0000287|GO:0016020|GO:0004674|GO:0051128|GO:0006468|GO:0003779|GO:0015629|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_32111_PI430048170 0.0221445664551635 0.7107277861136845.8228550401657 6.16976809982494 6.01950674012096 P P P 6.32228301431902 6.5473832732436 6.62439564876706 P P P LNCV6_32111_PI430048170 mRNA AAGGACTTCACAAAAACCTGTGGATAATGGAAGGGATGTTACGGTACAAACGTATATTTA NM_004230 RefSeq chr19 - 10221432 10231272 S1PR2 9294 sphingosine-1-phosphate receptor 2 GO:0000187|GO:0008284|GO:0090394|GO:0005178|GO:0001664|GO:0007186|GO:0005886|GO:0004930|GO:0003376|GO:0016021|GO:0038036|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135600_PI430048170 0.0239054447751163 1.42704217472102 7.10573551443857 6.95583318934629 7.02998838582073 P P P 6.71702248158365 6.39921818576258 6.41757145726614 P P P LNCV6_135600_PI430048170 mRNA GCTCCTATTTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGC NM_021123 RefSeq chrX + 49341210 49529981 GAGE7 2579 - GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130605_PI430048170 0.7351911672862070.9625568778347424.83468155538311 4.33928278756658 4.63582267490574 P P P 4.59056319815783 4.85269903366689 4.55555697419073 P P P LNCV6_130605_PI430048170 mRNA TAAATGTAAAGTCACTTTTTCATCAGTCTTAAAACCCAAAGGCTCTTTTCAGAGCCACCC NM_003537 RefSeq chr6 - 26031588 26032060 HIST1H3B 8358 "histone cluster 1, H3b"

GO:0005515|GO:0010467|GO:0046982|GO:0006325|GO:0006335|GO:0005576|GO:0005634|GO:0000228|GO:0003677|GO:0032776|GO:0043234|GO:0060968|GO:0016020|GO:0000183|GO:0007596|GO:0045814|GO:0040029|GO:0005654|GO:0000786|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131585_PI430048170 0.199781315422573 1.05725177972198 0.405492864820855 0.307312288836662 0.452399337139777 A A A 0.331606052883547 0.298144366552622 0.298014188304961 A A A LNCV6_131585_PI430048170 mRNA
CACTCCTTCTGTTTTGTTGCCGTTTATTTTTGTACTCAAATCTCTACATGGAGATAAATG NM_003695 RefSeq chr8 - 142784881 142786592 LY6D 8581 "lymphocyte antigen 6 complex, locus D"
GO:0035634|GO:0016020|GO:0009986|GO:0005886|GO:0030098|GO:0031225|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131970_PI430048170 0.10874892914714 0.519268239980013 2.31746775170161 3.01395078767086 3.64093629995173 A P P 3.90708246129017 4.10416665782511 4.08567151479073 P P P LNCV6_131970_PI430048170 mRNA
CACCCAGGAGCTGAAGGGATTGGAAAGGTTTGGATTCTTTGTAAATGTCCTGCTTTTCTT NM_003688 RefSeq chrX - 41514935 41923034 CASK 8573 "calcium/calmodulin-dependent serine protein kinase (MAGUK family), transcript variant 1"
GO:0005515|GO:0010839|GO:0005516|GO:0060170|GO:0005886|GO:0090288|GO:0015629|GO:0090280|GO:0016363|GO:0005829|GO:0016323|GO:0005737|GO:0061045|GO:0005911|GO:0030198|GO:0045944|GO:0007155|GO:0005730|GO:0004385|GO:0005524|GO:0042043|GO:0005604|GO:0042734|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110730_PI430048170 0.121324856028877 1.84132616009685 2.35897026235587 1.42520576347839 1.31178083562561 A A A 0.970085239164673 1.2467052102736 0.334326280747159 A A A LNCV6_110730_PI430048170 mRNA
ACATGCGCCTGATGTTTCGCAACCATAAAACATTTTACAAGGCTTCTGACTTTGGCCAGG NM_080424 RefSeq chr2 - 230168925 230220112 SP110 3431 "SP110 nuclear body protein, transcript variant c"
GO:0007165|GO:0006355|GO:0003682|GO:0005730|GO:0016032|GO:0008270|GO:0006338|GO:0005634|GO:0004871|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145760_PI430048170 0.282569603742176 0.859065463329061 0.254986014645931 0.275065529117641 0.353420709785403 A A A 0.387762682473352 0.781689974192169 0.33036947013898 A A A LNCV6_145760_PI430048170 mRNA
ACTCCCAGATGGTTTTATCAATAGCCTAGAGGTAAAGAACTGTCTTTTTCTCTGATTCTT NM_002664 RefSeq chr2 + 68365189 68397453 PLEK 5341 pleckstrin
GO:0005515|GO:0060305|GO:0033625|GO:0031529|GO:0042803|GO:0006904|GO:0005829|GO:0005737|GO:0010925|GO:0070493|GO:0002244|GO:0030836|GO:0032233|GO:0010572|GO:0005080|GO:0010920|GO:0045744|GO:0031532|GO:0043325|GO:0046488|GO:0030168|GO:0005576|GO:0032587|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132437_PI430048170 0.0428264201732432 0.629362182753615 3.06829105734005 3.66048752572616 3.42577845096983 A P P 3.8035788829693 4.05005729867136 4.31946174456685 P P P LNCV6_132437_PI430048170 mRNA
GGATCCTGATTCCCCATTAATCAAGATTTGTCAGACTTCACCTTCTATAATTAGAAAACA NM_002669 RefSeq chr4 - 154534996 154550433 PLRG1 5356 "pleiotropic regulator 1, transcript variant 1"
GO:0005515|GO:0008380|GO:0010467|GO:0034504|GO:1900087|GO:0003714|GO:0005634|GO:0071013|GO:0007165|GO:0016607|GO:0000398|GO:0005654|GO:0004871|GO:0005662 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54853_PI430048170 0.609544465616211 1.06764720603366 9.68705765471941 10.0552434975767 9.72085247929727 P P P 9.98099470423961 9.61114864483931 9.58189310392533 P P P LNCV6_54853_PI430048170 mRNA
CAGGCACTAACCCCAGGAAAGATGACAGCACATTGCCATAAAGTTTTGGTTGTTTTCTAA NM_007112 RefSeq chr1 - 155195587 155207981 THBS3 7059 "thrombospondin 3, transcript variant 1"

GO:0048471|GO:0003417|GO:0060346|GO:0043931|GO:0007160|GO:0005509|GO:0005576|GO:0008201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93140_PI430048170 0.0683105633256655 0.6531899442656236.20190009485883 5.60901523575434 5.59180456235079 P P P 6.27075071789399 6.58747263393515 6.45738643367717 P P P LNCV6_93140_PI430048170 mRNA
GCTCCCAAGACGCTCAGCAGCTTCTTCACCCCCCGGAAGCCAGCAGTCAAAAAAGAAGTGNM_000234RefSeq chr19 - 48115444 48170603 LIG1 3978 "ligase I, DNA, ATP-dependent, transcript variant 1"
GO:0042542|GO:0003909|GO:0005634|GO:0006303|GO:0009653|GO:0046872|GO:0043231|GO:0006302|GO:0005739|GO:0006273|GO:0006271|GO:0000723|GO:0000724|GO:0000722|GO:0006297|GO:0006298|GO:0033151|GO:0005794|GO:0005694|GO:0003910|GO:0006259|GO:0005524|GO:0003677|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95825_PI430048170 0.120056719241067 1.16946260372087 7.58836784746151 7.32336166172301 7.59997592773014 P P P 7.21991065585624 7.28219837803768 7.3459086051289 P P P LNCV6_95825_PI430048170 mRNA
TTGCTGGTTCACCTTGACGATCCAGAGAGGGCCATCCAGGATGCAATTTTAGAGGTCCTC NM_017802RefSeq chr7 + 726700 786479 DNAAF5 54919 "dynein, axonemal, assembly factor 5, transcript variant 1"
GO:0045505|GO:0036159|GO:0005737|GO:0031514|GO:0030030|GO:0036158|GO:0003341 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144020_PI430048170 0.2082432169159180.8446305844769390.267227930354866 0.2753678351183020.322483156384346A A A 0.4339954601659630.356320792502994 0.771625320738794A A A LNCV6_144020_PI430048170 mRNA
GTGAAGACTGCTCTACAGAGATTCATGACAAATCTGTGCTATTCCTTTAAAACAATGTAA NM_001005205 RefSeq chr11_JH159136v1_alt + 170963 172037 OR8J1 219477 "olfactory receptor, family 8, subfamily J, member 1" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130141_PI430048170 0.4444876889288961.15225107234109 0.967063937624922 0.4806182547150520.341161933333346A A A 0.53638302405638 0.375644842230358 0.332469980312863A A A LNCV6_130141_PI430048170 mRNA
TAGACAAGATCAAGCTAGAAAACAATCACGAGCTTGGGAGCTCTGTTTTTATTCATATTT NM_178857RefSeq chr8 - 10606349 10655107 RP1L1 94137 retinitis pigmentosa 1-like 1
GO:0035556|GO:0042461|GO:0005930|GO:0030030|GO:0005874|GO:0032391|GO:0045494|GO:0007601|GO:0070062|GO:0001750 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126663_PI430048170 0.25531191213196 1.58291102748665 0.438200218001168 1.68994006683612 1.32135561610659 A A A 0.4710705483512240.475874689290931 0.762218538404545A A A LNCV6_126663_PI430048170 mRNA
CAGGAAACATTTTAGAAAGTGCCAGATGACGCATCGATAATGCATACATTTGAACTTTTC NM_001100916 RefSeq chr8 - 30131670 30144684 MBOAT4 619373 membrane bound O-acyltransferase domain containing 4 GO:0016412|GO:0018191|GO:0005789|GO:0030176|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128518_PI430048170 0.1001086667718350.4563982530195120.271889507066293 0.2908586215715041.70501630049749 A A A 2.33431641129856 2.08340633885645 1.67281777707864 A A A LNCV6_128518_PI430048170 mRNA
TCTGTGTTGTGTGCGTGGCAGCCTCCAGGAATAAACATTCTTGTTGTCCTTTGTAAAAAA NM_016321RefSeq chr15 - 89471408 89496613 RHCG 51458 "Rh family, C glycoprotein, transcript variant 1"
GO:0005886|GO:0015696|GO:0030506|GO:0006873|GO:0008519|GO:0042592|GO:0031410|GO:0055085|GO:0006885|GO:0016323|GO:0016324|GO:0005887|GO:0015837|GO:0030855|GO:0072488|GO:0070634|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129576_PI430048170 0.2524584697615440.8965043947343426.55893333380756 6.58711186697116 6.31922212860378 P P P 6.52183897175489 6.80098024868016

6.61591654138699 P P P LNCV6_129576_PI430048170 mRNA
GATTACTGTGGTCTCTCTGACGGTCCAAGCAAAGGCTCTTTTCAGAGCCACCACCTTTTC NM_003529RefSeq chr6
+ 26020489 26020958 HIST1H3A 8350 "histone cluster 1, H3a"
GO:0005515|GO:0010467|GO:0046982|GO:0006325|GO:0006335|GO:0005576|GO:0005634|GO:0000228|GO:0003
677|GO:0032776|GO:0043234|GO:0060968|GO:0016020|GO:0000183|GO:0007596|GO:0045814|GO:0040029|GO:0
005654|GO:0000786|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131586_PI430048170 0.3579360937005960.8423686213321316.19777318259526
6.57250131094515 7.02557535096295 P P P 6.93675425282814 6.74384742333976
6.96701956823766 P P P LNCV6_131586_PI430048170 mRNA
GTAATGAGTGCTAAATGGGCACCATTATTCGAATCAGATACCTTTTATATTCTCTTTCCA NM_016144RefSeq chr5
+ 116084975 116293290 COMMD10 51397 COMM domain containing 10 GO:0005515 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_72474_PI430048170 0.4381867756479570.8230791535319230.44264984159473 0.453327402223271
0.375534938063388A A A 1.15423181366063 0.405619569929228 0.422882426140278A A A
LNCV6_72474_PI430048170 mRNA
TGAAAACTGCTGGGAGCCCATTGAGAAGTACATCAATGAGCAGTACGAGAAGTTCCTGAA NM_019106RefSeq chr22
+ 41976926 41998221 SEPT3 NA "septin 3, transcript variant B" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126995_PI430048170 0.3983872238641361.02434149369476 0.298183184052442
0.3172427776077640.401752961228149A A A 0.3213411833580640.302154234526965
0.291554475311657A A A LNCV6_126995_PI430048170 mRNA
GGTGGTGATCTGAATACAGCAGCAGTTTGAAAGTGTTCCGTTTTTAAATAAACAGTATGC NM_004857RefSeq chr14
+ 64465498 64474503 AKAP5 9495 A kinase (PRKA) anchor protein 5
GO:0005515|GO:0005516|GO:0005886|GO:0008179|GO:0030819|GO:0007268|GO:0006605|GO:0044281|GO:0010
739|GO:0005829|GO:0007165|GO:0006112|GO:0050796|GO:0051018 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127277_PI430048170 0.7272832588892430.9727857461860840.401375433225112
0.4200189908679390.446943794777708A A A 0.6268804832441120.345998763574056
0.399578181786201A A A LNCV6_127277_PI430048170 mRNA
ACGTTCATCACTTTAAACTGAACCTGGCAAGTTAATTTCCTCAGGAATGGGGATGTATTT NM_201435RefSeq chr12
+ 122774508 122827380 CCDC62 84660 "coiled-coil domain containing 62, transcript variant 2"
GO:0005737|GO:0030374|GO:0005886|GO:0071392|GO:0045944|GO:0030331|GO:0005654|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143128_PI430048170 0.0633288085457981 0.9570745813960260.426118912111068
0.3635718168140420.378175602645481A A A 0.4462475825172260.46737304824329
0.44476953235857 A A A LNCV6_143128_PI430048170 mRNA
GGAAATGCAAATTGTTATGTCTGTGTATCAGCTAGCTGTTGCTAGATAAAAAACCACTTA NM_001178097 RefSeq
chr12 + 92702842 92708549 C12orf74 338809 "chromosome 12 open reading frame 74, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138621_PI430048170 0.000408930245864133 1.53544025250585 12.0989106286146
11.9919444007732 12.1094940405694 P P P 11.4633415556064 11.4810685669314
11.4016898353539 P P P LNCV6_138621_PI430048170 mRNA
GGCTGTCAGTTACATTAAGGTGGTTGTTGTTGTTGTTTTAAACAAAATGGAGAAGCATAA NM_015503RefSeq chr16
+ 28863992 28874213 SH2B1 25970 "SH2B adaptor protein 1, transcript variant 2"
GO:0035556|GO:0005515|GO:0016020|GO:0007596|GO:0030032|GO:0006928|GO:0045840|GO:0005634|GO:0004
871|GO:2000278|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136044_PI430048170 0.3355915014442781.38632584532297 0.279407861232107
1.34339777788358 1.12483089499582 A A A 0.4384131598760440.650897029808799
0.436838776816383A A A LNCV6_136044_PI430048170 mRNA

GAGAAATCACAATGTAATCTAAAGCGGGACTGTCTCAAGAATAAGTCTTGGATATAGAAA NM_001166373 RefSeq chr4 - 163524297 164383255 MARCH1 NA "membrane-associated ring finger (C3HC4) 1, E3 ubiquitin protein ligase, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119045_PI430048170 0.0057206787083402 1.23605095870986 9.59738724887912 9.65011372427909 9.59618394683098 P P P 9.37619500749254 9.29898938390635 9.24909511760683 P P P LNCV6_119045_PI430048170 mRNA
CATAGTCCCTTTGGCCATCCTCTCACCCCAGAATATCCTAATAAACATTGTTTTCTTTTT NM_005264 RefSeq chr10 - 116056930 116273614 GFRA1 2674 "GDNF family receptor alpha 1, transcript variant 1" GO:0016167|GO:0005886|GO:0007411|GO:0005102|GO:0035860|GO:0031225|GO:0007166|GO:0070062|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130243_PI430048170 0.6073834915876280.9822790609130031 0.0225604138317 10.0032577866013 9.88351522900691 P P P 9.98122890098232 10.026793490309 9.98211985241823 P P P LNCV6_130243_PI430048170 mRNA
GTTTGTACAGACAGCCTGCGTGTTGTAAATAAAGCAGAGTGGGCTCTTTTGTGTTTATAA NM_024297 RefSeq chr17 - 7235027 7239506 PHF23 79142 "PHD finger protein 23, transcript variant 1" GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137487_PI430048170 0.0071008606002115 0.3414978746090485.746102134058 5.51267731594661 5.9558850200567 P P P 6.87572938849798 7.3036319055046 7.62352537405713 P P P LNCV6_137487_PI430048170 mRNA
GGAAGCCATTGTCTAATCAACTCTATCATTAGTGACTTGATGTCTCATACCTTAATTTTG NM_001199179 RefSeq chr3 + 130893990 131003202 ATP2C1 27032 "ATPase, Ca++ transporting, type 2C, member 1, transcript variant 5" GO:0005802|GO:0046872|GO:0016339|GO:0034220|GO:0006816|GO:0004871|GO:0043123|GO:0005794|GO:0030145|GO:0031532|GO:0032468|GO:0005509|GO:0006874|GO:0055085|GO:0005524|GO:0030026|GO:0007165|GO:0005388|GO:0008544|GO:0000139|GO:0016020|GO:0008152|GO:0070588|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133656_PI430048170 0.0667649172872614 0.9223732676203051 0.3734091414946 10.4816443924697 10.3817249889237 P P P 10.5080530668844 10.5410280292235 10.5397226576408 P P P LNCV6_133656_PI430048170 mRNA
GCTGTACTTAACCTTCTCCAACATACATCCTGCATTACATGAATGGATTATTCCTAATAA NM_001177515 RefSeq chr6_GL000251v2_alt - 3164238 3180362 ABHD16A 7920 "abhydrolase domain containing 16A, transcript variant 2" GO:0016787|GO:0008152|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128945_PI430048170 0.3623602136778630.8773804583544114.96060051665775 4.94677319541448 4.43798660128691 P P P 4.94528775544942 5.13118783385695 4.882155140324 P P P LNCV6_128945_PI430048170 mRNA
CTGTACAAGCTGCCCAACTTGAAATTTCTGGATGCCCAGAAAGTAACCAGACAAGAACGA NM_032024 RefSeq chr10 + 75782760 76557376 C10orf11 83938 chromosome 10 open reading frame 11 GO:0030318 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119916_PI430048170 0.85793881196067 0.9779825063841531 3.5652522520823 13.5603788134128 13.9137855977107 P P P 13.7222304800413 13.4992689344981 13.9137855977107 P P P LNCV6_119916_PI430048170 mRNA
GAGTTTCAGGCTCGTGCTAAGCTAGCGCCGTCGTCGTCTCCCTTCAGTCGCCATCATGAT NM_001286272 RefSeq chr13 - 45333470 45341284 TPT1 7178 "tumor protein, translationally-controlled 1, transcript variant 1" GO:0005515|GO:0045298|GO:0043066|GO:0005771|GO:0005509|GO:0006874|GO:0005634|GO:0042981|GO:0009615|GO:0005615|GO:0005737|GO:0006816|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139894_PI430048170 0.5013627009662440.9708054387297230.459479357937877 0.4807335340716260.32109366811719 A A A 0.409514402919357 0.510639597013365

0.472737470399804 A A A LNCV6_139894_PI430048170 mRNA
TTCATTTACACCTTGAGGAATGAGGAGGTAAAAAGTGCCATGAAGCAGCTCAGGCAGAGANM_001001912 RefSeq
chr14 + 21665082 21666024 OR4E2 NA "olfactory receptor, family 4, subfamily E, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_41244_PI430048170 0.0111099080332816 0.6570260952304 4.09291905189283
4.16870206638221 4.00877206399971 P P P 4.52108843749828 4.71061598997561 4.8430387333876
P P P LNCV6_41244_PI430048170 mRNA
TTCTAAAGTTCCTGTTGCTTCAGACAATGGATGAGCAATCACAAGGAATGCAAGGGCCAC NM_133494RefSeq chr1
+ 198156977 198322418 NEK7 140609 NIMA-related kinase 7
GO:0005815|GO:0005874|GO:0009966|GO:0005524|GO:0051225|GO:0046872|GO:0000910|GO:0007346|GO:0000
922|GO:0005737|GO:0004674|GO:0005654|GO:0006468 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133238_PI430048170 0.181271883722292 1.92344648112154 0.292235836145081
1.60029576492653 1.4640140272348 A A A 0.2964805881984590.265967716959227
0.282960168699582 A A A LNCV6_133238_PI430048170 mRNA
GGCTAAAGTAACTTGACCATATTTGATGCTTTTCTATGCTCATTTCAACTTGGCTTTTTG NM_001139514 RefSeq chrX
+ 86148450 86832602 DACH2 117154 "dachshund family transcription factor 2, transcript variant 2"
GO:0046545|GO:0006355|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_69211_PI430048170 0.0142020050544056 1.95866635778839 3.84825436457102
4.40548347041018 4.02929900777917 P P P 3.03954496483204 3.07113186709219
3.30493480774072 P P P LNCV6_69211_PI430048170 mRNA
CTTTCCTTTATGAAGGACCAAAGGTTATTTTCCGTTTTGCTCTGGCACTTTTTAAGTACA NM_144572RefSeq chr15 -
77994984 78077652 TBC1D2B 23102 "TBC1 domain family, member 2B, transcript variant 1"
GO:0005515|GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57025_PI430048170 0.2252666772405131.61887993525192 3.95648961285133 3.34990764897237
3.65577795229341 P P P 3.60597013614207 1.93109350524878 2.94182613259735 P A P
LNCV6_57025_PI430048170 mRNA
CGGGTGGGTGGTCAAATCACCACTTCTGTGTGATCTTGCTGGGATTCCTCCCTTAGGACT NM_016526RefSeq chr11
- 202923 207422 BET1L 51272 "Bet1 golgi vesicular membrane trafficking protein-like, transcript variant 2"
GO:0005484|GO:0030173|GO:0005794|GO:0016020|GO:0005795|GO:2000156|GO:0042147|GO:0031201|GO:0015
031|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145510_PI430048170 0.0127713005946694 1.98229049563349 5.27688185398948
5.55150417456041 5.41382681825508 P P P 4.36768231123478 4.7145114986316
4.15576852352283 P P P LNCV6_145510_PI430048170 mRNA
CTGGTTTTAAATGTTGGCCGTTGATGCAATTTAACCATTTAATTCCTGTTGCTCTATATG NM_207459RefSeq chr17 +
82359246 82363776 TEX19 400629 testis expressed 19 GO:0051321|GO:0005737|GO:0007283|GO:0030154
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130771_PI430048170 0.0246677121006452 1.27557044207434 10.4033579163684
10.1947965731246 10.173405871644 P P P 9.8358451168275 9.95749548757641
9.93330145833758 P P P LNCV6_130771_PI430048170 mRNA
GAACATCCCCTTGGATGATTTGCGGTTGCTTAGAATAAAACTTGCTACTAGCAAAAGAAA NM_012256RefSeq chr7
+ 149239650 149255609 ZNF212 7988 zinc finger protein 212
GO:0005515|GO:0003712|GO:0006355|GO:0006357|GO:0008270|GO:0005634|GO:0003677|GO:0006351|GO:0042
802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137630_PI430048170 0.2162087053632730.75347819044366 4.4805783614321
3.99501846969368 4.79418120353252 P P P 4.63704185430819 4.73989624572382 5.1703592807878
P P P LNCV6_137630_PI430048170 mRNA
CAAATGCATCTTTACACTCTTGCACAAAAGTTAAGGAATAAATGTCCACTGCTTTTGGTT NM_181838RefSeq chr5
+ 139561165 139628433 UBE2D27322 "ubiquitin-conjugating enzyme E2D 2, transcript variant 2"

GO:0000209|GO:0005515|GO:0006511|GO:0004842|GO:0034142|GO:0016567|GO:0016874|GO:0071456|GO:0061418|GO:0000151|GO:0002224|GO:0005524|GO:0005829|GO:0043234|GO:0002756|GO:0045087|GO:0035666|GO:0005654|GO:0070936|GO:0034138|GO:0006464|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133506_PI430048170 0.0168767489959332 0.46983086168869 7.23731227253349 6.75862586924863 6.96328967148387 P P P 7.66444112145063 8.15238946982251 8.36550941284672 P P P LNCV6_133506_PI430048170 mRNA CATCAGTACACTTGTCATTTCACATGTGTTTAATGTGACAGTTTTTCAGTACTGTATGTGNM_001247996 RefSeq chr8 - 130052104 130443660 ASAP1 50807 "ArfGAP with SH3 domain, ankyrin repeat and PH domain 1, transcript variant 2"
GO:0043547|GO:0005515|GO:0008060|GO:0006996|GO:0016020|GO:0032312|GO:0060271|GO:0005547|GO:0005546|GO:0008270|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110303_PI430048170 0.0729704300092794 1.29458529254417 6.2490270227736 6.62397291265795 6.47269888013855 P P P 6.05402826445871 6.12908703755801 6.06843582339268 P P P LNCV6_110303_PI430048170 mRNA TGGACGTGGAGAAGGTGACCACCTTCGAGCATCAGTACGTCAGTGCCATCAAGACCCTGT NM_002067RefSeq chr19 + 3094409 3124002 GNA11 2767 "guanine nucleotide binding protein (G protein), alpha 11 (Gq class)"
GO:0005886|GO:0005834|GO:0003924|GO:0030168|GO:0031683|GO:0005525|GO:0005765|GO:0046872|GO:0071467|GO:0006184|GO:0007507|GO:0031826|GO:0007165|GO:0001501|GO:0005737|GO:0007596|GO:0060158|GO:0045634|GO:0007188|GO:0001508|GO:0004871|GO:0070062|GO:0048066 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132837_PI430048170 0.0193336563735602 0.7104379099351265.49731227853649 5.28620786852234 5.58500417797589 P P P 5.784602261873 5.94840842860384 6.1126611808473 P P P LNCV6_132837_PI430048170 mRNA CCTCAGACTCAGACACAAGGCCTTTTACATGGAAATTTTACAAATTACTTCCATTTATGT NM_173570RefSeq chr3 + 113947900 113962980 ZDHHC23 254887 "zinc finger, DHHC-type containing 23"
GO:0018345|GO:0008270|GO:0016021|GO:0072659|GO:0019706 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143984_PI430048170 0.163753056256345 1.23489379271288 12.0232452434363 12.0035030962408 12.0042583945111 P P P 11.4699731174795 11.9729440771277 11.6283752871679 P P P LNCV6_143984_PI430048170 mRNA AGCCAGAGGCTGGGTTCATTTGTGTAACGACAATAAACGGTACTTGTCATTTCGGGCAAA NM_001006946 RefSeq chr2 - 20200796 20225433 SDC1 6382 "syndecan 1, transcript variant 1"
GO:0005515|GO:0042542|GO:0001657|GO:0005886|GO:0007603|GO:0044281|GO:0051591|GO:0005737|GO:0060009|GO:0006954|GO:0001948|GO:0030198|GO:0055002|GO:0042476|GO:0048627|GO:0030204|GO:0060070|GO:0030203|GO:0070062|GO:0043202|GO:0009986|GO:0005975|GO:0005796|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140073_PI430048170 0.0236158837710739 0.88762784814157 11.7579130408239 11.8504385318471 11.7883805225414 P P P 11.9749322633411 11.9692926171876 11.9699664808913 P P P LNCV6_140073_PI430048170 mRNA ATGAATATCAAAGCCCATATCCACATGTTGCTAGAGGGGCTTAGAGAACTACAAGGCCTG NM_153477RefSeq chrX - 47651791 47659180 UXT 8409 "ubiquitously-expressed, prefoldin-like chaperone, transcript variant 1"
GO:0005515|GO:0008017|GO:0005813|GO:0001106|GO:0048487|GO:0000226|GO:0005634|GO:0000122|GO:0006351|GO:0051297|GO:0005737|GO:0051015|GO:0047497|GO:0003682|GO:0000930|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134161_PI430048170 0.0159991747461024 0.6633443886542875.8405226105849 5.74914466953043 5.93508319140754 P P P 6.22165784461481 6.56639253059307

6.49667168347214 P P P LNCV6_134161_PI430048170 mRNA
CAATAGTTTCCCAATCACATAGCAGGCAAGAGATATTTTGTACTTTTTGATCCACTGTAA NM_032199RefSeq chr10
+ 61901253 62096948 ARID5B 84159 "AT rich interactive domain 5B (MRF1-like), transcript variant 1"
GO:0005515|GO:0030325|GO:0044212|GO:0006325|GO:0048705|GO:0005634|GO:0009791|GO:0010761|GO:0048
644|GO:0051091|GO:0035264|GO:0060021|GO:0045444|GO:0048468|GO:0000977|GO:0006357|GO:0001822|GO:0
003713|GO:0000122|GO:0003677|GO:0001227|GO:0006351|GO:0001889|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128930_PI430048170 0.5136667332794381.02908294163662 0.283917348431031
0.3093497700828750.445343381391078A A A 0.3272768944945750.29677215710066
0.295533728181714A A A LNCV6_128930_PI430048170 mRNA
CTAATGGATTCAATTACGGACTCTGGATATTTGCACTTATGTACTTGATACTGAATGCAT NM_021136RefSeq chr14
- 59595975 59870839 RTN1 6252 "reticulon 1, transcript variant 1"
GO:0005515|GO:0030182|GO:0005789|GO:0030176 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57097_PI430048170 0.000407529811813195 1.71145171715502 5.08141370059992
5.13449244650661 5.24528451910201 P P P 4.35542839050378 4.47735298690567
4.30198265100266 P P P LNCV6_57097_PI430048170 mRNA
TTTGTTCTGAACTTTCCTGTTACCTTTTCAGGGCTGACGTCACATGTAGGTGGCGTGTAT NM_004356RefSeq chr11
+ 2377316 2397419 CD81 975 "CD81 molecule, transcript variant 1"
GO:0001772|GO:0005515|GO:0008284|GO:0005886|GO:0006661|GO:0008283|GO:0030890|GO:0046488|GO:2000
145|GO:0050731|GO:0046718|GO:0031982|GO:0000187|GO:0008104|GO:0016020|GO:0005887|GO:0050776|GO:0
023026|GO:0043128|GO:0046813|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_133021_PI430048170 0.9421685783930691.01650001842997 5.8727091454739 5.4745033198599
5.42044899664564 P P P 5.44863642179445 5.69278918416758 5.58854180160586 P P P
LNCV6_133021_PI430048170 mRNA
GATACTAGATGTGACAATACTGTGAAAAGCAACACATGCTATATAAAACATTAGCACTGC NM_001144869 RefSeq
chr11 - 74491877 74493710 LIPT2 387787 lipoyl(octanoyl) transferase 2 (putative)
GO:0016415|GO:0005739|GO:0009249|GO:0016874|GO:0009107|GO:0033819 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129742_PI430048170 0.00133403969806675 1.59040047128273 6.4528721948474
6.4124873402131 6.28040731364606 P P P 5.64610052698013 5.83601908054213 5.6529051885818
P P P LNCV6_129742_PI430048170 mRNA
CTGTAGTTCCTTAGTTAGGTCTTAGCAATCAAACCAAATTGATGTCTCCCTTGACTCTTC NM_080677RefSeq chr17
+ 58083418 58090257 DYNLL2 140735 "dynein, light chain, LC8-type 2"
GO:0005515|GO:0008092|GO:0005813|GO:0006996|GO:0005886|GO:0008039|GO:0005874|GO:0006915|GO:0005
634|GO:0072372|GO:0016459|GO:0097193|GO:0005829|GO:0019886|GO:0003774|GO:1900740|GO:0030286|GO:0
016020|GO:0008152|GO:0006810|GO:0007017 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135905_PI430048170 0.0184124666554122 0.4142187639702644.35468393985316
4.74322510378942 4.66547861611989 P P P 5.4927097493659 5.71642371601024
6.28003804137945 P P P LNCV6_135905_PI430048170 mRNA
ATGTGAAATTAGTAGAATCAGGGAGGACGGGACTTATGCTGTGGTAGGCAACAGAAAAAA NM_031953RefSeq
chr4 + 185210129 185363966 SNX25 83891 sorting nexin 25
GO:0003674|GO:0034713|GO:0032801|GO:0038032|GO:0005575|GO:0060394|GO:0035091|GO:0015031|GO:0030
512|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112167_PI430048170 0.00271842624733004 0.5793793727162914.13509962613211
4.03226603228596 3.88568563696426 P P P 4.96880792659697 4.77524689201863
4.66561087955305 P P P LNCV6_112167_PI430048170 mRNA
GAACAGATTAACCTCATTTAGTTCATTAGCTTGCCTGTTGCTGCAATATTTGGTTTGTTANM_001139442 RefSeq chr9
- 121821924 122093606 TTLL11 158135 "tubulin tyrosine ligase-like family member 11, transcript variant 1"

GO:0005929|GO:0005737|GO:0016874|GO:0005856|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129841_PI430048170 0.4218044500070040.9776991450201920.370179535262055 0.4045255094140680.335905266511771A A A 0.4594879263630770.36156232561055 0.386180951639876A A A LNCV6_129841_PI430048170 mRNA TAGGTGGTAATCGTGGAAAATTTGAAAAATCTCATGTCAGTGTATTAAGATGGTGGAGAA NM_183422RefSeq chr13 - 44432142 44576565 TSC22D1 8848 "TSC22 domain family, member 1, transcript variant 1"
GO:0005515|GO:0043066|GO:0008284|GO:0006355|GO:0005737|GO:0043065|GO:0003700|GO:0006366|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144397_PI430048170 0.00255479416476189 0.6113757846396491 0.2435763424619 10.0930291619344 10.0423911724082 P P P 10.6808788647125 10.9382886102577 10.884521862893 P P P LNCV6_144397_PI430048170 mRNA CCCCAGCTCCCCTCAGTGCTGCTGTCAGTGTAGCAAATAAAGTCATGATATTTTCCTGGC NM_022089RefSeq chr1 - 16985957 17011972 ATP13A2 23400 "ATPase type 13A2, transcript variant 1"
GO:0005515|GO:0071287|GO:0008152|GO:0016021|GO:0005765|GO:0016887|GO:0005764|GO:0005524|GO:0046872|GO:0006812 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130012_PI430048170 0.000833863883983672 2.55327336028816 6.07985956918019 6.07314174009416 5.84121065671366 P P P 4.52443410471227 4.85758652164439 4.54283604395615 P P P LNCV6_130012_PI430048170 mRNA CTGTTAGAATGAAATGGTTCCCATAAATAAGGGGCATGAGCCCTTCCTCACGACAAAAAA NM_016582RefSeq chr11 - 60937082 60951785 SLC15A3 51296 "solute carrier family 15 (oligopeptide transporter), member 3, transcript variant 1"
GO:0015833|GO:0016021|GO:0015031|GO:0005765|GO:0055085|GO:0043231|GO:0015293|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139281_PI430048170 0.0458180164839426 2.03350099561718 2.22993414850997 1.30863182352579 1.92397594920194 A A A 0.5055169997432410.973887360055166 1.00530691923248 A A A LNCV6_139281_PI430048170 mRNA TAAGGCCATTCCATCAAACTGAAGATGGCAGCAAGTTGTCCTCACTTCTTCATTGAGCAC NM_002754RefSeq chr6 + 36130483 36144524 MAPK13 5603 "mitogen-activated protein kinase 13, transcript variant 1"
GO:0032755|GO:0005515|GO:0048010|GO:0048011|GO:0006355|GO:0006950|GO:0006970|GO:0007265|GO:0005524|GO:0006351|GO:0005829|GO:0035556|GO:0007049|GO:0018105|GO:0000165|GO:0004674|GO:0050729|GO:0004707 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133714_PI430048170 0.3855658988527220.9316645719893551 2.4652282228976 12.2176717954567 12.3087267686927 P P P 12.3406696812603 12.5820578690508 12.374153951825 P P P LNCV6_133714_PI430048170 mRNA CATCTCCTCGGTATAAATCATGTTTATAAGTTATGGAAGAACCGGGACATTTTACAGAAA NM_001128917 RefSeq chr19 + 44891219 44903689 TOMM40 10452 "translocase of outer mitochondrial membrane 40 homolog (yeast), transcript variant 1"
GO:0006626|GO:0005742|GO:0008320|GO:0005739|GO:0046930|GO:0005737|GO:0005654|GO:0015288|GO:0016021|GO:0031307|GO:0071806|GO:0044267|GO:0006811|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132519_PI430048170 0.0538256779101694 1.04969244316826 0.38922968466074 0.4310052809344690.361528451659419A A A 0.3018125100213030.33627755993606 0.334363126092044A A A LNCV6_132519_PI430048170 mRNA GGCATTTCTCCTAGGACAAAAACCTTTGGAATTTTCCAAGTAATAGAAGTATCTTACTGA NM_030959RefSeq chr6_GL000256v2_alt - 682547 684416 OR12D3 81797 "olfactory receptor, family 12, subfamily D, member 3"
GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_145426_PI430048170 0.0906843528551443 1.57953261726277 3.57642204470861
3.80760376549003 3.03277746953026 P P P 2.74558661354379 2.67695597732356
3.08691196604333 P P P LNCV6_145426_PI430048170 mRNA
TTATTATAATCGTCAGCCTCTTCAATGGCGTAGGAAAGAAGAAACAAATGCTTGAATCTC NM_080912RefSeq chr17
- 7101321 7114811 ASGR2 433 "asialoglycoprotein receptor 2, transcript variant H2'"
GO:0005515|GO:0009100|GO:0031647|GO:0055088|GO:0030246|GO:0004873|GO:0030282|GO:0016021|GO:0007
166|GO:0006898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131336_PI430048170 0.0542472504331519 1.20462250720075 5.24952239148424
5.16530278407384 5.41527569336199 P P P 5.13885063956089 4.96616179817551
4.92139991067572 P P P LNCV6_131336_PI430048170 mRNA
TCAGTGTGCATAAGCAAGTATCAGACCTCAGAATGTTTGAGTTATTTTGTCTTAGATATC NM_031215RefSeq chr20
- 62388629 62407283 CABLES2 81928 Cdk5 and Abl enzyme substrate 2 GO:0007049|GO:0051301
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141219_PI430048170 0.3358107904761031.39007690422338 0.333510216502405
1.32917125468384 0.416693303636124A A A 0.29426031313594 0.274202968097463
0.308817293312592A A A LNCV6_141219_PI430048170 mRNA
ACTCTCAGGGACCAAAATATAATTTTCAAAAGTCAAAGAGAAGGCTAGGTTTTACATGGT NM_001085447 RefSeq
chr2 - 169645424 169694421 CCDC173 129881 coiled-coil domain containing 173 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127391_PI430048170 0.9581578198048790.9986522176432610.501080539389291
0.2688383096060270.312606899272613A A A 0.4359544303296310.348321871869436
0.311954201991583A A A LNCV6_127391_PI430048170 mRNA
CCCTTCATACTGTGTATAAAATTGCAATCTAGTGAAATAAACCGTATGCAATGGACCATT NM_001293274 RefSeq
chr1 + 64505913 64693058 CACHD1 57685 "cache domain containing 1, transcript variant 2"
GO:0006816|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131991_PI430048170 0.6354262076554041.30551902050216 2.10245831238096
0.48466096505715 2.25431416368461 A A A 2.21573522658275 1.06018864785077
0.362195678160979A A A LNCV6_131991_PI430048170 mRNA
CTGAAGAGACTGAAGGCCAGAATCCGGAGGGAGGCATCCTCAGGCTGCTGGCTACAGTGA NM_001242672
RefSeq chr1_KI270762v1_alt - 192152 352839 TTC34 NA tetratricopeptide repeat domain 34 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126955_PI430048170 0.00853243907360006 0.4760326255645044.05505332167585
4.39251675282268 4.58728737297558 P P P 5.501837078773 5.2674929760072
5.51430913547712 P P P LNCV6_126955_PI430048170 mRNA
ATTTTATCAGGGACTTGAACAAAGACCTCACTCTTTTTCACTTGTCTTATGTCGAGAGAA NM_005603RefSeq chr18
- 57646425 57803095 ATP8B1 5205 "ATPase, aminophospholipid transporter, class I, type 8B, member
1"
GO:0005515|GO:0000287|GO:0005794|GO:0005886|GO:0005783|GO:0007605|GO:0032534|GO:0060119|GO:0032
420|GO:0031526|GO:0055085|GO:0021650|GO:0005524|GO:0045332|GO:0016324|GO:0034220|GO:0005887|GO:0
006855|GO:0015721|GO:0004012|GO:0007030|GO:0008206|GO:0045892 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_141278_PI430048170 0.1015681386312450.5634875561070834.38475693175826
4.33505049968679 4.49867137950386 P P P 4.76740541217772 5.07700644763729
5.70099343105158 P P P LNCV6_141278_PI430048170 mRNA
CAGGAGTGAAATTCCTTCACTGTCGTGGATGTGGTTATTATTCTAGATAATAATGACATT NM_017904RefSeq chr1
- 54784550 54801268 TTC22 55001 "tetratricopeptide repeat domain 22, transcript variant 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140663_PI430048170 0.04227177829882 0.3629089782462114.71475554614816
3.45705273090195 4.03188521645644 P P P 5.43388534033064 5.6131305047506

5.79487767146452 P P P LNCV6_140663_PI430048170 mRNA
GAACTAGTTTTGCAAAAAACACCTAATGTTGTATAATAATGCCCCAATGATCTTGCTGGT NM_002072RefSeq chr9
- 77716273 78031449 GNAQ 2776 "guanine nucleotide binding protein (G protein), q polypeptide"
GO:0005515|GO:0005886|GO:0003924|GO:0007202|GO:0005765|GO:0009791|GO:0046872|GO:0035412|GO:0007
507|GO:0016322|GO:0005737|GO:0045634|GO:0004871|GO:0070062|GO:0048066|GO:0042711|GO:0031965|GO:0
005834|GO:0050821|GO:0030168|GO:0007215|GO:0005525|GO:0031683|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143466_PI430048170 0.5152338136825881.04152082483967 0.279442411738857
0.2942799802248260.497380902747615A A A 0.3216837778410110.280758736179142
0.302730756228712A A A LNCV6_143466_PI430048170 mRNA
GACATGGACTGTTGCCATTAATACTTTTGGATTCCATATAACCCTTAACACAATAACTTC NM_175571RefSeq chr7
+ 150450629 150479395 GIMAP8155038 "GTPase, IMAP family member 8"
GO:0005739|GO:0005737|GO:0005794|GO:0005783|GO:0005654|GO:0005525|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_46849_PI430048170 0.0344361174090578 0.5734490032506154.72250327539621 4.9166130252212
5.07371763894841 P P P 6.05360659846543 5.59242519297428 5.41831179812236 P P P
LNCV6_46849_PI430048170 mRNA
GACTTCAAAGCTCATTGCTGAAAAATCAGAGGCTAAAATTGCACATAAAAGAACCAGATA NM_024854RefSeq chr12
+ 21437603 21471248 PYROXD1 79912 pyridine nucleotide-disulphide oxidoreductase domain 1
GO:0016491|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133761_PI430048170 0.0024497532965553 0.3908379218213167.83674438642976
7.95737536332189 8.31519553751954 P P P 9.33887529794871 9.27533357616776
9.58604361588616 P P P LNCV6_133761_PI430048170 mRNA
CATACCCCTGGTAACCCTGTGATATTATTTTTAAACATTTTGCTAATGGATCTCTGTTCT NM_024738RefSeq chr12 -
116713319 116738070 C12orf49 79794 chromosome 12 open reading frame 49 GO:0005576 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_130691_PI430048170 0.00697324955105078 1.394815529323 6.63388842243232
6.82301167116349 6.71509341284105 P P P 6.38426306300089 6.16119730047627
6.18187561832589 P P P LNCV6_130691_PI430048170 mRNA
CTTACTGGCTTACCACATTAAATGATTTCTCTCTCCTAACTCAGCTCAAATGGGCAGCCA NM_000121RefSeq chr19
- 11377204 11384342 EPOR 2057 "erythropoietin receptor, transcript variant 1"
GO:0038162|GO:0007507|GO:0005515|GO:0046697|GO:0007165|GO:0007420|GO:0005887|GO:0005576|GO:0042
802|GO:0004900 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136390_PI430048170 0.0545721449809143 0.5033835481685890.282671190978342
1.26760650786852 0.485074869701924A A A 1.41895675224946 1.81411054120328
1.92203022211067 A A A LNCV6_136390_PI430048170 mRNA
CTGAGAGTCAGGGTGGAGATGAGGTGCTCAATTAAACATTACTGTTTTCCATGCAAAAAA NM_013270RefSeq chr3
- 46712115 46717883 PRSS50 29122 "protease, serine, 50"
GO:0005737|GO:0004252|GO:0005783|GO:0006508|GO:0004298 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141208_PI430048170 0.25744500565442 1.01934387620831 0.304629548207316
0.2600140099419560.318680147432191A A A 0.2738328399988080.257653651266966
0.269514423465907A A A LNCV6_141208_PI430048170 mRNA
CTGGGGGTAGGGAAACTTCTAGTGGCAATGATAAAACCAGCAGCAATGATAATAGAAGGC NM_030642RefSeq
chr22_KI270876v1_alt + 32638 44249 APOL5 80831 "apolipoprotein L, 5"
GO:0008035|GO:0006629|GO:0005737|GO:0006869|GO:0042157|GO:0005576|GO:0005575|GO:0008289 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143643_PI430048170 0.000294090379123875 0.5699687431836925.85299338598669
5.89793538220186 5.96977897694863 P P P 6.80341334667754 6.70963136968445

6.63845527047162 P P P LNCV6_143643_PI430048170 mRNA
CCACAGCAAGAAACCTGACAATATTGTTGCTTTCTTCAAAAGTAATTTTGACTGATCTCA NM_198495 RefSeq chr7
- 144266673 144269299 CTAGE4 100128553 "CTAGE family, member 4"
GO:0008150|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67430_PI430048170 0.8050786888046581 1.04228242105943 4.1464747925042 4.54569176428185
4.66143893551853 P P P 4.47846170383684 4.4193555092747 4.32120247728332 P P P
LNCV6_67430_PI430048170 mRNA
CGGCGGGTGAAGCTGCAGCTCTGGGATACTTCAGGCCAGGGAAGATTTTGTACCATATTC NM_006822 RefSeq chr17
- 82657066 82698722 RAB40B 10966 "RAB40B, member RAS oncogene family"
GO:0009306|GO:0016567|GO:0005886|GO:0003924|GO:0005525|GO:0006886|GO:0072659|GO:0006904|GO:0006
184|GO:0017157|GO:0032482|GO:0019003|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78952_PI430048170 0.00421398488898178 1.49164498777285 3.71463421436302
3.92777748809621 3.70897993017102 P P P 3.30645620004161 3.15347431576652
3.16666829152385 P P P LNCV6_78952_PI430048170 mRNA
GACTCATTTTTGATATTCTATTGCGGATACAACAGATCATCTATTGTCACAAGCTAACCA NM_145032 RefSeq chr7
- 102812860 103074568 FBXL13 222235 "F-box and leucine-rich repeat protein 13, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145167_PI430048170 0.1617745061325210.6016452844677670.556971810958048
0.5556069327534540.332274682999285 A A A 1.75705717932016 0.97029891978796
0.714986478728939 A A A LNCV6_145167_PI430048170 mRNA
AATCTCACCTGCTTCCTTCCAGACAGTGTCGCTAAGTGCATTTCACAGTTTTTGGATCTG NM_020981 RefSeq chr2
+ 167818671 167870856 B3GALT1 8708 "UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase,
polypeptide 1" GO:0009312|GO:0000139|GO:0008499|GO:0006486|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134615_PI430048170 0.4894812209734250.9434640939138010.833157858116
10.7003469457055 10.6430295592469 P P P 10.6398320759406 10.9394109880282
10.8398744486331 P P P LNCV6_134615_PI430048170 mRNA
GAGATCATCATTGCAAAGTTCTCTGTTCCTGAGGAACTAAATTTAAGGAAAAAATGGGAT NM_080668 RefSeq chr11
- 65077454 65084143 CDCA5 113130 cell division cycle associated 5
GO:0005515|GO:0007076|GO:0000790|GO:0005886|GO:0005694|GO:0005634|GO:0071922|GO:0005829|GO:0006
302|GO:0008278|GO:0007067|GO:0000082|GO:0005737|GO:0003682|GO:0005654|GO:0007080|GO:0000278|GO:0
000775|GO:0051301|GO:0007064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137257_PI430048170 0.2008972614529330.5633036945753462.20294141650026
0.3360925966852471.2798452682119 A A A 2.24996371805583 2.66088580651736 1.8655446680266
A P A LNCV6_137257_PI430048170 mRNA
GTTCACTTTTATTTAAATAAACTTGTGTGGTAAAAGTACATGCCATGTGTCCCTCAACTG NM_012326 RefSeq chr2
+ 26970370 27027219 MAPRE3 22924 "microtubule-associated protein, RP/EB family, member 3,
transcript variant 1"
GO:0008017|GO:0005515|GO:0005881|GO:0048471|GO:0007067|GO:0005737|GO:0015630|GO:0045737|GO:0030
496|GO:0035371|GO:0045893|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141247_PI430048170 0.1107601141487641.3289191456575 8.91467309424879
9.04225659201932 8.96694095846178 P P P 8.26062061673296 8.817034857746
8.56499370551401 P P P LNCV6_141247_PI430048170 mRNA
TTAATTACTAATATTATTGAATGCCTTAGAGGAGGCCGGGCGAGCCCGGTGTTCTGAAGA NM_152236 RefSeq chr22
+ 29306994 29312789 GAS2L1 10634 "growth arrest-specific 2 like 1, transcript variant 2"
GO:0008017|GO:0097067|GO:0001725|GO:0030308|GO:0001578|GO:0005874|GO:0046966|GO:0005737|GO:0045
647|GO:0010629|GO:0051726|GO:0007026|GO:0007050|GO:0005856|GO:0008093|GO:0009267 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136596_PI430048170 0.0762653427376091 0.5366251449018640.249719411938847

0.5432012102988320.328943456315498A A A 1.76264774255483 0.999562556640964
0.910179266883689A A A LNCV6_136596_PI430048170 mRNA
TTTCCTCAGGTAACAGTTTTCCCCCACAACAGGCAGGCAGCCCTCTTAAGCGTCCATTTC NM_001136233 RefSeq
chrX - 24310861 24313315 SUPT20HL2 NA suppressor of Ty 20 homolog (S. cerevisiae)-like 2 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135922_PI430048170 0.2392524654970691.02138075228283 0.30687428783838
0.2935940228125220.354699453160522A A A 0.2995158386530670.284356125005592
0.280381139760309A A A LNCV6_135922_PI430048170 mRNA
TCTTTTGTTCTAACTTCAGCTTCACTGACACTGGGTTGAGCACTACTGTATGTGGAGGGT NM_207517RefSeq chr15
+ 83654085 84039841 ADAMTSL3 57188 "ADAMTS-like 3, transcript variant 1"
GO:0006508|GO:0005578|GO:0008270|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67334_PI430048170 0.1572469525910741.50273138456553 1.24606224492042 1.99954175133001
1.97416871602851 A A A 1.01289066664671 0.8494556952583861.60131650128422 A A A
LNCV6_67334_PI430048170 mRNA
TTTGTGGCCCAGAAAACTGAACGATTATTTTGTTCCTCCGTAGTCCAAAGGGCAGAGTTG NM_015059RefSeq chr15
+ 62647310 62844630 TLN2 83660 talin 2
GO:0005515|GO:0005886|GO:0005158|GO:0045202|GO:0003779|GO:0015629|GO:0001726|GO:0005916|GO:0005
737|GO:0051015|GO:0005198|GO:0005911|GO:0005200|GO:0007043|GO:0007155|GO:0005925|GO:0007016 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128670_PI430048170 0.5787525519109731.11479013106237 2.5022308708497
2.35925717693731 1.89191484178067 A A A 2.42340215951764 2.07754056682846
1.77772170735687 A A A LNCV6_128670_PI430048170 mRNA
GGCCACAGGTCCCACTCTAGTGAAGGTCAATGTCTCAGAATAAAAGCTGTATTTTTACAC NM_001025598 RefSeq
chr1 - 161046941 161069970 ARHGAP30 257106 "Rho GTPase activating protein 30, transcript variant 1"
GO:0043547|GO:0051056|GO:0007264|GO:0016023|GO:0043231|GO:0005829|GO:0005096 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134700_PI430048170 0.0040372765519843 4.1898352282293 5.85064909289642
5.9214129236384 5.69456776072078 P P P 3.8974693989317 3.94857094676815
3.35848581805399 P P P LNCV6_134700_PI430048170 mRNA
TATCATGGTGGTGTCGTGCATCTGCTGGAGCCCAATGCTGGTGTTGGTGGCGCTGGCCGT NM_000955RefSeq chr19
- 14472465 14475362 PTGER1 5731 "prostaglandin E receptor 1 (subtype EP1), 42kDa"
GO:0007186|GO:0005886|GO:0005887|GO:0032496|GO:0004957 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138523_PI430048170 0.00555902435517801 0.5240189424387325.94847333683218
5.68864751728584 5.83057803665466 P P P 6.53784802637265 6.74483980107511 6.9624068131318
P P P LNCV6_138523_PI430048170 mRNA
GTGCCATTAAACCACCTCCAGATGAGTGGAGGAACATCACTTTTTAATTTTTTAATTGTA NM_001282925 RefSeq
chr2 + 203328238 203432173 ABI2 10152 "abl-interactor 2, transcript variant 1"
GO:0005515|GO:0031209|GO:0017124|GO:0006928|GO:0018108|GO:0030175|GO:0032403|GO:0003677|GO:0030
027|GO:0005829|GO:0048365|GO:0005737|GO:0016601|GO:0016477|GO:0008154|GO:0007010|GO:2000601|GO:0
019900|GO:0005856|GO:0070064|GO:0031625|GO:0008093 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_65647_PI430048170 0.00436078044073729 0.5180398029574277.82350046290718
7.96561971186144 8.13286143979477 P P P 9.07006421972409 8.67862237937629
9.00676071522848 P P P LNCV6_65647_PI430048170 mRNA
GCTGTGTGGAAACATCTATCCTATAGATCATCCTATTCTTATGTGTCTTTGGTTATCAGA NM_012413RefSeq chr2
+ 37344609 37373322 QPCT 25797 glutaminyl-peptide cyclotransferase
GO:0016603|GO:0008270|GO:0017186|GO:0006464|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_93824_PI430048170 0.301462155453324 0.737835493440202 4.32120247728332 2.96772725158145 3.59203956707423 P P P 4.35232891944089 4.10720312380397 4.03377507895062 P P P LNCV6_93824_PI430048170 mRNA AGCTCTACCCTTCTCCAAAAGAAGAGCCAAGAGAAGGTCCTTTTCTACAAATATCAGAGC NM_001300970 RefSeq chr19 - 36445118 36489902 ZNF566 84924 "zinc finger protein 566, transcript variant 5" GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_142912_PI430048170 0.392803602965424 1.96136557461056 2.44473393524972 0.605799939800429 0.523201446343562 A A A 0.57737903531414 0.481757720025166 0.481081728629377 A A A LNCV6_142912_PI430048170 mRNA GCAGCTCTCTGTGTATTACCCTGGAAAACTGAAATAAACAATAAAAATCGATGTTTTCCT NM_001282492 RefSeq chr6 - 24797320 24798896 C6orf229 NA chromosome 6 open reading frame 229 NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139260_PI430048170 8.00236652989328e-05 6.57061212225923 7.39677544005593 7.6153656551021 7.77104250594855 P P P 5.04649473444597 4.64372259002817 4.93964698902742 P P P LNCV6_139260_PI430048170 mRNA CATGGGCAGGTACTGACTGAAGATGCAATCCAACCAAAGCCATTACATTTTTTGAGTTAG NM_001860 RefSeq chr9 + 113150957 113164142 SLC31A2 1318 "solute carrier family 31 (copper transporter), member 2" GO:0006878|GO:0005887|GO:0005770|GO:0005375|GO:0035434|GO:0055037|GO:0006825 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_104642_PI430048170 0.426811086415795 1.19570039454603 3.46631433908548 2.89926297599456 3.4157470856219 P A P 3.09610296003852 2.49597655450531 3.35277328236843 P A P LNCV6_104642_PI430048170 mRNA ATTCCTAAAGGGATCTTAAAGACTGGCTGGATGAATAAGCATCTGAATCTGGTGCCAGCC NM_021942 RefSeq chr4 + 183659266 183713594 TRAPPC11 60684 "trafficking protein particle complex 11, transcript variant 1" GO:0005794|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133034_PI430048170 0.00740115308645056 4.95184831057592 2.24392240361018 2.87725315934884 2.81112542051638 A A A 0.378580796972949 0.331848695521568 0.377393656426674 A A A LNCV6_133034_PI430048170 mRNA TGAAGGAAGGTGTTGATTACAGAGTGAAGATCTCCTTCAAGGTCCACAGGGAGATTGTCA NM_001176 RefSeq chr16 + 280605 283003 ARHGDIG 398 Rho GDP dissociation inhibitor (GDI) gamma GO:0043547|GO:0032880|GO:0051056|GO:0007162|GO:0016020|GO:0007264|GO:0016023|GO:0007266|GO:0005094|GO:0005829|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_136821_PI430048170 0.985701702875998 1.01677582211735 0.315871314438761 0.951718829933561 0.295924928951244 A A A 0.479209689929117 0.40882633021889 0.689138703048375 A A A LNCV6_136821_PI430048170 mRNA ACCCATTCATTTACAGTCTGAGAAATAAAGACATTAAGGGAGCCCTAAGAAAACTCTTGA NM_001004451 RefSeq chr9 - 122476957 122477926 OR1J1 NA "olfactory receptor, family 1, subfamily J, member 1" NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_135609_PI430048170 0.0111658291643011 1.2707740819168 11.1712342498879 11.1521127355106 11.0983125431691 P P P 10.8030756443362 10.8766839723325 10.7003469457055 P P P LNCV6_135609_PI430048170 mRNA CAAGCTTCGCAAGAGCATGTGGAAGGACCGGAATCTGGACGTGGTCCGCAAGAAGCAGAA NM_024321 RefSeq chr19 + 35629077 35637685 RBM42 79171 RNA binding motif protein 42 GO:0005737|GO:0048025|GO:0000166|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_142626_PI430048170 0.0359226888032161 1.40094718990032 10.3556473140783 10.2975735078542 10.1488972115747 P P P 9.91726900838822 9.8695779331543 9.53455300573734 P P P LNCV6_142626_PI430048170 mRNA

TGGGACTGACTGGCTCCAGACAGACCATGTTCTACACAGAGGTGACAGATGCCCAGCGTA NM_177533 RefSeq chr14 - 105172936 105181323 NUDT14 256281 nudix (nucleoside diphosphate linked moiety X)-type motif 14 GO:0005515|GO:0005737|GO:0047631|GO:0008768|GO:0008152|GO:0046872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127111_PI430048170 0.245576974886887 0.799702438834076 4.77493198059111 5.1981845879554 4.43910945998162 P P P 5.2269503132054 5.2396736890379 5.00148235874083 P P P LNCV6_127111_PI430048170 mRNA
GGGGATTCTTAGGATTTTTCTACATTCTGTATATTTCTTCTCAAACCTCCAAATGTCCTT NM_000530 RefSeq chr1 - 161304734 161309972 MPZ 4359 myelin protein zero
GO:0005886|GO:0005887|GO:0005198|GO:0043209|GO:0007268|GO:0045217 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144813_PI430048170 0.759295766602621 0.983625960091272 0.345107883242702 0.349120579992372 0.271423395110985 A A A 0.461594214398118 0.293480197844263 0.275977301208921 A A A LNCV6_144813_PI430048170 mRNA
TTTGGCAGTTGTCTGCATTAACCTGTTCATACACCCATTTTGTCCCTTTATTGAAAAAAT NM_022893 RefSeq chr2 - 60457193 60553498 BCL11A 53335 "B-cell CLL/lymphoma 11A (zinc finger protein), transcript variant 1"
GO:0032463|GO:0046982|GO:0003714|GO:0016925|GO:0005634|GO:0000122|GO:0000978|GO:0048671|GO:0046872|GO:0042803|GO:0006351|GO:0048672|GO:0001078|GO:0005737|GO:0030217|GO:0030517|GO:0045944|GO:0010976|GO:0030183|GO:0050773|GO:0010977|GO:0005654|GO:2000171 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135368_PI430048170 0.08950604595352 1.09634506182877 0.561541699683913 0.564641723939102 0.549462340864949 A A A 0.345945131027555 0.431655762045046 0.496062781327618 A A A LNCV6_135368_PI430048170 mRNA
AACTACTGTACCAAACCTCAGAAGTCTTATCTGGTAGGATTTTCTGTCTAATAGTGATAT NM_000549 RefSeq chr1 + 115029823 115034309 TSHB 7252 "thyroid stimulating hormone, beta, transcript variant 1"
GO:0051592|GO:0043627|GO:0016486|GO:0007186|GO:0005179|GO:0033189|GO:0007267|GO:0005576|GO:0044267|GO:0009653 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139972_PI430048170 0.0327741727584571 0.58241763768419 9.51888916009742 9.33929998188615 9.2215291223084 P P P 9.7680888864609 10.3134542303054 10.2904122887359 P P P LNCV6_139972_PI430048170 mRNA
TTGGGCTCAGTTCCCTGGGTCATCAGCCATCAAATCTTGTTGAGTTTAAAAAATAAACAG NM_014580 RefSeq chr9 + 127397137 127407891 SLC2A8 29988 "solute carrier family 2 (facilitated glucose transporter), member 8, transcript variant 1"
GO:0008286|GO:0001666|GO:0005886|GO:0005975|GO:0005765|GO:0055085|GO:0005536|GO:0008021|GO:0015758|GO:0005887|GO:0005355|GO:0007141|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79872_PI430048170 0.0421184374342006 0.716290628275645 5.08608150687139 5.12712519324392 4.74620445272819 P P P 5.68724367386395 5.38235167191719 5.33777387867676 P P P LNCV6_79872_PI430048170 mRNA
TTTTAAGAAAGGACAGCATTCCTGTGACCTCTGCCTACCATCCATAAAATACTCATTCCC NM_147189 RefSeq chr8 + 57994553 58149718 FAM110B 90362 "family with sequence similarity 110, member B"
GO:0005739|GO:0005737|GO:0005815 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145044_PI430048170 0.00244102219858256 0.484160568395514 4.68108329761446 4.66396079296575 4.96401202870996 P P P 5.63428836719834 5.78171225637113 6.02521465800062 P P P LNCV6_145044_PI430048170 mRNA
GGACACACAGAGTATTGGTCCTAAAGTCCAGAGACAGAGCACTAATTAGAAAACATTCAG NM_004075 RefSeq chr12 - 106991364 107093857 CRY1 1407 cryptochrome circadian clock 1

GO:0005515|GO:0043130|GO:0003904|GO:0042826|GO:0019915|GO:2000001|GO:0006094|GO:0035257|GO:0005634|GO:2000850|GO:0000989|GO:0005739|GO:0018298|GO:0009882|GO:0003690|GO:0000166|GO:0033762|GO:0001046|GO:0031397|GO:0043153|GO:0032868|GO:0045744|GO:0019901|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127183_PI430048170 0.127354062854202 0.871542166691993 14.5045621533062 14.5883612374088 14.4904481224677 P P P 14.5700418653215 14.8492246713325 14.7474233293648 P P P LNCV6_127183_PI430048170 mRNA CTCTCACTGCATTTGGTCAGGGGGGCATGAATAAAGGCTACAGGCTCCAACGTGAAAAAA NM_175744 RefSeq chr1 - 112701126 112707403 RHOC 389 "ras homolog family member C, transcript variant 1"
GO:0005515|GO:0044319|GO:0051056|GO:0005886|GO:0007264|GO:0005634|GO:0005525|GO:0032154|GO:0005829|GO:0043297|GO:0000910|GO:0007411|GO:0004871|GO:0043123|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101962_PI430048170 0.311852735367901 1.06528011743482 0.393243930824551 0.597162458241987 0.405747897428032 A A A 0.379374115519251 0.355847576488408 0.396136284445027 A A A LNCV6_101962_PI430048170 mRNA AACTGTGCTACTCCTCACCATCTGCAGCCTTGAAGGTCTTACTTTGAAAAGTCAAAGGAG NM_001643 RefSeq chr1 - 161222292 161223628 APOA2 336 apolipoprotein A-II
GO:0005515|GO:0043627|GO:0007603|GO:0060192|GO:0018206|GO:0030300|GO:0010903|GO:0042803|GO:0034361|GO:0006457|GO:0034364|GO:0055102|GO:0044255|GO:0070062|GO:0006656|GO:0042632|GO:0033344|GO:0002526|GO:0046982|GO:0045416|GO:0043691|GO:0034366|GO:0051384|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132039_PI430048170 0.00711815262297889 0.537146831787407 5.85139188334676 6.08683017978394 6.2206007895164 P P P 6.77323028324375 6.85709168099532 7.20504365137484 P P P LNCV6_132039_PI430048170 mRNA TTGTATTTGAAAGTATGACCTCACAGTCTTCATTTGTCCATAGCAAACATATGTGTGTGT NM_018366 RefSeq chr4 + 6716114 6717660 BLOC1S4 55330 "biogenesis of lysosomal organelles complex-1, subunit 4, cappuccino"
GO:0070527|GO:0005515|GO:0048490|GO:0005737|GO:0031083|GO:0032438|GO:0050885|GO:0006892|GO:0061024|GO:0008089|GO:0031175|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135268_PI430048170 0.232353661042308 0.7747471448972 6.76556544308622 6.95358055155073 7.06907699508122 P P P 6.90971291060282 7.28657316259371 7.62480568899966 P P P LNCV6_135268_PI430048170 mRNA CAGGAGCCAGAGAAATATGAATATACCAAAGTTGTTTGTTTAGCCTCCAACTTAAATTAC NM_001039091 RefSeq chrX + 12791354 12824227 PRPS2 5634 "phosphoribosyl pyrophosphate synthetase 2, transcript variant 1"
GO:0000287|GO:0016208|GO:0031100|GO:0005524|GO:0042803|GO:0016310|GO:0006139|GO:0006167|GO:0043531|GO:0016301|GO:0004749|GO:0006015|GO:0030246|GO:0002189|GO:0019003|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135486_PI430048170 0.0441290098829727 1.14576845679082 0.704803515951327 0.857926470174307 0.839474309002588 A A A 0.576134948690591 0.633897385546958 0.607437005117696 A A A LNCV6_135486_PI430048170 mRNA ACAGCACTTACAATTTTCCCTCTTCACTTGGTTCTTGTACTCTACAAAATATAGCTTTCA NM_001041 RefSeq chr3 - 164978897 165078495 SI 6476 sucrase-isomaltase (alpha-glucosidase)
GO:0004574|GO:0004575|GO:0005794|GO:0005886|GO:0005975|GO:0044281|GO:0005903|GO:0016324|GO:0009405|GO:0030246|GO:0044245|GO:0016021|GO:0070062|GO:0004558 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129904_PI430048170 0.0332230348333555 0.844496149049814 8.81807909034065 8.88713611300957 8.70688350504678 P P P 9.01994755898163 9.05151820562685 9.07727731915382 P P P LNCV6_129904_PI430048170 mRNA

ATGCTGCTGGTGCTCCATTAAAGTTTTACTCTGTGTTGCACTATATGTGTTCATGATAAA NM_000628 RefSeq chr21 + 33266359 33297234 IL10RB 3588 "interleukin 10 receptor, beta" GO:0005515|GO:0007165|GO:0051607|GO:0006955|GO:0004920|GO:0006954|GO:0005886|GO:0032002|GO:0019221|GO:0004872|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130969_PI430048170 0.0564207380039988 2.41070120366092 1.92699232172071 2.99323312363343 2.21199038086847 A A A 1.3242693232738 0.402048507262559 1.57379145483271 A A A LNCV6_130969_PI430048170 mRNA
GTCAGATTTCATGTCACTAAACAAGAAATCTGACAATAGTGCCAGGAAACTAATTTCCTG NM_001287426 RefSeq chr7 + 48088602 48108733 UPP1 7378 "uridine phosphorylase 1, transcript variant 3" GO:0046135|GO:0006139|GO:0044206|GO:0055086|GO:0044281|GO:0043097|GO:0042149|GO:0046108|GO:0009166|GO:0006206|GO:0004850|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127535_PI430048170 0.313547869573913 0.843666434062454 0.37369701948745 0.254945624354237 0.303439827671385 A A A 0.276651775554989 0.855424863307392 0.477429345741876 A A A LNCV6_127535_PI430048170 mRNA
CACGTAATACCATTGCAGAAAGAAAAGACAGTTCCAAATGATAAATTTTAGAGTTGTTTT NM_001167830 RefSeq chr1 - 93149741 93180689 TMED5 50999 "transmembrane emp24 protein transport domain containing 5, transcript variant 2" GO:0005515|GO:0005801|GO:0005793|GO:0005794|GO:0033116|GO:0090161|GO:0005789|GO:0016021|GO:0015031|GO:0070971 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132723_PI430048170 0.0121474398517264 1.25252104914378 11.554105314338 11.6900592468143 11.6937040133408 P P P 11.3351873916379 11.2902677249284 11.3417077418445 P P P LNCV6_132723_PI430048170 mRNA
CGGAAAGGAACTTCTCAGTTTTATTGGGGGTGTCTAAATTTCCTTTCATATGTTCAAATA NM_024067 RefSeq chr7 + 6590020 6608726 C7orf26 79034 "chromosome 7 open reading frame 26, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145183_PI430048170 0.395625268967191 32.7031248984303 0.482089141475266 6.8771133827746 0.41681164420771 A P A 0.265908695397205 0.351719521657504 0.262399640691947 A A A LNCV6_145183_PI430048170 mRNA
GCTTCCATTGACCATATGAAGGCCACCAATTAAATGGTTGTGTTAATCCAACATGTAAAA NM_017699 RefSeq chr3 + 113532370 113629575 SIDT1 54847 "SID1 transmembrane family, member 1" GO:0051033|GO:0016021|GO:0033227 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127908_PI430048170 0.814597715731822 0.980940605874226 10.9710925215087 10.9844156104369 10.7914084731841 P P P 10.871251873757 11.1034585172251 10.8494525383788 P P P LNCV6_127908_PI430048170 mRNA
CTGGCTGTGAGTGGTTTGTACATGCTACAATAAATGCAGCTGGCAGCATTGTGCAAAAAA NM_012171 RefSeq chr5 + 176647386 176659058 TSPAN17 26262 "tetraspanin 17, transcript variant 1" GO:0004842|GO:0016567|GO:0072594|GO:0000151|GO:0016021|GO:0019899 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132903_PI430048170 0.0806737611099083 1.1943398514573 9.91176409924089 10.0155571311049 9.72653019851998 P P P 9.7401594573033 9.63942536839756 9.51124752326804 P P P LNCV6_132903_PI430048170 mRNA
CCATCTGTGTCATGCTTATGTATTATGGCAAGAAGAGGAAAACTGGATTAATAAATACGT NM_144638 RefSeq chr3 + 44861908 44865667 TMEM42 131616 transmembrane protein 42 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129135_PI430048170 0.300169003059466 1.39488001803862 8.46796964199481 8.5712819056241 8.38233985430788 P P P 8.74072539215335 7.53468028802602

7.25324113421285 P P P LNCV6_129135_PI430048170 mRNA
CAGGGCTGTATGGAATAATAATTTAATGCTCACTGTGGCCCTGACTGAAAGTCAAGCTCA NM_013334 RefSeq
chr3 - 49721475 49723974 GMPPB 29925 "GDP-mannose pyrophosphorylase B, transcript variant 1"
GO:0005739|GO:0005737|GO:0009298|GO:0006488|GO:0005525|GO:0044267|GO:0004475|GO:0070062|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143395_PI430048170 0.02971222386323 1.22997908862442 11.3942374122316
11.2395846073936 11.1612107355583 P P P 10.9497052654432 11.0439180379768
10.9121160250568 P P P LNCV6_143395_PI430048170 mRNA
GGTGTGACTTGTAAACTGTCTAGTGTTTGCATTAAATAAAATGGCACCGAGCAGAAAAAA NM_001242614 RefSeq
chrX - 150766335 150898816 CD99L2 83692 "CD99 molecule-like 2, transcript variant 5"
GO:0005886|GO:0016021|GO:0007155|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69088_PI430048170 0.0636801214169862 0.67571914938865 4.78715399164889
4.18706274630353 4.63453102522765 P P P 5.29075920965632 4.91882039296751
5.13679983340078 P P P LNCV6_69088_PI430048170 mRNA
ATGACAGCTGTGGTGAAAATTGAAAAAGGAGTTGGTGGCAATAATGGGGGCAATGGTAAT NM_138473 RefSeq
chr12 + 53380194 53416442 SP1 6667 "Sp1 transcription factor, transcript variant 1"
GO:0005515|GO:0010467|GO:0003700|GO:0006367|GO:0044212|GO:0042826|GO:0030324|GO:0000981|GO:0048706|GO:0005634|GO:0044281|GO:0043353|GO:0048596|GO:0046872|GO:0042803|GO:0005737|GO:0003690|GO:0032993|GO:0045944|GO:0016032|GO:0007179|GO:0001046|GO:0044255|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127467_PI430048170 0.0193468604910048 1.44844394431548 6.31571109995142
6.56788118258278 6.67320848685034 P P P 5.85960435708175 6.04164998990148
6.06632319671163 P P P LNCV6_127467_PI430048170 mRNA
GGAATCTTTTAGTAAAATAGCAGTGTTTTTTGTTGTTTTTGCATTGGATTTGGGGAGTGG NM_001278248 RefSeq
chr1 + 95234154 95247225 RWDD3 25950 "RWD domain containing 3, transcript variant 5"
GO:0005515|GO:0005737|GO:0033235|GO:0032088|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142673_PI430048170 0.259915046768104 1.48265264379695 1.45575120347351
0.51670152494335 1.5610204148474 A A A 0.413279586826488 1.05320032887873
0.483638150958337 A A A LNCV6_142673_PI430048170 mRNA
TATCAGTAAGCTGATGGTACATGCATTTTCTAGAATAGAGCTGGGACTTCCCATGTGGCC NM_016173 RefSeq chr3
+ 50569477 50584990 HEMK1 51409 HemK methyltransferase family member 1
GO:0006306|GO:0005739|GO:0006479|GO:0008276|GO:0008170|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135448_PI430048170 0.236051205477822 1.04246048665625 0.331131740637926
0.300271257614528 0.419839264406057 A A A 0.294047644388318 0.27258446645704
0.307108026708773 A A A LNCV6_135448_PI430048170 mRNA
CACGTATTTTCCATGATGGGATAAATGTTTTCATTTCAAGTGCCAATGTGTGAACTGTAA NM_001242729 RefSeq
chr4 + 105552619 105680913 ARHGEF38 54848 "Rho guanine nucleotide exchange factor (GEF) 38, transcript variant 1" GO:0005737|GO:0032321|GO:0005089 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131112_PI430048170 0.265171005734691 1.1133096654686 11.8603042643809
12.1057870788103 12.1868820793679 P P P 11.8796814552081 11.8647761177534 11.961729427599
P P P LNCV6_131112_PI430048170 mRNA
TAGATGCTGTTGTTTGAATGTTACATACTTCTATTTGTGCCACATCTCCCCTCCACTCCC NM_138820 RefSeq chr5 +
176388782 176389750 HIGD2A 192286 "HIG1 hypoxia inducible domain family, member 2A"
GO:0043066|GO:0070469|GO:0005743|GO:0016021|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_135695_PI430048170 0.0143440962042383 1.73908105904472 6.89805082631663
7.3216129217653 6.93529482246276 P P P 6.47781235806297 6.27772627227102
6.00500662155513 P P P LNCV6_135695_PI430048170 mRNA
AAATTCACCTTCGATGTTGAGAAATCGGAGATTCAGACTTTCCACCTGCAGAATGACCCC NM_003116RefSeq chr20
+ 35615886 35621043 SPAG4 6676 sperm associated antigen 4
GO:0005737|GO:0031514|GO:0005198|GO:0006998|GO:0090286|GO:0016021|GO:0007283|GO:0005635|GO:0005
856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142579_PI430048170 0.396209130536397 0.71949265972868 0.32750213936511
1.99569591775902 0.434173787746519 A A A 0.858459558844934 1.83544720561927
1.91951291579094 A A A LNCV6_142579_PI430048170 mRNA
TACATGTTCCATGTGGCACGCCCAGGTGTGCTAATAAACGTTCATCTTCAGAACAAAAAA NM_001252065 RefSeq
chr11 - 61513715 61580872 SYT7 9066 "synaptotagmin VII, transcript variant 1"
GO:0005215|GO:0030054|GO:0005886|GO:0005509|GO:0031045|GO:0006887|GO:0005764|GO:0005544|GO:0050
796|GO:0045956|GO:0001778|GO:0030672|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143273_PI430048170 0.0689330363268432 1.74409724199227 4.43058803318599
5.1546821012141 5.08287130825752 P P P 4.46771422358242 4.11581704305264
3.67318364192533 P P P LNCV6_143273_PI430048170 mRNA
ACTTTATCCATGAAAATGAAGCAATGGCAGGTGGGAGGCTCTTCCCAATGTGCTTTCTTC NM_005492RefSeq chr20
+ 23491100 23496018 CST8 10047 "cystatin 8 (cystatin-related epididymal specific), transcript variant
1" GO:0010951|GO:0005737|GO:0004869|GO:0009986|GO:0005576 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134847_PI430048170 0.63788320924099 1.38098770534708 1.86502607286121
0.318805438088406 0.323597211992808 A A A 0.410611019293161 0.328706393741696
0.896881224029042 A A A LNCV6_134847_PI430048170 mRNA
TTTGAGGTGAGTTCTGATATCTCAAACACCAGCATCAGGGCCAGGGCAGACAAAATAAGA NM_001142946 RefSeq
chr11 - 2296276 2301913 C11orf21 29125 "chromosome 11 open reading frame 21, transcript
variant 1" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129876_PI430048170 0.416407749519185 0.374773397577393 0.485639265548297
0.507932794093312 0.401437147787365 A A A 3.04713554817077 0.441783213135487
0.516835971715921 P A A LNCV6_129876_PI430048170 mRNA
AAATGCTGTCTTGTGAGCATGAAGTGAACGGGCTGTTTTGCTCCAGCCACTTTTCTTGTA NM_133445RefSeq chr9
- 101569351 101738580 GRIN3A 116443 "glutamate receptor, ionotropic, N-methyl-D-aspartate 3A"
GO:0005515|GO:0043005|GO:0030054|GO:0017146|GO:0005234|GO:0045471|GO:0045202|GO:0030425|GO:0042
802|GO:0034220|GO:0004972|GO:0045211|GO:0043025|GO:0042165|GO:0006816|GO:0051721|GO:0005262|GO:0
060134|GO:0035249|GO:0014069|GO:0016358|GO:0035235|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106921_PI430048170 0.0138969786603781 1.17907600966895 13.9676540676177
14.0541075358915 14.1123508560733 P P P 13.7401851685402 13.8697316676238
13.8119726818629 P P P LNCV6_106921_PI430048170 mRNA
AGGTGTGTGCGCCATCATTGGGGGCATGTTCACAGTGGCTGGACTCATCGATTCGCTCAT NM_198398RefSeq chr20
+ 35542028 35557634 ERGIC3 51614 "ERGIC and golgi 3, transcript variant 1"
GO:0005794|GO:0016020|GO:0033116|GO:0005789|GO:0016021|GO:0016192 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144235_PI430048170 0.0355899818157981 5.52831562897788 11.8686100566345
11.9245685086971 11.7652497649524 P P P 11.3017232891643 11.4258555311605
10.9602348785742 P P P LNCV6_144235_PI430048170 mRNA
ATATTTTTGAGGCTGGGTGACGAGAAAATCTAGAGACATGAGGGACATAAATGGGCCTGG NM_001001410 RefSeq
chr16 - 1349239 1351872 TSR3 115939 "TSR3, 20S rRNA accumulation, homolog (S. cerevisiae)"

GO:0030490 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134866_PI430048170 0.00189402919879648 0.70582823959733 4.63243516288671
4.69772341625859 4.75321755160471 P P P 5.09790219945835 5.22986583522104
5.26083468611973 P P P LNCV6_134866_PI430048170 mRNA
ATACACAGTCTTCGAATACATCGAGAGTGGGATCATTAATCCCCTGCCCAAGAAAATCCC NM_152572RefSeq chr9
- 132725577 132878811 AK8158067 adenylate kinase 8
GO:0006165|GO:0004127|GO:0021591|GO:0004550|GO:0009142|GO:0004017|GO:0005524|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128873_PI430048170 0.9144868076483381.27728576709901 0.3584196127209562.5602490599251
0.99026304779715 A A A 0.9245651225367551.06687954210112 1.67068815917364 A A A
LNCV6_128873_PI430048170 mRNA
GTTGAAAACTCAGACTGCTTTTGTGATGTTTCAAATGAATAAAACTATCCTCCCCTCGTT NM_017938RefSeq chrX
- 120258649 120311536 TMEM255A 55026 "transmembrane protein 255A, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128549_PI430048170 0.00966820591843654 0.5206776979801015.23651047656483
4.88176697787117 4.7116056742116 P P P 5.87782640107761 6.10042924652922
5.69862707280603 P P P LNCV6_128549_PI430048170 mRNA
ACTTAAACCTCCTGCTGTGCCTCGCATCCTATGCTTAATAAAAGAACATGCTTGAATATC NM_016373RefSeq chr16
+ 78099412 79212667 WWOX 51741 "WW domain containing oxidoreductase, transcript variant 1"
GO:0005515|GO:0050662|GO:2001238|GO:0005886|GO:0030178|GO:0048705|GO:0071560|GO:0005634|GO:0005
829|GO:0005739|GO:0005737|GO:0045944|GO:0046983|GO:2001241|GO:0016055|GO:0008202|GO:0001105|GO:0
048037|GO:0005794|GO:0097191|GO:0001649|GO:0005902|GO:0072332|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138616_PI430048170 0.6263978263329610.8410096229323692.52660780135851
1.70606648743985 2.47055083428681 A A A 1.80256740729658 2.8779208956698
2.69644495582833 A P P LNCV6_138616_PI430048170 mRNA
TCCCATTTCTATTGGTGACCAACTTGCAAATGGATAAAACACAGGAAAATCCTGCCCCCC NM_052874RefSeq chr16
- 30989255 31010638 STX1B 112755 syntaxin 1B
GO:0010468|GO:0016081|GO:2000463|GO:0019901|GO:0005815|GO:0005886|GO:0019904|GO:0005819|GO:0010
807|GO:0031201|GO:0005634|GO:0006886|GO:0012505|GO:0005829|GO:0008021|GO:0005484|GO:0016020|GO:0
000149|GO:0009405|GO:0031629|GO:0016021|GO:0001956|GO:0048278 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_139073_PI430048170 0.5494081787955281.03445557261433 0.300338467535237
0.30941178514242 0.496680326729694A A A 0.3324952248555260.290806869853999
0.344598082851184A A A LNCV6_139073_PI430048170 mRNA
AATAAAGACGTGAAGGATGCTTTCTGGAAGTTAATACATACACAAGTTCCATTTCACTGA NM_001004735 RefSeq
chr11 + 55795555 55796500 OR5D14 NA "olfactory receptor, family 5, subfamily D, member 14"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108103_PI430048170 0.4739153695489571.15969230493027 0.319847575710048
0.3243953969015870.947650947487498A A A 0.3633495919912820.316082644732858
0.364931333911188A A A LNCV6_108103_PI430048170 mRNA
CATGGGGTCATATATTGCTTCATGTGTAAGGATTATGTATATGACAAAGACATAGAACAG NM_201286RefSeq chrX
- 55484615 55489198 USP51 158880 ubiquitin specific peptidase 51
GO:0004197|GO:0016578|GO:0016579|GO:0006355|GO:0004843|GO:0061136|GO:0000124|GO:0043161|GO:0008
270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130848_PI430048170 0.8989290916805440.9864735088532380.2972564415585
0.3001723506280690.508888179552637A A A 0.3073554073604460.26887970977381
0.579165824109294A A A LNCV6_130848_PI430048170 mRNA
GCTTCTATGAGATTTACTCCAACACAAATAGGACTGAATTTATTGTGAAGTAACATTGGC NM_001004196 RefSeq

chr3 + 112333068 112362811 CD200 4345 "CD200 molecule, transcript variant 2"
GO:0005515|GO:0005886|GO:0005887|GO:0050776 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117045_PI430048170 0.00949336372746556 0.3932060897908724.34276320345269
3.97480659776358 3.65125498440691 P P P 5.29296851462135 5.22946647541587
5.54911491208826 P P P LNCV6_117045_PI430048170 mRNA
ATGGGATAAACGCTTATCCACTCACTCACCCTTCCGAACTCTTAACATCAATGGGCAAAT NM_203342RefSeq chr1
+ 28887090 29120046 EPB41 2035 "erythrocyte membrane protein band 4.1, transcript variant 4"
GO:0005515|GO:0005516|GO:0008091|GO:0005794|GO:0030036|GO:0005886|GO:0008015|GO:0030507|GO:0003
779|GO:0005634|GO:0014731|GO:0043231|GO:0032092|GO:0043234|GO:0005545|GO:0030866|GO:0005200|GO:0
030863|GO:0019898. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143058_PI430048170 0.3726846775384731.04842712381592 0.327068673640577
0.3312675268842010.502659622241454A A A 0.3226990958936260.291981999748891
0.348134687411873A A A LNCV6_143058_PI430048170 mRNA
AAGACTGTAAGTGTAGAATTGAGCAACTGTCTTCTATCAATAAAGGCTGAATGGCAAAAA NM_213596RefSeq chr12
- 109277977 109309220 FOXN4 121643 forkhead box N4
GO:0001947|GO:0006355|GO:0060579|GO:0003700|GO:0003682|GO:0008016|GO:0010842|GO:0005634|GO:0045
893|GO:0001158|GO:0035881|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143061_PI430048170 0.0421910529786666 0.6120762915495197.98343857462598
7.92809174622026 8.26925792647196 P P P 8.46343350378132 8.70447529095252
9.09093910732753 P P P LNCV6_143061_PI430048170 mRNA
CCATGTACCTTTATTGAGCTTAATTATAATACTGTCAAATTGCCACGATCTCACTAAAGG NM_003137RefSeq chr6
- 35833033 35921180 SRPK1 6732 "SRSF protein kinase 1, transcript variant 1"
GO:0008380|GO:0005515|GO:0006397|GO:0048024|GO:0000287|GO:0005886|GO:0005783|GO:0005634|GO:0050
684|GO:0005524|GO:0016363|GO:0035556|GO:0005737|GO:0004672|GO:0007059|GO:0004674|GO:0045087|GO:0
016032|GO:0005654|GO:0006468|GO:0035092|GO:0045070|GO:0045071 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_145476_PI430048170 0.2393679387881690.9349235658502841 0.5114520609877
10.6105415119238 10.721839006956 P P P 10.6822904691418 10.696548127715
10.7626389379236 P P P LNCV6_145476_PI430048170 mRNA
TTTCCTAAGGTAATAGGGGGTTTATTTCATTTAGGCCCCAGTTGGTAGGTTTTAAAATAA NM_001303095 RefSeq
chr1 - 156721890 156728439 ISG20L281875 interferon stimulated exonuclease gene 20kDa-like 2
GO:0005515|GO:0004527|GO:0090305|GO:0042254|GO:0005730|GO:0005654 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144239_PI430048170 0.3625487229533950.9637806636362320.288440819553563
0.40655299634864 0.311006650734422A A A 0.4624858476610050.354773106187371
0.34827977164974 A A A LNCV6_144239_PI430048170 mRNA
TGGTGCAAAACAGGCTGATTGACATATACAAAAATGTTATGCTATTCTTTGCAAAAGGGA NM_181840RefSeq chr10
+ 117197488 117210299 KCNK18338567 "potassium channel, two pore domain subfamily K, member 18"
GO:0071435|GO:0015271|GO:0005886|GO:0005887|GO:0007268|GO:0005267|GO:0015269|GO:0006813|GO:0071
467 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129593_PI430048170 0.26062221671622 0.8285405094228695.49709518479972
5.24705036667857 5.71881368195809 P P P 5.45533692044374 5.86073983145602
5.95245137854764 P P P LNCV6_129593_PI430048170 mRNA
GTGTCTGCTGCGATAAAATGAGGTTGTCTGTAGTATTTAAGGAGAAAAGAGATAAGTTTT NM_001271948 RefSeq
chr5 - 146589504 146878785 PPP2R2B 5521 "protein phosphatase 2, regulatory subunit B, beta,
transcript variant 10"
GO:0005739|GO:0005515|GO:0007165|GO:0050790|GO:0008601|GO:0006915|GO:0000159|GO:0005741|GO:0005
856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90513_PI430048170 0.0328438859009842 1.08119739968379 0.551216496582449

0.4713140754956130.472833283708939A A A 0.3627879900277150.386839634577853
0.408933546285191A A A LNCV6_90513_PI430048170mRNA
TTTTGGGGGCAAGAGACAAGTTTTGAGAGATCCCGGTTTTCTAGCAGGTCATCTTCCAAA NM_001288780RefSeq
chr17 - 62704904 62808381 MARCH10 NA "membrane-associated ring finger (C3HC4) 10, E3 ubiquitin
protein ligase, transcript variant 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128121_PI430048170 0.0162188625313138 0.3374886063553963.10995991396371
3.58809497554859 3.96488761154804 P P P 5.01361173254 5.19363154026296 5.26997586557302 P
P P LNCV6_128121_PI430048170 mRNA
ATTCTCAGTGTTTGAGAGGTACAAGGGAAGAAAGGACTATGTGGATCCCTTGTGGCTATG NM_001160223RefSeq
chr8 - 42853294 42896723 RNF170 81790 "ring finger protein 170, transcript variant 1"
GO:0016567|GO:0016874|GO:0005789|GO:0008270|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_73243_PI430048170 0.0404648462820042 0.5297143323327655.15090149090109
4.37417169935315 4.7934730842577 P P P 5.60992404270928 5.86536458655724
5.68472290995284 P P P LNCV6_73243_PI430048170mRNA
ATCCAAAAAGAGACAACAGAGCAGCGTGCTCTTGAGGAACAAGAGAAACAAGAAAGAGCT NM_001174150
RefSeq chr3 + 93980138 94055678 ARL13B 200894 "ADP-ribosylation factor-like 13B, transcript variant
3"
GO:0005515|GO:0060170|GO:0006996|GO:0021830|GO:0007264|GO:0021532|GO:0021943|GO:0072372|GO:0070
986|GO:0009953|GO:0005525|GO:0035058|GO:0007224|GO:0001947|GO:0005622|GO:0042384|GO:0005929 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144691_PI430048170 0.0964665273264435 1.34905362203297 11.3173861377313
11.6632287461324 11.1622441353014 P P P 10.911766595471 10.9311697609925 11.046763647911
P P P LNCV6_144691_PI430048170 mRNA
ATTTCTTATCCCGTTTGTTACATTTTGAGGATAATAAAGGTGTGTGATCTGGTTTGGTAC NM_030567RefSeq chr5
+ 177446794 177456286 PRR7 80758 "proline rich 7 (synaptic), transcript variant 1"
GO:0030054|GO:0045211|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70640_PI430048170 0.0932331521262418 1.33192030748226 3.97597159226713 4.4243846715381
4.20052527829464 P P P 3.52415375779943 3.98984988340855 3.84266529221244 P P P
LNCV6_70640_PI430048170mRNA
TCAAAACAATAGCTCAGTTGACCCTTGTATGAGAAACTTGGATGAGTGTGAGGTGTGCCG NM_138402RefSeq chr2
+ 230327178 230403730 SP140L 93349 SP140 nuclear body protein-like
GO:0006355|GO:0003682|GO:0008270|GO:0006338|GO:0005634|GO:0003677 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_104391_PI430048170 0.0329462694471413 1.6862988130346 6.54272558572544
5.98969160907585 6.29770063008232 P P P 5.20244998136977 5.79933498891705
5.55797265563705 P P P LNCV6_104391_PI430048170 mRNA
GCTTCAACTTTTCCATCTGCTCCTAAATAGAGAAAGAGCAAATAAAGAGATAGTTTGTGA NM_001014442RefSeq
chr13 + 23888888 23892103 C1QTNF9B-AS1 NA "C1QTNF9B antisense RNA 1, transcript variant 1"NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88967_PI430048170 0.0133470200763462 1.26707506565045 10.66152990913
10.7412718891552 10.5532966582124 P P P 10.4248330574221 10.2781204002696
10.2274317544085 P P P LNCV6_88967_PI430048170mRNA
TTTTGCAAATATTTTGAGAGACATTGATTTTTCTCCCCGTGCTCCCCCGTTCTTCCCTGC NM_020310RefSeq chr17 -
2384059 2400964 MNT 4335 MAX network transcriptional repressor
GO:0000977|GO:0003700|GO:0008285|GO:0006366|GO:2001234|GO:0003714|GO:0007569|GO:0003713|GO:0005
634|GO:0007275|GO:0000122|GO:0001227|GO:0003682|GO:0051726|GO:0046983|GO:0005654 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127032_PI430048170 0.6094401936605641.08526952258953 5.58171890475553

5.42697809725912 5.14107414355215 P P P 5.64665480262398 5.13852664098577
4.95247622893196 P P P LNCV6_127032_PI430048170 mRNA
CAGTTCTTGGATGGCGTTCTCCTATCTACCTTCCTTCAACTGCTCTGCATATAATAAGCA NM_000486 RefSeq chr12
+ 49950740 49958881 AQP2 359 aquaporin 2 (collecting duct)
GO:0005802|GO:0071280|GO:0009651|GO:0005886|GO:0051928|GO:0030136|GO:0009992|GO:0005764|GO:0016
323|GO:0016324|GO:0042594|GO:0034220|GO:0033762|GO:0015250|GO:0015793|GO:0032496|GO:0005372|GO:0
030042|GO:0006833|GO:0015254|GO:0070062|GO:0030658|GO:0005791|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130409_PI430048170 0.0316278466376005 1.4514326487674 8.29092136287989
8.38024401316913 8.33604172810993 P P P 7.98726837094752 7.61316646380856
7.77114729781417 P P P LNCV6_130409_PI430048170 mRNA
AGGATGTCGTCTTTGGTGAGATCTCTATTATATCTTGTATGGTTTGCAAAAGGGCTTCCT NM_003141 RefSeq chr11
- 4384896 4393696 TRIM21 6737 tripartite motif containing 21
GO:0005515|GO:0004842|GO:0032479|GO:0006513|GO:0016567|GO:0003723|GO:0016874|GO:0090086|GO:0019
221|GO:0005634|GO:0046598|GO:0005829|GO:0042802|GO:0031648|GO:0070206|GO:0051091|GO:0005737|GO:0
000932|GO:0032481|GO:0060333|GO:0000209|GO:0032897|GO:0032088|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_15763_PI430048170 0.0399936993063626 2.88263656554366 2.31027952226957
1.76904245100601 2.97551053752784 A A P 0.918954040742821 0.663308485115127
1.10902149458753 A A A LNCV6_15763_PI430048170 mRNA
AGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCACAGAAGCTAA NM_001282506 RefSeq
chr3_KI270937v1_alt - 61317 73536 MUC20 200958 "mucin 20, cell surface associated, transcript variant
1"
GO:0000187|GO:0016324|GO:0048012|GO:0009925|GO:0006493|GO:0005796|GO:0031528|GO:0016266|GO:0051
260|GO:0005576|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142259_PI430048170 0.343186545665288 1.38937961341522 3.01783237500836
3.38590548388952 2.49709054232088 A P A 2.67425747578153 2.99184246477224
1.62231894962281 A P A LNCV6_142259_PI430048170 mRNA
GCTTGTTCTGGGCTCAGGGAGGGAGGGCGGTGGACAATAAACATCTGAGCAGTGAAAAAA NM_004479 RefSeq
chr9 - 137030173 137032840 FUT7 2529 "fucosyltransferase 7 (alpha (1,3) fucosyltransferase)"
GO:0046920|GO:0042355|GO:0005794|GO:0016020|GO:0032580|GO:0008417|GO:0002522|GO:0002361|GO:0006
486|GO:0016021|GO:0036065 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134779_PI430048170 0.949238474184997 0.999935510521735 9.00926248288486
8.87876293671418 8.56394237754916 P P P 8.89239391008621 8.86860173610085
8.72087450507679 P P P LNCV6_134779_PI430048170 mRNA
CTGCCTCAGGAGACTCTGATTTTATATTTGAGAAAAATAAAGGCGTTCAATCTGCAAAAA NM_013312 RefSeq chr19
- 12763002 12775620 HOOK2 29911 "hook microtubule-tethering protein 2, transcript variant 1"
GO:0005515|GO:0030897|GO:0005813|GO:0008333|GO:0005874|GO:0007032|GO:0045022|GO:0015031|GO:0007
040|GO:0070695|GO:0042802|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143382_PI430048170 0.437402077016263 0.762655167296395 0.446193755870915
0.611391325655467 2.38667062399292 A A A 1.19079667362599 2.20206190173651
1.91166116193527 A A A LNCV6_143382_PI430048170 mRNA
TAAACTGCATGGATATATCTTGGCAGAATCAGAAGTGTGGTTTTACACCAATAAAACAGC NM_001286611 RefSeq
chr6 - 138904014 138988261 REPS1 85021 "RALBP1 associated Eps domain containing 1, transcript
variant 3" GO:0005515|GO:0017124|GO:0005905|GO:0005886|GO:0005509|GO:0006898 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_60444_PI430048170 0.722661649824911 1.04457146456275 3.43060350960676 4.01364552552356
4.05502135277607 P P P 4.4887340401562 2.56811214414769 3.73510494126313 P A P
LNCV6_60444_PI430048170 mRNA

CCTTTTGTATATGATGTCACTGTGACCTCTTTGAAATATAGTGATGGCTTTTACCTACTT NM_006260 RefSeq chr13 + 95677138 95794989 DNAJC3 5611 "DnaJ (Hsp40) homolog, subfamily C, member 3" GO:0043066|GO:0051087|GO:0031205|GO:0031982|GO:0005790|GO:0030968|GO:0051787|GO:0051607|GO:0005737|GO:0016020|GO:0051603|GO:0001933|GO:0004860|GO:0005788|GO:0006469|GO:0006987|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140032_PI430048170 0.42125838504924 0.6127771868252370.379031732028535 0.2606412953432770.27906443096415 A A A 0.3083912829703540.307982685667016 1.84043577288583 A A A LNCV6_140032_PI430048170 mRNA
GGGCCAGAGAGCATGCACACGGTGTCCTGGTTAAATAAAGTCATCCCAACATTCAAAAAA NM_003465 RefSeq chr1 - 203216078 203229732 CHIT1 1118 "chitinase 1 (chitotriosidase), transcript variant 1" GO:0008061|GO:0009617|GO:0006032|GO:0006955|GO:0008843|GO:0005764|GO:0005615|GO:0004568|GO:0000272 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108302_PI430048170 0.0041981477809668 2.44067111514618 4.05783118580902 3.5562818070545 3.91001833185687 P P P 2.78031538401553 2.63178999143139 2.24330856524775 P P A LNCV6_108302_PI430048170 mRNA
ATGCGGTGCCATCAACAAAAATGGTCTTCAAGCCTCAAGCTGTGAAGTTCCTTTACACTG NM_005810 RefSeq chr12 + 8989624 9010744 KLRG1 10219 "killer cell lectin-like receptor subfamily G, member 1" GO:0006968|GO:0006954|GO:0005886|GO:0045087|GO:0050776|GO:0030246|GO:0004872|GO:0016021|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134075_PI430048170 0.6201771378471810.965576148305529 0.558296699944861 0.5003586408283520.272177028503626 A A A 0.4135825292494760.571350296031205 0.508734907477016 A A A LNCV6_134075_PI430048170 mRNA
AGTTCCCACCTGATATGTAGTTGGAGATGGGCAAATACAGCGTCCTTGAAGCATCATTTT NM_001142368 RefSeq chr1 + 109668021 109683997 GSTM2 2946 "glutathione S-transferase mu 2 (muscle), transcript variant 2" GO:0006805|GO:0070458|GO:0042178|GO:0005102|GO:0071313|GO:0006749|GO:0010881|GO:0044281|GO:0004364|GO:0014809|GO:0042803|GO:0005829|GO:0060316|GO:0043295|GO:0005737|GO:0016529|GO:0018916|GO:0010880|GO:0060315|GO:0055119|GO:0019899|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129168_PI430048170 6.77991257125765e-05 0.5870476597035459.12897319068133 9.18909977668026 9.17069631980539 P P P 9.88271543701093 9.93225617163572 9.97822459371373 P P P LNCV6_129168_PI430048170 mRNA
TGTCGACTTGGGGAGGTGATTTCTTTCCTGGTTCTATATGTGAAGCAAAATAAATGTTTT NM_002225 RefSeq chr15 + 40405484 40421313 IVD 3712 "isovaleryl-CoA dehydrogenase, transcript variant 1" GO:0005739|GO:0034641|GO:0008470|GO:0005759|GO:0050660|GO:0009083|GO:0005654|GO:0044281|GO:0006552|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133350_PI430048170 0.0302699838732593 0.7552590693850071 1.9662662446297 11.864325196005 11.6436728356291 P P P 12.2837275437582 12.3248828267281 12.0881948320944 P P P LNCV6_133350_PI430048170 mRNA
GGAGGGTAGGGGTGGTAATAAACTTCTCCAAACGATCGTTGTCATTTTAGACAGAAAAAA NM_032515 RefSeq chr2 + 241558730 241574138 BOK 666 BCL2-related ovarian killer GO:0005515|GO:0051400|GO:0031966|GO:0046982|GO:0008630|GO:0048709|GO:0006919|GO:0008283|GO:0006915|GO:0005634|GO:0005741|GO:0051402|GO:0042803|GO:0097192|GO:0005739|GO:0005737|GO:0072332|GO:0000139|GO:0007420|GO:1900119|GO:0005789|GO:0016021|GO:0008584 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142198_PI430048170 0.65262001531841 0.9113841978705515.40380147530037 5.52847078094293 5.72091921665999 P P P 5.83537226585577 5.89793538220186 5.25707286704134 P P P LNCV6_142198_PI430048170 mRNA
ATACATGCTCTGTCTCCTCTCTTGGAATGCATGAACTTTGATTCCTTCAGGCCCTTGTCA NM_080751 RefSeq chr20

+ 2536606 2641784 TMC2 117532 transmembrane channel-like 2
GO:0005245|GO:0050910|GO:0060005|GO:0070588|GO:0016021|GO:0032426 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_91387_PI430048170 0.229052860219415 1.21040331404542 4.56818810446411 4.37680596946075
4.90651993567121 P P P 4.22001194386035 4.33402020106419 4.50700014651252 P P P
LNCV6_91387_PI430048170 mRNA
TTTGGAGCCGTGAGAGGGTTGAACTATCTGCACCAAAATGGCTGTATTCACAGGAGTATT NM_001206864 RefSeq
chr2 + 201451668 201480851 STRADB 55437 "STE20-related kinase adaptor beta, transcript variant 2"
GO:0008286|GO:0005515|GO:0007254|GO:0005634|GO:0005524|GO:0005829|GO:0035556|GO:0032147|GO:0000
902|GO:0005737|GO:0004672|GO:0004702|GO:0006611|GO:2001240|GO:0006468|GO:0007050|GO:0000278 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137624_PI430048170 0.0424783530170014 1.48478850958629 11.4459387441431
11.9054073139295 11.5818600184321 P P P 11.1810782148454 11.0399278601538
11.0359434499859 P P P LNCV6_137624_PI430048170 mRNA
CAAAGCATCCACCATGGTGGATGGACTGAAGTGTGTATATTTTCTTGATCTATTTTTTAA NM_001136053 RefSeq
chr3 - 127573063 127590759 TPRA1 131601 "transmembrane protein, adipocyte asscociated 1,
transcript variant 1" GO:0006629|GO:0007186|GO:0004930|GO:0007568|GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_145628_PI430048170 0.169902064917139 0.840152917949737 10.9991043776251
10.8811457057363 10.8672641942634 P P P 10.9641294062508 11.3758351565674
11.1352137688537 P P P LNCV6_145628_PI430048170 mRNA
GCAGAAGCTGAGACGTGACTGTCTAGGAGTAACACTCATTAAAGCTTTCATTTTGGCACC NM_001172668 RefSeq
chr16 - 31060847 31073502 ZNF668 79759 "zinc finger protein 668, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138734_PI430048170 0.11268629779113 0.3891361848787062.14396074105771
0.3042162229487340.316176662373798 A A A 2.73698846070139 2.42189983244689
2.51217449672441 A A P LNCV6_138734_PI430048170 mRNA
TGTTACCACAGATTCCCTTGTGTCCGGAGAGATTCCCTAGCTCTAATGACAGCTTTTTTG NM_003601 RefSeq chr4
+ 143513462 143557489 SMARCA5 8467 "SWI/SNF related, matrix associated, actin dependent regulator
of chromatin, subfamily a, member 5"
GO:0005515|GO:0000793|GO:0010467|GO:0005634|GO:0006302|GO:0042393|GO:0000183|GO:0016584|GO:0006
338|GO:0016589|GO:0043596|GO:0016887|GO:0006352|GO:0006357|GO:0043044|GO:0006334|GO:0005730|GO:0
004386|GO:0031491|GO:0031213|GO:0005524|GO:0003677|GO:0034080|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_72763_PI430048170 0.1945736793037881.2073092772716 6.60797223186654 6.90141303727795
6.81449780822428 P P P 6.45444445386345 6.25510673926205 6.7677238242122 P P P
LNCV6_72763_PI430048170 mRNA
GAGGGTGGGAGTTGGTAAAGAGTAGGGTATTTCTATAACAGATATTATTCAGTCTTATTT NM_003341 RefSeq chr3
+ 23805892 23891640 UBE2E1 7324 "ubiquitin-conjugating enzyme E2E 1, transcript variant 1"
GO:0000209|GO:0005515|GO:0006511|GO:0007094|GO:0004842|GO:0033523|GO:0016567|GO:0032020|GO:0016
874|GO:0019221|GO:0051437|GO:0000151|GO:0005634|GO:0051436|GO:0031145|GO:0005524|GO:0051439|GO:0
005829|GO:0005654|GO:0070936|GO:0000278|GO:0010390|GO:0042296 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_51994_PI430048170 0.2721637832801721.1379363671158 7.79749195869667 7.56070833191848
7.71265538713433 P P P 7.29910007938719 7.7368807206255 7.45081795821864 P P P
LNCV6_51994_PI430048170 mRNA
CACGACCCACATAAAATCTACGAGTTTGTGAACTCAGGAGTTGGGGACTTTTCCCAGCCA NM_001197123 RefSeq
chr19 - 49659568 49665875 IRF3 3661 "interferon regulatory factor 3, transcript variant 3"

GO:0097300|GO:0005515|GO:0050689|GO:0003700|GO:0034142|GO:0044212|GO:0006366|GO:0019221|GO:0045
351|GO:0005634|GO:0050715|GO:0042803|GO:0042802|GO:0005829|GO:0071888|GO:0002756|GO:0051607|GO:0
005737|GO:0060337|GO:0071359|GO:0016032|GO:0032481|GO:0043123|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136421_PI430048170 0.56916841612292 1.06437025355142 8.63300452436034
8.71854326457771 8.56622697357018 P P P 8.80387193679813 8.52501026181201 8.2742716022739
P P P LNCV6_136421_PI430048170 mRNA
AGATGCTAACCTCGACTGAAGACGCCTCCCTGTCTCCAGCAAAGAGTCCCCTCTATTTCT NM_001134888 RefSeq
chr14 - 100880654 100884847 RTL1 NA retrotransposon-like 1 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130391_PI430048170 0.0255943123506786 1.09545149251321 10.6144120121664
10.5882060115464 10.5545453655334 P P P 10.4549589641044 10.5035017907583 10.402999415033
P P P LNCV6_130391_PI430048170 mRNA
TTGTTTTTTGTTAACGTATTACTCAGAGTCACCCAAGCCTCTTGGCTGAGGGTGAAGGTG NM_152833RefSeq chr9
- 136114580 136118885 C9orf69 90120 "chromosome 9 open reading frame 69, transcript variant 1"
GO:0005515|GO:0008284|GO:0007049|GO:0005737|GO:0048524|GO:0016032|GO:0005634|GO:0016021|GO:0005
525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132629_PI430048170 0.0311253769709873 1.57382674725605 5.0202206695675
5.51345089827244 5.25882925166888 P P P 4.50098726349968 4.67794087314791
4.68544225615232 P P P LNCV6_132629_PI430048170 mRNA
AACTTCATTGAAAAAACCTAGCCCTGTACAGCTGCCCTTTTAAAGAGGTGGCCATTGCAG NM_001282062 RefSeq
chr16 - 30005513 30013596 DOC2A 8448 "double C2-like domains, alpha, transcript variant 1"
GO:0017158|GO:0005544|GO:0005515|GO:0043005|GO:0005215|GO:0030054|GO:0007268|GO:0030672|GO:0016
079|GO:0005764|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144364_PI430048170 0.2219359484716191.18123074469292 7.25438838437088
7.59503003932612 7.30177159922123 P P P 7.35871273112857 7.15015548663744
6.91094751537776 P P P LNCV6_144364_PI430048170 mRNA
TTTTGGAGATTAGACTATTTGGATTCATGTGTAGCTGCCCTGTCCCCTGGGGCTTTATCT NM_014257RefSeq chr19
+ 7763148 7769605 CLEC4M 10332 "C-type lectin domain family 4, member M, transcript variant 1"
GO:0010468|GO:0019062|GO:0009988|GO:0046790|GO:0005576|GO:0005537|GO:0019079|GO:0046872|GO:0006
897|GO:0035556|GO:0046968|GO:0005737|GO:0030369|GO:0030193|GO:0016020|GO:0019882|GO:0005887|GO:0
045087|GO:0019048|GO:0042605|GO:0007159|GO:0030246|GO:0004872|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137788_PI430048170 0.0769095773309865 0.6965204806904115.67153035776474
5.05558555040369 5.33847760263412 P P P 5.66489209582968 5.91781668527953
6.08371088457134 P P P LNCV6_137788_PI430048170 mRNA
TGTTTAGCAAGTGTTAGGTACTGTATTTGAACCAATAAATGTGAATCCTTCTGCACATGG NM_033334RefSeq chr9
- 124517274 124771310 NR6A1 2649 "nuclear receptor subfamily 6, group A, member 1, transcript
variant 1"
GO:0010467|GO:0005667|GO:0006367|GO:0007276|GO:0008283|GO:0003707|GO:0000122|GO:0007283|GO:0000
978|GO:0003677|GO:0042803|GO:0043565|GO:0001077|GO:0045944|GO:0043401|GO:0005654|GO:0008270|GO:0
004879|GO:0030522. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128081_PI430048170 0.5744394436039480.9505730725034828.62360279804737
8.67714039223328 8.90851046357858 P P P 8.69470263011814 8.76419247984437 8.9713539602527
P P P LNCV6_128081_PI430048170 mRNA
GAAGTCCTTACCTCTTTATATTGTTTGCAGGTTTAAATAAAACAGTGTGGTGCCATTTTG NM_144563RefSeq chr2
+ 88691657 88750935 RPIA 22934 ribose 5-phosphate isomerase A
GO:0004751|GO:0019693|GO:0005975|GO:0009405|GO:0044281|GO:0048029|GO:0006098|GO:0009052|GO:0043
231|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_134694_PI430048170 0.4838683607997430.8626946014823014.99893922926393
5.08908764525074 4.9082436096532 P P P 5.57341396449991 5.13253736130768
4.83959055491921 P P P LNCV6_134694_PI430048170 mRNA
TTCTCAGTAAGAAACTCGTGGAGGGGCTGTCCGCTCTGGTGGTGGACGTTAAGTTCGGAG NM_001113756 RefSeq
chr22 - 50525752 50530085 TYMP 1890 "thymidine phosphorylase, transcript variant 3"
GO:0009032|GO:0055086|GO:0044281|GO:0043097|GO:0001525|GO:0006220|GO:0004645|GO:0005161|GO:0030
154|GO:0005829|GO:0006260|GO:0016154|GO:0046135|GO:0006935|GO:0016763|GO:0006206|GO:0008083 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137343_PI430048170 0.8303108825485151.12273998806986 2.99896467524258
1.52285582450272 0.328072031566912P A A 2.0616589342542 1.32718549491337
2.04056704255852 A A A LNCV6_137343_PI430048170 mRNA
TTATGGTTAAAAGTGGGGGATGGGGTAAATTATGCTGCTTTAATTCCAGATGATGTTTTA NM_138335RefSeq chr4
- 44701794 44726634 GNPDA2 132789 "glucosamine-6-phosphate deaminase 2, transcript variant 1"
GO:0005737|GO:0004342|GO:0016787|GO:0005975|GO:0006044|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140865_PI430048170 0.1113175814403421.20709774955286 8.74875080743744 8.9778652316987
9.08755212292341 P P P 8.71224273228036 8.63726982249758 8.66946684843776 P P P
LNCV6_140865_PI430048170 mRNA
TAAAAAGAACTACCTTTGTTCTCTCCCATCCTGCTCAGGTCTTTTCAGCAGTCTCATCAT NM_032351RefSeq chr17
+ 38297022 38323218 MRPL4584311 "mitochondrial ribosomal protein L45, transcript variant 1"
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0005743|GO:0005840 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135832_PI430048170 0.0536243754508688 1.22492194806034 9.34522647896255
9.25819410431599 9.3366492601739 P P P 8.89512420242779 9.16842483747841
8.98649588640208 P P P LNCV6_135832_PI430048170 mRNA
AGAAGCGATGCTTTAGTGGCCTAACCCAGGGTCAAATACAGCTCTTTCTAGCAAAATCAG NM_003388RefSeq chr7
+ 74289474 74405943 CLIP2 7461 "CAP-GLY domain containing linker protein 2, transcript variant 1"
GO:0005881|GO:0051010|GO:0005875|GO:0035371 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132862_PI430048170 0.0102679287964986 0.75776770817605710.3655562167431
10.1782663225179 10.1589613154242 P P P 10.6085791839484 10.7208165477761
10.5791548433557 P P P LNCV6_132862_PI430048170 mRNA
TTCTTTCTGCTTCTAAGACTTTGCCAAATGCCCTGGGTCTAAGAAAGAAAGAGACCCGCT NM_173481RefSeq chr19
+ 751145 764318 MISP 126353 mitotic spindle positioning
GO:0007067|GO:0005886|GO:0003779|GO:0005856|GO:0005938|GO:0005925|GO:0051301|GO:0043231 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130178_PI430048170 0.1517321079478741.06982597408677 0.488175289517777
0.44693603349247 0.530500289676236A A A 0.3107471009930850.390659248721894
0.468951654623861A A A LNCV6_130178_PI430048170 mRNA
GAGCTGAAGGTCGCCATGAAGAAGACTTGCTTCACCAAACTCTTTCCACAGAACTGCTGA NM_001004466 RefSeq
chr19 + 15794048 15794996 OR10H5 NA "olfactory receptor, family 10, subfamily H, member 5"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140174_PI430048170 0.0595230125666648 0.5684237765332244.15324287256788
3.92344253984671 4.1032132410104 P P P 4.4539466145789 4.86358285229667
5.21730601621443 P P P LNCV6_140174_PI430048170 mRNA
TAGAAACTGGCTTCTTGTCATCATTTCAACATCCACTCAAACGCTCACCCCTGAAAGTGG NM_018340RefSeq chr16
- 12659798 12803887 CPPED155313 "calcineurin-like phosphoesterase domain containing 1, transcript
variant 1" GO:0005737|GO:0016311|GO:0004721|GO:0046872|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131129_PI430048170 0.7999219702717050.7736307262858170.627761682199999

0.8905665393734891.16154343630256 A A A 0.6290581407768742.1465272266717
0.390682908424738 A A A LNCV6_131129_PI430048170 mRNA
CTAGCAAACCAGATAAGAAAAGATGTTAATGCCCATTCCCTAACTTATGTCTTAGACCAA NM_207469 RefSeq chr20
+ 257735 261095 DEFB132 NA "defensin, beta 132" NA . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_132671_PI430048170 0.1945786593938581.16278975519748 9.38272928003649
9.45917342006474 9.45937208574574 P P P 8.98771735927742 9.23187424646361
9.40068389801569 P P P LNCV6_132671_PI430048170 mRNA
GGCGAGACGCAGCTTTGTCCTGGGAGACGTTCATATTGGAATCTATTTAACTGCTAAAGA NM_018216 RefSeq chr1
- 2508530 2526628 PANK4 55229 pantothenate kinase 4
GO:0004594|GO:0016310|GO:0005737|GO:0015937|GO:0005524 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144576_PI430048170 0.2097177759633360.6406930780967526.97880349015765
5.98485616655067 6.31781829020581 P P P 6.52812160466436 7.60335385139857
7.06041132706712 P P P LNCV6_144576_PI430048170 mRNA
GGGCCACCTTCAACACCTGTCTTCTTGTTTCTAACATGTACTTTCTAATAATCTCTTACT NM_001080835 RefSeq chr2
- 240041812 240042982 PRR21 643905 proline rich 21 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145580_PI430048170 0.0260051026331197 2.8049991936601 1.48967377242219
2.34005431678082 1.86396348598607 A A A 0.5164976461201810.412456374324954
0.424929431518713 A A A LNCV6_145580_PI430048170 mRNA
ATCAGTTGCAGGTGCCAATGACTAACTTTTTGAATTCTATGTTGGCATTAACAATAAAGC NM_000624 RefSeq chr14
+ 94581368 94593120 SERPINA5 5104 "serpin peptidase inhibitor, clade A (alpha-1 antiproteinase,
antitrypsin), member 5"
GO:0097181|GO:0097182|GO:0004867|GO:0097183|GO:0007283|GO:0005539|GO:0002020|GO:0032190|GO:0005
615|GO:0036024|GO:0036025|GO:0036026|GO:0031091|GO:0031094|GO:0008201|GO:0002080|GO:0070062|GO:0
031210|GO:0005576|GO:0036029|GO:0036028|GO:0036027|GO:0010951|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136847_PI430048170 0.0224582940526081.07001319466259 0.385574609268763
0.3757847586925070.322713515064027 A A A 0.24645442300897 0.300917647450656
0.243882443522072 A A A LNCV6_136847_PI430048170 mRNA
GTCAAATGAAACAAGCTCTTGTGTAAATAGACTTCTGTGCCTAATAGTGACATTGTTTCA NM_004709 RefSeq chrX
+ 145827409 145829852 TMEM257 9142 transmembrane protein 257
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143204_PI430048170 0.00210974670629222 1.66643338611699 10.6820370032811
10.8064277140719 10.9238459304306 P P P 9.92307369140516 10.1833232393054
10.0937443401714 P P P LNCV6_143204_PI430048170 mRNA
TTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGATGTGGCTCAGTTTC NM_024006 RefSeq chr16
- 31090853 31094955 VKORC1 79001 "vitamin K epoxide reductase complex, subunit 1, transcript
variant 1"
GO:0060348|GO:0017187|GO:0048038|GO:0017144|GO:0007596|GO:0005789|GO:0016021|GO:0047057|GO:0044
267|GO:0042373|GO:0055114|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135900_PI430048170 0.0188268292126078 3.3232469083216 2.52012982431565
1.71864723230314 1.85402950255489 A A A 0.3075122670799810.298478045617036
0.418894793407615 A A A LNCV6_135900_PI430048170 mRNA
AGACACTCCTGCATGTCTTTCTGCTTCTGGGGTGTGGTTCCAGAACCGCAGGACCAAGTG NM_152568 RefSeq chr8
- 41646309 41647359 NKX6-3 157848 NK6 homeobox 3
GO:0043565|GO:0002067|GO:0006355|GO:0030857|GO:0001709|GO:0005634|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_133597_PI430048170 0.4965588346501930.8388941527765250.332709699717821
0.2819926831344560.394451215885535A A A 0.2886845124292741.04827932168271
0.296190605262257A A A LNCV6_133597_PI430048170 mRNA
GACACTACTGATGTCTGTCATACAGTTATTCTTCAGAAGTTCTCTGAGATGTCAAATATA NM_014178RefSeq chr14
- 24809654 25049889 STXBP6 29091 "syntaxin binding protein 6 (amisyn), transcript variant 1"
GO:0045920|GO:0005737|GO:0035542|GO:0016021|GO:0016192 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144088_PI430048170 0.3604204523501830.7001303236704480.398960577175476
0.4040789306475290.341872110362846A A A 0.43265765653647 0.4568832310592711.5166421122841
A A A LNCV6_144088_PI430048170 mRNA
CTTTTTGATCTTGTGCTATGAAACAATCTTCCAAAGAACTGTATAAGGTGGTCATAAGTG NM_000550RefSeq chr9
+ 12693385 12710266 TYRP1 7306 tyrosinase-related protein 1
GO:0005515|GO:0033162|GO:0042470|GO:0046982|GO:0005507|GO:0043438|GO:0032438|GO:0030318|GO:0042
803|GO:0042438|GO:0016021|GO:0016716|GO:0030669|GO:0010008|GO:0055114 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134310_PI430048170 0.1617819966690221.1044434945695 0.581303678828788
0.3587983862232520.535081988083031A A A 0.2812826149417970.388231609406592
0.382646596560787A A A LNCV6_134310_PI430048170 mRNA
CATTGCTTACTGTAAAGAGTCCAGGTAACTGACTTTATTCAGTTACTTCCTGTTCAATAA NM_000843RefSeq chr5
- 178978328 178995123 GRM6 NA "glutamate receptor, metabotropic 6" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_144697_PI430048170 0.0648450758947365 1.52863383341047 7.77556956979456
8.38670742720534 7.91046624871872 P P P 7.53268228878896 7.52572098464112
7.23116404789611 P P P LNCV6_144697_PI430048170 mRNA
ACTGGCCTTGGTCACTTTGTATTTCTGTCTTGGTTGGAAATACCATCAGCCTTCCTTGCTNM_001198721 RefSeq chr22
+ 44676807 44737681 PRR5 55615 "proline rich 5 (renal), transcript variant 6"
GO:0007049|GO:0001934|GO:0014068|GO:0031932 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142153_PI430048170 0.0079472577823846 1.15381859960123 0.759845974483735
0.8160275663944680.793885480960978A A A 0.6422080372083530.549014573390948
0.557997685213374A A A LNCV6_142153_PI430048170 mRNA
CTTCCAGGCACTTGGACACTAAAATCTACTATGTAGGTGCAAACTATTTTTCTCTTTTCTNM_023014RefSeq chr1 +
12857085 12861909 PRAMEF2 65122 PRAME family member 2
GO:0043066|GO:0008284|GO:0048387|GO:0045596|GO:0042974|GO:0045892 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_114216_PI430048170 0.9019432051341621.01977527582483 2.57923611504697
2.85507300917104 3.64230024119146 A A P 3.02254503907784 3.08823179076449
3.09917663024611 P P P LNCV6_114216_PI430048170 mRNA
ATATCCCTTTGCCAGACATCAGTCAGCTGAGTTTACCATCAGCTATGATAATGAGAAGGA NM_173674RefSeq chr6
+ 117482656 117569857 DCBLD1 285761 "discoidin, CUB and LCCL domain containing 1"
GO:0070492|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126914_PI430048170 0.8884488374661141.14481328063784 2.07672337561146
0.6872542294745860.543502152412901A A A 1.60665889249593 0.531338537750749
0.905972236371775A A A LNCV6_126914_PI430048170 mRNA
GACATGAGCCATTTGAGGGGAGAGGGAACGGAAATAAAGGAGTTATTTGTAATGACTAAA NM_004304RefSeq
chr2 - 29192773 29921611 ALK238 anaplastic lymphoma receptor tyrosine kinase
GO:0005515|GO:0008283|GO:0042981|GO:0018108|GO:0005524|GO:0038061|GO:0043234|GO:0000187|GO:0007
165|GO:0016310|GO:0004704|GO:0051092|GO:0046777|GO:0048666|GO:0005887|GO:0004713|GO:0004714|GO:0
007169|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138668_PI430048170 0.0182871222495841 0.3052408577305362.49195747955455

2.31907301547723 3.1912619262993 A A P 4.40061227109173 4.34279259135298
4.54159640484945 P P P LNCV6_138668_PI430048170 mRNA
CTTGAAAGAAAATACCAAGGAACAGGAAACTGATCATTAAAGCCTGAGTTTGCTTTCAAA NM_001735 RefSeq chr9
- 120952335 121050276 C5 727 complement component 5
GO:0005515|GO:0030449|GO:0004866|GO:0005615|GO:0006957|GO:0010760|GO:0000187|GO:0006956|GO:0006
954|GO:0050921|GO:0006935|GO:0005579|GO:0006958|GO:0019835|GO:0090197|GO:0070062|GO:0008009|GO:0
002523|GO:0006950|GO:0006874|GO:0005102|GO:0005576|GO:0042593|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_52890_PI430048170 0.2550288057537481.1185955792375 5.31734537688063 5.47734829125585
5.61041005120573 P P P 5.31536189684505 5.45375054698388 5.14980523252885 P P P
LNCV6_52890_PI430048170 mRNA
GTGTCCCAGCTTGCCCGCCCAAGGGCCCAGGCGACGTTCCGCTGTCCCCTGGAGCTCCCT NM_001144936 RefSeq
chr11 - 63759891 63768641 C11orf95 65998 chromosome 11 open reading frame 95 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_131977_PI430048170 0.0547111996805490.7801372906898611 1.4086687006628
11.3307277546843 11.5234449120207 P P P 11.6916488046738 11.6519739406036
11.9779668172263 P P P LNCV6_131977_PI430048170 mRNA
ACCTGTATCCACTATTAGGAGGTAAAAATCAATAAAATGGCCCATTCATTTGTGTTGTAG NM_173614 RefSeq chr16
+ 16232594 16294811 NOMO2 NA "NODAL modulator 2, transcript variant 2" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_108710_PI430048170 0.1408403542377571.23798843270814 12.6487877046776 13.091307910673
12.9868582710726 P P P 12.4636114738658 12.6591215100599 12.705128075871 P P P
LNCV6_108710_PI430048170 mRNA
CCCTCAGTTGTCCTATTCCTTCCTAGCTTCCCTGCAATAAAATCAAGCTGCTTTTGTTGG NM_004045 RefSeq chr5
- 151742821 151758649 ATOX1 475 antioxidant 1 copper chaperone
GO:0032767|GO:0006878|GO:0005507|GO:0005375|GO:0035434|GO:0016531|GO:0016530|GO:0006979|GO:0000
302|GO:0006825|GO:0015680|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126933_PI430048170 0.4142830883783971.014652606459 0.333791783925383
0.3134207933536720.265549834726014 A A A 0.285377658452720.289572563245385
0.27566746583859 A A A LNCV6_126933_PI430048170 mRNA
CTGTGCTTTGTCCATAGGTTGATTCTACAATCTGAAAATCAATAAACAGCATTTGCATGA NM_014336 RefSeq chr17
- 6423736 6435199 AIPL1 23746 "aryl hydrocarbon receptor interacting protein-like 1, transcript
variant 1"
GO:0005515|GO:0018343|GO:0043066|GO:0007603|GO:0005634|GO:0001918|GO:0001917|GO:0005737|GO:0001
895|GO:0006457|GO:0051082|GO:0007601|GO:0030823 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116175_PI430048170 0.1708739089195250.7408953232176740.398313061930352
0.3655355882222860.396009109146474 A A A 0.746121541116503 0.482805096202008
1.14998378335741 A A A LNCV6_116175_PI430048170 mRNA
GTGCAAGAGGAAAACCAAGCAGTGTCTTCTACGTGGCAGAAATAAAGCCTATGACTAATC NM_173526 RefSeq chr14
+ 67189392 67228550 FAM71D 161142 "family with sequence similarity 71, member D"
GO:0005737|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145141_PI430048170 0.0593427480625845 0.7153748108564861 0.6498272435555
10.8359847167282 10.3314150520651 P P P 11.1974399208129 11.202931490603
10.8890835914412 P P P LNCV6_145141_PI430048170 mRNA
GTCTACCATGGGGCCCAGGAGTTGGGGAAACACAATAAAGGTGGCATACGAAGGAAAAAA NM_001166237
RefSeq chr8 + 143553386 143563061 GSDMD 79792 "gasdermin D, transcript variant 2" GO:0031668
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124463_PI430048170 0.00386515030621709 0.7034949800251381 1.1609729047717
11.0497697207991 10.9751088810399 P P P 11.693172713126 11.5185774294064

11.4940737045534 P P P LNCV6_124463_PI430048170 mRNA
AAGGATCCACTGGGTGAATCCTCCCTCTCAGAACCAATAAAATAGAATTGACCTTTTAGA NM_001303007 RefSeq
chr6_GL000256v2_alt - 3026332 3029561 DDAH2 23564 "dimethylarginine
dimethylaminohydrolase 2, transcript variant 1"
GO:0005515|GO:0005813|GO:0043066|GO:0007263|GO:0003824|GO:0006809|GO:0045429|GO:0005739|GO:0005
737|GO:0000052|GO:0006527|GO:0016597|GO:0016403|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127411_PI430048170 0.523743102996997 0.674837041596587 0.411239659565722
0.317053417886363 0.468561074743805 A A A 1.77973402602452 0.310476801736051
0.255028700786784 A A A LNCV6_127411_PI430048170 mRNA
GCTGCACTTACCATTTGTCATATGATGGCACTTGACTACATATGGCTTTAGAAATAAAAT NM_032735 RefSeq chr12
- 69653608 69699416 BEST3 144453 "bestrophin 3, transcript variant 1"
GO:0043271|GO:0008150|GO:0003674|GO:0005886|GO:0034707|GO:0005254 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143645_PI430048170 0.00451233111987345 0.661296338344694 7.5875863942287
7.4967037426146 7.42834272345701 P P P 8.0346519808195 8.2460845277433
8.01464327130718 P P P LNCV6_143645_PI430048170 mRNA
CAGCATCAAAATGTGGTGTTCTTGTTAAGTAATTGATCGTGGTCTTTGCTTTAATCTTAG NM_018396 RefSeq chr7
+ 128476728 128502924 METTL2B 55798 methyltransferase like 2B GO:0016427|GO:0030488 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133009_PI430048170 0.318616508073639 1.39874623217929 3.23815839642864 3.2287782175233
3.25656549220876 P P P 1.69117210576711 2.95124843437368 3.21993029467212 A P P
LNCV6_133009_PI430048170 mRNA
ACTCTTCCAGAAACCTTAGAGCAGATGCAGAAAGTGAAATGGTTCAGATCTGGGAAAAAA NM_003059 RefSeq chr5
+ 132294451 132344206 SLC22A4 6583 "solute carrier family 22 (organic cation/zwitterion transporter),
member 4"
GO:0005515|GO:0007589|GO:0015695|GO:0005886|GO:0015491|GO:0015697|GO:0030165|GO:0055085|GO:0015
651|GO:0005524|GO:0005739|GO:0016324|GO:0000166|GO:0005887|GO:0006641|GO:0008513|GO:0015879|GO:0
006814|GO:0009437|GO:0015226|GO:0015293 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_140381_PI430048170 0.132186558568759 0.831249047495374 6.42613476649653
6.37503786697796 6.74169370990851 P P P 6.77754293771497 6.75286564509319
6.83899129517916 P P P LNCV6_140381_PI430048170 mRNA
ATCCCTTATTTCTTATCTTATTCTGATTCTGGCCATGCTACAAACATGTTCTCACCTGCC NM_001346 RefSeq chr3
- 186147200 186362234 DGKG 1608 "diacylglycerol kinase, gamma 90kDa, transcript variant 1"
GO:0005886|GO:0005509|GO:0030168|GO:0005524|GO:0007205|GO:0043231|GO:0035556|GO:0007165|GO:0016
310|GO:0005737|GO:0003951|GO:0048666|GO:0007596|GO:0004143 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136475_PI430048170 0.615545548931173 0.929490565493647 0.348803424954984
0.534155421043889 0.410340109526871 A A A 0.823598154684176 0.380349148884392
0.363335573297934 A A A LNCV6_136475_PI430048170 mRNA
CCAGTTTTGACAGGTCAGATTTTCATATGTATAGGTATAAATAGCCAACACTCAGTGAAC NM_130446 RefSeq
chr3 - 183487530 183555711 KLHL6 89857 kelch-like family member 6 GO:0050853|GO:0002467
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102378_PI430048170 0.465329209386153 1.4030347926849 1.5676570688528
0.40009940751915 0.287568826174671 A A A 0.482707361786809 0.375259121430187
0.297227715862341 A A A LNCV6_102378_PI430048170 mRNA
ATGTGTGAGGCCTTTTATTGTGAGAGTGGACAGACATCCGAGATTTCAGAGCCCCATATT NM_000280 RefSeq
chr11 - 31784791 31811353 PAX6 5080 "paired box 6, transcript variant 1"

GO:0005515|GO:0004842|GO:0000790|GO:0003700|GO:0006366|GO:0000981|GO:0001654|GO:0001755|GO:0000
132|GO:0007224|GO:0003309|GO:0021796|GO:0003690|GO:0021798|GO:0007411|GO:0021797|GO:0022027|GO:0
009887|GO:0019901|GO:0023019|GO:0001709|GO:0021549|GO:0003322|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133440_PI430048170 0.6671610160457 1.20064461638268 1.53043994431624
1.34448756794828 2.48168626074838 A A A 1.43494939862339 1.67820842869907
1.70888232907811 A A A LNCV6_133440_PI430048170 mRNA
CCCTGCTACTGGCTTTATTGCAATATTTATTTTCATCTACAATAGTTGCACATCTACTCA NM_024859 RefSeq chrX
+ 49162842 49168156 MAGIX 79917 "MAGI family member, X-linked, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139256_PI430048170 0.0169902945640238 0.609709015592872 5.83401272794471
5.80865851207343 6.01519814395745 P P P 6.34167661598777 6.6607035964332
6.77205221988282 P P P LNCV6_139256_PI430048170 mRNA
TTACTTAAGGTTATGGAGTAAACTAGCTTGGACCTTGGGCTGCAGGACGACTAGGATTCA NM_030571 RefSeq
chr5 + 142108758 142154443 NDFIP1 80762 Nedd4 family interacting protein 1
GO:0005515|GO:0048302|GO:0045732|GO:0048471|GO:0032713|GO:0032410|GO:0002761|GO:0048294|GO:0042
130|GO:0006879|GO:0045619|GO:0002829|GO:0031398|GO:0004871|GO:0043123|GO:0005938|GO:0050699|GO:0
005576|GO:0051224|GO:0007165|GO:0000139|GO:0050728|GO:0010629|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_62592_PI430048170 0.2944946411359681.27863427723119 2.12897762791457 1.66880573193241
2.45569216365735 A A A 1.81667561070729 1.78577100185343 1.69026525627503 A A A
LNCV6_62592_PI430048170 mRNA
TTCTATACGGAGCTGCTTCGGAAGAAGGTGGACACTCAGCCAGGGGCGGCCGGTGAAGCA NM_003933 RefSeq
chr16 + 1334503 1349441 BAIAP3 8938 "BAI1-associated protein 3, transcript variant 1"
GO:0007186|GO:0008022|GO:0007269 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135137_PI430048170 0.4375494136473440.8031982274781420.284280732581384
0.2897212480200640.434652244556571 A A A 0.3524671698896060.301195344094898
1.14532529681882 A A A LNCV6_135137_PI430048170 mRNA
GATTCAGTTCAAGGTCCTGAAAAAAGAAAAACATTTTACTCTGTGTACCTTGTGTCTTTC NM_021010 RefSeq chr8
- 7055299 7056739 DEFA5 1670 "defensin, alpha 5, Paneth cell-specific"
GO:0030133|GO:0005796|GO:0045087|GO:0050832|GO:0031640|GO:0019731|GO:0005576|GO:0005615|GO:0034
774 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136407_PI430048170 0.0788386712298474 1.56157795380311 3.39828464668296
3.36790883063968 3.83764256502068 P P P 2.51703581209232 2.81869025254026
3.28380801117043 A P P LNCV6_136407_PI430048170 mRNA
GTGGCTGTATTTTTTGTATACCGATTTCTGGATGGAATGCACACTGTTATCTGTTTAGTT NM_001361 RefSeq chr16 +
72008743 72025417 DHODH 1723 dihydroorotate dehydrogenase (quinone)
GO:0048039|GO:0007565|GO:0043065|GO:0044205|GO:0042493|GO:0010181|GO:0005743|GO:0055086|GO:0044
281|GO:0090140|GO:0005739|GO:0046134|GO:0042594|GO:0031000|GO:0007595|GO:0008144|GO:0031304|GO:0
043025|GO:0004152|GO:0005654|GO:0016021|GO:0006207|GO:0006206|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137364_PI430048170 0.5659702063933481.09730074692204 8.80751957740764
9.24525110314095 9.35915691622049 P P P 9.08639947847415 8.89752335930417
9.07517025399854 P P P LNCV6_137364_PI430048170 mRNA
TGAGAAATAAAAACACATCTTGGGAAGTGGGAATCCTGGAGTTTATGCCATTTGCAATAT NM_001135674 RefSeq
chr8 + 42541621 42552997 SMIM19 114926 "small integral membrane protein 19, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145237_PI430048170 0.0369767267898370.8244597474997849.75754374418234
9.70392139079138 9.93225617163572 P P P 10.0400122986694 10.0032577866013

10.1891008477107 P P P LNCV6_145237_PI430048170 mRNA
GGAAGACTCTCACTGTAAAAACAGCTGTAGGTATAATGTATATTCCCAGAGAATTGTATT NM_178868 RefSeq chr3
+ 32238678 32370321 CMTM8 152189 CKLF-like MARVEL transmembrane domain containing 8
GO:0005737|GO:0006935|GO:0005634|GO:0016021|GO:0005615|GO:0005125 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137397_PI430048170 0.6077153113879430.82698994471158 1.6428602711096
0.3801308792282110.322406701705448 A A A 0.371156431640587 1.64293649599671
1.29012789150503 A A A LNCV6_137397_PI430048170 mRNA
GCAAAGCAGCTCAACAAGAGAAAAAGCTCTAGTTATAGGGCTTAAATTGATTTCTATTTC NM_012416 RefSeq chr9
- 6011018 6015640 RANBP6 26953 "RAN binding protein 6, transcript variant 1"
GO:0005515|GO:0005737|GO:0005634|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137415_PI430048170 0.993831696953317 1.00308968827841 0.555938991552712
0.4118455245375290.245311343864381 A A A 0.365632446979222 0.439195983408292
0.410654070718282 A A A LNCV6_137415_PI430048170 mRNA
TATATGCTGGTACATGCTTTAAACATGGAGGTAACCCCACACGAGACATTCAGTGACAGG NM_014981 RefSeq chr3
- 108380368 108529322 MYH15 22989 "myosin, heavy chain 15"
GO:0005516|GO:0032982|GO:0003774|GO:0008152|GO:0003779|GO:0030016|GO:0005524 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127058_PI430048170 0.11199406806913 0.5452321674620250.431574111380458
0.43076359384988 1.53648456629144 A A A 1.82598319600744 2.1038106512657
1.27642857398892 A A A LNCV6_127058_PI430048170 mRNA
TGAATTTCTCAAGCCATTAGGAGAGAGAGAAATTGGGAGTGGTCCCCAAAGACCCTTCAA NM_175834 RefSeq chr12
- 52821446 52834293 KRT79 338785 "keratin 79, type II"
GO:0005198|GO:0045095|GO:0019899|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123590_PI430048170 0.90273559732265 1.06585191453465 2.98375122588999 1.1841801963735
2.57846965029329 A A A 2.14343543409811 2.57417983869111 2.25827508814207 A A A
LNCV6_123590_PI430048170 mRNA
ACAAAGAGAAATTCCTGCCAGACAATCCCGAAGAAGATTTCGGAAAATTAACTATAAAGG NM_001164386 RefSeq
chr5 - 131423920 131635236 RAPGEF6 51735 "Rap guanine nucleotide exchange factor (GEF) 6,
transcript variant 1"
GO:0005515|GO:0070300|GO:0005886|GO:0030033|GO:0007265|GO:0030139|GO:0032854|GO:0072659|GO:0043
087|GO:0005829|GO:0005085|GO:0016324|GO:0030742|GO:0017016 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_126552_PI430048170 0.3259908251089661.06419972654151 14.7414763789164
14.7012409326551 14.8770845443472 P P P 14.6134662335807 14.6316618333344
14.8035780367698 P P P LNCV6_126552_PI430048170 mRNA
AAGCGAATGCGCAGGCTGAAGCGCAAAAGAAGAAAGATGAGGCAGAGGTCCAAGTAAACC NM_001035267
RefSeq chr12 + 56116589 56117832 RPL41 6171 "ribosomal protein L41, transcript variant 2"
GO:0010467|GO:0003735|GO:0003723|GO:0006614|GO:0019083|GO:0019058|GO:0006415|GO:0006412|GO:0006
413|GO:0005829|GO:0006414|GO:0000184|GO:0016032|GO:0022625|GO:0044267 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141089_PI430048170 0.2033971720816570.7506655290891434.17886360309976
3.64585543718641 3.49951231230737 P P P 4.34311925443189 4.41656470758465
3.82957966337618 P P P LNCV6_141089_PI430048170 mRNA
AAGAGAAAGGGTGACCCCTTGGTCTCCAGGAAGGAGAAGAAGCAGCGTTGTAGCCAGTAG NM_001099338
RefSeq chr10 + 87225447 87234976 NUTM2A NA NUT family member 2A NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_142161_PI430048170 0.2732411623719220.8563737104314247.80972151162725 8.1100122091806
8.34618977371546 P P P 8.23314245401421 8.24481968485869 8.49336973352469 P P P

LNCV6_142161_PI430048170 mRNA
CTTTTGTTTCCTAAGAGATAATGGCATGGTTTCATATGTTATACTTTGGACAGACAGAGT NM_020197 RefSeq chr1
+ 214281221 214337134 SMYD2 56950 SET and MYND domain containing 2
GO:0005515|GO:0008285|GO:0010452|GO:0000993|GO:0006325|GO:0018027|GO:0005634|GO:0000122|GO:0018
026|GO:0016279|GO:0046872|GO:0006351|GO:0005829|GO:0002039|GO:0005737|GO:0046975|GO:0005654|GO:0
043516 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136492_PI430048170 0.0395290112753469 0.5056556032842473.12131314028137
2.38960301634621 3.0375074200074 P A P 3.75866774952677 3.98604877486097
3.85082908732902 P P P LNCV6_136492_PI430048170 mRNA
TTTGAGGGGGTAGGAGGAGGGAGAAACAGCCTGTGTTTTTTATGCAATAAAGTCATCAAC NM_001258248 RefSeq
chr17 - 47844913 47851150 SP6 NA "Sp6 transcription factor, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136446_PI430048170 0.00362252452953756 0.6078225778499798.65516247438962
8.35162693052553 8.50680092588457 P P P 9.1377198135973 9.18750854227336
9.35045927123232 P P P LNCV6_136446_PI430048170 mRNA
GCATCCATGTCAGTGGTGCTATGCTGGTTACAACTTGAGATTTTTGAAATAAAAAATTTG NM_014872 RefSeq chr9
- 37438102 37465410 ZBTB5 9925 zinc finger and BTB domain containing 5
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_57109_PI430048170 0.0324407457374972 0.8131479261761513 13.1657830538451
13.1193406127831 13.2726783064926 P P P 13.4259985497632 13.3966697527244
13.6239283448425 P P P LNCV6_57109_PI430048170 mRNA
ATGTAGGTTCGTGTCGTCGTTGGCTCTGAGACATTGATAATAAATTTTTCTCAACAGTGA NM_001194997 RefSeq
chr11 - 3000921 3057451 CARS 833 "cysteinyl-tRNA synthetase, transcript variant 5"
GO:0006423|GO:0005515|GO:0010467|GO:0005737|GO:0000049|GO:0004817|GO:0005524|GO:0046872|GO:0042
803|GO:0006418|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142752_PI430048170 0.00415471372028738 1.59126946843903 9.04954759365305
9.20242400706745 9.01503948462322 P P P 8.50144896479369 8.49934975912679
8.24825532548195 P P P LNCV6_142752_PI430048170 mRNA
CCAGCTTGTGGTAACTTACTGTCACATAGCTCTGACGTTTTGTTGTAATAAATGTTTTCA NM_018438 RefSeq chr1
+ 11664092 11674352 FBXO6 26270 F-box protein 6
GO:0005515|GO:0006986|GO:0004842|GO:0016567|GO:0031146|GO:0030433|GO:0005737|GO:0001948|GO:0006
281|GO:0006508|GO:0006516|GO:0030246|GO:0000077|GO:0019005 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_131489_PI430048170 0.3330141942080190.8667391270528250.250385956753692
0.3436292554388680.2797614497391 A A A 0.7810374931387440.366036981271553
0.298576892876038 A A A LNCV6_131489_PI430048170 mRNA
GGACTGCAATATCAACAACAAGTTGTTTCAAACAGCATCAAAATACAACTTCATTGCTAC NM_021815 RefSeq chr2
+ 107986513 108013983 SLC5A7 60482 "solute carrier family 5 (sodium/choline cotransporter), member 7,
transcript variant 1"
GO:0033265|GO:0015220|GO:0005886|GO:0008292|GO:0015871|GO:0007268|GO:0007274|GO:0055085|GO:0007
269|GO:0007271|GO:0043025|GO:0005307|GO:0016021|GO:0006814 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142889_PI430048170 0.4546784660115211.15837670819764 8.3544487811692 8.7788818346947
9.04058069683397 P P P 8.57704153958705 8.3446793179073 8.67722527095402 P P P
LNCV6_142889_PI430048170 mRNA
CCTGTGACTGATTCACAGAGGCATTTTGTGTGTGTGTGCTTATTTTAATTTTGTTCTTAT NM_001276722 RefSeq chr11
+ 36594492 36659291 C11orf74 119710 "chromosome 11 open reading frame 74, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_135662_PI430048170 0.0354900782788327 0.6332205184687948.25309943704808
8.28930362146004 8.60166655905503 P P P 8.90923827357333 8.83176157104648
9.35077140970371 P P P LNCV6_135662_PI430048170 mRNA
CTGTTTGTTTACCCGTTCTTCTTTGGCTGTATCTGATGACAGTATAAGATGTTCTTAATA NM_001303411 RefSeq chr18
- 35989823 36067594 RPRD1A 55197 "regulation of nuclear pre-mRNA domain containing 1A,
transcript variant 2" GO:0070940|GO:0016591 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139104_PI430048170 0.4084559416712280.5301829853809420.500077294874805
0.4680007346219010.252149327705934A A A 0.3989107014730152.27112807211642
0.461826339970172A A A LNCV6_139104_PI430048170 mRNA
CTCTCTGAGTAAAAACTCATACATGCAGAAAATTGTCTTTGCTCGAAATGATAATGCCAA NM_144649RefSeq chr8
- 132709945 132760668 TMEM71 137835 "transmembrane protein 71, transcript variant 1" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140006_PI430048170 0.000480960026616374 0.1472373126028018.05338036820484
7.71145165727167 8.15127519418178 P P P 10.4532987604586 10.6347186481907
11.0812930190756 P P P LNCV6_140006_PI430048170 mRNA
GCTATCTGTGCAGCAGTTTCTCTACAGTTGTGCATAAATGTTTTTACTATAAAATGAGCT NM_001256910 RefSeq
chr10 + 68956439 68985069 DDX21 9188 "DEAD (Asp-Glu-Ala-Asp) box helicase 21, transcript variant
2"
GO:0004004|GO:0003725|GO:0016020|GO:0008152|GO:0005730|GO:0005634|GO:0009615|GO:0043330|GO:0005
524|GO:0001649 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126905_PI430048170 0.8810721298299590.9644679463802337.38438300576514
7.26368187655766 7.53653527256466 P P P 7.06206611128345 7.54712460410774 7.6753191431303
P P P LNCV6_126905_PI430048170 mRNA
GCTAACGTTAAATGCTGCTATACAACTGCTTTGCAACAGTTGCTGGTATATTTAAATCAT NM_001178083 RefSeq
chr11 + 44095548 44245430 EXT2 2132 "exostosin glycosyltransferase 2, transcript variant 3"
GO:0005783|GO:0015012|GO:0044281|GO:0015014|GO:0046872|GO:0030154|GO:0042803|GO:0033692|GO:0030
203|GO:0070062|GO:0008375|GO:0050508|GO:0050509|GO:0005794|GO:0001707|GO:0046982|GO:0005975|GO:0
016757|GO:0015020|GO:0006024|GO:0007165|GO:0001503|GO:0000139|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130119_PI430048170 0.00257060519487912 0.2568477595259017.57915261148499
6.91186589699179 7.13540284650821 P P P 8.7689302964069 9.229925293978
9.49992193875368 P P P LNCV6_130119_PI430048170 mRNA
GTTTGGACCACATCTCTTTGGAAAATAGTTTGCAACATATTTAAGAGATACTTGATGCCA NM_005242RefSeq chr5
+ 76819007 76835315 F2RL1 2150 coagulation factor II (thrombin) receptor-like 1
GO:0005515|GO:0043311|GO:0070963|GO:0046330|GO:0050900|GO:0060100|GO:0046328|GO:0051607|GO:0046
329|GO:0030836|GO:0031274|GO:0070374|GO:0043123|GO:0090195|GO:0043122|GO:2000484|GO:0090198|GO:0
072608|GO:0031681|GO:0030335|GO:0005794|GO:0004930|GO:0050702|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132874_PI430048170 0.5186621183217020.9457595071983430.464410022388038
0.5042212127410540.422572640018419A A A 0.4408375926561830.728172459580255
0.445555536460981A A A LNCV6_132874_PI430048170 mRNA
CGTGTTCTGTTGGGGATAAAATTGCACAATAAATGTCAAGTCTCTGTTAAGTGTTTTAAC NM_207406RefSeq chr4
- 42110852 42152878 BEND4 389206 "BEN domain containing 4, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139442_PI430048170 0.1186853858061230.7429993778494415.5634349336399
15.0530981811772 15.0049989504239 P P P 15.7591531891094 15.7757562677193
15.4128153689741 P P P LNCV6_139442_PI430048170 mRNA
CGGCGGCTGAATCTAAGAATACGCGGTCTCCTGAGAACTTCAAAAAACAAAAACAAAAAA NM_003542RefSeq
chr6 + 26103947 26104337 HIST1H4C 8364 "histone cluster 1, H4c"

GO:0005515|GO:0010467|GO:0006325|GO:0005634|GO:0045653|GO:0000723|GO:0000183|GO:0000786|GO:0070062|GO:0035574|GO:0035575|GO:0046982|GO:0006334|GO:0006335|GO:0005576|GO:0006336|GO:0000228|GO:0003677|GO:0032776|GO:0034080|GO:0043234|GO:0016020|GO:0045814|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128657_PI430048170 0.6025728204426561.01707567198829 0.438442791795741 0.4845516702906920.447006236326049A A A 0.3793836352813720.403378079289132 0.510946226719659A A A LNCV6_128657_PI430048170 mRNA GTGAAACTCGACTAACTTTGGCCTTTGTGTATTTCCTGAAGGTAATATTGTTAACTGTTA NM_198956RefSeq chr7 - 20782273 20786889 SP8 221833 "Sp8 transcription factor, transcript variant 2" GO:0006355|GO:0009954|GO:0005634|GO:0030326|GO:0009953|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143668_PI430048170 0.3748454980085541.30833590759251 3.54425282132332 2.84559572762194 2.56343992883967 P A A 2.97840378018048 2.52996104560805 2.39839328751342 P P P LNCV6_143668_PI430048170 mRNA AATCTGGCCACCTCATCCACTACATCTGGATTGAGTGTACTGCAACAAAGAAAAACATTA NM_152686RefSeq chr5 - 139410202 139439525 DNAJC18 202052 "DnaJ (Hsp40) homolog, subfamily C, member 18" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141341_PI430048170 0.8303767368802291.01521993074508 12.1132582568943 11.9077723487679 11.8855343279304 P P P 11.9000310302111 12.0244533574671 11.9247701398964 P P P LNCV6_141341_PI430048170 mRNA GCTTCAGCTCCTGTAAACAGCCAGGTTAATAAAAGCACATGCCGTGAAGTTTCGAAAAAA NM_017503RefSeq chr9 + 133356544 133361165 SURF2 6835 "surfeit 2, transcript variant 1" GO:0008150|GO:0003674|GO:0005886|GO:0005730|GO:0005634|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139472_PI430048170 0.0129075677055078 0.2717060204258030.377476765857784 0.5566579722321410.423536758451494A A A 1.95687809778576 2.75275604745274 2.17267450756217 A P A LNCV6_139472_PI430048170 mRNA CTCCCCTAACTCAATCCCTGGTACATTCCTAATAAAGCAGTTTTGAGGAAAATCAAAAAA NM_016438RefSeq chr17 + 44847901 44850480 HIGD1B 51751 "HIG1 hypoxia inducible domain family, member 1B, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128147_PI430048170 0.3190889909191850.671697259992835 0.426890279008036 0.3506064163077331.18424379012264 A A A 1.65188099046753 1.47837139821381 0.43731404231251 A A A LNCV6_128147_PI430048170 mRNA TGTGTGAGTTAACAACAGGAATGAAGCCTAACAGTTTATATCTCCCCATATGCTTATTAC NM_001145678 RefSeq chr5 - 94150850 94618604 KIAA0825 285600 "KIAA0825, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91372_PI430048170 0.2705507237126831.13956866738118 6.20088003905587 6.59203699987687 6.31034436240081 P P P 6.02997738338716 6.25809305074522 6.26618776046473 P P P LNCV6_91372_PI430048170 mRNA TTCTCATTGAGAATGGAGTAGCTGAGCGGCAAAGATCTCTCTTTGTTGTAGTTGGGGATC NM_024662RefSeq chr11 + 34105563 34146911 NAT10 55226 "N-acetyltransferase 10 (GCN5-related), transcript variant 1" GO:0008150|GO:0008080|GO:0016020|GO:0008152|GO:0005730|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135079_PI430048170 0.000279311472291985 0.6956077995278854.5991333780286 4.617646614059 4.70337954126454 P P P 5.17161116739626 5.1121166127899 5.20793396682322 P P P LNCV6_135079_PI430048170 mRNA ATTTCACAGAAGTGCCTGAGACGCGGAGACATGGCTGGTGTTAAATGGAGCTATTCAATA NM_001303474 RefSeq chr7 + 1055274 1059269 GPR146 115330 "G protein-coupled receptor 146, transcript variant 1" GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_132212_PI430048170 0.0353848829535672 1.24143906807659 6.65990727125874
6.85839838352899 6.91368363742704 P P P 6.39609699445869 6.57205811115818
6.53407089115202 P P P LNCV6_132212_PI430048170 mRNA
AACCTGTGTTTGTATTGGAGATGTGTCTACTATTGGGGGAAGAGGTTCTCGTAATCGCTC NM_025224RefSeq chr20
- 63743667 63805503 ZBTB46 140685 zinc finger and BTB domain containing 46
GO:0006355|GO:2001200|GO:0045656|GO:0030853|GO:0005634|GO:0003676|GO:0045650|GO:2001199|GO:0046
872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69358_PI430048170 0.00500702250232256 0.6441933937192856.18065926219224
6.39306239384216 6.3933151421489 P P P 7.02393912469323 6.78718825942511
7.05489422961015 P P P LNCV6_69358_PI430048170 mRNA
TGAAATTCTGTTGGCAGAAGCAGCATTTTGAAGAAATAAAAGGTTCACTGCAGCTGACCC NM_152392RefSeq chr2
+ 61177419 61187551 AHSA2 130872 "AHA1, activator of heat shock 90kDa protein ATPase homolog 2
(yeast)" GO:0051087|GO:0032781|GO:0001671 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129622_PI430048170 0.1660671789789550.9164696510108889.85618646031999
9.87740193730367 9.87839708223044 P P P 9.87777466358638 10.0498953228617
10.0549911778606 P P P LNCV6_129622_PI430048170 mRNA
CCCCACTCTTGCTTGTGTTTCTTCTTTATGTAAATTGTGTGATGTTTCAATAAATCAGTC NM_005500RefSeq chr19 +
47130822 47210636 SAE1 10055 "SUMO1 activating enzyme subunit 1, transcript variant 1"
GO:0005515|GO:0043008|GO:0016567|GO:0046982|GO:0016925|GO:0004839|GO:0031510|GO:0005634|GO:0043
085|GO:0008022|GO:0019948|GO:0043231|GO:0005829|GO:0007346|GO:0019950|GO:0005654|GO:0008047|GO:0
044267|GO:0043687. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130252_PI430048170 0.0390473208454156 0.6218825198415331 0.0809241383442
10.0187482848856 10.2439816229442 P P P 10.5561715265021 10.6978994726803
11.0987264980044 P P P LNCV6_130252_PI430048170 mRNA
CAAGGAATGGAATTTCCATCCTGAGCCAGTTCAGTTAGGTGTCAATTGATACTATTTTAA NM_001009993 RefSeq
chr2 - 131047875 131093431 FAM168B 130074 "family with sequence similarity 168, member B"
GO:0030424|GO:0048471|GO:0005886|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128846_PI430048170 0.8242353551119141.00778218027854 0.522585778584624
0.5525257762847130.434401025584836A A A 0.5506050378000020.462773747741343
0.463398380576782A A A LNCV6_128846_PI430048170 mRNA
TCTGGTCTTTCTCATGCGTAGGGAGCAGTGTGAATGAAAGTGAAGTCAAACGGACAGTTT NM_020685RefSeq chr3
+ 62319042 62336213 C3orf14 57415 "chromosome 3 open reading frame 14, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122813_PI430048170 0.2997013095220610.7912438208931753.78565865391645 3.1509856798609
4.10744168079787 P P P 3.9725762535304 4.12001608535851 4.11717887106766 P P P
LNCV6_122813_PI430048170 mRNA
TTACGAGACATGGGCATCGTAGATATTCTACACAAACTGAGTCAGTCACCAGATTCAAAC NM_015396RefSeq chr3
+ 138187247 138298386 ARMC8 25852 "armadillo repeat containing 8, transcript variant 2" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_130095_PI430048170 0.3790619341266441.56455774355638 1.65094787082117
0.3507653937118190.283235968759382A A A 0.25559004151581 0.275929451425599
0.257611455037435A A A LNCV6_130095_PI430048170 mRNA
GGGTATGTGTGCATTAAATGAGTTTCACAGTAGATTGAATGCTTCAACTTCACTTCAATA NM_004820RefSeq chr8
- 64595971 64798791 CYP7B1 9420 "cytochrome P450, family 7, subfamily B, polypeptide 1"
GO:0050679|GO:0006805|GO:0005506|GO:0006699|GO:0008396|GO:0060740|GO:0044281|GO:0055085|GO:0005
789|GO:0008206|GO:0033783|GO:0016125|GO:0033147|GO:0055114|GO:0008203|GO:0020037 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_73356_PI430048170 0.00310899711264924 0.2630120736223550.475507769330273

0.9683638395843550.290298894947442A A A 2.59316518434874 2.08100681241016
2.82986873477793 A A P LNCV6_73356_PI430048170 mRNA
AGTTACCTCAGTATCTTTAGGTTGTGGCAGAATGTATTATTAGATAAGAGCCTGACTAGA NM_017577RefSeq chr3
+ 113838833 113947174 GRAMD1C 54762 "GRAM domain containing 1C, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129682_PI430048170 0.1812038232458310.9452658553966140.248491360330021
0.3300535405318980.29171910258964 A A A 0.4498424471714540.348016187663395
0.313683248155299A A A LNCV6_129682_PI430048170 mRNA
GAGCAAAGTCCTGTTTGGAAAACACTTCAGAAGATAAAACTGAATAGTGATTCAGTTAAC NM_001012425 RefSeq
chr1 + 92218015 92245810 C1orf146 NA chromosome 1 open reading frame 146 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_103487_PI430048170 0.5222217806902671.08490527926993 4.69129890753809
4.89457745576824 5.07339338714854 P P P 4.9145461867362 4.8797153221451
4.50247286541348 P P P LNCV6_103487_PI430048170 mRNA
AAACTTCTGACTCTGTTAAAAAAGAACCTGTTCTTGCCCAGCCTGCAGTCAGCAACTCTG NM_005085RefSeq chr9
+ 131125560 131234670 NUP2148021 nucleoporin 214kDa
GO:0005515|GO:0007077|GO:0005215|GO:0010467|GO:0019221|GO:0019058|GO:0005634|GO:0044281|GO:0006
606|GO:0005829|GO:0008645|GO:0043231|GO:0006406|GO:0015758|GO:0005643|GO:0006611|GO:0051726|GO:0
016032|GO:0005975|GO:0019083|GO:0055085|GO:0010827|GO:0005487|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142426_PI430048170 0.2066748511761421.05487108070468 0.452815046388083
0.3112806101674160.349124402531803A A A 0.2715198207256590.331356374954456
0.282181747592114A A A LNCV6_142426_PI430048170 mRNA
GATGTAAAGGCTGCTGTCAAAAACATACTGTGTAGGAAAAACTTTTCTGATGGAAAATGA NM_001004483 RefSeq
chr9 + 104569167 104570130 OR13C8NA "olfactory receptor, family 13, subfamily C, member 8" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144429_PI430048170 0.0923435494145533 0.9151463650761789.65814851226232
9.69825662679682 9.58366828504753 P P P 9.71442000451422 9.7447542460672
9.86271963996706 P P P LNCV6_144429_PI430048170 mRNA
GACTGCTGGAGTCAGGACATTTTATAGAGCCTTTTCCAGTTTTACTAAAAAATTTTTCCA NM_001163812 RefSeq
chr10 + 100987535 100994401 C10orf256652 "chromosome 10 open reading frame 2, transcript variant
2"
GO:0042645|GO:0006996|GO:0006390|GO:0002020|GO:0005524|GO:0034214|GO:0003697|GO:0005759|GO:0006
268|GO:0043139|GO:0051260|GO:0007005|GO:0006264 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132517_PI430048170 0.00415974242688015 0.2552045675090572.78062520354603
2.14424861562709 2.98256807087856 A A P 4.22200026414049 4.86267289504405
4.77937433634672 P P P LNCV6_132517_PI430048170 mRNA
GGAACTTCTATATGAGGATGCTGTGATCTAAAAATTAAATCTCAGTGGGCGGAGAAAAAA NM_004457RefSeq chr2
+ 222861013 222943401 ACSL3 2181 "acyl-CoA synthetase long-chain family member 3, transcript
variant 1"
GO:0005811|GO:0014070|GO:0048471|GO:0001676|GO:0005794|GO:0019901|GO:0051047|GO:0005783|GO:0007
584|GO:0042998|GO:0019904|GO:0005741|GO:0034379|GO:0005524|GO:2001247|GO:0004467|GO:0016020|GO:0
007420|GO:0005789|GO:0006633|GO:0016021|GO:0044539|GO:0005778 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140185_PI430048170 0.6486341311539690.9457133947187390.291750845275201
0.2794300695370040.435480316849779A A A 0.2952953044129310.261196825529949
0.661896263311602A A A LNCV6_140185_PI430048170 mRNA
TCAGTCCTACAGCAAGTTTGACACAAAATCGCACAACGATGACGCACTGCTCAAGAACTA NM_022557RefSeq chr17
- 63880211 63881942 GH2 2689 "growth hormone 2, transcript variant 2"

GO:0005179|GO:0005576|GO:0060397 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135085_PI430048170 0.7871257110025851.01584885281681 0.27630490894948
0.2817269504200950.470620678229142A A A 0.3428261354875530.292818532575339
0.333073036059297A A A LNCV6_135085_PI430048170 mRNA
GGTATACAAATCTGTCTACATGAAGTTTACAGATTGGTAAATATCACCTGCTCAACATGT NM_005807RefSeq chr1
+ 186296272 186314562 PRG4 10216 "proteoglycan 4, transcript variant A"
GO:0071425|GO:0006955|GO:0008283|GO:0042127|GO:0045409|GO:0030247|GO:0005615|GO:0006898|GO:0005
044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134411_PI430048170 0.0091009615001932 2.11769484391342 4.53220088650158
4.39295676139639 4.29032019890668 P P P 3.57551754510921 3.30953111685367
3.04445864572998 P P P LNCV6_134411_PI430048170 mRNA
TATTTATTCCCTCACCTTCTGCAGGGCTCCGTGCGGGCTGAAATTAAAGATTTCTTAGAG NM_002068RefSeq chr19
+ 3136031 3163769 GNA15 2769 "guanine nucleotide binding protein (G protein), alpha 15 (Gq
class)"
GO:0001664|GO:0005886|GO:0005834|GO:0003924|GO:0030168|GO:0007202|GO:0031683|GO:0005525|GO:0007
204|GO:0046872|GO:0006184|GO:0007596|GO:0060158|GO:0007207|GO:0007188|GO:0004871 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135958_PI430048170 0.2296788749888920.4396917915075770.284087361680618
0.6506048123826020.406138255042368A A A 2.29756111789096 0.32696386186248
1.67026900494534 A A A LNCV6_135958_PI430048170 mRNA
TGTGGCTGGTCAAGTCACTGATTTACCTTGGGCTTTATTTGATATAAATCATGTAAATCA NM_001199356 RefSeq
chr18 - 49481177 49492565 RPL17-C18orf32 NA "RPL17-C18orf32 readthrough, transcript variant 2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97011_PI430048170 0.0453143815693423 1.13506772262081 0.637481341472147
0.7472557642861310.765710405006014A A A 0.63003045872514 0.477435044967058
0.49301072047688 A A A LNCV6_97011_PI430048170 mRNA
CTGGGGAGTTAACTAGCTTAACAAAAGATGCTTAGCTTTTGTAAAAGAACAAGTGTTTCA NM_001114086 RefSeq
chr6 - 45898452 46080348 CLIC5 53405 "chloride intracellular channel 5, transcript variant 1"
GO:0005515|GO:0006821|GO:0007565|GO:0005244|GO:0005794|GO:0005815|GO:0007605|GO:0060088|GO:0034
707|GO:0002024|GO:0032420|GO:0015629|GO:0005254|GO:0008104|GO:0050885|GO:0006810|GO:0034765|GO:0
005938|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133708_PI430048170 0.3321435152637370.87333226806393 5.51672985434035
5.26117799631036 4.96209751242437 P P P 5.43455773122027 5.60781798554797
5.32238770037775 P P P LNCV6_133708_PI430048170 mRNA
TGGGCTTCCTGACCCCTGCCTATATCTATGAAATTTGCTGTTGGAGTGCTTATTATAACT NM_053278RefSeq chr6
+ 132552692 132553721 TAAR8 83551 trace amine associated receptor 8
GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0001594 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142497_PI430048170 0.3245868456716660.6956608166281543.80870132421366
2.79905921884973 2.03377965920816 P A A 3.92316931022313 3.58527717429436
3.14755733034565 P P P LNCV6_142497_PI430048170 mRNA
GCACCCCTATGCCCACTCTAATATTCAACAATTATAGACAATTTGCCCTATCATTTATTTNM_006193RefSeq chr7 -
127610291 127615726 PAX4 5078 paired box 4
GO:0043066|GO:0060041|GO:0042493|GO:0045597|GO:0001206|GO:0000122|GO:0051591|GO:0003677|GO:0006
351|GO:0030154|GO:0003690|GO:0031018|GO:0007623|GO:0009887|GO:0000980|GO:0005654 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139937_PI430048170 0.00368836808726093 0.5478940150657491 4.1860724441228
14.110542034335 13.9453921669246 P P P 14.9176404462693 14.9929781548489 14.944864163661
P P P LNCV6_139937_PI430048170 mRNA

TGAGCGGGAGGCAGAGTTTGCCTTCCTTTCTCCAGGACCAATAAAATTTCTAAGAGAGCT NM_000852 RefSeq chr11 + 67583594 67586653 GSTP1 2950 glutathione S-transferase pi 1 GO:0005515|GO:2001237|GO:0006805|GO:0005886|GO:0032691|GO:0048147|GO:0006749|GO:0005634|GO:0044281|GO:0032872|GO:0071638|GO:0005615|GO:0019207|GO:0032873|GO:0005829|GO:0043409|GO:0005739|GO:0005622|GO:0005737|GO:0043407|GO:0070373|GO:0035726|GO:0043508|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136117_PI430048170 0.5167033633184010.9082986999201261 0.6260521271154 10.1495065867821 10.1054879012238 P P P 10.6375423248831 10.4733233813853 10.2151430311061 P P P LNCV6_136117_PI430048170 mRNA
ATCAGCTCCCTGTCCTCCTTTCTTCCCTCGTTATTGATCTATAGACATTAGGAAGGGAGT NM_001145809 RefSeq chr19 + 50203627 50310544 MYH14 79784 "myosin, heavy chain 14, non-muscle, transcript variant 3" GO:0005516|GO:0030424|GO:0006200|GO:0042641|GO:0008360|GO:0007605|GO:0031032|GO:0030898|GO:0019228|GO:0030426|GO:0005737|GO:0000146|GO:0051015|GO:0007411|GO:0016460|GO:0070062|GO:0030048|GO:0001725|GO:0048013|GO:0005524|GO:0071625|GO:0016020|GO:0003009|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141496_PI430048170 0.0971599010641010.500241344998803 1.62425354155067 0.3142661371918081.31643386626493 A A A 2.17750421348056 2.53151404719596 1.73176679217842 A P A LNCV6_141496_PI430048170 mRNA
TTCCATGCCAAAGTCCCCCAAGATCTGGATATCTGGGGACAAGATGGTGGCCTCAGGCCT NM_001127893 RefSeq chr19 + 44671451 44684355 CEACAM19 56971 "carcinoembryonic antigen-related cell adhesion molecule 19, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135740_PI430048170 0.0491445203593021 0.3424947366560561.31485011496251 0.2690732939245880.316496967775133 A A A 2.79119130361408 1.37745927440425 2.2921694062552 P A A LNCV6_135740_PI430048170 mRNA
CTTATAGGGGATTCACATTTGGCCCCTGAGATTGCATTTGATACCATTTTATTTAGAATA NM_182609 RefSeq chr19 - 53235384 53254858 ZNF677 NA zinc finger protein 677 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79777_PI430048170 0.4987045267532870.818850934543751 0.326756918665993 0.296086923686231 0.423798569623134 A A A 0.293326376656418 1.14377945722504 0.30362285878416 A A A LNCV6_79777_PI430048170 mRNA
CTTACGTTATCCCCAATGCATTGTAAATGTCAAACTTTTGGAAAATAAAGCCTGCGTGCC NM_014237 RefSeq chr8_KI270822v1_alt + 335201 480684 ADAM18 8749 "ADAM metallopeptidase domain 18, transcript variant 1" GO:0016020|GO:0006508|GO:0008270|GO:0007275|GO:0016021|GO:0007283|GO:0004222|GO:0030154|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_34722_PI430048170 0.5718227391482982.53418369782558 0.318462544971005 3.3089683266094 0.272279107829126 A P A 0.256390931119838 0.258133410821176 1.31555425128267 A A A LNCV6_34722_PI430048170 mRNA
TCAGTTCATAAACGCACGCTGTGCACATCCCCTGTGCTTGGCAAGGGGCCTGGATAGAAG NM_001289922 RefSeq chr22 - 49620455 49657542 C22orf34 NA "chromosome 22 open reading frame 34, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144912_PI430048170 0.4281100085741330.897872941766509 2.95683207848414 3.08756000773238 3.55039099471878 A P P 3.41096800881148 3.31268661441836 3.40469107906313 P P P LNCV6_144912_PI430048170 mRNA
TAGCATAAAACAGTGGGGTTGGATCCCATGAATAACATTATAAAGGTTCTGGGGTTTTTT NM_002901 RefSeq chr11 + 32090930 32105726 RCN1 5954 "reticulocalbin 1, EF-hand calcium binding domain" GO:0005515|GO:0005783|GO:0005509|GO:0005788|GO:0043010|GO:0001701 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144637_PI430048170 0.0367713890687047 0.4016177918185551.95634479081621

2.40945009107922 1.24004031847795 A A A 2.80590098356411 3.64415246967526
3.21365434995903 P P P LNCV6_144637_PI430048170 mRNA
GTAGAAGTCACTGCCTTCTGAGTTTTCAAATAGATAACCACCTTTAATATTACACTGCTT NM_020771 RefSeq chr6
- 104728092 104859919 HACE1 57531 "HECT domain and ankyrin repeat containing E3 ubiquitin protein
ligase 1, transcript variant 1"
GO:0030334|GO:0005515|GO:0004842|GO:0006355|GO:0017137|GO:0016567|GO:0005783|GO:0016874|GO:0005
634|GO:0006351|GO:0048365|GO:0007049|GO:0016601|GO:0042787|GO:0000139|GO:0032580|GO:0007030|GO:0
061025|GO:0070936. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106930_PI430048170 0.476543263265264 0.719381043587177 0.409987081641347
0.299574741798613 0.301564645237229 A A A 1.50349664411382 0.308802365760111
0.259590974837827 A A A LNCV6_106930_PI430048170 mRNA
TTCCAAATTTCAACATCTACCCCCAAAACATAGGTGTCTGAGAGACTCCAGCATTTTCGG NM_002233 RefSeq chr11
- 30009740 30017030 KCNA4 3739 "potassium channel, voltage gated shaker related subfamily A,
member 4"
GO:0005251|GO:0005515|GO:0030424|GO:0005886|GO:0007268|GO:0030955|GO:0005887|GO:0005249|GO:0008
076|GO:0034765|GO:0051260|GO:0016021|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_114874_PI430048170 0.000152698088494094 0.284584834410315 6.16002454352915
5.90406190532917 6.21137541816103 P P P 7.78921474967193 7.86740374726863
8.06255115003559 P P P LNCV6_114874_PI430048170 mRNA
CTTTGGTGATTGAGGGAAATAATGTCTCTACTTGTAATTTATTGTGACCCTTTTTCACTG NM_018126 RefSeq chr4 +
41935119 41960807 TMEM33 55161 transmembrane protein 33
GO:0042470|GO:0008150|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142045_PI430048170 0.142955365159509 0.722037295279171 4.29214441816381
3.69149852514716 3.61414543386521 P P P 4.35079777724685 4.39536390097079
4.36018152828018 P P P LNCV6_142045_PI430048170 mRNA
AGAGCCTTCCCGCACCCGTCAGAAGCTCAGAGCCTTCTTGGACCCTTTAAAGATGTCCCT NM_004977 RefSeq chr19
- 50315507 50329377 KCNC3 3748 "potassium channel, voltage gated Shaw related subfamily C,
member 3"
GO:0005251|GO:0031594|GO:0005886|GO:0046928|GO:0007268|GO:0032809|GO:0032590|GO:0005249|GO:0008
076|GO:0051260|GO:0034765|GO:0043679|GO:0016021|GO:0030673|GO:0006813|GO:0071805 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_89324_PI430048170 0.945948921877389 0.981196456933623 7.1340388112942 7.23439465753527
7.35008214734698 P P P 7.56010249418005 7.04662492788743 7.14950546478064 P P P
LNCV6_89324_PI430048170 mRNA
CAGAAACCATAACACCGATGATTCTGATGATTTTTATGACTAACGTGCTGTGACATTGGT NM_018474 RefSeq chr20
+ 21125982 21246620 KIZ 55857 "kizuna centrosomal protein, transcript variant 1"
GO:0005515|GO:0005813|GO:0005737|GO:0019901|GO:0042995|GO:0007051 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135786_PI430048170 0.474421066745644 0.901948918567145 5.53299943869561
5.58036425446839 5.13329595464701 P P P 5.76875595112025 5.6030223882815
5.32807636519564 P P P LNCV6_135786_PI430048170 mRNA
TCCGAGTGGCCTTCTCCGACTACCAGCACTTTGCCTTGCTGTACTTGGAGATGCGGAAAG NM_207510 RefSeq chr9
+ 136982992 136985758 LCNL1 NA lipocalin-like 1 NA . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_127935_PI430048170 0.135233444669715 0.452427282814192 0.278380378190757
0.533378535199264 2.16203866043814 A A A 1.80375930235174 2.44228609624018
2.77516431564881 A A P LNCV6_127935_PI430048170 mRNA
GTAAAGTCCATTGTTTTTATTGTCCTGAGTTGTCTTAAACCTGCAAAATATACACTACCC NM_001199942 RefSeq

chr6 + 83067665 83168471 DOPEY1 23033 "dopey family member 1, transcript variant 2"
GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144555_PI430048170 0.2267574865326511.12246807392584 9.69660046140007
9.45644453367063 9.50336158981142 P P P 9.2173145801279 9.53213127209532
9.40110901851916 P P P LNCV6_144555_PI430048170 mRNA
GGGGCAGAGGAAAAGAAGAAGTGTTACTGCATTTTGTACAAAATAAATACAGTCATATGT NM_001286076 RefSeq
chr1 - 27891525 27914797 RPA2 6118 "replication protein A2, 32kDa, transcript variant 2"
GO:0005515|GO:2000001|GO:0005634|GO:0010569|GO:0006302|GO:0034605|GO:0000082|GO:0006271|GO:0003
697|GO:0000723|GO:0000724|GO:0000722|GO:0006297|GO:0006298|GO:0005662|GO:0031625|GO:0000781|GO:0
019903|GO:0035861|GO:0003684|GO:0006260|GO:0047485|GO:0006281|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140284_PI430048170 0.0118888487036272 0.5742049991806137.45645038621967
7.00190548424271 7.37457279758378 P P P 7.96280579793741 8.00431252240259
8.28466503842398 P P P LNCV6_140284_PI430048170 mRNA
TTGTTTTTCATCTCTTCCTCCCTATGGGTATTAGAAAGGACAGTTGAAAATAAGGGGGAA NM_017826RefSeq chr13
- 36168207 36214615 SOHLH2 54937 "spermatogenesis and oogenesis specific basic helix-loop-helix
2, transcript variant 1"
GO:0006355|GO:0048477|GO:0046983|GO:0007275|GO:0005634|GO:0007283|GO:0003677|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141192_PI430048170 0.0682501869689099 2.7277022065055 2.77947010243704
3.17204063114791 2.87474946534132 A P A 1.92628419616623 0.461684659641243
1.73662594377516 A A A LNCV6_141192_PI430048170 mRNA
CTATACCCCTGGACTCTAGTTATGGGGGCTAATAAATGTTATATACTGTTTAAGGTAAAA NM_001142285 RefSeq
chr10 + 78033759 78056813 RPS24 6229 "ribosomal protein S24, transcript variant d"
GO:0000462|GO:0010467|GO:0006364|GO:0015935|GO:0019058|GO:0034101|GO:0005634|GO:0006412|GO:0006
413|GO:0006414|GO:0005829|GO:0005737|GO:0000184|GO:0000166|GO:0016032|GO:0042274|GO:0003735|GO:0
006614|GO:0019083|GO:0005730|GO:0006415|GO:0016020|GO:0022627|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130366_PI430048170 0.0181892171923241.47485667193018 8.36634713330858 7.9932962990995
8.23465754850088 P P P 7.51737570189938 7.5856215816349 7.816727690127 P P P
LNCV6_130366_PI430048170 mRNA
GTTTCTTCTTTGGAAACCATCACTATTGAGAGATGGGAAAAACCTGAATGTATAAAGCAT NM_170662RefSeq chr3
- 105658264 105869043 CBLB 868 "Cbl proto-oncogene B, E3 ubiquitin protein ligase"
GO:0005515|GO:0045732|GO:0004842|GO:0016567|GO:0005886|GO:0046642|GO:0016874|GO:0005509|GO:0006
607|GO:0050860|GO:0005829|GO:0035556|GO:0007165|GO:0042110|GO:0005737|GO:0006955|GO:0002669|GO:0
008270|GO:0001784|GO:0005654|GO:0004871|GO:0007166 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_130401_PI430048170 0.6429554280396260.66743736997316 0.321975953097048
1.45154997621154 2.00514915619059 A A A 2.77900296155473 1.93723075503679
0.369281092057404P A A LNCV6_130401_PI430048170 mRNA
TCCTGTGACAGAGGCAGTGGTCAGCAAGATGGTGCCTCCGACTGTGGCTATGGCTCTGGA NM_178433RefSeq chr1
+ 152613810 152614098 LCE3B 353143 late cornified envelope 3B GO:0031424 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_128444_PI430048170 0.6276358398127740.9317572559875717.37380826992273
7.50000011170721 7.7806367640597 P P P 7.53213627342889 7.48387931355179
7.93176223294068 P P P LNCV6_128444_PI430048170 mRNA
GACTGGATGTGTATAAAGGAATTATGTTGTCATGTGCCTTTAACCAGCTTTAGTAATTAC NM_032927RefSeq chr4
- 4235541 4248242 TMEM128 85013 "transmembrane protein 128, transcript variant 3"
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_143577_PI430048170 0.1454830101499590.7083499683871871 4.2052742357868
13.5887628417134 13.4511413154777 P P P 14.3057071922688 14.3135993282208
14.2331024635619 P P P LNCV6_143577_PI430048170 mRNA
GCAGTCCCCCTCCTCCTCTTTATCTACATTACTTCCCGAAAATAAATGCAAATTAATGAA NM_014562RefSeq chr2
+ 63050801 63057831 OTX1 5013 "orthodenticle homeobox 1, transcript variant 1"
GO:0022037|GO:0001077|GO:0042472|GO:0048852|GO:0045944|GO:0030901|GO:0005634|GO:0009952|GO:0000
978 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128902_PI430048170 0.7351652774507570.9706925187335556.36443807798241
6.52600574978021 6.87337174011308 P P P 6.67721888025948 6.61034958595795 6.6518923723166
P P P LNCV6_128902_PI430048170 mRNA
GCAGGTCATTAAAGATCATGTGACCAATTGTGCATTCAGTTTTCAGAATTCTTTGCTATA NM_018139RefSeq chr14
- 49625173 49635230 DNAAF2 55172 "dynein, axonemal, assembly factor 2, transcript variant 1"
GO:0005515|GO:0005737|GO:0071973|GO:0060285|GO:0032526|GO:0070286 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130437_PI430048170 0.3464118495500430.8215485849111034.27312520014511
4.07028856471899 3.96274133859655 P P P 4.77691242543779 4.14106092422103
4.16207868577985 P P P LNCV6_130437_PI430048170 mRNA
CTCCCTGCATGTGTAACACCCCTTCTTGCTGTCTCTTAGTAAATAAACGACCCAAAGCAG NM_001265587 RefSeq
chr19 - 17816512 17821574 INSL3 3640 "insulin-like 3 (Leydig cell), transcript variant 1"
GO:0048471|GO:0043066|GO:0008284|GO:0008285|GO:0001664|GO:0005158|GO:0030819|GO:0005102|GO:0007
267|GO:0005576|GO:0001556|GO:0007283|GO:0002020|GO:0001701|GO:0005615|GO:0007193|GO:0005179|GO:0
008584 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52750_PI430048170 0.7224426156626921.32333238858685 2.20579994693962 0.54179375336324
0.456166649222511 A A A 1.54238212858824 0.4351011984061670.441644419279065 A A A
LNCV6_52750_PI430048170 mRNA
TCTGCAATCACCACCGGGAACTTTGGGAGGCTGGGAAGATGGAGCCAAACCAATGTGTGG NM_017670RefSeq
chr11 + 63985852 63998420 OTUB1 55611 "OTU deubiquitinase, ubiquitin aldehyde binding 1,
transcript variant 1"
GO:0005515|GO:0071108|GO:2000780|GO:0043130|GO:0004843|GO:0006974|GO:0019784|GO:0005737|GO:0006
281|GO:0006508|GO:0031625|GO:0002376|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139549_PI430048170 0.8653773516101480.8768538781547650.5914703849270180.9507968558389
0.63384268595334 A A A 0.2952775714301381.60126023531469 0.517234700768117 A A A
LNCV6_139549_PI430048170 mRNA
GTCAAGGGGGATATCAGAATAGTCACAAGTTAAAGCGTCTGAATTGATGTTAAAGTTTTA NM_030933RefSeq chr1
- 182899864 182953418 SHCBP1L 81626 SHC SH2-domain binding protein 1-like NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133779_PI430048170 0.3067816247103881.12260936212127 0.493686440590584
0.5278230237046090.857296564202714 A A A 0.4961106876266380.452201982664612
0.458155712187375 A A A LNCV6_133779_PI430048170 mRNA
CTCCCACTTCTTGGGAGGGTTACATTTTTTAAGTCTTAATCATTTGTGACATATGTATCT NM_000878RefSeq chr22 -
37125839 37149922 IL2RB 3560 "interleukin 2 receptor, beta"
GO:0007165|GO:0043066|GO:0004911|GO:0006461|GO:0016020|GO:0005886|GO:0005887|GO:0019221|GO:0016
032|GO:0038110|GO:0019976|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126842_PI430048170 0.3867262956213150.99177470166681 0.338377384393187
0.3671527809325340.339652975471497 A A A 0.3641654321739690.371636547673613
0.345183011835591 A A A LNCV6_126842_PI430048170 mRNA
ATTTAGGGACTTTTCAAAACAACTGCTGAGCTAATAAATCCTAGCATTTCTCAGGTCAAA NM_001034845 RefSeq
chr4 + 171813423 173040407 GALNTL6 NA polypeptide N-acetylgalactosaminyltransferase-like 6
NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139626_PI430048170 0.3516673605041510.8540442086148555.63555043998288
5.49628864943193 5.91089464424859 P P P 5.77618121055847 5.69578572422397
6.22641980364739 P P P LNCV6_139626_PI430048170 mRNA
AATGTATCACTGGCCCGTGTATCAATGACCCACATATCAATGACCCACGTATCAATGACC NM_001104629 RefSeq
chr4 + 37453929 37593510 C4orf19 55286 "chromosome 4 open reading frame 19, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136639_PI430048170 0.47256247485834 1.22257594363645 0.470917542324295
1.17378390760713 0.286382563206436A A A 0.3625813537352340.433633576081372
0.422408302601169A A A LNCV6_136639_PI430048170 mRNA
ATAGGAAAGAAACTTGAGCGGTATACTCAGAATGGTGAGAGCCCTGAATTTTGCAGACCG NM_001286820 RefSeq
chr4_KI270896v1_alt - 361898 364788 FRG2 448831 "FSHD region gene 2, transcript variant 1"
GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_39420_PI430048170 0.4195090907154411.39195508713648 1.76293024171489 2.91703409218112
2.93546509111036 A A P 2.1694004062797 1.90361227652764 2.3562448704788 A A A
LNCV6_39420_PI430048170 mRNA
TTAAAAAAGAAAGACAGGGAAGTGTCTCATGCGGGAGCCTCCATGTCATCTGCTTCATCA NM_002892RefSeq chr14
+ 58298503 58373733 ARID4A 5926 "AT rich interactive domain 4A (RBP1-like), transcript variant 1"
GO:0003700|GO:0006357|GO:0006366|GO:0044212|GO:0080182|GO:0006325|GO:0005634|GO:0007283|GO:0003
677|GO:0048821|GO:0045944|GO:0017053|GO:0036124|GO:0006349|GO:0005654|GO:0045892|GO:0034773 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54867_PI430048170 0.0606607300649883 1.32242469991703 10.2025722591962
10.5948816043682 10.4307245123781 P P P 10.1766790219948 10.0306081261464
9.81530712932561 P P P LNCV6_54867_PI430048170 mRNA
AGTCTCCAGGAAGATGCAGGCCTGCTCTCCCTCCTGTACCTGCCAACAGGATTTTTCTCC NM_001105203 RefSeq
chr1 + 155320848 155331118 RUSC1 23623 "RUN and SH3 domain containing 1, transcript variant 1"
GO:0000209|GO:0005515|GO:0030054|GO:0005794|GO:0005874|GO:0014069|GO:0003779|GO:0005634|GO:0009
967|GO:0031410|GO:0005737|GO:0045211|GO:0005070|GO:0015630|GO:0016023|GO:0005769 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134166_PI430048170 0.0429667771639852 0.5379514218062776.25042283018306
6.08087834242773 6.36129416624973 P P P 6.67302883744867 7.25246344100479
7.37204505138155 P P P LNCV6_134166_PI430048170 mRNA
AATTATGAGATGGTGGGAACCAGAGCAACTCAGGTGCATGATACAAGGAGAGGTTGTCAT NM_006187RefSeq
chr12 + 112938432 112973249 OAS3 4940 "2'-5'-oligoadenylate synthetase 3, 100kDa"
GO:0003725|GO:0005515|GO:0005886|GO:0001730|GO:0019221|GO:0009615|GO:0005524|GO:0005615|GO:0046
872|GO:0005829|GO:0043231|GO:0051607|GO:0005737|GO:0006139|GO:0060337|GO:0005654|GO:0060700|GO:0
060333|GO:0045071. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69315_PI430048170 0.9503981139535041.13040039878379 7.98256070124778 9.26054413328015
7.83200978608681 P P P 8.52394603554949 8.28701833402513 8.1672271119976 P P P
LNCV6_69315_PI430048170 mRNA
CCTGGGCCACTGACGCTCTGGCCTCTGTGGGAATCACACTGGGCTGACCTGGCATTGGGA NM_031209RefSeq chr19
+ 10701435 10713367 QTRT1 81890 queuine tRNA-ribosyltransferase 1
GO:0005739|GO:0005634|GO:0046872|GO:0008479|GO:0006400|GO:0008616 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_4775_PI430048170 0.9594280584836651.16636464460877 2.64747922605793 1.97597782668347
0.252016941149031A A A 2.03462734363445 1.24718319455533 1.72023431531653 A A A
LNCV6_4775_PI430048170 mRNA
TAGATCATCACTCTAAGGACACCACCCTCATCCACCAAATATTTGGAGGCTACTGGAGAT NM_001256867 RefSeq
chr4 + 9363128 9364721 USP17L30 NA ubiquitin specific peptidase 17-like family member 30
NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133172_PI430048170 0.0160407550127994 0.7606120151675348.52760641273846
8.53134136343477 8.75536281191059 P P P 8.9170903758394 9.08886026127209
8.99953236328618 P P P LNCV6_133172_PI430048170 mRNA
GAATTTCTGGACTTTAGCCCACCAGTTTGTCTGGTTGACTAACCTGCTGAGAGCTAAAAT NM_152344RefSeq chr17
- 44034634 44067619 LSM12 124801 LSM12 homolog (S. cerevisiae) NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135561_PI430048170 0.7260220203576360.9958628586595520.348571161587148
0.3609592128827740.313770177595621A A A 0.3471076496318580.35940103454486
0.335046024931274A A A LNCV6_135561_PI430048170 mRNA
CCAAATTGCAGATTATTCTGCAGAGAGGGAATTGCATGTTTGTGTTGTATATTTAGTATG NM_004370RefSeq chr6
- 75084325 75205907 COL12A1 1303 "collagen, type XII, alpha 1, transcript variant long"
GO:0005595|GO:0005576|GO:0035987|GO:0005615|GO:0031982|GO:0031012|GO:0001501|GO:0022617|GO:0030
020|GO:0030198|GO:0030199|GO:0030574|GO:0005788|GO:0007155|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138132_PI430048170 0.6409583319247960.9155883124952010.314802290416792
0.3090894174555910.488932521176558A A A 0.3037971108027510.271983920139862
0.850077828512858A A A LNCV6_138132_PI430048170 mRNA
GCAGCCATGAGGAAGTTGGTCACCAAATATATTTTGTGTAAAGAGAAGTGAAAGATAAAT NM_001004719 RefSeq
chr15_KI270852v1_alt + 403072 404156 OR4M2 NA "olfactory receptor, family 4, subfamily M, member 2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139913_PI430048170 0.2755981356955161.09906696480621 7.73403586657878
7.78028975521987 7.66152967160847 P P P 7.40132000278703 7.62144617542059
7.72777198090076 P P P LNCV6_139913_PI430048170 mRNA
CCCTAAACATTCACCTTGACCTTATTTATGACTTTACGTGCAAATGTTTTGACCATATTGNM_001202RefSeq chr14 -
53949735 53956836 BMP4 652 "bone morphogenetic protein 4, transcript variant 1"
GO:0033088|GO:0005515|GO:0001657|GO:0034504|GO:0001658|GO:0033085|GO:0003139|GO:0009791|GO:0005
615|GO:0007281|GO:0007224|GO:0035990|GO:0002062|GO:0030198|GO:0035993|GO:0010942|GO:0003279|GO:0
002320|GO:0030501|GO:0010453|GO:0001843|GO:0003323|GO:0030509|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131290_PI430048170 0.3435708056100810.7365468731643381.33056279790163
0.4293792222882451.7679272815669 A A A 1.77605772280424 2.02665708088542
1.24320465906514 A A A LNCV6_131290_PI430048170 mRNA
GCTTATGCCAAATGTCATCAAAAAGCCAGAATGCTACTACAGTAATGTAAAGGATTATTG NM_004593RefSeq chr3
- 185914569 185938136 TRA2B 6434 "transformer 2 beta homolog (Drosophila), transcript variant 1"
GO:0048026|GO:0005515|GO:0000166|GO:0000398|GO:0000381|GO:0000375|GO:0005634|GO:0003729 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72204_PI430048170 0.0466941834350183 1.82356677585819 2.74153382522868
2.06913002701829 2.42965510500259 A A A 1.07470476934303 1.83224529760842
1.70303792741624 A A A LNCV6_72204_PI430048170 mRNA
TTCGAGCTGCGCATCGTGGATCTGATTAAACCCGTGGGTGCTGGCTGCCAAGTCTTCGAA NM_000853RefSeq
chr22_KI270879v1_alt - 270307 278486 GSTT1 2952 "glutathione S-transferase theta 1, transcript
variant 1"
GO:0004602|GO:0006805|GO:0006749|GO:0044281|GO:0004364|GO:0070062|GO:0055114|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141098_PI430048170 1.61913503646931e-05 0.21067684231097 0.378093366029359
0.4039747150991830.314421473915491A A A 2.55246892746101 2.57989669055817
2.70185656254293 A P P LNCV6_141098_PI430048170 mRNA
GGTTTCTCTAATTGCTAATCACAACCCCACTGGGTCATGTTTGACATTTTATAATGAAAA NM_018241RefSeq chr4
+ 147617387 147635521 TMEM184C 55751 transmembrane protein 184C GO:0016021 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_133956_PI430048170 0.3854890485386141.04247640405674 11.6979171327263
11.6370877733372 11.5553391009949 P P P 11.4777768986052 11.6139910011222
11.6177112610742 P P P LNCV6_133956_PI430048170 mRNA
CCCTGTTTGCACCTCGATTTGTTTGCTGAAAATGTGAAATAGTAAAAATGAAATAACTGG NM_012478RefSeq chr17
- 75845698 75855420 WBP2 23558 WW domain binding protein 2
GO:0005515|GO:0001105|GO:0000790|GO:0071442|GO:0045944|GO:0045815|GO:0071391|GO:0000979|GO:0031
490|GO:0045184 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137594_PI430048170 0.3965187371448380.8911105248974840.282829512322101
0.2978040576112060.384141377252414A A A 0.7579120654897830.313638112811583
0.350949993691475A A A LNCV6_137594_PI430048170 mRNA
CATTCTCCACTGTTTGTTGTTGTTTACCTACACCCTCAATAAATGGTTCTTTAACCTAAA NM_001032726 RefSeq chrX
+ 70282171 70285002 RAB41 NA "RAB41, member RAS oncogene family" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_67435_PI430048170 0.1175360022609230.6527803937131221.20255135340579 1.36259612781001
2.05824663951788 A A A 2.05420308397355 2.00594606033864 2.50470326554455 A A P
LNCV6_67435_PI430048170 mRNA
CTGATCAGAGTTACTCTGATCTGAAGATTTTGGCGTTCAAGGCATTAAGATAATAGCCTG NM_001143823 RefSeq
chr18 - 5289018 5296195 ZBTB14 7541 "zinc finger and BTB domain containing 14, transcript
variant 1"
GO:0043565|GO:0005515|GO:0005737|GO:0003700|GO:0044212|GO:0005654|GO:0005634|GO:0000122|GO:0045
892|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129264_PI430048170 0.9873022788640890.9996544807442330.503795977632419
0.5259213620355010.411542307501016A A A 0.5385485927128860.450850530414251
0.454165889061417A A A LNCV6_129264_PI430048170 mRNA
CCGGGTTCACGAACTTGGTGCATTTCCTTCCAGACTTTTAAAAAGAAGATATTTAGGGAA NM_000923RefSeq chr19
- 18207960 18248200 PDE4C 5143 "phosphodiesterase 4C, cAMP-specific, transcript variant 1"
GO:0007165|GO:0004115|GO:0072372|GO:0005615|GO:0046872|GO:0006198|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132015_PI430048170 0.2525611956149060.8535566806467759.70563342402814
9.34134583772371 9.69004317864897 P P P 9.69164942982443 9.67770111607292
10.0498953228617 P P P LNCV6_132015_PI430048170 mRNA
TAGGGCAGCAGAGTGGAGCGATTTAGAAAGAACATTTTAAAACAATCAGTTAATTTACCA NM_006527RefSeq chr4
- 1692730 1712741 SLBP 7884 stem-loop binding protein
GO:0005515|GO:0006369|GO:0010467|GO:0006398|GO:0006366|GO:0008334|GO:0033260|GO:0031124|GO:0005
634|GO:0003729|GO:0005829|GO:0005737|GO:0006406|GO:0030529|GO:0005654|GO:0071204|GO:0051028|GO:0
071207|GO:0071208. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130611_PI430048170 0.1735192457357610.4569494355725170.467110764845958
0.83430252240476 0.524309120395753A A A 0.6252346358919732.08689130766806
2.09889477424376 A A A LNCV6_130611_PI430048170 mRNA
AGGCTTCCCTTGTCCTACGGTTGGGGACAAAGCAAGAATAAATAATGCTAATGAGGTCTG NM_138403RefSeq chr7
- 101613324 101629296 MYL10 93408 "myosin, light chain 10, regulatory" GO:0005739|GO:0005509 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130584_PI430048170 0.0108572366100668 0.4204622987522764.34704562243841
4.48552600904496 4.95147745003581 P P P 5.4574390508662 5.90429574044377
6.15863075839239 P P P LNCV6_130584_PI430048170 mRNA
CTAGTCTACTAGAGTACATTTGGCTAAGTAGATAACTTACCTAAATTTGCTCCAAAGCTA NM_002907RefSeq chr12
- 21468909 21501669 RECQL 5965 "RecQ helicase-like, transcript variant 1"
GO:0005515|GO:0043140|GO:0005634|GO:0006310|GO:0003677|GO:0005524|GO:0003678|GO:0006260|GO:0000

733|GO:0004003|GO:0006281|GO:0016020|GO:0005654|GO:0032508 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54785_PI430048170 0.265787898383772 1.45360596988546 0.243631388441881 0.943534181128912 1.30675909541677 A A A 0.419605586527908 0.334041269667103 0.311914281147358 A A A
LNCV6_54785_PI430048170 mRNA
TGGAGCAGCATTAACTAAGAAAGACCTGAAGAACCTCCTTGAAAGGGAATTTGGAGCTGT NM_007113 RefSeq chr1 - 152106316 152115454 TCHH 7062 trichohyalin GO:0008150|GO:0005509|GO:0031424|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141358_PI430048170 0.00788640164322701 2.12444508709338 7.96276300527528 7.99131019748736 7.98554236409202 P P P 6.8193844741101 7.08238769625412 6.7555595346397 P P P LNCV6_141358_PI430048170 mRNA
TGCAGAAACCGCTGGGTGGAGAAGAAGCCGATAAAGTCTATGAATCAACCTGCCAAAAAA NM_016339 RefSeq chr17 + 40177988 40195656 RAPGEFL1 51195 "Rap guanine nucleotide exchange factor (GEF)-like 1, transcript variant 3" GO:0043547|GO:0005085|GO:0016020|GO:0007186|GO:0007264|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142973_PI430048170 0.147311250753232 0.587864424655545 7.33943464878661 7.19186413472338 7.0130908557495 P P P 7.28722755256021 8.3665826773371 8.00936546264489 P P P LNCV6_142973_PI430048170 mRNA
AAGTAAACTTGTCCCTGCAACTGCCTTAGTAAACCCAAAGGCTCTTTTCAGAGCCACTCA NM_003523 RefSeq chr6 + 26183795 26184230 HIST1H2BE 8344 "histone cluster 1, H2be"
GO:0046982|GO:0050830|GO:0019731|GO:0006334|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0005615|GO:0003677|GO:0070062|GO:0002227 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133673_PI430048170 0.149351584683943 1.15909288906549 12.978900583728 12.9340068244904 12.674506774932 P P P 12.6524302505851 12.7140147109353 12.5979635312242 P P P LNCV6_133673_PI430048170 mRNA
AACCCAGAGCTCCCCAGTGTGGATACTAATAAACCTCTTGGAGCACACTCTCAGAAAAAA NM_006556 RefSeq chr1 - 154924731 154937008 PMVK 10654 phosphomevalonate kinase
GO:0016310|GO:0006695|GO:0016020|GO:0016126|GO:0070723|GO:0004631|GO:0019287|GO:0044281|GO:0005524|GO:0070062|GO:0005829|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133529_PI430048170 0.172783597679217 0.568666985743501 2.771289437136 1.16369633791372 1.74453428183758 A A A 2.69443825566326 2.94088065303977 2.94220228642568 P P P LNCV6_133529_PI430048170 mRNA
GCCACCCTGGTTGTGTTCATAATTACCATTGAGAAATGTCACTGTTATTAAAATACATTC NM_001286569 RefSeq chr2 - 135196968 135530730 ZRANB3 84083 "zinc finger, RAN-binding domain containing 3, transcript variant 3"
GO:0005515|GO:0048478|GO:0004520|GO:0003677|GO:0005524|GO:0003678|GO:0006974|GO:0000733|GO:0006281|GO:0008270|GO:0031297|GO:0000737|GO:0009411|GO:0043596|GO:0070530|GO:0045910 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133542_PI430048170 0.279312235092458 0.881791710721264 9.76572404899173 10.1704739434786 10.0622161290946 P P P 10.1821217013203 10.0460190592888 10.3304863202442 P P P LNCV6_133542_PI430048170 mRNA
GGGCCTTTGCTGTGTTTCCCTTGGTGGATTTTTGTGTTTTGTAAGTTGTCTATTTTGATA NM_153451 RefSeq chr11 - 69665563 69675397 ORAOV1 220064 oral cancer overexpressed 1 GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130737_PI430048170 0.0263717380631983 0.468205900355181 2.13970244888593 2.89895244028464 2.57947375915621 A A A 3.24870769922509 3.6043012744117 4.03929122607082 P P P LNCV6_130737_PI430048170 mRNA
ACTGCCCTGCTGTAATTAAACATTCTGTACCACATCTGTATTAAAAAGACATTGCTGACC NM_001130048 RefSeq chr13 - 98793486 98978084 DOCK9 23348 "dedicator of cytokinesis 9, transcript variant 2"

GO:0005515|GO:0008150|GO:0016020|GO:0032321|GO:0007596|GO:0007264|GO:0017048|GO:0005089|GO:0012
505|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130253_PI430048170 0.77711903495475 1.0540451293533 6.50793982720154
6.96522537253328 7.08758182332456 P P P 6.6400564455048 6.71846109057278
7.00989257403127 P P P LNCV6_130253_PI430048170 mRNA
GATAACCATATCCCCCCAGTGCTCATCAAAGTAGGACAATAAAAATCCATCCATCTCAGT NM_032117 RefSeq chr4
+ 153344648 153415095 MND1 84057 "meiotic nuclear divisions 1 homolog (S. cerevisiae), transcript
variant 1" GO:0051321|GO:0006310|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143936_PI430048170 0.2002402763707660.9861333260074850.335981599731405
0.3691788931318740.343776309195936A A A 0.3754074164966670.380756041715425
0.353271812476212A A A LNCV6_143936_PI430048170 mRNA
AAGACTCAAGTCTGTATGTACACTGGGGAGAAGCAGCCTGTTGAGTAAGATGAGAGAGAT NM_178861 RefSeq
chr13 - 98175784 98177267 RNF113B 140432 ring finger protein 113B GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132293_PI430048170 0.4119734634671730.8982568778789540.266700740882169
0.43128829765778 0.301247397728242A A A 0.7480647236336090.374737557835577
0.305827460005064A A A LNCV6_132293_PI430048170 mRNA
GCACGGTGAGCTCAGCACCCACAGAGAGACTTCTTGTGATTAAAAGAAACAAACCCATGC NM_001040032 RefSeq
chr8 + 10672636 10700593 C8orf74 NA chromosome 8 open reading frame 74 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136916_PI430048170 0.1548586991837650.4038109267063622.12741146619474
1.17908879582916 0.27369433322945 A A A 1.57552355547102 2.55050854790866
3.40361330958633 A A P LNCV6_136916_PI430048170 mRNA
GTGATGGGTGTAGTCATTAGCAAAGCATTTAAATCACTTGAGTATTTTGTCATGGTTCAT NM_003338 RefSeq chr10
+ 58334978 58370753 UBE2D17321 "ubiquitin-conjugating enzyme E2D 1, transcript variant 1"
GO:0005515|GO:0006511|GO:0007094|GO:0010467|GO:0004842|GO:0006367|GO:0034142|GO:0016874|GO:0061
418|GO:0000151|GO:0031145|GO:0005829|GO:0002756|GO:0005737|GO:0031398|GO:0007179|GO:0034138|GO:0
000209|GO:0051437|GO:0071456|GO:0051436|GO:0000122|GO:0030509|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_65039_PI430048170 0.00994368355466887 1.27187569076215 13.3932227813297
13.4787376884158 13.3056780545694 P P P 13.0065852073266 13.0854495814727
13.0488392172873 P P P LNCV6_65039_PI430048170 mRNA
ATCACGGCCGGTGATGCAGGCCTGAGTGTGTGCGGGAGACCAAATAAACCGGCTTGGGTG NM_015953 RefSeq
chr19 - 49555467 49580572 NOSIP 51070 "nitric oxide synthase interacting protein, transcript variant
1"
GO:0005515|GO:0005737|GO:0051001|GO:0000139|GO:0050999|GO:0046209|GO:0005654|GO:0005634|GO:0044
281|GO:0043086|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144665_PI430048170 0.3235281178574941.02502114617372 0.333417569816545
0.2516606868874860.332586269582009A A A 0.2734158673356950.262587842649953
0.276183169234917A A A LNCV6_144665_PI430048170 mRNA
TCGCCAGCGCATCATTAAGAAGTTTCAGTTTATAAAGTCACTTAGGTGTTTTTGGAAGGA NM_001005237 RefSeq
chr11 - 4923373 4924339 OR51G1 79324 "olfactory receptor, family 51, subfamily G, member 1
(gene/pseudogene)" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_119670_PI430048170 0.7348600309637031.13473108847452 3.64521226266559
4.72540197970745 4.12484974922239 P P P 4.28776383860201 4.02108361297473
3.80181603302227 P P P LNCV6_119670_PI430048170 mRNA
AGTCTCTTAAACAAAAGCAAAAGAATAAGCTTCGGGCGCTGTAGTACCTGCCAGCTTTCG NM_001199771 RefSeq

chr12 + 55720366 55724742 RDH5 5959 "retinol dehydrogenase 5 (11-cis/9-cis), transcript variant 1"
GO:0007603|GO:0042572|GO:0005789|GO:0005788|GO:0004745|GO:0007601|GO:0001523|GO:0044297|GO:0055
114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143375_PI430048170 0.0256116258722856 0.1852339091146240.502062713241477
1.85279276695519 2.29161171049176 A A A 3.75530208383078 3.97837565019121
4.60353832183232 P P P LNCV6_143375_PI430048170 mRNA
GGCTTGACATTATTATAACACGCATTTTGTGTTCCAGTTTAATAAAACGGTTTCTGAGTC NM_152240RefSeq chr3
- 179017224 179071868 ZMAT3 64393 "zinc finger, matrin-type 3, transcript variant 2"
GO:0005515|GO:0043065|GO:0005730|GO:0006915|GO:0008270|GO:0015031|GO:0040008|GO:0006974 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128703_PI430048170 0.3995347095916071.44380026231876 1.52470687604439
0.2759898914256360.435527432960417A A A 0.3530067293310620.299084512298736
0.334117281942176A A A LNCV6_128703_PI430048170 mRNA
CACTACCATCCTCTTGTAATTTTCCAGTTAGATTAATGGGGTTTGTTTTCAGGATTTTTG NM_170692RefSeq chr1 +
178093728 178479513 RASAL2 9462 "RAS protein activator like 2, transcript variant 2"
GO:0005515|GO:0005099|GO:0046580|GO:0007165|GO:0005737|GO:0032320|GO:0031235 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138844_PI430048170 0.0262230574030951.46707021603898 5.60566648218694
5.99309266843608 5.95140199110613 P P P 5.2841605353654 5.46136053430075
5.16032304146923 P P P LNCV6_138844_PI430048170 mRNA
TAAGTTAAGGGGCAGATTACCAATAAAGAACTGAATGAATTCATCCCCCCGGCCACCTCT NM_006569RefSeq chr2
- 27100593 27119127 CGREF1 10669 "cell growth regulator with EF-hand domain 1, transcript variant 1"
GO:0030308|GO:0008285|GO:0005509|GO:0006950|GO:0007050|GO:0005576|GO:0007155 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131796_PI430048170 0.0178817135106318 0.5633539536181 6.56515875659272
6.31311065326793 6.17211066435861 P P P 7.19812102282946 7.19351846117453 7.1700208439709
P P P LNCV6_131796_PI430048170 mRNA
ATCAGACAGCTCTGTAGCCTGACAAGAAATAAAACCACCCGTTTTCAGATGGGCAAAAAA NM_170607RefSeq chr17
+ 42567059 42573203 MLX 6945 "MLX, MAX dimerization protein, transcript variant 3"
GO:0005515|GO:0006355|GO:0000977|GO:0003700|GO:0046982|GO:0005634|GO:0044281|GO:0000122|GO:0001
227|GO:0003677|GO:0042803|GO:0006351|GO:0006913|GO:0005737|GO:0031325|GO:0006112|GO:0045892|GO:0
008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142336_PI430048170 0.4475792216211420.540026880965051 0.42743203774159
0.4659775979559590.444593216491437A A A 2.29779987170264 0.390261560919241
0.422745748164902A A A LNCV6_142336_PI430048170 mRNA
ATGCCTCCAGAAAGCATATTGCCCGGTGATGAAAAGGATCAGAAAATATACACTATATTT NM_001289973 RefSeq
chr8 - 6808519 6835644 XKR5 389610 "XK, Kell blood group complex subunit-related family,
member 5, transcript variant 2" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141600_PI430048170 0.00394540667589855 0.87887817258692 12.9417866208977
12.9178682779977 12.8766301962386 P P P 13.0520703404547 13.1268959806946
13.1157410877003 P P P LNCV6_141600_PI430048170 mRNA
GGACTTGTATTAGAGTCAGAGTCTTTTTATTTAGGCCAGTTGTCAAGTGTCAATAAAAGC NM_006303RefSeq chr7
+ 6009250 6023834 AIMP2 7965 aminoacyl tRNA synthetase complex-interacting multifunctional
protein 2
GO:0005515|GO:0010467|GO:0008285|GO:0016020|GO:0031398|GO:0006915|GO:0005634|GO:0060510|GO:0006
418|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145216_PI430048170 0.4081766500970290.9783142325003720.476006944340174
0.3784418913082180.435216082526393A A A 0.4253361207787550.488572420839764
0.471567966010477A A A LNCV6_145216_PI430048170 mRNA

CTCTACGCCTTTCTAGATGACAACTTCCGGAAGAACTTCCGCAGCATATTGCGGTGCTGA NM_005286RefSeq chr20 - 64105829 64106831 NPBWR2 2832 neuropeptides B/W receptor 2 GO:0005515|GO:0043005|GO:0005886|GO:0007268|GO:0038003|GO:0008188|GO:0004985|GO:0007186|GO:0042923|GO:0005887|GO:0007187|GO:0007218|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_130500_PI430048170 0.0382185044765269 0.26339144483183 3.69490098825351 2.33177652792991 2.62357036582646 P A A 4.92664967118826 4.9005354128518 4.97251046779315 P P P LNCV6_130500_PI430048170 mRNA
GTCTCTGATACCTGAAAAGTACATGTAAATGGTGATGGTGAAATAATACTGCAGTTAACT NM_004537RefSeq chr12 - 76045382 76085033 NAP1L1 4673 "nucleosome assembly protein 1-like 1, transcript variant 2" GO:0006260|GO:0005515|GO:0042470|GO:0008284|GO:0016020|GO:0006334|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_73886_PI430048170 0.814736409047685 1.02280106061309 4.80359291716248 5.01293153628406 4.64280600654528 P P P 5.25171656820298 4.46032756002789 4.53506589194391 P P P LNCV6_73886_PI430048170 mRNA
AGATATTCTAGCTGGGTTTGGATTTCTCACCCTGCTCCTTGGTCTTGACTGCGTGAAATT NM_006580 RefSeq chr3 + 190387871 190412143 CLDN16 10686 claudin 16 GO:0005515|GO:0007588|GO:0015693|GO:0016338|GO:0005886|GO:0005198|GO:0015095|GO:0016021|GO:0006875|GO:0005923|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_98583_PI430048170 0.26396855162153 0.743200291242882 4.57534268909336 4.9411207910486 4.97073265794157 P P P 4.87368443913377 5.07242819793331 5.71810909815434 P P P LNCV6_98583_PI430048170 mRNA
AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGT NM_000629 RefSeq chr21 + 33324908 33359822 IFNAR1 3454 "interferon (alpha, beta and omega) receptor 1" GO:0005515|GO:0032729|GO:0005886|GO:0019221|GO:0045351|GO:0009615|GO:0007259|GO:0051607|GO:0042110|GO:0060337|GO:0060338|GO:0004905|GO:0050718|GO:0005887|GO:0004904|GO:0016021|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_133056_PI430048170 0.135283098399841 1.03513123896579 0.382452377079868 0.390626968191408 0.449631097686448 A A A 0.351007606824335 0.336398246576508 0.386341005591205 A A A LNCV6_133056_PI430048170 mRNA
CCAAGTTGAATCCCATCATCTATAGTTTGAGGAACAAAGAAGTAAAAAAGGCAGTGAAGA NM_001004747 RefSeq chr11_JH159136v1_alt + 62948 63971 OR5T3 NA "olfactory receptor, family 5, subfamily T, member 3" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_134302_PI430048170 0.0184874139724529 2.58014211425431 7.67682756075206 7.94446375852132 7.56287724845929 P P P 6.81360540681916 6.20031474087074 5.95523196425109 P P P LNCV6_134302_PI430048170 mRNA
CAAAACCCTCCCAGTGTGTGTCCGTCTCTCATCTCAATAAAAGAATTTATTTTATTCTGA NM_024877 RefSeq chr19 - 40222207 40226690 CNTD2 79935 cyclin N-terminal domain containing 2 NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_142823_PI430048170 0.0910483144203945 0.322774754562171 2.46777972801355 0.457167872581498 0.408465866440528 A A A 2.62384536793941 3.42057016215196 3.10976244082609 A P P LNCV6_142823_PI430048170 mRNA
GAGCTGTCATTGAAATAGACATCTGTTTAAGAAGCGATACTTAGATGAACCTCTGTATTT NM_173206 RefSeq chr18 - 46815709 46917532 PIAS2 9063 "protein inhibitor of activated STAT, 2, transcript variant alpha" GO:0005515|GO:0016874|GO:0016925|GO:0003713|GO:0060766|GO:0005634|GO:0050681|GO:0003677|GO:0006351|GO:0045667|GO:0016607|GO:0045944|GO:0016605|GO:0008270|GO:0045893|GO:0030521|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_127526_PI430048170 0.767640811476464 0.989747848453876 0.438689759929065 0.47346362167212 0.378561191924088 A A A 0.516715810507846 0.402192072740949

0.41525569040349 A A A LNCV6_127526_PI430048170 mRNA
CACAGGAATGTATCACAACTTAACCGTTCCCGTTTGTTAGACTAGTTTCTTATTAATGTT NM_004795 RefSeq
chr13 + 33016432 33066145 KL 9365 klotho
GO:0008286|GO:0005886|GO:0005615|GO:0055074|GO:0007173|GO:0005499|GO:0004871|GO:0070062|GO:0002
526|GO:0048011|GO:0004566|GO:0030501|GO:0005975|GO:0017134|GO:0048015|GO:0007568|GO:0005576|GO:0
005104|GO:0006112|GO:0005179|GO:0005887|GO:0008543|GO:0045087|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135455_PI430048170 0.00462143461548376 0.753335806389166 7.65043691948898
7.65755605037438 7.71145165727167 P P P 8.02663806052563 8.04857850969058
8.16692545453613 P P P LNCV6_135455_PI430048170 mRNA
CATAAAGGAGAAAGCCCTGATTGATATGTATATAGAAGGTATAGCAGATTTGGGTGAAAT NM_000846 RefSeq
chr6 - 52750086 52763563 GSTA2 2939 glutathione S-transferase alpha 2
GO:0006805|GO:0030855|GO:0006749|GO:0044281|GO:0004364|GO:0070062|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_94355_PI430048170 0.0360934709624177 0.483958630963378 4.17230962122567
4.53917391020292 5.01429532823032 P P P 5.6823329217829 5.50669132297943
5.78815634694666 P P P LNCV6_94355_PI430048170 mRNA
GTGTCAATCAGTTTATCATCAGTAGGACTCAAGCTCTAATGTTGCACATTGATTCTTTTA NM_002270 RefSeq chr5
+ 72816590 72914388 TNPO1 3842 "transportin 1, transcript variant 1"
GO:0005515|GO:0010467|GO:0005737|GO:0006996|GO:0008536|GO:0016032|GO:0008139|GO:0005634|GO:0072
372|GO:0070062|GO:0005829|GO:0000060 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142797_PI430048170 0.223535141469413 1.06577010458841 0.561485164295877
0.721227544110453 0.565173728212804 A A A 0.494544470038086 0.535111690796125
0.547836897916364 A A A LNCV6_142797_PI430048170 mRNA
TACTACTTGTTCCTCTCACCTCTTGGTGGTGGGAATGTACTATGGAGCAGCTTTGTTCAT NM_001004689 RefSeq
chr1 + 248203067 248204006 OR2M3 NA "olfactory receptor, family 2, subfamily M, member 3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137663_PI430048170 0.0680623703419612 1.34163052045508 5.37995059481246
5.37724246457798 5.00960597830536 P P P 4.94792941137519 4.95273278412718
4.59660642483112 P P P LNCV6_137663_PI430048170 mRNA
GGTTAAGAAATACCTTTAAATTTAGGTAAATAAAGCTCAAGGAGGTGGGGCTGTCAAAAA NM_005223 RefSeq chr16
+ 3652938 3658095 DNASE1 1773 deoxyribonuclease I
GO:0005515|GO:0004520|GO:0006915|GO:0005634|GO:0005576|GO:0003779|GO:0005635|GO:0004530|GO:0000
737|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131022_PI430048170 0.0141291378214792 0.4028656261096 2.46418728848894
2.03806650515146 1.75342347496273 A A A 3.0006227491576 3.80370320567088
3.36352595888045 P P P LNCV6_131022_PI430048170 mRNA
ACCAGGCCATTCATTATTCCTCAAGTGTTAATATACTGACTTATGCAGTATTCAAACCAT NM_015040 RefSeq chr2
+ 208266266 208358751 PIKFYVE 200576 "phosphoinositide kinase, FYVE finger containing, transcript variant
2"
GO:0005515|GO:0048471|GO:0034504|GO:0043813|GO:0044281|GO:0046872|GO:0005829|GO:0035556|GO:0005
911|GO:0042147|GO:0000285|GO:0006661|GO:0036092|GO:0031410|GO:0005524|GO:0006898|GO:0016308|GO:0
032288|GO:0046854|GO:0000139|GO:0031901|GO:0031902|GO:0045121|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138652_PI430048170 0.873880617974556 1.08684883495076 0.264734281330296
0.276956845209327 1.25197292401636 A A A 0.376853976500669 0.887439486323919
0.337063032395451 A A A LNCV6_138652_PI430048170 mRNA
GAGGCTGTGGAGAAATAAGGACACATATATGGGAATGGAATGCAAAAGTTAAACTTTGGTNM_014412 RefSeq chr1
+ 174999755 175012027 CACYBP 27101 "calcyclin binding protein, transcript variant 1"

GO:0005515|GO:0043005|GO:0060416|GO:0007568|GO:0045740|GO:0030877|GO:0042803|GO:0044297|GO:0005737|GO:0005641|GO:0071277|GO:0060548|GO:0005654|GO:0055007|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145456_PI430048170 0.42555413490387 1.7102247389147 2.07688803633428 0.4592376724135470.389426573520599A A A 0.4512742482817630.407024379406338 0.425992026011478A A A LNCV6_145456_PI430048170 mRNA GGATGAAATCTTTGCAAAGGGTTTCCCTGGCACTCAAACAGAATAAATAGGCTTATAAAG NM_001185106 RefSeq chr3 + 111674675 111846447 PLCXD2 257068 "phosphatidylinositol-specific phospholipase C, X domain containing 2, transcript variant 1" GO:0016042|GO:0007165|GO:0008081|GO:0004871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133240_PI430048170 0.3202118762468080.69228250679039 0.411650768009179 0.5393148412564670.267081694649759A A A 0.3291306015997321.50460615604745 0.735764483501682A A A LNCV6_133240_PI430048170 mRNA GCTTGGTAAATTAAGCAGCTTTTGTATCTTCCCCTTTGACTTTAGGTAATAAAGCATCCA NM_001017920 RefSeq chr2 + 158795316 158815984 DAPL1 92196 death associated protein-like 1 GO:0006915|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127909_PI430048170 0.0902771917173135 0.6506367727282 7.30001371792959 7.19796512740778 7.18962411574791 P P P 7.42967063606372 8.01394800818334 8.02979472705125 P P P LNCV6_127909_PI430048170 mRNA TGTGCTCTGCATCTTATATTCCAGCAGGGTCTTCCAATGCATGGTTTAATAACTACTAGA NM_030927RefSeq chr10 + 80454281 80522635 TSPAN14 81619 "tetraspanin 14, transcript variant 1" GO:0045747|GO:0051604|GO:0009986|GO:0005886|GO:0097197|GO:0016021|GO:0019899|GO:0090002 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131854_PI430048170 0.0155027648176434 0.77620812570575311.2115869920297 11.4004741549226 11.1944066013807 P P P 11.6556062994346 11.7290850853633 11.5196528778095 P P P LNCV6_131854_PI430048170 mRNA GCTGGTAATAAACGAGGCCACAAATCATGCTTGTTAATAAATTGTGTGGTTCAAATCTGA NM_017723RefSeq chr9 + 137277827 137282641 TOR4A 54863 "torsin family 4, member A" GO:0051085|GO:0016021|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126958_PI430048170 0.8064237431967540.9601387385425829.86729691487531 9.88922619696408 9.7184829873544 P P P 10.101859226714 9.92938728363763 9.5772868805067 P P P LNCV6_126958_PI430048170 mRNA TCCAGAAGCTATTCTCTGAACGTATTGATGTGTTCAGCCCTGTGGAGTTCAACAAGGTGT NM_013265RefSeq chr11 + 65096114 65111860 VPS51 738 "vacuolar protein sorting 51 homolog (S. cerevisiae), transcript variant 1" GO:0005515|GO:0003674|GO:0005794|GO:0006869|GO:0006914|GO:0042147|GO:0016021|GO:0015031|GO:0000938 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144319_PI430048170 0.1474097603991850.778102124837962 7.39287678802738 6.9700655195181 7.0222568322183 P P P 7.24281493151617 7.75678179897232 7.46297375540013 P P P LNCV6_144319_PI430048170 mRNA CATCCGATTCCCCTGTATCAGTCACTGACAGTTAATAAACCTTTGCAAACGTTCAAAAAA NM_001278691 RefSeq chrX + 48255316 48267444 SSX1 6756 "synovial sarcoma, X breakpoint 1, transcript variant 1" GO:0006355|GO:0003714|GO:0005634|GO:0003676|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135082_PI430048170 0.3132298133894511.20270015970683 0.769389649471421 0.94612646076845 0.331620077592873A A A 0.4255756753233910.459479357937877 0.430200154136031A A A LNCV6_135082_PI430048170 mRNA TACTGCTTTGTCAGCAAGACTTTCCGGGCCACTGTCCGACAGGTCATCCACGATGCCTAC NM_181790RefSeq chr17 + 74367505 74372600 GPR142 350383 G protein-coupled receptor 142

GO:0005737|GO:0030054|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102400_PI430048170 0.5296757487441421.85550950768072 0.281483365253514
2.44962396707228 0.383914743581059A A A 0.372602058004747 0.31337513701489
0.819714637801321A A A LNCV6_102400_PI430048170 mRNA
TTCCTTCTTGTGGACCATTAAGCGAGACCCACCATCTTACTTCTTTGGCACAATCCATGT NM_001277053 RefSeq
chr2 - 84821666 84881245 TRABD2A 129293 "TraB domain containing 2A, transcript variant 1"
GO:0017147|GO:0031301|GO:0005887|GO:0018158|GO:0008152|GO:0030178|GO:0006508|GO:0060322|GO:0016
055|GO:0004222|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68250_PI430048170 0.0286459252940518 2.05652083514419 6.20861505926993
5.56797979700452 6.15448144092975 P P P 4.8262567834219 5.01892358016474
5.03894056555869 P P P LNCV6_68250_PI430048170 mRNA
TACACTTGTGAGGAGCCATATTACTACATGGAAAATGGAGGAGGTGGGGAGTATCACTGT NM_201442 RefSeq chr12
+ 7060675 7071031 C1S 716 "complement component 1, s subcomponent, transcript variant 1"
GO:0005515|GO:0006956|GO:0004252|GO:0045087|GO:0006958|GO:0005509|GO:0006508|GO:0072562|GO:0005
576|GO:0070062|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136745_PI430048170 0.727558433285527 1.15144696340052 1.31562786282032
0.350475050154381 0.285865671233377A A A 0.248980610224787 0.843325305087455
0.427872876876804A A A LNCV6_136745_PI430048170 mRNA
CAAACAATGAAAGACTTGGAAAAGGCCCTTTCAAATATCTTACCTAAGGAGAATCAAATC NM_001195790 RefSeq
chr17 - 35474922 35487739 SLFN12L NA schlafen family member 12-like NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_128737_PI430048170 0.161772509529393 0.930732035215376 0.262229518190825
0.301258530229654 0.282154756849596A A A 0.472126922605753 0.372801321902907
0.306850505613779A A A LNCV6_128737_PI430048170 mRNA
TACTAGGAATCTCATTTGCATTTGCATAGACTATACACATGGGGTGGAAAGGCCAGGCCT NM_001278381 RefSeq
chr17 - 43875358 43907942 MPP2 4355 "membrane protein, palmitoylated 2 (MAGUK p55
subfamily member 2), transcript variant 9"
GO:0007165|GO:0016020|GO:0005887|GO:0046939|GO:0004385|GO:0030165 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138574_PI430048170 0.384781562343758 1.0734263614853 4.84511908426842
4.80284521256517 5.01488281580855 P P P 4.65688321113052 4.75099936958411
4.94232213317536 P P P LNCV6_138574_PI430048170 mRNA
CTGTACATATCAGAAGCAAATAAAGAGCTCCACGTGCATCATTTCTTTCCCCACCCAGTT NM_001242896 RefSeq
chr22 + 31754022 31907034 DEPDC5 9681 "DEP domain containing 5, transcript variant 4"
GO:0043547|GO:0035556|GO:0048471|GO:0005765|GO:0005829|GO:0005096 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_52154_PI430048170 0.6526189701171 0.821914242927243 1.76013654722521 2.0439068433345
1.63881280217373 A A A 1.26916693375446 2.29060964400333 2.49167149768501 A A P
LNCV6_52154_PI430048170 mRNA
TACCAGAGTCCTACAGCCATGTTCTTGCAGAGTTTGAATCTCTGGATCCATTACTCTCAG NM_181507 RefSeq chr11
- 18278669 18322174 HPS5 11234 "Hermansky-Pudlak syndrome 5, transcript variant 1"
GO:0031084|GO:0006996|GO:0007596|GO:0043473 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129479_PI430048170 0.243110153139045 0.777314292785195 10.2374326230132
10.2893950230305 10.2559643651886 P P P 10.9699209270736 10.2662436518773
10.5496117394995 P P P LNCV6_129479_PI430048170 mRNA
ATGTGGAAGGTCATGATTTACCTGCATCTGAGAAACACCAGGATGTTACCTCCTAAAAAA NM_017947 RefSeq chr18
+ 36187516 36268722 MOCOS 55034 molybdenum cofactor sulfurase
GO:0006767|GO:0005575|GO:0044281|GO:0016829|GO:0005829|GO:0032324|GO:0043545|GO:0006766|GO:0006

777|GO:0030170|GO:0008265|GO:0016740|GO:0030151 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143617_PI430048170 0.715626471156249 1.85532096164421 3.74236809719061
0.819714637801321 1.65695591566481 P A A 1.90225942892141 1.74108602866195
1.47700762696644 A A A LNCV6_143617_PI430048170 mRNA
GGGACAGAGTCAAGGCTCAGAGAATAAAGGTAGCTAATCTCATCATAATATTTTTATTAG NM_001291780 RefSeq
chr20 + 57391397 57409330 RBM38 55544 "RNA binding motif protein 38, transcript variant 3"
GO:0006397|GO:0008380|GO:0008285|GO:0010830|GO:0005634|GO:0003729|GO:0030154|GO:0005829|GO:0007
049|GO:0000166|GO:0043484|GO:0005654|GO:0007050|GO:0003730|GO:0006978|GO:0070935|GO:0006977 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129267_PI430048170 0.339644471369080 9.22786999324997 10.689611629073 10.426614202455
10.6623449714755 P P P 10.5736747978626 10.7764150740424 10.7809332630766 P P P
LNCV6_129267_PI430048170 mRNA
ATTTTCTGGTGTGGCCTTCACCGGTGCCAAGGAGAATTTTTCCCTAGATTGGTGTAAACA NM_012145 RefSeq chr2
- 241675741 241686968 DTYMK 1841 "deoxythymidylate kinase (thymidylate kinase), transcript variant 1"
GO:0009041|GO:0043627|GO:0015949|GO:0008283|GO:0050145|GO:0055086|GO:0005634|GO:0044281|GO:0006
233|GO:0006227|GO:0005524|GO:0006235|GO:0004798|GO:0005829|GO:0046940|GO:0005739|GO:0005758|GO:0
007049|GO:0071363|GO:0005759|GO:0046939|GO:0045445|GO:0046686 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_122372_PI430048170 0.719057878389082 0.972003343964007 0.581360246408021
0.557337869871715 0.313026769991489 A A A 0.396422570563272 0.632322354329846
0.550987486344056 A A A LNCV6_122372_PI430048170 mRNA
TTCTTTCCTGAGCTTTCTATGCACCAAGACCTCAGCCAGGGACATGAGGTCCAGCTGCCC NM_001037814 RefSeq
chr22 - 16961935 17008222 GAB4 NA "GRB2-associated binding protein family, member 4" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138598_PI430048170 0.0112652657715604 1.99868769261993 7.47848853447685
7.87469308713257 7.63767484400161 P P P 6.96665173756334 6.61645709648411
6.37679685511833 P P P LNCV6_138598_PI430048170 mRNA
GCCTGAGATATAAGTTGTACTGCGTATGCAGTTTTTCCTCCAAAAATTAAATTGCTTTTG NM_022449 RefSeq chr2
- 237574321 237591126 RAB17 64284 "RAB17, member RAS oncogene family, transcript variant 1"
GO:0005515|GO:0005886|GO:0002415|GO:0032456|GO:0003924|GO:0030139|GO:0006886|GO:0030425|GO:0032
402|GO:0032401|GO:0005622|GO:0051489|GO:0016323|GO:0016324|GO:0045056|GO:0030100|GO:0043025|GO:0
046847|GO:0032482|GO:0070062|GO:0042470|GO:0051963|GO:0005525|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131406_PI430048170 0.323705972369636 1.11074569472205 5.81790077055635
5.88383591754859 5.77889295812038 P P P 5.87862358424747 5.67074645456736
5.44635654223843 P P P LNCV6_131406_PI430048170 mRNA
GAATACTTCCAATCAGGATATGCCCCTGCCTTATTTTTTCTAAGGTCTACTTTTACTACT NM_016302 RefSeq chr3 -
3149632 3179717 CRBN 51185 "cereblon, transcript variant 1"
GO:0005515|GO:0032463|GO:0016567|GO:0090073|GO:0005730|GO:0005634|GO:0046872|GO:0005737|GO:0016
020|GO:0004176|GO:0043161|GO:0031464|GO:0034766 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132782_PI430048170 0.484179437484643 0.809273995762001 0.37917455575451
0.256443730919062 0.28046430853796 A A A 0.263661341001115 1.12699223298411
0.262374522522983 A A A LNCV6_132782_PI430048170 mRNA
TTGAAAAGAGAAGAGAATGCCCAGCTTAATAGCAAGGAGGTAGAGGAGACCCTTCAGAAG NM_031907 RefSeq
chrX - 133025478 133028272 USP26 83844 ubiquitin specific peptidase 26
GO:0005515|GO:0004197|GO:0016579|GO:0004843|GO:0061136|GO:0043161|GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128127_PI430048170 0.000312404707284901 0.410366821066585 6.30668934933159
6.15575513462466 6.40347000477425 P P P 7.45580242304938 7.5341677187186 7.7279552739054

P P P LNCV6_128127_PI430048170 mRNA
ACAGAACTCAATGACTTGTCATGAGGTTTTCATATGAGCTACACATTGTGTACATTGATT NM_005907 RefSeq chr6
- 119177200 119349766 MAN1A1 4121 "mannosidase, alpha, class 1A, member 1"
GO:0005793|GO:0005794|GO:0005783|GO:0004571|GO:0005509|GO:0015923|GO:0005737|GO:0000139|GO:0016
020|GO:0016021|GO:0044267|GO:0070062|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140879_PI430048170 0.000298974011752693 2.95273997886461 11.5243921815277
11.4994601703284 11.6498508148183 P P P 9.96944003078446 10.0227643609402
9.99938604302803 P P P LNCV6_140879_PI430048170 mRNA
GCCTTCTCCTTTGTCTTTGTTTCACTCTGTGTTTCCAATAAACTCATTGTAGCGAATCAA NM_002284 RefSeq chr12 +
52301864 52309163 KRT86 3892 "keratin 86, type II" GO:0005198|GO:0045095|GO:0005615|GO:0070062
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132354_PI430048170 0.34951312394648 1.03594222984995 0.298144366552622
0.2611759197644350.398910701473015 A A A 0.2825320080163980.248191629010844
0.277981534696922 A A A LNCV6_132354_PI430048170 mRNA
CTGGTTGGATTTCTCACCAGGATTGTCTATAGAAGTTAACTGATTTATGATTGTTAACAC NM_001146265 RefSeq
chr7 - 113080412 113087778 GPR85 54329 "G protein-coupled receptor 85, transcript variant 1"
GO:0007165|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141882_PI430048170 0.3552936498422910.8339767032408120.441778964542078
0.4132006813676320.242575983874618 A A A 0.3689431936925310.44244690219491
0.995464860704566 A A A LNCV6_141882_PI430048170 mRNA
TACTTCTTCCATTTCTTTGGCATCGTGGACAGCGTCATAATCGCCATGATGGCTTATGAC NM_001004456 RefSeq
chr19 + 9093244 9094186 OR1M1 NA "olfactory receptor, family 1, subfamily M, member 1"NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58762_PI430048170 0.4054655617326841.28441470138741 1.19787377665364 0.317545230689893
0.353121224419485 A A A 0.2951483002172150.3136056775616650.357211760588239 A A A
LNCV6_58762_PI430048170 mRNA
CATACCATTCTTTTCTTGCCCCAAACTCCAAATAAACCACAAAAAGAAAGAAAAGCTTC NM_006446 RefSeq chr12
+ 21131193 21239796 SLCO1B1 10599 "solute carrier organic anion transporter family, member 1B1"
GO:0016323|GO:0016020|GO:0005886|GO:0015347|GO:0005887|GO:0015721|GO:0015711|GO:0043252|GO:0008
206|GO:0044281|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132956_PI430048170 0.1268736475323070.6397040440811418.26380047760359
7.96645353990585 8.29889601139038 P P P 8.2810174607143 8.95884915034713
9.11664936434649 P P P LNCV6_132956_PI430048170 mRNA
TCTGCCAGAGACGGGCCCAGAAGACTAAAGCTTCACTATAACGTGACTACAACTAGATTA NM_014791 RefSeq chr9
+ 36572861 36677683 MELK 9833 "maternal embryonic leucine zipper kinase, transcript variant 1"
GO:0030097|GO:0005515|GO:0043065|GO:0005886|GO:0008283|GO:0005509|GO:0008631|GO:0006915|GO:0018
108|GO:0005524|GO:0008289|GO:0061351|GO:0046777|GO:0016020|GO:0004674|GO:0000086|GO:0004715|GO:0
005938 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131814_PI430048170 0.0470525976638443 2.31961943571831 9.49838764310985
9.56645440344621 9.41946940255726 P P P 8.80666061904293 7.97209954538841
7.87650896567674 P P P LNCV6_131814_PI430048170 mRNA
TTTTCTAAGAGTCTGTGAACCCAGGAGCCTCTCGCTCTGGCTTTAAGATGCTATGACTAA NM_001242348 RefSeq -
- 0 0 --- NA - NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129943_PI430048170 0.3747533454041070.6962373641765620.361017625886639
0.4263894697384930.356739587869914 A A A 0.2730527604941051.52285582450272
0.615525845011658 A A A LNCV6_129943_PI430048170 mRNA
AATGATGTGTGCTTCAGTTTATTGCACTTTTCAAATACTCCAGTTTTTTGTGTGCGTGTG NM_001267598 RefSeq chr12

+ 16347642 16377189 MGST1 4257 "microsomal glutathione S-transferase 1, transcript variant 8"
GO:0005515|GO:0006805|GO:0005783|GO:0042493|GO:0005743|GO:0045177|GO:0006749|GO:0010243|GO:0005
634|GO:0005741|GO:0044281|GO:0004364|GO:0042803|GO:0071449|GO:0004602|GO:0005739|GO:0070207|GO:0
043295|GO:0032496|GO:0005789|GO:0033327|GO:0016021|GO:0005778|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138524_PI430048170 0.2590341387335790.5564371515163070.444570954639476
2.39763536772341 1.81878942498881 A A A 2.97849988175441 2.83715913091097
1.69060452568691 P P A LNCV6_138524_PI430048170 mRNA
TGCAAGTCCCAACTTTGAATAAAACAGATGATGTCCTGTGACTGCCCCACAGAGATAAGG NM_016428RefSeq chr17
+ 49210226 49223225 ABI3 51225 "ABI family, member 3, transcript variant 1"
GO:0030334|GO:0005622|GO:0005515|GO:0005737|GO:0016020|GO:0006928|GO:0018108|GO:0030027 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144955_PI430048170 0.7135699758198081.12858155913469 4.45772319977198 3.7764800577242
3.48304000596208 P P P 4.03465695075298 3.81309674259557 3.46929171875071 P P P
LNCV6_144955_PI430048170 mRNA
CCTCCCCTTGAGAGTCATCAGAAAAATACATTAGGAAAATGTGTTTAGAAATAAAAGCAC NM_001278694 RefSeq
chr14 - 105049388 105065550 GPR132 29933 "G protein-coupled receptor 132, transcript variant 1"
GO:0000082|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137494_PI430048170 0.9677591031156920.9961269671499770.434879407051934
0.4756149846237540.439626417413082A A A 0.3806952828938590.399416490644803
0.578749238775818A A A LNCV6_137494_PI430048170 mRNA
TAATTCACATTGGAGAGAAACCACCTGCTTGTCTTCTATGTGGGAAGGCCTTCAGTCTGT NM_001193630 RefSeq
chr8 + 7926336 7952413 ZNF705B NA zinc finger protein 705B NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137590_PI430048170 0.1686192861391060.8380021635077621 0.3696026168859
10.4785864485969 10.6377424572674 P P P 10.9534384055806 10.5371617660416 10.742926920012
P P P LNCV6_137590_PI430048170 mRNA
GTTGGGGGAGCTGATAAGGTTTTTGTACAGTATTTTCTCCTTCGTTGTATTGATTTTTGT NM_016545RefSeq chr1 +
181088501 181090843 IER5 51278 immediate early response 5 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144625_PI430048170 0.2388149695158381.13112504757225 7.84816001454702 8.058669422713
8.04228546104924 P P P 8.01265973293242 7.65560680624436 7.73195707031075 P P P
LNCV6_144625_PI430048170 mRNA
GTTAAAAGAGAGAGATGTGCTGTCAGTTTTCCTTCCGGATGTACCAGAAACTGAGAGCTA NM_178859RefSeq chr15
+ 65045369 65053396 SLC51B 123264 "solute carrier family 51, beta subunit"
GO:0043234|GO:0005215|GO:0070863|GO:0031647|GO:0046982|GO:0005886|GO:0015721|GO:0090314|GO:0060
050|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62562_PI430048170 0.0161193777153527 1.28972021572624 8.64676191514452
8.54099565543921 8.40626198915285 P P P 8.18991777109627 8.23359195693752
8.07473581631494 P P P LNCV6_62562_PI430048170 mRNA
ACGGCCCAGCAAAAGCGATGCTGAGAGGGGAAACAGTCCAGAGTCCAACAGCAGAACTTG NM_001005920
RefSeq chr16 - 681666 684439 JMJD8 339123 jumonji domain containing 8 GO:0070062 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_132040_PI430048170 0.7458901403755531.05787341409875 0.26527601417948
0.3016057118803160.780552417858971A A A 0.4739451535528170.375617413306608
0.308848759077885A A A LNCV6_132040_PI430048170 mRNA
GTGTAAAGAAAGTGAAAACCCTATTAATATCTGCTCACATCAACTCAACATCAGAGTTCA NM_001277403 RefSeq
chr19 + 23116974 23147212 ZNF730 100129543 zinc finger protein 730

GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129243_PI430048170 0.0369774756343631.25637424154084 10.4967233132525
10.4273968330136 10.4612082769904 P P P 9.98399061896102 10.2132249050889
10.1902852501626 P P P LNCV6_129243_PI430048170 mRNA
GTTAAAGTCCTATGAATGTGTGTGTGTGTGTGCTATTAAAACTGCTTTTTCTCAGTTTGA NM_018121RefSeq chr10
+ 100912568 100965134 FAM178A 55719 "family with sequence similarity 178, member A, transcript
variant 1" GO:0005634|GO:0005615|GO:0000785|GO:0043231 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134132_PI430048170 0.7624112329197821.01339653323979 0.401596792386224
0.5316639203509910.432797139486401A A A 0.5278593803452390.388206439692377
0.391154554241556A A A LNCV6_134132_PI430048170 mRNA
CTCCAAAGACTTTCTTACGGTATAATACATGTTGTTTAGGATTGTGTTTCTTAGTCACTGNM_052913RefSeq chr6 +
130437116 130443065 TMEM200A 114801 "transmembrane protein 200A, transcript variant 4" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98271_PI430048170 0.6009462602634760.974308710944033 1.55696878731688 1.70594775770111
1.66409488376696 A A A 1.77640653618304 1.62979388956376 1.6325948015864 A A A
LNCV6_98271_PI430048170 mRNA
ATTGCCTTTCGTTTCCCTATTCAAGGCCAAGGCTAGATTCTCTTCATTGTCTCCATTTCT NM_173499RefSeq chr15 +
96783406 96785615 SPATA8 145946 "spermatogenesis associated 8, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_82717_PI430048170 0.0598807212182201 0.8226528581494553.36581310664293
3.35246763129866 3.55306587181162 P P P 3.55037022489836 3.83522259365248
3.72534180657816 P P P LNCV6_82717_PI430048170 mRNA
TATTCCTCTTATTACTGTAAAATCATGCCTAGATCTTTTGGAGCTGTGTTCTACACCTTT NM_018427RefSeq
chr16_KI270853v1_alt + 575340 609661 RRN3 54700 "RRN3 RNA polymerase I transcription factor
homolog (S. cerevisiae), transcript variant 1"
GO:0010467|GO:0008283|GO:0042254|GO:0005730|GO:0006361|GO:0005634|GO:0006360|GO:0001701|GO:0007
000|GO:0048872|GO:2000142|GO:0005654|GO:0070063|GO:0045893|GO:0007028 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143233_PI430048170 0.2534586519898340.85347895247716310.1574214684703
9.75023220589976 9.64682973376411 P P P 10.164942721322 10.1087700033113
10.0143630580807 P P P LNCV6_143233_PI430048170 mRNA
TCCCCCTCAGACCTCCAAAGGGCAACAGAAGAGTATTAATAAACGTGAAAACTTAAAAAA NM_004220RefSeq chr16
+ 3135055 3142804 ZNF213 7760 "zinc finger protein 213, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133738_PI430048170 0.8719386706380690.9850004199470236.48592798003442
6.34922062218742 6.57549386646029 P P P 6.41368650999708 6.38715945223312
6.66726781078642 P P P LNCV6_133738_PI430048170 mRNA
CTGAAGCCTTTCTCCTTTTCTGTCACTTGCAAATTCCAAATTATAGCTAATAAAGATGAC NM_014845RefSeq chr6
+ 109691220 109825431 FIG4 9896 FIG4 phosphoinositide 5-phosphatase
GO:0005515|GO:0043813|GO:0006661|GO:0043812|GO:0036092|GO:0005783|GO:0044281|GO:0032288|GO:0000
139|GO:0048666|GO:0004438|GO:0016311|GO:0031901|GO:0031902|GO:0010976|GO:0043473|GO:0007626|GO:0
007033|GO:0055037|GO:0006644|GO:0010008|GO:0031642 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_129001_PI430048170 0.00032046388713601 3.26193443393718 8.3657154261071
8.5922119576318 8.42936056895414 P P P 6.95284103378194 6.65028729099266
6.65526759738072 P P P LNCV6_129001_PI430048170 mRNA

GAAACAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAAACAGATATTATTT NM_003809RefSeq chr17 + 7549057 7557890 TNFSF12 8742 "tumor necrosis factor (ligand) superfamily, member 12, transcript variant 1"
GO:0005515|GO:0005164|GO:2001238|GO:0048471|GO:0045732|GO:0005102|GO:0006915|GO:0001525|GO:0097190|GO:0005125|GO:0005615|GO:0045766|GO:0030154|GO:0007165|GO:0006955|GO:0001938|GO:0005887|GO:0043542 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140699_PI430048170 0.8885957002078891.06712511393426 0.247637183617615 0.30174928962461 1.1772405496448 A A A 0.9049722676186130.356640834481372 0.303247380810058A A A LNCV6_140699_PI430048170 mRNA
CTTTCTTCTCTTCCACATGTGCATATTCTGAGAACCAGACTTGGGGGATAGTAGCTTCTC NM_001282136 RefSeq chr6 + 77690655 77924759 MEI4 NA meiosis-specific 4 homolog (S. cerevisiae) NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127976_PI430048170 0.0940228378095832 0.4590520345828820.351800110011031 0.4183324559644920.349389756395804A A A 0.7444728562737811.61700235826116 1.89675589561586 A A A LNCV6_127976_PI430048170 mRNA
CCCTCGAAAAACAAAAATCCCTGGCTAATCCTGAAATATATTTAACTTGAAGTCTTTGGA NM_001267609 RefSeq chr1 - 168079541 168137667 GPR161 23432 "G protein-coupled receptor 161, transcript variant 1"
GO:0030666|GO:0060170|GO:0007186|GO:0004930|GO:0030819|GO:0007275|GO:0072372|GO:0016021|GO:0055037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145723_PI430048170 0.4599418289941910.8958865635967596.08207582227895 5.58212697428984 5.85262180564347 P P P 5.8919950400309 6.26351750880493 5.84256305453015 P P P LNCV6_145723_PI430048170 mRNA
TGCAACCACTGAACCTGTGGACTGTGTTCAAACAAATGCCAGCAGAACACAAAAGGCGAC NM_175066RefSeq chr12 - 132136594 132144335 DDX51 317781 DEAD (Asp-Glu-Ala-Asp) box polypeptide 51
GO:0016020|GO:0006364|GO:0005730|GO:0004386|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128020_PI430048170 0.8017191636764931.01260434542205 0.417094757597238 0.53218860322585 0.468672977652283A A A 0.5328061707037230.502588427101888 0.321759135786796A A A LNCV6_128020_PI430048170 mRNA
TCACTGGTGAGGTCTCAAAAGAGATAGAAGAGGATGGTTATGTAGTTGGGGAAAGAAATTNM_152338RefSeq chr16 + 29778239 29781648 ZG16 653808 zymogen granule protein 16
GO:0031012|GO:0042589|GO:0005796|GO:0005578|GO:0030246|GO:0060205|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137929_PI430048170 0.0728002742373498 0.9383021995418940.303218939793777 0.3119594898225960.315951303341454A A A 0.4516820185672240.393020187569503 0.360601756160984A A A LNCV6_137929_PI430048170 mRNA
TGAGTTTGCCTTGTTAATCTTCAATAGTTTTACCTACCCCAGTCTTTGGAACCCTAAATANM_002909RefSeq chr2 + 79120457 79123419 REG1A 5967 regenerating islet-derived 1 alpha
GO:0008284|GO:0030246|GO:0008083|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140741_PI430048170 0.0098436287243566 0.5049028459086158.98760638054416 9.16180397609874 9.326218235934 P P P 9.93092973334466 10.029193851435 10.4409473547198 P P P LNCV6_140741_PI430048170 mRNA
TCTATTTGCACTGTGCCTTTCAACTCCAGAAACATTCTGAAGATGTACTTGGATTTAATT NM_001153RefSeq chr2 + 69741994 69826464 ANXA4 307 annexin A4
GO:0012506|GO:2000483|GO:0048471|GO:0043066|GO:0004859|GO:0031965|GO:0051059|GO:0005886|GO:0006357|GO:0009986|GO:0005509|GO:0005634|GO:0032088|GO:0043086|GO:0042802|GO:0005544|GO:0007165|GO:0005737|GO:0030855|GO:0070062|GO:0048306 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129978_PI430048170 0.1650382780233010.8505868641151176.24312700385963 6.01760361168992 6.20925634632015 P P P 6.4376226157536 6.17567538957134

6.54285775807476 P P P LNCV6_129978_PI430048170 mRNA
TTCCTGCTGTAAAATAATTTTTAAAACCTTGACATTTCAAAGACTGCCTTGAAAGGTCGC NM_018025RefSeq chr19
+ 33080879 33130412 GPATCH1 55094 G patch domain containing 1
GO:0000398|GO:0071013|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138441_PI430048170 0.6155769311613420.9238789425150322.67614939826786
3.34469307231765 3.40127491384875 A P P 3.0935194716219 3.33123109453578
3.42621474040709 P P P LNCV6_138441_PI430048170 mRNA
ACTTTTGAGAAATCTACGTTTCCCAAGTTTTATGGGAACTGGCTATTCCTTGTCCCGGCA NM_018728RefSeq chr15
- 52192317 52295798 MYO5C 55930 myosin VC
GO:0005516|GO:0003774|GO:0008152|GO:0003779|GO:0016459|GO:0005524|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_74332_PI430048170 0.2212877584734940.7536671695296510.5377226407966940.631253939173634
0.516323326208066A A A 1.1057126029436 1.20375985095814 0.509615619610016A A A
LNCV6_74332_PI430048170 mRNA
ATGTCATACGTGAAAGAGACAGTGGACAGATTGCTCAAAGGATATGACATTCGCTTGCGG NM_000812RefSeq chr4
+ 47031277 47426430 GABRB1 2560 "gamma-aminobutyric acid (GABA) A receptor, beta 1"
GO:0005230|GO:0030054|GO:0005886|GO:0004890|GO:0034707|GO:0007268|GO:0055085|GO:0005254|GO:0007
165|GO:0034220|GO:0005887|GO:0045211|GO:0006810|GO:0071420|GO:0006811|GO:0015276 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145396_PI430048170 0.140162796208398 1.08704084440672 0.555519897806631
0.4661353062428660.607377662963688A A A 0.339643056890351 0.412362247493667
0.513999683761288A A A LNCV6_145396_PI430048170 mRNA
GCAATACTGCACCTGGTGATCACAAAGATAATGTTCTACTTCTGATAGAAATAATTTCTC NM_012082RefSeq chr8
+ 105318918 105804539 ZFPM2 23414 "zinc finger protein, FOG family member 2"
GO:0005515|GO:0030324|GO:0045599|GO:0005634|GO:0007506|GO:0005737|GO:0003221|GO:0045944|GO:0048
568|GO:0001085|GO:0060548|GO:2000195|GO:0001105|GO:0003714|GO:0060412|GO:0000122|GO:0003677|GO:0
001701|GO:0006351|GO:0001078|GO:0007596|GO:0003148|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136243_PI430048170 0.4145090536821620.7986941297136820.304700662947113
0.3189723147445260.380951043625847A A A 1.14100861809212 0.319973188790953
0.361859671079354A A A LNCV6_136243_PI430048170 mRNA
CCCACATATAAATGTACTTTTCCTTCCAGAAAAATTTCCCTTGAGGAAAAATGTCCAAGA NM_002974RefSeq chr18
- 63637258 63644319 SERPINB4 6318 "serpin peptidase inhibitor, clade B (ovalbumin), member 4,
transcript variant 1"
GO:0030162|GO:0010951|GO:0005737|GO:0004867|GO:0010466|GO:0019899|GO:0005615|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138138_PI430048170 0.185529524418356 1.14847671512817 12.5213773527075 12.607931542589
12.8184672073067 P P P 12.4707008122603 12.286679473039 12.5914207403609 P P P
LNCV6_138138_PI430048170 mRNA
CTTGATCAGTGAACACTAACATTTTGGGGACAACTTAGTCAATTGGTTTTCCTTACAACA NM_001033088 RefSeq
chr15 + 90265662 90272211 NGRN 51335 "neugrin, neurite outgrowth associated, transcript variant
2" GO:0030182|GO:0005634|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127258_PI430048170 0.799382228108118 1.04545410760888 0.86245866512205
0.4061085872170090.35758788622609 A A A 0.443755686904796 0.633629911153712
0.401138745235656A A A LNCV6_127258_PI430048170 mRNA
AGCATCAAGTAATTCGTTAGATGCTTGTTAAATGAAGTGGGTAGGTGAACAAAGTTAACG NM_153448RefSeq chrX
- 104250037 104254918 ESX1 80712 ESX homeobox 1
GO:0043565|GO:0005737|GO:0000977|GO:0060713|GO:0060716|GO:0051726|GO:0005634|GO:0000122|GO:0045
892|GO:0001227|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_92352_PI430048170 0.2961935718527171.079876310007 9.18848400853116 9.05795229396943
9.01574063261394 P P P 8.93401057914433 9.12195590354695 8.86703193639731 P P P
LNCV6_92352_PI430048170 mRNA
TCTACAGGACACTATCAAGAGGTATAATCTGCAGATGTTGGAAGCTGAGGGCAGCATGAA NM_025207 RefSeq chr1
+ 154983293 154993111 FLAD1 80308 "flavin adenine dinucleotide synthetase 1, transcript variant 1"
GO:0006771|GO:0005737|GO:0005886|GO:0003919|GO:0006766|GO:0005759|GO:0006777|GO:0006767|GO:0044
281|GO:0005524|GO:0006747|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137169_PI430048170 0.5781382386419650.9694606289961990.487979683158854
0.4994559294451550.29709522390538 A A A 0.4051780506669870.534001488875374
0.485482129420189 A A A LNCV6_137169_PI430048170 mRNA
CTTTTCTTTCTTACTGGGAAATTGAAGTAGCATGTCCTCTGAGTTGCATGTTTTAGATAA NM_025145 RefSeq chr10
- 104129887 104232362 CFAP43 80217 cilia and flagella associated protein 43 GO:0042995 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_136681_PI430048170 0.9471779541072861.00175667703765 12.2089943271248
12.2347750775188 12.1612904762219 P P P 12.1963973152676 12.290337378113
12.1057870788103 P P P LNCV6_136681_PI430048170 mRNA
ATACTTTGTGAGCAGCGGTTCCATCGCAGTGAACGCCGACTCTTCGGTGCAGTTGTTGGC NM_001687 RefSeq chr19
+ 1241749 1244825 ATP5D 513 "ATP synthase, H+ transporting, mitochondrial F1 complex, delta
subunit, transcript variant 1"
GO:0005215|GO:0015986|GO:0006200|GO:0022857|GO:0005743|GO:0044281|GO:0005524|GO:0005753|GO:0006
119|GO:0022904|GO:0005739|GO:0006754|GO:0043531|GO:0046961|GO:0046933|GO:0042776|GO:0005759|GO:0
000275|GO:0046688|GO:0016887|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143627_PI430048170 0.0273509147919811 0.6470052331401748.75644101350321
8.539453525152 8.4119745814405 P P P 8.91093473736669 9.36306551893296 9.2993590736264
P P P LNCV6_143627_PI430048170 mRNA
CATGCTGGTGGTGCCTGAGGTCTGATGGCCTCTAATAAACTGTGTCCTATATGCAAAAAA NM_016573 RefSeq chr19
- 19629472 19643667 GMIP 51291 "GEM interacting protein, transcript variant 1"
GO:0035556|GO:0005622|GO:0005515|GO:0051056|GO:0034259|GO:0032321|GO:0007264|GO:0046872|GO:0005
100|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51039_PI430048170 0.1002603592209380.8217045436425988.20723213197058 8.30871945097388
8.19297659671753 P P P 8.36401760003967 8.70858007408987 8.467062331558 P P P
LNCV6_51039_PI430048170 mRNA
TTCAGACAAACAGGAAACTTCTGCAGTCAGGAAGGCTCCTGTACCCTTCTTCTTTTCCTA NM_001164277 RefSeq
chr11 - 119024350 119030906 SLC37A4 2542 "solute carrier family 37 (glucose-6-phosphate
transporter), member 4, transcript variant 1"
GO:0005215|GO:0005783|GO:0005975|GO:0030176|GO:0015760|GO:0044281|GO:0042593|GO:0055085|GO:0008
645|GO:0015152|GO:0015758|GO:0016020|GO:0005789|GO:0006810|GO:0009405|GO:0006006|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143811_PI430048170 0.3722984019250731.06717112986056 11.9474722665253
11.8628730740512 11.7233927425798 P P P 11.6519739406036 11.878688945704
11.7210724797988 P P P LNCV6_143811_PI430048170 mRNA
CATTCACCTTTCTCCTAGAATGCTGTTGTAAATAAACAAATGGATCCCTGGAAACTTTAA NM_002768 RefSeq chr16
- 89644430 89657785 CHMP1A 5119 "charged multivesicular body protein 1A, transcript variant 2"
GO:0005515|GO:0007076|GO:0000815|GO:0016458|GO:0015031|GO:0016363|GO:0042803|GO:0045014|GO:0000
910|GO:0007034|GO:0006508|GO:0016192|GO:0070062|GO:0006997|GO:0000794|GO:0005815|GO:0019904|GO:0
010824|GO:0006351|GO:0012505|GO:0000920|GO:0008270|GO:0007080|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135752_PI430048170 0.1845086304292411.33803463557875 5.93184104998685
6.44615125015233 6.61362537888635 P P P 5.78470986811085 6.00292607728947

6.01610685971817 P P P LNCV6_135752_PI430048170 mRNA
CTCAGAGGTTATGTGTTCTAACTATTATCAAATGAATAAATCCTCTCTATCACATCCCCC NM_017425 RefSeq chr11
+ 124673843 124694791 SPA17 53340 sperm autoantigenic protein 17
GO:0007338|GO:0005516|GO:0005737|GO:0016020|GO:0003351|GO:0031514|GO:0072372|GO:0007283|GO:0007
339 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101449_PI430048170 0.25668683606402 0.7894094860250024.57510757126569
4.36307538498895 5.06120296519532 P P P 4.68764535792306 5.19445869946594
5.17669456979978 P P P LNCV6_101449_PI430048170 mRNA
TATGTATCATAGGTACTGGGAAGAATACAGCAAGGGTGCAGACTATATGGACTGCTTATA NM_001198779 RefSeq
chr10 - 35008550 35074330 CUL2 8453 "cullin 2, transcript variant 2"
GO:0005515|GO:0006511|GO:0008285|GO:0016567|GO:0061418|GO:0071456|GO:0097193|GO:0005829|GO:0000
082|GO:0016032|GO:0031462|GO:0005654|GO:0007050|GO:0031625 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133050_PI430048170 0.00107942467773319 1.93794070464902 10.7933795048592
11.0750498872006 10.8823239859156 P P P 10.0924861697709 9.9190153729705
9.88129460497424 P P P LNCV6_133050_PI430048170 mRNA
GGGAAAAGGGTTTTAGTAGAAGGGTGAATCGTATTTTACACAGCGGTCTTATTTATATAA NM_005740 RefSeq chr22
- 38778507 38794156 DNAL4 10126 "dynein, axonemal, light chain 4"
GO:0005929|GO:0048011|GO:0005737|GO:0003774|GO:0030286|GO:0005886|GO:0008152|GO:0005874|GO:0007
017 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143510_PI430048170 0.0109017019355033 0.4200457496025144.01128496207076
3.6647454521915 4.14800860702448 P P P 5.2420652376201 5.21828139375486 5.1585107283103
P P P LNCV6_143510_PI430048170 mRNA
AGGGAGAATACACATCTTTCTTGGAAGCTGGGAGTGTGTTCTCATTTCATGTCCATTCAG NM_017849 RefSeq chr2
- 96250207 96266013 TMEM127 55654 "transmembrane protein 127, transcript variant 1"
GO:0003674|GO:0032007|GO:0017137|GO:0005737|GO:0008285|GO:0005886|GO:0007032|GO:0016021|GO:0005
769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127263_PI430048170 0.9499731734178411.01108374043684 7.57432495608996
7.72936140898171 7.99627461897061 P P P 7.77969998777623 7.60263676439649
7.88760315061417 P P P LNCV6_127263_PI430048170 mRNA
CTACCCAGCATTCTGGTTTTTATGTTTTTTATGATCTATGCAGACAACTGTGTATTCTGT NM_001199297 RefSeq chr5
- 176905004 177006779 UIMC1 51720 "ubiquitin interaction motif containing 1, transcript variant 1"
GO:0005515|GO:0031572|GO:0005634|GO:0045739|GO:0006351|GO:0006302|GO:0042393|GO:0046965|GO:0070
531|GO:0010212|GO:0070537|GO:0045892|GO:0070530 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127237_PI430048170 0.7475013955753560.9895697392712250.276915805178133
0.2823896681348880.405751527460003 A A A 0.3630209579884750.306568772564623
0.343990610222592 A A A LNCV6_127237_PI430048170 mRNA
CTCTTAGACGAGTCATGGATTTGTACTGAAGTATTTACGTTTTCCACTTTTCTCCTTTAA NM_005210 RefSeq chr2 -
208142572 208146153 CRYGB 1419 "crystallin, gamma B"
GO:0005737|GO:0005212|GO:0070309|GO:0005634|GO:0005575|GO:0007601 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133086_PI430048170 0.00768633997130532 1.16988027681417 11.5983585362285
11.5259489538904 11.537192591665 P P P 11.2590810920246 11.3621415460681
11.3598701458499 P P P LNCV6_133086_PI430048170 mRNA
CTGTTTGCTTTGTGGATCCTGGGATAACATGTATATGTGTACACATGCCTATTCTGCCAA NM_005371 RefSeq chr12
- 57768567 57772131 METTL1 4234 "methyltransferase like 1, transcript variant 1"
GO:0005515|GO:0005737|GO:0000049|GO:0030488|GO:0005730|GO:0008176|GO:0005654|GO:0005634|GO:0043
527|GO:0006400 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139174_PI430048170 0.2249053882238750.77766876418606 5.34881022914802

5.14278271019294 5.64301562317846 P P P 5.50263505649673 5.57188109641294
6.11239943570698 P P P LNCV6_139174_PI430048170 mRNA
CCATCTTCTATTACCAGCACTTACAAGCACTGTGAAAACTGATCATGACAAATAAGTAAA NM_022899RefSeq chr3
- 53867065 53882202 ACTR8 93973 ARP8 actin-related protein 8 homolog (yeast)
GO:0005515|GO:0031011|GO:0007067|GO:0006355|GO:0006281|GO:0006338|GO:0006310|GO:0005634|GO:0005
524|GO:0006351|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137951_PI430048170 0.4034420486649560.93858832673123 7.01369011020926
7.19706987646819 7.13953856249245 P P P 7.28714380720778 7.2798826131011
7.05140183125823 P P P LNCV6_137951_PI430048170 mRNA
TCAGTTAATGATGAGTGACTATATTTACCAAAGCCCCTACCTGCTGCTGGGTCCCTTGTA NM_007286RefSeq chr5
+ 150640644 150659230 SYNPO 11346 "synaptopodin, transcript variant 1"
GO:0005515|GO:0005737|GO:0001725|GO:0043197|GO:0045211|GO:0032233|GO:0051492|GO:0043204|GO:0014
069|GO:0003779|GO:0005923|GO:0015629 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131470_PI430048170 0.0584716108877453 0.6694692219389651 0.0055587048486
10.1722146725084 10.5829429428246 P P P 10.7923430762755 10.7729455977946
10.9850621635295 P P P LNCV6_131470_PI430048170 mRNA
GTCTAGGTCTTTGATATTGCTCTTTTGGTTAACACTAAGCTTAAGTAGACTATACAGTTG NM_006667RefSeq chrX
+ 119236244 119244466 PGRMC1 10857 "progesterone receptor membrane component 1, transcript
variant 1"
GO:0005515|GO:0016020|GO:0007411|GO:0005783|GO:0005789|GO:0005730|GO:0016021|GO:0005496|GO:0070
062|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55125_PI430048170 0.177403414487093 1.07093441457126 0.5121151080895180.391562993748811
0.521511621935095 A A A 0.2985303244612930.3797893220987190.449893057301128 A A A
LNCV6_55125_PI430048170 mRNA
GGTGCACCAAATTGTCTACCCTCTTCTAAGAACATCAAGTTTTTCACTTTATTCTTACTT NM_178527RefSeq chr1 -
173500464 173603094 SLC9C2 284525 "solute carrier family 9, member C2 (putative)"
GO:0015299|GO:0016021|GO:0006814 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143703_PI430048170 0.298035151305751 1.23036764236209 1.00319095600942
0.3754582040526570.471298639453866 A A A 0.3381564180255980.321098248910861
0.375013659600505 A A A LNCV6_143703_PI430048170 mRNA
GATGTACCCCAAAGCTCTGAAGATATTTATTTCAGAGAAAACAATGCTAATGTGTGAGAT NM_001145664 RefSeq
chr2 - 101397360 101474703 RFX8 NA "RFX family member 8, lacking RFX DNA binding domain"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145603_PI430048170 0.00832699167988181 0.57844993671283513.2092099004528
13.3932227813297 12.9809505977698 P P P 13.8492584781476 14.0453667737687
14.0769519564572 P P P LNCV6_145603_PI430048170 mRNA
CGTGCCTCCCGAGAAATTTGTCTTTTTGTATAAATGACAAAGTGTTGAAAATGTATTTCC NM_006640RefSeq chr17
+ 77319514 77500596 SEPT9 NA "septin 9, transcript variant 3" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_77487_PI430048170 0.4833820134572521.23631865498338 6.59778371810338 5.71409006462557
6.39341631488398 P P P 6.65905295225367 5.36459122456032 5.54037435119246 P P P
LNCV6_77487_PI430048170 mRNA
CATGGCACTGCACTGTTTAGTACAGCTGTTGAAATGAAGATAAAACAATCAGCAGAACAA NM_001199917 RefSeq
chr6 - 83164873 83193936 PGM3 5238 "phosphoglucomutase 3, transcript variant 1"
GO:0030097|GO:0000287|GO:0019255|GO:0006041|GO:0005575|GO:0007283|GO:0004610|GO:0006048|GO:0005
829|GO:0006493|GO:0004614|GO:0006487|GO:0006488|GO:0044267|GO:0043687|GO:0018279 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132709_PI430048170 0.3771927816189270.7147643623236260.467676666946689
0.4390276758309950.245340898956619 A A A 0.3831380228995910.475812706771933

1.48283056112429 A A A LNCV6_132709_PI430048170 mRNA
CCTACTTTGGTAGGTGAAGAAACTAATGCAAATAATTCTTATGTGCACTAAACCTTGCTA NM_005833 RefSeq chr9
+ 125200582 125234159 RABEPK 10244 "Rab9 effector protein with kelch motifs, transcript variant 1"
GO:0005886|GO:0010008|GO:0006898|GO:0043231|GO:0006904|GO:0005768 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133588_PI430048170 0.0945689435629527 1.07181866491654 0.649162308855501
0.730259534190961 0.606950043209085 A A A 0.594339773606145 0.549667035224138
0.544392236994513 A A A LNCV6_133588_PI430048170 mRNA
TCCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAGTGGCCTTGAAAAAATTGCTGAT NM_001004485 RefSeq
chr9 + 104504262 104505222 OR13F1 NA "olfactory receptor, family 13, subfamily F, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94384_PI430048170 0.0992859952408347 1.33121145394544 6.66321020258579
6.24010703834925 6.31078201765831 P P P 6.15572036337927 6.10863920571146
5.70734169078182 P P P LNCV6_94384_PI430048170 mRNA
TAGCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCT NM_013443 RefSeq chr9
- 127885320 127899648 ST6GALNAC6 30815 "ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6, transcript variant 1"
GO:0001665|GO:0006677|GO:0008373|GO:0009312|GO:0005886|GO:0006687|GO:0009988|GO:0005737|GO:0009100|GO:0000139|GO:0001574|GO:0016021|GO:0006488|GO:0044267|GO:0043687|GO:0018279 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140580_PI430048170 0.2047536283230820.66199675844391 6.55783683301137
5.68075145663857 5.50471550968986 P P P 6.84518339338755 6.74731889328684 6.04384101668 P
P P LNCV6_140580_PI430048170 mRNA
GCCCGTGCCCTTTTCTAAACGCGTCTGTATGCAGTCAATAAAACAATCGATTTGAAAAAA NM_001130136 RefSeq
chr15 + 74129373 74136802 ISLR2 57611 "immunoglobulin superfamily containing leucine-rich repeat 2, transcript variant 1" GO:0009986|GO:0005886|GO:0045773|GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_139940_PI430048170 0.8142737461234820.865715645772083 3.96440094273151
3.80900946550417 3.17123295947952 P P P 4.14080101029467 4.28622518341767
2.90218069182236 P P P LNCV6_139940_PI430048170 mRNA
ATGAAGCCATATCTGCCTGCCTTTTCCTAAGGAGAGTCCACCCTAATTAATGTCCATTCC NM_001012503 RefSeq
chr11 + 71527266 71528164 KRTAP5-7 NA keratin associated protein 5-7 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_136452_PI430048170 0.0063996493787179 1.24989811385492 12.1985075057258
12.2125584973602 12.2800865648055 P P P 11.991382482751 11.8879220512356
11.8437367125892 P P P LNCV6_136452_PI430048170 mRNA
AAAGTTATTATAATAATGGGTAATTTGTCAATAAAGCATTCCTTTGGGGGAAAGTCCGCC NM_199360 RefSeq chr20
+ 63865227 63891545 TPD52L2 7165 "tumor protein D52-like 2, transcript variant 1"
GO:0005515|GO:0048471|GO:0005737|GO:0046982|GO:0042127|GO:0042803 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139618_PI430048170 0.0553427574727737 1.617833993649 4.77243660530837
4.50132247216678 4.68964991273518 P P P 4.12429821641753 4.15412639455734
3.53603059633412 P P P LNCV6_139618_PI430048170 mRNA
GGCAGATGTCCCAATCCTGGAGGTCATCCATTAGGAATTAAATTCTCCAGCCTCAAAAAA NM_001284286 RefSeq
chr22 + 31122922 31134697 INPP5J 27124 "inositol polyphosphate-5-phosphatase J, transcript variant 2"
GO:0031115|GO:0017124|GO:0052658|GO:0043647|GO:0005886|GO:0006661|GO:0052659|GO:0044281|GO:0004445|GO:0001726|GO:0034485|GO:0005829|GO:0030426|GO:0005737|GO:0043198|GO:0033137|GO:0046856|GO:0010977|GO:0006644. NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139788_PI430048170 0.1798419681419083.59589606536274 0.299321109032577
2.51142203186949 2.61902577481371 A A A 0.2891393455429230.266769053376301
0.276523067660956A A A LNCV6_139788_PI430048170 mRNA
ATAGCCCAAAGCTCACTGTGTAATTAGCATTTAGAAGCTGAAGATCCCCAACTGCTCCAG NM_003357RefSeq chr11
+ 62419034 62423206 SCGB1A1 7356 "secretoglobin, family 1A, member 1 (uteroglobin)"
GO:0005515|GO:0032714|GO:0032713|GO:0005635|GO:0034021|GO:0005615|GO:0071774|GO:0042130|GO:0032
496|GO:0030141|GO:0009410|GO:0034097|GO:0032689|GO:0070062|GO:0005791|GO:0043488|GO:0007565|GO:0
007566|GO:0042493|GO:0010193|GO:0050727|GO:0051384|GO:0019834|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127072_PI430048170 0.1134024656581550.7451680421840057.04592580515174
7.03994661200654 7.05988736365514 P P P 7.20186873736954 7.72421652953478 7.4454195164694
P P P LNCV6_127072_PI430048170 mRNA
TATTTATGGCTCTTTAAGGTGACCGCCACCTTGGTCCTAGTGTCTATTCCCTGGAATTCA NM_001024807 RefSeq
chr19 + 35868498 35879797 APLP1 333 "amyloid beta (A4) precursor-like protein 1, transcript variant 1"
GO:0005515|GO:0006378|GO:0048471|GO:0005794|GO:0005886|GO:0030818|GO:0046914|GO:0006915|GO:0031
696|GO:0031695|GO:0007193|GO:0031694|GO:0006417|GO:0042802|GO:0005604|GO:0006897|GO:0007399|GO:0
030198|GO:0009887|GO:0071874|GO:0030900|GO:0016021|GO:0007155|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129253_PI430048170 0.2034756365690591.05225591774434 14.0914338711183
14.0812527626529 14.110542034335 P P P 13.9650295277055 14.0990566720422 13.995391032046
P P P LNCV6_129253_PI430048170 mRNA
TTTTCATAACTTATGTTTTTATATGGTTGCATTTACGCCAATAAATCCTCAGCTGGGGTC NM_001536RefSeq chr19 +
49677151 49688450 PRMT1 3276 "protein arginine methyltransferase 1, transcript variant 1"
GO:0005515|GO:0019919|GO:0006355|GO:0016571|GO:0008168|GO:0006325|GO:0018216|GO:0005634|GO:0008
170|GO:0031175|GO:0042802|GO:0042054|GO:0035242|GO:0005829|GO:0045653|GO:0044020|GO:0005737|GO:0
043985|GO:0006479|GO:0005654|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122741_PI430048170 0.176350494695542 1.47752755050816 3.54069948970952
3.33629002995997 3.52915057256056 P P P 2.71106566855954 3.43183665172463
2.37459090943985 A P A LNCV6_122741_PI430048170 mRNA
GTCTGCTGTCAGTAAATGGCTGCAGGAGCCGAAGTGGTAAACTCCTCGGTCTCCAGAAAT NM_000796RefSeq chr3
- 114128651 114179052 DRD3 1814 "dopamine receptor D3, transcript variant a"
GO:0005515|GO:0032416|GO:0090325|GO:0042995|GO:0042220|GO:0051584|GO:0050883|GO:0002016|GO:0007
611|GO:0035483|GO:0007612|GO:0032467|GO:0060134|GO:0019904|GO:0035240|GO:0043278|GO:0045840|GO:0
000122|GO:0002031|GO:0032922|GO:0019216|GO:0007186|GO:0005887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130361_PI430048170 0.361840968201086 0.855757482415251 3.51188336787405
3.83850221995279 4.10205296267676 P P P 3.7857348436491 4.07602243111612
4.28219772923515 P P P LNCV6_130361_PI430048170 mRNA
CAGAAATCTCACTGGAGAGAAACTGTATGAATGTAGAGAATCTGGGAATACCTTTCTGAA NM_006631RefSeq chr19
- 9412425 9435578 ZNF266 10781 "zinc finger protein 266, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130791_PI430048170 0.3587676954786271.12694564504067 5.9642726643006
6.05202789451424 5.74244898811207 P P P 6.02153180651773 5.54884101585532
5.64408594470924 P P P LNCV6_130791_PI430048170 mRNA
AGCTGGAGACTTCCAGCTCCAGCTCCCACTCAAGATAATAAAGATAATTTTTCAATCCTC NM_019101RefSeq
chr6_GL000254v2_alt + 2997765 3000082 APOM 55937 "apolipoprotein M, transcript variant 1"
GO:0042632|GO:0033344|GO:0016209|GO:0043691|GO:0034366|GO:0009749|GO:0034361|GO:0034384|GO:0005
543|GO:0034365|GO:0005887|GO:0034364|GO:0034362|GO:0034375|GO:0034380|GO:0042157|GO:0034445|GO:0

005319|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143692_PI430048170 0.661928522445991 1.01722162692491 0.360517107027032
0.42597726068406 0.356199178220522 A A A 0.345234609605705 0.443024505599247
0.276741610195423 A A A LNCV6_143692_PI430048170 mRNA
TTGTAATTTGGGACCTGTCGTGGCTCCTTGATTTGAAGTAAACATTTTTGGCAGAAGGGC NM_182542 RefSeq chr13
- 45541296 45615739 ERICH6B 220081 glutamate-rich 6B NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142461_PI430048170 0.64995458541594 0.824230526924011 0.564888163996178
1.20343714792929 0.279578971253984 A A A 1.65926492250209 0.565380105405878
0.509002742751697 A A A LNCV6_142461_PI430048170 mRNA
ATGTCTTTGTAGAGCTACCTGGAAATTGGGAGGCAGGGGGAATAAAGGAAATCATTTGTC NM_015174 RefSeq chr19
- 3804023 3869029 ZFR2 23217 "zinc finger RNA binding protein 2, transcript variant 1"
GO:0008270|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142203_PI430048170 0.00611044200963371 0.50332907319342 9.28867239482915
9.11395399750324 9.59816279230845 P P P 10.2286910464131 10.2174984900199
10.5437502491631 P P P LNCV6_142203_PI430048170 mRNA
ACTCACAGCCTTTTTACTTTTTTCCCCTAACTTTAGCAATGTAGTATCTTGAGCCATTAA NM_006016 RefSeq chr6 -
109366513 109382559 CD164 8763 "CD164 molecule, sialomucin, transcript variant 1"
GO:0030097|GO:0005515|GO:0008285|GO:0005886|GO:0005576|GO:0007275|GO:0005765|GO:0005764|GO:0007
165|GO:0006955|GO:0007162|GO:0007517|GO:0005887|GO:0007155|GO:0010008|GO:0007157|GO:0005768 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127923_PI430048170 0.00603866364346154 0.347516718591167 3.07850759463536
3.04431950532186 2.98502725682519 P P P 4.79132293306861 4.32919214062164
4.52593146523752 P P P LNCV6_127923_PI430048170 mRNA
AATAGGGGTGTCTAAAAGACCCACCCTGGTGTAGACTCTTTATGGGAAAAAAGGAAAAAA NM_014597 RefSeq chr1
- 93869457 93879206 DNTTIP2 30836 "deoxynucleotidyltransferase, terminal, interacting protein 2"
GO:0006355|GO:0005730|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137279_PI430048170 0.000730688161011799 0.441202780122985 5.96327003601083
5.83643308674291 6.1371711259567 P P P 7.14399009824469 7.07283664800691
7.27039734340501 P P P LNCV6_137279_PI430048170 mRNA
TTCTTAATACTGTCATGTGACTTATGAGGAAACGGTTTGAACTTGTCTCGGAGGCATGGT NM_001099791 RefSeq
chr20 + 45363099 45376802 SYS1 90196 "Sys1 golgi trafficking protein, transcript variant 2"
GO:0005802|GO:0030173|GO:0043001|GO:0006895|GO:0000042 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144810_PI430048170 0.686043591103551 1.34475405548936 0.303617053267996
1.94837477018198 0.386922201646911 A A A 1.15659142229067 0.31794050074672
0.360981305258483 A A A LNCV6_144810_PI430048170 mRNA
TCTGTGAGAGTTACTACTTTGTAACTTATGGTTTCTGCTTCAGTATTGTGTTGGTTCTGT NM_198584 RefSeq chr8 +
85245486 85284073 CA13 377677 carbonic anhydrase XIII
GO:0043209|GO:0015701|GO:0008270|GO:0044281|GO:0004089|GO:0006730|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141223_PI430048170 0.692315591891907 1.02370647901601 8.44104311085742
8.59797201725142 8.66054201586322 P P P 8.4931821678726 8.51944656725196 8.5924491883877
P P P LNCV6_141223_PI430048170 mRNA
GTATGAAGAGGAAGTCTGGATCACTTAAACTGACTAGTTATTTCCGGGTCATAATTTTAA NM_197956 RefSeq chr9
- 128061232 128067320 NAIF1 203245 nuclear apoptosis inducing factor 1
GO:0005739|GO:0003674|GO:0030308|GO:0005886|GO:0005654|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137723_PI430048170 0.0229368068689459 0.47283240091271 8.23199593113148

8.17622884412447 8.35828789926547 P P P 9.22084359134973 9.04489392114066
9.67384994799073 P P P LNCV6_137723_PI430048170 mRNA
AATGATACACCTCTGACCCCAGCGTTCTGAATAAAATGCTAATTTTGGATCTGGAAAAAA NM_001792 RefSeq chr18
- 27950962 28177446 CDH2 1000 "cadherin 2, type 1, N-cadherin (neuronal)"
GO:0005515|GO:0008013|GO:0005886|GO:0048514|GO:0045202|GO:0016342|GO:0005916|GO:0016339|GO:0042
692|GO:0016324|GO:0005913|GO:0014704|GO:0005911|GO:0007155|GO:0090090|GO:0007156|GO:0007157|GO:0
070062|GO:0097150|GO:0045295|GO:0045294|GO:0019903|GO:0034329|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136817_PI430048170 0.1930506312598481.1803720994289 6.71177983831422
6.79243385417643 6.53415282658436 P P P 6.64538960860327 6.45507672039361
6.19744924237811 P P P LNCV6_136817_PI430048170 mRNA
CAGAAGACAAAATTGTAAGCCAGAGTCAACAAATTAAATAAATTACCCCCTCCTCCAGAT NM_004847 RefSeq
chr6_GL000256v2_alt + 2914502 2916307 AIF1 199 "allograft inflammatory factor 1, transcript
variant 2"
GO:0048471|GO:1900087|GO:0005884|GO:0071447|GO:0005634|GO:0071673|GO:0048678|GO:0071672|GO:0032
870|GO:0005829|GO:0045429|GO:0003674|GO:0005737|GO:0051015|GO:0006954|GO:0031668|GO:0051602|GO:0
042102|GO:0030041|GO:0097178|GO:0043204|GO:0051017|GO:0001774|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138154_PI430048170 0.2537825309384130.7450036000181160.320512482242778
0.3646447053050620.293041842715658A A A 0.5098826159961780.426374440090243
1.18983225323305 A A A LNCV6_138154_PI430048170 mRNA
GAAAGCTGCACTCAGAGGGAGGAGTTTTTCTTACATAATTTGCAATTTCAGGAATTTAAT NM_000901 RefSeq chr4
- 148078763 148442520 NR3C2 4306 "nuclear receptor subfamily 3, group C, member 2, transcript variant
1"
GO:0005515|GO:0010467|GO:0006355|GO:0003700|GO:0006367|GO:0003707|GO:0043565|GO:0043235|GO:0007
165|GO:0005789|GO:0043401|GO:0005654|GO:0008270|GO:0005496 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128956_PI430048170 0.6063873566943591.37220997772391 2.32943334770335
1.07670992378402 0.424744762839076A A A 1.84838464552956 0.336327229891128
0.394604501919382A A A LNCV6_128956_PI430048170 mRNA
GTGCTGATTATCAGAGCCATCCTCAGAATACCCTCAGTCTCTAAGAAATACAAAGCCTTC NM_002548 RefSeq chr17
- 3092057 3092996 OR1D2 4991 "olfactory receptor, family 1, subfamily D, member 2"
GO:0007338|GO:0050911|GO:0007608|GO:0004984|GO:0007186|GO:0006935|GO:0005886|GO:0005887|GO:0004
930|GO:0006928|GO:0016021|GO:0000060 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127082_PI430048170 0.4101798570426042.93731593043039 0.428990459932207
3.21020345000842 0.530493464534531A P A 0.5489945233029780.398419876361366
0.400244989033486A A A LNCV6_127082_PI430048170 mRNA
GCTGAACCGACACTCAAAACGCTACTGAGTCACAATAAAGATTGTTTTAAAGAGTAAAAA NM_021801 RefSeq chr11
+ 4988193 4992429 MMP26 56547 matrix metallopeptidase 26
GO:0030574|GO:0006508|GO:0005578|GO:0008270|GO:0004222 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_109622_PI430048170 0.0845592675656541 1.84067302983082 6.52931302535166
6.7191009834117 6.69952234413951 P P P 6.15684836566289 5.84216547382589
5.13607610719723 P P P LNCV6_109622_PI430048170 mRNA
AGTCATCTGTATCTTCGTCTCTTTCCTCAGCTTTGACTACAAACTGGTGCAGAAGGTGTG NM_007224 RefSeq chr12
+ 57216794 57226449 NXPH4 11247 neurexophilin 4 GO:0003674|GO:0007218|GO:0005576|GO:0005575
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130677_PI430048170 0.5150539473811261.10091828483006 2.98155638340198
3.17634085941182 2.71189355667731 P P A 2.82357577137302 3.06108106004148 2.5636173111739

P P P LNCV6_130677_PI430048170 mRNA
ATGCGTATGACCTCATCTTCCTTCGTATCCTACTGCACTCCAGGACTATGCCAATTTATG NM_001195545 RefSeq
chr17 + 39941473 39944734 LRRC3C 100505591 leucine rich repeat containing 3C GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95531_PI430048170 0.00428202691058832 0.356406591394181 4.4702410725273
4.96903487823918 4.75084809493862 P P P 6.13864032519934 6.22366729047203
6.32959386095124 P P P LNCV6_95531_PI430048170 mRNA
TGTTGTGTTTTTAGAGGTGCTATCTCCAGTTCCTTGCACTCCTGTTAACAAGCACCTCAG NM_014585 RefSeq chr2
- 189560589 189580811 SLC40A1 30061 "solute carrier family 40 (iron-regulated transporter), member 1"
GO:0005515|GO:0043066|GO:0005886|GO:0005771|GO:0003158|GO:0060586|GO:0055085|GO:0009653|GO:0008
021|GO:0005622|GO:0006879|GO:0034395|GO:0016323|GO:0060345|GO:0005737|GO:0005887|GO:0045944|GO:0
005381|GO:0016021|GO:0002260|GO:0034755 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137313_PI430048170 0.0540109175887356 0.547262662722749 3.19964693224276
3.17027353049159 3.43215652894831 P P P 3.70358672236082 4.11563867925249
4.49807232828917 P P P LNCV6_137313_PI430048170 mRNA
TTCTCTTCTGAAGTGTGAATTTGTAAACTGATTGTTTAATTGTCAGAGGGACTTTTGGAC NM_017696 RefSeq chr6
- 118813448 118931738 MCM9 254394 "minichromosome maintenance complex component 9, transcript variant 1"
GO:0006260|GO:0000724|GO:0004386|GO:0005634|GO:0007292|GO:0005524|GO:0003677|GO:0006974 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141735_PI430048170 0.542522470885046 1.39418879547858 2.22262720084969
0.411556227055639 1.52311753754045 A A A 0.425224207603012 1.88049870390943
0.420627109007093 A A A LNCV6_141735_PI430048170 mRNA
ACACCTGCACCCAGAACCCCATCAAGGTCTTGGTCAGGCTGAGAAAGAGACTGTCACCTG NM_001017437 RefSeq
chr22 + 30356637 30376829 CCDC157 NA coiled-coil domain containing 157 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141741_PI430048170 0.00287900775981973 2.95813002767315 5.71642371601024
5.92693093740246 6.28538137978338 P P P 4.27838527506173 4.37556531081517
4.61741554815404 P P P LNCV6_141741_PI430048170 mRNA
CCTACTGTTTGTATTTGCAAACTGAGCTTGTTGGAGGGAAGGCATTATTTTTTAAAATAC NM_003645 RefSeq chr15
+ 50182195 50236392 SLC27A2 11001 "solute carrier family 27 (fatty acid transporter), member 2, transcript variant 1"
GO:0001676|GO:0006699|GO:0070251|GO:0097089|GO:0030176|GO:0044281|GO:0005739|GO:0001561|GO:0050
197|GO:0008206|GO:0031957|GO:0005779|GO:0044539|GO:0005778|GO:0042760|GO:0044255|GO:0070062|GO:0
015245|GO:0006635|GO:0005102|GO:0005524|GO:0004467|GO:0005789|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135244_PI430048170 0.0364019139693358 2.20155785978283 5.16726237653903
5.88478744337531 5.79947073009328 P P P 4.581670103378 4.49640461165037
4.45565534473144 P P P LNCV6_135244_PI430048170 mRNA
CTCCAGTCAAGAATGTCACTGGTTGGCATGATATTCTTAGTTCTATTTTTCCTTCTTTAA NM_024074 RefSeq chr19 +
16661126 16689005 TMEM38A 79041 transmembrane protein 38A
GO:0031965|GO:0033017|GO:0005267|GO:0016021|GO:0071805|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141539_PI430048170 0.0701024729835899 0.416910104575965 10.1346090200747
8.90101836348437 8.89670899958645 P P P 10.8498735423835 10.7416555974594
10.4802090686759 P P P LNCV6_141539_PI430048170 mRNA
CCTTCCTCCCCCCAAAACTATACTGTTATTTTTCTATGTAAGCAAATTGTTTGAAATGCT NM_018211 RefSeq chr1 +
64745094 64833231 RAVER2 55225 "ribonucleoprotein, PTB-binding 2"
GO:0005737|GO:0000166|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139125_PI430048170 0.0104118772195625 0.5282395846440247.6074040496118
7.33472096163035 7.72551452489984 P P P 8.18182130013191 8.52865459595509
8.69953277790516 P P P LNCV6_139125_PI430048170 mRNA
CCCAAGCTATTTGCTCACATTAACAAATTAAAGTGCCTGAAGCATAATTCATTCTTTACC NM_181784RefSeq chr2
- 65310850 65432522 SPRED2 200734 "sprouty-related, EVH1 domain containing 2, transcript variant 1"
GO:0005515|GO:0005886|GO:0019901|GO:0007275|GO:0010801|GO:0090311|GO:0030291|GO:0000188|GO:0005
737|GO:0043517|GO:0005654|GO:0005173|GO:0030658 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137320_PI430048170 0.35001555360127 1.05859381035088 0.689157493602379
0.7502870615064710.66151293099166 A A A 0.75505035721155 0.545285397695365
0.545285397695365A A A LNCV6_137320_PI430048170 mRNA
CACTCTATGTTTCATTAATCTCAACTGGCAGCAATAAATATTCTCAGCAAGTTTGACTTG NM_031955RefSeq chr3
- 172889356 173141268 SPATA16 83893 spermatogenesis associated 16
GO:0005794|GO:0007275|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134122_PI430048170 0.2410116442348470.9357312762850857.449579944653
7.57372203403466 7.64081406778144 P P P 7.73100013189011 7.59614601485648
7.62747564048846 P P P LNCV6_134122_PI430048170 mRNA
TTTGAGTAAATATGTGTCCTCCCCACTGAGCTTTGTTTTCTGTTTCATTATGTCCATTGT NM_024303RefSeq chr19 -
56221309 56228290 ZSCAN5A 79149 zinc finger and SCAN domain containing 5A
GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0003677|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144164_PI430048170 0.5318041640428081.19366126999767 1.13565153269042
0.3770508025505060.277999997150252A A A 0.4953122689853080.391457411852662
0.29058700754816 A A A LNCV6_144164_PI430048170 mRNA
GATGAAAATGGTTAAATGTTTGTGATGGGAGCTCTGTACTCAATGGCATAACAATGTTTA NM_024415RefSeq chr5
+ 55738016 55817146 DDX4 54514 "DEAD (Asp-Glu-Ala-Asp) box polypeptide 4, transcript variant 1"
GO:0010467|GO:0048471|GO:0004386|GO:0005634|GO:0007275|GO:0007283|GO:0030317|GO:0003676|GO:0005
524|GO:0032880|GO:0033391|GO:0005737|GO:0034587|GO:0071546|GO:0071547|GO:0007141 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129621_PI430048170 0.0944645923542621.24500345549564 8.94258013865115
9.07623002902051 8.77576532305331 P P P 8.80912376858652 8.61209326270178
8.41346256667022 P P P LNCV6_129621_PI430048170 mRNA
TGTTAAGTAATTTAAGTCAAGGAAACTGCTAACGTGTTCCCTCCTCCCTTGGCTTTTAAA NM_153252RefSeq chrX
- 80669487 80809734 BRWD3 254065 bromodomain and WD repeat domain containing 3
GO:0006357|GO:0008360|GO:0007010|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128156_PI430048170 0.286074301175117 0.988515394908065 0.327267034197729
0.362124778949279 0.35280465589864 A A A 0.372924617744572 0.372390321561693
0.346948410418986 A A A LNCV6_128156_PI430048170 mRNA
CAAATTCTTGTTTACAGTAACAAAGTCTATCGGTGCAGTTTAGGACTGTGAATCTATAGT NM_001077706 RefSeq
chr6 + 138796110 138904070 ECT2L 345930 "epithelial cell transforming 2 like, transcript variant 1"
GO:0032321|GO:0005089 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140905_PI430048170 0.00735291527610915 0.281320079609877 6.32531247176557
5.7837846808889 6.43767387828302 P P P 7.53801700145753 7.95138973157158
8.47425384255427 P P P LNCV6_140905_PI430048170 mRNA
CTGCGTTGACTACTGCTATCAGGATTGTGTTGTGTGGAATATTCATCTACATAAATTTTA NM_006283 RefSeq chr8
+ 38787203 38853028 TACC1 6867 "transforming, acidic coiled-coil containing protein 1, transcript
variant 1"
GO:0005515|GO:0021987|GO:0005815|GO:0008283|GO:0019904|GO:0000226|GO:0032886|GO:0005634|GO:0005
737|GO:0007049|GO:0015630|GO:0022027|GO:0045111|GO:0051301|GO:0022008 . NA - . NA NA

NA NA NA NA NA NA NA
LNCV6_89062_PI430048170 0.023375975973107 1.1230780169877 5.33733312596818
5.30268077618626 5.38360522977285 P P P 5.10564497664694 5.18495453196786
5.22908822486958 P P P LNCV6_89062_PI430048170 mRNA
CCATATGATCACAGTCGTGTTAAACTGCAAAATGCTGAGAATGATTATATTAATGCCAGT NM_002828 RefSeq
chr18 - 12792301 12884335 PTPN2 5771 "protein tyrosine phosphatase, non-receptor type 2,
transcript variant 1"
GO:0008286|GO:0005515|GO:0008285|GO:0005886|GO:0005783|GO:0042527|GO:0019221|GO:0042524|GO:0005
634|GO:0035335|GO:0060334|GO:0060336|GO:0050922|GO:0060339|GO:0030183|GO:0070104|GO:0070373|GO:0
004725|GO:0060333|GO:0019905|GO:2000587|GO:0030971|GO:0042518|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134690_PI430048170 0.0152263409133494 2.5971359027234 3.00132510777938
3.74581350613067 3.71983398539976 P P P 2.55291263308057 2.02717670404488
1.75600076185534 A A A LNCV6_134690_PI430048170 mRNA
AGGCATTCCTTCAGTCCCCTGGGGAGGTTCAGATGCTCAGACTCCCTGATACCACCTTTC NM_018280 RefSeq
chr22 - 46050458 46054144 PRR34 55267 proline rich 34 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_95956_PI430048170 0.709396969208527 0.946037653429231 3.90564565399315
3.25472595149051 3.00272415014333 P P P 3.57665120477962 3.27408447599372
3.6779221801629 P P P LNCV6_95956_PI430048170 mRNA
GTACAGGAAAACAAAGGGCATGCTGTATCTTTGAAAGAAGCGCAAAAAGTGAATAGACTG NM_017576 RefSeq
chr9 - 83836698 83921465 KIF27 55582 "kinesin family member 27, transcript variant 1"
GO:0008017|GO:0005871|GO:0003351|GO:0005874|GO:0003777|GO:0005524|GO:0007224|GO:0042384|GO:0005
929|GO:0005737|GO:0008152|GO:0021591|GO:0016887|GO:0070062|GO:0007018 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_127914_PI430048170 0.262910332167749 0.91102808507737 0.572671590806327
0.484418649451447 0.31845467781328 A A A 0.735294996317373 0.538203399678901
0.505943590524442 A A A LNCV6_127914_PI430048170 mRNA
GCCCAGCTTCATGTGCTAGGGGGCATGATAATGATAATAAAGGAATTGTATCTAGGACTA NM_001080509 RefSeq
chr12 + 30926903 30996602 TSPAN11 441631 tetraspanin 11 GO:0016021 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_64246_PI430048170 0.711472348631495 1.03686013624865 12.0492130906327
12.274842377459 11.9865350181871 P P P 12.2479132762512 11.8876175432073
12.011083200071 P P P LNCV6_64246_PI430048170 mRNA
GAGACGGTCAGTGAAGAGTCGAACGTGCTCTGCCTCTCCAAGTCCCCCAACAAGCACAAC NM_001961 RefSeq
chr19 - 3976055 3985463 EEF2 1938 eukaryotic translation elongation factor 2
GO:0005515|GO:0010467|GO:0005886|GO:0003924|GO:0005634|GO:0003746|GO:0006412|GO:0006414|GO:0005
829|GO:0005737|GO:0002244|GO:0070062|GO:0016235|GO:0019901|GO:0008494|GO:0045727|GO:0005525|GO:0
010628|GO:0016020|GO:0030529|GO:0009405|GO:0005844|GO:0044267|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_91094_PI430048170 0.290527474696689 0.85320799721685 7.46283637475827
7.58892946248475 7.89411857381009 P P P 7.7806367640597 7.70315723839138
8.1444057915955 P P P LNCV6_91094_PI430048170 mRNA
GCTGTGTTTGCTTATTCTTTAGTTGAACACACTATGAAGAATTCCAGGTGTACTAGTGAA NM_175623 RefSeq
chr12 + 69739389 69823204 RAB3IP 117177 "RAB3A interacting protein, transcript variant alpha 2"
GO:0005515|GO:0017112|GO:0005813|GO:0006996|GO:0033365|GO:0032851|GO:0005634|GO:0006893|GO:0030
027|GO:0036064|GO:0005829|GO:0042384|GO:0006612|GO:0005856 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_79586_PI430048170 0.0189976893986528 0.616894234916676 4.24749501976753

4.66500744754503 4.35071387081068 P P P 4.92128350291644 5.05978312485594
5.36923898707008 P P P LNCV6_79586_PI430048170 mRNA
TGGATTTATCCTGCAGCTCAAGCAGCTTCTTGCCTGTGGTAATACCAAGTTTGAGGCATT NM_001001924 RefSeq
chr8 - 17643793 17800917 MTUS1 57509 "microtubule associated tumor suppressor 1, transcript
variant 1"
GO:0005739|GO:0005794|GO:0005886|GO:0005815|GO:0071375|GO:0005874|GO:0005819|GO:0005634|GO:0010
758|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60564_PI430048170 0.411482982805394 1.41536053796347 0.529325307103132
0.290786378962881 1.55334968922635 A A A 0.631253939173634 0.270704825835761
0.265879298698951 A A A LNCV6_60564_PI430048170 mRNA
ATGTGGAAAAATACCTATTCTAGAAAAAAGAAATGCCAGCAAACCCCAAGGCCGAATTGT NM_000131 RefSeq chr13
+ 113105787 113120681 F7 2155 "coagulation factor VII (serum prothrombin conversion accelerator),
transcript variant 1"
GO:0005515|GO:0051897|GO:0043627|GO:0005886|GO:0004252|GO:0031100|GO:0005615|GO:0050927|GO:0001
948|GO:0006508|GO:0010641|GO:0060416|GO:0030335|GO:0005796|GO:0005509|GO:0005102|GO:0005576|GO:0
031982|GO:0002690|GO:0017187|GO:0007596|GO:0030194|GO:0007598|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139980_PI430048170 0.704594371025065 0.803616709445958 0.28502257982123
2.38727485143122 2.42685361196488 A A A 0.863676839143389 2.66505597402326
2.71268520789424 A P P LNCV6_139980_PI430048170 mRNA
CCCATTTCTCACTGAGAAGATTGTGAATATTTCCATATGGATTTTCTATTGTTACTCTGG NM_006931 RefSeq chr12 -
7919227 7936296 SLC2A3 6515 "solute carrier family 2 (facilitated glucose transporter), member 3"
GO:0005886|GO:0005975|GO:0006767|GO:0044281|GO:0055085|GO:0008645|GO:0019852|GO:0015758|GO:0006
766|GO:0009405|GO:0016021|GO:0005355|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67176_PI430048170 0.116387601683005 1.23374949604906 10.3016287217362 10.4117418854803
10.4016724160282 P P P 9.8460787438012 10.0599769040685 10.2711433857439 P P P
LNCV6_67176_PI430048170 mRNA
AACATCCTCCTGCCACTTAGGAGGAAACACCTCCCTATGGTACCATTTATGTTTCTCAGA NM_001143842 RefSeq
chr12 + 47963546 47968878 TMEM106C 79022 "transmembrane protein 106C, transcript variant 1"
GO:0008150|GO:0003674|GO:0005789|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_76212_PI430048170 0.102176077339413 1.32708745212818 6.31900060350362 6.64358474521301
6.83853939692067 P P P 6.31421950559676 6.04185076823386 6.25325191460653 P P P
LNCV6_76212_PI430048170 mRNA
GGTCAGGAGGATTATATTCTCATGATTCAGCATGTGTATAGAAAGACTTTCTTTTACGAT NM_024632 RefSeq chr5
+ 154445956 154461053 SAP30L 79685 "SAP30-like, transcript variant 1"
GO:0010467|GO:0006355|GO:0045814|GO:0006325|GO:0005730|GO:0040029|GO:0005654|GO:0003677|GO:0046
872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139002_PI430048170 0.725946801772567 0.994051525794524 0.414862922616795
0.418731835246292 0.370613669113463 A A A 0.439837110372472 0.381805712606032
0.408296290520194 A A A LNCV6_139002_PI430048170 mRNA
TTAAGTTTACTCCTACTGCTGACCCAAGTGAAATTCCTTCTCCAGTCACAGTGTCAACCT NM_181337 RefSeq chr6
+ 24356902 24358284 KAAG1 353219 kidney associated antigen 1 GO:0006955|GO:0005575 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_133550_PI430048170 0.401820835762699 0.827034106458329 4.33434313493926 4.6546758363382
3.8472890776666 P P P 4.917776315621 4.51663778439224 4.2580541573315 P P P
LNCV6_133550_PI430048170 mRNA
TTCCCCGGCCCGTGAACAAATGTACAATTCTCTATTCTGACATTACAGACCACCGGATAA NM_006011 RefSeq chr15
+ 92393909 92468728 ST8SIA2 8128 "ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2"

GO:0003828|GO:0009311|GO:0005975|GO:0007399|GO:0030173|GO:0000139|GO:0007411|GO:0006491|GO:0001574|GO:0006486|GO:0033691|GO:0055037|GO:0006488|GO:0044267|GO:0005769|GO:0006464|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140014_PI430048170 0.727872983143584 1.02888741325581 11.238589841466 11.3858287948723 11.3173861377313 P P P 11.1217174039111 11.161506787979 11.5071506013237 P P P LNCV6_140014_PI430048170 mRNA
GGGTTTTATATGCAACTTATTGTATCTGAATTCCTGTAGCACACCTCATAGGTATGATTT NM_005231 RefSeq chr11 + 70398505 70436584 CTTN 2017 "cortactin, transcript variant 1"
GO:0005515|GO:2001237|GO:0005884|GO:0006886|GO:0030426|GO:0006930|GO:0005737|GO:0030516|GO:0030838|GO:0043197|GO:0008076|GO:0048041|GO:0048870|GO:0030041|GO:0005856|GO:0005938|GO:0070062|GO:0031532|GO:0001726|GO:0030027|GO:0006898|GO:0097062|GO:0005905|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138625_PI430048170 0.115611629677399 0.944538496068074 0.261473728120405 0.271048936482774 0.323636887720915 A A A 0.430794810325991 0.350791300597993 0.320030954423333 A A A LNCV6_138625_PI430048170 mRNA
ACTCTCAAATGAGCATTTCTACCTCTGTGGAACTGAAATAAAAACAAGTCTTCCATGAGT NM_021118 RefSeq chrX + 83861125 83886700 CYLC1 1538 "cylicin, basic protein of sperm head cytoskeleton 1, transcript variant 1"
GO:0033150|GO:0043159|GO:0005198|GO:0005200|GO:0007275|GO:0005634|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131989_PI430048170 0.329751530593182 0.705272964604342 0.446556914437006 1.56133811303394 1.43593976661217 A A A 1.91956948418064 1.05414958732609 2.03333137097312 A A A LNCV6_131989_PI430048170 mRNA
GGTTGTTCGTTGTTGTCATTTGTTATAGTGCTACTCCACTTTAGACACCATAGCTAAAAT NM_004972 RefSeq chr9 + 4985244 5128183 JAK2 3717 Janus kinase 2
GO:0005515|GO:0042503|GO:0033160|GO:0019221|GO:0006325|GO:0030154|GO:0042127|GO:0032496|GO:0032024|GO:0005856|GO:0042169|GO:0038083|GO:0033194|GO:0022408|GO:0030335|GO:0032760|GO:0019901|GO:0014068|GO:0018108|GO:0033209|GO:0031234|GO:0007186|GO:0005654|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66398_PI430048170 0.93346553159949 0.986381630248378 5.1633695119011 5.09417264787057 5.29425307516796 P P P 5.3594772451486 4.95940843166092 5.26964972690049 P P P LNCV6_66398_PI430048170 mRNA
TGCCTTCATGCCCTTAATAGATGATTCTGATGATGAAATTGAGGAATTCATGGTAACTTC NM_032824 RefSeq chr2 + 112055222 112119318 TMEM87B 84910 transmembrane protein 87B GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137921_PI430048170 0.0325729275007421 0.457139948665139 2.96002782695631 2.23180824053426 2.05510528047582 P A A 3.16564534391233 3.67318364192533 3.87359996027799 P P P LNCV6_137921_PI430048170 mRNA
GCCCATCTCAAAAGCTAATATTGATTCTTCTGTTCCATCAGCTTTCATTGTTAAGTAGAA NM_001010000 RefSeq chr18 + 6834432 6915713 ARHGAP28 79822 Rho GTPase activating protein 28
GO:0043547|GO:0051056|GO:0030054|GO:0007264|GO:0005654|GO:0005829|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140261_PI430048170 0.168507921722534 0.701397450868728 4.6729563068973 4.37867310820381 4.16849896762472 P P P 4.42772527512336 5.19890414241595 5.062348986417 P P P LNCV6_140261_PI430048170 mRNA
TTGAGAAAATAGCCATTCAGCTCAGGAAGGCTTCTAAGTAAAGGATGGATTTGGAAAAAA NM_003920 RefSeq chr12 - 56416372 56449416 TIMELESS 8914 timeless circadian clock
GO:0005515|GO:0000790|GO:0046982|GO:0030324|GO:0005730|GO:0005634|GO:0000122|GO:0042803|GO:0006351|GO:0006974|GO:0007067|GO:0009582|GO:0042127|GO:0009628|GO:0015630|GO:0042752|GO:0007623|GO:0

048754|GO:0045892|GO:0002009|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126724_PI430048170 0.1844318792275770.9312947525940190.267486319122438
0.3229056992310510.276280627347565A A A 0.4834114866056950.383222461304356
0.303055463716985A A A LNCV6_126724_PI430048170 mRNA
CTCTGAGAAGCTTTCTCTGCTGCAGCTGTGTATAAAATATTTAAAATGTTGTATGGTGTA NM_001704RefSeq chr6
+ 68635739 69389511 ADGRB3 NA adhesion G protein-coupled receptor B3 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_74346_PI430048170 0.4946729774347690.8715738882222696.53106057465487 6.29232807544493
5.92428175544387 P P P 6.6921285818749 6.57250131094515 6.06886539228484 P P P
LNCV6_74346_PI430048170 mRNA
GCTGCTGGCTTCTCCTGTGCTCTACACGGACCTGAATTACAGCATAAACAACTTGAGCAT NM_207330RefSeq chr4
+ 48016773 48037063 NIPAL1 NA NIPA-like domain containing 1 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137549_PI430048170 0.0101188698024712 0.6280918448916 0.515003392472388
0.4370069847107850.52931239538194 A A A 1.03890377600203 1.32629601592684 1.1151126134125
A A A LNCV6_137549_PI430048170 mRNA
TGGAAACTGGAATAATGTAATGATTGGAGGCACAGACTCTGGCCTTCAGCTATGTCCTTG NM_001134462 RefSeq
chr2 + 73202257 73211212 NOTO NA notochord homeobox NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133133_PI430048170 0.8493943485502631.12477496831731 1.61930469679861
0.26820859922447 0.413556714823962A A A 0.3743315607538220.304988084182341
1.29556121423003 A A A LNCV6_133133_PI430048170 mRNA
GCAGATGGAGGGGGAGATTATTTATGGAGAGATAAAATTATTCATTCGATACATTCAGTT NM_032602RefSeq chr6
+ 89894468 89896100 GJA10 84694 "gap junction protein, alpha 10, 62kDa"
GO:0005243|GO:0005886|GO:0050908|GO:0007276|GO:0007268|GO:0005922|GO:0016021|GO:0055085|GO:0007
416 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132271_PI430048170 0.4406668826731050.32076658453557 0.507222775731708
0.5356271594775540.433365264010195A A A 3.38306275240428 0.445343381391078
0.449350071994321P A A LNCV6_132271_PI430048170 mRNA
TGCAGTTATTTTAACTCAGTATAGGAGCTAGAGGAAGAGATTTCCGAAGTCTGCACCCCG NM_016951RefSeq chr16
+ 66552562 66566287 CKLF 51192 "chemokine-like factor, transcript variant 1"
GO:0008009|GO:0016020|GO:0008283|GO:0030593|GO:0048247|GO:0005576|GO:0048246|GO:0016021|GO:0032
940|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133206_PI430048170 0.4069763682671370.92901214051014 0.304778217429908
0.3156273991373480.393029343048054A A A 0.3709200324336730.316451418339067
0.626966432001162A A A LNCV6_133206_PI430048170 mRNA
TCTGTTGTCTTAAGCAGAGAAAGACATCTAAATGGTGTCAGGACATTTCAGTACTTCTGC NM_016046RefSeq chr10
- 97435908 97446011 EXOSC151013 exosome component 1
GO:0005515|GO:0010467|GO:0003723|GO:0006364|GO:0005730|GO:0043928|GO:0004532|GO:0005634|GO:0000
178|GO:0005829|GO:0005737|GO:0000176|GO:0005654|GO:0000288 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140143_PI430048170 0.00118647650526259 1.62236888697563 10.0657619675216
10.1030079421485 9.89931792179179 P P P 9.27596825999035 9.42604634182034
9.27450034323507 P P P LNCV6_140143_PI430048170 mRNA
AGACCCAAGCCTGACCCCATCCGAGTGGAATTTGAGTCCTAAAGAAATAAAAGAGTCGAT NM_001039496 RefSeq
chr11 + 64300390 64304767 TEX40 25858 testis expressed 40
GO:0005737|GO:0007283|GO:0030154|GO:0007140 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126637_PI430048170 0.7066753084477720.9881621187315730.449982654881189
0.4450611659159610.442181286232761A A A 0.5007853999440820.497851283552084

0.38726308557095 A A A LNCV6_126637_PI430048170 mRNA
CAGCAAGAATATTCATTAAGGATATTTTCTAAAACCCACACTTGAGAAAACCACCCAATG NM_016591 RefSeq chr5
- 75027463 75030899 GCNT4 51301 "glucosaminyl (N-acetyl) transferase 4, core 2"
GO:0003829|GO:0005975|GO:0016266|GO:0008109|GO:0002121|GO:0048872|GO:0042403|GO:0000139|GO:0006
493|GO:0060993|GO:0048729|GO:0016021|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130953_PI430048170 0.0450519681331156 0.3710159274478385.657193523755
5.72451303456934 5.92907231116989 P P P 6.54543276591792 7.19295128940055
7.66556663518405 P P P LNCV6_130953_PI430048170 mRNA
ACTTGGTCTTCTTTCAAGTTGTTTGTATGAAGATGCTGTACCCACTTGAACAGTCCTCAG NM_006089 RefSeq chrX
- 18239312 18354724 SCML2 10389 "sex comb on midleg-like 2 (Drosophila), transcript variant 1"
GO:0031519|GO:0006355|GO:0003700|GO:0005634|GO:0009653|GO:0003677|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132560_PI430048170 0.4380354672146340.9558778862977960.343288914689212
0.4277150411994810.323972118472487A A A 0.5250161286171990.449227502293396
0.309977083946924A A A LNCV6_132560_PI430048170 mRNA
TAACACATCACCACAGACTGACGGCTTTTCACAATAAATCAGTTTTCTTCGCTCAAAAAA NM_198461 RefSeq chr2
- 100273290 100322733 LONRF2164832 LON peptidase N-terminal domain and ring finger 2
GO:0004176|GO:0006508|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127576_PI430048170 0.35508348947264 0.91199617204904 9.81957550562694
9.52381535285641 9.47656287721694 P P P 9.88594348614028 9.69164942982443
9.65468307346148 P P P LNCV6_127576_PI430048170 mRNA
TGATAGATATATAAGGACCCTCCTCCCTCACTTATATTCTATTAAATCCTATCCTCAACTNM_020318 RefSeq chr1 +
176463170 176842834 PAPPA260676 "pappalysin 2, transcript variant 1"
GO:0005622|GO:0016020|GO:0060349|GO:0006508|GO:0008270|GO:0005576|GO:0044267|GO:0001558|GO:0030
154|GO:0008237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127656_PI430048170 0.3930730275716070.6442850487738120.3645180850901
0.3704069417148750.356180346765938A A A 0.4142508357102051.7454137583192
0.385080882299926A A A LNCV6_127656_PI430048170 mRNA
GCAGGATTTAAAATATGAGGCCCAATTGGATTATGGTGCCATATTTTACTTTCTAGGAAG NM_024806 RefSeq chr11
+ 122882527 122959722 C11orf63 79864 "chromosome 11 open reading frame 63, transcript variant 1"
GO:0035082|GO:0032053|GO:0007420|GO:0033326 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142843_PI430048170 0.0571637338627676 0.49159600506766911.8167782805097
10.9226189645456 10.9009399972429 P P P 12.4198319618431 12.378504307887
12.0940967696864 P P P LNCV6_142843_PI430048170 mRNA
CCCCTCCCCCTGGCCAGTTTTATATTTTAATCACACATTGAAAAATTCATTAACTTATTC NM_031889 RefSeq chr4 +
70628743 70646819 ENAM 10117 enamelin GO:0097186|GO:0005578|GO:0031214 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131191_PI430048170 0.0223223559168016 0.6877590936672479.69626724363183
9.79899035446971 9.73741507017008 P P P 10.133619948409 10.2435763424619
10.4583078325825 P P P LNCV6_131191_PI430048170 mRNA
TACTTCAGAGGTGGTCTCTTCTTTCTTGTAATAAAAGCAATATTTATGCGGAAAGCAAGC NM_003621 RefSeq chr11
+ 7513764 7653765 PPFIBP28495 "PTPRF interacting protein, binding protein 2 (liprin beta 2),
transcript variant 1" GO:0005622|GO:0003674|GO:0005615 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_142869_PI430048170 0.0316403933485679 1.27963556763792 7.56734592146984
7.65393813950008 7.83340836319949 P P P 7.33204908374897 7.27632078458784
7.38977773428135 P P P LNCV6_142869_PI430048170 mRNA
CTGCTTTTCTGTTAAGCATCGATAGGTAAGTTGATGGATAAAAGTTACTATGTAAGCCTA NM_014170 RefSeq chr3

+ 112990952 113001374 GTPBP8 29083 "GTP-binding protein 8 (putative), transcript variant 1"
GO:0005739|GO:0000917|GO:0005525|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139463_PI430048170 7.366612985507e-05 0.2420641444539668.0567519521694
7.8031823605968 7.84136285428765 P P P 10.0934171682245 9.78638078005122
9.95794878371012 P P P LNCV6_139463_PI430048170 mRNA
CACCCTATCTCCTCTGTATTTTTGTAGTGGAATTTCTATTTAAGGGGCTCATTAAAGCATNM_001145862 RefSeq chr1
- 149928650 149936898 MTMR11 10903 "myotubularin related protein 11, transcript variant 1"
GO:0016791|GO:0016311|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138408_PI430048170 0.4453165201917910.4888627514245390.341326661629852
0.3489886820205170.27391446803787 A A A 0.2738881872766390.2886031351226422.3894775583068
A A P LNCV6_138408_PI430048170 mRNA
GCAGATTAGTCCTGTAATGAACACCAACTAATGTAAATCAAATTCATTCTGGTGATGGTA NM_001100117 RefSeq
chr8 + 103500747 104254428 RIMS2 9699 "regulating synaptic membrane exocytosis 2, transcript
variant 1"
GO:0005515|GO:0097151|GO:0048786|GO:0017137|GO:0030054|GO:2000463|GO:0048791|GO:0006886|GO:0046
872|GO:0044325|GO:0010628|GO:0042734|GO:0017156|GO:0017157|GO:0019933|GO:0042391|GO:0030073|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108087_PI430048170 0.0636320591761933 1.80850434265608 3.60495365650458
3.84573909297445 3.6231829760857 P P P 2.28261233488795 3.06518174422893
3.04543723328765 A P P LNCV6_108087_PI430048170 mRNA
ACAAGTCGGACACAGGCAAACCTTATTACTATAACAACCAGAGTAAAGAGTCCCGCTGGA NM_012272 RefSeq chr12
+ 49623619 49644669 PRPF40B 25766 "PRP40 pre-mRNA processing factor 40 homolog B (S.
cerevisiae), transcript variant 2" GO:0008380|GO:0006397|GO:0016607 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_128123_PI430048170 0.0153796230650445 0.7926327175577791 2.9471745013908
12.9231625850651 12.9390276306254 P P P 13.197780788403 13.2624244707727
13.3509792021545 P P P LNCV6_128123_PI430048170 mRNA
CTGGGTGGGTTCAGAGGGCAATTTCTCTTTTATGTGTACATATGCTAAATAAACATAATT NM_012111 RefSeq chr14
+ 77458029 77469472 AHSA1 10598 "AHA1, activator of heat shock 90kDa protein ATPase homolog 1
(yeast)"
GO:0005515|GO:0005737|GO:0005783|GO:0051087|GO:0006950|GO:0032781|GO:0001671|GO:0070062|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74202_PI430048170 0.0657544310499631.67987353244669 4.7965752593475 4.06147351663811
4.2318822844464 P P P 3.8052116156309 3.66436943795377 3.4607484821904 P P P
LNCV6_74202_PI430048170 mRNA
AAAGAGAGAGAGAGATCTTGAGAGAGAAATGCTGTTCGTTCAAAAGTGGAGTTGTTTTAA NM_001145847 RefSeq
chr4 - 15968225 16083971 PROM1 8842 "prominin 1, transcript variant 2"
GO:0005515|GO:0072112|GO:0005793|GO:0045296|GO:0005886|GO:0009986|GO:0042622|GO:0005783|GO:0060
042|GO:0042805|GO:0032420|GO:0031528|GO:0010842|GO:0045494|GO:0005615|GO:0031982|GO:0060219|GO:0
005903|GO:2000768|GO:0072139|GO:0016324|GO:0005887|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132638_PI430048170 0.3200755362413421.56186436317356 1.58220512132033
1.46396042358809 0.275920345985167 A A A 0.4970882423717010.397809075737438
0.790525035110953 A A A LNCV6_132638_PI430048170 mRNA
ACAGATGAACACACGGGGGTTGATACCAAGGAGCTAGAAGATATTGCAGCTGACATTAAA NM_174901 RefSeq
chrX - 13035616 13044798 FAM9C 171484 "family with sequence similarity 9, member C"
GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134519_PI430048170 0.2522373066103841.08518622065099 14.644955262437
14.4303167481185 14.4223875269475 P P P 14.3788805044533 14.4377814347348

14.3366067434873 P P P LNCV6_134519_PI430048170 mRNA
GTAGAACTAAAGGCTGTTCCAAGAATGTGGGGTGGGGAAAGTAAATGCTAAGACTAAAAA NM_017838RefSeq
chr5 - 178149464 178153960 NHP2 55651 "NHP2 ribonucleoprotein, transcript variant 1"
GO:0005737|GO:0030515|GO:0015030|GO:0005730|GO:0005732|GO:0005654|GO:0031118 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_91495_PI430048170 0.1924218770025781.5201697035699 6.23558567415663 6.6018522108031
6.59294448118474 P P P 6.490422649911 5.25839077996239 5.60812473634516 P P P
LNCV6_91495_PI430048170 mRNA
GTGGTATCCTTACAATCATCCTGCTTCTTGTACATCACTGAATTTTCATCTCATTGATTA NM_018266RefSeq chr3 -
119428959 119463682 TMEM39A 55254 "transmembrane protein 39A, transcript variant 1" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131436_PI430048170 0.6614411329661851.16908098293561 0.434631963628294
0.5370158679257311.46484833128828 A A A 0.3109629628066790.346810329640544
1.16739229250496 A A A LNCV6_131436_PI430048170 mRNA
AGTTTGCTCAGATGGAGGTGAAGGTGGTCATGGCAAAGCTGCTGCAGAGGCTGGAGTTCCNM_006668RefSeq chr14
+ 99684417 99727301 CYP46A1 10858 "cytochrome P450, family 46, subfamily A, polypeptide 1"
GO:0006707|GO:0006805|GO:0005506|GO:0005783|GO:0006699|GO:0008395|GO:0033781|GO:0044281|GO:0007
399|GO:0005789|GO:0008206|GO:0016021|GO:0016125|GO:0055114|GO:0020037 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128298_PI430048170 0.00757944388265082 0.5390651510615783.73041950469109
3.67983643635809 3.3264086090916 P P P 4.22562905528391 4.54188339575942
4.64396390698305 P P P LNCV6_128298_PI430048170 mRNA
GCAGCGTGAAAATAAATACTTTAACTCAGGGGTCACTACAGGAAGACCCCGTTGAAAAAA NM_001003845 RefSeq
chr2 + 170715346 170717988 SP5 389058 Sp5 transcription factor
GO:0043565|GO:0006355|GO:0060349|GO:0005634|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140109_PI430048170 0.00775099755713645 0.5755451160944257.89641314009312
7.55250874646475 7.78221524027572 P P P 8.56879420436833 8.4657271260962
8.60499020281904 P P P LNCV6_140109_PI430048170 mRNA
TAAGGTGTGATTATCTTTCCCTGTCCATGTGCTTATTGAAAGAAGATAGTGAACAAATGA NM_005570RefSeq chr18
- 59327823 59359276 LMAN1 3998 "lectin, mannose-binding, 1"
GO:0005515|GO:0005537|GO:0030017|GO:0046872|GO:0006457|GO:0033116|GO:0007030|GO:0032527|GO:0044
220|GO:0018279|GO:0070062|GO:0012507|GO:0005793|GO:0010638|GO:0006888|GO:0016020|GO:0000139|GO:0
007596|GO:0034498|GO:0005789|GO:0016021|GO:0051082|GO:0007029|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143715_PI430048170 0.0340828007733281 0.2468137528430963.17398573094849
1.80631951995746 2.78708327640947 P A A 4.67065209509484 4.68881575808017
4.77840782700427 P P P LNCV6_143715_PI430048170 mRNA
GCAACCAGTAAATATTTTTGAGTAAATGAATGAAATCTTTATTGCCGGTGTTCTGTGCAC NM_177538RefSeq chr2
+ 203238440 203305840 CYP20A1 57404 "cytochrome P450, family 20, subfamily A, polypeptide 1"
GO:0004497|GO:0016020|GO:0005506|GO:0016705|GO:0016021|GO:0055114|GO:0020037 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135089_PI430048170 0.4003315391522821.0328687026354 0.452912894588924
0.3115621512169830.371004259322178A A A 0.2895247294617570.336171986556294
0.372124306829966A A A LNCV6_135089_PI430048170 mRNA
TGTCTCTATCCATGACTTCAACTTCAACTATCGCATTCAGTGCTGCACTAGCACAGTCAA NM_006093RefSeq chr11
- 57376768 57381150 PRG3 10394 proteoglycan 3
GO:0042554|GO:0017148|GO:0001694|GO:0019370|GO:0006955|GO:0045575|GO:0045416|GO:0030246|GO:0042
119 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_136672_PI430048170 0.00610377225184351 0.7307331808065447.34445141466152
7.48762100081879 7.41090384086215 P P P 7.93079941941535 7.92558766969026
7.73981986854275 P P P LNCV6_136672_PI430048170 mRNA
CCCCGCACGTTTGTATTGTGTATAAATACATTCATTAATAAATGCATATTGTGACCGTTC NM_001185080 RefSeq
chr7 - 101232091 101238820 CLDN15 24146 "claudin 15, transcript variant 1"
GO:0016338|GO:0070830|GO:0005198|GO:0034329|GO:0016021|GO:0005923|GO:0016328|GO:0045216|GO:0042
802|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133816_PI430048170 0.0841961296432861 1.38498121396723 9.48998279295174
9.53999203063076 9.99037663629521 P P P 9.12509630964126 9.14600081969576 9.3798796850837
P P P LNCV6_133816_PI430048170 mRNA
GCTTTTTGTTTGTTTATGTTACAGAATGCTGCAATTCAGGGCTCTTCAAACTTGTTTGAT NM_014713RefSeq chr2 -
20032649 20052028 LAPTM4A 9741 lysosomal protein transmembrane 4 alpha
GO:0005794|GO:0006810|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121944_PI430048170 0.7188817960626591.07238939035528 0.937304212094365
0.5378942286626550.300192113039889A A A 0.4000684308334360.607567359896306
0.53053324966219 A A A LNCV6_121944_PI430048170 mRNA
CTGAAGAGGACATGTCAAATATTACAGATCCACAGATGTGGGATTTTGATGATCTAAATT NM_000634RefSeq chr2
- 218162844 218166993 CXCR1 3577 chemokine (C-X-C motif) receptor 1
GO:0070098|GO:0005886|GO:0004930|GO:0002407|GO:0004918|GO:0019959|GO:0031623|GO:0006954|GO:0006
935|GO:0007186|GO:0016020|GO:0004950|GO:0038112|GO:0016021|GO:0007166 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134926_PI430048170 0.4036908790854471.46771283172198 1.69908894537953
0.3573257535288871.63767878980568 A A A 0.4981180824046531.35862150136011
0.29674851116733 A A A LNCV6_134926_PI430048170 mRNA
GGCATAAACTACAGAGCCTCATTGCCATGAGGTATTGTACAAAGTTTTAATACATTTTGT NM_007325RefSeq chrX
+ 123184242 123490915 GRIA3 2892 "glutamate receptor, ionotropic, AMPA 3, transcript variant 1"
GO:0030054|GO:0005886|GO:0005234|GO:0035249|GO:0007268|GO:0007215|GO:0030425|GO:0030666|GO:0035
235|GO:0034220|GO:0045211|GO:0004971|GO:0032281|GO:0006810 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128668_PI430048170 0.0176774415923003 0.3212169884212613.1226597438965
2.29779987170264 2.7848117180688 P A A 3.84810994663355 4.24906261963795
4.92890031935097 P P P LNCV6_128668_PI430048170 mRNA
GGAGATATCTTGTGGTTTAAAGCAAATGTCCCACTGAAAGTGATTCAAATATCAACAGAA NM_001142685 RefSeq
chr11 - 128965059 129192198 ARHGAP32 9743 "Rho GTPase activating protein 32, transcript variant 1"
GO:0005515|GO:0051056|GO:0030054|GO:0007264|GO:0014069|GO:0015629|GO:0005829|GO:0043547|GO:0000
139|GO:0043197|GO:0045211|GO:0005789|GO:0035091|GO:0005938|GO:0010008|GO:0005096 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138341_PI430048170 0.00738047313370535 2.11776128536852 1.49402588928954
1.52948282079778 1.15612539809422 A A A 0.39450005699838 0.275448969107861
0.287678489436979A A A LNCV6_138341_PI430048170 mRNA
TAGGAATAAGGAGATTAAAAATGCCATGAGGAAAGCCATGGAAAGGGACCCCGGGATTTC NM_001001954
RefSeq chr11 - 59421978 59422953 OR5A2 NA "olfactory receptor, family 5, subfamily A, member 2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88646_PI430048170 0.5371840556997631.06053610894593 4.09136655142222 4.13532321628047
4.26261042663819 P P P 3.84960484890398 4.09004295685836 4.27020174490197 P P P
LNCV6_88646_PI430048170 mRNA
TCTAGAGATTAACGACTCCGAAGAGGTTGCAAGTATTTATACTCCAACCCCAAGACACCA NM_020153RefSeq chr11
- 118544527 118566076 IFT46 56912 "intraflagellar transport 46, transcript variant 1"
GO:0005813|GO:0006996|GO:0031514|GO:0050821|GO:0072372|GO:0031512|GO:0008022|GO:0036064|GO:0007

224|GO:0042384|GO:0003674|GO:0005929|GO:0008150|GO:0005737|GO:0042073|GO:0030992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128788_PI430048170 0.3050776336932891.05751007403008 13.4797334741849 13.547180808684 13.4167395688686 P P P 13.2891969661643 13.4787376884158 13.4300074124505 P P P
LNCV6_128788_PI430048170 mRNA
CTCCCCTTTGGGGGTGTGTGTGTGTGTTTTAATTTTCTTTATGGAAAAATTGACAAAAAA NM_003367RefSeq chr19 + 35268992 35279815 USF2 7392 "upstream transcription factor 2, c-fos interacting, transcript variant 1"
GO:0005515|GO:0003700|GO:0019086|GO:0046982|GO:0006366|GO:0003705|GO:0055088|GO:0043425|GO:0005634|GO:0000978|GO:0042803|GO:0043565|GO:0003690|GO:0007595|GO:0045944|GO:0000430|GO:0000432|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143958_PI430048170 0.2059455246374031.07223461644068 12.011083200071 12.080897564102 11.8975062920714 P P P 11.9292994077212 11.9352150297459 11.8264465973279 P P P
LNCV6_143958_PI430048170 mRNA
GTGGGGCTGGACCAGGGCCCTGGAGGCCAATAAAGAGCTTTCTGGGTAGACCCTAAAAAA NM_172251RefSeq chr19 + 3762666 3767565 MRPL54116541 mitochondrial ribosomal protein L54
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0005743|GO:0005840 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134304_PI430048170 0.6218129177823 0.9354716517273393.04238358406826 3.73769198855634 3.57767408045231 P P P 3.46193058353905 3.63316225422105 3.63266282781911 P P P LNCV6_134304_PI430048170 mRNA
GAATATGCACCTGACATGCATTTAGTGCAAAGCCTGAGAAAGCTTCAAACAATATATAAA NM_016403RefSeq chr11 - 94962621 94973612 CWC15 51503 CWC15 spliceosome-associated protein
GO:0008380|GO:0005515|GO:0010467|GO:0000398|GO:0003723|GO:0005681|GO:0005654|GO:0005634|GO:0071013 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73470_PI430048170 0.9405679187958870.9888705685902595.65513645786128 5.41283153338436 5.37834260532871 P P P 5.37652360064718 5.72894803142484 5.37585128374713 P P P
LNCV6_73470_PI430048170 mRNA
AAGGTGTCTGAGTTTGTGGCGTCTAAGCCAGGCACGTGTGTGAAGGTGCTGACCATCGAG NM_032548RefSeq chr3 + 127672937 127680926 ABTB1 80325 "ankyrin repeat and BTB (POZ) domain containing 1, transcript variant 1" GO:0005737|GO:0005886|GO:0005730|GO:0003746|GO:0006414 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127602_PI430048170 0.00442439600709441 0.71769081476968 9.98951286268856 10.0766727230926 10.0672754717986 P P P 10.5854059172775 10.4139864428462 10.5653291778233 P P P LNCV6_127602_PI430048170 mRNA
GGCGGCTGTCCCTGTGCATCCTTTGATTACTCTCATGCTGCATTTACTGTTTACATTTGT NM_001025579 RefSeq chr17 + 8435851 8468177 NDEL1 81565 "nudE neurodevelopment protein 1-like 1, transcript variant 1"
GO:0005515|GO:0008017|GO:0008090|GO:0007100|GO:0001833|GO:0045773|GO:0000132|GO:0005635|GO:0005829|GO:0051642|GO:0005737|GO:0007059|GO:0048680|GO:0047496|GO:0021799|GO:0043203|GO:0006508|GO:0031252|GO:0060053|GO:0060052|GO:0005813|GO:0005871|GO:0043014|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144395_PI430048170 0.3798558367230350.8315761909657055.56028901128691 5.18002622546381 4.86485949285284 P P P 5.28367463653915 5.84100198279909 5.28923893554615 P P P LNCV6_144395_PI430048170 mRNA
TACGGCTCCCGCTTCTTCTGTGGCTGTGGCTATGGATGCGGCTCTGGCTACTACTATTGA NM_181604RefSeq chr21 - 30598685 30598874 KRTAP6-2 NA keratin associated protein 6-2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74383_PI430048170 0.00157148790653858 0.3416524101458123.90376586325159 3.46029553424989 3.87475402205336 P P P 5.01836407375771 5.37099143037846

5.49724446021561 P P P LNCV6_74383_PI430048170 mRNA
CAGTGTCTGTTCTTCATTTCTATAGCCAAAGCTGTTAGTTAAAATCCCAAATCTATAGCA NM_001267843 RefSeq
chr4 - 55427900 55545932 CLOCK 9575 "clock circadian regulator, transcript variant 1"
GO:0005515|GO:0003700|GO:0001190|GO:0006366|GO:0000982|GO:0006325|GO:0005634|GO:0009648|GO:0007
283|GO:0043231|GO:0005829|GO:0051092|GO:0045944|GO:2000074|GO:0046983|GO:0004871|GO:0001046|GO:0
004402|GO:0005667|GO:0042634|GO:0006355|GO:0006357|GO:0016573|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_37303_PI430048170 0.0152950068669047 0.612713129187181 8.88292009967657
8.54337962383452 8.7851049806641 P P P 9.41669620822983 9.49752754332181
9.43692244887406 P P P LNCV6_37303_PI430048170 mRNA
CTACAATGGTGAAAACAGTCCTGTTCACAAAGAAAAACGAGAAGCGGCGAAGAAAAAACA NM_001194995
RefSeq chr12 + 123233480 123257959 C12orf65 91574 "chromosome 12 open reading frame 65,
transcript variant 3" GO:0005739|GO:0006415|GO:0003747 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_137022_PI430048170 0.984246919261093 1.00235986167472 0.2646923317209
0.273852210793191 0.439665243249551 A A A 0.352487377584607 0.299839160916085
0.322004344114262 A A A LNCV6_137022_PI430048170 mRNA
GAGTAGTGTGTTTGCATTTGTGAATAATCTTACTCACAGCAAGTAAACGTAATAAAAGCC NM_003412 RefSeq chr3
+ 147409393 147416719 ZIC1 7545 Zic family member 1
GO:0007389|GO:0042472|GO:0003700|GO:0021510|GO:0005634|GO:0003677|GO:0046872|GO:0006351|GO:0030
154|GO:0005737|GO:0007420|GO:0008589|GO:0007628|GO:0042307|GO:0005654|GO:0045893 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_34008_PI430048170 0.346735785908442 1.62170820760075 0.980164991702607 2.57430257499839
2.10788445519789 A A A 0.39677418444563 1.0195796389291 2.07147374675213 A A A
LNCV6_34008_PI430048170 mRNA
TATGGGAATCTCTATTTCTAGGCCCTTCTGCAAGGTATTCCTGCTCTTTCCAGGAACCAT NM_182832 RefSeq chr21
- 41175230 41185239 PLAC4 191585 placenta-specific 4 NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129968_PI430048170 0.0164084120165321 1.14677778309493 0.733434897877264
0.791958784792446 0.779289421581441 A A A 0.640830823815047 0.527578092825011
0.541507570625031 A A A LNCV6_129968_PI430048170 mRNA
AAGATGAAGGAAATCACTGAGACAGTGACCAACACAGTCACAAATGCCATCACCCATGCA NM_001146157
RefSeq chr10 + 87020288 87024730 FAM25A 643161 "family with sequence similarity 25, member A"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115585_PI430048170 0.0748798330841325 1.93865046824738 2.69188883968142
2.81911150098221 3.26387793540862 A A P 2.17506390836132 1.2616132526047
2.32608792197425 A A A LNCV6_115585_PI430048170 mRNA
AATCAGATACCACCGTTGAAAGCTCCCATTCAGATGCCTCAGTTCAAGTGCTAATCACTG NM_015120 RefSeq chr2
+ 73385757 73609919 ALMS1 7840 Alstrom syndrome 1
GO:0005515|GO:0005813|GO:0006996|GO:0005814|GO:0051492|GO:0005634|GO:0005829|GO:0003674|GO:0005
929|GO:0000922|GO:0005737|GO:0000086|GO:0016197|GO:0005654|GO:0000278 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136255_PI430048170 0.0107931677154618 0.712485016239591 7.84380414482158
7.58252125488011 7.75268582442387 P P P 8.3474479690126 8.08080402864421
8.21773568421547 P P P LNCV6_136255_PI430048170 mRNA
CCGGATGGGGCTGAGGGGAGAAAGAATTATTAAACAATAAATACTTTCAAGACAATTTTA NM_001037171 RefSeq
chrX - 23703659 23743290 ACOT9 23597 "acyl-CoA thioesterase 9, transcript variant 1"
GO:0052689|GO:0005739|GO:0006637|GO:0003986 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128711_PI430048170 0.0126121582107414 0.302172575776937 0.347903213751988

1.05383945295903 0.576778325557823 A A A 2.74523338739519 2.56202281252842
1.76888476625075 P P A LNCV6_128711_PI430048170 mRNA
TACCAGAATGACTATGTCTGTGTTTCTTAGGAATGTTGAAGCTTTTTGTGAAAACTGTAC NM_020802 RefSeq chr11
+ 101915014 102001065 CEP126 NA KIAA1377 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131288_PI430048170 0.311609712472771 0.8404883821583874.47954758206606
3.85471199453561 4.43889052344691 P P P 4.62342268026948 4.35557697615089
4.61119963200472 P P P LNCV6_131288_PI430048170 mRNA
TGCTGACTTAACTGTAAAACCAAAAGAAAAGTCCAAAAAGAAAGTGGAAGCCAAGTCTAT NM_015262 RefSeq chr10
+ 45727199 45792964 FAM21C 253725 "family with sequence similarity 21, member C, transcript variant 1"
GO:0005515|GO:0005886|GO:0043325|GO:0080025|GO:0005547|GO:0070273|GO:0005546|GO:0032266|GO:2000813|GO:1900024|GO:0031901|GO:0071203|GO:0042147|GO:0010314|GO:0005769|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144520_PI430048170 0.00282265547029194 0.159162155870973 3.10111697820993
2.09184136079625 2.80645299013457 P A A 4.95131727967538 5.43524120109394
5.65655996137988 P P P LNCV6_144520_PI430048170 mRNA
GCGGTGAAAAAAGAAAGAGAGTCAAGAATTTTGTTGGATTGTGTTTGTGTGTGCATATAT NM_016613 RefSeq chr4
- 158124579 158172566 FAM198B 51313 "family with sequence similarity 198, member B, transcript variant 2" GO:0005794|GO:0000139|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64861_PI430048170 0.000280340180645394 2.47764794788753 14.1262237094712
14.3405912437658 14.0845566525336 P P P 12.9998755433996 12.8340054502495
12.7955966437331 P P P LNCV6_64861_PI430048170 mRNA
GTCCCATCACAAGCCCGGGGAGGGATCCCGCCTTTGAAAATAAAGCTGTTATGGGTGTCA NM_006423 RefSeq chr19
- 41956680 41959376 RABAC1 10567 Rab acceptor 1 (prenylated)
GO:0005515|GO:0030054|GO:0005794|GO:0016020|GO:0005886|GO:0016021|GO:0008022|GO:0070064|GO:0042802|GO:0008021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131207_PI430048170 0.123375111807064 2.97421757845259 4.30567655468626
3.96488761154804 4.04458573733752 P P P 3.60162303302524 0.940769267034515
1.76078861423496 P A A LNCV6_131207_PI430048170 mRNA
TGTCACAAAATCAGATATTTCCCTTTATTCCAGATTTCCTGGACACTTTCACCCAATTAT NM_001139443 RefSeq chr11
+ 61949883 61963594 BEST1 7439 "bestrophin 1, transcript variant 2"
GO:0030321|GO:0006821|GO:0005886|GO:0034707|GO:0055085|GO:0005254|GO:0005829|GO:0016323|GO:0034220|GO:0016020|GO:0050908|GO:0051924|GO:0016021|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131680_PI430048170 0.203777982772703 0.906275673771158 0.538203399678901
0.531721636492367 0.300815690932587 A A A 0.687465661407501 0.594229242301535
0.522674488427758 A A A LNCV6_131680_PI430048170 mRNA
GGCCTTTTGACAATTCATGTAAGAGATGCTGAATTTCCAAAGCTGATAAATGCTCTAAAT NM_139318 RefSeq chr14
- 62706576 63045238 KCNH5 27133 "potassium channel, voltage gated eag related subfamily H, member 5, transcript variant 1"
GO:0023014|GO:0005516|GO:0005886|GO:0009986|GO:0010389|GO:0007268|GO:0000155|GO:0005622|GO:0000160|GO:0005887|GO:0005249|GO:0008076|GO:0042391|GO:0034765|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137294_PI430048170 0.0437061198070246 1.41060741569378 11.5176019755013
11.6875443816962 11.5394321991826 P P P 11.3261360119049 11.0023190332344
10.8978986361318 P P P LNCV6_137294_PI430048170 mRNA
TTTTCTCTTCATCCTGTCTCTCTCCTCCTTACTCTTGGATAAATAAACAGCCTGTGAGCA NM_003098 RefSeq chr20 -
33407956 33443892 SNTA1 6640 "syntrophin, alpha 1"
GO:0050998|GO:0005515|GO:0005516|GO:0031594|GO:0030054|GO:0003779|GO:0060307|GO:0030165|GO:0003

117|GO:0016328|GO:0044325|GO:0042383|GO:0005622|GO:0043234|GO:0005737|GO:0006936|GO:0002027|GO:0
007528|GO:0045211|GO:0016013|GO:0051117|GO:0005856|GO:0086005|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130528_PI430048170 0.4384456342537611.08817136040664 10.1179302699743
10.1234261255958 10.3850374852838 P P P 10.0607869752996 9.89550230010842
10.2930410943603 P P P LNCV6_130528_PI430048170 mRNA
AGTGAAGTATACCATGCACCAAAATAAACTTTACTGTGTGTACCTAACTGCTCCTGGAAA NM_018244RefSeq chr20
- 35302565 35412142 UQCC1 55245 "ubiquinol-cytochrome c reductase complex assembly factor 1,
transcript variant 1" GO:0005515|GO:0034551|GO:0005743|GO:0016023|GO:0070131 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_69148_PI430048170 0.3798094155321241.31404731315253 2.63935801727085 2.72079211041108
3.56903750500368 A A P 2.35035994878778 2.54003090741098 2.97721210760582 A P P
LNCV6_69148_PI430048170 mRNA
AAATCAGTGATGGAGAAGGGAGAAAAAGGACCTCATCTACCTGCAGCAATGAGTCCCTAA NM_014832RefSeq
chr13 - 75284663 75482114 TBC1D49882 "TBC1 domain family, member 4, transcript variant 1"
GO:0032869|GO:0005737|GO:0061024|GO:0032851|GO:0016192|GO:0031339|GO:0030659|GO:0005097|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106145_PI430048170 0.6506813206798551.0453516835854 7.89449696036338
7.99804032383779 8.23006496116024 P P P 7.90397209919987 7.90670714126297 8.1289403361778
P P P LNCV6_106145_PI430048170 mRNA
GAAGAATTGATGTATGCCTCTTTGCCTCTGCTTTGTCATGCCATTAAGCTCACAATAAGG NM_001276506 RefSeq
chr11 + 112086823 112095801 SDHD 6392 "succinate dehydrogenase complex, subunit D, integral
membrane protein, transcript variant 4"
GO:0048039|GO:0006099|GO:0005743|GO:0009055|GO:0005740|GO:0044281|GO:0046872|GO:0005739|GO:0022
904|GO:0005749|GO:0000104|GO:0016021|GO:0044237|GO:0020037 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132931_PI430048170 0.31211262534284 1.26397548922219 1.01928416617915
0.2765851998330380.441524734263349A A A 0.2907275385129450.253543141359563
0.288035610438897A A A LNCV6_132931_PI430048170 mRNA
GTGCCAAGATAACCCTTTAACGGCAACACTTTCTTAAATGAAGACTATTTCTTTCATGAA NM_145016RefSeq chr11
- 58834065 58844524 GLYATL2 219970 glycine-N-acyltransferase-like 2
GO:0005739|GO:0005783|GO:0047961|GO:0008152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133577_PI430048170 0.00921817196441656 1.40715834917282 11.9046632821222
11.7718872975015 11.6324843793514 P P P 11.1675284346065 11.3364797809995
11.3331123856906 P P P LNCV6_133577_PI430048170 mRNA
GCCCCGGGTCTGTACAATACGGTTTGCTATAAAACTCAAAATCTTCCAGCCGGGAAAAAA NM_001099784 RefSeq
chr16 + 30924574 30948783 FBXL19 54620 "F-box and leucine-rich repeat protein 19, transcript variant
1" GO:0043161|GO:0008270|GO:0003677|GO:0019005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132472_PI430048170 0.0012598631961314 10.9612200424823 5.57223444719977
5.58827663933468 5.3240282115868 P P P 1.64043660788309 2.02131347624798
2.38049872258178 A A P LNCV6_132472_PI430048170 mRNA
CCCACTAACTAGCATTCCTTTAAAGAGACTGGGAAATGTTTTAAGCAAATCTAGTTTTGT NM_001287005 RefSeq
chr9 + 93058687 93085136 SUSD3 203328 "sushi domain containing 3, transcript variant 2"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140171_PI430048170 0.0302152601385648 0.4803607289958993.18212278665012
3.61085133877658 3.87260880973683 P P P 4.16146206486285 4.65442542025225
4.98837915143981 P P P LNCV6_140171_PI430048170 mRNA
CTACATTTCTTGCAAAGTACATTCCTTTCTGTGGTATTTTGTCCTGTAACTGAAGTATAG NM_006933RefSeq chr21 +
34073522 34106262 SLC5A3 6526 "solute carrier family 5 (sodium/myo-inositol cotransporter), member 3"

GO:0043576|GO:0006020|GO:0005886|GO:0005887|GO:0007422|GO:0006810|GO:0016021|GO:0006814|GO:0055085|GO:0005367|GO:0015798 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136007_PI430048170 0.909114910083044 1.00276262864671 0.298365690523442 0.337282320147469 0.389589663430675 A A A 0.356781272953069 0.337689601377408 0.320046921907675 A A A LNCV6_136007_PI430048170 mRNA
TTTGGAGGGATTTTGTGATGCAGAATATCTAAGTCATAGAAATAGAAGACAGGTGGAATA NM_004056 RefSeq chr8 - 60188863 60281395 CA8 767 carbonic anhydrase VIII
GO:0005737|GO:0048015|GO:0008270|GO:0004089|GO:0006730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113917_PI430048170 0.133662480970977 0.768884006192992 4.45280549397522 4.80671071796523 4.25141916261941 P P P 4.91544282037865 4.8931147825582 4.89528767397862 P P P LNCV6_113917_PI430048170 mRNA
AATTCAGAGTCTCTCATCTCAGCACATGACATTTTGTCATGGATCAAGCAGGAGGAGCAG NM_003575 RefSeq chr7 + 149195461 149226248 ZNF282 8427 "zinc finger protein 282, transcript variant 1"
GO:0006355|GO:0008270|GO:0005634|GO:0045892|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131999_PI430048170 0.211602784061537 0.844826169031918 3.79555657404489 3.50465570728165 3.84900677351169 P P P 3.74959773055339 4.16936424515436 3.95278068904657 P P P LNCV6_131999_PI430048170 mRNA
ATCGGCTTCAGTGATGGTTTTTGTGGGCATTTATTGTGTGTGTGTAAGAAATTTCATATG NM_152573 RefSeq chr9 - 82979584 83063128 RASEF 158158 RAS and EF-hand domain containing
GO:0006184|GO:0048471|GO:0009306|GO:0017157|GO:0005509|GO:0003924|GO:0032482|GO:0019003|GO:0005525|GO:0006886|GO:0012505|GO:0006904 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142114_PI430048170 0.447644105849701 0.748837196984055 0.392542557237646 0.304781429310298 0.343872555826241 A A A 1.37364190141494 0.306672490939842 0.344002118659649 A A A LNCV6_142114_PI430048170 mRNA
CCATGAACACACCGGTAAATAAAACATAGTCCAAGTGGAAGAATTCATTAATAAGGAACT NM_206933 RefSeq chr1 - 215622893 216423396 USH2A 7399 "Usher syndrome 2A (autosomal recessive, mild), transcript variant 2"
GO:0005515|GO:0035315|GO:0060171|GO:0060113|GO:0002142|GO:0007605|GO:0005518|GO:0032421|GO:0048496|GO:0045494|GO:0005604|GO:0001917|GO:0005737|GO:0016324|GO:0032391|GO:0017022|GO:0016021|GO:0007601|GO:0050953|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74295_PI430048170 0.174129400602464 0.875884158343327 10.8730418552118 10.8604551361481 11.0812930190756 P P P 11.0443778388538 11.0343378178528 11.303961454197 P P P LNCV6_74295_PI430048170 mRNA
TTTCTTTTAAACTGGCATTCTTGCCTAATGATGTTATCTAGGCACCATTGGAGACTGAAA NM_005339 RefSeq chr4 + 39698043 39782790 UBE2K 3093 "ubiquitin-conjugating enzyme E2K, transcript variant 1"
GO:0005515|GO:0006511|GO:0004842|GO:0016874|GO:0034450|GO:0005634|GO:0032434|GO:0015629|GO:0005524|GO:0005737|GO:0019787|GO:0070059|GO:0043161|GO:0045111|GO:0070936|GO:0031625|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134050_PI430048170 0.226115139753646 1.05550859187697 10.7203819363069 10.7634707781097 10.6177069762561 P P P 10.5701161241428 10.6765909387253 10.622934315301 P P P LNCV6_134050_PI430048170 mRNA
CTCCCCACATTCCCACCTCTAAGAATAAATAAGTTTTCCTTTTGTTTTCCACTCAAAAAA NM_015665 RefSeq chr12 - 53307455 53321628 AAAS 8086 "achalasia, adrenocortical insufficiency, alacrimia, transcript variant 1"
GO:0007077|GO:0010467|GO:0019221|GO:0019058|GO:0005634|GO:0044281|GO:0005635|GO:0015031|GO:0008645|GO:0003674|GO:0005737|GO:0015758|GO:0005643|GO:0016032|GO:0007612|GO:0046822|GO:0005813|GO:0031965|GO:0005975|GO:0019083|GO:0055085|GO:0010827|GO:0006913|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_134405_PI430048170 7.78102302292532e-05 0.3455594984945093.5205254860594
3.37401024315685 3.5908155277714 P P P 4.93803740046561 5.09519902326881
5.05492175281604 P P P LNCV6_134405_PI430048170 mRNA
GTTCAGGATGGGCAATAAATTATTTCTAAAGGAGGTCTAAAAGTGGAAAGAATGGTTTGA NM_006572RefSeq chr17
- 65009288 65056802 GNA13 10672 "guanine nucleotide binding protein (G protein), alpha 13,
transcript variant 1"
GO:0005515|GO:0005886|GO:0008360|GO:0003924|GO:0006928|GO:0005634|GO:0007266|GO:0031526|GO:0031
702|GO:0007204|GO:0046872|GO:0030154|GO:0004871|GO:0070062|GO:0030334|GO:0031584|GO:0042470|GO:0
001569|GO:0005834|GO:0030168|GO:0005525|GO:0031683|GO:0001701|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131473_PI430048170 0.000514021562185827 0.3531296436963237.54881625837365
7.21823207858569 7.36832471268161 P P P 8.79037999511402 8.7522268623985
9.09238664308516 P P P LNCV6_131473_PI430048170 mRNA
CAAATCCTGAGAGTGTTTTAATTGTTGGACAACATATTCTCAAGAATGGACTTTCCTTAC NM_001040436 RefSeq
chr12 - 32746543 32755953 YARS2 51067 "tyrosyl-tRNA synthetase 2, mitochondrial"
GO:0005739|GO:0004831|GO:0010467|GO:0072545|GO:0000049|GO:0005759|GO:0070184|GO:0043039|GO:0006
412|GO:0005524|GO:0042803|GO:0006418 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140360_PI430048170 0.1169745601449681.51997679727865 4.3468999366569
4.42738872419668 4.11993490981902 P P P 4.15280320660811 3.29263523954245
3.51047319738495 P P P LNCV6_140360_PI430048170 mRNA
CTCTGAGTGTAAACTACATGGTAGGTTGTGAAGGATGCAAATATCGAATCAATCATTTTT NM_152571RefSeq chr9
+ 136483494 136486067 C9orf163 158055 chromosome 9 open reading frame 163 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127629_PI430048170 0.1309428411610961.30019604686951 2.92601700920431
3.12051078402399 3.46112500417813 P P P 2.92867304400917 2.87356449408793
2.59971459929408 P P P LNCV6_127629_PI430048170 mRNA
TTTGTTTACCATCACAGCATGTGAGGTCATGGCCTCCCAGATCAAAGTATGCTGTCATTC NM_031949RefSeq chr6
+ 167325085 167342689 TTLL2 83887 tubulin tyrosine ligase-like family member 2
GO:0016874|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139599_PI430048170 0.2298390271752411.44095396311838 0.5310119168961
1.34081204869584 0.489945683164687A A A 0.2837021025491060.373463170755759
0.28976544625463 A A A LNCV6_139599_PI430048170 mRNA
ATCTGAAGCACAAGTATGAGACGGCACTCAAGGTGGGCAGCACCACCAATGAAGCTGCCG NM_003395RefSeq
chr1 - 227921463 227947975 WNT9A 7483 "wingless-type MMTV integration site family, member 9A"
GO:0007093|GO:0008285|GO:0072498|GO:0071300|GO:0045597|GO:0005578|GO:0007267|GO:0061072|GO:0048
704|GO:0005576|GO:0007275|GO:0005615|GO:0061303|GO:0005109|GO:0045880|GO:0045165|GO:0030182|GO:0
032331|GO:0035115|GO:0016055|GO:0043154|GO:0090090|GO:0060070|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128814_PI430048170 0.0130824729164187 0.4537320379040995.68048911701353
5.33145574204816 5.56157949732431 P P P 6.28495022692692 6.72816702999664
6.92917400480892 P P P LNCV6_128814_PI430048170 mRNA
CTAACACAAGACCCTGTAAATACATGATAATTGCACACAGATTTTACATATTTGCAGACC NM_001206998 RefSeq
chr22 + 28883766 29057488 ZNRF3 84133 "zinc and ring finger 3, transcript variant 1"
GO:0005515|GO:0006511|GO:0004842|GO:0016567|GO:0005886|GO:0016874|GO:0072089|GO:0005109|GO:2000
051|GO:0038018|GO:0005887|GO:0008270|GO:0090090|GO:0060070|GO:0060071 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134702_PI430048170 0.7598996767238461.46249997057617 2.52593981493786
0.3128057191277010.432752249893704A A A 0.56869685641266 1.58249691312562

0.301361509112599 A A A LNCV6_134702_PI430048170 mRNA
GGAATTTAAAAGAGGACATCAGAAGAGCTGGAGATGCAAGCTCTAGGCTGCGCTTCCAAA NM_031282 RefSeq
chr1 - 157573748 157598080 FCRL4 83417 Fc receptor-like 4
GO:0005515|GO:0005886|GO:0016021|GO:0070062|GO:0002376 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_103371_PI430048170 0.4549427619297320.5479673042800430.430478333162198
0.3848061482006080.410627118505878 A A A 0.308235179058459 2.23311001982956
0.409632428732334 A A A LNCV6_103371_PI430048170 mRNA
GAGGACTGGATGATATGGCATTTTGGTCCACTAATATTTACCATCTAACAAGCTTCATGT NM_001503 RefSeq chr6
- 24425833 24489622 GPLD1 2822 glycosylphosphatidylinositol specific phospholipase D1
GO:0008286|GO:0051044|GO:0008285|GO:0051047|GO:0002042|GO:0004630|GO:0010897|GO:0005765|GO:0005
615|GO:0071467|GO:0043231|GO:0010907|GO:0005622|GO:0010983|GO:0005737|GO:0071397|GO:0002062|GO:0
035701|GO:0071277|GO:0006507|GO:0070633|GO:0070062|GO:0032869|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142731_PI430048170 0.0126970598333874 0.6444786414588764.32069947772941
4.27686858189888 4.07651063964802 P P P 4.98870982958476 4.9394125454969
4.63394863547976 P P P LNCV6_142731_PI430048170 mRNA
CATCTATCAAGCAACACAGCCCCTTATCCCAGATAGAAAAGTGTCTCAAATGCATTCTAC NM_001284338 RefSeq
chr15 - 55826918 55917131 NEDD4 4734 "neural precursor cell expressed, developmentally down-
regulated 4, E3 ubiquitin protein ligase, transcript variant 3"
GO:0005515|GO:0043130|GO:0006513|GO:0016874|GO:0019221|GO:0031698|GO:0031175|GO:0031623|GO:0070
534|GO:0034644|GO:0042787|GO:0010766|GO:0010768|GO:0070063|GO:0070064|GO:0000785|GO:0005938|GO:0
070062|GO:0050847|GO:0005794|GO:0019904|GO:0014068|GO:0051592|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133216_PI430048170 0.000573825864855238 3.11654861607771 9.42025661946554
9.57971355114144 9.47570526571806 P P P 7.81594884096394 8.02046414224653
7.70617837722182 P P P LNCV6_133216_PI430048170 mRNA
CCTTGCCACCCGTGGTTGGATCTTGTTTTATATCTGCAAATAAATAGCTTGTTTGGAAGC NM_030812 RefSeq chr1
+ 17755312 17827063 ACTL8 81569 actin-like 8 GO:0005737|GO:0030855|GO:0005856 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145273_PI430048170 0.1364596336558031.56145048652438 5.44760977580576
5.81756301606185 4.92993819432917 P P P 5.11242553590014 4.82393859973526
4.36966829794085 P P P LNCV6_145273_PI430048170 mRNA
GCCTGTGGGATGCCTTGTGGGACGTCTCTTTCTATTCAATAAACAGATGCTGCAGCCTCA NM_203347 RefSeq chr9
- 136759633 136764513 LCN15 389812 lipocalin 15
GO:0006629|GO:0005215|GO:0036094|GO:0006810|GO:0005576 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141127_PI430048170 0.0702463163249086 0.6547798397920917.40864450199076
7.47499176535262 7.63705808890239 P P P 7.83779810333688 8.00243652802481
8.45122313424091 P P P LNCV6_141127_PI430048170 mRNA
ACTCAACGATCAGATTCACGGACCCAGAGCTTTTCCATGTGTTTATATTGTAAATATTTT NM_001105244 RefSeq
chr18 + 7567315 8406861 PTPRM 5797 "protein tyrosine phosphatase, receptor type, M, transcript
variant 1"
GO:0031290|GO:0005515|GO:0048471|GO:0045296|GO:0042493|GO:0010842|GO:0035335|GO:0031175|GO:0030
027|GO:0042802|GO:0007165|GO:0010596|GO:0005737|GO:0005913|GO:0006470|GO:0001937|GO:0005001|GO:0
005887|GO:0005911|GO:0045909|GO:0016525|GO:0007156|GO:0004725 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_136004_PI430048170 0.4071168767631250.8843844234195140.266182635824921
0.2848523609655490.423852431759643 A A A 0.35829715298051 0.794116933231145

0.308412835983645 A A A LNCV6_136004_PI430048170 mRNA
TCTCAGCTTGGGGAGTGAACACTTTCCGTTTTCATGCAGAATAAATCTAATTCCTTTGGA NM_173479 RefSeq chr19
+ 33132091 33175797 WDR88 126248 WD repeat domain 88 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129944_PI430048170 0.792859543223417 0.989603512150008 0.440163060978618
0.404292517194651 0.260541701110393 A A A 0.349716434086801 0.408689944215127
0.397341152542641 A A A LNCV6_129944_PI430048170 mRNA
TTGTGTTATACTGGGAGACAGGCCAATGTTTCCATTAATAGACAAGAGCACCACCACGCT NM_001204366 RefSeq
chr4 + 139665767 139740745 MGST2 4258 "microsomal glutathione S-transferase 2, transcript variant
2"
GO:0019370|GO:0006805|GO:0005886|GO:0010243|GO:0044281|GO:0005635|GO:0043085|GO:0004364|GO:0004
464|GO:0043231|GO:0004602|GO:0006750|GO:0005789|GO:0032496|GO:0016021|GO:0008047|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138080_PI430048170 0.367878199669052 0.874573312463625 10.7253477944623
10.8076474031212 11.0337634447375 P P P 10.7669746783177 11.0642165318715 11.286902319355
P P P LNCV6_138080_PI430048170 mRNA
GTTTCTTTAGTCAGGGTCTTTGCAGATTCTAAAGTTATACATGAATACATCAAAGTGGAC NM_005805 RefSeq chr2
+ 161308274 161411717 PSMD14 10213 "proteasome (prosome, macropain) 26S subunit, non-ATPase,
14"
GO:0006511|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0006303|GO:0031145|GO:0046
872|GO:0005829|GO:0034641|GO:0000082|GO:0070536|GO:0000724|GO:0016032|GO:0090090|GO:0070062|GO:0
006977|GO:0000209|GO:0043066|GO:0000502|GO:0006521|GO:0051437|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_74635_PI430048170 0.492735681319123 1.1145999687746 5.92045909579435 6.19705355530264
6.47816313547935 P P P 5.95109622936331 5.95465952727698 6.2528551619644 P P P
LNCV6_74635_PI430048170 mRNA
ATGTGGATATCACTCTTTATCGCAATGGTTATCATGGGGACCTGAATGAGACATTTTTTG NM_015143 RefSeq chr4
+ 98995636 99062809 METAP1 23173 methionyl aminopeptidase 1
GO:0070084|GO:0007603|GO:0005634|GO:0018206|GO:0022400|GO:0046872|GO:0006417|GO:0005829|GO:0070
527|GO:0005737|GO:0022626|GO:0004177|GO:0070006|GO:0006508|GO:0008235|GO:0031365|GO:0016056 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108464_PI430048170 0.0864550259108080 0.721467890325137 3.47714195902803
3.40544223866212 2.96347396984079 P P P 3.7933150123963 3.9679904205628
3.51344570803908 P P P LNCV6_108464_PI430048170 mRNA
GAACCCAAAATGGAATGAAGAATTTTATTTCAGGTAAACCCATCTAATCACAGACTCCTA NM_001144967 RefSeq
chr18 + 58044377 58401540 NEDD4L 23327 "neural precursor cell expressed, developmentally
down-regulated 4-like, E3 ubiquitin protein ligase, transcript variant j"
GO:0005515|GO:0010467|GO:0004842|GO:2000810|GO:0009651|GO:0006513|GO:0006367|GO:0016874|GO:2000
650|GO:0006883|GO:0019058|GO:0060306|GO:0015459|GO:2001259|GO:2000009|GO:0005622|GO:0030104|GO:0
034220|GO:0042787|GO:0010765|GO:0010038|GO:0007179|GO:0003085|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132947_PI430048170 0.538576307331034 1.03607224538223 0.300187191990321
0.309393739733625 0.499778209016841 A A A 0.33115082545048 0.289671579941345
0.34353867756857 A A A LNCV6_132947_PI430048170 mRNA
GAGAGGATGCACCTCAGGAAATTTACCAAGACCTAATTATATTGATGGAAGAATATTTAC NM_001080518 RefSeq
chr10 + 88724543 88752756 LIPK NA "lipase, family member K" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_142573_PI430048170 0.712162432909199 1.19237850381957 0.381009945269641
0.348276107418172 1.5298456782317 A A A 0.305253361743294 1.04403127236202

0.360475248816968 A A A LNCV6_142573_PI430048170 mRNA
GGTCCATGGTGGAAGACGATAACCCTGTGAAATACTTTATAAAATGTCTTAATGTTCAAA NM_002371 RefSeq chr2
+ 95025654 95053992 MAL 4118 "mal, T-cell differentiation protein, transcript variant a"
GO:0005515|GO:0005783|GO:0042552|GO:0006915|GO:0045176|GO:0007417|GO:0055085|GO:0030154|GO:0008
289|GO:0016505|GO:0016324|GO:0005887|GO:0045121|GO:0001766|GO:0019911|GO:0005768|GO:0015267|GO:0
019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126810_PI430048170 0.0210741984411615 0.54351347452557 9.1614144723348
8.92348249375748 8.94380248367786 P P P 9.54197468148395 10.0641228519496
10.0181063843558 P P P LNCV6_126810_PI430048170 mRNA
CCTTTGCGGCTCTGTACACATTTTTAAACCTGGCAAAAGATGAAGAGAATATTGTAAATA NM_020795 RefSeq chr17
+ 7408182 7419864 NLGN2 57555 neuroligin 2
GO:0052689|GO:0030054|GO:2000311|GO:0035418|GO:0045202|GO:0005615|GO:0097116|GO:0016337|GO:0002
087|GO:0045211|GO:0050885|GO:0004872|GO:0050839|GO:0097119|GO:0007158|GO:0035641|GO:0051965|GO:0
097151|GO:2000463|GO:0009986|GO:0051968|GO:0050804|GO:0072553|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142085_PI430048170 0.1661380364797621.02111569291916 0.319159061859592
0.28819933027743 0.270995253690185 A A A 0.2616907514631090.265053726819841
0.261581000300217 A A A LNCV6_142085_PI430048170 mRNA
CTCCAATCACGGGTTAAGAAGATTCCCAAATGACTGTAAAATTAAATACAAGCATGTTGA NM_001145475 RefSeq
chr12 - 50327311 50396622 FAM186A NA "family with sequence similarity 186, member A" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143977_PI430048170 0.0304373985237612 1.07261681292183 0.348174204054324
0.4107852068485820.337964999332281 A A A 0.2520365868945070.28649048324608
0.255827706968688 A A A LNCV6_143977_PI430048170 mRNA
TGAAGGATCAGAGGACTGAAAAATGATTCTGCAACTCTCTTAAAGTTAGAAATGTTTCTG NM_017716 RefSeq chr11
+ 60492777 60507428 MS4A12 54860 "membrane-spanning 4-domains, subfamily A, member 12,
transcript variant 1" GO:0070588|GO:0015279|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_92469_PI430048170 0.8786150388825461.11251422861865 1.56710049939166 0.549977307006043
0.291706629251635 A A A 0.5060470439154460.5483049265224041.13565153269042 A A A
LNCV6_92469_PI430048170 mRNA
CACCCTGCTTGCTTTGTGGCTATCATCAAAATCACCAACCAAAAGATTCACCTTTGGATT NM_013309 RefSeq chr15
- 45482480 45522804 SLC30A4 7782 "solute carrier family 30 (zinc transporter), member 4"
GO:0071577|GO:0005737|GO:0055069|GO:0005385|GO:0061088|GO:0005770|GO:0009636|GO:0016021|GO:0010
008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136671_PI430048170 0.0268236319310397 0.3379560229314111.170729800757
0.473284023329345 1.26843648964487 A A A 1.83857082904224 3.00003955334683
2.66006109815673 A P P LNCV6_136671_PI430048170 mRNA
CAGTGGGGTTGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAA NM_144492 RefSeq chr21
- 36460620 36480090 CLDN14 23562 "claudin 14, transcript variant 1"
GO:0016338|GO:0006461|GO:0070830|GO:0005886|GO:0005783|GO:0005198|GO:0034329|GO:0016021|GO:0005
923|GO:0045216|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90433_PI430048170 0.00121393149821238 0.463856394206713 9.72397979227 9.4377446525319
9.73414626088009 P P P 10.697102519093 10.6563512666722 10.8766839723325 P P P
LNCV6_90433_PI430048170 mRNA
TTTCATGTCATCCTGTTGGCACTGATGAAGAACCCTTACAGTTCAGGGTTCCTGGAACTT NM_212482 RefSeq chr2
- 215360455 215436068 FN12335 "fibronectin 1, transcript variant 1"
GO:0005515|GO:0008360|GO:0005518|GO:0045773|GO:0072562|GO:0050900|GO:0035987|GO:0002020|GO:0005
615|GO:0033622|GO:0016324|GO:0022617|GO:0030198|GO:0034446|GO:0031093|GO:0007155|GO:0008201|GO:0

070062|GO:0005793|GO:0005605|GO:0009611|GO:0005577|GO:0030168|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102887_PI430048170 0.00206540956319375 10.8748705925222 3.51060944944891 4.01917555791411 4.45088626277874 P P P 0.388053758511548 0.808070596056309 0.575864451248052 A A A LNCV6_102887_PI430048170 mRNA AAGGAATGTTATCAGTATTAAGCTAATGGTCCTGTTATGTCATTGTGTTTGTGTGCTGTT NM_005025 RefSeq chr3 + 167735722 167825569 SERPINI1 5274 "serpin peptidase inhibitor, clade I (neuroserpin), member 1, transcript variant 1" GO:0010951|GO:0004867|GO:0007422|GO:0007417|GO:0030155|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130036_PI430048170 0.250583255513021 0.947991301674371 9.82607783984586 9.6681227303792 9.68828455451811 P P P 9.76990044719339 9.83838345523484 9.80972153841911 P P P LNCV6_130036_PI430048170 mRNA TGTTTTTCCAGAGCTTTCTGGGATGTGGGAAAATAAATTACACTGAAGCAGTTGAAAAAA NM_032111 RefSeq chr6 - 44113635 44127454 MRPL1464928 mitochondrial ribosomal protein L14 GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0005840 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132740_PI430048170 0.198235798855889 0.546717504829974 3.04563456597345 2.27817560669877 2.37824691991981 A A A 2.50960063020762 3.77286341401234 3.81977239707956 A P P LNCV6_132740_PI430048170 mRNA CGCTTGGGGGTAAGTGGAATGATTTGCTAATATTGAGAATCTGTTGTATCAAACATAATA NM_213590 RefSeq chr13 + 49997006 50018467 TRIM13 10206 "tripartite motif containing 13, transcript variant 3" GO:0005515|GO:0004842|GO:0016874|GO:0032897|GO:0030433|GO:0097038|GO:0009653|GO:0051865|GO:0007165|GO:0005737|GO:0051092|GO:0045087|GO:0005789|GO:0043161|GO:0008270|GO:0004871|GO:0016021|GO:0043123|GO:0010332|GO:0010942|GO:0016239 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130726_PI430048170 0.255651560007378 1.05160362311803 0.565803167601543 0.688676169487185 0.54327579171743 A A A 0.52387555132852 0.527394346519657 0.532981834068141 A A A LNCV6_130726_PI430048170 mRNA GTTTCAATAAGCCCTTAAGTTAAGGGCTGATTGCACTTAGAAATAAGTTGCACTTAGAAA NM_001017975 RefSeq chr1 - 91260765 91404869 HFM1 164045 "HFM1, ATP-dependent DNA helicase homolog (S. cerevisiae)" GO:0000712|GO:0004386|GO:0003676|GO:0005524|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79675_PI430048170 0.0831677842829450 0.62275994052404 6.75461763951973 6.04185076823386 6.00547813909315 P P P 7.07041992043063 7.2040860889603 6.65088415656489 P P P LNCV6_79675_PI430048170 mRNA TCTGTGTGTGTGTGTGAACCATCATTTTTTGATCATCATGACCAATGAAACATTGACTCC NM_001283053 RefSeq chr8 - 27235322 27258439 STMN4 81551 "stathmin-like 4, transcript variant 2" GO:0043005|GO:0030424|GO:0005737|GO:0005794|GO:0051493|GO:0031110|GO:0015631|GO:0031175|GO:0007019|GO:0030426 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128948_PI430048170 0.0248241814366476 1.50497758804651 9.62804897994042 9.61257022349997 9.68316119188245 P P P 8.88674923777666 9.00676071522848 9.23946304399839 P P P LNCV6_128948_PI430048170 mRNA GGCCACTTACTGCCCTCTGTAAAAGATGTTAACATTTCTAGTTTTCTTTTAGTGTGAATT NM_021254 RefSeq chr21 - 32601673 32612608 C21orf59 56683 "chromosome 21 open reading frame 59, transcript variant 1" GO:0005634|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144449_PI430048170 0.224266925690848 0.826836913151868 0.302837772172806 0.313428446139592 0.286672050254369 A A A 0.488591272004238 0.845705611114252 0.344702000040257 A A A LNCV6_144449_PI430048170 mRNA AAAGAGTTCTGTTCAGACTTCTGAAGAGCAGCCTGTGGCTACAAATCTATGCTGATAAAT NM_001300939 RefSeq chr5 + 138083891 138091541 WNT8A 7478 "wingless-type MMTV integration site family, member 8A,

transcript variant 2"
GO:0090263|GO:0005578|GO:0044324|GO:0005576|GO:0005615|GO:0044335|GO:0005109|GO:0014034|GO:0030182|GO:0061317|GO:0060021|GO:0032526|GO:0060070|GO:0048018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135852_PI430048170 0.3791888588993271.42556287918124 0.608963989040793 0.5013914154738051.65719630635496 A A A 0.42386040784519 0.573789273966892 0.531472459210307 A A A LNCV6_135852_PI430048170 mRNA GAAGAGATGAACTGTGTATTTAACTTAAGCTATTGCTCTTAAAACCAGGGAGTCAGAATA NM_002922 RefSeq chr1 + 192575726 192580029 RGS1 5996 regulator of G-protein signaling 1
GO:0043547|GO:0007165|GO:0005516|GO:0006955|GO:0005737|GO:0005886|GO:0038032|GO:0007193|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139436_PI430048170 0.0209198936698803 0.661724801824794 11.4346518553967 11.4468278555438 11.4852230280764 P P P 11.9160584600398 12.2227019396068 11.9977939423881 P P P LNCV6_139436_PI430048170 mRNA GCTACCGCTTAAACGACTCAGCATCTCGACTTCCCAAATCAAAGGCCCTTTTCAGGGCCG NM_003545 RefSeq chr6 + 26204644 26205021 HIST1H4E 8367 "histone cluster 1, H4e"
GO:0005515|GO:0010467|GO:0006325|GO:0005634|GO:0045653|GO:0000723|GO:0000183|GO:0000786|GO:0070062|GO:0035574|GO:0035575|GO:0046982|GO:0006334|GO:0006335|GO:0005576|GO:0006336|GO:0000228|GO:0003677|GO:0032776|GO:0034080|GO:0043234|GO:0016020|GO:0045814|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108277_PI430048170 0.000462605674159447 2.90080967863434 8.49510404390434 8.39484379015321 8.52468365958112 P P P 7.03676742268966 6.98142335721298 6.77754293771497 P P P LNCV6_108277_PI430048170 mRNA AGTCCCCTGTGAATCAAGATTTGGGCATGTTCTTGGTCACCATTTCCTGCTACACCAGAG NM_001122955 RefSeq chr11 - 62690261 62707707 BSCL2 26580 "Berardinelli-Seip congenital lipodystrophy 2 (seipin), transcript variant 1" GO:0016042|GO:0003674|GO:0050995|GO:0019915|GO:0045444|GO:0030176|GO:0034389 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127007_PI430048170 0.32361882286938 1.04708280852654 0.487259088115334 0.317803560391968 0.401344483925639 A A A 0.286030258690396 0.350455097142706 0.374331560753822 A A A LNCV6_127007_PI430048170 mRNA CGCCTTGCTCTTGAAAGTGCAGTATTTTTCTACATCATGTCAAGAATGATTCAATGTAAA NM_001145271 RefSeq chr8 + 24384284 24406013 ADAMDEC1 27299 "ADAM-like, decysin 1, transcript variant 2"
GO:0007162|GO:0006955|GO:0006508|GO:0008270|GO:0005576|GO:0005575|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144553_PI430048170 0.00110191744369243 0.244285699772417 0.454792153880068 0.551728622604088 1.03479253713757 A A A 2.47987668833407 2.66840293725733 3.01119740213793 A P P LNCV6_144553_PI430048170 mRNA AGCTTCTTTTTCCAAAAGAAAAACTAGTTGCAGTCAGGGAGCCAGCGAAAAGACAAAAAA NM_013347 RefSeq chrX + 96883907 96885451 RPA4 29935 "replication protein A4, 30kDa"
GO:0000082|GO:0003697|GO:0033260|GO:0006270|GO:0006310|GO:0005654|GO:0005634|GO:0006289|GO:0000077|GO:0000278|GO:0005662 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137400_PI430048170 0.0477441482219738 0.596502461860379 6.903060269598 6.83848913057473 7.21947768237847 P P P 7.4466996966964 7.58552018490774 8.10753923715105 P P P LNCV6_137400_PI430048170 mRNA CTCACAAGTTTAACTGTTGTATTATAACAGTATTACATGTCAACGGTGTGGTTATGACCT NM_005493 RefSeq chr6 - 13621497 13711564 RANBP9 10048 RAN binding protein 9
GO:0005515|GO:0006461|GO:0007411|GO:0007020|GO:0005875|GO:0008536|GO:0005634|GO:0019899|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136765_PI430048170 0.774057523167142 0.978865383212584 0.316136394680747

0.501533495815485 0.353659711381343 A A A 0.533832094693154 0.448090947351366
0.276842037351364 A A A LNCV6_136765_PI430048170 mRNA
CTATGACTTCACAGACGTTACTGCTTAGGATGAAACCAAAATAGGCATTTAAGTAAAAGA NM_001109763 RefSeq
chr16 - 27787528 28063509 GSG1L 146395 "GSG1-like, transcript variant 1"
GO:0030054|GO:0005886|GO:2000311|GO:0016021|GO:0032279 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_70988_PI430048170 0.764157676188737 1.03014659398358 0.338825451556272
0.350288078858393 0.65308157709193 A A A 0.43991333162975 0.410820295046834
0.384893987781152 A A A LNCV6_70988_PI430048170 mRNA
GGGGGAAGAAGAGTTTTTGGACCCATAGATGTTTGGATGATGTCTCTAATTTGTCATTTA NM_020157 RefSeq
chr20 + 16748352 16752164 OTOR 56914 otoraplin GO:0001502|GO:0007605|GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142709_PI430048170 0.553215153276562 0.966546953687387 0.47349098377712
0.470578511980234 0.259750463497725 A A A 0.400646309799211 0.50502335859477
0.453765140509511 A A A LNCV6_142709_PI430048170 mRNA
TACCTCTTAGTGTACCCTATGTACCTGAATTTGCTTGGCTTCTTTGAGAATGAAATTGAA NM_001166400 RefSeq
chrX + 149881140 149885835 MAGEA8 4107 "melanoma antigen family A8, transcript variant 1"
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_140887_PI430048170 0.835377746642253 0.979851872630075 0.302505002574631
0.281390798436554 0.452287131339333 A A A 0.561423412738291 0.256734507843798
0.29259980115179 A A A LNCV6_140887_PI430048170 mRNA
GCACTGGGCAGTCTGCAGATTATGTCATGGATGTCAAATAAAAATTGAGACAACATGAAA NM_001004698 RefSeq
chr1 + 247491067 247492409 OR2W5 NA "olfactory receptor, family 2, subfamily W, member 5
(gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131364_PI430048170 0.00119816327666522 1.95264509221189 7.1047671673513
7.28075839970208 7.05916813567919 P P P 6.13577251537078 6.1718357406431
6.24811473526978 P P P LNCV6_131364_PI430048170 mRNA
ATGGTGGGGCCCCCAGCACCCTCTGTTAGTGCCGCAATAAATGCTCAATCATGTGCCAGA NM_003673 RefSeq
chr17 + 39665345 39666554 TCAP 8557 titin-cap
GO:0030240|GO:0005515|GO:0030018|GO:0001756|GO:0051373|GO:0060048|GO:0007512|GO:0005829|GO:0003
300|GO:0050982|GO:0036122|GO:0014898|GO:0055003|GO:0008307|GO:0030674|GO:0048769|GO:0055008|GO:0
030049|GO:0030916|GO:0045214|GO:0035994|GO:0035995|GO:0031432|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_49657_PI430048170 0.31077964508944 0.842531970525203 6.17617028948441
5.58803547226166 5.54430840783962 P P P 6.12414651137195 6.10498628548657
5.90028659511662 P P P LNCV6_49657_PI430048170 mRNA
GCTGCATTTGCCCCCTTCCCAACGCAGTTCAAAGCAATTTGAAATAAAGTCGTTCTCATA NM_001145140 RefSeq
chrX + 71763289 71767201 CXorf49 NA chromosome X open reading frame 49 NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_94064_PI430048170 0.185331402819199 0.913095980472028 10.173405871644
10.3554904033803 10.1305944144799 P P P 10.3419598109715 10.4243708486119
10.2936182100131 P P P LNCV6_94064_PI430048170 mRNA
TCTTCTCGGTAGAAGGGAGAAGGACAGAGCTCTCTTCAATAAATTCGTCAGGTCAAAGCA NM_016044 RefSeq
chr2 + 95402699 95413131 FAHD2A 51011 fumarylacetoacetate hydrolase domain containing 2A
GO:0016787|GO:0008152|GO:0046872 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_136573_PI430048170 0.0197936443251228 3.18164822845615 4.32468833391417
3.38571317498323 3.98560531940784 P P P 2.21510217993311 2.16439037284505

2.44259623439695 A A P LNCV6_136573_PI430048170 mRNA
AGGCCTCAAAAACATACGTAACGAAAAGGCCTAGCGAGGCAAATTCTGATTGATTTGAAT NM_139072 RefSeq
chr2 - 229357628 229714570 DNER 92737 delta/notch-like EGF repeat containing
GO:0005515|GO:0007220|GO:0005886|GO:0005509|GO:0048741|GO:0005112|GO:0007417|GO:0007416|GO:0030
425|GO:0006897|GO:0007219|GO:0030276|GO:0043025|GO:0010001|GO:0016021|GO:0001764|GO:0005769|GO:0
004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97952_PI430048170 0.0574508947315387 1.41869749940315 5.26830132442413
5.37834260532871 5.73344400909788 P P P 4.80395207717102 4.8598371460615
5.21005598734249 P P P LNCV6_97952_PI430048170 mRNA
ACAGCTTGACAAACTGAAGAAGGAAAAGCAGCAAAGGCAGTTTCAGCTTGACAGTCTCGA NM_016343 RefSeq
chr1 + 214603188 214664571 CENPF 1063 "centromere protein F, 350/400kDa"
GO:0005515|GO:0007094|GO:0048471|GO:0008283|GO:0005634|GO:0005635|GO:0015031|GO:0042803|GO:0030
154|GO:0016363|GO:0005829|GO:0005737|GO:0051382|GO:0007059|GO:0000086|GO:0051726|GO:0016202|GO:0
000785|GO:0051310|GO:0042493|GO:0010389|GO:0005819|GO:0030496|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138291_PI430048170 0.5048259316474080.9822561187865040.483125955784184
0.3771641088496960.448318647185157A A A 0.4389349120503310.49108841495201
0.45760077035591 A A A LNCV6_138291_PI430048170 mRNA
CACCTCAGATCATTGTTAGTCTTACTTAGCAGAAAATGTATAAACACTTACCAGGTAGTA NM_177531 RefSeq chr8
+ 109362476 109531271 PKHD1L1 93035 polycystic kidney and hepatic disease 1 (autosomal recessive)-
like 1 GO:0006955|GO:0004872|GO:0016021|GO:0005615|GO:0005829 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132263_PI430048170 0.5001764175076540.9783327397227660.265142475804219
0.2748386040144160.383798280562407A A A 0.3732348532832690.311245069697272
0.336467755366465A A A LNCV6_132263_PI430048170 mRNA
AAACCCCATTATCTACACTCTGAGAAACAAAGATGTGAAAGGGGCCTTGAGGACCCTGAT NM_001013355 RefSeq
chr1 + 248521646 248522597 OR2G6 NA "olfactory receptor, family 2, subfamily G, member 6" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139206_PI430048170 0.2308600482151630.7905842131531985.26956807162656
5.16944495831942 4.86958553608989 P P P 5.79493042245721 5.29966026674087
5.18522346469699 P P P LNCV6_139206_PI430048170 mRNA
GTATTGGCGTCTCTCCAAGTCGACACTTTTCCTGATCCCACTCTTTGGAATTCACTACAT NM_000823 RefSeq chr7
+ 30964020 30979531 GHRHR 2692 growth hormone releasing hormone receptor
GO:0005515|GO:0060124|GO:0043627|GO:0008284|GO:0005886|GO:0030819|GO:0005637|GO:0016520|GO:0033
143|GO:0008340|GO:0016363|GO:0005640|GO:0048609|GO:0007190|GO:0030104|GO:0005737|GO:0019838|GO:0
048469|GO:0030252|GO:0040018|GO:0030141|GO:0051246|GO:0032868|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135741_PI430048170 0.00487041939308563 1.41636231767766 9.75781719831958
9.82755069034794 9.60741610223092 P P P 9.31566988799881 9.18476114568848
9.19064794463564 P P P LNCV6_135741_PI430048170 mRNA
CCTCACAGGCGCTGTGAATTTTTGTACAAGTCTTGTAATTATCGAATCAACAACTTGTTT NM_020247 RefSeq chr1
+ 226940236 226987545 ADCK3 56997 aarF domain containing kinase 3
GO:0005739|GO:0006744|GO:0004674|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130816_PI430048170 0.00572146804050625 0.1732646758235683.29699062875731
2.93894738514924 2.93156404083968 P P P 5.05114338133198 5.53905942202622
6.03048142213332 P P P LNCV6_130816_PI430048170 mRNA
GATCATCATTGCTTCCCACATAGGAAAAATAAAATGTCTTCAGACTTGATGTGACTCAAA NM_001163335 RefSeq
chrX + 38006581 38128820 SYTL5 94122 "synaptotagmin-like 5, transcript variant 2"

GO:0005515|GO:0017137|GO:0016020|GO:0006887|GO:0006886|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111845_PI430048170 0.0069402071754173 1.69786463487022 3.6502605807575 4.01931391191007 3.93126796253781 P P P 3.25472595149051 3.07652018835737 2.99096940825477 P P P LNCV6_111845_PI430048170 mRNA TTTGACCTGGAGCCGGACACCTACTGCCGCTATGACTCGGTCAGCGTGTTCAACGGAGCC NM_002593 RefSeq chr7 + 100602258 100608176 PCOLCE 5118 procollagen C-endopeptidase enhancer
GO:0031012|GO:0016504|GO:0005515|GO:0010952|GO:0005518|GO:0006508|GO:0007275|GO:0008201|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133962_PI430048170 0.1011151079961650.79602909071889 10.8551791679913 10.625150832208 10.7837020538216 P P P 10.8398744486331 11.1429115929086 11.2476833854666 P P P LNCV6_133962_PI430048170 mRNA GGTGCCAGGGGTACATTTTTGCACTGAAATCTAAAGATGTTTTAAAAAACACTTTTCACA NM_004776 RefSeq chr20 - 49632945 49713884 B4GALT5 9334 "UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5"
GO:0005975|GO:0016266|GO:0044281|GO:0008378|GO:0046872|GO:0042339|GO:0000139|GO:0006493|GO:0018146|GO:0032580|GO:0009405|GO:0016021|GO:0044267|GO:0030203|GO:0070062|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_50936_PI430048170 0.1891823881694660.9589330985043820.2471780488107670.269250023289332 0.343527449685359 A A A 0.3966245991948280.3238015735581830.321526556219396 A A A LNCV6_50936_PI430048170 mRNA TTGAGTAGAGACAAGCTCTGGGCTTTGAGAGCTGAATAGCATTTTTCTCCTGCCTCATCA NM_015297 RefSeq chr9 + 34958194 34982544 KIAA1045 23349 "KIAA1045, transcript variant 1" GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140925_PI430048170 0.9212344050800810.9480662463011961.46322240835049 0.3317593046077461.3739860301267 A A A 1.86279368289153 0.785848754613757 0.685606059165939 A A A LNCV6_140925_PI430048170 mRNA CTCCGCACACCGTGAAAAAACTGGAAATGGGCATTGTAGTCTTTAATTAATAAAAACACC NM_001080444 RefSeq chr21 + 39745406 39802096 IGSF5 150084 "immunoglobulin superfamily, member 5"
GO:0043005|GO:0016337|GO:0050767|GO:0009986|GO:0005886|GO:0005911|GO:0043025|GO:0016021|GO:0005923|GO:0030165 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144781_PI430048170 0.0172271924721429 1.82146347620541 5.26257253173752 4.84706979404696 4.79373733687341 P P P 4.02349341578739 4.08890213073332 4.23455432979179 P P P LNCV6_144781_PI430048170 mRNA TAAACCCGCAATCTGCTCCAGATTCAAGCAGTAATATTTCAGCAAGAGGAGGTGGTCATG NM_138350 RefSeq chr1 + 6625149 6635586 THAP3 90326 "THAP domain containing, apoptosis associated protein 3, transcript variant 2" GO:0005515|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135902_PI430048170 0.9334813494439431.07573388093945 2.44254510224334 2.08089576227516 3.20857820317577 A A P 2.55361268666988 2.69596676232428 2.38648076232116 P P P LNCV6_135902_PI430048170 mRNA TGAAATGTACTCCCTTGGAAAGGAGGTCAGGGTTCTGAAGCTAGACATTGATGAACGAGT NM_001042633 RefSeq chr20 + 45833830 45843275 SNX21 90203 "sorting nexin family member 21, transcript variant 4"
GO:0035091|GO:0015031|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141680_PI430048170 0.0578507199016838 1.0387470439819 0.42759598270659 0.4691708751079990.450244550674889 A A A 0.3681758798664740.390104510082153 0.423950113365917 A A A LNCV6_141680_PI430048170 mRNA GTGAACATGTACAAGGAAGTGATGGAGAGAGATCACCTTCAAGACATACAGAGGAAAAGA NM_024867 RefSeq chr5 + 35617886 35814611 SPEF2 79925 "sperm flagellar 2, transcript variant 1"

GO:0009566|GO:0060541|GO:0035082|GO:0005794|GO:0002177|GO:0097225|GO:0046983|GO:0010259|GO:0007283|GO:0002520|GO:0048702|GO:0048854 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137578_PI430048170 0.129388219108855 1.05294089191758 12.0379713952708 11.9762045384777 12.0821546976656 P P P 11.9409226676497 11.9655446571611 11.9683910421929 P P P LNCV6_137578_PI430048170 mRNA
TAGGGAGAATGAATGTGCAACGTGGCTGAAATCTATTTTGTGTAATAAAAGGTGATACAA NM_152274 RefSeq chrX - 153587924 153599177 FAM58A 92002 "family with sequence similarity 58, member A, transcript variant 1"
GO:0005515|GO:0006355|GO:0019901|GO:0045860|GO:0016591|GO:0030295|GO:0000079|GO:0043410 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136138_PI430048170 0.9221413794541 1.00205507325856 0.352748206589714 0.336080129716723 0.276380868214815 A A A 0.320142742362429 0.330294809239992 0.306903560720837 A A A LNCV6_136138_PI430048170 mRNA
TAATGTCTCCTTTTAAGGAGACGAATGTACCAGAAAAATAATAAAGCAAAGAAGCTTCGG NM_152548 RefSeq chr5 + 95391343 95450440 FAM81B 153643 "family with sequence similarity 81, member B" GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142790_PI430048170 0.13929589514815 0.331351005920697 0.405496677028028 0.41335271045831 0.375996553425665 A A A 0.636729940686954 2.23094784452558 2.50688502228959 A A P LNCV6_142790_PI430048170 mRNA
GTGCTCAGACAGGTAACCACTGCTGCTACTGTTTTTATTTGTTTGTTTGTTCAATTTTAT NM_020734 RefSeq chr12 + 8699784 8777191 RIMKLB 57494 "ribosomal modification protein rimK-like family member B, transcript variant 1" GO:0005737|GO:0072591|GO:0072590|GO:0005524|GO:0046872|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137974_PI430048170 0.176510385185965 1.13472251616876 0.673706414266719 0.379912761325732 0.61576876650297 A A A 0.283137981497319 0.410433735181903 0.440483976816516 A A A LNCV6_137974_PI430048170 mRNA
TGCTTTGAACAACTGAAACGAGAACTGTCAAAGTCAAGGCAGACTATGGACTGTGCCACA NM_021833 RefSeq chr4 - 140559895 140568805 UCP1 7350 "uncoupling protein 1 (mitochondrial, proton carrier)"
GO:0022904|GO:0005739|GO:0006357|GO:0050873|GO:0017077|GO:0005743|GO:0044281|GO:0016021|GO:0006839|GO:0044237|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134390_PI430048170 0.0473178255133644 1.96433079579921 10.1160678081774 10.6147779288817 11.0121568324802 P P P 9.95227223441142 9.24310244211834 9.67597928460686 P P P LNCV6_134390_PI430048170 mRNA
TGTTGAACATCAACTGGGGAATTGAAGCCAATAAACCTTCCTTCTTAACCATTCAAAAAA NM_000669 RefSeq chr4 - 99336491 99353045 ADH1C 126 "alcohol dehydrogenase 1C (class I), gamma polypeptide"
GO:0004022|GO:0006805|GO:0006069|GO:0008270|GO:0044281|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127157_PI430048170 0.482579587719902 0.701299532398141 0.529438009027381 0.502992979197344 0.438225772685732 A A A 0.411289924491534 1.73163604059271 0.443608773084409 A A A LNCV6_127157_PI430048170 mRNA
GGCCCAACAGGATCATCTCATTGCATGATTTTCTTTACTTTTGAAGTAAAAGGAGATTTA NM_152599 RefSeq chr17 - 8797109 8799349 MFSD6L 162387 major facilitator superfamily domain containing 6-like
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128894_PI430048170 0.00428026147982514 0.260028335612646 6.56366482567992 6.13305008937714 6.35418207664942 P P P 7.82992353580558 8.42217180765009 8.56126146527756 P P P LNCV6_128894_PI430048170 mRNA
CTATTTGAAAAGGAGATGTACTTGGACGTTTCTGTAAATCTTGAGATAAACTGTTTGGAG NM_006888 RefSeq chr14 + 90396982 90408275 CALM1 801 "calmodulin 1 (phosphorylase kinase, delta)"
GO:0005515|GO:0005513|GO:0007603|GO:0030017|GO:0006936|GO:0007173|GO:0043274|GO:0016056|GO:0010

800|GO:0005813|GO:0032465|GO:0006996|GO:0019901|GO:0005975|GO:0008179|GO:0005509|GO:0019904|GO:0
030168|GO:0022400|GO:0010801|GO:0044325|GO:0031432|GO:0000922|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131517_PI430048170 0.2956584582443281.49418322476075 1.62546369313135
0.5915622989150660.558817663838018A A A 0.3528817946949730.444988042263649
0.506802655137506A A A LNCV6_131517_PI430048170 mRNA
AACAAGGCCATAAAGGTGGCTCTGGGGATGTTGATAAAGGGAAAGCTCACCAAAAAGTAA NM_001001966
RefSeq chr1 - 247814799 247815729 OR14A16 NA "olfactory receptor, family 14, subfamily A, member
16" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141650_PI430048170 0.00694161483830468 0.7369272125535458.77454829247993
8.87140572517391 8.89998376738442 P P P 9.21333666887711 9.23751922452851
9.41110191927023 P P P LNCV6_141650_PI430048170 mRNA
GAACCTGTTGAATTGCATGCTGGGAAGCATCAGTTGTCAAAATATGTTATATACTTCCAT NM_153698RefSeq chr9
- 96641250 96655317 AAED1 195827 AhpC/TSA antioxidant enzyme domain containing 1 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_82274_PI430048170 0.0887329303655686 1.40406822211903 3.8096502435195
3.94344628702305 4.30638863286701 P P P 3.5271328868172 3.24845018056845
3.80777478826158 P P P LNCV6_82274_PI430048170 mRNA
ACTCTGGCTCCTTCACCATCACGGGCAACAACAGCAACTTTGCTCAGAGGTTCCAGGGCA NM_001278116 RefSeq
chrX - 153861513 153886174 L1CAM 3897 "L1 cell adhesion molecule, transcript variant 4"
GO:0005886|GO:0043621|GO:0050900|GO:0042802|GO:0050850|GO:0006935|GO:0007411|GO:0043195|GO:0007
159|GO:0033691|GO:0007155|GO:0007156|GO:0007157|GO:0022409|GO:0009986|GO:0033631|GO:0007399|GO:0
042734|GO:0034109|GO:0005178|GO:0007596|GO:0016021|GO:0005925|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_76340_PI430048170 0.0208516323680823 1.56194138484666 8.1407237903448
7.87431695064896 7.90018604544156 P P P 7.42176736368614 7.48661181384474
7.05578656751847 P P P LNCV6_76340_PI430048170 mRNA
AATCACAACTGGGTACAAGACATTTCGCCACCTGCATGACCCAGCCTGGCGGAAGAGGGA NM_007255RefSeq
chr5 + 177600117 177610345 B4GALT7 11285 "xylosylprotein beta 1,4-galactosyltransferase,
polypeptide 7"
GO:0005794|GO:0030145|GO:0005975|GO:0048147|GO:0003831|GO:0044281|GO:0006029|GO:0008378|GO:0006
024|GO:0000139|GO:0032580|GO:0009405|GO:0046525|GO:0043206|GO:0006487|GO:0016021|GO:0030204|GO:0
030203|GO:0006464. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145003_PI430048170 0.00121255150972964 3.12594701227768 8.84792729567476
8.60619667467444 8.48663105262668 P P P 7.19732056996722 7.07954771702526
6.71150784679567 P P P LNCV6_145003_PI430048170 mRNA
TGTGAATGCCGCGTCCTGTCCTGGTGACAGGAGAACAATGTTGGTGAACGTCGCAAAAAA NM_001009939 RefSeq
chr22 + 19718434 19723322 SEPT5 NA "septin 5, transcript variant 2" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_83610_PI430048170 0.7323458779230721.06580339420822 4.02304490695603 3.61161220511519
4.20096175374007 P P P 3.29336825237165 4.20686901809107 3.97342331191642 P P P
LNCV6_83610_PI430048170 mRNA
AGAACTTTTCTTTGAAATGTCCCAAACATAAGAGGCTGCCGTAGTAATCCACCCCAACGG NM_030665RefSeq chr17
+ 17681472 17811451 RAI1 10743 retinoic acid induced 1
GO:0005739|GO:0001501|GO:0040015|GO:0006357|GO:0008270|GO:0005654|GO:0005634|GO:0045893|GO:0035
326|GO:0032922 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81217_PI430048170 0.0810715070695407 2.27440584097015 3.21228479223896
2.93703532221706 3.08660075731802 P P P 1.14723472506535 2.54278124658954
1.64854919514089 A P A LNCV6_81217_PI430048170 mRNA

AAAGAAAAGAGCCAGCTGCAGAATAGCCGAGACCTGGCCCAGAATGAGCAGCGCATCCTG NM_138424RefSeq chr9 - 114091637 114099057 KIF12 113220 kinesin family member 12 GO:0008017|GO:0008150|GO:0003674|GO:0005871|GO:0005737|GO:0008152|GO:0005874|GO:0003777|GO:0016887|GO:0005524|GO:0070062|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_67255_PI430048170 0.285136425895437 2.1549439637033 0.406122468569042 1.72096914428662 2.53957230374114 A A A 0.5823405059247990.368424929109543 1.03881190772452 A A A LNCV6_67255_PI430048170 mRNA

TCTTGAAGAGATGAAGAAAGGACACCTCGAAAGAGAGTGCATGGAAGAGACCTGCTCATA NM_000504RefSeq chr13 + 113122798 113149529 F10 2159 coagulation factor X GO:0005515|GO:0051897|GO:0030335|GO:0004252|GO:0005886|GO:0005796|GO:0005509|GO:0005576|GO:0031233|GO:0017187|GO:0005543|GO:0007596|GO:0007597|GO:0007598|GO:0006508|GO:0005788|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_145438_PI430048170 0.0183407224977996 1.87280188307755 6.11559384211515 6.50834236398374 6.56161577174167 P P P 5.5379424530213 5.42684501519704 5.54201195536496 P P P LNCV6_145438_PI430048170 mRNA

TAGTCTCTCTAGGTCATAGCTTTCATGTCCATTGAAGAATTACCAAGCCCAGCAAGTAAA NM_052892RefSeq chr16 - 81100878 81220370 PKD1L2 114780 "polycystic kidney disease 1-like 2 (gene/pseudogene), transcript variant 1" GO:0005509|GO:0030246|GO:0016021|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_115962_PI430048170 0.294409417709763 1.16446880775874 5.27271288430549 5.29805718959245 5.14862239505176 P P P 4.66561087955305 5.13842131042025 5.20340190827085 P P P LNCV6_115962_PI430048170 mRNA

ATAGTGCGAGCCAACGACATCCTGAAGCTGCCTTACAGCACCTTCCGCACCTACGTGTTC NM_005994RefSeq chr17 + 61399895 61409466 TBX2 6909 T-box 2 GO:0005515|GO:0060045|GO:0008284|GO:0060596|GO:0005634|GO:0048596|GO:0060021|GO:0005667|GO:0007569|GO:0035909|GO:0003203|GO:0007521|GO:0000122|GO:0000978|GO:0003677|GO:0060560|GO:0006351|GO:0003151|GO:0043565|GO:0048738|GO:0001078|GO:0060465|GO:0003148|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_129252_PI430048170 0.0314009270592451 .24708033319608 6.08614167549322 5.85735963187797 5.95402977033112 P P P 5.7806621548741 5.62568663634711 5.53383699411793 P P P LNCV6_129252_PI430048170 mRNA

AAGCATTTGTTATGATTTCCCTGAATTAATTCATCCCACGCATCCTCCCTGAGGCACCTG NM_001012710 RefSeq chr11 + 71565562 71566620 KRTAP5-10 NA keratin associated protein 5-10 NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_129891_PI430048170 0.0555742602134721 1.33344960985907 8.35149052592439 8.36375550550773 8.65859371058914 P P P 7.80877630674477 8.12173665453009 8.1912053278277 P P P LNCV6_129891_PI430048170 mRNA

CATGGTATGAATTCAGAGTGTGACTTAAGGGTCAATTCAAAGCAGTATTTTGACTTTTCA NM_015960RefSeq chr10 + 99732200 99756137 CUTC 51076 cutC copper transporter GO:0005737|GO:0055070|GO:0051262|GO:0005507|GO:0005730|GO:0005654|GO:0005634|GO:0006825 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_132716_PI430048170 0.390086419175316 1.46889460247925 0.362704965065224 1.58693716002481 0.407223115789796 A A A 0.3030093514807020.400739018513859 0.344186070695463 A A A LNCV6_132716_PI430048170 mRNA

GTTCTTGATGTACCAGCATACATAAACATATTAGGCTGTATTGTAAGTTTCCTGCATGTA NM_001145287 RefSeq chr6 + 154086506 154132354 OPRM1 4988 "opioid receptor, mu 1, transcript variant MOR-1K1" GO:0005515|GO:2000310|GO:0042220|GO:0007218|GO:0032496|GO:0070374|GO:0031681|GO:0005794|GO:0004930|GO:0019904|GO:0060079|GO:0004979|GO:0033554|GO:0071315|GO:0070848|GO:0042923|GO:0005887|GO:0007187|GO:0042060|GO:0070588|GO:0045121|GO:0031635|GO:0005925|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_112373_PI430048170 0.3571799241106620.8462242451549496.05934889571895
5.76579090807016 5.44260080125936 P P P 6.09821312807282 6.21088134918587
5.69804864405287 P P P LNCV6_112373_PI430048170 mRNA
TCCTCATCTCCCTCAAGGATGGCTACGTACCCCCAAAGAGCCGGGAGCTGAGGGTCAACC NM_001193333 RefSeq
chr16 + 30183409 30189076 CORO1A 11151 "coronin, actin binding protein, 1A, transcript variant 1"
GO:0006909|GO:0005515|GO:0008092|GO:0030424|GO:0030036|GO:0005886|GO:0005884|GO:0008360|GO:0051
279|GO:0006928|GO:0005634|GO:0042803|GO:0043524|GO:0005737|GO:0051015|GO:0048873|GO:0030833|GO:0
005911|GO:0042102|GO:0030670|GO:0071353|GO:0006816|GO:0007015|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134425_PI430048170 0.3675270713409851.32143101429615 1.24463867505244
0.3095557134523270.428791127259888A A A 0.3483451973931640.312670633022052
0.304085880605694A A A LNCV6_134425_PI430048170 mRNA
GGCAGGCTTCATCTGAAAAACTGTAATTGGAGAACTAGCTCAAAATAAATCTTGAAATAC NM_181599RefSeq chr21
+ 30396073 30396820 KRTAP13-1 140258 keratin associated protein 13-1 GO:0005882 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127240_PI430048170 0.2006579896442731.15768479042668 12.1252649849396
11.7745259317739 11.9389018432009 P P P 11.5524736192645 11.8209715752583
11.8356630588942 P P P LNCV6_127240_PI430048170 mRNA
GTAAAGTTACAACACACCCTCTTGCTAAAGACAAAATGATGAATGGAGGTCATTACACCT NM_007262RefSeq chr1
+ 7961653 7985282 PARK7 11315 "parkinson protein 7, transcript variant 1"
GO:0005515|GO:0045560|GO:0050681|GO:0042803|GO:0032757|GO:0042802|GO:0043523|GO:0005758|GO:0043
524|GO:0003690|GO:0003697|GO:0050787|GO:0005759|GO:0006508|GO:0051444|GO:0031397|GO:0042743|GO:0
000785|GO:0005507|GO:0003713|GO:0001047|GO:0005747|GO:0019955|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141394_PI430048170 0.3605363120510831.55706616411809 1.72233515589457
0.4293126204648130.448307016330884A A A 0.3321949160221960.352103090984604
0.405932654456965A A A LNCV6_141394_PI430048170 mRNA
CAGACTCTGAATGCATGACCTTTGGTACATGCCTGTTAATATTCATGTTCTGAAAATATT NM_014208RefSeq chr4
+ 87608528 87616873 DSPP 1834 dentin sialophosphoprotein
GO:0005737|GO:0001501|GO:0071460|GO:0001503|GO:0030198|GO:0005518|GO:0005509|GO:0005578|GO:0007
275|GO:0005576|GO:0031214|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138143_PI430048170 0.6659770854045860.9493706527671480.343783613176195
0.3772718526639510.296380618220639A A A 0.26611035659588 0.287092609309
0.656013942376837A A A LNCV6_138143_PI430048170 mRNA
GAGAGGCAGCATTTGTTTTCCAGTTAAAACTCTACCTCATTGTGATTATTATCCAATACA NM_001098612 RefSeq
chr19 - 51642552 51646879 SIGLEC14 NA sialic acid binding Ig-like lectin 14 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134014_PI430048170 0.0237950968010751 0.4894617809837773.49295814075929
2.85925156588213 3.49145819268409 P A P 3.94348098270453 4.37081409108135
4.62823700414069 P P P LNCV6_134014_PI430048170 mRNA
AAGCCAGCTTGCACTCTCTGCTTTCATCTTTTTGAAGCAATAACTATTACATAAATCAGT NM_001025247 RefSeq
chr1 - 229599193 229626047 TAF5L 27097 "TAF5-like RNA polymerase II, p300/CBP-associated factor
(PCAF)-associated factor, 65kDa, transcript variant 2"
GO:0006355|GO:0003700|GO:0043966|GO:0006366|GO:0030914|GO:0003713|GO:0006325|GO:0005654|GO:0005
634|GO:0004402|GO:0033276 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142562_PI430048170 0.3410256126324340.608653790975426 0.436974303824951
0.4894439439113990.465290512828915A A A 0.7695546840494390.401287863194695
1.91594520166443 A A A LNCV6_142562_PI430048170 mRNA

GAAGCATTTTTAACTGGGTAGAATCTGACTGTGGCTTGAAATAAAAAGCTCTCAGAAAAA NM_000727 RefSeq chr17 + 67044535 67056795 CACNG1 786 "calcium channel, voltage-dependent, gamma subunit 1" GO:0006936|GO:0005245|GO:0070588|GO:0006810|GO:0034765|GO:0070296|GO:0005891 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127164_PI430048170 0.0566253582718011.15261684305661 0.616121620274673 0.7645730535326720.797023080125762 A A A 0.6271590195910380.459656486665927 0.476574898115714 A A A LNCV6_127164_PI430048170 mRNA
TATACTTTAAGGAACAAGGATATGAAAGAGGCTCTGAGGAAACTTCTCTCGGGAAAATTG NM_001001914 RefSeq chr1 + 247605585 247606515 OR2G3 NA "olfactory receptor, family 2, subfamily G, member 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132941_PI430048170 0.762131014893296 1.01724655903551 0.269152607832929 0.2835210009401510.464434768476509 A A A 0.3434863558351460.296977731197317 0.310562140887375 A A A LNCV6_132941_PI430048170 mRNA
AACCACATGTTGTCTCCAAGCTGGTGGGAGCAGTGAAATCTGTAACATGCAAGATATTGA NM_001161334 RefSeq chr1 - 149782688 149812373 HIST2H2BF NA "histone cluster 2, H2bf, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140529_PI430048170 0.754254982198432 1.00609229858749 0.345998763574056 0.3234176104361980.268380214140063 A A A 0.3070168757748290.31342420857162 0.292085417058933 A A A LNCV6_140529_PI430048170 mRNA
CTTTGGAATTTCACAGCGTGCTAAAATAACAGATTTCTCAGAAGTCTTTCAGCAAGATAA NM_000091 RefSeq chr2 + 227164564 227314792 COL4A3 1285 "collagen, type IV, alpha 3 (Goodpasture antigen)" GO:0005515|GO:0008285|GO:0008283|GO:0006919|GO:0008015|GO:0007605|GO:0005587|GO:0072577|GO:0005576|GO:0032836|GO:0005604|GO:0010951|GO:0005178|GO:0022617|GO:0030198|GO:0005198|GO:0007411|GO:0008191|GO:0030574|GO:0016525|GO:0005788|GO:0007155|GO:0007166|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140168_PI430048170 0.0835291581282206 1.26834509884843 8.56845475493555 8.48405029689287 8.35808507284213 P P P 7.8819595431501 8.28231979165929 8.1952178194938 P P P LNCV6_140168_PI430048170 mRNA
TCTCCCTGACCAGGGACCAAGCACAGGGCATTTAGAGCTTTTTAGAATAAACTGGTTTTC NM_138477 RefSeq chr15 - 42723561 42737219 CDAN1 146059 codanin 1 GO:0005515|GO:0005737|GO:0008104|GO:0031497|GO:0005886|GO:0006325|GO:0005634|GO:0016021|GO:0008156|GO:0012505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131920_PI430048170 0.237443539780705 1.04850481648528 0.343886101834546 0.3363718704468350.463059758836301 A A A 0.3092001933827110.290162638512709 0.342010370531477 A A A LNCV6_131920_PI430048170 mRNA
CTAATTCGAGATTGTGAAGCAACACTTCTAAATTCAAAGACATAGAGTTGTCAAATCAGG NM_030772 RefSeq chr1 - 38874066 38881626 GJA9 81025 "gap junction protein, alpha 9, 59kDa" GO:0007154|GO:0005922|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72014_PI430048170 0.822972574739186 1.13825967123511 0.5037179703478292.06010908034005 0.642771182980976 A A A 1.83202535298113 0.4583986290030780.42930137105975 A A A LNCV6_72014_PI430048170 mRNA
CTGTATTATAACACTGTGAACAAGAACATCAGCAGCAGCAGAATTGTCAGCCTTCCTGCG NM_001290047 RefSeq chr22 + 17369365 17558155 CECR2 27443 "cat eye syndrome chromosome region, candidate 2, transcript variant 1" GO:0005515|GO:0060122|GO:0005719|GO:0043044|GO:0097194|GO:0001843|GO:0005634|GO:0001842|GO:0007338|GO:0000910|GO:0006309|GO:0007010|GO:0090102|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136694_PI430048170 0.802920625265272 1.07649473723446 0.344699671074468 1.10401979129446 0.368554000545294 A A A 0.3900188221016630.335731953963358

0.850657559804531 A A A LNCV6_136694_PI430048170 mRNA
GGAACTGTTAGTGAGTCAAGACAAACACATCTGAAATAAAGGAACTGTGTATTAACATGT NM_144665 RefSeq chr11
- 95165512 95231082 SESN3 143686 "sestrin 3, transcript variant 1"
GO:0032868|GO:0005634|GO:0042593|GO:0051896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133610_PI430048170 0.844205216366374 0.9639974272658 0.258810429203863
0.298391274976799 0.84272210641549 A A A 0.37095656854217 0.310916191611179
0.882512630356067 A A A LNCV6_133610_PI430048170 mRNA
CATTGTAAGCATAAGCTTTAGAAGTAAAGCATTTGCGTTTGCAGTGCATCAGATACATTT NM_002260 RefSeq chr12
- 10430605 10435993 KLRC2 3822 "killer cell lectin-like receptor subfamily C, member 2"
GO:0043235|GO:0005515|GO:0007165|GO:0006968|GO:0005886|GO:0005887|GO:0045087|GO:0002228|GO:0030
246|GO:0023024|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129626_PI430048170 0.00354818173411197 1.41510643239282 7.86716504962523
7.85961222498537 8.04167010184265 P P P 7.39495051315517 7.37153098417756
7.50323568888179 P P P LNCV6_129626_PI430048170 mRNA
CTGTACTGGTAAGACTTGTATCTCCATCCACCTGAAGGAGAATTGCTGGCTCATTTTCAG NM_181786 RefSeq chr19
+ 37334677 37364456 HKR1 284459 "HKR1, GLI-Kruppel zinc finger family member"
GO:0006355|GO:0007275|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135841_PI430048170 0.0256979968097134 1.29740740965405 10.1283993747677
10.2489163776223 10.2374326230132 P P P 9.67266276599283 9.94265884093068
9.86241360108967 P P P LNCV6_135841_PI430048170 mRNA
TCTTGAGGGAAGGAAAAGCCAGACTTTGGGTTTGTTTTTTGGGGGAATTATTGGTTTTTT NM_001080495 RefSeq
chr7 - 5306791 5423546 TNRC18 84629 trinucleotide repeat containing 18
GO:0005739|GO:0031965|GO:0006342|GO:0005737|GO:0000976|GO:0031507|GO:0003682|GO:0005654|GO:0005
634|GO:0000785|GO:0005677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145516_PI430048170 0.0684659105326509 1.18250670373504 9.59191495926611
9.50810590242374 9.60180823238768 P P P 9.36229077543564 9.17547270465141
9.42856459236608 P P P LNCV6_145516_PI430048170 mRNA
GGGTTGGGGGAGTCAGCATGATTATATTTTAATGTAGAAAATGTGACATCTGGATATAAA NM_001693 RefSeq chr8
+ 20197192 20221696 ATP6V1B2 526 "ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2"
GO:0008286|GO:0042470|GO:0046034|GO:0051701|GO:0005886|GO:0015078|GO:0033180|GO:0005765|GO:0055
085|GO:0001726|GO:0005524|GO:0043231|GO:0005829|GO:0012505|GO:0006879|GO:0033572|GO:0005902|GO:0
046961|GO:0015991|GO:0016021|GO:0090382|GO:0070062|GO:0015992 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_145599_PI430048170 0.0600893868624617 0.612234316584285 0.454414742993325
0.468743173183297 0.462690349871406 A A A 1.4064138554037 1.22921494760574
0.810873277485413 A A A LNCV6_145599_PI430048170 mRNA
GAGAAAGTTCACTTTTCCAGTGGCTCAAAAATTTGTTTTAGGTCAGAGATTTTAAGTGGT NM_001080463 RefSeq
chr11 + 103109430 103479863 DYNC2H1 79659 "dynein, cytoplasmic 2, heavy chain 1, transcript variant
2"
GO:0007368|GO:0005886|GO:0009953|GO:0030326|GO:0005829|GO:0019886|GO:0045880|GO:0003774|GO:0008
105|GO:0016485|GO:0007030|GO:0016887|GO:0035721|GO:0070062|GO:0006996|GO:0005794|GO:0021522|GO:0
005930|GO:0005874|GO:0045177|GO:0072372|GO:0031512|GO:0003777|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_101255_PI430048170 0.985593473778758 1.02315557141121 0.49623530474674
0.576338957633825 1.6726846643134 A A A 1.56928667947778 0.465304794156804
0.681363653123649 A A A LNCV6_101255_PI430048170 mRNA
GACATGAGAATTTACAGCTAAGAAAAGACCATAAAAGTGTGGATGCATGTAAGGTGTACA NM_001287533 RefSeq
chr7 + 65373798 65401135 ZNF92 168374 "zinc finger protein 92, transcript variant 4"

GO:0006355|GO:0003700|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126811_PI430048170 0.1669688063834660.4226237073869020.411304208089763 0.4214525859053770.43650949794516 A A A 2.27368014170015 1.68777476511399 0.546711593774302A A A LNCV6_126811_PI430048170 mRNA AAACACTAACGGAAACCCATGGAGTTTGTCCTTTGTAAAAATTTTAAACACAGTGTCTTG NM_181303RefSeq chrX + 71144830 71171201 NLGN3 54413 "neuroligin 3, transcript variant 1"
GO:0052689|GO:0005515|GO:0030054|GO:0048709|GO:2000310|GO:0045202|GO:0030139|GO:0048675|GO:0005615|GO:2000331|GO:0002087|GO:0004872|GO:0030534|GO:0007612|GO:0061001|GO:0060024|GO:0050839|GO:2000969|GO:0007158|GO:0051965|GO:2000463|GO:0009986|GO:0051968|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127424_PI430048170 0.2901268613767160.5701674012706140.42740289399278 0.4203478323272270.36596813635054 A A A 1.97401711989927 0.534687663959509 0.667940100758572A A A LNCV6_127424_PI430048170 mRNA TGCCTCTCATAAAGCTGCTTGGACATTTTAAGTGTTTTGTAATATGCATTGAAGTGTTGA NM_018040RefSeq chr1 - 217426992 217631102 GPATCH2 55105 "G patch domain containing 2, transcript variant 1"
GO:0010923|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137694_PI430048170 0.4336349853603370.8398097167228980.417598893241385 0.4557590051393110.463427852518162A A A 1.10595738307437 0.461298394410338 0.418152879159171A A A LNCV6_137694_PI430048170 mRNA TGAGGTACAGCAGGACCTTTCTAGGAAATGTGGCATACAAAACATTTTTATCTCATAAAA NM_017945RefSeq chr3 + 112562009 112584437 SLC35A5 55032 "solute carrier family 35, member A5"
GO:0015780|GO:0005338|GO:0000139|GO:0008643|GO:0005351|GO:0016021|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143295_PI430048170 0.2544545727950161.04988019056083 0.350442046441371 0.3526164892224390.484013324302028A A A 0.3215761113067650.3019356657762 0.356453223858274A A A LNCV6_143295_PI430048170 mRNA AAAGATGTCACCAGGGCTCTGAGGAGCATGATGCAGTCAAGAATGAACCAAGAAAAGTAG NM_001005495 RefSeq chr1_KI270892v1_alt + 123768 124725 OR2T3 NA "olfactory receptor, family 2, subfamily T, member 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128774_PI430048170 0.5729359826371481.16620454805005 0.36922561885772 0.3336993747356471.12852855125598 A A A 0.4865429382428080.438715128542522 0.385698106635489A A A LNCV6_128774_PI430048170 mRNA CTGAGCTTCCTTATGTTTCACACATTGTATTTGAACACAAAACATTAACAACTCCACTCA NM_001077RefSeq chr4_GL000257v2_alt - 222753 247016 UGT2B17 7367 "UDP glucuronosyltransferase 2 family, polypeptide B17"
GO:0052696|GO:0052695|GO:0016020|GO:0009813|GO:0001972|GO:0005789|GO:0015020|GO:0016021|GO:0032870|GO:0008202|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133792_PI430048170 0.2952700023395410.2626567800111620.375685799314691 0.33550787610331 0.325830179500273A A A 1.07898935747332 3.46966834033698 0.405858609294339A P A LNCV6_133792_PI430048170 mRNA ATCACGGAACATCCAGGATACTAATGTGGACTTCTCTGCATTGTGTAAGAACCAATTCAA NM_001122962 RefSeq chr20 - 1474590 1491587 SIRPB2 284759 "signal-regulatory protein beta 2, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145592_PI430048170 0.0197278514725480.9446895308924180.395555316254948 0.3461455003549960.344583085437603A A A 0.4622060933390270.449988639590051 0.420621270710533A A A LNCV6_145592_PI430048170 mRNA CGTGGCTATTGTTTATGGATTCATATGTAAGGTAGGGTCTTTTTTGCATATAGACTCCAG NM_004956RefSeq chr7 - 13891230 13990017 ETV1 2115 "ets variant 1, transcript variant 1"

GO:0005515|GO:0003700|GO:0006357|GO:0006366|GO:0000981|GO:0005634|GO:0000978|GO:0030154|GO:0001077|GO:0007517|GO:0007411|GO:0045944|GO:0048935|GO:0007638 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137062_PI430048170 0.3640489572590961.14331304280555 0.872579524338652 0.427748200636961 0.407633376302021 A A A 0.390417127135791 0.37745473954835 0.409647271786032 A A A LNCV6_137062_PI430048170 mRNA
TCCATACGAAATGCAAACCTTTGATTCTGTATGCTGTGATCTAGTGAAAAACTCCAATAT NM_152470 RefSeq chr18 + 46334223 46460820 RNF165 494470 "ring finger protein 165, transcript variant 1" GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135847_PI430048170 0.0656058707076321.04395066547875 0.338087751416627 0.337536074470412 0.280912141751117 A A A 0.247293965425075 0.273232733636442 0.250454379102639 A A A LNCV6_135847_PI430048170 mRNA
AACAAACTCATGTCTTCGTCTGTTGTCTGTACATTCTCCGTTAATGTTTCTCGCATTTAT NM_001282775 RefSeq chr1 - 240775513 241357230 RGS7 6000 "regulator of G-protein signaling 7, transcript variant 3" GO:0031681|GO:0005886|GO:0005834|GO:0038032|GO:0044292|GO:0005634|GO:0005829|GO:0035556|GO:0043547|GO:0005737|GO:0007186|GO:0004871|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128271_PI430048170 0.00116177818892366 2.32469946102323 5.0197360839112 5.38027207012202 5.23979389837582 P P P 3.85383916381307 4.08574982654529 4.06069607577694 P P P LNCV6_128271_PI430048170 mRNA
TAGGAGCAGTGAGTGACAAAGCCTCTGAAAGATGCATCATCTCTTCCTCACACCCATTTA NM_005631 RefSeq chr7 + 129188871 129213544 SMO 6608 "smoothened, frizzled class receptor" GO:0005515|GO:0017147|GO:0034504|GO:0060248|GO:0021696|GO:0001755|GO:0007228|GO:0005113|GO:0007224|GO:0031069|GO:0043231|GO:0001947|GO:0021794|GO:0071397|GO:0060644|GO:0003140|GO:0048589|GO:0070062|GO:0060684|GO:0050679|GO:0005794|GO:0001708|GO:0004930|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130817_PI430048170 0.7036390121140491.02882774794455 7.44744667894545 7.5185991314529 7.62340136508828 P P P 7.33256189663364 7.45598498311727 7.66376408715144 P P P LNCV6_130817_PI430048170 mRNA
TCTTTTGTTTCCCACCCCCCTGACATGTATGTGTGCTTTAATAAAGCTTTCTCACTTGTC NM_080737 RefSeq chrX - 100674490 100731534 SYTL4 94121 "synaptotagmin-like 4, transcript variant 1" GO:0005215|GO:0005813|GO:0017137|GO:0005886|GO:0050714|GO:0006887|GO:0042043|GO:0006886|GO:0008021|GO:0045921|GO:0005737|GO:0071985|GO:0005543|GO:0005654|GO:0008270|GO:0030141|GO:0046676|GO:0030658|GO:0005768|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130564_PI430048170 0.9222104213544130.8648299784409041.68609595558062 1.97804134338365 2.26353835938444 A A A 0.5977585550769492.07478975718988 3.01829182575962 A A P LNCV6_130564_PI430048170 mRNA
CAACAACTTACATCTCAGTCACTCCAAAAAACTGGCATGGGTAAACCAGCTATTACTAAG NM_182482 RefSeq chr21 + 10413531 10491615 BAGE2 NA "B melanoma antigen family, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133107_PI430048170 0.000343356003749594 2.02684359641613 8.58345370749329 8.7367595445671 8.7268750293303 P P P 7.75733133357445 7.53834208697394 7.69011522201439 P P P LNCV6_133107_PI430048170 mRNA
CAGCTTCATACTTCATGAAATCCTGGGTTTTCTTAACCATCTTTTCCTCATTTTCAATGG NM_005423 RefSeq chr21 - 42346357 42351099 TFF2 7032 trefoil factor 2 GO:0005515|GO:0030334|GO:0008284|GO:0019722|GO:0070098|GO:0043031|GO:0007586|GO:0005615|GO:0031723|GO:0050728|GO:0060455|GO:0070374|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129005_PI430048170 0.0845628544533713 0.7496915932519024.57082649374833 4.27389118527643 4.05591288924447 P P P 4.57469624987428 4.78569055994634 4.82160750183047 P P P LNCV6_129005_PI430048170 mRNA

CATAGCATGGCACAACTAAAAATCTAAGCCTGAAACCTGAAAAAAGAGATATGACAAGGG NM_177995 RefSeq chr9 + 94030793 94109856 PTPDC1 138639 "protein tyrosine phosphatase domain containing 1, transcript variant 2" GO:0030030|GO:0005654|GO:0008138|GO:0035335|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53445_PI430048170 0.756726210997263 1.0893731438736 0.3065345545576531.07626639923641 0.33536027247652 A A A 0.8805882322946160.2425454371802590.268831713807976 A A A LNCV6_53445_PI430048170 mRNA
TAGAATAAAAAACAGAACTGAACTTAGCCTTCCCAGGGAAGGAACCATGCCCCACACATC NM_001010881 RefSeq chr1 + 11762192 11789585 C1orf167 284498 chromosome 1 open reading frame 167 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142599_PI430048170 0.0277674252718555 1.24989496992946 8.95635461710252 9.00825418082347 8.95042787860923 P P P 8.68576580291959 8.73195090621018 8.52447896508854 P P P LNCV6_142599_PI430048170 mRNA
GTGGACAGACATATCTGCATATTTATCAATAAAGCCTTTTGCTCCTTCTCGCTTAAAAAA NM_024954 RefSeq chr10 + 97498881 97571210 UBTD1 80019 ubiquitin domain containing 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131319_PI430048170 0.00435532475177301 0.51827798732932 6.81952947580047 6.52390808293533 6.83637286815611 P P P 7.57870968971466 7.52331678161165 7.91191643625029 P P P LNCV6_131319_PI430048170 mRNA
GAATTTTATGGTCCCTTTCTTTGATGGTGCTTGCAGGTTTTCTAGGTAGAAATTATTTCA NM_000332 RefSeq chr6 - 16299111 16761490 ATXN1 6310 "ataxin 1, transcript variant 1" GO:0005515|GO:0008344|GO:0005634|GO:0043621|GO:0016363|GO:0042802|GO:0043231|GO:0008266|GO:0005737|GO:0045944|GO:0042272|GO:0051168|GO:0006396|GO:0048286|GO:0060079|GO:0000122|GO:0008022|GO:0003677|GO:0006351|GO:0042326|GO:0034046|GO:0043569|GO:0008542|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145290_PI430048170 0.4785109891557430.7939494667011390.937896691714109 1.61670311507139 0.319167156450588 A A A 1.81520247951421 0.812818286720769 1.36245015705451 A A A LNCV6_145290_PI430048170 mRNA
GAAGTACTGACTTTACCAAAAGAATCATCAAGAAAGCTATTTATATAAACCCCCTCAGTC NM_015082 RefSeq chr5 - 133196459 133612532 FSTL4 23105 follistatin-like 4 GO:0005509|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137455_PI430048170 0.0320300090026759 1.36635288079271 4.98211065653089 4.8220455125394 4.84977138169507 P P P 4.44750172619715 4.59959858799205 4.23833199763534 P P P LNCV6_137455_PI430048170 mRNA
AAGGGACTACAAACCAACTTTCGACTTCTGAAAAGAAGGCTACGGGAGATTCTCCAGTGA NM_152426 RefSeq chr22 + 39021112 39033251 APOBEC3D 140564 "apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3D" GO:0016814|GO:0051607|GO:0005737|GO:0000932|GO:0045087|GO:0045869|GO:0008270|GO:0010529|GO:0070383 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128163_PI430048170 0.00399146406640542 0.4503123809878276.31816521178293 5.84878599852363 6.12670794838341 P P P 7.01540204251768 7.24054585440357 7.48980956832191 P P P LNCV6_128163_PI430048170 mRNA
GGCTGGTCTGCATGCTGGAAGAGGTTGAGAGTTTTGGAATTGATTCCATGCTAAATGTCA NM_018263 RefSeq chr2 - 25739383 25878443 ASXL2 55252 additional sex combs like transcriptional regulator 2 GO:0000790|GO:0045672|GO:0048704|GO:0000122|GO:0003677|GO:0042975|GO:0006351|GO:0046872|GO:0007512|GO:0035360|GO:0045944|GO:0045600|GO:0005654|GO:1900159 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138589_PI430048170 0.1762803371306910.8213666954313851 3.0065852073266 12.847954215498 12.7070922332593 P P P 13.3875072276162 13.0803232510687 12.9216587605353 P P P

LNCV6_138589_PI430048170 mRNA
CGTCTCCCTCTCTGCAGCCTGTGTAAGCTATTATAATTAAAATGGTTTTCCGGGAAAAAA NM_031229RefSeq chr20
+ 408064 430966 RBCK1 10616 "RanBP-type and C3HC4-type zinc finger containing 1, transcript variant 2"
GO:0000209|GO:0005515|GO:0042346|GO:0043130|GO:0050852|GO:2001238|GO:0004842|GO:0003700|GO:0016
874|GO:0071797|GO:0032088|GO:0097039|GO:0051092|GO:0016032|GO:0008270|GO:0043161|GO:0043123|GO:0
060546 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140121_PI430048170 0.0305339383459711 1.25022502830356 14.865168762042
14.9667609290617 15.0732579793175 P P P 14.6598213593156 14.6578657770493
14.6282263205683 P P P LNCV6_140121_PI430048170 mRNA
AAAGAAGATGAAGAAGTCTTCAGGGGAGATTGTCTACTGTGGGCAGGTGTTTGAGAAGTC NM_000980RefSeq chr19
+ 17859877 17863324 RPL18A 6142 ribosomal protein L18a
GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0006415|GO:0006412|GO:0006
413|GO:0005829|GO:0006414|GO:0000184|GO:0016020|GO:0016032|GO:0022625|GO:0044267 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141431_PI430048170 0.0218282131679094 0.880940663102805 12.6463280675119
12.7786170806102 12.7147612462018 P P P 12.8517654030568 12.9271977679732
12.9113331539995 P P P LNCV6_141431_PI430048170 mRNA
CATCCCTCCCTGATATTGTATTGAAAATATTATGCACACTGTTCATGCTTCTACTAATCANM_022833RefSeq chr9 -
127505337 127569117 FAM129B 64855 "family with sequence similarity 129, member B, transcript variant
1"
GO:0043066|GO:0005737|GO:0005912|GO:0005886|GO:0005730|GO:0005654|GO:0005634|GO:0015629|GO:0070
062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134414_PI430048170 0.160301090953759 0.630304979071019 3.83764256502068
2.74457948823373 3.07053831281126 P A P 4.26162308058898 4.03427720585101
3.46961162546067 P P P LNCV6_134414_PI430048170 mRNA
GTCTGTGAGCTATTAATGTTATTAATTTTCATAAAAGCTGGAAAGCAGCTGCCTGTTTCA NM_001136493 RefSeq
chr1 + 39955111 39969968 MFSD2A 84879 "major facilitator superfamily domain containing 2A,
transcript variant 1"
GO:0045056|GO:0005737|GO:0015914|GO:0005886|GO:0005887|GO:0060856|GO:0005789|GO:0015908|GO:0005
548|GO:0055085|GO:0015293 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139412_PI430048170 0.245456874774296 0.940147866506518 0.254473551399878
0.354860518443822 0.277467922027731 A A A 0.480266156244086 0.374441371145084
0.295148300217215 A A A LNCV6_139412_PI430048170 mRNA
TCACGCACTATGTGGGAAGGGCGTGTTTTTAAATTAATAAAGTGTGTCACCATTAGCCAT NM_144669RefSeq chr12
+ 128853535 128984964 GLT1D1 144423 glycosyltransferase 1 domain containing 1
GO:0005737|GO:0009058|GO:0016757|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128611_PI430048170 0.302683551638481 1.05062285324086 0.498091183416724
0.328530241917565 0.422225105315448 A A A 0.288543447639146 0.357383975988544
0.392250370251056 A A A LNCV6_128611_PI430048170 mRNA
GGGAGGATACCTTCTCTTCTGTGGTGTGCCATTTGCTTTGGATTCAGGTTTCTAGAGTAA NM_001005193 RefSeq
chr19 - 9102268 9103306 OR7G2 NA "olfactory receptor, family 7, subfamily G, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130004_PI430048170 0.0111070486887879 0.331771056644671 5.42943525337789
5.50059844281287 5.70717752975424 P P P 6.94256007267029 6.83781269142002
7.54247281268335 P P P LNCV6_130004_PI430048170 mRNA
GAAAGCCCATAATGTATTTAGAAACAGGAATCCTCAGAGCAATTCTCTGTATTCTCATAT NM_004666RefSeq chr6
- 132680857 132714055 VNN1 8876 vanin 1
GO:0033089|GO:0002526|GO:0034235|GO:0005886|GO:0015939|GO:0006928|GO:0002544|GO:0031225|GO:0017
159|GO:0016337|GO:0006954|GO:0045087|GO:0016021|GO:0006979|GO:0070062 . NA - . NA NA NA

NA NA NA NA NA NA
LNCV6_133354_PI430048170 0.0950079693229274 1.15203996591126 9.66072062450002
9.75781719831958 9.70687038525306 P P P 9.58604361588616 9.35198451730482
9.56502278350328 P P P LNCV6_133354_PI430048170 mRNA
CATACTTAGCAAATCTAACACATGAAATGTAACATCTGCATATGGAGAACCGTGTTACTT NM_017592RefSeq chr19
+ 39391322 39400563 MED29 55588 mediator complex subunit 29
GO:0005515|GO:0006355|GO:0016592|GO:0005654|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_108891_PI430048170 0.0474875996278142 2.27924043918552 3.7046925383869
3.48261581580119 3.60200835367354 P P P 2.5987868826493 2.70179222094021
1.76063215354432 A P A LNCV6_108891_PI430048170 mRNA
AAGCGACACTGGGTTGGAAACACTTGGCTCTCTCATGAGTATTAAAATTCTATTTCAATC NM_130897RefSeq chr16
+ 80540951 80550809 DYNLRB2 83657 "dynein, light chain, roadblock-type 2, transcript variant 1"
GO:0006996|GO:0008152|GO:0005874|GO:0006810|GO:0072372|GO:0005868|GO:0003777|GO:0070062|GO:0007
018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144350_PI430048170 0.0115977778675440.5482895011033012.1800144899619
11.8789665520295 11.6863617661632 P P P 12.7382213826502 12.948586125941
12.6894912580734 P P P LNCV6_144350_PI430048170 mRNA
CTCTGTGACTGAGAGCCCTAGTGTGATGAGAACTAAAGAGAAAGCCAGACCCCTAAAAAA NM_021198RefSeq
chr2 + 218399754 218405941 CTDSP1 58190 "CTD (carboxy-terminal domain, RNA polymerase II,
polypeptide A) small phosphatase 1, transcript variant 1"
GO:0005515|GO:0006470|GO:0045665|GO:0006357|GO:0001933|GO:2000134|GO:0005634|GO:0046872|GO:0070
062|GO:0008420 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128519_PI430048170 0.474012713561863 1.28618557528929 0.422539271708138
0.400636018582385 1.3893342364501 A A A 0.43086437604288 0.471970734764453
0.454260837692301 A A A LNCV6_128519_PI430048170 mRNA
CAAAACTTGCTGAACAAATGGCTGGATGAGTGAAACAGGAATGGAGCAAGCCAGTACAGT NM_144968RefSeq
chrX + 53422855 53429828 RIBC1 158787 "RIB43A domain with coiled-coils 1, transcript variant 2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127887_PI430048170 0.314045386656055 0.816300121047098 9.35458178437784
8.73311262826961 8.56845475493555 P P P 9.34349858012243 9.31589385673727
8.96969272874915 P P P LNCV6_127887_PI430048170 mRNA
CTCCCCTGACCTCTGCCCTTTCTACATAAAGCAGGTTGGAGTTTTTCTCATTTCAAAAAA NM_207307RefSeq chr3
- 129401320 129428651 EFCAB12 90288 EF-hand calcium binding domain 12 GO:0005509 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_130167_PI430048170 0.133736600994973 1.19015792119437 8.26440944522789
8.61548735269729 8.39327661054791 P P P 8.22349390738355 8.1763623371583 8.1407237903448
P P P LNCV6_130167_PI430048170 mRNA
TTTATTTCCGTTTTTGTTTCTGGTTACTGTGAATCCCAGAGGAGTCTCTCCCTGTGCCCA NM_032442RefSeq chr17 -
7315631 7329319 NEURL4 84461 "neuralized E3 ubiquitin protein ligase 4, transcript variant 1"
GO:0005515|GO:0005814 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144154_PI430048170 0.0281140887263096 0.228867120579659 1.93169698602725
0.341736142240886 1.55885830776282 A A A 3.09881282250083 3.75232381858206
3.70445628154233 P P P LNCV6_144154_PI430048170 mRNA
GTAGTTGGAACCACTTAGTCTTTAGGTGCAAGACTGTTGTTAGATAGTACTGAGAAAAAA NM_001270520 RefSeq
chr14 + 59188662 59371405 DAAM1 23002 "dishevelled associated activator of morphogenesis 1,
transcript variant 2"
GO:0005515|GO:0005737|GO:0001725|GO:0030036|GO:0016020|GO:0005886|GO:0017048|GO:0003779|GO:0042
802|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_128198_PI430048170 0.0151139986136052 1.99933118106237 3.67133734720966
3.42241343842882 3.24456345636661 P P P 2.4463613619085 2.45701535550046
2.46835331892289 A P P LNCV6_128198_PI430048170 mRNA
TGTGTGTGCTCGTGTATATGGGGTGGGGAACATGAGACTTCCTGTGACCAGTCCACCCTG NM_002390RefSeq chr17
+ 44759199 44781846 ADAM11 4185 ADAM metallopeptidase domain 11
GO:0031012|GO:0005178|GO:0005886|GO:0007229|GO:0006508|GO:0008270|GO:0016021|GO:0004222|GO:0008
237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136540_PI430048170 0.78414656449701 1.01527745253813 0.318480920787483
0.3138160729118420.489847232737582A A A 0.3054966829392840.429126726187072
0.325895259672234A A A LNCV6_136540_PI430048170 mRNA
TCAGAGAATTTATGGCTCTGTATCCAATAAAAAAGATGGTGAAACTGGTCTATCTGCCAA NM_001080410 RefSeq
chr2 - 73254681 73269630 FBXO41150726 F-box protein 41 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129246_PI430048170 0.1231728407782820.8897893104700198.95239448314574
8.86112325731569 8.89802313549068 P P P 9.05061279389232 8.96163451730972
9.19636028425611 P P P LNCV6_129246_PI430048170 mRNA
TGTGTTTTTGGCTGTCCTGTCTATTGGATGTGATATGTTATGGATGTGATGTGTTAGTGTNM_001242481 RefSeq chr11
- 65996544 66002166 EIF1AD 84285 "eukaryotic translation initiation factor 1A domain containing,
transcript variant 1" GO:0003743|GO:0005654|GO:0045111|GO:0006413|GO:0043231 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_57049_PI430048170 0.0120640941851874 0.8285172012662974.8222246063297
4.97001045574388 4.95707866410113 P P P 5.20146821615662 5.24572566084216
5.11799938099276 P P P LNCV6_57049_PI430048170 mRNA
ATTCATCATGGACAAGAGCGAAGCCATCACGTCTGTGGACGACGCCATCCGGAAGCTGGT NM_022772RefSeq chr11
+ 706119 727727 EPS8L2 64787 EPS8-like 2
GO:0005886|GO:0035023|GO:0003779|GO:0032587|GO:0007266|GO:0031982|GO:0032855|GO:0043234|GO:0005
737|GO:1900029|GO:0032321|GO:0005089|GO:0030676|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_61010_PI430048170 0.0197710450997598 0.4788679703587484.30351141996472
3.55541743687584 3.81390686051153 P P P 4.82304592595482 4.78607747336111
5.29494980511024 P P P LNCV6_61010_PI430048170 mRNA
GGAACTGGAAGAAATATTGGATGTGATTGAACCTTCACAATTTGTTAAAATCCAAGAACC NM_006246RefSeq chr14
- 63373891 63543361 PPP2R5E 5529 "protein phosphatase 2, regulatory subunit B', epsilon isoform,
transcript variant 1" GO:0005515|GO:0007165|GO:0050790|GO:0005737|GO:0008601|GO:0000159 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136859_PI430048170 0.2110591998948231.17858519880333 9.93135328315646
9.95733395719405 9.7422592679411 P P P 9.89633697067086 9.56389224678781
9.42796290574964 P P P LNCV6_136859_PI430048170 mRNA
GAGATGGCCTTGCTCCTCCTCGCTGTACCCCCAGTAAAGAGCTTTCTCACATGCAAAAAA NM_004714RefSeq chr19
- 39825346 39834233 DYRK1B9149 "dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B,
transcript variant a"
GO:0005515|GO:0003713|GO:0005634|GO:0007520|GO:0018108|GO:0005524|GO:0004672|GO:0004674|GO:0004
712|GO:0006468|GO:0004713|GO:0045893|GO:0060612 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131606_PI430048170 0.0206478600078867 1.65578749653166 10.6634183048605
10.8233347286162 10.9017558940898 P P P 9.81888309366642 10.0376956312846
10.3162484531042 P P P LNCV6_131606_PI430048170 mRNA
CCTGGGCTTGTGTACCTCAGTGGTTTTTGTGTACTTTTTTCAATAAAATATCAAAGTTGA NM_014174RefSeq chr11
- 134248278 134253366 THYN1 29087 "thymocyte nuclear protein 1, transcript variant 1"
GO:0005737|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_141721_PI430048170 0.2017378833814010.3078208841712580.377429751311165
0.2773878339398310.278680047972837A A A 0.2573331462265742.11976579557655
2.71299097266835 A A P LNCV6_141721_PI430048170 mRNA
CACCTTGCTTGTGCTTAAACACTTATGTTCATCTAGTGTAGAATACATGGCTACTTGTTTNM_016116RefSeq chr7 +
95485900 95540231 ASB4 51666 "ankyrin repeat and SOCS box containing 4, transcript variant 1"
GO:0035556|GO:0004842|GO:2001214|GO:0031462|GO:0031466|GO:0031625|GO:0051865 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130235_PI430048170 0.2414387298885251.5976665346227 2.31471445652845
2.38369811853236 2.104586537559 A A A 0.5049350816854971.43185229300404
2.30898021488483 A A A LNCV6_130235_PI430048170 mRNA
GCTTGAAGTTTTCCAGGAGTCGCATTTTAAAAGTGTTTGTACACATTTTAACACTTGGAT NM_032528RefSeq chr2
- 106801599 106887107 ST6GAL2 84620 "ST6 beta-galactosamide alpha-2,6-sialyltranferase 2, transcript variant 1"
GO:0009311|GO:0000139|GO:0032580|GO:0007275|GO:0016021|GO:0006488|GO:0044267|GO:0040007|GO:0003835|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127000_PI430048170 0.0394741015901160.5977946216063873.56092940697133
3.32346165783214 3.07101292970268 P P P 3.81662871714422 3.91125471304935 4.420219404399
P P P LNCV6_127000_PI430048170 mRNA
CTGATGCTTTCTCCAGAATGAAGAGTCCCAATTTGTATATCAGTGTTAAGAAGAAAACAA NM_005188RefSeq chr11
+ 119206275 119308149 CBL 867 "Cbl proto-oncogene, E3 ubiquitin protein ligase"
GO:0005515|GO:0004842|GO:0017124|GO:0003700|GO:0016567|GO:0005886|GO:0016874|GO:0005634|GO:0016600|GO:0005829|GO:0005737|GO:0007173|GO:0007179|GO:0004871|GO:0006355|GO:0043066|GO:0005509|GO:0042059|GO:0014068|GO:0046875|GO:0008543|GO:0048260|GO:0001784|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_76082_PI430048170 0.0231447638091631 0.5695177282020956.96594937723615
6.72015456382431 6.48742822426345 P P P 7.51480267082512 7.60559643520709
7.52767052534232 P P P LNCV6_76082_PI430048170 mRNA
TAGCCCCCTCTAACATTTTTCATCAGCCTATGGCAAGTGGTTTTGTGGATTTTTCTAAAG NM_020690RefSeq chr5
+ 140401813 140549578 ANKHD1-EIF4EBP3 404734 ANKHD1-EIF4EBP3 readthrough NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136380_PI430048170 0.00166913663478189 0.4489701922876983.59839970793811
3.70680293151776 3.94692857003727 P P P 4.93716153246348 4.69660176537131
5.08082868192022 P P P LNCV6_136380_PI430048170 mRNA
GTCAACATAGTTCCAATGGCTCCTTTCTGACCTGCTTTCATGTTTTAATGTTTGTTTAAT NM_005447RefSeq chr12 -
85804552 85836540 RASSF9 9182 Ras association (RalGDS/AF-6) domain family (N-terminal) member 9
GO:0005515|GO:0007165|GO:0005215|GO:0016197|GO:0006605|GO:0070062|GO:0012510|GO:0005829|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98984_PI430048170 0.53516911164977 0.9002990103573239.57030571591018 10.0944256240437
10.241352721422 P P P 10.1245536031107 9.9128041039586 10.3696026168859 P P P
LNCV6_98984_PI430048170 mRNA
CTAAGCAAACTACAAACCAGGAAAATGAAGGGGTTGAAGAAGCGACCTGCAGAAAGGATA NM_032194RefSeq
chr6 + 110982016 111028263 RPF2 84154 "ribosome production factor 2 homolog (S. cerevisiae), transcript variant 1" GO:0000463|GO:0005730|GO:0000027|GO:0005634|GO:0019843 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_142926_PI430048170 0.0884765431444882 1.06146560711602 0.466884794162237
0.5573563337758410.516523195581429A A A 0.3751630922435610.43594269936759
0.471273663935402A A A LNCV6_142926_PI430048170 mRNA
CTGTACAAGTCTCTATACAATGTCTTTATCCCTGTGGGCAGCAAGCAATGATGATAATGA NM_015567RefSeq chr13
+ 87672614 87679615 SLITRK5 26050 "SLIT and NTRK-like family, member 5"

GO:0043235|GO:0048813|GO:0021756|GO:0007268|GO:0043588|GO:0030534|GO:0016021|GO:0007625|GO:0007409|GO:0072358|GO:0009410 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138346_PI430048170 0.5892428036712520.8808570040877928.11811907327131 7.77590400211278 7.95904957426538 P P P 7.73981986854275 8.04195514294848 8.52911373815078 P P P LNCV6_138346_PI430048170 mRNA
GTCGCCTTAGCATGTTTGCTGAACACCTTGTGGAAGCAAAAATCTGAAAATGTGAATAAA NM_005688RefSeq chr3 - 183919935 184017939 ABCC5 10057 "ATP-binding cassette, sub-family C (CFTR/MRP), member 5, transcript variant 1"
GO:0005886|GO:0005975|GO:0042626|GO:0044281|GO:0055085|GO:0005524|GO:0016020|GO:0005887|GO:0006810|GO:0009405|GO:0015711|GO:0030213|GO:0030212|GO:0008514|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130484_PI430048170 0.2207696880857451.32432797592418 4.91956573420997 4.73542261851667 5.23406107710625 P P P 4.04829868015552 4.73626111650834 4.81702653026585 P P P LNCV6_130484_PI430048170 mRNA
GGATGACTTGTTCATTTTTCTCTCCCTCTTTTTCTCTGTATATTTATGACCAGAGCAAAA NM_004789RefSeq chr9 + 124011609 124033163 LHX2 9355 LIM homeobox 2
GO:0021987|GO:0060041|GO:0006366|GO:0001843|GO:0048675|GO:0005634|GO:0009953|GO:0021978|GO:2000678|GO:0043565|GO:0001076|GO:0021772|GO:0007411|GO:0045944|GO:0003682|GO:0007498|GO:0008270|GO:0045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138660_PI430048170 0.2764835083220390.4074466011762270.337895058501984 0.3183746926077830.41390110982997 A A A 0.3267877271901411.1049710824455 2.59144991890602 A A P LNCV6_138660_PI430048170 mRNA
CTCTGGATTCAGCCTTCTTTTTCTGGACTCTGGACTTTCTCTAATAATAAATAGTTCTTC NM_002630RefSeq chr6 - 41736710 41747401 PGC 5225 "progastricsin (pepsinogen C), transcript variant 1"
GO:0007586|GO:0006508|GO:0004190|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143196_PI430048170 0.00318375315644714 0.4126798822369924.82822036651004 4.70982198935978 5.21115811746122 P P P 6.08151287312184 6.07299163084924 6.44251120297081 P P P LNCV6_143196_PI430048170 mRNA
GTGTCACTGTTACATTTCCCCCAAGAAGTTCAATAAACCAGCTTAGCCACAAAGAAAAAA NM_031296RefSeq chr4 + 139453806 139475915 RAB33B 83452 "RAB33B, member RAS oncogene family"
GO:0005515|GO:0050678|GO:0005794|GO:0005796|GO:2000156|GO:0003924|GO:0006914|GO:0048705|GO:0006891|GO:0005525|GO:0001558|GO:0006886|GO:0006184|GO:0000139|GO:2000785|GO:0032482|GO:0019003|GO:0070062|GO:0000042. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106810_PI430048170 0.0453994326233811 1.24952026938882 4.54950725372155 4.71724887421525 4.41928504923804 P P P 4.34305255340001 4.19819604968419 4.19103222802472 P P P LNCV6_106810_PI430048170 mRNA
AACTCAGGGTCTTCATTTTCCGTGGAACTCAAAGTCTTCTTGCTCTGTGGAACTTGGAGT NM_001113434 RefSeq chr17 - 21528309 21551678 C17orf51 339263 chromosome 17 open reading frame 51 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132982_PI430048170 0.0588989456684396 1.04822700949254 0.338249426586218 0.3527315707565910.287433523277033A A A 0.2482265303564950.2754103992457 0.251583576408048A A A LNCV6_132982_PI430048170 mRNA
GGTGAGAGGCCTTTGGAAACAGAAATGATTTCTATTTCTGTAAACAGCAATGTTTACTAA NM_138693RefSeq chr7 - 130732553 130734033 KLF14 136259 Kruppel-like factor 14
GO:0045944|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127688_PI430048170 0.1957430289150150.5438933198187350.31167448103082 0.2526949785421350.36334604060185 A A A 0.273093313616 1.46271425310105

1.52258226355396 A A A LNCV6_127688_PI430048170 mRNA
ACATGTATCTATGGAAATCCAAAATGCATCTGGGTGCAGCACTAAATAAATTCTCCATCC NM_005553 RefSeq chr11
+ 71548419 71549607 KRTAP5-9 3846 keratin associated protein 5-9
GO:0005515|GO:0008544|GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139702_PI430048170 0.26790819976543 1.65176217812354 3.09401635464973
2.57170127935971 2.83778477213825 P A A 2.99458234894085 1.80963902892103
0.697213947629481 P A A LNCV6_139702_PI430048170 mRNA
AGTTTCAGAACATATGCTAAATGCGAGAGGCCCACCCGGGGTAAATACATCACTGATAAT NM_001243541 RefSeq
chr17 - 78890579 78903217 CEP295NL NA "KIAA1731 N-terminal like, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67324_PI430048170 0.15093316930455 0.764631514431933 0.30653781113587 3.84560880703959
3.79500010451453 P P P 3.83496987602012 3.99344898908464 4.29984174899906 P P P
LNCV6_67324_PI430048170 mRNA
CCTTAGAGGAAGTGATAGTGGGCAGAGCAGAAAACGCCTGTGTTCCACCGTTCACCATCG NM_001482 RefSeq chr15
- 45361123 45378782 GATM 2628 glycine amidinotransferase (L-arginine:glycine amidinotransferase)
GO:0007584|GO:0015068|GO:0016813|GO:0005743|GO:0043434|GO:0044281|GO:0042246|GO:0005758|GO:0034
641|GO:0006601|GO:0006600|GO:0006979|GO:0046689|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_99674_PI430048170 0.148056360423556 1.22672779471353 3.48509226346766
3.77019475495132 3.56737221892506 P P P 3.57479051003407 3.12557947203607
3.21263999338264 P P P LNCV6_99674_PI430048170 mRNA
ACATTGAGAGGCGTGACGGAGGCATCCCTGCGGACCCCAACAACGTCTTCCTGTCCACAG NM_005309 RefSeq
chr8 + 144504081 144507172 GPT 2875 glutamic-pyruvate transaminase (alanine
aminotransferase)
GO:0034641|GO:0004021|GO:0042853|GO:0030170|GO:0008652|GO:0044281|GO:0070062|GO:0005829 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_128228_PI430048170 0.000768286761103678 0.419387436601125 8.19454256793137
8.01786003182519 8.30997793191304 P P P 9.24583844407563 9.43958331607588
9.59203537979852 P P P LNCV6_128228_PI430048170 mRNA
GTCCCCAGTCTGCAAAAGAAGCACAATTCTATTGCTTTGTCTTGCTTATAGTCATTAAAT NM_005180 RefSeq
chr10 + 22321209 22331485 BMI1 648 "BMI1 proto-oncogene, polycomb ring finger"
GO:0005515|GO:0000792|GO:0010468|GO:0048103|GO:0004842|GO:0030890|GO:2001234|GO:0000151|GO:0048
704|GO:0005634|GO:0048146|GO:0005737|GO:0006959|GO:0051443|GO:0071535|GO:0021903|GO:0035102|GO:0
030097|GO:0031519|GO:0007379|GO:0016573|GO:0016574|GO:0000122|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127955_PI430048170 0.0809303806892348 1.04181992902723 0.453820265397652
0.513658502823289 0.465655513133315 A A A 0.387025541743024 0.420717015790707
0.448123729882519 A A A LNCV6_127955_PI430048170 mRNA
GTGCTCCTACAAGTGCTTCATCTCTGTGCCTGAAATTCTATAAATGTTGCAATCATGAAA NM_006652 RefSeq
chr20 - 45512460 45515624 SPINT3 NA "serine peptidase inhibitor, Kunitz type, 3" NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_133018_PI430048170 0.00625882528881703 1.69775238831843 8.93095796237254
9.03992619280312 8.67748639589657 P P P 8.22805626519085 8.1595376959922
7.98246582054399 P P P LNCV6_133018_PI430048170 mRNA
TACCTCACAGGCTACTATGTGCACAAGTGCAAATAAATGCTGCCCCGCATGCACGCGGGG NM_001163724 RefSeq
chr1 + 3772786 3775982 SMIM1 388588 "small integral membrane protein 1 (Vel blood group), transcript
variant 1" GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136252_PI430048170 0.529782332588688 1.35037746107952 0.461013868026685
1.59726831480095 0.278589541057255 A A A 0.358355411276913 0.625993604177883

0.414697884963667 A A A LNCV6_136252_PI430048170 mRNA
GCGCAAAGATTGTACAAATCAAACTGGTGGATAATAAAGTCGTGGATGACTCACTGACAA NM_001137560 RefSeq
chr6 + 44270742 44279445 TMEM151B NA transmembrane protein 151B NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_135679_PI430048170 0.0133398869838604 0.747987511892181 10.0850149910293
10.2794344214505 10.2058673367871 P P P 10.7017706780116 10.6612257010594
10.459187904182 P P P LNCV6_135679_PI430048170 mRNA
GTAGCCAGGTGCTTTTGTAGATCTTGTGTTTTAGGTTGGGCATTTTCACTCTTCTGCCTT NM_001287237 RefSeq
chr8 - 144850165 144853067 COMMD5 28991 "COMM domain containing 5, transcript variant 4"
GO:0005515|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133313_PI430048170 0.0543640328711212 1.22316377530976 13.0395227857652
13.0059564150845 13.0256303573894 P P P 12.5957711227955 12.847954215498
12.7446529638245 P P P LNCV6_133313_PI430048170 mRNA
AAGGGGGCAGGAGTCAGCAATAAAGCTATGTCTGATATTTTCCTTCACTAATATGAATAA NM_001191003 RefSeq
chr10 + 104254193 104267464 GSTO1 9446 "glutathione S-transferase omega 1, transcript variant
3"
GO:0005515|GO:0006805|GO:0014810|GO:0042178|GO:0010881|GO:0044281|GO:0004364|GO:0045174|GO:0005
829|GO:0060316|GO:0019852|GO:0050610|GO:0005737|GO:0010880|GO:0060315|GO:0016491|GO:0071243|GO:0
070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132147_PI430048170 0.0661680813511366 0.856792881090685 12.5373051683662
12.4172740817698 12.626688797102 P P P 12.6246455290004 12.7841670933695
12.8404366787835 P P P LNCV6_132147_PI430048170 mRNA
AACTACCTTCAACTCCATCATGAAGTCTGATGTGGACATCCGCAAAGACCTGTACACCAA NM_001277406 RefSeq
chr2 - 130462815 130509235 POTEI 653269 "POTE ankyrin domain family, member I"
GO:0003674|GO:0001895|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133591_PI430048170 0.84047727937509 0.9909166984788 0.499471067141892
0.484312086442872 0.420769825554971 A A A 0.382790538194355 0.531235384797483
0.52634997621805 A A A LNCV6_133591_PI430048170 mRNA
GCAGTTTGTAGACACCAGTAATTTTAAGAACCTGCTTAGCTTCTGTGTTGTATTTAAGTT NM_001033050 RefSeq
chr12 - 106977290 106987166 MTERF2 80298 "mitochondrial transcription termination factor 2,
transcript variant 1"
GO:0042645|GO:0006355|GO:0003690|GO:0044212|GO:0005759|GO:0042803|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_63687_PI430048170 0.729396229323825 1.07310827071676 3.07717237238134
2.70710795702884 2.40839253998294 A A A 2.91389873386891 2.34805953291368
2.64825531272973 P A P LNCV6_63687_PI430048170 mRNA
ATGTTTACAACCCCAGCACCGGGGTCTTCACGGCTCCTTATGATGGGCGCTACCTGATCA NM_032048 RefSeq
chr18 + 2847029 2914092 EMILIN2 84034 elastin microfibril interfacer 2
GO:0031012|GO:0005515|GO:0008150|GO:0005581|GO:0005578|GO:0030023|GO:0005576|GO:0007155 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_136232_PI430048170 0.102133544875264 0.813816617377185 5.28880690438846
4.90590369517354 5.19645846046558 P P P 5.30209174581124 5.53293348515128
5.46523165528527 P P P LNCV6_136232_PI430048170 mRNA
TCTCACAATGTCCATTCCCCTAGCTCCTGTGCTATGAATATCATATTAATAAATAGCCTA NM_001303251 RefSeq
chr5 - 160393147 160400097 ZBED8 63920 "zinc finger, BED-type containing 8, transcript variant 1"
GO:0005654|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59436_PI430048170 0.000696093779531343 2.03870832794068 10.2066774078874
10.3167619540592 10.4762122235981 P P P 9.44327217591765 9.18540518401257

9.28907068171052 P P P LNCV6_59436_PI430048170 mRNA
TATGTAGTAGACAGTTGTGACCGAGACCGAATTGGCATTTCCAAATCAGAGTTAGTTGCC NM_001177 RefSeq
chr12 - 101393119 101407820 ARL1 400 "ADP-ribosylation factor-like 1, transcript variant 1"
GO:0005802|GO:0031584|GO:0005794|GO:0007264|GO:0019904|GO:0003924|GO:0005525|GO:0046872|GO:0006
184|GO:0005737|GO:0000139|GO:0034067|GO:0007030|GO:0042147|GO:0048193|GO:0009404|GO:0008047|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103615_PI430048170 0.1910769065939 1.59134466174732 3.47102215024022
3.22162867286128 4.29474767596722 P P P 2.98100459246931 2.78500377935991
3.37514865487055 A P P LNCV6_103615_PI430048170 mRNA
AGCAGTATCACTGTGAAAACTGTGGAATTTGATTGGTCCAAAGGAAGATTTTTTCCATTG NM_001278539 RefSeq
chr4 - 75479036 75514430 RCHY1 25898 "ring finger and CHY zinc finger domain containing 1, E3
ubiquitin protein ligase, transcript variant 9"
GO:0005515|GO:0004842|GO:0016567|GO:0016874|GO:0032436|GO:0005102|GO:0000151|GO:0005634|GO:0042
803|GO:0051865|GO:0002039|GO:0005737|GO:0042787|GO:0016607|GO:0031398|GO:0005654|GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141788_PI430048170 0.0744271624715828 0.493588456373413 3.39483499479707
2.31207109146366 3.06497275861411 P A A 3.99924689699562 4.09291905189283
3.93255682357848 P P P LNCV6_141788_PI430048170 mRNA
GGTCTGAAAGAGCTCTTACGGTTTCTGATAGAACTATATAGGACTACCTTTTAAGATTAA NM_032864 RefSeq
chr1 + 52404546 52418320 PRPF38A 84950 pre-mRNA processing factor 38A
GO:0008380|GO:0006397|GO:0005515|GO:0031965|GO:0005634|GO:0071011 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_143345_PI430048170 0.00236019506976503 0.398692802248648 4.45201407101896
4.11111646895774 4.50670919847263 P P P 5.55533988076995 5.51806890488346
5.96371567039864 P P P LNCV6_143345_PI430048170 mRNA
GCAGACATAGTACCTGGTCAGAACTATGCCTCGGTTTATTTATCATTTTGAAATAAAATC NM_024617 RefSeq
chr9 - 86287732 86354487 ZCCHC6 79670 "zinc finger, CCHC domain containing 6, transcript
variant 1" GO:0071044|GO:0031123|GO:0008270|GO:0050265 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_2769_PI430048170 0.107802299633904 1.15585565343862 6.32826517067628
6.58930518277835 6.43509198371654 P P P 6.28252122922726 6.33113060815614
6.11535153101188 P P P LNCV6_2769_PI430048170 mRNA
TGGAAATGAGAAGGAACCCAGCATGTGTGGCTCAGCCCCTTCTGTGTTCCCCTCCTGCAA NM_006515 RefSeq
chr3 + 4303303 4317265 SETMAR 6419 "SET domain and mariner transposase fusion gene, transcript
variant 1"
GO:2000373|GO:0005515|GO:0000793|GO:0071157|GO:0090305|GO:0008283|GO:0005634|GO:0015074|GO:0006
303|GO:0042800|GO:0004803|GO:0042803|GO:0003690|GO:0003697|GO:2001034|GO:0000729|GO:0051568|GO:0
010452|GO:0035861|GO:0006313|GO:0044547|GO:0004519|GO:2001251|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134460_PI430048170 0.0417865195133582 1.13709812083911 12.7669226904465
12.6480670661894 12.6230171454963 P P P 12.5723267556906 12.4908017918575
12.4188503940934 P P P LNCV6_134460_PI430048170 mRNA
CTCTCCCACATTGTCTTGCTAAATATAGACTTGGTAATTAAAATGTTGATTGAAGTCTGG NM_015388 RefSeq chr6
- 43511826 43516990 YIPF3 25844 "Yip1 domain family, member 3"
GO:0030133|GO:0005794|GO:0005886|GO:0005654|GO:0016021|GO:0030154|GO:0043231 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_120313_PI430048170 0.275290798968869 0.775179078839367 4.74572738149058
3.95068023027803 3.91489071937898 P P P 4.39477855236615 4.55880966550111
4.87824362715163 P P P LNCV6_120313_PI430048170 mRNA

ACAACAAAAGTATGGATATGGGAAACCAACATCCTTCTATTAGTAGGCTTCAGGAAATCC NM_001015049 RefSeq chr14 - 103556543 103562318 BAG5 9529 "BCL2-associated athanogene 5, transcript variant 1" GO:0090083|GO:0005515|GO:0048471|GO:0019901|GO:0016234|GO:0051087|GO:0061084|GO:0005634|GO:0032435|GO:0005739|GO:0016020|GO:0006457|GO:0070997|GO:0051444|GO:0031397|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145547_PI430048170 0.0459351327316596 1.0360237751938 0.379341951198105 0.350007288779286 0.357218255405781 A A A 0.294253920784112 0.300051192534158 0.338844596462933 A A A LNCV6_145547_PI430048170 mRNA
ATGCCAAGAAAGATGTTGTGAACACAAAGATGTTTGAGGAGCTCAAGAGCCGTCTGGACANM_003278RefSeq chr3 + 45026266 45036071 CLEC3B 7123 "C-type lectin domain family 3, member B" GO:0001652|GO:0071310|GO:0005509|GO:0071560|GO:0005576|GO:0030282|GO:0005615|GO:0031012|GO:0001501|GO:0005737|GO:0001503|GO:0010756|GO:0030246|GO:0008201|GO:0070062|GO:0036143 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131594_PI430048170 0.00228532788612182 0.34382074392746 5.337867577762 5.04669236630825 5.5260312931772 P P P 6.60979494456583 6.74608195169463 7.15760732126605 P P P LNCV6_131594_PI430048170 mRNA
CCAAAGGTAGTCTAGTCTAGAACGATAAGTTAATACGTGTTGGCTTTTCTAATTTGTACT NM_001938RefSeq chr1 + 93345920 93362591 DR1 1810 "down-regulator of transcription 1, TBP-binding (negative cofactor 2)" GO:0005515|GO:0046982|GO:0003714|GO:0006325|GO:0005634|GO:0000122|GO:0003677|GO:0006351|GO:0043565|GO:0043966|GO:0005671|GO:0017025|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140935_PI430048170 0.0524390233905350.411051033799497 3.44616130449208 3.96093808606379 4.68432345065107 P P P 5.57227073265365 5.19329943968511 5.41895585301099 P P P LNCV6_140935_PI430048170 mRNA
GGTGACAGGTACATGGCAATTCATTATACCCTCCTATTTTCCTATGTTTACATTATTCAT NM_024795RefSeq chr2 - 227362157 227379306 TM4SF20 79853 transmembrane 4 L six family member 20 GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130660_PI430048170 0.0773749129576959 0.863346876156079 10.6285527737491 10.6822904691418 10.5643703877369 P P P 10.6954288452314 10.8894816548286 10.9186353141922 P P P LNCV6_130660_PI430048170 mRNA
TGAGATCCGCGTGCTTATGCTCCTGTACTCTTCAGAGAAGAAAATCTTCATTGGCCTCAT NM_017432RefSeq chr19 + 49851119 49860744 PTOV1 53635 prostate tumor overexpressed 1 GO:0048471|GO:0006355|GO:0005886|GO:0005634|GO:0006351|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144005_PI430048170 0.481082491933445 1.11406669757219 6.46899576304641 6.5976234378093 6.47238644348921 P P P 6.60177346212577 6.47728530330313 5.90513480971191 P P P LNCV6_144005_PI430048170 mRNA
TCACGAGAATTTCAGGCTCTTCTCTCCGGCTCCAGCCTGTGCCTGTGATTGTCCAGGTGT NM_057088RefSeq chr12 - 52789684 52796108 KRT3 3850 "keratin 3, type II" GO:0005882|GO:0005198|GO:0045104|GO:0030855|GO:0045095|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137602_PI430048170 0.0717430004614389 1.03313415333327 0.395987820806477 0.409994772815611 0.441345896433568 A A A 0.358352447775807 0.351573765329453 0.396290305032865 A A A LNCV6_137602_PI430048170 mRNA
GGATTTAGTTCAGTTTAGCTCACACAGGTGTTTGCTGACATTCATTGGCCATTTAATACA NM_018018RefSeq chr12 - 46764760 46825997 SLC38A4 55089 "solute carrier family 38, member 4, transcript variant 1" GO:0015171|GO:0005886|GO:0005887|GO:0006865|GO:0006814|GO:0055085|GO:0003333|GO:0015293|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91494_PI430048170 0.588990321789417 0.963237505061223 0.299934106339926 0.464455157540322

0.319473040883982 A A A 0.526807502795051 0.433607761893724 0.280583856493864 A A A
LNCV6_91494_PI430048170 mRNA
AGAATATGCCGACAAGGTCTTCACCTACATCTTCATCATGGAGATGCTGCTCAAATGGGT NM_000334 RefSeq chr17
- 63938553 63972918 SCN4A 6329 "sodium channel, voltage gated, type IV alpha subunit"
GO:0006936|GO:0086010|GO:0005886|GO:0005887|GO:0005248|GO:0035725|GO:0034765|GO:0001518|GO:0006
814|GO:0019228 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128889_PI430048170 0.207135615787098 1.03213223554682 0.345919534262832
0.357172884927444 0.277389837684142 A A A 0.277221096791318 0.292760432515065
0.274837073703838 A A A LNCV6_128889_PI430048170 mRNA
CTCAATACATGGAATTTACTGGGGCATTTAACTTGTTCATGAAAATAGAGTGAGTCATTG NM_182762 RefSeq chr7
- 20134655 20217390 MACC1 346389 metastasis associated in colon cancer 1
GO:0006355|GO:0005737|GO:0051781|GO:0005634|GO:0008083|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137015_PI430048170 0.0251537161920753 0.787372921947463 11.0815111776947
11.2697729607349 11.1358575020478 P P P 11.6355372053673 11.5074071611351
11.3735178062761 P P P LNCV6_137015_PI430048170 mRNA
CGCCCTGCTGTATGATATTAATGTGGAAGGTCATCAATAAAGGGGAATTGTGTTGGTGAA NM_001257363 RefSeq
chr9 - 129094793 129110791 CRAT 1384 "carnitine O-acetyltransferase, transcript variant 2"
GO:0005739|GO:0004092|GO:0005782|GO:0005783|GO:0006810|GO:0005743|GO:0005102|GO:0044281|GO:0033
540|GO:0019254|GO:0044255|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143719_PI430048170 0.29423971343266 0.59182997085043 1.14100861809212
3.10667603806866 2.94844837846487 A P P 2.60339153869658 3.62931150236558
3.68619440057459 A P P LNCV6_143719_PI430048170 mRNA
TGCCAATTGAGTATCTTCTTTGCTTTGTTTTTGCTGCAGCCTCAGGCAAACAGATGGGGT NM_000932 RefSeq chr11
+ 64251522 64269452 PLCB3 5331 "phospholipase C, beta 3 (phosphatidylinositol-specific), transcript
variant 1"
GO:0005516|GO:0043647|GO:0005509|GO:0007268|GO:0044281|GO:0005829|GO:0003073|GO:0016042|GO:0035
556|GO:0004629|GO:0043234|GO:0016020|GO:0004435|GO:0005654|GO:0004871 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_100382_PI430048170 0.157963845211411 0.753760994423164 4.26098374607672 3.7241891249272
3.91442436096704 P P P 4.03033181090686 4.58472583924953 4.5006477282623 P P P
LNCV6_100382_PI430048170 mRNA
TAAACATAGCCTAAATATTGGTGATTACAATCGAACGGTCGGGAAAGGCCCTGGTTCTCG NM_014494 RefSeq chr16
+ 24729727 24826226 TNRC6A 27327 trinucleotide repeat containing 6A
GO:0005515|GO:0010467|GO:0048011|GO:0048015|GO:0016441|GO:0005829|GO:0035068|GO:0035278|GO:0000
166|GO:0007173|GO:0007219|GO:0000932|GO:0008543|GO:0045087|GO:0035195|GO:0005654|GO:0038095|GO:0
009267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145051_PI430048170 0.0154245239106864 0.723028813963236 7.20127526637925
7.02620821910102 7.20457782790566 P P P 7.78160014266294 7.54423768769337
7.50085887186222 P P P LNCV6_145051_PI430048170 mRNA
TTGTGATTTGCTGTTCTGTAGGCGTGTTGTGGATTCTTTCCATCAACTGCTGATTTCATC NM_080750 RefSeq chr20 +
62844565 62846191 DPH3P1 100132911 diphthamide biosynthesis 3 pseudogene 1 GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136952_PI430048170 0.000267827372217107 0.378640414758895 5.27170554214277
5.40322050671244 5.53967333228874 P P P 6.81966120159846 6.65234546912668
6.94361090827441 P P P LNCV6_136952_PI430048170 mRNA
GGAATTTTACATAAATCTTTGTTAATTACTGAGTGGGCAAGTAGACTTCCTGTCTTTGCT NM_006714 RefSeq chr6
+ 122789048 122809719 SMPDL3A 10924 "sphingomyelin phosphodiesterase, acid-like 3A, transcript
variant 1" GO:0005515|GO:0008150|GO:0006685|GO:0016798|GO:0004767|GO:0005615|GO:0070062 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128823_PI430048170 0.00145367841658005 1.67832427880314 11.1689276902494
11.1732960104574 11.1556954816948 P P P 10.4821163525824 10.3932395654623
10.3793884760101 P P P LNCV6_128823_PI430048170 mRNA
TTGTTGATTCTTGTCTGGCTAATAAATCATCACCAACTGCCTTCTCCTACAGGGAAAAAA NM_001161441 RefSeq
chr1 - 156806242 156816848 SH2D2A 9047 "SH2 domain containing 2A, transcript variant 1"
GO:0005515|GO:0048010|GO:0007165|GO:0017124|GO:0005737|GO:0008283|GO:0005070|GO:0009967|GO:0001
525|GO:0030154|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133823_PI430048170 0.16726124600411 1.05751141006368 0.471644783365564
0.4160034208555860.485621577855386A A A 0.3084711245922460.374055513939119
0.446360347242454A A A LNCV6_133823_PI430048170 mRNA
TTTTATGTTCTGCTCACAGACATTGCTTTCAAATGTTAGCTGCTGAAATCCACAATAAAC NM_005208RefSeq chr17
+ 29246856 29254484 CRYBA11411 "crystallin, beta A1"
GO:0005515|GO:0003674|GO:0005737|GO:0005212|GO:0002088|GO:0005634|GO:0007601|GO:0042803 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78928_PI430048170 0.000697489174297808 1.32908151576942 14.0433222595022
14.0481171558856 14.0563749468414 P P P 13.6433581110254 13.6110386338303 13.661703697614
P P P LNCV6_78928_PI430048170 mRNA
ACCAAATGCTGTCTTCTCTTTCTCCAATCAAGAAATAATAATCCCTCGAGTTTACAAAAC NM_003302RefSeq chr7
+ 100867327 100873454 TRIP6 7205 thyroid hormone receptor interactor 6
GO:0005515|GO:0005149|GO:0006355|GO:0030335|GO:0005886|GO:0005634|GO:0006351|GO:0046966|GO:0045
323|GO:0005737|GO:0008588|GO:0048041|GO:0008270|GO:0005856|GO:0019900|GO:0005925 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_57213_PI430048170 0.00411231846202471 0.455305080349364 11.600719097637
11.5264075395037 11.935521381234 P P P 12.6145281540025 12.753319208094 13.091307910673
P P P LNCV6_57213_PI430048170 mRNA
TTTGTGGGTGTGAAACAAATGGTGAGAATTTGAATTGGTCCCTCCTATTATAGTATTGAA NM_001172705 RefSeq
chr11 - 10797045 10807996 EIF4G2 1982 "eukaryotic translation initiation factor 4 gamma, 2,
transcript variant 3"
GO:0005515|GO:0008219|GO:0016281|GO:0016020|GO:0019221|GO:0006446|GO:0003743|GO:0007050|GO:0008
135|GO:0006413|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128041_PI430048170 0.0891443968878515 0.8363528276272575.88848280980624
6.02061246540565 5.94243134271603 P P P 6.07571769813123 6.37608703269046
6.15936253732817 P P P LNCV6_128041_PI430048170 mRNA
CAAGCCTGTGATGACATGGTGCTGATTCTGGGGGGCATTAAAGCTGCTGTTTTAAAAGGC NM_000094RefSeq chr3
- 48564072 48595160 COL7A11294 "collagen, type VII, alpha 1"
GO:0005515|GO:0004867|GO:0005590|GO:0005576|GO:0035987|GO:0005615|GO:0042802|GO:0005604|GO:0031
012|GO:0010951|GO:0008544|GO:0022617|GO:0030198|GO:0030574|GO:0005788|GO:0007155 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_94359_PI430048170 0.0657599522944549 1.25028340750363 8.01602238974832
8.04228546104924 8.07149588203342 P P P 7.66297402953826 7.58954653718958
7.89336949218076 P P P LNCV6_94359_PI430048170 mRNA
TGAATTAGTGGCCCAATGGAACTATTGTACTCTAAGTCAGGAAATATTAAGACGACCAAT NM_001283035 RefSeq
chr20 + 56468584 56518886 RTFDC1 51507 "replication termination factor 2 domain containing 1,
transcript variant 1" GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_128067_PI430048170 0.20402911146727 0.4510995165201240.381556563355436
3.00443301615808 2.58101321276677 A P A 3.72423151656471 3.42997276673386 3.3143491979133
P P P LNCV6_128067_PI430048170 mRNA

TCCTTTGCTTCCCTTTTTTCCTTTCCACCTTCTCACATGGAATGAGGGTTTGAGAGAGCA NM_000394RefSeq chr21 + 43169007 43172810 CRYAA 1409 "crystallin, alpha A"
GO:0005515|GO:0005212|GO:0043066|GO:0032387|GO:0005634|GO:0046872|GO:0042802|GO:0042026|GO:0005737|GO:0051260|GO:0051082|GO:0007601|GO:0050896|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82254_PI430048170 0.9924574873090450.9564655579340725.07292326757305 4.59711447452944 4.41829329915042 P P P 5.31872777612854 4.7443828659709 4.01211884126581 P P P LNCV6_82254_PI430048170 mRNA
CACCTTCTCCAGTCTCTCTTCGGACAGCCAGTAATTCCCGGGCAAGGCCAGAGACTTCAA NM_001129826 RefSeq chrX + 152759217 152760222 CSAG3 NA "CSAG family, member 3, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54846_PI430048170 0.0558113784755716 2.21112707773457 3.64633758676954 4.58475890605587 4.28927207821606 P P P 3.66676889828608 2.68195114142875 2.64177671083652 P P P LNCV6_54846_PI430048170 mRNA
TAATGTTTGGTACCAAACTTGGGGGCCAAAAAGGGCAGTGCTCAGGACTCCCTGGCCCCT NM_004952RefSeq chr1 + 155078871 155087538 EFNA3 1944 ephrin-A3
GO:0005005|GO:0048013|GO:0046875|GO:0005886|GO:0007411|GO:0005887|GO:0007267|GO:0005576|GO:0031225 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145711_PI430048170 0.4308731385231930.9267175676238880.288048982048599 0.2956334630129250.45049161844371 A A A 0.34744367015147 0.653265511968972 0.346603188417613A A A LNCV6_145711_PI430048170 mRNA
TGAGAGACCGGAGTATGATCCTCAGTGCGAGGACAAATAAAAGTAGTGATTATGTCCACC NM_001081552 RefSeq chr8 + 7847879 7863797 SPAG11A NA sperm associated antigen 11A NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137113_PI430048170 0.6723922151312450.8900984781064750.388654468427598 0.3888779715387420.338097661674741A A A 0.2459475269693010.994597584319838 0.24322149989107 A A A LNCV6_137113_PI430048170 mRNA
CAAGCTCTAGAGTGCTCCAGGAAAAGTTATATTCAGTATATGAATAAGTGTTATTCTCCA NM_182920RefSeq chr3 - 64515654 64687689 ADAMTS9 56999 "ADAM metallopeptidase with thrombospondin type 1 motif, 9"
GO:0005783|GO:0005578|GO:0007275|GO:0015031|GO:0005615|GO:0031012|GO:0006508|GO:0006516|GO:0008270|GO:0045636|GO:0004222|GO:0016192|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134446_PI430048170 0.0320148646522715 1.5837859788622 4.66966734848833 4.6641902136274 4.52863799301075 P P P 3.66022147496665 4.10042742425086 4.07520900105468 P P P LNCV6_134446_PI430048170 mRNA
TATTTGTAATGACTTCTGGCAAAAGCACGTGTCCTGGCCGGATGTAACTGTTCTCCTTTC NM_001242837 RefSeq chr11 + 925808 1012245 AP2A2 161 "adaptor-related protein complex 2, alpha 2 subunit, transcript variant 1"
GO:0072583|GO:0005515|GO:0048011|GO:0035615|GO:0048013|GO:0019901|GO:0005886|GO:0030122|GO:0042059|GO:0007268|GO:0006886|GO:0050690|GO:0005829|GO:0008289|GO:0030666|GO:0003674|GO:0019886|GO:0007173|GO:0007411|GO:0008565|GO:0016023|GO:0016032|GO:0030669 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142633_PI430048170 0.1915037769570620.9669371143719 0.292224270534331 0.3194893228400550.356110391160118A A A 0.3871378835208650.323542893863402 0.402172603988692A A A LNCV6_142633_PI430048170 mRNA
GCAAAAGGAATGTTGCACTAAAATGCAACATTGTCCTAACATTAGTCTGTGCATTTCAAA NM_213608RefSeq chr2 - 196804414 196810276 C2orf66 401027 chromosome 2 open reading frame 66 GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137270_PI430048170 0.3852305088909451.24246637332094 0.271685803904112 1.07385313047573 0.432426847656698A A A 0.3519311012301920.309977830690517

0.305761088897967 A A A LNCV6_137270_PI430048170 mRNA
TATGAGAGAAAAAGCATAATAAATCAGAAACAATATAAAAAGCTTTCAGAAAAGATAAAA NM_001012755 RefSeq
chrX - 104099213 104157027 SLC25A53 NA "solute carrier family 25, member 53" NA . NA -
NA NA NA NA NA NA NA NA NA
LNCV6_138841_PI430048170 0.681573237470866 1.10083971135522 3.09305950093236
2.54058999908424 1.84760766034555 P A A 0.4927231530628662.77183526989752
3.01242198311126 A P P LNCV6_138841_PI430048170 mRNA
GGCATCCAGGACCTTTAGGGAGGCATTTAATAAACACTTAATAAATAACAAAACTACCTT NM_153026 RefSeq chr12
- 42458337 42589770 PRICKLE1 144165 "prickle homolog 1 (Drosophila), transcript variant 1"
GO:0005515|GO:0031965|GO:2000691|GO:0032436|GO:0031398|GO:0001843|GO:0008270|GO:0005634|GO:0006
606|GO:0090090|GO:0045892|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94329_PI430048170 0.64212845996814 1.04797840453494 8.00034663722022 8.02759899967645
7.9831003947993 P P P 7.61495297172051 8.0532622430142 8.09334220333778 P P P
LNCV6_94329_PI430048170 mRNA
GCCAGTTTGAGCCTAATCTGATTCTTACAGTTTTACCTTCTTGAACCAATGTAAAAGTTT NM_016395 RefSeq chr15
+ 65530488 65578355 HACD3 NA 3-hydroxyacyl-CoA dehydratase 3 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130555_PI430048170 0.5169380995780620.9536554638802469.57003283379631
9.78537849238028 9.78016035741227 P P P 9.74887665357197 9.68558095379989
9.90762112563943 P P P LNCV6_130555_PI430048170 mRNA
CCCCTCTTTTGTTAAATAATATGGCTATGCTTAAAAGGTTGCATACTGAGCCAAGTATAA NM_004064 RefSeq chr12
+ 12717269 12722382 CDKN1B 1027 "cyclin-dependent kinase inhibitor 1B (p27, Kip1)"
GO:0005515|GO:0030308|GO:0007605|GO:0032403|GO:0007173|GO:0010942|GO:0032355|GO:0006977|GO:0071
285|GO:0048839|GO:0019903|GO:0008656|GO:0005072|GO:0008543|GO:0045930|GO:0045087|GO:0030544|GO:0
005654|GO:0000278|GO:0045892|GO:0038095|GO:0046686|GO:0060770|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_119829_PI430048170 0.9611796784370090.9971016707195612.6599456989064
12.4625709037817 12.687691156462 P P P 12.2788180708186 12.7870288986486
12.7165822429334 P P P LNCV6_119829_PI430048170 mRNA
GGTGGTGGTATTCTGTCATTTACACACGTCGTTCTAATTAAAAAGCGAATTATACTCCAG NM_006312 RefSeq chr12
- 124324410 124567464 NCOR2 9612 "nuclear receptor corepressor 2, transcript variant 1"
GO:0005515|GO:0010467|GO:0006367|GO:0042826|GO:0003714|GO:0006325|GO:0005112|GO:0005634|GO:0044
281|GO:0000122|GO:0003677|GO:0016363|GO:0006351|GO:0016604|GO:0072365|GO:0047485|GO:0016020|GO:0
007219|GO:0017053|GO:0003682|GO:0005654|GO:0007179|GO:0044255 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132895_PI430048170 0.6930775512890990.9692134225381771.69552560338092
0.3529613956504752.70509959875882 A A A 2.14265364920081 1.52989597304718
2.03011056239019 A A A LNCV6_132895_PI430048170 mRNA
CAGAAATCCTTACACCAAGTTGCACATATTCCATAATAAAGTGCTGTGTTGTGAATGAAA NM_000825 RefSeq chr8
- 25419257 25425040 GNRH1 2796 "gonadotropin-releasing hormone 1 (luteinizing-releasing
hormone), transcript variant 1"
GO:0010468|GO:0007565|GO:0043066|GO:0008285|GO:2001223|GO:0045471|GO:0007267|GO:0031960|GO:0005
576|GO:0007275|GO:0042698|GO:0005615|GO:0007165|GO:0005179|GO:2000354|GO:0005183 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144396_PI430048170 0.5664029021645261.15904658850367 0.443614430692607
1.09760708876057 0.285127464106897 A A A 0.3468415069719570.403853953753634
0.561912301899846 A A A LNCV6_144396_PI430048170 mRNA
CCTGGGGACAAAGCCTCCAAAAAGCCATCCAGAGGGAGAAGGAAACTGACAGCCACTGAG NM_080833 RefSeq
chr20 - 62410236 62427573 RBBP8NL 140893 RBBP8 N-terminal like GO:0005615 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_142295_PI430048170 0.7822664093776690.9821251427944150.274706275836412
0.4981747729330680.338040519826959A A A 0.5024297316087380.395254506139935
0.292981416181158A A A LNCV6_142295_PI430048170 mRNA
TATTTCAAACTGCACGTATGCAGACAGACCAGGAAGGAGGTTCTATGTAGTTGCATGTGA NM_002935RefSeq chr14
+ 20891402 20892348 RNASE36037 "ribonuclease, RNase A family, 3"
GO:0004519|GO:0050830|GO:0019731|GO:0005576|GO:0004540|GO:0003676|GO:0005615|GO:0070062|GO:0006
401|GO:0002227 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139825_PI430048170 0.2062046804903091.06480253871086 0.543554200451442
0.6984397189582670.557209269577994A A A 0.4743413747766940.519340775415111
0.538172104716362A A A LNCV6_139825_PI430048170 mRNA
GGTGTCTCCAACTCCTACCCCATTGCATGGGTTGTTGCGGACATCCAATAAAGATTTTTT NM_014571RefSeq chr1
- 39623430 39639676 HEYL 26508 hes-related family bHLH transcription factor with YRPW motif-like
GO:0071773|GO:0005515|GO:0000988|GO:0003700|GO:0000983|GO:0006366|GO:0072014|GO:0003181|GO:0003
184|GO:0005634|GO:0035914|GO:0050683|GO:0032835|GO:0042803|GO:0060317|GO:0005737|GO:0007219|GO:0
045944|GO:0014031|GO:0046982|GO:0003198|GO:0001106|GO:0060412|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_71878_PI430048170 0.211291475278301 1.02621950869082 0.3315049524778160.327556845143204
0.267715182473764A A A 0.2688806078120070.2795817940277430.267146412620918A A A
LNCV6_71878_PI430048170 mRNA
GGGTTTGTTGTAAACCAATGAACATTTGCTAGTTGTATCAAATCTTGGTACGCAGTATTT NM_058186RefSeq chr21
+ 41316733 41357727 FAM3B 54097 "family with sequence similarity 3, member B, transcript variant 1"
GO:0006915|GO:0005576|GO:0030073|GO:0005615|GO:0005125|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136094_PI430048170 0.0670028066359442 0.5481719015665764.09015293808996
4.29353173114145 5.03395644310089 P P P 5.03570791788014 5.65758136833228
5.43729827146207 P P P LNCV6_136094_PI430048170 mRNA
AGAAAAGAGAGGCAATGCCAAGCTGCTTCATCAACTGTTAATACTTCTTCCAGCCCGCAA NM_024121RefSeq chr2
- 120217470 120223408 TMEM185B 79134 transmembrane protein 185B GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_9387_PI430048170 0.0109373762162081 0.7642716525178988.22635197888444
8.05735206737731 8.26835344931663 P P P 8.4938000214734 8.60856088854723
8.61846075538075 P P P LNCV6_9387_PI430048170 mRNA
AGCGACTGGATTCTGGAGTCCATCTAGAGGGTCTTGGGAGGGATGTGACTGTTGGGAAGC NM_198552RefSeq chr1
- 231018957 231040249 FAM89A 375061 "family with sequence similarity 89, member A" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_132902_PI430048170 0.22279215220731 0.6819846085590230.351437803893933
0.3305573483640540.26996096190169 A A A 0.3140872655650650.827233157942551
1.30169260153212 A A A LNCV6_132902_PI430048170 mRNA
AGCTCCGCGCCAGGATGGCGCAGGAACTCAATAAAGTGCTTTGAAAATGCTGAGAAAAAA NM_000505RefSeq
chr5 - 177402137 177409576 F12 2161 coagulation factor XII (Hageman factor)
GO:0005515|GO:0016540|GO:0004252|GO:0005886|GO:0051919|GO:0005576|GO:0005615|GO:0051787|GO:0051
788|GO:0030194|GO:0007596|GO:0010756|GO:0016485|GO:0045087|GO:0002542|GO:0007597|GO:0002353|GO:0
006508|GO:0070009|GO:0042730|GO:0031638|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_142956_PI430048170 0.0234833343004863 3.34087644299292 1.80252846238346
2.99640700600615 2.45292887993004 A P A 0.33557140647369 0.302673151464156
1.36531263907129 A A A LNCV6_142956_PI430048170 mRNA
AATGATGTAATTTATTGTTGCGTTCCTCTGGAAGCTGTGACTGGAATAAACCCCCGCGTG NM_003508RefSeq chr7

+ 73433778 73436120 FZD9 8326 frizzled class receptor 9
GO:0042813|GO:0017147|GO:0048471|GO:0046982|GO:0005886|GO:0009986|GO:0004930|GO:0031527|GO:0042803|GO:0007399|GO:0007405|GO:0005737|GO:0007186|GO:0030183|GO:0007611|GO:0016021|GO:0060070|GO:0035567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138643_PI430048170 0.0037474880642941 5.43190625498024 2.83182442245692 2.71414328879565 3.22724705404302 A A P 0.509237585766769 0.467838188315334 0.522538408641934 A A A LNCV6_138643_PI430048170 mRNA
GCTTCTACCACCTTTGCAATTGTCATTTATCTTTCACTCCCTGAATAAAGTATCTATGCA NM_006945 RefSeq chr1 - 153039724 153041118 SPRR2D 6703 small proline-rich protein 2D
GO:0005737|GO:0008544|GO:0031424|GO:0001533 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62416_PI430048170 0.00988837293698413 0.494411685135815 7.93725443671361 7.60635178541365 7.90220676511725 P P P 8.50421014049946 8.9178356964122 9.04163410272977 P P P LNCV6_62416_PI430048170 mRNA
AGATTGTTGCTGCACATAGTTGCCTTTGTATCTCTGTATGAAATAAAAGGTCATTTGTTC NM_003870 RefSeq chr15 + 90388240 90502243 IQGAP1 8826 IQ motif containing GTPase activating protein 1
GO:0005515|GO:0005516|GO:0030054|GO:0001817|GO:0032403|GO:0007173|GO:0045860|GO:0070062|GO:0019901|GO:0019903|GO:0005509|GO:0005547|GO:0030496|GO:0043086|GO:0031234|GO:0043547|GO:0032320|GO:0008543|GO:0036057|GO:0005654|GO:0043539|GO:0005925|GO:0030424|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134458_PI430048170 0.0597712113374026 1.58045208307228 10.0275663566837 10.0323336171433 10.1585533298665 P P P 9.02163069427533 9.55804988278335 9.59368582579321 P P P LNCV6_134458_PI430048170 mRNA
GCGTTTCTTCTTGTACTTATGTGGTTTTTTGGCTTTTAATACAGACATTTTCCTCCAGAA NM_015444 RefSeq chr3 - 45224463 45226322 TMEM158 25907 transmembrane protein 158 (gene/pseudogene)
GO:0042277|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135867_PI430048170 0.33480324679227 0.841438676399887 0.382282667240604 0.407589147019074 0.311485774347913 A A A 0.398304031141931 0.429245658427466 0.952925931387205 A A A LNCV6_135867_PI430048170 mRNA
TCTATTTTTCATGTCCATTAAAACAGGCCAAGTGAGTGTGGAAGGCCTGGCTCATGTTGG NM_002412 RefSeq chr10 + 129467189 129767519 MGMT 4255 O-6-methylguanine-DNA methyltransferase
GO:0045471|GO:0042493|GO:0003908|GO:0005509|GO:0008168|GO:0009636|GO:0005634|GO:0045739|GO:0003677|GO:0071479|GO:0051593|GO:0003684|GO:0006306|GO:0071407|GO:0060644|GO:0043281|GO:0006281|GO:0006307|GO:0016020|GO:0009008|GO:0060548|GO:0005654|GO:0034599|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134031_PI430048170 0.254020415935049 1.17232756345608 0.950318351130814 0.928988267431 09 0.556463096334605 A A A 0.423591974894404 0.80130657477383 0.528935155515848 A A A LNCV6_134031_PI430048170 mRNA
AAGGTGAAGGCATCTGAGGCATTACAAAGTGAAGTTGACACAGACCTCCATACTTTATAA NM_138806 RefSeq chr3 - 112922684 112975090 CD200R1 131450 "CD200 receptor 1, transcript variant 1"
GO:0043235|GO:0005515|GO:0005886|GO:0050776|GO:0016032|GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92795_PI430048170 0.0255111725832396 0.558335098012759 2.74953244418739 2.55002752074147 2.39642503672527 A A A 3.08255996458735 3.70618867084852 3.38412693732738 P P P LNCV6_92795_PI430048170 mRNA
AAGTGTACAGAGGCTTCTGGCAACACGGATTGCCGTCTACCTGATGACCTTTCTCATCGT NM_001297427 RefSeq chr4 + 932386 958655 TMEM175 84286 "transmembrane protein 175, transcript variant 6"
GO:0016021|GO:0005765 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54454_PI430048170 0.93239429070885 1.01887778823959 0.404807593102341 0.384271260990381 1.34439647579159 A A A 0.514180850709531 0.708806862063854 1.00716535522272 A A A

LNCV6_54454_PI430048170 mRNA
AACATCAGACACTGGATCAACCCTAAAAAGGAGTCCATCCACAGCATCCAAGGATCCATA NM_001122961 RefSeq
chr1 - 109105950 109113857 C1orf194 127003 chromosome 1 open reading frame 194 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_136412_PI430048170 0.484222375029573 1.02050354261374 0.518310366539038
0.447565443936656 0.535019925691972 A A A 0.469857851259451 0.518316745926164
0.424848473959954 A A A LNCV6_136412_PI430048170 mRNA
AGCTTCACCTGGAGAGCTGCTTTTGCTCAGTAAATTCAACTTCCATGTTTTATCTTTTTT NM_033495 RefSeq chrX -
117897812 117973738 KLHL13 90293 "kelch-like family member 13, transcript variant 1"
GO:0000910|GO:0007067|GO:0004842|GO:0016567|GO:0031463 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_49993_PI430048170 0.211198537070123 0.837375628753855 3.32351577246132 3.67600293507573
3.83771521752272 P P P 3.87648927929694 3.77827762501855 3.98966190469003 P P P
LNCV6_49993_PI430048170 mRNA
GCGTTGTGAGCCAGTCTGTCTGTGATTATTTCTTTGAAGCTCAAGAGAAAGCTGCTGATG NM_207012 RefSeq chr10
- 74120256 74151068 AP3M1 26985 "adaptor-related protein complex 3, mu 1 subunit, transcript variant
1"
GO:0005515|GO:0048490|GO:0030131|GO:0017137|GO:0005794|GO:0006622|GO:0008089|GO:0005765|GO:0005
764|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129427_PI430048170 0.221822698600034 1.04644452343698 0.59312649175548
0.672834292763573 0.543813587795203 A A A 0.563297592319511 0.527107378560002
0.525511997601027 A A A LNCV6_129427_PI430048170 mRNA
AATGTAATGCGATTTTATTACTGGCGTGGATTAAACTTATGAATGTTTCCGGGAGGTTAA NM_002315 RefSeq chr11
- 8224303 8263878 LMO1 4004 "LIM domain only 1 (rhombotin 1), transcript variant 1"
GO:0045944|GO:0008270|GO:0005634|GO:0000122 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142038_PI430048170 0.551627445350559 0.906950228525162 0.469526212513276
0.532854368079511 0.459736388559556 A A A 0.419835130434018 0.946502181402778
0.457710200073162 A A A LNCV6_142038_PI430048170 mRNA
GAACAAGTCAAGTGGAAAGTGGAGAAATTATCTGTATAATTTTGGACACATACAATGCAG NM_005328 RefSeq chr8
- 121613030 121641390 HAS2 3037 hyaluronan synthase 2
GO:0008284|GO:0030335|GO:0001822|GO:0070295|GO:0071498|GO:0045226|GO:0085029|GO:0036120|GO:0005
887|GO:0060349|GO:0071356|GO:0071347|GO:0030213|GO:0050501|GO:0035810|GO:1900625|GO:0001570 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127750_PI430048170 0.748348098636768 0.966885745598856 13.5286882122629
13.3487050818052 13.2483491029949 P P P 13.2155919227458 13.5575981203049
13.4901445201665 P P P LNCV6_127750_PI430048170 mRNA
AGAGCCGGGTTTCATCTGGAATTAACTGGATGGAAGGGAAAATAAAGCTATCTAGCGGTG NM_198949 RefSeq chr7
+ 2242221 2251145 NUDT1 4521 "nudix (nucleoside diphosphate linked moiety X)-type motif 1,
transcript variant 2B"
GO:0046061|GO:0006203|GO:0006200|GO:0003924|GO:0005634|GO:0044281|GO:0046872|GO:0005829|GO:0005
739|GO:0035539|GO:0006195|GO:0005737|GO:0030515|GO:0005759|GO:0008413|GO:0006979|GO:0070062|GO:0
055086|GO:0050072|GO:0006184|GO:0006281|GO:0034656|GO:0042262|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126968_PI430048170 0.00563480467602394 1.70975692247536 9.48605193337398
9.85295606481314 9.664310653169 P P P 9.04203478745445 8.7259408354508 8.9198486429187
P P P LNCV6_126968_PI430048170 mRNA
TTCTCTTGGAACAACATCACTGATTCATTGGATCCTGCCACCCTGAGTGCCACATTTCAA NM_001256609 RefSeq
chr1 - 156292686 156295689 GLMP 112770 "glycosylated lysosomal membrane protein, transcript
variant 5"

GO:0030374|GO:0003700|GO:0044212|GO:0045944|GO:0005634|GO:0016021|GO:0004879|GO:0005765|GO:0030522|GO:0005764|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62901_PI430048170 0.2228295898806730.7177968471331633.66501882108481 2.89073763440469 3.3138570292589 P A P 3.837735398124 3.31554316575524 4.13783546936082 P P P
LNCV6_62901_PI430048170 mRNA
AACAAGACCAAGAAAAAGAAGTCATCAAGATTACCACCTGAGAAACCAAAGCACCAGACT NM_004774RefSeq chr17 - 39404284 39451274 MED1 5469 mediator complex subunit 1
GO:0005515|GO:0010839|GO:0010467|GO:0006367|GO:0033160|GO:0006702|GO:0000981|GO:0045618|GO:0032993|GO:0042809|GO:0045444|GO:0042789|GO:0006590|GO:0000785|GO:0044255|GO:0003712|GO:0003406|GO:0016922|GO:0001104|GO:0003713|GO:0030331|GO:0001892|GO:0001047|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90974_PI430048170 0.7615487972187560.8617437525048061.47765703817461 0.350655218256778 1.20528135570715 A A A 1.45653352681511 1.74863433171164 0.358815674134762A A A
LNCV6_90974_PI430048170 mRNA
AAGAAAAATTGCACTAAAAATCCACCTGTCCTCATCATGAATGACAGCGAGGGGCCTGTG NM_020436RefSeq chr20 - 51784043 51802509 SALL4 57167 spalt-like transcription factor 4
GO:0000792|GO:0001833|GO:0001843|GO:0003281|GO:0000122|GO:0030326|GO:0003677|GO:0046872|GO:0006351|GO:0043231|GO:0043234|GO:0005737|GO:0045944|GO:0005654|GO:0035019 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145041_PI430048170 0.00391980562862952 0.7022255371911777.95516088712397 7.98742499743345 7.83907631290348 P P P 8.4073316465283 8.45377785486123 8.45421503968881 P P P LNCV6_145041_PI430048170 mRNA
GGTGTGTTTCTCCCACAATTTGTTTGTGAATATTCACTTGTTTTATAAATGTCTGACCTG NM_021117RefSeq chr11 + 45847405 45883248 CRY2 1408 "cryptochrome circadian clock 2, transcript variant 1"
GO:0005515|GO:0043130|GO:0003904|GO:0005634|GO:0000989|GO:0071949|GO:0018298|GO:0005737|GO:0009882|GO:0003697|GO:0043153|GO:0000976|GO:2000118|GO:0019902|GO:0009785|GO:0005576|GO:0000122|GO:0042593|GO:2000323|GO:0003677|GO:0006351|GO:0032922|GO:0003914|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129768_PI430048170 0.4477287540317711.23131133070232 1.09983649219251 1.0442208689699 1.73816592190636 A A A 1.31787063366188 1.24152385401282 0.341922062361448A A A
LNCV6_129768_PI430048170 mRNA
TGATACCATTTGTGAGAAAGAAGCTCCCAAGTCATCATTACTCAGAAAGCAGACCCAGCC NM_199339RefSeq chr17 + 7420359 7421632 SPEM1 374768 spermatid maturation 1
GO:0005737|GO:0007291|GO:0030317|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73169_PI430048170 0.4575838995976221.47769266931889 1.65580242868765 0.359026375001185 0.25091202802925 A A A 0.3277423503096830.3578092927861360.343772690348956A A A
LNCV6_73169_PI430048170 mRNA
GGTCACAAACAGTAAAGTGTTCCTGTCTACCTGGAAAAGTGGCTGGAACAACAAGAAACC NM_213609RefSeq chr3 + 68004215 68545620 FAM19A1 407738 "family with sequence similarity 19 (chemokine (C-C motif)-like), member A1, transcript variant 1"GO:0005783|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_30975_PI430048170 0.0586845391268072 1.38234659648932 6.82532110255671 6.67946520330901 6.40357137677792 P P P 6.15259265202268 6.23912230958703 6.14465447040882 P P P LNCV6_30975_PI430048170 mRNA
ATGAGGATTCCATGTTCAAGAAAGGCTGGGAAATCTCTCCCCTCCTAGGGATTCAAAACA NM_001278587 RefSeq chr17 + 73737853 73756557 LOC100134391 NA uncharacterized LOC100134391 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128338_PI430048170 0.41639580134 0.9368782830586621 0.8138056366759 10.9058041578672 10.7840581430037 P P P 10.7562349465647 11.0436510630476 10.9734763896252 P P P

LNCV6_128338_PI430048170 mRNA
CTACACTTGGCCTGTTTTTCCAACCTATTTAATAGACATTAAAGCTAAACACACATTCCT NM_001126121 RefSeq
chr17 - 75272979 75289449 SLC25A19 60386 "solute carrier family 25 (mitochondrial thiamine
pyrophosphate carrier), member 19, transcript variant 1"
GO:0030302|GO:0005743|GO:0005634|GO:0016021|GO:0055085|GO:0030233 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134386_PI430048170 0.4125340966497921.66924414871905 0.368490304396811
0.3692781136847621.9345816053871 A A A 0.3554223762802580.329105125848761
0.380396622549709A A A LNCV6_134386_PI430048170 mRNA
GAGATCTTTCCTAATGGGAGCAAAAGGTTTGAATAATTTATATGTGAGCAAAACGGTGTT NM_001370RefSeq chr2
+ 84516454 84819589 DNAH6 1768 "dynein, axonemal, heavy chain 6"
GO:0001539|GO:0008152|GO:0005874|GO:0005858|GO:0003777|GO:0016887|GO:0005524|GO:0007018 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136693_PI430048170 0.00219533171509102 0.5453521735783061 2.3270857041764
12.1075560734547 12.3606726337001 P P P 12.954281689132 13.2476722360681
13.2130080975411 P P P LNCV6_136693_PI430048170 mRNA
TCTTTGGCTTTGCTACCAGTTCCATATGATGAGAAATAAACGTTCGCTGAGGTTTTGTTT NM_031459RefSeq chr1
+ 28259451 28282491 SESN2 83667 sestrin 2
GO:0005515|GO:0032868|GO:0032042|GO:0005737|GO:0006635|GO:0046323|GO:0043491|GO:0006914|GO:0070
328|GO:2000479|GO:0005634|GO:0009749 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127136_PI430048170 0.3178452341590020.8825839595574566.82674638351294
6.95106336816665 7.13448946883531 P P P 6.92927326462019 7.15512669467062 7.3540374625109
P P P LNCV6_127136_PI430048170 mRNA
CAGTCTCCACAAACCCTGTTTTAGTAGTAAGGTTTTCTTTTTCTATTGTACAAGTCAATGNM_006982RefSeq chr12 +
85280257 85301783 ALX1 8092 ALX homeobox 1
GO:0005515|GO:0005667|GO:0000977|GO:0003700|GO:0005794|GO:0046982|GO:0006366|GO:0003714|GO:0001
843|GO:0048704|GO:0007275|GO:0005634|GO:0030326|GO:0000122|GO:0009952|GO:0001228|GO:0007420|GO:0
001502|GO:0045944|GO:0014031|GO:0060021|GO:0005654|GO:0045893 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132351_PI430048170 0.000235014095237424 0.4895081921784666.75356170652657
6.57925086082227 6.58776556725157 P P P 7.55298577689966 7.74346346731254
7.71545630078486 P P P LNCV6_132351_PI430048170 mRNA
CCCCTAGGGAAGAAAGAAGGACTGGGTTTAGCAAAAATGATTTGGTAATTAAAGTTTATT NM_207344RefSeq chr12
+ 56468516 56470983 SPRYD4 283377 SPRY domain containing 4
GO:0005739|GO:0008150|GO:0003674|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141549_PI430048170 0.1047339344805760.7983257710082563.25623863524691
3.02867976636269 3.18150372961568 P A P 3.44010495269415 3.69973521503868 3.2791724737904
P P P LNCV6_141549_PI430048170 mRNA
GATTGCCTTATTTACTGCTGCGAACATTCTTGCACACATGCCCTGGTACGTGTGTGTGTT NM_175871RefSeq chr19
+ 11374706 11376951 SWSAP1 126074 SWIM-type zinc finger 7 associated protein 1
GO:0005515|GO:0006200|GO:0003697|GO:0000724|GO:0050821|GO:0005634|GO:0097196|GO:0016887 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142185_PI430048170 0.7459753885909110.9632514687382310.475054437264559
0.5606705318246190.49239758423045 A A A 0.4040374997355810.787828607951216
0.46987972631851 A A A LNCV6_142185_PI430048170 mRNA
AAGAAGAGCTAATTATGCAAAAGTGGCTTTCTCACTTATTCTGTTACAGAATACGGAACC NM_001130711 RefSeq
chr12 - 9913226 9932381 CLEC2A NA "C-type lectin domain family 2, member A, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134156_PI430048170 0.4247045841197310.7084583726468211.32236362686254

0.6064540728698552.06434116457664 A A A 2.20832726019368 1.04458017130342
2.29228437535429 A A A LNCV6_134156_PI430048170 mRNA
GGCGGGAAATGCACTAATTGTGCTCTTCCTTATAAATGGTACATATTACTGACACAGACA NM_021097RefSeq chr2
- 40112145 40430304 SLC8A1 6546 "solute carrier family 8 (sodium/calcium exchanger), member 1,
transcript variant A"
GO:0060401|GO:0008092|GO:0005516|GO:0030018|GO:0060402|GO:0005886|GO:0006883|GO:0009791|GO:0060
048|GO:0005432|GO:0046872|GO:0055074|GO:0071436|GO:0048747|GO:0016323|GO:0010649|GO:0006936|GO:0
014704|GO:0044557|GO:0006811|GO:0035050|GO:0051481|GO:0010882|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145622_PI430048170 0.5326117955093990.9709268442715310.467323308504346
0.4870149782511140.314984088706274A A A 0.4078889369975570.516594630818636
0.476516661166584A A A LNCV6_145622_PI430048170 mRNA
GGATCTGCAGATGATGGAGAACTACCTAGGCTTCATCTTTTCAACATATGTCTACACAAC NM_173658RefSeq chr3
+ 44584963 44596065 ZNF660 285349 zinc finger protein 660
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144873_PI430048170 0.4008308601332491.12814236422209 7.5448242122403
7.35116967030461 7.50621725071772 P P P 6.91584407269904 7.50115832839836
7.40506187864848 P P P LNCV6_144873_PI430048170 mRNA
GAACCGTGAACAAAACTGTGTTTTGAGTTTAGCTGACATTAAAGAAAAAAGTTCATCACG NM_001197294 RefSeq
chr5 - 147390807 147510056 DPYSL3 1809 "dihydropyrimidinase-like 3, transcript variant 1"
GO:0051219|GO:0017124|GO:0030336|GO:0016812|GO:0051491|GO:0048678|GO:0005615|GO:0044297|GO:0030
027|GO:0005829|GO:0030426|GO:0035374|GO:0031941|GO:0071345|GO:0007411|GO:0010976|GO:0010977|GO:0
051260|GO:0051764|GO:0051017|GO:0070382|GO:0006208 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_134578_PI430048170 0.00165598880562522 0.3710068256846998.78587641379909
8.50625937474045 8.33205900752003 P P P 10.2327305796861 9.77775782809148
9.90280208099129 P P P LNCV6_134578_PI430048170 mRNA
GCTTGGCTACTGTAGGTGTCCAATAAACAGTAGATGGAAACTGGGTCTCCACCCAAAAAA NM_198055RefSeq chr19
- 58561916 58573575 MZF1 7593 "myeloid zinc finger 1, transcript variant 2"
GO:0005515|GO:0006355|GO:0003700|GO:0044212|GO:0005634|GO:0000122|GO:0000978|GO:0006351|GO:0042
803|GO:0046872|GO:0001078|GO:0001077|GO:0045944 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106050_PI430048170 0.0792751315997769 1.15451894968608 7.75896025580835
7.80676967459721 7.8552358134329 P P P 7.4609844122362 7.63797002506769
7.69176875593755 P P P LNCV6_106050_PI430048170 mRNA
CCTTTTGTTTCACTTTTGCCCCCTTCTTGGGAACATTTGACCAAAAATAATCCTCATTTC NM_014760RefSeq chr3 +
10248492 10281222 TATDN2 9797 TatD DNase domain containing 2
GO:0006308|GO:0004536|GO:0043229|GO:0005654|GO:0016888|GO:0006987|GO:0044267|GO:0000737|GO:0046
872|GO:0030968 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128563_PI430048170 0.7797648324458910.9813673049054016.75792831504803
6.50659890103128 6.42406976992129 P P P 6.53729417725437 6.58590072380629
6.66520746659821 P P P LNCV6_128563_PI430048170 mRNA
GGGCCCAGAATCGTATCCCAAAGCCCTCCCATGGCCTAGAAAATAAATAAGTTATTGTTT NM_020209RefSeq chr19
+ 4278600 4290723 SHD 56961 Src homology 2 domain containing transforming protein D
GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99754_PI430048170 0.25701356661512 0.8515435071724877.26439490057764 7.34191356917343
6.93794605664922 P P P 7.61135364017974 7.44343799016906 7.18434278604418 P P P
LNCV6_99754_PI430048170 mRNA
GACCTAAAACAGTGTCTCCCCTGGGAACCTACTCCCCACCCAGCATTTGCTAAGTCTGAT NM_001144994 RefSeq

chr2 + 231037565 231049712 C2orf72 257407 chromosome 2 open reading frame 72 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139423_PI430048170 0.00280822288128743 2.38097694487768 5.79889387143875
5.74124989165521 5.69189325860973 P P P 4.35748960377577 4.66989104611408
4.43329544038615 P P P LNCV6_139423_PI430048170 mRNA
GGGATGTCCGCTATATCCAAAATTACAGCTATTGGCAAATAAACGAGATGGATAAAGGTG NM_005167 RefSeq chr1
- 112709993 112715328 PPM1J 333926 "protein phosphatase, Mg2+/Mn2+ dependent, 1J"
GO:0006470|GO:0004722 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136772_PI430048170 0.0862113088815425 1.29432472146182 11.5864320767679
11.9649975008033 11.8844948345935 P P P 11.2519342422845 11.4091164266836
11.6561741873904 P P P LNCV6_136772_PI430048170 mRNA
GTACCTATCCCTTTCGATTTGGCTTTACCTTCATCTATCTTGATCCTTTCCTGGCCAAAT NM_002764 RefSeq chrX +
107628423 107651026 PRPS1 5631 "phosphoribosyl pyrophosphate synthetase 1, transcript variant 1"
GO:0000287|GO:0005975|GO:0006221|GO:0044281|GO:0005524|GO:0042803|GO:0009156|GO:0034418|GO:0005
829|GO:0007399|GO:0016310|GO:0046101|GO:0006144|GO:0016301|GO:0004749|GO:0009405|GO:0006015|GO:0
006164 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130432_PI430048170 0.0906808304145569 2.71750867757872 3.07729667165951
3.80630360445617 2.48396110333543 P P A 0.624046290376142 1.58131709775919
2.53080081359776 A A P LNCV6_130432_PI430048170 mRNA
AGGAAAAAAGAAAGGGAGAGAGAGGAAAATAGAGGGTTGTCCACTCCTCACATTCCACGA NM_003867 RefSeq
chr8 + 22042752 22048808 FGF17 8822 "fibroblast growth factor 17, transcript variant 1"
GO:0008286|GO:0048011|GO:0008284|GO:0048015|GO:0005111|GO:0007267|GO:0005576|GO:0005105|GO:0005
615|GO:0007399|GO:0007165|GO:0007173|GO:0008543|GO:0045087|GO:0008083|GO:0038095 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133782_PI430048170 0.362914627388432 1.49057117224812 0.430174189213004
1.81744139143996 1.44518400177667 A A A 1.14848425619387 0.59374082827875
0.453491240407459 A A A LNCV6_133782_PI430048170 mRNA
CCAGCAGATCTGTGGAGACAAAACAAGCAACACCTTAAAAGAGTTTTATTTCTGAAAATA NM_001330 RefSeq chr16
+ 30896606 30903560 CTF1 1489 "cardiotrophin 1, transcript variant 1"
GO:0005146|GO:0048861|GO:0008284|GO:0007517|GO:0048666|GO:0008283|GO:0007267|GO:0005576|GO:0005
615|GO:0005125|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131345_PI430048170 0.451752036310593 0.56520107673073 1.76560009048205
0.340904183785445 0.379832933571108 A A A 1.56977841955033 2.66286314726325
0.330456786360319 A P A LNCV6_131345_PI430048170 mRNA
TTCCGGTGTGAAGATAAGTGATAAGGTAAAGAATGATGCCAGTAAGTATAGTAGAAACAC NM_001008226 RefSeq
chr15 + 82262810 82284926 SAXO2 NA stabilizer of axonemal microtubules 2 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133836_PI430048170 0.00426974719154766 0.302135242048361 4.66783347789833
4.24571469731571 4.41179387821005 P P P 5.79765711671162 6.1415415462094
6.51014363276741 P P P LNCV6_133836_PI430048170 mRNA
GCTTCTATTGGAACATTTGTATACTCGCAACTATATTTCTGTAAACAGCTGCAGTCAAAA NM_138714 RefSeq chr16
+ 69565965 69704666 NFAT5 10725 "nuclear factor of activated T-cells 5, tonicity-responsive, transcript
variant 1"
GO:0005515|GO:0007588|GO:0007165|GO:0005737|GO:0001077|GO:0003700|GO:0006366|GO:0045944|GO:0005
634|GO:0001816|GO:0000978|GO:0070884 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69507_PI430048170 0.199634640888445 0.519206834825413 0.463812850740203 0.479606020129663
0.386276986141442 A A A 1.88643321828201 0.422263684542318 1.49671372766713 A A A
LNCV6_69507_PI430048170 mRNA
AGCAAAGCCAATGTGATTTATTGAATGAAAGCACTGGACAATTACCAACAACTTGTTCCT NM_153228 RefSeq chr17

+ 56153474 56482646 ANKFN1 162282 ankyrin-repeat and fibronectin type III domain containing 1
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141674_PI430048170 0.0897136440835763 0.412502929603699 0.28280281040214
0.292458176313767 1.5448892381564 A A A 1.26870975097049 2.08484834698102
2.66445909865788 A A P LNCV6_141674_PI430048170 mRNA
GTGGCTGGTCAAGTCACTGATTTACCTTGGGCTTTATTTGATATAAATCATGTAAATCAA NM_001035005 RefSeq
chr18 - 49481177 49487274 C18orf32 497661 "chromosome 18 open reading frame 32, transcript
variant 2" GO:0007165|GO:0004871|GO:0043123 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127784_PI430048170 0.180391988832245 0.817663066322669 5.98296502463644
6.18698073559693 6.07955070361729 P P P 6.29604167020268 6.15403131358635
6.63483389115013 P P P LNCV6_127784_PI430048170 mRNA
GGAGGAATGGAAATAGTCTAGTCAGCTTATTTGTCAAGAAAAATGTCAACCTTGGTAATT NM_007189 RefSeq chr7
- 151211483 151227374 ABCF2 10061 "ATP-binding cassette, sub-family F (GCN20), member 2, transcript
variant 1"
GO:0005215|GO:0016020|GO:0008152|GO:0006810|GO:0005740|GO:0043190|GO:0016887|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145197_PI430048170 0.474905867058662 1.59737136428556 0.351158189448521
2.17413552822392 1.97466054404109 A A A 1.08662742042564 1.33340980287249
0.526754429807356 A A A LNCV6_145197_PI430048170 mRNA
TCGCTGTTTAGTTACTAGATGAACAAATCCACAGAATGGGTAAAGAGTAGAATCTGAACT NM_024501 RefSeq chr2
+ 176188578 176190907 HOXD1 3231 homeobox D1
GO:0043565|GO:0006355|GO:0030182|GO:0048706|GO:0005634|GO:0019233|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128207_PI430048170 0.283700926959886 1.23091841145791 3.26470931385428
3.23065373390666 3.68606176912516 P P P 2.95398581668431 2.80994354118993
3.47626772355219 P P P LNCV6_128207_PI430048170 mRNA
GGAAGAACAAGATGCCATAATGCCTATGAAGACTTCTTTAACAATCTTGTTTGGGTTTTT NM_024885 RefSeq chrX
- 101268252 101293071 TAF7L 54457 "TAF7-like RNA polymerase II, TATA box binding protein (TBP)-
associated factor, 50kDa, transcript variant 1"
GO:0008150|GO:0003674|GO:0006355|GO:0005737|GO:0006367|GO:0005669|GO:0007275|GO:0007283|GO:0030
154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51950_PI430048170 0.435507269892603 3.4885249898814 0.529543789224187 4.39901678785202
4.42091811814972 A P P 2.55897696841341 0.432774872997939 2.42198351309466 A A A
LNCV6_51950_PI430048170 mRNA
AGCTGCTGGACAAGTTCTCAAAGAAGCTGCAGCCGGAGCCAAACAGTGTCACTCCCACCA NM_033388 RefSeq chr11
+ 72814405 72829635 ATG16L2 89849 autophagy related 16-like 2 (S. cerevisiae)
GO:0000421|GO:0005654|GO:0015031|GO:0000045 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128705_PI430048170 0.107301957026379 0.964538742692899 0.443115945638432
0.374010057617932 0.396113810315543 A A A 0.435400127025414 0.476328109398041
0.458352428954531 A A A LNCV6_128705_PI430048170 mRNA
CTCCAGCATTCTGGTGATGTATTCTTTGAATACGTAATATGGAAACTAACAAAATTGACC NM_207102 RefSeq chr3
+ 48372218 48394725 FBXW12 NA "F-box and WD repeat domain containing 12, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95665_PI430048170 0.00948759909583371 0.705902486026884 8.4435839296233
8.54123474597995 8.62519680852748 P P P 8.94862381768166 8.96486523569864
9.19610536542558 P P P LNCV6_95665_PI430048170 mRNA
TGGCTGTTTCTACTACTGAATGAATCTTTGAAAAGCTGGTAAAAGACATGACCATGAAGA NM_152773 RefSeq chr3
- 196291218 196318294 TCTEX1D2 255758 Tctex1 domain containing 2 GO:0005515 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_133629_PI430048170 0.3441985197684520.8492376210534513.2525104871574
12.6094068543414 12.6010741454368 P P P 13.2295854193947 13.0375943967095
12.9930037857013 P P P LNCV6_133629_PI430048170 mRNA
CCCGACACATTTGTTAAAATCAAACCTGAATAAAACTACAAGTTTAATATGAAGCCCCCA NM_001970RefSeq chr17
+ 7307536 7312463 EIF5A 1984 "eukaryotic translation initiation factor 5A, transcript variant B"
GO:0005515|GO:0008284|GO:0003723|GO:0005634|GO:0003746|GO:0005829|GO:0006452|GO:0005737|GO:0045
905|GO:0006406|GO:0005643|GO:0005642|GO:0006611|GO:0017070|GO:0045901|GO:0070062|GO:0008612|GO:0
006915|GO:0006913|GO:0047485|GO:0016020|GO:0005789|GO:0043022|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144141_PI430048170 0.0244498149477983 0.5033477958589123.40125939268693
3.40488700433293 3.74791331991832 P P P 4.23205234326869 4.33132400117833
4.89729948771984 P P P LNCV6_144141_PI430048170 mRNA
TATCTTCTCTCGTTCACTTACTGGCATAGACTGCAGTTCTCTGACAGGCTTGTTTCCACTNM_033117RefSeq chr9 -
122239554 122264864 RBM18 92400 "RNA binding motif protein 18, transcript variant 1"
GO:0000166|GO:0003723 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75477_PI430048170 0.0112393288014782 0.6720858064223947.19875867586342
7.31529842922858 7.46244474087541 P P P 7.72966832281692 7.8930084109886
8.06618115036374 P P P LNCV6_75477_PI430048170 mRNA
GTGATAGTACATGGCTAACGTCAGAAATTCATAACCCTCTGGCTGTGGGACAGTATGTCA NM_153706RefSeq chr5
+ 56909259 56917338 SETD9 133383 "SET domain containing 9, transcript variant 1"
GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136186_PI430048170 0.4187044483424241.01408125753609 0.311632091987142
0.3358699846072430.37697192722617 A A A 0.3360430329432120.324749477162015
0.303733198112901A A A LNCV6_136186_PI430048170 mRNA
GTAGTTCCCTTACTAAATCCTTTCATTTATAGCCTGAGAAATAGGGAAGTAATAAGTGTC NM_001004736 RefSeq
chr3 + 98469479 98470576 OR5K1 NA "olfactory receptor, family 5, subfamily K, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131663_PI430048170 0.0144455113720179 0.4629557950428347.90893026601554
7.52919952223421 7.67908723417416 P P P 8.44480315227056 8.83756439012162
9.11608741598636 P P P LNCV6_131663_PI430048170 mRNA
GTACTTGTCTCAATGGGAATGGTGTAAAAAACAAAAGGCCTTATGTGATCTGTATCATAG NM_004491RefSeq chr19
+ 46918675 47005076 ARHGAP35 2909 Rho GTPase activating protein 35
GO:0051056|GO:0000977|GO:0007264|GO:0035024|GO:0008360|GO:0003714|GO:0001843|GO:0005634|GO:0000
122|GO:0015629|GO:0005525|GO:0001227|GO:0003677|GO:0005100|GO:0006351|GO:0005829|GO:0032321|GO:0
007411|GO:0010976|GO:0043010|GO:0030900|GO:0045892|GO:0043116 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_134412_PI430048170 0.71646549844305 0.9715614042467054.13951983786504
3.82713171814649 3.814605279693 P P P 4.0061670951052 3.86956645413641
4.04842235315664 P P P LNCV6_134412_PI430048170 mRNA
ATTGCTGTGTCCTTGCTGCTACCCTGGTCCATGCTGCCAGACGTGGTGGATGACTTTCAG NM_001080473 RefSeq
chr2 + 24010082 24024275 MFSD2B NA major facilitator superfamily domain containing 2B NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128793_PI430048170 0.00331503109301146 0.65313011314831811.3063686757923
11.236577622154 11.3492099862723 P P P 11.8314797841396 11.8628730740512
12.0352586996539 P P P LNCV6_128793_PI430048170 mRNA
CCTGGACGACATTGGGTTTTTCCTCTAGGAGAATACAAGCCTTAATAAACAATACTATTT NM_017798RefSeq chr20
- 63195429 63216186 YTHDF154915 YTH N(6)-methyladenosine RNA binding protein 1 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_128304_PI430048170 0.7417975996431231.14518253930389 1.30691907160905

3.00091005347911 2.34115460657748 A P A 0.5938165066381242.74111400878106
2.42767383663168 A P P LNCV6_128304_PI430048170 mRNA
CTATCTCTCATTGTTTTGGAAACAAGGTGTGATTATGCTATACTATAACCAGCCCTTAAT NM_003419RefSeq chr19
+ 36850357 36879575 ZNF345 25850 "zinc finger protein 345, transcript variant 1"
GO:0006355|GO:0003700|GO:0006366|GO:0006359|GO:0005634|GO:0000122|GO:0006383|GO:0003677|GO:0046
872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132755_PI430048170 0.0394516439694309 1.2130052927386 13.523001459322
13.6146686313356 13.7636850943339 P P P 13.2842099326778 13.3155777869909 13.469225697923
P P P LNCV6_132755_PI430048170 mRNA
CGTCTTGTGAAATTGTGTAGAGTGTTTGTGAGCTTTTTGTTCCCTCATTCTGCATTAATA NM_022807RefSeq chr15 +
24823646 24978582 SNRPN 6638 "small nuclear ribonucleoprotein polypeptide N, transcript variant 4"
GO:0008380|GO:0005515|GO:0003723|GO:0030532|GO:0005681|GO:0009725|GO:0005685|GO:0005686 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129987_PI430048170 0.3765031238510021.02746611733583 0.561511721540817
0.6230917863327010.506745287254951A A A 0.5510345878003750.520815798092148
0.504184255492115A A A LNCV6_129987_PI430048170 mRNA
TATATCAAAGAGCTGTGCAACCTCTTCGAGGCCCACAAACTTAAGTTCAACATCCCTGCT NM_025098RefSeq chr11
+ 75717888 75731286 MOGAT2 80168 monoacylglycerol O-acyltransferase 2
GO:0050892|GO:0005783|GO:0019432|GO:0005789|GO:0003846|GO:0016407|GO:0006651|GO:0016021|GO:0006
071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140496_PI430048170 0.5910390260826510.9855074250931681 3.4511413154777
13.4961484815745 13.5213057776113 P P P 13.4588321643036 13.5138885785469
13.5582168033812 P P P LNCV6_140496_PI430048170 mRNA
TACTAATTCGCATCTGGAAGCTCAGCAAGTGCACAAGCCTTACTTTGGTTACCGTGGAAA NM_014604RefSeq chr17
- 3662892 3668679 TAX1BP3 30851 "Tax1 (human T-cell leukemia virus type I) binding protein 3,
transcript variant 1"
GO:0005515|GO:0008285|GO:0005886|GO:0008013|GO:0030178|GO:0005634|GO:0007266|GO:0008022|GO:0015
629|GO:0032864|GO:2000009|GO:0005737|GO:0016055|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130807_PI430048170 0.1824593136932280.9500021864324680.279830691436004
0.2758577879704810.308290290192786A A A 0.4332879837267440.341193821371086
0.308797134286118A A A LNCV6_130807_PI430048170 mRNA
TGGTACACGGGGGTACACACCTGTATCCCTCCGTGAATAAGCATCTGGTGGACCCCCAGA NM_198697RefSeq chr21
+ 44657931 44658341 KRTAP12-3 NA keratin associated protein 12-3 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130192_PI430048170 0.9932697004911381.00129215596208 0.313199560950513
0.5255891694266320.388451871599544A A A 0.4997559323758880.380842466268787
0.344536331136331A A A LNCV6_130192_PI430048170 mRNA
CTTCATGGTCAAGCTCTAAGACACAACGAGCTCTGTTATTCAAGAAATCAATTCCAGTGG NM_152611RefSeq chr20
- 6040545 6054080 LRRN4 164312 leucine rich repeat neuronal 4
GO:0007616|GO:0005887|GO:0008542|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129362_PI430048170 0.0671073248726504 1.18050377275388 12.361022473419
12.6043726106387 12.5637653395552 P P P 12.3418259076265 12.1860389037135 12.290337378113
P P P LNCV6_129362_PI430048170 mRNA
TGGGGATTACCATTGTTCCTGGAGTACTCCTACCCTTAGTTGAATTTCCTTATTAAAGTT NM_170783RefSeq
chr6_GL000256v2_alt + 1360161 1363828 ZNRD1 30834 "zinc ribbon domain containing 1,
transcript variant a"
GO:0010467|GO:0006363|GO:0006362|GO:0006361|GO:0006360|GO:0003676|GO:0006139|GO:0005736|GO:0045
814|GO:0001054|GO:0040029|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_94977_PI430048170 0.8352710602260280.9831840029205366.52380753307673 6.69991930615098
6.87416386545543 P P P 6.64310819897416 6.66626169290376 6.87198747560458 P P P
LNCV6_94977_PI430048170 mRNA
CAAATACGATAGATCAGTGGGATACAACAGGCCTTTACAGCTTCTCTGAACAAACCAGGT NM_001003652 RefSeq
chr18 - 47833094 47931146 SMAD2 4087 "SMAD family member 2, transcript variant 2"
GO:0005515|GO:0001657|GO:0010467|GO:0000790|GO:0006367|GO:0003700|GO:0046332|GO:0009791|GO:0048
701|GO:0048589|GO:0003690|GO:0007179|GO:0017015|GO:0031625|GO:0001706|GO:0001707|GO:0019902|GO:0
023019|GO:0000122|GO:0000978|GO:0032924|GO:0060039|GO:0001701|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139637_PI430048170 0.0269054774818635 0.7844651936866217.69613365090395
7.55387372186988 7.52919952223421 P P P 7.78590479589094 8.04085910555503
7.99615417267488 P P P LNCV6_139637_PI430048170 mRNA
CCCATTCCATCTCTTGAAAAAATGTAGTCTTTGAATGTGTGAAAATCTAGGGACATTCAA NM_019892 RefSeq
chr9 - 136428614 136439804 INPP5E 56623 "inositol polyphosphate-5-phosphatase, 72 kDa"
GO:0006996|GO:0005886|GO:0006661|GO:0005930|GO:0072372|GO:0004445|GO:0044281|GO:0001726|GO:0005
829|GO:0004439|GO:0008150|GO:0046855|GO:0032580|GO:0046856|GO:0005856|GO:0006644 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137843_PI430048170 0.263746806771007 0.560112423297608 1.28147531362047
0.416588103867086 1.75014160917461 A A A 1.00774735230634 2.36643478087087
2.47544179337921 A A P LNCV6_137843_PI430048170 mRNA
CCAGAGCAGAGGGCATAAACTGCAACAATCAATATTAAATGAATGTTGACATAAACTGAA NM_006733 RefSeq
chrX + 101099808 101162989 CENPI 2491 centromere protein I
GO:0034080|GO:0005515|GO:0005737|GO:0006334|GO:0000776|GO:0007548|GO:0005654|GO:0005634|GO:0000
278|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138785_PI430048170 0.253465661138898 0.737769965793463 3.39062910037941
2.95826671931253 3.79994244361365 P A P 3.38751557089765 4.15316908616255
3.94217071980697 P P P LNCV6_138785_PI430048170 mRNA
TTGCCAGGTAGGAAATATGTTCCATATCTTTACTTATCATTGCATTTCAGATGGGAACTA NM_006080 RefSeq chr7
- 83958342 84194901 SEMA3A 10371 "sema domain, immunoglobulin domain (Ig), short basic
domain, secreted, (semaphorin) 3A"
GO:0030424|GO:0021828|GO:0048843|GO:0021675|GO:0048846|GO:0030425|GO:0007413|GO:0021772|GO:0007
411|GO:0060666|GO:0004872|GO:2001224|GO:0050919|GO:0006915|GO:0005576|GO:0048485|GO:0021785|GO:0
048813|GO:0045499|GO:0016020|GO:0002027|GO:0048841|GO:0060385|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131624_PI430048170 0.00505027982104273 0.267279379457164 1.45120636329684
1.15499671545347 2.01153279109633 A A A 3.52763972558602 3.16852354422863
3.71411159271054 P P P LNCV6_131624_PI430048170 mRNA
GGAGTTTTTCTACCCTGTAAAAATTAACTTTGTGGTTCCCAGTAATTACAGTAAGGAGTT NM_015295 RefSeq
chr18 + 2655886 2805017 SMCHD1 23347 structural maintenance of chromosomes flexible hinge domain
containing 1 GO:0001740|GO:0051276|GO:0060821|GO:0005524 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143914_PI430048170 0.38183112828117 1.42822657711443 0.622053069303315
0.514299287247634 1.68116999489743 A A A 0.42415298320248 0.606519611997087
0.544631445326839 A A A LNCV6_143914_PI430048170 mRNA
GCTAAGCAGAAAAGAAATTTGGACCTTGAAACCAGCAGTTCAACATATATACTTTTTGCA NM_183061 RefSeq
chr3 - 112140904 112294227 SLC9C1 285335 "solute carrier family 9, subfamily C (Na+-transporting
carboxylic acid decarboxylase), member 1"
GO:0034220|GO:0005886|GO:0031514|GO:0015299|GO:0007275|GO:0030317|GO:0016021|GO:0007283|GO:0006
814|GO:0055085|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_144764_PI430048170 0.350937997520205 1.32443959156531 2.90517334396396
3.29177401345906 2.47525227948696 A P A 1.80238142724339 2.9443410438174
2.60015563080253 A P P LNCV6_144764_PI430048170 mRNA
TGCCAGCTGTTGTGCACCTTCCTGAGAAATAAATATCCTCTAAATTTTCAAACCAAAAAA NM_014858 RefSeq
chr1 + 205227909 205273343 TMCC2 9911 "transmembrane and coiled-coil domain family 2,
transcript variant 1" GO:0005515|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_129104_PI430048170 0.00473666278506141 0.324498583397595 0.472273040870003
0.485821796741642 0.358661144356748 A A A 2.31746775170161 1.83736483729014
1.99422657972716 A A A LNCV6_129104_PI430048170 mRNA
GGGGATTTGAGTTTTACATCTTTCATAGTCTATTTAATGTGGCATCTGTATTTATCCCCA NM_004299 RefSeq chrX
- 75053171 75156340 ABCB7 22 "ATP-binding cassette, sub-family B (MDR/TAP), member 7,
transcript variant 1"
GO:0006879|GO:0005739|GO:0015886|GO:0015232|GO:0006810|GO:0005743|GO:0042626|GO:0044281|GO:0016
021|GO:0055085|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115718_PI430048170 0.735202394139482 1.02924819432561 8.55849080537011
8.59876982213599 8.44091739502748 P P P 8.63257250189312 8.58146969666868
8.23199593113148 P P P LNCV6_115718_PI430048170 mRNA
GGGAGGGGAATTGTTTGGACTATTGTTCTTCAGGATTGGAATAAAACAATCTTATTTTGG NM_199341 RefSeq
chr19 + 48170691 48197620 C19orf68 374920 chromosome 19 open reading frame 68
GO:0005515|GO:0006511|GO:0007275|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131058_PI430048170 0.000301038068834923 7.12908492487305 3.11055988263512
3.68736943087052 3.22762936839719 P P P 0.355677695596373 0.802843369091809
0.387848137021196 A A A LNCV6_131058_PI430048170 mRNA
AGTGTTTGGCTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCCCACCCG NM_052863 RefSeq
chr5 - 180590104 180591487 SCGB3A1 92304 "secretoglobin, family 3A, member 1"
GO:0030308|GO:0042127|GO:0005615|GO:0005125|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_134818_PI430048170 0.0445436572409993 0.817466388592617 12.253841527901
12.2042231641811 12.2583996727275 P P P 12.3926497017279 12.6157824190793
12.5714242002595 P P P LNCV6_134818_PI430048170 mRNA
GAATCTGTTTTCAGCTCTTGCATTGCATAGATGAACCTCAGCATGTAAAGAACTATTTTT NM_025215 RefSeq
chr12 + 131929267 131943861 PUS1 80324 "pseudouridylate synthase 1, transcript variant 1"
GO:0009982|GO:0005739|GO:0005667|GO:0000790|GO:0030374|GO:0004730|GO:0045944|GO:0005730|GO:0005
634|GO:0031119 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144521_PI430048170 0.0275166142388158 1.12702723830107 0.698893060140707
0.758196559606753 0.736884656704095 A A A 0.632341434293041 0.514767298431303
0.527003088270941 A A A LNCV6_144521_PI430048170 mRNA
TAAGTGTGATCAATCTTTTCTCTGCTGACTTGGTATAAATGTTTTCTTCCAGCCTCTAAA NM_001129908 RefSeq
chr3 + 42979266 43057716 FAM198A 729085 "family with sequence similarity 198, member A"
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127201_PI430048170 0.112578881628423 1.06697617780468 0.45923286277553
0.521302055609183 0.527781412571797 A A A 0.341686402008744 0.41259014671176
0.471518977637984 A A A LNCV6_127201_PI430048170 mRNA
ATCCTTGTGAAATGAATTTGTGATGACATACGCATGTGTAAATAAACTTTTCAGATGGCC NM_001128202 RefSeq
chr10 - 125655693 125683144 TEX36 387718 testis expressed 36 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_72453_PI430048170 0.0291181051142161 1.30605226642115 11.0604895764177

10.9855299595976 11.2171426457909 P P P 10.7105164595838 10.6905419360539 10.7161032222144 P P P LNCV6_72453_PI430048170 mRNA TTTGAAAAACAGCAGATTGGCTCAAGTGCGATGCCATATAAGCGGAATCCCATGCGTTCA NM_000026 RefSeq chr22 + 40346499 40366571 ADSL 158 "adenylosuccinate lyase, transcript variant 1" GO:0009168|GO:0051262|GO:0070626|GO:0004018|GO:0055086|GO:0044208|GO:0044281|GO:0005829|GO:0006167|GO:0006144|GO:0008152|GO:0006164|GO:0006189 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140921_PI430048170 0.133777705905058 0.67757629170502 3.87466632740653 3.79226156707314 4.61216433451272 P P P 4.89929431917478 4.57060268027942 4.61972835779692 P P P LNCV6_140921_PI430048170 mRNA TAACTCCTCACTGTACTGATTTACTGGCGCATGAAATTCTATTAAAAATGCATTCTTCTG NM_001170961 RefSeq chrX - 131273505 131289429 IGSF1 3547 "immunoglobulin superfamily, member 1, transcript variant 3" GO:0005515|GO:0007165|GO:0006355|GO:0016020|GO:0034711|GO:0005576|GO:0004872|GO:0016021|GO:0015026 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140387_PI430048170 0.0704946910829745 0.621507897547181 5.77043771257657 5.28948948508965 5.72431543195906 P P P 5.87662977932216 6.30034053972628 6.61842774238053 P P P LNCV6_140387_PI430048170 mRNA GCACTTGCCCCACTGTAAATATACAGCATGTAAAATTTCTATAGTATATAAATGGCAGCA NM_032172 RefSeq chr7 + 6104918 6161564 USP42 84132 ubiquitin specific peptidase 42 GO:0005515|GO:0004197|GO:0016579|GO:0004843|GO:0061136|GO:0043161|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135803_PI430048170 0.0133472097624411 0.411280813609955 5.61813125227221 5.69588151563588 5.66309105320431 P P P 6.618636086046 7.03122351017353 7.12509312303954 P P P LNCV6_135803_PI430048170 mRNA AAACAGTCTTGTTAAGGTGAAAGGGGTCCTTGGTGATGGATCATTATTTCAAAAAAGAAA NM_018989 RefSeq chr5 + 146203599 146289221 RBM27 54439 RNA binding motif protein 27 GO:0006397|GO:0005737|GO:0016607|GO:0000166|GO:0005654|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136323_PI430048170 0.0638228324784397 1.22241565423934 10.4481977150374 10.6439966954183 10.4963837849473 P P P 10.3903474007354 10.0751459139672 10.2439816229442 P P P LNCV6_136323_PI430048170 mRNA CCAGTAAGTGTACCTTGTACTTTATAAATAAACCTCAAGCAGCTCAAGGTTGTCCTTCTA NM_001161 RefSeq chr9 + 34329505 34343713 NUDT2 318 "nudix (nucleoside diphosphate linked moiety X)-type motif 2, transcript variant 1" GO:0005739|GO:0008803|GO:0006139|GO:0004081|GO:0006915|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132060_PI430048170 0.107850768540364 0.565026115265737 2.79114086476239 1.66775000539076 2.54922902616422 A A A 3.02185595761591 3.17315579660768 3.4712303459953 P P P LNCV6_132060_PI430048170 mRNA GCTACAGAGTAACATGATTCAGGGGAGGAAAAGTTCCTTAGAGTTACTTTTATAATTCTT NM_130434 RefSeq chr15 - 65445659 65517697 DPP8 54878 "dipeptidyl-peptidase 8, transcript variant 1" GO:0006955|GO:0005737|GO:0016020|GO:0006508|GO:0008236|GO:0005654|GO:0008239 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140756_PI430048170 0.00797112826106521 0.423208537422462 4.92519740841398 4.99249435007176 5.49001216550606 P P P 6.28798898114987 6.30902104672559 6.58165664756382 P P P LNCV6_140756_PI430048170 mRNA CTTCCGAGAAACTTTTCTGATCAGTTTGCGAGTTTTGATGAGTTTTGTAAGGTTTTTGTT NM_001083893 RefSeq chr14 - 30893798 31026401 STRN3 29966 "striatin, calmodulin binding protein 3, transcript variant 1"

GO:0005515|GO:0005516|GO:0003700|GO:0005794|GO:0005886|GO:0000159|GO:0005634|GO:0000122|GO:0032403|GO:0030425|GO:0043234|GO:0005737|GO:0045944|GO:0043025|GO:0005654|GO:0033147|GO:0051721|GO:0045892|GO:0032355|GO:0070016 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134494_PI430048170 0.0704320670024803 1.62684342068635 4.19993037115965 4.88157375472923 4.55383456499395 P P P 4.24985980985118 3.70727242971624 3.55669442679692 P P P LNCV6_134494_PI430048170 mRNA
GCAAACAGTGATGGAAGGCTGTTGTCTTGGTGTATCCCTTGCCTCATAGTCAATATATTT NM_001304331 RefSeq
chr1 + 203026520 203078736 PPFIA4 8497 "protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4, transcript variant 1"
GO:0005622|GO:0005515|GO:0048786|GO:0009986|GO:0045202|GO:0007268|GO:0014047|GO:0007269|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126746_PI430048170 0.598876814923571 1.46872318423556 0.275157926434354 0.281177332029507 1.92997854850456 A A A 0.342076707184524 0.292091995767285 0.810434603264889 A A A LNCV6_126746_PI430048170 mRNA
GTTGCTCTGGTCTGGGAAGAATGTATTTGTTTTGCACTATAATAAATGCGATTAAGTCCA NM_203405 RefSeq
chr21 - 30319130 30320289 KRTAP26-1 NA keratin associated protein 26-1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130872_PI430048170 0.213264432889787 2.354764470117 8.7636032858633 10.3529591232222 8.58471470408242 P P P 8.39894843323899 8.10958718166731 8.17622884412447 P P P LNCV6_130872_PI430048170 mRNA
AAGAGGCTGGACTATATCACAGCTGAAATTAAGCGATACGAATCCCAGCTTCGGGATCTT NM_001185181 RefSeq
chr6_GL000255v2_alt + 4484058 4485358 PFDN6 10471 "prefoldin subunit 6, transcript variant 1"
GO:0005737|GO:0006457|GO:0016272|GO:0051087|GO:0051084|GO:0051082|GO:0051131|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110570_PI430048170 0.0086408971355461 0.714137125115465 7.98637253493214 7.9398675286267 8.12206206334186 P P P 8.44158743015566 8.4073316465283 8.65062306573968 P P P LNCV6_110570_PI430048170 mRNA
CCTTATAATTACTCCAGACTCTCCTATCCAGCCTGTTGGGAATGGACCCAGTGATACAAA NM_003584 RefSeq
chr2 - 73762197 73780157 DUSP11 8446 dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)
GO:0004651|GO:0016791|GO:0006396|GO:0016607|GO:0016070|GO:0003723|GO:0005634|GO:0008138|GO:0035335|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145691_PI430048170 0.0383371958774824 0.59245841636734 2.3774180437104 2.89198837523458 2.82405535716311 A A A 3.0982412480475 3.52274823479367 3.72190286275462 P P P LNCV6_145691_PI430048170 mRNA
ACTGTGATCAACCCCATGCTGAACCCACTTATCTACAGCCTCAGAAATACTGATGTTCAG NM_012373 RefSeq
chr17 + 3420567 3421533 OR3A3 8392 "olfactory receptor, family 3, subfamily A, member 3"
GO:0050911|GO:0007165|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127256_PI430048170 0.0432701598270472 1.52978621739183 10.1352310442768 10.5791548433557 10.2729196943964 P P P 9.7050309951174 9.72875447000098 9.74955281520933 P P P LNCV6_127256_PI430048170 mRNA
ATTTCCTAGACGTACGTCAACTGTATGTACATACCGGGGCTCCTCTCCTAACATATATGT NM_001495 RefSeq
chr8 - 21692017 21788834 GFRA2 2675 "GDNF family receptor alpha 2, transcript variant 1"
GO:0031953|GO:0016167|GO:0005886|GO:0035860|GO:0031225|GO:0007169|GO:0019898|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142108_PI430048170 0.496975532377083 0.792437886715257 1.12504577447627 0.34003638466925 1.10006073501744 A A A 1.77479710792616 0.71511479321971 0.99371928112286 A A A LNCV6_142108_PI430048170 mRNA

GGGTGGGGATTCTCTTGTTTCTAAATCTTACACTTTCAGTTTCTTCTGTGTCTTAAATAT NM_001031732 RefSeq chr4_GL000257v2_alt - 4028 43748 YTHDC1 91746 "YTH domain containing 1, transcript variant 1" GO:0005515|GO:0016604|GO:0003723|GO:0006376|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137192_PI430048170 0.120948980549833 0.851928029816987 12.5932305809648 12.3403789961139 12.430754606097 P P P 12.8373633491238 12.5287000740222 12.6868707101339 P P P LNCV6_137192_PI430048170 mRNA
GGCTTTCTGAGTTTTTGTGGAATTAAAGTGCTGCTGCTGCGAAGGCTGAGGCTGAAAAAA NM_017622 RefSeq chr17 - 8188332 8190246 C17orf59 54785 chromosome 17 open reading frame 59 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136377_PI430048170 0.994812952869917 1.01750894349507 4.21538104566197 4.8978350516264 5.00935754928202 P P P 4.40019850566895 4.77765019514543 4.93853947247445 P P P LNCV6_136377_PI430048170 mRNA
CCTTCTTTGGTTGTGTTGCTCAGTGTGTAAGTGTTTGTTTCCAGGATATTTTCTTTTTAA NM_182663 RefSeq chr1 + 206507529 206589284 RASSF5 83593 "Ras association (RalGDS/AF-6) domain family member 5, transcript variant 1" GO:0035556|GO:0005515|GO:0005737|GO:1900180|GO:0008285|GO:0005874|GO:0031398|GO:0006915|GO:0005634|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131020_PI430048170 0.0699550590403445 0.361839567377665 1.34325146263827 2.51565917946399 2.81603777541728 A A A 3.74239199214913 3.89780061178975 3.8062451659045 P P P LNCV6_131020_PI430048170 mRNA
TAGTTGTCATTGAAGGTGTGAACATACCCTACCTCTACTCTACATGTGGAAGACCTGACC NM_032102 RefSeq chr11 + 95066876 95071224 SRSF8 10929 "serine/arginine-rich splicing factor 8, transcript variant 1" GO:0008380|GO:0006397|GO:0005515|GO:0000166|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130855_PI430048170 0.321829385204665 0.8979751176938476.27246584258588 6.43276319408734 6.31049421073173 P P P 6.71049717947577 6.39319327922328 6.35574897575907 P P P LNCV6_130855_PI430048170 mRNA
TTTTTGAAACAGGCTTCCTCCTTCAGGAGAGATCATGCGGACTAAACTGTAGCAATTCCA NM_018295 RefSeq chr7 + 135148013 135166215 TMEM140 55281 transmembrane protein 140 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128865_PI430048170 0.144613286496281 0.860026961114761 8.24770025525732 7.99089947284965 8.01212372178181 P P P 8.34941319795059 8.42138237409703 8.13133928053592 P P P LNCV6_128865_PI430048170 mRNA
TCAACAAGTTTGTGCAGTTCATCCATAAGTACATTACCTACAATGCCCCAGCAGCCATCT NM_001080453 RefSeq chr7 - 1470276 1504382 INTS1 26173 integrator complex subunit 1 GO:0034474|GO:0031965|GO:0016020|GO:0001833|GO:0032039|GO:0016021|GO:0043154|GO:0016180 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58935_PI430048170 0.187438898022517 1.70086256143053 3.56407034859118 4.09946129268919 4.01154871319995 P P P 2.11429316684883 3.2891901240459 3.63336097268668 A P P LNCV6_58935_PI430048170 mRNA
AAAGATTTTCTGCACATTAAAGAGAAGTACAGCAATGACTGGTGGATCGGGCGGCTAGTG NM_000725 RefSeq chr12 + 48818470 48828943 CACNB3 784 "calcium channel, voltage-dependent, beta 3 subunit, transcript variant 1" GO:0050852|GO:0051899|GO:0005245|GO:0019901|GO:0007268|GO:0008331|GO:0005891|GO:0005829|GO:0016324|GO:0016020|GO:0007411|GO:0007528|GO:0070588|GO:0006810|GO:0006816 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131820_PI430048170 0.054981369668311 0.919492160684866 0.358006632921698 0.325849766207197 0.30927061745327 A A A 0.483484580291011 0.487462167024995

0.383492520399895 A A A LNCV6_131820_PI430048170 mRNA
TCTCTCTGATGAGAACAGATTGTCTATAAAATCCCACAGTCCTTGGGAAGTTGGGGACCA NM_030956 RefSeq chr4
- 38772238 38782990 TLR10 81793 "toll-like receptor 10, transcript variant 1"
GO:0005886|GO:0002224|GO:0006955|GO:0006954|GO:0016020|GO:0002755|GO:0045087|GO:0050729|GO:0034
166|GO:0050707|GO:0016021|GO:0034146|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139864_PI430048170 0.3551511732367520.8746240679275516.49010442567856
6.23900000687273 6.61325802763606 P P P 6.45346202022965 6.5407867415276
6.91083991279609 P P P LNCV6_139864_PI430048170 mRNA
CTCTTTGGGTTAGTGTGGTATGTACAAGCTCACTCTTGTTGAAAATTAGAAAATAGTTGA NM_006371 RefSeq chr3
+ 33113957 33147773 CRTAP 10491 cartilage associated protein
GO:0018400|GO:0061077|GO:0030198|GO:0005783|GO:0032991|GO:0050821|GO:0005578|GO:0005788|GO:0007
283|GO:0032403|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95128_PI430048170 0.0179151258936107 1.48859938705885 7.83524070338293
7.80614680332052 8.11803590420136 P P P 7.36615476446766 7.27513651909888 7.41384607961 P
P P LNCV6_95128_PI430048170 mRNA
ATAGCAGTGCAGGAACAAACAGCACTTGCCAGCAAAGTCTGTGTGTACTGTTAAGTGTGT NM_001243689 RefSeq
chr12 + 51048298 51060424 LETMD1 25875 "LETM1 domain containing 1, transcript variant 3"
GO:0005515|GO:0005741|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137556_PI430048170 0.00516702565183387 0.5734521269410737.8051524877848
7.5055368799145 7.71123952151864 P P P 8.50071137729164 8.27437993938365
8.64565495024419 P P P LNCV6_137556_PI430048170 mRNA
CCTACCTTTGTACTTCAAACTCATGGAAGGATAACCACCTTCATGTTTTGAAATAAATGT NM_001001418 RefSeq
chr17_KI270909v1_alt - 207819 218757 TBC1D3C 414060 "TBC1 domain family, member 3C"
GO:0005886|GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136576_PI430048170 0.5280795471535590.6173832452048690.542010190392937
0.6856060591659393.3313372594168 A A P 0.6013837005807753.37069103315394
3.23356967524649 A P P LNCV6_136576_PI430048170 mRNA
GTACCTTTCTCTATGTCAAGTTTTGTGTCAGACATGGGAAATCATGTATTTGTTCAATTG NM_001184743 RefSeq
chr6 + 28281536 28302549 PGBD1 84547 "piggyBac transposable element derived 1, transcript
variant 1" GO:0006355|GO:0003700|GO:0016020|GO:0005634|GO:0006898|GO:0005044 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_145687_PI430048170 0.8320605815691031.01722549136408 10.6430295592469
10.5461891735334 10.4277770790595 P P P 10.2619433035227 10.7145782437763
10.5389770084437 P P P LNCV6_145687_PI430048170 mRNA
GGGACCATCTGATGTGATGTGAATACTCTTCCCACATACATTAAACACACTTAAGTGAGA NM_194255 RefSeq chr21
- 45514714 45542471 SLC19A1 6573 "solute carrier family 19 (folate transporter), member 1,
transcript variant 1"
GO:0005542|GO:0016020|GO:0005886|GO:0006766|GO:0005887|GO:0015884|GO:0006767|GO:0046655|GO:0044
281|GO:0008517|GO:0015350|GO:0051958 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137060_PI430048170 0.00939380661586003 0.4063653708986526.10786892705898
5.39862906971671 5.81979397958902 P P P 6.78303700777951 7.04216076823878
7.41452274290748 P P P LNCV6_137060_PI430048170 mRNA
CTGCTTGAAGCAAGGCCCAAGTTGAGAATACAGTAAAGGAAACTCATGAAAGTGGAAAAA NM_001098638
RefSeq chr11 + 74748867 74842413 RNF169 254225 ring finger protein 169
GO:2000780|GO:0016567|GO:0016874|GO:0035861|GO:0031491|GO:0008270|GO:0005654|GO:0005634|GO:0070
530|GO:0006974 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135739_PI430048170 0.0269229817458437 0.3867752477857362.09106552941197
2.11846754194749 2.23453729041089 A A A 3.01572627295282 3.79213937870754
3.64033583881439 P P P LNCV6_135739_PI430048170 mRNA

GTTAGGTATATCTGTGTAGTGTGGAGGGAAAAAGCTAGGAAAGAAATACACCAAATTATT NM_001039891 RefSeq
chrX - 46497724 46545457 ZNF674 641339 "zinc finger protein 674, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142671_PI430048170 0.0504304610712998 0.83831735917801311.9721112160391
12.0752652586618 11.8504385318471 P P P 12.2232540977639 12.1936118559564
12.2524007662669 P P P LNCV6_142671_PI430048170 mRNA
CTGATGTGGTAGGCTAGCAATATTTTGGTTAAAATCATGTTTGTGACTGTAACCATTTGT NM_001012614 RefSeq
chr4 - 1211439 1249120 CTBP1 1487 "C-terminal binding protein 1, transcript variant 2"
GO:0005515|GO:0090241|GO:0003700|GO:0008285|GO:0005634|GO:0035067|GO:0019079|GO:0042803|GO:0005
829|GO:0051287|GO:0017053|GO:0070491|GO:0007030|GO:0051726|GO:0005667|GO:0001106|GO:0019904|GO:0
000122|GO:0008022|GO:0006351|GO:0016616|GO:0031065|GO:0050872|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137497_PI430048170 0.0733710999391795 0.3869586692120241.88095138237532
0.33390243440181 1.03403571945027 A A A 2.75637894074283 2.52573176775567
2.47294905685335 A A P LNCV6_137497_PI430048170 mRNA
TATGGTGCTCTGTACCCTATGGGTGCTAAATAAAGGCTTGCTACTGGCAACTGGAAAAAA NM_031915 RefSeq chr13
+ 49444292 49495003 SETDB2 83852 "SET domain, bifurcated 2, transcript variant 1"
GO:0005694|GO:0006325|GO:0005634|GO:0070986|GO:0003677|GO:0001947|GO:0007067|GO:0007059|GO:0046
974|GO:0005654|GO:0008270|GO:0045892|GO:0051301|GO:0051567 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_135191_PI430048170 0.8184596070273150.9653108673982071.5200336219419
2.13147457775106 1.80092819285504 A A A 2.11636398033354 1.59699737962422
1.91022609493277 A A A LNCV6_135191_PI430048170 mRNA
TCCCCTAAAGTCTGTCAAGAACTAAAGGCCCGCAACAGAATAGATTGGGTCTACATTTGC NM_000678 RefSeq chr20
- 4220630 4249012 ADRA1D 146 adrenoceptor alpha 1D
GO:0004937|GO:0008284|GO:0005886|GO:0008283|GO:0007267|GO:0007275|GO:0006259|GO:0001994|GO:0001
986|GO:0007186|GO:0005887|GO:0071875|GO:0007188 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143678_PI430048170 0.1556036856133721.66666087348482 0.355738671628003
1.21263926714221 1.31467622628677 A A A 0.2818266355910860.278895073281226
0.289061221279051 A A A LNCV6_143678_PI430048170 mRNA
CATTGGACTGACTGAGGACACTGATACAAAATTTAAAATAAAGGGACACATCACAACCAA NM_001134382 RefSeq
chr3 - 12897042 13073117 IQSEC1 9922 "IQ motif and Sec7 domain 1, transcript variant 1"
GO:0043547|GO:0005802|GO:0005086|GO:0030036|GO:0016020|GO:0032012|GO:0005634|GO:0016192 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124214_PI430048170 0.01229350328583 0.3752239079186941.33857949200541
1.76025835312973 1.52728782466843 A A A 3.36883752603234 2.59743733541073
2.82120290392952 P P P LNCV6_124214_PI430048170 mRNA
AGGATGATCTAGTAATGGGCTCTTCCAAATCGCATCTGGTAGGTTCATAGCCATGAGTCA NM_001012279 RefSeq
chr6 - 127438405 127519355 SOGA3 387104 SOGA family member 3
GO:0010506|GO:0016021|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129842_PI430048170 0.0218892299619937 2.14709778651988 11.5394321991826
11.5898712163996 11.7548776921378 P P P 10.8880082713598 10.2139754682907
10.3974789093741 P P P LNCV6_129842_PI430048170 mRNA
CTTCCACCCAAGTCCGCATCTGTGTGTATCATCAATAAAGTTGTGTGCTTTGATTGGCAG NM_001184768 RefSeq
chrX - 101615117 101618001 ARMCX6 54470 "armadillo repeat containing, X-linked 6, transcript
variant 3" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141519_PI430048170 0.37551248008071 1.61433157773418 2.01378161242542
0.37758078472465 1.57708193525431 A A A 0.4922435756856550.906880849369099

0.905327149734061 A A A LNCV6_141519_PI430048170 mRNA
CCTGGTTCAGAGGAAGATGTTTTGAAGAATGAGGGAAAGCCAGGCACAAAGGGAAGCCAG NM_001042371
RefSeq chr16 - 2211601 2214821 PGP 283871 phosphoglycolate phosphatase
GO:0008967|GO:0000287|GO:0005975|GO:0016311|GO:0035335|GO:0004725 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126918_PI430048170 0.72738913747706 0.9374229760607350.389206276505642
0.3763498460443480.565773521547605 A A A 0.8717385302870490.340062636900962
0.339267715789977 A A A LNCV6_126918_PI430048170 mRNA
GGCAATAACTGCTTTAGATACTCTGAAAAAATTTCTCAGAAGTCAAGATATGAATGACGG NM_145720RefSeq chr4
- 152769353 152779764 TIGD4 201798 tigger transposable element derived 4 GO:0005634|GO:0003677
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142630_PI430048170 0.0066664014762211 0.5540345485778725.13765229400519
5.18367348895931 4.85358652626317 P P P 5.77524329191389 6.15231692437737
5.79261557720187 P P P LNCV6_142630_PI430048170 mRNA
CTGTCTTCTTTGCATCTGGCACACAGTAGATGCTCAATAAATGCCTGTGGAATGAAAAAA NM_198458RefSeq chr19
- 58354356 58362848 ZNF497 162968 "zinc finger protein 497, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144250_PI430048170 0.0020324029367605 0.5022262166983128.53329501115717
8.1937106443621 8.3075652134647 P P P 9.21133560162 9.5287631940316 9.27635068122641 P
P P LNCV6_144250_PI430048170 mRNA
TATATTGTGGATTTGGACAGCGACACAGCAGACAAGTTCCTGCAGCTGTTTGGAACCAAA NM_033452RefSeq chr17
- 75874163 75878575 TRIM47 91107 tripartite motif containing 47
GO:0005737|GO:0008270|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133981_PI430048170 0.3659865117798360.7086392095447170.272291371993881
0.3102212581989550.334459545067164 A A A 0.3992217809826530.3251650232390491.4123501424459
A A A LNCV6_133981_PI430048170 mRNA
CTCCTAAAAGGTTATCTTTCAATGTCTATTTCAGTATCTACTTCACTGTCAGTTCAAGAG NM_001004303 RefSeq
chr1 - 56718803 56819696 C1orf168 199920 chromosome 1 open reading frame 168 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_89585_PI430048170 0.0811697718267471 0.7614778082994115.99884406604868
5.74176192221904 5.97181015008982 P P P 6.52416927600213 6.06559087218593
6.27905249176016 P P P LNCV6_89585_PI430048170 mRNA
GAAAGAAGCATCAGATTTTGTGGGAATGATGCTAGCTGCTGCCACCTCAAAAACTTGTGC NM_001104647 RefSeq
chr3 + 140941819 140979943 SLC25A36 55186 "solute carrier family 25 (pyrimidine nucleotide carrier),
member 36, transcript variant 1"
GO:0005739|GO:0051881|GO:0005743|GO:0006864|GO:0016021|GO:0015218|GO:0007005|GO:0055085|GO:0032
355 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131273_PI430048170 0.0834636910338976 1.04431608516422 0.390674838492176
0.4072107862267890.459909290199523 A A A 0.3403608378370240.339496607373827
0.390576528416506 A A A LNCV6_131273_PI430048170 mRNA
CATGGGTGATCAACCAAAACTGAGCCTTAGAAATACAGGGTTCATTTAGAAATAAGTATT NM_001162491 RefSeq
chrX + 100969707 100990831 ARL13A NA "ADP-ribosylation factor-like 13A, transcript variant 3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144199_PI430048170 0.1712740734485230.7437978181150575.76542119153996
5.28254013282761 5.43696083828537 P P P 5.83606769675856 6.28101413674049
5.60924952267174 P P P LNCV6_144199_PI430048170 mRNA
AGCTCCAAGTGAGCTCTCGCAGCTGCCAGCAATCCAAAGGCTCTTTTCAGAGCCACTCAC NM_003527RefSeq chr6
+ 27893424 27893891 HIST1H2BO 8348 "histone cluster 1, H2bo"

GO:0046982|GO:0006334|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0003677 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127662_PI430048170 0.0166399483624355 1.54080458276068 8.18914760153328
7.93586603790691 7.8130498266482 P P P 7.57174227982258 7.29718790032874
7.19741919690632 P P P LNCV6_127662_PI430048170 mRNA
CAGGCCCGTCAGCATCACTGATGGGAATAAAAGTATTAATGCTTTGTGACAGCCAAAAAA NM_145160RefSeq chr15
+ 67542682 67807117 MAP2K5 5607 "mitogen-activated protein kinase kinase 5, transcript variant 1"
GO:0005515|GO:0030307|GO:0005634|GO:0046872|GO:0005829|GO:0005622|GO:0007507|GO:0000187|GO:0045
944|GO:2001240|GO:0090051|GO:0070375|GO:0034115|GO:0043154|GO:0004708|GO:0050679|GO:0051247|GO:0
071499|GO:0048011|GO:0060761|GO:0045415|GO:0005819|GO:0018108|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143995_PI430048170 0.260638485867865 1.05830661791084 10.5944620857759
10.7172021576476 10.769328072941 P P P 10.6004299011569 10.6074365082261
10.6331888456654 P P P LNCV6_143995_PI430048170 mRNA
AGCATAAGGTTTATCTCAAGTCTCAATTGAACTGCCTCCTCTTGTCAGGCAGGGACAACT NM_018093RefSeq chr11
- 62832904 62840156 WDR74 54663 WD repeat domain 74
GO:0008150|GO:0003674|GO:0016070|GO:0005730|GO:0001825|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134857_PI430048170 0.653521475532942 1.04740042067787 9.73328405723556
9.59026547958152 9.92519900108759 P P P 9.52798137243333 9.65275318122351 9.8667177198721
P P P LNCV6_134857_PI430048170 mRNA
GCAGTGTTTTCTAGAACAACTTAAGCAAATTATACTGAAAGCTGCTGTGGTTATTTCAGT NM_001199241 RefSeq
chr2 + 142877625 143042316 KYNU 8942 "kynureninase, transcript variant 3"
GO:0006569|GO:0030429|GO:0044281|GO:0034516|GO:0043420|GO:0042803|GO:0005829|GO:0005739|GO:0097
053|GO:0034641|GO:0005737|GO:0019805|GO:0019441|GO:0030170|GO:0005654|GO:0019442|GO:0034341|GO:0
034354 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67731_PI430048170 0.379559545826889 1.12872786632482 10.8548058027984 11.0538781528248
11.2620460889729 P P P 10.9038390511724 10.6323622893834 11.1011673471632 P P P
LNCV6_67731_PI430048170 mRNA
TGTATGGATCACAAGTGCAGCATTCCTTAATTCCTTCTGCTATATGTCACACAGTTGTTA NM_001284RefSeq chr5
+ 115841921 115914081 AP3S1 1176 "adaptor-related protein complex 3, sigma 1 subunit"
GO:0030133|GO:0008286|GO:0005515|GO:0005215|GO:0048490|GO:0005794|GO:0030123|GO:0008565|GO:0008
089|GO:0030119|GO:0006886|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142067_PI430048170 0.164501615896767 0.787011449424328 8.67203815506398
8.72504950625829 9.07727731915382 P P P 8.9073007035284 9.15204754298348
9.43727421531135 P P P LNCV6_142067_PI430048170 mRNA
GCGTGTCTTTACCTGTTCACTTAAGAGCACATTTTACAATATGGGATAAGCTATTGGAAA NM_080794RefSeq chr21
- 25585655 25607489 MRPL3954148 "mitochondrial ribosomal protein L39, transcript variant 2"
GO:0070124|GO:0070125|GO:0008150|GO:0070126|GO:0032543|GO:0006996|GO:0000166|GO:0005761|GO:0005
743 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135554_PI430048170 0.00900133161292282 0.837563197773868 9.40704110804491
9.34061089062602 9.45018261899883 P P P 9.64936289347747 9.58687865328001
9.72744565945505 P P P LNCV6_135554_PI430048170 mRNA
CTTAAAACGCGCACACAACTCTAGAGAGTGTTAAGAATAATGTTACTTGGTTAATGTGTT NM_018975RefSeq chr16
+ 75647736 75657443 TERF2IP 54386 "telomeric repeat binding factor 2, interacting protein"
GO:0005515|GO:0000781|GO:0006355|GO:0030870|GO:0048239|GO:0042162|GO:0010833|GO:0005634|GO:0000
228|GO:0005635|GO:0031848|GO:0010569|GO:0006351|GO:0005737|GO:0051092|GO:0000723|GO:0032205|GO:0
005654|GO:0043123|GO:0007004|GO:0070198|GO:0000784|GO:0000783 . NA - . NA NA NA NA NA
NA NA NA NA

LNCV6_143043_PI430048170 0.2340331618662290.72623572409147 0.293732407516738
0.3350332534547290.420516716292061A A A 0.2909385353131030.8811140585886481.1391464951506
A A A LNCV6_143043_PI430048170 mRNA
GACTGCAGAACAAGGTGAATTTGTATATGAAAAATAAGTGATGGAAACGTGGGATTCTTA NM_001256424 RefSeq
chr11 - 106674011 107018445 GUCY1A2 2977 "guanylate cyclase 1, soluble, alpha 2, transcript variant 1"
GO:0035556|GO:0007165|GO:0005737|GO:0007596|GO:0006182|GO:0030828|GO:0004383|GO:0005525|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134254_PI430048170 0.1241415128824271.33704879186258 11.2246306052031
11.7447442267641 11.4167792343562 P P P 11.329323022237 10.994998497909
10.8034778413587 P P P LNCV6_134254_PI430048170 mRNA
AAGAGAGGAGATTCTATGTGCTTTTATCAGAAAGTTTGAGTTCCCTGCCCCTCTGCCTTC NM_007160RefSeq
chr6_GL000252v2_alt + 853454 854517 OR2H2 7932 "olfactory receptor, family 2, subfamily H, member 2" GO:0050911|GO:0007618|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0006952|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127703_PI430048170 0.0373694674741396 0.7716468680505646.75391261899667
6.87062144302458 6.94256007267029 P P P 7.05290436874914 7.25100672019001
7.37343288712482 P P P LNCV6_127703_PI430048170 mRNA
TAGAACAGTTTTGTATTCTACTCCCTACAAGCCATTTTGAACTTCTGCCCTCACCGGACT NM_003170RefSeq chr17
+ 28662283 28702231 SUPT6H6830 suppressor of Ty 6 homolog (S. cerevisiae)
GO:0005515|GO:0006397|GO:0008380|GO:0006355|GO:0003700|GO:0045191|GO:0061086|GO:0005634|GO:0050684|GO:0003677|GO:0006351|GO:0042393|GO:0032968|GO:0016032|GO:0006338|GO:0051028|GO:0010793|GO:0051147 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129951_PI430048170 0.4863154240756931.37724602402472 1.54855030951824
0.3946708964230530.282492292648136A A A 0.5047258048596530.402378923011137
0.288194899807122A A A LNCV6_129951_PI430048170 mRNA
TAGAGGAAGTCTTTGTCAGCCCTTATAGCTATCATGTGAATAAAGTTAAGTCAACTTCAA NM_003063RefSeq chr11
- 107707374 107712061 SLN6588 sarcolipin
GO:0004857|GO:0016529|GO:0051924|GO:0051117|GO:0033017|GO:0006816|GO:0070296|GO:0016021|GO:0043242|GO:0043086|GO:0090281 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116664_PI430048170 0.1218374957140620.77789506157584 7.46867209801459
7.23022639445049 6.95271215035939 P P P 7.73618655396631 7.64753457667716 7.3770680617387
P P P LNCV6_116664_PI430048170 mRNA
TACCTTGTCTCCCATGCCATCCCTTGTTACTCCCTGGATGGGGACAATGTCCGTCATGGC NM_001015880 RefSeq
chr10 + 87659718 87747705 PAPSS2 9060 "3'-phosphoadenosine 5'-phosphosulfate synthase 2, transcript variant 2"
GO:0006805|GO:0050427|GO:0050428|GO:0005975|GO:0016779|GO:0044281|GO:0005524|GO:0005829|GO:0060348|GO:0016310|GO:0001501|GO:0004020|GO:0007596|GO:0000103|GO:0004781|GO:0009405|GO:0030203 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145348_PI430048170 0.00155718612111752 1.80060966732676 8.79443384577086
8.87998991385623 9.067916119838 P P P 8.0200223603912 7.99757346263188
8.18559279371918 P P P LNCV6_145348_PI430048170 mRNA
CAGTCATGGCCAAATGTTCAATATGAGTCTCAATAAACTGAATTTTTCTTGCGAATGTTG NM_000640RefSeq chrX
- 115003974 115017644 IL13RA2 3598 "interleukin 13 receptor, alpha 2"
GO:0007165|GO:0004896|GO:0019221|GO:0016021|GO:0004871|GO:0005615 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132376_PI430048170 0.0194213701513922 0.4799879827334712.78329086237588
2.51931645013776 3.02248390461686 A A P 3.57454959053423 4.23689794471256
3.63767973641069 P P P LNCV6_132376_PI430048170 mRNA

GATAACTGTAAAGGGACCCATGCTGATAGACTGGAAATAGAAGTAAATGTGTTTATTGAA NM_003640RefSeq chr9 - 108867519 108934328 IKBKAP 8518 "inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein"
GO:0045859|GO:0005515|GO:0006368|GO:0030335|GO:0006357|GO:0000993|GO:0005730|GO:0006325|GO:0008023|GO:0007165|GO:0033588|GO:0005737|GO:0006955|GO:0006461|GO:0000123|GO:0006468|GO:0008607|GO:0004871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138731_PI430048170 0.0631130551121248 1.11424784716595 0.612827892439281 0.7175280840016670.713755339447342A A A 0.6205654540790260.470495911147343 0.482389851315053A A A LNCV6_138731_PI430048170 mRNA
CTGTTTGCCTAATACATAATTGCCTTGTGCTGTGTACCTTGGAGCAGGGCCTTACATAGT NM_001098844 RefSeq chr10 + 17752260 17800867 TMEM236 NA transmembrane protein 236 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128462_PI430048170 0.8455090811844151.01768018978218 1.24409488123025 0.8139267272264850.455177884733594A A A 0.3473084623943811.49203185120056 0.397361051722891A A A LNCV6_128462_PI430048170 mRNA
AACCGACAGGAAGAAACTTTGGAATAAGGAAGAGAAGATTGACCAAACCATCCAAATGCC NM_000870RefSeq chr5 - 148481551 148654527 HTR4 3360 "5-hydroxytryptamine (serotonin) receptor 4, G protein-coupled, transcript variant b"
GO:0008284|GO:0005737|GO:0004993|GO:0016020|GO:0007186|GO:0005886|GO:0007187|GO:0005887|GO:0032098|GO:0007268|GO:0007210|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138559_PI430048170 0.0763665045611886 0.7505306998663575.39812225169942 4.94714566109078 5.00533119009028 P P P 5.48082848400002 5.42605560467989 5.71237292132358 P P P LNCV6_138559_PI430048170 mRNA
TAGCCACACCTGCAATGTAAAATGGAAGAAAATGCAAAGAAACCAAATGTGCCGAGTGAA NM_057159RefSeq chr9 - 110873773 111038085 LPAR1 1902 "lysophosphatidic acid receptor 1, transcript variant 2"
GO:0005515|GO:0005886|GO:0035025|GO:0030139|GO:0007202|GO:0071673|GO:0007204|GO:0001965|GO:0000187|GO:0005543|GO:0043197|GO:0043198|GO:0051482|GO:0043123|GO:0060999|GO:0043065|GO:0009986|GO:0004930|GO:0042552|GO:0071453|GO:0032060|GO:0030165|GO:0007186|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138820_PI430048170 0.0115415582833369 0.1355213009154522.02949546807401 0.2978628350914 0.992606511184088A A A 3.49951231230737 4.34863503986533 4.47217493700123 P P P LNCV6_138820_PI430048170 mRNA
GCAGTCACATTTCAAATAAAAGTCTGGGAAAGCAACACATCATCGCCAACTTTTAATTTT NM_033119RefSeq chr16 + 50548329 50640860 NKD1 85407 naked cuticle homolog 1 (Drosophila)
GO:0001754|GO:0005515|GO:0045732|GO:0005886|GO:0005509|GO:2000096|GO:0000159|GO:0090249|GO:0030165|GO:0007525|GO:0005737|GO:0016055|GO:0090090 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127801_PI430048170 0.4423520661224820.64720208492577 1.27092616454345 0.670948624567 1.82802132639931 A A A 2.40189332584557 0.7525168283069282.23414571239608 A A A LNCV6_127801_PI430048170 mRNA
TTTCTATCATTCCATGGAGAAAGCTGTGTTCCAATGAATCCTACCTCTTGCCCAGTCCCA NM_014405RefSeq chr17 + 66964863 67033402 CACNG4 27092 "calcium channel, voltage-dependent, gamma subunit 4"
GO:0030666|GO:0051899|GO:0005886|GO:0005245|GO:0005887|GO:0032281|GO:2000311|GO:0070588|GO:0006810|GO:0007268|GO:0019226|GO:0005891 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104397_PI430048170 0.0766449039011812 1.31601636285857 6.52737589657227 6.77262128242397 6.96157743309419 P P P 6.17884305868633 6.35974256275864 6.54395737509758 P P P LNCV6_104397_PI430048170 mRNA
CTTGGAGCAGCATTTCATGTTCTTTTGCTGTTTTGTGCTTTGCCGATTTTGGATTTTATT NM_022753RefSeq chr1 + 32817517 32858879 S100PBP 64766 "S100P binding protein, transcript variant 1"
GO:0005634|GO:0048306 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133942_PI430048170 0.986372142281193 0.999806744102848 0.323241839817559
0.327742350309683 0.401285678427431 A A A 0.367504145332054 0.319427758738221
0.366986482110429 A A A LNCV6_133942_PI430048170 mRNA
GCTCTTTGAGGTCAGGTATGTATTTCTTTCCCATATAGATAGTATTTTGTACATACCAGTNM_018651 RefSeq chr3 +
44555174 44572158 ZKSCAN7 55888 "zinc finger with KRAB and SCAN domains 7, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_100781_PI430048170 0.182495989409624 3.27353669210246 0.363391834163569
2.09664609319791 2.72658228344461 A A A 0.299188965526961 0.294467049268578
0.338690935738862 A A A LNCV6_100781_PI430048170 mRNA
ACAATCTCTGGTGAAACCTCAGAAAAGAGATATGCTTTTGTCTTAGATGGATGTCAGCAG NM_001242394 RefSeq
chr6 + 158650013 158764876 SYTL3 94120 "synaptotagmin-like 3, transcript variant 2"
GO:0005544|GO:0017137|GO:0006887|GO:0042043|GO:0006886|GO:0019897|GO:0012505 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_98152_PI430048170 0.479467847748188 1.15365375460913 3.69271843060913 3.56989574000534
3.92031474036769 P P P 2.95056763879262 3.49569008930812 3.96488761154804 A P P
LNCV6_98152_PI430048170 mRNA
TGTTGAAGAAAATATTCAAGAAGTTGTTGGGCATATCACTGAAGGTGTGTGCAGGCCTCT NM_001145079 RefSeq
chr13 + 39655626 39791665 COG6 57511 "component of oligomeric golgi complex 6, transcript
variant 2" GO:0070085|GO:0000139|GO:0017119|GO:0006891|GO:0015031 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106706_PI430048170 0.0199329461865255 0.759905112342671 5.42645665393034
5.41216017474545 5.66343499847578 P P P 5.78693869998519 5.98476010777608
5.92564704630224 P P P LNCV6_106706_PI430048170 mRNA
ATTGATTGAAAGTGGGAAGGAAGAAGGAATGAAGATTGACCTCATCGATGGCAAAGGCAG NM_020382 RefSeq
chr12 + 123384156 123409353 SETD8 387893 SET domain containing (lysine methyltransferase) 8
GO:0005515|GO:0005694|GO:0003714|GO:0005730|GO:0034968|GO:0005634|GO:0000122|GO:0018026|GO:0016
279|GO:0006351|GO:0018024|GO:0002039|GO:0007067|GO:0005654|GO:0043516|GO:0000278|GO:0045892|GO:0
051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129952_PI430048170 0.680901549510142 0.978437434336884 0.48843582822607
0.436026946886696 0.259198956685479 A A A 0.378152014444272 0.468676974024202
0.439571368032037 A A A LNCV6_129952_PI430048170 mRNA
GAGCATGAGGAGTGAAACGCTCTGTTTAGTATGTATAACTTAAAAGGAACACATACAATT NM_014438 RefSeq chr2
- 113022090 113052867 IL36B 27177 "interleukin 36, beta, transcript variant 1"
GO:0032755|GO:0006955|GO:0005149|GO:0006954|GO:0045087|GO:0019221|GO:0005576|GO:0005615|GO:0005
125|GO:0045582 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129931_PI430048170 0.948335841646782 1.00397746627251 0.420328966401467
0.639110659898884 0.568663378870071 A A A 0.654843513487546 0.56048964823299
0.391974616032104 A A A LNCV6_129931_PI430048170 mRNA
GCCCAAGGGATCCATAATAATAATTGCTTGGCCAGCCATGTGGCCTGCTGGCGTAAAAAA NM_004173 RefSeq chr22
- 21028717 21032558 SLC7A4 6545 "solute carrier family 7, member 4"
GO:0006520|GO:0015802|GO:0006810|GO:0015174|GO:0016021|GO:0003333 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_66302_PI430048170 0.770584642926635 0.941767533235373 1.96594345708106 1.36079397739663
2.68458477612173 A A A 2.48238597880481 1.64735818504874 2.31643208015081 A A A
LNCV6_66302_PI430048170 mRNA
ATCGGAGCCCCTGCACAAAATGAAATAAAGGAAGTGGAAATTGGCACTCAGTTCTTGGCT NM_003856 RefSeq chr2
+ 102337249 102346100 IL1RL1 9173 "interleukin 1 receptor-like 1, transcript variant 2"
GO:0005515|GO:0032754|GO:0004896|GO:0043032|GO:0002113|GO:0005576|GO:0035556|GO:0031012|GO:0007

165|GO:0002114|GO:0006955|GO:0050729|GO:0002826|GO:0004908|GO:0005057|GO:0016021|GO:0032689|GO:0
009897|GO:0090197|GO:0043124 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90998_PI430048170 0.1002741186312630.5928441410592153.17215597972316 3.36073515742185
3.73098406058613 P P P 3.59929289548728 4.43296230156881 4.40666183258387 P P P
LNCV6_90998_PI430048170 mRNA
TATACTCAGACCAGTTACTCCACAGAAGTTCCAAGTACTTACCGTTCATCTGGCAACAGC NM_004874RefSeq chr8
+ 38176587 38213301 BAG4 9530 "BCL2-associated athanogene 4, transcript variant 1"
GO:0005515|GO:0051897|GO:0043066|GO:0005886|GO:2001145|GO:0051087|GO:0005634|GO:0072659|GO:0051
291|GO:0005829|GO:0045785|GO:0035556|GO:0033138|GO:0010763|GO:0030838|GO:0071364|GO:0006457|GO:0
090367|GO:0071356|GO:0051496|GO:0097178|GO:0005057 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_139945_PI430048170 0.0573570902129747 0.8460269627694931 1.6047893348615
11.5531697596423 11.4086687006628 P P P 11.7750348985901 11.8743311049312
11.6383417073333 P P P LNCV6_139945_PI430048170 mRNA
CCTACTTTTTGGTCAGCTACGTCTCTAGAATAAGATGGTATCTGAAGTCCTTCCAAAAAA NM_001930RefSeq chr19
- 12675716 12681887 DHPS 1725 "deoxyhypusine synthase, transcript variant 1"
GO:0005515|GO:0008284|GO:0008612|GO:0051289|GO:0050983|GO:0042102|GO:0042593|GO:0044267|GO:0006
412|GO:0043687|GO:0034038|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134455_PI430048170 0.13763656372054 1.08538799388019 0.500436999932138
0.6356737621417570.58303922893044 A A A 0.3615284516594190.469701764822642
0.531399760531937A A A LNCV6_134455_PI430048170 mRNA
GTCCATGATATTTGCTAAGCTAGGTGTGTCTAAGAGTATTTTAAACCCTTATGGATTTTC NM_001130103 RefSeq
chr10 + 69801887 69959148 COL13A1 1305 "collagen, type XIII, alpha 1, transcript variant 1"
GO:0005515|GO:0005886|GO:0005576|GO:0005600|GO:0030154|GO:0001958|GO:0016337|GO:0007160|GO:0022
617|GO:0030198|GO:0005911|GO:0030574|GO:0005788|GO:0008201|GO:0001763 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_62063_PI430048170 0.0509516247158549 0.7133579007720784.58893575693021
4.69238637248609 4.64277953763302 P P P 4.89862629616143 5.31391001834395
5.14540723022544 P P P LNCV6_62063_PI430048170 mRNA
ATAATAACTTGGCCTGCAGCCAGTTACCTACTGCGAGCCGGCCTTCTGGTGCTCCATCTC NM_005902RefSeq chr15
+ 67065856 67195195 SMAD3 4088 "SMAD family member 3, transcript variant 1"
GO:0005515|GO:0000987|GO:0000988|GO:0001657|GO:0010467|GO:0030308|GO:0000790|GO:0003700|GO:0006
367|GO:0000983|GO:0008013|GO:0001756|GO:0005518|GO:0032916|GO:0030878|GO:0001947|GO:0009880|GO:0
003690|GO:0006810|GO:0016202|GO:0007179|GO:0002520|GO:0017015|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132468_PI430048170 0.4809704849609890.9341670884668826.69175638183635
6.75184521953235 6.41879147966425 P P P 6.81131562503132 6.79017750295367
6.56424431976895 P P P LNCV6_132468_PI430048170 mRNA
TCATTATCATCAACAATATCTCAGGCTGCTGGTCCCTCCTCAATCAATGAGGAGACCCTT NM_001097611 RefSeq
chr1 - 46545643 46551215 KNCN 148930 kinocilin
GO:0060091|GO:0016324|GO:0043025|GO:0032437|GO:0016021|GO:0036064 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130893_PI430048170 0.0899249870791167 0.7936413188568177.20678093134133
6.86676199553115 6.87559643862883 P P P 7.27706851859052 7.5083193052885
7.16973313028092 P P P LNCV6_130893_PI430048170 mRNA
GTATGAGAATAAAATGATTTCCACCATCAGGATTCTCCCATGCCCCCCTTTATTAAAAAA NM_183238RefSeq chr12
- 132921432 132956282 ZNF605 100289635 "zinc finger protein 605, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_130381_PI430048170 0.5958368302087950.9462604816664480.565504080028699
0.3004273079189740.517239908888795A A A 0.655182817294051 0.629644780563373
0.328715315642249A A A LNCV6_130381_PI430048170 mRNA
GTGGTTGATGAATTATGGCTGTAAATAACACTATAGTTTAATAAGCCCACCATTCTGAGT NM_001001933 RefSeq
chr1 + 75128433 75161533 LHX8 NA "LIM homeobox 8, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138634_PI430048170 0.1086470113545810.7656942138341759.07006421972409
9.09975338259771 9.32362001486226 P P P 9.35145482156508 9.43636390720953
9.82853593426551 P P P LNCV6_138634_PI430048170 mRNA
GTATTTTCTGACCACATAAAGGCTTCTTCTCTTTGTAATAAAGTAGAAAAGCTCTCCTCA NM_001199303 RefSeq
chr12 + 70243713 70354993 CNOT2 4848 "CCR4-NOT transcription complex, subunit 2, transcript variant 1"
GO:0005515|GO:0010467|GO:0001104|GO:0006357|GO:0006366|GO:0001226|GO:0005634|GO:0031047|GO:0000122|GO:0001829|GO:2000036|GO:0030014|GO:0006417|GO:0005829|GO:0004535|GO:0005737|GO:0016020|GO:0010606|GO:0033147|GO:0000289|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142479_PI430048170 0.5145155635695750.947263362995781 10.0472299967525
9.91363815101689 9.68984859992078 P P P 9.88864582311133 10.0335542789777
9.98163075813703 P P P LNCV6_142479_PI430048170 mRNA
GAGCCCCCTGGCATTTCTGCAATGCAAATAAAGAGGGTACTTTTTCTGAAGTGTAAAAAA NM_006440RefSeq chr22
- 19875517 19941992 TXNRD2 10587 "thioredoxin reductase 2, transcript variant 1"
GO:0005515|GO:0050661|GO:0050660|GO:0045340|GO:0005739|GO:0050787|GO:0005759|GO:0000305|GO:0004791|GO:0045454|GO:0000302|GO:0016152|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143045_PI430048170 0.1093638990985580.6299608924038745.91837812403476
5.81064711988325 6.23269647200335 P P P 6.1249821904628 6.91360519827578
6.83449530011984 P P P LNCV6_143045_PI430048170 mRNA
TCTTTCTGAGGTCCAGGGTCCTTATATGAAGAGATTCATATATATGAAGAGATTCGTCTA NM_018283RefSeq chr13
+ 48037566 48047222 NUDT15 55270 "nudix (nucleoside diphosphate linked moiety X)-type motif 15, transcript variant 1"
GO:0006184|GO:0035539|GO:0034656|GO:0006203|GO:0055086|GO:0044281|GO:0008413|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143829_PI430048170 0.3142677968623911.03382523534436 0.302952089179761
0.2556694355169830.377714406498233A A A 0.275616129679061 0.24426905356371
0.274884910047322A A A LNCV6_143829_PI430048170 mRNA
CCCATCCTTATTAGCTCTACTGGAATTTTCATACACGTAAATGCAGAAGTTACTAAGTAT NM_020975RefSeq chr10
+ 43077068 43130349 RET 5979 "ret proto-oncogene, transcript variant 2"
GO:0005515|GO:0001657|GO:0060041|GO:0005886|GO:0097021|GO:0071300|GO:0001755|GO:0001838|GO:0030155|GO:0043231|GO:0061146|GO:0005737|GO:0000165|GO:0033619|GO:0004872|GO:2001241|GO:0072300|GO:0007156|GO:0007158|GO:0035799|GO:0030335|GO:0042551|GO:0006919|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_33254_PI430048170 0.9103217987277391.06176384323739 0.476098219185235 0.500942832153104
1.67897067958161 A A A 0.481887543003901 1.53607777407821 0.445717876260811 A A A
LNCV6_33254_PI430048170 mRNA
TAATTAGCAAGCAGCAGTTTCTCTCCAATTCATCACGGTCGCTGTTTAATTAGCCGAGCC NM_182584RefSeq chr20
- 32631624 32651981 C20orf203 284805 chromosome 20 open reading frame 203 GO:0005737 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134669_PI430048170 0.2671529511755131.03770540608219 0.512037886563315
0.60382974693899 0.490992266624883A A A 0.475362151285365 0.481569679824863
0.492199301596518A A A LNCV6_134669_PI430048170 mRNA
CATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGGGAAA NM_001005286

RefSeq chr1 - 247711828 247712755 OR6F1 NA "olfactory receptor, family 6, subfamily F, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134120_PI430048170 0.9766681851306451.00027476836789 3.39681240016791
3.64483792703676 3.93954724548383 P P P 3.9825170835188 3.64206584896506
3.33376215963568 P P P LNCV6_134120_PI430048170 mRNA
AGGATTTCATTCTAAGCAGGGGCTACAGGACGCCACGTTTCCTTGAGAATATGTATATCG NM_001242936 RefSeq
chr4 + 76214039 76283783 FAM47E 100129583 "family with sequence similarity 47, member E,
transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145480_PI430048170 0.0800181791376580.7761823513047539.0865446432407
8.76538749688009 8.66701500426927 P P P 9.17152197713674 9.33020599647707
9.14061882456225 P P P LNCV6_145480_PI430048170 mRNA
TGCGTTATATTGTATAATACCAACGTAAGGAAATAAACCTTTGGAATTGTTGGGCTGGTG NM_003565RefSeq chr12
+ 131894733 131923162 ULK1 8408 unc-51 like autophagy activating kinase 1
GO:0005515|GO:0043005|GO:0031102|GO:0048675|GO:0007265|GO:0032403|GO:0048671|GO:0031175|GO:0005
829|GO:0021707|GO:0031623|GO:0005737|GO:0070969|GO:0046777|GO:0042594|GO:0008104|GO:0031669|GO:0
043025|GO:0000045|GO:0030659|GO:0016239|GO:0017137|GO:0005776|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130287_PI430048170 0.0235549488098450.5912899632626145.5182839148648
4.98411209450207 5.08667685342921 P P P 6.00477234027484 6.10823954864871
5.78946330711786 P P P LNCV6_130287_PI430048170 mRNA
ACAGTTGCTTCTCAGCTCAGCTGTGCCAGGATCTTGTTGAGTCAGGTCAGCTGCCCACAG NM_024866RefSeq chr22
+ 50481555 50486437 ADM2 79924 "adrenomedullin 2, transcript variant 1"
GO:0010628|GO:0007631|GO:0005179|GO:0007586|GO:0006468|GO:0005576|GO:0045776|GO:0007189|GO:0001
525|GO:0032403|GO:0045766 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142135_PI430048170 0.49596585483404 0.7990696102886350.374012840699165
0.2722307967568240.406077285638938A A A 1.2225341076417 0.29105097899044
0.303762008846902A A A LNCV6_142135_PI430048170 mRNA
CTTGGGACGATAAAGAGAACTGTAAACTTAATTTTGTAGTTAGAGAAGATGAACCCAAAC NM_001288707 RefSeq
chr22 - 17580156 17589192 LOC101929372 NA uncharacterized LOC101929372 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_68482_PI430048170 0.1043662393915720.4733433904884352.21701258906209 0.92558907798463
2.24697709718453 A A A 2.79001073895413 3.17924586831951 2.97980817871618 P P P
LNCV6_68482_PI430048170 mRNA
TATGACTCAGGTGAGGACACAAGCTGTAAAGGCCACATTGATCTGGCTGAAGTAGAAATG NM_030962RefSeq chr11
- 9778666 10294207 SBF2 81846 SET binding factor 2
GO:0005515|GO:0005774|GO:0017112|GO:0051262|GO:0019902|GO:0042552|GO:0032851|GO:0042803|GO:0016
791|GO:0019208|GO:0016020|GO:0016311|GO:0035091 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129098_PI430048170 0.1425463994783310.8534376629816649.68558095379989 9.3656356778252
9.37322242559228 P P P 9.60224563605355 9.75391842262854 9.7718884664109 P P P
LNCV6_129098_PI430048170 mRNA
CACAGAGCAAGGCGGGCAGGGAACGGTTATTTTTCTAAATAAATGCTTTAAAAGAAAAAA NM_006399RefSeq chr14
+ 75522440 75546991 BATF 10538 "basic leucine zipper transcription factor, ATF-like"
GO:0005515|GO:0002320|GO:0003700|GO:0006357|GO:0030330|GO:0072539|GO:0045190|GO:0042832|GO:0005
634|GO:0060218|GO:0001816|GO:0072540|GO:0006351|GO:0006974|GO:0043565|GO:0005737|GO:0045064|GO:0
043011 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135935_PI430048170 0.2888703120278551.10422031822595 9.59265106545721
9.56448255463867 9.40932661454995 P P P 9.54636952300005 9.38063627750005
9.19579689399618 P P P LNCV6_135935_PI430048170 mRNA
CGCCCCAGGCGTCACTCAGTGATCACGGGTAAAGAGAACTGTTTCAAAAAGCTTAAAAAA NM_003660RefSeq chr19

+ 49119388 49151030 PPFIA3 8541 "protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3, transcript variant 1"
GO:0005515|GO:0048786|GO:0009986|GO:0007268|GO:0048172|GO:0014047|GO:0007269|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140053_PI430048170 0.9807043542116311.00122928565151 8.70858007408987
8.66953133461803 9.0543597105626 P P P 8.56183010311216 9.04872303523839
8.80751957740764 P P P LNCV6_140053_PI430048170 mRNA
TCAATGTGGGCAGTTCAGTCGTCTGGGTTTTTTCCCCTTTTCTGTTCATTTCATCTGGCT NM_005184RefSeq chr19 +
46601254 46610782 CALM3 808 "calmodulin 3 (phosphorylase kinase, delta)"
GO:0005515|GO:0005513|GO:0007603|GO:0030017|GO:0006936|GO:0007173|GO:0043274|GO:0016056|GO:0010
800|GO:0005813|GO:0032465|GO:0006996|GO:0019901|GO:0005975|GO:0008179|GO:0005509|GO:0019904|GO:0
030168|GO:0022400|GO:0010801|GO:0044325|GO:0031432|GO:0000922|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_62070_PI430048170 0.35328290134381 0.9471896748023729.89136986880826 9.98013926815009
10.1221604483722 P P P 10.0638393719312 10.0468844203144 10.1260067864961 P P P
LNCV6_62070_PI430048170 mRNA
ATTGAAAGTGTGCGTCAAAGAACATAAATATCAGTGGATTTTCTCTGTGTATATGTGCAG NM_001143936 RefSeq
chr15 + 67521183 67527303 C15orf61 145853 chromosome 15 open reading frame 61 GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134563_PI430048170 0.0194635298961817 0.92649392017178412.8057706705676
12.8813820506171 12.8544791588397 P P P 12.9549059698952 12.9355560335343
12.9822435204721 P P P LNCV6_134563_PI430048170 mRNA
CATGTGGAAGGGCTCTGAGCTGTGTCCTCCTTCATTAAAAGTTTTTATGTCTCGTGTCAG NM_012469RefSeq chr20
+ 63981077 64033100 PRPF6 24148 pre-mRNA processing factor 6
GO:0000244|GO:0005515|GO:0008380|GO:0010467|GO:0000245|GO:0003723|GO:0003713|GO:0005634|GO:0050
681|GO:0071013|GO:0071001|GO:0006403|GO:0016607|GO:0016020|GO:0000398|GO:0045944|GO:0000375|GO:0
043021|GO:0005654|GO:0005681|GO:0005682|GO:0046540 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_119900_PI430048170 0.7322844183410760.6125521036998872.34030228515339
1.63710182476322 2.36024224401224 A A A 0.7402352171217713.16089217493521
3.47416984805859 A P P LNCV6_119900_PI430048170 mRNA
ATTCGTGTGCAGAATGAAGGAACTGGAAAAAGTTCTTGGTGGATGCTCAATCCAGAGGGT NM_002015RefSeq chr13
- 40555663 40666597 FOXO1 2308 forkhead box O1
GO:0005515|GO:0001659|GO:0006366|GO:0071732|GO:0045599|GO:0000981|GO:0035947|GO:0000989|GO:0007
173|GO:0045444|GO:0031625|GO:2000177|GO:0032869|GO:0000122|GO:0008543|GO:0045087|GO:0005654|GO:2
000377|GO:0045893|GO:0045892|GO:0038095|GO:0010508|GO:0008286|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133737_PI430048170 0.2306000822722341.15656482902296 14.7276947499819
14.6379608581595 14.6749436600491 P P P 14.7163389830249 14.373379617518
14.2860674911971 P P P LNCV6_133737_PI430048170 mRNA
TCATTGTTACTGCCTTGTGAGATAAAAACTGATTAAACCTTTGTGGCTGTGGTTGGCTGA NM_002862RefSeq chr20
+ 25248069 25298012 PYGB 5834 "phosphorylase, glycogen; brain"
GO:0005737|GO:0016020|GO:0005975|GO:0030170|GO:0009405|GO:0008184|GO:0006006|GO:0044281|GO:0005
980|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141824_PI430048170 0.28097325757989 0.9236049902911711.9105409887774
11.7599168870764 11.9683910421929 P P P 11.9364987539279 11.9169766641917
12.1277389151326 P P P LNCV6_141824_PI430048170 mRNA
TCTGCCATCAGTGAAAATTCTTAAACTTGGAGCAACAATAAAAAGCTTCCAGAACAGATC NM_001697RefSeq chr21
- 33903452 33915854 ATP5O 539 "ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit"

GO:0005215|GO:0005886|GO:0006200|GO:0022857|GO:0005743|GO:0005634|GO:0044281|GO:0005753|GO:0005739|GO:0022904|GO:0006754|GO:0046933|GO:0042776|GO:0008144|GO:0016887|GO:0044237|GO:0070062|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127037_PI430048170 0.00142110292979102 0.4367231140879096.87611696787342 6.69925034556813 6.76132907132943 P P P 8.11380952496716 7.78960395765928 8.00587554881051 P P P LNCV6_127037_PI430048170 mRNA GAAATTATTAATCATCCTCTGTGTGGCTCATGTTTTTGCTTTTCAACACACAAAGCACAA NM_000715RefSeq chr1 + 207104261 207144972 C4BPA 722 "complement component 4 binding protein, alpha" GO:0044216|GO:0005515|GO:0030449|GO:0045732|GO:0005886|GO:0045087|GO:0006958|GO:0045959|GO:0072562|GO:0005576|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132958_PI430048170 0.30090082953004 1.05756304714029 0.454401406353577 0.6115469756193320.554237814571855A A A 0.5598397801182890.406006332880891 0.411119052763538A A A LNCV6_132958_PI430048170 mRNA CTGGTGAGGAATTATCATGTGTTCATTCCCATTTTAGAGCGTGAAACTCCTACATTAGAA NM_003829RefSeq chr9 - 13105703 13279564 MPDZ 8777 "multiple PDZ domain protein, transcript variant 1" GO:0005515|GO:0043220|GO:0042552|GO:0014069|GO:0031410|GO:0008022|GO:0016327|GO:0030425|GO:0005737|GO:0016324|GO:0045211|GO:0016032|GO:0005923|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128138_PI430048170 0.4064483296894610.8950351080757130.366208612840145 0.3906691528307660.337175830518897A A A 0.7905077975497830.356619098063676 0.38537470886168 A A A LNCV6_128138_PI430048170 mRNA GATTTTGAACTCTAGACAGATGGCCTTATAGATTTGGAAAATGAGTACTTGACTGAAATG NM_001029860 RefSeq chr8 - 100133359 100145871 FBXO43NA "F-box protein 43, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130876_PI430048170 0.00272203551695722 3.91949717200034 6.59285077200514 6.85316659933796 6.74161697843866 P P P 5.0861839336016 4.54770039523679 4.58907932277694 P P P LNCV6_130876_PI430048170 mRNA GGGCTCTGGAATCCCTTTGTAAATAGGTGTGTTGAATTTGTTTTGAAGTGAATAAAATTC NM_018088RefSeq chr12 - 8221259 8227618 FAM90A1 55138 "family with sequence similarity 90, member A1" GO:0008270|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127718_PI430048170 0.7244199565001980.7794426473716671.8546630302451 0.4668755736676242.05737904548132 A A A 0.5513849284216352.44759559372289 2.27286501333918 A P A LNCV6_127718_PI430048170 mRNA CTTAGGAACTCAGAAGTGAAGAATACTTTGAAGAGAGTGCTGGGAGTAGAAAGGGCTTTANM_030908RefSeq chr6 - 131699643 131701401 OR2A4 NA "olfactory receptor, family 2, subfamily A, member 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105331_PI430048170 0.0489063347907456 0.3151848572215871.18709944334736 2.3038927018382 2.74611964163754 A A A 3.54368503399881 3.96854254137366 4.07558368649415 P P P LNCV6_105331_PI430048170 mRNA TATACCAAACATTATCTCCGCGAAAGATATCAAGAGATGAGGTGTCCCTAGAGGATTCCT NM_001169117 RefSeq chr4 + 26860690 27025381 STIM2 57620 "stromal interaction molecule 2, transcript variant 3" GO:0005515|GO:0032237|GO:0005886|GO:0051928|GO:0005783|GO:0005246|GO:0005509|GO:0070588|GO:0006874|GO:0005789|GO:0015279|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134756_PI430048170 0.3070557039803621.02033761067879 0.321879831121965 0.24854293204773 0.284719744091947A A A 0.2578897906064350.251931146880825 0.25910368309827 A A A LNCV6_134756_PI430048170 mRNA AAATTCATGAGGGTCCAGAAGTTGTTCCTCTGGATTCAGGTTGTTAAAGGGACTAATGAG NM_183059RefSeq chr1 - 211476521 211492917 RD3 NA "retinal degeneration 3, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_134096_PI430048170 0.00656584869504432 0.4441008648269635.17338012289815
4.58918990969012 4.94383773718731 P P P 5.8557317061544 6.14704085039884
6.24764995777918 P P P LNCV6_134096_PI430048170 mRNA
CCAAAGCTGAGTGTTTTAAAGAATGAACATATCTGGAAATCCTTGCTCTCAAAACAAAAC NM_006420RefSeq chr20
+ 48921737 49036693 ARFGEF2 10564 ADP-ribosylation factor guanine nucleotide-exchange factor 2
(brefeldin A-inhibited)
GO:0005802|GO:0005515|GO:0034237|GO:0048471|GO:0030054|GO:0050811|GO:0006887|GO:0015031|GO:0010
256|GO:0005829|GO:0032279|GO:0035556|GO:0005085|GO:0005086|GO:0043197|GO:0001881|GO:0032280|GO:0
005879|GO:0007032|GO:0016192|GO:0005815|GO:0032760|GO:0006893|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_82940_PI430048170 0.3345613715091350.9575938276533030.2698589976159920.397604566247065
0.298653428377915A A A 0.4659387774885260.358205071564361 0.329016904689429A A A
LNCV6_82940_PI430048170 mRNA
ACATGTACGACATCTTCAACTTGAATGACAAGGCTTTGTGCTTCACCAAGTGCAGGCAGT NM_170776RefSeq chr16
+ 57668244 57689378 ADGRG3 NA adhesion G protein-coupled receptor G3 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_126695_PI430048170 0.7778537518074671.1746735937228 0.281440040211929
0.4352575168141321.56982985219799 A A A 0.4746357439393310.364628458199861
1.02566646417924 A A A LNCV6_126695_PI430048170 mRNA
CCATAAGACCATGTGGGTTTCCATGGTGGCTATCAATAAAACTCCTTAGGAAAACTTAAA NM_001253837 RefSeq
chr10 - 100288145 100330486 PKD2L1 9033 "polycystic kidney disease 2-like 1, transcript variant 2"
GO:0008092|GO:0005515|GO:0060170|GO:0005886|GO:0005783|GO:0005272|GO:0008324|GO:0071468|GO:0007
224|GO:0042802|GO:0043231|GO:0070207|GO:0050982|GO:0035725|GO:0005227|GO:0071805|GO:0006812|GO:0
001581|GO:0005262|GO:0005261|GO:0009986|GO:0005509|GO:0031513|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133882_PI430048170 0.0460824876865742 0.36121450969016 1.80683937562525
1.71069051762064 1.97284285799974 A A A 3.64948175929607 3.47461549824845
2.57281288428828 P P P LNCV6_133882_PI430048170 mRNA
CAGTCACATACTAACTTTTCAGATTTGTTCTTGTGTTTCAGAAAAAAGTGCTCAGCATGA NM_006895RefSeq chr2
+ 137964237 138016364 HNMT 3176 "histamine N-methyltransferase, transcript variant 1"
GO:0035902|GO:0043005|GO:0007585|GO:0002347|GO:0046539|GO:0051384|GO:0006972|GO:0014075|GO:0042
220|GO:0032259|GO:0005737|GO:0007420|GO:0005654|GO:0070555|GO:0070062 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_133736_PI430048170 0.792355601135939 0.993321542917102 0.372840874277157
0.352537151715573 0.260922117264425 A A A 0.330239595172984 0.353246251261189
0.334157890121096 A A A LNCV6_133736_PI430048170 mRNA
GTCGAGCAAGTTCTGTTGATATATTGTGTCATGCAAAGAAAACTGTATTTGTGGTTAGAA NM_001297750 RefSeq
chr12 - 10069553 10099065 CLEC1A 51267 "C-type lectin domain family 1, member A, transcript
variant 4" GO:0005622|GO:0005887|GO:0030246|GO:0006952|GO:0007166|GO:0004888 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_141872_PI430048170 0.000344663619920082 1.55238147115173 13.1935801073368
13.2295854193947 13.2994282940421 P P P 12.539321969592 12.5995565011557
12.6788781545896 P P P LNCV6_141872_PI430048170 mRNA
TCCTTGAAATGTGTGTGTGTTTGTGTCAAGAGGAGTTGTGTTCTTTGTAAATAAAGGTTA NM_018405 RefSeq
chr17 - 31851864 31859307 COPRS 55352 "coordinator of PRMT5, differentiation stimulator"
GO:0005515|GO:0042393|GO:0006355|GO:0005737|GO:0007517|GO:0043985|GO:0005886|GO:0006325|GO:0005
654|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111473_PI430048170 0.000777337615913004 0.632158256884636 4.15741457958299
4.10648665769992 4.28111277047283 P P P 4.78756175587805 4.9158394726819

4.82918893430204 P P P LNCV6_111473_PI430048170 mRNA
TGTGGATGGATGAGTACGCAGAGTACATTTACCAGCGCCGGCCTGAATACCGCCACCTCT NM_198321 RefSeq
chr5 + 154190734 154420983 GALNT10 55568 polypeptide N-acetylgalactosaminyltransferase 10
GO:0004653|GO:0006493|GO:0000139|GO:0030246|GO:0016266|GO:0016021|GO:0044267|GO:0046872|GO:0043
687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140962_PI430048170 0.0216547456389813 1.40249437332342 6.51981353226767
6.30905161526169 6.51336154048205 P P P 5.94574256720351 6.13876092783823
5.78129885674122 P P P LNCV6_140962_PI430048170 mRNA
TAGCAGAAGGCTTTTGATTTTTCTCTTGCCTGAGGCTTGAATCTGACAAACCCTTGGTGG NM_003214 RefSeq
chr6 - 35473596 35497084 TEAD3 7005 TEA domain family member 3
GO:0005515|GO:0010467|GO:0005667|GO:0007565|GO:0006367|GO:0003700|GO:0006357|GO:0045944|GO:0001
085|GO:0005654|GO:0035329|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145318_PI430048170 0.0556405244081238 0.5819382921900423.92134714349606
3.39780134213755 3.11539181844366 P P P 4.49923743567073 4.07946359214328
4.28671829340865 P P P LNCV6_145318_PI430048170 mRNA
TTTATGCTGAAGGGCTCTGATTGGGCAAAATAAAATACTCTAATCTCTCCTGAAACTAAA NM_001127715 RefSeq
chr6 + 147204357 147390476 STXBP5 134957 "syntaxin binding protein 5 (tomosyn), transcript variant 2"
GO:0010468|GO:0045921|GO:0005737|GO:0030054|GO:0030193|GO:0017157|GO:0017075|GO:0015031|GO:0006
887|GO:0030659|GO:0005892|GO:0008021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94579_PI430048170 0.8357263188562960.97595683102579 7.60377604619031 7.79332194953909
7.99108188455684 P P P 8.01052978425104 7.62383260699593 7.85910331101422 P P P
LNCV6_94579_PI430048170 mRNA
ATTGTCACAGTAGCTTATTTGAACTTGAGACCATTGTAAGCATGACCCAACCTACCACCC NM_004331 RefSeq chr8
+ 26383006 26413128 BNIP3L 665 BCL2/adenovirus E1B 19kDa interacting protein 3-like
GO:0005515|GO:0043066|GO:0043065|GO:0046982|GO:0005783|GO:0035694|GO:0005741|GO:0031224|GO:0005
635|GO:0042803|GO:0042802|GO:0005739|GO:0051607|GO:0016032|GO:0016021|GO:0005521 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138013_PI430048170 0.3054949436695860.9822103766697790.316692858368122
0.33585765859813 0.357596349801668A A A 0.3908084450852580.3293131487034
0.367337327811877A A A LNCV6_138013_PI430048170 mRNA
GGAGTCATGCATTTTGCTTTGGACACAGTGTTTTATCACCTGTTCATTTGAAGAAAAATA NM_004460 RefSeq chr2
- 162170683 162243535 FAP 2191 "fibroblast activation protein, alpha, transcript variant 1"
GO:0005515|GO:0010710|GO:0005886|GO:0004252|GO:0060244|GO:0002020|GO:0005615|GO:0071158|GO:0010
716|GO:0042803|GO:0005737|GO:0071438|GO:0051603|GO:0046983|GO:0006508|GO:0007155|GO:0009986|GO:0
031258|GO:0045178|GO:0045177|GO:0051917|GO:0032587|GO:0001525|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127945_PI430048170 0.9647630001548770.9975749924485931 0.5650412902589
10.4946076155936 10.4654344408119 P P P 10.4648487899683 10.4644955495269
10.6035688585629 P P P LNCV6_127945_PI430048170 mRNA
GTGCTAGTACATCATTCATGATCACCTTAATGCTCATGAGACTATATTTATGATCAGTGA NM_020383 RefSeq chr10
- 109864765 109923553 XPNPEP1 7511 "X-prolyl aminopeptidase (aminopeptidase P) 1, soluble,
transcript variant 1"
GO:0005737|GO:0030145|GO:0004177|GO:0070006|GO:0006508|GO:0010815|GO:0042803|GO:0070062|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135808_PI430048170 0.0115372406013456 0.28708725319545 6.19119170437566
5.42187603978402 5.69938732301765 P P P 7.57701572505521 7.53392771351095
7.70438704321035 P P P LNCV6_135808_PI430048170 mRNA
GTTGGACATACATTCCAAGCTTTTCAACTCTAGGAGAAAAAGAAAATCATGTTTTCCTGT NM_022763 RefSeq chr3
+ 172039627 172400702 FNDC3B 64778 "fibronectin type III domain containing 3B, transcript variant 1"

GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57010_PI430048170 0.6603940085896310.9313871107564938.1444057915955 7.7839728859904
7.74568317452115 P P P 8.07195899678978 8.21286330470304 7.68000078325611 P P P
LNCV6_57010_PI430048170 mRNA
CGCTCGAGGATTTAAAAGCAACAAGAAGAAAACCAAACAATGCTGATAGACTCAGAAAAG NM_145806RefSeq
chr10 + 133308888 133313162 ZNF511 118472 "zinc finger protein 511, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_117840_PI430048170 0.1252707345300840.91614396838377 6.31631979188855
6.31320539334877 6.28661665408978 P P P 6.35078195677879 6.41712721663516
6.52227390659266 P P P LNCV6_117840_PI430048170 mRNA
CCTGGGGATGACCCTTAAAAGTCTCCCGTCACCCCCAGTATTGGGGGGAAGCTGACTATT NM_002536RefSeq chrX
+ 48539686 48562609 TBC1D25 4943 "TBC1 domain family, member 25"
GO:0005515|GO:0005776|GO:0006914|GO:0032851|GO:0031410|GO:0005097 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126932_PI430048170 0.3667025254946220.8742221748793350.360784427798575
0.3788117835716410.30882777550681 A A A 0.3624476321261110.384880913465385
0.833320834750948A A A LNCV6_126932_PI430048170 mRNA
GGTGAATACATTTATGCCTTTGTCCATCGAATCCCGCCATCATATGTGAAGATGATTCAA NM_001190441 RefSeq
chr19 + 39655893 39660647 LGALS16 148003 "lectin, galactoside-binding, soluble, 16"
GO:0006915|GO:0070234|GO:0005575|GO:0030395 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141728_PI430048170 0.0348886206437185 0.847088581189434 10.5167080913311
10.4974373933754 10.3311604803509 P P P 10.7786118792058 10.6537404801973
10.6340143234261 P P P LNCV6_141728_PI430048170 mRNA
TTTTTGCCTAATGTCCCTGCCTCTAGGTTCATAATGAATTAAAGGTTCATGAACGCTGCG NM_015015RefSeq chr19
+ 4969112 5153597 KDM4B 23030 lysine (K)-specific demethylase 4B
GO:0006355|GO:0030054|GO:0006325|GO:0051213|GO:0008270|GO:0005654|GO:0005634|GO:0005925|GO:0006
351|GO:0055114|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127561_PI430048170 0.1480369509240480.8903667441659918.93698335931743
8.73135789840319 8.86544547628875 P P P 8.96276984833128 8.9210766516424
9.14961617882791 P P P LNCV6_127561_PI430048170 mRNA
GCGAAAGATCAGATGAGATTTAATGAAGACCCAGTGTAAAGAATAAATGAATCTTACTCC NM_000236RefSeq chr15
+ 58431975 58568874 LIPC 3990 "lipase, hepatic"
GO:0042632|GO:0004806|GO:0043691|GO:0030169|GO:0070328|GO:0004620|GO:0005615|GO:0034372|GO:0034
374|GO:0034382|GO:0034364|GO:0034373|GO:0034375|GO:0006633|GO:0034638|GO:0019433|GO:0034185|GO:0
008201|GO:0008203. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142086_PI430048170 0.0840800474129947 3.0374464259619 2.89543890174649
2.5650518380511 1.22527873509099 A A A 1.15780917053112 0.370621666069514
0.716824563472373A A A LNCV6_142086_PI430048170 mRNA
ATGAAAGAAACGGAGGCTTCCTACAAGGCCCAGAACCTCTACATCTTCCTGGAAAACATT NM_032130RefSeq chr12
- 49587504 49605650 FAM186B 84070 "family with sequence similarity 186, member B, transcript
variant 1" GO:0043234 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58518_PI430048170 0.6710289238864880.9766609299732338.41387117820785 8.56845475493555
8.61952513596609 P P P 8.65664866923717 8.54498780155579 8.50601646688768 P P P
LNCV6_58518_PI430048170 mRNA
GCTCCTTTCCACCAGTGATTTGTATTAAGACAGCACTTATATTGTACAATACTTCAGACT NM_003845RefSeq chr12
+ 4590071 4613888 DYRK4 8798 "dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4,
transcript variant 1"
GO:0005515|GO:0005737|GO:0004674|GO:0018108|GO:0005634|GO:0004712|GO:0004713|GO:0005524|GO:0046

872|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131598_PI430048170 0.0281063738145990.6409089464189798.32186031668449 7.8896213819933
7.95034058237798 P P P 8.7608709998453 8.60433632978275 8.75559086714847 P P P
LNCV6_131598_PI430048170 mRNA
CATTCTCTAGGAACAGCTGCGACTCATAAAGACCAAGAAGCATAAATAAACTTTCAAAAA NM_001286837 RefSeq
chr2 - 3544891 3558371 RNASEH1 246243 "ribonuclease H1, transcript variant 2"
GO:0005739|GO:0006369|GO:0000287|GO:0004523|GO:0003723|GO:0005634|GO:0004540|GO:0006264|GO:0003
676|GO:0042803|GO:0006401 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127766_PI430048170 0.5945432162073110.90190745742849 0.454201692975915
0.3190191724437220.353185499207151 A A A 0.8857725667728340.332410189849546
0.276946873065407 A A A LNCV6_127766_PI430048170 mRNA
GTGATGAGGTGGATTGATACTTTCTACTTTGCATTAAAATTATTTTCTAGCCTGCAGTCT NM_001077693 RefSeq
chr5 - 139448553 139462743 ECSCR 641700 "endothelial cell surface expressed chemotaxis and
apoptosis regulator, transcript variant 1"
GO:0005737|GO:0006935|GO:0005886|GO:0006915|GO:0016021|GO:0001525|GO:0030154 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_68513_PI430048170 0.0103366364882541 0.6127458608881786.38606426318775
6.33221379458924 6.62467496736728 P P P 7.03490183173055 7.03217432820669
7.38381011502552 P P P LNCV6_68513_PI430048170 mRNA
GACTGGGTTGTTTCAATCTAACAGTCAAAGGTCATGCTAAATGTGTAGAAGTTGTAAAAA NM_001527 RefSeq chr6
- 113936155 113971195 HDAC2 3066 "histone deacetylase 2, transcript variant 1"
GO:0000792|GO:0005515|GO:0010467|GO:0000790|GO:0003700|GO:0005657|GO:0006325|GO:0042220|GO:0034
605|GO:0016581|GO:0016580|GO:0031072|GO:0045347|GO:0001103|GO:0043044|GO:0019213|GO:0031492|GO:0
001047|GO:0000122|GO:0045786|GO:0000978|GO:0016358|GO:0032922|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129537_PI430048170 0.16278069382542 0.6278328275512920.322168302849245
0.3201908331649160.494260451531701 A A A 0.5431644131785721.5326407916046
0.905475034310115 A A A LNCV6_129537_PI430048170 mRNA
CTCAGATTGGTAATGCCAGAAAAAATTTTAAGAGGACTCACCAAAAGTACTAGATCTATG NM_152275 RefSeq chr2
- 177614297 177618966 TTC30A 92104 tetratricopeptide repeat domain 30A
GO:0042384|GO:0005929|GO:0042073|GO:0030992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93935_PI430048170 0.1197438250178541.53185353618836 3.24761200963164 4.02202270869583
3.5272471991499 P P P 2.99657949620741 3.10136066211717 2.95771417945544 P P P
LNCV6_93935_PI430048170 mRNA
AGATCTGTAACGTGGTGGCCATCCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCA NM_001066 RefSeq chr1
+ 12167002 12209220 TNFRSF1B 7133 "tumor necrosis factor receptor superfamily, member 1B"
GO:0005515|GO:0051044|GO:0048471|GO:0005886|GO:0008630|GO:0007568|GO:0005576|GO:0005634|GO:0097
191|GO:0033209|GO:0050779|GO:0006955|GO:0071222|GO:0005031|GO:0006954|GO:0071363|GO:0050728|GO:0
043196|GO:0043025|GO:0045121|GO:0016021|GO:0031625 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_142802_PI430048170 0.4594297480819292.28730679197377 3.32113578969919
0.7699378582050670.925120498981837 P A A 0.2811533499572581.51961059072608
0.897566108684811 A A A LNCV6_142802_PI430048170 mRNA
GGCTGTGGCCGTCTTTGTACTCTGGTGATTTTTAAAAATTGAATCTTTGTACTTGCATTGNM_001177999 RefSeq chr4
+ 25656463 25678746 SLC34A2 10568 "solute carrier family 34 (type II sodium/phosphate
cotransporter), member 2, transcript variant 3"
GO:0043627|GO:0005886|GO:0007568|GO:0019904|GO:0035435|GO:0031528|GO:0031526|GO:0031402|GO:0055
085|GO:0031982|GO:0001701|GO:0044341|GO:0005436|GO:0016324|GO:0015321|GO:0005887|GO:0030643|GO:0
042301|GO:0009750|GO:0006817|GO:0035725|GO:0016021|GO:0032355|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_145109_PI430048170 0.7610265064906911.00229443313124 0.32931679443409
0.3524181937750950.348707667225975A A A 0.3473119589804720.347433143527688
0.325777374638927A A A LNCV6_145109_PI430048170 mRNA
CTGTGCTACTGTCTTTGGAAAAATGTTTGTCTCAGTTGGAAATAATAAAAGATTCACCTG NM_001819RefSeq chr20
+ 5911327 5925359 CHGB 1114 chromogranin B (secretogranin 1)
GO:0005515|GO:0005179|GO:0005576|GO:0030141 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132839_PI430048170 0.2897979827035711.01990944919569 0.452962255346013
0.4905838214373790.421808204422745A A A 0.4248244723946860.417699519229407
0.438254166248811A A A LNCV6_132839_PI430048170 mRNA
GAACCATGTAGCTGAGATGTATTTGTTTAGATGAAAAGTCTACACTGGTTCTTAATGTGA NM_178566RefSeq chr9
- 14611070 14693482 ZDHHC21 340481 "zinc finger, DHHC-type containing 21"
GO:0018345|GO:0005794|GO:0005886|GO:0018230|GO:0050999|GO:0044281|GO:0000139|GO:0048733|GO:0016
409|GO:0008270|GO:0046209|GO:0016021|GO:0001942|GO:0019706 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145437_PI430048170 0.910007516850095 1.07943638881483 2.77558912436909
0.5103886082964321.03590843274325 A A A 2.24040511194308 0.6932896409397861.6872842439454
A A A LNCV6_145437_PI430048170 mRNA
GAAGGAATGGGTGCTTTGTGATGGATAAAAGGCATTAAATAAAACCACGTTTACATTTTG NM_005244RefSeq chr20
+ 46894623 47188844 EYA2 2139 "EYA transcriptional coactivator and phosphatase 2, transcript
variant 1"
GO:0005515|GO:0005813|GO:0006355|GO:0000287|GO:0016576|GO:0005634|GO:0035335|GO:0006351|GO:0097
192|GO:0005739|GO:0005737|GO:0007501|GO:0006281|GO:0014706|GO:0004725 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_39331_PI430048170 0.8620883857284880.9819704517124346.78953981784441 6.58574700328213
6.48788115741313 P P P 6.45425621435645 6.79453539279856 6.68900278580907 P P P
LNCV6_39331_PI430048170 mRNA
GACTTTCCATGGTGAGATTGCTAGTGTCTCAGAGAATAAAGGACAGAACCAGTCCAAGTC NM_001204911 RefSeq
chr16 + 58001372 58013570 USB1 79650 "U6 snRNA biogenesis 1, transcript variant 3"
GO:0034477|GO:0008380|GO:0006397|GO:0000175|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142213_PI430048170 0.591184837775093 0.8869009049717627.83182690048907
7.80239756272103 8.06269225921139 P P P 7.60367962605565 8.20650346850386 8.3225891035217
P P P LNCV6_142213_PI430048170 mRNA
GTGGCCACCTGCTGACTATTTGTGGTTTAAAATAAAAGGTTTACTTGTCTGCAGAAAAAA NM_001201362 RefSeq
chr6 - 79201244 79234738 HMGN3 9324 "high mobility group nucleosomal binding domain 3,
transcript variant 3" GO:0046966|GO:0008150|GO:0005737|GO:0031492|GO:0005654|GO:0000785|GO:0016568
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_43655_PI430048170 0.1348604722137071.35375218259713 3.87854519767812 3.82608200404063
4.3623958934998 P P P 3.61759864080805 3.5974662783037 3.60365571780986 P P P
LNCV6_43655_PI430048170 mRNA
TTAACCTGTGTCTTACTTCCTCAGCTGCCTTCTGAACCTACTTGTCAAGAGAATCTGCCT NM_018214RefSeq chr6
+ 53794979 53924121 LRRC1 55227 leucine rich repeat containing 1 GO:0005737|GO:0016020 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130411_PI430048170 0.71773437271658 1.13507881747515 0.341922062361448
0.46887000298206 1.29608683556009 A A A 0.4871434713044420.853613937664291
0.368082265724435A A A LNCV6_130411_PI430048170 mRNA
TATTGTCTGGAGACATAGAATTAGTCCAAACGGTGTCACCTCCAGGAAGCCTTACTGTCA NM_001287807 RefSeq
chr20 - 44461762 44465344 C20orf62 NA chromosome 20 open reading frame 62 NA . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_131402_PI430048170 0.6034683317669390.9636923511150740.542891953280669
0.5138999143665840.275179266392758A A A 0.4090367704419270.581417615238617
0.511063832379988A A A LNCV6_131402_PI430048170 mRNA
CCAGAAAAGATTTTCTCTTGATGGTTTCTTCAACAGGAAACAGATATTGGAATAGTGTAC NM_001195685 RefSeq
chr2 + 149329984 149474145 LYPD6 130574 "LY6/PLAUR domain containing 6, transcript variant 1"
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132411_PI430048170 0.00589200281865401 0.5231126631788018.03339390872961
7.87067911885774 8.30728415738586 P P P 8.90583894858071 8.96499938935771
9.16597397549795 P P P LNCV6_132411_PI430048170 mRNA
GATGGGAATGCTGTATCTGTGGAAGTCATGTTATACTGGATTCATTTCCAATTAAATACT NM_007145RefSeq chr19
+ 36214601 36238773 ZNF146 7705 "zinc finger protein 146, transcript variant 1"
GO:0006355|GO:0005737|GO:0003700|GO:0005730|GO:0008270|GO:0005634|GO:0008201|GO:0003677 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135840_PI430048170 0.0104031878815895 1.6956642577597 10.0971702892066
10.2590290941189 9.94952457382247 P P P 9.38421573222968 9.31086267569216
9.34077213497314 P P P LNCV6_135840_PI430048170 mRNA
GAGCGGCCAGCTTGGCCTTTGCCTTAATAAATGTGCTTTATTTTCTCTTCAGTGAAAAAA NM_001145023 RefSeq
chr17 - 47837680 47841333 SCRN2 90507 "secernin 2, transcript variant 2"
GO:0008150|GO:0003674|GO:0006508|GO:0006887|GO:0016805|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141379_PI430048170 0.6892007242096930.8425338509065740.928192292784707
2.34669295011437 1.02592839646557 A A A 2.47799544516648 1.67203596921711
0.966971315028128P A A LNCV6_141379_PI430048170 mRNA
TCACCATCTCGCAGCAGCTCGGCTTGGAGCTCAACACCGTCAGCAACTTCTTCATGAACG NM_001080488 RefSeq
chr19 + 1753662 1775445 ONECUT3 NA one cut homeobox 3 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127121_PI430048170 0.1174480203245431.30014020443189 9.26054413328015
9.73855796321537 9.52601248790612 P P P 8.9647321283123 9.04203478745445
9.38606976865699 P P P LNCV6_127121_PI430048170 mRNA
CACATGCATATGTGTGTATGTGTGTATATCTTTCCCCCCATCAATTGGTACAATTTTTAANM_001003940 RefSeq chr15
- 40087890 40108874 BMF 90427 "Bcl2 modifying factor, transcript variant 1"
GO:0005515|GO:0032464|GO:0001669|GO:0005886|GO:2001234|GO:0043276|GO:0006915|GO:2001244|GO:0005
741|GO:0016459|GO:0097193|GO:0005829|GO:1900740|GO:0090200 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138135_PI430048170 0.1907349413551392.25266091805924 1.09424845827458
0.8220153185533142.47506477330042 A A A 0.6704154092862290.366986482110429
0.400035266820931A A A LNCV6_138135_PI430048170 mRNA
GAAGTAAAGAAGGCTTTAGCGAATGTAATTAGCAGGAAAAGGACCTCTTCCTTTCTGTGA NM_003697RefSeq chr11
- 55993680 55994625 OR5F1 338674 "olfactory receptor, family 5, subfamily F, member 1"
GO:0050911|GO:0007608|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130686_PI430048170 0.9991347789361781.00842877726747 7.52146512755776
7.06491823033902 7.43160248573315 P P P 7.31730678209652 7.29389002720762
7.40731054160781 P P P LNCV6_130686_PI430048170 mRNA
TTACATTTGAGTCTCTGTACCTGCTTGGAAGAAATAAAAATACGTGTGAATTCCATCTCA NM_007055RefSeq chr10
- 77975148 78029540 POLR3A11128 "polymerase (RNA) III (DNA directed) polypeptide A, 155kDa"
GO:0032728|GO:0010467|GO:0006386|GO:0006385|GO:0003899|GO:0032549|GO:0003677|GO:0006383|GO:0006
351|GO:0005829|GO:0051607|GO:0016020|GO:0001056|GO:0045087|GO:0003682|GO:0005666|GO:0032481|GO:0

005654|GO:0008270. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128374_PI430048170 0.1501373048950430.9638474472744960.268500488136529
0.3068527312656470.332666730922905A A A 0.4005541415960020.325257414531538
0.341203748277069A A A LNCV6_128374_PI430048170 mRNA
ATTACACCTTTGGCCAACCCATTTGTGTATAGCCTCCACAATAAGGATGTCAAGGGTGCA NM_001004450 RefSeq
chr9 - 122628578 122629535 OR1B1 NA "olfactory receptor, family 1, subfamily B, member 1
(gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144804_PI430048170 0.0868082921181111 1.18007756393095 9.44405852790623
9.70030255155124 9.45713271281434 P P P 9.3204758401597 9.36253187730776
9.21241333512443 P P P LNCV6_144804_PI430048170 mRNA
AGATTCAGCAGTGTGTGAGAAGAGCAGCCTTCCTTTGTCCCTGTGGTATTCATAAAGTAC NM_032118RefSeq chr2
+ 74421757 74425755 WDR54 84058 WD repeat domain 54 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_130558_PI430048170 0.9750310870053020.9971553118210775.07067848198088
5.25834071247557 5.20323516080712 P P P 5.06768496187514 5.16849709561379
5.30493365207412 P P P LNCV6_130558_PI430048170 mRNA
AAGCAAGTTTACCCTCAGAGTTATGCTTTTCCAAAGAGGCTGATGTCTTTGTTTTTGTTT NM_015107RefSeq chrX
- 53936679 54044174 PHF8 23133 "PHD finger protein 8, transcript variant 2"
GO:0005515|GO:0032454|GO:0032452|GO:0006325|GO:0005634|GO:0035064|GO:0000082|GO:0045943|GO:0071
557|GO:0061188|GO:0071558|GO:0031965|GO:0035574|GO:0035575|GO:0005506|GO:0005730|GO:0006351|GO:0
051864|GO:0070544|GO:0007420|GO:0003682|GO:0016706|GO:0008270|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145099_PI430048170 0.57434568571122 1.03878977525957 9.90563147021603
9.85681431912013 9.78665693573361 P P P 9.96139494715846 9.72415566444636
9.68558095379989 P P P LNCV6_145099_PI430048170 mRNA
TAACTTGTTTCTTGACGACCACCTCATGTGGCCAATAAATGGACTGGGAGCGTTTTAGCT NM_022450RefSeq chr16
- 58058 72631 RHBDF1 64285 rhomboid 5 homolog 1 (Drosophila)
GO:0004252|GO:0008283|GO:0015031|GO:0042058|GO:0000139|GO:0016477|GO:0019838|GO:0061136|GO:0005
789|GO:0006508|GO:0050709|GO:0050708|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142670_PI430048170 0.3489791335168871.02845677737887 0.297622800559364
0.2866997352193850.39014726042638 A A A 0.29842539339281 0.275893138547035
0.28086553399075 A A A LNCV6_142670_PI430048170 mRNA
CATGAGGACATCTAGCTCAATACAAAATGAAGATGAAGCCACCAGTATGGAGCTGATTGC NM_006514RefSeq chr3
- 38697345 38794010 SCN10A6336 "sodium channel, voltage gated, type X alpha subunit, transcript
variant 1"
GO:0086010|GO:0005248|GO:0019228|GO:0019233|GO:0086067|GO:0060371|GO:0086069|GO:0002027|GO:0044
299|GO:0055117|GO:0001518|GO:0034765|GO:0035725|GO:0006814|GO:0007600|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128075_PI430048170 0.2020680658977820.5022238137503130.309989836722764
0.2945616529320690.341923428286224A A A 0.29897518495499 1.3742279566325
1.85267267008226 A A A LNCV6_128075_PI430048170 mRNA
AGGAATCTCCCTATCCCTGGAGAGTCCAGGAATCTATATTAAAACATGAAACAAAGCAAA NM_015279RefSeq chr12
+ 64824571 64881018 TBC1D30 23329 "TBC1 domain family, member 30"
GO:0017137|GO:0005886|GO:0033126|GO:0032851|GO:0072372|GO:0036064|GO:0005097 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135435_PI430048170 0.4537830621957210.9062243429382036.21107895813256
6.06159613743364 6.18630754359843 P P P 6.36397976677714 6.01177053097293
6.47443923409472 P P P LNCV6_135435_PI430048170 mRNA
AATGCTGCCCAATCTTCACCAGCTTCAGAAATCTGACCTTTGCCGATGCTGCAATAAAGT NM_080599RefSeq chr10

- 11920021 12043170 UPF2 26019 "UPF2 regulator of nonsense transcripts homolog (yeast), transcript variant 1"
GO:0005515|GO:0001889|GO:0010467|GO:0048471|GO:0005737|GO:0006406|GO:0000184|GO:0003723|GO:0031100|GO:0005634|GO:0035145|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137028_PI430048170 0.8046356398699921.08824365035661 2.37246930846093
0.4491755479128150.262112369387486A A A 0.9334634878319 1.56733077967867
1.16446417757392 A A A LNCV6_137028_PI430048170 mRNA
CAGTGCCAACAACATCTCATGAAATTTAAAATAAATCCCCAAGGCATCAGAAACGTAAAA NM_032296RefSeq chr16
+ 2911978 2951208 FLYWCH1 84256 "FLYWCH-type zinc finger 1, transcript variant 1"
GO:0005737|GO:0005654|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107353_PI430048170 0.7145844153257021.08286366679833 5.47834849731082
4.88592710475855 4.84836613246106 P P P 5.08063350453805 5.11483014845464
4.73261427244982 P P P LNCV6_107353_PI430048170 mRNA
TGCCTGCTTCTCCTCAGAGGAGCATGAGACCCATTTCCAGAACCCTGGGAACACGAGACT NM_018354RefSeq chr20
- 1180560 1184473 TMEM74B 55321 "transmembrane protein 74B, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133330_PI430048170 0.5960987419190580.8803841676537530.912837741499674
0.3579850953030371.75727149958949 A A A 1.62276874128794 0.903631556093316
1.31254126528177 A A A LNCV6_133330_PI430048170 mRNA
GGATCTTGTAAACAGGGCATATATCAAAGATGACCTTATAATATGTACCCGAATATACAG NM_006255RefSeq chr14
+ 61321442 61550980 PRKCH 5583 "protein kinase C, eta"
GO:0004699|GO:2000810|GO:0005886|GO:0010744|GO:0030168|GO:0060252|GO:0050861|GO:0005524|GO:0070528|GO:0046872|GO:0005829|GO:0007165|GO:0005737|GO:0051092|GO:0045618|GO:0005911|GO:0007596|GO:0034351|GO:0006468|GO:0004697|GO:0019899|GO:0017160|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128511_PI430048170 0.8820135502612830.9952547865727770.264809321255461
0.2831878354973870.414304063124057A A A 0.3630123579138980.314613470429486
0.309305449802507A A A LNCV6_128511_PI430048170 mRNA
CTTTTGACAGCTTCATTTTATTTTTGACGTCACTTTTTGGCCATGTAAACTATTTGTGGC NM_021020RefSeq chr8 -
20246164 20255292 LZTS1 11178 "leucine zipper, putative tumor suppressor 1"
GO:0005515|GO:0006355|GO:0003700|GO:0030054|GO:0016242|GO:0014069|GO:0003677|GO:0044297|GO:0006351|GO:0048814|GO:0005737|GO:0007049|GO:0016324|GO:0043197|GO:0043198|GO:0045211 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54035_PI430048170 0.4513076972009340.8966110289164974.68151307757755 4.69829590893117
4.9929880957804 P P P 4.70888633769311 4.9037261025668 5.20965344445853 P P P
LNCV6_54035_PI430048170 mRNA
CTGCTCTTATTAGTTAAACACAGTTGTGTGGAATCACTGTTCCTGGTTAGAAATTTCTGC NM_018087RefSeq chr1
- 53765460 53838552 NDC1 55706 "NDC1 transmembrane nucleoporin, transcript variant 1"
GO:0007129|GO:0031965|GO:0005737|GO:0016020|GO:0005643|GO:0031081|GO:0017056|GO:0051028|GO:0007283|GO:0051292|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138446_PI430048170 0.0730851418201038 0.6178606184075455.98172325387305
5.95454274829062 6.10231228677341 P P P 6.29212907653768 6.79189097812553
6.96202854706636 P P P LNCV6_138446_PI430048170 mRNA
CACCAAATTCATGTACAGCATGCATCACGGATCAATAGACTGTACTTATTTTCCAATAAA NM_000877RefSeq chr2
+ 102142775 102179874 IL1R1 3554 "interleukin 1 receptor, type I, transcript variant 1"
GO:0005515|GO:0005886|GO:0009986|GO:0050727|GO:0005576|GO:0002020|GO:0005161|GO:0004909|GO:0006955|GO:0016020|GO:0005887|GO:0004908|GO:0004871|GO:0070555|GO:0070498|GO:0007166|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137741_PI430048170 0.1780970536091191.34401368428474 4.30097859150246

4.44820431710518 4.2737985824901 P P P 4.27203974162658 3.89407076310533
3.47421528471971 P P P LNCV6_137741_PI430048170 mRNA
TTCTATGGTAGTACCTACAGATCTGCCCTTCTTCTTCTAAAGGGTAAGTCATAATCTGTG NM_007351 RefSeq chr4
+ 89894900 89954629 MMRN1 22915 multimerin 1
GO:0007596|GO:0002576|GO:0030168|GO:0031093|GO:0005576|GO:0007155 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129745_PI430048170 0.1842217047750671.08499133881408 0.554483418536506
0.38769560170151 0.551144704020406 A A A 0.2934876726652540.390739396688778
0.457564175206479 A A A LNCV6_129745_PI430048170 mRNA
CCACAATTGCAGGAAAACAATGTAGTTCTGAGTCTAATAGTGATAAAGAATGCAGTTTGA NM_025235 RefSeq chr10
+ 91798393 91865475 TNKS2 80351 "tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase
2"
GO:0000209|GO:0005515|GO:0048471|GO:0090263|GO:0005634|GO:0005635|GO:0046872|GO:0003950|GO:0005
829|GO:0070213|GO:0006471|GO:0032212|GO:0005737|GO:0035264|GO:0000139|GO:0040014|GO:0016055|GO:0
019899|GO:0070198|GO:0000242|GO:0000784 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95279_PI430048170 0.6022936969753550.9643255540123430.2817471945831130.468543697737217
0.313489502500996 A A A 0.5198957835703220.4192422321281340.278753642599587 A A A
LNCV6_95279_PI430048170 mRNA
AACAGGTCAAGACATGAAAATACAAGCCAGGTACCATTGCAGGAGTCCAGGACAAGAAAG NM_002016 RefSeq
chr1 - 152302174 152325203 FLG 2312 filaggrin
GO:0005882|GO:0005515|GO:0030216|GO:0005198|GO:0005509|GO:0061436|GO:0016023|GO:0007275|GO:0005
634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118714_PI430048170 0.7206754213405451.22859442956896 0.312559213280313
0.261192170913555 1.55093857797807 A A A 0.6224067324817010.255162241717754
0.712205873634096 A A A LNCV6_118714_PI430048170 mRNA
AATTAGTAGTGAGAAGGAACTTAAGAATTTAACAGAATTAGAAGATGAACATTTGGCAAA NM_002533 RefSeq chr1
- 224227333 224330189 NVL 4931 "nuclear VCP-like, transcript variant 1"
GO:0005739|GO:0005737|GO:0016020|GO:0005886|GO:0005730|GO:0005634|GO:0005524 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142232_PI430048170 0.00932584065728966 0.5717202888699287.16071669667475
6.75577517664758 7.01390112445427 P P P 7.62097476667397 7.70016016889471
8.02530265236487 P P P LNCV6_142232_PI430048170 mRNA
CAGGGTAATTGCCACTTTACTTGTGCAATACTGCTGTAAATAACTGCAGATTTTTAAACA NM_001204108 RefSeq
chr2 + 111120913 111168445 BCL2L11 10018 "BCL2-like 11 (apoptosis facilitator), transcript variant
13"
GO:0008017|GO:0005515|GO:0034976|GO:0030879|GO:0048538|GO:0007283|GO:0048536|GO:0097141|GO:0097
140|GO:0043525|GO:1900740|GO:0043029|GO:0002262|GO:0048066|GO:0032464|GO:0070242|GO:2001244|GO:0
060139|GO:0001701|GO:0045787|GO:0043280|GO:0048070|GO:0007420|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131070_PI430048170 0.1284538672599790.7254031963069139.01961704317194
8.59997245747727 8.31451187243611 P P P 9.18476114568848 9.21805096732449
8.99930661655518 P P P LNCV6_131070_PI430048170 mRNA
CCCACTTTTCAGTGCCTCCCCTGCTCATCTCCAATAAAATAAAAGCACTTATGGAAAAAA NM_014070 RefSeq
chr6_GL000255v2_alt - 2369221 2370554 C6orf15 29113 chromosome 6 open reading frame 15
GO:0008150|GO:0003674|GO:0005540|GO:0030198|GO:0043236|GO:0005575|GO:0005614|GO:0001968|GO:0008
201|GO:0070052 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133878_PI430048170 0.42202080962857 0.5994128418309320.310957303049324
1.13249447893732 0.826211793740693 A A A 2.22897026169244 0.299073822271431
1.46816665204306 A A A LNCV6_133878_PI430048170 mRNA

AAGCAGTAAAAGTAAATGAATCCCACCTTTACTAAAACACTTTCTCTGAACCCCCCTTGC NM_005386 RefSeq chr20 + 37521204 37523688 NNAT 4826 "neuronatin, transcript variant 1" GO:0009249|GO:0007420|GO:0030182|GO:0006810 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_141959_PI430048170 0.00604471629895503 0.44456734007832 3.42605057128435 3.19623318216819 3.76504368680373 P P P 4.42397363661782 4.69983550932758 4.80324314092794 P P P LNCV6_141959_PI430048170 mRNA
TCGGGTGGGGAGAAAAAGCCCTAAATCAGAATGTTTATATTTGCCTAAAGATGTCCTTAA NM_018287 RefSeq chr10 - 31805397 31928876 ARHGAP12 94134 "Rho GTPase activating protein 12, transcript variant 1" GO:0043547|GO:0051056|GO:0007264|GO:0002011|GO:0005829|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108475_PI430048170 0.4216933134711110.94937546153882 0.324337306461576 0.5240238790507890.392775165380417 A A A 0.5006723915986440.379494170832537 0.585598909444573 A A A LNCV6_108475_PI430048170 mRNA
CCCTGAAGGTCGTGCCGGAAGGAATCAGAATGAACAAAACTGTGGCTGTTCGCACCCTGGNM_000064 RefSeq chr19 - 6677834 6720682 C3 718 complement component 3 GO:0005515|GO:0030449|GO:0005886|GO:0004866|GO:0072562|GO:0001970|GO:0005615|GO:0006957|GO:0006956|GO:0006955|GO:0006954|GO:0006958|GO:0006631|GO:0001798|GO:0070062|GO:0045745|GO:2000427|GO:0005102|GO:0005576|GO:0010884|GO:0010866|GO:0010575|GO:0031715|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142684_PI430048170 0.0341429447501158 1.85340617057875 1.5946950409469 1.70455617440301 1.75504002793169 A A A 0.43319075426404 1.08971643686354 0.791407489843473 A A A LNCV6_142684_PI430048170 mRNA
GGTGCCTAAAAACTCAAGAACCATTGATAAGTGAGATCACTCAAAATGAGCTGATATATT NM_024592 RefSeq chr4 + 55346220 55373099 SRD5A3 79644 steroid 5 alpha-reductase 3 GO:0003865|GO:0005783|GO:0006702|GO:0019348|GO:0016095|GO:0044281|GO:0016628|GO:0047751|GO:0005789|GO:0016021|GO:0006488|GO:0044267|GO:0006489|GO:0008202|GO:0055114|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138582_PI430048170 0.4140321199940741.50784196235683 1.9734299247324 0.3569613123888431.33878294020966 A A A 0.3195855271446961.37950008553971 0.357826236053296 A A A LNCV6_138582_PI430048170 mRNA
TTTCTTGCCTCCAGTTGGTTCAGAAAATGACTGAGGCCTGGAGAATAATAGACCTGTGCT NM_001101330 RefSeq chr2 - 43675152 43676322 C1GALT1C1L NA hCG1645220 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106745_PI430048170 0.0190155703474640.6080818788522923.44549656348417 2.97642058470523 3.28787268445481 P A P 3.89030270783762 3.90178066800927 4.0996864072706 P P P LNCV6_106745_PI430048170 mRNA
ATCTAACTAGAAGGGATACCCTTCCATTTCAAAGAACAGAATGCTAAGGAAGCTGTGGCA NM_001204180 RefSeq chr8 - 123226188 123274487 ZHX1-C8orf76 NA ZHX1-C8orf76 readthrough NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94340_PI430048170 0.8186763612904350.9716070914130984.94473626434935 4.44195261560214 5.26003782896325 P P P 4.70713840816619 4.98211065653089 5.16112516299175 P P P LNCV6_94340_PI430048170 mRNA
AGAGATTATTCATGATCGAATCAAGAGGGAATATGGACTGGAGACCTATCTCGGGCCTCT NM_001281302 RefSeq chr5 - 74721203 74767371 GFM2 84340 "G elongation factor, mitochondrial 2, transcript variant 4" GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0005759|GO:0003924|GO:0032790|GO:0005525|GO:0003746 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67423_PI430048170 0.00512038977664529 1.78700285902089 6.73748374421639 7.06457356482206 7.02859880287011 P P P 6.31375804580257 5.94536759295397 6.05552666056771 P P P LNCV6_67423_PI430048170 mRNA

TATCTTGAAAACAATCTTCCAGTAGTTCTGACGATACTTGGAGCCTGGTCCACGTGCATC NM_001145526 RefSeq chr17 + 78187316 78207701 AFMID 125061 "arylformamidase, transcript variant 1" GO:0034641|GO:0006569|GO:0019441|GO:0004061|GO:0005634|GO:0044281|GO:0034354|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145454_PI430048170 0.0114499124240264 0.306153637680876 0.258621392118227 0.328679876608573 0.276528407559762 A A A 2.03559523148329 1.61953281935277 2.26106734334701 A A A LNCV6_145454_PI430048170 mRNA
CTACTTTGGTTTTGTTGTTGTTTTGATTTGTTTTTGGCTAAGTAGAGGACATGGACTAGT NM_001291867 RefSeq chrX + 17375419 17735993 NHS 4810 "Nance-Horan syndrome (congenital cataracts and dental anomalies), transcript variant 3" GO:0016324|GO:0005737|GO:0002088|GO:0005923|GO:0005925|GO:0030154|GO:0030027 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135870_PI430048170 0.747638254424079 0.98801885963491 0.370806699533887 0.464354429275212 0.351378587076655 A A A 0.484797571872667 0.370409266749107 0.383306157378611 A A A LNCV6_135870_PI430048170 mRNA
CACAGACTTAGTGTTTGAAAACTGTGTTTTAAAAACAGAAACAGATTGATGGGTAACAGG NM_144777 RefSeq chr13 + 77535673 77645263 SCEL 8796 "sciellin, transcript variant 1" GO:0005515|GO:0005737|GO:0008544|GO:0030216|GO:0008270|GO:0009790|GO:0001533|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139636_PI430048170 0.0100217010293818 0.688995470265578 8.40973431326672 8.19096870900993 8.12217701782238 P P P 8.78644890499804 8.87120697059254 8.68753303855985 P P P LNCV6_139636_PI430048170 mRNA
TCCTGCTGCCTTCCCACCCCCGTTCTTGGGTATGTTCAATAAAAGGATTGTTTTCCTAGA NM_003577 RefSeq chr10 + 133230273 133231558 UTF1 8433 undifferentiated embryonic cell transcription factor 1 GO:0005515|GO:0006357|GO:0045944|GO:0003713|GO:0071837|GO:0005634|GO:0008584|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143359_PI430048170 0.538503703529277 1.01216539431787 0.353708127905268 0.351947284720746 0.41478789144507 A A A 0.364390893420842 0.32706804111245 0.377073760754831 A A A LNCV6_143359_PI430048170 mRNA
CCCACAAATCTATTGTATTAGTTGCCTTCTATAACAATAAATCTTCACTGAGCAAAAGGC NM_001546 RefSeq chr6 + 19837369 19842200 ID4 3400 "inhibitor of DNA binding 4, dominant negative helix-loop-helix protein" GO:0005515|GO:0008284|GO:0022010|GO:0045599|GO:0005634|GO:0007405|GO:0005737|GO:0000082|GO:0045944|GO:0001085|GO:0046983|GO:0045444|GO:0021895|GO:0006357|GO:0003714|GO:0000122|GO:0006351|GO:0045669|GO:0048712|GO:0021766|GO:0045665|GO:0048715|GO:0007623|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98551_PI430048170 0.0569038389443294 0.732535915248495 6.78959774159056 6.39997113466033 6.8220929018824 P P P 6.95529028828549 7.19967201769459 7.22566729048754 P P P LNCV6_98551_PI430048170 mRNA
TCTCACACCACATTTCCTCAAAGCTAATCTGAATTCTGTAGGCTAAAAATATTCATGTAG NM_004798 RefSeq chr20 + 32277650 32335008 KIF3B 9371 kinesin family member 3B GO:0005515|GO:0008017|GO:0007368|GO:0007100|GO:0016939|GO:0072383|GO:0005829|GO:0019886|GO:0008574|GO:0015630|GO:0061024|GO:0005876|GO:0090307|GO:0007052|GO:0016887|GO:0070062|GO:0007018|GO:0005813|GO:0006996|GO:0005873|GO:0032467|GO:0030496|GO:0072372|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133794_PI430048170 0.740869756487725 1.09197048233334 0.402507902895952 0.405010448561873 1.11877632622608 A A A 0.819058417230534 0.422499264598338 0.38656210839266 A A A LNCV6_133794_PI430048170 mRNA
CCTATTCCTGAAAATATGATGGTTAGCAAAGTTTGAGATAACTAGAGCCTGTAATCCATC NM_001007033 RefSeq

chr12 + 8455994 8478330 CLEC6A NA "C-type lectin domain family 6, member A" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127518_PI430048170 0.0029989170223218 0.3675615620914966.52235654089996 6.85678499037131 6.84616411293326 P P P 7.94315082222422 8.095682632313 8.48694493699801 P P P LNCV6_127518_PI430048170 mRNA
AGCCAGGGTTTTTTCCCCTAATTTGTATCATTGCTATATGTGTTATTGTACCAAACTACANM_020696RefSeq chr3 - 44748743 44761681 KIAA1143 57456 KIAA1143 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130405_PI430048170 0.52937381332889 1.10003644234586 11.6235078159129 11.6398595031704 11.8944848972863 P P P 11.1569062902342 11.7007929791118 11.8209715752583 P P P LNCV6_130405_PI430048170 mRNA
GGATTTGCTTGGGATACAGAAGAGGCCATGTGTCTCAGAGCTGTTAAGGGCTTATTTTTT NM_198433RefSeq chr20 - 56369388 56392295 AURKA 6790 "aurora kinase A, transcript variant 1"
GO:0005515|GO:0072686|GO:0072687|GO:0051642|GO:0046777|GO:0071539|GO:0031625|GO:0000780|GO:0005813|GO:0032465|GO:0019901|GO:0005819|GO:1900195|GO:0030496|GO:0045840|GO:0046605|GO:0035174|GO:0045120|GO:0000278|GO:0051301|GO:0032091|GO:0043146|GO:0048471|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128267_PI430048170 0.0203837467938204 0.6991554935769778.97155988715874 8.8898533519294 8.66953133461803 P P P 9.16168529292556 9.50940402502799 9.40377767052414 P P P LNCV6_128267_PI430048170 mRNA
TGCAGAGACAGGAAGCTGGAGATGTCTTTATAAAGTCACACCTTTACAGACTGTAAAAAA NM_022092RefSeq chr16 + 788621 798074 CHTF18 63922 "CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)"
GO:0006260|GO:0005737|GO:0016020|GO:0051985|GO:0005654|GO:0007283|GO:0005524|GO:0003677|GO:0007140|GO:0007131 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140968_PI430048170 0.9446861561511651.00576668264105 0.271795864542339 0.2803564911058460.475347104402517A A A 0.3412271132489040.34737563316594 0.323223168996612A A A LNCV6_140968_PI430048170 mRNA
AGCCATACTTCTGAGGGAAGACTGGCTGGCAATAAAGTCAAATTAAGTGACCACAAAAAANM_033438RefSeq chr1 - 159951491 159954254 SLAMF989886 "SLAM family member 9, transcript variant 1"
GO:0004872|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138527_PI430048170 0.3146379019954531.05278760764429 0.605377225690119 0.4448325980326290.596435398485701A A A 0.4204114356304420.537930166779458 0.468810064261227A A A LNCV6_138527_PI430048170 mRNA
AAGGAGCTTCCTTTTAAATTTTGTCTGTAGGAAATGGTTGAAAACTGAAGGTAGATGGTG NM_021146RefSeq chr1 + 11189288 11195981 ANGPTL7 10218 angiopoietin-like 7 GO:0005576|GO:0006979 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_11560_PI430048170 0.767639809255493 1.10744706107493 1.81043055861636 1.99362871643964 1.04777381663921 A A A 1.73539985352231 1.3582065347088 1.45235329603467 A A A LNCV6_11560_PI430048170 mRNA
ACAACTAGAGAAAGAAGAATGCATGCAATGTGTTCCCTGTAGTCCAAGAACCAGGGTAGCNM_001301317 RefSeq chr1 + 151540308 151583577 TUFT1 7286 "tuftelin 1, transcript variant 3"
GO:0030345|GO:0005737|GO:0042476|GO:0005576|GO:0030282 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118510_PI430048170 0.1997765400541290.7903275866827138.52911373815078 8.2411052729554 8.07023555030277 P P P 8.9210766516424 8.57196849447137 8.34445918216123 P P P LNCV6_118510_PI430048170 mRNA
AGCCAGTGACCCAGCCCCACCAATGGGCCTCCAGAGACCCCAGGAACAATAAAATGTCTTNM_002963RefSeq chr1 - 153457743 153460661 S100A7 6278 S100 calcium binding protein A7
GO:0005515|GO:0051238|GO:0005783|GO:0005509|GO:0010820|GO:0005576|GO:0005634|GO:0001525|GO:0071

624|GO:0005829|GO:0050829|GO:0005737|GO:0050786|GO:0008544|GO:0030216|GO:0045087|GO:0032496|GO:0
008270|GO:0090026|GO:0070374|GO:0000302|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_55449_PI430048170 0.3696802408963391.19169654332511 7.32884065198275 7.98357291235384
7.53886041643835 P P P 7.63460367432053 7.25705148895627 7.24466653541353 P P P
LNCV6_55449_PI430048170 mRNA
TGACGTGGATTTTAATGAATTTGGACTCCATGTGGATTTGGTCGTCTCCCTGATTCCGAG NM_025179RefSeq chr1
- 208022242 208244320 PLXNA25362 plexin A2
GO:0005515|GO:0030334|GO:0021935|GO:0005886|GO:0001756|GO:0060037|GO:0002116|GO:0005622|GO:0051
642|GO:0017154|GO:0005887|GO:0007411|GO:0071526|GO:0021915|GO:0060174 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144166_PI430048170 0.3783793252510521.03226844936661 0.379404707929438
0.2434592819323660.29075355361949 A A A 0.26123095223715 0.256138802042058
0.262101832947219A A A LNCV6_144166_PI430048170 mRNA
TACCCTGAGGACACGATATCAGAGGTCATAAGAAGATCATTCAATTTAACCAAATATTGA NM_181610RefSeq chr21
- 30496855 30497110 KRTAP19-4 NA keratin associated protein 19-4 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127522_PI430048170 0.4305133716254610.96951282313379 0.416167047867878
0.4392555691613470.291329824683228A A A 0.4010427845035820.462399640945217
0.420980326901128A A A LNCV6_127522_PI430048170 mRNA
GTAAATCAACAACCTGCATAATAAATAAAAGGCAATCATGTTATAGGAGAAAGGCTGGCA NM_152321RefSeq chr12
- 14914026 14938549 ERP27 121506 "endoplasmic reticulum protein 27, transcript variant 1"
GO:0034976|GO:0009986|GO:0006457|GO:0005783|GO:0005788|GO:0003756 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137095_PI430048170 0.0782061768020808 0.6638283136957984.17061999928987
4.39646378688386 3.91398098140543 P P P 5.0929492760801 4.69417705578873 4.4292712606134
P P P LNCV6_137095_PI430048170 mRNA
ATCCTACTTCTCCTGCTGCTGCATAAAGAATCTCAACCTTCATTTTATTTGAACACGGAC NM_152432RefSeq chr11
+ 100687675 100990925 ARHGAP42 143872 Rho GTPase activating protein 42
GO:0043547|GO:0005622|GO:0007165|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143782_PI430048170 0.6321588535695450.8820985732740698.67026386532024
8.84223676730753 9.08619179050037 P P P 8.54668813460051 9.09073895150079
9.40755393765985 P P P LNCV6_143782_PI430048170 mRNA
CAGCCTTAAGTATTTACATGCTCCCAGGTCATTGTCAGTTTATGGTATTATGTTGTTTTA NM_005792RefSeq chr16 -
82148161 82170224 MPHOSPH6 10200 M-phase phosphoprotein 6
GO:0005515|GO:0005737|GO:0000460|GO:0003723|GO:0000176|GO:0005730|GO:0005634|GO:0000178 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139283_PI430048170 0.0281669297431726 0.4087284738580273.12510974152074
2.10252550033325 2.44371347944172 A A A 3.67473802279014 3.61647505431987
4.33115724752392 P P P LNCV6_139283_PI430048170 mRNA
AAAGAACTCATACTCTATGTGTCCCCTATAAATTTTAGGAATGTTAGGGAGCCAATGGAA NM_001008727 RefSeq
chr19 - 9565727 9584533 ZNF121 7675 zinc finger protein 121
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129907_PI430048170 0.1502246076576671.05289581891685 0.441416194739768
0.4472472459378260.472074052921088A A A 0.3218043640550020.374159594243669
0.439457894081475A A A LNCV6_129907_PI430048170 mRNA
TGCTGACAACTTCCAGAGAAGCCATGGTTTTTTGTATTGGTCATAACTCAGCCCTTTGGG NM_001558RefSeq chr11
+ 117986390 118001483 IL10RA 3587 "interleukin 10 receptor, alpha, transcript variant 1"

GO:0019969|GO:0005515|GO:0004920|GO:0005886|GO:0019221|GO:0032496|GO:0004872|GO:0016021|GO:0004871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140603_PI430048170 0.0073221262252479 0.2918009964681035.2337478041179 4.68515366344326 5.46849491067251 P P P 6.86300217432518 6.79793017712422 7.1413673907597 P P P LNCV6_140603_PI430048170 mRNA
TAAGAAATCATTCAGATCATCCCCCCTTTTTAAGTAGTGTGAATTGCAAAACCCAACATA NM_013437RefSeq chr8 - 104489230 104589024 LRP12 29967 "low density lipoprotein receptor-related protein 12, transcript variant 1"
GO:0005515|GO:0005041|GO:0007165|GO:0005905|GO:0005887|GO:0016021|GO:0040008|GO:0006898|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59253_PI430048170 0.4767985909295791.07108311074853 6.71254772649384 6.81127897095727 7.05810738635536 P P P 6.67253717007642 6.77822272812952 6.85069859360406 P P P LNCV6_59253_PI430048170 mRNA
AGAGACCTTAAGTGCTAAACTTAGTGGAGTTTGTGACCAGAGAATTGGCATTTTCTACAA NM_014999RefSeq chr12 + 71754877 71787370 RAB21 23011 "RAB21, member RAS oncogene family"
GO:0005515|GO:0005802|GO:0012506|GO:2000643|GO:0003924|GO:0005525|GO:0032154|GO:0006886|GO:0030100|GO:0032580|GO:0048260|GO:0008152|GO:0017157|GO:0005789|GO:0009898|GO:0032482|GO:0019003|GO:0005925|GO:0030659|GO:0005769|GO:0070062|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107156_PI430048170 0.0102375141839877 0.7878201923637015.79053556521331 5.75683431613825 5.94282205201119 P P P 6.08993208474957 6.21598359057892 6.21960190937353 P P P LNCV6_107156_PI430048170 mRNA
TAGACATCAAGCCCTACATAGCTGAGTATGACTCACCGCAAAATGTGATGGAGCCTTTAG NM_016481RefSeq chr9 - 97904488 97922570 C9orf156 51531 chromosome 9 open reading frame 156
GO:0016787|GO:0008152|GO:0016032 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139572_PI430048170 0.8018396424346840.9915207208456880.403508969504547 0.3744578790791730.250199855805306A A A 0.3329374864629270.375554676949649 0.360758400141767A A A LNCV6_139572_PI430048170 mRNA
CCATACTCTATAATAGTTACATTGAGTGCCACATAATGCTGATACTTGTCTAATGTTGAG NM_000769RefSeq chr10 + 94762680 94853206 CYP2C19 1557 "cytochrome P450, family 2, subfamily C, polypeptide 19"
GO:0019369|GO:0018676|GO:0006805|GO:0017144|GO:0018675|GO:0044281|GO:0043231|GO:0004497|GO:0005737|GO:0016712|GO:0008202|GO:0046483|GO:0008392|GO:0005506|GO:0008395|GO:0019373|GO:0016098|GO:0052741|GO:0019825|GO:0042738|GO:0097267|GO:0016491|GO:0005789|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113139_PI430048170 0.1194607940231330.8187830536930050.433050151721344 0.3957373622843160.397972315742222A A A 0.7851719210246970.809198469726099 0.474497479249831A A A LNCV6_113139_PI430048170 mRNA
TGTAGGTTTCTAGAGATGGAATTCACGTCAGAAAATTCCAACTTCTGTTATCCCTGCCCC NM_001101387 RefSeq chr17 - 10822474 10838101 PIRT NA phosphoinositide-interacting regulator of transient receptor potential channels NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133508_PI430048170 0.2659105756503981.03744417846751 0.450823615113478 0.3577057619113980.405428237299688A A A 0.2999316258457020.347310210688486 0.407114684550822A A A LNCV6_133508_PI430048170 mRNA
ACTGGACAAATACACTGAACTTTGATGAGTACATTGCCAGCTGGAAGGAAATTGCTACAA NM_152587RefSeq chr11 - 108382999 108467531 C11orf65 160140 chromosome 11 open reading frame 65 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140586_PI430048170 0.4418506142772190.9740844299612570.397955527236681 0.4171711094569950.288371950499028A A A 0.3864350060144210.435756057594828 0.397805151910226A A A LNCV6_140586_PI430048170 mRNA

CTCATTCTCAAAGCTCGTAACATCCACCTGGCCAATCTTAAGATGTGGATAGAGTTCTTT NM_172250 RefSeq chr4 + 145619387 145660035 MMAA 166785 methylmalonic aciduria (cobalamin deficiency) cblA type GO:0009236|GO:0009235|GO:0006635|GO:0016787|GO:0006766|GO:0005759|GO:0019626|GO:0006767|GO:0044281|GO:0005525|GO:0044255 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_142694_PI430048170 0.0224257991379966 0.6400120447682656.59085415766922 6.1741719229103 6.45016404984001 P P P 7.03750357637068 6.98981465818264 7.14554448882627 P P P LNCV6_142694_PI430048170 mRNA
CTCGTTCAAACAAATTATGACCACACACACTGAAGAGTATGTTTGTCTCTTGTGGTGTAA NM_032828 RefSeq chr19 + 57849812 57865123 ZNF587 84914 "zinc finger protein 587, transcript variant 1" GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109276_PI430048170 0.0807074419884541 1.05322640816885 0.449718070736242 0.5173709457376040.491716899489223 A A A 0.3664874705980180.415092140318759 0.452304617390473 A A A LNCV6_109276_PI430048170 mRNA
ACATATTGTTCACTGTTGTAACCACCTTGCAGGATTTCAGTCTATAAACTAGGTGAGAAT NM_007190 RefSeq chr10 + 119892572 119944658 SEC23IP 11196 "SEC23 interacting protein, transcript variant 1" GO:0007338|GO:0012507|GO:0005801|GO:0001675|GO:0005793|GO:0005737|GO:0007030|GO:0097038|GO:0070971|GO:0006886|GO:0046872|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134417_PI430048170 0.9236626870852690.99595672181627414.8407157286467 14.933810966719 15.0474544066442 P P P 14.9202514239861 14.9003120302304 15.0233517439809 P P P LNCV6_134417_PI430048170 mRNA
GTGGTGACTTGCGGATTTATGTTTCAGTGTACTGGAAACTTTCCATTTTATTCAAGAAAT NM_001826 RefSeq chr1 + 154974641 154979249 CKS1B 1163 "CDC28 protein kinase regulatory subunit 1B, transcript variant 1" GO:0005515|GO:0000082|GO:0008283|GO:0016538|GO:0005654|GO:0000079|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70150_PI430048170 0.2061593674381530.8243660691262024.04265221618271 3.56538636126134 3.57592601121343 P P P 3.86353180942245 3.99242387671032 4.19734121337286 P P P LNCV6_70150_PI430048170 mRNA
CAGCAGAAATTAAGATTAGAAACTGACTGCTTCAGGGCTCAGCTGGAAGAAGAAAAAAGA NM_033395 RefSeq chr11 + 93661649 93730356 CEP295 85459 centrosomal protein 295kDa GO:0005813|GO:0005737|GO:0005814|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135300_PI430048170 0.3347300378231180.9259467472691987.46342192330023 7.31075515083811 7.14877788543037 P P P 7.37191832999513 7.39751648750783 7.50041182795899 P P P LNCV6_135300_PI430048170 mRNA
ACAGTTGTATCTAACCGCATGTGCTGTTGTGCCTAATGCTCTATAAAGCATGTTAAACAG NM_001105537 RefSeq chr2 - 218637915 218659540 ZNF142 7701 "zinc finger protein 142, transcript variant 1" GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0005575|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138269_PI430048170 0.7883522078350230.9738343763315767.9773288712513 8.18462371693399 8.20790683874136 P P P 7.96342701597589 8.23692577642842 8.27561890807572 P P P LNCV6_138269_PI430048170 mRNA
CACACCGTTATGCATTACTCTGTGTCTACTATTATGTGTGCATAATTTATACCGTAAATG NM_005931 RefSeq chr6_GL000254v2_alt + 2840010 2853071 MICB 4277 "MHC class I polypeptide-related sequence B, transcript variant 1" GO:0030881|GO:0050689|GO:0005886|GO:0009408|GO:0009986|GO:0002429|GO:0046703|GO:0042267|GO:0046629|GO:0003823|GO:0001913|GO:0019882|GO:0050776|GO:0019835|GO:0016032|GO:0016021|GO:0032526|GO:0006979 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131740_PI430048170 0.0327239639383925 2.1988393879728 1.68232001696771 2.34974001066989 2.21482338978012 A A A 1.00530691923248 1.35815926313811

0.398426990961416 A A A LNCV6_131740_PI430048170 mRNA
AGCAGACTATACCTCTTCTGTCCGCTGACTTGCCCAATAAATAATTCTGCAGAGAAAAAA NM_001256613 RefSeq
chr3 + 184097063 184106995 HTR3E 285242 "5-hydroxytryptamine (serotonin) receptor 3E, ionotropic,
transcript variant 4" GO:0005230|GO:0034220|GO:0005886|GO:0016021|GO:0055085 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_88928_PI430048170 0.0696072478060192 2.19109261625229 3.13198492018392
2.47699069691379 3.67416928843823 P A P 2.38648076232116 1.76725498285036
1.90111667641469 A A A LNCV6_88928_PI430048170 mRNA
ATTTTGTTGTCCTGGGCGAGTATGACCGATCATCAAACGCAGAGCCCTTGCAGGTTCTGT NM_001907 RefSeq chr16
- 67929569 67931875 CTRL 1506 chymotrypsin-like
GO:0004252|GO:0007586|GO:0006508|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139968_PI430048170 0.000851542978298408 0.282027730278596 7.26398790370411
7.01087127217301 7.53261320406886 P P P 8.86221683306002 9.15111258847814
9.28747764358876 P P P LNCV6_139968_PI430048170 mRNA
GGCCATGGGAACTCTGTTTATGCCCTGTTTTAATGTTTCTGTTTTATGTTTTACTGTTAA NM_018124 RefSeq chr16 -
74621398 74666881 RFWD3 55159 ring finger and WD repeat domain 3
GO:0005515|GO:0004842|GO:0016567|GO:0016874|GO:2000001|GO:0035861|GO:0005634|GO:0002039|GO:0005
737|GO:0006281|GO:0010212|GO:0016605|GO:0008270|GO:0031571 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133517_PI430048170 0.138337165633495 1.44030699196867 12.4791530318775
13.1639078160911 13.0600533806966 P P P 12.370329730649 12.3403789961139
12.4980863639174 P P P LNCV6_133517_PI430048170 mRNA
GAAAAGCCTACAAACTCATTGATATAAAAGCTTAACAAAGGTACTCCCCGCCCCCCGCCC NM_006355 RefSeq chr6
+ 25962688 25987329 TRIM38 10475 tripartite motif containing 38
GO:0050687|GO:0016874|GO:0019221|GO:0005575|GO:0046598|GO:0005829|GO:0032648|GO:0051091|GO:0051
092|GO:0008270|GO:0043161|GO:0004871|GO:0070936|GO:0043123|GO:0045070|GO:0060333 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127851_PI430048170 0.358206477145642 0.841886676352928 0.499455929445155
0.458398629003078 0.397611502340588 A A A 1.04940772516382 0.531509389401186
0.444516358643519 A A A LNCV6_127851_PI430048170 mRNA
CTCCGCCCAAAGCAAGACACTCCAGCAATGCAAAGGTTAAAATAAAAGTCAAAATAAAGA NM_019855 RefSeq
chr19 - 48029382 48044054 CABP5 56344 calcium binding protein 5
GO:0007165|GO:0005509|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127181_PI430048170 0.0152053998719586 3.47009326480127 3.85451286937339
2.7384722071244 3.12269966213091 P A P 1.69850380278672 1.78447320231514
0.934487817239941 A A A LNCV6_127181_PI430048170 mRNA
CTCTTCTGCTTTTACTGGGGGATCTTTAATTTGCTGTGTGCCATGTGGAAGTATCGGGAA NM_001168272 RefSeq
chr3 + 4493347 4847840 ITPR1 3708 "inositol 1,4,5-trisphosphate receptor, type 1, transcript
variant 3"
GO:0005515|GO:0031088|GO:0005783|GO:0005637|GO:0044281|GO:0007202|GO:0009791|GO:0007173|GO:0050
882|GO:0006816|GO:0031094|GO:0031095|GO:0005955|GO:0048010|GO:0001666|GO:0048011|GO:0051209|GO:0
005220|GO:0048016|GO:0032469|GO:0005730|GO:0015085|GO:0014069|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134431_PI430048170 0.156542010438315 0.662243594111965 4.59227662681565
3.95563518508694 3.81457554479853 P P P 5.19749455513957 4.44025149273269
4.50433987640623 P P P LNCV6_134431_PI430048170 mRNA
ACCGCTATGCTGTTGAGAGTGCCCTGCTCCACTTACAAAAGGATGGGGCCTATACCGTGC NM_198482 RefSeq chr2
+ 85434794 85437029 SH2D6 NA SH2 domain containing 6 NA . NA - . NA NA NA NA NA
NA NA NA NA

LNCV6_59650_PI430048170 0.86459222106127 0.94961191316021 0.3945432260436120.683723698718262
0.422253097787419 A A A 0.3177441814524460.3293105076958870.988498919306213 A A A
LNCV6_59650_PI430048170 mRNA
ATCAACAACAAAATGTGGAATGTAAGAAAGCTCAGCCAAAGGAGGTGATGTCGCCAACGG NM_002442 RefSeq
chr12 - 120341329 120369180 MSI1 4440 musashi RNA-binding protein 1
GO:0008266|GO:0005737|GO:0000166|GO:0003723|GO:0030855|GO:0005634|GO:0009725|GO:0005844|GO:0007
399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139841_PI430048170 0.0106490209161072 1.35927583786165 11.2600971277392
11.3621415460681 11.402399049874 P P P 10.9411162171131 10.7553957233028
10.9926717881471 P P P LNCV6_139841_PI430048170 mRNA
GCTCTGCTCTAAAATTGTTGACATTCATGTCTCTGAGTTACAAAAGTGCTAATTCACTAC NM_001098522 RefSeq
chr11 + 20363856 20383783 HTATIP2 10553 "HIV-1 Tat interactive protein 2, 30kDa, transcript
variant 4"
GO:0005515|GO:0043066|GO:0006357|GO:0051170|GO:0003713|GO:0045765|GO:0006915|GO:0005634|GO:0001
525|GO:0005635|GO:0030154|GO:0005737|GO:0016020|GO:0016491|GO:0016032|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137710_PI430048170 0.00143571817922183 0.5140120703729996.75785815225915
6.8208697160212 7.04578404731792 P P P 7.81280164284901 7.69870200475538
7.99403261370399 P P P LNCV6_137710_PI430048170 mRNA
GTATGATGTAGGTAAAAATATATACCTTCGGGTCGCAGTTCACCATTTATATGTGGTATT NM_003263 RefSeq chr4
- 38796254 38804791 TLR1 7096 toll-like receptor 1
GO:0045410|GO:0034130|GO:0046982|GO:0005886|GO:0042535|GO:0007165|GO:0006955|GO:0006954|GO:0016
020|GO:0042116|GO:0005887|GO:0045087|GO:0042495|GO:0002755|GO:0035354|GO:0030670|GO:0050707|GO:0
004872|GO:0071727|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135217_PI430048170 0.3272468433032560.9206760044325264.80043031145024
5.13318455481445 4.90916329344337 P P P 5.0661521365249 5.07449922817183
5.07998013963096 P P P LNCV6_135217_PI430048170 mRNA
TGGTTCCCACACGAAGTCATCTCTTAATCATCATTAGCAATAGCAGTTCCCTTCCAAGGC NM_002213 RefSeq chr3
- 124761948 124887305 ITGB5 3693 "integrin, beta 5"
GO:0090136|GO:0005515|GO:0002474|GO:0005886|GO:0009986|GO:0043149|GO:0042590|GO:0035987|GO:0045
335|GO:0043235|GO:0005178|GO:0006936|GO:0007160|GO:0007229|GO:0030198|GO:0034684|GO:0002479|GO:0
004872|GO:0007179|GO:0031252|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_104216_PI430048170 0.0529649467883318 1.90099815932979 4.17808622962905
5.07040628804591 4.51985385931261 P P P 3.44830111275534 4.03202823627173
3.58385248101628 P P P LNCV6_104216_PI430048170 mRNA
TCTTGTCAATGATGGCGGTCACAGCAGGTGCCGACTTCTGCTATGCCATCGAGGTAAGCT NM_001290018 RefSeq
chr16 + 68311113 68357266 PRMT7 54496 "protein arginine methyltransferase 7, transcript variant 3"
GO:0019918|GO:0019919|GO:0005886|GO:0006325|GO:0005634|GO:0008469|GO:0030154|GO:0005829|GO:0042
393|GO:0043046|GO:0006355|GO:0016571|GO:0043393|GO:0005730|GO:0034969|GO:0035241|GO:0018216|GO:0
008757|GO:0016277|GO:0000387|GO:0006351|GO:0035243|GO:0035242|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144013_PI430048170 0.9202944109451551.01243602228078 6.42282048993182 6.4451870206608
6.80204368255597 P P P 6.47180625662663 6.35221290399237 6.78880031958717 P P P
LNCV6_144013_PI430048170 mRNA
TATTATTCTGTTGACCTATTTGCCTTACTATGAGCTGAGGGTAGTTCAATATGCTCACTC NM_015962 RefSeq chr14
+ 74713146 74736687 FCF1 51077 FCF1 rRNA-processing protein
GO:0000462|GO:0032040|GO:0005730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134264_PI430048170 0.7739180236894550.95031028582004 0.44354565388845

0.4966772592578950.500396206135887A A A 0.3422012532668530.398588428224046
0.862708464710853A A A LNCV6_134264_PI430048170 mRNA
GAAAAGGATAAACTATCACACATTCACGACCAAAAAGAGACAAGTGAGCTATATATCTAG NM_001037730 RefSeq
chr20 + 31257663 31259632 DEFB115 NA "defensin, beta 115" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_58705_PI430048170 0.26260085334891 1.56473382694614 1.57663991894408 1.45638011025363
0.41817411285249 A A A 0.5464636752451540.49088550367924 0.720861409323964A A A
LNCV6_58705_PI430048170 mRNA
GAAATGAATGTGTTTCCAGGCTTTCCTGGTGGTTTATGGCATTCTCCAAACTCCTATGCA NM_006143RefSeq chr12
- 12661060 12696187 GPR19 2842 G protein-coupled receptor 19
GO:0007186|GO:0005887|GO:0004930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142410_PI430048170 0.0869694643765937 0.5871076799945281.15627482270991
0.3408808515527890.280473058699511A A A 1.47145177849195 1.55720101719824
1.20566494766858 A A A LNCV6_142410_PI430048170 mRNA
ACTTAATGTCCATCTTCCACACCCCACATATATATAGATATAGATACAGATGCATATGTC NM_001277285 RefSeq
chr11 - 133908624 133956754 IGSF9B NA "immunoglobulin superfamily, member 9B" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132239_PI430048170 0.0484882916462174 1.27070244425974 9.97665994191385
9.96005670805377 10.0883577506039 P P P 9.47722098339661 9.79309593327418 9.7032072560631
P P P LNCV6_132239_PI430048170 mRNA
AGAAAATGGAAGGTCACTATGTTCATGCTGGGAACATCATTGCAACACAGCGCCATTTCC NM_016504RefSeq chr17
- 50367866 50373201 MRPL2751264 mitochondrial ribosomal protein L27
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0006412|GO:0005
762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145579_PI430048170 0.3740530202246940.9410136062486560.526720215053835
0.5106509048246920.27648679949812 A A A 0.5183167459261640.567837704939551
0.503387070822687A A A LNCV6_145579_PI430048170 mRNA
TTTCACAACAGGCTGGTTGTACCGAGTAAACAACACGATGCCATGAAGACCCTGAAAAAA NM_001289032 RefSeq
chr14 + 94561419 94569913 SERPINA4 5267 "serpin peptidase inhibitor, clade A (alpha-1
antiproteinase, antitrypsin), member 4, transcript variant 1" GO:0010951|GO:0004867|GO:0005615|GO:0070062
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144325_PI430048170 0.0212457091233778 0.5784077985125437.42228066356116
7.22153798341098 7.64857485379843 P P P 8.10338905582025 8.00120155751524
8.53236423788994 P P P LNCV6_144325_PI430048170 mRNA
GAGCATACCCTTGTATAGCTTCAGGTGCTAGAATTAAAATTGATCTGTTATCACAAGAAA NM_012250RefSeq chr11
- 14277919 14359184 RRAS2 22800 "related RAS viral (r-ras) oncogene homolog 2, transcript variant 1"
GO:0006184|GO:0005515|GO:0030335|GO:0016020|GO:0005886|GO:0005783|GO:0003924|GO:0007265|GO:0005
525|GO:0005925|GO:0001649|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142511_PI430048170 0.000461990321174158 0.2223106122757529.30161542388513
8.90685938697199 9.26253624095641 P P P 11.0568193387601 11.3259879406454
11.5807128522445 P P P LNCV6_142511_PI430048170 mRNA
GTCTAACGTGGTGTGGGAGAGAATTTACAAGTCCTTTATTGAAAGAATAATTGTTGCAAA NM_006325RefSeq chr12
+ 130871993 130877678 RAN 5901 "RAN, member RAS oncogene family, transcript variant 1"
GO:0005515|GO:0010467|GO:0030036|GO:0007264|GO:0019058|GO:0003924|GO:0007286|GO:0005634|GO:0050
681|GO:0044281|GO:0006606|GO:0032092|GO:0005829|GO:0005737|GO:0005643|GO:0034629|GO:0006611|GO:0
016032|GO:0007052|GO:0000785|GO:0070062|GO:0042470|GO:0019904|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_116414_PI430048170 0.1882742881309480.9498320465186330.442583318833714
0.3929960168269590.318830614433129A A A 0.5156093529771950.448318647185157

0.414073637422952 A A A LNCV6_116414_PI430048170 mRNA
ACCACGCTCAGGATTCACTCCACTACGAAGGCCGTGCTTTGGACATCACTACGTCTGACC NM_021044 RefSeq chr12
- 49089420 49094819 DHH 50846 desert hedgehog
GO:0005515|GO:0005886|GO:0042552|GO:0005509|GO:0007267|GO:0007286|GO:0050810|GO:0005615|GO:0005
113|GO:0030238|GO:0006508|GO:0033327|GO:0008233|GO:0008270|GO:0032355 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140433_PI430048170 0.3354577210930730 0.6424083545543270 0.326405612793744
0.33122510759759 0.493813316327704 A A A 0.3314999651075460 0.670849851112701
1.70128585105702 A A A LNCV6_140433_PI430048170 mRNA
GTGCACAGTGGACACAGGAATTGAACAAAGTTTACCATGATTAACATTATGTTTTCTTAG NM_006544 RefSeq chr14
- 57202475 57268899 EXOC5 10640 exocyst complex component 5
GO:0005737|GO:0047485|GO:0006996|GO:0006892|GO:0061024|GO:0015031|GO:0006887|GO:0044267|GO:0017
160|GO:0048278|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132765_PI430048170 0.0643381423528575 0.6427754621058822.52964065042837
2.35497372909252 2.62682380408818 A A A 2.92942055746057 3.49482393216796
2.93743011632563 P P P LNCV6_132765_PI430048170 mRNA
GGATCTGTTTCTGTAGTCGAGGACAACTGTGATGTAACTTTGAATTAAACAAACAAAACA NM_173802 RefSeq chr12
+ 31659186 31669082 METTL20 254013 "methyltransferase like 20, transcript variant 1"
GO:0005759|GO:0006479|GO:0008276 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144730_PI430048170 0.3132411933345490 0.4282714968833340 0.261777972812693
0.2783491726387460 0.390169827693795 A A A 0.37691230498778 2.52660780135851
0.705543738082687 A P A LNCV6_144730_PI430048170 mRNA
ATTGAGGAAACGATGCGGGACAAATGATGGTCTTCACGGTGGGATGGACCTCGTCAGCTGNM_022046 RefSeq chr19
- 51077896 51084245 KLK14 43847 kallikrein-related peptidase 14
GO:0009566|GO:0045745|GO:0045744|GO:0004252|GO:0006508|GO:0070684|GO:0005615|GO:0070062|GO:0048
730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127871_PI430048170 0.0124484047621266 4.8653312641741 3.13667671551576
2.21832736805503 3.02384118402014 P A P 0.4175814314876890 .623367308920999
0.641249907120812 A A A LNCV6_127871_PI430048170 mRNA
AAGAAGTGTTTGGAATGTGCTGTAAGAATGGAGGAAGTCGTTTCCACTGTCAGCATCCTC NM_152718 RefSeq chr11
- 61258285 61295316 VWCE 220001 von Willebrand factor C and EGF domains
GO:0008284|GO:0005509|GO:0005576|GO:0009966 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92670_PI430048170 0.0216818741095277 2.04744523124598 4.80221562421767
5.28197730486163 5.53224260936873 P P P 4.27030791154636 4.39964712742972
3.89030270783762 P P P LNCV6_92670_PI430048170 mRNA
TATGGCCTCATTTTAGCTGCTTCAGTGTGTTGGAGCTGTTACTTGCTCCTTCATTTCCTG NM_001267782 RefSeq chr11
- 46396411 46594069 AMBRA1 55626 "autophagy/beclin-1 regulator 1, transcript variant 1"
GO:0005515|GO:0005776|GO:0008285|GO:0005930|GO:0006914|GO:0030154|GO:0005829|GO:0043231|GO:0045
335|GO:0005739|GO:0005737|GO:0043524|GO:0043552|GO:2000785|GO:0021915|GO:0031625 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_76038_PI430048170 0.0787701322645519 0.770003003417419 12.059631416373
12.0008831572685 12.3023291908639 P P P 12.5642133727722 12.2524007662669
12.6641999621898 P P P LNCV6_76038_PI430048170 mRNA
GCCCTGTGTCTGGCACCTACATCCTTGATGATTGTTCTCTTACCCATTCTGGAATTTTTT NM_004134 RefSeq chr5 -
138554881 138575629 HSPA9 3313 heat shock 70kDa protein 9 (mortalin)
GO:0005515|GO:0042645|GO:0043066|GO:0006626|GO:0005730|GO:0005524|GO:0005739|GO:0005737|GO:0006
457|GO:0006611|GO:0051082|GO:0005925|GO:0044267|GO:0031625|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140218_PI430048170 0.0398590834991466 0.9320402879374280.355239682292697

0.32288045933788 0.310808222472999 A A A 0.47690284748116 0.427777069284028
0.387841705134608 A A A LNCV6_140218_PI430048170 mRNA
CTTCGGCACTGATGGAATTTGATTTCGATGACCAACTGCAAAACAATCTCATTATATTTA NM_020722 RefSeq chr4
+ 56170194 56330724 KIAA1211 57482 KIAA1211 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144508_PI430048170 0.199250688985192 1.34288074599059 9.34861316183811
9.18860475194031 9.51937989290377 P P P 9.37262241452446 8.52305215294931
8.76730272100702 P P P LNCV6_144508_PI430048170 mRNA
ACAGAGTTCAGCAATTTTGATTAAATTAAGACTTGGGGGTGAAACTTTCCAGTTTACTGA NM_004184 RefSeq chr14
- 100333787 100375590 WARS 7453 "tryptophanyl-tRNA synthetase, transcript variant 1"
GO:0005515|GO:0010467|GO:0008285|GO:0045765|GO:0005634|GO:0001525|GO:0005524|GO:0006412|GO:0005
829|GO:0006418|GO:0006436|GO:0004830|GO:0005737|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127460_PI430048170 0.544379556284660 0.750401534556769 2.37518348507644
2.62158898919451 3.23428149668776 A A P 2.57394035170815 2.74241976729525
3.90779632372533 A A P LNCV6_127460_PI430048170 mRNA
CATAGCAAAGTCACTTTTATAACAGTTTACCACTATGCTTGATTATAATGTGAAAGGCGG NM_017742 RefSeq chr18
+ 62523424 62578585 ZCCHC2 54877 "zinc finger, CCHC domain containing 2, transcript variant 1"
GO:0005737|GO:0008270|GO:0035091|GO:0003676 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143864_PI430048170 0.160418744594379 0.909047594834723 10.719722501844
10.8090843944969 10.5805242778443 P P P 10.8034778413587 10.8519773719934
10.8748147648873 P P P LNCV6_143864_PI430048170 mRNA
GGAGTTACAGTCCCTTTTGGCCCTCACATCCAATAAAGAGACTGATACCACTGGAAAAAA NM_005469 RefSeq
chr20 - 45841720 45857409 ACOT8 10005 acyl-CoA thioesterase 8
GO:0052815|GO:0052689|GO:0005515|GO:0006637|GO:0005782|GO:0006699|GO:0043649|GO:0016290|GO:0005
102|GO:0044281|GO:0036109|GO:0033559|GO:0047617|GO:0005739|GO:0016032|GO:0008206|GO:0033540|GO:0
044255|GO:0016559|GO:0033882 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134001_PI430048170 0.115689944095797 1.3580134632908 13.0554296014199
13.2288079954774 13.0803232510687 P P P 13.0059564150845 12.5770443807314
12.3931688964629 P P P LNCV6_134001_PI430048170 mRNA
AATTGAGGGAGAGACCTTTCTTCCTTGTTGAGGGTGAAAAATAAATAAGAATTACATGTC NM_133491 RefSeq
chr17 - 7626237 7627876 SAT2 112483 spermidine/spermine N1-acetyltransferase family member 2
GO:0032920|GO:0005737|GO:0032919|GO:0032918|GO:0009447|GO:0004145|GO:0070062|GO:0046204 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_118530_PI430048170 0.949012528079784 1.00578281560867 7.0501316165548
6.50386619647945 6.37150609641173 P P P 6.83775471658098 6.63264081512163
6.50311081081196 P P P LNCV6_118530_PI430048170 mRNA
ATGCCTGCCTGTGATCTTCCTCTCCTTGGGATTTGGCCTGGATACAGTAGAGGTGTGCCC NM_014215 RefSeq
chr1 - 156840872 156858920 INSRR 3645 insulin receptor-related receptor
GO:0043235|GO:0046777|GO:0031532|GO:0005887|GO:0030238|GO:0043560|GO:0018108|GO:0004714|GO:0071
469|GO:0007169|GO:0005524|GO:0043548 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_129557_PI430048170 0.468891600433775 0.970091248185604 0.419632551291753
0.438215479881114 0.280012177641519 A A A 0.394932786539836 0.460819086183789
0.417879332453235 A A A LNCV6_129557_PI430048170 mRNA
TGACATGAACAGTTTCTTCTGTGAGGACAGTTGGCTATTGAAATAAAATGAGCAATGGAA NM_033067 RefSeq
chr1 + 53459398 53467487 DMRTB1 63948 "DMRT-like family B with proline-rich C-terminal, 1"
GO:0000987|GO:0006355|GO:0003700|GO:0007548|GO:0005634|GO:0046872|GO:0042803|GO:0006351 . NA

- . NA NA NA NA NA NA NA NA NA
LNCV6_128744_PI430048170 0.0443655345498053 0.62935544109605 12.0159673408848
11.8088739031328 11.6316512811841 P P P 12.374153951825 12.8166539676317
12.2288288594563 P P P LNCV6_128744_PI430048170 mRNA
TAGAAAGTTCCTTTGGCCAACTGCTTAGAAGCCCAACACAACCCAAAGGCTCTTTTCAGA NM_005321 RefSeq
chr6 + 26156330 26157115 HIST1H1E 3008 "histone cluster 1, H1e"
GO:0005515|GO:0005720|GO:0006334|GO:0016584|GO:0005634|GO:0000786|GO:0031490|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_132968_PI430048170 0.0684319837697523 1.79566357391694 1.68891073623799
2.08603709374008 1.58922457249699 A A A 0.468833692576059 0.808911505670675
1.43282065252516 A A A LNCV6_132968_PI430048170 mRNA
AGGAGTGGGTCCAGAGGTACATGAAGAACCTGGACGCCAAGCAGAAGAAGGCTTCCCCTA NM_002991 RefSeq
chr7 - 75811795 75813715 CCL24 6369 chemokine (C-C motif) ligand 24
GO:0008009|GO:0030335|GO:2000418|GO:0008360|GO:0007267|GO:0005615|GO:0032855|GO:0045766|GO:0007
165|GO:0006955|GO:0006954|GO:0001938|GO:0006935|GO:0030838|GO:0050729|GO:0007010|GO:0048245 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126959_PI430048170 0.0118604294258562 0.592552995266035 5.59207132018621
5.58690097144242 5.95149198183783 P P P 6.25527014788386 6.45890685218345
6.68088879556583 P P P LNCV6_126959_PI430048170 mRNA
GTCATGAACATGAAATACAAACACGATGGCTTCGAAATGTCTTTCAATAAATGTTTCTGC NM_024094 RefSeq chr8
- 119833940 119855930 DSCC1 79075 DNA replication and sister chromatid cohesion 1
GO:0006260|GO:0005515|GO:0031390|GO:0034421|GO:0034088|GO:0003689|GO:0005654|GO:0000785|GO:0006
275|GO:0000775 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140325_PI430048170 0.334766057161905 0.472441737505897 0.387966019234972
0.306250338757279 1.49502405104192 A A A 0.255984309941729 2.52246994544635
2.14189067256803 A P A LNCV6_140325_PI430048170 mRNA
TGCAAAGAGTTGTTTAACTTGCATGGTGCCACCCAATAAATATCTGTGCAATTGAAAAAA NM_144696 RefSeq chr1
+ 179365719 179554735 AXDND1 126859 "axonemal dynein light chain domain containing 1, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136805_PI430048170 0.107660105735486 0.589490192805733 11.3778208348411
12.3556608938509 12.2183653035808 P P P 12.9201007215573 12.8353063229293
12.6506470727289 P P P LNCV6_136805_PI430048170 mRNA
CCCTAGGGTCCCCAGCCCTACTCCCGCCGCTCTGAAAATAATAAACGACTTTATTCTTGG NM_032344 RefSeq chr11
+ 64226273 64230016 NUDT22 84304 "nudix (nucleoside diphosphate linked moiety X)-type motif 22,
transcript variant 1" GO:0016787|GO:0008152|GO:0005654 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_143986_PI430048170 0.0800583243636931 1.48932844445374 11.8614642713482
12.2207772408033 11.862602490716 P P P 11.7786408973273 11.2881299312432
11.0965421085412 P P P LNCV6_143986_PI430048170 mRNA
CCGTGTGGGCCGTGCTGTGTCCTTATGTCATTGTAATATAAATACAGATTTTTATATCTC NM_006454 RefSeq chr4
- 2247432 2262012 MXD4 10608 MAX dimerization protein 4
GO:0005515|GO:0008285|GO:0003714|GO:0046983|GO:0005634|GO:0000122|GO:0003677|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139627_PI430048170 0.0110456732423264 1.61822781085635 8.31679100543799
8.63782769376215 8.5858207866721 P P P 7.86425858717871 7.74305173192294
7.86658966512283 P P P LNCV6_139627_PI430048170 mRNA
GCTGTTATTCATACACACTTTCCACTTCAAATATACCCAAATATGGCTTTCCTCACTTAANM_024328 RefSeq chr14 +
23555981 23559581 THTPA 79178 "thiamine triphosphatase, transcript variant 1"
GO:0006772|GO:0000287|GO:0016787|GO:0006766|GO:0016311|GO:0042357|GO:0006767|GO:0044281|GO:0006

091|GO:0042723|GO:0050333|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89142_PI430048170 0.8450894073581821.13552642225753 2.59442218877228 1.81958780447982
0.512140229485374 A A A 1.71293724755519 2.36989124955178 0.305471603587019 A A A
LNCV6_89142_PI430048170 mRNA
AAACACTGGAGTCTGAAAACAAGGTCAAACTCTCCATCCCATCCATGATGTGGGAACATG NM_012276 RefSeq
chr19_KI270938v1_alt - 315569 321554 LILRA4 23547 "leukocyte immunoglobulin-like receptor,
subfamily A (with TM domain), member 4" GO:0005515|GO:0016021|GO:0002376 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_137510_PI430048170 0.1713650518431111.16400195910125 0.739561406966646
0.3934626969358730.672302075858729 A A A 0.2817551754720960.421102446709546
0.461894949103143 A A A LNCV6_137510_PI430048170 mRNA
GAGTTTAGATTGTGAGTCCATGTTTTGTCTGTTGTGCCTATAAAGGAAATTTGAAATCTG NM_080283 RefSeq chr17
- 68974631 69060995 ABCA9 10350 "ATP-binding cassette, sub-family A (ABC1), member 9"
GO:0005739|GO:0005215|GO:0008152|GO:0006810|GO:0016021|GO:0016887|GO:0005524 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_92292_PI430048170 0.4444661652232271.0803545838419 6.73288075428879 6.93529482246276
6.96560628358539 P P P 6.89096361442566 6.53497018776944 6.85813800403956 P P P
LNCV6_92292_PI430048170 mRNA
CTCCAAAATGAGGTTAACTGCCTCATATGTGGGACAGAATCTAGAAAGTTTGATCCATTC NM_006537 RefSeq chr15
+ 63504510 63594640 USP3 9960 "ubiquitin specific peptidase 3, transcript variant 1"
GO:0016578|GO:0000790|GO:0006355|GO:0004843|GO:0000122|GO:0004197|GO:0042393|GO:0006281|GO:0031
647|GO:0061136|GO:0003682|GO:0043161|GO:0008270|GO:0001046|GO:0000278 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_68234_PI430048170 0.2742749713307680.5566634183227241.75053025935338 0.633986481011333
2.02660815929016 A A A 2.4997465369719 1.36668655511465 2.98498725937175 A A P
LNCV6_68234_PI430048170 mRNA
CTTTAAAAGCTTTAGGACATCCAGCTATGCTAAGTAAAGTCTTAGGAGGTTCCTTTGCTG NM_001039590 RefSeq
chrX + 41085634 41236579 USP9X 8239 "ubiquitin specific peptidase 9, X-linked, transcript variant
3"
GO:0005515|GO:0021698|GO:0010467|GO:0016579|GO:0006367|GO:0004843|GO:0048675|GO:0009791|GO:0005
829|GO:0030426|GO:0005737|GO:0007059|GO:0007179|GO:0070410|GO:0045177|GO:0000122|GO:0007292|GO:0
030509|GO:0001701|GO:0006351|GO:0004197|GO:0021766|GO:0007067|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_53744_PI430048170 0.2803531510063570.7667831374547077.85426822610218 6.82029594789817
7.14554448882627 P P P 7.8502863483896 7.75595309986855 7.54605341417119 P P P
LNCV6_53744_PI430048170 mRNA
CTTCCAACTTCAAAAAAGCCAAGAGAGTCAAAACAGAGGATGAAAAAGAGAAAGACCCAG NM_004964 RefSeq
chr1 + 32292106 32333623 HDAC1 3065 histone deacetylase 1
GO:0005515|GO:0010467|GO:0000790|GO:0006367|GO:0003700|GO:0044212|GO:0006325|GO:0010832|GO:0007
219|GO:0016581|GO:0016580|GO:0007179|GO:0000785|GO:0001103|GO:0000976|GO:0001106|GO:0043044|GO:0
019213|GO:0031492|GO:0060766|GO:0001047|GO:0000122|GO:0045786|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145046_PI430048170 0.4254522025804070.6986874101119231.55116685753496
1.03497384677493 0.918549832385598 A A A 0.8120667556407311.73456995877988
2.24760993372019 A A A LNCV6_145046_PI430048170 mRNA
CTCAGACTAACCATAGTAATAATACACATTTCTGTGAGTGCTGACTTGTCTTTGCAATAT NM_001079858 RefSeq
chrX - 18989306 19122637 ADGRG2 NA "adhesion G protein-coupled receptor G2, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132534_PI430048170 0.5727064265061431.10397928108758 0.336022250713809

0.8872606224061380.364954392434839A A A 0.49063841297278 0.371516858898509
0.363560977372907A A A LNCV6_132534_PI430048170 mRNA
GGCAACAAAACTTGTGGTCTTTACTTTTGAATAGCTACCCAAGAAAAGGTTTTAAAGGTA NM_006682RefSeq chr7
- 77193370 77199833 FGL2 10875 fibrinogen-like 2 GO:0005577|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132440_PI430048170 0.1549117485571681.29279460859462 7.01628978982033
6.69572502211217 6.88115082057805 P P P 6.66852657004703 6.11535153101188
6.65028729099266 P P P LNCV6_132440_PI430048170 mRNA
CCACATACCCAGCACCCATGAAATAAAAGATTCATCTGTAATTGGGATTCAAAGTGATTA NM_007107RefSeq chr3
- 156539552 156555200 SSR3 6747 "signal sequence receptor, gamma (translocon-associated protein gamma)" GO:0010467|GO:0005784|GO:0006614|GO:0030176|GO:0044267|GO:0006412 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_70853_PI430048170 0.819059892097105 1.0277459975221 9.72998431692895 9.33755429962867
9.46206871730414 P P P 9.49728309415926 9.57064106215218 9.36393710099333 P P P
LNCV6_70853_PI430048170 mRNA
TTGTGTCTGGAATCATCACACCTATCCATGAGCAGTGGGAAAAGGCTAATGTAAGCAGTC NM_006814RefSeq chr20
+ 1118596 1167782 PSMF1 9491 "proteasome (prosome, macropain) inhibitor subunit 1 (PI31), transcript variant 1"
GO:0005515|GO:0006511|GO:0002474|GO:0010467|GO:0004866|GO:0005783|GO:0090263|GO:0044281|GO:0031145|GO:0005829|GO:0034641|GO:0005737|GO:0000082|GO:0016032|GO:0090090|GO:0006977|GO:0000209|GO:0005839|GO:0043066|GO:0006521|GO:0051437|GO:0042590|GO:0006915|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134435_PI430048170 0.00478691576751404 1.13030828069754 4.83160856825792
4.76284522145105 4.78690211811124 P P P 4.60846833613403 4.63696792661386
4.60641399778003 P P P LNCV6_134435_PI430048170 mRNA
GATAGGGGGAGGGTTGGAAAATTTATTTTTATGAAACAGAGGGAAGACTTTATTGTTGTT NM_201403RefSeq chr1
- 46607714 46616891 MOB3C 148932 "MOB kinase activator 3C, transcript variant 2" GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129731_PI430048170 0.6459096847785290.9766935726309591 0.6850089131159 10.515140324142
10.4791129811461 P P P 10.5379470072882 10.6464979590843 10.6033036495972 P P P
LNCV6_129731_PI430048170 mRNA
TTTTGGATGGTAGAGTGTGTGCACTGACTGTGAGTCGAATAAACAATTGAGACGAAAAAA NM_032809RefSeq chr9
+ 129036973 129072072 FAM73B 84895 "family with sequence similarity 73, member B"
GO:0060348|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141274_PI430048170 0.00656725273741124 0.7552660847776515.3625358149706
5.32034115954834 5.50524743653772 P P P 5.82120716514685 5.69851502642443
5.88369518093253 P P P LNCV6_141274_PI430048170 mRNA
CAGTTTCTGGCATCAGTGTACTATTTATAGTCTATAGCATACATTACTTGCAAATGGGAA NM_024926RefSeq chr7
+ 139133743 139191986 TTC26 79989 "tetratricopeptide repeat domain 26, transcript variant 1"
GO:0042384|GO:0005813|GO:0042073|GO:0006996|GO:0030992|GO:0072372|GO:0015031|GO:0036064|GO:0007224 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143524_PI430048170 0.0471408798307846 1.19942933727 12.6010741454368
12.7746501535332 12.5840403668432 P P P 12.381028705671 12.4143568487957
12.3849170070934 P P P LNCV6_143524_PI430048170 mRNA
GCTGTGGGCCTCATCCTTCACTCAGTTGTGAAATAAACCGCTCCTTGCCCCGATAAAAAA NM_001667RefSeq chr11
+ 65014112 65022185 ARL2 402 "ADP-ribosylation factor-like 2, transcript variant 1"
GO:0005515|GO:0031116|GO:0005813|GO:0007264|GO:0031113|GO:0010811|GO:0003924|GO:0005634|GO:0072372|GO:0005525|GO:0016328|GO:0051297|GO:0005758|GO:0007049|GO:0070830|GO:0051457|GO:0007021|GO:0008152|GO:0019003|GO:0005095|GO:0034260|GO:0070062 . NA - . NA NA NA NA NA NA NA NA

NA
LNCV6_136791_PI430048170 0.5585454663036651.03133324820968 9.0668582433585
8.90489122848024 9.01368901235583 P P P 8.97640941620821 9.02374622281454
8.85096757817433 P P P LNCV6_136791_PI430048170 mRNA
TCAGGAGTTATCTGGTGACAATATCGATCAAATTAAGTTTGCAGCCATCGGCCCCACTAC NM_000375RefSeq chr10
- 125788577 125823268 UROS 7390 uroporphyrinogen III synthase
GO:0071418|GO:0005739|GO:0048037|GO:0006780|GO:0006778|GO:0044281|GO:0006782|GO:0004852|GO:0071
243|GO:0046677|GO:0006783|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62550_PI430048170 0.000602255709679806 0.6456429962015512.3153293689081
12.4532112065109 12.3575241016145 P P P 12.9866433301914 13.0554296014199
12.9798263050151 P P P LNCV6_62550_PI430048170 mRNA
CTCCACAGTGGCTTCCGACTCAGGCTCCAATGGACCAAATAAAAGCGTTTTGTTTTGTAA NM_005632RefSeq chr16
+ 527855 554636 CAPN15 6650 calpain 15
GO:0006355|GO:0005737|GO:0004198|GO:0003700|GO:0006508|GO:0008270|GO:0008233|GO:0008234 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139578_PI430048170 0.2773999187821210.8276858244421947.36853410744127 7.4009057574013
7.43506819642904 P P P 7.31606516784291 7.87349712315027 7.77521453465722 P P P
LNCV6_139578_PI430048170 mRNA
ACAAGAAAGCAGAAATATTTTTACCGGGGTCGCCTGGATTGGGATGAGAACACATCAGCT NM_001294338 RefSeq
chr1_GL383519v1_alt - 67890 78552 CLK2 1196 "CDC-like kinase 2, transcript variant 1"
GO:0045721|GO:0005515|GO:0005634|GO:0018108|GO:0005524|GO:0046777|GO:0016607|GO:0004674|GO:0010
212|GO:0004712|GO:0005654|GO:0006468|GO:0043484|GO:0004713|GO:0032526 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134478_PI430048170 0.34315033470021 0.8366261140673953.58154941831494
3.04350657438308 3.02104874969729 P P P 3.75595523561487 3.48585177996095 3.1943800960554
P P P LNCV6_134478_PI430048170 mRNA
TTTATCTGTCCACCCCTCACAGACTAGGACCCTCAAATAAAGCTGTTTTATATCAAAAAA NM_020387RefSeq chr1
+ 156061174 156070504 RAB25 57111 "RAB25, member RAS oncogene family"
GO:0003382|GO:0005515|GO:0008284|GO:0031268|GO:0003924|GO:0031410|GO:0005525|GO:0006887|GO:0006
886|GO:0032402|GO:0031143|GO:0006184|GO:0031489|GO:0016023|GO:0060627|GO:0032482|GO:0055037|GO:0
010634|GO:0019003|GO:0031260|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132136_PI430048170 0.1091494621169520.7451905917156151 2.2642057970035
12.2516551429894 12.4312083746326 P P P 12.4091421558749 12.8852621777877
12.8826293266279 P P P LNCV6_132136_PI430048170 mRNA
GCTGTGGTATTTTTGTTTTGTTTTTGTCTTTTAAATTAAGCCTCGGTTGAGCCCTTGTAT NM_181801RefSeq chr20 +
45813032 45816957 UBE2C 11065 "ubiquitin-conjugating enzyme E2C, transcript variant 4"
GO:0010994|GO:0005515|GO:0007094|GO:0006511|GO:0004842|GO:0016567|GO:0016874|GO:0031145|GO:0005
829|GO:0051488|GO:0008054|GO:0005737|GO:0019787|GO:0005680|GO:0031625|GO:0010458|GO:0031536|GO:0
051437|GO:0051436|GO:0005524|GO:0051439|GO:0070979|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127900_PI430048170 0.8574567996541380.9848256024885615.29902761679534
4.81346466126387 4.72522463447685 P P P 5.16506194522871 4.89295528295831 4.8970661297397
P P P LNCV6_127900_PI430048170 mRNA
CAGCCCCCAGGAGAGCCCTCCACAGCCTGTCAATAAATTTTTTGTAGGCCAACACATGCA NM_001304360 RefSeq
chr1 - 1921950 2003837 CFAP74 85452 cilia and flagella associated protein 74
GO:0035082|GO:0005930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93299_PI430048170 0.00526827971174942 0.4619211156894695.89514566638471
5.66023407497462 5.38431113341265 P P P 6.85001624671668 6.58418072894406
6.87566493196735 P P P LNCV6_93299_PI430048170 mRNA

TGTTAACCAACAGCCGCCAGGGCTTCCTGTTGAAATAAATATATAGCAACAAAGGAAAAA NM_002748 RefSeq chr15 + 52019213 52066265 MAPK6 5597 mitogen-activated protein kinase 6 GO:0005515|GO:0007165|GO:0007049|GO:0005737|GO:0046982|GO:0019901|GO:0004674|GO:0000165|GO:0006468|GO:0005634|GO:0005524|GO:0004707 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130149_PI430048170 0.321507422399176 1.31930192493819 4.54641420167475 5.4792163308228 5.10954172076991 P P P 4.63861325019525 4.61673271288684 4.82008924867756 P P P LNCV6_130149_PI430048170 mRNA
GAGATGCTGCAACAGTTCTTGATTTAGCAGCAGTTATTCTCTTGTTTACATAGTTATGTT NM_001042496 RefSeq chr15 - 34229995 34337760 SLC12A6 9990 "solute carrier family 12 (potassium/chloride transporter), member 6, transcript variant 5" GO:0015079|GO:0071476|GO:0005886|GO:0015379|GO:0019901|GO:0010107|GO:0001525|GO:0071477|GO:0055085|GO:0035827|GO:0016323|GO:0035826|GO:0005887|GO:0016021|GO:0006813|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119828_PI430048170 0.00478767886542751 0.642236439064959 5.87430709252564 5.59039372954985 5.73659504446308 P P P 6.46268799442223 6.38080830910632 6.28259427853425 P P P LNCV6_119828_PI430048170 mRNA
ACACAGGAGAGAAACCCTATAAATGTTATGAGTGTGGGAAGGCGTTCAGTCAGAGTTCGA NM_152437 RefSeq chr12 + 123973214 124015439 ZNF664 144348 "zinc finger protein 664, transcript variant 1" GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134716_PI430048170 0.40799066857194 4.00797249427412 0.319644290888035 3.57212354349242 0.276082130277331 A P A 0.255409384748455 0.253645922432494 0.257159990779554 A A A LNCV6_134716_PI430048170 mRNA
ACCATATTGGGAACAGCCAAAAGAAGTTATAGAACAAGAATTTAAGGTGACTCTATCTGA NM_052939 RefSeq chr1 - 157678187 157700857 FCRL3 115352 Fc receptor-like 3 GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144406_PI430048170 0.00677069081429587 1.30930032828264 12.7082493246587 12.860793554036 12.7966144153118 P P P 12.4271697811338 12.4049998642518 12.3705908334481 P P P LNCV6_144406_PI430048170 mRNA
TTCAACAAAGGGGGTGAAGTGTCCTACTAAAAAGAATAAATGTTGGCAGTGAATTAAACA NM_002812 RefSeq chr19 + 38374549 38383824 PSMD8 5714 "proteasome (prosome, macropain) 26S subunit, non-ATPase, 8" GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0034641|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0000502|GO:0043066|GO:0005838|GO:0006521|GO:0042590|GO:0051437|GO:0006915|GO:0042981|GO:0051436|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103717_PI430048170 0.349254483993094 0.929556648548542 12.3385123946731 12.5082702993847 12.2207772408033 P P P 12.3849170070934 12.5702548252712 12.4367051665769 P P P LNCV6_103717_PI430048170 mRNA
AGATTGTACCCAGATAGCTGGGATTGGAAGTGAGGAGGTTTCTCACCCCACAGATAACCC NM_001301339 RefSeq chr22 - 23765833 23767972 CHCHD10 400916 "coiled-coil-helix-coiled-coil-helix domain containing 10, transcript variant 1" GO:0005739|GO:0005758|GO:0003674|GO:0006754|GO:2000984|GO:0007005|GO:0006119 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144400_PI430048170 0.657639328126061 0.947025792809961 9.5538422748877 9.54330863256475 9.57355251935845 P P P 9.40614812575325 9.61043674542481 9.85479300073464 P P P LNCV6_144400_PI430048170 mRNA
TGTCAATCAAAAGGTTTGCAATGATTTCCTTCCTGCCAAAAATAAACATGTGAAACTGCA NM_001008392 RefSeq chr3 + 37862177 37984469 CTDSPL 10217 "CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like, transcript variant 1"

GO:0008150|GO:0003674|GO:0016311|GO:0001933|GO:2000134|GO:0005634|GO:0004721|GO:0046872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142481_PI430048170 0.676349672222914 0.989497715654189 0.436346829367702 0.446749573703507 0.366746601444869 A A A 0.476676677524641 0.400779087234262 0.418287473893122 A A A LNCV6_142481_PI430048170 mRNA
GACTCTTGTTCTTGTCTGATCTCTTGTCAAATTGTTATTTTGTAATGAACTGCGTCTCCT NM_001136504 RefSeq chr1 - 202590596 202643453 SYT2 127833 "synaptotagmin II, transcript variant 2"
GO:0005544|GO:0005515|GO:0005215|GO:0030054|GO:0042584|GO:0005886|GO:0005509|GO:0009405|GO:0006810|GO:0030672|GO:0016021|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136449_PI430048170 0.0430358387963143 0.255033520782518 2.46597507378691 1.15105522002648 2.67941700426263 A A A 4.38515535716217 4.17307651706984 4.04913715264905 P P P LNCV6_136449_PI430048170 mRNA
CTGGGATGTAACTATCTTACATGTTTACATAAGAAATAATAAACTGGAGGTGGGAATGGA NM_006626 RefSeq chr9 - 122908055 122913328 ZBTB6 10773 zinc finger and BTB domain containing 6
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131032_PI430048170 0.484314545284292 0.905597057416235 0.476943619957797 0.518209299853251 0.422771398693215 A A A 0.461205130433636 0.440818107065835 0.898807238523218 A A A LNCV6_131032_PI430048170 mRNA
CTGAGGCCAATAGGTGCCTAGTAAATGTTAACTGTTCTTGGAAAAAATAAAAACATCAGT NM_001332 RefSeq chr5 - 10971840 11904043 CTNND2 1501 "catenin (cadherin-associated protein), delta 2, transcript variant 1"
GO:0005515|GO:0006355|GO:0005634|GO:0007275|GO:0006351|GO:0007165|GO:0005737|GO:0016337|GO:0005912|GO:0048167|GO:0043204|GO:0007612|GO:0007155|GO:0001763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76396_PI430048170 0.301611281051231 0.911719347708011 9.86093779394749 9.74680551796521 9.86805553664281 P P P 9.90762112563943 9.82086652574234 10.1323506969957 P P P LNCV6_76396_PI430048170 mRNA
TGCCTTGAAGGAAAAAAGAACCTATTTTTGTGCATCATTTACCAATCATGCCACACAAGC NM_018434 RefSeq chr5 - 179955066 180072118 RNF130 55819 "ring finger protein 130, transcript variant 1"
GO:0005737|GO:0004842|GO:0016567|GO:0016874|GO:0006915|GO:0008270|GO:0005654|GO:0005634|GO:0016021|GO:0012501 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134581_PI430048170 0.192570995851974 1.08104034764386 0.728919215914658 0.543813587795203 0.666551192017101 A A A 0.44335963952526 0.576476506274403 0.583999420847132 A A A LNCV6_134581_PI430048170 mRNA
CCCCACTTTTTGTTGCTTTCTAGACTTGTGTGTAGAAAGAAGATTAATGATCACTTAAAG NM_203371 RefSeq chr11 + 26994080 26997085 FIBIN 387758 fin bud initiation factor homolog (zebrafish)
GO:0005794|GO:0005783|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127301_PI430048170 0.115776750529982 1.29789335592528 3.97011494278796 4.33021202559863 4.32388162345086 P P P 4.06621436214947 3.56242162278649 3.8518289807447 P P P LNCV6_127301_PI430048170 mRNA
TCCAAGCCAACAAGGCTACACTGGTGTGTCTCATGAATGACTTTTATCCGGGAATCTTGA NM_020070 RefSeq chr22 - 23573125 23580308 IGLL1 3543 "immunoglobulin lambda-like polypeptide 1, transcript variant 1"
GO:0006955|GO:0016020|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137373_PI430048170 0.303365419558213 0.604934494125734 3.26647833312579 0.460499342380771 1.63983566863602 P A A 2.50635579378425 3.44648300637277 2.75488739529717 A P P LNCV6_137373_PI430048170 mRNA
TACATCACCTTCTCAGCTCTTGACCTCAGAAAGTATCCAAACCAAGGAGGAGAAACCTGT NM_016341 RefSeq chr10 + 93993988 94328391 PLCE1 51196 "phospholipase C, epsilon 1, transcript variant 1"

GO:0045859|GO:0005515|GO:0019722|GO:0043647|GO:0005886|GO:0008283|GO:0007200|GO:0007265|GO:0046578|GO:0044281|GO:0006940|GO:0001558|GO:0007204|GO:0032835|GO:0007205|GO:0005829|GO:0005085|GO:0007507|GO:0004629|GO:0000187|GO:0005737|GO:0007173|GO:0007010|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128592_PI430048170 0.839233104669493 0.982085354691637 12.6514997348213 12.7640464690612 12.6551073035233 P P P 12.5459789437222 12.8517654030568 12.7376169845131 P P P LNCV6_128592_PI430048170 mRNA TGGAAATAAACCTGCGTGTGGGTGGAGTGTTAGGACCAACGGTTTCCTAGGAGTAAAAAA NM_001206950 RefSeq chr17 + 82228405 82239499 SLC16A3 9123 "solute carrier family 16 (monocarboxylate transporter), member 3, transcript variant 1"
GO:0031965|GO:0005886|GO:0008028|GO:0044281|GO:0015129|GO:0050900|GO:0015629|GO:0055085|GO:0015718|GO:0016020|GO:0035879|GO:0005887|GO:0006090|GO:0007596|GO:0015355|GO:0044237|GO:0015293 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145524_PI430048170 0.0093375248132598 1.18441984122092 0.79055909259006 0.844032334933006 0.859029701913695 A A A 0.660084493892191 0.539759012847717 0.559216708227961 A A A LNCV6_145524_PI430048170 mRNA GCCATCTTACAGGGAAAAGTTATAACCACTATTCCCCTATAACATAATGCTAATGATTGT NM_025153 RefSeq chr5 - 160563119 160852212 ATP10B 23120 "ATPase, class V, type 10B"
GO:0005515|GO:0000287|GO:0005886|GO:0005783|GO:0008152|GO:0004012|GO:0005789|GO:0016021|GO:0006886|GO:0005524|GO:0045332|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139860_PI430048170 0.310981152614634 0.847300799945407 0.253797337721951 0.282417208043784 0.29256381711743 A A A 0.82224366189234 0.359145079893851 0.307278477105359 A A A LNCV6_139860_PI430048170 mRNA ATTCTACAAAGTCTTATTGCTTGTACAGACAGCCATCTACTCTGTCGTGGGCTATGCCTC NM_001010873 RefSeq chr6 + 41042497 41044337 TSPO2 NA "translocator protein 2, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131228_PI430048170 0.982900119353449 1.0001979024641 9.12781725012915 9.06071772504354 9.15970969711667 P P P 9.15922891703306 9.0179723253747 9.16712288585226 P P P LNCV6_131228_PI430048170 mRNA CTACTTTTGTGGTGTGGGAGGGGAATGCTATGGAAGTATGTAATAATTTCTAATGTATAT NM_001256409 RefSeq chr1 + 53946325 53968168 LRRC42 115353 "leucine rich repeat containing 42, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138699_PI430048170 0.109388061956518 0.826770213612577 12.7395915424647 12.4406839320128 12.7878047716002 P P P 12.807655519296 12.9403582906321 13.0565740736994 P P P LNCV6_138699_PI430048170 mRNA TTCAATTACCGACGCAGACGCCCAGAAAACCCTAAACCACAAGATGGCAAAGAGACAAAA NM_004559 RefSeq chr1 + 42682394 42702349 YBX1 4904 Y box binding protein 1
GO:0005515|GO:0008380|GO:0010467|GO:0003700|GO:0006366|GO:0010494|GO:0003723|GO:0005634|GO:0043231|GO:0005737|GO:0003690|GO:0003697|GO:0045944|GO:0051781|GO:0051154|GO:0070062|GO:0006355|GO:0031965|GO:0070934|GO:0000122|GO:0000978|GO:0003677|GO:0001701|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134105_PI430048170 0.315619823153469 1.23768300172921 0.294744686693455 0.997602534161801 0.499564100958693 A A A 0.331642432774104 0.288543447639146 0.341157662560486 A A A LNCV6_134105_PI430048170 mRNA GATTTCCAAGTGCCAATATTTCTGATATAACAAACTACATGTAATCCATCACTAGCCATG NM_000315 RefSeq chr11 - 13492053 13496020 PTH 5741 parathyroid hormone
GO:0010468|GO:0006366|GO:0003705|GO:0045453|GO:0045471|GO:0030819|GO:0007267|GO:0031856|GO:0031857|GO:0033280|GO:0007266|GO:0051428|GO:0005615|GO:0071774|GO:0034645|GO:0046326|GO:0045944|GO:0071107|GO:0010288|GO:0030501|GO:0045725|GO:0046058|GO:0042493|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_144430_PI430048170 0.5380758766592691.21196231163367 0.280391098093234
0.3051894454240981.16877541022952 A A A 0.413056762586451 0.359550218944104
0.335810696872044 A A A LNCV6_144430_PI430048170 mRNA
TGCTAAGTAGAACATCAAAATTCAGGAGACTAAGAGAGCTGCTTAGGAGGAGAAAGGAGA NM_001282301
RefSeq chr16 - 60358454 60359763 LOC729159 NA UPF0607 protein ENSP00000381418-like NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131729_PI430048170 0.1360843342372941.19123930710172 4.198042127441
4.31819594879075 4.14093035978494 P P P 4.18293736008243 3.81021771869747
3.88482500304789 P P P LNCV6_131729_PI430048170 mRNA
TGAATTCAGAACCTTCTAATGAAAACTCCATGCCTCTGGTCCTTGGACTCTTGTCCATGG NM_181334RefSeq chr22
+ 44702197 44862784 PRR5-ARHGAP8 553158 PRR5-ARHGAP8 readthrough NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_145577_PI430048170 0.3095686669743031.02097621476391 0.30364440522715
0.2825595254402230.356566422276166 A A A 0.299820155455097 0.276164097767509
0.277828283248249 A A A LNCV6_145577_PI430048170 mRNA
CCCTTTGTTCTCATGAGCTGTGACCCCAGTGTATACAGGTTTTGTTTTGCCTGGAAAAGA NM_173857RefSeq chr19
- 53266759 53267665 VN1R4 317703 vomeronasal 1 receptor 4
GO:0016503|GO:0007186|GO:0005886|GO:0016021|GO:0019236 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141942_PI430048170 0.6912425417164481.23285685901404 1.68685039199726
2.18749175297307 0.451285503514595 A A A 2.05106920258334 0.951534581710206
0.419184511304241 A A A LNCV6_141942_PI430048170 mRNA
AGAAGACATGGTGACTGTGGTGGAGGACTGGATGAACTTCTACATCAACTATTACAGGCA NM_016633RefSeq chr16
+ 31527881 31528803 AHSP 51327 alpha hemoglobin stabilizing protein
GO:0030097|GO:0030492|GO:0020027|GO:0005833|GO:0006457|GO:0050821|GO:0051082 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134147_PI430048170 0.0413224321435759 1.22294402652454 7.88938004501013
7.84778127933396 8.05833913674815 P P P 7.61641761688626 7.65677521506827
7.65955332674402 P P P LNCV6_134147_PI430048170 mRNA
ACCAACAAGAATTACCAATCACCCACAACCAGGAGGACCTTTGAGACCATCTTTGAGGAA NM_024031RefSeq chr16
+ 30650919 30656413 PRR14 78994 proline rich 14 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135369_PI430048170 0.00613154915738471 2.2664311673538 1.7130898729864
1.96535746079536 1.79258857831282 A A A 0.339776021010937 0.834592165969912
0.72181535345398 A A A LNCV6_135369_PI430048170 mRNA
CCACCATGAAGAAATATATTGGTGATGAGTTCTATTGAGGAATTTTGAAAAGAGAGAAGG NM_001201536 RefSeq
chr1 - 222557901 222589933 TAF1A 9015 "TATA box binding protein (TBP)-associated factor, RNA
polymerase I, A, 48kDa, transcript variant 3"
GO:0005515|GO:0010467|GO:0006366|GO:0006363|GO:0006362|GO:0000120|GO:0006361|GO:0005634|GO:0006
360|GO:0003677|GO:0043231|GO:0000183|GO:0045814|GO:0015630|GO:0040029|GO:0005654 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130638_PI430048170 0.000383850673565728 0.737479321213141 12.3292645710493
12.2995574861062 12.3566576945771 P P P 12.7165822429334 12.8018748115357
12.7841670933695 P P P LNCV6_130638_PI430048170 mRNA
GCTTCTCTGCTCAGTGTCTACTAACGACCGACATTTGCTAATGTAAATAATAGTAAATTA NM_183373RefSeq chr6
- 3722601 3752012 PXDC1 221749 PX domain containing 1 GO:0035091 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_127731_PI430048170 0.1366475492432851.21777800501003 9.34584379187789

9.72348111532887 9.65529657553089 P P P 9.36306551893296 9.10671154237581 9.4112747211748
P P P LNCV6_127731_PI430048170 mRNA
GGGTGTAGGAAGGCCCTTTTTACATACTCTTTTCTCATGAGAGCTCACTATTTTAACAAT NM_000387 RefSeq chr3
- 48856922 48898993 SLC25A20 788 "solute carrier family 25 (carnitine/acylcarnitine translocase),
member 20" GO:0005739|GO:0005737|GO:0006853|GO:0005743|GO:0044281|GO:0016021|GO:0044255 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132363_PI430048170 0.0832621908556522 1.05330586952177 0.459081307241181
0.5349280717723940.494413220838514 A A A 0.37684397709466 0.42690700244754
0.459693028781291 A A A LNCV6_132363_PI430048170 mRNA
CTCTTCTTTTGTGTGACAGAAGTCAGCAACCAAATTTCATCTTGTTAGAACCATTTTGTTNM_001168221 RefSeq chr2
- 201487420 201619182 ALS2CR11 151254 "amyotrophic lateral sclerosis 2 (juvenile) chromosome region,
candidate 11, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133289_PI430048170 0.0337655599035690.431467836485285 2.75699194509206
2.47432289898866 1.85559130703277 A A A 3.02758966712713 3.8750241208535
3.81838277461914 P P P LNCV6_133289_PI430048170 mRNA
AAACATGACCAGAGAAGCATGTGACTCAGATAATGTTCCCCGGAAGTTGCAGAGCAATCT NM_001142386 RefSeq
chrX + 24465226 24550466 PDK3 5165 "pyruvate dehydrogenase kinase, isozyme 3, transcript
variant 1"
GO:0004740|GO:0005515|GO:0010510|GO:0035357|GO:0044281|GO:0005524|GO:0010906|GO:0071398|GO:0005
739|GO:0004672|GO:0018105|GO:0004674|GO:0006090|GO:0005759|GO:0006006|GO:2000377|GO:0071333|GO:0
044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68959_PI430048170 0.1781811883202641.2082908054105 7.3808116850403 7.13172991555874
7.57751933983293 P P P 7.12854241518009 7.07863776301878 7.09785761512806 P P P
LNCV6_68959_PI430048170 mRNA
AAAGGACAACATTGACATCACCCTACAGTGGCTTATTCAACACTCGAAGTCACGGAGAAG NM_138795 RefSeq chr1
- 202133403 202144743 ARL8A 127829 "ADP-ribosylation factor-like 8A, transcript variant 1"
GO:0007264|GO:0043014|GO:0003924|GO:0048487|GO:0030496|GO:0051233|GO:0005525|GO:0005765|GO:0005
737|GO:0007067|GO:0007059|GO:0016020|GO:0008152|GO:0031902|GO:0070062|GO:0051301 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_82997_PI430048170 0.1086495203813070.761249958653615 5.52004863957595 5.13009591828809
5.110520058595 P P P 5.84567508039907 5.71111518560228 5.38447231591807 P P P
LNCV6_82997_PI430048170 mRNA
ATCTTTCTCCCTCTACTCACGGAATTTCTGTCTATTAAGGTGACAGAACTGAAGGGCCTG NM_001193523 RefSeq
chr16 + 67529636 67546788 FAM65A 79567 "family with sequence similarity 65, member A,
transcript variant 3" GO:0008150|GO:0003674|GO:0005737|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_65984_PI430048170 0.00211036372831478 0.6360914298583856.51621215369531
6.64996981463189 6.41605294566459 P P P 7.16978690353685 7.27132217539641
7.10383330630347 P P P LNCV6_65984_PI430048170 mRNA
AGCTGAAAAATTGTAGAGTGCCCATGGGGTAGAAGTAGAATCCTTTTATACTTTGGTTCC NM_144579 RefSeq chr2
- 72942035 73071836 SFXN5 94097 sideroflexin 5
GO:0015746|GO:0034220|GO:0015137|GO:0005743|GO:0016021|GO:0055072 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128329_PI430048170 0.2638472177118560.8656888317544590.248025977816504
0.2620222006347330.348475511193931 A A A 0.4005078731239540.73633427697511
0.312530267908052 A A A LNCV6_128329_PI430048170 mRNA
CTCTTGCATTCTGTTTGGTTGCCCTTTAGTTTCCTAGTAAATGCTCCTTTTGAAAAACTC NM_175733 RefSeq chr11 +
7251949 7469045 SYT9 143425 synaptotagmin IX
GO:0005215|GO:0030054|GO:0050796|GO:0045956|GO:0006810|GO:0031045|GO:0030672|GO:0016021|GO:0046

872|GO:0042802|GO:0030667 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74928_PI430048170 0.00152527733843036 1.76067031578643 10.4619432179501
10.4999509967395 10.3777867701536 P P P 9.59997614462067 9.52925751146782
9.75541052344752 P P P LNCV6_74928_PI430048170 mRNA
GGCTGCAGCAGTGGTTAAGGAGTAACACCTTCTTGTATTAAGGAATTTTAAACTAAATAA NM_004564 RefSeq chr4
- 151670655 151761023 GATB 5188 "glutamyl-tRNA(Gln) amidotransferase, subunit B"
GO:0005739|GO:0032543|GO:0050567|GO:0070681|GO:0030956|GO:0006412|GO:0005524|GO:0008135 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142283_PI430048170 0.0101840408317197 0.5247887964751599.61317097704915
9.24124155762804 9.13781293226083 P P P 10.1253795876325 10.3743813051315
10.3158310576903 P P P LNCV6_142283_PI430048170 mRNA
GGCGTTTCTTTGCCGATTTTTGAATGTGATTTTAAAGAGTGAAAAATGAGACTATGCGTT NM_001619 RefSeq chr11
+ 67266433 67286558 ADRBK1 156 "adrenergic, beta, receptor kinase 1"
GO:0005515|GO:0005886|GO:0038032|GO:0007202|GO:0060048|GO:0031694|GO:0005829|GO:0007507|GO:0031
623|GO:0005737|GO:0004703|GO:0007173|GO:0018105|GO:0045988|GO:0018107|GO:0048011|GO:0003108|GO:0
007217|GO:0072372|GO:0007213|GO:0005524|GO:0007165|GO:0033605|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132853_PI430048170 0.4300032191830451.04143019512655 0.322760482109186
0.32809499725662 0.496750535967835 A A A 0.33021517178897 0.296011240928905
0.352002889358675 A A A LNCV6_132853_PI430048170 mRNA
CACATGTGGCATCTCTGCTGACAAACAAAAACAGACTTTTAGTTTCAATTTACATAGAGT NM_001159279 RefSeq
chr7 + 57450176 57473559 ZNF716 441234 zinc finger protein 716
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136704_PI430048170 0.796995783929267 1.08881342690923 1.2136721302299
3.36356702784686 1.36490426068025 A P A 2.19728569177074 2.53706877190594
1.83131058844354 A P A LNCV6_136704_PI430048170 mRNA
GCACAGGATTGTATATACCAAGCCATAGGCACTTACTGTAGTCAAAGAGGAACATTTTTA NM_001291306 RefSeq
chr5 - 176386023 176388762 NOP16 51491 "NOP16 nucleolar protein, transcript variant 5"
GO:0005730|GO:0042273|GO:0005634|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133090_PI430048170 0.0227742858965221 0.1821897321743051.96989258036464
1.15811379722408 2.66710779425721 A A A 4.65637509212195 4.31629879117895
4.55293279268834 P P P LNCV6_133090_PI430048170 mRNA
CCAGTTTACTGTGTGGTTTTATCTTCAGGTACAGATAGTTTGTGGTACTACTTGAAAATA NM_001079802 RefSeq
chr9 + 105558129 105641118 FKTN 2218 "fukutin, transcript variant 1"
GO:0005801|GO:0005794|GO:0008285|GO:0005783|GO:0005634|GO:0060049|GO:0005615|GO:0035269|GO:0007
399|GO:0007517|GO:0046329|GO:0000139|GO:0016021|GO:0016740 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139164_PI430048170 0.0069399173315564 1.84642148103743 9.52663394959084
9.7787927949313 9.60650049466956 P P P 8.96232247548705 8.7467493767454
8.52760641273846 P P P LNCV6_139164_PI430048170 mRNA
AAACTTGCTCTGTTTTGTAAGAGCGTGTTCCTTTTCCTCTTTTTTGTCACTTTAAAGACC NM_138499 RefSeq chr10 +
132397197 132417854 PWWP2B 170394 "PWWP domain containing 2B, transcript variant 1" GO:0005654
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127043_PI430048170 0.3061892295051421.12670079935533 8.97988196453568
9.19087428924402 9.10836305931075 P P P 9.15543184101228 8.87769553567794
8.70071903986278 P P P LNCV6_127043_PI430048170 mRNA
GCTTTAAGGATCACAGAGACACAAAGAAAATTTGAACCCTACGCTTCTCCCATCCCACTT NM_014149 RefSeq chr7
- 135183837 135211564 WDR91 29062 WD repeat domain 91 NA . NA - . NA NA NA NA NA

NA NA NA NA
LNCV6_139703_PI430048170 0.0879991806631896 0.9304978490873820.347811534021314
0.331343952989297 0.302345511083551 A A A 0.4925688374681670.429701117516587
0.368715090826679 A A A LNCV6_139703_PI430048170 mRNA
GCCTTGCCAATTTATTGCATTCTGACTCTGGAAAATGTCCTAGTTCTTAGTTAATAAACA NM_001085455 RefSeq
chr21 - 30281308 30282958 KRTAP24-1 NA keratin associated protein 24-1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_135310_PI430048170 0.4031786431185991.05143421062165 0.292818532575339
0.2874776340461820.4877967389267 A A A 0.3008743751230210.262226430701083
0.296767987771354 A A A LNCV6_135310_PI430048170 mRNA
TGTCTCGCTTCTACTACTACTACAGAAGATGGGAATATTAGGATCCTATTGAATGCCTTG NM_001004751 RefSeq
chr11 + 4639714 4640838 OR51D1 390038 "olfactory receptor, family 51, subfamily D, member 1"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139377_PI430048170 0.0117074315238303 0.6190335116544429.27053225166769
9.22171797284556 9.53367433496192 P P P 10.0148832248391 9.83470881961078
10.2428464235668 P P P LNCV6_139377_PI430048170 mRNA
GATGTAACCTGGAAACTATGCTTTACATGGCAATCAAAGCCTTTTGATCATGTACATTTT NM_007240RefSeq chr1
+ 161749767 161757164 DUSP1211266 dual specificity phosphatase 12
GO:0005737|GO:0006470|GO:0033133|GO:0008270|GO:0005634|GO:0008138|GO:0019900|GO:0035335|GO:0006
464|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138074_PI430048170 0.0030757130893451 0.6281320108902811 2.7525470695989
12.542243698853 12.6671072536148 P P P 13.3966697527244 13.1670495058365
13.4060140465467 P P P LNCV6_138074_PI430048170 mRNA
CATAAGGCATCTCAGTCAAATCCCCATCACTGTCATAAATTCAAATAAAATGTCTGAACA NM_003680RefSeq chr1
- 32775238 32818032 YARS 8565 tyrosyl-tRNA synthetase
GO:0004831|GO:0010467|GO:0000049|GO:0005153|GO:0006437|GO:0006915|GO:0005634|GO:0006428|GO:0004
822|GO:0005524|GO:0005615|GO:0005829|GO:0006418|GO:0007165|GO:0005737|GO:0004871 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_74381_PI430048170 0.2183154685849691.08580564494741 8.99421340377964 9.03856435174635
9.16578379694276 P P P 9.07185748531974 8.87061105619829 8.89693610020922 P P P
LNCV6_74381_PI430048170 mRNA
CTTCTCTCCAACATAATTATGTTAATATGGTCCTCATTTTTCTTTTGGTGCAGAACCGTT NM_018475RefSeq chr4 +
55395912 55426175 TMEM165 55858 "transmembrane protein 165, transcript variant 1"
GO:0005794|GO:0035751|GO:0006874|GO:0005765|GO:0032588|GO:0043231|GO:0000139|GO:0031901|GO:0031
902|GO:0006487|GO:0016021|GO:0010008|GO:0032472 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143254_PI430048170 0.1087107962874980.7014845373411799.89006448007494
9.97733385657724 10.4574699759083 P P P 10.367786025433 10.5355021976323
10.9574904815912 P P P LNCV6_143254_PI430048170 mRNA
CTCTAAACCTGTTATTTCTGTGCTAATAAACGAGATGCAGAACCCTTGAATGTTGAAAAA NM_004725RefSeq chr10
+ 123154243 123165370 BUB3 9184 "BUB3 mitotic checkpoint protein, transcript variant 1"
GO:0005515|GO:0007094|GO:0051321|GO:0051436|GO:0031145|GO:0051439|GO:0005829|GO:0000070|GO:0071
173|GO:0000777|GO:0000776|GO:0005654|GO:0000278|GO:0008608|GO:0051301 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134851_PI430048170 0.000474780055481353 0.1683620771302144.62131891023844
4.1085261294671 4.58368023677154 P P P 6.69810218542603 6.99589452444086
7.31832693534392 P P P LNCV6_134851_PI430048170 mRNA
GTGGGAATCTTTGATGCCAGAAATTTATAAAGAGGTTCTGTATCTTCACACCTTGAATAA NM_002605RefSeq chr15
+ 84981973 85139141 PDE8A 5151 "phosphodiesterase 8A, transcript variant 1"

GO:0006355|GO:0000160|GO:0009187|GO:0004115|GO:0004114|GO:0004871|GO:0046872|GO:0070062|GO:0006198|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140213_PI430048170 0.4105619598218391.06639192461739 10.973753561686 10.7710856839812 10.9267369156288 P P P 10.7069345445128 10.959687937911 10.7201702829939 P P P LNCV6_140213_PI430048170 mRNA TGGTCCTACTGCCTACTTCACGCTGTGCAATGTGGTCATGCGGCATGACATCCCAGACCT NM_033416RefSeq chr2 + 130342915 130346624 IMP4 92856 "IMP4, U3 small nucleolar ribonucleoprotein" GO:0005515|GO:0030515|GO:0006364|GO:0032040|GO:0005730|GO:0042134|GO:0034457 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142821_PI430048170 0.00359729653913604 3.9033494059435 4.00180659532781 3.85791549196917 3.37975019076778 P P P 1.29234053113961 1.92659984704295 2.08222700511356 A A A LNCV6_142821_PI430048170 mRNA CTTTGGCCCTGAGAAGGTTTTTAAATGTGTTATTTACTTCTCTAAACATGACGATTGCTA NM_001024401 RefSeq chr16 + 28292518 28323849 SBK1 388228 SH3 domain binding kinase 1 GO:0005737|GO:0004674|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67467_PI430048170 0.5774577727485581.23736109020336 1.94784310905535 2.95879093522 3.121265004303 A P P 2.95343045492568 2.74140719196944 1.00029668377214 P P A LNCV6_67467_PI430048170 mRNA TGAACCACCCCGAGCGCGGGGCGCGGTGCTCACAGCCACGGTACTGGCTCGGAGGGAGGA NM_003259RefSeq chr19 + 10289978 10296778 ICAM5 7087 "intercellular adhesion molecule 5, telencephalin" GO:0006909|GO:0005515|GO:0016337|GO:0005178|GO:0005886|GO:0005887|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144617_PI430048170 0.0201935625446298 6.46665435841212 6.20595123275241 6.10561913759252 6.20297948744391 P P P 2.60687193248219 4.01211884126581 3.48922645509155 A P P LNCV6_144617_PI430048170 mRNA GCCTTGGAAATCCAGATCTTTAAAATTTTATGTATTTATTAACATCGCCATTGGACCCCA NM_139155RefSeq chr10 + 70672802 70762439 ADAMTS14 140766 "ADAM metallopeptidase with thrombospondin type 1 motif, 14, transcript variant 1" GO:0030198|GO:0030199|GO:0030574|GO:0006508|GO:0005578|GO:0008270|GO:0005576|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141780_PI430048170 0.1420973533730511.08161123536553 0.666551192017101 0.7863763863990580.628087967502008A A A 0.5822767498705390.591840239270206 0.572046920749168A A A LNCV6_141780_PI430048170 mRNA CGTCAGTTGTGATAGAGTTCTAGATTGGCAATGCAGTTACATTGTTTCTTCTTTGAAAAT NM_198512RefSeq chrX + 70177482 70205703 DGAT2L6 NA diacylglycerol O-acyltransferase 2-like 6 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136897_PI430048170 0.9319459712338370.9921616961323970.30234870888568 0.3091309109067390.517021991775877A A A 0.5501802862082460.277508867006599 0.330646135019685A A A LNCV6_136897_PI430048170 mRNA ATCCTAGCCAAATATCTCAGTTACATTTACCATACAGTTTCCTTTGTGAAAGAACAGTAG NM_001037317 RefSeq chr1 - 98890244 99004893 LPPR5 163404 "lipid phosphate phosphatase-related protein type 5, transcript variant 1" GO:0016787|GO:0008152|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127762_PI430048170 0.24371410029943 1.21954734511913 7.36939217747518 6.98616999188809 6.84360105880172 P P P 6.85059575689975 6.97258982768781 6.53473223516581 P P P LNCV6_127762_PI430048170 mRNA CTTGTCCTGGGCCTGCCCCTGTGTATTCACCACCAATAAATCAGACCATGAAACCAGTGA NM_000118RefSeq chr9 - 127815011 127854773 ENG 2022 "endoglin, transcript variant 2" GO:0005515|GO:0070278|GO:0048844|GO:0048845|GO:0005615|GO:0030155|GO:0042803|GO:0005114|GO:0001

947|GO:0070022|GO:0003084|GO:0048745|GO:0042127|GO:0007179|GO:0017015|GO:0030336|GO:0009986|GO:0
003273|GO:0031960|GO:0000122|GO:0030509|GO:0005072|GO:0043235|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_104071_PI430048170 0.0017941034567539 1.72137669653733 5.16190158537664
5.23122546958191 5.10359065514593 P P P 4.36282356401394 4.50491726891908
4.27148008490996 P P P LNCV6_104071_PI430048170 mRNA
AAGATGATTATAAAGGAATATCGGATTCCTCTGCCAATGACCGTGGAGGAGTACCGCATC NM_001300801 RefSeq
chr12 - 122983479 123110489 PITPNM2 57605 "phosphatidylinositol transfer protein, membrane-
associated 2, transcript variant 2"
GO:0008152|GO:0005509|GO:0006810|GO:0016021|GO:0043231|GO:0012505|GO:0008289 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142379_PI430048170 0.1372670118924650.2121293950627423.55150176492004
0.4552324295232240.256500594725346P A A 3.97600918172192 5.52231453114084
2.50344075599047 P P P LNCV6_142379_PI430048170 mRNA
ACCCAGCTTGGGCAGAGTGCACCTGAGATTTGATAAGATCATTAAATATTTACAAAGCAA NM_183062RefSeq chr1
+ 227815716 227846470 PRSS38 339501 "protease, serine, 38" GO:0004252|GO:0006508|GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133806_PI430048170 0.3042991125747730.7123586238238390.323724554722145
0.3207024570232230.313458708591936A A A 0.4595807768500240.40665874900356
1.35268697222013 A A A LNCV6_133806_PI430048170 mRNA
AATCACATAGCCAATGATGTGTGAGTGAGAAACCTATCAGGTTTGTCCTGAGGATATAGC NM_017833RefSeq
chr21_GL383581v2_alt - 92183 95613 DNAJC28 54943 "DnaJ (Hsp40) homolog, subfamily C, member
28, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137500_PI430048170 0.7508791422694880.9883898040454450.316865674110251
0.2466791384544550.295293266600579A A A 0.2607044965817150.384058282373313
0.262001146411919A A A LNCV6_137500_PI430048170 mRNA
CAAAAGCTATCATTGTCACCCTAAATGTGGAATAAAATAAGATGCATCGACGTAGACAAA NM_003121RefSeq chr19
+ 50418937 50431052 SPIB 6689 "Spi-B transcription factor (Spi-1/PU.1 related), transcript variant 1"
GO:0043565|GO:0005737|GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0030154 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135982_PI430048170 0.6018026974196990.9774143538709690.51748769290368
0.56563486739446 0.435922525444645A A A 0.5220949304580140.621177442460586
0.473675231528119A A A LNCV6_135982_PI430048170 mRNA
GAGAGCACTAATCATTTCTGTTTGAGTTCCACTAACACTTCAAAATCAGAACTATGTTCT NM_001002294 RefSeq
chr1 + 171090876 171117819 FMO3 2328 "flavin containing monooxygenase 3, transcript variant 2"
GO:0050661|GO:0034899|GO:0006805|GO:0004499|GO:0017144|GO:0050660|GO:0005789|GO:0044281|GO:0016
021|GO:0016597|GO:0055114|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144757_PI430048170 0.3942827716670721.30181143194962 0.372478920328125
0.3421027705652851.24167668919697 A A A 0.3044006256606160.303503909224172
0.395735900158722A A A LNCV6_144757_PI430048170 mRNA
AAGCTATTCAATATCAGCAGCATTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTC NM_152459RefSeq chr16
- 5044121 5066145 C16orf89 146556 "chromosome 16 open reading frame 89, transcript variant 1"
GO:0016020|GO:0042803|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_41168_PI430048170 0.8090285100883921.02535000868087 2.28964145369731 2.41254128193683
2.10831117305076 A A A 2.51480554223027 1.90633970153555 2.23340759298908 P A A
LNCV6_41168_PI430048170 mRNA
ATCCATCCCTGAGAACAGGAACCTAACGGAGCTGGTGGTGGCCGTGACTGACGAGAACAT NM_024898RefSeq
chr19 - 6467203 6481808 DENND1C 79958 "DENN/MADD domain containing 1C, transcript variant
1" GO:0017112|GO:0030136|GO:0032851|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_127453_PI430048170 0.5278336222429470.8927172706705080.96814360380283
0.4731889328015340.415323304922133A A A 0.6095302523263770.631324104862247
1.11472515536351 A A A LNCV6_127453_PI430048170 mRNA
AGAAACAAGGACATGTTGAAGGCTTTGAGGAAACTAATATCTAGGATACCATCTTTCCAT NM_001001958 RefSeq
chr19 - 9126011 9126950 OR7G3 390883 "olfactory receptor, family 7, subfamily G, member 3"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93633_PI430048170 0.2816161741258281.62568210641758 1.99203934725824 0.870572255449629
0.728711016272839A A A 0.5887060818117630.6398697722732990.612523929024335A A A
LNCV6_93633_PI430048170 mRNA
TCACCTGGTTCAATAAAGGACTCTAAAACTGAAGCCTCAGGTAATATTGCAATTAGAAAA NM_198529RefSeq chr17
+ 29941604 30108452 EFCAB5 NA "EF-hand calcium binding domain 5, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134959_PI430048170 0.0583885141460616 0.7339789096883946.68240889209394
6.55211583667814 7.01087127217301 P P P 7.0686747512749 7.19413335728099
7.34710974669513 P P P LNCV6_134959_PI430048170 mRNA
CTCAGTCATTTCTTTACAAGAAAATGATTGAATCTGTTTTAGGTGACAGCACAATGGACA NM_018221RefSeq chr2
- 74156083 74178868 MOB1A 55233 MOB kinase activator 1A
GO:0005515|GO:0035329|GO:0046872|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129900_PI430048170 0.0355504921353714 0.69653844771028 9.33079037539471
8.97348566941334 8.97911856921158 P P P 9.62421247345308 9.69342768614133 9.5575068764968
P P P LNCV6_129900_PI430048170 mRNA
GTTTGGATTTTGATCTCAATGTGTAAAATGACAGAGATGTAACAAGCTCATAGGGTATCA NM_016276RefSeq chr20
+ 43566096 43585633 SGK2 10110 "serum/glucocorticoid regulated kinase 2, transcript variant 2"
GO:0015459|GO:0032411|GO:0005634|GO:0005575|GO:0055085|GO:0001558|GO:0005524|GO:0005829|GO:0035
556|GO:0034220|GO:0004674|GO:0042127|GO:0006468|GO:0006979|GO:0017080 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_111838_PI430048170 0.6182910499870060.9272496801393531 4.1554610091337
14.9915793442871 14.8803808570599 P P P 14.8492246713325 14.7871918659034
14.8508579788749 P P P LNCV6_111838_PI430048170 mRNA
GGGGAAGGCTTCGCTGTCTATCAGCTGTGATTTGTAAAAATAAAATCTTTAAATCTCTCG NM_003910RefSeq chr7
+ 99408977 99419616 BUD31 8896 BUD31 homolog (S. cerevisiae)
GO:0003700|GO:0006357|GO:0000398|GO:0005681|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131137_PI430048170 0.4753395584807861.0212515654127 0.295480419819848
0.3228225289414520.407140977154895A A A 0.3305295458414420.309618883706103
0.296437143420724A A A LNCV6_131137_PI430048170 mRNA
CACGTGTATCCAGAGCAAGGAAACTGGGAAGCTTCCATTTGGAAATTCTTTTTCAGGAAG NM_001220493 RefSeq
chr17 - 9771433 9791297 DHRS7C 201140 "dehydrogenase/reductase (SDR family) member 7C,
transcript variant 1" GO:0014801|GO:0010880|GO:0033017|GO:0005576|GO:0004745|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132649_PI430048170 0.3196335413875460.8517852870542290.492173146766464
0.5031392280835240.300822669137821A A A 0.4342561811692970.539376222829644
0.968537964278966A A A LNCV6_132649_PI430048170 mRNA
GCTTCAGGAAAACTGCTCTTTTGTAAAAAGAATAGCGATGACATTTTCTAATGTGCAGAA NM_030965RefSeq chr1
+ 76867500 77064052 ST6GALNAC5 81849 "ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-
acetylgalactosaminide alpha-2,6-sialyltransferase 5"
GO:0001665|GO:0009312|GO:0008373|GO:0000139|GO:0006688|GO:0016021|GO:0006488|GO:0044267|GO:0043

687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140492_PI430048170 0.0242888299232711 0.7919848310024219.79024183167355
9.71787996235489 9.78438905939527 P P P 10.1470156277115 9.97105162699702
10.1764911221238 P P P LNCV6_140492_PI430048170 mRNA
CCCTCGCTTTATACTTGCATTTCGCTTTTCAGTAAAAACAGTCAAGTTACTGAGTTCTCA NM_198531RefSeq chr18
+ 79069274 79378282 ATP9B 374868 "ATPase, class II, type 9B"
GO:0005802|GO:0048471|GO:0000287|GO:0005886|GO:0006890|GO:0005524|GO:0045332|GO:0006897|GO:0004
012|GO:0008152|GO:0072600|GO:0016021|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127605_PI430048170 0.00733536122386133 0.3821229984340245.69222440714275
5.32314599674961 5.94737947487636 P P P 6.95520867273203 7.00122216622734
7.22271699120791 P P P LNCV6_127605_PI430048170 mRNA
CTTTTAAAGTTTTGCTGAAGAATGTGTCTGTGGTTAGGATAGCACAAGCATTAACTTTTG NM_032145RefSeq chr6
- 145798135 145814785 FBXO3084085 F-box protein 30 GO:0004842|GO:0016567|GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129650_PI430048170 0.5329001418923431.41904800354133 2.22329197034175
3.75754691093623 2.47374193761162 A P A 2.84964931512372 2.17670302587394
2.32384425970286 P A P LNCV6_129650_PI430048170 mRNA
GAACAAGTTGCTAAAGATGAGAATGAACAAAGCATATTCAGGGCATGTTTAATAGACTGA NM_032487RefSeq chr3
- 169766922 169769895 ACTRT3 84517 actin-related protein T3 GO:0005737|GO:0005856|GO:0001673 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137875_PI430048170 0.00587443324003393 0.4607062940357033.50878647174452
3.7241652904552 4.05250385714468 P P P 4.66464591181786 5.06839071320865
4.93040003860685 P P P LNCV6_137875_PI430048170 mRNA
TTATTTGTAGAATATGGCAAAAGCATTTACAGCTCATCATGTATCTATCTGCTCCTGTTC NM_001171110 RefSeq
chrX + 93674012 93712274 FAM133A 286499 "family with sequence similarity 133, member A,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136344_PI430048170 0.3056577847437831.04954679648317 0.486535901945433
0.31462340792213 0.395221962604857A A A 0.2831627407543060.34886523030036
0.359017338631732A A A LNCV6_136344_PI430048170 mRNA
CTTCTGTCACCACGTCATCTTTCCAGGATTAACCTTGACCAGTAAAAAGCTCTGTAATAG NM_152453RefSeq chr15
+ 37934606 37951422 TMCO5A 145942 transmembrane and coiled-coil domains 5A GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131934_PI430048170 0.0262738765376812 0.3735762534148394.071347657484
4.2117770916409 4.41003248159727 P P P 5.0946002874718 5.7052718586126 6.0260617800201
P P P LNCV6_131934_PI430048170 mRNA
GACTTTGTTTATTTAAAGTTTCTTGCTGTGAAAAAGAACTCCCTACCTGTGAGTTCCTTT NM_020647RefSeq chr8 -
74234703 74321327 JPH1 56704 junctophilin 1
GO:0014701|GO:0003674|GO:0030018|GO:0060402|GO:0007517|GO:0005886|GO:0060314|GO:0030314|GO:0016
021|GO:0008307 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137083_PI430048170 0.0115679403111115 0.42131562536053 0.586569408955746
0.5011540175147360.300452787503027A A A 1.70696279900063 1.35808019234637
2.00665145734841 A A A LNCV6_137083_PI430048170 mRNA
GATGCTGATGATGTGCCTTATTCAGATTAGTTGGCCATTACCAGAATAAAGAATAAATCT NM_001199260 RefSeq
chr1 - 179839966 179877806 TOR1AIP2 163590 "torsin A interacting protein 2, transcript variant 3"
GO:0031965|GO:0005737|GO:0005783|GO:0005789|GO:0051117|GO:0005634|GO:0032781|GO:0016021|GO:0007
029|GO:0001671|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131162_PI430048170 0.7213820360826831.13304294337794 1.27151780881193 1.2210844377342
0.289139345542923A A A 1.11100025403619 0.2998004465471440.907407949456606A A A
LNCV6_131162_PI430048170 mRNA

TCAGCTTCAAGTCCGTTGAGAAGAAAATGACAGACATGCTAAAAGAGGAAGAAGAGAGGC NM_001039374 RefSeq chr9 + 136796337 136807741 CCDC183 84960 coiled-coil domain containing 183 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128395_PI430048170 0.2025565277898241.84825960522079 0.357107989711222 1.13802913731984 1.7866946987665 A A A 0.3130709373914020.300062949455187 0.352701753817308A A A LNCV6_128395_PI430048170 mRNA
TTCTCTGGAATGCAAGGAGGAGACTTCATTTACTTCCCAATAAACTTCATTTCTCTGGCA NM_021013RefSeq chr17_GL383564v2_alt + 57879 62596 KRT34 3885 "keratin 34, type I" GO:0005882|GO:0008544|GO:0005198|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129393_PI430048170 0.0268118156986368 0.6925068214959536.78460213101334 7.14279530122312 7.07658902270551 P P P 7.74842142595107 7.44097240137536 7.4041525164187 P P P LNCV6_129393_PI430048170 mRNA
GAAAGGTGGAGTCAGTTTGTATCAGTTAATAGGATGTTCATATTCCAAGGATATTAGTTG NM_032119RefSeq chr5 + 90558799 91164216 ADGRV1 NA "adhesion G protein-coupled receptor V1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135084_PI430048170 0.4183909056366390.4247850724736870.269843142948048 0.2949670521524450.414297748109833A A A 0.3617814577582482.66451443215782 0.308695616640818A P A LNCV6_135084_PI430048170 mRNA
GGAAGCCATTGGTTTAAGCAAAAGATAATTGGCTTATGGAATTGTGTTTTGTGCCGTTAG NM_181791RefSeq chr7 + 37740393 37741311 GPR141 353345 G protein-coupled receptor 141 GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65083_PI430048170 0.1986671791800724.80992759550489 0.3524387129071933.54229094861777 2.27254342129007 A P A 0.2937166070852840.2842614815601010.320215869792388A A A LNCV6_65083_PI430048170 mRNA
TCCAATGACATGTGTGCTAGAGCTTACTCTGAGAAGGTGACAGAGTTCATGTTGTGTGCT NM_001002231 RefSeq chr19 + 50873432 50880567 KLK2 3817 "kallikrein-related peptidase 2, transcript variant 2" GO:0022617|GO:0004252|GO:0030198|GO:0006508|GO:0005576|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140929_PI430048170 0.4914667390332541.30572389136605 1.41006254386108 0.4251919749981820.292258495833524A A A 0.4981482154853930.392516363577749 0.352050297143116A A A LNCV6_140929_PI430048170 mRNA
GAAGGTGCTGAAAATGACTTTTTTGTAAATGTCTGAAGGACACTGTCTTATACCATACCA NM_001177483 RefSeq chr10 - 21125762 21146559 C10orf113 NA "chromosome 10 open reading frame 113, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129038_PI430048170 0.1588365625924861.07961971878369 0.49614495414578 0.5144675396407460.569280116409338A A A 0.3209868814608320.416647549884695 0.505782384857859A A A LNCV6_129038_PI430048170 mRNA
CAGTCTAACTCCTATATCATGTTGTCTGCTTTCTAATAAACTCAATACTCCTACCATAGA NM_033032RefSeq chr17_JH159146v1_alt - 203890 204709 KRTAP2-2 NA keratin associated protein 2-2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138410_PI430048170 0.0478035211837119 1.3520101574578 8.31543995939194 8.46958287376976 8.44643462552826 P P P 7.73701845444578 8.11787214837721 8.04819757941114 P P P LNCV6_138410_PI430048170 mRNA
TTTAAATGGAATTTATTCTATCAACTGCCTGAGAGGACACAATGGGGGAGGGGCTTCGGA NM_020753RefSeq chr17 - 75500259 75515583 CASKIN2 57513 "CASK interacting protein 2, transcript variant 1" GO:0008150|GO:0003674|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133094_PI430048170 0.0279192617158996 0.94784339596976 0.404675912474998 0.3506762621736180.354096455072719A A A 0.4589640222391070.455258561183739

0.427495865858684 A A A LNCV6_133094_PI430048170 mRNA
GTCTGAAGTCATTCAGAAGTGGTTTGAGGTTTCTGTTTTTTGGTGGTTTTTGTTTGTTTT NM_000909 RefSeq chr4 - 163323964 163332795 NPY1R 4886 neuropeptide Y receptor Y1
GO:0005515|GO:0007631|GO:0005886|GO:0007193|GO:0019233|GO:0003151|GO:0004983|GO:0005887|GO:0007187|GO:0007218|GO:0040014|GO:0008217|GO:0001602|GO:0001601|GO:0006006|GO:0007626 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127516_PI430048170 0.5899726172048960.9162506204675740.452211824667165
0.5107953669732270.519691852531114 A A A 0.9333435009578050.406947035265721
0.461925411908828 A A A LNCV6_127516_PI430048170 mRNA
GAGAGTGATTCAAATGATTCAAATTCCATGACATTGGAAAAAGGTCATCATAGCTCTAAC NM_005039 RefSeq chr12_KI270904v1_alt - 546785 550553 PRB1 5542 "proline-rich protein BstNI subfamily 1, transcript variant 1" GO:0008150|GO:0003674|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129974_PI430048170 0.6730275355824680.8652974864289291.91331326265673
0.5086874185574140.342143012335061 A A A 1.66035311822233 0.408374921149662
1.57249640970802 A A A LNCV6_129974_PI430048170 mRNA
CCTTATGGATGCAAGAAAAGTAGCCACATCTTTAGTCACCATTCATATTTTACTGAACAA NM_001242802 RefSeq chr19 - 36818321 36838027 ZNF790 388536 "zinc finger protein 790, transcript variant 4"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143893_PI430048170 0.0330189652675388 0.6543186386280056.45407532773751
5.99136624959149 6.43013587671409 P P P 6.81189565025658 6.80632109259196
7.11619283859888 P P P LNCV6_143893_PI430048170 mRNA
AACAAGCATCACTGCCCTCACTAATAACATTGTGACTTTGCTGTCAAGTGTAGAGTCCCC NM_001012989 RefSeq chrX + 143884070 143885250 UBE2NL 389898 -
GO:0070534|GO:0005737|GO:0019787|GO:0005634|GO:0031625|GO:0006301|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143597_PI430048170 0.54941829262973 1.03988590812571 0.278933401462039
0.2907041078076850.505156356789942 A A A 0.3245767392464140.280791492834784
0.311224062813593 A A A LNCV6_143597_PI430048170 mRNA
GAGCATTACGATCCACGATTATTGATGTTGACATGTCCATGTAGTAATTTTTCTTCAAGT NM_032553 RefSeq chrX + 79170971 79172229 GPR174 84636 G protein-coupled receptor 174
GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141292_PI430048170 0.0302524877187456 1.1807531828379 8.91671319279465
8.78903940330757 8.86683932530421 P P P 8.6596259277644 8.68589338200522
8.50421014049946 P P P LNCV6_141292_PI430048170 mRNA
AGGGGTGTGAAATAGAATTTATTGTGGCTCTGATTATGTACACGTGAGATGGCCTGGCTG NM_001130144 RefSeq chr11 - 65538558 65558228 LTBP3 4054 "latent transforming growth factor beta binding protein 3, transcript variant 1"
GO:0050431|GO:2000741|GO:0005509|GO:0005576|GO:0030502|GO:0031012|GO:0060430|GO:0046849|GO:0030198|GO:0045780|GO:0060349|GO:0007179|GO:0032331|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144681_PI430048170 0.8606426562427470.9891091357575921 1.9783617775874
11.7927020546173 11.674478159489 P P P 11.7344290689134 11.9046632821222
11.8647761177534 P P P LNCV6_144681_PI430048170 mRNA
CACATAATCCTCTTCTTCATCCTCATATGAAATAAATGAAGAGAGCTTCCTCATTCAAAC NM_001355 RefSeq chr22_KI270879v1_alt - 207728 216194 DDT 1652 "D-dopachrome tautomerase, transcript variant 1"
GO:0005737|GO:0004167|GO:0042438|GO:0033981|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134599_PI430048170 0.0970928454800750.7681898028179464.76489706154093

4.82024032884599 4.53901629268773 P P P 4.90554914740733 5.35261453314304
4.98183104313888 P P P LNCV6_134599_PI430048170 mRNA
TCTGATCTGTGTGTGAGTGTGTGTGAACTTCTGAAAGACAATATTAAAGAGACTTAGTTG NM_030651 RefSeq
chr6_GL000253v2_alt - 3453363 3456944 PRRT1 80863 proline-rich transmembrane protein 1
GO:0009607|GO:0030054|GO:0005886|GO:0045202|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139967_PI430048170 0.0384440607699993 0.6955635856096079.01994755898163
9.01300487792192 9.41989309623426 P P P 9.55238587758045 9.60765685609221
9.88086788088518 P P P LNCV6_139967_PI430048170 mRNA
GACATTGCTGCTCTTGGTGGTGTTATCTAATTTTTGTGATAGGGAAACAAATTCTTTTGA NM_022457 RefSeq chr1
- 175944825 176207244 RFWD2 64326 "ring finger and WD repeat domain 2, E3 ubiquitin protein ligase,
transcript variant 1"
GO:0005515|GO:0005813|GO:0016567|GO:0016874|GO:0032436|GO:0005829|GO:0005737|GO:0000139|GO:0016
607|GO:0010212|GO:0005654|GO:0008270|GO:0005925|GO:0006977 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_76387_PI430048170 0.1075098173487490.9633603676797667.83065770007588 7.87349712315027
7.85426822610218 P P P 7.94760625752853 7.89241622428097 7.87936381667368 P P P
LNCV6_76387_PI430048170 mRNA
GTTCCCCTAAGGCACTTTTAAAGATACTCTGTAAGAACCATTAACAATAAACTTACTGTC NM_016175 RefSeq chr5
- 179837265 179858840 C5orf45 51149 "chromosome 5 open reading frame 45, transcript variant 1"
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139694_PI430048170 0.2331080057510950.7536193591201154.95445977208461
5.27620941318719 5.44324294835994 P P P 5.17723773200892 5.72491002257804
5.93604578255705 P P P LNCV6_139694_PI430048170 mRNA
GATGTTAATCAGGTCTCTCAAGTTTCATGGAGTCTATGCTGATCCTTTAATTGACAAATA NM_001174072 RefSeq
chr5 - 80138726 80256082 SERINC5 256987 "serine incorporator 5, transcript variant 1"
GO:0006665|GO:0015194|GO:0005794|GO:0043209|GO:0042552|GO:0015825|GO:0005789|GO:0051347|GO:0016
021|GO:0008654|GO:0006658|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91592_PI430048170 0.0318182581873561.20190028519842 9.83937324756164 9.87608921617178
10.0386733536658 P P P 9.62116878345909 9.62581418030608 9.71705094830742 P P P
LNCV6_91592_PI430048170 mRNA
ATTCAACAGGAGCTACAAACAGCCAAGAAGTATGGGACCAAGAATAAGAGAGCTGCCCTA NM_014169 RefSeq
chr14 - 24209580 24213830 CHMP4A 29082 charged multivesicular body protein 4A
GO:0005515|GO:0000815|GO:0097320|GO:0019058|GO:0005634|GO:0006900|GO:0042803|GO:0008289|GO:0005
829|GO:0042802|GO:0005737|GO:0007034|GO:0016197|GO:0016032|GO:0051117|GO:0061024|GO:0051260|GO:0
030659|GO:0070062|GO:0006997|GO:0030496|GO:0000920|GO:0031902|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141176_PI430048170 0.3587064356924121.13393155744998 7.73935319375945
8.12792323737841 8.12447099802938 P P P 7.6402426462284 7.7790992514664
8.03394299387123 P P P LNCV6_141176_PI430048170 mRNA
AACTTCACTCCTGTTTCATGTTCACTGGTATTTGGTGCATTTGCTTGTAATACAGTTTTT NM_152379 RefSeq chr1 -
231223762 231241187 C1orf131 128061 "chromosome 1 open reading frame 131, transcript variant 1"NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126930_PI430048170 0.00226390203073299 3.44479302723594 2.36124498347408
2.56299387514518 2.77947010243704 A A A 0.8581409761622880.797083692377965
0.722352936063959 A A A LNCV6_126930_PI430048170 mRNA
GCAAGTGTTGTAGACTAACAAAGATACTCCAAAATACAATGGCTTAAAGAATGTGGTCAT NM_001142537 RefSeq
chr11 + 63507986 63516774 LGALS12 85329 "lectin, galactoside-binding, soluble, 12, transcript
variant 4" GO:0005739|GO:0005634|GO:0097193|GO:0030395 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_138651_PI430048170 0.0864563358002145 0.60977639290111412.7096101479619
11.9587618548037 12.0046757728895 P P P 12.916689360588 13.0458965994459
12.9770813245763 P P P LNCV6_138651_PI430048170 mRNA
GGACCCCCTTCCCCCTCACCTCCAGGCAGGGACAGAATAAATGTTTGTATGGATTTTAGA NM_020695 RefSeq
chr19 - 1815245 1848453 REXO1 57455 "REX1, RNA exonuclease 1 homolog (S. cerevisiae)"
GO:0004527|GO:0090305|GO:0005654|GO:0003676 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144133_PI430048170 0.196879453881244 1.60650024660179 1.68887583333072
2.24895176697311 2.04590608727087 A A A 1.59331384829506 1.68253112449297
0.388223893190515 A A A LNCV6_144133_PI430048170 mRNA
GGTGTGCACATGTTTGCATGAAGGAATTCAGGCCTTATTAAATATTCTCAGAGGGGGAAA NM_153002 RefSeq
chr3 - 120165480 120244295 GPR156 165829 "G protein-coupled receptor 156, transcript variant 1"
GO:0007186|GO:0005886|GO:0004965|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_109966_PI430048170 0.21926188944406 1.10747889837316 10.3589527838311
10.5090521564118 10.3953190182716 P P P 10.1544864198026 10.4395715425579
10.2158655052615 P P P LNCV6_109966_PI430048170 mRNA
TGGGCCAGACGCTGGTGTGGTGTCTGCACAAGGAGTGACCTTCTCATGCTGATTTGCAGA NM_005258 RefSeq
chr15 + 40764086 40767713 GCHFR 2644 GTP cyclohydrolase I feedback regulator
GO:0004857|GO:0005515|GO:0042470|GO:0031965|GO:0050999|GO:0005634|GO:0044281|GO:0051291|GO:0030
425|GO:0005829|GO:0006809|GO:0043234|GO:0009890|GO:0005737|GO:0030742|GO:0046209|GO:0043105|GO:0
016597|GO:0044549|GO:0042133 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131351_PI430048170 0.200870671530388 2.30171002509282 1.74730367865802
0.460161350307487 2.32429736192584 A A A 0.467418264699718 0.689424263239714
0.306720857896989 A A A LNCV6_131351_PI430048170 mRNA
TAAGTCAGCAAACTGCGGGAATACTGTCTCTTCTATGTATTTTGTGAATAGTAAGCATAA NM_000441 RefSeq
chr7 + 107660634 107717807 SLC26A4 5172 "solute carrier family 26 (anion exchanger), member 4"
GO:0007605|GO:0015698|GO:0031526|GO:0015111|GO:0006885|GO:0032880|GO:0016324|GO:0015116|GO:0015
108|GO:0008272|GO:0008271|GO:0016021|GO:0015705|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130302_PI430048170 0.198717991680382 1.79788217723757 0.571635069493769
1.89027760630634 1.71137148303163 A A A 0.879738043609178 0.714376096267727
0.297681096375648 A A A LNCV6_130302_PI430048170 mRNA
AGAATGTTTTTAAAAATAGGTAGTGGAGCCATAGCCCTCACCATAGACACCTCTGAGCCC NM_003630 RefSeq
chr6 + 143450780 143490614 PEX3 8504 peroxisomal biogenesis factor 3
GO:0005515|GO:0005783|GO:0045046|GO:0055085|GO:0003333|GO:0043231|GO:0005829|GO:0008289|GO:0043
234|GO:0015171|GO:0016020|GO:0032994|GO:0046983|GO:0007031|GO:0005654|GO:0005779|GO:0016557|GO:0
005778|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73122_PI430048170 0.632368757987022 0.977483332673336 15.5230137151772
15.5083284199389 15.4614129385349 P P P 15.4649877504665 15.6361932541317
15.4847049615393 P P P LNCV6_73122_PI430048170 mRNA
GGCGCTCCGGCCCCGCGCTCCCTCCCTCTGCCTTTCATTCCCAGCTGTCAACATCCTGGA NM_001166243 RefSeq
chr3 - 59749309 61251459 FHIT 2272 "fragile histidine triad, transcript variant 2"
GO:0005515|GO:0006355|GO:0047710|GO:0005634|GO:0032435|GO:0003824|GO:0006351|GO:0042802|GO:0005
829|GO:0005739|GO:0006260|GO:0005737|GO:0072332|GO:0000166|GO:0016787|GO:0031625|GO:0006163|GO:0
009117|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54481_PI430048170 0.566024098963096 0.924201567894966 6.65196522837049
6.54105519940212 7.18397738660079 P P P 6.87149623646304 6.85064605113088

7.07041992043063 P P P LNCV6_54481_PI430048170 mRNA
TGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCAT NM_178454 RefSeq chr1
- 111117331 111140216 DRAM2 128338 DNA-damage regulated autophagy modulator 2
GO:0005737|GO:0005794|GO:0010506|GO:0006915|GO:0016021|GO:0005765|GO:0005764|GO:0043231 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_137828_PI430048170 0.281085627799726 1.05371118754526 0.52366967326534
0.348354461393298 0.450012930212325 A A A 0.401239979620462 0.366661845883406
0.33222388971654 A A A LNCV6_137828_PI430048170 mRNA
GTTTCTATATTGATTGTATGCCTGGTATAATAAAGGAAAAGACTGCCTTATTGTCCCCTT NM_005288RefSeq chr13
- 26755200 26760785 GPR12 2835 G protein-coupled receptor 12
GO:0007186|GO:0005887|GO:0004930|GO:0006874|GO:0031210 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128102_PI430048170 0.0422441179018651 0.6264519107021027.43924025177903
7.16509240411479 7.42592738743629 P P P 7.73178242944846 7.95499819878534
8.32162081320601 P P P LNCV6_128102_PI430048170 mRNA
TTTGTCCCGATTGGGTCCCAGATACACAAAATGTACAAATGTAAACTTGCTCATTTTATT NM_004257RefSeq chr2
- 105264389 105329714 TGFBRAP1 9392 "transforming growth factor, beta receptor associated protein
1, transcript variant 1"
GO:0005515|GO:0007165|GO:0050790|GO:0006355|GO:0005737|GO:0005083|GO:0016020|GO:0046332|GO:0007
179|GO:0016192|GO:0006886|GO:0005160 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136666_PI430048170 0.1933163081465890.9311836761021250.256845936335652
0.2706513096243120.36759062190729 A A A 0.3904303348155720.495913596719089
0.314078272082296A A A LNCV6_136666_PI430048170 mRNA
TTCTTTGTGGGGAGCCTCAGAAAGAAAAGGCTGAAGGAATCTCTCAGAGTGATTCTCCAA NM_052967RefSeq
chr6_GL000256v2_alt - 795776 796913 MAS1L 116511 "MAS1 proto-oncogene like, G protein-coupled
receptor" GO:0005737|GO:0007186|GO:0005886|GO:0004930|GO:0005654|GO:0016021 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_144932_PI430048170 0.00132886997466677 0.38697470336211 10.0926510927714
9.95397458078934 10.189407912295 P P P 11.3278718354534 11.329323022237 11.669971396508
P P P LNCV6_144932_PI430048170 mRNA
GGTGCATGTAAATACAGTATGCTCTTTGGATGTAAATCTTAGAAATGCAGTGTGAATGTA NM_001876RefSeq chr11
- 68754882 68841931 CPT1A 1374 "carnitine palmitoyltransferase 1A (liver), transcript variant 1"
GO:0014070|GO:0001676|GO:0006635|GO:0004095|GO:0042493|GO:0006853|GO:0005743|GO:0005741|GO:0044
281|GO:0042802|GO:0071398|GO:0005739|GO:0050796|GO:0016020|GO:0030855|GO:0032000|GO:0006006|GO:0
006641|GO:0007623|GO:0051260|GO:0042755|GO:0031307|GO:0009437|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_49730_PI430048170 0.0497255806112150.5997374790109488.99743341244191 8.83735629200878
9.17525424508774 P P P 9.41812229191323 9.64786581335313 10.0934171682245 P P P
LNCV6_49730_PI430048170 mRNA
TGACATTCTCAGTGATAATGGAGGTTTCACTGTGAAGCATCACCAGCAGATCCTTGTTTT NM_001290205 RefSeq
chr3 - 53283424 53347627 DCP1A 55802 "decapping mRNA 1A, transcript variant 3"
GO:0005515|GO:0010467|GO:0016787|GO:0016020|GO:0000184|GO:0000932|GO:0043928|GO:0005634|GO:0042
802|GO:0005829|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96700_PI430048170 0.1213882442283090.7611549315621143.67687179013484 3.7457358956018
4.18428122024098 P P P 4.25702935601679 4.28526398479197 4.29961185540627 P P P
LNCV6_96700_PI430048170 mRNA
AGAACTTTCTGTTACCAGAAGACACTCACATTCAGAATGCTCCATTTCAAGTGTGTTTCA NM_031885RefSeq chr16
- 56484346 56520096 BBS2 583 Bardet-Biedl syndrome 2
GO:0005515|GO:0038108|GO:0060170|GO:0021987|GO:0051216|GO:0043001|GO:0007288|GO:0045494|GO:0032

402|GO:0036064|GO:0005829|GO:0008104|GO:0040015|GO:0042311|GO:0045444|GO:0030534|GO:0040018|GO:0
014824|GO:0001103|GO:0034464|GO:0006996|GO:0033365|GO:0031514|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130219_PI430048170 0.2961589578027670.9695616596461550.391953176452745
0.4174105831807290.310085483797125A A A 0.4057969020890040.442146598593004
0.407164005455864A A A LNCV6_130219_PI430048170 mRNA
TTAATAAACAGAAATCTCCAGAACCTCTGAAACACATTCTTGAAGCCCAGCTTTCATATC NM_001115131 RefSeq
chr5 - 41142145 41261438 C6 729 "complement component 6, transcript variant 2"
GO:0005515|GO:0030449|GO:0006956|GO:0005579|GO:0045087|GO:0019835|GO:0006958|GO:0005576|GO:0001
970|GO:0001701|GO:0045766|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143592_PI430048170 0.0743903977204751 2.01184263737844 3.42172220250346
3.32997207250936 2.50158775950979 P P A 2.19969987682187 1.48891778650014
2.52084319841903 A A P LNCV6_143592_PI430048170 mRNA
GGGCGGGAGTGGGAAGGCTAAGAATCTGCTTAGTAAATGGTTTGAACTCTCTCCAAAAAA NM_001130861 RefSeq
chr22 - 19523023 19525337 CLDN5 7122 "claudin 5, transcript variant 1"
GO:0016338|GO:0005886|GO:0005911|GO:0005198|GO:0016021|GO:0005923|GO:0070062|GO:0042802 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127819_PI430048170 0.00563687060218016 0.2854170191994986.22120676672927
5.82573971586422 6.21446814301589 P P P 7.41173835521619 8.08733235631286
8.11910375595919 P P P LNCV6_127819_PI430048170 mRNA
CTTCATATGGCTAAGTTGTAGTTTGGCAGAGTTAACAGCATAAGAATAAACATGCTGTAA NM_153695RefSeq chr9
- 96385942 96418387 ZNF367 195828 zinc finger protein 367
GO:0003700|GO:0006357|GO:0005654|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144573_PI430048170 0.3186686005759551.0921676559399 8.15408881536281
8.14707438948565 7.92397821053536 P P P 8.08012563185721 7.96686119110801
7.79394095522987 P P P LNCV6_144573_PI430048170 mRNA
AATGTTTTGCTCCGTGCTGACGCCTCCCTCGGCACCGTCCTGTCTGTGTTGTGGACTGGG NM_001013638 RefSeq
chr16 + 805442 813861 PRR25 NA proline rich 25 NA . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_142345_PI430048170 0.0688471007520479 0.4799480268016330.49015745722617
1.4834135504782 0.52594874906371 A A A 2.03083066551854 1.36490426068025
2.34780018819049 A A A LNCV6_142345_PI430048170 mRNA
CCTGTTCTCTGGTTATGAAATGTGTTAAAGACAAGGTGCAAATTTAAAACAATGCCTGTA NM_015065RefSeq chr11
- 108505430 108593647 EXPH5 23086 exophilin 5
GO:0045921|GO:0017137|GO:0071985|GO:0050714|GO:0003334|GO:0006886|GO:0005768 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132105_PI430048170 0.1716209442029271.10910252155429 11.0757138970283
10.9121160250568 10.8880082713598 P P P 10.6850089131159 10.9189969933466
10.8214455521275 P P P LNCV6_132105_PI430048170 mRNA
CCATTAAAGACTGTGAAGGTAGAATGTTTGTAAAGCTCTTAACAGTATGTAAGCCTTCAA NM_006589RefSeq
chr1_GL383519v1_alt - 52227 60506 FAM189B 10712 "family with sequence similarity 189, member
B, transcript variant 1" GO:0005515|GO:0008150|GO:0050699|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128983_PI430048170 0.0111300790259186 0.9508517624220030.368641159138875
0.3655247635256290.331448705024961A A A 0.4448364843425330.431711916479547
0.407231275001495A A A LNCV6_128983_PI430048170 mRNA
GGCAGCATTTCATTTGTAAAGCACTTGGGTAACCCTTTGTTCTTGCAATAACAATATTAT NM_001011709 RefSeq
chr10 + 116427911 116477956 PNLIPRP3 NA pancreatic lipase-related protein 3 NA . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_128513_PI430048170 0.2381663620585291.12028727941434 5.79969529670512
5.84417216407422 5.94601139937138 P P P 5.89960944546978 5.5706658210488
5.60901523575434 P P P LNCV6_128513_PI430048170 mRNA
TAAAAATTGGAGGAGGCTTGGCCCTCAGCCCTTATATCTCTCTCTTTTTCACTCTCTTCC NM_001282533 RefSeq
chr20 - 3162616 3173592 LZTS3 9762 "leucine zipper, putative tumor suppressor family member
3" GO:0005737|GO:0030054|GO:0045211|GO:0014069|GO:0005856 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_121855_PI430048170 0.8930579383210841.10148371251532 2.07066335667289
0.4360811541870470.336449416797241A A A 1.2746126370756 0.918100338769868
0.910261918643589A A A LNCV6_121855_PI430048170 mRNA
TAGGGAGAATTAAGTCACACTGGTCTCTATAAGATAATCTGATGAATTCTGCATCTTTGA NM_178123RefSeq chr2
- 179101691 179264623 SESTD1 91404 SEC14 and spectrin domains 1
GO:0005515|GO:0005545|GO:0070300|GO:0043325|GO:0080025|GO:0070273|GO:0001786|GO:0031210|GO:0005
546|GO:0034704|GO:0032266|GO:0010314 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143193_PI430048170 0.0662800323703995 0.6836998541596551 0.6901999811577
10.2529828101558 10.1085500913944 P P P 10.7761780296002 11.0404803779997
10.9338445538831 P P P LNCV6_143193_PI430048170 mRNA
TATCCTCCCACCGCCTCCGTTAACACGATCCTGAATAAATCTTGAGAACCCCAGAAAAAA NM_001352RefSeq chr19
- 48630559 48637550 DBP 1628 D site of albumin promoter (albumin D-box) binding protein
GO:0001889|GO:0001077|GO:0000977|GO:0006357|GO:0045944|GO:0007623|GO:0005634|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131952_PI430048170 0.1326836856484171.26591077106555 11.9121771665339
11.9021354619812 12.1735902180749 P P P 11.7813207083161 11.3452067377406
11.8120618237729 P P P LNCV6_131952_PI430048170 mRNA
GACAACTGTTGCATGCCAAGTTTTTTGTGTGTGTGAAACACTTCAAAACTGATTTAAAAG NM_006815RefSeq chr12
+ 123584528 123598141 TMED2 10959 transmembrane emp24 domain trafficking protein 2
GO:0005515|GO:0005793|GO:0035459|GO:0005794|GO:0030137|GO:0005783|GO:0072661|GO:0001893|GO:0048
208|GO:0048598|GO:0006886|GO:0048205|GO:0043231|GO:0006888|GO:0042589|GO:0030663|GO:0033116|GO:0
032580|GO:0005789|GO:0007030|GO:0016021|GO:0034260 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_129895_PI430048170 0.0811054462714466 1.07940237502377 0.602578501191822
0.5198692875811210.638837046910693A A A 0.4161245210460310.493438462791165
0.521533062656304A A A LNCV6_129895_PI430048170 mRNA
TTCCTTCTGCACTGTATAAAAGGACCATTTGAGGATGTTTTGCCTTTTGTGTATTTTTTC NM_001451RefSeq chr16 +
86510526 86514464 FOXF1 2294 forkhead box F1
GO:0006366|GO:0001756|GO:0003705|GO:0007224|GO:0007507|GO:0016337|GO:0030198|GO:0060438|GO:0043
305|GO:0000977|GO:0030335|GO:0048286|GO:0051150|GO:0000122|GO:0001701|GO:0045198|GO:0060441|GO:0
072189|GO:0071345|GO:0072001|GO:0045893|GO:0060446|GO:0051145|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_52553_PI430048170 0.7907061087339021.02456840501425 3.53979120376971 3.47102215024022
3.4090000090013 P P P 3.69465086590233 3.04416953692378 3.50395905858375 P P P
LNCV6_52553_PI430048170 mRNA
ATGTGAAAAACCCTTGACACGATTGCATGTCACTTACGAAGGTACCATAGAAGAAAATGG NM_003631RefSeq chr10
- 49818274 49942027 PARG NA "poly (ADP-ribose) glycohydrolase, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_133138_PI430048170 0.0324444122611933.62574423823914 3.4642924508854
4.86698559878342 3.75351860808226 P P P 1.75526376495552 2.69526007104324
2.31027952226957 A P P LNCV6_133138_PI430048170 mRNA

CAGCCTTACTGGTACTTTTTCTCATGTATCACAGGTTACTTCTTATGTATATTAAAGTGG NM_001105576 RefSeq chrX
+ 119758612 119760202 SOWAHD 347454 sosondowah ankyrin repeat domain family member D NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143239_PI430048170 0.00177714854985977 1.47559965467487 5.76054595987127
5.59425990204957 5.69878845986114 P P P 5.2347766280117 5.05996579009636
5.07317177435389 P P P LNCV6_143239_PI430048170 mRNA
TGCTGTTGGTGAATAAATCAGTCTACTGGAACTCCAAGGACTGGATGTAAGCAGATCTTT NM_014037 RefSeq chr19
- 49289634 49325217 SLC6A16 28968 "solute carrier family 6, member 16"
GO:0005622|GO:0005328|GO:0005326|GO:0006836|GO:0016021|GO:0055085 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130211_PI430048170 0.179561920022219 1.42734866668146 1.62297976706308
1.88296337360539 2.03263931354027 A A A 1.74292817716423 1.35856533545782
0.763020003505985 A A A LNCV6_130211_PI430048170 mRNA
TATTGTAATATATGGGATTAGATTCATCTATGGAGGGCAGAGTGGGCTGCCTGGGGATTG NM_005456 RefSeq chr11
+ 45885495 45906465 MAPK8IP1 9479 mitogen-activated protein kinase 8 interacting protein 1
GO:0005515|GO:0048471|GO:0045202|GO:0005634|GO:0005829|GO:0042802|GO:0046328|GO:0005737|GO:0016
192|GO:0008432|GO:0043508|GO:0006355|GO:0031966|GO:0044302|GO:0031434|GO:0009967|GO:0031435|GO:2
001243|GO:0044294|GO:0007258|GO:0044295|GO:0044297|GO:0005789|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142081_PI430048170 0.218727253312281 1.87859313078909 0.95795544656294
1.95036899603407 0.463533353645222 A A A 0.343097493411075 0.327742350309683
0.380492673437062 A A A LNCV6_142081_PI430048170 mRNA
GCTGTGGGCATTAGTTCAGAAGCACTACCTGCATCTTAATTTTCAAAACTTAAGTTTTAT NM_001042519 RefSeq
chr2 + 190180862 190203484 C2orf88 84281 "chromosome 2 open reading frame 88, transcript variant
1" GO:0034237|GO:0005886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142212_PI430048170 0.492015771210749 1.10937979718991 12.6386726857083
12.8580423044775 13.142203685908 P P P 12.6283964393678 12.5843898331379
12.9866433301914 P P P LNCV6_142212_PI430048170 mRNA
ATTTGAACATGTAGTGTACGTGCTGTTGAGTTGTGAACTGGTGGGCCGTATGTAACAGCT NM_004965 RefSeq chr21
- 39342314 39349121 HMGN1 3150 high mobility group nucleosome binding domain 1
GO:0050678|GO:0006357|GO:0006325|GO:0031492|GO:0005634|GO:0003677|GO:0048597|GO:0000720|GO:0005
737|GO:0010225|GO:0040034|GO:0032786|GO:0006283|GO:0010224|GO:0000785 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127708_PI430048170 0.0961744106057140 .9426562621173418.75883220557077
8.73505676222913 8.80284121765205 P P P 8.89195205843714 8.78903940330757
8.87012353095778 P P P LNCV6_127708_PI430048170 mRNA
ATAGGCACCGTATTTCACAAAACTCTGTACTGTGAGCTCTAGACTCTAGATAGTAAAAAA NM_000940 RefSeq chr7
- 95359871 95396375 PON3 5446 paraoxonase 3
GO:0047856|GO:0019439|GO:0005615|GO:0042803|GO:0046872|GO:0043231|GO:0009605|GO:0046226|GO:0010
124|GO:0004063|GO:0018733|GO:0016311|GO:0004064|GO:0046395|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128678_PI430048170 0.000996775842554287 1.70198823691825 8.14418304380962
7.95773365083016 8.0370419909706 P P P 7.22148658825842 7.40945670455956
7.20327849742226 P P P LNCV6_128678_PI430048170 mRNA
GGGGACCGAGTTTGTACATTTTCCATTTTGGAATTTTGAGTTCCAATTGTTGTAAAACTT NM_025251 RefSeq chr8
- 144529178 144605695 ARHGAP39 80728 Rho GTPase activating protein 39
GO:0051056|GO:0007411|GO:0007264|GO:0005634|GO:0005856|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130990_PI430048170 0.42307028900754 1.02373989894588 0.296931463432472

0.3189878409833390.405037324316365A A A 0.3242394403844940.304170615178964
0.293101874236403A A A LNCV6_130990_PI430048170 mRNA
GTGTGTTCATTTGTCAGTGAATCGTACAGGATTTGTAAAGTGTTCATAAATTGAGCTTTC NM_130768RefSeq chr7
- 117363221 117427523 ASZ1 136991 "ankyrin repeat, SAM and basic leucine zipper domain containing 1,
transcript variant 1"
GO:0010467|GO:0007165|GO:0005737|GO:0034587|GO:0071546|GO:0007275|GO:0031047|GO:0007283|GO:0004
871|GO:0030154|GO:0043046|GO:0007140 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136102_PI430048170 0.48757170021961 1.56502872573229 0.304203584560873
1.88415843604159 0.321891700041402A A A 0.4695795229409120.359240119253424
0.354845984572536A A A LNCV6_136102_PI430048170 mRNA
AATTAACCACTCAATTCAATAGTAAAAGCCATGCTTGGATGTTTCTTTTGCATGTTGCCT NM_144770RefSeq chr21
+ 14216144 14228372 RBM11 54033 RNA binding motif protein 11
GO:0008380|GO:0006397|GO:0008266|GO:0016607|GO:0000166|GO:0000381|GO:0007275|GO:0005654|GO:0005
634|GO:0034599|GO:0042803|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143869_PI430048170 0.000534806172509044 0.4374390374861967.89652253041304
7.66755345131885 7.82699086712371 P P P 8.9988212236869 8.8339134056421
9.13103585665572 P P P LNCV6_143869_PI430048170 mRNA
CAATGCTTCACATCATATTGTGCTGCAGTTTCCATCATTTTTAAAGGACAGAGACATAAA NM_001142300 RefSeq
chr2 + 207711539 207756172 CCNYL1151195 "cyclin Y-like 1, transcript variant 1"
GO:0019901|GO:0000079 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125429_PI430048170 0.158646576630057 1.17794008310529 14.4466661261208 14.695432397812
14.8116892702957 P P P 14.4978326100348 14.2740781672976 14.4860024250734 P P P
LNCV6_125429_PI430048170 mRNA
TTTTTGAGGAAGACGCGGTCGTAAGGGCTGAGGATTTTTGGTCCGCACGCTCCTGCTCCT NM_001146227 RefSeq
chr8 - 56068179 56074581 RPS20 6224 "ribosomal protein S20, transcript variant 1"
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0006415|GO:0006412|GO:0006
413|GO:0005829|GO:0006414|GO:0005737|GO:0002181|GO:0000184|GO:0016020|GO:0022627|GO:0016032|GO:0
044267|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139942_PI430048170 0.0612387235035693 0.7939199687964566.28960499990417
6.09955351677299 5.9427314015569 P P P 6.49617174560694 6.36575732499185 6.486117952975
P P P LNCV6_139942_PI430048170 mRNA
GCTAAAATCTGTAAGATGAAGGTGACAACAAAAGTCAACCGTCATGACAAAATCAATGGA NM_001277324 RefSeq
chr16 + 14750812 14765448 NPIPA2 NA "nuclear pore complex interacting protein family, member A2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144290_PI430048170 0.3880323769155270.5399627737071360.348135575225955
1.14610612460639 0.808000280673578A A A 0.3463105495749491.52635448375446
2.47162258825198 A A P LNCV6_144290_PI430048170 mRNA
GTCATGCTTTCTATTATAATAACTTGGCTTCGGTTATCCATCAAATGCACACTTATACTG NM_001127217 RefSeq
chr13 - 36844830 36920272 SMAD9 4093 "SMAD family member 9, transcript variant a"
GO:0005515|GO:0030618|GO:0001657|GO:0003700|GO:0051216|GO:0045597|GO:0005634|GO:0046872|GO:0005
829|GO:0005622|GO:0035556|GO:0005737|GO:0001880|GO:0007179|GO:0005667|GO:0001666|GO:0030509|GO:0
003677|GO:0006351|GO:0060348|GO:0071407|GO:0005654|GO:0006468|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131188_PI430048170 0.1887804030239860.9311505933790580.270507992004242
0.3280892510799760.275589015822221A A A 0.48694137694149 0.387623003927279
0.303198663413444A A A LNCV6_131188_PI430048170 mRNA
TTTATAGTTTCCGCAACAAGGAAATTAAGGAGGCCATGGTGAGGGCACTTGGAAGAACCA NM_001004134 RefSeq
chr12 - 48202338 48203292 OR10AD1 NA "olfactory receptor, family 10, subfamily AD, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_132548_PI430048170 0.00824787707668143 1.27241275065397 9.20333654131969
9.30866841548796 9.20303046907856 P P P 8.78884228985587 8.90983759443213
8.97036693294622 P P P LNCV6_132548_PI430048170 mRNA
GTCAGGCAGACGTTTATACAACACCACGGTGCTTTTATACATTGTGCTTATTTTAATAAA NM_003684RefSeq chr1
- 46557406 46604294 MKNK1 8569 "MAP kinase interacting serine/threonine kinase 1, transcript variant
1"
GO:0035556|GO:0005515|GO:0009651|GO:0018105|GO:0008543|GO:0004674|GO:0006446|GO:0006468|GO:0005
634|GO:0005524|GO:0097192|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127840_PI430048170 0.1043386300764750.4921295355625520.398029066743875
1.85453378046911 1.03676342325636 A A A 2.11622594828892 2.48740363897916
2.08798138277376 A P A LNCV6_127840_PI430048170 mRNA
GGAATGCTCTACGTGCTCAGAACTGAATTAAAATGGCATTATGTCAATAGAGAATTCAAA NM_152334RefSeq chr15
- 101653751 101724442 TARSL2 123283 threonyl-tRNA synthetase-like 2
GO:0008150|GO:0006435|GO:0003674|GO:0005737|GO:0004829|GO:0005575|GO:0005524 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136567_PI430048170 0.0454735822555633 0.0792572666262825 0.498472829724602
0.4740055717711320.254117641222396A A A 3.16677483308334 5.1189492375932
2.73679361466715 P P P LNCV6_136567_PI430048170 mRNA
ACTGTAATTGAAAATGTTTCCGATGTGTGGAAGAAATGAAGACTGCTTTGTGTCTGCAAA NM_212559RefSeq chrX
- 100913441 100928909 XKRX 402415 "XK, Kell blood group complex subunit-related, X-linked"
GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131159_PI430048170 0.0119565836783275 6.41396046028837 2.71999329133099
2.75164556412145 3.84782106738142 A A P 0.7834277373070910.352095772488916
0.405418433995843A A A LNCV6_131159_PI430048170 mRNA
AATGTTGTAGAAGGTGGTGGATACTTGAGCCCTATCCAACTCCGGTTCCCAAAGGAAAAT NM_001195257 RefSeq
chr8 - 12310961 12318316 LOC100133267 NA "defensin, beta 130-like" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_128624_PI430048170 0.1471580912122831.21569428381938 12.5120396820002
12.5149473761548 12.7255974213845 P P P 12.1868820793679 12.136019699307
12.5572738587135 P P P LNCV6_128624_PI430048170 mRNA
GGCCTTGGCCGTGTAATGTGAGGTTTACCTGATTCTCTAATGAAATAAATACCTAAGTTA NM_016071RefSeq chr7
- 141006160 141014679 MRPS33 51650 "mitochondrial ribosomal protein S33, transcript variant 1"
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0006412|GO:0005
763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137158_PI430048170 0.2628833896709561.23575754874416 0.5991512948612391.1724125198746
0.640705290994253A A A 0.6105362891587680.47363419341743 0.48122987104134 A A A
LNCV6_137158_PI430048170 mRNA
CGTATATATACACGTGTGGTTCTATTTAGGTGGGGAAAAAATGAAAAAGCAGGGACAACA NM_152996RefSeq chr1
+ 76074703 76630984 ST6GALNAC3 256435 "ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-
acetylgalactosaminide alpha-2,6-sialyltransferase 3, transcript variant 1"
GO:0006677|GO:0009100|GO:0008373|GO:0006687|GO:0000139|GO:0016021|GO:0006488|GO:0044267|GO:0043
687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131599_PI430048170 0.5414745136333431.11957999257917 0.888954390432558
0.35541350525479 0.296101386092791A A A 0.4491755479128150.347310210688486
0.328819062189978A A A LNCV6_131599_PI430048170 mRNA
TAGGTCCTGAGGGCACAGCCTAGCTGAGTGCAAAGAAATATAGGATGCTTAGAAAGCATANM_032899RefSeq chr8
+ 123179046 123208965 FAM83A 84985 "family with sequence similarity 83, member A, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128494_PI430048170 0.3536281586452251.61338454109952 0.418912778831741

1.16565611584217 2.03439023002483 A A A 0.5457870326820260.988127676252442
0.394788862590264A A A LNCV6_128494_PI430048170 mRNA
AGGTACTTCCTGTTATAGTAAAAGAAAAAGAGTATTGGTGGCCGTTACCTATCATGACAA NM_000294RefSeq chr16
+ 30748298 30761176 PHKG2 5261 "phosphorylase kinase, gamma 2 (testis), transcript variant 1"
GO:0005516|GO:0004689|GO:0005975|GO:0005978|GO:0005964|GO:0005977|GO:0050321|GO:0044281|GO:0005
575|GO:0006091|GO:0005524|GO:0005829|GO:0045819|GO:0004674|GO:0009405|GO:0006006|GO:0006468|GO:0
005980 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134225_PI430048170 0.1839869535073490.7210265928413534.54108515120378
3.89886923475753 4.54732447835872 P P P 4.43499711011809 4.8415859840629
5.13352167393619 P P P LNCV6_134225_PI430048170 mRNA
GGGAAGTTCCTACAGTACACAGAAATAAAAGCTAATGTTACTATGAATGCGCATTACTTT NM_152636RefSeq chr11
+ 28108250 28333507 METTL15 196074 "methyltransferase like 15, transcript variant 2"
GO:0071424|GO:0070475 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90153_PI430048170 0.0177291002752250.6548679941113355.46010908903575 5.47772610727314
5.53718697028543 P P P 6.0676845675442 5.95301254345627 6.26966219294787 P P P
LNCV6_90153_PI430048170 mRNA
TTACTAGCTTGAAACAAGCTGCCCTGGTTAAAGCGCCTCTCATTCCGACTTTGAACACAA NM_032842RefSeq chr7
- 130164714 130205498 TMEM209 84928 "transmembrane protein 209, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135906_PI430048170 0.7606959844465750.7629627341763151.45750893053115
0.4157738972930450.88130843652541 A A A 2.25535444199358 0.723872621981942
0.418180950754999A A A LNCV6_135906_PI430048170 mRNA
CTGTAATAACTTCTAGGTATTCGAAACCTGTGATTTCTGTGCCATTTTCTGTAAAGATAC NM_182894RefSeq chr14
+ 74239471 74262738 VSX2 NA visual system homeobox 2 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_133520_PI430048170 0.000310291845677045 1.32114364214332 9.41333107420495
9.46180683028884 9.42550004252192 P P P 9.00617481088154 9.01186397901477
9.07661253679235 P P P LNCV6_133520_PI430048170 mRNA
GAGAGTGTGACCCTCTCCTGTAAAGTATTTATCCCACCCATTAATATAATTTCTGTATAA NM_171982RefSeq chr8
- 27284885 27311319 TRIM35 23087 "tripartite motif containing 35, transcript variant 1"
GO:0003674|GO:0005737|GO:0043065|GO:0008285|GO:0045930|GO:0045087|GO:0006915|GO:0008270|GO:0005
654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142036_PI430048170 0.9175217309694841.00405987769318 0.300998918625653
0.3086269700083890.424601453685334A A A 0.3561513430273730.307428797215529
0.355922542448311A A A LNCV6_142036_PI430048170 mRNA
AAACAAGCAGTCAGCATCTGGTGGTAGAGTTTTGCTTGGTCATTAAACTCTTAGAACTTA NM_203494RefSeq chr15
- 50500561 50546705 USP50 NA ubiquitin specific peptidase 50 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138869_PI430048170 0.00613813242586116 2.38224274423673 6.2246635537095
6.52940199930407 6.43591104417917 P P P 5.44927181614035 4.89339044627543
5.04871231096838 P P P LNCV6_138869_PI430048170 mRNA
AGATACAGCAGAGCTCACAGTGAGTCAGAAAGTCTCCACTTTCTGAACATAGCTCTATAA NM_017881RefSeq chr9
- 75061199 75088217 NMRK1 54981 "nicotinamide riboside kinase 1, transcript variant 1"
GO:0016310|GO:0050262|GO:0009435|GO:0005524|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_71941_PI430048170 0.0411462419338777 1.41273066666256 7.74378646659855
7.97861446688708 7.88398099708974 P P P 7.54499172850145 7.10839377196075
7.43239811088071 P P P LNCV6_71941_PI430048170 mRNA
TCTCAGAACACAAACAAAACCTGTGAAGAGTGCCTGAAGAACGTCTCCTGAACTTTGAGG NM_004339RefSeq chr21

- 44849584 44873903 PTTG1IP 754 "pituitary tumor-transforming 1 interacting protein, transcript variant 1"
GO:0003674|GO:0005737|GO:0016020|GO:0007275|GO:0005634|GO:0004872|GO:0016021|GO:0006606|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138963_PI430048170 0.32522519602337 1.20065884661124 1.128679431975 0.6187069463788870.533906165576733A A A 0.5813602464080210.490511771139052 0.490268382242477A A A LNCV6_138963_PI430048170 mRNA
GACATGATATAGTCAGCTGCCTTTTAAGAGGTCTTATCTGTTCAGTGTTAAGTGATTTAA NM_001759RefSeq chr12 + 4273735 4305356 CCND2 894 cyclin D2
GO:0005515|GO:0031965|GO:0019901|GO:0005730|GO:0045737|GO:0005634|GO:0005829|GO:0007049|GO:0000307|GO:0001934|GO:0005654|GO:0000785|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141486_PI430048170 0.2677936505201430.81120807142021 6.45133633232739 5.89728452069733 5.73444236951938 P P P 6.53854175898194 6.33076280319977 6.20016572105327 P P P LNCV6_141486_PI430048170 mRNA
GCTTTCTCCCTGCCTTGATTGAGCTTGAGTGATGTGGAATAAATTGTCCGTCTCTTCTTTNM_153007RefSeq chr17 + 8339869 8346045 ODF4 146852 outer dense fiber of sperm tails 4
GO:0031514|GO:0007275|GO:0016021|GO:0007283|GO:0030154|GO:0001520 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59554_PI430048170 0.00523429672089843 0.7662780618304648.41669212716143 8.43466999291462 8.5705646325841 P P P 8.89584546893754 8.80519925273618 8.87644834018022 P P P LNCV6_59554_PI430048170 mRNA
GCCAACTCAGGAAATGAAAGGACGATTCTTATTTCCACTGCGGTTACTTTTGTGGATGTG NM_001082538 RefSeq chr12 + 110614026 110649131 TCTN1 79600 "tectonic family member 1, transcript variant 1"
GO:0021523|GO:0006996|GO:0021956|GO:0036038|GO:0001701|GO:0005615|GO:0021537|GO:0001841|GO:0005829|GO:0016020|GO:0008589|GO:0060271|GO:0021904|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124218_PI430048170 0.1061729560370671.08907153467955 0.65034562664825 0.5338981940050620.685637303903621A A A 0.4327070026209390.518487467991961 0.551144704020406A A A LNCV6_124218_PI430048170 mRNA
TGAGCAGGTCTGCAGTTGGTTGGTGGAGAAAAATTTAGGAGAGCTAGTTCATAGATTTCA NM_001258275 RefSeq chr6 - 130144301 130365425 SAMD3 154075 "sterile alpha motif domain containing 3, transcript variant 3" GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127207_PI430048170 0.2621156862244981.05069240558101 0.568705691760435 0.5500801139575440.481592927880658A A A 0.5532870968820050.410813422167993 0.419233601123739A A A LNCV6_127207_PI430048170 mRNA
ATATGTGACAATACCGGTATCACCACGGTTTCAAGGGACATCTTCAGAGCCAACATCTAC NM_000502RefSeq chr17 + 58192727 58205174 EPX 8288 eosinophil peroxidase
GO:0032753|GO:0004601|GO:0032693|GO:0032714|GO:0042744|GO:0002215|GO:0072677|GO:0006979|GO:0046872|GO:0070062|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142447_PI430048170 0.3078038330972090.756643239135438 0.295934702225433 0.2771685955991720.393070358878768A A A 0.2921962495615430.560530082044956 1.17653213973694 A A A LNCV6_142447_PI430048170 mRNA
TCCTGGCATTCCATGTAGAATAGGTAGAGAATATTTAACCAATGAGCAAATAAATGTTGG NM_001098475 RefSeq chr1 + 154502218 154548147 TDRD10 126668 "tudor domain containing 10, transcript variant 1"
GO:0000166|GO:0003723 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126813_PI430048170 0.2993153431628760.7469721560708612.45236761813893 3.4358971521146 3.51290264118106 A P P 3.39507731324925 3.52013544116236 3.91688439497853 P P P LNCV6_126813_PI430048170 mRNA
GGGAAACAAGCAGTAGAGGCTGTTGGTTAATCTTGGCACAAGTTTAATTACAGGTTTTTT NM_024894RefSeq chr2

- 10570765 10689987 NOL10 79954 "nucleolar protein 10, transcript variant 1" GO:0005730 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128772_PI430048170 0.5261336553124760.95943205687205 8.09474489331654
8.27120870519838 8.05059619798726 P P P 8.15143630165374 8.31038640088199
8.13704116564023 P P P LNCV6_128772_PI430048170 mRNA
GACAAGAAGTTCCATTTGATGTCAATAAAGCAAAGTACTTGCCTACTTTTTTGAAGCTGA NM_020639RefSeq chr21
- 41739368 41767089 RIPK4 54101 receptor-interacting serine-threonine kinase 4
GO:0005515|GO:0005737|GO:0051092|GO:0016020|GO:0004674|GO:0006468|GO:0005634|GO:0005524|GO:0002
009 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131067_PI430048170 0.3784133901104720.9364027531720199.84754275767072
9.82829000374877 9.57251009649736 P P P 9.83288163005736 9.89648875047757
9.81815854662947 P P P LNCV6_131067_PI430048170 mRNA
CTACCTGATGCCCCTTCCCCAATTTGGGGACTTTTTGATAATATAAATATATCTGTATAT NM_001040118 RefSeq
chr11 - 72685068 72752389 ARAP1 116985 "ArfGAP with RhoGAP domain, ankyrin repeat and PH
domain 1, transcript variant 3"
GO:0005515|GO:0005802|GO:0051056|GO:0030037|GO:0005794|GO:0005886|GO:0007264|GO:0008360|GO:0005
547|GO:0051491|GO:0031410|GO:0031702|GO:0005100|GO:0005829|GO:0051497|GO:0008060|GO:0032312|GO:0
032580|GO:0043089|GO:0001921|GO:0008270|GO:0051270 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_145561_PI430048170 0.0563298804756071 0.5656926863028764.24361995965441
4.1558143888316 4.89227217273947 P P P 5.21585782234531 5.2244836500429
5.42432683133334 P P P LNCV6_145561_PI430048170 mRNA
GACACTTGGAAATGAAGTTCTTCCTGAAAATATCACTGCAATAAAATACGTACTACGTCA NM_006190RefSeq chr2
- 200910170 200963701 ORC2 4999 "origin recognition complex, subunit 2, transcript variant 1"
GO:0000792|GO:0005515|GO:0000808|GO:0005886|GO:0005634|GO:0000122|GO:0003688|GO:0006260|GO:0000
082|GO:0016020|GO:0006270|GO:0005654|GO:0005664|GO:0000278|GO:0000939 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_105443_PI430048170 0.2609600913136351.06581777629978 10.9148926024439
10.9546091597441 11.046763647911 P P P 10.7638789127948 10.94366863945
10.9292018094905 P P P LNCV6_105443_PI430048170 mRNA
AGGACGACATCCTCATGGATCTCATCTGAATCCCCAACACCCAATAAAGTTCCTTTTTAA NM_030973RefSeq chr19
+ 49818278 49836980 MED25 81857 mediator complex subunit 25
GO:0005515|GO:0010467|GO:0006367|GO:0048147|GO:0000122|GO:0042974|GO:0035563|GO:0071158|GO:0046
965|GO:0045944|GO:0005654|GO:2001178|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_36716_PI430048170 0.1579641489105871.19690956837608 8.25103442312087 8.57967194701506
8.35162693052553 P P P 8.32874253571355 8.13569022103063 7.93275491084119 P P P
LNCV6_36716_PI430048170 mRNA
GCTGCGGCACCGCAGGCCTGAGCCACCCCTTCTCTGCTGTCTCCTTCTCTTCCTCAGGGC NM_015554RefSeq chr15
+ 69160633 69272205 GLCE 26035 glucuronic acid epimerase
GO:0005794|GO:0005975|GO:0047464|GO:0015012|GO:0044281|GO:0006024|GO:0000139|GO:0009405|GO:0016
857|GO:0050379|GO:0016021|GO:0030203|GO:0030210 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132454_PI430048170 0.5059801952111751.02635411855825 0.430121454889783
0.2794611130441520.326782205860213A A A 0.2816270605521790.320446282659778
0.325446784753377A A A LNCV6_132454_PI430048170 mRNA
TGGTACACCATGTTTACTGCAAACCAATCATCCAAACAATTTCATTTTGCAAATTAGCCC NM_138803RefSeq chr2
- 158171356 158456753 CCDC148 130940 "coiled-coil domain containing 148, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136539_PI430048170 0.0172374102294443 1.77180885710416 5.91864248407062
5.98198649204858 5.68654240675179 P P P 5.33227613448249 4.93861403902723

4.80353755449089 P P P LNCV6_136539_PI430048170 mRNA
GCTCACATGTTGGGAATCCCTGGAATAAAATGCTTGTTCAGTGTGATGGAGCGGCAAAAA NM_001244676 RefSeq
chr2 + 88170294 88186637 THNSL2 55258 "threonine synthase-like 2 (S. cerevisiae), transcript variant 2"
GO:0046360|GO:0005575|GO:0005125|GO:0005615|GO:0009088|GO:0003674|GO:0008150|GO:0005737|GO:0009071|GO:0016311|GO:0030170|GO:0070905|GO:0004795 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91955_PI430048170 0.63673612456524 1.03236857060456 0.7286174254607050.539880660575808
0.524229205002417 A A A 0.4352160825263930.6329861266690480.588375403733699 A A A
LNCV6_91955_PI430048170 mRNA
TGAGGAAGTTCGCAAAGAAGTGAAGCTCTGAAAGTATCAGCTGAGAGATTTACAGATGAC NM_013266 RefSeq chr10
- 65912517 67696191 CTNNA3 29119 "catenin (cadherin-associated protein), alpha 3, transcript variant 1"
GO:0005916|GO:0005515|GO:0016337|GO:0005737|GO:0051015|GO:0045296|GO:0005856|GO:0030027 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137991_PI430048170 0.5718053707197210.9394102563019345.83010905083075
5.44450794378562 5.29587813285272 P P P 5.68278751341692 5.57271725201971
5.63724593306305 P P P LNCV6_137991_PI430048170 mRNA
ATATACGAGTTCTATTTGGAGTTGGGAAAATTCCTAGCAATGGCTCCCTCCAATGGGAAA NM_152592 RefSeq chr14
- 95417493 95475836 SYNE3 161176 "spectrin repeat containing, nuclear envelope family member 3"
GO:0005791|GO:0005640|GO:0005515|GO:0051015|GO:0016020|GO:0090150|GO:0008360|GO:0007010|GO:0034993|GO:0090286|GO:0016021|GO:0005635 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135531_PI430048170 0.0834260573026070.2929036893063012.7046610028255
0.3998201377780180.969249236441151 A A A 3.12411240397854 3.86902712008569
3.33842726736609 P P P LNCV6_135531_PI430048170 mRNA
GGAAAGAACTATGTTAGGTCTGATTCATGTGAAGAAGATGTTGCAAAGGATTTATTTCAC NM_018429 RefSeq
chr5_KI270897v1_alt + 985598 1097797 BDP1 55814 "B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB"
GO:0010467|GO:0006355|GO:0005737|GO:0003682|GO:0005654|GO:0005634|GO:0006383|GO:0003677 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138800_PI430048170 0.4318524263126721.1627882735705 6.44735255925913
6.45155239936795 6.56821759958583 P P P 5.68828770796715 6.45880847480605
6.52980148146429 P P P LNCV6_138800_PI430048170 mRNA
AGTCCAGCCATAAGCTATTTTGCCAACATGTCAGAGTAATCTGTATTTTTGTATGTGATT NM_005983 RefSeq chr5
+ 36152042 36184040 SKP2 6502 "S-phase kinase-associated protein 2, E3 ubiquitin protein ligase, transcript variant 1"
GO:0000209|GO:0005515|GO:0004842|GO:0071460|GO:0016235|GO:0008283|GO:0005730|GO:0005634|GO:0048661|GO:0031145|GO:0042802|GO:0005829|GO:0000082|GO:0005737|GO:0000086|GO:0051726|GO:0033148|GO:0005654|GO:0000278|GO:0019005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141266_PI430048170 0.2093049154266950.8043018430686298.38636053682167
8.49949154636435 8.22424491748704 P P P 8.98823609412946 8.5947865158863
8.42353342220362 P P P LNCV6_141266_PI430048170 mRNA
ATGAAGTCATCCACTCCTGCATCTGGTTGGTCTTTATTGAGCACCTACTATATGCAGAAG NM_001928 RefSeq
chr19_KI270868v1_alt + 38544 42489 CFD 1675 complement factor D (adipsin)
GO:0004252|GO:0030168|GO:0005576|GO:0005615|GO:0006957|GO:0006956|GO:0007596|GO:0045087|GO:0002576|GO:0006508|GO:0008236|GO:0031093|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137331_PI430048170 0.0262602631423548 0.7122791652337536.67400229784871
6.58734046071136 6.32344243019709 P P P 7.09949509718228 7.04301415569369
6.92813948913954 P P P LNCV6_137331_PI430048170 mRNA
GTCCCCACACAACCCTCACCCCTGGCTGTGAGAATCCTGAGGCACCTTGATGCATTTTTT NM_001142675 RefSeq

chr11 - 867858 915058 CHID1 66005 "chitinase domain containing 1, transcript variant 1"
GO:0005515|GO:0005802|GO:0006032|GO:0005770|GO:0005975|GO:0005634|GO:0005615|GO:0005764|GO:0008
061|GO:0070492|GO:0016020|GO:0045087|GO:1900016|GO:0004568|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132567_PI430048170 0.1964321943597910.9420896136894130.361640082970654
0.3771426331758250.316428903758606A A A 0.5103312140228250.446590261151217
0.352834593094788A A A LNCV6_132567_PI430048170 mRNA
CTACATTCTGAAAGCACAATTTTCCATTCATCTTTTTGGATGTAAACTTTTATCCCCGAC NM_139167RefSeq chr8 -
14089863 15238283 SGCZ 137868 "sarcoglycan, zeta"
GO:0048738|GO:0042383|GO:0060047|GO:0005737|GO:0007517|GO:0016012|GO:0061024|GO:0055001|GO:0016
021|GO:0005856|GO:0046716 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142219_PI430048170 0.0245454324504398 1.40715367207475 6.45574796555067
6.64771434720898 6.82314777234674 P P P 6.18242378640071 5.99212192774488
6.28216701891527 P P P LNCV6_142219_PI430048170 mRNA
GAAGCGTATTACTGGGTATAGTATGTGACTCCTCTTCTCAGACTAATAAATTATCTTTTG NM_017714RefSeq chr20
- 13389388 13638936 TASP1 55617 "taspase, threonine aspartase, 1"
GO:0006508|GO:0045893|GO:0004298 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139034_PI430048170 0.5990870785948970.7110602609659980.674903215045807
0.5648802805168680.82159620973405 A A A 0.4364765392726581.99317604931565
0.562374158909153A A A LNCV6_139034_PI430048170 mRNA
GTTTTTGGTGTAAGCACAGGATAAAAAAGGAGAGCGTCAAAGAAAAGAGACATAACACCT NM_173812RefSeq
chr12 - 63558912 63668574 DPY19L2 283417 dpy-19-like 2 (C. elegans)
GO:0000030|GO:0007286|GO:0018406|GO:0005637|GO:0007275|GO:0005634|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_79751_PI430048170 0.1760935748455061.25853216678569 7.51979256909597 7.22314014254542
7.76704604388498 P P P 7.2523621981187 7.19637311303733 7.113614210165 P P P
LNCV6_79751_PI430048170 mRNA
TTTCTGGGAATAATACTGGGGGTTTTGTTTTTGTTTTTGAACTGTCTCAAATGTTCTCCC NM_001105214 RefSeq chr8
+ 38105792 38140080 ASH2L 9070 "ash2 (absent, small, or homeotic)-like (Drosophila), transcript
variant 2"
GO:0005515|GO:0030097|GO:0043627|GO:0006355|GO:0008284|GO:0044212|GO:0006366|GO:0006325|GO:0005
634|GO:0003677|GO:0042800|GO:0046872|GO:0006351|GO:0006974|GO:0035097|GO:0048188|GO:0045944|GO:0
005654|GO:0051568. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134546_PI430048170 0.0679228209040954 1.58604468741926 6.20516485816769
6.55889908316027 5.89358718957072 P P P 5.8937949058395 5.51796878681332
5.25420115595557 P P P LNCV6_134546_PI430048170 mRNA
CATTAACTTATGGCTTCCTAGAAAAAGTGGACTTGAAATGTCTGCCCCGGTACCCAAGTC NM_001100631 RefSeq
chr1 - 13223331 13226109 PRAMEF22 NA PRAME family member 22 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_143566_PI430048170 0.0853079596897338 1.07439287372169 5.51926432765606
5.51350601045051 5.54115729118044 P P P 5.48842112061213 5.39261566342451
5.38001953790082 P P P LNCV6_143566_PI430048170 mRNA
ATAATCTTAGAAAGTGAGAGGAGGTCACTGAAACCTGGCCTGAGGTTTGAAGAAGATGGA NM_001105520
RefSeq chr17 + 6651738 6653298 C17orf100 388327 chromosome 17 open reading frame 100
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128154_PI430048170 0.10706369894034 1.06969064869351 0.467562947837716
0.5571063157189490.534279119459963A A A 0.3542348466184520.429408326141166
0.482352846903421A A A LNCV6_128154_PI430048170 mRNA
ACTACTTTAATATTGGCCAAAAAGCTAGATATGGCATCAGGTAGACTAGTGGAAAGTTAC NM_021007RefSeq chr2

+ 165293830 165392310 SCN2A 6326 "sodium channel, voltage gated, type II alpha subunit, transcript variant 1"
GO:0030424|GO:0086010|GO:0005886|GO:0042552|GO:0005248|GO:0031226|GO:0034706|GO:0030315|GO:0033270|GO:0051402|GO:0019228|GO:0033268|GO:0014704|GO:0005887|GO:0035725|GO:0034765|GO:0001518|GO:0006814|GO:0008627. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130750_PI430048170 0.413600500623377 1.05310700878686 0.302075232190637 0.30607841517342 0.512738461527675 A A A 0.310288578247649 0.272879391999429 0.32350922981509 A A A LNCV6_130750_PI430048170 mRNA
ATGAAGATTCCACCAATGTGGCTTTCACCATCTCTATGCTTTTGGGCAACCTCAACAGCT NM_000707 RefSeq chr1 - 206109848 206117048 AVPR1B 553 arginine vasopressin receptor 1B
GO:0042277|GO:0045907|GO:0007186|GO:0005886|GO:0005887|GO:0005000|GO:0005080|GO:0007202|GO:0007204|GO:0032870|GO:0001992|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129487_PI430048170 0.835769443975756 1.00892576067224 0.529907963605276 0.463567879611237 0.374153657601133 A A A 0.38633364717826 0.47761032832248 0.467720135186022 A A A LNCV6_129487_PI430048170 mRNA
TCTAGAGGACATGCATACTTTCCACATTATATACTCCAACTGGTTAATATGCTAATCTGA NM_004784 RefSeq chr4 + 118034344 118258634 NDST3 9348 N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3
GO:0000139|GO:0019213|GO:0016021|GO:0015012|GO:0030210|GO:0015016 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142158_PI430048170 0.540383524151138 0.977617413289857 8.99930661655518 9.02777687603461 9.14961617882791 P P P 9.09951832854533 9.10818343166932 9.07117088905157 P P P LNCV6_142158_PI430048170 mRNA
TCAAAAAGCAATCTGGAAGAAAGCCCTGTGCTTTGGGGGAGTAAGAATGTGTGTGCAGAA NM_000182 RefSeq chr2 - 26190634 26244726 HADHA 3030 "hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit"
GO:0042645|GO:0005515|GO:0032868|GO:0006635|GO:0042493|GO:0035965|GO:0005743|GO:0003857|GO:0044281|GO:0032403|GO:0005739|GO:0051287|GO:0016508|GO:0016509|GO:0016507|GO:0003985|GO:0004300|GO:0006644|GO:0000062|GO:0044255|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141550_PI430048170 0.103671551528833 0.485701001460543 0.301566625437105 1.76744406321893 0.985709775910857 A A A 1.57379145483271 2.45833169095164 2.3649924335256 A P P LNCV6_141550_PI430048170 mRNA
GAACCATACTACCATCTCCAGGCCCAAACTCTGAAATAAAGACATGAGCATGAGCACAAA NM_001160213 RefSeq chr16 - 72119096 72172450 PMFBP1 83449 "polyamine modulated factor 1 binding protein 1, transcript variant 2" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130223_PI430048170 0.164277510290911 1.77662264552885 1.51637409464371 1.3739860301267 0.403188449205145 A A A 0.364988839502262 0.313397331652059 0.359420901699475 A A A LNCV6_130223_PI430048170 mRNA
GCGCTGTTTCCTTCACAAATTAGACATTGGTTTGGGAAACAATGTAGCCTCGTTAAACAT NM_005440 RefSeq chr17 + 43025240 43032041 RND2 8153 Rho family GTPase 2
GO:0005515|GO:0007165|GO:0047485|GO:0007264|GO:0008152|GO:0003924|GO:0005525|GO:0002080|GO:0005769|GO:0048672 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99479_PI430048170 0.0100920874430532 1.24530452629317 3.9322084515464 4.02731081278024 3.96464260355968 P P P 3.64068354525565 3.58014652985419 3.75027991431433 P P P LNCV6_99479_PI430048170 mRNA
TGACTATGGCTACAAAAGCTGGGAAGCCTTCTCTAACCTCTCCTATTATACTAGAGCCCT NM_000963 RefSeq chr1 - 186671811 186680427 PTGS2 5743 prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
GO:0019369|GO:0006693|GO:0035633|GO:0019674|GO:0010042|GO:0042803|GO:0071636|GO:0031622|GO:0034644|GO:0004601|GO:0001516|GO:0032496|GO:0051926|GO:0007613|GO:0007612|GO:0006979|GO:0032355|GO:0

042633|GO:0007566|GO:0051968|GO:0031394|GO:0051384|GO:0045786|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126041_PI430048170 0.1714002941435991.39562992581833 3.00349184170139 3.37163194801673 3.74581350613067 P P P 3.03677145141162 2.53995913487046 3.12971218922819 P P P LNCV6_126041_PI430048170 mRNA TGCAGTCATTTCAGTTTGATTTCATTGGAGACACTCTGACTGATGATGAAATTAACATCG NM_002547RefSeq chrX - 68042343 68433457 OPHN1 4983 oligophrenin 1
GO:0051966|GO:0051056|GO:0030036|GO:0030054|GO:0007264|GO:0003779|GO:0048488|GO:0015629|GO:0005100|GO:0005829|GO:0007399|GO:0006930|GO:0007165|GO:0005543|GO:0043197|GO:0035255|GO:0032321|GO:0007411|GO:0030100|GO:0043195 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142753_PI430048170 0.9507293038998131.10187831601339 1.48962727877381 3.41776557934439 3.33877279224661 A P P 2.43936870438417 2.68576765742225 3.25867112578321 A P P LNCV6_142753_PI430048170 mRNA GTTCGTTTTTGGTTCTGAGGATGTGATATCCGTACTTACTGATACTAAAGCCAAATTTAA NM_001200050 RefSeq chr1 + 182789448 182830384 NPL80896 "N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase), transcript variant 2"
GO:0008747|GO:0006488|GO:0044267|GO:0019262|GO:0043687|GO:0018279|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144425_PI430048170 0.4716409820294130.79751254103794 0.306776396249289 0.2915345844007620.353274833488268A A A 1.17401953859286 0.28329154921884 0.279930042316282A A A LNCV6_144425_PI430048170 mRNA GGCCCTCAGTGTTGTACTATTTGTCTCGGTCCTTGTGTCTAAGGAGCAATGCAGAAAAAA NM_007264RefSeq chr12 + 56994570 56996685 GPR182 11318 G protein-coupled receptor 182
GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0007166|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142076_PI430048170 0.1741430316616 1.29575315668473 9.80124037027588 9.70831888375523 9.72583330416197 P P P 8.98096762784508 9.64341333465847 9.4149690964422 P P P LNCV6_142076_PI430048170 mRNA CTGCCCAAGATATGTATTCTCTGACACTCTTATTTGGTCATAAAACAATAAATGGTGTCA NM_002561RefSeq chr17 - 3673227 3696404 P2RX5 5026 "purinergic receptor P2X, ligand gated ion channel, 5, transcript variant 1"
GO:0035590|GO:0004931|GO:0010524|GO:0005524|GO:0050850|GO:0005639|GO:0007399|GO:0007165|GO:0034220|GO:0005887|GO:0006810|GO:0001614|GO:0005216|GO:0006812|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129128_PI430048170 0.8662433879196280.96519509472148 5.00458715738145 5.09805742643183 4.53864752040432 P P P 4.74494566164839 5.3007673012746 4.73296812393398 P P P LNCV6_129128_PI430048170 mRNA CTGCTGAGTCTGTCTGATGTTTTGGTTGTGTGAATAAATATAATTCCCCTCTGGAAAAAA NM_001276501 RefSeq chr6_GL000256v2_alt - 3506970 3509120 GPSM3 63940 "G-protein signaling modulator 3, transcript variant 1" GO:0008150|GO:0003674|GO:0050790|GO:0005737|GO:0008277|GO:0005575|GO:0005092 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137302_PI430048170 0.0242238786468988 0.5134074598537635.97000777058795 5.41751247124674 6.07065261717866 P P P 6.5095404071303 6.72155321292903 7.12526708397182 P P P LNCV6_137302_PI430048170 mRNA GAAGATGGTAGAAATGTACTATGTTTATGCTTCTACATCCAGTTTGTACAAGCTGGAAAA NM_014247RefSeq chr4 + 159267845 159360149 RAPGEF2 9693 Rap guanine nucleotide exchange factor (GEF) 2
GO:0005515|GO:0070300|GO:2001214|GO:0048022|GO:0045202|GO:0031697|GO:0032854|GO:0031175|GO:0046582|GO:0007218|GO:0000165|GO:0048167|GO:0045860|GO:0043025|GO:0070374|GO:0005088|GO:2000481|GO:0019901|GO:0005509|GO:0030165|GO:0019992|GO:0043234|GO:0007186|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_134706_PI430048170 0.0883458801363047 1.21705456352042 2.7875428983447
2.57117293142404 2.89324201353213 A A A 2.41452899492427 2.50853932251989
2.49535964585638 A A P LNCV6_134706_PI430048170 mRNA
AAATTTAGAATTTCTCATTGGGAGAGTAAGGTACCCCCATCCCAGAATGATAACTGCACA NM_031281 RefSeq chr1
- 157513376 157552520 FCRL5 83416 "Fc receptor-like 5, transcript variant 1"
GO:0043235|GO:0005886|GO:0050859|GO:0016021|GO:0051280 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_60765_PI430048170 0.00345006103888879 0.458596041258937 4.96152493831575
4.51495270198058 4.86368146399712 P P P 5.73873856834548 5.90856779525103
6.08352570557534 P P P LNCV6_60765_PI430048170 mRNA
TCCAAAGAGCAGCTTCTCAGATCTTCAGTGTTCACTGGTAAATTTCTAACAGTGTATTTG NM_015382 RefSeq chr14
- 31100114 31207523 HECTD1 25831 HECT domain containing E3 ubiquitin protein ligase 1
GO:0005515|GO:0005737|GO:0004842|GO:0042787|GO:0016874|GO:0001843|GO:0005634|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145346_PI430048170 0.0375354392807381 0.635707460666108 9.63958632278008
9.57895565887573 9.81066366118342 P P P 10.1251048574503 10.2002301772017
10.6232215514411 P P P LNCV6_145346_PI430048170 mRNA
GGTAGTCTTCAACCAGGGATTGTTTCTGTTTAACTTCTTATAGGAAAGCTTGAGTAAAAT NM_001560 RefSeq chrX
+ 118727595 118794533 IL13RA1 3597 "interleukin 13 receptor, alpha 1"
GO:0005515|GO:0005886|GO:0030890|GO:0002639|GO:0016515|GO:0005898|GO:0035772|GO:0007166 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130246_PI430048170 0.579609909080771 1.14139233688606 1.82090484265189
2.17132528541357 1.75810187663905 A A A 2.32067235576526 1.84948792255889
0.491479443364006 A A A LNCV6_130246_PI430048170 mRNA
ACATTTGAAGAAGAACGGCTCCTCTATTGCCGCTTCCTGGACAACAAGCTATTGTTATCC NM_001031854 RefSeq
chr11 + 44047980 44059977 ACCSL NA 1-aminocyclopropane-1-carboxylate synthase homolog
(Arabidopsis)(non-functional)-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143817_PI430048170 0.00320952403760084 0.367318526044472 4.15333043834989
3.56532688891518 3.93403473651365 P P P 5.08528527511687 5.39498171421207
5.53158934959034 P P P LNCV6_143817_PI430048170 mRNA
ATGGCACTTGGAGTGCATCATAGTTCTACAGTTTGTTTTTGTTTTCTTCAAAAAAGCTGT NM_016441 RefSeq chr2
+ 36356226 36551135 CRIM1 51232 cysteine rich transmembrane BMP regulator 1 (chordin-like)
GO:0010951|GO:0005886|GO:0004867|GO:0005010|GO:0048009|GO:0016021|GO:0030165|GO:0001558|GO:0070
062|GO:0007399|GO:0005520 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144310_PI430048170 0.0218933415763845 0.636571663450929 9.8704160453209
9.44929497140008 9.46003278707426 P P P 10.0460190592888 10.3565728316772
10.3517067208704 P P P LNCV6_144310_PI430048170 mRNA
CCTCGGTAGCCCCACTTTCCTTGCTGTGTGGACTTGAAACAAAATAAAATGTGTTGCTTC NM_001103161 RefSeq
chr1 - 20719731 20732640 SH2D5 400745 "SH2 domain containing 5, transcript variant 1"
GO:0030054|GO:0045211|GO:0014069 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138569_PI430048170 0.615107887304363 1.00719796211453 0.340182152600937
0.321652860128637 0.283597726953964 A A A 0.309877220480678 0.313249509319648
0.291747231044257 A A A LNCV6_138569_PI430048170 mRNA
GGGCTTAAGGCTAATTTGAGTTGAAGGGTATTTGTAATATTTGATTTGCTTTTAGCAGAG NM_145175 RefSeq chr2
+ 14632685 14640044 FAM84A 151354 "family with sequence similarity 84, member A" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_63134_PI430048170 0.301851861432263 2.56547899323073 2.59496935384696 2.8966480889737
0.325728472064479 A A A 1.66196062336367 0.383033850809374 0.353607341426917 A A A

LNCV6_63134_PI430048170 mRNA
AGGACATTACTGGTTGTTCTGGCTGGTTTGAAAAGCACAAATAAACTTGGGATGTGGTTC NM_003726RefSeq chr17
- 48133439 48430232 SKAP1 8631 "src kinase associated phosphoprotein 1, transcript variant 1"
GO:0005515|GO:0050852|GO:0017124|GO:0005886|GO:0019901|GO:0019903|GO:0005634|GO:0009967|GO:0032
403|GO:0005737|GO:0005911|GO:0045944|GO:0005070|GO:0045893|GO:0042169 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128446_PI430048170 0.7305689094162520.9927487131175090.430983343482444
0.4391543073862820.371132449530649A A A 0.460259575400881 0.396222888791926
0.416493345453759A A A LNCV6_128446_PI430048170 mRNA
TCAGGAAGGCTTGTGTTAGGGACAATCTCAGACTATTATCATGGGCCAAACCTGAGAGAT NM_033516RefSeq chr9
+ 6328348 6330918 TPD52L3 89882 "tumor protein D52-like 3, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134079_PI430048170 0.3919287560228060.3590961670042990.401783173761094
0.26500508313716 0.293386602351843A A A 0.4810534764888162.96476192502967
0.304984717056585A P A LNCV6_134079_PI430048170 mRNA
CTCTGTAAATGGTTGGATTTCATTTCACCCTTAAAGGGATGCTTAAAGGAGAAGATAATA NM_002409RefSeq chr22
+ 39457319 39492196 MGAT3 4248 "mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-
acetylglucosaminyltransferase, transcript variant 1"
GO:0000139|GO:0016021|GO:0003830|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144081_PI430048170 0.1126616550652191.20425548813081 8.43057165620908
8.12685922950255 8.13269653108286 P P P 8.12581259964302 7.91236304566577
7.85453452016448 P P P LNCV6_144081_PI430048170 mRNA
TTCTAACCGAAGACAAGACAGACACCCATGTTCATAAATAAATAAAAGTAAGCCTAAGCA NM_020798RefSeq chr11
+ 78188811 78214711 USP35 57558 ubiquitin specific peptidase 35
GO:0004197|GO:0016579|GO:0004843|GO:0061136|GO:0043161 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140270_PI430048170 0.4914106243123991.02157606376009 0.501215940104188
0.4579390126733710.392931742655055A A A 0.37024762144416 0.444359626619811
0.445855749227287A A A LNCV6_140270_PI430048170 mRNA
CTTGTAGGAATACTAACATGGTATAGATTATCTGAGTGTTCCACAGTTGTATGTCAAAAG NM_006790RefSeq chr5
+ 137867855 137887851 MYOT 9499 "myotilin, transcript variant 1"
GO:0042383|GO:0005515|GO:0030018|GO:0006936|GO:0051393|GO:0003779|GO:0015629|GO:0008307 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138202_PI430048170 0.9553039350627641.06651467819226 1.86312769755829
0.5626194399694980.623709726548217A A A 0.5437423330882571.59706255495092
0.813627432341542A A A LNCV6_138202_PI430048170 mRNA
GGAGGGGGTTGGAGTTTTGAACGTAGTAAGCCTTACCTTAATAGAATTAAATTCATGAAA NM_022076RefSeq chrX
+ 44844002 44844888 DUSP2163904 dual specificity phosphatase 21
GO:0000188|GO:0005737|GO:0031314|GO:0005759|GO:0005634|GO:0008138|GO:0035335|GO:0017017|GO:0004
725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145077_PI430048170 0.7086211807147590.9690848722886669.09561446564862
8.87149767391928 8.96456815739423 P P P 8.87325794465153 9.16825826058211
9.01982944359593 P P P LNCV6_145077_PI430048170 mRNA
CCCTGAGGTTGTACTGTAAACATCATAGTGACTTGTCTTTTCAAATATATTCCCACTATT NM_001127464 RefSeq
chr16 + 88427470 88440757 ZNF469 84627 zinc finger protein 469
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138070_PI430048170 0.0789802423308463 0.3782165737169340.437850392748881

0.4535717478526081.96420052914897 A A A 2.45775567662212 2.81864448096323
2.31335920194493 A P A LNCV6_138070_PI430048170 mRNA
CACGCTGTATTAGATGTGTGTAAATTAGCCAAAGGTTATTTTACAAAGTGAGACATTGGT NM_015902RefSeq chr8
- 102252273 102412689 UBR5 51366 "ubiquitin protein ligase E3 component n-recognin 5, transcript
variant 1"
GO:2000780|GO:0000209|GO:0005515|GO:0050847|GO:0043130|GO:0006511|GO:0004842|GO:0033160|GO:0008
283|GO:0016874|GO:0003723|GO:0090263|GO:0034450|GO:0005634|GO:0035413|GO:0006974|GO:0005737|GO:0
006281|GO:0042787|GO:0016020|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_134278_PI430048170 0.7988246821331960.9859018092161419.70047994657655
9.76955572206777 9.8422812715566 P P P 9.7602376103409 9.7090264138639
9.90107421821029 P P P LNCV6_134278_PI430048170 mRNA
TTATATTCCGGAGGTAGAAGGCGTAGAACAGGTTATGGATGATGAATCAGATGAAAAAGANM_015700RefSeq chr2
- 69396112 69437628 NFU1 27247 "NFU1 iron-sulfur cluster scaffold, transcript variant 1"
GO:0005739|GO:0005515|GO:0005737|GO:0051539|GO:0016226|GO:0005506|GO:0005654|GO:0005634|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_21581_PI430048170 0.1380810617915560.8151177756455466.76451944173032 6.34148765995452
6.43175490545588 P P P 6.81681885018197 6.97248393055529 6.65045278863044 P P P
LNCV6_21581_PI430048170 mRNA
ATCTCTGTGGAGCGGGGAACGGGACAGTTGTGTAAAAATCCAAAATACAATTCTGACTAT NM_012079RefSeq chr8
- 144314582 144326919 DGAT1 8694 diacylglycerol O-acyltransferase 1
GO:0005515|GO:0016746|GO:0019915|GO:0003846|GO:0055089|GO:0050252|GO:0044281|GO:0034379|GO:0035
336|GO:0042572|GO:0005789|GO:0019432|GO:0004144|GO:0006641|GO:0036155|GO:0016021|GO:0006644|GO:0
044255|GO:0046474|GO:0046339 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130938_PI430048170 0.3683355716820061.13982211870496 0.474700978121801
0.4905049253178210.933294899027481 A A A 0.5127012162247050.428232813474805
0.438112902746746 A A A LNCV6_130938_PI430048170 mRNA
AAACAGGAAAATACCTGCAACGTCACCATAGAAGGCTTGGATGCCGAGAAGTGTTACTCT NM_022148RefSeq chrY
- 1190495 1212723 CRLF2 64109 "cytokine receptor-like factor 2, transcript variant 1"
GO:0005886|GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139492_PI430048170 0.31708175205903 0.9772588957647420.372168057734505
0.3979756004269770.312521864928675 A A A 0.3866426682120240.414536797222824
0.382160722084821 A A A LNCV6_139492_PI430048170 mRNA
CGTATATATGGCAGACCACAGGACTTCTGTCCAAGAGAACTGAGTTCAACTCCATCTATG NM_001245RefSeq chr19
- 51519529 51531856 SIGLEC6 946 "sialic acid binding Ig-like lectin 6, transcript variant 1"
GO:0016020|GO:0005887|GO:0007267|GO:0030246|GO:0005576|GO:0007155 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131791_PI430048170 0.00110169929260565 0.4403379683726245.43608875193279
5.10730817744618 5.24138024485838 P P P 6.24449941591744 6.5036330213408
6.58423312921567 P P P LNCV6_131791_PI430048170 mRNA
CTAGCTCTGTCCTGCTACCTAAAGGATATAAAGAAATACTATTGCTCTAGAATGTATTAC NM_020830RefSeq chr2
- 223875342 223945387 WDFY1 57590 WD repeat and FYVE domain containing 1
GO:0008150|GO:0005545|GO:0008270|GO:0005634|GO:0005769|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131166_PI430048170 0.7138181402257451.00581149427976 0.343848115853147
0.3260634857473580.281155605713712 A A A 0.31290109259932 0.318172955159861
0.295537665986988 A A A LNCV6_131166_PI430048170 mRNA
GCTGCTGGAAACCATGCAAAATGTTTTGAATTGCCCTTAAAATATGGAAAATGTTTTCTG NM_015215RefSeq chr1
+ 6785323 7769706 CAMTA1 23261 "calmodulin binding transcription activator 1, transcript variant

1" GO:0006355|GO:0005737|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129739_PI430048170 0.0486853742401636 1.13573960292609 13.2448385103377 13.3227944848908 13.4096376848397 P P P 13.0735522642843 13.2264459616535 13.1268959806946 P P P LNCV6_129739_PI430048170 mRNA GCTGTTACACAGTGTCATTGTTGATGTTAAATTAAAGTCATATTCTTGCTTCTCTCCAGA NM_001198909 RefSeq chr7 + 128862802 128865849 ATP6V1F 9296 "ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F, transcript variant 2"
GO:0005515|GO:0008286|GO:0051701|GO:0015078|GO:0016469|GO:0033180|GO:0042624|GO:0055085|GO:0005829|GO:0006879|GO:0033572|GO:0016020|GO:0046961|GO:0008152|GO:0015991|GO:0090382|GO:0016471|GO:0070062|GO:0015992. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140616_PI430048170 0.0330561885207242 1.3143501249213 9.03704391340522 9.013111872393 9.07824765145006 P P P 8.64181898917927 8.78537786568161 8.50531661338627 P P P LNCV6_140616_PI430048170 mRNA TTCCCTGATGCAGTACTTATTATGTTGGATAATCAGAAACTGGTGCCTCAGCCTCGTGTG NM_016049 RefSeq chr14 - 24138964 24141588 EMC9 51016 ER membrane protein complex subunit 9
GO:0072546|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133058_PI430048170 0.00845054661938704 0.38850193900345 4.26006556294456 3.88357617936646 4.16994984764295 P P P 5.09196557298528 5.47692502629649 5.78134611715278 P P P LNCV6_133058_PI430048170 mRNA GCCACACCCAGGCAATTTAATATCCATGGTCTTCTATAATGTTTATACCACATTGTAAAT NM_016631 RefSeq chr21 - 32733898 32771858 PAXBP1 94104 "PAX3 and PAX7 binding protein 1, transcript variant 1"
GO:0001078|GO:0007517|GO:0045944|GO:0031062|GO:0005634|GO:0014842|GO:0000122|GO:0000978|GO:2000288|GO:0006351|GO:0008134|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130457_PI430048170 0.376645408295575 2.96552358116152 3.1549522278978 0.489972734453241 0.537475823232522 P A A 0.322035889033678 0.402991247480272 0.479458228255317 A A A LNCV6_130457_PI430048170 mRNA CCTGGCAAACACTGACATTACATCATTATCATGATTTAAAGGAAATAGTACTAGAGAAGG NM_021023 RefSeq chr1 + 196774799 196794073 CFHR3 10878 "complement factor H-related 3, transcript variant 1"
GO:0072562|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142254_PI430048170 0.186939795824106 1.25887453672428 4.43952761956219 4.36168415297103 4.13361873264795 P P P 3.96456682899488 4.27686858189888 3.64545990199055 P P P LNCV6_142254_PI430048170 mRNA GTAATGAGCACCTGGATATGTCAATTAAAATGCCCATTTGTGAAGCTTACTCAATAAAAC NM_021133 RefSeq chr1 - 182573633 182589259 RNASEL 6041 "ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)"
GO:0005515|GO:0006397|GO:0003723|GO:0006364|GO:0019221|GO:0019843|GO:0004521|GO:0005575|GO:0005524|GO:0046872|GO:0016363|GO:0005829|GO:0005739|GO:0051607|GO:0060337|GO:0004672|GO:0045944|GO:0006468|GO:0045071. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145749_PI430048170 0.0170015443664563 0.350052254186164 3.8034981191306 3.90858428681655 3.95260194978426 P P P 5.01961296626034 5.33607827728173 5.759855568294 P P P LNCV6_145749_PI430048170 mRNA TATCTGTTCTTTGTGTGTAAAGAGTAACAATAAAAGAACACCAGTGTACCCACCGTATAG NM_001291476 RefSeq chr17_KI270857v1_alt - 1848854 1882558 DDX52 11056 "DEAD (Asp-Glu-Ala-Asp) box polypeptide 52, transcript variant 2" GO:0016020|GO:0008152|GO:0005730|GO:0004386|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129902_PI430048170 0.00249415882650573 0.376095047837842 10.2968272302959 10.0150738762354 9.7680888864609 P P P 11.3219243378641 11.6561741873904 11.3591911490487 P P P LNCV6_129902_PI430048170 mRNA GTGTGTGATGTGAAGCCAATTCAGACAGGCAAATAAAAGTGACCTTTTACACTGAAAAAA NM_130444 RefSeq chr21

+ 45455509 45513720 COL18A1 80781 "collagen, type XVIII, alpha 1, transcript variant 3"
GO:0005515|GO:0008284|GO:0005581|GO:0008285|GO:0005615|GO:0046872|GO:0042802|GO:0022617|GO:0030198|GO:0030574|GO:0009887|GO:0007155|GO:0070062|GO:0030335|GO:0042493|GO:0005576|GO:0001525|GO:0005604|GO:0031012|GO:0005198|GO:0001886|GO:0051599|GO:0005788|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145321_PI430048170 0.10520398126877 1.21717774066124 7.05679096227793 7.39404919139939 7.35105200045324 P P P 7.11729539292759 6.85568360276515 6.98923837093008 P P P LNCV6_145321_PI430048170 mRNA
ATGTTAGAATGAACAAATGCTAAAGAGATGTTCCTCTCCTTCTTCCCTACTCCCCAACTC NM_005659RefSeq chr22 - 19449940 19479215 UFD1L 7353 "ubiquitin fusion degradation 1 like (yeast), transcript variant 1"
GO:0005515|GO:0006511|GO:0001501|GO:0004843|GO:0005102|GO:0043161|GO:0005634|GO:0032403|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143413_PI430048170 0.2942532614411790.9054795405622510.3470263048536 10.4063336408777 10.6860823067821 P P P 10.6553452687244 10.5264449536578 10.7047470612392 P P P LNCV6_143413_PI430048170 mRNA
GGCTGATGTGTTATGGGCAGTATGGATGTCTTCATTTGTTGCTTCTGTTTTTCATCTTTT NM_024779RefSeq chr12 + 57591158 57603428 PIP4K2C 79837 "phosphatidylinositol-5-phosphate 4-kinase, type II, gamma, transcript variant 1" GO:0046854|GO:0005737|GO:0016020|GO:0005524|GO:0016309|GO:0070062|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102136_PI430048170 0.941520579808372 1.00477260176681 8.55343628174905 8.43310161036901 8.35220420687242 P P P 8.51464949463841 8.41951311884005 8.38807843709262 P P P LNCV6_102136_PI430048170 mRNA
TCAGCTTCAGGAGGCCTGCTTCCCACCTGGCCCCATCAGGCTGCAGGTCACACTTGAAGA NM_030974RefSeq chr8 - 144098632 144104237 SHARPIN 81858 "SHANK-associated RH domain interactor, transcript variant 1"
GO:0005515|GO:0030054|GO:0030262|GO:0031424|GO:0014069|GO:2000348|GO:0071797|GO:0005634|GO:0010803|GO:0032403|GO:0097039|GO:0030425|GO:0042802|GO:0005829|GO:0005737|GO:0007420|GO:0050728|GO:0051260|GO:0005654|GO:0008270|GO:0007005|GO:0043123|GO:0031593 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80106_PI430048170 0.142842602854982 1.42134626994752 3.77965667833869 4.12406642976965 4.38398888711205 P P P 3.22476941468364 3.51452369655833 3.98578456952742 P P P LNCV6_80106_PI430048170 mRNA
TACAGACCATGCACATGAACCACTGGACGCTGGGGTATCCCAATGTGCACGAGATCACCC NM_001286841 RefSeq chr8 + 98944402 98952104 OSR2 116039 "odd-skipped related transciption factor 2, transcript variant 3"
GO:0001656|GO:0008284|GO:0033687|GO:0048793|GO:0005634|GO:0048704|GO:0009790|GO:0030154|GO:0046872|GO:0036023|GO:0002062|GO:0061029|GO:0045944|GO:0042476|GO:0060021|GO:0042474|GO:0050679|GO:0030501|GO:0072498|GO:0001823|GO:2000543|GO:0000122|GO:0010628|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141494_PI430048170 0.50297813412582 1.12218787378529 5.70670620511473 5.32823515617702 5.39964353896545 P P P 4.87041108237137 5.62442404123519 5.37072326307222 P P P LNCV6_141494_PI430048170 mRNA
GGAAGTTTGTTGGTCTTTATTAGATAAATTTCCAGAGACCTGTCCATAATACCCAACAGA NM_138420 RefSeq chr14 - 104937253 104978357 AHNAK2 113146 AHNAK nucleoprotein 2
GO:0042383|GO:0005515|GO:0030018|GO:0005737|GO:0005886|GO:0043034|GO:0030315|GO:0001778|GO:0005634|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75042_PI430048170 0.665954507279738 1.10008181538075 3.74677621061793 3.81374733557617 3.09855001227603 P P A 4.07837713695456 3.40922610871475 2.39371762286509 P P A LNCV6_75042_PI430048170 mRNA
TAATTTGAATGAAATTACACTTGACAGCCTGTCTCCAAGCAAACAAGAGGAACGAGGGAG NM_201591 RefSeq

chr4 - 175632936 175813114 GPM6A 2823 "glycoprotein M6A, transcript variant 2"
GO:0005515|GO:0043005|GO:0005262|GO:0003407|GO:0005886|GO:0051491|GO:0030175|GO:0044295|GO:0007
416|GO:0031982|GO:0048863|GO:0043197|GO:0048812|GO:0070588|GO:0043025|GO:0016021|GO:0001764|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138078_PI430048170 0.132020051145974 1.20576455033988 5.55330499824205
5.50415223500007 5.54966336995552 P P P 5.08813431608134 5.20769259354518
5.4744637871209 P P P LNCV6_138078_PI430048170 mRNA
TCTAGTTTTGGAGTAGAGGGGAGATGTTTTCTCAAACTTAGGGCAGTCCTGAGATGCTCA NM_001270482 RefSeq
chr17 + 32444462 32483319 PSMD11 5717 "proteasome (prosome, macropain) 26S subunit, non-
ATPase, 11, transcript variant 1"
GO:0005515|GO:0006511|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005
829|GO:0043248|GO:0034641|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0
000502|GO:0043066|GO:0005838|GO:0006521|GO:0051437|GO:0042590|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_108110_PI430048170 0.642630497782081 0.979358757323018 11.5580071228688
11.5082927100728 11.3858287948723 P P P 11.4572928028959 11.5137080243753
11.5744194474011 P P P LNCV6_108110_PI430048170 mRNA
ACTCCCCAGATGCCACCTGAGAGGAGCTTCTGTTTGGCATTCCAGATGGAAGGACAGGCA NM_001301855 RefSeq
chr17 + 75667115 75708062 SAP30BP 29115 "SAP30 binding protein, transcript variant 1"
GO:0005515|GO:0010467|GO:0006355|GO:0045814|GO:0040029|GO:0006915|GO:0005654|GO:0005634|GO:0045
111|GO:0010942|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132752_PI430048170 0.822575645715743 0.951913636536498 5.89248959051563
5.73137157811335 5.8246791879677 P P P 6.20342279113531 5.82964299887979
5.56046826921212 P P P LNCV6_132752_PI430048170 mRNA
TCTGGCATAGGGGTACTGGTCTCTAATAAACATCAGCTGCTGCTCCCCCAAACCAAAAAA NM_173525 RefSeq
chr11 + 6205567 6211135 C11orf42 160298 chromosome 11 open reading frame 42 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_74641_PI430048170 0.763598370582773 1.0634506013124 0.380234429805063
0.905226112232029 0.280571919959842 A A A 0.25698812245106 0.799579313839384
0.252924000775011 A A A LNCV6_74641_PI430048170 mRNA
AAGTTATTGGGCATCTTGAAACCATATTGATGCCCTGGCATCCTGCCACATGAACTATGG NM_000673 RefSeq
chr4 - 99412260 99435510 ADH7 131 "alcohol dehydrogenase 7 (class IV), mu or sigma
polypeptide, transcript variant 2"
GO:0006805|GO:0010430|GO:0045471|GO:0006069|GO:0006068|GO:0005576|GO:0044281|GO:0019841|GO:0001
523|GO:0005829|GO:0004022|GO:0004031|GO:0009617|GO:0035276|GO:1900116|GO:0042573|GO:0004024|GO:0
042572|GO:0008270|GO:0004745|GO:0048019|GO:0055114 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132390_PI430048170 0.194662373394013 1.04672929006936 0.456047374194773
0.400059502135833 0.444986187630071 A A A 0.307806860000884 0.362601551166585
0.430983343482444 A A A LNCV6_132390_PI430048170 mRNA
TGTTTTAAACAGCTCTTCTTGCAATGGTAGAGGCTCTTCAATTAAACAGAGATGGTAACA NM_001128159 RefSeq
chr17 - 508667 714856 VPS53 55275 "vacuolar protein sorting 53 homolog (S. cerevisiae), transcript
variant 1" GO:0005515|GO:0048471|GO:0005794|GO:0042147|GO:0015031|GO:0010008|GO:0000938 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_133002_PI430048170 0.632443710391012 0.805184600038215 3.4656971705839
1.797150183027 1.55234870551972 P A A 1.95387509658628 3.62677280651595
2.44696862179042 A P P LNCV6_133002_PI430048170 mRNA
CCCCACTCCACTCGCACGTGATTACAGTCTGTAAAGGTGTGACTTTATAAAGACAAAAAA NM_016541 RefSeq
chr16 - 798040 800733 GNG13 51764 "guanine nucleotide binding protein (G protein), gamma 13"

GO:0031681|GO:0006112|GO:0050909|GO:0005886|GO:0071377|GO:0005834|GO:0007200|GO:0044281|GO:0004871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130134_PI430048170 0.2331591939906681.15606286543548 0.69246960341602 0.2826244818746940.470577384059532A A A 0.2964048184042250.258349308878793 0.292195385556536A A A LNCV6_130134_PI430048170 mRNA TATGGGTTCTGGTGGCTAGAGAGAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACA NM_145273RefSeq chr17 + 43847147 43863629 CD300LG 146894 "CD300 molecule-like family member g, transcript variant 1"
GO:0016323|GO:0016324|GO:0002414|GO:0001791|GO:0032585|GO:0016021|GO:0070062|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93551_PI430048170 0.9123111256316821.00275726894082 7.91864333868992 7.88073500584892 7.94865564441442 P P P 7.96005426985447 7.9216834714556 7.85315555573561 P P P LNCV6_93551_PI430048170 mRNA TGCCCGTGTGGCGCTGATTGGATTTCCCTCTGTGGTCCACATTCTTGAGTCTGATGACCT NM_001388RefSeq chr17 + 18087866 18107985 DRG2 1819 developmentally regulated GTP binding protein 2
GO:0005739|GO:0007165|GO:0005737|GO:0016020|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135030_PI430048170 0.0643889839095873 0.4882803389049484.55393550055741 3.84185657853297 4.97969148220796 P P P 5.12014516856871 5.5439617558034 5.92263244715192 P P P LNCV6_135030_PI430048170 mRNA CAGCTGGGTCCAGATATCAGGTGTTCTAAATCTAAGAATGTAAGAACAATCTTAATAGAA NM_004298RefSeq chr5 - 37291632 37371126 NUP1559631 "nucleoporin 155kDa, transcript variant 2"
GO:0007077|GO:0005215|GO:0010467|GO:0031965|GO:0005975|GO:0019083|GO:0019221|GO:0019058|GO:0044281|GO:0005635|GO:0006606|GO:0055085|GO:0010827|GO:0008645|GO:0006406|GO:0016020|GO:0015758|GO:0005643|GO:0009405|GO:0086014|GO:0017056|GO:0016032|GO:0006998|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53946_PI430048170 0.2901491611238710.9008638095591984.2815664606251 4.08953896899471 4.10325353306814 P P P 4.2808458563558 4.14607665426618 4.4868055306313 P P P LNCV6_53946_PI430048170 mRNA ATGATTGTGAAGTGGTGGAAATGGATCCAAAATAATAAGTGACTTCTCTACCAAAGCATA NM_021639RefSeq chr1 - 45627303 45686630 GPBP1L1 60313 GC-rich promoter binding protein 1-like 1
GO:0003700|GO:0005634|GO:0045893|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82771_PI430048170 0.1222788101212790.9237525133770241 3.6370299062428 13.6647826225386 13.6908302792748 P P P 13.692874088506 13.7874686520293 13.8516607243858 P P P LNCV6_82771_PI430048170 mRNA TGTCGGACTATGTAATTGTAACTATACCTCTGGTTCCCATTAAAAGTGACCATTTTAGTT NM_004960RefSeq chr16 + 31180109 31194871 FUS2521 "FUS RNA binding protein, transcript variant 1"
GO:0008380|GO:0005515|GO:0010467|GO:0005737|GO:0000166|GO:0000398|GO:0003723|GO:0008270|GO:0005654|GO:0005634|GO:0003677|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127352_PI430048170 0.5355992807229270.9363511907032660.300181782722025 0.26504951483402 0.355954979519024A A A 0.2825274612650960.622942685597775 0.273637387258289A A A LNCV6_127352_PI430048170 mRNA CAGCAGTATTACTTGTAACGCAATTCAGGGATATTAAAGGGACTTTGGCCACTCAAAAAA NM_033129RefSeq chr20 - 661595 676179 SCRT2 85508 scratch family zinc finger 2
GO:0001078|GO:0000790|GO:2001222|GO:0000122|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142390_PI430048170 0.2302905386695171.73732806361512 1.68641125474751 2.42111524175296 2.7070808192584 A A A 2.4227687977863 0.498932645797971

0.940261235298491 A A A LNCV6_142390_PI430048170 mRNA
AGCAGATGCCTCTTGTTTTAATATATTAAAATTTTGCAAAGCCCTTTGAGCTACTGCCTT NM_032777 RefSeq chr8
+ 37796882 37843986 ADGRA2 NA adhesion G protein-coupled receptor A2 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_139502_PI430048170 0.3531780267454980.7462575227975380.484808053119169
0.4596174957326810.418992091877559 A A A 1.40810114484392 0.514807183030644
0.512890803345059 A A A LNCV6_139502_PI430048170 mRNA
GCCCAACCTGTATGGCGGGTCTGTACTTATTTTGTTTACCCCCAATTTAAAACGTTTTTT NM_014442 RefSeq chr19 -
51450996 51458454 SIGLEC8 27181 sialic acid binding Ig-like lectin 8
GO:0005515|GO:0007165|GO:0030246|GO:0016021|GO:0007155|GO:0004888 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138047_PI430048170 0.1129449314913881.0441164986365 0.410488189048429
0.4236754230079380.438845246551325 A A A 0.3257092866080470.350951671593382
0.408390682995231 A A A LNCV6_138047_PI430048170 mRNA
GCGGTAATTGGTGATACTTCTTTGAATGTAGATTTCCAATCACATCTTTAGTGTCTGAAT NM_017545 RefSeq chr20
- 7882983 7940446 HAO1 54363 hydroxyacid oxidase (glycolate oxidase) 1
GO:0052852|GO:0052853|GO:0005782|GO:0010181|GO:0005102|GO:0044281|GO:0052854|GO:0034641|GO:0046
296|GO:0001561|GO:0008891|GO:0003973|GO:0047969|GO:0046487|GO:0006979|GO:0005777 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144889_PI430048170 0.00705463053201181 0.7181454729092318.38864490059216
8.15127519418178 8.32508256791447 P P P 8.84201943902331 8.66745043800309
8.79325122163682 P P P LNCV6_144889_PI430048170 mRNA
TCGTGATTTCCAGATCTCCGCAAATGACTTCATTGCCAAGAAGAGAAGAAAATGCATTTA NM_001008566 RefSeq
chr22 - 26525747 26565404 TPST2 8459 "tyrosylprotein sulfotransferase 2, transcript variant 1"
GO:0016020|GO:0000139|GO:0007342|GO:0005783|GO:0060468|GO:0016021|GO:0008476|GO:0006478|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134040_PI430048170 0.00123963618199816 0.7158158966392591 0.4648487899683
10.3929851229798 10.3178989890907 P P P 10.7968924238658 10.8880082713598
10.9380574853284 P P P LNCV6_134040_PI430048170 mRNA
TATAGTTAGTTTTATAACCCTGAATGCCCCCACCCTTCCCCTAAGCACACAGGGGTTAAA NM_001199898 RefSeq
chr17 + 50094736 50111369 PDK2 5164 "pyruvate dehydrogenase kinase, isozyme 2, transcript
variant 2"
GO:0031670|GO:0008286|GO:0004740|GO:0010510|GO:0005967|GO:0010565|GO:0044281|GO:0042593|GO:0005
524|GO:0042803|GO:0010906|GO:0006885|GO:0005739|GO:0006111|GO:0005737|GO:0004672|GO:0072332|GO:0
006090|GO:0005759|GO:0034614|GO:0006006|GO:0005654|GO:0006468|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134110_PI430048170 0.4380070817823791.20142130375573 1.61505440098239
1.58235616346688 1.80420111229744 A A A 1.96255482207043 1.2871355678803
0.688061416218499 A A A LNCV6_134110_PI430048170 mRNA
AACAGTTCTTCCTGGAGACCCTGAAGAAAGGGTCCTACAATTTGACATCTCATTCAGCCT NM_001080542 RefSeq
chr17 - 75910536 75941038 FBF1 85302 Fas (TNFRSF6) binding factor 1
GO:0090162|GO:0043297|GO:0005515|GO:0043296|GO:0042384|GO:0005813|GO:0000922|GO:0006996|GO:0005
814|GO:0045095|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138324_PI430048170 0.0819125886018112 0.8926186218400268.58887544652123
8.74848952218022 8.70740796889741 P P P 8.92592027182795 8.74817881399967
8.86146810976925 P P P LNCV6_138324_PI430048170 mRNA
TCACAGCGCCACTCCTACTTTGTATGCTCATAGTTTAAATTTTTGTAGGAAACTTTCAAT NM_001136105 RefSeq
chr11 + 111299250 111308735 COLCA2 120376 "colorectal cancer associated 2, transcript variant 3"
GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_140820_PI430048170 0.447356904187192 0.978202574776881 0.373560890728918
0.410560549810283 0.337227049299922 A A A 0.464255785438592 0.364134421491385
0.387361070198099 A A A LNCV6_140820_PI430048170 mRNA
GGCATCTAACTGTTACACCAAATCTTAAGTGAATAAAACTTTACCAAGGCTTCTCAGTTA NM_004673 RefSeq chr1
- 178849534 178871080 ANGPTL1 9068 angiopoietin-like 1
GO:0005102|GO:0007169|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96328_PI430048170 0.566479656235337 0.935543660432614 2.71870132963429 3.05477419914752
2.55476478835317 A A A 2.72898341078897 2.99294591725585 2.92753418626161 A P P
LNCV6_96328_PI430048170 mRNA
GCCGCTAATGTCTTTGTTAGTGACAGTGCATTTTGTAGTACTGTACAAGTGTTGTGCTAA NM_012330 RefSeq chr10
+ 74826412 75032622 KAT6B 23522 "K(lysine) acetyltransferase 6B, transcript variant 1"
GO:0005515|GO:0070776|GO:0006355|GO:0016573|GO:0006325|GO:0006334|GO:0005634|GO:0003677|GO:0006
351|GO:0043966|GO:0005654|GO:0008270|GO:0016407|GO:0045893|GO:0000786|GO:0045892|GO:0004402|GO:0
008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117203_PI430048170 0.021250129159418 0.70164941496166 7.86439995313959
7.96122162347452 8.09428261388886 P P P 8.42936056895414 8.32819327548074
8.68181923878908 P P P LNCV6_117203_PI430048170 mRNA
TAATTCTTGGATTTTCTTCACTGCAGGGCTTTGGGTGGAGAAATAAAACTCTTCAAATGC NM_001185039 RefSeq
chr17 - 75941510 75979434 ACOX1 51 "acyl-CoA oxidase 1, palmitoyl, transcript variant 3"
GO:0006629|GO:2000189|GO:0000038|GO:0006693|GO:0016401|GO:0005886|GO:0005782|GO:0050660|GO:0005
634|GO:0044281|GO:0006091|GO:0007283|GO:0043231|GO:0005739|GO:0071949|GO:0044255|GO:0005778|GO:0
005777|GO:0016559|GO:0005504|GO:0019395|GO:0055088|GO:0005730|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143744_PI430048170 0.0283680808633671 1.13723860931106 10.2629082466865
10.3085357564874 10.205562432303 P P P 10.0423911724082 10.1574214684703
10.0185777296758 P P P LNCV6_143744_PI430048170 mRNA
CAGTGAGAGGTGTGGCCCCACACCGATTTATGATATTAAAATCTCAACTCCCACAAAAAA NM_032353 RefSeq chr17
+ 42773435 42779600 VPS25 84313 vacuolar protein sorting 25 homolog (S. cerevisiae)
GO:0005515|GO:0000814|GO:0006355|GO:0005730|GO:0005634|GO:0043328|GO:0006351|GO:0042803|GO:0005
829|GO:0005739|GO:0005198|GO:0016197|GO:0061024|GO:0005654|GO:0010008|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137073_PI430048170 0.226113211628943 1.12273555506483 13.1486735622766
12.9909930208018 12.838371327394 P P P 12.6863136854935 12.888620768072
12.9084292443961 P P P LNCV6_137073_PI430048170 mRNA
AGGTCTCACCCCTGTGGCCTGTGATTATGAATAAAGATTATCTTTGTAAAGATCAAAAAA NM_003731 RefSeq chr9
+ 137188601 137190370 SSNA1 8636 Sjogren syndrome nuclear autoantigen 1
GO:0005813|GO:0042073|GO:0006996|GO:0000086|GO:0060830|GO:0005634|GO:0000278|GO:0036064|GO:0042
802|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140145_PI430048170 0.371824988740116 0.844562044697081 0.385744852507952
0.253601128049553 0.289948794475109 A A A 0.903325237589399 0.407902891845492
0.273901750317244 A A A LNCV6_140145_PI430048170 mRNA
GGGTCACTTCTCATTTTCTTTGCTGACTTACCTTTTTACTGACCGTTGTGAATTTCTGTC NM_005739 RefSeq chr15 -
38488100 38564806 RASGRP1 10125 "RAS guanyl releasing protein 1 (calcium and DAG-regulated),
transcript variant 1"
GO:0002437|GO:0043303|GO:0005886|GO:0005509|GO:0030168|GO:0032252|GO:0007265|GO:0032862|GO:0001
816|GO:0014066|GO:0042629|GO:0030154|GO:0005829|GO:0008289|GO:0005085|GO:0007165|GO:0016020|GO:0
000139|GO:0047496|GO:0007596|GO:0045087|GO:0005789|GO:0038095 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_128626_PI430048170 0.198034522776199 0.800171903855996 6.23696355401533

6.05107741987347 6.62122985945318 P P P 6.40712129174598 6.6411936933479
6.85140187847919 P P P LNCV6_128626_PI430048170 mRNA
CACAGGGAAAAGACTTAATATTTTTGACATGATGGCAGTTACTAAAGAAGCACCTGAAAC NM_005830 RefSeq chr13
- 40729295 40771211 MRPS31 10240 mitochondrial ribosomal protein S31
GO:0070124|GO:0005739|GO:0005515|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0019
904|GO:0005743|GO:0005730|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131082_PI430048170 0.2446744433617580.8608530171183921 2.4771804657135
12.0001312548572 12.1305252499726 P P P 12.3571923398271 12.4095971154105
12.5272304268431 P P P LNCV6_131082_PI430048170 mRNA
TGAGTACCAAGCCATGTAATGGTAACTTGGACTTTAATAAAAGGGAAATGAGTTTGAACT NM_004255 RefSeq chr15
- 74920275 74938154 COX5A 9377 cytochrome c oxidase subunit Va
GO:0022904|GO:0004129|GO:0005743|GO:0009055|GO:0044281|GO:0055085|GO:0046872|GO:0044237|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129493_PI430048170 0.000327617654323339 4.61879979070673 4.87281406990309
5.35595612321071 5.15376136563034 P P P 3.14221678987631 2.76093246504462
2.87002578207601 P P P LNCV6_129493_PI430048170 mRNA
TCATGCAGATGCAGTCTGAATTCCTTGCCTGAATTAAATTTATGTATCCTCTCCAAAAAA NM_001166663 RefSeq
chr1 - 160830159 160862902 CD244 51744 "CD244 molecule, natural killer cell receptor 2B4, transcript
variant 2"
GO:0005515|GO:0007165|GO:0005886|GO:0007596|GO:0004872|GO:0016021|GO:0050900|GO:0009897 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139445_PI430048170 0.0489635641804884 0.56880954158353 4.76007578239313
4.45938964871654 5.26500893257103 P P P 5.41553210109078 5.66820617896053
5.91609979863025 P P P LNCV6_139445_PI430048170 mRNA
CCCTTCAAAACTGTACAAAGAAGACGACTGTTTTCCATTTCCATTTAAACATTTTTAGCC NM_001301778 RefSeq
chr20 + 62143719 62182510 SS18L1 26039 "synovial sarcoma translocation gene on chromosome 18-
like 1, transcript variant 2"
GO:0016604|GO:0000780|GO:0071565|GO:0050775|GO:0000777|GO:0000776|GO:0005634|GO:0045893|GO:0016
358|GO:0006351|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138792_PI430048170 0.00751219640486918 1.69410655743616 10.1966229441284
10.1598241079203 10.1267384966452 P P P 9.2799416007696 9.54775342417594
9.36156646037712 P P P LNCV6_138792_PI430048170 mRNA
GGTCTCTACAAGTGACAGATGTGTTGTTTTCAACAGTATTATTAGGTTATGAATAAAGCC NM_018053 RefSeq chr1
+ 27959461 27968096 XKR8 55113 "XK, Kell blood group complex subunit-related family, member 8"
GO:0005886|GO:0016021|GO:0043652|GO:0070782 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95066_PI430048170 0.49925964838784 0.789958974527192 0.381435479739434 0.392849701945078
0.465118080761438 A A A 1.32201936650642 0.32826149236265 0.381724882231116 A A A
LNCV6_95066_PI430048170 mRNA
ATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGTACAGT NM_198946 RefSeq chr9
- 136744017 136748528 LCN6 158062 lipocalin 6 GO:0007338|GO:0005576 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_129913_PI430048170 0.339403971582361 0.851179916392885 5.03619479024525
5.49846815976358 4.95591759730059 P P P 5.4017375134612 5.64655107816059
5.16009892162477 P P P LNCV6_129913_PI430048170 mRNA
TTTGGATCAATAGAAGGGCAACCCCATCCCACTGCCTGTGTCTGTTGAGCCCTGGCCTAG NM_001167670 RefSeq
chr20 + 2816329 2817158 TMEM239 100288797 transmembrane protein 239 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112274_PI430048170 0.0144210821210502 0.604629136799541 3.73684007423745
3.43651991397281 3.71411159271054 P P P 4.38315406288946 4.37550229417177

4.32468833391417 P P P LNCV6_112274_PI430048170 mRNA
AATGCTGATTCTTCATCTGTCCCTCATGGAGCAGTCTATTATCCAGTAATGTCAGATCCC NM_001257231 RefSeq
chrX + 111681169 111760647 ALG13 79868 "ALG13, UDP-N-acetylglucosaminyltransferase subunit,
transcript variant 7"
GO:0004577|GO:0006508|GO:0005789|GO:0030246|GO:0008234|GO:0006488|GO:0044267|GO:0030259|GO:0043
687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132692_PI430048170 0.2212022381151381.08950785713595 0.602932537330426
0.8265867891706390.632142555942956A A A 0.5063400933636240.598731391207597
0.594089712309418A A A LNCV6_132692_PI430048170 mRNA
GATTCTGGAGCCTTTCTCATCATAAGACTGTGGAAAATACACAGTCGTTTAAGTTAAAAA NM_012309RefSeq chr11
- 70467855 71224796 SHANK2 22941 "SH3 and multiple ankyrin repeat domains 2, transcript variant
1"
GO:0005515|GO:0043005|GO:0060170|GO:0017124|GO:0008328|GO:0030054|GO:0005886|GO:0005883|GO:0060
291|GO:0060292|GO:0031526|GO:0030426|GO:0016324|GO:0030160|GO:0043197|GO:0045211|GO:0043025|GO:0
007613|GO:0030534|GO:0007612|GO:0035640|GO:0014069|GO:0005575|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131871_PI430048170 0.00991146023161442 1.32891659184484 10.0260065109919
10.205562432303 10.0468844203144 P P P 9.72689208285073 9.68044260136623
9.64598703887114 P P P LNCV6_131871_PI430048170 mRNA
TTTGTGAACTGGGGCATCAATCATCTTTTGATAAATGGATCAGTTTTAGGACTTTCAGAA NM_006567RefSeq chr6
+ 5261350 5771583 FARS2 10667 "phenylalanyl-tRNA synthetase 2, mitochondrial"
GO:0010467|GO:0000287|GO:0000049|GO:0006432|GO:0005759|GO:0004826|GO:0005524|GO:0008033|GO:0006
418 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144455_PI430048170 0.0453571538485438 0.2184803733559012.20229463142423
0.9332948990274810.29037456337604 A A A 3.34328659765608 3.73835279965663
3.57373147982136 P P P LNCV6_144455_PI430048170 mRNA
GCCTAAAATTTTGTTGGATTGGGACTAAAATGTTCTATTAGCCAATGAATAACGTCCAAG NM_001018067 RefSeq
chr1 - 67407809 67430440 SERBP1 26135 "SERPINE1 mRNA binding protein 1, transcript variant 1"
GO:0005515|GO:0043488|GO:0048471|GO:0005737|GO:0016020|GO:0005886|GO:0042981|GO:0005634|GO:0003
730|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54469_PI430048170 0.0242307148934311 0.7026667296944768.31344873163076
8.30775599376415 8.54045348834128 P P P 8.78068083138085 8.78277155207737
9.11207081438332 P P P LNCV6_54469_PI430048170 mRNA
CTTATTAACAGGAAATGCTAAGGTACCTTCTCTGTGGAACAATCTGCAATGTCTAAATCG NM_001242673 RefSeq
chr1 + 109984764 110023742 AHCYL110768 "adenosylhomocysteinase-like 1, transcript variant 2"
GO:0005515|GO:0006378|GO:0005783|GO:0032412|GO:0005829|GO:0004013|GO:0008150|GO:0044070|GO:0010
765|GO:0006611|GO:0006730|GO:0031440|GO:0033353|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130552_PI430048170 0.3766486918756791.04845383966546 5.35732215208665
5.31807564884571 5.46806670407448 P P P 5.25921334662925 5.41720695427091
5.26069727644694 P P P LNCV6_130552_PI430048170 mRNA
GATGTTGTGCCCCAGACCTGCCTGCATGGTTCCATCCATTACTCATGGCCTCAGCCTCAT NM_022478RefSeq chr14
- 23047060 23057538 CDH24 64403 "cadherin 24, type 2, transcript variant 1"
GO:0016337|GO:0070097|GO:0008013|GO:0005886|GO:0045294|GO:0005911|GO:0034329|GO:0005509|GO:0016
021|GO:0007156|GO:0045216|GO:0034332 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138423_PI430048170 0.8934982025475741.02770732868048 6.69289707433982
6.19349868292184 6.63264081512163 P P P 6.42069494379006 6.45056356743636
6.57444326479504 P P P LNCV6_138423_PI430048170 mRNA
TTTGACACCAATAATTTTCAAGGAAGAAAATCTTAGGACTATGTATAGCCAGGACAGGCA NM_020191RefSeq chr3

+ 139344018 139357045 MRPS22 56945 mitochondrial ribosomal protein S22
GO:0070124|GO:0005739|GO:0070125|GO:0008150|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005
761|GO:0005743|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132619_PI430048170 0.0314580491632471.50459815892069 5.11379251192906 5.3131870082722
5.17395417376808 P P P 4.73301957121621 4.73835216908402 4.33239346583588 P P P
LNCV6_132619_PI430048170 mRNA
GTGGCTGAGAGCCACCTGCCCGGTGAGTCCTCTATTCAGTTCTGTCCTCACAATCACTGA NM_001287262 RefSeq
chr1 - 228510358 228512288 BTNL10 NA butyrophilin-like 10 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_135227_PI430048170 0.0218759671259222 1.34955675681081 10.0599769040685
10.2117903477172 10.1181451437539 P P P 9.519125814098 9.76572404899173
9.79602213626434 P P P LNCV6_135227_PI430048170 mRNA
GATGCAGTGGCTCTCCATTGCCACTCTGATTCCTCCTTTCTTTTGGTCACAGAGAAAGGG NM_144582RefSeq chr2
- 70985937 70994871 TEX261 113419 testis expressed 261
GO:0006888|GO:0030134|GO:0030173|GO:0097020|GO:0030176 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_126807_PI430048170 0.34612531301812 1.04527916017509 0.302146667963743
0.2776969926615020.44119475232971 A A A 0.2906451362277850.254366817802845
0.289514538880552A A A LNCV6_126807_PI430048170 mRNA
GACACAGCTGAATCACCCATGAGAAGGTCAAATATGTGTAATAAATGAATTTGCTTCAAA NM_002772RefSeq chr21
- 18269115 18403653 TMPRSS15 5651 "transmembrane protease, serine 15"
GO:0005903|GO:0004252|GO:0006508|GO:0016021|GO:0006898|GO:0005044 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132319_PI430048170 0.3198909643376691.10138682871602 5.00355546525988
5.00431216655111 4.7089795624325 P P P 4.64614287566056 4.82589397813634
4.83855785373704 P P P LNCV6_132319_PI430048170 mRNA
GACAAACACACCTTTTTATACCAATCAGTATCCTCTGTTCATTAAAACTGGCTATCCATT NM_144994RefSeq chr2
- 96837913 96844021 ANKRD23 200539 ankyrin repeat domain 23
GO:0005737|GO:0014704|GO:0005654|GO:0030016|GO:0015629|GO:0031432|GO:0009612 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127557_PI430048170 0.66045648562031 1.11480166253854 2.4027935641116
2.48122857916745 3.12017908642919 A A P 1.51877078510415 2.73113793936756
3.00839626051712 A P P LNCV6_127557_PI430048170 mRNA
GAAGCTTTGCAAATTGAATTCTCAGTGAGTTGTATATTTATACACCTGGCTTGAAGCCTT NM_006033RefSeq chr18
+ 49562030 49592908 LIPG 9388 "lipase, endothelial"
GO:0042632|GO:0006629|GO:0032376|GO:0005794|GO:0009986|GO:0007584|GO:0008283|GO:0043691|GO:0004
620|GO:0004465|GO:0005615|GO:0050746|GO:0010983|GO:0034375|GO:0055091|GO:0008970|GO:0008201|GO:0
009395|GO:0005769. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143205_PI430048170 0.5050313948532440.9659146155785212 0.0857485675546
12.0345284032365 12.055438470441 P P P 11.9892223431042 12.1742880184879
12.1556625977531 P P P LNCV6_143205_PI430048170 mRNA
GGGCTCCCACCTACCTTTTATTTAAGCCAGTATTCTTTGTTCCTGCTTGTAATAAAACTT NM_032283RefSeq chr1 +
26826709 26855720 ZDHHC18 84243 "zinc finger, DHHC-type containing 18"
GO:0018345|GO:0005794|GO:0016409|GO:0008270|GO:0034613|GO:0016021|GO:0019706 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130272_PI430048170 0.5108006719090090.94837704454406 0.537009736407115
0.5139163325893540.276344358235951A A A 0.4080958898599970.643820641330959
0.509180483572751A A A LNCV6_130272_PI430048170 mRNA
GTATTTTCCCCAAATGGTGATGATGAGCAGTGCTTTGCATGAAACTAGATTTTATCAATT NM_004885RefSeq chr4

+ 72031803 72148201 NPFFR2 10886 "neuropeptide FF receptor 2, transcript variant 1"
GO:0042277|GO:0005886|GO:0004930|GO:0007268|GO:0015629|GO:0008188|GO:0032870|GO:0009582|GO:0007
186|GO:0005887|GO:0007218|GO:0043408|GO:2000479|GO:0045761|GO:0031628 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_117273_PI430048170 0.4972586618165291.02974289993809 0.284954553894825
0.3093034704937780.443155473532344A A A 0.3252667416161360.2956201811057270.2945428326789
A A A LNCV6_117273_PI430048170 mRNA
ATATCCTCTTGAGCCAAACTGTTTGGGTCTCGTTGCTTCATGGTATGGTCTGGATTTGTG NM_020182RefSeq chr20
- 57648391 57709975 PMEPA1 56937 "prostate transmembrane protein, androgen induced 1,
transcript variant 1"
GO:0005515|GO:0010991|GO:0005886|GO:0050699|GO:0070412|GO:0060394|GO:0000139|GO:0031901|GO:0007
179|GO:0016021|GO:0010008|GO:0030512|GO:0030521 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129689_PI430048170 0.0494622468484834 1.16613950957986 9.74336716497663
9.8102553210433 9.79095360660682 P P P 9.47346402891453 9.6695573467714
9.53003203973384 P P P LNCV6_129689_PI430048170 mRNA
TCTCCCGTGCCCACTTGGCTATTTACTTATTTATTTATTGTGTGCCAGTGATGGTGGGTG NM_020315RefSeq chr22
+ 37658729 37666932 PDXP 57026 "pyridoxal (pyridoxine, vitamin B6) phosphatase"
GO:0005515|GO:0007088|GO:0032465|GO:0032361|GO:0000287|GO:0031258|GO:0005886|GO:0031247|GO:0030
496|GO:0032587|GO:0015629|GO:0032154|GO:0071318|GO:0004647|GO:0030027|GO:0005829|GO:0006470|GO:0
030836|GO:0031072|GO:0004721|GO:0070938|GO:0033883|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144864_PI430048170 0.0807375676961652 1.28274629625489 10.1354915616513
10.1594831819455 9.87919628385952 P P P 9.93186752323727 9.6268632979875
9.52210375761458 P P P LNCV6_144864_PI430048170 mRNA
ATGGAGCTGGAGCAGCCCGCCTAGAACCCAGTCTAATGAGAACTCCAGAAAGCTGGAGCA NM_004031RefSeq
chr11_KI270832v1_alt - 142447 145621 IRF7 3665 "interferon regulatory factor 7, transcript variant d"
GO:0005515|GO:0032479|GO:0034142|GO:0016064|GO:0006366|GO:0000982|GO:0019221|GO:0045351|GO:0005
634|GO:0005829|GO:0002756|GO:0005737|GO:0060337|GO:0045655|GO:0045944|GO:0032481|GO:0034138|GO:0
032607|GO:0060333|GO:0032608|GO:0032728|GO:0032727|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136569_PI430048170 0.00292089167077494 0.4353397156140314.70945533768202
4.60831032292582 5.04529057047601 P P P 5.82964299887979 6.05736795390219
6.09821312807282 P P P LNCV6_136569_PI430048170 mRNA
TTTTGACTTTGTGCAGGACAGAAAGTTGTGTAGGTATGACTGTTCTACTTTTCAGTTTTC NM_020928RefSeq chr5
+ 61332272 61546172 ZSWIM6 57688 "zinc finger, SWIM-type containing 6"
GO:0048812|GO:2001222|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128333_PI430048170 0.190466577219381 0.8340466314475044.81645976481377
4.32441351968001 4.49860107222259 P P P 4.75048832976669 4.74625686359714
4.96121830440981 P P P LNCV6_128333_PI430048170 mRNA
GAACTAGTATCACTTATCTCAGCAAAAGAGATTGTTTGCATGGAAAGATTAATAGCACTG NM_015214RefSeq chr8
+ 38231490 38262769 DDHD2 23259 "DDHD domain containing 2, transcript variant 1"
GO:0016042|GO:0005793|GO:0005737|GO:0005794|GO:0016787|GO:0005815|GO:0046872|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142865_PI430048170 0.1101018832533231.34046343007562 12.0050157545532 11.919524693441
11.5074071611351 P P P 11.6328082615409 11.3712624451609 11.1695085384724 P P P
LNCV6_142865_PI430048170 mRNA
CCCAGCTGTGACACGTTTTGATCAAAGGAGAAACAATAAAGGGATAAACCATAAATAAAA NM_198335RefSeq chr11
- 62624825 62646726 GANAB 23193 "glucosidase, alpha; neutral AB, transcript variant 3"
GO:0033919|GO:0042470|GO:0017177|GO:0005794|GO:0016020|GO:0006457|GO:0030246|GO:0005788|GO:0044

267|GO:0070062|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137915_PI430048170 0.00903376334464922 0.4845499057077963.66665586477779
3.10802635526108 3.51953062430628 P P P 4.35547819482889 4.38891713152224 4.7141335785083
P P P LNCV6_137915_PI430048170 mRNA
TCAGCAAATATTTGTATTACTGCTTGATTCTGTGACAGTCACAATAGATGTAGAGAAGGC NM_018257RefSeq
chr20_KI270870v1_alt + 164285 183433 PCMTD2 55251 "protein-L-isoaspartate (D-aspartate) O-
methyltransferase domain containing 2, transcript variant 1" GO:0004719|GO:0005737|GO:0006479 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_132699_PI430048170 0.000563174945248867 0.4826769736026027.13695848237402
7.05140183125823 7.31282518583575 P P P 8.17428031902747 8.12595677899425
8.35568783280536 P P P LNCV6_132699_PI430048170 mRNA
GAAGTCCTAACTTCCACTATTCTAGAAAGTATAGTGGTGATTTGTGTGCAAAGATTTGAA NM_004514RefSeq chr17
+ 82519717 82604607 FOXK2 3607 forkhead box K2
GO:0005515|GO:0006355|GO:0000287|GO:0003700|GO:0006357|GO:0005634|GO:0000978|GO:0006351|GO:0043
231|GO:0043565|GO:0001077|GO:0045944|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142937_PI430048170 0.00562121841988754 3.63712450354928 2.8079643319836
2.90934381530662 3.59292012037267 A A P 0.7859553004698061.57328823363767
1.38321545568585 A A A LNCV6_142937_PI430048170 mRNA
TGGTTTGAGGTGATCTCGCAAAGTTATTCTTCCACCATGGCCAACAACGAAGGACTTTTC NM_006169RefSeq chr11
+ 114295812 114312516 NNMT 4837 nicotinamide N-methyltransferase
GO:0008112|GO:0006805|GO:0042493|GO:0031100|GO:0010243|GO:0044281|GO:0032259|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133003_PI430048170 0.00555204327182878 0.5348235231650126.11398679583142
5.9310614345259 6.35197392750347 P P P 6.93609220264319 6.91418496488956
7.25977966401999 P P P LNCV6_133003_PI430048170 mRNA
GAAGGATCACTTTACAGGCAACGCTCATTTTAAGCAACCCTTAAGAAATGTTTATGTTTC NM_139248RefSeq chr3
- 185507781 185552581 LIPH 200879 "lipase, member H"
GO:0052689|GO:0016042|GO:0005886|GO:0004620|GO:0008201|GO:0005615 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_78560_PI430048170 0.3032004975387971.87218100538781 0.2731475352192650.780026012051267
2.01690525135956 A A A 0.3362140416084620.2926404367072730.306939149992366A A A
LNCV6_78560_PI430048170 mRNA
TTCTATGCTGAAGCAGATTCTGAACGTCTTAAAATCTGTTCATTATCAGATGCTGAAAGA NM_001170905 RefSeq
chr7 + 64313872 64356634 ZNF736 728927 "zinc finger protein 736, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130025_PI430048170 0.9015521553810581.02656095732001 3.98348130944095
3.04289646602011 2.42169808155595 P P A 3.37724857364671 2.74830808165174
3.52931860135268 P P P LNCV6_130025_PI430048170 mRNA
AGGGGCAGCAGGGGGTGTGTTTGTGGACAAATAAATTTGTAAAGTCCGAGGATTAAAAAA NM_022567RefSeq
chrX + 41447459 41475652 NYX 60506 nyctalopin
GO:0005622|GO:0008150|GO:0003674|GO:0005578|GO:0007601|GO:0050896 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133038_PI430048170 0.0957140694489109 0.60301406799861 6.07797808326576
5.75763468836499 6.01087854334224 P P P 6.27659194885355 6.52244544793148
7.12134321754439 P P P LNCV6_133038_PI430048170 mRNA
CCGATCCTTTGTCCAGAAGAAGCCCATGGAATATTGAATGTAATACATTTAGTCAATTAA NM_020336RefSeq chr20
+ 38472805 38578861 RALGAPB 57148 "Ral GTPase activating protein, beta subunit (non-catalytic),
transcript variant 1" GO:0032859|GO:0017123|GO:0046982|GO:0061024|GO:0032484|GO:0060178 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_116863_PI430048170 0.7627692754037811.03082041356387 3.90422218925316
3.93055899997346 3.69413321445202 P P P 4.30562111015938 3.7494573933947
3.11247534390648 P P P LNCV6_116863_PI430048170 mRNA
AGAAAACTGCATAAAGAAGGTGATCCTGGCCTCGGGGAGTTCCTGGTGTGTGCCTCCAGC NM_001271863 RefSeq
chr1 - 205336064 205357090 KLHDC8A 55220 "kelch domain containing 8A, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144055_PI430048170 0.1908973760274540.88646385499514 5.30209174581124
5.55679091251665 5.607882032929 P P P 5.64574132945744 5.63011051053842
5.72876758498449 P P P LNCV6_144055_PI430048170 mRNA
CTTTTTATTTGGCTTGGAGTTCTTCAAAGCATTGAAGTGTGTTCATAGTCCAGGTTTTTT NM_198896RefSeq chr11 -
73675637 73761156 RAB6A 5870 "RAB6A, member RAS oncogene family, transcript variant 2"
GO:0005515|GO:0005802|GO:0005794|GO:0006890|GO:0019904|GO:0003924|GO:0072385|GO:0031410|GO:0005
525|GO:0005829|GO:0031489|GO:0018125|GO:0000139|GO:0016020|GO:0034498|GO:0019882|GO:0034067|GO:0
042147|GO:0032482|GO:0019003|GO:0070062|GO:0000042 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_104221_PI430048170 0.6507545553468221.0682622923415 5.67737377614413
5.58877369118873 5.34051099761046 P P P 5.77462455511745 5.44375924465023
5.02758462487157 P P P LNCV6_104221_PI430048170 mRNA
TATTGACTGTCTTTCCCCCTGTCCTCGACAGAAGAGTGGGAGGTGAGAAGCCCGTCTCCT NM_001178061 RefSeq
chr1 - 151131686 151146664 SEMA6C 10500 "sema domain, transmembrane domain (TM), and
cytoplasmic domain, (semaphorin) 6C, transcript variant 1"
GO:0005886|GO:0007411|GO:0030215|GO:0004872|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_104111_PI430048170 0.0273830937214088 2.81176390843498 1.94202692496341
2.2542290401659 2.964702943141 A A P 0.5165734527407170.61356654119968 1.5256285054247
A A A LNCV6_104111_PI430048170 mRNA
CATGCGAGTAAACATTTACGGGCACCATAGATAAAAGGCTTGTGTTTTAATCCTCATCCT NM_001282575 RefSeq
chr20 - 50081123 50115959 UBE2V1 7335 "ubiquitin-conjugating enzyme E2 variant 1, transcript
variant 12"
GO:0005515|GO:0050852|GO:0034142|GO:0070423|GO:0000151|GO:0005634|GO:0035370|GO:0030154|GO:0006
301|GO:0035872|GO:0005829|GO:0070534|GO:0005737|GO:0051092|GO:0019787|GO:0002755|GO:0043123|GO:0
031625|GO:0070062|GO:0031624|GO:0000209|GO:0031371|GO:0006355|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145062_PI430048170 0.12690213123274 1.05519474484498 10.4293111863937
10.5389770084437 10.4709480957651 P P P 10.3932395654623 10.3912229998129
10.4241396886643 P P P LNCV6_145062_PI430048170 mRNA
TCTGTACTGTCATGCCCGTCTCTGGAATGTCCACTCCCAGAGCCTGCCCCAGCCCTTCGA NM_015603RefSeq chr19
+ 47256473 47271953 CCDC9 26093 coiled-coil domain containing 9 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145284_PI430048170 0.3683819599057550.7647590700586710.484412977747698
0.4485313343025870.24743178913863 A A A 0.38851524356546 0.4894264740772711.2945975185577
A A A LNCV6_145284_PI430048170 mRNA
GCTCTGCATAGGGTAACATAGTAATTTAACAATAAAAACTTACCGTGCTTGTGTCCAAAA NM_015237RefSeq chr1
+ 92167051 92184723 KIAA1107 23285 KIAA1107 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_93291_PI430048170 0.3066032134742871.80931936871865 0.4976002739226642.26168094399605
1.64705672807465 A A A 0.4706848796158440.8999163847275920.933611663515281 A A A
LNCV6_93291_PI430048170 mRNA

TTTAACATTTCGCCACCTACTGAAGACATCATTTGGGACCAAGCTGATGAGCCCTTGAAG NM_021813 RefSeq chr6 - 89926527 90296908 BACH2 60468 "BTB and CNC homology 1, basic leucine zipper transcription factor 2, transcript variant 1" GO:0005737|GO:0001206|GO:0005634|GO:0000980|GO:0000122|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141222_PI430048170 0.9265023385597360.9216165386708471.78162605416072 0.47212189573548 0.469981284748057 A A A 0.326542525265977 0.611340487903887 1.98436477188687 A A A LNCV6_141222_PI430048170 mRNA
CCTGAAACAGGAATGGGGCAAAGAGAAAGGAGAGCCAGGAGCATTTAAAAATCAGCATCT NM_000890 RefSeq chr11 + 128891417 128918056 KCNJ5 3762 "potassium channel, inwardly rectifying subfamily J, member 5"
GO:0005515|GO:0005242|GO:0005886|GO:0015467|GO:0008076|GO:0010107|GO:0007268|GO:0034765|GO:0006813 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67131_PI430048170 0.262767971931211 0.846603592910643 0.456243327078381 0.33862056423459 0.329619090098572 A A A 0.465798632131405 0.440316705463491 0.89578214724105 A A A LNCV6_67131_PI430048170 mRNA
GTTGAAAAATGCGGTTAAAAAGGTGATGGGTATCTTTAAGAGCAGCTTATTCCAAGCTTT NM_001142699 RefSeq chr11 - 83455012 85627270 DLG2 1740 "discs, large homolog 2 (Drosophila), transcript variant 1"
GO:0005515|GO:0008328|GO:0030054|GO:0005886|GO:0044224|GO:0097120|GO:0004385|GO:0007268|GO:0014069|GO:0019233|GO:0045197|GO:0007399|GO:0016323|GO:0035255|GO:0016020|GO:0045211|GO:0008076|GO:0010923|GO:0046939|GO:0043113 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139272_PI430048170 0.00463502363447064 0.3554804957038926.63921320314773 6.30560949815199 6.98553471743347 P P P 7.87488629155832 8.11857715284493 8.43771511167439 P P P LNCV6_139272_PI430048170 mRNA
GTGCTCTTACACAGTATGCATCATATTGTTGTCTGTGAAATTAAAGGACATTTGATAGTC NM_005171 RefSeq chr12 + 50764005 50821160 ATF1 466 activating transcription factor 1
GO:0005515|GO:0014070|GO:0003700|GO:0034142|GO:0006366|GO:0003705|GO:0005634|GO:0051403|GO:0032403|GO:0043623|GO:0002756|GO:0045944|GO:0002755|GO:0032025|GO:0034138|GO:0048011|GO:0000977|GO:0038124|GO:0046982|GO:0038123|GO:0034134|GO:0045740|GO:0002224|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145555_PI430048170 0.0193259563757093 0.6406458787419738.60191195642096 8.17470668241077 8.27701301785172 P P P 9.07041303269329 9.13580798444228 8.78644890499804 P P P LNCV6_145555_PI430048170 mRNA
CCTGCGTCTAACTTTTGACGCTATAAATAGGTTCAAGAAACTAATAAAACGTTCTGGTTT NM_001272036 RefSeq chr8 + 144517964 144525175 LRRC14 9684 "leucine rich repeat containing 14, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137979_PI430048170 0.164594962023477 1.02822769958486 0.379716879790252 0.384160906618083 0.437025633797569 A A A 0.357462540676628 0.337124248266221 0.386124284605591 A A A LNCV6_137979_PI430048170 mRNA
CATTTTACCCAGACATGGTGAACCGTGATACTAAGATGGCATCGAATCCTAGAAAGTGCA NM_022052 RefSeq chrX - 103075820 103093094 NXF3 56000 nuclear RNA export factor 3
GO:0005515|GO:0005737|GO:0006406|GO:0000166|GO:0016973|GO:0042272|GO:0005654|GO:0005634|GO:0003729 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132547_PI430048170 0.318202900027426 0.820838852545856 4.92410321200887 4.40042976894091 4.36940599202444 P P P 5.20037330468305 4.69359632868767 4.65822091023314 P P P LNCV6_132547_PI430048170 mRNA
TGTGGGTGTCCTTTCCCTGTCAAACTCATTAAAAATTCCTTTGTTGCCAGTGCCAAAAAA NM_001168465 RefSeq chrX - 20006712 20116996 MAP7D2 256714 "MAP7 domain containing 2, transcript variant 1"
GO:0005737|GO:0005198|GO:0015630|GO:0005874|GO:0000226 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133562_PI430048170 0.9247925599109061.00297688054112 0.366466767961282
0.3403826781581710.256792205412022A A A 0.3132495093196480.32886110240182 0.3108613454618
A A A LNCV6_133562_PI430048170 mRNA
AAACAGGGCTTTTTTCCCCTTTATGAAAAAAGTACACAGAAGTGTTGAAACGATTCAAGT NM_001206671 RefSeq
chr11 - 8106049 8169043 RIC3 79608 "RIC3 acetylcholine receptor chaperone, transcript variant
3"
GO:0000139|GO:0044183|GO:0006457|GO:0005789|GO:0033130|GO:0016021|GO:0007204|GO:0043623|GO:0007
271 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132640_PI430048170 0.7000369784592281.3173437717412 2.17188589378372
1.87026008546158 3.56073050207878 A A P 2.3649924335256 1.76297381265827
2.72419774890631 A A P LNCV6_132640_PI430048170 mRNA
GGTATTACTGTTTGTGTGTTTGAGTTTACTGCACATGTTTGTGTTTGTGTATATGTGTCT NM_153838RefSeq chr6 +
47698552 47722021 ADGRF4 NA adhesion G protein-coupled receptor F4 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_129516_PI430048170 0.000957341028924205 0.4562681960859274.98883743017681
4.73733496697587 5.04593472141764 P P P 6.10203301004578 5.92069775080825
6.15359671782996 P P P LNCV6_129516_PI430048170 mRNA
TGGGGTGGGGGGAGGAAAATTTTTACTTTCCATCTTAATGTAACCTTATGCTATTCTGTA NM_178517RefSeq
chr17_KI270857v1_alt + 770458 774205 PIGW 284098 "phosphatidylinositol glycan anchor biosynthesis,
class W"
GO:0006501|GO:0016746|GO:0016254|GO:0005789|GO:0016021|GO:0072659|GO:0044267|GO:0043687|GO:0006
505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143625_PI430048170 0.759555740155385 1.06219725971679 5.15579455900938
4.52113503826398 4.9054576888246 P P P 4.91791655058594 4.72459807040068
4.74009716926463 P P P LNCV6_143625_PI430048170 mRNA
ATGCTTTTGCTACCCCGTTAACAGAAGAATATACAGAACTGTCTTAGGCGAAAGTATGTA NM_001254728 RefSeq
chr14 + 31026642 31096450 AP4S1 11154 "adaptor-related protein complex 4, sigma 1 subunit,
transcript variant 5" GO:0005215|GO:0005905|GO:0005794|GO:0008565|GO:0015031 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_133327_PI430048170 0.157686106077551 1.10732880962465 10.6596197143065 10.821726821279
10.8373653860872 P P P 10.5082719915483 10.6432459209415 10.7243633513725 P P P
LNCV6_133327_PI430048170 mRNA
ATCGATGCCTTTTAGTTTTTCCAATGATTTTTACACTATATTCCTGCCACCAAGGCCTTT NM_001199207 RefSeq chr7
+ 74453789 74602593 GTF2IRD1 9569 "GTF2I repeat domain containing 1, transcript variant 3"
GO:0014886|GO:0006355|GO:0005737|GO:0003700|GO:0006366|GO:0006357|GO:0003705|GO:0007275|GO:0005
654|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142141_PI430048170 0.140742608421871 1.22930559673893 11.6717165647686
11.6985549931402 11.6416967685626 P P P 11.1136723950396 11.5616019589329
11.4084305878893 P P P LNCV6_142141_PI430048170 mRNA
TCCACCCAGACAAGCAATAAAAGTGGTCTCCTCCCTGTGCATGCTTCTGCTTTCAAAAAA NM_022908RefSeq chr3
- 52524368 52535077 NT5DC2 64943 "5'-nucleotidase domain containing 2, transcript variant 2"
GO:0016311|GO:0008253|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130949_PI430048170 0.5707613092692481.01776963292366 0.507288075478107
0.5654868574548630.44032521125454 A A A 0.4971073233205730.468786348688466
0.473529428389612A A A LNCV6_130949_PI430048170 mRNA
GCTATCTCATTTTGCATTAAACTTTAAGCAGGACAGATTGCTGAAGCCATGATATTTAAG NM_198081RefSeq chr6
- 107702156 107824317 SCML4 256380 "sex comb on midleg-like 4 (Drosophila), transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128588_PI430048170 0.1726792089486760.9273273677877616.07752651022033

6.06954142387539 6.23540192545574 P P P 6.22254566734219 6.30234756820708
6.18786224665101 P P P LNCV6_128588_PI430048170 mRNA
AATCTAGAGCATTGAGCACTTTATCTCCCACGACTCAGTGAAGTTTCTCCAGTCCCTAGT NM_016151 RefSeq chr16
+ 29973866 29988405 TAOK2 9344 "TAO kinase 2, transcript variant 1"
GO:0030036|GO:0008360|GO:0031572|GO:0046330|GO:0005634|GO:0032874|GO:0051403|GO:0001558|GO:0030
425|GO:0005737|GO:0000186|GO:0048041|GO:0006612|GO:0005856|GO:0004709|GO:0030659|GO:0006950|GO:0
005730|GO:0006915|GO:0031434|GO:0005524|GO:0006974|GO:0043235|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137865_PI430048170 0.0449986831924124 1.1146062604734 0.592572966487288
0.7139985437765650.584594165721236 A A A 0.4232609135007540.532630984610337
0.467246347661767 A A A LNCV6_137865_PI430048170 mRNA
AGTTATGTTCTGCTTTGCTTGGCACAAAATAAATGTAACCTGGAGGCTCCAAGTATTCAC NM_032600 RefSeq chr3
+ 107377340 107378634 CCDC54 84692 coiled-coil domain containing 54 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_108705_PI430048170 0.9279464792574690.9946033215781330.280706996961404
0.5259006544251120.365394860830273 A A A 0.5042851228134970.395352040933594
0.299322232566868 A A A LNCV6_108705_PI430048170 mRNA
CTGGTCAAAGGCTCCTACATGTTAGAGCCTTTTACAGACTCACTGCGTTGAGTCTAACAA NM_015564 RefSeq chr5
- 138869389 138875368 LRRTM226045 leucine rich repeat transmembrane neuronal 2
GO:0030054|GO:0050808|GO:0045211|GO:0060291|GO:0016021|GO:0060076|GO:0042043|GO:0002091 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133826_PI430048170 0.00134864326256924 1.97512526164821 7.0783824744793
7.08019448986333 6.85519811928031 P P P 5.99217020454073 6.19151537466042
5.87805831271813 P P P LNCV6_133826_PI430048170 mRNA
GCCCCAGACACCTTCCCTGAGGACACTCAATAAAGGTTCCTGAATCTTCCTGCCAAAAAA NM_057093 RefSeq chr2
- 218990189 218993405 CRYBA21412 "crystallin, beta A2, transcript variant 2"
GO:0008150|GO:0003674|GO:0005212|GO:0002088|GO:0005575|GO:0042803 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127543_PI430048170 0.0986703140027416 0.849500442852937 10.4583078325825
10.1610111283459 10.258821201503 P P P 10.5924444229752 10.4983394705934
10.5074933867066 P P P LNCV6_127543_PI430048170 mRNA
ATTGGGAATGTATGACCAATCTTAGACCCTGAAAAATGGCAGAAAATACATGGAAATTTG NM_017860 RefSeq chr1
+ 151047782 151051395 C1orf56 54964 chromosome 1 open reading frame 56
GO:0005737|GO:0005654|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91880_PI430048170 0.00335122527957971 1.2377812002284 7.76360278794462 7.8356525330907
7.88292809611023 P P P 7.50709862299274 7.46623365848441 7.58552018490774 P P P
LNCV6_91880_PI430048170 mRNA
TGTCTACAACAAAAGCAATTTTAGTCGATTTCACGCGGACTCCGTGTGCAAAGCCTCGAA NM_024050 RefSeq chr19
+ 17309527 17323297 DDA1 79016 DET1 and DDB1 associated 1 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129855_PI430048170 0.0635804911924653 1.26424956125006 10.2111825881419
10.428675269792 10.0724572242838 P P P 10.0332634427571 9.84426004740927
9.83359336743766 P P P LNCV6_129855_PI430048170 mRNA
TAGGGCTGGGGCAGCTCCCAGAGAATGAATAGTGCTGTTTCCTATTGGACTGATAAAAAA NM_001610 RefSeq chr11
- 47239301 47248847 ACP2 53 "acid phosphatase 2, lysosomal, transcript variant 1"
GO:0001501|GO:0016020|GO:0016311|GO:0003993|GO:0016021|GO:0005765|GO:0007040|GO:0005764|GO:0070
062|GO:0043202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144827_PI430048170 0.376600982373485 1.04655439659842 0.329191245857991
0.3334048984169830.499956409762503 A A A 0.3255644089890970.29502307421866

0.351134551203242 A A A LNCV6_144827_PI430048170 mRNA
TGTCCTTTTAAGAAGGGAGATATGAATCCAATAAATAAACTCAAGTCTTGGCTACCTGGA NM_080629 RefSeq chr1
- 102876466 103108496 COL11A1 1301 "collagen, type XI, alpha 1, transcript variant B"
GO:0042472|GO:0055010|GO:0005592|GO:0007605|GO:0050840|GO:0048704|GO:0005576|GO:0006029|GO:0035
987|GO:0046872|GO:0035989|GO:0001503|GO:0002063|GO:0022617|GO:0001502|GO:0030198|GO:0050910|GO:0
030199|GO:0030574|GO:0005788|GO:0030674|GO:0007601|GO:0005201 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142472_PI430048170 0.1606238284490090.7038166062798513.96110761308742
3.30378985478035 4.13681739738089 P P P 4.41678007866513 4.28767384561209
4.34085051813693 P P P LNCV6_142472_PI430048170 mRNA
GGAGGGAATGCTACTGATAATTTGTAGATAATATTCTTTAAGACTTAGGGGAACCATTGA NM_001746 RefSeq chr5
+ 179698928 179731638 CANX 821 "calnexin, transcript variant 1"
GO:0072583|GO:0005515|GO:0002474|GO:0030424|GO:0009306|GO:0005783|GO:0032839|GO:0019886|GO:0001
948|GO:0043197|GO:0006457|GO:0043025|GO:0071556|GO:0044233|GO:0070062|GO:0018279|GO:0005791|GO:0
042470|GO:0007568|GO:0005509|GO:0048488|GO:0005790|GO:0043234|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135795_PI430048170 0.8071579141806681.11984278548229 0.395125881761874
0.4012722056228621.39026660607742 A A A 0.83903067110576 0.355368585453682
0.701548465522999 A A A LNCV6_135795_PI430048170 mRNA
CTCATGCTTGCAAAACTAGAGACCCCTAAGGCAGAACTGAGAATAAACATGTTTACTTTG NM_004816 RefSeq chr9
+ 69329324 69392454 FAM189A2 9413 "family with sequence similarity 189, member A2, transcript
variant 1" GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134424_PI430048170 0.1535446156691841.04088403035066 0.354032644141533
0.3324615590018120.421470090634692 A A A 0.3035797454506350.291992624618632
0.34002855829645 A A A LNCV6_134424_PI430048170 mRNA
CTAGAAGGTGGTTCCATTCATCTTGTTATCAGCCATTCTGTAGATCTGGTTTCTACTGAC NM_181622 RefSeq chr21
- 30425392 30425912 KRTAP13-3 337960 keratin associated protein 13-3 GO:0005882 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138702_PI430048170 0.1789965739733191.18186695936878 0.566066950043599
0.7544438675743410.968194610058467 A A A 0.4812042055966150.54741626622781
0.563661399156513 A A A LNCV6_138702_PI430048170 mRNA
TGTACACGTGGGCGTCGTGGTCATCAAAGCAGTGTCCTCAGGCTTCTACGTGGCCATGAA NM_001300812 RefSeq
chr19 + 639894 643703 FGF22 27006 "fibroblast growth factor 22, transcript variant 2"
GO:0008286|GO:0048011|GO:0005794|GO:0009986|GO:0048015|GO:0005730|GO:0005104|GO:0005576|GO:0005
615|GO:0030154|GO:0007173|GO:0008543|GO:0045087|GO:0008083|GO:0038095 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137318_PI430048170 0.0320865354401649 1.22556704307741 9.23768070215447
9.26645518241986 9.19154842199285 P P P 8.86668985373617 8.87856100407187
9.06259373606252 P P P LNCV6_137318_PI430048170 mRNA
AAAGCGATTTGAGATGCCAATACCTGTGAATACCTGTTAATAAAGAGCTGTTAAATAGAC NM_001508 RefSeq chr2
+ 132416573 132646596 GPR39 2863 G protein-coupled receptor 39
GO:0007186|GO:0005886|GO:0005887|GO:0004930|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139269_PI430048170 0.0664525699135735 0.83883288109147 13.4186932268042
13.5286882122629 13.6576887533345 P P P 13.6409895564352 13.8588364347769
13.8647410446687 P P P LNCV6_139269_PI430048170 mRNA
AAGTTGCCATATAGATGTGAACTGCTCAACACACAGATCTCCTACTCCATCCAGTCCTGA NM_002083 RefSeq chr14
- 64939151 64942905 GPX2 2877 "glutathione peroxidase 2, transcript variant 1"

GO:0004602|GO:0005737|GO:0001659|GO:0002862|GO:0051702|GO:0009609|GO:0009055|GO:0000302|GO:0070062|GO:0055114|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127378_PI430048170 0.5478298443813610.8579582771923881.67148647383916 0.30798348200054 0.302834955552498A A A 1.48891778650014 1.08347141309734 0.737783226248963A A A LNCV6_127378_PI430048170 mRNA
AATAAGGAAGAAAGAAAACATGCCAAGCTGAGCATGCTGCTCCAAATAAATATCTGCTTT NM_001199799 RefSeq chr3 - 121987322 122022280 ILDR1 286676 "immunoglobulin-like domain containing receptor 1, transcript variant 1" GO:0070506|GO:0005886|GO:0090277|GO:0016021|GO:0006898|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136656_PI430048170 0.00546307395189357 0.2451913003608484.99249435007176 4.60532591873164 5.39936577614002 P P P 6.53642790556947 7.00512299918986 7.49154488771943 P P P LNCV6_136656_PI430048170 mRNA
AAACTCAGATGTTCTCCAACTTACACTAATGTCTGGTTTTCTTGAACTATGTGAGAGAAA NM_001104554 RefSeq chr15 + 69314402 69407637 PAQR5 54852 "progestin and adipoQ receptor family member V, transcript variant 1" GO:0048477|GO:0007275|GO:0004872|GO:0016021|GO:0005496 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135473_PI430048170 0.0109722688088317 0.4053891965221317.42979670817441 7.20869753990132 7.54144475665383 P P P 8.39060255957282 8.57751279396855 9.05565255319598 P P P LNCV6_135473_PI430048170 mRNA
GGACAAATGTGCTTGGTTTTACTATTATGTAATCACAACTTACTTTCTGCTTGTAGTTGCNM_021038RefSeq chr3 + 152268039 152465779 MBNL1 4154 "muscleblind-like splicing regulator 1, transcript variant 1" GO:0008380|GO:0003725|GO:0005515|GO:0005813|GO:0010494|GO:0003723|GO:0006376|GO:0005634|GO:0030326|GO:0001701|GO:0046872|GO:0007399|GO:0005737|GO:0000381|GO:0007519|GO:0000380|GO:0045445|GO:0043484|GO:0005654. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141958_PI430048170 0.2448550247516821.27691292920785 1.17277007428908 0.6098691946425090.538977775133439A A A 0.3841180706351180.462829576257435 0.501063549694654A A A LNCV6_141958_PI430048170 mRNA
GCAGAAGGGAAACTTCAATTACAGTATAACTGGTCTGATCTGTTCTACATATTAAAGTTC NM_001013643 RefSeq chr1 + 116694111 116706603 C1orf137 NA chromosome 1 open reading frame 137 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140984_PI430048170 0.0600777410011907 0.8329006358471181 0.6623449714755 10.4205990695301 10.4235013128745 P P P 10.8640473379176 10.7744985466433 10.6660313346624 P P P LNCV6_140984_PI430048170 mRNA
GAGGCTGCTTAGCCACATGGGAGGTGCTCAGTAAAGGAGAGCAATTCTTACAGGAAAAAA NM_030578RefSeq chr19 - 41354416 41364173 B9D2 80776 B9 protein domain 2 GO:0005515|GO:0042384|GO:0005813|GO:0006996|GO:0043015|GO:0016020|GO:0036038|GO:0005634|GO:0000278|GO:0036064|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132097_PI430048170 0.00252054639262368 0.3382969286168955.76494530448914 5.56457876605912 5.77180715756501 P P P 6.98302132587351 7.32574797861573 7.45298961382824 P P P LNCV6_132097_PI430048170 mRNA
GTTTTATGTTCCTGAAGCTATCTTGTTCTCTGTTAAAGCTACTAATTGTCTCAGTGTAAG NM_018143RefSeq chr17 - 41848518 41865431 KLHL11 55175 kelch-like family member 11 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128559_PI430048170 0.0872481394880286 0.4326265789375950.319679470921411 0.4733678502176930.335822613673847A A A 0.8020453891453251.6912800703991 2.01372147497057 A A A LNCV6_128559_PI430048170 mRNA
ATGGGAGGAGAAGCCCATACTGCTACTATAACTTGTGTATGTTAAATGTCTGTTTTAAAA NM_002674RefSeq chr12 - 102196458 102197836 PMCH 5367 pro-melanin-concentrating hormone GO:0007631|GO:0030354|GO:0007218|GO:0007268|GO:0007275|GO:0005634|GO:0005576|GO:0007283|GO:0030

154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143017_PI430048170 0.0686567563487678 0.7956167796536617.0958690523501
7.29924572643153 7.43637119528566 P P P 7.52701480044619 7.51071498953799
7.78656249387871 P P P LNCV6_143017_PI430048170 mRNA
TTGCTCAAAAAATGAGCTCGCATTTGTCAATGACAGTTTCTTTTTTCTTACTAGACCTGTNM_004346RefSeq chr4 -
184627695 184649475 CASP3 836 "caspase 3, apoptosis-related cysteine peptidase, transcript variant alpha"
GO:0005515|GO:0007605|GO:0051402|GO:0097200|GO:0007507|GO:0043525|GO:0030198|GO:0006508|GO:0043
029|GO:0009411|GO:0030889|GO:0035329|GO:0043281|GO:0045165|GO:0008233|GO:0005654|GO:0008625|GO:0
001782|GO:0005886|GO:0045736|GO:0046007|GO:0001836|GO:0005634|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134410_PI430048170 0.1883176566198431.33698622271187 4.03844305914163
4.04092427593323 4.64608381763496 P P P 4.09144201574113 3.84343670169548
3.57629090120748 P P P LNCV6_134410_PI430048170 mRNA
GTTTTCACCGTCGTATGAGAGGACTATTCATGATAGGCTGTATTTGCTGACAGCCTACTT NM_032779RefSeq chr2
- 74472831 74483230 CCDC142 84865 coiled-coil domain containing 142 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_144480_PI430048170 0.1976237085370280.4991171996721370.362592761578433
0.3646415305977390.454954247074816A A A 0.3475783361236391.75318340353625
1.70424518532456 A A A LNCV6_144480_PI430048170 mRNA
CTCTGAACAGCTAGATAAGCATAGAGAATTTCTGTTATACCAAGCATAAAGTACACCTAA NM_017416RefSeq chrX
+ 104566314 105767829 IL1RAPL2 26280 interleukin 1 receptor accessory protein-like 2
GO:0004910|GO:0019221|GO:0004908|GO:0016021|GO:0007417 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_100045_PI430048170 0.2820663091331871.13431855437967 4.94854236919378
5.32155967971725 5.20163908831613 P P P 4.90661669800165 4.86384588443126
5.16216229218138 P P P LNCV6_100045_PI430048170 mRNA
AAATTGTAACCTGAAGCACATCGATGAAGTTATCTATCCGTGCCCTGTGGAGCCAAAAAA NM_001271783 RefSeq
chr12 + 29149002 29335616 FAR2 55711 "fatty acyl CoA reductase 2, transcript variant 1"
GO:0005782|GO:0008611|GO:0005789|GO:0044281|GO:0016021|GO:0080019|GO:0035336|GO:0050062|GO:0044
255|GO:0005778|GO:0055114|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143332_PI430048170 0.0358629458253295 1.42121161704931 7.77943910479286
8.15543082902495 8.11339299507051 P P P 7.43305861697868 7.50010849744355
7.61634286980965 P P P LNCV6_143332_PI430048170 mRNA
AGAGGCCTTTCAGTTCCTTTTCTGTCCTTCCCCTTCTTAACACAAGCTCAAATTTTCTAA NM_004840RefSeq chrX -
136665550 136781344 ARHGEF6 9459 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
GO:0005515|GO:0051056|GO:0048011|GO:0043065|GO:0007264|GO:0034329|GO:0030032|GO:0007254|GO:0006
915|GO:0097190|GO:0030027|GO:0005829|GO:0043547|GO:0005622|GO:0005911|GO:0032321|GO:0005089|GO:0
005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107945_PI430048170 0.00627939114409383 1.56409384652065 7.26134730123765
7.2203275361962 7.45572366720066 P P P 6.7122254301836 6.68229190317531
6.61635438846403 P P P LNCV6_107945_PI430048170 mRNA
AGAGAAATACGCAGTGCCTGTGCTCAGGACAAAGAAGAAGTTTCTCGAGTGGATGCAAAA NM_006810RefSeq
chr3 + 123067008 123162106 PDIA5 10954 "protein disulfide isomerase family A, member 5, transcript
variant 1"
GO:0034976|GO:0006457|GO:0005783|GO:0016491|GO:0005789|GO:0005788|GO:0003756|GO:0045454|GO:0006
987|GO:0044267|GO:0055114|GO:0030968 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138195_PI430048170 0.6643912664326471.02773169321148 0.705705182591973
0.5309388621745860.512074474570238A A A 0.43484987972893 0.619527263451542
0.577529375088895A A A LNCV6_138195_PI430048170 mRNA

CTCACTACTCCATAGGTTAATTGAATTCCTGGTTGAGAAACTAACTTGTTTTGTTTTCCANM_001040429 RefSeq chr13
+ 57631654 57728931 PCDH17 27253 protocadherin 17
GO:0005515|GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_59017_PI430048170 0.1867142997836411.25634278339832 8.22470411334057 8.46139390623575
8.14652455205936 P P P 8.22917827749302 7.95941304940441 7.60912960070072 P P P
LNCV6_59017_PI430048170 mRNA
TCACTGATAAAACTCTCAATGAGGAGCAGCTCTCCCCATGAGCAAGTTCTTGCCTTCATT NM_001242696 RefSeq
chr12 - 52205580 52210855 C12orf80 NA chromosome 12 open reading frame 80 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129194_PI430048170 0.4531601094233650.9723771158590010.405954613198585
0.4244519491531710.283800051505086A A A 0.3889943924754260.44499122162995
0.404888048591009A A A LNCV6_129194_PI430048170 mRNA
CATCCAAAAAGGCGATTTGGTATCCCCATGGATCGGATTGGTAGAAACCGGCTTTCAAAT NM_198184RefSeq chr3
+ 191212532 191250121 OSTN NA osteocrin NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136579_PI430048170 0.0937598026733618 0.7012695896304264.60705684163353
4.30801386373846 4.66693843194516 P P P 4.68601151543311 5.07925848607356
5.31011759101013 P P P LNCV6_136579_PI430048170 mRNA
GCCGAATGTGATGTTCCGCTTTGTGTTGTTCCGTGCTTTGAAATTTACCACACGAAAAAA NM_152595RefSeq chr15
+ 34102072 34104390 PGBD4 161779 piggyBac transposable element derived 4 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136684_PI430048170 0.2584067609896291.03840990173386 0.571070160018217
0.6448419638292990.525767717847652A A A 0.5503269192715950.515121340880661
0.515329451714355A A A LNCV6_136684_PI430048170 mRNA
GTAGCTGTGAAGGCCATTAAAAAGACAAACTTAATGTACAGAGCATTTATTCAGATCAAG NM_152745RefSeq chr7
+ 8433954 8752963 NXPH1 30010 neurexophilin 1 GO:0005102|GO:0005576 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_128795_PI430048170 0.0910011434037932 1.09944404579588 0.529459665447094
0.36223056528027 0.472431275631847A A A 0.2741797446704060.370946714110394
0.311998818668193A A A LNCV6_128795_PI430048170 mRNA
TTCCTGGTGTCTGCTGTTGAGCTGGACAATGGAAGAACTGAAAGTCTATACTCAATGCTG NM_198687RefSeq chr21
+ 44573728 44575371 KRTAP10-4 NA keratin associated protein 10-4 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141813_PI430048170 0.0182470172581572 0.5635612665934943.52010691657631
3.41727896758027 3.73107152253279 P P P 4.1032132410104 4.36073695974082
4.65217115175947 P P P LNCV6_141813_PI430048170 mRNA
TTACCCATGATAGGACTTTTGTGATATGGCTAATCTCAGTACACATTTCAACTTAAAACC NM_017768RefSeq chr1
- 70144801 70205678 LRRC40 55631 leucine rich repeat containing 40 GO:0016020 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127895_PI430048170 0.5389112062558090.8622197502332942.44664998336642
3.27064647114272 3.04077564884313 A P P 3.57194807342104 2.92476310678178 2.9210946595557
P P P LNCV6_127895_PI430048170 mRNA
GGTATGAAAAACCATCATCCTGAACAGCAAAGCTCCCTGCTAAACCTCTCTTCGACGAAA NM_001256869 RefSeq
chr8 - 12132416 12134009 USP17L7 NA ubiquitin specific peptidase 17-like family member 7 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138418_PI430048170 0.0255023515793439 0.6508049645151044.9334514644135
4.63336920762482 5.08473314252068 P P P 5.33811808591232 5.44418450880335
5.73455870507685 P P P LNCV6_138418_PI430048170 mRNA
GGCAGCAGCATTTGAGTCCATGAATGCTATGGTCATTAAAATAATTGATTATACTTTCCT NM_022497RefSeq chr3

- 15048511 15065309 MRPS25 64432 mitochondrial ribosomal protein S25
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0005743|GO:0005840 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64233_PI430048170 0.14210913039612 1.40255249937059 5.15489025887362 5.43442390086468
5.22970346445171 P P P 4.36515674551109 5.16545186421325 4.72738292785179 P P P
LNCV6_64233_PI430048170 mRNA
AGACAAAAGGTAAAGACGCAACGTTTCCAACTCTCGGGACGCCAAGGCCGCAGGACTGGA NM_205843 RefSeq
chr19 + 3359562 3469217 NFIC 4782 "nuclear factor I/C (CCAAT-binding transcription factor),
transcript variant 2"
GO:0003700|GO:0006366|GO:0000981|GO:0005730|GO:0005634|GO:0000122|GO:0000978|GO:0006260|GO:0001
077|GO:0003690|GO:0045944|GO:0042475|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122136_PI430048170 0.00147691237859497 1.5951628604938 4.88825171547072
4.66594925199441 4.7818709490298 P P P 4.1708517688539 4.00204912468637
4.14495157799328 P P P LNCV6_122136_PI430048170 mRNA
TGCCTTCCTAGAGCTCATGGACCATGGCATTGTCTCCTGGGACATGGTTTCAATCACCTT NM_133171 RefSeq chr20
- 46366050 46406632 ELMO2 63916 "engulfment and cell motility 2, transcript variant 1"
GO:0005515|GO:0048010|GO:0030971|GO:0017124|GO:0005737|GO:0016020|GO:0060326|GO:0045087|GO:0006
915|GO:0005856|GO:0038096|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78328_PI430048170 0.97741714036832 0.983635711288494 1.14870084726156 0.394023831348248
0.426990527312899 A A A 0.319504178760366 0.463711554555744 1.22017370605449 A A A
LNCV6_78328_PI430048170 mRNA
TAATTCCTCAATGCAACACACACACATATGCCAGGGTTGGTCAAATGGGAAGAGAGCCTT NM_001202481 RefSeq
chr7 - 30651942 30700103 CRHR2 1395 "corticotropin releasing hormone receptor 2, transcript
variant 3"
GO:0005515|GO:0015056|GO:0005794|GO:0005886|GO:0009986|GO:0005783|GO:0005179|GO:0071376|GO:0005
887|GO:0016525|GO:0043950|GO:0007188|GO:0043951 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142267_PI430048170 0.796694161051994 1.29420721372303 0.396644690911639
2.87523937698665 2.21473771689087 A A A 2.36643478087087 1.91933397981955
0.41583959504637 A A A LNCV6_142267_PI430048170 mRNA
GTTGGCATTTCTGTAAACTGCCTGTCCATGCTCTTTGTTTTTAAACTTGTTCTTATTGAA NM_006610 RefSeq chr1 -
11026522 11047239 MASP2 10747 "mannan-binding lectin serine peptidase 2, transcript variant 1"
GO:0005515|GO:0004252|GO:0005509|GO:0001855|GO:0005576|GO:0001867|GO:0006956|GO:0045087|GO:0006
958|GO:0006508|GO:0008233|GO:0048306|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128352_PI430048170 0.533997664724803 1.60331693407408 0.416392815466222 2.2550460992834
0.489222815011513 A A A 0.315705488976704 0.291896506960216 1.14813701358039 A A A
LNCV6_128352_PI430048170 mRNA
CTTTCACATATAGCACAGGGGAAGGTAAAATGGAAGGGCTGCTAATTGAGACATATAATT NM_004984 RefSeq chr12
+ 57550063 57584771 KIF5A 3798 kinesin family member 5A
GO:0005515|GO:0008017|GO:0048471|GO:0005871|GO:0005874|GO:0007268|GO:0005524|GO:0005829|GO:0030
705|GO:0019886|GO:0003774|GO:0008104|GO:0016020|GO:0007411|GO:0007596|GO:0008574|GO:0008152|GO:0
016887|GO:0007018. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130710_PI430048170 0.0210790218219916 1.53100609989855 6.41078953074643
6.72868272655083 6.6671515513163 P P P 6.18194944142193 6.02448734994551
5.74218393103547 P P P LNCV6_130710_PI430048170 mRNA
TTAAAAGCTTTATTAGTCTCTACCAGGAGGAAGCCCTCTCTCTTGCACAGGTGACTCTCA NM_001080523 RefSeq
chr19 - 4890436 4902867 ARRDC5 645432 arrestin domain containing 5 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141638_PI430048170 0.200158935177138 0.850510652868425 0.371723520243433
0.337910800953831 0.325282209858078 A A A 0.464343624095547 0.434986660857642

0.806476396843041 A A A LNCV6_141638_PI430048170 mRNA
GTTGTTCAGGTACAAACATGACAAACAACTCTAGCTATGACTCTTAATGTTCAATTGCAA NM_002830 RefSeq chr2
+ 119759630 119984898 PTPN4 5775 "protein tyrosine phosphatase, non-receptor type 4
(megakaryocyte)"
GO:0008092|GO:0005515|GO:0005737|GO:0006470|GO:0009898|GO:0005856|GO:0035335|GO:0004726 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_142463_PI430048170 0.243271360224662 0.843441161922393 0.792219843686843
0.507422894878195 0.285462302776845 A A A 0.576309769189898 0.82516622767703
0.94171657210335 A A A LNCV6_142463_PI430048170 mRNA
GACGTTGAATGGGACATAGAACTGTCCTACATTTATGTCAAAGTATATATTTGAATCGCT NM_020879 RefSeq
chr7 + 77122616 77295204 CCDC146 57639 coiled-coil domain containing 146 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_138789_PI430048170 0.347760135999816 0.879281680209776 0.276212724050983
0.281345788915326 0.407507935624769 A A A 0.362300991666373 0.777354062849336
0.343116003568536 A A A LNCV6_138789_PI430048170 mRNA
GAGTGTTGGTGTTAAGCATGAAACAAACAGCAGCTGTTGTCCTTAAAAATGAATTGACCT NM_012431 RefSeq
chr7 - 83363905 83649163 SEMA3E 9723 "sema domain, immunoglobulin domain (Ig), short basic
domain, secreted, (semaphorin) 3E, transcript variant 1"
GO:0005515|GO:0001569|GO:0008360|GO:0002040|GO:0005576|GO:0005615|GO:2000249|GO:0016020|GO:0050
808|GO:0007411|GO:0016525|GO:0071526|GO:0004872|GO:0030215|GO:0001953 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_139920_PI430048170 0.00929352575650188 2.41102631235107 1.86483160111626
2.17231484901673 1.4847114853113 A A A 0.688250047990779 0.742382829467457
0.329612565505714 A A A LNCV6_139920_PI430048170 mRNA
TTGAGCCTCAAAAAGTGAAGGAAAAGATGAAGAACGCCTGATGCCAACTGTTCAGCTGTC NM_002903 RefSeq
chr17 - 9897709 9905367 RCVRN 5957 recoverin
GO:0007165|GO:0007603|GO:0005509|GO:0051924|GO:0031284|GO:0022400|GO:0007601|GO:0030425|GO:0016
056|GO:0008048 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141839_PI430048170 0.00299126681597144 0.372098718813664 4.86756794996502
4.30990351326111 4.70198063653775 P P P 5.86724076162727 6.02507590876295
6.28931794789086 P P P LNCV6_141839_PI430048170 mRNA
GCCATTTCCCTACTTATAAGATGTCTCAATCTGAATTTATTTGGCTACACTAAAGAATGC NM_012238 RefSeq
chr10 + 67884668 67918390 SIRT1 23411 "sirtuin 1, transcript variant 1"
GO:0005515|GO:0010467|GO:0030308|GO:0000790|GO:0006364|GO:0006325|GO:0032071|GO:0007283|GO:0010
906|GO:0003950|GO:0034605|GO:0033158|GO:0006979|GO:0031937|GO:0016239|GO:0032868|GO:0017136|GO:0
031393|GO:0005719|GO:0003714|GO:0007569|GO:0019213|GO:0033553|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129509_PI430048170 0.779297056793029 1.0046298119426 0.346532861416946
0.330231524217899 0.281814828004852 A A A 0.31640441923627 0.323149425059889
0.299715347462548 A A A LNCV6_129509_PI430048170 mRNA
TTTGGTCAAAGTGCTTAGCAGAGCTGGACTCAGGCAAATGTGCTGACTACATAGAAACTG NM_001004699 RefSeq
chr19 + 8730953 8732009 OR2Z1 NA "olfactory receptor, family 2, subfamily Z, member 1" NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_129147_PI430048170 0.357165646649266 1.02542764039443 0.425444265423696
0.426534658813769 0.338699910188102 A A A 0.329840258256017 0.370858207139986
0.382522837691483 A A A LNCV6_129147_PI430048170 mRNA
GACTCAGACTGTTTCAGGCTCCAGGACAGGAAGTGCAGTGTAGGCAAAATTGCAAAAATT NM_006820 RefSeq
chr1 + 78620381 78646145 IFI44L 10964 interferon-induced protein 44-like
GO:0051607|GO:0006955|GO:0005737 . NA - . NA NA NA NA NA NA NA NA

NA
LNCV6_43442_PI430048170 0.0487264876734649 2.75860273183376 1.72946713791673
3.00589424620682 2.79132051907272 A P A 1.58910981244527 0.868929301000869
0.83874621951544 A A A LNCV6_43442_PI430048170 mRNA
AGCTACAGGCTCTAGAATTTTATTAAATGCCATCTCTCACTACCATATTTTTCTTTCCTG NM_001195637 RefSeq
chr11 - 22846922 22860426 CCDC179 100500938 coiled-coil domain containing 179 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134321_PI430048170 0.54291793707278 0.880281153601259 2.7643509680165
1.50562192330537 1.60628342028205 A A A 2.11833209230804 2.46152188031371
2.18680457337856 A A A LNCV6_134321_PI430048170 mRNA
ATTTGTAAATATTTCTATTGGACCCAATTCTCCTCGGAATTGGCTGGCACCTCTGGCTGC NM_080607 RefSeq
chr20 + 37903096 37945345 VSTM2L 128434 V-set and transmembrane domain containing 2 like
GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51837_PI430048170 0.979406918809291 0.979090779219165 7.16700426298783
7.37879236080749 7.50879717622165 P P P 6.98671313379865 7.36865676169413
7.71895497742106 P P P LNCV6_51837_PI430048170 mRNA
ACATTGTAGGTTATCATGTGATTGTTCCATGTAGTTCCTGTCTTCTTTCCTGCAACAACA NM_207418 RefSeq chr1
+ 145095999 145112692 FAM72D 728833 "family with sequence similarity 72, member D" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54516_PI430048170 0.844643264435566 1.02869992003987 6.91702491563555
6.50249893496164 6.55831452904705 P P P 6.66038788129564 6.61722953721289
6.61325802763606 P P P LNCV6_54516_PI430048170 mRNA
CAGCATTTCAGAACCAGGTTCTCCTTCGAGGAACAGAGAAAATGAAACCAGCAGACAGAA NM_017744 RefSeq
chr1 - 112523518 112619418 ST7L 54879 "suppression of tumorigenicity 7 like, transcript variant 1"
GO:0030308|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113327_PI430048170 0.22864062191164 4.41850364607464 0.557686846701508
2.61623750661578 3.80824860088246 A A P 0.766287014672558 0.570349421597395
0.770190525408205 A A A LNCV6_113327_PI430048170 mRNA
ACAAATGGCTGGAAATTGAATCCAGTTGTGGGTGCAGTCTACAGTCCCGAATTCTATGCA NM_018723 RefSeq
chr16 + 6019130 7713338 RBFOX1 54715 "RNA binding protein, fox-1 homolog (C. elegans) 1, transcript
variant 4"
GO:0008380|GO:0006397|GO:0005802|GO:0005515|GO:0005737|GO:0000166|GO:0003723|GO:0050885|GO:0050
658|GO:0043484|GO:0005634|GO:0008022 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_53912_PI430048170 0.269299569539867 0.833626515635561 0.251951763008521
0.301026769149389 0.313629029467359 A A A 0.420338309557441 0.851814858452111
0.326817365634776 A A A LNCV6_53912_PI430048170 mRNA
ATATCGACCATATAAATGTGATCAGTGCAGCCGGGAGTTCATGAGGTCTGACCATCTCAA NM_173484 RefSeq
chr1 + 44118849 44135137 KLF17 128209 Kruppel-like factor 17
GO:0003700|GO:0044212|GO:0006357|GO:0007276|GO:0005634|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141630_PI430048170 0.697276629093077 0.987723359383638 0.441952615602137
0.462934423350532 0.3700311669459 A A A 0.505095026661491 0.404339482007103
0.418508052546721 A A A LNCV6_141630_PI430048170 mRNA
TGTCTTGCAAGCAAAGCACGTATTAAATATGATCTGCAGCCATTAAAAAGACACATTCTG NM_000371 RefSeq
chr18 + 31591766 31599023 TTR 7276 transthyretin
GO:0005515|GO:0007603|GO:0046982|GO:0070327|GO:0005576|GO:0070324|GO:0001523|GO:0005615|GO:0042
802|GO:0043234|GO:0005737|GO:0005179|GO:0030198|GO:0042572|GO:0006810|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_141679_PI430048170 0.0636084425071821 0.653829819161715 3.93332130921735 3.94762704236912 4.48630516531574 P P P 4.50804003602203 4.67126798731803 5.04491077396866 P P P LNCV6_141679_PI430048170 mRNA CTTCAGGGGTAAATTATCCTAGTTACCAAGTCCTATTTGGACATAAAGAAAATCCTACTT NM_014396RefSeq chr7 - 38723942 38909200 VPS41 27072 "vacuolar protein sorting 41 homolog (S. cerevisiae), transcript variant 1" GO:0005515|GO:0008017|GO:0033263|GO:0030897|GO:0005770|GO:0005798|GO:0035542|GO:0005765|GO:0005829|GO:0003674|GO:0008150|GO:0051020|GO:0016020|GO:0015630|GO:0006623|GO:0048193|GO:0008270|GO:0042144|GO:0016192|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135790_PI430048170 0.155549314119803 1.17797819685883 5.33723689409882 5.17583028645353 5.11963478341336 P P P 4.97277489446664 5.16298641213151 4.77028630389764 P P P LNCV6_135790_PI430048170 mRNA TTAAAGGAAATCCATGTGTGGTTAAGCTCTGTGTGGGTGTGTGCATGTGCACAGTTAGTG NM_015347RefSeq chr12 - 130396135 130517865 RIMBP2 23504 RIMS binding protein 2 GO:0030054|GO:0005886|GO:0010923|GO:0045202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142162_PI430048170 0.416144174552304 1.07419152056913 10.3795632050451 10.2739274129453 10.4322426127777 P P P 10.2465279782607 10.0740295090209 10.4370300240684 P P P LNCV6_142162_PI430048170 mRNA GCAGACATGGTTTGCAAACCACAAGAATCATTAGTTGTAGAGAAGCACGATTATAATAAA NM_001167740 RefSeq chr1 - 245749339 246507342 SMYD3 64754 "SET and MYND domain containing 3, transcript variant 1" GO:0001162|GO:0000993|GO:0006325|GO:0006334|GO:0034968|GO:0014904|GO:0000979|GO:0046872|GO:0018024|GO:0045184|GO:0005737|GO:0033138|GO:0045944|GO:0005654|GO:0006469|GO:0071549 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129151_PI430048170 0.00663199157981555 4.72294455134558 4.66188534005437 4.3365070358735 4.72012429952193 P P P 1.84528289015415 2.22539149878633 2.79671908095606 A A P LNCV6_129151_PI430048170 mRNA ACTCAATATTGGGTGAGTTGGTCTGAACAAGGTGGGGATAAAGTAGAGTGGAAATAATGT NM_015253RefSeq chr17 + 6070613 6124427 WSCD1 23302 WSC domain containing 1 GO:0008152|GO:0008146|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130915_PI430048170 0.417614664789553 12.5051189070896 5.66441390869068 0.516876303304604 0.55657606870684 P A A 0.433587466277036 0.555413550988739 0.553461594948482 A A A LNCV6_130915_PI430048170 mRNA GAGGTGAAGAAAGCTGTGTTGAAACTGAGAGACAAAGTAGCACATTCTCAGGGAGAATAA NM_001001953 RefSeq chr11 + 124023012 124023948 OR10G9 NA "olfactory receptor, family 10, subfamily G, member 9" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127608_PI430048170 0.0388687894817093 1.12138151498536 0.66155215047396 0.739534620828929 0.731381815747058 A A A 0.629353822122878 0.49565338184355 0.509105132248358 A A A LNCV6_127608_PI430048170 mRNA CACTCCTGTTTCATTAATCACTTAACAGTAGTTGTTAGGACTAATTTGATACACTTGTGG NM_206832RefSeq chr17 - 30316347 30334047 TMIGD1 NA transmembrane and immunoglobulin domain containing 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133865_PI430048170 0.00105894244700174 4.4612741702496 2.90078184542963 2.65151741270358 2.72491841493761 A A A 0.607799791431549 0.325895259672234 0.837519181926446 A A A LNCV6_133865_PI430048170 mRNA GGCTAAATGCACCAAGAAAGCTTCTTCAGAGTGAAGAATCTTAATGCTTGTAATTTAAAC NM_001271368 RefSeq chr9 + 122370529 122395703 PTGS1 5742 "prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase), transcript variant 7" GO:0019371|GO:0006629|GO:0019369|GO:0006805|GO:0004666|GO:0051213|GO:0005634|GO:0044281|GO:0046872|GO:0043231|GO:0005737|GO:0004601|GO:0006954|GO:0001516|GO:0042127|GO:0005789|GO:0008217|GO:0

006979|GO:0070062|GO:0055114|GO:0020037|GO:0001750 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140204_PI430048170 0.511423597639542 1.04833529173542 10.3225850477949 10.1309320278111 10.0819758143866 P P P 10.1343389729171 10.1935421980052 10.0085300507049 P P P LNCV6_140204_PI430048170 mRNA AGTCACCTTTGATACAACCAAGTCGGATGGGCAGTTTAAGAAGACAGCCAGTAACAGCAA NM_003313 RefSeq chr8_KI270816v1_alt - 102657 107602 TSTA3 7264 tissue specific transplantation antigen P35B GO:0050662|GO:0005737|GO:0042356|GO:0019835|GO:0007159|GO:0019673|GO:0009055|GO:0042351|GO:0016853|GO:0070062|GO:0055114|GO:0050577 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139762_PI430048170 0.639088453557837 1.03201672745582 10.110469215576 10.1913379153047 10.2639057708893 P P P 10.1442268779547 9.99349015467907 10.2813410670075 P P P LNCV6_139762_PI430048170 mRNA GACTCGGAACTCCTCGTCTTACTTTGTGCTCCATGTTTTGTTTTTGTATTTTGGTTTGTA NM_033489 RefSeq chr1 - 1635225 1659097 CDK11B 984 "cyclin-dependent kinase 11B, transcript variant 5" GO:0005515|GO:0006355|GO:0008283|GO:0006915|GO:0005634|GO:0050684|GO:0001558|GO:0005524|GO:0005737|GO:0007067|GO:0004672|GO:0004674|GO:0051726|GO:0006468|GO:0004693 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141134_PI430048170 0.304365466189411 0.674126108813057 0.457049556110515 0.378216580446694 1.8229786303406 A A A 2.14062276432502 1.30707737809283 1.21962277845925 A A A LNCV6_141134_PI430048170 mRNA CAGTTACATTCAGCAGAAAAAGTGACATTTAATGGAAAGCAAAACAAATCAGGTCCTGAT NM_001009881 RefSeq chr1 - 52423275 52553090 ZCCHC11 23318 "zinc finger, CCHC domain containing 11, transcript variant 1" GO:0032755|GO:0005515|GO:0005730|GO:0031123|GO:0032088|GO:0001816|GO:0005615|GO:0050265|GO:0010587|GO:0010586|GO:0005737|GO:0019827|GO:0031054|GO:0071044|GO:0008270|GO:0031664|GO:0070102|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130945_PI430048170 0.509700926915537 1.463024129834 2.41340588074722 2.8437737538683 1.12606229709678 A A A 2.17565201888774 1.30824009215203 1.60681639590646 A A A LNCV6_130945_PI430048170 mRNA TATCTAAACCAGCCTTGGGAAATTACAGTGTTTTACAATAAACAGAAAGCCAAGCGGAAA NM_001282540 RefSeq chr17 - 15565481 15619704 CDRT1 374286 "CMT1A duplicated region transcript 1, transcript variant 2" GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145012_PI430048170 0.300890778380607 1.18764283683032 11.5924339888471 11.7058480555889 11.871315798664 P P P 11.8204651323838 11.1543359700885 11.3833623857913 P P P LNCV6_145012_PI430048170 mRNA AATGTGCCAGGAGCCATAGGAATATCTGTATGTTGGATGACTTTAATGCTACATTTTAAA NM_004281 RefSeq chr10 + 119651369 119677817 BAG3 9531 BCL2-associated athanogene 3 GO:0005515|GO:0008625|GO:0043005|GO:0030018|GO:0043066|GO:0005886|GO:0021510|GO:0051087|GO:0050821|GO:0032403|GO:0097192|GO:0005829|GO:0005737|GO:0006457|GO:0007420|GO:0071260|GO:0010664 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133513_PI430048170 0.00231635702276863 0.225490125341284 2.33414742823597 2.65422891391003 1.88543926400421 A A A 4.17597668647043 4.55715987715535 4.64658549381386 P P P LNCV6_133513_PI430048170 mRNA GACCTAGGTCATCTATGAACCCTCTTTGTGTCTAATAAACATATCTGTAAAGGCAAAAAA NM_004226 RefSeq chr2 - 196133582 196171612 STK17B 9262 serine/threonine kinase 17b GO:0035556|GO:0005793|GO:0046777|GO:0004672|GO:0005886|GO:0004674|GO:0006915|GO:0006468|GO:0005634|GO:0015629|GO:0005524|GO:2000271 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89648_PI430048170 0.387808228708807 1.09860332729514 5.04913061645336 4.93905775184017 5.08501504415958 P P P 4.71255341235041 5.14125504542294 4.77847450059157 P P P

LNCV6_89648_PI430048170 mRNA
AATCTGGACGAGGCTAGAGAACAGAAAGAAAAGAGTCCTCCAGACCAGCCTGCGGTCCCC NM_001286645
RefSeq chr4 + 2844149 2930075 ADD1 118 "adducin 1 (alpha), transcript variant 5"
GO:0005516|GO:0048471|GO:0020027|GO:0030036|GO:0005886|GO:0071300|GO:0005634|GO:0042803|GO:0006
921|GO:0006884|GO:0005829|GO:0030968|GO:0032092|GO:0045807|GO:0051016|GO:0042608|GO:0051015|GO:0
048873|GO:0043197|GO:0035264|GO:0045111|GO:0051017|GO:0046982|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137692_PI430048170 0.16357396590422 1.05022577294044 0.505834880277519
0.6134467860076470.519006057146519A A A 0.4497798641908270.480129292041311
0.498270103333466A A A LNCV6_137692_PI430048170 mRNA
GAGAAACGCAAGCAGACTGGATTGGGATAGAAGTATTTGTGTACCTGGATTAATGAACTA NM_000243RefSeq chr16
- 3242027 3256627 MEFV 4210 "Mediterranean fever, transcript variant 1"
GO:2001056|GO:0005875|GO:0005874|GO:0032691|GO:0071641|GO:0003779|GO:0005634|GO:0001726|GO:0030
027|GO:0035872|GO:0005829|GO:0006954|GO:0032695|GO:0050728|GO:0045087|GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132668_PI430048170 0.135549621684661 1.15800645779031 11.3716597722323
11.4403825651977 11.2841172281677 P P P 11.3111160278361 11.1527816075893
10.9829490243819 P P P LNCV6_132668_PI430048170 mRNA
GCCGCTGTGTCTCCTTTGTATCCTAAATCTTTATTTTTCTAGGACATGTTATGCCTCCAT NM_175875RefSeq chr19 -
45764784 45769239 SIX5 147912 SIX homeobox 5
GO:0043565|GO:0005515|GO:0005737|GO:0005794|GO:0002088|GO:0007286|GO:0005654|GO:0045892|GO:0006
351|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134682_PI430048170 0.865678946811476 1.0129311381177 8.57591975552617
8.66038988994051 8.90622529970602 P P P 8.59122822995602 8.35232774226351
9.06969773659926 P P P LNCV6_134682_PI430048170 mRNA
GAGCTGCTCATGTGTGAGTTATTATCACTGCTGTCTTTCTATTGAGTTACAAATCTATATNM_017646RefSeq chr1 -
39841030 39883505 TRIT1 54802 tRNA isopentenyltransferase 1
GO:0005739|GO:0052381|GO:0005575|GO:0005524|GO:0046872|GO:0008033 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143704_PI430048170 0.341264182321691 1.78216608345244 1.58431434462267
2.15235921482635 0.345311671584324A A A 0.7921443080976140.547641649259033
0.762614578754559A A A LNCV6_143704_PI430048170 mRNA
GCAGTTATTGCTGTCAAAAGCCTGTTCTCTCAACTGCTGTCAATAAAATTAAAGATACAG NM_004188RefSeq chr9
+ 132945544 132991687 GFI1B 8328 "growth factor independent 1B transcription repressor, transcript
variant 1"
GO:0005515|GO:0030097|GO:0005667|GO:0006366|GO:0008283|GO:0005634|GO:0000122|GO:0003677|GO:0016
363|GO:0046872|GO:0001085|GO:0051569|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131341_PI430048170 0.0114687766315084 0.9432345844302260.372168057734505
0.3475290142331530.328843126340939A A A 0.4576632776269050.43489079091867
0.408834480368616A A A LNCV6_131341_PI430048170 mRNA
ACCTGCGGGTCAAGACAGTGACCTTCGAATACTGAAGAAAGGTCTTTGTGAGAAGAAAGT NM_012190RefSeq chr3
- 126103560 126180802 ALDH1L1 10840 "aldehyde dehydrogenase 1 family, member L1, transcript
variant 2"
GO:0005739|GO:0016155|GO:0009058|GO:0008168|GO:0004029|GO:0016742|GO:0003824|GO:0032259|GO:0006
730|GO:0070062|GO:0055114|GO:0009258 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145128_PI430048170 0.2970083499238420.8811784073649427.95610748746075
8.18260350005501 8.32654393938513 P P P 8.171579478174 8.30207506215348
8.53873634728365 P P P LNCV6_145128_PI430048170 mRNA
GGATGGACAGTGGGAAAACAAAATAAGTCAATGGAAACCTGATTTGTTTTTCAGTTACTT NM_018321RefSeq chr5

+ 34915714 34925682 BRIX1 55299 "BRX1, biogenesis of ribosomes"
GO:0005730|GO:0000027|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128007_PI430048170 0.0334122662296913 1.25797459735804 12.0994121954247
11.9561615885089 12.2323459722447 P P P 11.7712790611312 11.6610743897043
11.8680379242373 P P P LNCV6_128007_PI430048170 mRNA
AAGGCGACCAGTTTTCGTTGTATTGTTGTTCAATTAAATGGTGATATAGGGAAAAGAGAA NM_001278636 RefSeq
chr13 - 49660675 49691487 EBPL 84650 "emopamil binding protein-like, transcript variant 2"
GO:0005783|GO:0005789|GO:0016125|GO:0016021|GO:0047750 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_126804_PI430048170 0.5911373701716751.08251220871805 6.26975861418564
6.06367507178647 6.34974656161784 P P P 5.71148783999677 6.08652365231037
6.46029399957248 P P P LNCV6_126804_PI430048170 mRNA
GGGACTGGTTAAAGTCCCCCAGAAACTACAATAAAGAACAACTTTTGTTTTAACTCTTAA NM_000947RefSeq chr6
+ 57317616 57646850 PRIM2 5558 "primase, DNA, polypeptide 2 (58kDa), transcript variant 1"
GO:0051539|GO:0003896|GO:0003677|GO:0046872|GO:0000082|GO:0006271|GO:0000723|GO:0006270|GO:0000
722|GO:0006269|GO:0005654|GO:0000278|GO:0032201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99751_PI430048170 0.0658531964949456 0.8856722335191318.25399005386544 8.2328939128954
8.39615163813962 P P P 8.46033882404155 8.55577398383132 8.39327661054791 P P P
LNCV6_99751_PI430048170 mRNA
AGGCCACAGCTGCCCTATTCACTTCTAAGGGCCCTGTTTTGAGATTGTTTGTTCTAATTT NM_005104RefSeq
chr6_GL000256v2_alt + 4367906 4430762 BRD2 6046 "bromodomain containing 2, transcript
variant 1"
GO:0005515|GO:0005737|GO:0006357|GO:0003682|GO:0006334|GO:0070577|GO:0005634|GO:0007283|GO:0006
351|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132322_PI430048170 0.5823980778450761.01757970818099 0.33252638846234
0.2763118379661650.385890509558898A A A 0.3591543966522410.268320183184353
0.292366978579261A A A LNCV6_132322_PI430048170 mRNA
CTGCTTTTCAGAATGTAGTCCTGGTTCTTCTAAATATGCTTGACAATGTGGATAAATCTA NM_001010905 RefSeq
chr6 + 127577173 127591818 C6orf58 352999 chromosome 6 open reading frame 58 GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132137_PI430048170 0.1042592701306930.390921850286337 2.2055667394894
0.5020226445291330.299138821104339A A A 2.90218069182236 2.02531913571332 2.8120823337913
P A P LNCV6_132137_PI430048170 mRNA
CACTGGAATCGTGGCTCCCAAAAAGATGCTTTAATTGTGTGGTGCTTTTATAGTTTAGCT NM_003337RefSeq chr5
+ 134371175 134392108 UBE2B 7320 ubiquitin-conjugating enzyme E2B
GO:0005515|GO:0006344|GO:0006511|GO:0004842|GO:0000790|GO:0006513|GO:0016567|GO:0033522|GO:0005
886|GO:0033503|GO:0005657|GO:0007288|GO:0016874|GO:0005634|GO:0007283|GO:0006301|GO:0070534|GO:0
005737|GO:0019787|GO:0070193|GO:0060070|GO:0000785|GO:0009411|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128032_PI430048170 0.6030606176793720.821785352407176 0.574199703301687
0.4632879862381471.50009353113305 A A A 1.2406102677393 1.68208939651091
0.44309224606862 A A A LNCV6_128032_PI430048170 mRNA
ATGAAGGCAGCAATAAAGAGAGTATGCAAACAGCTAGTGATTTACAAGAGGATCTCATAA NM_001005277 RefSeq
chr5 + 181367286 181368225 OR4F16 NA "olfactory receptor, family 4, subfamily F, member 16" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142966_PI430048170 0.6269229240037010.969573956948661 0.517752564748356
0.5213352264080220.305064727960052A A A 0.4001808548074840.571286699733458
0.511668413727977A A A LNCV6_142966_PI430048170 mRNA
AGATGGAAAGCTCTAAGATCTTCTATTTTGGGGAAGACATGAAAGCGCTGAGCTGAGGGA NM_175062RefSeq chr5

- 180100794 180209130 RASGEF1C 255426 "RasGEF domain family, member 1C"
GO:0043547|GO:0005622|GO:0005085|GO:0051056|GO:0007264 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141992_PI430048170 0.3606309773791110.8717180765669730.357720079355874
0.4923721166933450.37376586772438 A A A 0.6748684234464780.80840674412292
0.289747841868627A A A LNCV6_141992_PI430048170 mRNA
GTAATCTGATGACTTAGAGGAGGAGATTAACCTTTCAGGCTCTTTTGAATTTGGTTTTTA NM_152524RefSeq chr2
+ 200526141 200584095 SGOL2 151246 "shugoshin-like 2 (S. pombe), transcript variant 1"
GO:0005515|GO:0030892|GO:0000777|GO:0005654|GO:0051754|GO:0000278|GO:0000775|GO:0051301|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135763_PI430048170 0.3831268961044870.90652466255432 0.274475020200345
0.2797569932803650.404873338103212A A A 0.3635050968928640.306396429988814
0.687755284802469A A A LNCV6_135763_PI430048170 mRNA
CCACACTGTACTGTTCAAGTCAATGTTAATAAAGCATTTCAAAACCAGCTGCTTTATTCA NM_012253RefSeq chrX
+ 154295673 154330363 TKTL1 8277 "transketolase-like 1, transcript variant 1"
GO:0006772|GO:0005737|GO:0006007|GO:0005634|GO:0046872|GO:0004802 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129670_PI430048170 0.6652500822260090.9716693645903950.271126189171142
0.4774554238304960.317772115708926A A A 0.5050547032227490.399377842502624
0.28622305388161 A A A LNCV6_129670_PI430048170 mRNA
TCCTGAGTGTTAGAAGTGTTATTGGCAAAGCAATCCAATAAAATAAGCTACCTATGATGC NM_001126063 RefSeq
chr6 - 73223544 73225452 KHDC1L NA KH homology domain containing 1-like NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129367_PI430048170 0.6976369032952380.9312456173688543.20015491594573 2.1065857895873
3.49929580455904 P A P 2.86729917002154 3.10553108579324 3.42395060623799 P P P
LNCV6_129367_PI430048170 mRNA
TGAGGATCTGTTACCTGCATGTGCCAATTATGGAAATAAAATCTTCTAGTCTTTACTGGA NM_001289967 RefSeq
chr18 - 58670008 58671873 LOC101927322 NA uncharacterized LOC101927322 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137559_PI430048170 0.00890620079743612 0.1384627483032141.15601340040151
2.18653737463383 1.98224809232584 A A A 4.548378258075 4.76640611141848
4.74899176955585 P P P LNCV6_137559_PI430048170 mRNA
AAGCGCCTTAATATATCCCTTTGTGGAAGGCACTACACAGTTTACTTTTATATTGTATTG NM_004690RefSeq chr6
- 149658152 149718256 LATS1 9113 "large tumor suppressor kinase 1, transcript variant 1"
GO:0005515|GO:0000287|GO:0005815|GO:0019901|GO:0000819|GO:0045736|GO:0051220|GO:0035329|GO:0005
524|GO:0005829|GO:0033138|GO:0000922|GO:0007067|GO:0030833|GO:0009755|GO:0030216|GO:0004674|GO:0
000086|GO:0043254|GO:0006468|GO:0090090|GO:0051301 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_142819_PI430048170 0.0482433549266262 2.12647360870956 1.94218992891192
0.9745312703384191.73671576989072 A A A 0.9239635296262760.279903227263908
0.247398509280158A A A LNCV6_142819_PI430048170 mRNA
CACCAGGATGAACACTGAAGCTTTTGTACCTGATATAAGTATGCTTACTTCTTTTAGAAA NM_173651RefSeq chr2
+ 185738627 185833289 FSIP2 401024 fibrous sheath interacting protein 2 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_130700_PI430048170 0.0035443258699592 2.88845319663948 7.49015011220832
7.75352988422153 7.4685208683767 P P P 6.04934346334017 6.03874168598811
6.05098871708291 P P P LNCV6_130700_PI430048170 mRNA
TGGCGCTTGGATCTGGGGTGGGAGTAACAGGGCAGAAATGATTAAAATGTTTGAGCACAANM_002773RefSeq chr16
- 31131432 31135830 PRSS8 5652 "protease, serine, 8"

GO:0005515|GO:0005886|GO:0004252|GO:0010765|GO:0006508|GO:0008236|GO:0005576|GO:0016021|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136332_PI430048170 0.0897351397973199 1.11652929019927 6.3046646606965 6.39522007144638 6.5006293791888 P P P 6.22664692273501 6.30711964245153 6.19399919958092 P P P LNCV6_136332_PI430048170 mRNA
CAATGGGTGCACAATAAATAACAGGTCAACAAAGAGGGAGGTGTGTCAGTGTGTGAGGAA NM_012455 RefSeq chr2 + 113173982 113203100 PSD4 23550 pleckstrin and Sec7 domain containing 4
GO:0043547|GO:0005802|GO:0005086|GO:0030054|GO:0005543|GO:0016020|GO:0005886|GO:0030182|GO:0032012|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64178_PI430048170 0.00729349810755435 1.94055471776404 6.65088415656489 6.61248134367528 6.43884789624229 P P P 5.657193523755 5.79452893801678 5.35554831734373 P P P LNCV6_64178_PI430048170 mRNA
GTCCGCCTCGGGCACCGCGTCCAACCTCAGAGTTTGCAAATAAAGGTTGCTTAGAAGGTG NM_017573 RefSeq chr19 - 1481427 1490450 PCSK4 54760 proprotein convertase subtilisin/kexin type 4
GO:0004252|GO:0006508|GO:0016021|GO:0007340|GO:0007339|GO:0048240|GO:0002080 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131465_PI430048170 0.00586594980820952 2.14679740289661 5.26074099057384 4.92765788061894 5.00213406035402 P P P 4.0058840986806 3.97801146681585 3.92031474036769 P P P LNCV6_131465_PI430048170 mRNA
ATAGCTTGAAAGGCCTGGCCAGGGGAGGAGCACAGATATTTTCCTGTATAATTCCAGAAT NM_001134387 RefSeq chr7 + 6577433 6588979 ZDHHC4 55146 "zinc finger, DHHC-type containing 4, transcript variant 1" GO:0005794|GO:0008152|GO:0008270|GO:0016021|GO:0019706 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129709_PI430048170 0.7899394641114241.01412392272257 0.306081556091131 1.47736613464387 2.21436870591153 A A A 1.60545348140993 1.30483566034438 1.59809280818769 A A A LNCV6_129709_PI430048170 mRNA
GTCTGTGGTTCATTATTCTCAATATGAATCATACCAAGATATTTGTGCCTCATCTCGAAA NM_004506 RefSeq chr6 + 122399550 122433119 HSF2 3298 "heat shock transcription factor 2, transcript variant 1"
GO:0005737|GO:0003700|GO:0000977|GO:0006366|GO:0045944|GO:0003713|GO:0001162|GO:0005634|GO:0007283|GO:0001228|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133760_PI430048170 0.00320079505567858 0.3145611421251115.74895564345255 5.13623842516751 5.26799277886533 P P P 6.68883866882347 7.16630420622451 7.30794029969531 P P P LNCV6_133760_PI430048170 mRNA
GCTTGGTTCTTTAAAGATTTGGAGAAGATATGTAAATTACCAAGGCACTTGGTTTTTCTG NM_013390 RefSeq chr9 - 71683365 71768884 TMEM2 23670 "transmembrane protein 2, transcript variant 1"
GO:0007275|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139662_PI430048170 0.000585359077057791 1.82460683742367 9.50713834214043 9.37009909443609 9.57314256620201 P P P 8.73505676222913 8.51815879795918 8.5933159201582 P P P LNCV6_139662_PI430048170 mRNA
TGAGAACATTCGAAAGGACCTGGAGACCCGTAAGAAACAGAAGGAAGATGTGGAAGTTGT NM_139286 RefSeq chr9 - 113267010 113275589 CDC26 246184 cell division cycle 26
GO:0005515|GO:0007094|GO:0051437|GO:0051436|GO:0031145|GO:0051439|GO:0005829|GO:0007067|GO:0070979|GO:0005680|GO:0005654|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133649_PI430048170 0.0111538107473065 0.58670048795770211.8045124888141 11.6966855502966 12.064979433984 P P P 12.5587830556001 12.4367051665769 12.8688096000354 P P P LNCV6_133649_PI430048170 mRNA
CTTATGTCCACTTTACAAAAGAAAACAGCATTGTGATTACTCCCAGGGACCGTATTTTAT NM_002047 RefSeq chr7 + 30594564 30634032 GARS 2617 glycyl-tRNA synthetase
GO:0010467|GO:0015966|GO:0005524|GO:0006426|GO:0004820|GO:0005829|GO:0006418|GO:0005737|GO:0005

759|GO:0046983|GO:0005654|GO:0030141|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61972_PI430048170 0.0869235148623950.6272291139013963.75631417405552 2.90963513123211
3.32850949479514 P A P 3.87451551293111 3.85099839492746 4.35357442340657 P P P
LNCV6_61972_PI430048170 mRNA
TACTGGGAACAGAATACAACCCATATAAATCAGATGCAGGTGGTAGTCACATCACCAGAG NM_001270528 RefSeq
chr15 + 58987665 59097419 RNF111 54778 "ring finger protein 111, transcript variant 1"
GO:0000209|GO:0005515|GO:0007389|GO:0010467|GO:0006367|GO:0016567|GO:0032184|GO:0016874|GO:0005
730|GO:0046332|GO:0005634|GO:0006351|GO:0043234|GO:0005737|GO:0045944|GO:0031398|GO:0005654|GO:0
007179|GO:0008270|GO:0045893|GO:0030579|GO:0030511 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_134209_PI430048170 0.0190996159275103 0.6266930048771321 0.5924444229752
10.8396008945743 10.8304141910199 P P P 11.1856256218773 11.4313980085487
11.6448909522899 P P P LNCV6_134209_PI430048170 mRNA
GTATGTGGATGGGGAAGTTTTGTTTCTCCTCTTAGCATTTGTTTCTATAACCAGAAATAA NM_001037165 RefSeq
chr7 + 4682298 4771443 FOXK1 221937 forkhead box K1
GO:0005515|GO:0030308|GO:0000977|GO:0006357|GO:0006366|GO:0000981|GO:0005730|GO:0005634|GO:0030
154|GO:0007517|GO:0005654|GO:0045893|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63552_PI430048170 0.5907418304647930.9046770593611443.90887261858223 3.55182613809356
3.99466781582819 P P P 3.59058986419678 4.07797854597999 4.18995301230876 P P P
LNCV6_63552_PI430048170 mRNA
TACCTGAAAATCTTCACAACTGATCATTATCTCCTTCTCTTTGAGACCTGACTGAAAAAA NM_001256071 RefSeq
chr17 + 80260860 80398781 RNF213 57674 "ring finger protein 213, transcript variant 3"
GO:0005737|GO:0004842|GO:0016567|GO:0016020|GO:0006200|GO:0016874|GO:0005730|GO:0008270|GO:0016
887|GO:0051865 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130842_PI430048170 0.6521973020491660.9874403412543390.276420057343421
0.3078687568864240.390036987644681 A A A 0.3752187083815770.335547225627688
0.320099609500108 A A A LNCV6_130842_PI430048170 mRNA
CCTTCAACACTGGACACGTCGAGCATTTTGTAGCTTAATTAAACCTCATGTAAGGCCAAA NM_001005339 RefSeq
chr10 - 119499826 119542710 RGS10 6001 "regulator of G-protein signaling 10, transcript variant 1"
GO:0043547|GO:0005737|GO:0043197|GO:0005886|GO:0043025|GO:0038032|GO:0043679|GO:0005634|GO:0005
096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138403_PI430048170 0.6986861575852411.05682569997762 4.84107014593977
4.91540138826041 4.49265554589502 P P P 4.82971436425978 4.8093554455148
4.35766248971489 P P P LNCV6_138403_PI430048170 mRNA
AGCTATTCCCTCCAGCATCTGGTTCTGTACAAAAATTAAATGCTTATTTGTTTAAGTCTC NM_002405 RefSeq chr22
- 37469062 37486440 MFNG 4242 "MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase,
transcript variant 1"
GO:0045747|GO:0033829|GO:0007389|GO:0030173|GO:0008152|GO:0005615|GO:0046872|GO:0032092 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58240_PI430048170 0.4691998794016831.33905768091436 1.50167284494932 0.308306368731682
0.505054703222749 A A A 0.3078604723952330.6872042039688960.323340532664644 A A A
LNCV6_58240_PI430048170 mRNA
GGACGGACGTGGGCCAGTGCGAGCCCAGAGGGCCCGAAGGCCGGGGCCCACCATGGCCCA NM_012104 RefSeq
chr11 - 117285685 117316256 BACE1 23621 "beta-site APP-cleaving enzyme 1, transcript variant a"
GO:0008798|GO:0005515|GO:0005802|GO:0030424|GO:0005794|GO:0009986|GO:0005886|GO:0005770|GO:0005
783|GO:0005771|GO:0050435|GO:0001540|GO:0005887|GO:0006508|GO:0016021|GO:0004190|GO:0006509|GO:0
019899|GO:0030659|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133660_PI430048170 0.00226542721706746 1.37748754881655 5.7337452435438
5.69129267195113 5.78550312371153 P P P 5.19532600760988 5.27311624612074

5.35320576743086 P P P LNCV6_133660_PI430048170 mRNA
GAAGAAGCTCTTTTGGGTATCAACACCTAGGTCGCCAGTGAAATAGAACACAGAACAGGANM_000747RefSeq chr17
+ 7445086 7457613 CHRNB1 1140 "cholinergic receptor, nicotinic, beta 1 (muscle)"
GO:0030054|GO:0045202|GO:0007274|GO:0055085|GO:0005892|GO:0007271|GO:0048747|GO:0035095|GO:0007
165|GO:0034220|GO:0006936|GO:0003009|GO:0005887|GO:0045211|GO:0015464|GO:0042391|GO:0042166|GO:0
050877|GO:0001941|GO:0004889|GO:0006812|GO:0015267|GO:0015276 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129851_PI430048170 0.8647737232429680.9775124742376722.95693925844838
3.69149852514716 3.45692577758882 A P P 3.30712144620534 3.71321776961063
3.22962639922217 P P P LNCV6_129851_PI430048170 mRNA
TTTCATCAAGGATTTTCTACCGGTGGTGCCGCACCCCTACGAGCCTCCTGAACCGTCCTT NM_001161546 RefSeq
chr5 - 139391945 139395196 PROB1 NA proline-rich basic protein 1 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130170_PI430048170 0.0563978067125069 0.6486894976559428.27030280276705
7.6702138728347 7.82152453092083 P P P 8.25702531608992 8.7509303647734 8.650838441264
P P P LNCV6_130170_PI430048170 mRNA
GCTGTGTACAAAGAGATGTGAAATACTTTCAGGCAAAAATAAACTGTAAGTGACTCATCA NM_198390RefSeq chr16
+ 81445169 81711763 CMIP 80790 "c-Maf inducing protein, transcript variant 1"
GO:0005515|GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139154_PI430048170 0.7276608596452410.8792422320796511.64674153954079
1.20845389469847 0.32803485280719 A A A 1.8171972073489 1.37499159565325
0.584657258281278A A A LNCV6_139154_PI430048170 mRNA
TGCAGCTTCCGGGAGCTGCTTCTTGAGGACGGATACAATGTTTACCAGTCCGAAGCCCAC NM_019113RefSeq chr19
+ 48756086 48758325 FGF21 26291 fibroblast growth factor 21
GO:0005515|GO:0007165|GO:0008284|GO:0046326|GO:0007267|GO:0010988|GO:0005576|GO:0005104|GO:0070
374|GO:0045716|GO:0008083|GO:0090080 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2684_PI430048170 0.2856687188261620.5245657843609110.45450055079269 0.328335588285264
0.38633649856773 A A A 0.2933300065545111.03718738937133 2.077185392542 A A A
LNCV6_2684_PI430048170 mRNA
AATGAAATGCTAAAAGAGCCCTTGCTAAGTCACATGCAAATGGTTACGGAGATCGTGGTA NM_207338RefSeq chr15
- 66547467 66565497 LCTL NA "lactase-like, transcript variant 1"NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138000_PI430048170 0.0127058587076923 0.5895574672778 6.25954888293833
6.03316542260563 6.50041116399511 P P P 7.02825511232067 6.88559158859624
7.18809855103027 P P P LNCV6_138000_PI430048170 mRNA
CAACCACCATTTCAGCTATTAAAAACTCCTGTTATCTCCTTGTTTGAATTTCAGGTCATT NM_001243776 RefSeq chr11
+ 95790460 95832693 CEP57 9702 "centrosomal protein 57kDa, transcript variant 2"
GO:0008017|GO:0005515|GO:0005813|GO:0005794|GO:0006996|GO:0043015|GO:0034453|GO:0017134|GO:0005
874|GO:0007286|GO:0005634|GO:0042803|GO:0005829|GO:0005737|GO:0008543|GO:0000086|GO:0015630|GO:0
051260|GO:0005654|GO:0000278|GO:0000060 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106372_PI430048170 0.6716483612043390.9802191971167180.26692135580862
0.2869414164942380.419072119896541A A A 0.4380989708605880.31385773047328
0.308471124592246A A A LNCV6_106372_PI430048170 mRNA
ATTATTCGCTGAAACATACAGGTTTTAATTTTTACGAGGCTAAGGCCACGGCCGCCTCAC NM_152658RefSeq chr19
- 36034984 36054762 THAP8 199745 THAP domain containing 8 GO:0003677|GO:0046872 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_133974_PI430048170 0.1883257989743720.72899767755879 0.412136028919516
0.4040987371105110.379246655565892A A A 1.21739845208627 0.474951332334526
0.773606632333205A A A LNCV6_133974_PI430048170 mRNA

CATAATACCATGCTATAGGAGACTGGGCAAAACCTGTACAATGACAACCCTGGAAGTTGC NM_032208RefSeq chr2
+ 69013143 69249327 ANTXR184168 "anthrax toxin receptor 1, transcript variant 1"
GO:0005515|GO:0022414|GO:0005886|GO:0009986|GO:0031258|GO:0031532|GO:0005518|GO:0031527|GO:0046
872|GO:0007165|GO:0051015|GO:0009405|GO:0034446|GO:0016021|GO:0010008|GO:0070062|GO:0004888 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141281_PI430048170 0.7983844431939520.9906272966927590.259008503686037
0.2685907120046590.415674128316778A A A 0.3618142030857160.305986450350283
0.321055423696526A A A LNCV6_141281_PI430048170 mRNA
AGTTTGTACACTAAAACTAAGTTTTTGGCTGACTGTCATATTGTGGTCCTTAATCTTGAG NM_032132RefSeq chr1
- 150698058 150720888 HORMAD1 84072 "HORMA domain containing 1, transcript variant 1"
GO:0000794|GO:0007126|GO:0060629|GO:0048477|GO:0005694|GO:0051598|GO:0001824|GO:0051177|GO:0042
138|GO:0005634|GO:0007283|GO:0007130 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139057_PI430048170 0.3083955618780031.2788160941913 4.9809848730451
5.32016061289536 5.68198530365607 P P P 4.58666938104313 4.88988396755252
5.40616474689679 P P P LNCV6_139057_PI430048170 mRNA
TATCTGAAATTCCTATTTCCTGTTAACATAGGAGGTGTGTGCAGACTTTATTAATGTGAG NM_001023570 RefSeq
chr3 - 121769762 121835079 IQCB1 9657 "IQ motif containing B1, transcript variant 1"
GO:0005515|GO:0005516|GO:0005813|GO:0006996|GO:0048496|GO:0045494|GO:0005829|GO:0045171|GO:0042
384|GO:0015630|GO:0032391|GO:0005654|GO:0019899|GO:0070062|GO:0001750 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_125079_PI430048170 0.0484908146715754 0.8321920943515146.65683800723118
6.46142719554082 6.70511753269883 P P P 6.92688675109111 6.78982710982725
6.90925229690573 P P P LNCV6_125079_PI430048170 mRNA
ATGAATGTAGTGAGTGTGGGAAAGCCTTCAGTCTTAACTCCAACCTTGTCCTGCATCAGA NM_001287054 RefSeq
chr7 + 100015571 100041689 ZKSCAN1 7586 "zinc finger with KRAB and SCAN domains 1, transcript
variant 2" GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_127253_PI430048170 0.4038554123386351.11826170060282 7.03728373991518
6.55671020169299 6.85095463265047 P P P 6.60075315319179 6.79182281671446
6.60012105118862 P P P LNCV6_127253_PI430048170 mRNA
GTTGCAGGGTTTAAAAACATCCATTAACATGAAAGCTAATAAACCTGTCAGAGAACAAGA NM_024946RefSeq chr16
- 57152465 57186064 FAM192A 80011 "family with sequence similarity 192, member A" GO:0005634
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74239_PI430048170 0.2631676192074751.13121457326372 6.02468554495936 5.84619307845836
6.11248902933858 P P P 5.97155359338731 5.59398608145262 5.87086969776738 P P P
LNCV6_74239_PI430048170 mRNA
TTACGGAAGAGGGCTATTTGCATATTCAGATGCATCTTGTCAAAGGGGAAGACCTTGCTG NM_015187RefSeq chr4
- 25747426 25863031 SEL1L3 23231 "sel-1 suppressor of lin-12-like 3 (C. elegans), transcript variant 1"
GO:0005654|GO:0005634|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127813_PI430048170 0.00577727437181009 2.28219859733235 4.68544225615232
4.20833308749786 4.35989840422356 P P P 3.11850497386503 3.34483323024112
3.25200863756107 P P P LNCV6_127813_PI430048170 mRNA
CTAGAAATGGCCAGAGTTTTTGACAGACAGAGTGTAGTCTCCTTATTAGAAGAAAGGAAA NM_145235RefSeq chr10
+ 125896538 126009592 FANK1 92565 fibronectin type III and ankyrin repeat domains 1
GO:0005737|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141299_PI430048170 0.0267026590232278 0.9508522596973130.404031503057652
0.3618171969071450.354883024033224A A A 0.4505109738178430.455725869683527
0.433009633562485A A A LNCV6_141299_PI430048170 mRNA
ACCAAGTTTTACTTTGAACAGAGCTGGTAGGGAGACAGGAAACTGCGTTTTAGCCTTGTG NM_032556RefSeq chr2

+ 113072317 113075850 IL1F10 84639 "interleukin 1 family, member 10 (theta), transcript variant 1"
GO:0005149|GO:0019221|GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57451_PI430048170 0.0336265479438549 1.21076651890289 10.4723313897919
10.5160969189489 10.5752943649678 P P P 10.2345602971998 10.1352310442768
10.3592673004485 P P P LNCV6_57451_PI430048170 mRNA
TATCCCTAACCACAGCTCAAAATCGCTATCATCTTTAGGCAAATTAAAATCTATGTGGCA NM_139178 RefSeq chr11
+ 43880806 43920275 ALKBH3 221120 "alkB, alkylation repair homolog 3 (E. coli)"
GO:0005515|GO:0031418|GO:0008283|GO:0043734|GO:0005634|GO:0008198|GO:0035552|GO:0005739|GO:0005
737|GO:0006281|GO:0006307|GO:0005654|GO:0051747 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142898_PI430048170 0.0038448888965082 1.56321190385774 9.86479683884062
10.0429269296104 10.0225604138317 P P P 9.33577453833766 9.29956383928126
9.36711897390641 P P P LNCV6_142898_PI430048170 mRNA
TTGAAAGGTCAAGACCGTGAACTGAAAAAAGTGTTGGCCTTTTTGCGGGACCAGATTTTT NM_018090 RefSeq chr1
+ 16440671 16460089 NECAP 255707 "NECAP endocytosis associated 2, transcript variant 1"
GO:0005622|GO:0030125|GO:0005905|GO:0005886|GO:0015031|GO:0006897 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140907_PI430048170 0.718825903990516 1.08607958911545 2.65784553459903
1.91685023178542 2.19658086930729 A A A 1.85935113674976 2.11250158868387
2.47383335586464 A A P LNCV6_140907_PI430048170 mRNA
TACTCAAAGGGGGAGGGTGGCTATAAATGGTTTGCAAATTTATATCTATTATCACATCTT NM_001042749 RefSeq
chrX + 123960559 124102655 STAG2 10735 "stromal antigen 2, transcript variant 1"
GO:0005515|GO:0051321|GO:0005886|GO:0005694|GO:0032876|GO:0005730|GO:0005634|GO:0015629|GO:0005
829|GO:0007067|GO:0016020|GO:0019827|GO:0003682|GO:0007062|GO:0005654|GO:0045111|GO:0000278|GO:0
000785|GO:0000775|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134998_PI430048170 0.0206138503029485 1.38279357641631 5.13830866715208
5.31819462289412 4.98917648242964 P P P 4.7990283153617 4.53710147860377
4.71341969339084 P P P LNCV6_134998_PI430048170 mRNA
GGGAGGGGGAGAGAGCAAGGAGATCGGTATCTTTGTAATAAAACTGCAATTTTATAAATT NM_153631 RefSeq chr7
- 27106189 27127020 HOXA3 3200 "homeobox A3, transcript variant 2"
GO:0006355|GO:0008284|GO:0003700|GO:0051216|GO:0048704|GO:0048538|GO:0001525|GO:0030878|GO:0009
952|GO:0006351|GO:0048645|GO:0043565|GO:0060017|GO:0021615|GO:0001974|GO:0071837|GO:0005654|GO:0
010159 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138910_PI430048170 0.540242714025113 1.29646868748279 0.292290658627683
0.975409222675043 1.66070048311523 A A A 0.295329652874519 0.397833530978138
1.23581353726742 A A A LNCV6_138910_PI430048170 mRNA
CACTTGTAAAGATAGATAGCAGAACTAAGCTTGGTAAAAGCCCATGATTGTTTGTATACT NM_030816 RefSeq chr1
- 70259001 70354734 ANKRD13C 81573 ankyrin repeat domain 13C
GO:0010869|GO:0048471|GO:0005783|GO:0005789|GO:0005102|GO:2000209|GO:0006621 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131215_PI430048170 0.00543794913840251 1.44308223347694 10.8525907582721
10.9862319620791 11.0154127292044 P P P 10.3945011016565 10.4327687607867
10.4442065101475 P P P LNCV6_131215_PI430048170 mRNA
GGGGCTTGTCCTTCCTTTGCAGCTGTTTTGAATGTAGTTTTCCTTTTCTATTTATTTGCA NM_015260 RefSeq chr19 +
16829386 16880353 SIN3B 23309 "SIN3 transcription regulator family member B, transcript variant 1"
GO:0001741|GO:0005515|GO:0000806|GO:0016575|GO:0001106|GO:0000805|GO:0005634|GO:0044281|GO:0000
122|GO:0006351|GO:0048738|GO:0005737|GO:0016580|GO:0007519|GO:0030849|GO:0003682|GO:0005654|GO:0
004407|GO:0044255. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133949_PI430048170 0.0516237849325058 1.39077468643778 9.97756721734247
10.0959144012482 9.99152564885231 P P P 9.78571725128278 9.44048360168481

9.38004147167876 P P P LNCV6_133949_PI430048170 mRNA
TTGAATCCTCATTAAAGGTTTCTTTACCCACCCTGAGGCTGTATTGATCACAGACCTGGC NM_016494RefSeq chr2
+ 85595713 85597708 RNF181 51255 ring finger protein 181
GO:0004842|GO:0016874|GO:0008270|GO:0051865 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134703_PI430048170 0.0100585418666558 3.5357809493064 3.02783541886546
3.70568011933227 3.5452878486351 P P P 2.04689419714023 1.0065133497413
1.65871396733717 A A A LNCV6_134703_PI430048170 mRNA
AAGACAGAGGAAGGAGATTGATGCCAGAGAACACAAACGCTTCAGGAGAAATTCAAGCCT NM_173855RefSeq
chr12 - 121651386 121669654 MORN3 283385 MORN repeat containing 3 GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132662_PI430048170 0.0997077376489587 1.09679332631405 0.57329114246808
0.6848772219832240.666879878350568A A A 0.6070079821381150.452747233867312
0.462662956632191A A A LNCV6_132662_PI430048170 mRNA
GCTCTTATAGTTGGTAAGTTTTATGAAGTGTTTGCTGAGGAATTCTGTCATCTTTAACAG NM_175710RefSeq chr1
+ 207645112 207723691 CR1L 1379 complement component (3b/4b) receptor 1-like
GO:0043235|GO:0005737|GO:0016020|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136073_PI430048170 0.178205193093868 1.01428159689202 0.31357937477614
0.2780066998943980.297293062078154A A A 0.2819986356512860.273743898064174
0.271961696483664A A A LNCV6_136073_PI430048170 mRNA
CAACATACTGGTCAAACATTTTCTCACCAGAGAGCTTCTACCACAAGGATATTTAAAAGA NM_001003927 RefSeq
chr17 - 31316409 31321749 EVI2A 2123 "ecotropic viral integration site 2A, transcript variant 1"
GO:0007165|GO:0016021|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132157_PI430048170 0.2634305496831090.7888690689120156.49509383445174
6.49974319436149 6.79633701028552 P P P 6.56372290757216 6.90262970181729
7.28270929666901 P P P LNCV6_132157_PI430048170 mRNA
AACAGACTCATTACAAATGGTTACCTTGTTATTTAACCCATTTGTCTCTACTTTTCCCTG NM_001211RefSeq chr15 +
40161008 40221136 BUB1B 701 BUB1 mitotic checkpoint serine/threonine kinase B
GO:0005515|GO:0007094|GO:0007093|GO:0048471|GO:0008283|GO:0034501|GO:0051233|GO:0031145|GO:0005
829|GO:0005737|GO:0005680|GO:0007091|GO:0005815|GO:0006915|GO:0051436|GO:0005524|GO:0051439|GO:0
000940|GO:0007067|GO:0004672|GO:0004674|GO:0000777|GO:0000776|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131152_PI430048170 0.5110911702464880.7938602497510780.432635744196082
0.2985635891644950.868006210043834A A A 1.43895646286778 0.324988092945844
0.664142682255966A A A LNCV6_131152_PI430048170 mRNA
GACCTGGTTGTCAGCCAAAGTCCTACAATGTGAAAAGAGTTAGATACTATTTTACTATAA NM_030967RefSeq
chr17_JH159146v1_alt - 189951 190854 KRTAP1-1 81851 keratin associated protein 1-1
GO:0008150|GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131360_PI430048170 0.0900439101549766 0.3101520100460443.16828634513991
1.27659224660373 1.11553914100119 P A A 3.70083548018487 4.03164030068115
3.85040623148515 P P P LNCV6_131360_PI430048170 mRNA
CCCGTACCAAAAAGTAGAGTGGAGCCTCTTTGCACTACTACTATCAATAAATTTTAAATC NM_002645RefSeq chr11
- 17086575 17169807 PIK3C2A 5286 "phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit
type 2 alpha"
GO:0008286|GO:0005886|GO:0030136|GO:0071583|GO:0005634|GO:0044281|GO:0006887|GO:0005829|GO:0005
737|GO:0007173|GO:0016303|GO:0070062|GO:0005794|GO:0006661|GO:0036092|GO:0048015|GO:0005524|GO:0
031982|GO:0006897|GO:0014829|GO:0046854|GO:0016020|GO:0035005|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130229_PI430048170 0.1750868681134431.11025958700531 9.47785161031221
9.52444014494609 9.28177195917713 P P P 9.33789008752555 9.29603904622331

9.20561166932297 P P P LNCV6_130229_PI430048170 mRNA
ATGCCAGAAGGTGGCCAGTTTTGCTTTATGATCTTATGAAGGAAGATTTGTGACCCTACG NM_001947RefSeq chr3
- 52048920 52056445 DUSP7 1849 dual specificity phosphatase 7
GO:0005515|GO:0048011|GO:0038124|GO:0034142|GO:0038123|GO:0034134|GO:0002224|GO:0051403|GO:0035
335|GO:0005829|GO:0000188|GO:0002756|GO:0045087|GO:0043407|GO:0002755|GO:0035666|GO:0034166|GO:0
005654|GO:0034146|GO:0034138|GO:0034162|GO:0004725|GO:0017017 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_131111_PI430048170 0.7790063898477541.00917815076846 0.508901359852804
0.5504208354195590.425694005603824A A A 0.5160042174543790.464620002122883
0.467047447915751A A A LNCV6_131111_PI430048170 mRNA
GCACAGGGTTCCCTTATGTAGATGTACACATGGCATTGCATATAGAGATTAAATTATTAT NM_001039762 RefSeq
chr10 - 127135425 127196158 FAM196A 642938 "family with sequence similarity 196, member A" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145744_PI430048170 0.3347470866585250.8480497446467438.53502946235765 8.2711539125523
7.95861080871494 P P P 8.74981424311649 8.4931821678726 8.24889373221891 P P P
LNCV6_145744_PI430048170 mRNA
AGCCCCGAGAGGGAGCCTGTCGTCTCCCAGGGAATAAAGGAGTGCGTTCTGTTCAAAAAA NM_003978RefSeq
chr15 + 76995123 77037330 PSTPIP19051 proline-serine-threonine phosphatase interacting protein 1
GO:0005515|GO:0048471|GO:0001725|GO:0005826|GO:0019903|GO:0003779|GO:0032154|GO:0035872|GO:0030
027|GO:0005829|GO:0006897|GO:0007165|GO:0006954|GO:0016020|GO:0045087|GO:0001931|GO:0007155 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135027_PI430048170 0.0144476543359317 0.41467108065638 4.98272302975255
5.02424099023479 5.4382551977232 P P P 5.98969160907585 6.42651186496167
6.77782960449265 P P P LNCV6_135027_PI430048170 mRNA
TCATGGACCAAAGGGTTTACTTGACAAATTTGTGTGACAGACTCCGAACAATTCCTTTAC NM_002915RefSeq chr13
+ 33818068 33837507 RFC3 5983 "replication factor C (activator 1) 3, 38kDa, transcript variant 1"
GO:0046683|GO:0005515|GO:0003689|GO:0005634|GO:0003677|GO:0006260|GO:0006271|GO:0006281|GO:0000
723|GO:0006283|GO:0000722|GO:0000731|GO:0006297|GO:0005654|GO:0005663|GO:0006289|GO:0000278|GO:0
016887|GO:0032201. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138084_PI430048170 0.735647012983944 1.00294526103109 0.340264147712999
0.3456697480536360.315387539144137A A A 0.3337690804507810.338747576507146
0.316159126269605A A A LNCV6_138084_PI430048170 mRNA
CGCCCTTTTCTAGGCTTTTTGTATCATTTCTTAGTACATTGTAATAGATTCAAACCAGTC NM_000774RefSeq chr19 +
41114447 41128376 CYP2F1 1572 "cytochrome P450, family 2, subfamily F, polypeptide 1"
GO:0008392|GO:0006805|GO:0070330|GO:0005506|GO:0008395|GO:0019373|GO:0009636|GO:0044281|GO:0018
931|GO:0043231|GO:0004497|GO:0005737|GO:0019825|GO:0042738|GO:0005789|GO:0016712|GO:0018979|GO:0
055114|GO:0020037. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132913_PI430048170 0.1870671371532890.6169833167317291 3.6834619870774
12.3257530184347 12.5472668589107 P P P 13.6663223986479 13.7763473510331
13.5879245671732 P P P LNCV6_132913_PI430048170 mRNA
ACCCCCACCCCCGCATTTTTGTGTGTTGAAATTCTTGAAGGTTACATTAAATAAAACAAA NM_001427RefSeq chr7
+ 155458128 155464831 EN22020 engrailed homeobox 2
GO:0043565|GO:0016020|GO:0048666|GO:0045944|GO:0030901|GO:0007275|GO:0005634|GO:0030902 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132639_PI430048170 0.1273791354362791.04927683828417 0.548194264455043
0.4863723412656570.518884230622015A A A 0.3894432780054460.472853034666951
0.481843638661946A A A LNCV6_132639_PI430048170 mRNA
GATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCATAAAGACTTCCT NM_001017403 RefSeq
chr1 + 202193989 202319761 LGR6 59352 "leucine-rich repeat containing G protein-coupled receptor

6, transcript variant 1"
GO:0005515|GO:0030335|GO:0005886|GO:0004930|GO:0090263|GO:0030177|GO:0031982|GO:0032588|GO:0005
737|GO:0007186|GO:0005887|GO:0005654|GO:0016055|GO:0004888 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128776_PI430048170 0.00117150141399018 0.2943085272876254.52099764022226
4.09857423784251 4.60975466673191 P P P 5.90986416959216 6.24716160610928
6.37671910599018 P P P LNCV6_128776_PI430048170 mRNA
GATAGTGTGTGGAATTTTATTTTGAAGGATAAGACCATGGGAAAATTGTGGTAAAGACTG NM_001258316 RefSeq
chr3 + 172750684 172821474 ECT2 1894 "epithelial cell transforming 2, transcript variant 2"
GO:0045859|GO:0005515|GO:0072686|GO:0070301|GO:0007264|GO:0005634|GO:0015031|GO:0032154|GO:0042
803|GO:0043231|GO:0005829|GO:0032147|GO:0000910|GO:0005737|GO:0070830|GO:0005911|GO:0043089|GO:0
071277|GO:0051260|GO:0004871|GO:0043123|GO:0005089|GO:0051056|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143131_PI430048170 0.1801223272607440.68088736385051 0.453154061188223
0.4434512351462470.251144586177948A A A 0.3871766770945991.23601260963998
1.06521199493107 A A A LNCV6_143131_PI430048170 mRNA
GCAAGAGAATTCAACCTCAAGAAACCCTTGAATTAGGACATCCCATATAGACAGATTTTT NM_001080406 RefSeq
chr12 - 27081056 27082522 C12orf71 NA chromosome 12 open reading frame 71 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140004_PI430048170 0.00290516106161672 2.48998436251529 9.1436660276298
9.15771665754493 9.01186397901477 P P P 7.55850005293631 7.93176223294068
7.85280912638468 P P P LNCV6_140004_PI430048170 mRNA
TCAGAGGCGTACAACTAGTTGGCGATTAGACTTGTTATGTGATGTTACCAGCCTGAAATG NM_022463RefSeq chr17
- 799312 979758 NXN 64359 "nucleoredoxin, transcript variant 1"
GO:0030178|GO:0004791|GO:0005634|GO:0031397|GO:0072358|GO:0016055|GO:0047134|GO:0030154|GO:0055
114|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130928_PI430048170 0.0852156216812093 0.4727125294574981.55987011924667
2.3050641635591 2.97047937609943 A A P 3.63967773590898 3.06293297094176
3.63825262758346 P P P LNCV6_130928_PI430048170 mRNA
CTGTCTTGTAAAAAAGTTGAGGGGACTAAAAGTTTATGACTCTGATATGGAAGTTGTCAT NM_152415RefSeq chr8
+ 17246891 17298024 VPS37A 137492 "vacuolar protein sorting 37 homolog A (S. cerevisiae), transcript
variant 1"
GO:0005813|GO:0000813|GO:0019082|GO:0019058|GO:0019068|GO:0015031|GO:0043231|GO:0005737|GO:0016
197|GO:0031902|GO:0061024|GO:0016032|GO:0005654|GO:0043162|GO:0010008 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_101529_PI430048170 0.2518790700334550.90873940962337 6.78199564884487 6.6538654307699
6.95510856529989 P P P 6.84840703116794 6.93626928823023 7.03062796502763 P P P
LNCV6_101529_PI430048170 mRNA
GCTGCTACCAGAATCTTTTATTTGCAAAGAGAAACTAGGGGAAAATGTAGCCAACATATA NM_012179RefSeq chr22
+ 32474719 32498831 FBXO7 25793 "F-box protein 7, transcript variant 1"
GO:0005515|GO:0006511|GO:0004842|GO:0016567|GO:0000422|GO:0019901|GO:0045736|GO:0006626|GO:0000
151|GO:2000134|GO:0005634|GO:0005829|GO:0005739|GO:0043234|GO:0005737|GO:0031647|GO:0045620 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64968_PI430048170 0.0104006135299851 1.41278617716209 5.79671619151482
5.78744687432983 5.79481071217203 P P P 5.34751454096186 5.34137495055922
5.18894668529811 P P P LNCV6_64968_PI430048170 mRNA
TTTACCTTGTTTTGTGGGGACTGGAGAGACAAGTAAACTCTCAGAGTAACTGTCCCCTCT NM_001039885 RefSeq
chr19 + 46746045 46758575 FKRP 79147 "fukutin related protein, transcript variant 2"
GO:0042383|GO:0005791|GO:0005794|GO:0016010|GO:0000139|GO:0016485|GO:0016021|GO:0005615|GO:0035

269|GO:0016740 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142957_PI430048170 0.0206714183381938 0.3964431545643024.08016872402649
3.23688697765759 3.66319563566651 P P P 5.15142285557648 4.86601627728304
5.07459555917369 P P P LNCV6_142957_PI430048170 mRNA
GCTCACTAGGATTTTGCTGAACATTAAAAAGTGTGATAGCGATATTAGTGCCAATCAAAT NM_003506RefSeq chr8
+ 103298830 103332866 FZD6 8323 "frizzled class receptor 6, transcript variant 1"
GO:0042813|GO:0001736|GO:0005515|GO:0017147|GO:0042472|GO:0005886|GO:0009986|GO:0004930|GO:0030
168|GO:0001843|GO:0043433|GO:0016327|GO:0035880|GO:0033278|GO:0016324|GO:0007186|GO:0005887|GO:0
016021|GO:0090090|GO:0001942|GO:0060071|GO:0031625|GO:0030659|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136333_PI430048170 0.0426492295568619 1.81238293258885 3.02196323941406
2.9809556817115 2.33650625036906 A A A 1.79349564472044 2.27742769007361
1.72689034743015 A A A LNCV6_136333_PI430048170 mRNA
TTTCCAAGTGATGTCTTTCAGGGAAGCAGTGTTTGAAATAGATAGCGGGTACCTTCCCTG NM_001039958 RefSeq
chr15 + 89776357 89778751 MESP2 NA mesoderm posterior basic helix-loop-helix transcription factor 2
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133253_PI430048170 0.1207863990001270.6225418409775465.97043104289634 5.6329084147909
5.71919361891317 P P P 5.93003797341543 6.49312875624447 6.83287516529726 P P P
LNCV6_133253_PI430048170 mRNA
GCATTTGTACTTGAATAGTAGGATTTTAAAGGGCATTGATAGCATACCAAACAAAAGGCA NM_015409RefSeq chr12
+ 131949919 132080466 EP400 57634 E1A binding protein p400
GO:0016607|GO:0043967|GO:0043968|GO:0003682|GO:0035267|GO:0006325|GO:0004386|GO:0005654|GO:0000
812|GO:0005524|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_15807_PI430048170 0.0774701476162851.04226950788321 0.3889483026602090.389049477972382
0.429211372661282 A A A 0.3192232584271060.3258262180037110.382506790682035 A A A
LNCV6_15807_PI430048170 mRNA
ACAGTTATTGCTGTACCAGATTTGCAGTGTCCCACAAAATACTCCGGTATGTTGTACTGA NM_001145248 RefSeq
chr3_KI270784v1_alt - 54702 83194 FAM157A NA "family with sequence similarity 157, member A"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142729_PI430048170 0.0828394432773243 0.7032054581553656.97215780433579
6.80292685281405 6.96275107322111 P P P 7.6426268506545 7.09083120566442
7.48029407369737 P P P LNCV6_142729_PI430048170 mRNA
CGGGCCAAATAGCACATAACACCTGGTTATATATGAAATACTCATATGTTTATGACCAAA NM_003840RefSeq chr8
- 23135590 23164030 TNFRSF10D 8793 "tumor necrosis factor receptor superfamily, member 10d,
decoy with truncated death domain"
GO:0007165|GO:0043066|GO:0045569|GO:0006915|GO:0016021|GO:0004888 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137704_PI430048170 0.00591228381287963 1.69440816673759 3.08961455721464
3.26203186040985 2.95302377617242 P P P 2.50585765592189 2.36997442017043
2.13970244888593 A A A LNCV6_137704_PI430048170 mRNA
CCCCTGGAAAAACTTCCAAAAGTAGAGAAAATAAAGGACTCATTTCACATTTCCCCTACT NM_001130090 RefSeq
chr17 + 17972812 18016875 LRRC48 83450 "leucine rich repeat containing 48, transcript variant 1"
GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71390_PI430048170 0.0172265917287275 0.6032660906503315.80257275783193
5.86287672280246 5.87252201061721 P P P 6.51449772241461 6.41810475354592
6.77042557667966 P P P LNCV6_71390_PI430048170 mRNA
AACTTCAGACATTCCAGAATTGTCATGATGTTTACACTGTCTGAGTTAAAAATCCTGTTC NM_080821RefSeq chr20
+ 56358926 56368662 FAM210B 116151 "family with sequence similarity 210, member B" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA

LNCV6_93058_PI430048170 0.0250897027442766 1.72810061206424 5.02591492015886
5.13075813957515 5.58171890475553 P P P 4.27871371902105 4.64760098598348
4.48325094697537 P P P LNCV6_93058_PI430048170 mRNA
AGAGCAGAGGATCAGGTTTATGATGCTGCAGTCAGGTGGTTGAAATACGATGAACCTAAT NM_018846 RefSeq chr7
+ 23106297 23175419 KLHL7 55975 "kelch-like family member 7, transcript variant 2"
GO:0005737|GO:0016567|GO:0005886|GO:0031463|GO:0005730|GO:0005654|GO:0005634|GO:0042803 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131498_PI430048170 0.2278914803170550 0.1352944032659081 .27277331491328
0.82915855110531 1.74930449080122 A A A 5.51868583147733 1.50562192330537
2.83914569272694 P A P LNCV6_131498_PI430048170 mRNA
GTCACATTACATCAGACATCTCTTTATGCATGTGCATTCAAAAGGAAGAGTAGATAGAAT NM_009590 RefSeq chr17
+ 42844591 42850711 AOC2 314 "amine oxidase, copper containing 2 (retina-specific), transcript variant
2"
GO:0048038|GO:0005886|GO:0005507|GO:0052596|GO:0009055|GO:0052595|GO:0052594|GO:0052593|GO:0005
737|GO:0008131|GO:0006584|GO:0009308|GO:0007601|GO:0055114 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134755_PI430048170 0.00451371274237179 0.4272091303729283.87648927929694
3.51150866879471 4.04174485302478 P P P 5.00789910718615 4.8901184900595 5.2402137570073
P P P LNCV6_134755_PI430048170 mRNA
GATCATTTCACCTGATGTTTTTGAAGCATCCTAAGTACAGTAGAGTAGAAAACTGATTTC NM_203453 RefSeq chr9
+ 4662293 4665272 PPAPDC2 403313 phosphatidic acid phosphatase type 2 domain containing 2
GO:0016787|GO:0008152|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139964_PI430048170 0.0638272681806481 0.65259757440178 7.2282323562793
6.88859022582812 7.28412357256634 P P P 7.48913212052285 7.61432531955442
8.10089576166802 P P P LNCV6_139964_PI430048170 mRNA
GATGATGAATTTTCCTCGTATGGTCAGTAGTCTTGTAATAAAAAGCATGTAGAGTGTAGA NM_002613 RefSeq chr16
+ 2537963 2603190 PDPK1 5170 "3-phosphoinositide dependent protein kinase 1, transcript variant
1"
GO:0005515|GO:0019722|GO:0034122|GO:0005158|GO:0042995|GO:0046777|GO:0007173|GO:0016301|GO:0043
274|GO:0018107|GO:0010667|GO:0043122|GO:0043304|GO:0032869|GO:0019901|GO:0010518|GO:0030168|GO:0
003323|GO:0016004|GO:0008543|GO:0045087|GO:0005654|GO:0005925|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_94141_PI430048170 0.4584651603083331.58404489502627 0.2756950052618790.280807940156025
1.81697502463936 A A A 0.3443104726995550.2938250194771960.333494998428397 A A A
LNCV6_94141_PI430048170 mRNA
TTCTCATTCACAGTGCAGGGAGATACCTCAGTAGAAGCATACAGTCCAGTCTTCAACTAG NM_001303419 RefSeq
chr4 - 188091271 188105587 TRIML2 205860 "tripartite motif family-like 2, transcript variant 1"
GO:0016567|GO:0016874|GO:0032526 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127205_PI430048170 0.0571372958557334 0.4266292093283142.32528830307162
2.45412736375903 2.90931430600746 A A P 3.04637927115293 4.1032132410104
4.06633105487358 P P P LNCV6_127205_PI430048170 mRNA
GATCCCAATCAGAGGGATGGAGCTAATCTTTTTGCTGTTGAAATAAAATGAATTTATGAG NM_199420 RefSeq chr3
- 121431425 121546006 POLQ 10721 "polymerase (DNA directed), theta"
GO:0043142|GO:0003684|GO:0006261|GO:0006281|GO:0071897|GO:0003887|GO:0005654|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69235_PI430048170 0.2431008344813151.93741391646118 2.06519389629662 0.391920375112159
1.08736100035891 A A A 0.2857401595696310.4108797983395360.470429792366968 A A A
LNCV6_69235_PI430048170 mRNA
ATCATCGTGCACCCACAGTTCTACATCATCCAGACCGGGGCGGACATCGCCCTGCTGGAG NM_012217 RefSeq chr16

+ 1256271 1258493 TPSD1 23430 tryptase delta 1 GO:0004252|GO:0006508|GO:0008236|GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116542_PI430048170 0.5835273544487210.96247873500205 6.07571769813123
5.97818922175798 6.12791710012965 P P P 6.04947045936943 6.02819701205523
6.26189896389928 P P P LNCV6_116542_PI430048170 mRNA
CCTTTGCCGGGATGTTTCCATTGCTTCATGTTTCAGTAAACAAAAGGAGTTTGTGACCAA NM_031492RefSeq chr11
- 66664993 66677921 RBM4B 83759 "RNA binding motif protein 4B, transcript variant 1"
GO:0010628|GO:0008380|GO:0006397|GO:0005515|GO:0000166|GO:0005730|GO:0007623|GO:0008270|GO:0043
153|GO:0032922|GO:0006417 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129222_PI430048170 0.0181430516746937 1.7960435687282 5.4140718666836
5.20217855865833 5.62553921598468 P P P 4.61972835779692 4.54349918289608
4.57407516140286 P P P LNCV6_129222_PI430048170 mRNA
TCATGGAGTAACTTAAAAATACATATCTATCTTCCAGAACAAGCCACACAACAACACACC NM_152272RefSeq chr8
+ 23243636 23261999 CHMP7 91782 charged multivesicular body protein 7
GO:0000920|GO:0000815|GO:0045324|GO:0006997|GO:0016197|GO:0008565|GO:0019058|GO:0061024|GO:0016
032|GO:0007080|GO:0015031|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138315_PI430048170 0.4689837337538931.18569341896654 8.07399861370408
8.74118802715595 8.82203369683745 P P P 8.2281787935051 8.22695103548754
8.53291750264761 P P P LNCV6_138315_PI430048170 mRNA
ATTAAGATTGGAAGGGGACTTGATTATTTTAAGAAACCACAGAGTCGTTTTTCCCTTGGA NM_138798RefSeq chr2
- 99169262 99181029 MITD1 129531 "MIT, microtubule interacting and transport, domain containing 1"
GO:0005515|GO:0032091|GO:0000281|GO:0019904|GO:0030496|GO:0042803|GO:0043231|GO:0000920|GO:0071
985|GO:0031902|GO:0035091|GO:0019898|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140602_PI430048170 0.51523258981174 1.22370571756562 3.35547833578208 3.6702283218444
2.67061289562859 P P A 2.56579443629278 3.50428054579367 2.74467603143681 A P P
LNCV6_140602_PI430048170 mRNA
TTAATCCGCAGGCAGCCTGGAACAGTCTAGAGGAGATTTGTATAAAAAGTAGATACCAAG NM_001012502 RefSeq
chr9 + 127706991 127714024 C9orf117 286207 chromosome 9 open reading frame 117 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_135702_PI430048170 0.0578024681920491 1.25199881308555 4.79035718602394
4.46933433510583 4.5624318195821 P P P 4.41767015570722 4.19377253175441
4.24756426291256 P P P LNCV6_135702_PI430048170 mRNA
TTTTCTCCTGCATTGTGACTCACGAAATTGACCGCTACACAGCAATTGCCTATTGGGTAC NM_006120RefSeq
chr6_GL000256v2_alt - 4347848 4352360 HLA-DMA 3108 "major histocompatibility complex,
class II, DM alpha"
GO:0048839|GO:0016064|GO:0009986|GO:0005771|GO:0002503|GO:0042613|GO:0005765|GO:0015031|GO:0045
059|GO:0019886|GO:0016020|GO:0050778|GO:0031902|GO:0051085|GO:0023026|GO:0016021|GO:0045582|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131879_PI430048170 0.00735563126966233 0.2780265361629291.55585835572793
2.3978082088463 1.94525123007406 A A A 3.70249150940788 3.76777643002658
4.06537010413872 P P P LNCV6_131879_PI430048170 mRNA
CCTGAGGGTGCTTTGTGTAATATATTGTACACTACAGCATCTTATATTTTTTGAGTTGAG NM_012421RefSeq chr1
+ 40161368 40240921 RLF 6018 rearranged L-myc fusion
GO:0005515|GO:0051276|GO:0006355|GO:0045944|GO:0015074|GO:0008270|GO:0005634|GO:0045893|GO:0003
677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142488_PI430048170 0.0060977640283973 3.05952830412367 4.01159358634801
3.66586040375697 4.00938629100575 P P P 2.18699336257918 1.93214302003743
2.65857143548963 A A P LNCV6_142488_PI430048170 mRNA
TCTTGAGGTCCTAAAGGTATGATTCAGACCTTTCAGCCCTTTCCAGAACTTTGACCCTCT NM_032316RefSeq chr3

- 49422332 49429324 NICN1 84276 nicolin 1 GO:0005874|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130754_PI430048170 0.339569289636712 0.926966394208153 0.25942759164529 0.274776893450132 0.407165365383402 A A A 0.367112140165206 0.581303678828788 0.311532372081526 A A A LNCV6_130754_PI430048170 mRNA
CGCTTGGAAATAACTCAAATAAATTACAAGAAGCCTGTCTGTTCTTTGTGAGACTGTAAA NM_001303246 RefSeq chr3 + 141487046 141615363 RASA2 5922 "RAS p21 protein activator 2, transcript variant 1"
GO:0035556|GO:0005099|GO:0046580|GO:0007165|GO:0048471|GO:0005737|GO:0032320|GO:0031235|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127415_PI430048170 0.00539051268030343 0.543203717116077 8.81792048431407 8.40798029519182 8.57287110421054 P P P 9.32735637929752 9.55238587758045 9.57715527543189 P P P LNCV6_127415_PI430048170 mRNA
ATGAGTAGTTGGGGACTCCATTTCTAAGGAGACTAGGTAAATAAAATGACCTTTGACATT NM_004318 RefSeq chr8 - 61500555 61714640 ASPH 444 "aspartate beta-hydroxylase, transcript variant 1"
GO:0005515|GO:0007389|GO:0005513|GO:0008285|GO:0005886|GO:0042264|GO:0005783|GO:0010524|GO:0004597|GO:0030176|GO:0097202|GO:0060316|GO:0014701|GO:0010649|GO:0032237|GO:0006936|GO:0031647|GO:0010880|GO:0060314|GO:0071277|GO:0060021|GO:0033198|GO:0008307|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134637_PI430048170 0.18154076047596 0.966361285576988 0.293158233691461 0.343772690348956 0.325374190655592 A A A 0.41779311849897 0.33417143228453 0.357596349801668 A A A LNCV6_134637_PI430048170 mRNA
TAGTGCAGCCACATCCAGGTGTGCAAGTAGGGAGCCAGTTGGTAGATCAGAGGAAGGAAG NM_001136234 RefSeq chrX + 24362760 24365424 SUPT20HL1 NA suppressor of Ty 20 homolog (S. cerevisiae)-like 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69533_PI430048170 0.187518549495899 1.30278009383334 6.27318728607023 6.89181342749203 6.72015456382431 P P P 6.47838824735073 6.28885269659582 6.00219036874472 P P P LNCV6_69533_PI430048170 mRNA
TGCACGACCTCCAGATCCTCGACTTTCCACCCATCAGCGCCTTCCCTGTCAATACGCTCC NM_033315 RefSeq chr17 + 35731659 35743521 RASL10B 91608 "RAS-like, family 10, member B"
GO:0006184|GO:0005886|GO:0007264|GO:0090277|GO:0005525|GO:0003050 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138171_PI430048170 0.520838746396018 0.914226983330786 0.398233059948001 0.264124470993342 0.308377739358076 A A A 0.281105246100676 0.732846740860998 0.301666304991706 A A A LNCV6_138171_PI430048170 mRNA
GGTTTGACTGGCAAATTCACTTTTTACTCATTTATTCTCATTCATCATACCGCATCACAC NM_002159 RefSeq chr4 + 70050414 70058848 HTN1 3346 histatin 1
GO:0005515|GO:0050832|GO:0031640|GO:0005576|GO:0031214|GO:0042742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134048_PI430048170 0.000247404064190467 0.293978373557571 3.15499919894163 3.27320260039488 2.92900645311798 P P P 4.68288000597836 4.97726396979988 4.99579669214667 P P P LNCV6_134048_PI430048170 mRNA
CCATGTGTGATTTTTAAGATGTGCTGGGGAAAAATAAATCAATACCACAACCACCAAAAA NM_003659 RefSeq chr2 + 177392742 177543836 AGPS 8540 alkylglycerone phosphate synthase
GO:0008610|GO:0008762|GO:0005782|GO:0008611|GO:0005730|GO:0044281|GO:0043231|GO:0005739|GO:0071949|GO:0016020|GO:0008609|GO:0005778|GO:0044255|GO:0055114|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129901_PI430048170 0.00794703392394356 0.207333340744611 1.22456400013996 0.364342329766756 0.353624258842479 A A A 3.05003691864541 2.74716089773004 3.11209485221026 P P P LNCV6_129901_PI430048170 mRNA

TGGCAACTGGGAAGAAGTGGCCTCAAAGGCACTTAATTTGATTTTTATTTTTTAAATGCT NM_004850 RefSeq
chr2 - 11181651 11344585 ROCK2 9475 "Rho-associated, coiled-coil containing protein kinase 2"
GO:0005515|GO:0008625|GO:0030036|GO:0005886|GO:2000145|GO:0051492|GO:0005634|GO:0007266|GO:0051
893|GO:0030155|GO:0046872|GO:0005829|GO:0006939|GO:0000910|GO:0045616|GO:0007411|GO:0032956|GO:0
048010|GO:0005813|GO:0048013|GO:2000114|GO:0010825|GO:0001843|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_110350_PI430048170 0.457994563288389 0.28510037485953 0.257441249708755
0.31814030347788 1.46676657599678 A A A 0.474783857616373 0.730443018678126
3.92711090952212 A A P LNCV6_110350_PI430048170 mRNA
TCTCTGTGCTTCTACTGAGGACTGTGAAGTGGACCCCAGCAAATGTCCAGCCTCGGAGCT NM_022904 RefSeq
chr19 - 15451626 15464571 RASAL3 64926 RAS protein activator like 3
GO:0005099|GO:0046580|GO:0007165|GO:0005737|GO:0032320|GO:0016020|GO:0031235|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_129720_PI430048170 0.0422736916516701 0.802453622061715 7.83813029249573
7.96131887639944 7.99997661237129 P P P 8.40839966218802 8.13118680471981
8.20273286038106 P P P LNCV6_129720_PI430048170 mRNA
CCGTGAGCTTGGAAGCTTACTTTTGATTCTTAAAGCCTATGTTTTCTAAAATGAGACAAA NM_017905 RefSeq
chr13 + 113490992 113550229 TMCO3 55002 transmembrane and coiled-coil domains 3
GO:0015299|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139439_PI430048170 0.0254529072442946 0.805536308009443 5.00958455597346
4.96616179817551 4.86061540378889 P P P 5.36396400262493 5.27418971110559
5.12845934649321 P P P LNCV6_139439_PI430048170 mRNA
TCTTCTACAACCAGAGCCCCCCACAATGATGATTAAACACCTGACACATCTTGCAAAAAA NM_001206929 RefSeq
chr6_GL000250v2_alt - 3513569 3516924 AGER 177 "advanced glycosylation end product-specific
receptor, transcript variant 2"
GO:0005515|GO:0005886|GO:0009611|GO:0005576|GO:0031175|GO:0042802|GO:0050930|GO:0044548|GO:0051
092|GO:0006954|GO:0005887|GO:0045087|GO:0004872|GO:0007166|GO:0004888 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_142288_PI430048170 0.206498034321998 5.32059494385464 0.475024509914677
3.89555532937901 2.44537688860463 A P A 0.426357263157659 0.444053004598958
0.462416830347278 A A A LNCV6_142288_PI430048170 mRNA
CTGGCCTCAAGTTACCAGGTAGCCTGAACTTTGATTTTATTTTACCATTAAATTGCTTTA NM_001078173 RefSeq
chrX - 135020503 135022536 FAM127C NA "family with sequence similarity 127, member C" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132324_PI430048170 0.163009659285314 3.56591267533273 2.76227077829704
2.98828703885414 0.737544143126868 A A A 0.593871948474558 0.639300861377472
0.612277000062068 A A A LNCV6_132324_PI430048170 mRNA
TTAGCCACAGCCCAAATCTTCCAGGCAAATGTAATAAACGTGACATTGCCGTTAGCCAAA NM_032825 RefSeq
chr19 + 36605304 36628597 ZNF382 84911 "zinc finger protein 382, transcript variant 1"
GO:0005634|GO:0045892|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_139019_PI430048170 0.263860745530279 1.02255744398251 0.303469842507993
0.254702472868952 0.325674262899332 A A A 0.270209590535427 0.249290616008735
0.268617758104821 A A A LNCV6_139019_PI430048170 mRNA
TTTGCTTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTGATGGAGAGG NM_206966 RefSeq
chr5 - 147892707 147906538 C5orf46 389336 chromosome 5 open reading frame 46
GO:0008150|GO:0003674|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_124110_PI430048170 0.169841368422987 1.07934064244417 0.532018829745823

0.408374921149662 0.548270561350755 A A A 0.298419039021172 0.391176922413821
0.467666582127991 A A A LNCV6_124110_PI430048170 mRNA
GTACAGCGATTGGAGGTCGATGTAAAAATCAATGTGATGATAGTGAATTTAGGATTTCAT NM_001037498 RefSeq
chr6 - 50043574 50048651 DEFB112 NA "defensin, beta 112" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_133464_PI430048170 0.30603455743013 0.985737186684991 0.349844388320095
0.378046926634114 0.326872960040025 A A A 0.372166478637887 0.387568966756679
0.35750290992614 A A A LNCV6_133464_PI430048170 mRNA
GTTCTACTTACCTGTCAAAGCACATTCTACATGTACTGTAAACAGATACACTTTAGTAAG NM_207386 RefSeq
chr17 + 11241422 11564063 SHISA6 388336 "shisa family member 6, transcript variant 1"
GO:0032281 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145015_PI430048170 0.00900693161464971 0.827875306865353 12.3162694149429
12.1949556934166 12.2928851114504 P P P 12.4610203038949 12.6074775813517
12.5522303951769 P P P LNCV6_145015_PI430048170 mRNA
CTCTTCCTTCACAGTATTTAAGAAATAAAAGTCGGATTTTTCTGGCTGCTTTCTCTCTAA NM_004639 RefSeq
chr6_GL000256v2_alt - 2938303 2951978 BAG6 7917 "BCL2-associated athanogene 6, transcript variant 1"
GO:0005515|GO:0006511|GO:0030324|GO:0005634|GO:0009790|GO:0007283|GO:0032435|GO:0030154|GO:0043231|GO:0005829|GO:0005737|GO:0042127|GO:0006810|GO:0007130|GO:0031625|GO:0043066|GO:0001822|GO:0050821|GO:0045861|GO:0018393|GO:0042771|GO:0070059|GO:0007420|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130529_PI430048170 0.503413815212269 1.22001832706379 0.384911021042973
0.378738644898834 1.22944579951253 A A A 0.442078282741303 0.444564770730746
0.420584443987694 A A A LNCV6_130529_PI430048170 mRNA
AGAGATGCCTCGATTCCTCAGTTCAAACCCGAAATCCAGGTCTATGAGAACATCCATTTG NM_001003693 RefSeq
chr6_GL000256v2_alt + 3006198 3009889 LY6G6F 259215 "lymphocyte antigen 6 complex, locus G6F"
GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132486_PI430048170 0.182282306045878 1.11224424508237 14.8054059947843
14.9583364157898 15.0562130566324 P P P 14.7155759619385 14.7442577339201
14.9035109591796 P P P LNCV6_132486_PI430048170 mRNA
CAGGCTACTGGTTTGTATGATGTATTAGTAGAGCAACCCATTAATCTTTTGTAGTTTGTA NM_002574 RefSeq chr1
- 45511034 45521938 PRDX1 5052 "peroxiredoxin 1, transcript variant 1"
GO:0005515|GO:0042345|GO:0005782|GO:0008283|GO:0042267|GO:0034101|GO:0005634|GO:0032872|GO:0005615|GO:0042803|GO:0005829|GO:0005737|GO:0004601|GO:0001895|GO:0005759|GO:0019430|GO:0042744|GO:0070062|GO:0042470|GO:0005719|GO:0005730|GO:0008379|GO:0001501|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_120732_PI430048170 0.15163818382641 1.27007795359831 6.69521810500023
6.70198128320969 6.56085435222347 P P P 6.60758568516105 6.21050842164791
6.0514398986736 P P P LNCV6_120732_PI430048170 mRNA
CCTGCTGTTCTCCGGTGCTCTGTCCGAGGGACAGTTCTATTCACCCCCAGAATCCTTTGC NM_006804RefSeq chr17
+ 39637079 39664201 STARD3 10948 "StAR-related lipid transfer (START) domain containing 3, transcript variant 1"
GO:0005515|GO:0006629|GO:0006701|GO:0017127|GO:0030301|GO:0005765|GO:0005739|GO:0005737|GO:0015485|GO:0031902|GO:0016021|GO:0006839|GO:0008202|GO:0008203 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_95547_PI430048170 0.146251370325418 0.652587075149662 0.528531312907667 1.11472515536351
0.264502622598396 A A A 1.14938576381105 1.70873205314488 0.912679880816438 A A A
LNCV6_95547_PI430048170 mRNA
CGAGGAGGCCATTGAAAGACTGAAGGAAACAGAGAAGATCATAGCTGAGCTCAATGAGAC NM_001244008

RefSeq chr2 - 240713763 240820308 KIF1A 547 "kinesin family member 1A, transcript variant 1"
GO:0008017|GO:0043005|GO:0005871|GO:0005874|GO:0005524|GO:0030705|GO:0003774|GO:0005737|GO:0008
152|GO:0008574|GO:0043025|GO:0008089|GO:0016192|GO:0016887|GO:0007018 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144071_PI430048170 0.00675160274961283 0.49038302440363 6.07259076298349
5.98912935454324 6.06259964494308 P P P 6.90524530605035 7.03071476554556 7.2522473845046
P P P LNCV6_144071_PI430048170 mRNA
GCACACTTTCTGGTCACTTTGTACAATGTAGATTTGAAGTACAGTGGTGAAAACATTAAA NM_016231 RefSeq chr17
+ 28042661 28196378 NLK51701 nemo-like kinase
GO:0005515|GO:0006355|GO:0000287|GO:0030178|GO:0005634|GO:0005524|GO:0006351|GO:0005829|GO:0035
556|GO:0046777|GO:0004672|GO:0033136|GO:0000165|GO:0004674|GO:0018107|GO:0007179|GO:0005654|GO:0
006468|GO:0016055|GO:0042169|GO:0031625|GO:0008134|GO:0004707 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_126634_PI430048170 0.1055634325953191.70712851698047 3.15441132982404
3.13426283974847 3.23940015478837 P P P 2.93576799271557 2.01432452229677
2.07020668945906 P A A LNCV6_126634_PI430048170 mRNA
CAAGAGAATTGTCACACATGACACAAGATGTACATAATATCATGCTCACTGCAGTGTTAT NM_002348 RefSeq chr1
+ 160796073 160828255 LY9 4063 "lymphocyte antigen 9, transcript variant 1"
GO:0003674|GO:0004872|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126925_PI430048170 0.0273102172040748 1.68978669423575 10.3988149343787
10.3172805114234 10.2719264017552 P P P 9.84591929339996 9.44464543138857
9.38501148442422 P P P LNCV6_126925_PI430048170 mRNA
GTATATCCTTGCGATGTACAGTATCAGAAGGTGGTTTGACAGCATCATAAACAGGCTGAC NM_003256 RefSeq chr3
- 12153067 12159351 TIMP4 7079 TIMP metallopeptidase inhibitor 4
GO:0051045|GO:0042493|GO:0005578|GO:0043434|GO:0042698|GO:0002020|GO:0007417|GO:0005615|GO:0030
017|GO:0046872|GO:0048553|GO:0010951|GO:0008150|GO:0008191|GO:0032496|GO:0009725|GO:0034097 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129588_PI430048170 0.0432417825244190.74580291035561 9.0221948642184
8.79232282007694 8.84663852257373 P P P 9.08619179050037 9.37502255635142
9.45405865299602 P P P LNCV6_129588_PI430048170 mRNA
TATACAACTTTCAGAGCCTCTTGTATTTGGAAGGCTGGAAGGGCCCAGACTTTGGAATAG NM_001303448 RefSeq
chr1 + 24643102 24673281 SRRM1 10250 "serine/arginine repetitive matrix 1, transcript variant 1"
GO:0008380|GO:0006369|GO:0010467|GO:0006366|GO:0031124|GO:0005634|GO:0071013|GO:0003677|GO:0016
363|GO:0005829|GO:0006406|GO:0016607|GO:0000398|GO:0000375|GO:0005654 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_125244_PI430048170 0.8857872664437970.99022928926721814.527264296307 15.017977493984
15.0500057685567 P P P 14.8736548586409 14.7742617534001 15.03479939236 P P P
LNCV6_125244_PI430048170 mRNA
TTTCTGTAAGAAGTGTGGCAAGCACCAACCCCATAAAGTGACACAGTACAAGAAGGGCAA NM_001199973
RefSeq chrX + 101390889 101414140 RPL36A-HNRNPH2 NA "RPL36A-HNRNPH2 readthrough, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99099_PI430048170 0.774635266509985 1.01196045382799 0.276215205952891 0.306727758998639
0.430076928131217 A A A 0.349389756395804 0.311937466750314 0.304472316318064 A A A
LNCV6_99099_PI430048170 mRNA
TGATTTTTCCCAACCATTTCCATCAGTGAGTTTGCTGTCTGTGAGTCGTGCAAGCTTGGT NM_152250 RefSeq
chr8_KI270813v1_alt + 170773 172696 DEFB105A NA "defensin, beta 105A" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_143641_PI430048170 0.728526663958994 0.952533594663343 2.49687769630809
2.83294927312294 1.55420514609406 A A A 2.63214216808788 2.25744522246805

2.46164035440292 A A P LNCV6_143641_PI430048170 mRNA
CGGGAGCCCAGAGTGCACAGATCAGATATTTATTAAACATATAAATAAAACACAGTTTTC NM_001284406 RefSeq
chr3 - 12733529 12769457 TMEM40 55287 "transmembrane protein 40, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62569_PI430048170 0.3666198869333591.13654318692712 5.87862358424747 5.49665195236669
5.4579186735431 P P P 5.59039372954985 5.49530731159453 5.20466595146572 P P P
LNCV6_62569_PI430048170 mRNA
AGGTCAAGGTCATCCCCGTGCTCGAGGACAACTACATGTACCTGGTCATCGAGGAGCTCA NM_001290139 RefSeq
chr16 + 726935 729715 HAGHL 84264 "hydroxyacylglutathione hydrolase-like, transcript variant 4"
GO:0016787|GO:0008152|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129894_PI430048170 0.00335232062346155 0.3280199706176126.43375648199796
5.87801055963127 5.99932729933849 P P P 7.34180462830953 7.80606472193792
7.97633126868059 P P P LNCV6_129894_PI430048170 mRNA
CACTGAATTGTCAGGCTTTGATTGATAATTGTAGAAATAAGTAGCCTTCTGTTGTGGGAA NM_015691RefSeq chrX
+ 10015754 10144478 WWC3 55841 WWC family member 3
GO:0046621|GO:0035331|GO:0032947|GO:0000122|GO:0019900|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_83210_PI430048170 0.0432790857001931 1.1265685375772 6.97060451951273
6.83440318536175 6.94963507778914 P P P 6.76153255041999 6.76401757209282 6.7164869831095
P P P LNCV6_83210_PI430048170 mRNA
TGATCCTGTTTGGTGGCTTCCATGAAAGTACACGGGATTACATCTACTACAACGACGTGT NM_017566RefSeq chr16
- 87707811 87765992 KLHDC4 54758 "kelch domain containing 4, transcript variant 1" GO:0005515
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131885_PI430048170 0.4226274747604441.07587445611975 10.0234206886022
10.1534964043344 9.85071833299591 P P P 10.0439134825049 9.89271621801948
9.77800244595129 P P P LNCV6_131885_PI430048170 mRNA
CCTCCCCAGAACACTCAGAGGGACGGTCAACATCAGAGCACATTAAACGCTGGTGAAACC NM_152339RefSeq
chr16 - 89696356 89701713 SPATA2L 124044 spermatogenesis associated 2-like NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140845_PI430048170 0.9422477694861541.17734426568589 2.23903538722973
0.3978723117599170.308011974913246A A A 0.9052733580947121.25987163979408
0.93560093013717 A A A LNCV6_140845_PI430048170 mRNA
TTAGATTTGGAAAGCCCGGAAGAAGCTGCAGCAAACAAGTTCCGGATCAAATCCCCATTT NM_018676RefSeq chr13
- 52377167 52406494 THSD1 55901 "thrombospondin, type I, domain containing 1, transcript variant 1"
GO:0005737|GO:0009986|GO:0002244|GO:0005576|GO:0016021|GO:0071944 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_112249_PI430048170 0.1639322867786460.90047137063305411.0727438164202
11.0864200023503 11.2881299312432 P P P 11.3233694122397 11.1979698970422
11.3837536952944 P P P LNCV6_112249_PI430048170 mRNA
CTGTTATACCCCATATATTACCCCTTCATGTCCTAAAGAAGACATTTTCTCTTAGAGATTNM_001145408 RefSeq chrX
+ 71283191 71301171 NONO 4841 "non-POU domain containing, octamer-binding, transcript variant
1"
GO:0005515|GO:0006397|GO:0008380|GO:0005730|GO:0001047|GO:0005634|GO:0006310|GO:0016363|GO:0006
351|GO:0042802|GO:0042382|GO:0006281|GO:0016607|GO:0000166|GO:0016020|GO:0042752|GO:0007623|GO:0
005654|GO:0045892. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140045_PI430048170 0.0814493506074628 2.13460901100214 3.5288964095287
3.7407728876378 2.66030386276192 P P A 1.67979226962789 2.85575198508279
2.06661070580788 A P A LNCV6_140045_PI430048170 mRNA
CATGGATGAGACCAGAGGAGGTATGGATGGAAACAAGCTCTATGGAAAATAAAGCATGAG NM_144698RefSeq

chr1 - 145866559 145885866 ANKRD35 148741 "ankyrin repeat domain 35, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83629_PI430048170 0.00341554804832976 0.6405633875549498.85774949240405
8.62090727911378 8.66525981242223 P P P 9.50168318971653 9.30839713119875
9.26133656549408 P P P LNCV6_83629_PI430048170 mRNA
AGGGGACTGGCTCCTTTCCCAGTGTCCTTAAAATAAAGAAATGAAAATGCTTGTTGGCAC NM_001040078 RefSeq
chr17 + 18476784 18494945 LGALS9C 654346 "lectin, galactoside-binding, soluble, 9C" GO:0030246
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138701_PI430048170 0.00756270615891104 0.7430576971046821 0.5016715142012
10.4327687607867 10.4552241180433 P P P 10.9462699304735 10.9377994787231
10.7862645899163 P P P LNCV6_138701_PI430048170 mRNA
TAACACGTGCAATTATTTAAAAAGATTTCAATAAAACTGCCTGGCTGGCTCCGGGCCGCC NM_006285 RefSeq chr9
+ 35605283 35610041 TESK1 7016 testis-specific kinase 1
GO:0005515|GO:0004674|GO:0034329|GO:0018108|GO:0004712|GO:0007283|GO:0004713|GO:0005524|GO:0046
872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136676_PI430048170 0.402741016140018 1.48959854261085 2.42452764391733
3.93538745408563 3.35199286692938 A P P 2.84438525124951 2.39053745930617
3.05376856897912 P A P LNCV6_136676_PI430048170 mRNA
GGTCCAACTTTTGGATATTTAAAATTGATCCCTGTGTGGCTAACAGAATTAATGTTTCCA NM_001282380 RefSeq
chr15 - 89896531 89912687 ARPIN 348110 "actin-related protein 2/3 complex inhibitor, transcript
variant 2" GO:0030336|GO:0033058|GO:2000393|GO:0051126|GO:0030027 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136497_PI430048170 0.2337538675767540.9326631000328690.4708082423692110.424373652402
0.461572824491311 A A A 0.4836723710858770.4997941935701430.668097636935075 A A A
LNCV6_136497_PI430048170 mRNA
CAGCTTTAAACGAAGACAACCAAAAGAATGCAAACTGGATTTATCCGAGATATTTGACTT NM_130775 RefSeq chrX
+ 52812203 52818298 XAGE5 170627 "X antigen family, member 5" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_122987_PI430048170 0.2862515670465711.28077011849671 1.07654575578435
0.3139709745414740.836235075543948 A A A 0.46927474132941 0.411261176061293
0.375166800052799 A A A LNCV6_122987_PI430048170 mRNA
GCAGCAAACTGAAAGTAATGCAAACAGATGAATCCAATAAAGAAACAGCTAACCTACAAG NM_148894 RefSeq
chr4 - 13568741 13627704 BOD1L1 259282 biorientation of chromosomes in cell division 1-like 1
GO:0005654|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143094_PI430048170 0.0118736664671488 1.6277915729897 5.30218590201608
5.36443766941416 5.6331786294249 P P P 4.96760401003641 4.58157972609736
4.63249681801236 P P P LNCV6_143094_PI430048170 mRNA
GAAGGGCAAACATATTTCTTAATGAGAGGCAGTCCTTCATGTTTTGCAATAAAATGACTT NM_014157 RefSeq chr16
+ 58249935 58283830 CCDC113 29070 "coiled-coil domain containing 113, transcript variant 1"
GO:0005515|GO:0043234|GO:0042384|GO:0005737|GO:0034451|GO:0005654 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130414_PI430048170 0.2945850415693541.86134005966852 2.58787392525731
3.38555693963052 1.66083980108245 A P A 0.405123305208385 2.44625755346239
1.91429368980068 A A A LNCV6_130414_PI430048170 mRNA
AGCCTGGGCATCCTCAGGTGGTCAGGCGTAGATCACCAGAATAAACCCAGCTTCCCTCTT NM_001079 RefSeq chr2
+ 97713567 97739860 ZAP70 7535 "zeta-chain (TCR) associated protein kinase 70kDa, transcript variant
1"
GO:0046638|GO:0005515|GO:0050852|GO:0005886|GO:0050850|GO:0005829|GO:0035556|GO:0005737|GO:0006
955|GO:0005911|GO:0042101|GO:0046641|GO:0038083|GO:0045582|GO:0001772|GO:0005102|GO:0043366|GO:0

018108|GO:0005524|GO:0072678|GO:0045059|GO:0031234|GO:0002250|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133539_PI430048170 0.00686911376877343 1.459863962518 8.35696982423006 8.48320270312093 8.26214998314979 P P P 7.91211370412524 7.88829819710514 7.6597547692286 P P P LNCV6_133539_PI430048170 mRNA
GGAAAAGTCAAAGTGTTGCTGTGGCTCCATATTTCAACTAAAAATATATCTGTTGGAGAA NM_020248 RefSeq chr1 - 9848275 9910258 CTNNBIP1 56998 "catenin, beta interacting protein 1, transcript variant 1"
GO:0002528|GO:0005515|GO:0032091|GO:0072201|GO:0001658|GO:0008013|GO:0030178|GO:0030877|GO:0048662|GO:0005634|GO:0009952|GO:0043433|GO:0043392|GO:0005829|GO:0045669|GO:0060633|GO:0005737|GO:0045657|GO:0005654|GO:0016055|GO:0070016 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145251_PI430048170 0.0127111780919362 1.3072425140258 6.08646516269613 5.94142718724285 5.87079857261954 P P P 5.70670620511473 5.52724115110526 5.50501469634437 P P P LNCV6_145251_PI430048170 mRNA
GGAGGAACATCTGTTTGATTACTTTCTTTTGTGGAACTGGAAATTTCCATCGAGGAAATG NM_003501 RefSeq chr4 - 8366281 8440725 ACOX3 8310 "acyl-CoA oxidase 3, pristanoyl, transcript variant 1"
GO:0005739|GO:0016402|GO:0016020|GO:0005782|GO:0050660|GO:0005102|GO:0003995|GO:0044281|GO:0033540|GO:0044255|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134852_PI430048170 0.130537660936328 0.844298849592035 8.79812603129046 8.5788714310288 8.64984205982283 P P P 9.03777169123146 8.99614635603145 8.71305296951252 P P P LNCV6_134852_PI430048170 mRNA
CAGTCTTCTCTGGGCTTGAGGCTGCTCCTTGGCAGGCATTTAAAGTAAAAAATAAAATGG NM_001286796 RefSeq chr9 + 129608883 129636131 NTMT1 28989 "N-terminal Xaa-Pro-Lys N-methyltransferase 1, transcript variant 1"
GO:0035572|GO:0035573|GO:0005737|GO:0007059|GO:0018012|GO:0005654|GO:0005634|GO:0007051|GO:0018016|GO:0008276 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67591_PI430048170 0.585448842660189 0.906822716047574 0.329177647296222 0.306500432952781 0.436176945059274 A A A 0.839209029669405 0.273673170196996 0.314114110294181 A A A LNCV6_67591_PI430048170 mRNA
TTGTCCAGGATTTTAAGGATGTCAGACTGCTGTAGATGACTCAATAAATGTTTTGCCATT NM_001199635 RefSeq chr7 + 31052460 31111479 ADCYAP1R1 117 "adenylate cyclase activating polypeptide 1 (pituitary) receptor type I, transcript variant 1"
GO:0005515|GO:0043005|GO:0005886|GO:0030306|GO:0045471|GO:0010524|GO:0060732|GO:0007202|GO:0007283|GO:0030154|GO:0007190|GO:0004999|GO:0060548|GO:0004872|GO:0032355|GO:0046545|GO:0005791|GO:0048011|GO:0009986|GO:0008179|GO:0042493|GO:0033555|GO:0043235|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143868_PI430048170 0.266403968283346 0.518903297363152 2.6123683057908 1.25155166463198 3.01965616611244 A A P 2.35237727705766 4.10376002575977 3.27826953991042 A P P LNCV6_143868_PI430048170 mRNA
GGAAAGGACTTTGATTTCTCTTTGTTATTTAATCACTGATGTGGTCTAAACCCACGATAA NM_006267 RefSeq chr2 + 108719480 108785811 RANBP2 5903 RAN binding protein 2
GO:0007077|GO:0005515|GO:0000413|GO:0010467|GO:0003723|GO:0016874|GO:0019221|GO:0019058|GO:0044281|GO:0006606|GO:0005829|GO:0008645|GO:0005739|GO:0015758|GO:0006457|GO:0005643|GO:0008536|GO:0016032|GO:0031965|GO:0005975|GO:0016925|GO:0019083|GO:0003755|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131705_PI430048170 0.0681462771090789 0.913648106412604 0.245172668236012 0.286349775523172 0.311972941744895 A A A 0.424313986349771 0.333993676505041 0.473392962696838 A A A LNCV6_131705_PI430048170 mRNA
ATGTACATAGAACTTCCAAATGCTGAGCCCAGATCCAAAGTTGTCTTCTGTCCACGAGCA NM_014512 RefSeq chr19_KI270891v1_alt - 20939 114105 KIR2DS1 3806 "killer cell immunoglobulin-like receptor, two

domains, short cytoplasmic tail, 1"
GO:0007165|GO:0006955|GO:0005886|GO:0045087|GO:0050776|GO:0016021|GO:0004888 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_110721_PI430048170 0.465926037119627 1.38975710314397 0.305867121703281
0.331124716369445 1.5166421122841 A A A 0.391748476563012 0.327714263577828
0.363420057226595 A A A LNCV6_110721_PI430048170 mRNA
TTTTTGGCACATTCCTGTGCAAGGTGGTCTCACTCCTGAAGGAAGTCAACTTCTATAGTG NM_001557 RefSeq chr2
+ 218126012 218137253 CXCR2 3579 "chemokine (C-X-C motif) receptor 2, transcript variant 1"
GO:0005515|GO:0002438|GO:0008284|GO:0005886|GO:0007200|GO:0019959|GO:0007204|GO:0042629|GO:0005
622|GO:0031623|GO:0072173|GO:0006954|GO:0006935|GO:0033030|GO:0038112|GO:0010666|GO:0004871|GO:0
070098|GO:0009986|GO:0030593|GO:0002407|GO:0004918|GO:0045766|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133808_PI430048170 0.367556774223257 1.49831723081948 1.86752355489176
0.630966565757908 0.678011490992871 A A A 0.657169852379389 0.420118729393667
0.697590432050752 A A A LNCV6_133808_PI430048170 mRNA
TGGAGTCAGGACAAAGCAGATTCGAGAGAGAGTGCTGAGGATTTTTCTCAAGACCAATCA NM_001005168 RefSeq
chr11 - 5856748 5857702 OR52E8 NA "olfactory receptor, family 52, subfamily E, member 8" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134080_PI430048170 0.00551965122093797 0.622599872193574 10.1000078753861
9.79024183167355 9.92684632812589 P P P 10.4546500702585 10.7510674056318 10.663162539269
P P P LNCV6_134080_PI430048170 mRNA
GGCCCCTGCCTTAGGCCTACCTGATCAAAATAAAGCCTCAGCCACATTTGCTATAAAAAA NM_000850 RefSeq chr1
+ 109656075 109661709 GSTM4 2948 "glutathione S-transferase mu 4, transcript variant 1"
GO:0043295|GO:0005737|GO:0006805|GO:0018916|GO:0042178|GO:0006749|GO:0044281|GO:0019899|GO:0004
364|GO:0042803|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138117_PI430048170 0.707827460092764 1.16342421001241 1.88386450299622
0.471606461900596 1.5095392775937 A A A 0.505179905511169 1.90173424069239
0.72718799658065 A A A LNCV6_138117_PI430048170 mRNA
GCATGAGACGCTGTCAAATACAGACAAAGGATTTGAGATGTTCTCAATAAAAAGAAAATG NM_015833 RefSeq chr21
+ 45074577 45226563 ADARB1 104 "adenosine deaminase, RNA-specific, B1, transcript variant 2"
GO:0003725|GO:0005515|GO:0006397|GO:0010467|GO:0006396|GO:0030336|GO:0008285|GO:0003726|GO:0016
556|GO:0016553|GO:0003723|GO:0005730|GO:0005634|GO:0003729|GO:0046872|GO:0006382|GO:0051607|GO:0
005737|GO:0044387|GO:0004000|GO:0045087|GO:0051726|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_52065_PI430048170 0.0856013992428021 1.5976821673389 3.97278408305396
4.44021682511836 3.88723881535016 P P P 3.73795818749109 3.54329839638602
2.94031536704659 P P P LNCV6_52065_PI430048170 mRNA
TGAGAGCAACTTCGTACAGGTGACTCGGTTGGGAGAAGTTGCCAACGAGGTCACCATGGG NM_138411 RefSeq
chr19 - 50466784 50476746 FAM71E1 112703 "family with sequence similarity 71, member E1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134640_PI430048170 0.389015927776736 1.0140528660097 0.330168389430655
0.307053288251265 0.267734695499397 A A A 0.284275204109257 0.286578406283821
0.274364338719965 A A A LNCV6_134640_PI430048170 mRNA
ACCTTCACTGTTACATAAGGTACAGATATAAAATGCAGAAAAAGCATCAAGAATTCTGCC NM_178824 RefSeq chr3
- 167478684 167653501 WDR49 151790 WD repeat domain 49 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_128923_PI430048170 0.440281335214569 0.967501992900611 0.432492147777814
0.45551125973449 0.295117229897661 A A A 0.408772663933480 0.482243205004618
0.439306286048023 A A A LNCV6_128923_PI430048170 mRNA

CAGGAGGAAATTGTAAGATCAGTCTGGTACTGAATAAAATCCTGGCCTGATTGTCTTACC NM_001145350 RefSeq chr20 - 35526970 35529652 C20orf173 140873 "chromosome 20 open reading frame 173, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127001_PI430048170 0.00203353932709067 0.7679107117568176.81726840212785 6.80185452305664 6.71513543178179 P P P 7.1466615007724 7.23253141363777 7.09684286138339 P P P LNCV6_127001_PI430048170 mRNA
CCGACATATGTTGGTTATTCTTTTAGACATGTTTTTTGTTGTTGTTGTCACCTGGAACTT NM_006612RefSeq chr17 + 4997947 5028399 KIF1C 10749 kinesin family member 1C GO:0005515|GO:0008017|GO:0005871|GO:0005794|GO:0005783|GO:0006890|GO:0005874|GO:0005524|GO:0030705|GO:0003774|GO:0008152|GO:0008574|GO:0016192|GO:0016887|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134792_PI430048170 0.00647285559074469 1.46411646844431 7.49867012974474 7.65071382651234 7.60159475773345 P P P 7.03253802404243 7.03253802404243 7.03994661200654 P P P LNCV6_134792_PI430048170 mRNA
TTATTACCTCCACATTTTGAAGCAGTTCATGACCAGCATAGTGCTTTGGGGGCATTTTTT NM_014891RefSeq chr7 - 99394675 99408682 PDAP1 11333 PDGFA associated protein 1 GO:0007165|GO:0008283 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137745_PI430048170 0.0344744786609323 0.7347707134322987.22213992761045 7.29762201438115 7.58252125488011 P P P 7.73166478379023 7.78436983641577 7.93765796610149 P P P LNCV6_137745_PI430048170 mRNA
GGGCTTGCATTATAATTACTTGCCACTTGAATGTGTTTTGTGTAATGTTTTAACAGTGCTNM_015646RefSeq chr12 + 68610838 68660606 RAP1B 5908 "RAP1B, member of RAS oncogene family, transcript variant 1" GO:0005515|GO:0005886|GO:0008283|GO:0030033|GO:0003924|GO:0032403|GO:0005829|GO:0005622|GO:0005911|GO:0061028|GO:0070374|GO:0070062|GO:0005811|GO:2000301|GO:0032486|GO:2000114|GO:0030168|GO:0005525|GO:0006184|GO:0016020|GO:0045955|GO:0007596|GO:0045121|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127364_PI430048170 0.5866240188383170.7232549451742750.968194610058467 0.34439522583842 0.319069266671713A A A 1.83711330223681 0.336852164191232 0.432252848047281A A A LNCV6_127364_PI430048170 mRNA
AGGGTCAGAGTTTTCAAAACAAAAGCATCTTCCCTAGAAATTTTTGTGAATTGTTTGCAC NM_001276718 RefSeq chr15 + 40239090 40277487 PAK6 56924 "p21 protein (Cdc42/Rac)-activated kinase 6, transcript variant 5" GO:0035556|GO:0023014|GO:0005515|GO:0006355|GO:0005737|GO:0004702|GO:0007010|GO:0006915|GO:0006468|GO:0005634|GO:0000278|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127289_PI430048170 0.3723278253234590.8187458297248962.23067696680538 2.85785681851389 1.82086033232749 A A A 2.83495794665375 2.60962378062737 2.50162138669039 A A P LNCV6_127289_PI430048170 mRNA
ATGCTGCCTGCTCTGTTTACAATGGTTTGTGTTTTGTGGATACATATCAAATGCTGTAAT NM_153442RefSeq chr10 + 123666354 123697397 GPR26 2849 G protein-coupled receptor 26 GO:0005886|GO:0004930|GO:0016021|GO:0007189 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137088_PI430048170 0.9301600481427121.11730538980574 2.02582595566352 0.3736762344683690.25646625529305 A A A 0.34565900033523 0.384412922260078 1.72132912639953 A A A LNCV6_137088_PI430048170 mRNA
GGGACAGGAACAGAAACAGATGACTATTTTTCTTAGTATTCATATTAAGCAATGTGCATC NM_001256579 RefSeq chr21 - 14591391 14643107 LOC388813 NA uncharacterized protein ENSP00000383407-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135127_PI430048170 0.00137932653532892 4.77992847592881 3.69001976887477 3.94133327961628 3.41486924642998 P P P 1.81329626160167 1.30296218528485 1.11341813264769 A A A LNCV6_135127_PI430048170 mRNA

CTCCAGTCTGATTTTATAAAGTGCTGACGAGATTGGGAATAAAGAGGCATAAAGAAAAAA NM_182847 RefSeq chr2
+ 219514169 219538772 ASIC4 55515 acid sensing (proton gated) ion channel family member 4
GO:0034220|GO:0005887|GO:0005272|GO:0006810|GO:0035725|GO:0015081|GO:0005216 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127641_PI430048170 0.9377697603162270.9395928866771561.48189864800809
1.19874212500409 0.412486905509701 A A A 0.3045540689151572.02745086597405
0.604426733369571 A A A LNCV6_127641_PI430048170 mRNA
GATATTGACTCTCTTTATACCTACCCAAGCTGAACGACCCTCCTTTTCTTAAATAAAATA NM_006683 RefSeq chr14
+ 20745939 20748380 EDDM3A 10876 epididymal protein 3A GO:0007321|GO:0005615 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_142469_PI430048170 0.8830511233948551.01010935889073 12.8940553607465
12.6685375982546 12.7268791721342 P P P 12.6868707101339 12.776463362445
12.7900406387301 P P P LNCV6_142469_PI430048170 mRNA
ATAGGCTTGTTTCCAGAGTTGTCCTTATACAAAATGTATAAAAAGCAGTTTCTGGTGTGA NM_015971 RefSeq chr17
+ 75261667 75266376 MRPS7 51081 mitochondrial ribosomal protein S7
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0022627|GO:0003723|GO:0005
743|GO:0006412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134086_PI430048170 0.0170652606977091 0.6893036850432 5.8358498159809
5.77485130970304 5.51554126450804 P P P 6.19759172868535 6.42858141085747
6.11114054008317 P P P LNCV6_134086_PI430048170 mRNA
TCGCTCTGCAAATGTTTATTGAACATTTCTGAGATTTTAAGAGATTTTGTTGGCTGCTCC NM_021241 RefSeq chr19
- 15421506 15449951 WIZ58525 widely interspaced zinc finger motifs
GO:0070208|GO:0005515|GO:0010571|GO:0050821|GO:0005634|GO:0070984|GO:0046872|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135733_PI430048170 0.7131887274024560.9612784762316770.351284517427839
1.26542289311746 2.57271839378413 A A A 2.12412384903974 1.14050993834887
1.78779239682398 A A A LNCV6_135733_PI430048170 mRNA
CTGTATCCTTTCATAGCTTTTGAAAATGTGGGTGTACTATGTACTATGTGGATGTACTAC NM_001178099 RefSeq
chrX - 47974850 48003995 ZNF182 7569 "zinc finger protein 182, transcript variant 3"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_91943_PI430048170 0.4205723793953241.01359460926761 0.3122896212868290.33658393230828
0.375605181321127 A A A 0.3365785816335090.3255922306114080.304388631438502 A A A
LNCV6_91943_PI430048170 mRNA
GGAGGAGCTTCCTACTTTTGAGTTTCTCTGTGGAAATAAAACATGAATCTTGTTTCCCTA NM_033317 RefSeq chr19
- 35497216 35513658 DMKN 93099 "dermokine, transcript variant 2"
GO:0005515|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133864_PI430048170 0.0371590876350798 1.13010726338676 10.6814873328083
10.7472182819535 10.6232215514411 P P P 10.4209640986678 10.5636845572633
10.5366211992585 P P P LNCV6_133864_PI430048170 mRNA
ATTAACCCATGCATACTGTATGCCATAAACTCACTTTGGTATATCCGCGTCACATGCAGA NM_032646 RefSeq chr17
+ 74213556 74262018 TTYH2 94015 "tweety family member 2, transcript variant 1"
GO:0005515|GO:0005886|GO:0034707|GO:0005254 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135931_PI430048170 0.00992521490918526 0.4189324568096846.42641170080611
5.88867344593057 6.39548255310501 P P P 7.38509088806933 7.51530573688062
7.62620621317993 P P P LNCV6_135931_PI430048170 mRNA
GTTGCTTTAACTGAGGAGAAAAGAAAGCACACTGCCTAAATGTGTAAAAGAAAAATGCAG NM_016141 RefSeq chr3
- 32525970 32570874 DYNC1LI1 51143 "dynein, cytoplasmic 1, light intermediate chain 1"
GO:0005813|GO:0005886|GO:0005874|GO:0090267|GO:0003777|GO:0005524|GO:0000922|GO:0005737|GO:0007

067|GO:0016020|GO:0008152|GO:0000777|GO:0006810|GO:0016032|GO:0000776|GO:0005868|GO:0051301|GO:0
007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68092_PI430048170 0.7345641042134440.9424871134239070.3892597016214850.660427892023671
0.355704341217825 A A A 0.3733302683942590.3707598390311680.876539341929511 A A A
LNCV6_68092_PI430048170 mRNA
AGTTGTGAAGAAGCTGACTGTATAGACCCTGGGTGTTCTAATCATGGTGTGTGTATCCAC NM_001080477 RefSeq
chr4 + 182323983 182803024 TENM3 55714 teneurin transmembrane protein 3
GO:0030424|GO:0007165|GO:0046982|GO:0016020|GO:0097264|GO:0010976|GO:0048593|GO:0016021|GO:0007
156|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132410_PI430048170 0.1631027501567931.06905744255733 0.49977616842282
0.4103525028368780.52229349964377 A A A 0.30320932292042 0.381780061447917
0.456745181594448 A A A LNCV6_132410_PI430048170 mRNA
ACCAGCGGGGTGCTTGCCATTCTGAAGATAATAAAATGAATGTGTTGCAAATTGAAAAAA NM_016379RefSeq chrX
- 6533617 6535118 VCX3A 51481 "variable charge, X-linked 3A"
GO:0007420|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131451_PI430048170 0.0286717403823568 0.6494530816872927.16271340237707
6.6909188597753 6.99814419237337 P P P 7.46047855876488 7.67317289804146 7.6169379207746
P P P LNCV6_131451_PI430048170 mRNA
CTGTTGCTTCTTGGCCAGTGTAGTCAATAAGGGTCTTCTTTAACATCTAAGATAGAGGTT NM_017990RefSeq chr16
+ 70113625 70161281 PDPR 55066 pyruvate dehydrogenase phosphatase regulatory subunit
GO:0010510|GO:0005737|GO:0006090|GO:0005759|GO:0016491|GO:0044281|GO:0044237|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139136_PI430048170 0.0274494017356967 0.3002761008416180.64688428509606
0.5180996630337471.68330337395689 A A A 2.78399182951953 2.99764004591885
2.53723169734898 P P A LNCV6_139136_PI430048170 mRNA
CGCTCTGATTTAGCCTTAATTTTGTTAAATTTTTTAGAGATGAATGAAGTGCTGCTGTGG NM_015247RefSeq chr16
+ 50742049 50801935 CYLD 1540 "cylindromatosis (turban tumor syndrome), transcript variant 1"
GO:0005515|GO:0006511|GO:0005881|GO:2001238|GO:0042347|GO:0048471|GO:0004843|GO:0070423|GO:0035
872|GO:0036064|GO:0005829|GO:0002181|GO:0070536|GO:0045581|GO:2001242|GO:0016055|GO:0090090|GO:0
070064|GO:0032480|GO:0005813|GO:0070266|GO:0003735|GO:0019901|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138840_PI430048170 0.3071528474405040.9223656387196055.50839685288385
5.68949094794218 5.62199347578685 P P P 5.56478649834978 5.82624584973619
5.77142286849432 P P P LNCV6_138840_PI430048170 mRNA
TGCAGGCCCATGCCTGCTCAGGACACTGCAATGGAGACCTTCAACTCCCCATCTTTATCG NM_006150RefSeq chrX
- 49174802 49186400 PRICKLE3 4007 prickle homolog 3 (Drosophila)
GO:0005515|GO:0008150|GO:0008270|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139710_PI430048170 0.7301790797917281.03672566093498 9.32763942771743
9.48345737616767 9.68138325975728 P P P 9.45187710534706 9.29128802146646
9.59872811271002 P P P LNCV6_139710_PI430048170 mRNA
CAGTTAGTGTTGGAAAAACCTGGTGGTGTTTACAATGTTGCTAATCATTACAAAACATTC NM_001166118 RefSeq
chr7 - 33014112 33041165 NT5C3A51251 "5'-nucleotidase, cytosolic IIIA, transcript variant 4"
GO:0006213|GO:0000287|GO:0005783|GO:0046085|GO:0055086|GO:0044281|GO:0008665|GO:0005829|GO:0005
739|GO:0046135|GO:0005737|GO:0000166|GO:0016311|GO:0008253|GO:0006206|GO:0009117 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_102651_PI430048170 0.0147754829336526 0.38187491087388 6.11248902933858
5.42772667166848 6.2545465520281 P P P 6.91842803812407 7.41423590461684
7.66034537818992 P P P LNCV6_102651_PI430048170 mRNA
TTGCAGACAGACCGTCATATTCTAATAGCTCATGAAATTTGGGCAGCAGGGAGGAAAGTC NM_003392RefSeq chr3

- 55465714 55487642 WNT5A 7474 "wingless-type MMTV integration site family, member 5A, transcript variant 1"
GO:0032755|GO:0003700|GO:0044212|GO:0045599|GO:0043032|GO:0038031|GO:0001756|GO:0005110|GO:0005115|GO:0005615|GO:0007223|GO:0005109|GO:0001947|GO:0007411|GO:0016055|GO:0032729|GO:0010800|GO:0021891|GO:0003408|GO:0009986|GO:0005796|GO:0019904|GO:0001843|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106039_PI430048170 0.00630850832693449 1.65428652235122 4.21497221749501 3.92910719640793 3.99976013200987 P P P 3.17974511094261 3.52296302967736 3.25512815248005 P P P LNCV6_106039_PI430048170 mRNA
AAGCCCAGAGAGATCTCTACAGAGATGTGATGTTGGAGAACTACAAGAATCTCATTATAC NM_001077624 RefSeq chr19 - 9757474 9768734 ZNF846 NA zinc finger protein 846 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138390_PI430048170 0.0447606845482914 0.76757882376426 10.1878873341844 10.1544864198026 9.94886488526656 P P P 10.2864404777083 10.6355492973004 10.5041933200655 P P P LNCV6_138390_PI430048170 mRNA
CATTCATTCCCTGGCATTAATCCCTTAGAGGGAATAATAAAGCTTTTTATTTCTCTGTGA NM_021078RefSeq chr17 - 42113110 42121364 KAT2A 2648 K(lysine) acetyltransferase 2A
GO:0005515|GO:0072686|GO:0042826|GO:0006366|GO:0008283|GO:0001756|GO:0035948|GO:0006325|GO:0005615|GO:0021537|GO:0031647|GO:0035264|GO:0043997|GO:0016032|GO:0044154|GO:0006338|GO:0004402|GO:0016578|GO:0006357|GO:0030914|GO:0010484|GO:0003713|GO:0001843|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141825_PI430048170 0.1368677639504440.45931735935015 0.370770810475809 1.58431434462267 2.19095155510519 A A A 3.23356967524649 2.45808583102513 2.13219048206267 P P A LNCV6_141825_PI430048170 mRNA
TCCTAGTTCTCTTCCCACCTGTCAACCTGAATTAAAGTCTACACTGCCTTTGTGAAAAAA NM_002036RefSeq chr1 + 159204012 159206500 ACKR1 2532 "atypical chemokine receptor 1 (Duffy blood group), transcript variant 2"
GO:0070098|GO:0005886|GO:0004930|GO:0006952|GO:0019957|GO:0006954|GO:0007186|GO:0032642|GO:0004872|GO:0016021|GO:0055037|GO:0005769|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64830_PI430048170 0.0139648244416145 0.6896197509521989.69004317864897 9.8048740168027 9.77775782809148 P P P 10.1219555367211 10.3900005244437 10.3570547096149 P P P LNCV6_64830_PI430048170 mRNA
TTATTTATTACCTGGAGGCCTGTCCAGCACCCACCCTACCCCCATAAAGCATTGTTTACA NM_016154RefSeq chr19 + 40778218 40796944 RAB4B 53916 "RAB4B, member RAS oncogene family"
GO:0048471|GO:0005886|GO:0003924|GO:0005525|GO:0006886|GO:0006184|GO:0003674|GO:0030100|GO:0046323|GO:0032593|GO:0032482|GO:0019003|GO:0055037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135304_PI430048170 0.2721681288649481.25322731614032 4.62200514470952 4.37903577658424 4.19220823964662 P P P 4.49633014548134 3.71673359998992 3.9184538194365 P P P LNCV6_135304_PI430048170 mRNA
CTGGCTGCCTACTGGAATGTAAATATGTGATAAAATAATAAATGACAGCGGCAAAGCCTA NM_001080397 RefSeq chr1 + 8318084 8344167 SLC45A1 50651 "solute carrier family 45, member 1"
GO:0008643|GO:0016021|GO:0055085|GO:0015293 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131631_PI430048170 0.4696547530126140.5582922857230530.3032007095771980.310262835463 0.516810763900424A A A 2.17680938735415 0.27869885826825 0.332512773562511A A A LNCV6_131631_PI430048170 mRNA
AAATGAAAGTCCTGGAGTTTGTGGCCAAGCTCAATGATACCGTTGCCAGTACCTACAAGT NM_001277307 RefSeq chrX + 16167480 16171393 MAGEB17 NA melanoma antigen family B17 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64870_PI430048170 0.705394510483581 1.69748893560824 2.63834539365209 0.386866850971261

0.288415008809376 A A A 0.5669962201521720.6905887336244381.0442208689699 A A A
LNCV6_64870_PI430048170 mRNA
GCTCTCGCCATTTCCTAAGAGATACATTGTAAAATGTGACAGTAATACTGATTCTAGCAG NM_001130167 RefSeq
chr19 - 42752686 42765679 PSG8 440533 "pregnancy specific beta-1-glycoprotein 8, transcript
variant 2" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144675_PI430048170 0.1036018191014530.7553768452794823.52103207474075
3.04894857876915 3.51344570803908 P P P 3.98845626090767 3.67541889081845
3.65793603978625 P P P LNCV6_144675_PI430048170 mRNA
CTGTTTTAACGTAAGACAAACTGATAGCAACATTCTGTTGTTTTAAAGGAAGTGGGTCCG NM_001193388 RefSeq
chr16 - 1363204 1414720 UNKL 64718 "unkempt family zinc finger-like, transcript variant 1"
GO:0005515|GO:0005737|GO:0016567|GO:0016874|GO:0008270|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142944_PI430048170 0.1004666501002961.31578455042337 7.27259588454909
7.37001006740656 7.2600786767908 P P P 7.07746323954638 6.60264779920421
6.99420576522076 P P P LNCV6_142944_PI430048170 mRNA
CATGAGCAAGAACCACTTTATAGCTGGCATATATTTTTCCAGATTTTCTCTATGCATAAG NM_001286205 RefSeq
chr16 + 90022599 90044971 GAS8 2622 "growth arrest-specific 8, transcript variant 3"
GO:0003674|GO:0017137|GO:0008285|GO:0005794|GO:0031514|GO:0005874|GO:0034613|GO:0030317 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130217_PI430048170 0.0339949627728878 1.37098399862549 9.3136511672981
9.68946087800525 9.48640784686848 P P P 9.08196558737807 9.12877570881672
8.93034640687791 P P P LNCV6_130217_PI430048170 mRNA
TTTATTTATGTCATGTCGGGTGTGGGATCTTGAGCTCTGGCAGTGATGATGGTACTTCCT NM_001281504 RefSeq
chr19 + 10543893 10553423 ATG4D 84971 "autophagy related 4D, cysteine peptidase, transcript
variant 2"
GO:0006501|GO:0006995|GO:0000422|GO:0006915|GO:0051697|GO:0005829|GO:0004197|GO:0005737|GO:0016
485|GO:0005759|GO:0006612|GO:0006508|GO:0000045 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127431_PI430048170 0.0167908148532683 0.4481043833378355.6783073100675
5.20063519415305 5.58791954777231 P P P 6.23188151664102 6.66334646970384 6.9905327460799
P P P LNCV6_127431_PI430048170 mRNA
GTCATCTTACTGAAAGGAATAACACTTCTAAAGATCACCATTTCTGAGAAGTTCTTGGAA NM_015328RefSeq chr7
+ 129225013 129430211 AHCYL223382 "adenosylhomocysteinase-like 2, transcript variant 1"
GO:0004013|GO:0006730|GO:0033353|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142700_PI430048170 0.0824566137946165 1.29483301573652 8.49236355975636
8.85056181667839 8.64126711576732 P P P 8.39741993754004 8.42098577649344
8.03929195728628 P P P LNCV6_142700_PI430048170 mRNA
TAGGAAACTTTTCCTAAAAGGAAGTGGCAATTTTAACTAATCTCCCCTCCGCCGCTCCCA NM_016202RefSeq chr19
+ 55642051 55643470 ZNF580 51157 "zinc finger protein 580, transcript variant 1"
GO:0005515|GO:0006355|GO:0070301|GO:0005634|GO:0003677|GO:0002690|GO:0006351|GO:0032757|GO:0046
872|GO:0010595|GO:0010628|GO:0006954|GO:0001938|GO:0006935 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139065_PI430048170 0.5884828221263720.9662303216187950.506107317757394
0.4811278955707730.256407236258347 A A A 0.4039778952839420.52594874906371
0.472679944705104 A A A LNCV6_139065_PI430048170 mRNA
GAGATGGGATAGGATATTTACATATTGAGATGATGTATCTGATATTCCACCCATTCACAA NM_001135924 RefSeq
chr7 - 12330882 12404226 VWDE 221806 von Willebrand factor D and EGF domains GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140036_PI430048170 0.59787344847314 0.779028009956891 1.63682311399273
1.61939782837333 3.16287718758184 A A P 2.47166598111424 1.75193311698669

3.39471989013225 A A P LNCV6_140036_PI430048170 mRNA
ATCTGTTCAATGCCATTTGCGTTTCAATAAAGTTATCTCCTGTACTGTCCACTGAAAAAA NM_020443 RefSeq chr1
+ 201648321 201826974 NAV1 89796 "neuron navigator 1, transcript variant 1"
GO:0005737|GO:0001578|GO:0005874|GO:0001764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140429_PI430048170 0.2227110397183671.05153645918595 0.54029927861349
0.6619163238955610.535327390477947 A A A 0.4893410058592840.511078342600503
0.523021074032941 A A A LNCV6_140429_PI430048170 mRNA
GTATTATCTCTTTCTTCTTCTTGTGGTGATCATCTTGAATTACTGTGGGATGTAAGTTTC NM_001244014 RefSeq chr12
- 6693790 6700843 PIANP 196500 "PILR alpha associated neural protein, transcript variant 2"
GO:0016323|GO:0005912|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133183_PI430048170 0.2131883199503221.01103085729773 0.324850629733631
0.3375324018785520.346365539720838 A A A 0.3309363003032060.326664546664539
0.303598019583027 A A A LNCV6_133183_PI430048170 mRNA
TATATAAACCGCCCTTTTTGTATGCACCACGGGCGGCTTTTATATGTAATTGCAGCGTGG NM_002821 RefSeq chr6
+ 43076267 43161720 PTK7 5754 "protein tyrosine kinase 7 (inactive), transcript variant PTK7-1"
GO:0001736|GO:0005515|GO:0031532|GO:0071300|GO:0003401|GO:0090179|GO:0001843|GO:0018108|GO:0005
524|GO:0045198|GO:0007165|GO:0060026|GO:0016477|GO:0005887|GO:0005911|GO:0042060|GO:0010976|GO:0
090103|GO:0060484|GO:0004713|GO:0007155|GO:0060070|GO:0005925 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142893_PI430048170 0.0139816103944872 0.5812089247659236.12119368853427
6.39851250023626 6.58366268832259 P P P 7.12109226664512 7.06779035191732 7.2906841154836
P P P LNCV6_142893_PI430048170 mRNA
GTAAACTCTAGATTACTGTGTCAACCCAATACTATTTGGCCATAGATGTAAAAACTACCA NM_001002030 RefSeq
chr6 - 127288711 127343609 ECHDC1 55862 "ethylmalonyl-CoA decarboxylase 1, transcript variant
1" GO:0008152|GO:0016831|GO:0004492|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141510_PI430048170 0.7166321264950021.01241327438016 0.437449169569914
0.4216830927081940.314851139480707 A A A 0.33947340439292 0.389551944218139
0.393987600296619 A A A LNCV6_141510_PI430048170 mRNA
GAAGAAAGGCAAATCTGACTTTTTCTGTGCGCCTTAAACAATTCTTGTAACTTTCTTCAA NM_002234 RefSeq chr12
+ 5043918 5046788 KCNA5 3741 "potassium channel, voltage gated shaker related subfamily A,
member 5"
GO:0005515|GO:0005251|GO:0030018|GO:0048471|GO:1900087|GO:0005886|GO:0005783|GO:0055075|GO:0043
267|GO:0007268|GO:0043266|GO:0086091|GO:0019229|GO:0071435|GO:0015271|GO:0060372|GO:0086089|GO:0
014704|GO:0008076|GO:0097110|GO:0042391|GO:0051260|GO:2000288|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140048_PI430048170 0.0934841623062443 0.82663559033412512.0816830958454
11.7977288635592 11.7562430096398 P P P 12.0887666555374 12.2788180708186
12.1065652849587 P P P LNCV6_140048_PI430048170 mRNA
GATTTCAATAAATCTGTCCACTCCCCTTTTGTGGGGGTGAACGTTTTAACAGCCAAAAAA NM_001810 RefSeq chr20
- 3783850 3786690 CENPB 1059 "centromere protein B, 80kDa"
GO:0043565|GO:0006355|GO:0005694|GO:0003696|GO:0003682|GO:0019237|GO:0005634|GO:0000775 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67818_PI430048170 0.6265029311840650.9699676371675020.5194476340164910.468149878650107
0.25733053104385 A A A 0.4003996646836780.5162685211895340.471033078987846 A A A
LNCV6_67818_PI430048170 mRNA
AAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTGTGTCCTTCTT NM_205854 RefSeq
chr6_GL000255v2_alt - 2186501 2187327 SFTA2 389376 surfactant associated 2 GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_64817_PI430048170 0.176466137891493 1.17516083012073 6.69883609475789 6.61520211660586
6.3240509008025 P P P 6.37956591967638 6.34148765995452 6.24116744897091 P P P
LNCV6_64817_PI430048170 mRNA
TCTTGTGGAAACGTCCTCTTCAATGGTTACCTGCCGCCACCAGTGTTCCCAGTGAAGCGG NM_138392 RefSeq chr19
+ 40576850 40591399 SHKBP1 92799 SH3KBP1 binding protein 1 GO:0051260 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_137127_PI430048170 0.250162182008334 0.931485380576461 10.6478243005264 10.825156229364
10.8494525383788 P P P 10.8978986361318 10.9352130649573 10.8015050741173 P P P
LNCV6_137127_PI430048170 mRNA
TCTCTTTTACCTGCTCCTGTAAATACTCCCTTCTCCCAATAAAACTTGGTGTGTGTTCTC NM_022574 RefSeq chr7 -
100679506 100689247 GIGYF1 64599 GRB10 interacting GYF protein 1 GO:0048009 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_130962_PI430048170 0.253401644179843 0.913563518902035 8.34181307707894
8.17994300124119 8.26295135768406 P P P 8.53353875543238 8.26025333369926 8.3735957969864
P P P LNCV6_130962_PI430048170 mRNA
CACCAACCACACAAGTTTGTTGTGAGTCATAAATGGATAATGAATATAAATGCGCATTGA NM_206914 RefSeq chr12
+ 57772599 57782541 METTL21B 25895 "methyltransferase like 21B, transcript variant 2"
GO:0005622|GO:0005737|GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127892_PI430048170 0.000392453817748095 1.78540134822574 8.09992731459599
8.22470411334057 8.27007538145905 P P P 7.45256949086472 7.37181395430836
7.26049007102827 P P P LNCV6_127892_PI430048170 mRNA
AAAGCAACATTTGTCATGTGGTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCT NM_001142292 RefSeq
chr2 - 96705929 96740076 LMAN2L 81562 "lectin, mannose-binding 2-like, transcript variant 1"
GO:0006888|GO:0030134|GO:0005794|GO:0000139|GO:0006457|GO:0005789|GO:0016021|GO:0015031|GO:0005
537|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132731_PI430048170 0.0933364765488892 1.06417585280981 0.586070385615025
0.506708225374559 0.584673131197431 A A A 0.408203160221805 0.489582838692788
0.509882615996178 A A A LNCV6_132731_PI430048170 mRNA
GAAAAGAAGGCTGCATTTAGACACGGTCAAGCAATCAGTTCATGCATTTCTAAGACTGCT NM_001042705 RefSeq
chr3 + 159069251 159266307 IQCJ NA "IQ motif containing J, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136097_PI430048170 0.796794045977818 0.991113431302402 0.262080489151616
0.278939703516317 0.408638682927907 A A A 0.366372203491545 0.31545756522614
0.310296082837379 A A A LNCV6_136097_PI430048170 mRNA
TTTCTTCAGCAGAACTCTTGTCATGTAGTGTACATTTGATTAAAACCCATAGCCATGTAA NM_025184 RefSeq chrX
- 44147881 44343677 EFHC2 80258 EF-hand domain (C-terminal) containing 2 GO:0005509 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129046_PI430048170 0.0453479818574624 0.674751538297803 7.62559451864932
7.34330358440773 7.58079458632967 P P P 8.18559279371918 7.77473984734712
8.26177368858063 P P P LNCV6_129046_PI430048170 mRNA
CAGTAAAGCAATTGTTGCAAGATGAATGGCTAATATTTTGGTGCAGTGTTTGATGTTCAA NM_014646 RefSeq chr18
- 2916993 3011947 LPIN2 9663 lipin 2
GO:0006629|GO:0006646|GO:0003713|GO:0005634|GO:0044281|GO:0008195|GO:0006351|GO:0005829|GO:0009
062|GO:0045944|GO:0016311|GO:0005789|GO:0019432|GO:0006644|GO:0044255|GO:0046474|GO:0006656 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128885_PI430048170 0.508727627310971 0.975703561735227 14.8570749777845
14.7684701228387 14.9035109591796 P P P 14.8726953183056 14.8318046021362
14.9324781422081 P P P LNCV6_128885_PI430048170 mRNA
TCTAGGTTTTGGATACCATGAGTATGTATGTTTACCTGTGCCTAATAAAGGAGAATTATG NM_021158 RefSeq chr20

+ 380628 397559 TRIB3 57761 "tribbles pseudokinase 3, transcript variant 1"
GO:0008286|GO:0005515|GO:0034976|GO:0005886|GO:0045599|GO:0005634|GO:0044281|GO:0005829|GO:0032
092|GO:0007173|GO:0043405|GO:0016301|GO:0055106|GO:0051443|GO:0031625|GO:0044255|GO:0048011|GO:0
032869|GO:0019901|GO:0048015|GO:0003714|GO:0045717|GO:0005524|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139023_PI430048170 0.2692290137276080.628195616798 0.665552859465394
0.3262517912813980.335244387664052A A A 0.4573333767525121.7491468511438
0.843540518940689A A A LNCV6_139023_PI430048170 mRNA
GTGTAGCTCTCCATCTAAGTTTTGGATAAACTGAAGTGGCACTGTGACTTTAAAAATAAA NM_203436RefSeq chr12
+ 107774384 107776644 ASCL4 NA achaete-scute family bHLH transcription factor 4 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127663_PI430048170 0.0153218279422471 0.4882727306032436.15816660467502
5.60948037333978 6.23292605782638 P P P 6.78660182861438 7.10077778502742
7.25390876770119 P P P LNCV6_127663_PI430048170 mRNA
GACCGTTCTATTGTGTGGATGACCACATAAGAAGGCAATTTTAGTGTATTAATCATAGAT NM_001281435 RefSeq
chr17 + 12020817 12143831 MAP2K4 6416 "mitogen-activated protein kinase kinase 4, transcript
variant 2"
GO:0005515|GO:0030424|GO:0034142|GO:0005634|GO:0032839|GO:0051403|GO:0005829|GO:0005622|GO:0002
756|GO:0043525|GO:0002755|GO:0061049|GO:0043204|GO:0072709|GO:0034138|GO:0038124|GO:0038123|GO:0
034134|GO:0045740|GO:0007254|GO:0006915|GO:0018108|GO:0031435|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135400_PI430048170 0.00649125307648986 0.56199160442281411.1814122540541
10.9878358834732 11.1344480332169 P P P 11.7210724797988 11.9662662446297
12.0930578912282 P P P LNCV6_135400_PI430048170 mRNA
CAGGATCTATTTTTGGAGGTTTATTACGTATGTCTGGTTCTCAATTCCAACAGTTTAATG NM_005911RefSeq chr2
+ 85538977 85545280 MAT2A 4144 "methionine adenosyltransferase II, alpha"
GO:0005515|GO:0006805|GO:0006556|GO:0044281|GO:0032259|GO:0006730|GO:0005524|GO:0004478|GO:0048
269|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143265_PI430048170 0.0563811430770590.3362313066914293.48817516095088
2.57671992555126 1.94617070130901 P A A 4.20567584190072 4.55091964195321
4.37058651632726 P P P LNCV6_143265_PI430048170 mRNA
GCCTGAAGTAGGTGTTCAGAGTAATACTTTGCGTTATACTGAGAGAGAATCTGAATTTTA NM_133474RefSeq chr4
- 439983 499171 ZNF721 170960 zinc finger protein 721
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140405_PI430048170 0.3548939739509561.50279153194187 0.377026733073033
1.60628342028205 0.467587726847727A A A 0.3327609722927590.323812043499046
0.377700711761008A A A LNCV6_140405_PI430048170 mRNA
TATGCAATCCCTTCAAAGCAGCCAGAGTTCCACATTGAAATCCTATCAATCTGAAAGGCC NM_001085479 RefSeq
chr3 + 51826882 51830858 IQCF3 401067 "IQ motif containing F3, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_144340_PI430048170 0.7338031987231751.01145911112686 0.316732125960763
0.3210982489108610.433188795361372A A A 0.3536756685030560.309542500896538
0.360998155148135A A A LNCV6_144340_PI430048170 mRNA
GCACAACTATAACCTATGGGAATGATGTAGTAACACAGATTATTCATCTTGTTAGAGTTG NM_005420RefSeq chr4
- 69841211 69860152 SULT1E1 6783 "sulfotransferase family 1E, estrogen-preferring, member 1"
GO:0050294|GO:0008210|GO:0047894|GO:0007565|GO:0006805|GO:0004304|GO:0050427|GO:0051923|GO:0044
281|GO:0005496|GO:0008202|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144442_PI430048170 0.12795690629022 1.08109233685581 0.487881955761778

0.6043648948937550.566793077158375A A A 0.3541751049345030.451332985561509
0.514023425335129A A A LNCV6_144442_PI430048170 mRNA
GGTCTTATGCACAGGAACTAAAGGAAAAAGAGATCGAGTCACAAAAATTCAGGAAGAGGG NM_022573RefSeq
chrY + 6246222 6249012 TSPY2 NA "testis specific protein, Y-linked 2" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_145528_PI430048170 0.00825077479540383 2.34915296168636 4.2038166375518
4.6584434380393 4.75910122558743 P P P 3.25816486571489 3.00541945111849
3.64663690936636 P P P LNCV6_145528_PI430048170 mRNA
TTCTACTTTGATTTTATTGTTAGTGCATTGTCGTTCTTGTGTCAGTAGCAAGTTTCAGTG NM_005275RefSeq
chr6_GL000251v2_alt - 2021095 2037314 GNL1 2794 guanine nucleotide binding protein-like 1
GO:0007165|GO:0005198|GO:0042254|GO:0008152|GO:0003924|GO:0005634|GO:0005525|GO:0005615|GO:0006
974|GO:0002456 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137128_PI430048170 0.4079697003116991.46341116920344 1.50296472871911 0.2791973903596
0.271053300363646A A A 0.2517258377890530.2751042770999460.250767180517186A A A
LNCV6_137128_PI430048170 mRNA
GGCCTATTTCCATTCAGCTACAAAGTGGGAACAATTAAAAGCATTGTTTGATTTGTATTG NM_019891RefSeq chr1
- 236215121 236282039 ERO1LB 56605 ERO1-like beta (S. cerevisiae)
GO:0005515|GO:0005783|GO:0015035|GO:0003756|GO:0042593|GO:0022417|GO:0019471|GO:0006457|GO:0030
198|GO:0005789|GO:0016491|GO:0016671|GO:0045454|GO:0030070|GO:0051082|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144602_PI430048170 0.0101469572779896 1.27075621950631 15.9384289628982
15.7903407747963 15.8333333318826 P P P 15.4305708112217 15.4722053857075
15.6194197932382 P P P LNCV6_144602_PI430048170 mRNA
ACTGGAATCCTTTCAGCAAGACTTCTCTTTGCCTCAAATAAAAAGTGCTTTTGTGAGAAA NM_001628RefSeq chr7
- 134442354 134459136 AKR1B1 231 "aldo-keto reductase family 1, member B1 (aldose reductase)"
GO:0044598|GO:0044597|GO:0005975|GO:0043795|GO:0006950|GO:0009055|GO:0044281|GO:0005615|GO:0005
829|GO:0004032|GO:0004033|GO:0005737|GO:0006700|GO:0005654|GO:0008202|GO:0070062|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75045_PI430048170 0.00543265512656581 1.64960822361241 9.95015333456082
9.78048522453064 9.87203767108798 P P P 9.30911887589098 8.99731103969228 9.1176046203511
P P P LNCV6_75045_PI430048170 mRNA
CAGGATCAGGACACGTATCTGTCCCATTTCCAGATACATATGAAATAACGAAGAGTTATT NM_021928RefSeq chr4
+ 176319938 176332245 SPCS3 60559 signal peptidase complex subunit 3 homolog (S. cerevisiae)
GO:0010467|GO:0005787|GO:0050796|GO:0005783|GO:0006614|GO:0006508|GO:0005789|GO:0008233|GO:0016
021|GO:0044267|GO:0006412|GO:0006465 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139276_PI430048170 0.4685244563852530.9413585821648348.64664720713602
8.57803171332686 8.69210283981207 P P P 8.71291883065769 8.56795651893166 8.8825232782872
P P P LNCV6_139276_PI430048170 mRNA
GGAAGGTAAAAATAGTGGTGTGATCATGAACCAAAGGAATTTATGTTTTGTAACTTGGGT NM_021222RefSeq chr1
+ 151008390 151035713 PRUNE 58497 "prune exopolyphosphatase, transcript variant 1"
GO:0005515|GO:0005737|GO:0008152|GO:0004427|GO:0005634|GO:0005925|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136077_PI430048170 0.5878963474650487.06472765584448 0.616055103977007
0.5728764133464285.62189724019401 A A P 1.97373481610686 0.849683072508896
0.738174066331324A A A LNCV6_136077_PI430048170 mRNA
CATGATCCAGGAGCACATACCACAAACTACCACAATAAAAAAGCTGTTTTTGCTAAAAAA NM_020349RefSeq chr10
+ 97572440 97583886 ANKRD2 26287 "ankyrin repeat domain 2 (stretch responsive muscle), transcript variant 1"
GO:0000791|GO:0043619|GO:0005634|GO:0000122|GO:0043422|GO:0035914|GO:0030017|GO:0045662|GO:0005

829|GO:0031432|GO:0043231|GO:0006936|GO:0007517|GO:0016605|GO:0008307|GO:0031674 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54954_PI430048170 0.791092466001704 1.00962136304754 0.461816126881307 0.525617899008537 0.438911321074501 A A A 0.548699491842991 0.412116693897565 0.421415241772964 A A A
LNCV6_54954_PI430048170 mRNA
AGTTACGTGTTCCTAGCAGGACCAACTACAGTCTTCCCAAGGATTGAGTTATGGACTTTG NM_000567 RefSeq chr1 - 159712288 159714589 CRP 1401 "C-reactive protein, pentraxin-related"
GO:0005515|GO:0033265|GO:0051258|GO:0050830|GO:0045471|GO:0030175|GO:0005615|GO:0042803|GO:0030426|GO:0006954|GO:0015485|GO:0006958|GO:0045908|GO:0071277|GO:0008228|GO:0032930|GO:1900006|GO:0070062|GO:0010288|GO:0001666|GO:2000482|GO:0010745|GO:0007568|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139798_PI430048170 0.570269804548233 1.1954588706372 0.46654464068107 1.38408628827746 0.535698318509081 A A A 0.347342539572259 0.423983986727145 0.954546982275585 A A A LNCV6_139798_PI430048170 mRNA
AATCAAGTGGAGACAGAGTCGGTGGGAGACGTGACTTATCCAGCCCACAGGGACTGCTAC NM_021246 RefSeq chr6_GL000256v2_alt + 3014651 3017100 LY6G6D NA "lymphocyte antigen 6 complex, locus G6D"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140093_PI430048170 0.296281987446734 1.06913166568787 11.0394043772539 10.8513387361905 10.8618845630249 P P P 10.7243633513725 10.8936759357187 10.8478427040201 P P P LNCV6_140093_PI430048170 mRNA
CTCTTATTTCTCAGGGAGATCACAGCAACCTAAATAAACCAGATACCTTTTCTCAAAAAA NM_001384 RefSeq chr1 + 43969980 43973371 DPH2 1802 "DPH2 homolog (S. cerevisiae), transcript variant 1"
GO:0044267|GO:0017183|GO:0043687|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137264_PI430048170 0.419960970287503 1.05808850713268 8.14275599642718 8.09713758050142 8.10131600242338 P P P 7.93876890324624 8.19876980568579 7.94414062796624 P P P LNCV6_137264_PI430048170 mRNA
ATTCACAAAAGAAAAATACATTTTTTCCCCCAGGGGTGGGGCAAGGACAGTGGAGAGAGTNM_001303501 RefSeq chr19 + 1026274 1039068 CNN2 1265 "calponin 2, transcript variant 4"
GO:0030097|GO:0005516|GO:0001725|GO:0030336|GO:0031032|GO:0003779|GO:0010628|GO:0050765|GO:0032970|GO:0016020|GO:0005911|GO:0042127|GO:0042060|GO:0007010|GO:0071260|GO:0005856|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127331_PI430048170 0.148484468825088 1.07483597201781 0.481801368709541 0.519095155157271 0.55332642223221 A A A 0.327515897440801 0.415432202711506 0.494955719848492 A A A LNCV6_127331_PI430048170 mRNA
CCAGACCAACCCTGAGATTTTGTCAACCTGATTAAGTCAATATGAATGATTAAAAAGATG NM_024642 RefSeq chr9 + 98807698 98850081 GALNT12 79695 polypeptide N-acetylgalactosaminyltransferase 12
GO:0004653|GO:0006493|GO:0000139|GO:0030246|GO:0016266|GO:0016021|GO:0044267|GO:0046872|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63680_PI430048170 0.0869605768651039 0.650844486470309 5.05513374708724 5.36143074378051 5.48163213660012 P P P 5.4771013433069 6.0697954178589 6.1535045744094 P P P LNCV6_63680_PI430048170 mRNA
TTTAAAGACCTTGGGTATCCTTTTGCACTATCCAAAAGCTCCATGTACACAGTGGGGGCT NM_006101 RefSeq chr18 + 2571510 2616635 NDC80 10403 NDC80 kinetochore complex component
GO:0005515|GO:0000132|GO:0005634|GO:0005829|GO:0051315|GO:0007067|GO:0000070|GO:0007059|GO:0016020|GO:0000942|GO:0000777|GO:0005200|GO:0000776|GO:0008608|GO:0000278|GO:0007052|GO:0031262|GO:0000775|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106225_PI430048170 0.239422666172996 0.826700519947313 8.1301421951038 8.48531820499753 8.27396021399001 P P P 8.30728415738586 8.53236423788994 8.84485538690535 P P P LNCV6_106225_PI430048170 mRNA

GGAAGCATGGACGAGAACATGGAGCAAATGTTTTACAACCTGAACCTCAGAACTGTGATC NM_004225 RefSeq chr8 - 8784488 8893621 MFHAS1 9258 malignant fibrous histiocytoma amplified sequence 1 GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54771_PI430048170 0.0380275112116795 0.704347223508257 4.4974617443959 4.64271447016999 4.86400657057675 P P P 5.15413976481634 5.20819292650267 5.1820540921866 P P P LNCV6_54771_PI430048170 mRNA
CATCAAAAAAGGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGA NM_001135638 RefSeq chr1 + 151198544 151249531 PIP5K1A 8394 "phosphatidylinositol-4-phosphate 5-kinase, type I, alpha, transcript variant 1"
GO:0006909|GO:0005515|GO:0005886|GO:0072661|GO:0005634|GO:0044281|GO:0005829|GO:0010761|GO:0005737|GO:0048041|GO:0097178|GO:0006650|GO:0019900|GO:0006661|GO:0031532|GO:0032587|GO:0008654|GO:0032863|GO:0005524|GO:0030027|GO:0016308|GO:0046854|GO:0007165|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141781_PI430048170 0.226585005603387 1.54963746551855 2.30514794549093 3.13454452395715 3.40244320973713 A P P 1.88623328538415 2.80805724051728 2.31607862740875 A P A LNCV6_141781_PI430048170 mRNA
TTTGGCGAGGGTGTGGAGCCCGCCAACCTCAAGGCCTCCGTGGTTTTTAACCAGCTCTGA NM_006189 RefSeq chr11 + 77102839 77103331 OMP 4975 olfactory marker protein
GO:0030424|GO:0007608|GO:0007165|GO:0005737|GO:0043025|GO:0007268|GO:0005634|GO:0004871|GO:0022008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129832_PI430048170 0.200418272211595 0.587483607008146 1.94677439606528 0.258663317640914 0.650775586043227 A A A 1.60551756470622 2.2036828096899 1.85653273125389 A A A LNCV6_129832_PI430048170 mRNA
GGGCCATATTTATTAAAAGAGTTCTGTGTGGTCACATAGAGTTCCTTTGGGATTTCATCC NM_001297617 RefSeq chr5 - 60751788 60844274 ELOVL7 79993 "ELOVL fatty acid elongase 7, transcript variant 3"
GO:0005515|GO:0005783|GO:0019367|GO:0019432|GO:0005789|GO:0044281|GO:0035338|GO:0034626|GO:0016021|GO:0042761|GO:0044255|GO:0016740 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130465_PI430048170 0.161576624848802 0.346616749717112 3.64612670456513 0.31919340574038 2.20996500272496 P A A 3.81487782100544 4.31161355123237 4.25824993324083 P P P LNCV6_130465_PI430048170 mRNA
CTCCTTGACATTTCGTTCAAGTTATAGATTCAATGGAGCTATGTCTTGTTTTAAGTTGCT NM_181523 RefSeq chr5 + 68215755 68301821 PIK3R1 5295 "phosphoinositide-3-kinase, regulatory subunit 1 (alpha), transcript variant 1"
GO:0005515|GO:0034976|GO:0005159|GO:0005158|GO:0043560|GO:0050900|GO:0042993|GO:0033120|GO:0034644|GO:0007173|GO:0043551|GO:0046326|GO:0043559|GO:0043125|GO:0032869|GO:0030335|GO:0032760|GO:0005168|GO:0019903|GO:0030168|GO:0014065|GO:0008543|GO:0045087|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136342_PI430048170 0.559383396489961 0.908375614980125 0.425353667977398 0.469993783752994 0.471348415760119 A A A 0.912450977689066 0.380975970947294 0.427554327790645 A A A LNCV6_136342_PI430048170 mRNA
CTCGCAAGGATGTTGTCACGGTAGGAAATATTTATAACTTGTTTTGAAATCAAAAGAACC NM_152666 RefSeq chr1 - 242088386 242524696 PLD5 200150 "phospholipase D family, member 5, transcript variant 1"
GO:0008152|GO:0016021|GO:0003824 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143168_PI430048170 0.779388646553379 0.993454454966137 0.332547832146401 0.309499273069632 0.282043427058309 A A A 0.368577466838483 0.300020081149682 0.282927322906439 A A A LNCV6_143168_PI430048170 mRNA
TGAATATTGATAGTCCACATCACAAGCTGCATCTGTTTGAGAACCCAGCTTTCAGTGGCC NM_004076 RefSeq

chr22 + 25199849 25207359 CRYBB3 1417 "crystallin, beta B3" GO:0005212|GO:0007601 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_112209_PI430048170 0.990698185951377 0.997997776407685 2.76491545684255
3.19455353006104 2.57181003167129 A P A 2.8273071157295 2.48451918958964
3.20907322389515 P P P LNCV6_112209_PI430048170 mRNA
TCAGAAGGAATTGTATTTCATTCTCTGCAAATCAGTTTGTGTTTCAGGAGCTGGCTGCCA NM_001282628 RefSeq
chrX - 2934631 2964453 ARSE 415 "arylsulfatase E (chondrodysplasia punctata 1), transcript variant 1"
GO:0006665|GO:0001501|GO:0006687|GO:0005795|GO:0005788|GO:0004065|GO:0044281|GO:0044267|GO:0046
872|GO:0070062|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138705_PI430048170 0.876847431779762 0.99419297509604 0.46208277827944
0.493852759942706 0.395946065510567 A A A 0.534883511802329 0.41500566946838
0.425848840706401 A A A LNCV6_138705_PI430048170 mRNA
CATTTTGTTTTGAAAACATCTTCTGGACTTACACCAGAGCTTAGTGTCGTCTTTACTATG NM_002702 RefSeq
chr12 - 51186935 51198167 POU6F1 5463 "POU class 6 homeobox 1, transcript variant 1"
GO:0007507|GO:0006355|GO:0007517|GO:0003700|GO:0007420|GO:0005654|GO:0005634|GO:0015629|GO:0003
677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132422_PI430048170 0.173362738758316 0.688895169596496 2.69448145626186
1.76671048792088 2.2767005739652 A A A 2.99964054382132 2.41366010513658
3.00786229467952 P A P LNCV6_132422_PI430048170 mRNA
CAGGGGGTACATGAGTTTCTGAATTTTTAAAAAATGTTTTTGGTTTGGTTTTTCTGGGGA NM_001031695 RefSeq
chr22_KI270876v1_alt - 59733 161581 RBFOX2 23543 "RNA binding protein, fox-1 homolog (C. elegans)
2, transcript variant 1"
GO:0005515|GO:0006397|GO:0008380|GO:0016070|GO:0003714|GO:0003723|GO:0005634|GO:0021942|GO:0003
729|GO:0010724|GO:0048813|GO:0005737|GO:0000166|GO:0000381|GO:0042127|GO:0050885|GO:0005654|GO:0
045892|GO:0030520|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88252_PI430048170 0.15263288021887 1.59152568651979 2.42138036543022
2.57026978964587 2.64542452754652 A A A 2.43968297159452 1.65595137662207
1.2941956824093 P A A LNCV6_88252_PI430048170 mRNA
GAGTCAAGAGAAATTTATAGGAGGCCTTCGGGAGAATTAGAGCAAAGACTCTCAGGAGAA NM_031421 RefSeq
chr17 + 41930622 41965650 TTC25 83538 "tetratricopeptide repeat domain 25, transcript variant 1"
GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75842_PI430048170 0.082896358997645 1.31434025485688 2.5136683554279
2.44418710452379 2.64315259860457 A A A 2.22144013448755 2.30783135489636
1.85738123998961 A A A LNCV6_75842_PI430048170 mRNA
TTCTTCTTTACCCAGTGAACCTATATTTGAAAAAAGTGAAACAGAAATTCCCACTTGTGG NM_014819 RefSeq
chr5 - 109334708 109409974 PJA2 9867 "praja ring finger 2, E3 ubiquitin protein ligase"
GO:0034236|GO:0034237|GO:0004842|GO:0016567|GO:0030054|GO:0005886|GO:0007616|GO:0016874|GO:0014
069|GO:0010738|GO:0005737|GO:0000139|GO:0045211|GO:0005789|GO:0008270 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_135031_PI430048170 0.755661725405456 1.02400562393926 8.7954965621265
8.9093740001027 8.74786507454234 P P P 8.61422751569046 8.984304234988
8.73120564771238 P P P LNCV6_135031_PI430048170 mRNA
TCTGATCTGTGTGTGGGTTGACATTTTAGCTAATAAAGCCTTGCAGTGTTTGTTGGCAAA NM_001278791 RefSeq
chr7 - 74231501 74254458 RFC2 5982 "replication factor C (activator 1) 2, 40kDa, transcript variant
3"
GO:0005515|GO:0005794|GO:0003689|GO:0005634|GO:0005524|GO:0006260|GO:0006261|GO:0006271|GO:0006
281|GO:0000723|GO:0006283|GO:0000722|GO:0006297|GO:0005654|GO:0005663|GO:0006289|GO:0000278|GO:0
032201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103143_PI430048170 0.163261838221428 0.672409021669229 4.35836625238732

5.12037613439267 5.35076065632151 P P P 5.58541387342703 5.34170934648111 5.76439596468087 P P P LNCV6_103143_PI430048170 mRNA TGAAATCTATGACATTCTTCAGTCCTCCAATATGGCAGATGGTGATAGTTTTAATGAGAT NM_018120 RefSeq chr8 - 65602455 65634217 ARMC1 55156 "armadillo repeat containing 1, transcript variant 1" GO:0005739|GO:0046872|GO:0030001 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61213_PI430048170 0.011504092176171 0.523981300331745 6.53473223516581 6.57085874248815 6.99954978260644 P P P 7.3891049974346 7.61050247914094 7.90403564469197 P P P LNCV6_61213_PI430048170 mRNA TGGATTAATGCAAAAGGGGTAATAAAGACTGCAACATTCTCAGGACCAAATTAAACTGCT NM_024824 RefSeq chr14 + 88562908 88613509 ZC3H14 79882 "zinc finger CCCH-type containing 14, transcript variant 1" GO:0005515|GO:0005737|GO:0016607|GO:0005730|GO:0005654|GO:0005634|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90975_PI430048170 0.436929304533761 0.575009582857493 1.689187543067 0.89424813790893 0.29472597663925 A A A 0.336696710775189 2.3000319359748 2.25889796552318 A A A LNCV6_90975_PI430048170 mRNA ACACCTTAGCTGGATACAAAACATATTATGAAACAGAATGACTGTGATCTTTGATCCGAG NM_012340 RefSeq chr20 - 51386956 51542719 NFATC2 4773 "nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2, transcript variant 1" GO:0050853|GO:0005515|GO:0003700|GO:0005886|GO:0030890|GO:0005634|GO:0001816|GO:0015629|GO:0005829|GO:0005737|GO:0045944|GO:0006355|GO:0042493|GO:0000122|GO:0000978|GO:0003677|GO:0006351|GO:0006974|GO:0001078|GO:0001077|GO:0016477|GO:0030529|GO:0045087|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145087_PI430048170 0.0225822167450837 1.32654018224369 7.15945595568617 7.15564602902162 7.32537756929819 P P P 6.92932177731666 6.63568520970299 6.8434791432154 P P P LNCV6_145087_PI430048170 mRNA TTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAGAAGTCTTGCGCA NM_001472 RefSeq chrX + 49589528 49596837 GAGE2C NA - NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134643_PI430048170 0.856951574360481 1.01342085256554 11.3701472939211 11.1462817416004 11.370772033717 P P P 11.3122093702477 11.2091027018183 11.31703700437 P P P LNCV6_134643_PI430048170 mRNA AATAATGTAGTCCCCAAATACCTGAAAGCTGTCTTTAAAAATGCAGGTAAGCATGTGACT NM_032382 RefSeq chr16 - 69328620 69339623 COG8 84342 component of oligomeric golgi complex 8 GO:0016020|GO:0000139|GO:0017119|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142368_PI430048170 0.6229380945166 0.826063401483035 1.2871355678803 1.27744613977765 0.552662335465743 A A A 0.562556841498262 1.53838883737918 1.71495256722806 A A A LNCV6_142368_PI430048170 mRNA GCTACGGTTTTAATCATCCAGGGTGCCATTCCACCATAGAAGAGCAATCCTTTTAGGAAA NM_005314 RefSeq chrX + 16123300 16153518 GRPR 2925 gastrin-releasing peptide receptor GO:0004946|GO:0031989|GO:0007186|GO:0005886|GO:0008283|GO:0005887|GO:0042127|GO:0008528 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138945_PI430048170 0.0239046174459843 1.15831076027958 11.3826746370862 11.3971743976931 11.2716071734842 P P P 11.1419457558313 11.1147973259233 11.161506787979 P P P LNCV6_138945_PI430048170 mRNA CAGTGGAAAACGTGTCTCTTTAAAGCTGCTATGTGAACAGCTTTTACAGTCATTAAATTT NM_016408 RefSeq chr20 - 33358838 33401569 CDK5RAP1 51654 "CDK5 regulatory subunit associated protein 1, transcript variant 1"

GO:0005737|GO:0051539|GO:0019901|GO:0007420|GO:0045736|GO:0045664|GO:0005575|GO:0032403|GO:0046872|GO:0016740|GO:0006400 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132214_PI430048170 0.165808452433974 0.673030033310526 1.7262558403767 2.16447973186792 2.11721295572464 A A A 2.41079800328779 3.039686262417 2.1643280971681 A P A LNCV6_132214_PI430048170 mRNA
ACGCTGGCTGCTGTCATGCCATCTGGGTATGCATTAAACATTAATGATGATCAGCACTGA NM_002841 RefSeq chr3 + 61561568 62294898 PTPRG 5793 "protein tyrosine phosphatase, receptor type, G"
GO:0005515|GO:0007420|GO:0005887|GO:0005001|GO:0010977|GO:0007169|GO:0005615|GO:0035335|GO:0004725|GO:0070062|GO:0042802|GO:0010633 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134952_PI430048170 0.63896691253556 1.02306975034841 0.276194675531889 0.302308940592357 0.454918637252123 A A A 0.338531477847673 0.300639292165344 0.30174804118407 A A A LNCV6_134952_PI430048170 mRNA
TGTAAACAAAAATGAGAGCTTGAGTCAGAGGAAGCCGAGACAATATCCTTCCTCGACAAC NM_178129 RefSeq chrY - 1462572 1537144 P2RY8 286530 "purinergic receptor P2Y, G-protein coupled, 8"
GO:0005886|GO:0045028|GO:0035589|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136404_PI430048170 0.028257442932841 0.473538014490563 8.01959378608979 7.94967168686619 8.09815572470069 P P P 8.73552330552983 9.07705914260007 9.41452038218624 P P P LNCV6_136404_PI430048170 mRNA
GGAACGTGTTAGAAACTGTTTTGTGCTTTTATGGATGTCATACTTGACAATACATGTGTA NM_003909 RefSeq chr8 + 86514426 86561498 CPNE3 8895 copine III
GO:0006629|GO:0005544|GO:0005215|GO:0005737|GO:0004674|GO:0006468|GO:0016192|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135011_PI430048170 0.00843417342279383 0.436722771316633 7.11346123850961 6.50441215580648 6.86164561201871 P P P 7.68037288662344 8.23844574249217 8.15030622481097 P P P LNCV6_135011_PI430048170 mRNA
CTCTCCGGGGTGGTTAATAAAATGCAACACTTGGCATTTTTATGTTTTAAGAAAAACAGT NM_002293 RefSeq chr1 + 183023459 183145592 LAMC1 3915 "laminin, gamma 1 (formerly LAMB2)"
GO:0050679|GO:0005606|GO:0005576|GO:0043260|GO:0005615|GO:0005604|GO:0031012|GO:0043259|GO:0006461|GO:0007492|GO:0016477|GO:0022617|GO:0043208|GO:0007411|GO:0030198|GO:0031581|GO:0034446|GO:0007155|GO:0070062|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70266_PI430048170 0.94980520274886 1.01308638659369 5.39567424965534 5.2611420701397 5.7079515508246 P P P 5.30305136366607 5.4671923530495 5.56337852530987 P P P LNCV6_70266_PI430048170 mRNA
CTCCTGCTGAAACTCCTGTGAAAGAAAGACTTTTTATTGTGTTTAATCCTCATCCTTTAC NM_152945 RefSeq chr2 + 178112423 178129655 RBM45 129831 RNA binding motif protein 45
GO:0005737|GO:0000166|GO:0003723|GO:0005654|GO:0005634|GO:0030154|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144136_PI430048170 0.501732012450527 1.48729055103567 1.82485445975904 0.479361129203313 0.265197687303218 A A A 0.403861586824178 0.51331690425874 0.461554926570488 A A A LNCV6_144136_PI430048170 mRNA
CAACATGGTCCTAGCACTGCACACTCAGTTCTGCTCTAAGAAGCTGCAATAAAGTTTTTT NM_012387 RefSeq chr1 + 17308194 17364000 PADI4 23569 "peptidyl arginine deiminase, type IV"
GO:0005515|GO:0006355|GO:0005509|GO:0006334|GO:0016990|GO:0005634|GO:0004668|GO:0006351|GO:0018101|GO:0005737|GO:0045087|GO:0019827|GO:0006338|GO:0006464|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64996_PI430048170 0.730637611581106 0.862139271706836 1.78679135647695 0.339609604927559 0.906880849369099 A A A 0.4649701907834 1.92270435225754 1.30635761896037 A A A

LNCV6_64996_PI430048170 mRNA
CAGAAGAGAATCAAATAGTTTCCTCTTATGCTTCTAAAGTCTGTTTTGAGATCGAAGAAG NM_001184902 RefSeq
chr19 - 48208085 48255946 CARD8 22900 "caspase recruitment domain family, member 8, transcript
variant 4"
GO:0072559|GO:0043280|GO:0005515|GO:0005737|GO:0050718|GO:0006919|GO:0032089|GO:0005654|GO:0005
634|GO:0008656|GO:0042803|GO:0043124 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129429_PI430048170 0.00538564207040631 0.4444544669839966.00998529496366
5.69930037161044 6.11831545787223 P P P 6.99386994929092 6.90205693273346
7.41911439133224 P P P LNCV6_129429_PI430048170 mRNA
GGCTGGTTGTGACTCAGATCAGCTTAACTTTTTATATTATGTTATTTCACTAACTGCTAC NM_145254 RefSeq chr16 -
75443243 75464737 TMEM170A 124491 "transmembrane protein 170A, transcript variant 1" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143006_PI430048170 0.0411148537660352 0.6529976181909434.29007403395575
4.39575643831838 4.60261533782477 P P P 4.89411976653046 4.85632384642741
5.34692203268941 P P P LNCV6_143006_PI430048170 mRNA
TTTGTTTGTTTTGCTTTTTGTAGACTGCCATGTGCAAGTAAAATTCCTGCTTCTGCCATG NM_173464 RefSeq chr18 -
5954705 6414911 L3MBTL4 91133 l(3)mbt-like 4 (Drosophila)
GO:0006355|GO:0003700|GO:0008270|GO:0005634|GO:0006351|GO:0016568 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143476_PI430048170 0.5381417983161491.32810966859701 0.574882282153089
1.77840078272914 1.8844534163353 A A A 0.7770122840465311.19842563185524
1.30803607788538 A A A LNCV6_143476_PI430048170 mRNA
GATCCCCATTGGATATAAGGATGACTGGTAAAATCTCATTGCTACTTTAATCTATGTTTC NM_145046 RefSeq chr19
- 16479056 16496192 CALR3 125972 calreticulin 3
GO:0044183|GO:0006457|GO:0005509|GO:0030246|GO:0005788|GO:0051082|GO:0007283|GO:0030154 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144913_PI430048170 0.3489357016093910.6352934774024535.57863399458798
5.37640372621748 5.62511591358446 P P P 5.20466595146572 6.30573315210968
6.67686699594208 P P P LNCV6_144913_PI430048170 mRNA
CGGTTGTAAACAGTACACATGTCATTTTGTGATATAGGACTCCCAAATAAAAGTATCAGA NM_021738 RefSeq chr10
- 29457347 29634972 SVIL 6840 "supervillin, transcript variant 2"
GO:0005515|GO:0005886|GO:0032467|GO:0002102|GO:0030496|GO:0005634|GO:0015629|GO:0032154|GO:0005
737|GO:0051015|GO:0007519|GO:0071437|GO:0007010|GO:0043034|GO:0005925 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128210_PI430048170 0.6351871446257110.9107251373174481 1.0439180379768
11.2551922706065 11.5089236158576 P P P 11.1223329943347 11.286902319355 11.762494160911
P P P LNCV6_128210_PI430048170 mRNA
CTGACTTCACCATGTTTATTCCCTTTGCCTACAACCAGTTAATATCTGAGTAACTTATCT NM_020188 RefSeq chr16 -
80975801 81006897 CMC2 56942 C-x(9)-C motif containing 2 GO:0005739 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_138513_PI430048170 0.1545281234837441.19447251485341 6.35168385888504
6.41594842008165 6.0430290339723 P P P 6.03938949810591 6.1425572100569
5.87381221425572 P P P LNCV6_138513_PI430048170 mRNA
CCCCATTGTATTTATTTGCCTGCTGGAAAATCACATCCGGAAATAAAATAGAAATATGTC NM_001163257 RefSeq
chrX + 153764195 153779346 PLXNB3 5365 "plexin B3, transcript variant 2"
GO:0005515|GO:0030336|GO:0005886|GO:0019904|GO:0050918|GO:0005622|GO:0051022|GO:0007162|GO:0010
593|GO:0001938|GO:0017154|GO:0060326|GO:0007411|GO:0071526|GO:0016021|GO:0034260 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129854_PI430048170 0.00023720503443718 5.66070774128838 6.67268003059898

6.56905114487436 6.21158084366775 P P P 4.19136800954618 3.8924431627719
3.88429688042899 P P P LNCV6_129854_PI430048170 mRNA
CTCCTAAATCAAGCATCTTTCTGTTACTGATGTTCAATAAAAGAATAGTTGCCAAGGCTG NM_001111035 RefSeq
chr19 - 11574659 11578986 ACP5 54 "acid phosphatase 5, tartrate resistant, transcript variant 1"
GO:0050830|GO:0045453|GO:0003993|GO:0032691|GO:0032929|GO:0032720|GO:0006767|GO:0044281|GO:0005
764|GO:0008198|GO:0005829|GO:0008199|GO:0006771|GO:0045019|GO:0006766|GO:0032695|GO:0060349|GO:0
050728|GO:0016311|GO:0032496|GO:0016021|GO:0034097|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140140_PI430048170 0.0086274492600815 1.28403771462137 4.98030610169735
4.81735481622725 4.80545231620475 P P P 4.5876819209439 4.47361516744158
4.46311398464628 P P P LNCV6_140140_PI430048170 mRNA
TAATCTTTTGCAGGCCCGCTTCTCAATGAATGAGATACACCAGGATATGCACGTGCATCT NM_031908RefSeq chr5
- 160347767 160370641 C1QTNF2 114898 C1q and tumor necrosis factor related protein 2
GO:0070208|GO:0000187|GO:0005581|GO:0045725|GO:0046326|GO:0046321|GO:0005102|GO:0051260|GO:0005
615|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67815_PI430048170 0.000209634122178272 0.27191607005333 5.38920660927129
5.33679258600753 5.62463132587762 P P P 7.37934847308052 7.12178577265871
7.47921223417122 P P P LNCV6_67815_PI430048170 mRNA
ACATGGGGCTGAGTTTAAATGAAGAAGAAATACGTGCAAATGTGGCCGTGGTTTCTGGTG NM_005625RefSeq chr8
+ 58553168 58582860 SDCBP 6386 "syndecan binding protein (syntenin), transcript variant 1"
GO:0005515|GO:0005137|GO:0030036|GO:0005886|GO:0046330|GO:0007268|GO:0072562|GO:0005634|GO:0007
265|GO:0005615|GO:0042803|GO:0042802|GO:0005829|GO:0035556|GO:0005109|GO:0006930|GO:0005737|GO:0
001948|GO:0005912|GO:0019838|GO:0007411|GO:0006612|GO:0005856|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134994_PI430048170 0.0497096942034326 1.50353308585341 3.89018870964533
4.00073108078121 4.01093331830589 P P P 3.07646631570695 3.43100057689511
3.58621431695067 P P P LNCV6_134994_PI430048170 mRNA
CACTTCCCAGCCCAGCTGTGTTTTATGTAACCGAAAATAAAGATGCGTGGTGACAAAGAA NM_006896RefSeq chr7
- 27153718 27156677 HOXA7 3204 homeobox A7
GO:0048704|GO:0005634|GO:0000122|GO:0001525|GO:0000978|GO:0009952|GO:0006351|GO:0048863|GO:0043
565|GO:0045617|GO:0001077|GO:0045656|GO:0045944|GO:0002686|GO:0045892|GO:0001953|GO:0008134 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139845_PI430048170 0.3714788046508860.8813845300847311.3990695083021
11.2115869920297 11.2247162102749 P P P 11.1689276902494 11.6659947810437
11.5108024019611 P P P LNCV6_139845_PI430048170 mRNA
ACCTTGTGTCTTGTAGGGTATGGTATGTGGGACTTCGCTGTTTTTATCTCCAATAAAAAA NM_017899RefSeq chr12
- 117038922 117099446 TESC 54997 "tescalcin, transcript variant 1"
GO:0005515|GO:0033628|GO:0008285|GO:0032417|GO:0005886|GO:0071300|GO:0072661|GO:0005634|GO:0042
803|GO:0051604|GO:0005737|GO:0045654|GO:0030854|GO:0000287|GO:0005509|GO:0050821|GO:0032587|GO:0
019212|GO:0001726|GO:0030027|GO:0010628|GO:0030219|GO:0004860|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142536_PI430048170 0.14776228545789 0.7992261810433028.8206578661852
8.68943027160557 8.66895315915325 P P P 8.75825009147406 9.21108011033926 9.1443319852367
P P P LNCV6_142536_PI430048170 mRNA
GCTATCCCAAACTCTCAGCCTCTGTGAATAAAGTTGTTTTTTCATTAACCTCTCAAAAAA NM_005250RefSeq chr16
+ 86578508 86581698 FOXL1 2300 forkhead box L1
GO:0003700|GO:0006357|GO:0006366|GO:0030111|GO:0008301|GO:0000981|GO:0005634|GO:0007275|GO:0003
677|GO:0030166|GO:0043565|GO:0007507|GO:0061146|GO:0007495|GO:0009887 . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_127228_PI430048170 0.2936705863221050.8175720910890260.25655208221363
0.3755434638126520.288611127388439A A A 0.4670382284606290.940426506191052
0.31107921551323 A A A LNCV6_127228_PI430048170 mRNA
CTGCCAGATCACCAATCTAGATCTTTGTGCCAAACAAAATGAGATCTCATTAAAAGGTTA NM_017541RefSeq chr3
- 186538442 186544378 CRYGS 1427 "crystallin, gamma S" GO:0005212|GO:0002088|GO:0002009 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137094_PI430048170 0.0124296476271078 0.57269773479449 7.42909494341262
7.33529432071326 7.31469984844255 P P P 8.00128967740542 8.09699014064962
8.37005396386934 P P P LNCV6_137094_PI430048170 mRNA
AACAACAGATGAAAGCCAGTGAGCCTACTAACCGTGCCATCTTGCAAACTACACTTTAAA NM_025164RefSeq chr11
- 116843401 117098415 SIK3 23387 "SIK family kinase 3, transcript variant 1"
GO:0032880|GO:0005515|GO:0005737|GO:0001958|GO:0000287|GO:0035264|GO:0004674|GO:0060351|GO:0006
468|GO:0035108|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134016_PI430048170 0.00107223972099842 0.2750895958128168.88848319540611
8.93231048546394 9.03576474522663 P P P 10.8841992709453 10.5946121499903
10.9441628638149 P P P LNCV6_134016_PI430048170 mRNA
CCACTGGTTCTTATCTGCTAGCCTTTTACATACATGTGTACTATATTTGTTTATAGACTG NM_015141RefSeq chr3 +
32106510 32168715 GPD1L 23171 glycerol-3-phosphate dehydrogenase 1-like
GO:0005886|GO:0019674|GO:0044281|GO:0042803|GO:0005829|GO:0046168|GO:0060373|GO:0090038|GO:0051
287|GO:0010765|GO:0033137|GO:2000010|GO:0019432|GO:0006654|GO:0044255|GO:0070062|GO:0086005|GO:0
009331|GO:0005975|GO:0004367|GO:2000649|GO:0006734|GO:0044325|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145472_PI430048170 0.4986683643610991.20120551860093 0.380376303273288
1.10185107132702 0.263613892169946A A A 0.3437893256019120.407418470906387
0.349857906673439A A A LNCV6_145472_PI430048170 mRNA
CATCTTCTGCTCTTCTGTACATTTCTAGATGCAAATAACTCCTTCACCAGGCAGTGAGTG NM_153837RefSeq chr16
+ 57542688 57577188 ADGRG5 NA "adhesion G protein-coupled receptor G5, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141855_PI430048170 0.0546602922093241 0.80392944715870415.5998328096669
15.8611827673751 15.8482215926717 P P P 16.1273862878246 16.0965591354373
16.0433524516053 P P P LNCV6_141855_PI430048170 mRNA
GCTCCTCTACTCTTTGAGACATCACTGGCCTATAATAAATGGGTTAATTTATGTAACAAA NM_000998RefSeq chr2
+ 216498796 216501465 RPL37A 6168 ribosomal protein L37a
GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0005634|GO:0006415|GO:0006412|GO:0046
872|GO:0006413|GO:0005829|GO:0006414|GO:0000184|GO:0016032|GO:0022625|GO:0044267|GO:0005925|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141426_PI430048170 0.0968414256065225 0.7828428239213967.4843775666916
7.93368613115701 7.63675909665301 P P P 8.12767007568335 7.96352412035257
8.05525405137217 P P P LNCV6_141426_PI430048170 mRNA
AAGCAAAGCTAGGTAGCCATTTCTTCTGTTCTACCAAGTTATAATAGCATTCATTTCCCT NM_001888RefSeq chr16
- 21258517 21303136 CRYM 1428 "crystallin, mu"
GO:0050661|GO:0003714|GO:0007605|GO:0070327|GO:0005634|GO:0000122|GO:0070324|GO:0042803|GO:0005
739|GO:0047127|GO:0042403|GO:0005737|GO:0055114|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132738_PI430048170 0.44004238890719 0.8218603113882994.61988453868551 3.9193109994002
3.67939902480366 P P P 4.26292244234292 4.79916702175494 4.07684352450674 P P P
LNCV6_132738_PI430048170 mRNA
TCAATCTCCTATTGCTTGTCAGCCTGTGTGCGTGTGGTGCAGGAAATAAAGGATCTATAC NM_177977RefSeq chr17
- 41722638 41734646 HAP1 9001 "huntingtin-associated protein 1, transcript variant 2"

GO:0005515|GO:0030424|GO:0008090|GO:0030054|GO:0005783|GO:0007268|GO:0005634|GO:0006887|GO:0015031|GO:0015629|GO:0005764|GO:0005739|GO:0008104|GO:0050769|GO:0047496|GO:0017157|GO:0005856|GO:0048403|GO:0048011|GO:0005776|GO:0045742|GO:0016234|GO:0031587|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142264_PI430048170 0.2366644206422250.8044256139511516.57124908476403 6.02723320849175 5.90050015185768 P P P 6.34250955980945 6.64922688014994 6.52390808293533 P P P LNCV6_142264_PI430048170 mRNA CCCCCCACAGAGCTTGGTTGCATAACGTTTTTCCATTTGAAAGAAAGATCTAGATTCAAC NM_207414RefSeq chr8_KI270819v1_alt - 106284 122209 MROH5 389690 "maestro heat-like repeat family member 5, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137932_PI430048170 0.1637380608841020.6786192375365958.73505676222913 8.82323888861916 9.13092542299735 P P P 8.92873879689115 9.5598027295294 9.78048522453064 P P P LNCV6_137932_PI430048170 mRNA CTCATGATTCTTACTGAAGCTGTTGATGACAGGATATCATGGTGACGTTTTTGTAATGAA NM_018410RefSeq chr2 - 233836700 233854566 HJURP 55355 "Holliday junction recognition protein, transcript variant 1" GO:0005515|GO:0005730|GO:0006334|GO:0005634|GO:0003677|GO:0042802|GO:0034080|GO:0042393|GO:0005737|GO:0007049|GO:0007059|GO:0051101|GO:0043254|GO:0000777|GO:0005654|GO:0000775 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138491_PI430048170 0.9117637587598551.07358215562706 4.26351885461847 3.26321480657476 3.03458326927605 P P P 3.98119141873607 3.42938879716356 2.98178212995405 P P P LNCV6_138491_PI430048170 mRNA ATACTGACCTATAGGAGGCACTGCCCAGAGCTCCTAACTGGGGTGGGGTGCAAAGGAAAG NM_001012715 RefSeq chr9 + 129321015 129322603 C9orf106 NA chromosome 9 open reading frame 106 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129644_PI430048170 0.0692480222491665 0.78469838321 5.02270492037369 4.89744414748673 5.21640454972811 P P P 5.21153084467005 5.39282010296561 5.57652997315624 P P P LNCV6_129644_PI430048170 mRNA GAGGGAAAGGGGCTAAAGTCTCTTCTGTTGGTAATTTATTAGTTACTCTTGAAACAATAA NM_001289008 RefSeq chr5 - 88195205 88268879 TMEM161B 153396 "transmembrane protein 161B, transcript variant 3" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_22725_PI430048170 0.1151222752710710.44821575141863 0.4199007333753050.351261899086061 1.91429368980068 A A A 2.3650823745446 1.52015409396654 2.63701531808409 A A P LNCV6_22725_PI430048170 mRNA CAACAGTATCATCCAGCAAAGAAGTTCAAGATTCACTGTCTGTTGGAACATTGGCTCAAA NM_024688RefSeq chr10 + 32567722 32882864 CCDC7 79741 "coiled-coil domain containing 7, transcript variant 5" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137303_PI430048170 0.0436247987142113 0.7019364086035658.35237512289453 8.06368628753114 7.87389838226267 P P P 8.65450368591544 8.73635085258262 8.4573962704738 P P P LNCV6_137303_PI430048170 mRNA TGGCTGCTCTCCTTCCCAATAGTCACAAGATTTACCATGATAATAATAGGTTAAGACTTG NM_001098531 RefSeq chr12 - 47734669 47759106 RAPGEF3 10411 "Rap guanine nucleotide exchange factor (GEF) 3, transcript variant 1" GO:0005515|GO:0045859|GO:0008603|GO:0005886|GO:0008283|GO:0044281|GO:0032854|GO:0005085|GO:2000249|GO:0030552|GO:0061028|GO:0017034|GO:0070062|GO:0005952|GO:0032486|GO:0030168|GO:0001525|GO:0045766|GO:0012505|GO:0007165|GO:0006112|GO:0016020|GO:0050796|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138953_PI430048170 0.5969333635672181.03064721007605 0.415586881136275 0.5420101903929370.379176866701795 A A A 0.50608259901445 0.396277698983371 0.30160075663243 A A A LNCV6_138953_PI430048170 mRNA

GTGATATCCAGTGACATCTAACTTTCATGGATGTATGTGACAGTGTTTGTTCAAGTTAAA NM_001145718 RefSeq chrX - 120872597 120875925 CT47B1 643311 "cancer/testis antigen family 47, member B1"NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57987_PI430048170 0.00259865118850351 0.546306300311961 5.53178676189434 5.56839567244135 5.83780897084223 P P P 6.35321250265809 6.57164816913643 6.6346580498453 P P P LNCV6_57987_PI430048170 mRNA
AATGGGTAGTAGCCAAACTCACAAATTGGAGTGATGAACCTGCTTATACCTAAGGGCAGG NM_001039618 RefSeq chr11 - 85657563 85665138 CREBZF 58487 "CREB/ATF bZIP transcription factor, transcript variant 1" GO:0043565|GO:0005515|GO:0051090|GO:0003700|GO:0045814|GO:0005634|GO:0009615|GO:0045892|GO:0003677|GO:0006351|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112307_PI430048170 0.137199411025866 1.35833841671802 10.1795834933868 10.5401152813164 10.1074564367287 P P P 9.69131809110583 9.55949821828569 10.205562432303 P P P LNCV6_112307_PI430048170 mRNA
TTTCCTGGTCTTTGTGATCGTCCTCTTCTTCATTTACCACTTCATGCAGGCTGAAGAAGG NM_000117 RefSeq chrX + 154379236 154381523 EMD 2010 emerin GO:0005515|GO:0007077|GO:0031965|GO:0005783|GO:0007084|GO:0005874|GO:0048487|GO:0048147|GO:0005637|GO:0003779|GO:0005635|GO:0035914|GO:0035414|GO:0060828|GO:0046827|GO:0005640|GO:0006936|GO:0007517|GO:0071363|GO:0016020|GO:0016021|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139555_PI430048170 0.308558113377829 0.889298764677622 3.63204289315107 4.06573285102226 3.84943304230471 P P P 3.91626563883906 4.17157700972114 3.98750748244201 P P P LNCV6_139555_PI430048170 mRNA
CATGGCTACCCTTCACTTTTGGAGGGAGTTTTAAGTGATACAGATCTTTTTGCCAAGCAA NM_001278082 RefSeq chr5 - 151769792 151771508 LOC100652758 NA uncharacterized LOC100652758 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136873_PI430048170 0.000117025564587764 5.93632285688058 4.59181652787766 4.87270557536495 4.63063349573698 P P P 2.250849881579 2.2374081521638 1.88567978072596 A A A LNCV6_136873_PI430048170 mRNA
GAGGTTGAATAGGAGTTCTCCTGGAGCAACTTGAGGGTAATAATGATGATGATATAATAA NM_006179 RefSeq chr19 - 49061139 49063867 NTF4 4909 neurotrophin 4 GO:0008344|GO:0061193|GO:0005166|GO:0042490|GO:0007616|GO:0007267|GO:0005576|GO:0060384|GO:0043524|GO:0008052|GO:0008544|GO:0007402|GO:0048812|GO:0045664|GO:0005788|GO:0016023|GO:0007169|GO:0008083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129411_PI430048170 0.415543369831917 1.17522596499612 2.46152188031371 2.45126941202193 2.50585765592189 A A A 2.60180845766752 1.6574948900726 2.30688427878269 P A A LNCV6_129411_PI430048170 mRNA
ACTCCATGGAGATCCGCACCCCTGACATCAATCCTGCCTGGTACGCCAGTCGCGGGATCA NM_015893 RefSeq chr2 + 237566573 237567175 PRLH 51052 prolactin releasing hormone GO:0006629|GO:0032868|GO:0031861|GO:0005576|GO:0002023|GO:0048483|GO:0009749|GO:0005737|GO:0006112|GO:0001894|GO:0005179|GO:0007186|GO:0040014|GO:0045444|GO:0005184 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105126_PI430048170 0.00575000185276763 0.515296990476111 6.328707325901 6.27967600959974 6.67063193846957 P P P 7.14630136738011 7.41579725007792 7.58519767090067 P P P LNCV6_105126_PI430048170 mRNA
CATACTATCTGTATACATGTGCACATGCGGCATTTTACTATGAAATTTAATATGCTGGGT NM_017526 RefSeq chr1 + 65420447 65436007 LEPROT 54741 "leptin receptor overlapping transcript, transcript variant 1" GO:0060400|GO:0005794|GO:0000139|GO:0005102|GO:0016021|GO:0046426|GO:0010008|GO:2000009|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137911_PI430048170 0.00566389823469496 0.42442284733436 3.3880355220436

3.3549213457129 3.75791274089208 P P P 4.38878433676483 4.9233148066841
4.87554221498926 P P P LNCV6_137911_PI430048170 mRNA
CTCATGACTCTAAAAAGTGCATGGCTTGGGGCTATACTTTGTTTTGCAGTTTGTTGGTAT NM_001135187 RefSeq
chr2 + 227472171 227561222 AGFG1 3267 "ArfGAP with FG repeats 1, transcript variant 1"
GO:0005515|GO:0001675|GO:0045109|GO:0007289|GO:0003723|GO:0007275|GO:0042995|GO:0003677|GO:0043
231|GO:0043547|GO:0008060|GO:0006406|GO:0005643|GO:0032312|GO:0043025|GO:0016023|GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128464_PI430048170 0.0161572240842853 1.50922764466847 10.565501501987
10.9552580650324 10.742594493893 P P P 10.3276600469514 10.1181451437539 10.047682541463
P P P LNCV6_128464_PI430048170 mRNA
TCAGAATGATTTGCTGGATGGTTTTTGGACCTGTCAGTCTCCCCTCCCTGGTATATATGT NM_000871 RefSeq chr1
+ 19665286 19680966 HTR6 3362 "5-hydroxytryptamine (serotonin) receptor 6, G protein-coupled"
GO:0005515|GO:0032008|GO:0005886|GO:0042493|GO:0014050|GO:0014053|GO:0007268|GO:0060291|GO:0014
054|GO:0004969|GO:0030425|GO:0007210|GO:0014058|GO:0005929|GO:0004993|GO:0021795|GO:0005887|GO:0
007187|GO:0007612|GO:0032355|GO:0033603 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111940_PI430048170 0.457634499827113 1.52927754335968 1.51296014387796
0.3394848444022298 2.07345540121065 A A A 0.4969638692894941.19825462752075
0.799065472018318 A A A LNCV6_111940_PI430048170 mRNA
TGCAAAACGTTTCCAGGAATTGAAAGCACAAAGAGAAAGTAAAGAAGCCCTAGAGATTGA NM_023034 RefSeq
chr8 - 38275042 38382272 WHSC1L1 54904 "Wolf-Hirschhorn syndrome candidate 1-like 1,
transcript variant long"
GO:0005515|GO:0005694|GO:0016571|GO:0006325|GO:0005634|GO:0042800|GO:0006351|GO:0018024|GO:0005
654|GO:0008270|GO:0045892|GO:0046976|GO:0051568|GO:0070734 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127842_PI430048170 0.0117528099916457 1.22928935905929 0.827331541632494
0.8840388375338620.944210648982781 A A A 0.6866070492377950.518120818719633
0.554242890810271 A A A LNCV6_127842_PI430048170 mRNA
TTCCCTTTGTTTTTCCCTAGCATTGGTTTAAAGGTACATTACAGTATATAGATGGTTTCG NM_153216 RefSeq chr5 -
93740308 93741603 POU5F2134187 "POU domain class 5, transcription factor 2"
GO:0043565|GO:0006355|GO:0003700|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_62213_PI430048170 0.0936648430129402 0.5848845675650480.347787585805867
0.32078081168584 0.309506772065137 A A A 0.7308058608351160.913062624824952 1.5298456782317
A A A LNCV6_62213_PI430048170 mRNA
CAATCAATGTTTACAACCTCACCTGCAATAACTGTTCAGAAAACTGCAGTGATGTTCTGT NM_001145923 RefSeq
chr15 - 76348185 76861944 SCAPER 49855 "S-phase cyclin A-associated protein in the ER, transcript
variant 2" GO:0005737|GO:0005783|GO:0005654|GO:0005634|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_98305_PI430048170 0.4671007578402881.08774298605515 4.98115906465591 5.38646885202525
5.22221400560546 P P P 4.92690524785124 5.10883707652564 5.2049187185245 P P P
LNCV6_98305_PI430048170 mRNA
TACATGAACACCAACTTGGTGCAGGAGAACTTCAGCAGCCTCCTGACCCTGCTCTGGACC NM_199242 RefSeq chr17
- 75827225 75844717 UNC13D 201294 unc-13 homolog D (C. elegans)
GO:0005515|GO:0006909|GO:0033093|GO:0043304|GO:0017137|GO:0043320|GO:0005770|GO:0005764|GO:0045
921|GO:0051607|GO:0016020|GO:0055037|GO:0002432|GO:0002467|GO:0070382 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129087_PI430048170 0.7096804189429491.02490009954242 10.4654344408119
10.4807282786362 10.5890262490371 P P P 10.2968272302959 10.5701161241428
10.5492610064757 P P P LNCV6_129087_PI430048170 mRNA

TGTGTGGGAAGTAAGGGTGAGTCTCATATTCTTCTATTAAATTTGCCACAAGAATTGCAA NM_016417 RefSeq chr14 + 95534985 95544718 GLRX5 51218 glutaredoxin 5
GO:0030097|GO:0005739|GO:0051537|GO:0015035|GO:0009055|GO:0045454|GO:0005634|GO:0046872|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136591_PI430048170 0.9835758675004461.03388444245459 0.358527152647686 1.12966658543223 0.32712331919033 A A A 0.6619543926459020.753132830812645 0.380936456326862 A A A LNCV6_136591_PI430048170 mRNA
GATGAGTTGGCATTGATAGCAATAATGTAAAATTATGTCTTTGAGCTTTATTGGAAGGGG NM_001145082 RefSeq chr3 + 40477112 40490237 ZNF619 285267 "zinc finger protein 619, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128944_PI430048170 0.1089012514165220.3509128188445760.364915090033591 0.3217769309998341.41896565468009 A A A 1.01680472272143 2.70809763970576 2.65387635760976 A P P LNCV6_128944_PI430048170 mRNA
GTGGTTTTTGAAGTTCTTAGATACGTGTGTGTAGCTTTGTGTGGCATTATATATAGCATT NM_001159280 RefSeq chr15 + 43330355 43354555 ADAL 161823 "adenosine deaminase-like, transcript variant 1"
GO:0017144|GO:0004000|GO:0006144|GO:0006154|GO:0046103|GO:0043101|GO:0055086|GO:0043103|GO:0044281|GO:0046872|GO:0009117|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131501_PI430048170 0.33274848838109 1.28009977684724 3.88606965669891 4.06233632101528 3.95012527446079 P P P 2.86858635520435 3.81926692497181 3.93126796253781 P P P LNCV6_131501_PI430048170 mRNA
ATAAATTTGAGGTATGTGGGAAGCATGTGTAGCTATGTTGTACTCTCTAAACCTGCCCAG NM_020880 RefSeq chr19 + 57599884 57608269 ZNF530 348327 zinc finger protein 530
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_8625_PI430048170 0.0221653282626241 1.90369487684046 4.21478226328443 4.70041521061333 4.05656878921914 P P P 3.6630893448979 3.35614139164269 3.20857820317577 P P P LNCV6_8625_PI430048170 mRNA
ACGGCCGCTGAGTGAGGCGTCGGCTGTGTTTCTCACCGCGGTCTTTTCCTCCCACTCTTG NM_018017 RefSeq chr10 - 114122214 114174605 CCDC186 55088 coiled-coil domain containing 186 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109408_PI430048170 0.2283410495206610.8765416338570979.56645440344621 9.28772065097731 9.30130290815123 P P P 9.48859976030327 9.76855195560232 9.46600166438041 P P P LNCV6_109408_PI430048170 mRNA
ATGTCATGGTCAGGTTCAAGGGCAGCAGGAAAGACGAGATCCTGGGCATCGCCAACAACC NM_178443 RefSeq chr11 + 64206679 64223891 FERMT3 83706 "fermitin family member 3, transcript variant URP2LF"
GO:0070527|GO:0030054|GO:0005178|GO:0016020|GO:0007229|GO:0007159|GO:0002102|GO:0034446|GO:0033632|GO:0042995|GO:0070062|GO:0033622 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_38378_PI430048170 0.0939630740187111 1.1030420943897 0.614043577380627 0.5357477462601180.713134022070438 A A A 0.4197540662408960.491828303135193 0.530197455372876 A A A LNCV6_38378_PI430048170 mRNA
CTGTGGAGCTGGGGAAGAACTCAAAGGAAACAAGTTCCAGAGGATCGTGTTTATGAAGAA NM_000139 RefSeq chr11 + 60088663 60098467 MS4A2 2206 "membrane-spanning 4-domains, subfamily A, member 2, transcript variant 1"
GO:0051219|GO:0050663|GO:0005886|GO:0019901|GO:0051279|GO:0007202|GO:0007205|GO:0043306|GO:0032998|GO:0006955|GO:0019863|GO:0006954|GO:0005887|GO:0045087|GO:0045121|GO:0019767|GO:0042169|GO:0009897|GO:0038095|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88836_PI430048170 0.0402283915572256 2.2060741747153 10.6350393832037 11.4827119250871 10.9170223041296 P P P 10.0313246815308 9.8067453244042

9.89550230010842 P P P LNCV6_88836_PI430048170 mRNA
GGACGGGGATGTCAGGGAGGCAAGTGTGTTGTGTTACTGTGTCAATAAACTGATTTAAAG NM_002537 RefSeq chr15
- 64687573 64703281 OAZ2 4947 "ornithine decarboxylase antizyme 2, transcript variant 1"
GO:0005515|GO:0034641|GO:0008073|GO:0045732|GO:0006596|GO:0006521|GO:0006595|GO:0005634|GO:0090
316|GO:0044281|GO:0043086|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144851_PI430048170 0.99141648884473 0.9643162034586096.12201385222764
6.24721652622835 6.46971694123688 P P P 5.86240679719221 6.17134045229924
6.81582345613793 P P P LNCV6_144851_PI430048170 mRNA
GATAATGTACCCAAATACTATGGCCAGATAATAAATTGTGCTGCAAACAACATGTCTTGT NM_020799 RefSeq chr10
+ 88880186 88923502 STAMBPL1 57559 STAM binding protein-like 1
GO:0005515|GO:0016020|GO:0006508|GO:0046872|GO:0008237 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133620_PI430048170 0.3256650066721710.9835036832623690.334422473343977
0.3494743249112270.354263776053688 A A A 0.3994576898826640.336026993888773
0.374037702653304 A A A LNCV6_133620_PI430048170 mRNA
GCAGCATCCAAAATCTTAATGTGTTTCATTTGATGTTGTTAGATCAGAGAAGAAATTGGC NM_001290040 RefSeq
chr3 + 77040142 77649963 ROBO2 6092 "roundabout, axon guidance receptor, homolog 2
(Drosophila), transcript variant 4"
GO:0031290|GO:0001656|GO:0005515|GO:0001657|GO:0021891|GO:0051964|GO:0009986|GO:0061364|GO:0007
417|GO:0032870|GO:0042802|GO:0050925|GO:0007411|GO:0007420|GO:0016199|GO:0050772|GO:0016021|GO:0
030673|GO:0007156|GO:0008046|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142835_PI430048170 0.5005498286800441.90581687421884 2.39730861040185
2.98084125573419 0.334923700040673 A P A 1.21074253284069 1.95089680421732
0.472671454272776 A A A LNCV6_142835_PI430048170 mRNA
GCTCAATCTGTTAACAGGCTTCTGGCATGTAGATCAGTGGTCTCCAAGCTTTTGTGATTG NM_000623 RefSeq chr14
+ 96204797 96244329 BDKRB2 624 bradykinin receptor B2
GO:0005515|GO:0004947|GO:0009651|GO:0046982|GO:0005886|GO:0008015|GO:0002020|GO:0031702|GO:0007
204|GO:0019229|GO:0006939|GO:0006954|GO:0007186|GO:0033137|GO:0004435|GO:0005887|GO:0042311|GO:0
042310|GO:0008152|GO:0043114|GO:0007169|GO:0007166|GO:0050482|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_55421_PI430048170 0.2902649139271050.8464520496110750.3634265989173520.369133096728908
0.330685053344006 A A A 0.4400235794396590.89005063490785 0.402278678211941 A A A
LNCV6_55421_PI430048170 mRNA
AGTCAAGAAAATGAGATGTTTTCCATCAGAGACAGTGCACACAGGCGGTTTCTGCTATTC NM_001185156 RefSeq
chr1 + 206897442 206904139 IL24 11009 "interleukin 24, transcript variant 3"
GO:0008284|GO:0030336|GO:0008285|GO:0005783|GO:0042517|GO:0006915|GO:0005125|GO:0005615|GO:0046
427|GO:0043280|GO:0006955|GO:0071222|GO:0006954|GO:0033136|GO:0042060|GO:0071353|GO:0043154 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139926_PI430048170 0.00473535685717858 6.02392672904845 5.63293962021314
5.90736905019263 5.30928140441343 P P P 3.51290264118106 3.00446804357162
2.41773700466588 P P A LNCV6_139926_PI430048170 mRNA
CCCTGTGCTGTAGCTTCTTTCCAGGCCTTTCCCAAGGAGTAGCTGAAAGGAAGACGCGAT NM_206818 RefSeq
chr19_KI270938v1_alt - 69045 77107 OSCAR 126014 "osteoclast associated, immunoglobulin-like
receptor, transcript variant 1" GO:0005886|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144492_PI430048170 0.1494778149926771.13675173946701 6.82556601859334
6.62323997894997 6.54920321238035 P P P 6.53438342986849 6.4879634010768 6.433510637438
P P P LNCV6_144492_PI430048170 mRNA
TCTGGGTTTTACATCTCCTGTAAGAGTTTTGAAACCACTACAGGCTTTGACCCTCACAGG NM_003080 RefSeq chr6

+ 109440727 109443919 SMPD2 6610 "sphingomyelin phosphodiesterase 2, neutral membrane (neutral sphingomyelinase)"
GO:0006665|GO:0048011|GO:0006684|GO:0005886|GO:0006687|GO:0004767|GO:0044281|GO:0097190|GO:0046872|GO:0009612|GO:0035556|GO:0005887|GO:0005901|GO:0046513 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138263_PI430048170 0.00493411241066243 1.44515782831511 12.5995565011557 12.7408838987212 12.7500898921101 P P P 12.0232452434363 12.2341873366608 12.2341873366608 P P P LNCV6_138263_PI430048170 mRNA
CATATTTGATGTGTGTGTGTATGATGAGCCAATAAACCAGACTGTGTGCGTGGCAAAAAA NM_031946 RefSeq chr7 + 151086421 151144436 AGAP3 116988 "ArfGAP with GTPase domain, ankyrin repeat and PH domain 3, transcript variant 1"
GO:0007264|GO:0003924|GO:0005634|GO:0005525|GO:0071944|GO:0043547|GO:0006184|GO:0008060|GO:0005737|GO:0016020|GO:0032312|GO:0034614|GO:0043161|GO:0008270|GO:0000060|GO:0031593 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143970_PI430048170 0.1128781751393220.819531636668572 7.64857485379843 7.4614135524759 7.71963546705213 P P P 7.89068967504816 8.08556425406775 7.70137000268326 P P P LNCV6_143970_PI430048170 mRNA
TTTTATGCACAGCCTAGTTATCAAGGGGATGATTTGCCGACATGTTTGAGAACCCCCTAA NM_003131 RefSeq chr6 + 43171294 43181506 SRF 6722 "serum response factor (c-fos serum response element-binding transcription factor), transcript variant 1"
GO:0005515|GO:0000790|GO:0003700|GO:0006366|GO:0000983|GO:0003705|GO:0045597|GO:0010736|GO:0010735|GO:0030155|GO:0031175|GO:0042803|GO:0007507|GO:0001947|GO:0022028|GO:0048589|GO:0010669|GO:0042789|GO:0046016|GO:0008306|GO:0030336|GO:0001707|GO:0007616|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143116_PI430048170 0.2547058979427670.61521443472095 0.472867241329201 0.5490004397513590.724496608888933 A A A 0.5789216501557381.89327496035012 1.07814195312774 A A A LNCV6_143116_PI430048170 mRNA
GTGTCTGTGTATTTAGCATGTGTACTATAATCAGGTGATATAGTATTCCTTCAGTCTTTGNM_001007527 RefSeq chr5 - 36103311 36151913 LMBRD2 92255 LMBR1 domain containing 2 GO:0016020|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134900_PI430048170 0.3686550392822390.9743578865164760.502849260803122 0.3944538683479810.482030438081275 A A A 0.4969703437692790.499422421843653 0.497646766789823 A A A LNCV6_134900_PI430048170 mRNA
ACAACCTCAGCCCATGGTCAATGAATAAGCACTTTGAGAAAGTTACTATACTAATAACTA NM_001085401 RefSeq chr6 + 4079205 4130765 C6orf201 404220 "chromosome 6 open reading frame 201, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64336_PI430048170 0.00560577254153169 1.80893858576571 3.09299398417134 3.41471885390919 3.31576135867755 P P P 2.63001907787868 2.219039259524 2.39797518984179 P A P LNCV6_64336_PI430048170 mRNA
ACATTTCACTGTTAGACTCACAGGATGCTGGCCATTGGTCTTTCCCTTTGTGATCATCTT NM_001202409 RefSeq chr19 + 9323771 9343845 ZNF559 84527 "zinc finger protein 559, transcript variant 5"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131788_PI430048170 0.0585454118767266 0.1820919879704080.301661310935808 0.2601803383103660.341326661629852 A A A 1.45311375246144 2.85035165288314 3.37208812540873 A P P LNCV6_131788_PI430048170 mRNA
ACTGAGGCTGTAGAAGCAGCGAATTGTCTAGCCATTTAAGTTATTTTTGTAAAATTCAGC NM_001190848 RefSeq chr7 - 135387069 135510127 CNOT4 4850 "CCR4-NOT transcription complex, subunit 4, transcript variant 4"

GO:0005515|GO:0010467|GO:0004842|GO:0000166|GO:0016874|GO:0008270|GO:0005634|GO:0030014|GO:0000289|GO:0051865|GO:0005829|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131044_PI430048170 0.2900112581020420.69354521252592 2.78231675096247 2.6762327247861 2.56783616391008 A A A 3.76837490676251 2.87342731276188 2.75058028027431 P P P
LNCV6_131044_PI430048170 mRNA
GTGTTTATTCTTTTCCTGTGCCCCTCATAATGGAAGAAAGTAAACTGCTTATCCCGAGCC NM_003215RefSeq chr4 - 48135782 48269797 TEC 7006 tec protein tyrosine kinase
GO:0050853|GO:0005515|GO:0050852|GO:0010543|GO:0005102|GO:0042246|GO:0005524|GO:0046872|GO:0030154|GO:0031234|GO:0005829|GO:0008289|GO:0035556|GO:0002250|GO:0005911|GO:0007229|GO:0045087|GO:0042127|GO:0006468|GO:0005856|GO:0038083|GO:0004715|GO:0007169|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132123_PI430048170 0.0187027921372326 0.61977128463904310.2794344214505 10.1367737305051 10.0914890731511 P P P 10.6027597878309 11.003308719045 10.9472595964626 P P P LNCV6_132123_PI430048170 mRNA
AGCGCACTAGCATGTGATATTAGGGAGTTTGCAATAAATTATTGAGGCTGATGTAAAAAA NM_022094RefSeq chr3 - 9866709 9879056 CIDEC 63924 "cell death-inducing DFFA-like effector c, transcript variant 3"
GO:0005811|GO:0003674|GO:0006355|GO:0005783|GO:0097194|GO:0006915|GO:0042981|GO:0005634|GO:0034389|GO:0006351|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127982_PI430048170 0.4466400539749391.02237812429492 0.360927945976229 0.2462847206509680.296878715587603A A A 0.26873056780878 0.271551333701324 0.270312686369589A A A LNCV6_127982_PI430048170 mRNA
TACAAGACATTTTAGAAACTTCCTGGGGGGTTGGAAACAAACATCCCCCAGAGAAGTGCA NM_014907RefSeq chr9 + 37651054 37746904 FRMPD1 22844 FERM and PDZ domain containing 1
GO:0005886|GO:0005856|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134196_PI430048170 0.0217769687085601 0.6554362916591215.26888672443508 5.34308614125001 5.26790803427777 P P P 5.89120829232242 5.72363164088017 6.07351849799715 P P P LNCV6_134196_PI430048170 mRNA
GGCATTCCTAAATGATTGTGAGGGGTTGTCTTATAAATTTGGTTTGTTGTGGTAGAAAAA NM_017956RefSeq chr8 + 124450806 124453025 TRMT1255039 tRNA methyltransferase 12 homolog (S. cerevisiae)
GO:0016740|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138554_PI430048170 0.0057598153897687 0.4688485547455997.12849378431991 7.1667899140092 7.22298419135557 P P P 8.15477828674465 8.15921945456145 8.46224806594526 P P P LNCV6_138554_PI430048170 mRNA
GGTTAGAGGACACCAAAGATACTGGGTCATCAGCCATTAAGTATATCTATTTCAAAATTA NM_001282606 RefSeq chr12 - 66136935 66170072 TMBIM4 51643 "transmembrane BAX inhibitor motif containing 4, transcript variant 1" GO:0050848|GO:0005515|GO:0043066|GO:0005795|GO:0000139|GO:0006915|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143019_PI430048170 0.0758333479397055 0.79191372117363310.7317212322792 10.451565387362 10.3884046436111 P P P 10.8411748592231 10.9161563915045 10.8464955359598 P P P LNCV6_143019_PI430048170 mRNA
GCAGAGGGAGTGTGCGAATCTACCCTGACCAATGGGCTCAAGAATAAAGTATGATTTTTG NM_177552RefSeq chr16 + 30199227 30204329 SULT1A3 NA "sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141804_PI430048170 0.00844940106510455 0.65693175216427 10.2212271275663 10.5051729158482 10.2174984900199 P P P 11.0502092915251 10.9204786577019 10.8001918567749 P P P LNCV6_141804_PI430048170 mRNA
TTCTACTCAGGCACGGGCTACAAGCTGAGTCCCTTCACCTTCGCTGCCACAGATGACTAG NM_006019RefSeq chr11 + 68038994 68050899 TCIRG1 10312 "T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3, transcript variant 1"

GO:0008286|GO:0005215|GO:0008284|GO:0005886|GO:0005765|GO:0006879|GO:0005739|GO:0000220|GO:0033572|GO:0016324|GO:0007035|GO:0046961|GO:0030670|GO:0051117|GO:0090382|GO:0015986|GO:0070072|GO:0051701|GO:0055085|GO:0006968|GO:0005887|GO:0015991|GO:0010008|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136960_PI430048170 0.6263383742464890.5555663162547941.04112988022818 0.2986286305379840.470844156125013A A A 0.2978861889395640.266048511492807 2.58031575903176 A A P LNCV6_136960_PI430048170 mRNA CACATTTTCCTTGGATACACACTAACCCTGGTGTTTCTGTCCTTATAAGGCTGACTGCAC NM_212555RefSeq chr11 - 125776130 125778819 PATE2 NA prostate and testis expressed 2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132473_PI430048170 0.9109144738039961.00694523098681 0.26694149905451 0.2756851932232770.449570354288977A A A 0.3490044077159990.2975305983738 0.322699095893626A A A LNCV6_132473_PI430048170 mRNA GCTGGAAGCTTGATCAAGTCCTGTTTCTTCTTGACACAGACTGATTAAAAATTAAAAGAA NM_017982RefSeq chr1 - 223220818 223364202 SUSD4 55061 "sushi domain containing 4, transcript variant 1" GO:0030449|GO:0045959|GO:0045957|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130524_PI430048170 0.44236161729224 1.02277231925844 0.38536440017072 0.38950825844754 0.287676874195236A A A 0.3067447880547170.329288958424933 0.331217089935146A A A LNCV6_130524_PI430048170 mRNA TTCCTTCTGCAGCAAGTTCTTGAAATTCAATGAAGATCGGTGCTTCAGGGTGGACATGGT NM_198923RefSeq chr11 - 68980020 68980986 MRGPRD 116512 "MAS-related GPR, member D" GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127896_PI430048170 0.4592010066577860.46975932862035 0.39246296733665 0.35438355053322 0.390067813497311A A A 0.3056722067450940.3173538169398962.541845863071 A A P LNCV6_127896_PI430048170 mRNA CTTTAAGAAATCAGCAAGTGAAACAAGCTTTCAAGGACTCAGTCAAAAAGATTGTGAAAC NM_001005494 RefSeq chr12 + 55551226 55552156 OR6C4 NA "olfactory receptor, family 6, subfamily C, member 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144461_PI430048170 0.0165259820652405 0.3044802534944020.290783597682805 0.3012372408312420.426580189531421A A A 2.10356349245917 2.37872972191191 1.57546748467993 A P A LNCV6_144461_PI430048170 mRNA CATGCCAAGAGATTATGGATTTATGCATATTTTGTTTTGCTGTAGTACCATTCCTAGTTG NM_002538RefSeq chr5 + 69492291 69558104 OCLN 100506658 "occludin, transcript variant 1" GO:0005515|GO:0030054|GO:0005886|GO:0019904|GO:0006915|GO:0030139|GO:0031410|GO:0032259|GO:0045216|GO:0006921|GO:0016327|GO:0005829|GO:0016324|GO:0006461|GO:0070830|GO:0005198|GO:0005911|GO:0008119|GO:0046500|GO:0046498|GO:0005923|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108510_PI430048170 0.55520295146148 1.03675894334814 0.304332981616351 0.3092466903439460.514545304501389A A A 0.3127157599251570.340683414244091 0.32847825387209 A A A LNCV6_108510_PI430048170 mRNA TGATGACCCATGGCGTCTAAGATCAACGTACCAATCTCAAAAATACCAGGCTGAATTCCC NM_006669RefSeq chr19 + 54616929 54637530 LILRB1 10859 "leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1, transcript variant 1" GO:0046636|GO:0042803|GO:0042130|GO:0031623|GO:0051607|GO:0045077|GO:0051926|GO:0032609|GO:0030109|GO:0032689|GO:0042169|GO:2001199|GO:0030107|GO:2001202|GO:2001205|GO:2001193|GO:0042536|GO:0045786|GO:2000669|GO:0014063|GO:0072643|GO:0002767|GO:0002230|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136527_PI430048170 0.5167915824195450.71647076477051 0.54163295290729

0.7345645396722020.590339331694984A A A 0.43804457309969 1.8323748041198
0.622385802534092A A A LNCV6_136527_PI430048170 mRNA
CTGCTTGTCCGTGCACAATGTAATTCTAAACCTGGCTTGTTTCTCATTTAAATATATCTA NM_138995RefSeq chr2 +
170178144 170655164 MYO3B 140469 "myosin IIIB, transcript variant 2"
GO:0051491|GO:0003779|GO:0016459|GO:0005524|GO:0032433|GO:0032426|GO:0001917|GO:0000146|GO:0005
737|GO:0046777|GO:0018105|GO:0004674|GO:0018107|GO:0007601|GO:0050896|GO:0001750 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131581_PI430048170 0.0101247185851902 1.23396486334522 6.98401188337997
7.10177507119634 6.9381195029924 P P P 6.78595704798636 6.69353383851849
6.63548088585348 P P P LNCV6_131581_PI430048170 mRNA
GGGTCTTTATTCGATAGCATTTATTATGAGCTGTCCTTTCTAAATTGTATTCATTCCTCC NM_001271087 RefSeq chr1
- 151176299 151190213 VPS72 6944 "vacuolar protein sorting 72 homolog (S. cerevisiae), transcript
variant 1"
GO:0005515|GO:0043234|GO:0006325|GO:0005654|GO:0005634|GO:0000122|GO:0035019|GO:0003677|GO:0006
351|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139654_PI430048170 0.000501688727198068 2.14576267534069 6.08751492584434
6.06467185407487 6.11257826990741 P P P 4.97561505496058 5.06147092442425
4.92007673676604 P P P LNCV6_139654_PI430048170 mRNA
ACAGTGACTTTCTCAGAGGTGACAGAGATGATGGATGAGCAGCTGGATTTTCGTGATGAA NM_001099335 RefSeq
chr8 - 22219702 22232338 PHYHIP 9796 "phytanoyl-CoA 2-hydroxylase interacting protein,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134843_PI430048170 0.584440981719034 1.34174492702289 0.268077308816382
0.386986927982566 1.65281534219085 A A A 0.748510180755421 0.355307819329668
0.329221552676995A A A LNCV6_134843_PI430048170 mRNA
GATGGCCACAGGCCTCTCTATACACATTTACAGAATTTCACATAAAGGTTTACTCTGAAA NM_006686RefSeq chr9
- 108854588 108855995 ACTL7B 10880 actin-like 7BGO:0005737|GO:0005200|GO:0015629 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_49798_PI430048170 0.0635334607363335 1.38238669895205 4.89485267853013
5.36955244719467 5.1816840713408 P P P 4.48303129672516 4.69032350170678
4.88272814140733 P P P LNCV6_49798_PI430048170 mRNA
AAGTACTCTCATGGAGACAAGGACTTCACTGAGGATGTCAACTGTGCTTTTGAGTTCCTG NM_014815RefSeq chr17
- 40019096 40054636 MED24 9862 "mediator complex subunit 24, transcript variant 1"
GO:0003712|GO:0005515|GO:0010467|GO:0001104|GO:0006367|GO:0006357|GO:0016573|GO:0005634|GO:0051
291|GO:0046966|GO:0030374|GO:0030518|GO:0042809|GO:0016592|GO:0019827|GO:0004872|GO:0005654|GO:0
045893|GO:0030521|GO:0004402 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136939_PI430048170 0.570166248775053 1.11142855170295 4.71089173037862
4.69484370719298 5.0661521365249 P P P 4.1246290786954 4.70957931129507
5.06177598161436 P P P LNCV6_136939_PI430048170 mRNA
GGACTGTGGCTGGACATTCATCTAAATAAATTTGAATATACGACACTTTTCTCACTTGAA NM_018043RefSeq chr11
+ 70078301 70189546 ANO1 55107 "anoctamin 1, calcium activated chloride channel, transcript variant
1"
GO:0005515|GO:0006821|GO:0046982|GO:0005886|GO:0034707|GO:0007275|GO:0055085|GO:0042803|GO:0005
737|GO:0016324|GO:0034220|GO:0042391|GO:0005229|GO:0005227|GO:0006812|GO:0009897|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103573_PI430048170 0.0400736410171784 0.662624218317584 5.8279138465273
5.56730707784186 5.70842292870556 P P P 6.04976615923027 6.55822448829679
6.24243997447219 P P P LNCV6_103573_PI430048170 mRNA
AGCCAGTTCCTCATCAATGGGAAACCTTTCTATTTCCACGGTGTCAACAAGCATGAGGAT NM_000181RefSeq chr7
- 65960685 65982314 GUSB 2990 "glucuronidase, beta, transcript variant 1"

GO:0004566|GO:0005975|GO:0019904|GO:0005102|GO:0006027|GO:0044281|GO:0043231|GO:0016020|GO:0009405|GO:0030212|GO:0030214|GO:0030203|GO:0070062|GO:0043202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136322_PI430048170 0.1491900266275150.88234899422542 11.962116804681 11.852646673227 12.108701243606 P P P 12.0919344909775 12.080897564102 12.2937461275495 P P P LNCV6_136322_PI430048170 mRNA
CACCAGGCCTTCTTCACTAAGACTTTGTATTCAACTTAGTTTAATGTAGATTTGCCATTA NM_014142RefSeq chr10 - 12167573 12196144 NUDT5 11164 nudix (nucleoside diphosphate linked moiety X)-type motif 5
GO:0000287|GO:0017110|GO:0055086|GO:0005634|GO:0044281|GO:0050072|GO:0005829|GO:0005622|GO:0019303|GO:0030515|GO:0034656|GO:0047631|GO:0019144|GO:0009117|GO:0070062|GO:0009191 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79950_PI430048170 0.3357862622723170.716886304156843 1.95778226815418 0.881499264334258 0.276163085116173 A A A 1.41593142269503 2.05781697916098 1.50891056909364 A A A LNCV6_79950_PI430048170 mRNA
AAGAACAAGATCGGTCCCCTGTTTGAGGAATTAATGACCAAGTTAATAACTGAGACACCT NM_001195639 RefSeq chr8 + 68330721 68535827 C8orf34 116328 "chromosome 8 open reading frame 34, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135976_PI430048170 0.0633036003176143 1.18453768526256 9.47538068402991 9.31152771298136 9.39604311244944 P P P 9.23415603432914 9.2135516247545 8.99496032548892 P P P LNCV6_135976_PI430048170 mRNA
GGACTTGTCTCCTTTTCTGTGAAAATGCTTTGTAAAAAGTTGTTATTGTTTGCATAGAGC NM_001130677 RefSeq chr17_KI270857v1_alt - 2707024 2710253 C17orf96 100170841 chromosome 17 open reading frame 96 GO:0048663 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134742_PI430048170 0.0158013540610640.3864403475638797.21610317021494 6.92571816843415 7.20386657841756 P P P 8.04195514294848 8.51703640543881 8.81687805634136 P P P LNCV6_134742_PI430048170 mRNA
CCCCGGATATACTTTGCCAAACGAAATTTGAATTCTCTGAATAAATTGGTCATGTCTAAA NM_017813RefSeq chr8 - 56957928 56993871 IMPAD154928 inositol monophosphatase domain containing 1
GO:0052833|GO:0052832|GO:0005794|GO:0006021|GO:0008441|GO:0009791|GO:0046872|GO:0046854|GO:0001958|GO:0002063|GO:0016020|GO:0016311|GO:0008254|GO:0016021|GO:0030204|GO:0008934|GO:0042733 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137439_PI430048170 0.00697683083219108 0.4654253339480358.84387071045322 8.62554064058454 8.81907162020748 P P P 10.0275663566837 9.57355251935845 9.96654438467987 P P P LNCV6_137439_PI430048170 mRNA
CAACATAAACAATAGTAACTGAGCTATTAAAGGCAACCTCTCTGACTCCTTCTGCCTAAA NM_001204831 RefSeq chr3 - 43366325 43622068 ANO10 55129 "anoctamin 10, transcript variant 2"
GO:0005622|GO:0006821|GO:0034220|GO:0016020|GO:0005886|GO:0005229|GO:0016021|GO:0005227|GO:0055085|GO:0006812 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139182_PI430048170 0.3639620301353431.0535116422543 0.309853342225051 0.3061025893669520.494814014012727 A A A 0.30418648653483 0.270312686369589 0.318409595087048 A A A LNCV6_139182_PI430048170 mRNA
TCTCTGAAGTCATTTGTGAGCTTGTATGACTTTTGTATTTAGCAATGTTGCATGCTCACA NM_006823RefSeq chr8 + 78516100 78605267 PKIA 5569 "protein kinase (cAMP-dependent, catalytic) inhibitor alpha, transcript variant 1"
GO:0034236|GO:0005515|GO:2000480|GO:0005737|GO:0010389|GO:0042308|GO:0005634|GO:0004862|GO:0000122 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136046_PI430048170 0.0112996248150240.5330909997302428.62565667378157 8.63361853445046 8.76143593412076 P P P 9.43184623954823 9.46387110971457 9.81888309366642 P P P LNCV6_136046_PI430048170 mRNA

CTGGTCCCAAGTAGTAGTGTCTTCCTAGTATATTAGTTTGATTTAATATCTGAGAAGTGT NM_031850RefSeq chr3
+ 148697870 148743003 AGTR1 185 "angiotensin II receptor, type 1, transcript variant 4"
GO:0005515|GO:0004945|GO:0019722|GO:0005886|GO:0010873|GO:0007200|GO:0007266|GO:0007204|GO:0001
558|GO:0032430|GO:0019229|GO:0042312|GO:0003081|GO:0002018|GO:0051482|GO:0042127|GO:0033864|GO:0
031711|GO:0046982|GO:0001822|GO:0010744|GO:0050727|GO:0002034|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135791_PI430048170 0.00114402974629458 4.51434757074456 7.49369549665207
7.65244418862818 7.35713526360958 P P P 5.44738606392626 5.50090597136223
4.99513307355186 P P P LNCV6_135791_PI430048170 mRNA
GTTAAGGTTATCTGTCCATTGCCTTGTACGAAAGTCTCAAGAAAAGTCTACATCTTAAAA NM_015672RefSeq chr22
- 18606126 18611919 RIMBP3 85376 RIMS binding protein 3 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_137881_PI430048170 0.3859496918846160.81571048232008 5.12299346610509
4.56631945949065 4.11425221006792 P P P 5.18275856516346 4.99364711662464
4.63316622692072 P P P LNCV6_137881_PI430048170 mRNA
GTTATGACTCCCATGTTGAACCCCATTATCTACAGCCTGAGAAATAACGAGGTGAAGAAT NM_001004460 RefSeq
chr11 + 6869754 6870666 OR10A2341276 "olfactory receptor, family 10, subfamily A, member 2"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136053_PI430048170 0.2771785472506440.8453281568367543.15181875032615
3.20614161065439 2.99750465579541 P P P 3.65577795229341 3.20529121005237
3.17819275482543 P P P LNCV6_136053_PI430048170 mRNA
AACAAAATACAGAGCTCAGTGAGCCACCTGATTCTAAAGAGCGAGTCTGGAATCTTTCGG NM_033413RefSeq chr17
+ 47831626 47837713 LRRC46 90506 leucine rich repeat containing 46 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_137330_PI430048170 0.4523249299326 1.16869464598787 0.454920917710459
1.07438714787545 0.439017920838334 A A A 0.493222215954125 0.496045902928717
0.397019076263455 A A A LNCV6_137330_PI430048170 mRNA
TGCCCGCTTCCAAATCCATCTGCGTGTAGAATGTACTGTAGATTGTAAGAATGTAATATA NM_133448 RefSeq
chr12 - 129071725 129903667 TMEM132D 121256 transmembrane protein 132D
GO:0005515|GO:0010923|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_77587_PI430048170 0.247256724578561 1.02023025818476 0.306414474039273
0.284171857270048 0.345642973219097 A A A 0.29400312607668 0.27840379182437
0.277751973722262 A A A LNCV6_77587_PI430048170 mRNA
GTGGCTTAACACTTGTGAGAGTTACCAGCTTGAAAATGATGGTGTTGACTACCTCTTGAA NM_001004317 RefSeq
chr6 + 104957047 105083332 LIN28B 389421 lin-28 homolog B (C. elegans)
GO:0005515|GO:0006355|GO:0016235|GO:0003723|GO:0005730|GO:0031123|GO:0005634|GO:0003677|GO:0010
587|GO:0005739|GO:0005737|GO:0031054|GO:0005654|GO:0008270 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_108897_PI430048170 0.974327247414486 1.00509668478772 13.5867451998482
13.7109203054174 13.8773712154242 P P P 13.7258676982932 13.6607496997863
13.7787951489583 P P P LNCV6_108897_PI430048170 mRNA
ATCCAGAACCACCTGCAAGTGCTGCTGCTGCTGGTATTCGAGGCCATCGTGTACCGGCGC NM_001142864 RefSeq
chr16 - 88715337 88784964 PIEZO1 9780 piezo-type mechanosensitive ion channel component 1
GO:0008381|GO:0005261|GO:0050982|GO:0005886|GO:0005783|GO:0033116|GO:0042391|GO:0005789|GO:0016
021|GO:0033634|GO:0033625|GO:0006812 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141273_PI430048170 0.3608421676292340.627283231089391 0.305234330174475
0.302788231989879 0.29354590039105 A A A 1.71758898601522 0.403790706758331

0.354238514556853 A A A LNCV6_141273_PI430048170 mRNA
CAACATTTTACCCACACACAGATAAAGTTTTCCCTTGAGGAAACAACAGCTTTAAAAGAA NM_001301716 RefSeq
chr17 - 40553769 40561013 CCR7 1236 "chemokine (C-C motif) receptor 7, transcript variant 3"
GO:0002885|GO:0071731|GO:0046330|GO:0051491|GO:2000510|GO:2000147|GO:0031529|GO:0005622|GO:0032
649|GO:0030838|GO:0034695|GO:0043552|GO:0045860|GO:0032496|GO:0031274|GO:0070374|GO:0043123|GO:2
000525|GO:2000526|GO:0051209|GO:0070098|GO:0009986|GO:0004930|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_107961_PI430048170 0.223011664488887 1.21195867804432 3.57551754510921
3.38453237482215 3.0874446801514 P P P 3.06754831616683 2.85908050663786
3.29691324656083 P P P LNCV6_107961_PI430048170 mRNA
TCCAGCACCAAGCCATGTCCTCAGTGCAAGCACTTTACAACCTTCAAGAAAAAAGGACAT NM_001286398 RefSeq
chr6 + 124962544 125086338 RNF217 154214 "ring finger protein 217, transcript variant 1"
GO:0004842|GO:0042787|GO:0016874|GO:0008270|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145487_PI430048170 0.0173183489781588 0.37608613808727 4.48641694471172
3.86444221577658 4.37601839356809 P P P 5.13122268686797 5.69036280254025
6.06297664804096 P P P LNCV6_145487_PI430048170 mRNA
GAGTTTACGAAATTGTGTCATTATGGTCCCCATACAGTGGTATTTAACTTTTAAAGCAAC NM_002637 RefSeq chrX
- 72578813 72714181 PHKA1 5255 "phosphorylase kinase, alpha 1 (muscle), transcript variant 1"
GO:0005516|GO:0005886|GO:0004689|GO:0005975|GO:0005977|GO:0006091|GO:0044281|GO:0004553|GO:0005
829|GO:0009405|GO:0006006|GO:0006468|GO:0005980 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140201_PI430048170 0.320472177469931 1.03451694425093 0.301909978311777
0.257047620746561 0.382835810909028 A A A 0.277001317155306 0.244901628037868
0.275618771514791 A A A LNCV6_140201_PI430048170 mRNA
TTTAAGATGATGAGAAATTGTGCGCCTGCATCACAAGACTTGATTATGAAAGATAAAGTC NM_001244764 RefSeq
chr4 - 121131408 121227466 TNIP3 79931 "TNFAIP3 interacting protein 3, transcript variant 3"
GO:0002756|GO:0071222|GO:0034142|GO:0006954|GO:0043124|GO:0031593 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128064_PI430048170 0.238440070686869 1.06434871980707 0.514731451837897
0.329431376681264 0.432298822334185 A A A 0.282380000375296 0.362085118767694 0.3664981015663
A A A LNCV6_128064_PI430048170 mRNA
TGTTTGCCCTTTATTATGAATAGCTCATTACAGGTACTAAGGATTGTTTACTTCCGAACT NM_174910 RefSeq
chr6_KI270797v1_alt - 15320 26744 TCTE3 6991 t-complex-associated-testis-expressed 3
GO:0005737|GO:0003774|GO:0030286|GO:0016020|GO:0008152|GO:0005874|GO:0006810 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_75641_PI430048170 0.431438704744241 0.750697617483945 2.14030640393033 0.347278523710329
2.30034150381886 A A A 1.84321018063774 2.38369811853236 2.41196851036013 A A P
LNCV6_75641_PI430048170 mRNA
TCAGATCAATGAATTGAAGGAGCTGCAAAAAACCTTTGAAATCTCCATTGGGAGAAAAGA NM_001099271 RefSeq
chr5 - 75674198 75717488 POC5 134359 "POC5 centriolar protein, transcript variant 1"
GO:0007049|GO:0005813|GO:0005814 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140203_PI430048170 0.279113759781066 0.658011207894837 3.50778635392646
4.27704582245705 3.4749975661192 P P P 4.49021123039119 4.84928790816805
3.62627943845629 P P P LNCV6_140203_PI430048170 mRNA
ACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGATCAAT NM_012113 RefSeq chr1
+ 150257742 150265078 CA14 23632 carbonic anhydrase XIV
GO:0005886|GO:0015701|GO:0044281|GO:0016021|GO:0004089|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132917_PI430048170 0.000890309836652042 0.315354715766985 9.5606569423979

9.33644560010082 9.31001107887546 P P P 10.8909233980336 10.9839808129097
11.3067260004662 P P P LNCV6_132917_PI430048170 mRNA
ATATAGAGACCCCAGAGCTGTTGCACCCAATACACAGAGCTTCTTTGCAAAGGGAAAAAA NM_005120RefSeq chrX
+ 71118555 71142454 MED12 9968 mediator complex subunit 12
GO:0005515|GO:0010467|GO:0001190|GO:0006367|GO:0008013|GO:0030178|GO:0005634|GO:0090245|GO:0046
966|GO:0007507|GO:0030374|GO:0030518|GO:0042809|GO:0045944|GO:0004872|GO:0060070|GO:0060071|GO:0
003712|GO:0005813|GO:0001104|GO:0003713|GO:0019904|GO:0005730|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140365_PI430048170 0.0441437692999547 0.78965372910022 6.58743747894002
6.44480075087426 6.34750311366003 P P P 6.6390233230447 6.80602178850647
6.95021038647007 P P P LNCV6_140365_PI430048170 mRNA
CTTAGGTAACTGAAAGTTCCTACTCTCCCTTAAGGTATTAAATGACTCTTTTTCCAAAGA NM_001286458 RefSeq
chr16 - 8892093 8936729 USP7 7874 "ubiquitin specific peptidase 7 (herpes virus-associated),
transcript variant 3"
GO:0005515|GO:0016578|GO:0016579|GO:0004843|GO:0032088|GO:0005634|GO:0007275|GO:0008022|GO:0005
829|GO:0004197|GO:0051090|GO:0002039|GO:0010216|GO:0061136|GO:0006283|GO:0016605|GO:0016032|GO:0
043161|GO:0031625|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139233_PI430048170 0.0455022919177346 1.32590970998178 6.33007975268853
6.48249079108187 6.21033694067335 P P P 6.14859965300968 5.8588997572949
5.78086399704562 P P P LNCV6_139233_PI430048170 mRNA
GAGCCTGTGTATGTGTCATATTAACAATATAACAGAGTCTCCCCTCACAATGATTCATCC NM_001005216 RefSeq
chr6_GL000256v2_alt + 421173 422248 OR2J3 NA "olfactory receptor, family 2, subfamily J, member 3"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136362_PI430048170 0.0384323834645175 0.6322521160805335.84572755336014
5.6131305047506 6.01811236234023 P P P 6.17857492560708 6.49887725589311
6.75499020147443 P P P LNCV6_136362_PI430048170 mRNA
CAGGTTGAGAACTGCTAATGTATAGAATGACTAAACAGCTGTCTTTCAGGGTATCATTTT NM_138400RefSeq chr7
+ 156949722 156973182 NOM1 64434 nucleolar protein with MIF4G domain 1
GO:0005515|GO:0008150|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131947_PI430048170 0.00118550450908536 0.2782738024833216.80053072546994
7.04235395997457 7.3041515705386 P P P 8.83272037151774 8.80874783486103
9.07097302361112 P P P LNCV6_131947_PI430048170 mRNA
GATACAGTCACCAAGAATGTTTTGAGTTTTTTGAAAGACCCCAATTTAAGCCTTGCTTAT NM_016308RefSeq chr1
+ 47333796 47378839 CMPK1 51727 "cytidine monophosphate (UMP-CMP) kinase 1, cytosolic, transcript
variant 1"
GO:0006240|GO:0018963|GO:0004849|GO:0006222|GO:0004550|GO:0009220|GO:0005634|GO:0009142|GO:0044
281|GO:0006227|GO:0006225|GO:0005829|GO:0005737|GO:0022602|GO:0033862|GO:0070062|GO:0015949|GO:0
004127|GO:0005730|GO:0046705|GO:0055086|GO:0005524|GO:0006165|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144006_PI430048170 0.8228666367878791.03167791296328 2.3389534248219
2.34657112661381 2.79991243949187 A A A 2.86754012701582 2.04495867098001
2.36717934595297 P A P LNCV6_144006_PI430048170 mRNA
ACTCTGCTTTCGGAAGTGCTGTGGTCTGGGGGTCTTCATAATAAACCTCATTTGCAATTC NM_000423RefSeq chr12
- 52644557 52652175 KRT2 3849 "keratin 2, type II"
GO:0005882|GO:0051546|GO:0005794|GO:0031424|GO:0005634|GO:0005615|GO:0043616|GO:0032980|GO:0005
737|GO:0008544|GO:0016020|GO:0005200|GO:0045111|GO:0045095|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_109448_PI430048170 0.106815364262583 1.3683861201052 11.0737924569683
10.8142167392173 10.8541090547869 P P P 10.8072812557817 10.2599488860338

10.2593157068152 P P P LNCV6_109448_PI430048170 mRNA
TATCCAGGCTCCATGACAGTCTTGCCATAGAAAGAAAAATAAAGTAGCCAATTCTAAAAG NM_014752RefSeq chr11
+ 74949246 74979031 SPCS2 9789 signal peptidase complex subunit 2 homolog (S. cerevisiae)
GO:0010467|GO:0005787|GO:0050796|GO:0006614|GO:0006508|GO:0005789|GO:0008233|GO:0016021|GO:0044
267|GO:0006412|GO:0006465 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138750_PI430048170 0.0158553365046828 1.28759291029011 13.4654035950379
13.5391924420898 13.5519464083922 P P P 13.0626690005307 13.2718641584669
13.1213381931256 P P P LNCV6_138750_PI430048170 mRNA
TTTCTCTTTACTGGATGTTTATTTATAAAGATCTGGCCTGTTCCTGCGTCTGCGGAGCGG NM_001694RefSeq chr16
+ 2513869 2520223 ATP6V0C 527 "ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c, transcript
variant 1"
GO:0005515|GO:0008286|GO:0051701|GO:0030177|GO:0005765|GO:0055085|GO:0006879|GO:0033572|GO:0046
961|GO:0046933|GO:0015991|GO:0030670|GO:0016032|GO:0016021|GO:0090382|GO:0005925|GO:0033179|GO:0
010008|GO:0031625|GO:0070062|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140007_PI430048170 0.8637464408524250.97826304440964 8.88079427829836
8.73257798261911 8.98192355932369 P P P 8.65832676281149 8.96542943422513
9.04887689839655 P P P LNCV6_140007_PI430048170 mRNA
AAGATCTCTTCCCCCAAGAAAAAGTGTACAGACAGCTGGCAGTGGAGCCTGCTTTATTTA NM_001096RefSeq chr17
- 41866925 41919019 ACLY 47 "ATP citrate lyase, transcript variant 1"
GO:0005515|GO:0044262|GO:0006200|GO:0005886|GO:0015936|GO:0035338|GO:0044281|GO:0009346|GO:0046
872|GO:0005829|GO:0005739|GO:0006101|GO:0005737|GO:0019432|GO:0044255|GO:0070062|GO:0008610|GO:0
048037|GO:0003878|GO:0005524|GO:0006112|GO:0031325|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140442_PI430048170 0.00799821836804095 0.4886899403200445.40671318683123
5.28270123581497 5.63856102660954 P P P 6.26369586510375 6.36241100263298
6.77201147439203 P P P LNCV6_140442_PI430048170 mRNA
GTCTATGTACATACTGCTTATTGATGTGCTGTGATATGAGGGAATCTGAAATGTTTCATA NM_175876RefSeq chr1
- 231332730 231337872 EXOC8 149371 exocyst complex component 8
GO:0005515|GO:0006996|GO:0005886|GO:0005770|GO:0015031|GO:0030426|GO:0005829|GO:0005737|GO:0000
145|GO:0051601|GO:0016020|GO:0022617|GO:0001927|GO:0061024|GO:0007032|GO:0044267|GO:0017160 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130148_PI430048170 0.3052172913097620.9092443718092391 2.9113331539995
12.8181520075661 12.6698856840471 P P P 12.762417648835 13.0647069831795
12.9776941796525 P P P LNCV6_130148_PI430048170 mRNA
GTTTCCCTGTCTGTCTGTGTTAGTAGAAAAATAAAATCCTATGAAATCTGAGTACGTTGA NM_006598RefSeq
chr5_KI270792v1_alt - 68882 129739 SLC12A7 10723 "solute carrier family 12 (potassium/chloride
transporter), member 7"
GO:0019901|GO:0015379|GO:0005886|GO:0005887|GO:0006810|GO:0055085|GO:0006813|GO:0006884|GO:0006
811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130731_PI430048170 0.00884780987483737 0.70375917012453310.0711294942341
10.2337498409634 10.1986973170843 P P P 10.6223255027704 10.5685425064687
10.8253780738395 P P P LNCV6_130731_PI430048170 mRNA
CTGACTTACAGCAAGCGAGTTATCGTCTTCTGTATTTTGTAGACTTTCTAAATAAAGTCA NM_001161572 RefSeq
chr22 + 38201931 38216510 MAFF 23764 "v-maf avian musculoaponeurotic fibrosarcoma oncogene
homolog F, transcript variant 3"
GO:0043565|GO:0006355|GO:0003700|GO:0007567|GO:0006366|GO:0007596|GO:0005654|GO:0045604|GO:0035
914|GO:0001701 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133439_PI430048170 0.6364135049259541.04843107024707 9.30810076098402
9.19804401881929 9.4281897543209 P P P 9.15451367671744 9.05617480441795

9.49126090211105 P P P LNCV6_133439_PI430048170 mRNA
TTCGTTAGCCACAAAGAGAAATATCTGAAAGTCAACATGATGCTTCTTGCATATTATCCA NM_018077RefSeq chr7
- 128310382 128343908 RBM28 55131 "RNA binding motif protein 28, transcript variant 1"
GO:0008380|GO:0006397|GO:0000166|GO:0005730|GO:0005681 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129794_PI430048170 0.0576262106642011 0.5481408641893063.34740706759697
2.53523008072959 2.77826798645019 P A A 3.69546754903791 3.80478067936576
3.88058366132274 P P P LNCV6_129794_PI430048170 mRNA
GTATCAGACCTTTTAATGAATTTTCATGGATGCTGATTAAAAGACAAACCTGTGACTCAG NM_175918RefSeq chr4
+ 1391551 1395994 CRIPAK 285464 cysteine-rich PAK1 inhibitor
GO:0005515|GO:0043627|GO:0005737|GO:0051493|GO:0005886|GO:0005783|GO:0005634|GO:0033147|GO:0006
469 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138536_PI430048170 0.0961336620553610.8309087025397783.07349113449652
3.33914646113454 3.20993127342661 A P P 3.32632681991193 3.64690516975945 3.4449033228183
P P P LNCV6_138536_PI430048170 mRNA
GAGCAGATATGTATAATATGATCAGGATTGTCCTACAGTTGTAAATAAGAATAGGTCCTG NM_001009899 RefSeq
chr3 - 113648385 113696646 KIAA2018 205717 "KIAA2018, transcript variant 1"
GO:0016020|GO:0008152|GO:0005509|GO:0004571|GO:0046983|GO:0005634|GO:0003677 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144192_PI430048170 0.00548641198817759 1.26222710352992 12.6023358261387
12.7280766459175 12.6074775813517 P P P 12.2683514412486 12.4002417137818
12.2606126686798 P P P LNCV6_144192_PI430048170 mRNA
CGTTGAACACTTCCTTGCTTTTTTCACATGTTTTATGGAATTGTTCACCTGGTTTGAAAT NM_001282619 RefSeq chr3
+ 50226687 50259354 GNAI2 2771 "guanine nucleotide binding protein (G protein), alpha inhibiting
activity polypeptide 2, transcript variant 5"
GO:0005515|GO:0008284|GO:0005886|GO:0008283|GO:0003924|GO:0007268|GO:0007194|GO:0007193|GO:0046
872|GO:0005829|GO:0035556|GO:0005737|GO:0000186|GO:0051924|GO:0004871|GO:0070062|GO:0005813|GO:0
001664|GO:0007584|GO:0005834|GO:0030496|GO:0030168|GO:0007214|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128662_PI430048170 0.0046659432201455 0.3093182261023966.1043831062984
5.78244097976793 6.23870229235691 P P P 7.31832693534392 7.78778689979095
8.04399887243233 P P P LNCV6_128662_PI430048170 mRNA
TATAAGGCTAGTACCTGCTTTGTTGGGGTATGGTTGGCTCGTGTGCATTAAGTCAACAAA NM_033550RefSeq chr20
- 46684364 46689637 TP53RK 112858 TP53 regulating kinase
GO:0005515|GO:0002039|GO:0070525|GO:0016787|GO:0016020|GO:0004674|GO:0000408|GO:0006468|GO:0005
634|GO:0005524|GO:0008033|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142870_PI430048170 0.9435499347085620.9839650346154046.92799337265984
6.45032881957256 6.1009584859283 P P P 6.94963507778914 6.45653304494968
6.14872674626387 P P P LNCV6_142870_PI430048170 mRNA
GGTGGCATTGTTCTCCCTGACTTCATAATGAGCAAATGTTTCACATTTGAACTTAAGGAA NM_207335RefSeq chr3
+ 127923058 127987671 KBTBD12 166348 kelch repeat and BTB (POZ) domain containing 12 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140001_PI430048170 0.6810169800864110.9539103172638520.410836934512648
0.4427489123614270.457820671896093A A A 0.3400720207231750.733681169835815
0.411084514325938A A A LNCV6_140001_PI430048170 mRNA
ATTTTAAGTGTCTTCTGTGGTATATGTGGGAGGGCCATTAAGGAGTGGGTTTCACTCCCT NM_001004343 RefSeq
chr1 - 241995489 241999083 MAP1LC3C 440738 microtubule-associated protein 1 light chain 3 gamma
GO:0005515|GO:0006995|GO:0008017|GO:0005776|GO:0000422|GO:0000421|GO:0005874|GO:0050811|GO:0031
410|GO:0000407|GO:0005829|GO:0012505|GO:0031090|GO:0061025|GO:0000045|GO:0019898 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_128011_PI430048170 0.60451026621184 0.9652509298233290.537926274906808
0.4926794063536130.262870690732781A A A 0.4104736260063920.552161773909415
0.495201304643622A A A LNCV6_128011_PI430048170 mRNA
ATGGCTTCATGAGAACAGTAGAACCTTATGAATGTATACTAGCATACAAGGATCTCAAAT NM_001284361 RefSeq
chr2 - 197726878 197785010 BOLL 66037 "boule-like RNA-binding protein, transcript variant 4"
GO:0005515|GO:0005737|GO:0007126|GO:0000166|GO:0003723|GO:0045948|GO:0008494|GO:0007275|GO:0007
283|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141308_PI430048170 0.9639504380881730.8387918220831763.06137575814892
3.32109700747872 3.30623418867207 A P P 2.00795552729265 3.93489214468249
3.84236526271022 A P P LNCV6_141308_PI430048170 mRNA
CTGGATAAAGCAAGATTTCCTTTCAATAAACGCTGTCACCCAATGGGAATTTTGACTCTA NM_001252335 RefSeq
chr15 + 57376504 57550727 CGNL1 84952 "cingulin-like 1, transcript variant 1"
GO:0003774|GO:0008152|GO:0016459|GO:0005923 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107395_PI430048170 0.0356655497645394 0.7024471989428248.96694095846178
9.15172734891188 9.14752557301906 P P P 9.35013442819539 9.74253417468863
9.67977699436026 P P P LNCV6_107395_PI430048170 mRNA
TAACACTTCTTTTTCCCATATGTCATTCATTTCTCAAGTCTAAGAGTAGCAGTTACCATC NM_001163922 RefSeq chr19
- 51331540 51342124 VSIG10L 147645 V-set and immunoglobulin domain containing 10 like
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134635_PI430048170 0.00698721606827783 0.4737595150033887.21398520593502
6.98467106735028 7.31716475646166 P P P 7.94186954688811 8.32370106906664
8.45544517943557 P P P LNCV6_134635_PI430048170 mRNA
TCTGGGGCAATGAAACCCTGATCATGTTGTTGATGGTTAGCATATGTTTCTGAAAATTAA NM_019045 RefSeq chrX
+ 118346072 118449960 WDR44 54521 "WD repeat domain 44, transcript variant 1"
GO:0048471|GO:0005794|GO:0010008|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131493_PI430048170 0.3428402600714330.5025840538556230.424328589530559
0.4467326376565750.325362599824407A A A 0.5952603264246870.480046891461247
2.31310680063507 A A A LNCV6_131493_PI430048170 mRNA
GCAACCACAAGTTTAAATGAAGACAAGCTGAAACAACGCAAGCTGGTTTTATATTAGATA NM_001097604 RefSeq
chrX + 52495667 52500811 XAGE1E NA "X antigen family, member 1E, transcript variant a" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130228_PI430048170 0.0677797628297419 0.9509585835479860.298853633085711
0.32142531462785 0.333181184087632A A A 0.4322553428136210.382987017011647
0.355002427515849A A A LNCV6_130228_PI430048170 mRNA
ATATTATTTGTCTGTCAGCCTTTCAGTCATTCTTTTCTCTTGGAAAGGTAGGAGGCTGCC NM_033059 RefSeq
chr17_JH159146v1_alt - 266930 268104 KRTAP4-11 653240 keratin associated protein 4-11 GO:0045095
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141396_PI430048170 0.5799510980137270.9743688512939221 3.1281974475494
13.0527782587073 12.9930037857013 P P P 13.0090673634427 13.1718569280814
13.1040029401077 P P P LNCV6_141396_PI430048170 mRNA
CAGGTCTTCATCATGCCTTGTCTTTTTTAACTGAGAAAGGAGATTTTTTGAAAAGAGTAC NM_015629 RefSeq
chr19_GL949746v1_alt + 89902 106263 PRPF31 26121 pre-mRNA processing factor 31
GO:0000244|GO:0005515|GO:0015030|GO:0005690|GO:0005634|GO:0016607|GO:0000398|GO:0071339|GO:0043
021|GO:0005684|GO:0005687|GO:0046540|GO:0070990 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143621_PI430048170 0.4484330681459291.27434503918517 2.15139034092157
1.82919488906294 1.10676460617424 A A A 1.39038199778788 1.72686993536776
1.02358561417207 A A A LNCV6_143621_PI430048170 mRNA
GAACACAAAGGAAAGTATGGCATTCCAGAGCACGAGACTCTTGTTTTAAAATGACTTGAC NM_058165 RefSeq chr2

+ 222671737 222709930 MOGAT1 116255 monoacylglycerol O-acyltransferase 1
GO:0019432|GO:0005789|GO:0003846|GO:0004144|GO:0006651|GO:0016021|GO:0006071 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141477_PI430048170 0.2166156654373421.05491165883356 0.540234464017001
0.6704154092862290.540397156362668A A A 0.4840241550806460.512575148064032
0.526703023920184A A A LNCV6_141477_PI430048170 mRNA
GTCTATCATGACAGTAGAGATGACTGAGTTAAAAATCTGACTAATTCAGAGGAAATGAAC NM_005584RefSeq chr13
- 35473788 35476695 MAB21L1 4081 mab-21-like 1 (C. elegans)
GO:0008284|GO:0043010|GO:0005634|GO:0009653 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63486_PI430048170 0.15021690054112 0.6774295873907974.55679939199931 4.11320637706187
3.63069468436311 P P P 4.85236937099051 4.88071425481521 4.33816373624778 P P P
LNCV6_63486_PI430048170 mRNA
CCCACTGGCTCCCATCACAGGGCTTAGTGTGAAGCTCAGGGCAAGGGTGGACCTTTAAAT NM_001077620 RefSeq
chr17 + 76540038 76545376 PRCD 768206 "progressive rod-cone degeneration, transcript variant 1"
GO:0005737|GO:0016021|GO:0007601|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135782_PI430048170 0.0219191498664675 0.5540150628250269.55419426283375
9.24802938436511 9.49586368569569 P P P 9.95313729098035 10.3162484531042
10.5425403628771 P P P LNCV6_135782_PI430048170 mRNA
GTCCTCTGGCCACATAGTTTTAAAATTAGGTGATTGATTATATGACCGAATAGAACTATC NM_022132RefSeq chr5
+ 71587287 71658703 MCCC2 64087 methylcrotonoyl-CoA carboxylase 2 (beta)
GO:0005515|GO:0006768|GO:0006767|GO:0009083|GO:0044281|GO:0015936|GO:0005524|GO:0005829|GO:0005
739|GO:0034641|GO:0004485|GO:0006766|GO:0005759|GO:0006552 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_78931_PI430048170 0.3541390809127770.5663573299461590.4546509214777940.372131087842606
2.31987685622801 A A A 0.7975971337491162.75628214549835 2.32943334770335 A P A
LNCV6_78931_PI430048170 mRNA
TTATTTTCTCTCAATTCCCTACTGCCTGTTTCTTACTTTGAACCTGGAGGCAGCCTGCAGNM_005960RefSeq chr7 +
100949419 100968346 MUC3A 4584 "mucin 3A, cell surface associated"
GO:0030197|GO:0006493|GO:0005796|GO:0016266|GO:0005576|GO:0016021|GO:0044267|GO:0043687|GO:0005
201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132027_PI430048170 0.6471468781286 0.9445551728588349.73537507632427
9.88984156676884 10.2073196501787 P P P 9.87561677196826 9.97865831715404
10.2409222617251 P P P LNCV6_132027_PI430048170 mRNA
ACTTCATATTTGGGTAGGTTAAGCTGCCATACGTGTTCAGTGTGAATAGTGTTTAAGTTG NM_001033112 RefSeq
chr5 + 139342433 139369720 PAIP2 51247 "poly(A) binding protein interacting protein 2, transcript
variant 1"
GO:0005515|GO:0005737|GO:0045947|GO:1900271|GO:0007613|GO:0030371|GO:0007283|GO:0003729 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142100_PI430048170 0.0028581503452282 0.7164484700878158.76444413592084
8.62617663869496 8.59008017760649 P P P 9.20836797116059 9.17493262971786
9.04115370920912 P P P LNCV6_142100_PI430048170 mRNA
ATGGGTAACAGTATTGGGGCCAGATCCCTAAGCCCCCCAGCTGTAAATAGGCTGTGGCCA NM_001135999 RefSeq
chr9 + 35538631 35561898 RUSC2 9853 "RUN and SH3 domain containing 2, transcript variant 1"
GO:0005515|GO:0008150|GO:0017137|GO:0031410|GO:0070062|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137891_PI430048170 0.00920213427902097 0.5808405868179138.22424491748704
7.84736454529049 8.08500728711087 P P P 8.86286146667409 8.60924726914681 9.029978036544
P P P LNCV6_137891_PI430048170 mRNA
CAGCACCTCTTGGTTAAATAATGTATGCTGTGAGACATGAAATTAAAACAGACCTATGAA NM_005667RefSeq chr2

- 86603392 86623877 RNF103 7844 "ring finger protein 103, transcript variant 1"
GO:0005515|GO:0004842|GO:0016567|GO:0005783|GO:0016874|GO:0005789|GO:0008270|GO:0016021|GO:0030
433|GO:0007417 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110343_PI430048170 0.00929945852820098 1.48775580753565 6.51684205828702
6.82773837875849 6.62775424189456 P P P 6.20542975684509 5.99932729933849
6.05763070609079 P P P LNCV6_110343_PI430048170 mRNA
AGCTGGTGAGAGTATCACAGACTCCTGTTGCAACAGCATCAGGGCCCAACTTCTCCCTGG NM_001271043 RefSeq
chr19 + 13024580 13098796 NFIX 4784 "nuclear factor I/X (CCAAT-binding transcription factor),
transcript variant 1"
GO:0021707|GO:0006260|GO:0003700|GO:0006366|GO:0021680|GO:0048708|GO:0045944|GO:0003705|GO:0005
634|GO:0000122|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134284_PI430048170 0.540804929928439 0.864482197048637 3.17000400019115
2.06454501082629 0.47854268500856 P A A 2.7236991837112 2.255948578897
2.45412736375903 P A P LNCV6_134284_PI430048170 mRNA
CTATTAGTAGAACCAAATTTCTAAGCTGTGGCGTGCTGAAAATAAAATGCTTATGAAGCA NM_001463 RefSeq chr2
- 182833275 182866770 FRZB 2487 frizzled-related protein
GO:0042813|GO:0017147|GO:0010721|GO:0030308|GO:0043065|GO:0008285|GO:0004930|GO:0030178|GO:0005
615|GO:0070367|GO:0060029|GO:0061053|GO:0001501|GO:0016020|GO:0014033|GO:0045600|GO:0090103|GO:0
061037|GO:0016021|GO:0090090|GO:0035567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64953_PI430048170 0.0600434901949133 0.953830797701759 0.422603675442233
0.355512718553926 0.373469852674147 A A A 0.455326957249031 0.464892146144618
0.436647276587372 A A A LNCV6_64953_PI430048170 mRNA
TTGAACTTTTGGGTTCAAACTCAGAAGGAGTCACAGATCTTAGACTGTGGCTATGCCAGC NM_001002923 RefSeq
chr19 - 46039747 46041016 IGFL4 NA IGF-like family member 4 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133780_PI430048170 0.0486564521838079 0.751870773377523 12.618753050522
12.8523206780331 12.9891730460733 P P P 13.1712002584602 13.0999711010499
13.4266223916217 P P P LNCV6_133780_PI430048170 mRNA
AGTTAAGCGTGCATAAGTTAACTTCCAATTTACATACTCTGCTTAGAATTTGGGGGAAAA NM_004048 RefSeq
chr15_KI270849v1_alt + 34835 41507 B2M 567 beta-2-microglobulin
GO:0005515|GO:0002474|GO:0005886|GO:0019221|GO:0002237|GO:0055072|GO:0005615|GO:0042802|GO:0042
026|GO:0005737|GO:0001895|GO:0030670|GO:0016032|GO:0070062|GO:0060333|GO:0012507|GO:0002480|GO:0
033077|GO:0002481|GO:0005794|GO:0042612|GO:0042493|GO:0042590|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138548_PI430048170 0.2220754281220181 1.17146875613729 8.89622345336056
8.87170901573717 9.19106489150696 P P P 8.5375451543476 8.77031106252803
8.95801744153101 P P P LNCV6_138548_PI430048170 mRNA
AAGATGAAAGCTATTGGATGGGGAAAGAAGACTCTGGACCAGGTCTTAGAGGATGTAGAC NM_006554 RefSeq
chr2 + 176269394 176338025 MTX2 10651 "metaxin 2, transcript variant 1"
GO:0006626|GO:0005741|GO:0044267|GO:0006839 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70370_PI430048170 0.127117933449675 0.880243959179279 3.75160689807995 3.80027230969976
3.98680576399497 P P P 3.96653598297998 4.15827508216577 3.96823255631375 P P P
LNCV6_70370_PI430048170 mRNA
GCCAGTATCACAAATGAACTACAGACTGTTCAGAATGAGAAAACCCAACTCCAGGCACAT NM_001080539 RefSeq
chr2 + 196639631 196732806 CCDC150 284992 coiled-coil domain containing 150 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129466_PI430048170 0.241192362745975 1.32819863565342 3.00316420491163
3.11819538381498 2.37483811209431 A P A 2.18690950625799 2.42536597774703
2.71238275353014 A A P LNCV6_129466_PI430048170 mRNA

GTCCACAGACATCACATTTCTACTAAAAACAGGAAGCCCAGAAGCTTTGAAAGAAAGATA NM_033215 RefSeq chrX + 49269842 49288093 PPP1R3F 89801 "protein phosphatase 1, regulatory subunit 3F, transcript variant 1" GO:0005979|GO:0016020|GO:2001069|GO:2000465|GO:0019903|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139865_PI430048170 0.0105402125866522 1.07688737845694 0.391870896818811 0.4020092016747570.35479877198291 A A A 0.2454036381304690.307094092066834 0.275346180074441 A A A LNCV6_139865_PI430048170 mRNA
GTCACATACATGGTTGTCTTTATGTAACTTAATTTTTTCATCCGCAGGTGCCATTTTCAT NM_001164749 RefSeq chr14 + 32939252 33804176 NPAS3 64067 "neuronal PAS domain protein 3, transcript variant 1" GO:0001964|GO:0042711|GO:0007165|GO:0005737|GO:0046983|GO:0007626|GO:0005654|GO:0004871|GO:0045893|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142631_PI430048170 0.872222714831326 1.19378748807045 4.02505035795404 2.43357344611193 2.76597982691333 P A A 3.08166060729782 3.07689610075019 2.79843946795342 P P P LNCV6_142631_PI430048170 mRNA
AGCTGATGCATTGCTGGTCTCTCATCTGCAGCTTCCACAGAGTGCCAAGCCCCTCACTCA NM_001080468 RefSeq chr19 - 39202921 39204266 SYCN 342898 syncollin GO:0006887|GO:0030667|GO:0030658 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64211_PI430048170 0.00523929641975074 1.64274102411719 13.3614622925947 13.5402799867065 13.4797334741849 P P P 12.7261760375294 12.5899476986209 12.9053225035242 P P P LNCV6_64211_PI430048170 mRNA
AAGATGAGGTATTAATCCCCTCCATTGCTCTCCAAAAGCCAATAAAGTGATTACACCCGA NM_004152 RefSeq chr19 + 2269485 2273488 OAZ1 4946 "ornithine decarboxylase antizyme 1, transcript variant 1" GO:0005515|GO:0034641|GO:0008073|GO:0045732|GO:0006596|GO:0006521|GO:0006810|GO:0090316|GO:0044281|GO:0043086|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80351_PI430048170 0.909828230055276 0.986485596011282 0.559590192107922 1.0488956423389 0.490405486101626 A A A 0.300651571381401 1.35041153147954 0.303186844325059 A A A LNCV6_80351_PI430048170 mRNA
AATTTAGAGGGGCCACCTATCAACTCATCAGTGTTCAAAGAATATGCTGGGAGCATGGGT NM_001160354 RefSeq chr8 + 142700110 142704166 LY6K 54742 "lymphocyte antigen 6 complex, locus K, transcript variant 2" GO:0005737|GO:0005886|GO:0005730|GO:0005634|GO:0005576|GO:0031225 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139690_PI430048170 0.0255712918150034 0.70378015870922 9.40755393765985 9.19841794718044 9.41348291184587 P P P 9.7447542460672 9.71631464405904 10.0627751285627 P P P LNCV6_139690_PI430048170 mRNA
AAATACCTTCTCTAGGTAAGACACTTGGTAGATGAGAGACGGAAGGCATTGTCAAGAACC NM_006811 RefSeq chr20 - 44499259 44522085 SERINC3 10955 "serine incorporator 3, transcript variant 1" GO:0006665|GO:0015194|GO:0005794|GO:0005886|GO:0015825|GO:0016021|GO:0006658 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134466_PI430048170 0.21413277308617 0.795142715415477 5.68295325625371 5.73904837858547 6.02288294813979 P P P 5.80569125715182 6.41423156284241 6.17660993984938 P P P LNCV6_134466_PI430048170 mRNA
CAGCCCTGTTCCTGGTCCAAGTACTTTGTATTGTATACGTGAGTCATAATAATAAAAAGA NM_022658 RefSeq chr12 + 54009105 54012761 HOXC8 3224 homeobox C8 GO:0043565|GO:0003700|GO:0030182|GO:0015630|GO:0048705|GO:0005654|GO:0000122|GO:0009952|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_38410_PI430048170 0.222283154019137 1.17128142700132 12.3732933532898 12.6010741454368 12.8057706705676 P P P 12.2216770351764 12.3894483245919 12.503235382399 P P P LNCV6_38410_PI430048170 mRNA
TTGAAACCAAGTCTGTTTCTTGTTTTGTATTTTCTCTCTGGAAGTTGTAAGGAGGTGGTC NM_001204083 RefSeq

chr1 + 19596976 19629821 MINOS1 440574 "mitochondrial inner membrane organizing system 1, transcript variant 5" GO:0005739|GO:0008150|GO:0003674|GO:0005743|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55280_PI430048170 0.0409189021631321 0.613775474841491 4.61300390404949 5.00064651311374 5.200731437213 P P P 5.54273412249076 5.70373449951472 5.7337452435438 P P P LNCV6_55280_PI430048170 mRNA
TGAATGGTATTAAATTTTAGTCTCTGGAACATCCAAAACCAAGCAAAGGGATGTGACTAT NM_024529 RefSeq chr1 + 193121957 193254812 CDC73 79577 cell division cycle 73
GO:0005515|GO:0008285|GO:0033523|GO:0048147|GO:0050680|GO:0030177|GO:0005634|GO:0001711|GO:0031648|GO:0045638|GO:0045944|GO:0016055|GO:0006378|GO:0000993|GO:2000134|GO:0000122|GO:0006351|GO:0007049|GO:0071222|GO:0019827|GO:0032968|GO:0016593|GO:0005654|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131939_PI430048170 0.00585073564715881 0.462589698168217 7.36982792642377 7.42683724564237 7.11189968754776 P P P 8.45936877259814 8.40518160836899 8.39894843323899 P P P LNCV6_131939_PI430048170 mRNA
CACACCTGGGACTGTTTTTAATACATAGCAACAGACTGGGTTATTTATTTAAGATGTGTA NM_018964 RefSeq chr21 + 42499631 42581440 SLC37A1 54020 "solute carrier family 37 (glucose-6-phosphate transporter), member 1" GO:0005215|GO:0016020|GO:0008643|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138481_PI430048170 0.000314238244516109 6.40317648801489 5.15033735227076 5.15781377758642 5.32052409044447 P P P 2.32772395796863 2.72864296402107 2.51449560785256 A P P LNCV6_138481_PI430048170 mRNA
GCTGGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAACTGAGCTACGAAAAA NM_001327 RefSeq chrX - 154617608 154619271 CTAG1B NA cancer/testis antigen 1B NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139569_PI430048170 0.000900855262761114 0.39102756196921 6.00792634604285 5.88005786210821 6.25070190547029 P P P 7.34653811029525 7.24750540012169 7.60890495108267 P P P LNCV6_139569_PI430048170 mRNA
CCTGACTACTACCTTCATATTTCATTTCAAATTCAAACTTCTGAGGTTGCAGCATATATG NM_017988 RefSeq chr12 + 100267770 100340136 SCYL2 55681 SCY1-like 2 (S. cerevisiae)
GO:0005515|GO:0048471|GO:2000370|GO:0005794|GO:0008333|GO:0030136|GO:0005102|GO:0005524|GO:0004672|GO:0006468|GO:0090090|GO:0002092|GO:0010008|GO:2000286 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55518_PI430048170 0.568931012495115 0.95399144940134 7.17269085354767 6.81622671892533 7.11118923766367 P P P 7.15162918410083 7.12733578261434 7.0475203942237 P P P LNCV6_55518_PI430048170 mRNA
GTGTCAAGTGCTTACTGATTTGATTGATGAAGAAGTAAAAAGTGGCATCAAGAAGAACAG NM_138794 RefSeq chr1 + 219173830 219212865 LYPLAL1 127018 "lysophospholipase-like 1, transcript variant 1"
GO:0008150|GO:0002084|GO:0005737|GO:0004622|GO:0042997|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140527_PI430048170 0.170204633874812 1.03780710877124 0.348719600705798 0.313820744576595 0.404256906491824 A A A 0.296915981797438 0.284351120026328 0.326042674348655 A A A LNCV6_140527_PI430048170 mRNA
TTGCTTTTTGTCTGAGTGCCTAATTTTGTGTTTTGTGTCTGAGTGCCTCAGTTCCTCAAA NM_001184879 RefSeq chr1 - 160541093 160579516 CD84 8832 "CD84 molecule, transcript variant 1"
GO:0005515|GO:0005886|GO:0007596|GO:0005887|GO:0006952|GO:0004872|GO:0050900|GO:0007156|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145544_PI430048170 0.152015513389424 1.09121648807755 0.513528644259527 0.670097803317044 0.641702312585083 A A A 0.58729409469611 0.424642298244593

0.43452432761446 A A A LNCV6_145544_PI430048170 mRNA
CCACTTTGCAAACTTTAACTACACATGCTTGGAATTAAGTTTTAGCTGTTTTCATTGCTC NM_005752 RefSeq chr16 +
78022545 78032104 CLEC3A 10143 "C-type lectin domain family 3, member A, transcript variant 1"
GO:0001501|GO:0030246|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133356_PI430048170 0.0812055539076209 0.56088359700429311.0568193387601
10.2321006125212 10.1296642931853 P P P 11.4719813312834 11.4515741444046
11.1664651296865 P P P LNCV6_133356_PI430048170 mRNA
TCCCTCCCTTCCCTCTCCTTGAGTGCATTTTGAATTAAAGCCTATATTGAAAAGAAAAAA NM_175885 RefSeq chr11
- 82732003 82733864 FAM181B 220382 "family with sequence similarity 181, member B" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_138308_PI430048170 0.195706897328318 0.805789733687439 4.3585897852408
3.77983402213758 4.23825695901943 P P P 4.45639033999231 4.31443829154961
4.58957604827327 P P P LNCV6_138308_PI430048170 mRNA
CACCATGGACTTAGGCTTGATTAAAATGCTACACATTTAGAGCGTTTTGTAATTCCTTTT NM_213598 RefSeq chr19
+ 57320496 57330776 ZNF543 125919 zinc finger protein 543
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136690_PI430048170 0.555681938563713 1.00776886842849 0.317234247642752
0.344089286169311 0.367751819788748 A A A 0.343919426368188 0.336308070594183
0.315647984585663 A A A LNCV6_136690_PI430048170 mRNA
GTGGCTGTTTACCCACAATGAAAGAGTTCTAATAAAGATGTGCTGAAGTTGCAATATAAA NM_005249 RefSeq chr14
+ 28767071 28770277 FOXG1 2290 forkhead box G1
GO:0043565|GO:0005515|GO:0003700|GO:0007420|GO:0007568|GO:0005634|GO:0045892|GO:0003677|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96029_PI430048170 0.160008930655427 0.918384662763519 8.58606451413699 8.62473734487066
8.62138701352706 P P P 8.61927965932548 8.7788818346947 8.79631979010708 P P P
LNCV6_96029_PI430048170 mRNA
TATTTAATGCTGTAAAGTTGGACTGTTGTTCAATAAACCAGAGCAATGCATTAGCTCCTC NM_001171135 RefSeq
chrY - 2486413 2500539 ZBED1 9189 "zinc finger, BED-type containing 1, transcript variant 3"
GO:0008152|GO:0046983|GO:0000228|GO:0003677|GO:0046872|GO:0004803 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139320_PI430048170 0.219046397501581 1.04146719855355 0.33693724237931
0.30803564088907 0.419624821444314 A A A 0.296202158702027 0.27731310816117
0.317290579216007 A A A LNCV6_139320_PI430048170 mRNA
AGTTCGCTCATTCCAACTAATCATCATCTTCAAGTTTTCCACCAAGGTACCTACATTCTA NM_138697 RefSeq chr1
+ 6555277 6579757 TAS1R1 80835 "taste receptor, type 1, member 1, transcript variant 2"
GO:0050912|GO:0046982|GO:0007186|GO:0005886|GO:0008527|GO:0016021|GO:0050917 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_93784_PI430048170 0.718467903122355 1.09078822761828 3.49373013542928 2.83803262568191
3.53782849851207 P A P 3.16074661559077 3.37443156367345 3.03851057382266 P P P
LNCV6_93784_PI430048170 mRNA
AGAGTACATGGATGTGGTGGAGCAGCAGACAGAGAACCTGGAGCTGCACACCAATGCCCT NM_015089 RefSeq
chr6 + 43182183 43224587 CUL9 23113 cullin 9
GO:0005515|GO:0031461|GO:0006511|GO:0007088|GO:0005737|GO:0016567|GO:0000226|GO:0008270|GO:0005
524|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130980_PI430048170 0.567190262878411 0.924066979351152 9.94695999082491
9.94081070898785 9.92039082057451 P P P 10.3252269274625 9.90762112563943
9.87187703528731 P P P LNCV6_130980_PI430048170 mRNA
ATTCCTAATTCTGCCGTTGTAATGAGACTTGATTAAAACACCGCCACTTTTTTGCATTGC NM_181491 RefSeq chr9

- 133340900 133348156 MED22 6837 "mediator complex subunit 22, transcript variant c"
GO:0005515|GO:0005737|GO:0001104|GO:0006366|GO:0006357|GO:0016592 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140205_PI430048170 0.25239911348351 0.5675475807936862.95090137543059
2.10094099137115 2.92012005205578 A A P 2.54228199128854 3.54646307844431
4.08832155495209 A P P LNCV6_140205_PI430048170 mRNA
CCTGTACAGAACAGTACCTTGGCATTCAGCAGCTGTAATTGGGGAACATTAAAACAGTAA NM_022041RefSeq chr16
+ 81314965 81380198 GAN 8139 gigaxonin
GO:0005515|GO:0003674|GO:0005737|GO:0016567|GO:0031463|GO:0005856 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138187_PI430048170 0.6638773025969521.1509895310614 2.27652659120235
1.16714904514764 1.42946206852279 A A A 0.38656210839266 1.47540720451914
2.14170182694177 A A A LNCV6_138187_PI430048170 mRNA
CTACCACCTGAGTAGAGGGCTGAGGGCAGCTGGGGGAGGGGAATTAAAGCGTATTTAGTG NM_001282477
RefSeq chr9 - 137170927 137172046 TMEM210 100505993 transmembrane protein 210 GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65080_PI430048170 0.2156875433384631.21643727811849 4.11702423299771 4.54363177411426
4.60883900288103 P P P 4.30070337134358 4.07661538695865 4.0802746275593 P P P
LNCV6_65080_PI430048170 mRNA
CAACAAATGGGAAAAGTTAACATTTGCACCATCTTGCCATATTCAAAAACCTTGTGCTTA NM_001290149 RefSeq
chr19 - 50797692 50804853 C19orf48 84798 "chromosome 19 open reading frame 48, transcript
variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132954_PI430048170 0.7904398073458160.9821695671358565.66681821750243
5.34732236127399 5.385693436566 P P P 5.56810736988693 5.42559223498604
5.50201101420721 P P P LNCV6_132954_PI430048170 mRNA
AGGTGCTCACATTCCTTAAATTAAGGAGAAATGCTGGCATAGAGCAGCACTAAATGACAC NM_017411RefSeq chr5
+ 70049522 70077595 SMN2 6607 "survival of motor neuron 2, centromeric, transcript variant d"
GO:0005515|GO:0000245|GO:0010467|GO:0030018|GO:0015030|GO:0003723|GO:0005634|GO:0034660|GO:0000
387|GO:0042802|GO:0005829|GO:0007399|GO:0005737|GO:0032797|GO:0005654|GO:0005681|GO:0034719 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127175_PI430048170 0.0318644544730435 0.4585539688554648.1989438616627
8.09100820072133 8.35709148561967 P P P 8.87012353095778 9.39736324529406
9.65863684842713 P P P LNCV6_127175_PI430048170 mRNA
CCAAGTTGTGCTTTTCTGTTTTCAAGTGTAAATGATGTTGAGCAGAATGTTGTACTTGAA NM_021205RefSeq chr1
+ 228735076 228746669 RHOU 58480 "ras homolog family member U, transcript variant 1"
GO:0005515|GO:0051056|GO:0030036|GO:0005886|GO:0007264|GO:0008360|GO:0002102|GO:0003924|GO:0042
995|GO:0005525|GO:0046872|GO:0005829|GO:0006184|GO:0016601|GO:0000082|GO:0000139|GO:0007010|GO:0
005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145505_PI430048170 0.1677607732938810.6680394751599835.95723119133742
5.76042943898639 6.40957505187945 P P P 6.14624725474584 6.60220188618582
7.05984429217366 P P P LNCV6_145505_PI430048170 mRNA
TTTAGAACCTGCTTCTCTGATCTGTGTGTTTCCTCACTTCTCAATAAAAATGTCTTTTGC NM_001256279 RefSeq chr12
+ 132986347 133012568 ZNF26 7574 "zinc finger protein 26, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127890_PI430048170 0.2570641305215561.92021579503842 0.318519792677325
0.7883974211814711.96435568650982 A A A 0.2561011922996590.252587386686738
0.257693251848784A A A LNCV6_127890_PI430048170 mRNA
GTGATGCACTAATTGCATCAACAGGGTTATTTATGGATTCGTTATTGTCTCTCCAATTTTNM_001164434 RefSeq chr21

- 30590104 30590397 KRTAP22-2 NA keratin associated protein 22-2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139725_PI430048170 0.0448869384616985 0.7744379512825067.58826239535321 7.54805791892527 7.77991520260974 P P P 7.84723403016933 7.97961801815666 8.18614131819873 P P P LNCV6_139725_PI430048170 mRNA CCAGTTTTTGTATTTGTGAACTCATCTGTGGGAGGAGTAAAGAAAATCCAAAAGCATTTA NM_017426RefSeq chr4 - 76114658 76148515 NUP54 53371 "nucleoporin 54kDa, transcript variant 1" GO:0007077|GO:0010467|GO:0031965|GO:0005975|GO:0019083|GO:0019221|GO:0019058|GO:0044281|GO:0005635|GO:0006605|GO:0055085|GO:0010827|GO:0006913|GO:0008645|GO:0005737|GO:0015758|GO:0005487|GO:0005643|GO:0009405|GO:0016032|GO:0005654|GO:0051028|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132268_PI430048170 0.6522599281141010.9309295214274728.36936643843583 7.52678885758405 7.68730440723411 P P P 8.00514750150386 8.202093859225 7.80300945744833 P P P LNCV6_132268_PI430048170 mRNA GGAAACATGGTCCAGTTTTGTGTGTGTGCGTGTGTGTAAATGTGTACACACAGACATAAA NM_004621RefSeq chr11 - 101451563 101583928 TRPC6 7225 "transient receptor potential cation channel, subfamily C, member 6" GO:0005515|GO:0070301|GO:0005886|GO:0051928|GO:0007568|GO:0071456|GO:0030168|GO:0032414|GO:0055085|GO:0007204|GO:0070679|GO:0034220|GO:0007411|GO:0007596|GO:0036057|GO:0070588|GO:0015279|GO:0016021|GO:0006812. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126854_PI430048170 0.1375235604773531.21130917558556 7.03434962628039 6.97750800776862 7.28466357340102 P P P 6.72903280625612 6.67885970109665 7.04914862723209 P P P LNCV6_126854_PI430048170 mRNA GCCACAGATTCCCTTCTTTACTAAACAAATCCCATGGATTCTGATTTCTGGGTCTTAGGA NM_021977RefSeq chr6 + 160348372 160452579 SLC22A3 6581 "solute carrier family 22 (organic cation transporter), member 3" GO:0005515|GO:0019534|GO:0005329|GO:0005886|GO:0015695|GO:0015697|GO:0015872|GO:0032098|GO:0044281|GO:0055085|GO:0015101|GO:0015651|GO:0051615|GO:0016020|GO:0005887|GO:0006855|GO:0072488 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131479_PI430048170 0.4307673345406970.2030243847414560.496072328617335 0.5152715807367420.404949613079126A A A 4.15243182575125 0.443900464589285 0.448805472929372P A A LNCV6_131479_PI430048170 mRNA ACCATTCCAACCTGGGTTCATGAACACAATATCTGTTCAGATCCAGCCAATTTCAAAGAT NM_001005170 RefSeq chr11 + 4586790 4587905 OR52I2 NA "olfactory receptor, family 52, subfamily I, member 2"NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138085_PI430048170 0.1186914975440140.59645108173536 1.42260627664685 2.41625601677204 1.6660792371475 A A A 2.24323416593159 2.50988202497715 3.05902404508807 A P P LNCV6_138085_PI430048170 mRNA AGTGGAAACGTGCTAACTTTTTCTGTAAATCTGAAATAAAAGGTGCTGTTCCTTCCTCTG NM_133334RefSeq chr4 + 1900625 1948818 WHSC1 7468 "Wolf-Hirschhorn syndrome candidate 1, transcript variant 7" GO:2001032|GO:0005515|GO:0003289|GO:0034770|GO:0005694|GO:0048298|GO:0010452|GO:0006325|GO:0005634|GO:0000122|GO:0009653|GO:0003290|GO:0006351|GO:0018024|GO:0043565|GO:0060348|GO:0005737|GO:0003149|GO:0003682|GO:0070201|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136315_PI430048170 0.1780024849581830.68083394009222 0.258654795965063 0.2700877341606080.416277863992976A A A 1.09023874304106 1.07929936737705 0.317708182503844A A A LNCV6_136315_PI430048170 mRNA ATCATTAGGCTGAACTGTCTCTTATAGAATGAGGTCAAAGACACTCCCAGTTGCAGGGAG NM_152654RefSeq chr19 + 12969617 12974753 DAND5 199699 "DAN domain family member 5, BMP antagonist" GO:1900108|GO:0030514|GO:0016015|GO:0003140|GO:0003283|GO:0005576|GO:0003281|GO:0038101|GO:0061

371|GO:0030512 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92442_PI430048170 0.0722310085763922.96415043608923 2.77362853864403 4.3092582997959
3.65681069357191 A P P 2.08758283454174 2.38025715266603 1.923619097268 A A A
LNCV6_92442_PI430048170 mRNA
GATCTCCGGATGGGGAAATACGCAGGAAGGAAATGCCACCAAGCCCGAGCTCCTGCAGAA NM_182973 RefSeq
chr19 + 2389785 2426088 TMPRSS9 360200 "transmembrane protease, serine 9"
GO:0004252|GO:0005887|GO:0006508|GO:0031639 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59022_PI430048170 0.24119470031749 1.20701647275326 3.35080555484351 2.90650348462788
3.14979062998913 P A P 3.14931389374517 2.80063036464575 2.62706405236763 P P P
LNCV6_59022_PI430048170 mRNA
AACCTGGAGCCGTTGTTCGAGCAGTACATCAACAACCTCAGGAGGCAGCTGGACAGCATCNM_173086 RefSeq chr12
- 52468515 52473785 KRT6C 286887 "keratin 6C, type II"
GO:0005882|GO:0005198|GO:0045104|GO:0045095|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131720_PI430048170 0.1853828892254340.7436992946754585.2453185602717
5.70381952334283 6.06730599597186 P P P 6.07333646954745 6.08513911584983
6.24843132467273 P P P LNCV6_131720_PI430048170 mRNA
GCAAATCGGGCTTAATCTTAAAATTGGTGGTCATTTCAATGGTTGACATATTTGGCTATT NM_004280 RefSeq chr6
- 8079394 8102595 EEF1E1 9521 "eukaryotic translation elongation factor 1 epsilon 1, transcript
variant 1"
GO:0005515|GO:0010467|GO:0005737|GO:0043065|GO:0008285|GO:0043517|GO:0005634|GO:0070062|GO:0006
418|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141462_PI430048170 0.5072759852090561.54456558416322 2.75778447988013
0.7705615501546842.06253495352458 A A A 1.23929864026285 0.793425378381886
2.03345653921861 A A A LNCV6_141462_PI430048170 mRNA
CACTCTAACCTCTCCAGCTTATCTAACATGTCATAAACATAATAAATCTGTGTTGTCCAA NM_057157 RefSeq chr10
+ 93073474 93077884 CYP26A1 1592 "cytochrome P450, family 26, subfamily A, polypeptide 1,
transcript variant 2"
GO:0006805|GO:0005506|GO:0071300|GO:0044281|GO:0007417|GO:0009952|GO:0048384|GO:0014032|GO:0019
825|GO:0048387|GO:0006766|GO:0034653|GO:0001972|GO:0008152|GO:0005789|GO:0008401|GO:0055114|GO:0
020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138895_PI430048170 0.1262270490881090.9433014365385740.252761818287692
0.2673279231473820.31833871903074 A A A 0.4309182425756930.345848246865919
0.312516830862287 A A A LNCV6_138895_PI430048170 mRNA
CACTTTTGGAGATTCCCATTTCAGGGAGTTTCTTCTGGGGGTTAACATAACGTATCAATG NM_197965 RefSeq chr4
- 86823467 86849263 SLC10A6 NA "solute carrier family 10 (sodium/bile acid cotransporter), member
6" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114377_PI430048170 0.00736125441967796 0.5657139578829844.976770844775
4.82667847228332 5.08079507662992 P P P 5.79614281706669 5.77130665051856
5.79347828654789 P P P LNCV6_114377_PI430048170 mRNA
TAAAATGGTGGACAGGCACCAAAGCTATTTTCTCATCTGTCCTGTGGATGAGTGGAACTG NM_001143942 RefSeq
chr6 + 17281577 17293868 RBM24 221662 "RNA binding motif protein 24, transcript variant 1"
GO:0043488|GO:0005737|GO:0000166|GO:0010830|GO:0005634|GO:0003730|GO:0030154 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137499_PI430048170 0.0541957993486713 0.8492762352574 10.5279474017315
10.6115322034141 10.7009397484179 P P P 10.7629721743438 10.7989777222108
10.9811336471623 P P P LNCV6_137499_PI430048170 mRNA
AGACTTTGTTCTTAGAATGGAGCCTGTGTATCTACTATCTCCAGTTTGTATTATTTCTTG NM_001145415 RefSeq chr1
+ 150926338 150964744 SETDB1 9869 "SET domain, bifurcated 1, transcript variant 1"

GO:0005515|GO:0000790|GO:0005886|GO:0001833|GO:0006325|GO:0005634|GO:0000122|GO:0003677|GO:0006
351|GO:0043231|GO:0018024|GO:0060348|GO:0005737|GO:0036124|GO:0005654|GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134724_PI430048170 0.13124387238822 1.27693392724806 10.7350284905782
10.5767809805054 10.3240775736801 P P P 10.4003022072358 10.2505166415992
9.91449409013783 P P P LNCV6_134724_PI430048170 mRNA
GAAACTATTTATTGGTGCTCCTGTGATACCGAATTAAATACGGAGGAAAAACAGGAAAAA NM_198850RefSeq chr19
- 43475102 43504833 PHLDB3653583 "pleckstrin homology-like domain, family B, member 3"
GO:0019899 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130735_PI430048170 0.000547500686255685 0.41716934828752 5.31659265262842
5.13607610719723 5.24051920547046 P P P 6.49980143651255 6.45821126026447
6.52396773537353 P P P LNCV6_130735_PI430048170 mRNA
CTACTTTCAGTGAGAGTATGCCTTCACTATGTTAAAAAATAAGCTCATAAAACAGGGTAC NM_152387RefSeq chr2
- 200488960 200510069 KCTD18130535 potassium channel tetramerization domain containing 18
GO:0051260 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93361_PI430048170 0.9776997187953670.9991644341562781 0.4166561006776 10.3025420935788
10.2916995521804 P P P 10.1661974650033 10.4624618847505 10.3734091414946 P P P
LNCV6_93361_PI430048170 mRNA
AGTCATCTTTGATCAATTGGTCGTAACCCACAAAATCCTTCGGAAGGCCAGAGGAAACCT NM_018249RefSeq chr9
- 120388868 120580170 CDK5RAP2 55755 "CDK5 regulatory subunit associated protein 2, transcript
variant 1"
GO:0005515|GO:0008017|GO:0005516|GO:0048471|GO:0030054|GO:0044212|GO:0001578|GO:0000132|GO:0005
829|GO:0005737|GO:0007059|GO:0015631|GO:0000086|GO:0005856|GO:0000242|GO:0070062|GO:0022008|GO:0
090231|GO:0005813|GO:0005794|GO:0006996|GO:0019901|GO:0005874|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140573_PI430048170 0.6830185172698241.02368682343227 0.271858997239023
0.2878898242815580.473950866558565 A A A 0.3387114704133250.29447358771739
0.307703941930401 A A A LNCV6_140573_PI430048170 mRNA
GACAGAAACTAATCCTTACTATCCTATTAGGATACCACTTTTCATTGCAAAGTTTGTGTC NM_024812RefSeq chr8
+ 103140692 103230305 BAALC 79870 "brain and acute leukemia, cytoplasmic, transcript variant 1"
GO:0005737|GO:0016020 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138018_PI430048170 0.276231591199064 1.12423536624221 10.3707504234545
10.2298721744549 10.1340973550945 P P P 10.2930410943603 10.0076218880075
9.90903143359338 P P P LNCV6_138018_PI430048170 mRNA
ACCTTCTGAGCCTGCGCCCACACTATTGAAAACACTAATGAAAGTACTCCTCTGAAAAAA NM_138463RefSeq chr17
- 28724347 28726212 TLCD1 116238 "TLC domain containing 1, transcript variant 1"
GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131633_PI430048170 0.511550532918476 0.967469306924841 0.443391822433144
0.452126759427462 0.264284220056684 A A A 0.395982795616015 0.480504517174712
0.432884420807341 A A A LNCV6_131633_PI430048170 mRNA
CTCTCCATTTATTTAGTGATCGAAACACGATAGCATGGTAGTAAATTAGGCATTTCCTAA NM_182506RefSeq chrX
+ 27807989 27823014 MAGEB10 139422 melanoma antigen family B10 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_132887_PI430048170 0.275396411088689 1.03371920871136 0.438029131925957
0.350651748620941 0.391537882088435 A A A 0.299736141676817 0.339424450770023
0.397183044714665 A A A LNCV6_132887_PI430048170 mRNA
TGACCAAAGAAATGCACGAAATGTGAAGTTCTTTGTCACTGTCCTGTATATCAAGGAAAT NM_017533RefSeq chr17
- 10443290 10469559 MYH4 4622 "myosin, heavy chain 4, skeletal muscle"
GO:0003725|GO:0030048|GO:0005516|GO:0014823|GO:0030049|GO:0006200|GO:0003779|GO:0030016|GO:0005

524|GO:0030017|GO:0032982|GO:0000146|GO:0006936|GO:0061024|GO:0005859 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130424_PI430048170 0.25919095268169 1.0586040140417 0.503583482668471 0.3240714624459550.415822923060283 A A A 0.2823736144781140.356921697755181 0.361906634457209 A A A LNCV6_130424_PI430048170 mRNA TTGAGGAATAAGGATGATAAACTTGCCCTGGGCAAAACCCTGAAGAGAGTGCTCTTCTAA NM_001005196 RefSeq chr11 - 124423941 124424871 OR8B4 NA "olfactory receptor, family 8, subfamily B, member 4 (gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133828_PI430048170 0.0342853630854082 1.05898275165726 0.351687526248651 0.3685001756215050.301257008174934 A A A 0.2443416944382980.282291366340881 0.24731059652761 A A A LNCV6_133828_PI430048170 mRNA GAACTGGTCCGTGCACAGTCAGCACAAAAAACTCAAACGAATAAAAAAGAGAAAGTCTGG NM_001886 RefSeq chr22 + 26621963 26630672 CRYBA4 1413 "crystallin, beta A4" GO:0003674|GO:0005212|GO:0043010|GO:0005575|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128192_PI430048170 0.3093517962833841.0803227625134 0.537335996426861 0.2732336389172230.339683576334747 A A A 0.2861842484517350.268590712004659 0.274284127857601 A A A LNCV6_128192_PI430048170 mRNA AGTATCCTAAGAGTTAAGGCACATCAAACACAGGAGTCGAGAGAGTGCAGTTCAGGGAAA NM_000330 RefSeq chrX - 18639687 18672103 RS1 6247 retinoschisin 1 GO:0016062|GO:0043325|GO:0080025|GO:0070273|GO:0005547|GO:0005546|GO:0007275|GO:0010842|GO:0032266|GO:0005615|GO:0001786|GO:0007155|GO:0007601|GO:0010314|GO:0019897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145280_PI430048170 0.0526667264754438 1.23192354685794 5.24459984849369 5.21630546591114 5.27752720160895 P P P 5.09484142988042 4.88235863923939 4.84645695979203 P P P LNCV6_145280_PI430048170 mRNA GTTGCCAATTCCATTTTAAAATGCCACAGATGCGTGTTGCTCCCAGTCTGTGGTTAAACG NM_020225 RefSeq chr4 + 183905355 184017722 STOX2 56977 storkhead box 2 GO:0003674|GO:0001893|GO:0009790|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137758_PI430048170 0.0187017651748591 0.5122071222325019.66756025159466 9.6168678248367 9.73133925690199 P P P 10.3432814106749 10.6910189368621 10.8359847167282 P P P LNCV6_137758_PI430048170 mRNA CACTGGCCTCAATACCTTGTTTAGGATTTCTTCACCCTTTTGTCAAATTGTTATTTAAAG NM_001080826 RefSeq chr8 - 8317735 8381834 SGK223 157285 homolog of rat pragma of Rnd2 GO:0018108|GO:0005524|GO:0004715 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61152_PI430048170 0.5007552532508070.8338446282247530.3188324843278810.281310007817146 0.418183649918121 A A A 0.2895413135934961.07568048699686 0.293808935649294 A A A LNCV6_61152_PI430048170 mRNA TCGCCAAGCGGCGTTTGGCAATATCAGATATCCACTCTATTTATTTTTACCTAAGGAAAA NM_003239 RefSeq chr14 - 75958096 75982022 TGFB3 7043 "transforming growth factor, beta 3" GO:0005515|GO:0043627|GO:0043932|GO:0051491|GO:0030879|GO:0042704|GO:0048702|GO:0005615|GO:0005114|GO:0042802|GO:0043524|GO:0030198|GO:0042127|GO:0043025|GO:0051781|GO:0007179|GO:0048839|GO:0007565|GO:0030501|GO:0048286|GO:0046982|GO:0009986|GO:0045740|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136262_PI430048170 0.000383535911685465 0.3396273142317078.60137215092444 8.68023045763585 8.92788712286467 P P P 10.1745705186539 10.2126584791587 10.4949585590484 P P P LNCV6_136262_PI430048170 mRNA GTGCGTAATTGTAGATGCATGTACTTGTGTGTTTTGTGTAATTATTGAAGTGCAATGATG NM_012428 RefSeq chr15 - 73560002 73633412 NPTN 27020 "neuroplastin, transcript variant b"

GO:0009986|GO:0045743|GO:0060291|GO:0018108|GO:0005105|GO:0005524|GO:0007204|GO:0042734|GO:0010976|GO:0001934|GO:0016021|GO:0004714|GO:0050839|GO:0007156|GO:0007169|GO:0048170 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145106_PI430048170 0.2760055280893610.9502057166282039.75036104961586 9.59738724887912 9.59997614462067 P P P 9.67977699436026 9.7602376103409 9.73299424337882 P P P LNCV6_145106_PI430048170 mRNA GCCTGTGGAAGGGAGCCTTTTGCTACAATTTGTAACTTATTTTCTAAAGTCTATTTTGTA NM_014699RefSeq chr16 + 31074421 31083512 ZNF646 9726 zinc finger protein 646
GO:0005515|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137078_PI430048170 0.4394332912755680.8308991741712355.1801264396945 3.88996863360163 4.20272030838264 P P P 4.84671995723634 4.89528767397862 4.64981000860308 P P P LNCV6_137078_PI430048170 mRNA CCCCTCCACTGTCACATTGTAACTGAACTTCAGGATAATAAAGTGTTTGCCTCCAAAAAA NM_000759RefSeq chr17 + 40015360 40017813 CSF3 1440 "colony stimulating factor 3 (granulocyte), transcript variant 1"
GO:0051897|GO:0008284|GO:0019221|GO:0005130|GO:2000251|GO:0050731|GO:0007275|GO:0014068|GO:0042993|GO:0005125|GO:0005615|GO:0032092|GO:0033138|GO:0006955|GO:0071222|GO:0045639|GO:0030838|GO:0071345|GO:0045944|GO:0030851|GO:0019899|GO:0008083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121991_PI430048170 0.1150905327165511.39466049865194 6.18343199220765 6.57051659087586 6.06338767453608 P P P 6.10589367134078 5.78622688533664 5.46432710029232 P P P LNCV6_121991_PI430048170 mRNA AGACAAAGGATTGCCTGGTTCTTCTGGAGAGAAAGGGAATCCTGGAAGAAGGGTGATAAA NM_004369RefSeq chr2 - 237324011 237414207 COL6A31293 "collagen, type VI, alpha 3, transcript variant 1"
GO:0004867|GO:0005578|GO:0005576|GO:0005589|GO:0031982|GO:0005615|GO:0042383|GO:0031012|GO:0010951|GO:0007517|GO:0022617|GO:0007411|GO:0030198|GO:0030574|GO:0005788|GO:0007155|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142467_PI430048170 0.0265206141944858 0.6218572752343466.25822854117778 5.79574816256841 6.25735798268236 P P P 7.02005691131181 6.60712713838814 6.75701462090112 P P P LNCV6_142467_PI430048170 mRNA CTGCTGTCCTGTCAAATGCATCTTTTTATTTACATGTCCCTTAAATTAAAGCTGATCATG NM_003144RefSeq chr6 - 7281142 7313314 SSR1 6745 "signal sequence receptor, alpha, transcript variant 1"
GO:0005515|GO:0010467|GO:0008284|GO:0005783|GO:0006614|GO:0006613|GO:0005789|GO:0016021|GO:0006987|GO:0044267|GO:0006412|GO:0030968 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69302_PI430048170 0.0088476148691886 1.51197636559524 6.63888834606048 6.77911402936285 6.60616152873054 P P P 6.12687359462059 6.19952096841528 5.89743365953623 P P P LNCV6_69302_PI430048170 mRNA AGAGAAGCAGAAAATGTATATGGTGATGGAGTACTGCGTGTGTGGCATGCAGGAAATGCT NM_000455RefSeq chr19 + 1205798 1228435 STK11 6794 serine/threonine kinase 11
GO:0005515|GO:0030308|GO:0030111|GO:0007286|GO:0050731|GO:0030010|GO:0007409|GO:0001558|GO:0032403|GO:0046777|GO:0001894|GO:0051645|GO:0001944|GO:0070062|GO:0000287|GO:0043276|GO:0072332|GO:0042304|GO:0050772|GO:0008286|GO:0060770|GO:0050852|GO:0008285|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135704_PI430048170 0.6677840197942321.01881513743006 0.420796319521443 0.5409794908690340.454838643509559 A A A 0.5391377962143090.394736739194177 0.400040551247609 A A A LNCV6_135704_PI430048170 mRNA AGCAGCTGCAGGCGCTCGAGGCGCTTTTCGTGCAGAACCAGTATCCTGACGTGAGTACGC NM_005315RefSeq chr22 - 19148990 19150283 GSC2 2928 goosecoid homeobox 2
GO:0043565|GO:0003700|GO:0006357|GO:0005634|GO:0009653|GO:0003677 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_140867_PI430048170 0.1778549688998980.6962814715100861 1.1608190551458
10.8494525383788 11.1902395210576 P P P 11.0730545711321 11.6960254836151
11.9000310302111 P P P LNCV6_140867_PI430048170 mRNA
CCTGTTTTCCACACTCTGTCTTTGCAGTTTTGGTAATTCTGTGGTCTATTTATACAGATA NM_015354RefSeq chr9 +
128947692 129007096 NUP18823511 nucleoporin 188kDa
GO:0007077|GO:0010467|GO:0005975|GO:0019083|GO:0019221|GO:0019058|GO:0044281|GO:0005635|GO:0015
031|GO:0055085|GO:0010827|GO:0008645|GO:0015758|GO:0016020|GO:0005643|GO:0009405|GO:0016032|GO:0
051028|GO:0000278. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140575_PI430048170 0.0107488029666967 0.6418031127854386.87126866908118
6.76177542002828 7.11854436354165 P P P 7.42675689257802 7.51040155334367
7.73893206684553 P P P LNCV6_140575_PI430048170 mRNA
TCAGTTAGAACGTAGATACTGTAAAGTCCACACACACATTAAATCTTGTTTTCCTGAAAG NM_016823RefSeq
chr17_KI270862v1_alt - 363378 379182 CRK1398 "v-crk avian sarcoma virus CT10 oncogene homolog,
transcript variant II"
GO:0005515|GO:0008286|GO:0048010|GO:0048011|GO:0035020|GO:0048013|GO:0005886|GO:0006357|GO:0045
309|GO:0030168|GO:0005634|GO:0015629|GO:0005829|GO:0000186|GO:0005737|GO:0046875|GO:0007596|GO:0
045087|GO:0032956|GO:0005070|GO:0032319|GO:0042169|GO:0038096|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138838_PI430048170 0.2475236896505051.01712315829019 0.323524486336141
0.2984866089980050.2711099299859 A A A 0.2740536198223160.276833463606246
0.269216754131658A A A LNCV6_138838_PI430048170 mRNA
CGGTTTTGACTCTAAAACAGTGCGAATCTGACTTAAACCTGCAGTTTGATTAATAAAGAA NM_001195522 RefSeq
chrX + 40623565 40624139 MPC1L NA mitochondrial pyruvate carrier 1-like NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_131266_PI430048170 0.2902776610392241.03038454377712 0.308248714299517
0.2513384637390660.355432600445337A A A 0.2711913436265240.243849254284332
0.272132925292877A A A LNCV6_131266_PI430048170 mRNA
AATGTGGCTCACAGAAGGGATATCACCATTTTGTTCTGATGAAGGAAGGAGAACACCAGC NM_024318RefSeq
chr19_GL949752v1_alt - 213941 217725 LILRA6 79168 "leukocyte immunoglobulin-like receptor,
subfamily A (with TM domain), member 6, transcript variant 1" GO:0016021|GO:0002376 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_109113_PI430048170 0.1693918685978311.28939329587833 4.96616179817551
5.05167690918329 5.11774033394023 P P P 4.34290705625774 4.62634928183961
4.99558966444929 P P P LNCV6_109113_PI430048170 mRNA
TTTCTGTACTGAAGGTTTTAGTCCTCAATCAAACAGGAATAACGTGGGCTGAGGTGCTGC NM_001287801 RefSeq
chr1 + 235367359 235448968 TBCE 6905 "tubulin folding cofactor E, transcript variant 3"
GO:0008344|GO:0005874|GO:0051087|GO:0000226|GO:0009791|GO:0005737|GO:0048589|GO:0006457|GO:0014
889|GO:0051084|GO:0007023|GO:0048936|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143866_PI430048170 0.7774580808450591.03661677316392 7.28714380720778
7.59563754935093 7.70998591867583 P P P 7.44475526160078 7.38780682313593
7.62611395825568 P P P LNCV6_143866_PI430048170 mRNA
TGCTCACTGTCTGATGCAAATGTCTGGTCTATTTGTTAGTAAATAACAGGGAAATCATTT NM_138288RefSeq chr14
- 34432937 34462262 SPTSSA 171546 "serine palmitoyltransferase, small subunit A"
GO:0005515|GO:0004758|GO:0030148|GO:0005789|GO:0016021|GO:0017059 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130124_PI430048170 0.0284690598763377 0.9501384649886360.405269560824831
0.3581762679509380.355762215766566A A A 0.4527258002314840.456035279629557
0.432245007324985A A A LNCV6_130124_PI430048170 mRNA

GAGCTTTTGTTATAAACTTAATATTCAGAAGGCAAGGGTTATGATCCTGATGTGTCCTTT NM_001300737 RefSeq chr6 + 123803845 124825640 NKAIN2 154215 "Na+/K+ transporting ATPase interacting 2, transcript variant 3" GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127628_PI430048170 0.0147621071872116 0.4449574591423515.32251154703616 4.6065235600422 4.93449204758781 P P P 5.94173911232778 6.20190009485883 6.29142782077551 P P P LNCV6_127628_PI430048170 mRNA
GAGTTGCTTTGTTATGCCTTCAGCAAATAGCTTCATTTTGCCAATACTGAATAAAAGAGT NM_015360RefSeq chr5 + 55307747 55425581 SKIV2L223517 superkiller viralicidic activity 2-like 2 (S. cerevisiae) GO:0005515|GO:0000460|GO:0000398|GO:0005730|GO:0004386|GO:0005654|GO:0005634|GO:0071013|GO:0005524|GO:0000178 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142269_PI430048170 0.0199236661680351 0.7598328500120157.22612410672032 7.32055131748451 7.49918270604783 P P P 7.85280912638468 7.62436255194869 7.76175377172391 P P P LNCV6_142269_PI430048170 mRNA
CCTCTAATTCAGTATTCCATTTAATAAAAACAATACAGTGGCTGGAAAGGAGCATCAGAA NM_003149RefSeq chr3 + 36380486 36548006 STAC 6769 "SH3 and cysteine rich domain, transcript variant 1" GO:0035556|GO:0034605|GO:0005515|GO:0007165|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77228_PI430048170 0.0411300877237571 0.2762381850894360.264973206728697 1.98038340011226 0.719290935697416A A A 2.49410924519681 3.29878361737516 3.18902351562217 A P P LNCV6_77228_PI430048170 mRNA
TCAACTACAGACTCAGCATCCGCCAGTTGAACCAGCACAATGCGGTGGTCAAGGCCATCC NM_153487RefSeq chr6 - 37632507 37697990 MDGA1 266727 MAM domain containing glycosylphosphatidylinositol anchor 1 GO:0003674|GO:0005794|GO:0005886|GO:0007420|GO:0021799|GO:0001764|GO:0046658|GO:0005615|GO:0021527 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141820_PI430048170 0.0783294951971841.22415940004271 8.88234046940455 8.9748397827783 9.19197053548213 P P P 8.62698120149535 8.66182897710731 8.88848319540611 P P P LNCV6_141820_PI430048170 mRNA
AATGAGACAGCAGCAGAGCATCTCCTCTTAAGGATACGTGCCTTGGACTCATGTTTGAAT NM_032314RefSeq chr12 - 120503278 120529161 COQ5 84274 "coenzyme Q5 homolog, methyltransferase (S. cerevisiae)" GO:0005739|GO:0006744|GO:0008757|GO:0044281|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_1672_PI430048170 0.2362072186091240.7359524680535940.2991364174113110.321300058854769 0.400079546073644A A A 1.14236278744186 0.3068482799584770.780895458262943A A A LNCV6_1672_PI430048170 mRNA
CTCAAGATTCTGTAAAACCAAGCAAATGGGGGAAAAGTTAGTCAATCCTGTCATATAATA NM_198239RefSeq chr6 + 112054167 112069684 WISP3 8838 "WNT1 inducible signaling pathway protein 3, transcript variant 3" GO:0007165|GO:0005178|GO:0060548|GO:0007267|GO:0005578|GO:0007155|GO:0008201|GO:0008083|GO:0005615|GO:0001558|GO:0005520 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138208_PI430048170 0.0036425168730338 0.5478402832459045.18032313382019 4.87561773436493 4.97888355306262 P P P 5.92101200701687 5.93295800864887 5.79837355516548 P P P LNCV6_138208_PI430048170 mRNA
CGTTAAGCAACATTTGAAAGCTGTATGACCAAATAAAGAAGCACTTTTATACCGCCAAAA NM_015284RefSeq chr1 + 43389884 43454247 SZT2 23334 seizure threshold 2 homolog (mouse) GO:0003674|GO:0021540|GO:0043473|GO:0009791|GO:0007417|GO:0070062|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127598_PI430048170 0.169665000438855 2.03625880695492 13.8418095260872 14.0897715592418 13.7391104305632 P P P 13.8379813370285 11.9364987539279 11.9385146749093 P P P LNCV6_127598_PI430048170 mRNA
ACTTTGGGTTTGTAGGGGTCCTCAAGTGCCTTTGTGATTAAAGAATGTTGGTCTATGAAA NM_022044RefSeq chr22

+ 21642252 21644299 SDF2L1 23753 stromal cell-derived factor 2-like 1
GO:0051787|GO:0034976|GO:0016020|GO:0051087|GO:0051117|GO:0005788|GO:0042981|GO:0071712 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136643_PI430048170 0.7010935854506450.98079593690539 0.400636838239513
0.4699233018365950.399018109893479A A A 0.5255422320764820.483638150958337
0.338888455782947A A A LNCV6_136643_PI430048170 mRNA
TTCAATGCAGTTGCTCTGTTTATCTACCTGTCCAACATGTTTGACATCAACAGTCTGTGG NM_176881RefSeq chr7
+ 143183418 143184435 TAS2R39 259285 "taste receptor, type 2, member 39"
GO:0033038|GO:0007186|GO:0005886|GO:0016021|GO:0001580 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137522_PI430048170 0.0131623348947351.12328400032364 12.1080154815958
12.1047110024901 12.1327083001928 P P P 11.9538932932173 11.9011121408529
11.9861493424688 P P P LNCV6_137522_PI430048170 mRNA
GGTATCGTATTTTATCAGCTTACAGTTTAATGCCTAAGTTTCCCCTGGAAATAGCAAATA NM_018992 RefSeq
chr16 + 2682493 2709031 KCTD5 54442 potassium channel tetramerization domain containing 5
GO:0005515|GO:0016032|GO:0051260|GO:0005634|GO:0032403|GO:0005829 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_90254_PI430048170 0.19275055043027 0.846006649100235 17.2564257068282
16.9340403840515 16.8186528850799 P P P 17.2564257068282 17.2564257068282
17.2564257068282 P P P LNCV6_90254_PI430048170 mRNA
GACTGTGCAGGAGAAAGAGAACTAGTGCTGAGGGCCTCAATAAAGTTTGTGTTTATGCCA NM_033301 RefSeq
chr8 - 144789768 144792344 RPL8 6132 "ribosomal protein L8, transcript variant 2"
GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0005730|GO:0019843|GO:0006
415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0000184|GO:0016032|GO:0
022625|GO:0044267|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139711_PI430048170 0.406347963518448 1.45999806696946 0.402609950740911
1.87712778323471 1.28643240378954 A A A 1.31106080332143 0.367098717274953
0.401828309378627 A A A LNCV6_139711_PI430048170 mRNA
CTGTGGTTCCTTTTCCTCATGAAAATTGACAGGGCATTCCTCATTAAAAATACATATCTA NM_001282534 RefSeq
chr8 - 139617120 139703056 KCNK9 51305 "potassium channel, two pore domain subfamily K,
member 9, transcript variant 1"
GO:0005244|GO:0046982|GO:0005886|GO:0090102|GO:0007268|GO:0005267|GO:0034765|GO:0016021|GO:0006
813|GO:0071805|GO:0042803|GO:0008021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_135100_PI430048170 0.0232307218005881 1.07307937632836 0.468168911656218
0.482030438081275 0.522077349238387 A A A 0.347221801052906 0.397947862853981
0.421388130763533 A A A LNCV6_135100_PI430048170 mRNA
AACGTAGAGAGAATGCGGCATAACCACCAATAAAGGAGTCTTGATTTAACCCTGAAAAAA NM_022142 RefSeq
chr19 + 47994650 48025153 ELSPBP1 64100 epididymal sperm binding protein 1
GO:0007338|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128810_PI430048170 0.0144150678363686 0.941266376723575 0.366863982937405
0.342171417056513 0.325134890191915 A A A 0.460046338051089 0.431481223673934
0.404386172780925 A A A LNCV6_128810_PI430048170 mRNA
TTATTGCTGCGTGACTCTGTATTACTTTGGTGCATAAAAGTTGAACATTGTTGTTTACTGNM_002514RefSeq chr8 +
119416311 119424438 NOV 4856 nephroblastoma overexpressed
GO:0010468|GO:0030424|GO:0005578|GO:0007267|GO:0001558|GO:0030425|GO:0043231|GO:0007165|GO:0005
178|GO:0060548|GO:0043025|GO:0007155|GO:0008083|GO:0008201|GO:0005520 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_43558_PI430048170 0.0653940944530079 1.63243456107411 4.29905680991657

4.97897039722823 4.81669509804972 P P P 4.0190057484337 3.88207906544996
4.14446994949595 P P P LNCV6_43558_PI430048170 mRNA
TTTATTATCAAGACCCCAAAGGGTACCAGGGATCTTAGTCCTCAGCATATGGTTGTGAGG NM_012208 RefSeq chr5
+ 140691425 140699321 HARS2 23438 "histidyl-tRNA synthetase 2, mitochondrial, transcript variant 1"
GO:0010467|GO:0005759|GO:0006412|GO:0005524|GO:0004821|GO:0006427|GO:0006418 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131099_PI430048170 0.5946279880367490.7785054507146983.89455474047241
3.60512021818301 3.72110611727337 P P P 3.19782241592677 4.24610717768679
4.55596918793672 P P P LNCV6_131099_PI430048170 mRNA
GCCACTAGCTTGATTTTCTTTCTCCTCTGATTTCAGTTCACTGTTCAGTTTAGCATTAAA NM_001172303 RefSeq chr10
+ 27154823 27186919 MASTL 84930 "microtubule associated serine/threonine kinase-like, transcript variant 1"
GO:0005813|GO:0005634|GO:0005524|GO:0032154|GO:0034048|GO:0006974|GO:0005737|GO:0007067|GO:0004674|GO:0016301|GO:0000086|GO:0051726|GO:0005654|GO:0006468|GO:0000278|GO:0051721|GO:0051301 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104304_PI430048170 0.0701933174164633 1.29107643260675 13.3142242251336
13.6706348593095 13.5854874093953 P P P 13.2121670852511 13.1568472904284
13.1175633191862 P P P LNCV6_104304_PI430048170 mRNA
CACTCCCGCCCGAGGGGCAGGCCTCAAAGCCCGCCTTGGCCCCGCTTTCCCGCCCCTGAA NM_015720 RefSeq chr3
+ 127629158 127672810 PODXL2 50512 podocalyxin-like 2
GO:0005515|GO:0005887|GO:0005539|GO:0050901 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142256_PI430048170 0.000384818308653555 0.4226438502264394.61391064453901
4.51150725616328 4.78471850417764 P P P 5.79323037656821 5.86117501629218
5.98955121735742 P P P LNCV6_142256_PI430048170 mRNA
GACACTAGCTTGAAGTAAGAGGAGAATTATGCTTTTCTTTGCTTTTTCTACAAACCCTTA NM_001301055 RefSeq -
- 0 0 --- NA "prenylcysteine oxidase 1 like, transcript variant 2" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139856_PI430048170 0.0468995590505942 1.46927473523339 7.01301916602893
7.13800004781176 7.21662785142187 P P P 6.27410082472475 6.61345105894019
6.77737186599437 P P P LNCV6_139856_PI430048170 mRNA
ATTCTTTTGTAACGAGTCTTTCATGATGTGACTTTGAGGCCCCAACATGACAGCCACTGG NM_014964 RefSeq chr17
+ 19237376 19336715 EPN2 22905 "epsin 2, transcript variant 2"
GO:0005794|GO:0007219|GO:0048568|GO:0005654|GO:0030128|GO:0001701|GO:0043231|GO:0008289|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128553_PI430048170 0.4035806792121651.38278498222681 3.48615831564959
4.07753355990414 4.75189097827942 P P P 3.35829544608574 3.94991119857511
3.81653792905838 P P P LNCV6_128553_PI430048170 mRNA
GCTATGTTAGAACATAAGTACACAAAAGTCATCTGGCAAAACATTTACCTGTAGTTTTGC NM_175874 RefSeq chr12
+ 14803571 14823857 C12orf60 144608 chromosome 12 open reading frame 60 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133158_PI430048170 0.8969644850397361.00064657709015 1.04928852265718
1.20766529175036 0.291559730395404 A A A 1.57714930586088 0.491496888356218
0.27475344075604 A A A LNCV6_133158_PI430048170 mRNA
GTACAGGAAGTGTTGAGAGAGACAGTGAACAGAATCATGACCTTGATACAAAGGAAAACT NM_001005325
RefSeq chr11 - 123805407 123806349 OR6M1 390261 "olfactory receptor, family 6, subfamily M, member 1" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141067_PI430048170 0.197632056514993 0.463221337995853 0.276535831772843
0.280670180626826 0.420847689487112 A A A 0.357387241782257 1.38605905956566

2.08154267680746 A A A LNCV6_141067_PI430048170 mRNA
CATCATTGTATGTTATTTCCCACAACCCAGTTGGAGGGGCATGGCTTCCAATTTAGAGAC NM_016204RefSeq chr10
+ 47322489 47326270 GDF2 2658 growth differentiation factor 2
GO:0071773|GO:0005515|GO:0030308|GO:0051216|GO:0048514|GO:0060395|GO:0005615|GO:0032757|GO:0006
879|GO:0030513|GO:0045944|GO:0043408|GO:0048468|GO:0070062|GO:0001569|GO:0010862|GO:0042981|GO:0
001525|GO:0030509|GO:0032924|GO:0005160|GO:0005125|GO:0045766|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140248_PI430048170 0.1754297120408460.8551938399303879.69907070492112
9.58059393234201 9.93291279627664 P P P 9.8438256010603 9.90787532462349
10.1429649716517 P P P LNCV6_140248_PI430048170 mRNA
GGTGAATTCTACTTTTTATGTTGGAGTGGACCAATGTCTATCAAGAGTGACAAATAAAGT NM_005765RefSeq chrX
+ 40580963 40606636 ATP6AP2 10159 "ATPase, H+ transporting, lysosomal accessory protein 2"
GO:0005515|GO:0043005|GO:0002003|GO:0005886|GO:0030177|GO:0044297|GO:0032914|GO:0060323|GO:0043
408|GO:0048069|GO:0006508|GO:0004872|GO:0004190|GO:0016021|GO:0019899|GO:0044267|GO:0021903|GO:0
009897|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131608_PI430048170 0.0427494076455192 0.68496493481317 3.51165917991101
3.0010892742786 3.2197324491254 P P P 3.6370794641728 3.80353204393765
3.95754443890886 P P P LNCV6_131608_PI430048170 mRNA
TACTGAACCTAATGATGCAGATGGATGGCACATCAGTATAATAAATGATGGAAAACGGTT NM_033127RefSeq chr1
- 177929106 177969915 SEC16B 89866 SEC16 homolog B (S. cerevisiae)
GO:0010628|GO:0070863|GO:0000139|GO:0005789|GO:0007031|GO:0048208|GO:0070972|GO:0015031|GO:0007
029|GO:0043231|GO:0016559 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_36432_PI430048170 0.0507241918482148 0.8013124176593667.73372140827609
8.00034663722022 8.00355445336143 P P P 8.25440129795195 8.34509782344669
8.10276650786847 P P P LNCV6_36432_PI430048170 mRNA
GGTTTGCCCACTTGATTGAGAAAGATGTTCCAGTGAGGAACCCTGATCTCTCAGCCCCAA NM_006546RefSeq chr17
+ 48997411 49056145 IGF2BP1 10642 "insulin-like growth factor 2 mRNA binding protein 1, transcript
variant 1"
GO:0005515|GO:0017148|GO:0048027|GO:0030424|GO:0010467|GO:0048471|GO:0070934|GO:0010494|GO:0005
634|GO:0030175|GO:0003729|GO:0045182|GO:0030027|GO:0030426|GO:0005829|GO:0042035|GO:0005737|GO:0
043197|GO:0000166|GO:0030529|GO:0051028|GO:0003730|GO:0010610|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_55537_PI430048170 0.4827738138024320.8952118066842662.99434489758764 2.41335564435385
2.70110054305472 P A A 2.80919037348361 2.67410818323873 3.12515163137019 P P P
LNCV6_55537_PI430048170 mRNA
TTTCAAGTTCTTATTGAAAGTTGTCAGTGCAGCTGTCCAGGCCCAACATTCAGCCACAAA NM_012414RefSeq chr1
- 220148267 220272501 RAB3GAP2 25782 RAB3 GTPase activating protein subunit 2 (non-catalytic)
GO:0017112|GO:0017137|GO:0046982|GO:0005886|GO:0032851|GO:0043085|GO:0006886|GO:0043087|GO:0043
547|GO:0043234|GO:0005737|GO:0097051|GO:0030234|GO:0008047|GO:0005096 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137217_PI430048170 0.32298574017196 1.10817049841592 10.4752575197748
10.7402562270112 10.5394309066895 P P P 10.2492878024047 10.6182131088684
10.4327687607867 P P P LNCV6_137217_PI430048170 mRNA
CGCAGCAAGGAGTGATATGGTTTGTCTTTTTAAGACTGGACTTGCTTTATATTAAATTTG NM_013355RefSeq chr9
+ 128702522 128720920 PKN3 29941 protein kinase N3
GO:0005515|GO:0007165|GO:0048471|GO:0005794|GO:0004672|GO:0010631|GO:0006468|GO:0005634|GO:0004
697|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145260_PI430048170 0.1548397617420380.4982824253873382.45719602714443
2.36261627828202 2.12006639254009 A A A 4.0029398000504 2.94939996390558

2.65756215244777 P P P LNCV6_145260_PI430048170 mRNA
GGATTCTCTCTATTTCCTTTTATGGGTTATAGAAGTCCCTGCAGTTGGCTGTGTGTGGTG NM_024504 RefSeq chr8
- 70051650 70071327 PRDM14 63978 PR domain containing 14
GO:0005515|GO:0006355|GO:0001708|GO:0034972|GO:0008168|GO:0001827|GO:0003677|GO:0007281|GO:0046
872|GO:0006351|GO:0009566|GO:0000902|GO:0048873|GO:0044030|GO:0040037|GO:0040029|GO:0005654|GO:0
035019|GO:0030718. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133723_PI430048170 0.816004757119943 1.02610955347195 7.44855727377416
7.78778689979095 7.74616684563658 P P P 7.66181288826994 7.43946855480708
7.77308622448895 P P P LNCV6_133723_PI430048170 mRNA
GATAAGTGTAATTTTCTCTATAGGAGACCACGTTGCTACATCTGTTAATGCCTGTCAGTG NM_023075 RefSeq chr18
- 11883470 11908797 MPPE1 65258 "metallophosphoesterase 1, transcript variant 1"
GO:0006888|GO:0005801|GO:0008081|GO:0005793|GO:0034235|GO:0030145|GO:0005794|GO:0033116|GO:0005
654|GO:0016021|GO:0070971|GO:0006506 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98484_PI430048170 0.430526408137621 0.868673633806688 3.93380095249169 3.87803276010713
3.25596780873237 P P P 4.13375078228678 3.72354782221848 3.88280996848737 P P P
LNCV6_98484_PI430048170 mRNA
TAATAAGGCAGCTGAATGAAGGGAGGTAACGGACCCCTGAGAGGGGCACTGAAGTCTGCA NM_001114618
RefSeq chr5 - 180790540 180809817 MGAT1 4245 "mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-
acetylglucosaminyltransferase, transcript variant 1"
GO:0008375|GO:0003827|GO:0005975|GO:0001701|GO:0006049|GO:0031982|GO:0046872|GO:0000139|GO:0016
020|GO:0006486|GO:0016021|GO:0044267|GO:0070062|GO:0018279|GO:0043687 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144774_PI430048170 0.00240210406548508 1.45175954209381 4.60155182378776
4.76712905090033 4.77160813756674 P P P 4.27904902392306 4.08961226928853
4.15823346979099 P P P LNCV6_144774_PI430048170 mRNA
CCTTCTTCCAACCTTATTGCCTCATTTCCCCCTTGTAGTCAATGTTTTTTGGAAACACTG NM_001193362 RefSeq chr14
+ 69191765 69244020 EXD2 55218 "exonuclease 3'-5' domain containing 2, transcript variant 3"
GO:0008408|GO:0005737|GO:0090305|GO:0005634|GO:0003676 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135933_PI430048170 0.0141990728703667 1.42618620134929 11.3215084688439
11.3192956879824 11.2900579289965 P P P 10.9180861635834 10.7738348301968 10.693641440726
P P P LNCV6_135933_PI430048170 mRNA
GGTCCTAGCTGTTAGGGACATTTCCAAGCTGTTAGTTGCTGTTTAAAATAGAAATAAAAT NM_006293 RefSeq chr15
+ 41559021 41579338 TYRO3 7301 TYRO3 protein tyrosine kinase
GO:0005515|GO:0034122|GO:0060068|GO:0005634|GO:0042698|GO:0007283|GO:0005635|GO:0043524|GO:0046
777|GO:0034446|GO:0001779|GO:0007155|GO:0045824|GO:0023014|GO:0046982|GO:0030168|GO:0043277|GO:0
018108|GO:0005524|GO:0014065|GO:0070527|GO:0007165|GO:0005887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143933_PI430048170 0.163409603009124 1.03372075982217 0.337949076748568
0.348786800215148 0.276541191475117 A A A 0.268661589674576 0.28396606957384 0.2681007205355
A A A LNCV6_143933_PI430048170 mRNA
ATCTTCCTCTGTTTCTACAAAAGATTGTAAAACCCTTTTTAGGCAAGGGCCCAAGGACAG NM_020398 RefSeq chr20
- 45540625 45547426 EPPIN 57119 "epididymal peptidase inhibitor, transcript variant 1"
GO:0010951|GO:0005515|GO:0009986|GO:0004867|GO:0010466|GO:0005576|GO:0042742 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131601_PI430048170 0.00244688158653044 0.541821254617797 11.4562865572154
11.4224055083052 11.1800967732603 P P P 12.2995574861062 12.2790764354772
12.1429356773868 P P P LNCV6_131601_PI430048170 mRNA
CAGCACAAGGACCCAGCCTTTGTTCTGCACTTAATAAATGGTTTTGCTACTGCTAAAAAA NM_000213 RefSeq chr17

+ 75721435 75757818 ITGB4 3691 "integrin, beta 4, transcript variant 1"
GO:0005515|GO:0030056|GO:0005886|GO:0097186|GO:0009925|GO:0030198|GO:0048870|GO:0031581|GO:0004
872|GO:0046847|GO:0048333|GO:0007155|GO:0031252|GO:0070062|GO:0008305|GO:0001664|GO:0009986|GO:0
034329|GO:0009611|GO:0006914|GO:0048565|GO:0005604|GO:0043235|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143324_PI430048170 0.2204927160114680.7905033213725797.82303811092215 7.71528079506
8.01708621644501 P P P 7.8733576712677 8.13230264423891 8.51149591025807 P P P
LNCV6_143324_PI430048170 mRNA
TCCTCAAAAGCTACAAACCAGTGGTCTGCAAAATAAAGTGTGTTGGAAACCTCTAAAAAA NM_012247RefSeq chr10
- 13317437 13348298 SEPHS1 22929 "selenophosphate synthetase 1, transcript variant 1"
GO:0005515|GO:0016310|GO:0031965|GO:0005737|GO:0046982|GO:0005886|GO:0004756|GO:0005525|GO:0005
524|GO:0042803|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127597_PI430048170 0.2623731638419680.7009209678717160.390584598898997
0.3665986256218230.255071939743776A A A 0.38828911228854 0.618163151012776
1.36097634386458 A A A LNCV6_127597_PI430048170 mRNA
GCTGTAGAAGAAATCTGGTTTGAAACTGCCAAATCCTATGAATCTGGGATCTCCATGTGA NM_001013619 RefSeq
chr15 + 78507563 78533670 HYKK 123688 "hydroxylysine kinase, transcript variant 1"
GO:0016310|GO:0005737|GO:0047992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_4201_PI430048170 0.1447544592091 1.30301048542249 10.6674634481273 10.8633560724635
11.2277974219929 P P P 10.4942300811035 10.3828801227384 10.7655911005374 P P P
LNCV6_4201_PI430048170 mRNA
GCCTGGGATATGGGTTTTAAATGGACATTGTCTGTACCAGCTTCATTAAAATAAACAATA NM_003352RefSeq chr2
- 202206179 202238599 SUMO1 7341 "small ubiquitin-like modifier 1, transcript variant 1"
GO:0005515|GO:0019221|GO:0032436|GO:0045202|GO:0005634|GO:0030425|GO:0043433|GO:0060334|GO:0032
880|GO:0005737|GO:0090204|GO:0030578|GO:0031334|GO:0005643|GO:0019789|GO:0060021|GO:0031625|GO:0
060333|GO:0031965|GO:0016925|GO:0005730|GO:0043392|GO:0006281|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133146_PI430048170 0.0618536735100803 0.8979406469994517.85041867141665
7.80452181918712 7.86495021978678 P P P 8.04115781698478 7.90297528343057
8.03809912640098 P P P LNCV6_133146_PI430048170 mRNA
AGGGCATTTAATCAGGAGGAAAGGTTTGGAAAACTAACTCAGGTGTATTTATTGTTTAAG NM_000098RefSeq chr1
+ 53196428 53214197 CPT2 1376 carnitine palmitoyltransferase 2
GO:0005739|GO:0006635|GO:0004095|GO:0006853|GO:0005743|GO:0005730|GO:0005654|GO:0044281|GO:0044
255 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111975_PI430048170 0.0898891727180376 1.25544774990938 5.6065422637591
5.75593169773599 5.72843800795788 P P P 5.17378438722082 5.57985112530715
5.32760605461947 P P P LNCV6_111975_PI430048170 mRNA
ACAGCACAGGGAAACCAAAATGTCATCAGAGTCGGGAGCTGCCCAGAATCCCTCCCGAGA NM_018440RefSeq
chr8 - 80967810 81112068 PAG1 55824 phosphoprotein membrane anchor with glycosphingolipid
microdomains 1
GO:0005515|GO:0050852|GO:0050863|GO:0005886|GO:0050868|GO:0009967|GO:0035556|GO:0007165|GO:0007
173|GO:0005070|GO:0045121|GO:0016021|GO:0042169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100400_PI430048170 0.7079885847913790.9798325153319450.513455372596552
0.4514365613449290.275010366092084A A A 0.38838776205379 0.489409175307579
0.458906731915116A A A LNCV6_100400_PI430048170 mRNA
GCTTCCAAATGGTTACTTCCAACTGTAATTGATCAGAAATCATTTATTTTCCCTCAGGAA NM_001031715 RefSeq
chr15 + 67254799 67501804 IQCH 64799 "IQ motif containing H, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_133804_PI430048170 0.1752476475486351.05535256700963 0.471741536200173

0.4070138615721960.47688107865315 A A A 0.3067763962492890.371188778971328
0.44235205760465 A A A LNCV6_133804_PI430048170 mRNA
GTGAAGCTCTTATTTTGTAACCTGGGTAAATGTTAGTTTCTAGATTTTCGGCTTAACATC NM_145263RefSeq chr4
+ 52051330 52097306 SPATA18 132671 "spermatogenesis associated 18, transcript variant 1"
GO:0005515|GO:0005737|GO:0035694|GO:0036126|GO:0035695|GO:0005741|GO:0006974|GO:0043231 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131833_PI430048170 0.05017252199714 0.8614629638733712.6283964393678
12.5510404641556 12.4343628665284 P P P 12.7900406387301 12.728893371401
12.7461744612078 P P P LNCV6_131833_PI430048170 mRNA
TTAAGAGGCTTCCAGAGAAAACGGCACACCAATCAATAAAGAACTGAGCAGAAACCAACA NM_182905RefSeq
chr9 - 14510 29739 WASH1 100287171 WAS protein family homolog 1
GO:0005515|GO:0034314|GO:0030335|GO:0043014|GO:0003779|GO:0006887|GO:0000145|GO:0022617|GO:0031
901|GO:0071437|GO:0016197|GO:0071203|GO:0031274|GO:0042147|GO:0055037|GO:0055038|GO:0005769|GO:0
031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134967_PI430048170 0.1844584685254 1.11881464687305 8.75052443984254
8.78587641379909 8.71664532161528 P P P 8.41763166439964 8.69813592566002
8.63735623421143 P P P LNCV6_134967_PI430048170 mRNA
TCTTCTATTTAAGAGAACCTCAGATGATGTACCTGAGCCTCAGGGTTTTGTTTCAGAGGG NM_002180RefSeq chr11
+ 68903850 68940601 IGHMBP2 3508 immunoglobulin mu binding protein 2
GO:0005515|GO:0030424|GO:0003723|GO:0032575|GO:0005634|GO:0006412|GO:0008186|GO:0030426|GO:0005
737|GO:0003697|GO:0051260|GO:0032508|GO:0008094|GO:0006355|GO:0043141|GO:0000049|GO:0006310|GO:0
005524|GO:0003677|GO:0006351|GO:0003678|GO:0006260|GO:0006281|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135188_PI430048170 0.0834008917231606 0.6540002669501787.87672688946058
7.96499433716834 7.93668759826291 P P P 8.16743863613753 8.58112869650387
8.79953559553162 P P P LNCV6_135188_PI430048170 mRNA
TTTCACTTTCTGATCACGGTACGTCCATAAAGCCAGTATTACACTTAAATGAAGTATTCT NM_001136191 RefSeq
chr19 - 11164266 11197567 KANK2 25959 "KN motif and ankyrin repeat domains 2, transcript variant
2"
GO:0005739|GO:0005515|GO:0070563|GO:0043069|GO:0005737|GO:0008285|GO:0006915|GO:2000134|GO:0033
147|GO:0000122|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134836_PI430048170 0.282392963285097 0.6946166195279610.377452055647325
1.03918882299822 0.32456769571144 A A A 0.4726692883381621.19716242512773
1.56121573540475 A A A LNCV6_134836_PI430048170 mRNA
GCTTTCTAATTCCTTTCCTCCCTTATTGGTTACCTATGAATTGCTCAGTTCTAACAATGA NM_016200RefSeq chr7 +
118184031 118204039 LSM8 51691 "LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)"
GO:0005515|GO:0030629|GO:0000398|GO:0005681|GO:0046540|GO:0017070 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129754_PI430048170 0.7345858703141541.03546780891894 0.39058184760322
0.37190451044918 0.692982386000021 A A A 0.5786313883307690.382001679783268
0.356618450191341 A A A LNCV6_129754_PI430048170 mRNA
GGCTTACAACTTGCTAACCCCAAAAGAAGCAATAAATGTTAAGCAATTTTAGTAACCAGT NM_022568RefSeq chr6
- 134917389 134950122 ALDH8A1 64577 "aldehyde dehydrogenase 8 family, member A1, transcript
variant 1"
GO:0005622|GO:0005737|GO:0001758|GO:0042574|GO:0042573|GO:0042904|GO:0004029|GO:0070062|GO:0055
114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142648_PI430048170 0.2347674121264421.44563905321747 4.92406875996731
5.31140248078243 5.02301806298463 P P P 4.68804585747329 4.9826749681211
3.76180189832124 P P P LNCV6_142648_PI430048170 mRNA

TTTATTTATGCTGTGCCATTCAAAGCACATGTTCAAGAGAACAGAACACTCTCCCCGCCC NM_018943RefSeq chr22
+ 18110686 18131731 TUBA8 51807 "tubulin, alpha 8, transcript variant 1"
GO:0006184|GO:0051258|GO:0005737|GO:0005874|GO:0005200|GO:0003924|GO:0007017|GO:0005525 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132840_PI430048170 0.266336118484117 1.08192333116137 8.89878360840702
8.94258013865115 9.1305252606977 P P P 8.8833741454181 8.80116889757074
8.95319223119477 P P P LNCV6_132840_PI430048170 mRNA
GTGAGAAGAAGATTCAATCGTAACTGTGTCAACAGTATTGTGAAGTGATCATTTCTTGTA NM_014044RefSeq chr2
+ 98608578 98618514 UNC50 25972 unc-50 homolog (C. elegans)
GO:0000139|GO:0003723|GO:0005637|GO:0016021|GO:0015031|GO:0007166 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_102593_PI430048170 0.95884335509313 0.992043085599067 9.76990044719339
9.74281666237918 9.81947089993775 P P P 9.59152717736263 9.87953704791716
9.87811967290989 P P P LNCV6_102593_PI430048170 mRNA
TACCAACGGTGGAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAA NM_001065RefSeq chr12
- 6328756 6342117 TNFRSF1A 7132 "tumor necrosis factor receptor superfamily, member 1A"
GO:0005515|GO:0006693|GO:0033160|GO:0032715|GO:0019221|GO:0045202|GO:0002020|GO:0032403|GO:0005
615|GO:0043525|GO:0071392|GO:0032496|GO:0043123|GO:0042742|GO:0009986|GO:0032760|GO:0043279|GO:0
033209|GO:0043235|GO:0005031|GO:0005887|GO:0045121|GO:0008625|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129020_PI430048170 0.195914329058252 0.80078919173723 0.295750937921435
0.285215568907238 0.478353621190207 A A A 0.656308880474679 0.374634446513713
0.942458579296285 A A A LNCV6_129020_PI430048170 mRNA
TCCCACCTGATATGCAGTGCTTTTGACTATCTTATGCATGGTTTATTCCTCTGGCTTGGA NM_174934RefSeq chr11
- 118133376 118152915 SCN4B 6330 "sodium channel, voltage gated, type IV beta subunit, transcript variant 1"
GO:0005248|GO:0031226|GO:2000649|GO:0060307|GO:0086091|GO:0060048|GO:0044325|GO:0086067|GO:0014
704|GO:0010765|GO:0086002|GO:0001518|GO:0035725|GO:0086012|GO:0006814|GO:0086006|GO:0017080 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132180_PI430048170 0.0222418326453597 0.623834342873412 6.05883933449399
6.39842796009493 6.33238651335379 P P P 6.67675211855903 6.96622154734772
7.16904843154336 P P P LNCV6_132180_PI430048170 mRNA
CAAAACCATTTCTTCAGGTTAAATTGAGGCATTTTAATCTGCACAGTTTATCTTCTGCCA NM_005802RefSeq chr9
- 32540543 32552628 TOPORS 10210 "topoisomerase I binding, arginine/serine-rich, E3 ubiquitin protein ligase, transcript variant 1"
GO:0005515|GO:0006511|GO:0004842|GO:0034504|GO:0006513|GO:0016874|GO:0000151|GO:0005634|GO:0003
823|GO:0036064|GO:0035845|GO:0042127|GO:0019789|GO:0000930|GO:0051443|GO:0043066|GO:0046549|GO:0
008630|GO:0005814|GO:0016925|GO:0046548|GO:0030496|GO:0010842|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128070_PI430048170 0.894416981211343 0.954723803301507 1.73816592190636
0.38250900407326 0.246071429261245 A A A 0.365727433163111 1.757206915219 7
0.519038777394308 A A A LNCV6_128070_PI430048170 mRNA
TGTACCTTCTGCTCAATTTCCTTTCCTCATCCCAAATAAATGCCTTGTTACAAGAAAAAA NM_004084RefSeq chr8
- 6977648 6980092 DEFA1 1667 "defensin, alpha 1"
GO:0005796|GO:0050830|GO:0050832|GO:0005576|GO:0005615|GO:0002227|GO:0031012|GO:0051607|GO:0006
955|GO:0006935|GO:0045087|GO:0019731|GO:0031640|GO:0035578|GO:0070062|GO:0030520 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142176_PI430048170 0.328012869949211 1.47783809575813 2.97986910648423
2.21175806820837 3.04373572131757 A A P 2.81784363536797 2.30333099551471

1.04668010104359 P A A LNCV6_142176_PI430048170 mRNA
TTGGGCTGTGTGTGGATTGGATGGGGTGAGGGTACGGCCATTGTCCTCTTCTTAACGGGA NM_207397 RefSeq chr1
- 27379099 27383333 CD164L2 NA CD164 sialomucin-like 2 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_116056_PI430048170 0.4539673608241340.9771532429804810.363009366571594
0.4143525975964710.334898030894094A A A 0.466411863666676 0.362224859937766
0.382655449247396A A A LNCV6_116056_PI430048170 mRNA
CAGATTTTTTGGAACCAACTGAGGAATTCTGTACACAAAGCTTCAGCAAACACTTAGAGA NM_001012642 RefSeq
chr15 - 72159805 72197795 GRAMD2 196996 GRAM domain containing 2 GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_137651_PI430048170 0.1389677350832751.38340508955502 8.64034014854263
8.69634268660841 8.55519809540579 P P P 8.4771958497472 8.17562913680552
7.74616684563658 P P P LNCV6_137651_PI430048170 mRNA
TTTTACATCATGTCCTGAGCCTACCTTTCCCCCAAATTCTGGGGCCCACAGCCTAGGAGC NM_001077621 RefSeq
chr7 + 73667843 73672110 VPS37D 155382 vacuolar protein sorting 37 homolog D (S. cerevisiae)
GO:0000813|GO:0031902|GO:0019082|GO:0016197|GO:0019058|GO:0061024|GO:0016032|GO:0019068|GO:0015
031|GO:0010008|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134670_PI430048170 0.1100926271886690.9457877185718830.266403030126989
0.2752978523938770.326805287946238A A A 0.4301304671526480.353871110106945
0.324406265795228A A A LNCV6_134670_PI430048170 mRNA
TGAGTCTTCAGAGGGAATCTCATTCGTTTTATTGGGACTGACAACAAGTCCTGGACAGCA NM_080859 RefSeq chr9
+ 122800122 122801073 OR1K1 NA "olfactory receptor, family 1, subfamily K, member 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141746_PI430048170 0.9909012358433591.00569638121806 6.85604883281052
6.31405907371013 6.32826517067628 P P P 6.27037510277103 6.72629051369884
6.50981830431843 P P P LNCV6_141746_PI430048170 mRNA
TGCCCATGTGAATCTGGCAAGGTGTTTAACAGTGTGGGCTTGAAAGTCCAAACCAAAAAA NM_005094 RefSeq chr9
+ 128340559 128361470 SLC27A4 10999 "solute carrier family 27 (fatty acid transporter), member 4"
GO:0006629|GO:0015245|GO:0001579|GO:0001676|GO:0005886|GO:0007584|GO:0031526|GO:0055085|GO:0004
467|GO:0005902|GO:0016020|GO:0000166|GO:0005789|GO:0006810|GO:0043588|GO:0016021|GO:0015908|GO:0
031957|GO:0015909|GO:0044539|GO:0042760 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136280_PI430048170 0.1514137805510651.32770397889152 6.42344301003016
5.82997070935191 6.07845395982401 P P P 5.42575983492807 5.92082079435582
5.77667502958681 P P P LNCV6_136280_PI430048170 mRNA
TGGACAGTTGCATGGAAGCTGAGACTCTCACTGACAGTGAAACCCTCAAATGAACACAAT NM_174913 RefSeq chr14
+ 24299853 24309126 NOP9 161424 "NOP9 nucleolar protein, transcript variant 1"
GO:0008150|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105436_PI430048170 0.0722251889020643 1.22152751191639 10.5503886319615
10.3977491364022 10.6162973457171 P P P 10.0413143373449 10.3016287217362
10.3457000024865 P P P LNCV6_105436_PI430048170 mRNA
GCGCCTGACGATACGCTCTTCTATTGTCTTATTCTGGCAGGTTTTGACGTTTTAAATTTT NM_016080 RefSeq chr17 -
759308 782331 GLOD4 51031 glyoxalase domain containing 4 GO:0005739|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135324_PI430048170 0.0345428868539605 0.6134933083292796.68592536551021
6.84221769737982 6.83458547081024 P P P 7.20213803026516 7.7268143046756
7.50621725071772 P P P LNCV6_135324_PI430048170 mRNA
TTTTCTCGTGAGCTTAGGCCGCTGGTTTTGGTGATTTTTGTCTGATTGCAATGTCTGGAC NM_003512 RefSeq chr6
+ 26124144 26124690 HIST1H2AC 8334 "histone cluster 1, H2ac"
GO:0008150|GO:0003674|GO:0046982|GO:0005634|GO:0000786|GO:0003677|GO:0070062 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_135775_PI430048170 0.0788420004241006 1.11880777457264 9.18567277749674
9.23930765388064 9.05641201389704 P P P 9.0221948642184 8.92788712286467
9.04872303523839 P P P LNCV6_135775_PI430048170 mRNA
ATAAGAGGCTGGCCACCAAACAGAGCAGTGGCTAAATTGCAGTAGCAGCATATCTTTTTT NM_001008RefSeq chrY
+ 2841581 2866956 RPS4Y1 6192 "ribosomal protein S4, Y-linked 1"
GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0005634|GO:0007275|GO:0019
843|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0016020|GO:0000184|GO:0022627|GO:0
016032|GO:0044267|GO:0005844 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141878_PI430048170 0.0379312360597455 0.73186871322273211.1842321426108
11.3681227285338 11.0515354706506 P P P 11.6610743897043 11.6623029829733
11.6491097446243 P P P LNCV6_141878_PI430048170 mRNA
ATTTATTGTGTACTGACTCCATCTGCCCCGTCAAATAAAAAACCACAAGGTTCGAGCCGC NM_177938RefSeq chr3
+ 48989907 49007148 P4HTM 54681 "prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum),
transcript variant 3" GO:0031418|GO:0005506|GO:0005509|GO:0016706|GO:0005789|GO:0016021|GO:0055114
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70419_PI430048170 0.6182563526097720.9676814432309270.5344207369728610.482293637870517
0.261643959819083 A A A 0.4082355934398880.5369157717676270.486770827075522 A A A
LNCV6_70419_PI430048170 mRNA
TTATCACGGACTCTTCACTGAAAAATGATGCTCTCCATACTGGGAGCTGAGCTTTCTCTG NM_139163RefSeq chr2
- 201288270 201357398 ALS2CR12 130540 "amyotrophic lateral sclerosis 2 (juvenile) chromosome region,
candidate 12, transcript variant 1"
GO:0005515|GO:0003674|GO:0035686|GO:0036126|GO:0005575|GO:0043087|GO:0001520 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128680_PI430048170 0.4803977797076281.36939262310192 2.02127029637812
0.5915937334317331.36391237673999 A A A 1.44182622943911 0.928675538785244
0.405091437492313 A A A LNCV6_128680_PI430048170 mRNA
TATTAGGGCCCTGGGGAAGAAACAAGAGCCATTAAAATCTCTTTGGTTTGAAGCAAAAAA NM_001869RefSeq chr7
+ 130266862 130289797 CPA2 1358 carboxypeptidase A2 (pancreatic)
GO:0007039|GO:0006508|GO:0004180|GO:0008270|GO:0005576|GO:0004181 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127680_PI430048170 0.0607119895523938 0.7219619418894822.68583992978515
2.89159552706622 2.97920699246428 A A P 3.2840640845373 3.57067328847629
3.08594520504433 P P P LNCV6_127680_PI430048170 mRNA
TGACAAGATGGGCCTCAAGTTCTTGGGCACCAAGTACCTGGAGGTGACGCTGAGTGGCAT NM_053284RefSeq chr16
+ 631011 634116 WFIKKN1 117166 "WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain
containing 1"
GO:0048747|GO:0032091|GO:0010951|GO:0005515|GO:0001501|GO:0004867|GO:0008191|GO:0060021|GO:0005
576|GO:0043392 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135781_PI430048170 0.6839709517936851.11526560477061 1.52461595103279
2.28473882122428 1.34480378921332 A A A 0.7518264560185342.29161171049176
1.40402359830775 A A A LNCV6_135781_PI430048170 mRNA
GGAGGACAGAGAAAGGATACTAAATGAAACAACAGGGGAGATACAATATTATCTGGTTGC NM_001202425
RefSeq chr19 + 9324694 9382617 ZNF559-ZNF177NA "ZNF559-ZNF177 readthrough, transcript
variant 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139983_PI430048170 0.2921479192971871.23325764073802 0.457726307426734
0.6376291018302791.116258280804 A A A 0.5642456410402270.406312076279877
0.410381450299515 A A A LNCV6_139983_PI430048170 mRNA
GAAAAAGAGATCTGGCTCTGTGATAGGCAAATATGTGGACAGCAGAGGGATTCTTAGGAG NM_001144958

RefSeq chr12 - 3615327 3753200 CRACR2A 84766 "calcium release activated channel regulator 2A, transcript variant 1"
GO:0005515|GO:0032237|GO:0005737|GO:0005794|GO:0002115|GO:0016020|GO:0051928|GO:0005509|GO:0005730|GO:0005634|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140298_PI430048170 0.2732516322738351.02170548302818 0.326566320632219
0.25981569191043 0.27197856339383 A A A 0.2534169340964870.257928560259989
0.254952918668681A A A LNCV6_140298_PI430048170 mRNA
GTGGCAATGCTTTTGTGCATTACATCCTCTAGAGGGAACATAAAAAGATACCAATAAAAT NM_199051RefSeq chr1 - 190097666 190477629 BRINP3 339479 bone morphogenetic protein/retinoic acid inducible neural-specific 3
GO:0005739|GO:0071300|GO:0045930|GO:0045666|GO:0005783|GO:0043025|GO:0007050|GO:0005576|GO:0030425 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130214_PI430048170 0.4931266370735581.37373307860606 0.416134972669279
1.54477369860105 0.256956289754779A A A 0.3737419289525970.435630905206805
0.397051214087477A A A LNCV6_130214_PI430048170 mRNA
TTTCTTGAACACGATGAAGCCATAGCAACAAGTCTGGTCTAGAAAGAAGTCTCGGCGAGA NM_194287RefSeq chr14 + 76826381 76870302 LRRC74A NA leucine rich repeat containing 74A NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135238_PI430048170 0.1206172427723931.56900803343523 2.5815130642039
2.28803055912846 1.71069051762064 A A A 1.37520461916272 1.89004538021708
1.44004378471637 A A A LNCV6_135238_PI430048170 mRNA
TTCATGAATTCACCTTCCAGCTTCCTCAGAATAAAATGCTGCCTGGGTCAAGGACTCAAA NM_015717RefSeq chr2 - 70830211 70835823 CD207 50489 "CD207 molecule, langerin"
GO:0002474|GO:0051607|GO:0005886|GO:0031901|GO:0042590|GO:0030246|GO:0002479|GO:0030139|GO:0016021|GO:0030669|GO:0005537 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144255_PI430048170 0.5301179703325891.40864341644466 0.315885319094801
1.67068815917364 0.297892046901635A A A 0.5175617678611240.430242268069065
0.307411115595531A A A LNCV6_144255_PI430048170 mRNA
CTGAGTGGATATTACTCTGCATCACAATGAAGCCAACAGTCATATCTTCCGATGTGGAGA NM_024114RefSeq chr11 + 55262181 55271119 TRIM48 79097 tripartite motif containing 48 GO:0005622|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133943_PI430048170 0.3515248176143981.0433986286703 0.299087502365323
0.274038924755035 0.433628947364469A A A 0.2892998904159960.252357665046735
0.286094220961525A A A LNCV6_133943_PI430048170 mRNA
CCTGGGTTTAGGACCTATGTATGAAGGCCACCAATTTTTTAAAAATATCTGTGGTTTATT NM_002977RefSeq chr2 - 166195186 166375987 SCN9A 6335 "sodium channel, voltage gated, type IX alpha subunit"
GO:0005886|GO:0086010|GO:0005248|GO:0009636|GO:0009791|GO:0031402|GO:0019228|GO:0006954|GO:0001518|GO:0034765|GO:0035725|GO:0006814|GO:0048266 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144031_PI430048170 0.9547602118540181.07854910695917 0.419804035395117
2.05661676314576 1.46414658965169 A A A 0.6004167752943461.68352638964607
1.54953832430344 A A A LNCV6_144031_PI430048170 mRNA
ACCAAAATATTTTGGAAATATCAACCTTGTCTCGGGCACCTGGAGGGAGTCCCATAATCC NM_032561RefSeq chr22 - 37943049 37953647 C22orf23 84645 "chromosome 22 open reading frame 23, transcript variant 1"
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135491_PI430048170 0.6220821633924291.1231730207585 0.594763823079493
1.09041095870362 0.310015186772829A A A 0.3998756315670150.637997200420733
0.554483418536506A A A LNCV6_135491_PI430048170 mRNA
TTTTTATTAACCATGTCTAACTACGTATCTGTGCCACAGCTTGCAGTGAGGCAGGCCACT NM_001286527 RefSeq chr16 + 84368522 84464187 ATP2C2 9914 "ATPase, Ca++ transporting, type 2C, member 2, transcript

variant 1"
GO:0005515|GO:0005388|GO:0034220|GO:0000139|GO:0008152|GO:0070588|GO:0016021|GO:0055085|GO:0005
524|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134692_PI430048170 0.2698400286448631.16128883360584 0.280515799110517
0.7474127513309130.50895154527823 A A A 0.3257534127764190.280799963921367
0.320471411131426A A A LNCV6_134692_PI430048170 mRNA
CTGTTTAGCACAAATGTGCCCTACATACTGGAGATTAAATAAAGATTGTGAAGTCTGAAA NM_001122716 RefSeq
chrX + 126819763 126821785 PRR32 NA proline rich 32 NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_110647_PI430048170 0.5945330668744751.2381634466942 1.6269303092343
2.87312573703773 2.12880390768591 A A A 1.48189864800809 2.13647244814831
2.24913234395255 A A A LNCV6_110647_PI430048170 mRNA
CCGATTGACATGCGACACCAGGAAGGAAGGTACCATTACGAGCCTCATTCTGTCCACGGT NM_005270RefSeq chr2
+ 120797290 120992653 GLI2 2736 GLI family zinc finger 2
GO:0005515|GO:0007389|GO:0033089|GO:0003700|GO:0044212|GO:0021696|GO:0021965|GO:0030879|GO:0007
224|GO:0007507|GO:0048589|GO:0007411|GO:0002062|GO:0060603|GO:0060032|GO:0021938|GO:0045740|GO:0
000122|GO:0001701|GO:0001649|GO:0007418|GO:0001501|GO:0002076|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_103462_PI430048170 0.2939642907030970.7839359431490373.11639395300379
3.70212742363467 3.50266180725721 P P P 3.90929484618275 3.35178571485329
4.07802908771778 P P P LNCV6_103462_PI430048170 mRNA
TCTTCGGAAATACAAGGACTTCTGCATCCATGGAGAATGCAAATATGTGAAGGAGCTCCG NM_001945RefSeq chr5
- 140332842 140346603 HBEGF 1839 heparin-binding EGF-like growth factor
GO:0051545|GO:0051897|GO:0008284|GO:0005154|GO:0035313|GO:0051549|GO:0005886|GO:0030307|GO:0090
303|GO:0008016|GO:0005615|GO:0007173|GO:0008201|GO:0048011|GO:0030335|GO:0009986|GO:0048015|GO:0
005576|GO:0048661|GO:0030666|GO:0007165|GO:0007517|GO:0008543|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144529_PI430048170 0.0317499258406039 0.7799903358338988.21413484562553
8.38712997041152 8.36163451856955 P P P 8.57921258788059 8.84560462565298
8.60419848819154 P P P LNCV6_144529_PI430048170 mRNA
TGATTTTGCTTGTATTTCCGGAAGTGGGGTTGCTGGGTCATAGGGCAGGTGTAATTTTTT NM_173547RefSeq chr17
- 75888959 75897003 TRIM65 201292 "tripartite motif containing 65, transcript variant 1"
GO:0005622|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131374_PI430048170 0.00248775081536611 2.72847501018046 7.30198356523924
7.11439131955423 7.22716569776371 P P P 5.77827245524898 5.96109198130628 5.5345859847938
P P P LNCV6_131374_PI430048170 mRNA
TTCCATCTAGCTGCTAATGCCAAGTGTCCCTAAAGATGGAGGAATAAAGCCACCAATTCT NM_004143RefSeq chrX
- 72301637 72306987 CITED1 4435 "Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-
terminal domain, 1, transcript variant 1"
GO:0001656|GO:0005515|GO:0001658|GO:0043627|GO:0060711|GO:0003700|GO:0044212|GO:0060712|GO:0051
591|GO:0042803|GO:0043524|GO:0000578|GO:0042438|GO:0032496|GO:0070670|GO:0007179|GO:0071107|GO:0
032868|GO:0071104|GO:0071105|GO:0003713|GO:0060231|GO:0001890|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141596_PI430048170 0.0157958660200861 0.6985542451338037.06717582672017
6.80574705306232 6.77789893419118 P P P 7.22286540607456 7.47666480327026 7.5055368799145
P P P LNCV6_141596_PI430048170 mRNA
ACACGAGGGTGGAAATGAAAACTGGAACTTCCTTGTAAATTTAAACTTGGCAATAAAAGA NM_015226RefSeq chr16
+ 10944487 11182189 CLEC16A 23274 "C-type lectin domain family 16, member A, transcript variant 1"
GO:0006914|GO:0005765|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_124445_PI430048170 0.2547357670910380.7332256811832329.03440194906256
7.97300926172356 8.15921945456145 P P P 8.95936735434658 9.10921667105178
8.63532464286363 P P P LNCV6_124445_PI430048170 mRNA
TTCTTCCTCCCGCTGCTAAGCCGCTGTCCCTCCGCCATGGGAATAAAGAATAAGGATGGG NM_005007RefSeq
chr6_GL000255v2_alt + 2803426 2814673 NFKBIL1 4795 "nuclear factor of kappa light
polypeptide gene enhancer in B-cells inhibitor-like 1, transcript variant 1"
GO:0005515|GO:0071222|GO:0034122|GO:0007249|GO:0032720|GO:0042994|GO:0032088|GO:0005654|GO:0005
634|GO:0045111|GO:0031665|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136276_PI430048170 0.0140578828087878 0.7657025799722181 0.9821210886758
10.7887115364853 10.7551418437986 P P P 11.1550379767388 11.3280636717867
11.2032882463497 P P P LNCV6_136276_PI430048170 mRNA
CCCGCCCCGTGTGATTTGTTTCATTGTTAATATAATTTCCAGTTTAATAAACAAAACCCT NM_002503RefSeq chr19
+ 38899929 38908894 NFKBIB 4793 "nuclear factor of kappa light polypeptide gene enhancer in B-cells
inhibitor, beta, transcript variant 1"
GO:0005515|GO:0038124|GO:0034142|GO:0038123|GO:0034134|GO:0003713|GO:0005634|GO:0002224|GO:0006
351|GO:0005829|GO:0002756|GO:0007165|GO:0071222|GO:0051092|GO:0045087|GO:0002755|GO:0035666|GO:0
034166|GO:0032481|GO:0004871|GO:0034146|GO:0034138|GO:0034162 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142310_PI430048170 0.3868660994331881.12065605617517 10.2644487776068
10.4502443540619 10.6182131088684 P P P 10.0825477459227 10.1869265226404
10.5494322120669 P P P LNCV6_142310_PI430048170 mRNA
TGGACTCCAACCTTCCTTTTTTAAAATTTTCTCCAGCCCTGGGAGCAAGTTGCAGTCTTT NM_001287737 RefSeq
chr1 - 92074435 92075472 SETSIP NA SET-like protein NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141069_PI430048170 0.0201346645169712 0.94781080311506 0.398138365437596
0.3548271260452320.348774980578883A A A 0.4552324295232240.45191688695083
0.426916481958177A A A LNCV6_141069_PI430048170 mRNA
CCAGTGATTCGAGCTATATTTAAGTATTCAAGAAAGCCAGTCTTAACATTTCTAACTCTG NM_002544RefSeq chr17
- 31294649 31297362 OMG 4974 oligodendrocyte myelin glycoprotein
GO:0048011|GO:0005886|GO:0031102|GO:0048683|GO:0050771|GO:0031225|GO:0007155|GO:0050770|GO:0042
802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139734_PI430048170 0.0296571801756341 2.38244135088489 6.74659354682579
6.55012828166714 6.59055182103013 P P P 4.90737990683835 5.7721106080131
5.32904571736773 P P P LNCV6_139734_PI430048170 mRNA
CTGGGTGACGCATGCCTCTGGTCTAATAAACTGGGTTTCAACCATCTCCTCTTCAAAAAA NM_020039RefSeq chr12
+ 50057636 50083622 ASIC1 41 "acid sensing (proton gated) ion channel 1, transcript variant 1"
GO:0005515|GO:0005886|GO:0050915|GO:0055085|GO:0071467|GO:0070207|GO:0007165|GO:0015280|GO:0034
220|GO:0005887|GO:0006810|GO:0006816|GO:0035725|GO:0006814|GO:0009268 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141694_PI430048170 0.9564486722950331.03153402188086 1.96021507210107
0.34071181923666 1.10202246654408 A A A 0.2498498255746141.17884517620159
1.85909863417877 A A A LNCV6_141694_PI430048170 mRNA
CACAGGAAATGATCATAGACCTAAAAATAGTTTTTAAGGAAACCAGCTACACGGGGCAAC NM_004232RefSeq chr18
+ 70288900 70330198 SOCS6 9306 suppressor of cytokine signaling 6
GO:0001772|GO:0005515|GO:0016567|GO:0050868|GO:0019221|GO:0006952|GO:0007259|GO:0046426|GO:0005
737|GO:0004860|GO:0006469|GO:0010498|GO:0040008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144890_PI430048170 0.0677725204822629 0.7745539930262685.82198949335324
5.92644275768908 6.16914256138866 P P P 6.18601173231417 6.29109753029895
6.54455006680906 P P P LNCV6_144890_PI430048170 mRNA

GTGTTGACATTTGAGGATGGGTATGCAAGGAAAAAATATACTTCTGTTTACTTACTCTGA NM_032424RefSeq chr11 - 106007901 106022227 MSANTD4 84437 Myb/SANT-like DNA-binding domain containing 4 with coiled-coils GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137386_PI430048170 0.00273147091631098 0.4296117972387074.2862891419768 4.00540567706424 4.38491576269899 P P P 5.52510789519098 5.34395121799468 5.48436524002418 P P P LNCV6_137386_PI430048170 mRNA
CCTGTGATCTTTCTTCTCCCAGCTAAGAGTTCTTCAATAAATTTAAGAAATACCTGGTAA NM_016248RefSeq chr13 + 42272152 42323267 AKAP1111215 A kinase (PRKA) anchor protein 11
GO:0035556|GO:0005815|GO:0006928|GO:0010738|GO:0008157|GO:0051018|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130221_PI430048170 0.00761268198840723 1.58270177267799 10.9472595964626 11.2116583695112 10.9602348785742 P P P 10.3031150031275 10.5720581490659 10.2515716640127 P P P LNCV6_130221_PI430048170 mRNA
GCCTGGAGAGGATCTATGCTTGTTTGTTTTTGTAATCCATATCATAGTTGCTTTCTTTAA NM_001395RefSeq chrX + 153642442 153651326 DUSP9 1852 dual specificity phosphatase 9
GO:0005515|GO:0000188|GO:0005737|GO:0006470|GO:0007254|GO:0005634|GO:0004721|GO:0008138|GO:0035335|GO:0017017|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138599_PI430048170 0.372204473273132 1.36504879987849 2.27853138052882 2.67534443829109 2.87379843673813 A A A 1.0279873600648 2.99411754730834 1.84681280970565 A P A LNCV6_138599_PI430048170 mRNA
GAGATGACAAGTCAACATAGCATGGGATCTTGGCTAGACAAGGAAAGCGAGAGAACATTA NM_021072RefSeq chr5 - 45254949 45696118 HCN1 348980 hyperpolarization activated cyclic nucleotide gated potassium channel 1
GO:0030424|GO:0046549|GO:0005886|GO:0005222|GO:0005248|GO:0005267|GO:0007268|GO:0045176|GO:0030425|GO:0042802|GO:0030552|GO:0005887|GO:0005249|GO:0042391|GO:0035725|GO:0034765|GO:0016021|GO:0071320|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141547_PI430048170 0.383647327120022 1.08290916717455 11.5178532396679 11.4774896330669 11.6792855278164 P P P 11.5847005031751 11.2432204060813 11.488830541898 P P P LNCV6_141547_PI430048170 mRNA
TTAGCCATCTTACTTGGCTTTTTACTATTAACATGATGTACTAAAGTAGAGCCCTTTGAG NM_006070RefSeq chr3 + 100709330 100748967 TFG10342 "TRK-fused gene, transcript variant 1"
GO:0005515|GO:0007165|GO:0005737|GO:0004871|GO:0043123|GO:0070062|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142131_PI430048170 0.00934245422194815 0.435234003902296 3.894289567503 3.51709497751275 3.92016195244439 P P P 5.07371763894841 4.59441050362333 5.22559589586667 P P P LNCV6_142131_PI430048170 mRNA
CTCCAGTGATCAGAAACATTGATATCAATCCCTATTAAATTAGTGGGGGGAATATTAACT NM_019004RefSeq chr7 + 92246233 92401384 ANKIB1 54467 ankyrin repeat and IBR domain containing 1
GO:0005515|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143023_PI430048170 0.00553586353764738 1.81044671247581 11.1918622023341 11.1852154227229 11.1865253180977 P P P 10.2500713552158 10.2794344214505 10.4563256636039 P P P LNCV6_143023_PI430048170 mRNA
GTTTTCACTAAGTCGTTCCTACCATAACTGTGAATTTAAAGTAAAACCAGCTCAGAATCC NM_015933RefSeq chr3 + 48440275 48444129 TMA7 51372 translation machinery associated 7 homolog (S. cerevisiae) NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143084_PI430048170 0.6757108370362440.9574716523557178.75602684802846 8.79421412405352 8.74404097813318 P P P 8.59899177662692 8.89573082757081 8.96276984833128 P P P LNCV6_143084_PI430048170 mRNA
ACCCTGTTACTGTTTGAAAATGCATGCATGTTACGATGAATCTCCAACCTGAGGAAAAAA NM_003559RefSeq

chr17_KI270857v1_alt - 2801009 2835224 PIP4K2B 8396 "phosphatidylinositol-5-phosphate 4-kinase, type II, beta"
GO:0005886|GO:0006661|GO:0044281|GO:0005524|GO:0016309|GO:0005829|GO:0016308|GO:0035556|GO:0046854|GO:0005789|GO:0005654|GO:0005057|GO:0006644|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134350_PI430048170 0.61344672667589 0.6943656962211143.51776721777929 3.71570615938736 3.50356395716968 P P P 4.96135484288407 3.31497208550644 3.41204515658092 P P P LNCV6_134350_PI430048170 mRNA
CTTATCTGCTCTCCTTCTCTGACTTGACCATCATGACTAGAATGATTATCCCTTTACTGA NM_001099780 RefSeq chr14 + 23042166 23044060 PSMB11 NA "proteasome (prosome, macropain) subunit, beta type, 11" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134928_PI430048170 0.3356759048942780.6982297695157280.402001740770961 0.2960363677704150.335140511283406A A A 1.45664084737817 0.529941186922732 0.343657791974753A A A LNCV6_134928_PI430048170 mRNA
AGTAAACACTTTAGTTGCTTTCAGGGATGACACAAGCACACAATGATTTTTGCTTACAAT NM_001143RefSeq chrY - 6865917 6874027 AMELY 266 "amelogenin, Y-linked"
GO:0031012|GO:0030345|GO:0005578|GO:0031214 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139173_PI430048170 0.8865563769927 0.9701348116769417.13883545481937 7.01646047641887 6.6208520530077 P P P 7.31308543254897 6.87149623646304 6.70122618869323 P P P LNCV6_139173_PI430048170 mRNA
AACACATTGCACTCTCCCTACGGAACGCTGGGCTTGGACGCGCATTCCTCTTCCAACTGA NM_001199824 RefSeq chr19 - 55540655 55545543 SBK3 NA "SH3 domain binding kinase family, member 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138717_PI430048170 0.1838693687526660.7474180047974244.53424404497969 3.84622618120352 3.8649024021639 P P P 4.69730631699789 4.62854177735452 4.25230942914999 P P P LNCV6_138717_PI430048170 mRNA
CTGCTCCTCCAGCCTGCTGAATTTACTGAGTAAAGAAATAGCAAATATGATAGATGTTTT NM_006073RefSeq chr6 - 123216338 123637093 TRDN 10345 "triadin, transcript variant 1"
GO:0005515|GO:0060047|GO:0005886|GO:0005783|GO:0051279|GO:0031122|GO:0042803|GO:0060316|GO:0014701|GO:0010649|GO:0005737|GO:0006936|GO:0034220|GO:0010880|GO:0060315|GO:0030674|GO:0030314|GO:0006874|GO:0005102|GO:0033018|GO:0033017|GO:0014808|GO:0034704|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_43570_PI430048170 0.1452547038066661.14417227113076 9.105244480411 8.97036693294622 9.19867311248668 P P P 8.85300533563032 9.05768650498597 8.77478623614486 P P P LNCV6_43570_PI430048170 mRNA
TTGCCAAAAGTGCTAAAATCACAGTGAATGAGTGGAGCTTCTGGTGATGAAGGCCCTTTC NM_175932RefSeq chr11 + 236807 252984 PSMD13 5719 "proteasome (prosome, macropain) 26S subunit, non-ATPase, 13, transcript variant 2"
GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0034641|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0000502|GO:0043066|GO:0005838|GO:0006521|GO:0051437|GO:0042590|GO:0006915|GO:0042981|GO:0051436|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136977_PI430048170 0.4228268898918550.4382610277951590.434840985838513 0.4201809052377210.313150288218668A A A 2.66750088351392 0.386590249662717 0.391627512215066P A A LNCV6_136977_PI430048170 mRNA
ATATTGATTATGGTGACTGATAATGACAGCAATGCTATCACTCCCACCAGGGAGCCTTCC NM_001130992 RefSeq chr3 - 139526404 139539829 RBP1 5947 "retinol binding protein 1, cellular, transcript variant 2"
GO:0005215|GO:0007603|GO:0006776|GO:0016918|GO:0006810|GO:0005501|GO:0019841|GO:0001523|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_65687_PI430048170 0.0812878454885661 0.8013923206107825.20905162960775
5.51729942293286 5.37972647814317 P P P 5.82095644636635 5.75403610544337
5.48423659596813 P P P LNCV6_65687_PI430048170 mRNA
TCCTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAGCCATGCCCAGTGTC NM_138370RefSeq chr2
+ 42048020 42058528 PKDCC 91461 "protein kinase domain containing, cytoplasmic"
GO:0005794|GO:0030501|GO:0048286|GO:0042997|GO:0005576|GO:0018108|GO:0048566|GO:0030282|GO:0015
031|GO:0005524|GO:0030154|GO:0001501|GO:0004672|GO:0035264|GO:0060021|GO:0032332|GO:0004715 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133279_PI430048170 0.6330173369814551.22908917904302 3.1396330686972
1.64434923791522 2.01271901344265 P A A 2.69201457383704 0.358271155441327
2.39313403181464 A A P LNCV6_133279_PI430048170 mRNA
GCGGGGAGAGGGTACACAATGGGTATCTAATAAATACTTAAGAGGTGGAATTTGTGGAAA NM_000331RefSeq
chr11 + 18266260 18269976 SAA1 6288 "serum amyloid A1, transcript variant 1"
GO:0001664|GO:0030593|GO:0030168|GO:0050716|GO:0005576|GO:0050715|GO:0006953|GO:0007204|GO:0006
898|GO:0045785|GO:0034364|GO:0071682|GO:0050728|GO:0045087|GO:0050708|GO:0048247|GO:0048246|GO:0
008201|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113428_PI430048170 0.0115748564079520.6850133564944864.62103351797941
4.90394513418471 4.70335840619753 P P P 5.33222934251222 5.32904571736773
5.21630546591114 P P P LNCV6_113428_PI430048170 mRNA
CCCTCCATTCTTGCTGATGTATTCTGCATATTAGACATTGAGACAAATTGTTTAGAAGAA NM_001081550 RefSeq
chrX - 123600560 123733054 THOC2 57187 THO complex 2
GO:0008380|GO:0006397|GO:0005515|GO:0000347|GO:0006406|GO:0016607|GO:0016973|GO:0003723|GO:0000
346|GO:0005654|GO:0000445|GO:0046784 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140176_PI430048170 0.00132344283147393 4.51930598342867 5.57887729161002
6.06587208799645 6.25028297222157 P P P 4.06838763176257 3.51884179448393
3.80782131805753 P P P LNCV6_140176_PI430048170 mRNA
ATTTTCTTCCTGGGATTGGGGAGGGGATGATTCAGACCCCACATGGCCTCCAACCTTGGC NM_000453RefSeq chr19
+ 17871972 17895174 SLC5A5 6528 "solute carrier family 5 (sodium/iodide cotransporter), member 5"
GO:0005886|GO:0008507|GO:0005634|GO:0044281|GO:0015111|GO:0055085|GO:0031982|GO:0034641|GO:0071
371|GO:0006810|GO:0006590|GO:0035725|GO:0016021|GO:0071320|GO:0015705|GO:0070062|GO:0006811 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128652_PI430048170 0.00380883060145478 1.50032649439612 8.52614238473396
8.70331022816257 8.71583143845945 P P P 8.11339299507051 8.01052978425104
8.07137100685557 P P P LNCV6_128652_PI430048170 mRNA
GCCCGCTTACTGTTAAATCGTCCCTCTGTTGCTTTATCCTCTAAAATATGTTAAGGGATA NM_003450RefSeq chr16
+ 3401189 3409366 ZNF174 7727 "zinc finger protein 174, transcript variant 1"
GO:0005737|GO:0003700|GO:0044212|GO:0006366|GO:0000981|GO:0005654|GO:0005634|GO:0000122|GO:0015
629|GO:0045892|GO:0046872|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114827_PI430048170 0.4731698341223480.9892626789261660.3625147750148
0.3666154100321840.360959212882774A A A 0.4059393691489680.346021322700293
0.384221335433483A A A LNCV6_114827_PI430048170 mRNA
CATTCTCTCAGTACACTGTGGTGTCAGATATCAATCTTGCCAAAATAGATGATGATGCAA NM_000670RefSeq chr4
- 99123656 99144298 ADH4 127 "alcohol dehydrogenase 4 (class II), pi polypeptide"
GO:0005503|GO:0006805|GO:0006066|GO:0006069|GO:0006081|GO:0046164|GO:0044281|GO:0003960|GO:0019
841|GO:0001523|GO:0005829|GO:0004022|GO:0004032|GO:0051287|GO:0035276|GO:0019115|GO:0004024|GO:0
042572|GO:0016620|GO:0008270|GO:0004745 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138887_PI430048170 0.00606270742439264 1.5355092897121 11.4046202184534
11.5155275389363 11.7041672073519 P P P 11.0361001019334 10.8034778413587
10.9352130649573 P P P LNCV6_138887_PI430048170 mRNA

CATATAGTCTTTCTGGTTTCTGGAGATAACCCATCAATAAAAGCTGCTTCCTCTGGTAAA NM_016406 RefSeq chr1 + 161153743 161158856 UFC1 51506 ubiquitin-fold modifier conjugating enzyme 1 GO:0005515|GO:0071568|GO:0034976|GO:0071569|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130568_PI430048170 0.00428353810402857 0.3198885832474084.96647622760226 4.92542127557188 5.37494805776747 P P P 6.77925702779445 6.65954635780525 6.80120141108346 P P P LNCV6_130568_PI430048170 mRNA
GGTAACTTCTTGGCTTTCTTTTGTACCACAACTTATTTTACTACTGATATTTGACCTGGA NM_016230 RefSeq chr6 + 83859650 83960427 CYB5R4 51167 cytochrome b5 reductase 4 GO:0048471|GO:0004128|GO:0005783|GO:0050660|GO:0006801|GO:0006739|GO:0006091|GO:0042593|GO:0046872|GO:0016653|GO:0003032|GO:0003958|GO:0016174|GO:0048468|GO:0030073|GO:0046677|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145238_PI430048170 0.6729096034987130.9735209993367075.03322849991982 4.89354625752639 5.14458136501958 P P P 5.07317177435389 5.14718762267573 4.97277489446664 P P P LNCV6_145238_PI430048170 mRNA
CAAGGGCCACATTCACCTTTTCAGAGTGACTCAATCAAATTTGTAGTTTGTAAAAGTATT NM_000031 RefSeq chr9 - 113386311 113401338 ALAD 210 aminolevulinate dehydratase GO:0032791|GO:0005634|GO:0004655|GO:0044281|GO:0003824|GO:0006782|GO:0005829|GO:0006783|GO:0042802|GO:0006778|GO:0071353|GO:0008270|GO:0051260|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130459_PI430048170 0.2766409310628370.6301177590748630.484171651876643 1.51505572170093 2.63214216808788 A A A 2.47811214263977 2.65358439916386 2.24193071771717 A P A LNCV6_130459_PI430048170 mRNA
GTCTCTAGCTAAAACCAACTGTTTAGTTGACTTTTTAGTTATAGGATAAGTTGGAAGTCC NM_017673 RefSeq chr1 + 185157158 185291781 SWT1 54823 "SWT1 RNA endoribonuclease homolog (S. cerevisiae), transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63189_PI430048170 0.4169851126048270.9341405987958855.40197273841562 5.63698261581679 5.49656157459682 P P P 5.55017374853888 5.77047969186097 5.50527745284189 P P P LNCV6_63189_PI430048170 mRNA
TTCTGAGCCAGGCACATCAAATGTCAAGGAATTGACTGAACGAACTAAGAGCTCCTGGAT NM_001288968 RefSeq chr17 + 50426157 50474845 ACSF2 80221 "acyl-CoA synthetase family member 2, transcript variant 1" GO:0005739|GO:0016874|GO:0006631|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133611_PI430048170 0.6836128983058410.9626107726841810.301680750591228 0.3022090714228760.47162172124843 A A A 0.3255571177165910.603860124232605 0.297461770580065 A A A LNCV6_133611_PI430048170 mRNA
GCATAAGCTTTAGAGGTAAAGCGTTTGCATTTGCAGTGCATCAGATAAATTGTATATTTC NM_213658 RefSeq chr12 - 10446035 10454616 KLRC1 3821 "killer cell lectin-like receptor subfamily C, member 1, transcript variant 3" GO:0043235|GO:0005515|GO:0005886|GO:0005887|GO:0050776|GO:0030246|GO:0023024|GO:0007166|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136180_PI430048170 0.1046228058556271.43995604542819 2.81322247152209 3.2461689611233 2.88524374954953 A P P 2.85226940031832 2.19677368085484 2.26168094399605 P A A LNCV6_136180_PI430048170 mRNA
ATCTACACATTCATCGAGATTCCTGTTTGCGAGCCCTGGCGTCCATTTTTTGCTCATAAA NM_001145014 RefSeq chr19 + 55759140 55763175 RFPL4A NA ret finger protein-like 4A NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136588_PI430048170 0.000998586356797924 0.2440678217429524.53846490961223 3.94379023752035 4.26718569355497 P P P 5.98198649204858 6.35301657999331 6.52685092042943 P P P LNCV6_136588_PI430048170 mRNA

CTGTGTTAATTCTATCTCCAGTAGGCCTAATGCTTGAATAAGCAAGATGTCTAATCAATA NM_020474RefSeq chr18 + 35654568 35711834 GALNT1 2589 polypeptide N-acetylgalactosaminyltransferase 1 GO:0048471|GO:0005794|GO:0030145|GO:0016266|GO:0005576|GO:0004653|GO:0000139|GO:0006493|GO:0016020|GO:0018242|GO:0032580|GO:0030246|GO:0018243|GO:0016021|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132833_PI430048170 0.5042503610563650.7270378873857830.681375198321463 1.89734396024199 0.365352490611178A A A 1.64960143439006 2.15888978199622 0.583340320438205A A A LNCV6_132833_PI430048170 mRNA
ACCAAAACTGGTTGACTCTAACCTTGCCTTGCTGAGTAAAAATTCTGCTTTGGATGAGAA NM_001163391 RefSeq chr6 - 28388949 28399767 ZSCAN12 9753 "zinc finger and SCAN domain containing 12, transcript variant 1" GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132044_PI430048170 0.2012056753823522.1087789286551 0.39767182669514 1.50217018018239 2.08222700511356 A A A 0.33541916900137 0.358192203332722 0.518550413508501A A A LNCV6_132044_PI430048170 mRNA
TGAAGGACAAAATACAGATCCCAAGCTAAATCCCAAGGATGACGGCATCGTCTATGCTTC NM_013439RefSeq chr7 + 100373444 100400099 PILRA 29992 "paired immunoglobin-like type 2 receptor alpha, transcript variant 1" GO:0005515|GO:0007165|GO:0005886|GO:0016032|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67414_PI430048170 0.2154557044611890.8474771609889921.91210544656971 2.1462736459416 2.32379608881571 A A A 2.15710543848947 2.40918521013035 2.53606135739325 A P P LNCV6_67414_PI430048170 mRNA
AACCTCTACAAGGCCAGCGTGCTGAAGAAGGTGGCCGATATCCACAGAGCCTCCAAGGAT NM_004259RefSeq chr17 - 75626844 75667189 RECQL5 9400 "RecQ protein-like 5, transcript variant 1" GO:0008026|GO:0031965|GO:0000993|GO:0005730|GO:0005634|GO:0006310|GO:0006259|GO:0003676|GO:0005524|GO:0003678|GO:0051304|GO:0006260|GO:0005737|GO:0007067|GO:0006281|GO:0016591|GO:0005654|GO:0032508|GO:0034244|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138332_PI430048170 0.2956036314185410.5565594122693670.433014620474215 0.3703214708558580.402429679518128A A A 0.3046577375517381.97437879446264 0.969658887967094A A A LNCV6_138332_PI430048170 mRNA
ACATGGCTGTCAACAATGCCAGGAAAATATCTACAGAAGGAAAGAATCCCCTACGCCACT NM_198154RefSeq chr17 + 7355177 7357219 TMEM95 339168 transmembrane protein 95 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133608_PI430048170 0.3142807107776030.8205322896982740.483238454793921 0.4829327604120660.392641099753914A A A 1.1007527625797 0.523908495781528 0.510258286240215A A A LNCV6_133608_PI430048170 mRNA
CTCTGATCTGCTTTCTATAGATAATGAGGAAGAAATGGTAAGACGTAAATGTTTCAACAC NM_013431RefSeq chr12 - 10407383 10409757 KLRC4 8302 "killer cell lectin-like receptor subfamily C, member 4" GO:0006968|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137720_PI430048170 0.0364752127267866 0.3412839560054280.277049835853961 0.3772766657737370.484666120266176A A A 2.36928481501456 1.30286063629887 1.93444560743913 A A A LNCV6_137720_PI430048170 mRNA
CAGTTCACCCTCTTTGCCTAACAATCTCGGAAGGAAAATATATCACATCAATAATCAATA NM_016279RefSeq chr5 - 26880599 27038582 CDH9 1007 "cadherin 9, type 2 (T1-cadherin)" GO:0003674|GO:0016337|GO:0005886|GO:0034329|GO:0005509|GO:0016021|GO:0007156|GO:0045216|GO:0034332 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127657_PI430048170 0.0710629101790457 1.55603935023801 5.13714055012152 4.94792941137519 5.18875729452267 P P P 4.05068089858544 4.47420217314439 4.75985126395594 P P P LNCV6_127657_PI430048170 mRNA

ACAAGTGGCTGTTAACTGAGTCACCATATCCCAGTAAAGCTGAATTTTCTCACTAAAAAA NM_004627 RefSeq chr21 + 39380286 39397889 WRB 7485 "tryptophan rich basic protein, transcript variant 1" GO:0005789|GO:0005634|GO:0016021|GO:0071816 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_137277_PI430048170 0.3997866140342320.9594310513628470.268337032830137 0.41322000186752 0.299321109032577 A A A 0.473904988752577 0.365524763525629 0.320420836025796 A A A LNCV6_137277_PI430048170 mRNA
AAATAAAGGTACTTCTGGGCAGCCAGGCTGCACAGCATTTGCTTTCCTCTGAGATTCTAA NM_005588 RefSeq chr6 + 46793356 46839782 MEP1A 4224 "meprin A, alpha (PABA peptide hydrolase)" GO:0005515|GO:0005887|GO:0017090|GO:0007586|GO:0006508|GO:0008270|GO:0004222|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_133387_PI430048170 0.0241957575961620.3844000426602443.29263523954245 3.61072757889466 2.7822361861232 P P A 4.55016692346782 4.68832753059738 4.69804368813325 P P P LNCV6_133387_PI430048170 mRNA
GCAATGTCTAATTTGTATACACTTCAGTTAAATTTCCCTAAAACTTGAAAGGGGACCTTG NM_005385 RefSeq chr3 + 42600654 42648741 NKTR 4820 natural killer cell triggering receptor GO:0000413|GO:0016018|GO:0016020|GO:0006457|GO:0003755 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_99910_PI430048170 0.7050165277484720.9657426888066484.29622623949371 4.03720370453825 4.03595404972144 P P P 4.19220823964662 4.31568577371969 4.01220542140345 P P P LNCV6_99910_PI430048170 mRNA
CAGGACGGTCAGATAAGAATGTGCCTTTTGATGAAAGAACTTTATCTTTCTACAATGAAG NM_198507 RefSeq chr5 + 100535304 100586740 FAM174A 345757 "family with sequence similarity 174, member A" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_121292_PI430048170 0.6847610243946250.8965256638824753.02248390461686 2.3261935549828 2.59423143230515 A A A 2.82299861038102 3.2129526837342 2.3345538314821 P P A LNCV6_121292_PI430048170 mRNA
TGGAGAACCTGAAGACCAGCTGCCCACAGAGCCACCTTCAGGCATCTCAGAGAAGACAGA NM_004646 RefSeq chr19 - 35825371 35851993 NPHS1 4868 "nephrosis 1, congenital, Finnish type (nephrin)" GO:0005515|GO:0007588|GO:0072015|GO:0005886|GO:0019904|GO:0007254|GO:0030507|GO:0007520|GO:0042995|GO:0032836|GO:0043234|GO:0030838|GO:0051393|GO:0005887|GO:0007519|GO:0036057|GO:0045121|GO:0017022|GO:0007155|GO:0044062|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_133522_PI430048170 0.0157004561970808 0.5028614998957525.92353227117711 5.9774104089836 6.43401182335186 P P P 6.83106547578796 7.0215374695909 7.44424258002814 P P P LNCV6_133522_PI430048170 mRNA
CTGATGTCTTGCTGAATGCTGTGACTCATAGTTTACTTTTGTTCAAAATAGTTTGCACTT NM_015294 RefSeq chr17 - 58998199 59106905 TRIM37 4591 "tripartite motif containing 37, transcript variant 1" GO:0005515|GO:0035518|GO:0005164|GO:0048471|GO:0004842|GO:0016235|GO:0016874|GO:0032088|GO:0000122|GO:0046600|GO:0042803|GO:0051865|GO:0005829|GO:0051091|GO:0005737|GO:0051092|GO:0035098|GO:0003682|GO:0070842|GO:0008270|GO:0031625|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_137134_PI430048170 0.4213756982620630.8267176258304730.388634999795816 0.4032746312593120.459625276518768 A A A 0.3433362780111761.11243169422574 0.501725999573417 A A A LNCV6_137134_PI430048170 mRNA
CTGCCTTCTCAACTCCAAACTGACTCTTAAGAAGACTGCATTATATTTATTACTGTAAGA NM_000492 RefSeq chr7 + 117479962 117668664 CFTR 1080 "cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C, member 7)" GO:0005515|GO:0030321|GO:0006695|GO:0043627|GO:0005886|GO:0030324|GO:0043434|GO:0030301|GO:0031205|GO:0005254|GO:0032870|GO:0016323|GO:0005737|GO:0016324|GO:0015108|GO:0045909|GO:0042311|GO:0015106|GO:0006810|GO:0006833|GO:0034097|GO:0030659|GO:0070062|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_131597_PI430048170 0.1774887404864330.6717172344809273.76618063211472
3.86365156735939 4.03030797173724 P P P 4.76748283681827 3.89381310385407
4.59401092207595 P P P LNCV6_131597_PI430048170 mRNA
TACCAGCAACAGAGAAGCAAAGAATGGAGTTCAACCTTACACTATAAACATCTAATAGAT NM_144975RefSeq chr17
+ 35243066 35267742 SLFN5 162394 schlafen family member 5 GO:0005634|GO:0005524|GO:0030154
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140266_PI430048170 0.4894721378832021.1268509439914 0.687565095374497
0.7445398788967961.21493640391086 A A A 0.6187500089693350.992212511515617
0.537355215132386A A A LNCV6_140266_PI430048170 mRNA
AACCTGGTCACCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAA NM_152997RefSeq chr4
+ 70226070 70235251 FDCSP 260436 follicular dendritic cell secreted protein GO:0005576 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_128967_PI430048170 0.0115696086029491 1.44139011191128 10.308825649047
10.3874375787194 10.6101940553359 P P P 9.90582746874061 9.79139561155692
10.0338234957212 P P P LNCV6_128967_PI430048170 mRNA
CTGGCCTAATGAGCAATGTTCTCAATTTTCGTTTTCATTTTGCTGTATTGAGACCTATAA NM_003859RefSeq chr20 -
50934867 50958523 DPM1 8813 "dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic
subunit"
GO:0005515|GO:0006501|GO:0004582|GO:0033185|GO:0043178|GO:0005783|GO:0019348|GO:0019673|GO:0005
634|GO:0005537|GO:0035269|GO:0035268|GO:0004169|GO:0016020|GO:0005789|GO:0006488|GO:0044267|GO:0
006506|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135943_PI430048170 0.0207652177836729 0.4882889718294647.81231894692854
7.74642933566789 7.63980169440053 P P P 8.41042951480836 8.97640941620821 8.859858541136
P P P LNCV6_135943_PI430048170 mRNA
GCCTGCCAAGGACCTCATTTAGTTTGTGTATTAAAACCAAAAAGCTTTTGTCTTTAAGAA NM_016307RefSeq chr9
+ 129665640 129722672 PRRX2 51450 paired related homeobox 2
GO:0043565|GO:0045880|GO:0006355|GO:0042472|GO:0003700|GO:0051216|GO:0048844|GO:0042474|GO:0005
634|GO:0002053|GO:0030326|GO:0048701 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137052_PI430048170 0.000287808530977703 0.6203905908655993.83557160814894
3.76451017523633 3.81895159644468 P P P 4.47232659652752 4.44678633394419
4.56445540291856 P P P LNCV6_137052_PI430048170 mRNA
GCTTCTGCTGCTCTGTTGGCCTCTGAAGAGCAATATCTAATTTATTATTACTGTAATTTT NM_001271675 RefSeq chr6
+ 65301417 65305611 LOC441155 NA zinc finger CCCH-type domain-containing-like NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135899_PI430048170 0.5247259087485321.30667687718215 3.37188172532891
2.68217758808891 2.05449710642916 P A A 2.56032484427129 2.46039125993954
2.20523359506977 A A A LNCV6_135899_PI430048170 mRNA
ATCCGGGGGCGGCCCCGGGTGGGCGCGAGTCGCTTTGTATCATCAATAAATTATTTAACG NM_177400RefSeq chr10
- 132784815 132786033 NKX6-2 84504 NK6 homeobox 2
GO:0006355|GO:0003700|GO:0010455|GO:0010454|GO:0022010|GO:0045686|GO:0005634|GO:0000122|GO:0045
687|GO:0043565|GO:0031018|GO:0050885|GO:0021912|GO:0021913 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_135395_PI430048170 0.00848008150490016 0.4561797154427365.70334811543055
5.6685591181593 6.21945586895011 P P P 6.76864765548626 7.08332294933
7.17411758027752 P P P LNCV6_135395_PI430048170 mRNA
CACATTAAAGATGAGCTTGTTAAAAAGGAAAGCATATTTCTCTGATTGCCCTTATGGAGA NM_001287821 RefSeq
chr15 + 66505082 66549484 ZWILCH 55055 "zwilch kinetochore protein, transcript variant 2"
GO:0005515|GO:0007093|GO:0007067|GO:0000777|GO:0000776|GO:0000278|GO:0051301|GO:0005829 . NA

- . NA NA NA NA NA NA NA NA NA
LNCV6_138956_PI430048170 0.800492783266952 0.958718848281189 12.5770443807314
12.1827330531416 12.4033276895685 P P P 12.3755380780297 12.7373487943623
12.2078917334807 P P P LNCV6_138956_PI430048170 mRNA
AATGGTTGGTGTGTCATGGTGCCTCATCATTCTGGGGAGACTGAAAATACCTTCATCACT NM_080738 RefSeq
chr1 + 236395415 236484708 EDARADD 128178 "EDAR-associated death domain, transcript variant
B" GO:0007165|GO:0005737|GO:0061153|GO:0042475|GO:0001942|GO:0030154 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_89398_PI430048170 0.412516399237057 0.886515503941221 8.41801849963494
8.11237060678237 7.89897154850911 P P P 8.44643462552826 8.4470424388392
8.07357631882307 P P P LNCV6_89398_PI430048170 mRNA
TGGAAGTCCCCGGGAGCCTCTCCTTGCCTGGTGACCTACTAAAAATATAAAAATTAGCTG NM_000383 RefSeq
chr21 + 44285837 44298219 AIRE 326 autoimmune regulator
GO:0005515|GO:0006355|GO:0000977|GO:0044212|GO:0005634|GO:0001228|GO:0045182|GO:0006351|GO:0006
417|GO:0042802|GO:0042393|GO:0005737|GO:0006955|GO:0045944|GO:0003682|GO:0006959|GO:0008270|GO:0
045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142468_PI430048170 0.663412362840095 1.04340787151755 10.4262799574404
10.4307245123781 10.6944598967525 P P P 10.3727437424198 10.3363923744776
10.6537404801973 P P P LNCV6_142468_PI430048170 mRNA
AGTGGGCAAGACATGATTAATGAATCAGAATCCTGTTTCATTGGTGACTTGGATAAAGAC NM_007266 RefSeq
chr2 + 27628995 27650846 GPN1 11321 "GPN-loop GTPase 1, transcript variant 1"
GO:0005515|GO:0005737|GO:0008152|GO:0003924|GO:0005634|GO:0005525 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_116418_PI430048170 0.155577972466706 0.680190862493335 6.46290667493933
6.30122625695941 6.4643182773535 P P P 6.47381515491769 7.03421333050985
7.28064783428653 P P P LNCV6_116418_PI430048170 mRNA
AAGCGAAACACACAAACCAGCCTCAACTTACACTTGGTTACTCAAAAGAACAAGAGTCAA NM_001291869 RefSeq
chr3 - 185643738 185825039 IGF2BP2 10644 "insulin-like growth factor 2 mRNA binding protein 2,
transcript variant 3"
GO:0005515|GO:0017148|GO:0010467|GO:0048027|GO:0005634|GO:0009653|GO:0045182|GO:0005829|GO:0042
035|GO:0005737|GO:0000166|GO:0051028|GO:0003730|GO:0005856 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132566_PI430048170 0.503762529592532 1.21981891369072 2.02356024394054
2.31615385380894 2.34705897327861 A A A 2.21469933337186 2.46863171012097
0.495413417359682 A A A LNCV6_132566_PI430048170 mRNA
TTCCAGGGCCTGAGCAGCTGGATCTGGTACAAAGCAATCGGACATAGAGTTGGAGGGGGA NM_007102 RefSeq
chr1 + 42153420 42155824 GUCA2B 2981 guanylate cyclase activator 2B (uroguanylin)
GO:0007589|GO:0007588|GO:0006182|GO:0031284|GO:0045776|GO:0070062|GO:0008048 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145604_PI430048170 0.505636396067362 0.883940287909049 5.58137515127454
5.63514835336687 5.57739665029013 P P P 5.37012410822586 5.96371567039864
5.92222060841235 P P P LNCV6_145604_PI430048170 mRNA
GTCTGTTACGTTAACATGCTTTTCTAAAATTGCTTCACGTGTTAATTCATTTACTCCTGC NM_001300799 RefSeq chr5
- 132756003 132777375 SEPT8 NA "septin 8, transcript variant 6" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129251_PI430048170 0.0334384626804227 0.83670179343506 10.9465403165372
10.9988289788503 10.8131914358847 P P P 11.1621280905297 11.1612107355583
11.2125590039737 P P P LNCV6_129251_PI430048170 mRNA
CAGGGCCCCACCTCCCTCTCTCAGATATGTACAATAATTTAACACGGTTGCCTGAAAAAA NM_005735 RefSeq chr2

- 97655938 97664098 ACTR1B 10120 "ARP1 actin-related protein 1 homolog B, centractin beta (yeast)"
GO:0005515|GO:0019886|GO:0005813|GO:0005737|GO:0016020|GO:0005869|GO:0005524|GO:0070062|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137130_PI430048170 0.0529387046733070.5224010902913924.57262888883748
4.70186654059306 5.00371870891606 P P P 5.15827770814916 5.83698070380946
5.99800123482818 P P P LNCV6_137130_PI430048170 mRNA
GTCAGCATCTGACCATCTGTGACTATAAAGCTGTTATTCTTGTTATACCATTTGAAGTTT NM_001287248 RefSeq
chr15 + 90717326 90815462 BLM 641 "Bloom syndrome, RecQ helicase-like, transcript variant 4"
GO:0005515|GO:0007095|GO:0010165|GO:0048478|GO:0046632|GO:0005657|GO:0005634|GO:0000079|GO:0051
259|GO:0016363|GO:0002039|GO:0005737|GO:0004003|GO:0003697|GO:0000723|GO:0000724|GO:0046641|GO:0
051782|GO:0032508|GO:0016887|GO:0000729|GO:0008026|GO:0043140|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138834_PI430048170 0.3910192506945660.9032364296357130.32383377078525
0.3423458543578280.354011809035541 A A A 0.7249523112083930.332478535245185
0.370043353257361 A A A LNCV6_138834_PI430048170 mRNA
GGTAACAACTGCTGAGCTCAAAGATTTGTGATTGTTAAAACTTCTCTGGCATTTAATCAT NM_144967 RefSeq chrX
+ 131058241 131089883 ARHGAP36 158763 "Rho GTPase activating protein 36, transcript variant 1"
GO:0043547|GO:0051056|GO:0007264|GO:0005829|GO:0005096 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138753_PI430048170 0.0138384840237681 0.2031843727619730.503935362756308
1.17286723441546 1.87551534814089 A A A 3.28778823792278 3.48277317838426
3.92496400831474 P P P LNCV6_138753_PI430048170 mRNA
GGCTCATCTTCATACCTTTTTCCATTTTGAATCCTACAAAAATACTGCAAAAGACTAGTG NM_005898 RefSeq chr11
+ 34051682 34102610 CAPRIN1 4076 "cell cycle associated protein 1, transcript variant 1"
GO:0017148|GO:0005737|GO:0016020|GO:0010494|GO:0005887|GO:0000932|GO:0050775|GO:0003723|GO:0061
003|GO:0030425|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127719_PI430048170 0.0935761181470762 0.80179878810797511.37380904915
10.9887384081759 11.1165720449905 P P P 11.5312789410438 11.4977207146902
11.4313980085487 P P P LNCV6_127719_PI430048170 mRNA
AGCTTTTTTGTTGCTCCTCCCCACTGCCCCTTTTAATTTATTTGGTTGTTTGCGGAGGGA NM_003936 RefSeq chr2 +
218959627 218962155 CDK5R2 8941 "cyclin-dependent kinase 5, regulatory subunit 2 (p39)"
GO:0005886|GO:0071902|GO:0016534|GO:0016533|GO:0021549|GO:0000079|GO:0021819|GO:0008289|GO:0021
766|GO:0005737|GO:0045956|GO:0021722|GO:0001764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135804_PI430048170 0.605653504206256 1.03728436802566 14.1512594524672
13.9062755658641 13.91914250264 P P P 13.9503101416789 13.9515550431602
13.9296797496943 P P P LNCV6_135804_PI430048170 mRNA
TCCCCCTCCTTCCCCAAGAGAGGAAATAAAAGCCACCTTCGCCCTAGGGCCAAGAAAAAA NM_004095 RefSeq chr8
+ 38030501 38060365 EIF4EBP1 1978 eukaryotic translation initiation factor 4E binding protein 1
GO:0031929|GO:0005515|GO:0008286|GO:0010467|GO:0030324|GO:0045471|GO:0030371|GO:0006412|GO:0006
413|GO:0005829|GO:0043234|GO:0002192|GO:0045931|GO:0000082|GO:0005737|GO:0031333|GO:0002931|GO:0
008190|GO:0045947|GO:0005654|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75967_PI430048170 0.0552007452729756 1.13095393351088 10.3607622387825
10.4243708486119 10.2815031037432 P P P 10.0772381913654 10.241352721422
10.2136756948433 P P P LNCV6_75967_PI430048170 mRNA
GTTTTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTT NM_004199 RefSeq chr5
- 132192610 132227242 P4HA2 8974 "prolyl 4-hydroxylase, alpha polypeptide II, transcript variant 1"
GO:0016222|GO:0031418|GO:0005506|GO:0005783|GO:0009055|GO:0004656|GO:0005634|GO:0043231|GO:0005
737|GO:0018401|GO:0005788|GO:0016702|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142715_PI430048170 0.8267889123304290.968224626110213 2.76247458085005

1.95269282849967 2.24545590854972 A A A 2.23315466738781 2.21972473192829
2.71019879915448 A A P LNCV6_142715_PI430048170 mRNA
CCTGGGCCGAACCCTTGGCAGGCGGGCACCGAGGCTGTGGTGCTGCGTGCTCAGCGGTAA NM_001190479
RefSeq chr15 - 40281443 40282586 ANKRD63 NA ankyrin repeat domain 63 NA . NA -
NA NA NA NA NA NA NA NA NA
LNCV6_132342_PI430048170 0.2197194344073240.96763546041261 0.385881768710348
0.4104337351819030.31773312720849 A A A 0.4128281243130380.438792118666083
0.406207205429659A A A LNCV6_132342_PI430048170 mRNA
CTGTCTAGCTTAAACTACTACTCAAGCTGCTTAAGTTCTTAAGTATTGTTTGTAATCACC NM_001289045 RefSeq
chr6 - 143940299 144008416 PLAGL1 5325 "pleiomorphic adenoma gene-like 1, transcript variant 16"
GO:0000977|GO:0005794|GO:0006366|GO:0000981|GO:0006915|GO:0005634|GO:0001228|GO:0035914|GO:0003
677|GO:0046872|GO:0030154|GO:0043231|GO:0045944|GO:0005654|GO:0007050 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135126_PI430048170 0.6388269187834931.37616653295118 2.02037566704586
0.5351277864242770.459656486665927A A A 0.7602609793675590.439563744280663
0.963666840363297A A A LNCV6_135126_PI430048170 mRNA
CCTCAGAATCATCTGGGAAATAAAAATAGGATAGAGGAGTGTTAATGGTCACTTAGAATA NM_017419RefSeq
chr4_GL383527v1_alt - 1310 30896 ASIC5 51802 acid sensing (proton gated) ion channel family
member 5
GO:0015280|GO:0034220|GO:0005886|GO:0015252|GO:0035725|GO:0016021|GO:0055085|GO:0015992 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141707_PI430048170 0.4348600922711821.47059889191385 1.01295405579358
1.92190889979592 0.38411724153903 A A A 1.03028628069372 0.587953951173615
0.368280944027096A A A LNCV6_141707_PI430048170 mRNA
CCCAGGGGAATAGAGGAAACCAGGAATTCATTTCAAAATCATCAAAGTCTAAATTTAGAA NM_013391RefSeq chr5
- 78997563 79069674 DMGDH 29958 "dimethylglycine dehydrogenase, transcript variant 1"
GO:0005759|GO:0006544|GO:0009055|GO:0047865|GO:0006579|GO:0019695|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141366_PI430048170 0.1414897757108091.09132493267271 0.503365358718292
0.6224590560223280.599804323641778A A A 0.3452255810755370.459964006017851
0.538433537545113A A A LNCV6_141366_PI430048170 mRNA
CTTTGAAAGATGGAACCTCCAAGTGAATTACAACTTATTCTATCATTGATGAATTCAGCC NM_144629RefSeq chr2
- 197570802 197675860 RFTN2 130132 raftlin family member 2 GO:0005886|GO:0043330|GO:0033227 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130478_PI430048170 0.7189206144632750.9740181696124640.285393715567957
0.4958731863470260.333186642809537A A A 0.5245637167020250.425407561610261
0.276187368696474A A A LNCV6_130478_PI430048170 mRNA
CTGTGTCTTGGCTTCTTCAGTCGGTTTAATTAAAACAAACAGAACAATTTTCCCCAAAAA NM_032880RefSeq chr1
+ 18107745 18378483 IGSF21 84966 "immunoglobin superfamily, member 21" GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135093_PI430048170 0.7657210756736291.03605420726203 12.5939059345464
12.8947874542702 12.9885516466897 P P P 12.6717613756345 12.7449321997173
12.9242264134008 P P P LNCV6_135093_PI430048170 mRNA
TGCTTGTAATTTTTAAATTCATATCAATCATGGATGAGTCTCGATGTGTAGGCCTTTCCA NM_002792RefSeq chr20
- 62136726 62143458 PSMA7 5688 "proteasome (prosome, macropain) subunit, alpha type, 7"
GO:0005515|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0004
298|GO:0042802|GO:0034641|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0
005839|GO:0000502|GO:0043066|GO:0006521|GO:0051437|GO:0042590|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_128567_PI430048170 0.0964783864794522 1.08417988376231 12.7300552708726
12.8651052087476 12.7481684200262 P P P 12.6128685740628 12.6655813795102
12.7169475023334 P P P LNCV6_128567_PI430048170 mRNA
TTTCCTTTCATAAAGGAGTTGTGTCCCCAGCCCTTCCACTCCAGTAAAGAACTGAATTGG NM_020230RefSeq chr19
+ 10106222 10111299 PPAN 56342 peter pan homolog (Drosophila)
GO:0008380|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59901_PI430048170 0.0666292222819886 1.37832894903289 4.42494682694986
4.60824555518179 4.16532670493605 P P P 3.9516126600786 3.89947809414668
3.99117034120486 P P P LNCV6_59901_PI430048170 mRNA
ATTGCACAAGAAAAAGCCTTGAGAAAGACAGAATTGCTTGTGGACCGTGCATGTTCCACC NM_005932RefSeq chr13
- 23730188 23889448 MIPEP 4285 mitochondrial intermediate peptidase
GO:0005739|GO:0006627|GO:0005759|GO:0006508|GO:0004222|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126540_PI430048170 0.0453399978767731 0.64204816244143 5.72543620091898
6.02239637070918 5.5025035229412 P P P 6.38528747959378 6.37167583000439
6.45706809022531 P P P LNCV6_126540_PI430048170 mRNA
AGGATGGGATCAGCTCAGCAAAACGAACCTCTATATCCGAGGACTGCCTCCCCACACCAC NM_016836RefSeq chr2
- 160272150 160493807 RBMS1 5937 "RNA binding motif, single stranded interacting protein 1, transcript variant 1"
GO:0006260|GO:0005515|GO:0006396|GO:0003690|GO:0003697|GO:0000166|GO:0003723|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142231_PI430048170 0.0137533860671999 1.18820250604337 13.5318401905955
13.5122625505822 13.4274875608275 P P P 13.1551322933968 13.3087625273485
13.2592363878197 P P P LNCV6_142231_PI430048170 mRNA
GGGGTGGTGGTTGCCCTACCTGTTTTTGCCAAAAATAAATTGTTTAAAACTTTTCTTATT NM_138639RefSeq chr19
+ 49665141 49673916 BCL2L12 83596 "BCL2-like 12 (proline rich), transcript variant 1"
GO:0005515|GO:0002039|GO:0016020|GO:0045944|GO:0005634|GO:2000773 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127765_PI430048170 0.0506638758950104 0.614017192015513 9.73260228899296
9.50843855676412 9.86899677346926 P P P 10.0587084260988 10.3793884760101
10.7280270648802 P P P LNCV6_127765_PI430048170 mRNA
CATTGTAAAGGTGAACTTCTACCTCTGTATCTAAATGTATACCATCCACTTGTAAATGAC NM_172037RefSeq chr8
+ 73294601 73325285 RDH10 157506 retinol dehydrogenase 10 (all-trans)
GO:0008406|GO:0001656|GO:0007603|GO:0005634|GO:0048703|GO:0043583|GO:0005737|GO:0031076|GO:0060
431|GO:0014032|GO:0042574|GO:0042572|GO:0004745|GO:0002138|GO:0052650|GO:0001701|GO:0001523|GO:0
044297|GO:0005789|GO:0016021|GO:0035115|GO:0060449|GO:0007601|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_104415_PI430048170 0.144032878757306 0.817356864324104 8.98289558595248
8.82542111354747 8.73485100418503 P P P 9.17893983724333 9.32460762766306
8.89021760530965 P P P LNCV6_104415_PI430048170 mRNA
TGAACCCCCCAAATCAGGTCACGTAGAATCAAGAACTGTTTGGGATGAAATCACCATGTG NM_001243279 RefSeq
chr16 + 89093808 89155846 ACSF3 197322 "acyl-CoA synthetase family member 3, transcript variant 4"
GO:0005739|GO:0090409|GO:0006631|GO:0006633|GO:0090410|GO:0016878|GO:0005524 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137605_PI430048170 0.542304794563568 1.07207923487308 0.712572010447335
0.424321243163608 0.300865562399246 A A A 0.479044951483217 0.370506542823432 0.313474845727 1
A A A LNCV6_137605_PI430048170 mRNA
AACCACTTCATTCTTGAAAGCTGTGGCCAGCTTGTTATTTATAACAACCTAAATTTGGTT NM_000572RefSeq chr1
- 206767602 206772494 IL10 3586 interleukin 10

GO:0010468|GO:0032715|GO:0060670|GO:0005615|GO:0042130|GO:0045348|GO:0071392|GO:0002904|GO:0045347|GO:0044130|GO:0032689|GO:0042742|GO:0002875|GO:0032868|GO:0030886|GO:0030595|GO:0045191|GO:0007568|GO:0042536|GO:0030889|GO:0051384|GO:0005125|GO:0045355|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131354_PI430048170 0.00457916793603295 0.45284164676493210.483890160112 10.0782590614092 10.0035523452374 P P P 11.1081529541808 11.5457432681907 11.3551029168485 P P P LNCV6_131354_PI430048170 mRNA
GAGGAGCTCTGGCTAAGGCACAGTTTTCTAGAAATAAAACATTTATTCGGTTTTTAAACA NM_001243249 RefSeq chr16 - 85804 138698 NPRL3 8131 "nitrogen permease regulator-like 3 (S. cerevisiae), transcript variant 5"
GO:0048738|GO:0043547|GO:0008150|GO:0003674|GO:0035909|GO:0060021|GO:0003281|GO:0005575|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62976_PI430048170 0.0391641870769597 1.32075927038905 7.33842129476496 7.63797002506769 7.35031793039896 P P P 7.19351846117453 7.04541402832379 6.88787954453097 P P P LNCV6_62976_PI430048170 mRNA
TCTGTGGTCAGTGACTGTGTCTGGTCGGAAACACAGTGTCCGCCTCTGCTCCCCACGCCA NM_024927RefSeq chr17 - 42667914 42677030 PLEKHH3 79990 "pleckstrin homology domain containing, family H (with MyTH4 domain) member 3, transcript variant 1" GO:0007165|GO:0005856|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142919_PI430048170 0.0296224008088887 0.50235832959534 9.01914918870253 8.94108243802824 8.8013715021625 P P P 9.49600714792846 10.0661943831361 10.1100503928561 P P P LNCV6_142919_PI430048170 mRNA
TGTGGACAGCAGGGACCTGCGCTACCGTCTGTGGTCTCAATAAAGAAACCGACCACATGG NM_182924RefSeq chr7 - 1434358 1459473 MICALL2 79778 MICAL-like 2
GO:0043005|GO:0001725|GO:0017137|GO:0005886|GO:0031532|GO:0034333|GO:0032456|GO:0042805|GO:0032432|GO:0031175|GO:0005829|GO:0051015|GO:0070830|GO:0005911|GO:0031005|GO:0030041|GO:0034446|GO:0008270|GO:0005923|GO:0055037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97345_PI430048170 0.972756748831051 1.17190859391047 1.62087273159026 2.36046054665186 0.354339068866675 A A A 1.36989804106842 1.24612428370213 1.65112867114111 A A A LNCV6_97345_PI430048170 mRNA
CTATAATTTACCCAGATAGCCCCAGCAAGGTCAAAGACATATCATGTCCCAAGGAGAAAA NM_001201480 RefSeq chr2 + 178194480 178399433 OSBPL6 114880 "oxysterol binding protein-like 6, transcript variant 3"
GO:0005515|GO:0031965|GO:0005886|GO:0006869|GO:0097038|GO:0008289|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56438_PI430048170 0.257187382330515 1.31202072931149 5.27718044375339 5.44571064904134 5.50316239622841 P P P 5.19333380979308 5.30595909413311 4.40561258147037 P P P LNCV6_56438_PI430048170 mRNA
TCTACTTGCTGAAAGTGAGCATTGTTGATGCTCTTGAGAGCATCAGCCAGGACATTAATG NM_033500RefSeq chr10 + 69269999 69401881 HK1 3098 "hexokinase 1, transcript variant 5"
GO:0005515|GO:0001678|GO:0005975|GO:0097228|GO:0019318|GO:0005741|GO:0044281|GO:0004396|GO:0055085|GO:0005524|GO:0006096|GO:0005829|GO:0008645|GO:0005739|GO:0004340|GO:0008865|GO:0015758|GO:0009405|GO:0046835|GO:0045121|GO:0019158|GO:0051156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74653_PI430048170 0.2578181706179360.8760769816490420.2500401165219180.26283676311316 0.352412025736623 A A A 0.3987540422583760.6996142604742980.312503606673442 A A A LNCV6_74653_PI430048170 mRNA
GAGGCAGCTAATAATTCACTTGTTGTTACTACAACAAAACCATCTATAACAACACCAAAC NM_016242RefSeq chr4 - 100395340 100518093 EMCN 51705 "endomucin, transcript variant 1"
GO:0005886|GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_138920_PI430048170 0.4354890131493790.8169692084300039.01751168532069
8.70779756881452 8.32823606889034 P P P 9.17204311381366 9.25116215753183
8.46499383852074 P P P LNCV6_138920_PI430048170 mRNA
CCTGAGGCCCCCATCTCCTTAAAGAGTGTGGCAAAATAATGATTTTTAAATCTCAAAAAA NM_001278614 RefSeq
chr16 - 20333050 20352878 UMOD 7369 "uromodulin, transcript variant 3"
GO:0060170|GO:0008285|GO:0072218|GO:0072233|GO:0031225|GO:0005615|GO:0016323|GO:0016324|GO:0019
864|GO:0007159|GO:0007157|GO:0070062|GO:0048878|GO:0007588|GO:0010033|GO:0005794|GO:0005509|GO:0
031410|GO:0072372|GO:0072221|GO:0006968|GO:0000922|GO:0045121|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140654_PI430048170 0.9006914172782231.10700252907043 2.62961781652971
3.74969318777492 2.48762547558721 A P A 2.84325105824043 3.28843795499718
2.55120222040326 P P P LNCV6_140654_PI430048170 mRNA
GATGGGTGCCAGCCCTGCATTGCTGAGTCAATCAATAAAGAGCTTTCTTTTGACCCAAAA NM_020995 RefSeq chr16
+ 72063225 72077246 HPR 3250 haptoglobin-related protein
GO:0030492|GO:0008152|GO:0034366|GO:0072562|GO:0005576|GO:0003824|GO:0006898|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135298_PI430048170 0.1655121351437761.13281467259909 11.1892284594142
11.3400797656844 11.4861213729025 P P P 11.1944066013807 11.0733576710807
11.2190100614031 P P P LNCV6_135298_PI430048170 mRNA
GTAAAGGGTTTTGTTTCCTTCTCCCTTCCCCTTTTCCCTGTACTTTGTAATGTCAGTGTT NM_001135218 RefSeq chr1
- 28603095 28643092 TAF12 6883 "TAF12 RNA polymerase II, TATA box binding protein (TBP)-
associated factor, 20kDa, transcript variant 1"
GO:0005515|GO:0010467|GO:0006352|GO:0006368|GO:0003700|GO:0005669|GO:0006367|GO:0046982|GO:0006
366|GO:0030914|GO:0003713|GO:0006325|GO:0003677|GO:0033276|GO:0051091|GO:0043966|GO:0000125|GO:0
016032|GO:0005654|GO:0004402|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104928_PI430048170 0.3425508782912110.7607289447060541.35041153147954
1.54470554075816 2.58783317072344 A A A 1.98053560829697 2.58772849948623
2.35948898211408 A A A LNCV6_104928_PI430048170 mRNA
GCAGTGTTAGCTAATACATACCTTGAGCATAGAACTGAATGCTGTAATTCAGAGCCATTT NM_005401 RefSeq chr1
- 214348695 214551681 PTPN14 5784 "protein tyrosine phosphatase, non-receptor type 14"
GO:0003712|GO:0005515|GO:0030971|GO:0006355|GO:0008285|GO:0005634|GO:0035335|GO:0006351|GO:0001
946|GO:0005737|GO:0006470|GO:0005654|GO:0005856|GO:0046825|GO:0004725 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_142902_PI430048170 0.6467062894415941.06863884042566 3.01690486518139
2.86801299478979 2.88544108625133 A A P 2.97200293606702 2.28842505950112
3.10253938545324 P A P LNCV6_142902_PI430048170 mRNA
TTTACGTGGATAGGACTTTAGACACCACCCAGCCCAAACTTCCAAATAAAATATGGAACG NM_005472 RefSeq chr11
- 74454840 74467555 KCNE3 10008 "potassium channel, voltage gated subfamily E regulatory beta
subunit 3" GO:0008076|GO:0005249|GO:0060306|GO:0015459|GO:0071805 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138872_PI430048170 0.4005243962228050.6193487900477790.996484320321706
0.3670582614197380.340181278873005 A A A 2.07795112456668 0.398227221545268
0.854160726209695 A A A LNCV6_138872_PI430048170 mRNA
AATATGCCTAATCTGTAATCACATTTCTGAGTGTTCTCCTCTTTTTCTGTGTGAGGTTTT NM_000170 RefSeq chr9 -
6532463 6645692 GLDC 2731 glycine dehydrogenase (decarboxylating)
GO:0005739|GO:0030170|GO:0009055|GO:0006546|GO:0016829|GO:0004375|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131976_PI430048170 0.0844717442134329 1.0479428545539 0.416069919093548
0.4469219219577920.457407803656194 A A A 0.3356964963410240.364477556803376

0.416693303636124 A A A LNCV6_131976_PI430048170 mRNA
CAGACCCAAGGCTGTTTTGCAGTTTTCATATGTTGTTTGCTGAAGTCATTGTAATTTTTT NM_030797 RefSeq chr2 -
16549461 16665866 FAM49A 81553 "family with sequence similarity 49, member A" GO:0005622 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140372_PI430048170 0.0125656476716045 0.487507116980174 6.86437308435455
6.78824991766672 7.32134819528642 P P P 7.74670778717492 7.99059215620746
8.34284523330278 P P P LNCV6_140372_PI430048170 mRNA
GCCTGTGTGAGATCTGTGTCTTAAAACTTACTGGAATGGAAATCTATGAATTATTGCAAA NM_006345 RefSeq chr4
+ 41990505 42087534 SLC30A9 10463 "solute carrier family 30 (zinc transporter), member 9"
GO:0016922|GO:0030374|GO:0003700|GO:0045944|GO:0003682|GO:0008324|GO:0006829|GO:0005634|GO:0016
021|GO:0006289|GO:0005856|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135267_PI430048170 0.127925739120252 0.721637401314708 9.6369651965317
9.93135328315646 10.1269882308789 P P P 10.2704874783183 10.0857363205492
10.7177285384839 P P P LNCV6_135267_PI430048170 mRNA
CTGGCAAAATGGACTTTCTCAAAATAGGACTGCACGCTTGGTGTACTTTAAATGTTAATG NM_025196 RefSeq chr4
- 7060052 7068073 GRPEL1 80273 "GrpE-like 1, mitochondrial (E. coli)"
GO:0005739|GO:0050790|GO:0006457|GO:0005759|GO:0006626|GO:0051087|GO:0051082|GO:0044267|GO:0042
803|GO:0000774 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141220_PI430048170 0.912009994395263 0.94258455729685 1.20708665328713
0.488118633261395 0.530291525610191 A A A 0.335598330768599 0.608819491292418 1.4236707622309
A A A LNCV6_141220_PI430048170 mRNA
GTGACTCTAGTGATCTTTAACATACACAGAATGATCTACAGTGATCTTTAACATACTCAG NM_025059 RefSeq chr6
+ 151494039 151621193 CCDC170 80129 coiled-coil domain containing 170 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_144099_PI430048170 0.370740003178957 1.0296905991582 0.295259015246811
0.30189213139866 0.406706543757801 A A A 0.308736830230152 0.285389414578672
0.285705246707708 A A A LNCV6_144099_PI430048170 mRNA
AACTACCTCAACTGGTCAGAAACACAGATTGTATTCTATGAGTCCCAGAAGATGAAAAAA NM_000090 RefSeq chr2
+ 188974372 189012746 COL3A1 1281 "collagen, type III, alpha 1"
GO:0005515|GO:0021987|GO:0035025|GO:0005586|GO:0046332|GO:0005615|GO:0046872|GO:0007507|GO:0071
230|GO:0022617|GO:0007411|GO:0030198|GO:0030199|GO:0030574|GO:0007179|GO:0043206|GO:0034097|GO:0
009314|GO:2001223|GO:0060414|GO:0048407|GO:0007568|GO:0030168|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140658_PI430048170 0.280224363580446 1.4636528524711 3.87876538854325
2.79947981358883 3.00599996780965 P A P 2.44161024986568 2.92061988660521
2.86618806611287 P P P LNCV6_140658_PI430048170 mRNA
TGAGCTGAACAAGGAGCTGAAGCCCACCAAGCCCATGCAGTTCCTGGGTGATGAGGAAAC NM_000290 RefSeq
chr7 - 44062726 44065587 PGAM2 5224 phosphoglycerate mutase 2 (muscle)
GO:0048037|GO:0004082|GO:0004083|GO:0005975|GO:0046538|GO:0006094|GO:0006941|GO:0005634|GO:0044
281|GO:0007283|GO:0006096|GO:0005829|GO:0016311|GO:0009405|GO:0006006|GO:0004619|GO:0046689|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139419_PI430048170 0.933293650073205 0.967930785811298 1.1710098207505
0.436498571029355 1.47954480129507 A A A 1.46141898243119 1.33348126863015
0.413112923317071 A A A LNCV6_139419_PI430048170 mRNA
GACCGTTTTAAAGGATCTTTTTTAATGTTTTATGACTGCCTGTCTGTTTGAATACTGGCA NM_178177 RefSeq chr3 -
139560180 139678043 NMNAT3 349565 "nicotinamide nucleotide adenylyltransferase 3, transcript variant 1"
GO:0005739|GO:0000309|GO:0006766|GO:0004515|GO:0019674|GO:0009611|GO:0006767|GO:0044281|GO:0009
435|GO:0005524|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62025_PI430048170 0.0265988296085391 1.330646309662 8.27832717630892

8.21595696925699 8.51527110495282 P P P 7.79175384910561 7.94628248218752
8.04175395941048 P P P LNCV6_62025_PI430048170 mRNA
ATATGAAAGGGACTTCGAGAGGATTTCAACAGTGGTCCGAAAAGAAGTGATACGGTTTGA NM_003099 RefSeq chr15
+ 64095883 64144234 SNX1 6642 "sorting nexin 1, transcript variant 1"
GO:0005515|GO:0072673|GO:0045732|GO:0005154|GO:0005794|GO:0005158|GO:0006886|GO:0030027|GO:0043
231|GO:0042802|GO:0005829|GO:0031623|GO:0043234|GO:0016050|GO:0005737|GO:0016020|GO:0034498|GO:0
031901|GO:0042147|GO:0035091|GO:0010008|GO:0019898|GO:0030904 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_82959_PI430048170 0.2806648131874831.31605679240516 6.13451842386104 5.85280509063218
6.34670779325267 P P P 5.08881897349049 5.83262515829121 6.08990116187777 P P P
LNCV6_82959_PI430048170 mRNA
ATCCCTCTTACTGTAGATAACACTGCAAATCTTGGAATTTTGTTTTTTGCTGTTTCCAGA NM_001130487 RefSeq chr16
+ 58464089 58513619 NDRG4 65009 "NDRG family member 4, transcript variant 2"
GO:0035050|GO:0006950|GO:0048662|GO:0060038|GO:0014912|GO:0030154|GO:0005829|GO:0001947|GO:0005
739|GO:0003674|GO:0016323|GO:0005737|GO:0010976|GO:0005789|GO:0016049|GO:0070374|GO:0010642 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132825_PI430048170 0.67595977390509 0.9531215121541520.605523885962218
0.6515232294445680.569679355914077A A A 0.5939530362891490.905273358094712
0.505249024717613A A A LNCV6_132825_PI430048170 mRNA
GACTACATGTCTAGGAAACTGTTGAGATTCAAAGGAATCTCACTGTTCCTAAATAAATGT NM_014352 RefSeq chr11
+ 120240193 120319944 POU2F325833 "POU class 2 homeobox 3, transcript variant 1"
GO:0005515|GO:0005667|GO:0006357|GO:0005634|GO:0000978|GO:0006351|GO:0043922|GO:0043565|GO:0001
077|GO:0005737|GO:0008544|GO:0030216|GO:0045944|GO:0042060|GO:0046983|GO:0005654 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138978_PI430048170 0.1070312371812540.7722363645773246.55327960036548
6.55831452904705 6.76068251728971 P P P 7.08863897145323 6.70802988684685
7.16400231965213 P P P LNCV6_138978_PI430048170 mRNA
AGATGAAACTATATGTGCCACACTTTGCACTACTCATAATGATAACCTCAAGACTATCAG NM_030759 RefSeq chr10
+ 63133246 63155031 NRBF2 29982 "nuclear receptor binding factor 2, transcript variant 1"
GO:0010467|GO:0006355|GO:0005737|GO:0006367|GO:0005654 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131661_PI430048170 0.8580862044910780.9687152792170046.06267957883649
6.51050654952668 6.07632129136709 P P P 6.4991184844742 6.34049755636489
5.93737739075373 P P P LNCV6_131661_PI430048170 mRNA
AATAGTTAGTCACCTTCTGACCTTCTCCTCTTTCTCAAAGCCTTCTGTCCCTGGTTTTTG NM_013259 RefSeq chr3 +
111998738 112013888 TAGLN3 29114 "transgelin 3, transcript variant 1"
GO:0051015|GO:0005634|GO:0000122|GO:0007417 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114811_PI430048170 0.9901678217292561.00869362686869 9.21071805307144
8.70951328219781 8.5579868828404 P P P 9.01349231564017 8.96610895069158
8.48841907192494 P P P LNCV6_114811_PI430048170 mRNA
TTGCCTCTCCAAGATCTGCCGAGATGTACAGAAAACACTAGGACTAACTCAGCATGTTCA NM_030821 RefSeq chr4
- 109709988 109730086 PLA2G12A 81579 "phospholipase A2, group XIIA"
GO:0005794|GO:0005783|GO:0036149|GO:0005509|GO:0036148|GO:0005576|GO:0044281|GO:0016042|GO:0008
150|GO:0036150|GO:0047498|GO:0006644|GO:0006654|GO:0036151|GO:0046474|GO:0036152 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132366_PI430048170 0.7436678789774630.9705042314617641 1.8020588198469
11.3990695083021 11.3775020229632 P P P 11.575295940917 11.6853802090356
11.4810685669314 P P P LNCV6_132366_PI430048170 mRNA
TCTGAGACCCCCACCCCACGAACCAAATCCAAATAAAGTGACATTCCCAGCCTGAAAAAA NM_182965 RefSeq chr17

+ 76384608 76387860 SPHK1 8877 "sphingosine kinase 1, transcript variant 2"
GO:0005515|GO:0005516|GO:0070301|GO:0019722|GO:0030307|GO:0014075|GO:0017050|GO:0006457|GO:0031
398|GO:0032026|GO:0033198|GO:0007565|GO:0000287|GO:0030335|GO:0010803|GO:0045931|GO:0003951|GO:0
007420|GO:0010976|GO:0032570|GO:0051084|GO:0046834|GO:0001956|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138638_PI430048170 0.3299989654013040.9836793605982920.335840341044198
0.3504061186840540.354287316060079A A A 0.4000203245441970.33652705419099 0.374565083313
A A A LNCV6_138638_PI430048170 mRNA
GCTTTCATCACATTTTCTCTATTCTGACCTCTGTTATGAGAAATAAAAGTCACTGATTCCNM_001547RefSeq chr10 +
89301948 89309276 IFIT2 3433 interferon-induced protein with tetratricopeptide repeats 2
GO:0032091|GO:0005515|GO:0051607|GO:0005737|GO:0060337|GO:0043065|GO:0008637|GO:0035457|GO:0005
783|GO:0019221|GO:0009615|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119658_PI430048170 0.1579006580596 0.76479249658595 0.337874103177207
0.3244273312446330.294142608927068A A A 0.3534532313848850.875973195689261
0.83208174357812 A A A LNCV6_119658_PI430048170 mRNA
TGAATCTTAGTGACCAGCAGGTCAAGATCTGGTTTCAGAACCGGAGAATGAAAAAGAAAANM_173860RefSeq chr12
+ 53954929 53956566 HOXC12 3228 homeobox C12
GO:0043565|GO:0006355|GO:0007275|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_59034_PI430048170 0.0414939452807002 1.72537082494522 4.33986722013011
4.75469949428211 4.51817483986716 P P P 3.70057935686457 4.10951546388087
3.37867671453321 P P P LNCV6_59034_PI430048170 mRNA
TGATTGTGGAGTTGCACACGCTGTGTGACTGTAATTGCAGTGACACCCAGCCCCAGGCTC NM_000889RefSeq chr12
- 53191317 53207307 ITGB7 3695 "integrin, beta 7, transcript variant 1"
GO:0005515|GO:0008305|GO:0003366|GO:0005886|GO:0009986|GO:0007275|GO:0009615|GO:0050901|GO:0072
678|GO:0046872|GO:0043235|GO:0034669|GO:0007160|GO:0016020|GO:0001618|GO:0007229|GO:0030198|GO:0
050776|GO:0043113|GO:0034446|GO:0034113|GO:0007155|GO:0050839|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_61772_PI430048170 0.0289793773917943 0.6825509391301348.12947158547271
8.07992410335017 7.93904258475913 P P P 8.74817881399967 8.35665693353817
8.67405629170343 P P P LNCV6_61772_PI430048170 mRNA
TTTCCGCCCCATTGAGGATAATGAAAAGAGCAAAGATGTGAATGGACCCGAACCACTCAA NM_007236RefSeq chr15
+ 41231238 41281885 CHP1 11261 calcineurin-like EF-hand protein 1
GO:0008017|GO:0005515|GO:0005215|GO:0032417|GO:0015459|GO:0031122|GO:0071468|GO:0051259|GO:0017
156|GO:0006611|GO:0031397|GO:0060050|GO:0030203|GO:0070062|GO:0022406|GO:0005793|GO:0005975|GO:0
005509|GO:0090314|GO:0070885|GO:0042308|GO:0051453|GO:0005925|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_56340_PI430048170 0.51090886262639 1.05879564558605 10.1216050675415 9.93186752323727
10.1034238743686 P P P 9.76324189001843 10.0547817442963 10.0782590614092 P P P
LNCV6_56340_PI430048170 mRNA
CAGAAGATGACCTTAACACAGTAGCAGCTGGAACCATGACAGGCATGTTGTATAAATGTA NM_006327RefSeq chr10
+ 45972452 46003741 TIMM23100287932 "translocase of inner mitochondrial membrane 23 homolog
(yeast), transcript variant 1"
GO:0005744|GO:0005739|GO:0005515|GO:0015450|GO:0005758|GO:0006626|GO:0005743|GO:0031305|GO:0071
806|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145423_PI430048170 0.00422843232666784 2.92064627946942 9.27474880700267
9.55989317518131 9.39845829506986 P P P 8.18055268691379 7.7474934762706
7.61873383618125 P P P LNCV6_145423_PI430048170 mRNA
CTGGCGCCACCGAACCTGCACATCTCAACTTGTAACTCAATAAACAGAAGTGACAATCGG NM_024527RefSeq chr19

- 17292130 17303473 ABHD8 79575 abhydrolase domain containing 8
GO:0016787|GO:0008152|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129865_PI430048170 0.0752876202377156 0.7232361579769789.72744565945505
9.57715527543189 9.89271621801948 P P P 10.0652983176251 10.0103107411759
10.4917704395585 P P P LNCV6_129865_PI430048170 mRNA
CATAATGGTCAGAGGCGCATGAATTTGTGAAGGTGGAAATAAACTATTTGTAAAGTGAAA NM_001160210 RefSeq
chr7 - 96120219 96322147 SLC25A13 10165 "solute carrier family 25 (aspartate/glutamate carrier),
member 13, transcript variant 1"
GO:0005215|GO:0005975|GO:0005313|GO:0005509|GO:0005743|GO:0006094|GO:0044281|GO:0005739|GO:0051
592|GO:0015813|GO:0045333|GO:0006754|GO:0015810|GO:0005887|GO:0015183|GO:0006810|GO:0009405|GO:0
043490|GO:0006006. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114327_PI430048170 0.0144338925661555 0.4675360577148393.48626690945649
3.52352935914429 3.50861231611876 P P P 4.34755723752131 4.61534203783528
4.80941761706387 P P P LNCV6_114327_PI430048170 mRNA
TTTGTATCAGAGCAATTTTGCTTGCAGAAAGCTATGAAATAAAACACGTCCCTTAACTGC NM_001144769 RefSeq
chr6 - 56457986 56954628 DST667 "dystonin, transcript variant 2"
GO:0005882|GO:0005515|GO:0030424|GO:0030056|GO:0030018|GO:0045104|GO:0035371|GO:0005634|GO:0030
011|GO:0005635|GO:0015629|GO:0042803|GO:0005829|GO:0005737|GO:0009925|GO:0051010|GO:0030198|GO:0
048870|GO:0007010|GO:0015630|GO:0031581|GO:0007050|GO:0045111|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136257_PI430048170 0.1787281638424332.95116899779748 0.365923917148246
2.07175197373346 2.47862663831293 A A A 0.3088932486741770.302573629184127
0.353568020371521A A A LNCV6_136257_PI430048170 mRNA
ATCCTGAATTAGAATGAAGACCCTCCAGTGTATCATAGTGTCATGCCAACCATCTTTGCC NM_001004063 RefSeq
chr14 + 19935607 19936683 OR4K1 79544 "olfactory receptor, family 4, subfamily K, member 1"
GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137683_PI430048170 0.571655458433455 1.18774121330728 1.43341298340823
1.15894157844472 0.454902673942832A A A 1.11662292809036 0.834860587205059
0.439230121380394A A A LNCV6_137683_PI430048170 mRNA
TGGACTCCAAGAGCCCGGACGAGATCATTCTGGAGGAGAGCGACTCCGAGGAAAGCAAAA NM_001105574
RefSeq chr10 + 123136050 123137731 HMX3 NA H6 family homeobox 3 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_130138_PI430048170 0.0781305996243828 0.7184711278487928.18877006748088
8.24327031863823 8.53188800448685 P P P 8.49109280947887 8.8521253317271
9.02544699063279 P P P LNCV6_130138_PI430048170 mRNA
GCTTCAGTGTGTGTTTTTTAAGTTGCTGGGCATTACACTTACCAATTAAAGAATTTTGGA NM_001134793 RefSeq
chr11 + 125887059 125900646 HYLS1 219844 "hydrolethalus syndrome 1, transcript variant 2"
GO:0005813|GO:0005737|GO:0005886|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103281_PI430048170 0.0144477711959169 2.0750949348338 5.72995684611314
6.15003373354026 6.24462277544294 P P P 4.78847665083455 4.77796898360325
5.36697853489588 P P P LNCV6_103281_PI430048170 mRNA
TTTTTGGAATTTCGTAAGGCAAGAAGTGACATGCTTCTCTCCAGGAAGAATCAGCTCCTG NM_001483 RefSeq chr7
+ 55964576 56000182 GBAS 2631 "glioblastoma amplified sequence, transcript variant 1"
GO:0005739|GO:0005515|GO:0006754|GO:2000984|GO:0016020|GO:0005887|GO:0006119 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131506_PI430048170 0.0169596059605377 0.4365456715701022.29547114306246
2.90737900946556 2.35615137120486 A A A 3.80811677299557 3.61414543386521
3.79778877999264 P P P LNCV6_131506_PI430048170 mRNA

GACTGCTGGGTGGGTTTGGAGTTCTTGGCTTTAATCATTCATTACAAAGTTCAGCATTTT NM_001910RefSeq chr1
- 206009263 206023909 CTSE 1510 "cathepsin E, transcript variant 1"
GO:0019886|GO:0016540|GO:0007586|GO:0006508|GO:0004190|GO:0042803|GO:0070062|GO:0005768 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145264_PI430048170 0.0406617441833442 0.45597774774686 3.40344832063636
3.22815705350759 3.15347431576652 P P P 3.94899930893568 4.29293656074632
4.81886223231108 P P P LNCV6_145264_PI430048170 mRNA
AACATTTATTGTACATTCAGTGAGTTATAGTGTTAATAGTCTTGTGCTATGCAGCAGGTG NM_020228RefSeq chr11
- 129899705 130002835 PRDM10 56980 "PR domain containing 10, transcript variant 1"
GO:0006355|GO:0008168|GO:0005634|GO:0032259|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142178_PI430048170 0.848749148988366 1.03235929386154 0.341648291652829
0.304094848956791 0.794222870234771 A A A 0.294251195202175 0.27851500635109
0.734672050964402 A A A LNCV6_142178_PI430048170 mRNA
TGTGAAGATTCCTGACTTAGGGGTGGCTTTTGTTTACAAGATGCAAGAGGGGAAACCTGT NM_001004434 RefSeq
chr1 - 26038021 26046138 SLC30A2 7780 "solute carrier family 30 (zinc transporter), member 2,
transcript variant 1"
GO:0005737|GO:0005770|GO:0008324|GO:0006829|GO:0016021|GO:0005765|GO:0061090|GO:0055085 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139935_PI430048170 0.911128275642283 0.988048556638251 5.99240393506999
5.72038012348919 5.80082541266602 P P P 6.36158017461705 5.43796785368481
5.60399380836607 P P P LNCV6_139935_PI430048170 mRNA
AGCCACGTAGAAGCACCTTGAAATCTGTAAAACCACAAGAAAGTACTTTATAAAAGGTAT NM_032169RefSeq chr3
- 132558137 132660131 ACAD11 84129 "acyl-CoA dehydrogenase family, member 11"
GO:0017099|GO:0031966|GO:0050660|GO:0005634|GO:0070991|GO:0033539|GO:0004466|GO:0016772|GO:0005
777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144726_PI430048170 0.284460898675852 0.88757057699849 0.270176851929895
0.416826773809234 0.288664670490297 A A A 0.504739531638428 0.679431305091925
0.285308502294406 A A A LNCV6_144726_PI430048170 mRNA
CTTTAGTATATGCAAATGTACTGAAAGGGTAGTTCAAGTCTAAAATGCCATAACCCCTTT NM_007015RefSeq chr13
- 52703265 52739812 LECT1 11061 "leukocyte cell derived chemotaxin 1, transcript variant 1"
GO:0030948|GO:0001501|GO:0051216|GO:0001937|GO:0001886|GO:0016525|GO:0005578|GO:0016021|GO:0006
029|GO:0012505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135000_PI430048170 0.624147426846958 0.684743964500362 0.354234846618452
0.334539425290475 0.959069530092933 A A A 2.02014331278032 0.328256091580568
0.305364043437628 A A A LNCV6_135000_PI430048170 mRNA
CCTGTCATCAGCAACAGTAGAAGATGGGAAAAATAGAATATTTACCAAAATATCTGCCAT NM_001085480 RefSeq
chr6 - 116752196 116765723 FAM162B 221303 "family with sequence similarity 162, member B"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136985_PI430048170 0.526784142402761 0.80545818697794 4.37903577658424
3.92658207374833 3.90844674459221 P P P 4.63885513368239 4.68151307757755
3.67587011588396 P P P LNCV6_136985_PI430048170 mRNA
ATGGCAAGCCCTCGGCTCAGCTGCTTCTCCATTGGAATAAACTCTTGTTTCTCTAAAAAA NM_031474RefSeq chr12
- 2825347 2835055 NRIP2 83714 nuclear receptor interacting protein 2
GO:0005737|GO:0006508|GO:0005634|GO:0004190|GO:0000122|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144399_PI430048170 0.0100285809992438 0.296768505614193 3.99199643073805
3.54669342522921 3.84681103827817 P P P 5.01246468368155 5.65479458500666
5.87817257845735 P P P LNCV6_144399_PI430048170 mRNA

CAAAGTAAAACCATACAAAGCTAGTGTCAGTCTCTCTCATTGTTCACAAATAAAGGACTT NM_003201 RefSeq chr10
+ 58385142 58399230 TFAM 7019 "transcription factor A, mitochondrial, transcript variant 1"
GO:0042645|GO:0005515|GO:0010467|GO:0006996|GO:0003700|GO:0008301|GO:0006356|GO:0006391|GO:0005
634|GO:0006390|GO:0000978|GO:0005829|GO:0005739|GO:0006261|GO:0001077|GO:0045944|GO:0031072|GO:0
003682|GO:0005759|GO:0033108|GO:0006338|GO:0007005|GO:0045893|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135163_PI430048170 0.871889136841442 1.05715491103421 0.388478506533033
0.400694030942544 1.27024147108225 A A A 1.13963004022917 0.331685403427372
0.386144523087635 A A A LNCV6_135163_PI430048170 mRNA
CTGTACCTTCTGCTCAATTTCCTTTCCTCATCTCAAATAAATGCCTTGTTACAAGAAAAA NM_005217 RefSeq chr8
- 7015868 7018294 DEFA3 1668 "defensin, alpha 3, neutrophil-specific"
GO:0005796|GO:0050830|GO:0050832|GO:0005576|GO:0005615|GO:0002227|GO:0003674|GO:0051607|GO:0045
087|GO:0019731|GO:0031640|GO:0035578|GO:0070062|GO:0030520 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133715_PI430048170 0.633978118800919 1.14519548593218 1.1452793142417
0.39789840835805 0.305505807901876 A A A 0.295644942556916 0.763570495891961
0.305711386377281 A A A LNCV6_133715_PI430048170 mRNA
GAAAAGCACTGAAGATGATGCTGTTTGGTAAAATTTTCCAAAAAGATTCATCCAGGTGTA NM_138327 RefSeq chr6
- 132644983 132646003 TAAR1 134864 trace amine associated receptor 1
GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0001594 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_74609_PI430048170 0.149362017662034 1.35963880285656 5.36889991510979 6.00343534420798
5.82585476766308 P P P 5.30333989792517 5.03641834615313 5.55427275428675 P P P
LNCV6_74609_PI430048170 mRNA
ACACAGCAGAGGCACCCTCGTATGTTTTGAAAGTTGCCTTCTGAAAGGGCACAGTTTTAA NM_014883 RefSeq chr4
- 88725953 89057195 FAM13A 10144 "family with sequence similarity 13, member A, transcript
variant 1" GO:0043547|GO:0051056|GO:0007264|GO:0005829|GO:0005096 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_90392_PI430048170 0.0811703634175313 1.3035163951536 13.6809433115107
13.8532278328632 13.9987763956756 P P P 13.2476722360681 13.417170905471
13.7015089882626 P P P LNCV6_90392_PI430048170 mRNA
TTACATGGACATATGTAGCAACACAAGTCGGAATAGAATGGAACCTGTCCCCTGTTGGCA NM_001866 RefSeq chrX
+ 77899463 77905384 COX7B 1349 cytochrome c oxidase subunit VIIb
GO:0022904|GO:0005746|GO:0004129|GO:0005743|GO:0044281|GO:0016021|GO:0007417|GO:0055085|GO:0044
237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117053_PI430048170 0.229783386194795 0.67229828616241 0.400636838239513
0.373893534465748 0.247648362913821 A A A 1.40053173618263 0.791751014809243
0.362732266593656 A A A LNCV6_117053_PI430048170 mRNA
TGACTGCAAGCCAAGCACAGATGTATCTGAGGGCACAGATGCTCATCTTCACGCCCACGG NM_198040 RefSeq chr1
- 33323622 33375593 PHC2 1912 "polyhomeotic homolog 2 (Drosophila), transcript variant 1"
GO:0035102|GO:0031519|GO:0005515|GO:0000792|GO:0008270|GO:0007275|GO:0005654|GO:0005634|GO:0007
283|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137589_PI430048170 0.0177731214858810 0.329125648031912 3.55981410961822
3.42254525922386 3.72846023001989 P P P 4.63914011034808 5.25399058945676
5.51106278839774 P P P LNCV6_137589_PI430048170 mRNA
CAAATTGCTTGTACAATTTGAAATGGGCCTCAATGGTACTTCAAACCTTTTGATTATTCC NM_015035 RefSeq chr20
- 41178448 41300099 ZHX3 23051 zinc fingers and homeoboxes 3
GO:0005515|GO:0003700|GO:0046982|GO:0003714|GO:0005634|GO:0000122|GO:0003677|GO:0006351|GO:0030
154|GO:0042803|GO:0046872|GO:0045669|GO:0005654|GO:0045892 . NA - . NA NA NA NA NA NA

NA NA NA
LNCV6_134951_PI430048170 0.0229628250243133 0.7456203828411287.10261071955005
7.09695229034764 6.95264733550425 P P P 7.29971844366093 7.59152309456538
7.52058712228012 P P P LNCV6_134951_PI430048170 mRNA
TATACTCCACCCCTTTCTCAACGGTCCTTTTTTAAAGCACATCTCAGATTACCCAAAAAA NM_198282RefSeq chr5
- 139475527 139482790 TMEM173 340061 "transmembrane protein 173, transcript variant 1"
GO:0005515|GO:0048471|GO:0032479|GO:0033160|GO:0005886|GO:0035458|GO:0005741|GO:0002218|GO:0042
993|GO:0042803|GO:0032092|GO:0035438|GO:0042802|GO:0051607|GO:0045944|GO:0032481|GO:0030659|GO:0
031625|GO:0005777|GO:0032608|GO:0005794|GO:0019901|GO:0006915|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135251_PI430048170 0.4149748994624421.06746847382302 8.57967194701506
8.36689582649784 8.60542550086897 P P P 8.33257987236437 8.56159109250918
8.37654189060661 P P P LNCV6_135251_PI430048170 mRNA
TCGAGATCATCCGCAACACCCTCTACAAGGCCTACCTGGAGTCCTTCTACAAGTTCTGCA NM_004691RefSeq chr16
- 67438013 67481186 ATP6V0D1 9114 "ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1"
GO:0008286|GO:0005515|GO:0005765|GO:0032403|GO:0030968|GO:0006879|GO:0033572|GO:0016324|GO:0008
553|GO:0030670|GO:0043679|GO:0090382|GO:0033179|GO:0070062|GO:0005813|GO:0051701|GO:0055085|GO:0
008021|GO:0042384|GO:0016020|GO:0007420|GO:0015991|GO:0006987|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136558_PI430048170 0.2983117057301250.8269433524937160.447967741823853
0.46888477011065 0.294323333149853A A A 1.01942959710231 0.496639937828591
0.452249961792893A A A LNCV6_136558_PI430048170 mRNA
AGATCATCTGTTGCTATCCCCTGGGAGGCCTTTGTGACTTGTCTAGCAGATATTAAATGG NM_005912RefSeq chr18
- 60371330 60372768 MC4R 4160 melanocortin 4 receptor
GO:0005515|GO:2000821|GO:0032868|GO:0007631|GO:0005886|GO:0030819|GO:2000252|GO:0002024|GO:0005
634|GO:0004977|GO:0006112|GO:0042923|GO:0045780|GO:0004980|GO:0007188|GO:0016021|GO:0017046|GO:0
030073|GO:0031625. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143408_PI430048170 0.4590597515529111.00706109890516 0.33742078297542
0.3323466728966220.306152190898851A A A 0.3215483275730290.323900948485311
0.300092419455759A A A LNCV6_143408_PI430048170 mRNA
AGAATGTGTTGGTTTACCAGTGACACCCCATATTCATCACAAAATTAAAGCAAGAAGTCC NM_006074RefSeq chr11
+ 5689586 5710863 TRIM22 10346 "tripartite motif containing 22, transcript variant 1"
GO:0006355|GO:0016567|GO:0003700|GO:0015030|GO:0016874|GO:0003714|GO:0019221|GO:0005634|GO:0009
615|GO:0006351|GO:0005829|GO:0070206|GO:0051607|GO:0051091|GO:0005737|GO:0006955|GO:0051092|GO:0
016607|GO:0016032|GO:0005654|GO:0008270|GO:0043123|GO:0060333 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_127610_PI430048170 0.00467739097197344 1.40375050711325 7.57056526503404
7.50382322089477 7.3902358934038 P P P 7.10171345031466 7.01220577531332
6.87999751825858 P P P LNCV6_127610_PI430048170 mRNA
CATTTCTGTAATGATGGATCTCGCTCCCACTTTCCCCCAAGAACCTAATAAAGGCTTGTG NM_144615RefSeq chr19
- 4292227 4302431 TMIGD2126259 "transmembrane and immunoglobulin domain containing 2,
transcript variant 1"
GO:0005515|GO:0042104|GO:0007165|GO:0005886|GO:0031295|GO:0016021|GO:0001819|GO:0015026 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94657_PI430048170 0.1266775385721681.42011010099615 5.21819697239229 5.07160101193783
5.18665366947582 P P P 4.40134056970223 4.4023799690862 5.05570700987667 P P P
LNCV6_94657_PI430048170 mRNA
TGGATGTAGCTTTGCCCATTATTGAGAATTATAAGGATCGGTTGTTGGCAATTGGAGAGG NM_001146171 RefSeq
chr1 + 212791827 212816825 TATDN3 128387 "TatD DNase domain containing 3, transcript variant 5"

GO:0005739|GO:0006308|GO:0004536|GO:0043229|GO:0005634|GO:0016888|GO:0000737|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135787_PI430048170 0.0435382613908559 0.5351417767686133.38166367973658 3.85636460317311 4.22414603298089 P P P 4.3807265629259 4.84269579451111 4.99727930859264 P P P LNCV6_135787_PI430048170 mRNA
ATTCAGATGGTGCTAATTCAGACTCCAGACTGAATTTTAATTCAAGTTCTTTCTCAAGTC NM_000426RefSeq chr6 + 128883140 129516565 LAMA2 3908 "laminin, alpha 2, transcript variant 1"
GO:0030334|GO:0022011|GO:0005102|GO:0005606|GO:0005576|GO:0030155|GO:0005604|GO:0045995|GO:0042383|GO:0031012|GO:0032224|GO:0007517|GO:0043197|GO:0005198|GO:0007411|GO:0030198|GO:0007155|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_37689_PI430048170 0.00389806340386624 0.5553488986483265.21578024686196 5.08550255650893 5.40683992083786 P P P 6.19978062468635 5.87539677581373 6.17473790360434 P P P LNCV6_37689_PI430048170 mRNA
ATCCATTCCTAATGATGGTACATGCTTTCAGGAACACAGTTCTTATGGCAGAAATTCTCT NM_001271650 RefSeq chr3 - 28322352 28349127 AZI2 64343 "5-azacytidine induced 2, transcript variant 4"
GO:0005515|GO:0042110|GO:0005737|GO:0007249|GO:0044565|GO:0032640|GO:0097028|GO:0032609|GO:0000278|GO:0032635|GO:0032607 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129680_PI430048170 0.8820285288023560.9758413440626423.40144991363388 3.6756970186993 3.99908269540287 P P P 3.72308960027098 3.45043139517554 4.01542397337192 P P P LNCV6_129680_PI430048170 mRNA
CCTATAAGACAGTTTAAAGTGAGACCTGGAAAAACATTTGCTTTACCTTGAATAGATAGG NM_002098RefSeq chr6 - 42183283 42194956 GUCA1B 2979 guanylate cyclase activator 1B (retina)
GO:0007589|GO:0001917|GO:0007603|GO:0005509|GO:0007267|GO:0031284|GO:0022400|GO:0007168|GO:0007601|GO:0016056|GO:0008048 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129471_PI430048170 0.1673304344257570.5884356132415923.43421923372876 2.03586392841437 2.33854940015089 P A A 3.59820119743642 3.51344570803908 3.37904860352874 P P P LNCV6_129471_PI430048170 mRNA
AAAGCATGCTTCTCTCTCAAAAAGAAAAATTAAAGGATTTTATTGCCAGTCGTGTCAGTC NM_012120RefSeq chr6 + 47477788 47627260 CD2AP 23607 CD2-associated protein
GO:0005515|GO:0017124|GO:0005886|GO:0005730|GO:1900182|GO:0032911|GO:0015629|GO:0001726|GO:2000249|GO:0006930|GO:0007165|GO:0005737|GO:0007067|GO:0031941|GO:0006461|GO:0005911|GO:0005200|GO:0070062|GO:0051301. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94741_PI430048170 0.0291207260825557 1.21061255702413 10.7117353644631 10.7764150740424 10.7153670346512 P P P 10.488691233953 10.5369398992125 10.3447351231954 P P P LNCV6_94741_PI430048170 mRNA
TCTCATGGTCCGGAATGACACCCCCTGTGGAACCACCATTGGACCTATCTTGGCTTCTCG NM_012100RefSeq chr2 - 219373457 219387940 DNPEP 23549 aspartyl aminopeptidase
GO:0005737|GO:0004177|GO:0006508|GO:0072562|GO:0008270|GO:0005654|GO:0005634|GO:0008237|GO:0006518 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138933_PI430048170 0.2061243445544881.05797165115558 0.423993306242577 0.4451713742733090.564962770461239A A A 0.3909198508689250.387106259551548 0.416067936805574A A A LNCV6_138933_PI430048170 mRNA
CAGTAACCTCACTGAGAATGTTTTACAGTGATGGAAAATAAACTCTGTTCCAAGTTCAAA NM_139170RefSeq chr16 + 4734287 4749396 C16orf71 146562 chromosome 16 open reading frame 71 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144782_PI430048170 0.9014978109020931.2864171549685 2.59169788529253 2.97709811720315 0.606604571542564A A A 2.43416257618273 1.5544466624703 1.86740698455279 A A A LNCV6_144782_PI430048170 mRNA
GGGGCAGGGGCCAGATAGAAATTATTGGTTTTGTTTTTTAATTTTGTTTTTCCTGTTTTC NM_182947RefSeq chr12 +

57611434 57617245 ARHGEF25 115557 "Rho guanine nucleotide exchange factor (GEF) 25, transcript variant 1" GO:0005886|GO:0032321|GO:0030016|GO:0005089|GO:0030017|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132441_PI430048170 0.0638723543245642 1.07666434153591 0.458443602629223 0.3510372231514010.375273210116792A A A 0.26567932526174 0.337359589201707 0.262981706427437A A A LNCV6_132441_PI430048170 mRNA CACCGCAGATGGGAACCTTAATCTTTCTTTTCTAAAATTGATGCTATGAAAATTTGCGTT NM_001104548 RefSeq chr1 + 209428822 209432547 MIR205HG NA MIR205 host gene NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134752_PI430048170 0.0532002071430345 1.36925790900833 5.99329401551521 6.07134082781077 5.92222060841235 P P P 5.28457730405785 5.63655337816521 5.67796365196054 P P P LNCV6_134752_PI430048170 mRNA AGGCACTTCCCCGGCTTTTGAAGTTGTAACTATTTAGTGAAAAGTTGATAGATCATTTAA NM_019893RefSeq chr10 - 50187239 50248610 ASAH2 56624 "N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2, transcript variant 1" GO:0006665|GO:0005739|GO:0007165|GO:0017040|GO:0006687|GO:0005886|GO:0006672|GO:0006915|GO:0044281|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139479_PI430048170 0.00376183033866404 0.402572003848981 5.28537169999051 5.6017765319441 5.73199027682875 P P P 6.74619096894029 6.891893465356 6.94745011815419 P P P LNCV6_139479_PI430048170 mRNA TTGTATTTGGTCCACGTGGATTGGAAAACCTTTGCTTTGATTATACTTTTCTTTGGGCACNM_001139499 RefSeq chr7 - 32485332 32495258 LSM5 23658 "LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae), transcript variant 3" GO:0008380|GO:0006397|GO:0005515|GO:0010467|GO:0003723|GO:0043928|GO:0005681|GO:0005634|GO:0005829|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129091_PI430048170 0.171451420202169 0.943257792276896 0.245493472307019 0.31700206655688 0.292417515990804A A A 0.448177484571391 0.347561574428932 0.309326077142652A A A LNCV6_129091_PI430048170 mRNA AAGGCTCACAGATTTAAAGCATCATCTGTTCGATTGAAATTTTGCACCAGCGAAGAATTC NM_020996RefSeq chr12 - 4434141 4445614 FGF6 2251 fibroblast growth factor 6 GO:0008286|GO:0048011|GO:0008284|GO:0008283|GO:0048015|GO:0007267|GO:0005104|GO:0005576|GO:0001525|GO:0005615|GO:0042383|GO:0007165|GO:0007173|GO:0001502|GO:0008543|GO:0045087|GO:0051781|GO:0045445|GO:0008083|GO:0038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129492_PI430048170 0.48368418693006 0.780734994118759 0.334465380344225 0.290565196402785 1.17384455082845 A A A 0.291150562397808 1.1105714913934 1.42678412088987 A A A LNCV6_129492_PI430048170 mRNA ATGACAAAATCATCTTTGTGAAGGCCTCGCAGGAAGACCCAACACATGGGACCTATAACT NM_198053RefSeq chr1 - 167430639 167518610 CD247 919 "CD247 molecule, transcript variant 1" GO:0005515|GO:0050852|GO:0005886|GO:0031295|GO:0042803|GO:0050690|GO:0042802|GO:0005737|GO:0042105|GO:0042101|GO:0045087|GO:0050776|GO:0016032|GO:0016021|GO:0038096|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127746_PI430048170 0.44712680346899 1.41313617576386 1.56496561485796 0.362898682545837 0.346539952894019A A A 0.416399481649991 0.34349494044381 0.378634247120765A A A LNCV6_127746_PI430048170 mRNA AGCAAGTTTCTGAGTAACAGCTGAAAATGGCCTTGTTGCCTGTGTAGAGCAAGTTACGGT NM_001135721 RefSeq chr8 + 22275566 22356071 PIWIL2 55124 "piwi-like RNA-mediated gene silencing 2, transcript variant 1" GO:0010467|GO:0051321|GO:0048477|GO:0000966|GO:0045727|GO:0007275|GO:0007283|GO:0031047|GO:0034584|GO:0003729|GO:0033391|GO:0005737|GO:0034587|GO:0071546|GO:0043186|GO:0060903|GO:0005844|GO:0

030718|GO:0043046. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78373_PI430048170 0.00322929741035607 0.3719138731526223.61251622296315
3.52438380719296 3.9287317806301 P P P 4.77493198059111 5.24921030879093
5.29873339288797 P P P LNCV6_78373_PI430048170 mRNA
TCACTGAATGCGAAATGACGAAATCTAGCCCTTTGAAAATAACATTGTTTTTAGAAGAGG NM_018685 RefSeq chr7
+ 36389802 36453791 ANLN 54443 "anillin, actin binding protein, transcript variant 1"
GO:0007067|GO:0005826|GO:0000921|GO:0002244|GO:0000281|GO:0007096|GO:0005654|GO:0003779|GO:0015
629|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137412_PI430048170 0.0283368938185861 0.66109723491657 2.9462334094829
2.63405012279368 2.48789082865396 A A A 3.51608164732282 3.17580049911559
3.17892782988625 P P P LNCV6_137412_PI430048170 mRNA
CACCCCTTGTTAAACTTCTCTAACCAAAATACAAGTGTAGAAGAATGTCAGGCTAAAAAA NM_007247 RefSeq
chr17_KI270857v1_alt - 1753964 1848551 SYNRG 11276 "synergin, gamma, transcript variant 1"
GO:0005737|GO:0005794|GO:0030121|GO:0006886|GO:0006897 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133198_PI430048170 0.657231136233216 1.07740191942338 4.81225749937031
4.59432390715088 5.09489025859775 P P P 4.43100588287205 4.53958018198905
5.14528826900151 P P P LNCV6_133198_PI430048170 mRNA
GTAACTACTTTGAGTCTTTTCTGCATGATTGCTCTTTGAGAGAACTTTAACAAGGGAATT NM_052950 RefSeq chr13
+ 51584347 51762035 WDFY2 115825 WD repeat and FYVE domain containing 2 GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134218_PI430048170 0.0251744506514711 0.5400718701166467.3400395296909
7.17780088399361 7.29283572660395 P P P 8.02024493532953 7.9420943423135
8.46306145137958 P P P LNCV6_134218_PI430048170 mRNA
GCAGCTGCTGAAAATCAGCTTTGCCTTTAATTAAACCATGTTCTCTCCAACCAGAAAAAA NM_001174061 RefSeq
chr1 + 183472370 183554193 SMG7 9887 "SMG7 nonsense mediated mRNA decay factor, transcript
variant 5"
GO:0005515|GO:0010467|GO:0035303|GO:0005737|GO:0006406|GO:0000184|GO:0005634|GO:0045111|GO:0051
721|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139792_PI430048170 0.7102929223242670.9709909730790267.20527601790871
7.13256827475783 7.03718268810856 P P P 7.2964106016202 7.18720985885851
7.00929597661024 P P P LNCV6_139792_PI430048170 mRNA
TAGTCGCGATCTCCCAGTGAGCCATCACGATGCCCTTTTCAAATAAATGTTAATGTTGTC NM_014971 RefSeq chr2
+ 25042103 25159135 EFR3B 22979 EFR3 homolog B (S. cerevisiae) NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137135_PI430048170 0.9636765408822280.9923635147058457.21182244321891
7.38068674136501 7.43498732783397 P P P 7.55396585150355 7.19702415707479
7.29501506227538 P P P LNCV6_137135_PI430048170 mRNA
CATTTGTGTGGCTCTCAAACATCCCTTTGGAAGGGATTGTGTGTACTATGTAATATACTG NM_002448 RefSeq chr4
+ 4859664 4863933 MSX1 4487 msh homeobox 1
GO:0030308|GO:0034504|GO:0008285|GO:0006366|GO:0010463|GO:0042481|GO:0000982|GO:0021983|GO:0005
634|GO:2000678|GO:0009952|GO:0002039|GO:0030513|GO:0090427|GO:0005737|GO:0045944|GO:0060021|GO:0
042475|GO:0042474|GO:0051154|GO:0061312|GO:0005667|GO:0043066|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145113_PI430048170 0.3944155131289390.8797764359802140.974697188856667
0.6283605155331370.353396694522637 A A A 0.9789476611836190.913356925110138
0.667687643810806 A A A LNCV6_145113_PI430048170 mRNA
CAAAATGTACTCCTTTCACAGTGTTCTCCTCTTCTGAACTGTGCAGTTATCTATTAAATT NM_025212 RefSeq chr4 -
104468305 104494901 CXXC4 80319 CXXC finger protein 4

GO:0005737|GO:0030178|GO:0016023|GO:0008270|GO:0031410|GO:0007352|GO:0030165|GO:0016055|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125447_PI430048170 0.2571271261905390.5827323786451642.71428146093482 0.3514155648904630.253972611122718A A A 2.32233506984033 2.38899521877342 2.39459073793811 A A P LNCV6_125447_PI430048170 mRNA GCGGTTTCAAATTCCCTAAACATTTTAGATGATGATTATAATGGACAAGCCAAGTGTATG NM_001242318 RefSeq chr8 - 65714333 65841734 PDE7A 5150 "phosphodiesterase 7A, transcript variant 3" GO:0007165|GO:0004115|GO:0046872|GO:0006198|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130251_PI430048170 0.6022732220903060.8978582427364830.49852303882886 0.3355148695354590.430643002717761A A A 0.2903991004474690.952925931387205 0.401906565368841A A A LNCV6_130251_PI430048170 mRNA GTATCTTCTCTTTCCTCCTGTGATGAATCCCATTGTCTACAGTGTGAAGACCAAACAGAT NM_001005238 RefSeq chr11 - 4914718 4915663 OR51G2 NA "olfactory receptor, family 51, subfamily G, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133394_PI430048170 0.00788867596382772 0.5400232632151179.12252941876939 8.74556043874552 8.68382936184465 P P P 9.60864623430246 9.94477966825284 9.68338167831635 P P P LNCV6_133394_PI430048170 mRNA TCTGTCTCGCGGGCCGGGAAACTGCTCTGATGGGAAAATAAACAGCCCAAAACCAAAAAA NM_138422RefSeq chr19 + 1905371 1913447 ADAT3 113179 "adenosine deaminase, tRNA-specific 3" GO:0016787|GO:0008270|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141021_PI430048170 0.7615472893344270.945326263358877 0.380873673862979 0.3732647407963920.317678828998552A A A 0.2458629526277910.762094062326412 0.244019720475128A A A LNCV6_141021_PI430048170 mRNA ATGAGCGAATGAATTAGAAAAGAATAAAACCTACGTAATTAATGACCTTGGCAATGACAG NM_001304457 RefSeq chr19_KI270938v1_alt - 225382 232285 LILRB5 10990 "leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5, transcript variant 4" GO:0006952|GO:0016021|GO:0007166|GO:0004888|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134012_PI430048170 0.00498979563247604 0.47595072041104 7.21947768237847 6.94575941944367 7.15684961255475 P P P 7.91807579977278 8.21041451715152 8.38324707863971 P P P LNCV6_134012_PI430048170 mRNA CAGTGATGGGTGAAAACATTTTACCGGATTATGGAATGTTTACCAGAACATGTTTTGATT NM_014043RefSeq chr3 + 87227262 87255548 CHMP2B 25978 "charged multivesicular body protein 2B, transcript variant 1" GO:0005515|GO:0006997|GO:0019904|GO:0019058|GO:0005634|GO:0010824|GO:0015031|GO:0005829|GO:0000920|GO:0005622|GO:0005739|GO:0005737|GO:0007034|GO:0031902|GO:0016197|GO:0061024|GO:0016032|GO:0005654|GO:0007080|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144388_PI430048170 0.00536549156383234 1.74978708895098 10.5774969641834 10.4541680089105 10.7905196929226 P P P 9.78142785739696 9.7307907947937 9.90319205857552 P P P LNCV6_144388_PI430048170 mRNA CCTGCACTGGCATTTGGATGTGTGTTAATGCTATTTGTTTTGTCTTAAAAGTAAAACCTT NM_004344RefSeq chrX - 152827326 152830757 CETN2 1069 "centrin, EF-hand protein, 2" GO:0008017|GO:0005515|GO:0005813|GO:0032465|GO:0006996|GO:0007099|GO:0005814|GO:0005509|GO:0071942|GO:0007283|GO:0031683|GO:0036064|GO:0005829|GO:0005622|GO:0007067|GO:0032795|GO:0000086|GO:0032391|GO:0006289|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143430_PI430048170 0.000725040561116017 0.3712135625753354.583410969937 4.6858218807183 4.96119159723909 P P P 5.99366387130594 6.28875222246779 6.24664918137281 P P P LNCV6_143430_PI430048170 mRNA GATACATGTGGGCCTGTTAGTCTTCGAAGCTTCCAGATGGTTTGTGTTTTGAGGTACAAA NM_014904RefSeq chr10

- 118004915 118046603 RAB11FIP2 22841 RAB11 family interacting protein 2 (class I)
GO:0005515|GO:0017137|GO:0005886|GO:0019901|GO:0030010|GO:0015031|GO:0055085|GO:0042803|GO:0043231|GO:0003091|GO:0045055|GO:0035773|GO:0005654|GO:0006833|GO:0055038|GO:0030659|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80756_PI430048170 0.5822630753548280.772354232508281 2.06314993354037 3.06933271081302 2.48568365555071 A P A 2.5815130642039 3.65926145875085 2.2958885870673 A P A LNCV6_80756_PI430048170 mRNA
GAGGAGACTTCGGACCTTCTTTCACAACTGCAGAGCCTCCTGGGGCCACACCTTGACAAA NM_001145196 RefSeq chr9 + 42183658 42189887 SPATA31A6 NA "SPATA31 subfamily A, member 6" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129872_PI430048170 0.64193729689377 1.15272650498229 0.402565385279337 0.42730571410961 1.2507447488682 A A A 0.7487722090417860.45045783389575 0.412295216774072 A A A LNCV6_129872_PI430048170 mRNA
GTTCCCATTGCTCAATAAATGTGGATCATCAGAGACATTTATGAACAATGACAGAAGAAA NM_005304 RefSeq chr19 + 35358585 35360487 FFAR3 2865 free fatty acid receptor 3
GO:0014061|GO:0002879|GO:0005886|GO:0004930|GO:0090276|GO:0032722|GO:0045776|GO:0002720|GO:0007193|GO:0008289|GO:0071398|GO:2001275|GO:0002385|GO:0006954|GO:0007186|GO:0046885|GO:0005887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65276_PI430048170 0.00051127740654805 1.97368920432341 7.25170773275776 7.17689734902171 7.37651541060601 P P P 6.18082114873424 6.25822854117778 6.42005410792702 P P P LNCV6_65276_PI430048170 mRNA
TCTGAGGATGGCCTTTATGAGGGAGCTGGCAATTGAACATCATTCATCTAAATATGCACA NM_001098491 RefSeq chr19 + 57487710 57494680 ZNF419 79744 "zinc finger protein 419, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137044_PI430048170 0.000464558241281461 4.98110179338765 5.06035396703446 4.91724030631738 4.74240950887859 P P P 2.4700179568685 2.40363616705478 2.86924208812077 A A P LNCV6_137044_PI430048170 mRNA
TCCCACGCCAGGCCCAAGAGAGATTCTATGACATATATTATAGAGAGAATTCTATATCAA NM_001031690 RefSeq chr7 - 143353399 143362747 FAM131B 9715 "family with sequence similarity 131, member B, transcript variant a" GO:0005737|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65273_PI430048170 0.3289293715558090.7685449376522822.28020082859044 3.16865687637344 3.38506741841789 A P P 3.18032330623079 3.29183215325708 3.67304999739678 P P P LNCV6_65273_PI430048170 mRNA
ATTGGATACCTTCATTTGGGAAGAACCACAGAGTTCACATGGCAGAGGAGATCTTCACAT NM_001172773 RefSeq chr19 + 57389849 57402551 ZNF548 147694 "zinc finger protein 548, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134454_PI430048170 0.03854075561572 0.4351901695136951 1.6720693389805 10.7833989473689 10.7592990040566 P P P 12.4949661818727 12.390826771541 12.0994121954247 P P P LNCV6_134454_PI430048170 mRNA
CTCCCTCCCCAGCTCCACTAAGATTTTCACTTTAGCCATATTCTGATTTTTAAAAAGGAA NM_014485 RefSeq chr4 - 94298555 94342876 HPGDS 27306 hematopoietic prostaglandin D synthase
GO:0019369|GO:0019371|GO:0000287|GO:0006693|GO:0006805|GO:0005509|GO:0004667|GO:0044281|GO:0004364|GO:0042803|GO:0005829|GO:0007165|GO:0005737|GO:0007626 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142060_PI430048170 0.3076434089267151.12106401597796 8.53033018472221 8.33053681381963 8.62899754106286 P P P 8.11732327503313 8.36550941284672 8.50223524748182 P P P LNCV6_142060_PI430048170 mRNA

TAGGAGAAGAAATCCGCAGAAGCTTATTAAAGTTAAGAACAACATAGACGTTTGTCCTGA NM_031903 RefSeq chr7 + 42932339 42937854 MRPL3264983 mitochondrial ribosomal protein L32 GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005761|GO:0005743|GO:0015934|GO:0006412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127474_PI430048170 0.3463078734056091.17060261692226 6.59169776562791 7.15135976727648 6.71368474992376 P P P 6.60446009796165 6.56257145856577 6.66772570721037 P P P LNCV6_127474_PI430048170 mRNA
ACAACAAAACAAACACAAAACCACTGATCTGTGATTGCTCTCCCTTTGTGTCTACTGCCG NM_138703 RefSeq chrX - 75782987 75785244 MAGEE2 139599 melanoma antigen family E2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128633_PI430048170 0.0446359691609436 0.4043467981808595.03908098625592 4.6970031238607 4.95921288853976 P P P 5.60096508039693 6.16981579330941 6.67051927804686 P P P LNCV6_128633_PI430048170 mRNA
AGTGTTATCCTGCTCTCAGGCCAACAGGGGGAGCAAAATAGAAACATTCCAGATATAGCT NM_017612 RefSeq chr12 - 122471598 122501073 ZCCHC8 55596 "zinc finger, CCHC domain containing 8" GO:0005515|GO:0000398|GO:0008270|GO:0005654|GO:0005634|GO:0071013 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67921_PI430048170 0.55363093654021 1.19979019496771 3.2987162519002 2.33694202062057 2.55490461385549 P A A 3.32935472001257 2.16612175074548 1.47027810686483 P A A LNCV6_67921_PI430048170 mRNA
TATCAGAGGGGCTCCAGTACCTATTTGAGAACATCTCCCAGCTCACTGAAAAAGATGTCT NM_020393 RefSeq chr1 - 153330120 153348841 PGLYRP4 57115 peptidoglycan recognition protein 4 GO:0016019|GO:0050830|GO:0044117|GO:0042834|GO:0008745|GO:0005576|GO:0032827|GO:0005622|GO:0009253|GO:0002221|GO:0016020|GO:0045087|GO:0008270|GO:0016045|GO:0032689 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141893_PI430048170 0.349088761251036 0.908878745004664 0.378709147975252 0.366057969923272 0.263893635486776 A A A 0.68099550779198 0.372158676017468 0.347246902190725 A A A LNCV6_141893_PI430048170 mRNA
AAACAACTCCGGAATGTCGCTAGCTCCTTAGTAAATAAATGAATCTCTTTCTGGAAAAAA NM_019558 RefSeq chr2 + 176129739 176132695 HOXD8 3234 "homeobox D8, transcript variant 1" GO:0000977|GO:0045944|GO:0048705|GO:0005634|GO:0000122|GO:0008595|GO:0001228|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2805_PI430048170 0.00314021099655759 1.19734229065938 8.1937106443621 8.14062819681762 8.1744965541911 P P P 7.95987957784256 7.86483252947416 7.90352971289008 P P P LNCV6_2805_PI430048170 mRNA
TTGGTATTAAAGGCCACCATTTGCACAAATGTTCCTGTTTTGGGTAACTTGGATTATTGT NM_001272038 RefSeq chr1 - 153981616 153985366 RAB13 5872 "RAB13, member RAS oncogene family, transcript variant 2" GO:0034236|GO:0005802|GO:0005515|GO:0043005|GO:0035767|GO:0005886|GO:0032456|GO:0003924|GO:0030139|GO:0010737|GO:0006886|GO:0031175|GO:0005737|GO:0070830|GO:0016197|GO:0061024|GO:0032482|GO:0030659|GO:0070062|GO:0030658|GO:0032869|GO:0005794|GO:0031410|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137646_PI430048170 0.144429849360503 0.560950386358631 3.1949392494404 2.83570573392482 1.88330735119726 P A A 3.0907636260986 3.999663782825 3.47407674170588 P P P LNCV6_137646_PI430048170 mRNA
GAACAAAGTTGTCATTATAGGGTCTATAAACTTAAGTCTCCAGCTTATTTGAGACTGGCT NM_001204858 RefSeq chr8 - 73945137 73972287 TCEB1 6921 "transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C), transcript variant 3" GO:0005515|GO:0070449|GO:0006511|GO:0010467|GO:0006368|GO:0006357|GO:0006366|GO:0030891|GO:0071

456|GO:0061418|GO:0032403|GO:0005829|GO:0050434|GO:0032968|GO:0016032|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133851_PI430048170 0.0259013319666864 0.756693824439864 7.66393008538586 7.90365312480207 7.68561993437969 P P P 8.1942993540082 8.16106358960266 8.11580612133088 P P P LNCV6_133851_PI430048170 mRNA GCCCTGCATTTATGAGGCACCTACCTTCATTTTGCTAACGCTTATTCTGAATAAAAGTTT NM_015974 RefSeq chr13 - 20403666 20525873 CRYL1 51084 "crystallin, lambda 1"
GO:0005794|GO:0005886|GO:0005730|GO:0003857|GO:0005634|GO:0070403|GO:0042803|GO:0005829|GO:0050104|GO:0005737|GO:0006631|GO:0055114|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139038_PI430048170 0.00896274483792201 0.507550259378098 4.58530479962117 4.66306296079753 4.4676840131711 P P P 5.28381678798375 5.62053548515497 5.71842209110216 P P P LNCV6_139038_PI430048170 mRNA CTCGTTAAATTTTGCCAAATCAGTTGCCCCCAAAAGGGAATATGCTTTTCCTTATTTTTT NM_001080393 RefSeq chr3 + 72888233 72975371 GXYLT2 727936 glucoside xylosyltransferase 2
GO:0035252|GO:0016266|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142526_PI430048170 0.00279122090525922 2.19021359249464 12.2316355559511 12.6352549810924 12.3120144209691 P P P 11.3657524011342 11.3324506994541 11.10625910283 P P P LNCV6_142526_PI430048170 mRNA GCCTGGAAACGTGCCAGGACACTGTCCTGGTGCCCAGCCCAACGTGGTCCAACGTTTTTT NM_002513 RefSeq chr16 - 1770319 1771709 NME3 4832 NME/NM23 nucleoside diphosphate kinase 3
GO:0006241|GO:0004550|GO:0006915|GO:0042981|GO:0006220|GO:0009142|GO:0005524|GO:0046872|GO:0005829|GO:0005739|GO:0006165|GO:0006228|GO:0006183|GO:0006163|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145754_PI430048170 0.450845445104936 0.800486862494622 2.53810462781801 2.71737201542614 2.51924603034156 A A A 3.39969526894763 2.43428887919858 2.73869932066718 P A P LNCV6_145754_PI430048170 mRNA TATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTCTCCAGGCAACCAGCTCTAC NM_005091 RefSeq chr19 - 46019154 46023298 PGLYRP1 8993 peptidoglycan recognition protein 1
GO:0016019|GO:0050830|GO:0044117|GO:0042834|GO:0008745|GO:0005576|GO:0032827|GO:0009253|GO:0002221|GO:0006955|GO:0050728|GO:0045087|GO:0008270|GO:0016045|GO:0032689|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129071_PI430048170 0.0836395816351726 0.7330109146960975.09945007110559 5.20959418398838 5.45645178261382 P P P 5.55953178554187 5.52756286145447 5.99698040728494 P P P LNCV6_129071_PI430048170 mRNA ACTCCTAACATACATATGTTTGGGGAAGTATTCTATTCTATACTTGCCAATGTGGAGAAC NM_147156 RefSeq chr10 - 50305584 50623977 SGMS1 259230 sphingomyelin synthase 1
GO:0006665|GO:2001237|GO:0033188|GO:0005886|GO:0005783|GO:0006686|GO:0030148|GO:0006915|GO:0005634|GO:0044281|GO:0047493|GO:0010628|GO:0016310|GO:0030173|GO:0071222|GO:0006954|GO:0000139|GO:0016020|GO:0000138|GO:0016301|GO:0071356|GO:0016049 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140411_PI430048170 0.56120540611669 0.9541853814491320.497479777192783 0.4483255199186070.345921151810188 A A A 0.3713696503913190.449189461303251 0.662325681248791 A A A LNCV6_140411_PI430048170 mRNA TTCTTCCACTGACATAAAATGCCAGCTTGATCGTACAATAAATCTGTCTATTTACCTGGG NM_178460 RefSeq chr20 - 1534250 1557697 SIRPD 128646 signal-regulatory protein delta GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129862_PI430048170 0.1710900546705490.9135089910987741 3.0819541623262

13.1935801073368 13.2205961868164 P P P 13.1701135966533 13.3602626423252
13.3530631576056 P P P LNCV6_129862_PI430048170 mRNA
AGTTCATCTTTTTATATGGGGTTGTTGTCTCATTTTGGTCTGTTTTGGTCCCCTCCCTCG NM_006148 RefSeq chr17 +
38869858 38921770 LASP1 3927 "LIM and SH3 protein 1, transcript variant 1"
GO:0005515|GO:0051015|GO:0034220|GO:0015075|GO:0005070|GO:0009967|GO:0008270|GO:0030864|GO:0005
925|GO:0070062|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131903_PI430048170 0.00495100762646502 0.29535139149974 4.22083540297483
3.71202508224568 4.36793712850834 P P P 5.44095441210873 5.86165121514727
6.24462277544294 P P P LNCV6_131903_PI430048170 mRNA
GGCAGTCTTTCCTCTCTTACATTATTGGTAAGATTATACTAACAAAATGTTTCCCCTTGT NM_016937 RefSeq chrX +
24693946 24996985 POLA1 5422 "polymerase (DNA directed), alpha 1, catalytic subunit"
GO:0005515|GO:0008283|GO:0005658|GO:0003887|GO:0005634|GO:0005635|GO:0006303|GO:0046872|GO:0016
363|GO:0006273|GO:0000082|GO:0005737|GO:0006271|GO:0000083|GO:0006272|GO:0000723|GO:0000166|GO:0
001882|GO:0006270|GO:0000722|GO:0016032|GO:0000785|GO:0051539|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131198_PI430048170 0.3141236793917380.83302126847655 0.294854913291897
0.4272721868722020.318437188659449 A A A 0.4698189614465760.944472551346771
0.349830454755647 A A A LNCV6_131198_PI430048170 mRNA
TCACTGAGAAGACATAAGATGCTCTCCAGAGGGAGTAAGCCAAAAATCTACAAACTCTTA NM_002929 RefSeq chr13
+ 113667281 113735664 GRK1 6011 G protein-coupled receptor kinase 1
GO:0043066|GO:0007603|GO:0038032|GO:0022400|GO:0050254|GO:0005524|GO:0004672|GO:0004703|GO:0008
277|GO:0046777|GO:0060060|GO:0007601|GO:0008594|GO:0016056|GO:0042327 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130279_PI430048170 0.0893453298150463 1.16724251851475 10.3232726685449
10.1850454238183 10.4291031403102 P P P 10.0909866837971 10.0874220659751
10.1000078753861 P P P LNCV6_130279_PI430048170 mRNA
AAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATTCCAGGCTCTTTCCATAA NM_015959 RefSeq chr11
+ 57712522 57740973 TMX2 51075 "thioredoxin-related transmembrane protein 2, transcript variant 1"
GO:0008150|GO:0003674|GO:0045454|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136545_PI430048170 0.54372072813431 1.24148416177298 2.79995031570797
3.94788383803662 3.34006861102156 A P P 3.30432555790799 3.35815290855787 2.6002442174539
P P P LNCV6_136545_PI430048170 mRNA
ATATCTCAAATCTTCTGCAGGACATGAGCAAGCCCCTTGGCTCAGCATTTCTGTCTTTCT NM_005684 RefSeq chr1
+ 174448073 174449545 GPR52 9293 G protein-coupled receptor 52
GO:0007186|GO:0005887|GO:0004930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139342_PI430048170 0.00097285521693059 0.5371558832687517.3891049974346
7.44779860901857 7.2270564045511 P P P 8.18432079855892 8.31500430401457
8.26037645136832 P P P LNCV6_139342_PI430048170 mRNA
GAAGCCCATGGGAGAATTTTGGGGATGTTTTGGTCTTTTCTTCCTTTTGTAATAAAAATT NM_002181 RefSeq chr2
- 219054419 219060516 IHH NA indian hedgehog NA . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_107618_PI430048170 0.1940351038512610.93091383368504 5.52324803119056
5.61921373118588 5.43660844717172 P P P 5.57604720791008 5.60885191191834
5.70658281314113 P P P LNCV6_107618_PI430048170 mRNA
TCTCTGATCAGCGCGCTCTTCGCCCTTCTGCAGCAGCCGCTGTTTCTGGCCATGATGGGT NM_001284498 RefSeq
chr17_KI270861v1_alt - 0 58403 SLC43A2 124935 "solute carrier family 43 (amino acid system L
transporter), member 2, transcript variant 1"
GO:0005886|GO:0006865|GO:0016021|GO:0015179|GO:0055085|GO:0006811 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_136650_PI430048170 0.2855783294849890.8373572905947930.403998066578307
0.3327192364974260.366270917510192A A A 0.2986680116937250.864593987868565
0.653265511968972A A A LNCV6_136650_PI430048170 mRNA
GGTATTTTCTTGGAGAATGTAAGAACTTAACAATAAAGCTGAACTGGTGTTGTGAAACAG NM_001011544 RefSeq
chrX + 149688236 149717268 MAGEA11 4110 "melanoma antigen family A11, transcript variant 2"
GO:0005515|GO:0005737|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72409_PI430048170 0.0303754500006709 1.31966005373206 12.1466258966303
12.0635103574549 12.2768062277969 P P P 11.5790999100416 11.9027772517624 11.794050136879
P P P LNCV6_72409_PI430048170 mRNA
ATGTCAGACAACGAGGACAATTTTGATGGCGACGACTTTGATGATGTGGAGGAGGATGAANM_001301129 RefSeq
chr22 + 37953662 37969315 POLR2F 5435 "polymerase (RNA) II (DNA directed) polypeptide F,
transcript variant 2"
GO:0008380|GO:0010467|GO:0006386|GO:0006368|GO:0006367|GO:0006385|GO:0006366|GO:0006363|GO:0006
362|GO:0006361|GO:0005634|GO:0006360|GO:0006383|GO:0005829|GO:0005736|GO:0034587|GO:0005665|GO:0
016032|GO:0005666|GO:0032481|GO:0035019|GO:0005730|GO:0006370|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133696_PI430048170 0.6861775878881070.9709293734034520.604348130042076
0.5163596375890050.308473260372618A A A 0.4193382485696120.609187920130878
0.537782268237543A A A LNCV6_133696_PI430048170 mRNA
CATGTTCAAAAGAAGTTCATTCCTGTCTAAAGTGGGAAAGTTGCATTTAATGTTAGGGGT NM_002469RefSeq chr12
+ 80707628 80709477 MYF6 4618 myogenic factor 6 (herculin)
GO:0060415|GO:0003700|GO:0046982|GO:0006357|GO:0006366|GO:0001756|GO:0003705|GO:0070888|GO:0005
634|GO:0000978|GO:0001228|GO:0035914|GO:0042693|GO:0042692|GO:0051149|GO:0048743|GO:0007519|GO:0
045944|GO:0045663|GO:0043403|GO:0005654|GO:0045892 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_90838_PI430048170 0.5299118428126391.28681846838628 0.3778360803805941.41294010019078
0.279331952210015A A A 0.6813195706094060.2874472944926870.260743953302607A A A
LNCV6_90838_PI430048170 mRNA
TATCTGTATCCAGAGGAAATAGCCAAGGATATTCAAGGTGTGCCTGGGAAGTTTGAGCTG NM_000219RefSeq chr21
- 34446687 34512275 KCNE1 3753 "potassium channel, voltage gated subfamily E regulatory beta
subunit 1, transcript variant 2"
GO:0005251|GO:0005515|GO:0030018|GO:0005886|GO:0009986|GO:0007605|GO:0031433|GO:0015459|GO:0060
307|GO:0086091|GO:0005764|GO:0071435|GO:0086008|GO:0086009|GO:0006493|GO:0005249|GO:0008076|GO:0
086013|GO:0086002|GO:0086011|GO:0006487|GO:0071320|GO:0071805|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_69886_PI430048170 0.8782812047438310.9322880506528180.3507607553119170.529509307397912
1.62211110787797 A A A 0.8090374969190170.2712966604778611.70443732029956 A A A
LNCV6_69886_PI430048170 mRNA
GCGTGCACTGTTCGTATTTGGAGTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCA NM_001163075 RefSeq
chr17 + 78146352 78166283 C17orf99 100141515 chromosome 17 open reading frame 99
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137114_PI430048170 0.1652928925774250.6736406511930582.84218622096971
3.11164524551645 3.02657823899276 A P P 3.64562598311263 3.89457721325808
3.03302342614053 P P P LNCV6_137114_PI430048170 mRNA
CCCCCGGGATGGCTGCTTCCAAGTTGTTTGCAATTAAAGGTTCTGTATAAAACCAAAAAA NM_080386RefSeq chr2
+ 131476006 131482934 TUBA3D 113457 "tubulin, alpha 3d"
GO:0005515|GO:0051258|GO:0005874|GO:0003924|GO:0005634|GO:0005525|GO:0006184|GO:0005737|GO:0006
457|GO:0005200|GO:0051084|GO:0007017|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_128018_PI430048170 0.1847412178316461.68980729552423 1.52032878987289
1.40303070816614 0.41352187364313 A A A 0.360381882840952 0.320312950021364
0.602578501191822 A A A LNCV6_128018_PI430048170 mRNA
GGTAATGCTGACAGTTATCCTTGAATCTGACTATAGACATTTGTTATTCAGTGTGAAACA NM_001300778 RefSeq
chr12 + 133080202 133107672 ZNF140 7699 "zinc finger protein 140, transcript variant 4"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93974_PI430048170 0.0529041400336541 0.80817041293201 5.63068372612131
5.72321864352062 5.74946423179557 P P P 5.90547016443769 5.93521086930284
6.17211066435861 P P P LNCV6_93974_PI430048170 mRNA
ATTTAAACACTGACGGAGACATGAGGGTGACACCTGAGCCGGGAGCAGGTCCAACCCAAG NM_017660 RefSeq
chr19 + 19385832 19508932 GATAD2A 54815 "GATA zinc finger domain containing 2A, transcript
variant 2"
GO:0005515|GO:0010172|GO:0001568|GO:0003700|GO:0005634|GO:0012501|GO:0001701|GO:0001842|GO:0006
351|GO:0021506|GO:0043565|GO:0006306|GO:0016607|GO:0016581|GO:0005654|GO:0008270|GO:0030674|GO:0
045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_11479_PI430048170 0.0360079018366340.2629852431194741.65039028282983 0.599990894339371
2.21596270760048 A A A 3.60962500189196 3.1889200020183 3.81148027854533 P P P
LNCV6_11479_PI430048170 mRNA
GCATCTTAGCAGATAAGCCTATTAAAATTGTGCTTTTGTAACAATGTTGTGGTTGCTAGA NM_002614 RefSeq chr1
- 145670852 145707400 PDZK1 5174 "PDZ domain containing 1, transcript variant 1"
GO:0005515|GO:0005215|GO:0005886|GO:0008283|GO:0090314|GO:0031528|GO:0031526|GO:0005124|GO:0030
165|GO:0032403|GO:0044070|GO:0005737|GO:0016324|GO:0006810|GO:0045121|GO:0034767|GO:0015879|GO:0
015893|GO:0090002|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122923_PI430048170 0.4937713710005782.28059740350008 0.320628487857019
2.78270804683786 0.269882829147569 A A A 0.3231782542563920.720018070672692
0.257473514232429 A A A LNCV6_122923_PI430048170 mRNA
GATAATGATGCCTGGTGTATTGAAATCCTCAATAAATACTGCCAAGTGTGGATCAGTTGG NM_178335 RefSeq chr3
+ 191329084 191398670 CCDC50 152137 "coiled-coil domain containing 50, transcript variant 2"
GO:0005515|GO:0005737|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132284_PI430048170 0.3781934654080651.02966518130959 0.294794719459902
0.3034427015630070.409064657806528 A A A 0.31025933518449 0.286768575736142
0.286447564606385 A A A LNCV6_132284_PI430048170 mRNA
TTTATCCTTACCTTCTGCAATCAGACAGTTAAAACAGTGCTACAGGGGCAGATGCAGAGG NM_001001667 RefSeq
chr7_KI270803v1_alt + 1075407 1076349 OR6V1 NA "olfactory receptor, family 6, subfamily V,
member 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127734_PI430048170 0.0153434928581564 0.5747545620795459.48484873434666
9.39764978572556 9.02674266571342 P P P 10.1079823642132 10.231411247063
9.99704351016895 P P P LNCV6_127734_PI430048170 mRNA
CCCTGCCTGTGTGTGTTATTTCAAAGGAAAAGAACAAAAGGAATAAATTTTCTAAGCTCT NM_024103 RefSeq chr19
- 6440063 6459770 SLC25A23 79085 "solute carrier family 25 (mitochondrial carrier; phosphate
carrier), member 23"
GO:0005509|GO:0071277|GO:0005743|GO:0097274|GO:0051503|GO:0016021|GO:0043457|GO:0055085|GO:0051
282|GO:0002082 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130212_PI430048170 0.2088464100896281.17101612440668 5.98095232398502
6.10704245924933 6.26281613786673 P P P 5.62831862356717 6.00069022455192
6.01966544635113 P P P LNCV6_130212_PI430048170 mRNA
CCCATTCTTACTGATACTTTTGTCAGATATCACCCTGTCCTTAAATCATGATCACTTAAA NM_052936 RefSeq chrX + 108091668 108154671 ATG4A 115201 "autophagy related 4A, cysteine peptidase, transcript variant 1"

GO:0006995|GO:0006501|GO:0004197|GO:0005737|GO:0000422|GO:0016485|GO:0006612|GO:0006508|GO:0051697|GO:0008234|GO:0000045|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127905_PI430048170 0.63981039423855 1.03026267351609 0.277861056925828 0.286589642698453 0.497443668792421 A A A 0.332504333405817 0.285665086009198 0.325134890191915 A A A LNCV6_127905_PI430048170 mRNA
CGCCCACACTGATGGTTTTGCACTGGTTTTTGTGAATGTTTCTTACAAAAAGAAAAAGGA NM_130783 RefSeq chr11 + 44764425 44932426 TSPAN18 90139 tetraspanin 18 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97242_PI430048170 0.0312918764988346 0.780655524194636 5.88585000862206 5.69361412279091 5.9774104089836 P P P 6.34728863564595 6.12478548810048 6.16087687092405 P P P LNCV6_97242_PI430048170 mRNA
TCGAGCTGAGAAGGATGCTGAACAGAAGATTGAAGAACAGAAGACTTTAGACAAAGCAAG NM_016474 RefSeq chr3 + 14651745 14672659 CCDC174 51244 coiled-coil domain containing 174 GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137950_PI430048170 0.265616979797026 1.10546151684671 7.18754046086999 6.8888722334609 7.07051205193707 P P P 6.81642582263444 7.03414471915278 6.8689310948493 P P P LNCV6_137950_PI430048170 mRNA
CAGGGAAAGGGTTAGACAACTTGAAACATTGACCCTGTATAAAAATGCAAAATTCTCAAT NM_138572 RefSeq chr6 + 42050512 42080906 TAF8 129685 "TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 43kDa"
GO:0005515|GO:0048471|GO:0005669|GO:0046982|GO:0051457|GO:0045598|GO:0001833|GO:0005654|GO:0005634|GO:0045893|GO:0030154|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67849_PI430048170 0.979823190959469 1.13329626906302 2.32394808818925 0.512679306773786 0.898203966038254 A A A 0.681805153660499 1.70616914283201 1.29539292009088 A A A LNCV6_67849_PI430048170 mRNA
CCATGTTATGCAGGAGGAATTGGATAATGTTGTATGTGAATGCAATAAAAAGGAGGATGA NM_001286449 RefSeq chr15 + 56365423 56445997 TEX9 NA "testis expressed 9, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137124_PI430048170 0.788925228330405 1.08044043652575 3.18877233858342 2.30384244794184 2.77697295885701 P A A 2.46881688350211 3.02426003852903 2.50635579378425 A P P LNCV6_137124_PI430048170 mRNA
TAAAAACATCCCAGACAAGACAGTTTGATTATGGAGACTGTCCCCAAGCAGATTGGTGTG NM_015575 RefSeq chr2 + 232697304 232860577 GIGYF2 26058 "GRB10 interacting GYF protein 2, transcript variant 2"
GO:0017148|GO:0007631|GO:0008344|GO:0021522|GO:0009791|GO:0005737|GO:0048873|GO:0016020|GO:0035264|GO:0050881|GO:0050885|GO:0048009|GO:0031571|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127735_PI430048170 0.19828162352179 1.03269475649488 0.351007606824335 0.292045688878085 0.375937817319712 A A A 0.29083617574502 0.28130794026182 0.308752302008485 A A A LNCV6_127735_PI430048170 mRNA
GATTCTGTATCTTTTGGAAAAAAGCCGAGAGTTGAAGATAGTATATTTCTGGTAGTACTG NM_013386 RefSeq chr1 - 108134721 108200358 SLC25A24 29957 "solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24, transcript variant 1"
GO:0005739|GO:0005737|GO:0005509|GO:0071277|GO:0005743|GO:0015867|GO:0034599|GO:0016021|GO:0005347|GO:0055085|GO:0006839|GO:0010941 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144416_PI430048170 0.00287013075590688 0.215405332455805 1.92117948182019 2.17653932023412 2.71363548136541 A A A 4.64552951467255 4.24316788890677 4.64706540342349 P P P LNCV6_144416_PI430048170 mRNA
CATGTGTGTGAAAATGCAGGTTTTCTCTTAGAAATAAAGTGGTGACTTGTGCTGTAAAAA NM_052893 RefSeq chr6 - 38168450 38640148 BTBD9 114781 "BTB (POZ) domain containing 9, transcript variant 1"

GO:0042748|GO:0042428|GO:0008344|GO:0007616|GO:1900242|GO:0050951|GO:0060586 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90870_PI430048170 0.12919533273732 1.28281775731622 5.27826452120614 4.84742230229375 5.15933680164393 P P P 4.84819442870792 4.45797376030355 4.89577342413649 P P P LNCV6_90870_PI430048170 mRNA
AGAGTGTAACAAGGGATATGTCAAGGTAAAGCAGAGTTTGAGGAAGAGGCAAAGAACCCT NM_001195249 RefSeq chr9 - 32972605 33001576 APTX 54840 "aprataxin, transcript variant 7"
GO:0005515|GO:0003725|GO:0051219|GO:0000012|GO:0042542|GO:0000790|GO:0005634|GO:0046872|GO:0006302|GO:0005737|GO:0003690|GO:0031647|GO:0000785|GO:0008967|GO:0033699|GO:0005730|GO:0006974|GO:0003684|GO:0047485|GO:0003682|GO:0016311|GO:0046403|GO:0005654|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144244_PI430048170 0.1869047089341781.09899253447373 0.5615228004923540.7923467456812 0.625979425884361 A A A 0.4418832284911690.5519938427583880.583557112348688 A A A LNCV6_144244_PI430048170 mRNA
AACTTTTCCTACCCAGTTTAGCAAAACACCTGTTTTATGCAACAATACATCACAACAGGC NM_020369 RefSeq chr7 + 127593634 127601797 FSCN3 29999 "fascin actin-bundling protein 3, testicular"
GO:0005737|GO:0051015|GO:0007286|GO:0007015|GO:0030674|GO:0015629|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139340_PI430048170 0.00346405991050746 0.3612762623578822.8945013864137 2.99397473345815 2.72621819566926 A P A 4.06116083324247 4.58828988361232 4.33639075275766 P P P LNCV6_139340_PI430048170 mRNA
CCACTGTGTTTTATCTACTGTGTGTTGTGGTGGCCTGTTGGAGGCAAATAGATCAGATTT NM_013450 RefSeq chr2 - 159318978 159616601 BAZ2B 29994 "bromodomain adjacent to zinc finger domain, 2B, transcript variant 1" GO:0005515|GO:0006355|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140173_PI430048170 0.0351344811321041 0.7461413852742489.44386036602832 9.08073995124637 9.21655235435457 P P P 9.6357688087258 9.8065952945231 9.57999390778647 P P P LNCV6_140173_PI430048170 mRNA
GTGACACTCAAGCCCCTCTCATTTTTATCTGTCTACCTCCATTCTGAAGAGGGAGGTTTT NM_021095 RefSeq chr2 - 27199586 27212307 SLC5A6 8884 "solute carrier family 5 (sodium/multivitamin and iodide cotransporter), member 6, transcript variant 1"
GO:0012506|GO:0015887|GO:0005886|GO:0015939|GO:0006768|GO:0006767|GO:0044281|GO:0031526|GO:0055085|GO:0016020|GO:0005887|GO:0006766|GO:0008523|GO:0006810|GO:0015878|GO:0006814 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132952_PI430048170 0.00362843402248499 0.3766557984883527.15345914229432 6.68495643768157 6.7672656267839 P P P 7.93586603790691 8.38670742720534 8.49497442114246 P P P LNCV6_132952_PI430048170 mRNA
CCTTGCCTTTGAGTGGCTTTGAAACTTAATATAGTTTTTAAAAAGTGCAATGGGATGAGA NM_015459 RefSeq chr11 - 63624081 63671730 ATL3 25923 "atlastin GTPase 3, transcript variant 1"
GO:0006888|GO:0016020|GO:0005783|GO:0008152|GO:0007030|GO:0005789|GO:0003924|GO:0051260|GO:0016021|GO:0005525|GO:0007029|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144729_PI430048170 0.0874521949243805 1.65435205922435 4.16329503383768 4.78863577565907 4.55205843870664 P P P 4.21098440913421 3.74175801290497 3.29573737306491 P P P LNCV6_144729_PI430048170 mRNA
GGAAAGCCTCTATTTTTCTTTCTGAGAAACTGAGAAATTTGATTGACACAGGGGGGTGTA NM_003800 RefSeq chr6 - 88609896 88963629 RNGTT 8732 "RNA guanylyltransferase and 5'-phosphatase, transcript variant 1"
GO:0006396|GO:0010467|GO:0006366|GO:0008192|GO:0006370|GO:0005634|GO:0005525|GO:0035335|GO:0004651|GO:0050355|GO:0004484|GO:0016032|GO:0005654|GO:0008138|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133150_PI430048170 0.5077010916414961.12506387693481 0.3048492664469
0.88130843652541 0.36670296554003 A A A 0.2731968402879450.429091008885253
0.407577183127577A A A LNCV6_133150_PI430048170 mRNA
TCAAAATACAAGTGTGGGATGAAAAACCACCATCCTGAACAGCAAAGCTCCCTGCTAAAC NM_001256874 RefSeq
chr8_KI270813v1_alt + 24048 25641 USP17L4 NA ubiquitin specific peptidase 17-like family member
4 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126853_PI430048170 0.6806473968603811.45007398704367 2.23225935547235
0.5012652894006010.351435127693016A A A 1.15577491777394 0.535931509757512
0.504221212741054A A A LNCV6_126853_PI430048170 mRNA
GAAAGCAGCAATTTGCTGTTCTCAACCATTCTTTCAAGGCTTTTCATTGTTCAAAGTTAA NM_000493RefSeq chr6
- 116118921 116126133 COL10A1 1300 "collagen, type X, alpha 1"
GO:0005581|GO:0001958|GO:0001501|GO:0022617|GO:0051216|GO:0030198|GO:0030574|GO:0005578|GO:0005
788|GO:0005576|GO:0005938|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131133_PI430048170 0.00565457478348677 7.47690150564738 3.19362654683542
4.22543651438914 3.05746477126841 P P P 1.08120598788441 0.442728391118412
0.447802393694207A A A LNCV6_131133_PI430048170 mRNA
TCTTTGACAACAGCGACAACGTGGTGCTGCGGCAGTATGAGGACATGGTGGTGGACGAGT NM_021267RefSeq
chr19 - 18868545 18896144 CERS1 NA "ceramide synthase 1, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_115943_PI430048170 0.2683846289473221.42255754643826 4.20472332832286
4.35396932424037 4.52917616968249 P P P 4.43945082382707 3.777730753513
3.02774496586549 P P P LNCV6_115943_PI430048170 mRNA
CCACTGGAGTTCAAGTGGCTCCACAACAACAGGGAGCTGACCAAGTTCTCCCTGGAATAC NM_001144952 RefSeq
chr17 - 73334383 73644088 SDK2 54549 sidekick cell adhesion molecule 2
GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135195_PI430048170 0.219437956593922 1.03561276129205 0.525143620646536
0.474402552054350.454611268652997A A A 0.3795446298990830.45866512540038
0.463875961117937A A A LNCV6_135195_PI430048170 mRNA
CCAGATAGATAGGACAACTTCAGTTTATTCCAGCAAGAAAGAAAAGATTGTTATGCAAGA NM_001073RefSeq chr4
- 69200330 69214731 UGT2B11 10720 "UDP glucuronosyltransferase 2 family, polypeptide B11"
GO:0008210|GO:0052696|GO:0006805|GO:0009813|GO:0005789|GO:0015020|GO:0016021|GO:0032870|GO:0043
231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132120_PI430048170 0.31920744420392 1.02045231694119 0.321105043086454
0.2455395535070990.292250739741059A A A 0.2602443226416370.25066524506215
0.261341392043513A A A LNCV6_132120_PI430048170 mRNA
GCATAATGCAGACATTCTTGTATTTGGCTTTTGCTCACGTAGAGTGTCTGATTTTGGTGG NM_001001659 RefSeq
chr7 + 144129112 144130045 OR2A14135941 "olfactory receptor, family 2, subfamily A, member 14"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138313_PI430048170 0.0216663437847852 0.1727019326322930.531889615579505
0.6348385754416920.599870006894335A A A 3.16637754485653 2.33471299554662
3.59885050862133 P A P LNCV6_138313_PI430048170 mRNA
AGACCTTCCAGAAATACTACTGTGTAAGGGCCAGAAATATCTTCACTTGTCATTGTTATA NM_000353RefSeq chr16
- 71566850 71577095 TAT6898 tyrosine aminotransferase
GO:0006559|GO:0006536|GO:0009058|GO:0004838|GO:0051384|GO:0044281|GO:0005575|GO:0005829|GO:0005
739|GO:0034641|GO:0006103|GO:0030170|GO:0006572|GO:0046689|GO:0006979|GO:0016597|GO:0080130 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137986_PI430048170 0.0121450135702138 1.7704877130568 5.71160539890923
5.42645665393034 5.70073243531221 P P P 5.03254581127386 4.77411065697498 4.5343786308732

P P P LNCV6_137986_PI430048170 mRNA
ACTGTGTGCCTGTCTGCTGTAAGCCTGTCTGCTGCAAACCCATCTGCTGTGTGCCTGTCT NM_198690 RefSeq chr21
+ 44627122 44628378 KRTAP10-9 NA keratin associated protein 10-9 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136373_PI430048170 0.0679025221370003 2.69797975951966 2.05944019382733
3.01999623452908 3.02906587709952 A P P 0.380353582288919 2.05980310814702
1.07456617533208 A A A LNCV6_136373_PI430048170 mRNA
CCTCAGCAAGGGAGCCATACATTTTTGTAACATTTTGATATGTTTTAATGCATCTGACTT NM_014737 RefSeq chr20
- 4780023 4823645 RASSF2 9770 "Ras association (RalGDS/AF-6) domain family member 2, transcript variant 1"
GO:0048872|GO:0005515|GO:0045667|GO:0007049|GO:0005737|GO:0001501|GO:0046849|GO:0001503|GO:0038168|GO:0005634|GO:0045670 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128953_PI430048170 0.46549906201809 0.6706735821399261.3619566833863
2.03517695691813 1.70982107054974 A A A 3.02440366846038 2.03638546340596
1.36886992539756 P A A LNCV6_128953_PI430048170 mRNA
ATTTAAACTTTTCCTGCTGCTTTTGGTAACTTCTCACCTGGGGCCATATTTTACAGATTT NM_001282853 RefSeq chr10
+ 35336873 35572670 CCNY 219771 "cyclin Y, transcript variant 4"
GO:0005515|GO:0019901|GO:0005886|GO:0000086|GO:0000308|GO:0045737|GO:0016538|GO:0005634|GO:0016055|GO:0070062|GO:0060828|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56986_PI430048170 0.694376750599091 0.973484118156383 9.14725704252539 9.24925838669361
9.43279996869748 P P P 9.27248088152281 9.2635448786497 9.41890079466273 P P P
LNCV6_56986_PI430048170 mRNA
TCTCAGAAAATCGACCGATTAGATGGTGCACATGCCCCAGAGTTGACCAAAAAAGTTCAG NM_001199868 RefSeq
chr10 + 130136374 130180382 GLRX3 10539 "glutaredoxin 3, transcript variant 1"
GO:0005515|GO:0030018|GO:0051536|GO:0015035|GO:0009055|GO:0046872|GO:0010614|GO:0002026|GO:0005080|GO:0045454|GO:0005938|GO:0055114|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130871_PI430048170 0.419000128298988 0.522885137931594 0.293931246695978
0.333337312558872 0.394182285761045 A A A 0.357711062947707 0.335430241012749
2.24013544441429 A A A LNCV6_130871_PI430048170 mRNA
GTAACGCATTCATGAATTTCCAGTGTTCAGTAAATAGCAGCTATGTGTGTGCAAAATAAA NM_031950 RefSeq chr4
- 15960239 15963236 FGFBP2 83888 fibroblast growth factor binding protein 2
GO:0019838|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127536_PI430048170 2.61919443316065e-05 0.369305184295708 8.05784284410724
7.91353949996109 7.9420943423135 P P P 9.31457727787483 9.43739338227975
9.47222113391063 P P P LNCV6_127536_PI430048170 mRNA
AATACACTTCCCTCATGCCCTTCTATATAAAACTTAATACCATTAGTTCCCCATTCTTGA NM_001303062 RefSeq chr7
- 44577894 44582295 TMED4 222068 "transmembrane emp24 protein transport domain containing 4, transcript variant 6" GO:0007165|GO:0005789|GO:0016021|GO:0004871|GO:0043123|GO:0015031|GO:0070062
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131690_PI430048170 0.0774403159270289 1.45084705885945 4.16040863221031
3.57323773217498 3.75018395983119 P P P 3.23370686850421 3.47386596982898
3.21509723437618 P P P LNCV6_131690_PI430048170 mRNA
TGAAGGAAGATAGGTAGCCCAGAGAAGAAGTTTTGGACTTAACAACATACCAAGGCAGCT NM_014703 RefSeq
chr3 - 51395866 51500002 VPRBP 9730 "Vpr (HIV-1) binding protein, transcript variant 1"
GO:0005515|GO:0016567|GO:0033151|GO:0005730|GO:0005634|GO:0035212|GO:0000122|GO:0005524|GO:0006351|GO:0005737|GO:0008180|GO:0030183|GO:0016032 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142624_PI430048170 0.0155948830587098 0.541592303138587 2.28488709711087
2.77724859849237 2.78094814573752 A A A 3.24319163217562 3.53878459263861 3.7285224499726
P P P LNCV6_142624_PI430048170 mRNA

GCAGGAGAATTTGCACTGGTTGTGTTAAATGTATAAAAAGCTATATGTTCACCAGTTTAC NM_001013649 RefSeq chr2 - 85605252 85612056 C2orf68 388969 chromosome 2 open reading frame 68 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139084_PI430048170 0.6940721939387 0.9869782604363388.91124975876717 8.98612025260177 8.90657587342709 P P P 8.89092213175622 8.95635461710252 9.01223525197497 P P P LNCV6_139084_PI430048170 mRNA
TCTTATTGAGGCCCTGTACCTTCTGCTGTGTGTGTGTATATATAAAGCACCAGTCTGCTC NM_004651 RefSeq chrX + 47232914 47248328 USP11 8237 ubiquitin specific peptidase 11 GO:0005515|GO:0004197|GO:0016579|GO:0005737|GO:0004843|GO:0061136|GO:0043161|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126222_PI430048170 0.2138071668733880.4607163797347162.47354605276962 0.4852356574120480.450885713056761 A A A 1.49663209850157 2.40350119822961 3.31437863857867 A A P LNCV6_126222_PI430048170 mRNA
GATAATTCTGGTGGCTGTGTGGAGTATGTGTTGGAGATAACTACATAAAGAGACAAAAAA NM_004654 RefSeq chrY + 12701230 12860843 USP9Y 8287 "ubiquitin specific peptidase 9, Y-linked" GO:0004197|GO:0016579|GO:0005737|GO:0004843|GO:0016477|GO:0061136|GO:0070410|GO:0043161|GO:0007179|GO:0030509|GO:0008234|GO:0007283 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98806_PI430048170 0.0580572115417496 1.31194990247318 6.5951706871004 6.77412342098094 6.69753000969482 P P P 6.11052145057579 6.50812882584149 6.25007540281597 P P P LNCV6_98806_PI430048170 mRNA
AAGTCACCTTTCTCTCCAGTGCCACTACTGCGCTTTCGATGCAGAATAATTCAGCATTTG NM_023924 RefSeq chr5 - 863734 892824 BRD9 65980 "bromodomain containing 9, transcript variant 1" GO:0008150|GO:0006355|GO:0070577|GO:0005575|GO:0003676|GO:0006351|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126774_PI430048170 0.00281449377358999 0.8612890926595271 1.701133154848 11.7356538925722 11.6966855502966 P P P 11.8967509215611 11.9130286353796 11.9692926171876 P P P LNCV6_126774_PI430048170 mRNA
GAGGGCAGTTCACCAGCATCCATAGAGTAATAAAGTCACTGTGTGTAGACCCGGAAAAAAA NM_018337 RefSeq chr19 + 56141165 56160893 ZNF444 55311 "zinc finger protein 444, transcript variant 1" GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93253_PI430048170 0.0688043951246273 0.8636265463460226.30664782569461 6.43175490545588 6.41282645363938 P P P 6.62388353794413 6.46455936381103 6.69118233483174 P P P LNCV6_93253_PI430048170 mRNA
GGAGCAGCACCAAATGTTGTCTATACATATACTGGAAAGAGAATTGCATTATATATTGGA NM_001300947 RefSeq chr12 + 69239536 69274358 CPSF6 11052 "cleavage and polyadenylation specific factor 6, 68kDa, transcript variant 2" GO:0005515|GO:0006397|GO:0006378|GO:0051262|GO:0003723|GO:0005634|GO:0003729|GO:0042382|GO:0000166|GO:0016020|GO:0030529|GO:0005654|GO:0005849 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143491_PI430048170 0.0657473735242713 1.17372458690947 12.6342247794958 12.6157824190793 12.5021700442356 P P P 12.2054621102385 12.4023727559852 12.4435265795269 P P P LNCV6_143491_PI430048170 mRNA
GTATATAAACTTGGACAAAGAAACAAAAACCGGCACATGCGGTTACTGTGGGCTCCAGTT NM_004553 RefSeq chr5 + 1801381 1816051 NDUFS6 4726 "NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)" GO:0005743|GO:0009055|GO:0010259|GO:0044281|GO:0022904|GO:0005747|GO:0006936|GO:0035264|GO:0070584|GO:0006120|GO:0006631|GO:0072358|GO:0008137|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136700_PI430048170 0.00547962538865683 0.4590423207589835.51842041750516

5.16550961606441 5.35825136623565 P P P 6.73599749155511 6.21502038186796 6.4348800796364
P P P LNCV6_136700_PI430048170 mRNA
TAACCCATGCAGACCATTGTTTGATCTATGCTAACTTATCAACTTGGCTATTCAATAAAG NM_021982 RefSeq chr5
+ 134648784 134727911 SEC24A 10802 "SEC24 family member A, transcript variant 1"
GO:2000189|GO:0002474|GO:0012507|GO:0048471|GO:0030127|GO:0045714|GO:0050714|GO:0048208|GO:0044
281|GO:0006886|GO:0005829|GO:0006888|GO:0003674|GO:0019886|GO:0000139|GO:0005789|GO:0061024|GO:0
008270|GO:0044267|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130048_PI430048170 0.0452042927035521.43900759750985 8.92832659535143
9.13458932014966 9.16873625041334 P P P 8.35643905817174 8.44310572082514
8.82434600849964 P P P LNCV6_130048_PI430048170 mRNA
AAGAAGGGGTCTTGAGATCCCCTAAACTTGCATACCCAGTTTTTTGGATATTGTAATAAA NM_003581 RefSeq chr2
+ 105745062 105894274 NCK2 8440 "NCK adaptor protein 2, transcript variant 1"
GO:0005515|GO:0060734|GO:0008285|GO:0005783|GO:0030032|GO:0030159|GO:0005829|GO:0005737|GO:0007
172|GO:0007173|GO:0030838|GO:0007411|GO:0033137|GO:0045944|GO:0007176|GO:0042102|GO:0007015|GO:0
008093|GO:0012506|GO:0048010|GO:0048013|GO:0009967|GO:0006417|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143595_PI430048170 0.93469964817861 0.9809093704032851.34319147288912
0.3002130468409470.789497650502695A A A 0.3631959396766890.309430451231013
1.62218523450586 A A A LNCV6_143595_PI430048170 mRNA
ACTATTAGAAACAAGGAGGTGAAGGGAGCCTTAAGAAAGGCAATGACTTGCCCAAAGACT NM_001005188
RefSeq chr11 - 123753579 123754518 OR6X1 NA "olfactory receptor, family 6, subfamily X, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142509_PI430048170 0.0341224655456538 1.55211644120104 8.46007761283191
8.63100403108119 8.46818366695178 P P P 7.58580870873339 7.97849835256917
8.05613478389382 P P P LNCV6_142509_PI430048170 mRNA
GGGATTATGATGACTATGCGGACTTCTATATTGTCTTCATCTCATTGTGTGTATTATGTANM_001166131 RefSeq chr17
+ 50373219 50381459 EME1 146956 "essential meiotic structure-specific endonuclease 1, transcript
variant 1"
GO:0005515|GO:0005737|GO:0005720|GO:0006281|GO:0004519|GO:0090305|GO:0005730|GO:0006310|GO:0005
634|GO:0072429|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135696_PI430048170 0.3602719558745750.689418899069022 9.2130705117987
8.88302206361814 9.02275331252125 P P P 8.75644101350321 9.66984312479285
10.0404514043299 P P P LNCV6_135696_PI430048170 mRNA
CAATACCAAGACCAACTGGCATAGAGCCAACTGAGATAAATGCTATTTAAATAAAGTGTA NM_006461 RefSeq chr17
- 28577564 28599038 SPAG5 10615 sperm associated antigen 5
GO:0005515|GO:0072686|GO:0005815|GO:0051988|GO:0030496|GO:0005634|GO:0035371|GO:0000070|GO:0000
922|GO:0005737|GO:0007059|GO:0000777|GO:0000776|GO:0005654|GO:0007051|GO:0051301 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130460_PI430048170 0.3798988475883161.93748881844166 2.24298514153757 0.4050046375221
0.439924144086613A A A 0.3257195124880780.3355828774661480.391353288804536A A A
LNCV6_130460_PI430048170 mRNA
GGGGTGCATGAAGGTTTCTGAAAATTAACACTGCTTGTGTTTTTAACTCAATATTTTCCA NM_005214 RefSeq chr2
+ 203867787 203873960 CTLA4 1493 "cytotoxic T-lymphocyte-associated protein 4, transcript variant 1"
GO:0050853|GO:0005515|GO:0048471|GO:0005794|GO:0043065|GO:0005886|GO:0031295|GO:0030889|GO:0006
974|GO:0042130|GO:0006955|GO:0045334|GO:0050777|GO:0005887|GO:0045590|GO:0009897 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138918_PI430048170 0.0660737142643961 0.9589780259458690.395507424828457
0.3984676712058 0.341558699415157A A A 0.4345362480312530.453725287765835
0.429155835134056A A A LNCV6_138918_PI430048170 mRNA

AAGTACAGTGACTATTTCAAGCCATTTTCCACAGGAAAACGAGTGTGTGCTGGAGAAGGC NM_000773RefSeq chr10
+ 133527362 133539116 CYP2E1 1571 "cytochrome P450, family 2, subfamily E, polypeptide 1"
GO:0006805|GO:0017144|GO:0045471|GO:0031227|GO:0044281|GO:0043231|GO:0005739|GO:0004497|GO:0005
737|GO:0016712|GO:0008202|GO:0046483|GO:0008392|GO:0005506|GO:0008395|GO:0019373|GO:0010193|GO:0
010243|GO:0016098|GO:0000139|GO:0019825|GO:0042738|GO:0016709|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134433_PI430048170 0.7605952902828730.968342360269235 1.43075503149839
1.05660965385732 1.85377067829393 A A A 1.56792116139285 1.59108934218582
1.42605788648009 A A A LNCV6_134433_PI430048170 mRNA
GCCGTTAAAATATATTTCATAAGAAGTCTCAATCTCAAACTCTCCATCTCTCAATCCTCC NM_152448RefSeq chr15
+ 44956701 44979223 C15orf43 145645 chromosome 15 open reading frame 43 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144669_PI430048170 0.0124360216219779 0.4998653760104758.26503191265213
8.33618986855524 8.61772769629417 P P P 9.15565340697901 9.30080608181554
9.72583330416197 P P P LNCV6_144669_PI430048170 mRNA
CTCTGTACTGAATTTGTACTCTATTGCCATTAGATCTTACAATAATGTTCCACTCTGCAANM_003930RefSeq chr7 -
26667061 26864743 SKAP2 8935 "src kinase associated phosphoprotein 2, transcript variant 1"
GO:0005515|GO:0042113|GO:0007165|GO:0005737|GO:0008285|GO:0006461|GO:0005886|GO:0005070|GO:0009
967|GO:0005654|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141512_PI430048170 0.716189201089372 0.980571891647958 0.406492770103093
0.4646703578643070.380380367151467 A A A 0.5280788349203280.474823305891222
0.327439900636943 A A A LNCV6_141512_PI430048170 mRNA
CTGAAATCACTAACACATATAGGGCTTCCTTTGGTATCAAAGTACTTTACTTGGGTTAAT NM_031886RefSeq chr19
- 49067417 49072941 KCNA7 3743 "potassium channel, voltage gated shaker related subfamily A,
member 7"
GO:0005251|GO:0005886|GO:0008076|GO:0007268|GO:0051260|GO:0034765|GO:0016021|GO:0071805 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141475_PI430048170 0.0025545764086176 0.5943528391870945.36939575472905
5.27013837763582 5.08672192613451 P P P 5.89151271433016 6.1026276200284
5.99030943514994 P P P LNCV6_141475_PI430048170 mRNA
CTCTGAATTGTCACACTTTTCCCTTCCCCACCAGTTCTTTAATAAAAGTATTTGAAAGGC NM_144614RefSeq chr19
+ 7049339 7051735 MBD3L2 125997 methyl-CpG binding domain protein 3-like 2 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138938_PI430048170 0.2470738175288380.303392320081938 0.274858239543771
0.2960926029153020.356850294793823 A A A 0.403953180520792 1.2737236506769 3.0899771900058
A A P LNCV6_138938_PI430048170 mRNA
TTCCAACTTAGTGCATCCCTTTAGAAAGTAAGCAATCAGAAAACAAGCCTCGGCTGTGTG NM_144602RefSeq chr16
+ 49373807 49399431 C16orf78 123970 chromosome 16 open reading frame 78 GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52141_PI430048170 0.4073756146367691.22819494845122 4.44444963476051 4.46276574402311
3.71164504190953 P P P 3.88459466507341 3.98757114786607 3.97414136013344 P P P
LNCV6_52141_PI430048170 mRNA
AGAAGCACAGTCCACAGATATCTCTGCGACTTTACCTACTACACCTCTTTGTACCAGAGT NM_017712RefSeq chr19
+ 18340586 18369953 PGPEP1 54858 "pyroglutamyl-peptidase I, transcript variant 1"
GO:0016920|GO:0006508|GO:0008234|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133001_PI430048170 0.4276319203188141.15859420149698 3.26060991948603
3.59699086192961 3.73074790495332 P P P 3.62805090041488 3.3743837773791
2.89543890174649 P P P LNCV6_133001_PI430048170 mRNA
TCCTTTATCTCTGTGGACTTGTATATATTCTGGAAGGGGAACCACAGTTTCACCATCGCC NM_005453RefSeq chr6

- 33314404 33317735 ZBTB22 9278 "zinc finger and BTB domain containing 22, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140824_PI430048170 0.138219943625118 1.18036850783087 4.84349021926258
5.15563139104249 5.00789910718615 P P P 4.88232211590665 4.82657357005273
4.57962790315217 P P P LNCV6_140824_PI430048170 mRNA
AGAGATGAACCTAAATGAGATAGGAAGCCTGTCCCATAGCAGCCTTCCTCTCACTACTTT NM_014425 RefSeq chr9
+ 100099219 100301144 INVS 27130 "inversin, transcript variant 1"
GO:0005515|GO:0005516|GO:0001822|GO:0005874|GO:0005819|GO:0005634|GO:0009791|GO:0005737|GO:0016
020|GO:0031016|GO:0060971|GO:0016055|GO:0090090 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129094_PI430048170 0.321082276637161 0.838520286506334 3.5157912008213
3.11492647445605 2.76285227123842 P P A 3.52122588972094 3.2939715800009
3.42997276673386 P P P LNCV6_129094_PI430048170 mRNA
ATGTTCTTTCCAACCCCTGCCACATGTTCATGTGTCCTAAGTCTTCCTTGATGATGCATC NM_199254 RefSeq chr13
- 19422878 19536763 TPTE2 93492 "transmembrane phosphoinositide 3-phosphatase and tensin
homolog 2, transcript variant 3"
GO:0034220|GO:0006661|GO:0000139|GO:0016314|GO:0005789|GO:0044281|GO:0016021|GO:0008138|GO:0006
644|GO:0005216|GO:0035335|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131317_PI430048170 0.258463025656494 1.16947657211029 6.10448679294011 5.98517144497
6.34865277218341 P P P 5.71164912544374 6.17593448408227 5.85751096480401 P P P
LNCV6_131317_PI430048170 mRNA
TCATTAAAGGAGCTGTTTCCTGGGTAAATCTAGAGTGGGGTTTTGGTTCTTTATTTTCCC NM_001297590 RefSeq
chr19 + 45406208 45410766 CD3EAP 10849 "CD3e molecule, epsilon associated protein, transcript
variant 1"
GO:0010467|GO:0003899|GO:0005694|GO:0009303|GO:0006363|GO:0005730|GO:0006362|GO:0000120|GO:0006
361|GO:0005634|GO:0006360|GO:0005739|GO:0005737|GO:0005736|GO:0045814|GO:0040029|GO:0005654|GO:0
007169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133580_PI430048170 0.0975664572702404 0.302003636352566 0.369798304898986
1.12633944632985 2.77088685836771 A A A 3.51953062430628 3.37144139782804
3.61942410369454 P P P LNCV6_133580_PI430048170 mRNA
CTGTTTATCACTCCAGTGATTTTGAGTTTGCAGTTTCACAATCAGTTCTTCATTTCATGA NM_031442 RefSeq chrX -
34627063 34657288 TMEM47 83604 transmembrane protein 47
GO:0008150|GO:0003674|GO:0005886|GO:0005911|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143699_PI430048170 0.508400319800552 1.00797674614984 0.374885350241599
0.372226668862746 0.397258814484939 A A A 0.378748723646708 0.34359698535602
0.387397284220232 A A A LNCV6_143699_PI430048170 mRNA
CACAAATTCTGTTGCCTGGTGGAAAGAAGGCAAAGGCCTTCAGCAATCTATATTACCAGC NM_032782 RefSeq chr5
- 157085831 157109237 HAVCR2 84868 hepatitis A virus cellular receptor 2 GO:0016021|GO:0070062
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131252_PI430048170 0.0125117829987779 0.944945775356626 0.363273515579186
0.35048054755665 0.326815755282146 A A A 0.453256979451429 0.428809972163506
0.403398622566909 A A A LNCV6_131252_PI430048170 mRNA
CTGAGATCAAGTTTAGTAGGCAGGACTTGATCTCAAGTGGTCACAAAGTTTTCTAAAAAA NM_145315 RefSeq chr6
+ 108294893 108523048 LACE1 246269 lactation elevated 1 GO:0005739|GO:0005524 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141065_PI430048170 0.0417112841445888 1.04709058975253 0.424842563163776
0.448391514115499 0.396371054215521 A A A 0.325635324285858 0.362543389279568
0.382167732826891 A A A LNCV6_141065_PI430048170 mRNA

GCTGCACATGCATCAACAAATTACAACATGTTTTGTACACGAATAAACCCATTACAAGAA NM_001286099 RefSeq chr6 + 109978255 109980721 GPR6 2830 "G protein-coupled receptor 6, transcript variant 1" GO:0007186|GO:0005887|GO:0004930|GO:0003376|GO:0038036|GO:0007204 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138912_PI430048170 0.437228350980215 1.21825632499347 2.36393956200988 1.9055733588931 1.56095913236004 A A A 1.4348673115951 1.38802821820464 2.13815368294804 A A A LNCV6_138912_PI430048170 mRNA
TGTGATGGCATTTGCAGAAGCTCAGTAAAACACTATATACTGAATAACACCAAAATAAGC NM_017750 RefSeq chr2 - 85341954 85354698 RETSAT 54884 "retinol saturase (all-trans-retinol 13,14-reductase)" GO:0005640|GO:0031965|GO:0016020|GO:0042572|GO:0016491|GO:0005789|GO:0055114|GO:0051786 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145612_PI430048170 0.271588634642582 0.758184552311472 0.256427909298651 0.275151627708458 0.356965067273984 A A A 0.385525649115181 0.446921921957792 1.13179655645458 A A A LNCV6_145612_PI430048170 mRNA
TACCCAGTCCTTTCAAGGGGCCTCTTTTCTACTAATAAAGATGGATCAAGTCTCAAAAAA NM_012125 RefSeq chr15 + 33968887 34065086 CHRM5 1133 "cholinergic receptor, muscarinic 5" GO:0030054|GO:0005886|GO:0008283|GO:0015872|GO:0007197|GO:0019226|GO:0001696|GO:0007213|GO:0060304|GO:0016907|GO:0004435|GO:0005887|GO:0045211|GO:0008152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128319_PI430048170 0.796853308767201 0.979512435196114 1.76704051580135 1.32522377127475 2.05340772480068 A A A 1.09756439143681 0.888398811520767 2.6506467801601 A A P LNCV6_128319_PI430048170 mRNA
GCAAATCTCACTGGATATTTTTAAAGGTCTCCACAGAGTTTATGCCATATTGGAATTTTG NM_000204 RefSeq chr4 - 109740691 109802179 CFI 3426 complement factor I GO:0030449|GO:0004252|GO:0005576|GO:0005634|GO:0005615|GO:0006898|GO:0046872|GO:0016020|GO:0045087|GO:0006958|GO:0006508|GO:0005044|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129076_PI430048170 0.488983597219274 1.01274132157049 0.309828774947623 0.337508291937148 0.380595366927505 A A A 0.339830586334782 0.327525938070607 0.306464599538282 A A A LNCV6_129076_PI430048170 mRNA
GTTGGGCAATATGAAATTTTTAAAGGAGTAGAATACCAAATGATAGAAACAGACTGCCTG NM_000239 RefSeq chr12 + 69348353 69354233 LYZ 4069 lysozyme GO:0006954|GO:0001895|GO:0019835|GO:0008152|GO:0003796|GO:0005576|GO:0005615|GO:0042742|GO:0070062|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135421_PI430048170 0.138745139344986 0.979446972470599 0.317667918949996 0.354297576486018 0.35480067104561 A A A 0.387351878677283 0.377266484176401 0.352115457933485 A A A LNCV6_135421_PI430048170 mRNA
TTGGACCTGGTTTTGTTTTCCTGCAGCTGTTGACTTGTTGCCCTGAAGTACAATAAAAAA NM_001025199 RefSeq chr1 + 111229710 111243440 CHI3L2 1117 "chitinase 3-like 2, transcript variant 3" GO:0008061|GO:0006032|GO:0006955|GO:0005975|GO:0030246|GO:0005615|GO:0004568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118513_PI430048170 0.203550313392917 1.09194949199383 11.6519739406036 11.6757724220096 11.55170113303 P P P 11.358721520948 11.5414311882032 11.5913097757117 P P P LNCV6_118513_PI430048170 mRNA
TTCAATGAGTACTGGAGATTGATTGGGGAGCTGGCCAAGGAAATCAGGAAGAAGAAAGAC NM_001024210 RefSeq chr1 - 153618799 153634092 S100A13 6284 "S100 calcium binding protein A13, transcript variant 1" GO:0005515|GO:0050663|GO:0048471|GO:0043303|GO:0008284|GO:0005507|GO:0017134|GO:0008360|GO:0050703|GO:0005509|GO:0005634|GO:0005615|GO:0042803|GO:0042629|GO:0005829|GO:0008289|GO:0005737|GO:0050786|GO:0051602|GO:0008270|GO:0046688|GO:0043123|GO:0070062 . NA - . NA NA NA NA NA

NA NA NA NA
LNCV6_108683_PI430048170 0.172324908999895 1.03344502143373 0.33967423748752
0.350880047954417 0.27678305212988 A A A 0.270410292653743 0.286020378647867
0.269562416671893 A A A LNCV6_108683_PI430048170 mRNA
GAGAAATGTACATTACCATTGACTGGAAAGCAATGTGTCAACCGCATTATTACTGAAAAG NM_000436 RefSeq chr5
- 41730064 41870689 OXCT1 5019 3-oxoacid CoA transferase 1
GO:0014823|GO:0007584|GO:0035774|GO:0045471|GO:0042493|GO:0044281|GO:0042803|GO:0005739|GO:0007
507|GO:0042594|GO:0046952|GO:0007420|GO:0005759|GO:0046950|GO:0008260|GO:0009725|GO:0060612|GO:0
044255|GO:0042182. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142492_PI430048170 0.980797960725731 0.90151053477935 1.15804430015775
3.16042111068763 2.51480554223027 A P A 2.87435435351879 3.27985289323302
0.754722918674975 P P A LNCV6_142492_PI430048170 mRNA
CTCCTCGGCCACTTTCAGTGCGTCGGTTCGTTTTGATTCTTTTTCTTTTGTGCACATAAG NM_003988 RefSeq chr10 +
100745710 100829941 PAX2 5076 "paired box 2, transcript variant c"
GO:0005515|GO:0000987|GO:0001658|GO:0021554|GO:0070301|GO:0006366|GO:0044212|GO:0071300|GO:0034
451|GO:0048793|GO:0000982|GO:0001655|GO:0007409|GO:0005764|GO:0021650|GO:0072075|GO:0043069|GO:0
032993|GO:0072177|GO:0031667|GO:0050679|GO:0003406|GO:0035799|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145525_PI430048170 0.281919908538394 1.03962453516772 0.321812424580052
0.278840036671998 0.408137566792596 A A A 0.288128480503578 0.262870690732781
0.292445886061757 A A A LNCV6_145525_PI430048170 mRNA
GCCTTGCCTAAGACTGTTTCCTTTGTTCTAAAATAGGACTTAAATAAAATGAGCTCTGTA NM_144647 RefSeq chr5
- 35904295 35938779 CAPSL 133690 "calcyphosine-like, transcript variant 1" GO:0005737|GO:0005509
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129397_PI430048170 0.977054167312256 0.984475404755228 4.49707410186285
4.00961530848985 4.33872901496962 P P P 4.72878671881745 4.24895121053852 3.8402228485968
P P P LNCV6_129397_PI430048170 mRNA
TATAAGTTGGTTTCCAGCCCCCAGTGTCCTGACTTCTGTCTGCCACATGAGGAGGGAGGC NM_006907 RefSeq chr17
- 81932385 81937257 PYCR1 5831 "pyrroline-5-carboxylate reductase 1, transcript variant 1"
GO:0005515|GO:0055129|GO:0051881|GO:0008652|GO:0044281|GO:0042802|GO:0005739|GO:0034641|GO:0005
759|GO:0006561|GO:0034599|GO:0004735|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90652_PI430048170 0.345546613136666 1.08335183677965 10.5342497005379 10.3458391358538
10.6347186481907 P P P 10.3033508812441 10.3616603593731 10.5100929295179 P P P
LNCV6_90652_PI430048170 mRNA
GCACTTCTGTCTAGAAAATAATAATTGCAAGTTGTATAACTCAGGCGTCTTTGCATTTCT NM_001130089 RefSeq
chr16 - 75627723 75647687 KARS 3735 "lysyl-tRNA synthetase, transcript variant 1"
GO:0005515|GO:0010467|GO:0000049|GO:0005886|GO:0015966|GO:0005576|GO:0005634|GO:0004824|GO:0005
524|GO:0046872|GO:0017101|GO:0008033|GO:0005829|GO:0006418|GO:0005739|GO:0005737|GO:0005759|GO:0
006430|GO:0015630|GO:0016032|GO:0016597 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140749_PI430048170 0.018314824204457 1.4686076934195 8.09585551771284
8.36207648972764 8.02916656015505 P P P 7.81073624467266 7.52541718711399
7.48739496676453 P P P LNCV6_140749_PI430048170 mRNA
CACTGCCTCTATAGGGTAACCTGGAACATTCTCTAGGTTATATCAATATAAAACAATGTA NM_001267571 RefSeq
chr9 - 98198997 98255721 TBC1D25 5357 "TBC1 domain family, member 2, transcript variant 1"
GO:0005515|GO:0045296|GO:0030054|GO:0032851|GO:0016023|GO:0031410|GO:0005097 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131924_PI430048170 0.0937124480043634 0.628212045291269 5.1816840713408
4.8073834321779 5.46737328737251 P P P 5.38133286910932 5.89179042565533
6.16422828151282 P P P LNCV6_131924_PI430048170 mRNA

CAGGCAGAAATATTTAGTATCTAGTCAGTATCTGTAGCTACACTGTATAACTGTTCTTCA NM_004329RefSeq chr10 + 86756638 86925188 BMPR1A 657 "bone morphogenetic protein receptor, type IA" GO:0005515|GO:0035137|GO:0006366|GO:0051216|GO:0000981|GO:0001756|GO:0046332|GO:0042803|GO:0060914|GO:0048589|GO:0014032|GO:0004702|GO:0043025|GO:0048352|GO:0007179|GO:0023014|GO:0050679|GO:0001707|GO:0030501|GO:0003272|GO:0030509|GO:0060391|GO:0001701|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131127_PI430048170 0.0138850300808619 0.8199612890495528.19825856362507 8.10905090955496 8.18796176964721 P P P 8.35220420687242 8.51615635669098 8.48252174173221 P P P LNCV6_131127_PI430048170 mRNA
AGCCACGAACCAGACAAGCAGACAATCAGCGGACAATCGGTTCTGGACTCACCCCTCATC NM_017721RefSeq chr19 + 13906142 13930880 CC2D1A 54862 coiled-coil and C2 domain containing 1A GO:0007165|GO:0001078|GO:0005737|GO:0016020|GO:0005815|GO:0005634|GO:0004871|GO:0000122|GO:0043123|GO:0000978|GO:0006351|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139081_PI430048170 0.2689182622874140.84611084972297 9.0346967279432 8.93047745166858 9.30251696159328 P P P 9.03677071891756 9.45773535268834 9.48060206974249 P P P LNCV6_139081_PI430048170 mRNA
AGGTAGAAACGCCCTCCGTGTGTGCATATTTGTTGGTTCTCTGATTAAAGTTTTGAGTCT NM_015428RefSeq chr19 + 50025805 50048774 ZNF473 25888 "zinc finger protein 473, transcript variant 1" GO:0005515|GO:0010467|GO:0006369|GO:0006355|GO:0015030|GO:0006398|GO:0008334|GO:0006366|GO:0031124|GO:0005654|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136207_PI430048170 0.00777386786279037 0.4810192540344327.59335314844191 7.4647333327378 7.97849835256917 P P P 8.46725502226711 8.76754782131158 8.97534912285198 P P P LNCV6_136207_PI430048170 mRNA
GCCTGTCTGTGGCATTCTCTAGATGTTTCTTTTTTACACAATAAATTCCTTATATCAGCT NM_012319RefSeq chr18 - 36108530 36129394 SLC39A6 25800 "solute carrier family 39 (zinc transporter), member 6, transcript variant 1" GO:0071577|GO:0071578|GO:0031258|GO:0009986|GO:0005886|GO:0005385|GO:0005887|GO:0005783|GO:0006882|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132068_PI430048170 0.4179644190776361.5232811823633 1.68017107642034 0.3401314470140510.316630614920423A A A 0.3292355048918120.33180880558226 0.307376490081204A A A LNCV6_132068_PI430048170 mRNA
GGTTAAAATATGTGGGGAGTTGTGCCTATATAAATTCTTATGTGTGATGATTACTGCTAG NM_001195576 RefSeq chrX + 111876050 111903985 TRPC5OS 100329135 "TRPC5 opposite strand, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140349_PI430048170 0.8715666765668780.993062433536748 7.03871674181946 6.99728930227048 6.94911151693158 P P P 6.30816747424542 7.42315415734549 7.0726330268962 P P P LNCV6_140349_PI430048170 mRNA
TGACGTGGAACTACACACGAAGTGTAATTAGTGGGGGAAAAAATATTTTTTAAACAAAGG NM_080626RefSeq chr12 + 124993647 125025803 BRI3BP 140707 BRI3 binding protein GO:0005739|GO:0005741|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134082_PI430048170 0.3374687914955231.10602639688999 0.487510531266742 0.8245889220699550.502349783202759A A A 0.4831708532298740.509351107675995 0.40967080314357 A A A LNCV6_134082_PI430048170 mRNA
CTGTTCTTTTTTGTCTATTGGGTTATATAGGAATTCACAACGAAATCAGATGGCTCCTAA NM_001100917 RefSeq chr12 - 85014314 85036277 TSPAN19 144448 tetraspanin 19 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126971_PI430048170 0.0222854888785754 1.40323963614688 6.74095887502165 6.56342075450032 6.71257759991728 P P P 6.11099596815368 6.37808742242524 6.04594538447146 P P P LNCV6_126971_PI430048170 mRNA

ACTTTGAGGTCCGGCATGGCAATGAGGACACCATCAAGGAAATGCTGCGTATCCGGCGCANM_020196RefSeq chr19 - 7619524 7629553 XAB2 56949 XPA binding protein 2
GO:0005515|GO:0006281|GO:0016020|GO:0006283|GO:0000398|GO:0001824|GO:0005654|GO:0005634|GO:0006289|GO:0071013|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132678_PI430048170 0.235887158800393 1.23329439038092 4.36925777681974 4.06765950938426 4.09714864446857 P P P 3.55278714138268 4.21813844940549 3.79534062769592 P P P LNCV6_132678_PI430048170 mRNA
TGGAGCCACCCTACCTCAGGGCCTCTTGATATTTGAGGTAATAAATTCATTGTTCTGTAT NM_031900RefSeq chr5 - 34998100 35048135 AGXT2 64902 alanine--glyoxylate aminotransferase 2
GO:0016223|GO:0055086|GO:0044281|GO:0008453|GO:0019265|GO:0045429|GO:0005739|GO:0034641|GO:0046135|GO:0005759|GO:0019481|GO:0030170|GO:0047305|GO:0046487|GO:0009436|GO:0006206 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91537_PI430048170 0.0203402998763182 0.582320839515886 7.84434443088137 7.30001371792959 7.45465874006157 P P P 8.11947039625167 8.40982438673285 8.44424775744895 P P P LNCV6_91537_PI430048170 mRNA
AGCTTAAACAACTGTGAAGGTGCTGCTGGCAGCACATCTGAAAAATCAAGAAATGTGCCT NM_001102420 RefSeq chr9 - 72351424 72365247 ZFAND5 7763 "zinc finger, AN1-type domain 5, transcript variant a"
GO:0005515|GO:0048705|GO:0005575|GO:0001701|GO:0003677|GO:0003674|GO:0008150|GO:0010761|GO:0003016|GO:0005737|GO:0048745|GO:0060324|GO:0008270|GO:0048008|GO:0001944 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61908_PI430048170 0.768739755685447 1.0452772267454 6.49092760455432 6.5458269078565 6.94436655362297 P P P 6.35019179125939 6.68611643437394 6.76418311170635 P P P LNCV6_61908_PI430048170 mRNA
TTGGATAATAAGTGTTCTGTGTACCCCTTGACGTTTGACAAAAATGAAAACATGGCTGCC NM_016194RefSeq chr15 - 52120925 52191368 GNB5 10681 "guanine nucleotide binding protein (G protein), beta 5, transcript variant 2"
GO:0005515|GO:0007165|GO:0007603|GO:0005886|GO:0008152|GO:0051087|GO:0003924|GO:0022400|GO:0005634|GO:0004871|GO:0031682|GO:0016056 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143674_PI430048170 0.000619896179606343 1.19819504173228 0.859750809002817 0.896479178931592 0.895208506974188 A A A 0.65929453533256 0.606128228145993 0.603031639217953 A A A LNCV6_143674_PI430048170 mRNA
ACACACAGAAAATCTGAAAGAATCATACAATAAACATCAGTATATTCTCCACCTAAAAAA NM_133480RefSeq chr3 - 9783127 9793011 TADA3 10474 "transcriptional adaptor 3, transcript variant 2"
GO:0005515|GO:0072686|GO:0003700|GO:0006325|GO:0005634|GO:0005622|GO:0030374|GO:0031647|GO:0004402|GO:0016922|GO:0006357|GO:0030914|GO:0003713|GO:0019904|GO:0006351|GO:0033276|GO:0010628|GO:0007067|GO:0043966|GO:0031063|GO:0005671|GO:0005654|GO:0001932|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136777_PI430048170 0.146225307688606 1.32696832335118 3.54300562201627 3.22403144777114 3.30493480774072 P P P 2.58860774977939 2.93599784498508 3.26382023515232 P P P LNCV6_136777_PI430048170 mRNA
CAAACTAAAGACATCAGTTCATTGGTCAAATATTTGTTACCTGGAATGGAACTTGAAAGC NM_017662RefSeq chr9 - 74722494 74888094 TRPM6 140803 "transient receptor potential cation channel, subfamily M, member 6, transcript variant a"
GO:0005515|GO:0005262|GO:0005886|GO:0009636|GO:0031526|GO:0005524|GO:0055085|GO:0046872|GO:0016324|GO:0034220|GO:0004674|GO:0070588|GO:0006468|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132911_PI430048170 0.0488968823276802 0.748318404418228 8.64418190152238 8.84312093695337 8.72000438780274 P P P 9.37352692323259 9.05129029701222 9.01687689298165 P P P LNCV6_132911_PI430048170 mRNA

TGCTAACTGGATAAAGTTTGTGCAGCACATTCCTGAGTGTACGATATTGACCTGTAGCCC NM_001004354 RefSeq
chr9 - 137299630 137302251 NRARP NA NOTCH-regulated ankyrin repeat proteinNA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134786_PI430048170 0.0159643483564923 0.5361539751326635.29630425820428
5.18073089359283 5.44090337672223 P P P 5.88059202782276 6.34028455673446
6.35790266591523 P P P LNCV6_134786_PI430048170 mRNA
CCCCCTGTGCATAGTACGACCTTTACTGTCGTATTTTTGAAAAATTAAAAATACAGTGTT NM_001004439 RefSeq
chr15 - 68301703 68432153 ITGA11 22801 "integrin, alpha 11"
GO:0008305|GO:0038065|GO:0033627|GO:0005886|GO:0006929|GO:0005518|GO:0038064|GO:0046872|GO:0001
649|GO:0007517|GO:0007160|GO:0016020|GO:0034681|GO:0007229|GO:0030198|GO:0007155|GO:0005925 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129852_PI430048170 0.3886325661191881.11829082115884 9.60012418029114
9.55675555100428 9.48060206974249 P P P 9.69475450853372 9.20519902823465
9.19804401881929 P P P LNCV6_129852_PI430048170 mRNA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGA NM_016361 RefSeq chr1
- 147647365 147670512 ACP6 51205 "acid phosphatase 6, lysophosphatidic"
GO:0005739|GO:0005737|GO:0052642|GO:0016311|GO:0003993|GO:2001311|GO:0006644 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128171_PI430048170 0.2843961504203390.6099745750783221.65988597949069
0.4290185000429310.306964845250515A A A 2.0381289733748 1.87693238291681
0.709853632820577A A A LNCV6_128171_PI430048170 mRNA
CACAGCTTGTCCCCATCGTTCACCTTTAGAATTAAATATAAATTAACTCCTCACATTGAA NM_001001317 RefSeq
chr7 - 142252137 142258058 PRSS58 136541 "protease, serine, 58"
GO:0004252|GO:0006508|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131809_PI430048170 0.4459386172809091.0170894813921 0.354905360060543
0.3534474347645920.425402011196217A A A 0.3597537295659010.325125044034356
0.376244163745548A A A LNCV6_131809_PI430048170 mRNA
CTCATATTCATACTTGCTTGCTCAACCACTTATGCATCTATATTTAGCTAACATGAGTGA NM_001134734 RefSeq
chr1 + 34176951 34219130 C1orf94 84970 "chromosome 1 open reading frame 94, transcript variant
1" GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140693_PI430048170 0.7630749446207441.0472422322272 4.3881421125425 4.6024937991005
4.88750829298045 P P P 4.88767643711621 4.26531374060763 4.49972823488935 P P P
LNCV6_140693_PI430048170 mRNA
TTTCAGAGCCAGATCATTTCTTGGAAAGTGTAGGCTTACCTCAAATAAATGGCTAACTTA NM_000600 RefSeq chr7
+ 22727146 22732002 IL6 3569 interleukin 6
GO:0005515|GO:0032755|GO:0033160|GO:0009408|GO:0045599|GO:0008360|GO:0010996|GO:0009409|GO:0019
221|GO:0005615|GO:0031175|GO:0045079|GO:0031667|GO:0032868|GO:0045740|GO:0007568|GO:0030168|GO:0
042832|GO:0005896|GO:0006953|GO:0032722|GO:0005125|GO:0032966|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142832_PI430048170 0.0681210360234371 3.16369968191383 4.11694094881868
4.03275634444988 4.02524146113184 P P P 3.04097928773975 1.30530372218869
2.35125224848564 P A A LNCV6_142832_PI430048170 mRNA
TTTGCCGGCCTATGTGCTTTAACCTTAAGCTGATACTTTCCTTTAGGTGTCACTCTTGTT NM_001012979 RefSeq chrX
- 103273689 103276869 TCEAL5 340543 transcription elongation factor A (SII)-like 5
GO:0005515|GO:0006355|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140118_PI430048170 0.1219828386900250.6582731933697415.1840758055482
5.29381592330997 5.6224529842461 P P P 5.46741959073787 6.14287571107541
6.22401859400059 P P P LNCV6_140118_PI430048170 mRNA
GTAATCTACCCTCAGAGCCATGTATTTGAGAATGCTTCAATCATATTTTCCTATGTACTT NM_017785 RefSeq chr5

+ 169583633 169604777 SPDL1 54908 spindle apparatus coiled-coil protein 1
GO:0005515|GO:0031577|GO:0005815|GO:0034501|GO:0000132|GO:0005634|GO:0005829|GO:0000922|GO:0000
940|GO:0043515|GO:0007080|GO:0000278|GO:0019899|GO:0051301 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_131863_PI430048170 0.0193389412972890.5661124524598895.8868747334497
6.24356766329244 6.24168042598223 P P P 6.93963384568314 6.95338759280696
6.96985618543119 P P P LNCV6_131863_PI430048170 mRNA
CTTTGTGTTTAATATATCTGGGTGATGGATCACAACACATCAATAAACTGACTTACCCTA NM_001032410 RefSeq
chr21 + 29024616 29054486 USP16 10600 "ubiquitin specific peptidase 16, transcript variant 3"
GO:0043130|GO:0016578|GO:0004843|GO:0006357|GO:0003713|GO:0005634|GO:0006351|GO:0006974|GO:0004
197|GO:0042393|GO:0005737|GO:0007049|GO:0007067|GO:0061136|GO:0051289|GO:0035522|GO:0045944|GO:0
070537|GO:0043161|GO:0008270|GO:0045893|GO:0045901|GO:0051301 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_130858_PI430048170 0.2036483897702164.24534054623833 0.267725548177356
3.24000341668039 2.39673277152247 A P A 0.3470399370696580.29652485392921
0.321216324434131 A A A LNCV6_130858_PI430048170 mRNA
GAGTTGAAAATGCAACCAACTCTTGGCGAACTGTACAAACAAATCTTTGCTATACTTTAT NM_004262 RefSeq chr4
- 67820875 67883998 TMPRSS11D9407 "transmembrane protease, serine 11D"
GO:0007585|GO:0004252|GO:0005887|GO:0006508|GO:0008233|GO:0005576|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127382_PI430048170 0.4980309857427980.8418798906380054.70257859190525
3.67564583816229 3.74627961917649 P P P 4.73962878414512 4.25215183620993
4.02468358751968 P P P LNCV6_127382_PI430048170 mRNA
CACCCTCTCCATGCCCAACCTAAGATTGTGTGGGTTTTTTAATTAAAAATGTTAAAAGTT NM_000162 RefSeq chr7
- 44144270 44189423 GCK 2645 "glucokinase (hexokinase 4), transcript variant 1"
GO:0005515|GO:0032811|GO:0043266|GO:0006096|GO:0008645|GO:0015758|GO:0044320|GO:0032024|GO:0019
158|GO:0045821|GO:0051156|GO:0032869|GO:0000287|GO:0005975|GO:0019903|GO:0005978|GO:0006739|GO:0
070509|GO:0051594|GO:0043531|GO:0046835|GO:0005654|GO:0045180|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_111203_PI430048170 0.5116373018124760.8622070160319860.319452692997724
2.09013579907595 0.360718983263879 A A A 1.55962738835329 1.25695618914464
1.34325146263827 A A A LNCV6_111203_PI430048170 mRNA
TGTATCAAATTCAGCTCAGTCATAGCAAAGAAGAATGAAAGATGGCATTCAGATGGAATC NM_152544 RefSeq chr4
+ 8440804 8476555 TRMT44152992 tRNA methyltransferase 44 homolog (S. cerevisiae)
GO:0005737|GO:0008168|GO:0032259|GO:0046872|GO:0008033 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140656_PI430048170 0.6949693760835531.4035412037427 0.302604042205771
0.2857795883904542.0924778616806 A A A 0.2962839113312521.22930079067863
0.279067066492963 A A A LNCV6_140656_PI430048170 mRNA
AGCAGAATTGGGAGGGACTTTGTGGAGACAGGGCTGGACTTGAAAGGAAGAAGAAGTCTA NM_016346 RefSeq
chr15 + 71810547 71814929 NR2E3 10002 "nuclear receptor subfamily 2, group E, member 3,
transcript variant 1"
GO:0005515|GO:0010467|GO:0005667|GO:0008285|GO:0006367|GO:0060041|GO:0006366|GO:0003707|GO:0005
634|GO:0000122|GO:0045872|GO:0043565|GO:0007165|GO:0045944|GO:0043401|GO:0005654|GO:0008270|GO:0
004879|GO:0007602|GO:0042462|GO:0030522|GO:0007601 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_136915_PI430048170 0.1714435827346111.3208077303978 6.41757145726614
6.40684281133159 6.30044021006536 P P P 5.53416232228353 6.19971798038628
6.10420021243612 P P P LNCV6_136915_PI430048170 mRNA

GAGTAGACCACCAGTATGCTTAAATATGTGATACTTGTTAATGTAATACACCATTCAGGA NM_152485 RefSeq chr1 - 209779207 209784730 C1orf74 148304 chromosome 1 open reading frame 74 NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_140416_PI430048170 0.00418090515198744 0.29753724814885 5.63021552082887 4.99314302671495 5.38937877651541 P P P 6.65603739906682 7.17328287069922 7.40252180756696 P P P LNCV6_140416_PI430048170 mRNA
GCATCATGTGGAAGAATGGGAACTATGCTTACTTTATGAAGTGATGTATAACACAATGAA NM_006449 RefSeq chr2 - 37641881 37672199 CDC42EP3 10602 "CDC42 effector protein (Rho GTPase binding) 3, transcript variant 1" GO:0005519|GO:0005886|GO:0008360|GO:0007266|GO:0015629|GO:0005100|GO:0012505|GO:0007165|GO:0005737|GO:0030838|GO:0032321|GO:0031274|GO:0017049 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_109851_PI430048170 0.0811913967546937 0.864850895643013 6.02206400125485 5.89277346751486 5.96797036879442 P P P 6.1613283953245 6.0481934189592 6.29411158067472 P P P LNCV6_109851_PI430048170 mRNA
GAATGGTGGCTACAACCAACTCTGTGATATCTGGGCAGTAGGAATAACAGCAATTGAACT NM_198794 RefSeq chr14 - 50418492 50532658 MAP4K5 11183 "mitogen-activated protein kinase kinase kinase kinase 5, transcript variant 2" GO:0035556|GO:0005515|GO:0005737|GO:0005083|GO:0004672|GO:0005886|GO:0004702|GO:0004674|GO:0006468|GO:0007257|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_141559_PI430048170 0.0831622483647429 0.63840284253516 4.19145539732906 3.91752213980598 4.56389658008589 P P P 4.58632400264766 4.74347385736972 5.2678426939254 P P P LNCV6_141559_PI430048170 mRNA
TGAGGCTGTGAAAGCTGTCCACATTTTTGCTGTGTATTAAATAGCTGTGGGTCATCAAAA NM_007204 RefSeq chr1 + 111755567 111767577 DDX20 11218 DEAD (Asp-Glu-Ala-Asp) box polypeptide 20 GO:0000244|GO:0005515|GO:0010467|GO:0006396|GO:0043065|GO:0048477|GO:0019904|GO:0050810|GO:0005634|GO:0034660|GO:0000122|GO:0000387|GO:0003677|GO:0005524|GO:0005829|GO:0004004|GO:0005737|GO:0016020|GO:0032797|GO:0017053|GO:0005654|GO:0005856|GO:0034719 . NA - . NA NA NA NA NA NA NA NA NA NA LNCV6_127180_PI430048170 0.447147442265034 0.582065869160745 0.410159987434883 0.387070957557685 0.408037721345599 A A A 2.08059274629225 0.33643014486166 0.397080612265433 A A A LNCV6_127180_PI430048170 mRNA
CAATATTTTACACCATTGTGATTCCCTTGCTGAATCCCGTCATCTACAGTTTGAGGAACA NM_001004746 RefSeq chr11_JH159136v1_alt - 42854 43934 OR5T2 219464 "olfactory receptor, family 5, subfamily T, member 2" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA NA LNCV6_126864_PI430048170 0.918165208785455 1.07285469317453 0.439756453261549 1.2046620132432 2.47426474414415 A A A 1.97169553281428 1.51450457104954 0.858203849424207 A A A LNCV6_126864_PI430048170 mRNA
ATGTGAACTGCCAGACACCTTCCATTTCCCTTTCTATCTGTTTTTCTTGCTAGTTCCTGT NM_032599 RefSeq chr7 + 128715341 128731743 FAM71F1 84691 "family with sequence similarity 71, member F1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_133807_PI430048170 0.385332088483054 0.689019251286946 2.39371762286509 0.357462540676628 0.264718510341606 A A A 2.21623755205382 1.02067701983031 2.18723112260877 A A A LNCV6_133807_PI430048170 mRNA
AAGGAAAACACCCTTTCCAAAGCAAATTCCCCTCCAGCAAATAAAGCATGAAATATACAG NM_002418 RefSeq chr6 - 33794671 33804016 MLN 4295 "motilin, transcript variant 1" GO:0007186|GO:0005179|GO:0007267|GO:0005102|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_141302_PI430048170 0.00783152293293915 0.675659813705037 6.62142363435364 6.42136576604156 6.3911734617869 P P P 7.0783824744793 6.98647832771287 7.07513913791474 P P P LNCV6_141302_PI430048170 mRNA CAGCATATCCAAATATGTCAGCAATTTCAATAAACATGACTGTACTCAACAAACCAAGTG NM_181846 RefSeq chr19 + 58327018 58342346 ZSCAN22 342945 zinc finger and SCAN domain containing 22 GO:0008150|GO:0003674|GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131511_PI430048170 0.0623565166611273 0.67450388523868 7.5417440368004 7.38216099305986 7.27684495231386 P P P 7.62510948271685 8.06389962171201 8.17232390758687 P P P LNCV6_131511_PI430048170 mRNA GGGTATGGGCAAGAAATGACTGTAAATATTTCAGCCCCACATTATTTATAGAAAATGTAC NM_003682 RefSeq chr11 + 47269647 47330031 MADD 8567 "MAP-kinase activating death domain, transcript variant 4" GO:2001236|GO:0005515|GO:0017112|GO:0005886|GO:2001234|GO:0097194|GO:0032851|GO:0042981|GO:0005123|GO:0030295|GO:0000187|GO:0005737|GO:0032483|GO:0051726|GO:0016021|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52322_PI430048170 0.00982121219710374 1.74067211259722 1.42043479207177 1.16297404978257 1.13850224429866 A A A 0.413015227520846 0.483170853229874 0.443166703854979 A A A LNCV6_52322_PI430048170 mRNA AGGGAGGCTCTTTAGTAACCTAAAGGACAACTTGAAAGACACCCTCAAAGACACATCTTC NM_001256864 RefSeq chr1 + 65309534 65415869 DNAJC6 9829 "DnaJ (Hsp40) homolog, subfamily C, member 6, transcript variant 1" GO:0072318|GO:0017124|GO:2000369|GO:0006892|GO:0061024|GO:0045202|GO:0035335|GO:0004725|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140128_PI430048170 0.0911688057573459 1.89148391924699 2.96456417989337 2.25258066571369 3.27854421608906 A A P 1.97389482768345 2.14221115229296 1.77981301512588 A A A LNCV6_140128_PI430048170 mRNA ATTGGCCCAAGGGTGAGAACCAGTAGCATCTGCTGTCCATCAAGGCCCTGTGCTGCAACA NM_006678 RefSeq chr17 - 74541065 74546171 CD300C 10871 CD300c molecule GO:0007165|GO:0006968|GO:0005887|GO:0004888|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140123_PI430048170 0.5321705361698720.5665198104048990.419413403048408 1.51552449682204 1.35620570577459 A A A 0.5336347752163432.94726405354015 1.46777064363505 A P A LNCV6_140123_PI430048170 mRNA TGCTGTGTGGTGTGTTTCTTTCCCCACTGACAGTGAATAAAAGGTGCAACTGTGAAAAAA NM_016257 RefSeq chr1 - 39678647 39691710 HPCAL4 51440 "hippocalcin like 4, transcript variant 1" GO:0005622|GO:0007165|GO:0005246|GO:0019904|GO:0005509|GO:0008022|GO:0007417 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103360_PI430048170 0.0799549261340614 0.8374609871200897.77654752228584 7.47710064153665 7.57610323097395 P P P 7.82441634218684 7.98415116279779 7.79808789540025 P P P LNCV6_103360_PI430048170 mRNA CACGGCTGGTATTCTGCAGGCTGAATGCAGTCTCCAGACTGGAAACGCAGAGCGGCTCCT NM_017921 RefSeq chr17 - 81556884 81637153 NPLOC4 55666 "nuclear protein localization 4 homolog (S. cerevisiae), transcript variant 1" GO:0005515|GO:0005783|GO:0042175|GO:0007030|GO:0061025|GO:0008270|GO:0005634|GO:0030433|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83274_PI430048170 0.7373146263968571.01486305517688 5.72118738869365 5.57783922017552 5.67934051494018 P P P 5.61670830943393 5.71714237857353 5.58092316605657 P P P LNCV6_83274_PI430048170 mRNA

AACTCCACCACTTGTCCCAAGTGTGCCCGGCTCAGCCTGAGGAAGCAGTCGCTCTTCCAG NM_001242820 RefSeq chr16 + 89948730 89968060 DEF8 54849 "differentially expressed in FDCP 8 homolog (mouse), transcript variant 7" GO:0035556|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_101025_PI430048170 0.0693061512840197 1.13896219290792 14.7280795874122 14.7942764099206 14.9261094060188 P P P 14.5782740078966 14.5871761704368 14.7223811688627 P P P LNCV6_101025_PI430048170 mRNA
GCTGGTAGCTTCTATGTAATTCGCAATGATTCCATCTAAATAAAAGTTCTATGATCTGCA NM_001297565 RefSeq chr1 + 46303612 46316777 UQCRH 7388 "ubiquinol-cytochrome c reductase hinge protein, transcript variant 2" GO:0022904|GO:0009060|GO:0005739|GO:0005746|GO:0008121|GO:0006122|GO:0005743|GO:0044281|GO:0044237|GO:0055114|GO:0006119 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135109_PI430048170 0.739981485432085 1.02130398831253 12.2125584973602 12.2951176904979 12.1164313651137 P P P 12.120237877342 12.0839165572288 12.322612038818 P P P LNCV6_135109_PI430048170 mRNA
CCAGTGATGGATTCACCCCATCTCCCAAATAAAGTTTACTTGTTTTACATTCCATAAAAA NM_001199120 RefSeq chr6_GL000253v2_alt + 1655360 1657092 RPP21 79897 "ribonuclease P/MRP 21kDa subunit, transcript variant 1" GO:0004526|GO:0042493|GO:0005730|GO:0046872|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_140184_PI430048170 0.111978693628245 0.823364705617123 6.04694405037541 6.08961809501917 6.05854141205337 P P P 6.14994694940731 6.36860502411363 6.49698055592422 P P P LNCV6_140184_PI430048170 mRNA
CATGTCTGGGATAGACTGGTCTAGAATAAAAATGAAGTTTCCATTGCTTTGTTTGCTTTA NM_006788 RefSeq chr18 + 9475531 9538108 RALBP1 10928 ralA binding protein 1 GO:0005515|GO:0051056|GO:0007264|GO:0032855|GO:0043087|GO:0005829|GO:0048365|GO:0007165|GO:0006935|GO:0016020|GO:0043089|GO:0008152|GO:0006810|GO:0016887|GO:0017160|GO:0030675|GO:0043492|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_128921_PI430048170 0.00214566528972104 0.806149745370407 11.6116806562769 11.5616019589329 11.4980572683505 P P P 11.9092318219945 11.8193801255375 11.8761848838558 P P P LNCV6_128921_PI430048170 mRNA
TCTAGATGGCCTCATCTCTTCCTTCCACAAACTGTCTAGAACCAATAAAAGGAAACCTGC NM_018074 RefSeq chr19 + 4247113 4269088 CCDC94 55702 coiled-coil domain containing 94 NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_72628_PI430048170 0.22244016430878 0.578522287601993 0.339766407268598 0.289016706267425 1.72882694437997 A A A 0.980712656541206 2.2220871559918 1.76119100569442 A A A LNCV6_72628_PI430048170 mRNA
TAGTGAATCCAGGATAAGCGAGTGGACATTTCAACCCTTTACTAACCACTCTGTGGATGG NM_015931 RefSeq chr3 - 8619399 8652078 SSUH2 51066 "ssu-2 homolog (C. elegans), transcript variant 3" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_142261_PI430048170 0.142247098370786 1.13640378407155 7.76623029006563 7.60841562591605 7.52380748081407 P P P 7.31536757316568 7.46663717950374 7.56287724845929 P P P LNCV6_142261_PI430048170 mRNA
CCAGTCTTGAGAAACAGGTCAAGGACAGCTTCAAAAGAGATTCTAAATAAATGTTAATGT NM_152503 RefSeq chr20 - 37101225 37179588 MROH8 140699 "maestro heat-like repeat family member 8, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135892_PI430048170 0.00210374198582367 0.356104163466361 5.51426820596283 5.38620883587921 5.88764540909319 P P P 6.89868292369434 7.20606620769879 7.18066572606942 P P P LNCV6_135892_PI430048170 mRNA
TGCCCACAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAGTTTTTATATTTGTCAAT NM_002485 RefSeq chr8 - 89933335 89984671 NBN 4683 nibrin

GO:0005515|GO:0007095|GO:0007093|GO:0030870|GO:0008283|GO:0005657|GO:0001832|GO:0005634|GO:0006302|GO:0004003|GO:0000723|GO:0000724|GO:0050885|GO:0007050|GO:0032508|GO:0000784|GO:0031954|GO:0033674|GO:0051321|GO:0030330|GO:0045190|GO:0035861|GO:0005730|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137804_PI430048170 0.000340755163238526 2.45595753494879 13.4927653875779 13.223685522278 13.4259985497632 P P P 11.9673154937065 12.1399439473606 12.1524244989068 P P P LNCV6_137804_PI430048170 mRNA
TACCAAAGAAGAGTTTACAGACAATAAAATGGAAAGGTCCTGCTGTGGAAACTTACCCAA NM_001740RefSeq chr16 + 71358712 71390438 CALB2 794 "calbindin 2, transcript variant CALB2"
GO:0005737|GO:0051480|GO:0005509|GO:0005921|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135130_PI430048170 0.0121321327325613 1.38915608677971 13.6337288121043 13.5385509954716 13.5449856972557 P P P 13.2305330259162 13.0722692673068 12.9828288207758 P P P LNCV6_135130_PI430048170 mRNA
TTCTCCACTGTACAGAAGAGCCACCACTGGGATGGGGAATAAAGTTGAGAACATGAGTTT NM_021934RefSeq chr12 + 52069973 52077495 ATG101 60673 "autophagy related 101, transcript variant 1"
GO:0005515|GO:0000407|GO:0000045|GO:0032403|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132117_PI430048170 0.0222923809870038 0.4998467465862676.58844663164829 6.32391995270418 6.76784099309809 P P P 7.1832836997868 7.54373430228068 7.90013008082499 P P P LNCV6_132117_PI430048170 mRNA
GTTTAAATGTGTTGTCATTGTCTCCATTGTCTTTGTCCAGAGCCTATTATTATGGAAACANM_014089RefSeq chr13 + 25301527 25342423 NUPL1 9818 "nucleoporin like 1, transcript variant 1"
GO:0005515|GO:0007077|GO:0010467|GO:0031965|GO:0005975|GO:0019083|GO:0019221|GO:0019058|GO:0044281|GO:0005635|GO:0015031|GO:0055085|GO:0010827|GO:0006913|GO:0008645|GO:0015758|GO:0005487|GO:0005643|GO:0009405|GO:0016032|GO:0051028|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130845_PI430048170 0.8535625709700881.01284420455983 3.98762874749561 3.43278335657057 3.68730597044884 P P P 4.24571469731571 3.36634828161526 3.28676545162064 P P P LNCV6_130845_PI430048170 mRNA
TTACTCAGCAAGGCAAAAGAGGAACCACCAGCTGCTTCCCTGGATCAGCCCTCAGCACTG NM_001080413 RefSeq chr7 - 144397239 144410227 NOBOX NA NOBOX oogenesis homeobox NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139780_PI430048170 0.4064881858678942.73142849280368 0.318825563777456 2.87687274290852 0.271559162039237A A A 0.2567822639655750.259612566388455 0.25808915768111 A A A LNCV6_139780_PI430048170 mRNA
GCTTCTAAGAAATGCCATTGAGCATTGTTTCTTATTTAGTTTCTCAAAGATCTGTTCTGC NM_001164435 RefSeq chr21 - 30718524 30718777 KRTAP21-3 NA keratin associated protein 21-3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137928_PI430048170 0.00650325708436345 0.557658874983 7.2476232815255 6.93144248935008 6.94333049196124 P P P 7.64823041549658 8.05038941332599 7.94469644579195 P P P LNCV6_137928_PI430048170 mRNA
GTCCTGTCTTAAAAGTACAGTCTATATCTTGGAAATAAATAGCTTTCCTCAAGGCATGAA NM_001199417 RefSeq chr17_KI270857v1_alt + 2463785 2547694 ARHGAP23 57636 Rho GTPase activating protein 23
GO:0051056|GO:0032321|GO:0007264|GO:0005100|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144383_PI430048170 0.3358201371557380.3672835143720740.25801092220733 0.3127839606267940.279593778374132A A A 0.60348131161185 0.371690813225461 2.83378832252653 A A P LNCV6_144383_PI430048170 mRNA

CCTGGGTCATGCCATCCTACACCAAATTCCTGTTAAACAGAGGCATGATTTATTCCAGTG NM_153027RefSeq chr4
+ 164956947 164959121 FAM218A 152756 "family with sequence similarity 218, member A" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_111150_PI430048170 0.921483930656697 1.10037606098587 1.11565920746904
2.32838655694655 2.87154939674856 A A P 1.81845139276535 1.54162634541737
2.75408064975506 A A P LNCV6_111150_PI430048170 mRNA
TGATAATGAAAAGATCTGGAGGACACAGAATACCAGGCTTGAATTGCTGTGGTCAGGGAANM_002662RefSeq chr3
- 171600404 171810494 PLD1 5337 "phospholipase D1, phosphatidylcholine-specific, transcript variant
1"
GO:0005515|GO:0048471|GO:0007264|GO:0050830|GO:0032534|GO:0007265|GO:0004630|GO:0030139|GO:0044
281|GO:0005765|GO:0016324|GO:0006935|GO:0006654|GO:0006655|GO:0005794|GO:0016042|GO:0000139|GO:0
016020|GO:0070290|GO:0031902|GO:0005789|GO:0006644|GO:0035091|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138794_PI430048170 0.225860744474786 1.22176505506293 5.24793270207431
4.76251580918157 4.92658468283109 P P P 4.46683873459402 4.64580433955494
4.95717611929311 P P P LNCV6_138794_PI430048170 mRNA
GGTGCCCACAACTCACTCACCAAGATGTTTAACAGTAAGTAACAGTAAATGTAAAAGATT NM_004212RefSeq chr15
+ 45252229 45275934 SLC28A2 9153 "solute carrier family 28 (concentrative nucleoside transporter),
member 2"
GO:0015860|GO:0006139|GO:0016020|GO:0005886|GO:0005887|GO:0001882|GO:0015211|GO:0005415|GO:0055
085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131434_PI430048170 0.875461663983186 1.02875750795956 7.0093925618512
7.18936895104647 7.51757740437171 P P P 7.20274257219047 7.12090812762214
7.31035739067371 P P P LNCV6_131434_PI430048170 mRNA
TTAGTTCTGTGCTCTTCCTTATTTAGTGTTGTATCATAAATACTTTGATGTTTCAAACAT NM_005388RefSeq chr9 -
122818096 122828656 PDCL 5082 phosducin-like
GO:0035556|GO:0005515|GO:0007165|GO:0005737|GO:0008277|GO:0006457|GO:0061084|GO:0005057|GO:0032
403|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141641_PI430048170 0.0506419650308930 0.614903745079139 3.17308416797509
3.61764371494498 3.86817344802492 P P P 4.09069792031587 4.47197418026687
4.25917793656201 P P P LNCV6_141641_PI430048170 mRNA
GAACTCATTGCCTTCATCAATGTGTCTGTTTTTTAATTCCTCCTTTTTCCCTTGAAAGGA NM_144643RefSeq chr4 -
128883994 129093607 SCLT1 132320 "sodium channel and clathrin linker 1, transcript variant 1"
GO:0042384|GO:0005813|GO:0006996|GO:0045162|GO:0071439|GO:0030276|GO:0005814|GO:0008022|GO:0070
062|GO:0017080|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135710_PI430048170 0.0284027790480783 0.306454005061671 0.491406582586798
1.54463457735758 0.482293637870517 A A A 3.26561559652893 2.13855499632585
2.21567150476342 P A A LNCV6_135710_PI430048170 mRNA
GCTCTTCTATCTAATCAGTCAATATTTCCTTGGCCCTCAAGCCAACATTCATTTTTTATG NM_207322RefSeq chr15 +
62066976 62070917 C2CD4A 145741 C2 calcium-dependent domain containing 4A GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109567_PI430048170 0.294262109080724 1.084209516637 7.53581191273117
7.43946855480708 7.69188039716496 P P P 7.34620122620204 7.42176736368614
7.55294685200416 P P P LNCV6_109567_PI430048170 mRNA
ATTTCTTCTGGAAAACTGGAAACAAGATAGGGTTTAAACCAGCAGGAGGCATCCGCAGTG NM_015954RefSeq chr12
+ 15911171 16037381 DERA 51071 "deoxyribose-phosphate aldolase (putative), transcript variant 1"
GO:0009264|GO:0005737|GO:0004139|GO:0046121|GO:0046386|GO:0005634|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135545_PI430048170 0.162669791828161 1.25645909026241 12.374153951825

12.4785694278587 12.7189078067619 P P P 12.4116120102016 11.8727972156231
12.2686680673521 P P P LNCV6_135545_PI430048170 mRNA
ATACTGTTTAGGCCGCAGGAGAGTTTGGAATCCGGAATAAATACTACCTGGAGGTTTGTC NM_001282387 RefSeq
chr2 - 208236226 208254303 IDH1 3417 "isocitrate dehydrogenase 1 (NADP+), soluble, transcript
variant 3"
GO:0050661|GO:0000287|GO:0006099|GO:0005782|GO:0005102|GO:0006749|GO:0044281|GO:0048545|GO:0006
097|GO:0042803|GO:0004450|GO:0005829|GO:0005739|GO:0006102|GO:0008585|GO:0005737|GO:0051287|GO:0
006740|GO:0006103|GO:0006979|GO:0044255|GO:0070062|GO:0005777 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_136662_PI430048170 0.0101574768020911 0.74951840006253310.5130720503515
10.5978447681466 10.679578475051 P P P 10.9106733327671 10.9811336471623
11.1415862738244 P P P LNCV6_136662_PI430048170 mRNA
CCCCACTGACCTGAAGGTTCCATGTAACTGTATACACATGAATACTTAAATGCCAACATT NM_006990RefSeq chr1
- 27404225 27490187 WASF2 10163 "WAS protein family, member 2, transcript variant 1"
GO:0005515|GO:0031209|GO:0030036|GO:0030032|GO:0015629|GO:0032403|GO:0005829|GO:0005622|GO:0010
592|GO:0005911|GO:0070062|GO:0030048|GO:0072673|GO:0048010|GO:0001667|GO:0003779|GO:0001525|GO:0
001726|GO:0030027|GO:0051497|GO:0016601|GO:0035855|GO:0045087|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133920_PI430048170 0.0494305538470282 0.4649410042986716.28339878080391
6.46962819737437 6.11358726332731 P P P 6.80292685281405 7.7238006285216
7.52371562625734 P P P LNCV6_133920_PI430048170 mRNA
CTCATTGGTTCTCAAGGACTAACCTGTGGGGGAAAGCAATAGAGACACTCTTTTTCTCTC NM_001199172 RefSeq
chr17 + 76868715 76950389 MGAT5B 146664 "mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-
glucosaminyltransferase, isozyme B, transcript variant 3"
GO:0005515|GO:0030144|GO:0000139|GO:0016021|GO:0006487|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138837_PI430048170 0.2146669729699210.8705547601322339.95552238876625
9.94498456876713 9.92128965780522 P P P 10.3328272583205 10.0995066909942
9.96546777074238 P P P LNCV6_138837_PI430048170 mRNA
TCTAATGCAGCTGCTGGGGCCTGATGCCCTGAGTTGTTTGTGATTCAATAAAGAATCCAT NM_018389RefSeq chr11
+ 45805089 45813016 SLC35C1 55343 "solute carrier family 35 (GDP-fucose transporter), member C1,
transcript variant 1" GO:0045746|GO:0005794|GO:0000139|GO:0008643|GO:0016021|GO:0055085|GO:0030259
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134865_PI430048170 0.3059501397126920.3751302122637610.478058197125996
0.49904306832272 0.396875360303091A A A 1.07821415502529 0.42669530696004
2.91355702778223 A A P LNCV6_134865_PI430048170 mRNA
CCAGCCAGGAAGGAGCACTCTTATGGAAACAAGTTTTAATACAATTTTAAAATGTATTGC NM_001145128 RefSeq
chr6 - 109492855 109691212 AK9221264 "adenylate kinase 9, transcript variant 1"
GO:0031965|GO:0006186|GO:0005737|GO:0050145|GO:0005730|GO:0004550|GO:0006757|GO:0005654|GO:0005
634|GO:0006756|GO:0006174|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136245_PI430048170 0.6608760772505790.9300176916735164.94468059613881
2.89881191331914 3.18007458915026 P A P 3.51276342461165 4.56332798086078
3.98380779280951 P P P LNCV6_136245_PI430048170 mRNA
GGTATCCCTCCATGCCCTTCTGTAATAAATATCTGGAAAAAACATTAAACAATAGGCAAA NM_001143818 RefSeq
chr18 + 63887704 63903890 SERPINB2 5055 "serpin peptidase inhibitor, clade B (ovalbumin),
member 2, transcript variant 1"
GO:0010951|GO:0043066|GO:0005737|GO:0005886|GO:0007596|GO:0004867|GO:0005576|GO:0042730|GO:0005
615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144920_PI430048170 0.0708385682810601 1.13279781575116 8.80223183695747

8.7556743689666 8.71768784578476 P P P 8.60259847592823 8.6611214924475 8.4666038742591
P P P LNCV6_144920_PI430048170 mRNA
GCCATGGTGCTTTCCCCAAAAGTTGTGTTGCTTTTATCAGTTTTCTAACTTAATAAAAAG NM_022480RefSeq chr15
- 85759325 85794958 KLHL25 64410 kelch-like family member 25
GO:0005737|GO:0016567|GO:0042787|GO:0006446|GO:0031463 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130135_PI430048170 0.3985617394064740.6983205848629560.331812282622764
0.3594450792827220.347030806405628A A A 0.3568259798050121.52318990185261
0.385205710669314A A A LNCV6_130135_PI430048170 mRNA
GATATGCTCTGGGGCTTTCATGGGAATGATGAAGATGATAATGAGAAAAATGTTATCATT NM_001289086 RefSeq
chr17 - 74694308 74713000 CD300LF 146722 "CD300 molecule-like family member f, transcript
variant 6" GO:0005886|GO:0016021|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108515_PI430048170 0.3713768352465921.06871050511931 6.14445982038531
6.12124716014752 6.33961544197565 P P P 6.04918689939036 6.23564154724744
6.03414185721779 P P P LNCV6_108515_PI430048170 mRNA
AATCATTTCCTTGGCTGATAACCATATCCTGCTGTGGGATTTACAGGAAAGCTCGAGCCA NM_003310RefSeq chr2
- 3188969 3377882 TSSC1 7260 tumor suppressing subtransferable candidate 1 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129206_PI430048170 0.00303955987430247 0.3235865210719215.15597470360931
4.96098448410074 5.1970958981856 P P P 6.46777393618554 6.69236449450895
6.99857895959253 P P P LNCV6_129206_PI430048170 mRNA
AACAAATGGTGTATTGCTTTTCATACAAGTGTTTTCACAAAAGCCATTTGCCTAGGCAGC NM_021156RefSeq chr20
- 7977352 8019829 TMX4 56255 thioredoxin-related transmembrane protein 4
GO:0034976|GO:0006457|GO:0005783|GO:0003756|GO:0045454|GO:0016021|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142674_PI430048170 0.1889349893752380.6530583744592930.378456688819761
0.5426628557150010.364739009601283A A A 0.4942345047462761.49574521270087
0.973887360055166A A A LNCV6_142674_PI430048170 mRNA
AGAAAAAAGCACCAAAGGGAAGGCTTCCTATCTGTGTGGTGATGAATCGCATTTCCTGAG NM_001133RefSeq chr4
+ 73481744 73504001 AFM 173 afamin
GO:0051180|GO:0072562|GO:0005576|GO:0008431|GO:0005615|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145180_PI430048170 0.5686322630871970.9662934664978960.489873258547221
0.4892130509867540.268500488136529A A A 0.4056840073702910.525827340415538
0.473056419154592A A A LNCV6_145180_PI430048170 mRNA
CCCCATTTTAGTCTAATGGGAAGATACAGATGTGCAAGTCTGCTTTTTTGTTTTTTGTTA NM_033512RefSeq chr8 -
97273485 97277948 TSPYL5 85453 TSPY-like 5
GO:0005515|GO:0051897|GO:0008284|GO:0031398|GO:0006334|GO:0005634|GO:0071480|GO:0040008 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144812_PI430048170 0.0127605356150309 0.4375699635737663.81926692497181
3.13545790098924 3.22640923835184 P P P 4.32384032156508 4.64290023193144 4.8440919249172
P P P LNCV6_144812_PI430048170 mRNA
TGTGTCTGCCATTTCATTTGTACGCTTGTTCAAAACCAAGTTTGTTCTGGTTTCAAGTTA NM_138576RefSeq chr14 -
99169287 99271713 BCL11B 64919 "B-cell CLL/lymphoma 11B (zinc finger protein), transcript variant 1"
GO:0071678|GO:0003382|GO:0005515|GO:0043066|GO:0033077|GO:0008285|GO:0033153|GO:0046632|GO:0010
837|GO:0048538|GO:0005634|GO:0000978|GO:0003334|GO:0046872|GO:0043368|GO:0006351|GO:0031077|GO:0
019216|GO:0001077|GO:0045944|GO:0045664|GO:0021773|GO:0042475|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142375_PI430048170 0.5432928865477810.8381119799458080.435310686109608 0.4602933059633

0.475160561908706 A A A 0.3289150866696041.20343714792929 0.437861043171322 A A A
LNCV6_142375_PI430048170 mRNA
CTTCACATGGAAATAATAAAGCTCTTTATATGAGCTGTCCCACCAGCAACTTATATATGT NM_014594 RefSeq chr5
+ 179060605 179080690 ZNF354C 30832 zinc finger protein 354C
GO:0031965|GO:0006355|GO:0005737|GO:0003700|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141211_PI430048170 0.00886662940621768 3.00537690923588 6.46129823613739
6.68558510593873 6.64045986610436 P P P 5.3305585792921 4.98030610169735 4.6414442970043
P P P LNCV6_141211_PI430048170 mRNA
ACTGGAGAGTGTGGGGAATGGGAAGAAGCAGTTTACTTTAGACTAAAGAATATATTGGGGNM_145343 RefSeq chr22
+ 36253070 36267531 APOL1 8542 "apolipoprotein L, 1, transcript variant 2"
GO:0005515|GO:0006821|GO:0072562|GO:0005576|GO:0031224|GO:0005254|GO:0005615|GO:0006898|GO:0008
289|GO:0034361|GO:0034364|GO:0045087|GO:0006869|GO:0019835|GO:0042157|GO:0031640|GO:0008203 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138119_PI430048170 0.1051468557057341.21478849548468 11.1585301673986
11.3942374122316 11.3949710139256 P P P 11.2044289054384 11.0544548632016
10.8357666023921 P P P LNCV6_138119_PI430048170 mRNA
GGGAAGGGGGAACATGAGCCTTTGTTGCTATCAATCCAAGAACTTATTTGTACATTTTTT NM_001207014 RefSeq
chr11 + 75562055 75572804 SERPINH1 871 "serpin peptidase inhibitor, clade H (heat shock protein 47),
member 1, (collagen binding protein 1), transcript variant 1"
GO:0003433|GO:0006986|GO:0005793|GO:0004867|GO:0005783|GO:0005518|GO:0005615|GO:0010951|GO:0051
604|GO:0030198|GO:0030199|GO:0005788|GO:0032964|GO:0051082|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_98781_PI430048170 0.00172691607290283 1.72560426827207 6.69301292759375
6.48843319843429 6.73993001237262 P P P 5.95631950355298 5.71891060437524
5.88682641794284 P P P LNCV6_98781_PI430048170 mRNA
GAATCTAATAACTACAATACTTACCGGTCAAGGAAATACACCAGTTGGTATGTGGCACTG NM_002006 RefSeq chr4
+ 122826707 122898235 FGF2 2247 fibroblast growth factor 2 (basic)
GO:0060045|GO:0005515|GO:0001658|GO:0048598|GO:0005615|GO:0010764|GO:0007173|GO:0006935|GO:0032
958|GO:0043552|GO:0061045|GO:0030198|GO:0060548|GO:0009887|GO:0051781|GO:0070374|GO:0051209|GO:0
005125|GO:0042056|GO:0043536|GO:0008543|GO:0045087|GO:0042060|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130616_PI430048170 0.3268383270155571.04528181411787 0.474264181623044
0.3080235700274630.379294165523383 A A A 0.2821778720293640.34287639572098
0.348747885679854 A A A LNCV6_130616_PI430048170 mRNA
GTCCCGGAGCTCAAGGATCAGAGTAACACAATTTTCACTTTTTCTGTCTTTATGTAAGAA NM_021076 RefSeq chr22
+ 29480191 29491288 NEFH 4744 "neurofilament, heavy polypeptide"
GO:0008017|GO:0030424|GO:0019901|GO:0005883|GO:0000226|GO:0007409|GO:0005739|GO:0005737|GO:0045
502|GO:0005198|GO:0030031|GO:0005200|GO:0033693|GO:0048936|GO:0019894|GO:0030674 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141253_PI430048170 0.5666686110544291.14487057072511 0.296279564361955
0.3239851227034581.00134072254241 A A A 0.4223724185790420.377153741322912
0.351189216413905 A A A LNCV6_141253_PI430048170 mRNA
CAAAAATCTGAAAGAAACGTCTTTAGTGGCTTTAAGCCCCAAAACGTCCCTAAGGCGTCC NM_003004 RefSeq chr17
- 82321023 82334045 SECTM16398 secreted and transmembrane 1
GO:0007165|GO:0006955|GO:0005794|GO:0005886|GO:0007498|GO:0016021|GO:0004871|GO:0043123|GO:0005
615|GO:0005125|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142024_PI430048170 0.3916229767734080.9719321245206130.398116287403915
0.4215850779609510.297057482850181 A A A 0.3953001207020960.442529532231101

0.404723863777659 A A A LNCV6_142024_PI430048170 mRNA
AAGCCAGTATATGTTAAAAAGACTTAGGTTCAGGGGCATCAGTCCCTAAGATGTTATTTA NM_002177 RefSeq chr9
- 21140631 21142145 IFNW1 3467 "interferon, omega 1"
GO:0005132|GO:0019221|GO:0033141|GO:0045343|GO:0009615|GO:0005125|GO:0005615|GO:0005126|GO:0002
250|GO:0051607|GO:0042100|GO:0045087|GO:0006959|GO:0030183|GO:0007050|GO:0043330|GO:0002286|GO:0
002323 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145189_PI430048170 0.0355894345450842 0.6279319121062975.86216768465451
5.611580810346 6.13688775367099 P P P 6.37808742242524 6.3989379475429
6.84554445415768 P P P LNCV6_145189_PI430048170 mRNA
GTCCCCCATGTGGATATTTCTTATACTAATTGTATCATAAAGCCGTTTATTCTTCCTTGT NM_001030273 RefSeq chr11
+ 13277726 13387265 ARNTL 406 "aryl hydrocarbon receptor nuclear translocator-like, transcript variant
3"
GO:0005515|GO:0032007|GO:0001190|GO:0006366|GO:0045599|GO:0090263|GO:0000982|GO:0051879|GO:0090
403|GO:0005634|GO:0007283|GO:0050767|GO:0045944|GO:2000074|GO:0051726|GO:0004871|GO:0001046|GO:2
000772|GO:2001016|GO:0000060|GO:0005667|GO:0006355|GO:0000976|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127702_PI430048170 5.92573605174661e-06 1.92852618804228 10.3053129309195
10.3045833473904 10.2869700470352 P P P 9.32831099170726 9.36044738949172 9.3654059941805
P P P LNCV6_127702_PI430048170 mRNA
AGGACCTCAGTACTAAAGCCTGTTCTCTGGAGGAAATAAAGAAAATATGTTTGGAGGTGC NM_001267803 RefSeq
chr11 + 73876968 73927736 PAAF1 80227 "proteasomal ATPase-associated factor 1, transcript variant
1" GO:0005515|GO:0000502|GO:0016032 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70169_PI430048170 0.0247499392556642 1.46192202095534 7.56052123215048
7.66444112145063 7.4890116639456 P P P 7.01577240620081 7.21333950438072
6.81988509508635 P P P LNCV6_70169_PI430048170 mRNA
AAGGGTTCCAGAGAGAAGCTAGAAGTCCCCCTTGAATGACCCCCAGAGCCCCTCTGAGAA NM_024959 RefSeq
chr12 - 113298765 113335120 SLC8B1 80024 "solute carrier family 8 (sodium/lithium/calcium
exchanger), member B1"
GO:0005886|GO:0006851|GO:0051480|GO:0042593|GO:0055085|GO:0005432|GO:0042803|GO:0042383|GO:0050
796|GO:0032592|GO:0051560|GO:0070588|GO:0035725|GO:0086038|GO:0086036|GO:0030061|GO:0050896|GO:0
006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104788_PI430048170 0.59043535465578 1.07623500330092 8.36908364231139
8.84560462565298 8.60020990266808 P P P 8.61275468633497 8.31232815203652
8.59210298536838 P P P LNCV6_104788_PI430048170 mRNA
AATGAGCCAGATGTTTATGAAACTAGCGACCTACCTGAGGATGATCAAGCGGAGTTCGAT NM_006400 RefSeq chr12
- 57530049 57547331 DCTN2 10540 "dynactin 2 (p50), transcript variant 1"
GO:0005515|GO:0005813|GO:0006996|GO:0008283|GO:0005874|GO:0030507|GO:0031982|GO:0032402|GO:0030
426|GO:0005829|GO:0019886|GO:0003774|GO:0005737|GO:0007067|GO:0030286|GO:0016020|GO:0000086|GO:0
008152|GO:0000776|GO:0000278|GO:0005869|GO:0007052|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132747_PI430048170 0.3317079240135271.28392321991919 3.08399085220014
2.77668238931336 2.68764212959239 A A A 1.83016038554352 2.98930610078204
2.44968871351668 A P P LNCV6_132747_PI430048170 mRNA
GGCATCCATAATTGCTGCTAACCTAGACATTTCATAGTTACAGATTAAATCTACTTGACT NM_012337 RefSeq chr1
- 159872363 159900116 CFAP45 25790 cilia and flagella associated protein 45
GO:0005739|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102652_PI430048170 0.4762385406514751.10916618410731 5.59690513560807
5.44286743451896 5.85411200092768 P P P 5.35330470446322 5.78854094668483
5.27982845836392 P P P LNCV6_102652_PI430048170 mRNA

GAATTCATGTACAGTGGTGTGGAGAATAAGCAGGTGGTGATTATACATCACATGAGGCTG NM_033547RefSeq chr11 - 77878719 77994671 INTS4 92105 integrator complex subunit 4
GO:0005515|GO:0032039|GO:0016180 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132453_PI430048170 0.2013277149892730.48914164173268 0.3289943939354742.8421293185952
1.75929824939789 A A A 3.06313928900759 3.04420906363549 2.91496564154652 P P P
LNCV6_132453_PI430048170 mRNA
TAAAGTAATGGAACTTTGATGATGCCTTTGCTGGGCATTATGTGTCCATGCCAGGGATGC NM_033004RefSeq chr17 - 5514117 5584512 NLRP1 22861 "NLR family, pyrin domain containing 1, transcript variant 1"
GO:0005515|GO:0006919|GO:0072558|GO:0019904|GO:0050727|GO:0006915|GO:0005634|GO:0051402|GO:0005524|GO:0008656|GO:0035872|GO:0005829|GO:0005622|GO:0050718|GO:0045087|GO:0032495|GO:0019899|GO:0042742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128777_PI430048170 0.5570263538173930.9670293263913080.471553052912137
0.4612887888485450.254314244320256A A A 0.3963427377090170.497399468836318
0.446987892196721A A A LNCV6_128777_PI430048170 mRNA
TCTGAGCCATGGTCATGATGACTTAGGATTCTGGATCTCTTATGAATAACAAATTTATCC NM_001075RefSeq chr4_GL000257v2_alt - 580595 586024 UGT2B10 7365 "UDP glucuronosyltransferase 2 family, polypeptide B10, transcript variant 1"
GO:0006629|GO:0052696|GO:0009813|GO:0005789|GO:0015020|GO:0016021|GO:0032870|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128655_PI430048170 0.0108336945161714 1.58664066721953 4.88986661202076
5.12735566352486 5.18088488409026 P P P 4.27281923948725 4.29536438748799
4.62131891023844 P P P LNCV6_128655_PI430048170 mRNA
CTGCCCTTTTCATGTCTTGATTGTTGAATTCTTCTGTGAGATACTCCAAATATCCTAATA NM_001289972 RefSeq chr12 + 133037581 133063304 ZNF84 7637 "zinc finger protein 84, transcript variant 4"
GO:0006355|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134053_PI430048170 0.0534080833270696 2.30679265482979 5.08210070227479
5.23462879488949 4.9166130252212 P P P 4.37177281166374 3.21580293116712
3.81818334419305 P P P LNCV6_134053_PI430048170 mRNA
GCAGGAGCTCCAGGTGGGTGGCAGGGGCAGGTGAACAGAGCTATTTTCCGAATTAATATA NM_001103175
RefSeq chr16 - 3027866 3035541 CCDC64B 146439 coiled-coil domain containing 64B
GO:0017137 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141624_PI430048170 0.0916623370184916 0.7478487091818936.04115246774572
6.09069252231733 6.37810751379007 P P P 6.30768722773517 6.62821848235345
6.81084778748057 P P P LNCV6_141624_PI430048170 mRNA
TAGTATCACTAGCAGTAGTTCCTGCGACTCTTAGCAACACAACCCGAATATTTGCTCCCT NM_007219RefSeq chr20 - 3931420 4015407 RNF24 11237 "ring finger protein 24, transcript variant 1"
GO:0000139|GO:0008270|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141229_PI430048170 0.6991762700048070.7245065463142491.65082673762693
0.6544245418577981.23741595381588 A A A 0.6019980169526881.2017066213456
2.57119870404967 A A P LNCV6_141229_PI430048170 mRNA
TTTTACTCCATCCAGTGCTTAAAGCTGATCTAAGGACTTCGATGGTTCCAGCCTTCAAAG NM_031407RefSeq chrX - 53532095 53686729 HUWE1 10075 "HECT, UBA and WWE domain containing 1, E3 ubiquitin protein ligase"
GO:0000209|GO:0005515|GO:0004842|GO:0006513|GO:0016574|GO:0016874|GO:0005634|GO:0003677|GO:0030154|GO:0005737|GO:0042787|GO:0016020|GO:0006284|GO:0005654|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138158_PI430048170 0.0446669091455633 1.16425420687782 0.645574704436233
0.7854911269633330.825196627212367A A A 0.6379117518138370.470253721151348

0.490103018681672 A A A LNCV6_138158_PI430048170 mRNA
AAAGAATCTGTCTACCAACTCCTCATAGTGAGCCAGAAGCAGCCTCATAACCCTGAATGT NM_001720 RefSeq chr1
- 39758230 39788861 BMP8B 656 bone morphogenetic protein 8b
GO:0051216|GO:0010862|GO:0042981|GO:0030509|GO:0060395|GO:0005125|GO:0005160|GO:0005615|GO:0001
501|GO:0001503|GO:0070700|GO:0043408|GO:0048468|GO:0008083|GO:0040007 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127445_PI430048170 0.867499766609649 1.01285810043095 7.27167451429694
7.14417250471815 7.00905378518073 P P P 7.20297906313337 7.11409663312229
7.06087891361124 P P P LNCV6_127445_PI430048170 mRNA
CAGGACGCAGAGGACTCTAGGTTTAACATTTTGTACAAAATGGAACCTGTTAATCATATT NM_194284 RefSeq chr8
+ 8702155 8704107 CLDN23 137075 claudin 23
GO:0016338|GO:0070830|GO:0005886|GO:0005198|GO:0034329|GO:0016021|GO:0005923|GO:0045216|GO:0042
802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139934_PI430048170 0.392257526496621 0.963046837167215 8.64926504087182
8.74598842817892 8.58540106594531 P P P 8.7790582009598 8.69053873514984
8.67641081673156 P P P LNCV6_139934_PI430048170 mRNA
AAGGGGTTTTGGGGACACAGAAGAATAAGTAAACACATCTCGGAGGCTTTGTGGAAAAAA NM_001136538
RefSeq chr12 + 111686052 111757107 ACAD10 80724 "acyl-CoA dehydrogenase family, member 10,
transcript variant 1" GO:0005739|GO:0016787|GO:0050660|GO:0003995|GO:0055114|GO:0016772 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144768_PI430048170 0.321606829838945 1.11050312816759 0.799147969848654
0.598146338682377 0.463973759315577 A A A 0.650531136068551 0.367283830287752
0.392291408233637 A A A LNCV6_144768_PI430048170 mRNA
CTTGGTTGAAGTAAGAAAACTGTACCATCCTCTATCCTGTGTGCCATAATAAAATAGTAA NM_006158 RefSeq chr8
- 24950955 24956869 NEFL 4747 "neurofilament, light polypeptide"
GO:0005515|GO:0030424|GO:0051258|GO:0008090|GO:0045109|GO:0005883|GO:0007268|GO:0043434|GO:0005
829|GO:0030426|GO:0042802|GO:0040011|GO:0005737|GO:0043524|GO:0043274|GO:0014012|GO:0050885|GO:0
033693|GO:0030674|GO:0051412|GO:0019904|GO:0031133|GO:0009636|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_78405_PI430048170 0.0455177716681052 1.69419699383295 6.70228183881056
6.84734591889469 6.85488246738498 P P P 6.20799511698335 6.20690069024563
5.64265199879406 P P P LNCV6_78405_PI430048170 mRNA
GACCTGGAACCCAGGGACCCGAGTCCCGACCCGGATTATCGTGGCGCTTTTCCCGGCCGG NM_003718 RefSeq chr7
+ 39950359 40097134 CDK13 8621 "cyclin-dependent kinase 13, transcript variant 1"
GO:0070816|GO:0030097|GO:0005515|GO:0007088|GO:0008284|GO:0019908|GO:0005794|GO:0030332|GO:0007
275|GO:0005524|GO:0005615|GO:0008353|GO:0005737|GO:0004672|GO:0016607|GO:0000380|GO:0016032|GO:0
005654|GO:0004693. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112266_PI430048170 0.106657219259541 1.32346474505033 8.67641081673156
8.87204359836082 9.13206679190011 P P P 8.55477486804816 8.21093794380431
8.69613075224811 P P P LNCV6_112266_PI430048170 mRNA
GAATAAAAACAGGGTTGAATGAGTTCCAGAAAGCAGGGTTCTCAACCTCGTGGACAGCAA NM_001142418
RefSeq chrX - 103675497 103686818 MORF4L2 9643 "mortality factor 4 like 2, transcript variant 1"
GO:0005515|GO:0006281|GO:0045944|GO:0006325|GO:0005730|GO:0051155|GO:0005654|GO:0040008|GO:0006
351|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129280_PI430048170 0.35198671887223 0.919042453480152 15.6982996114748
15.3968197624887 15.4211852134286 P P P 15.4992358134484 15.708873323373
15.6844536894455 P P P LNCV6_129280_PI430048170 mRNA
GCTGTACATAGTCCTTTTATCTCCTTGTGGCCTATGAAACTGGTTTATAATAAACTCTTA NM_003091 RefSeq chr20 -
2461634 2470853 SNRPB 6628 "small nuclear ribonucleoprotein polypeptides B and B1, transcript

variant 2"
GO:0008380|GO:0005515|GO:0010467|GO:0006369|GO:0006366|GO:0008334|GO:0031124|GO:0034660|GO:0071
013|GO:0000387|GO:0034709|GO:0005829|GO:0000398|GO:0030532|GO:0005683|GO:0005654|GO:0005681|GO:0
071204|GO:0005687|GO:0034719|GO:0005685|GO:0005689|GO:0071208|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_5661_PI430048170 0.00330845987871157 0.4718116478918767.16578149438534
6.91969808956349 6.71826674492574 P P P 8.18124917885805 8.04318371522009
7.84585036607689 P P P LNCV6_5661_PI430048170 mRNA
GCCCCTCCCGAGACACCCGCTACCTGGTGTTAGCGGTGGACCGCCCTGCGGGGGCCTGGC NM_000479RefSeq
chr19 + 2249113 2252073 AMH 268 anti-Mullerian hormone
GO:0014070|GO:0042493|GO:0007568|GO:0001655|GO:0005102|GO:0007267|GO:0005576|GO:0005160|GO:0005
615|GO:0001546|GO:0007530|GO:0010628|GO:0007506|GO:0005737|GO:0051092|GO:0005179|GO:0001880|GO:0
007548|GO:0008083. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137746_PI430048170 0.0179258013620102 1.44018835237646 5.73506128789906
5.62623376680475 5.9725548486052 P P P 5.27872678832953 5.38559514304915
5.09828718224407 P P P LNCV6_137746_PI430048170 mRNA
ATTGATTAAAACCATTTTGTTCTAGGTGTGGCTGGTGGCATTTGTGGGGTGCAGATGGGT NM_001276252 RefSeq
chr1 + 27234515 27308633 WDTC1 23038 "WD and tetratricopeptide repeats 1, transcript variant 1"
GO:0004857|GO:0005515|GO:0008361|GO:0032869|GO:0016567|GO:0042826|GO:0045717|GO:0005634|GO:0000
122|GO:0043086|GO:0001701|GO:0055082|GO:0005829|GO:0042393|GO:0035264|GO:0006006 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144841_PI430048170 0.2710476211232780.82526881901436413.2604268422821
13.1150133768812 13.2452090993211 P P P 13.1198116544137 13.65689108652 13.619806924056
P P P LNCV6_144841_PI430048170 mRNA
GAATTCGGAACTGTCCTTTCCTTGGCTTTATGCACATTAAACAGATGTGAATATTCAAAA NM_005030RefSeq chr16
+ 23678821 23690367 PLK1 5347 polo-like kinase 1
GO:0005515|GO:0007077|GO:0008017|GO:0010997|GO:0000910|GO:0018105|GO:0016301|GO:0051443|GO:0046
677|GO:0010800|GO:0005813|GO:0006996|GO:0019901|GO:0000281|GO:0005819|GO:0043393|GO:0030496|GO:0
000122|GO:0000070|GO:0000922|GO:0000776|GO:0005654|GO:0030071|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143961_PI430048170 0.785795153359045 1.02068899569182 3.58026208549778
3.38627622727317 3.7344663057849 P P P 2.64390239374803 4.01115135350149
3.65864717751666 A P P LNCV6_143961_PI430048170 mRNA
CGCTGTTGCTCTGCTTTTGTCTTTATATACAGTAGTTTTTATAACAATGTCCCTAGGTTT NM_001099294 RefSeq chr22
- 44243676 44312851 KIAA1644 85352 KIAA1644 GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141553_PI430048170 0.2839793061565331.02675593790952 0.312964213323401
0.2481577998125870.335368076571002A A A 0.2684116161025180.245394632092821
0.269690031736028A A A LNCV6_141553_PI430048170 mRNA
TCACAGCTGACTTGAAGGAACGTTCTTGGTCCTGAATAAACCGATGCTCAGAGTGGTAAA NM_001080466 RefSeq
chr17 - 74356415 74361819 BTBD17 NA BTB (POZ) domain containing 17NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_92246_PI430048170 0.2159539983773260.7889434920825175.24254483762124 5.93386730789736
5.77540282939669 P P P 5.84127063177215 6.06985236794802 6.13733936686445 P P P
LNCV6_92246_PI430048170 mRNA
GCACGCCAACCACTCCAAAATTTTGAGTCTTGCATTACTTTTTGTTCCTTTTTTAAAAAC NM_001278480 RefSeq chr13
- 37009313 37059713 SUPT20H 55578 "suppressor of Ty 20 homolog (S. cerevisiae), transcript variant
3" GO:0005515|GO:0003712|GO:0007369|GO:0000124|GO:0006914|GO:0006325|GO:0005730|GO:0070461 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_134685_PI430048170 0.9053690063106630.9938496844263120.625747567645046
0.50750594547706 0.390811471035015A A A 0.4272913198444650.585927341000411
0.542487046529912A A A LNCV6_134685_PI430048170 mRNA
CCAGTTCCACGAGTGTACGTTTGGATTTTCAACTTGGTTTCGTATCTGCCAAAGCTTTGT NM_019066RefSeq chr15
- 23643548 23647846 MAGEL2 54551 melanoma antigen family L2
GO:0034314|GO:0005515|GO:0070534|GO:0004842|GO:0042752|GO:0042147|GO:0005634|GO:0045892|GO:0005
769|GO:0030904|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111851_PI430048170 0.8633691744251560.9943944919555774.47290199941757 5.2525711417587
5.19659996278634 P P P 5.02456842629928 5.0068121972359 5.03766503689873 P P P
LNCV6_111851_PI430048170 mRNA
AATCAGTTTCTGGAGCAGGAAACTCATCTCTTCAGCGCCATTAACAGCCATTTGCTGACT NM_021930RefSeq chr7
+ 105532084 105567677 RINT1 60561 RAD50 interactor 1
GO:0005515|GO:0007049|GO:0060628|GO:0005783|GO:0005789|GO:0048193|GO:0015031 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127760_PI430048170 0.0376459665863395 0.4212619707004982.97065508609059
2.40690423578801 2.08184208553499 A A A 3.75604262052413 3.78708118625113
3.80027230969976 P P P LNCV6_127760_PI430048170 mRNA
TTATCTACAATTCAGAACAGCCCAACCAAGAAAAGAAAGAAATACGAAAGAGGCCATTAANM_001009608 RefSeq
chr20 + 10435302 10623379 SLX4IP 128710 SLX4 interacting protein GO:0005515 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131027_PI430048170 0.0333871177375079 0.4047156310547431.43730276633848
1.76997480226577 1.00395345359112 A A A 2.27321364302262 2.46576555235935 3.2802787163958
A A P LNCV6_131027_PI430048170 mRNA
CTGCAAACGCAGAAAACAGATTACAGTCTCTTATCCATTTTTTGAAATCCAAAAACTACG NM_001078166 RefSeq
chr17 - 58000918 58007346 SRSF1 6426 "serine/arginine-rich splicing factor 1, transcript variant 2"
GO:0005515|GO:0008380|GO:0006369|GO:0010467|GO:0048024|GO:0006366|GO:0003723|GO:0031124|GO:0005
634|GO:0050733|GO:0071013|GO:0003729|GO:0060048|GO:0005737|GO:0006406|GO:0000166|GO:0035145|GO:0
070062|GO:0006397|GO:0043488|GO:0006355|GO:0006376|GO:0001701|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_54764_PI430048170 0.1835916197594690.8672527203727686.28233752398959 6.0854016748736
6.39045594728055 P P P 6.53636431049314 6.27570022160442 6.56194227681035 P P P
LNCV6_54764_PI430048170 mRNA
ATAGGTTGAAAACAATCATCTGTGAGTTTAGGAGTCTTAAGATCCTCACAGCACGGGAGC NM_001038707 RefSeq
chr1 - 151050970 151059649 CDC42SE1 56882 "CDC42 small effector 1, transcript variant 1"
GO:0006909|GO:0007165|GO:0005737|GO:0005886|GO:0005198|GO:0008360|GO:0005856|GO:0005095|GO:0043
086 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129230_PI430048170 0.4314029742191381.11449029505407 10.871251873757
10.8148354427167 10.7075952476522 P P P 10.9578528265136 10.5630281228109 10.339424701386
P P P LNCV6_129230_PI430048170 mRNA
TACTTTTTATACAAATCTCCTCTAGACTGTTCCAGGCTGCCTGCGGATTAAAGTGGGGGT NM_001002913 RefSeq
chr9 - 127713947 127715657 PTRH1 NA peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae) NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137725_PI430048170 0.1297362956028941.02716825534928 0.385437479836415
0.391201490334533 0.433014620474215A A A 0.3607347126934480.343127936001905
0.389855688945372A A A LNCV6_137725_PI430048170 mRNA
GAGTTTGTACTCATAGCCTTGGAACCTTAATTCGAAATGTACTGAAGAAAAAGTAACAGC NM_004361RefSeq chr18
+ 65750920 65880938 CDH7 1005 "cadherin 7, type 2, transcript variant b"
GO:0016337|GO:0005886|GO:0034329|GO:0005509|GO:0016021|GO:0007156|GO:0045216|GO:0034332 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_141995_PI430048170 0.00866791984121655 2.15161673786588 7.61029256370165
8.14886311334646 8.04759673315135 P P P 7.08644322405629 6.87044836058922
6.53588385042164 P P P LNCV6_141995_PI430048170 mRNA
ATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGGTCTTCAAGT NM_001037633 RefSeq
chr5 - 138946720 139198376 SIL1 64374 "SIL1 nucleotide exchange factor, transcript variant 1"
GO:0006457|GO:0005783|GO:0005788|GO:0051082|GO:0006886|GO:0005615 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135129_PI430048170 0.9820690901965070.9696325340021942.31335920194493 2.2365035374112
2.42363598518847 A A A 2.43129431584156 2.74444336246275 1.77582791898947 A P A
LNCV6_135129_PI430048170 mRNA
AGCTTGTACAGTCTGATTCTTTTTATCTGGGGTAGGGGGGCTTTTATGTTTGTCCGATGG NM_183377RefSeq chr17
- 33013087 33292988 ASIC2 40 "acid sensing (proton gated) ion channel 2, transcript variant MDEG2"
GO:0010468|GO:0005515|GO:0005886|GO:0007605|GO:0007268|GO:0035418|GO:0045202|GO:2001259|GO:0071
468|GO:0003026|GO:0019229|GO:0034220|GO:0043197|GO:0042391|GO:0043025|GO:0035725|GO:0051965|GO:0
022839|GO:0043066|GO:0005248|GO:0007417|GO:0050915|GO:0055085|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128700_PI430048170 0.7259630241658160.9783834162210010.29385969716923
0.3073957071499710.41349930766254 A A A 0.3141983933084750.500340622731943
0.288400981037333A A A LNCV6_128700_PI430048170 mRNA
TCTGTATTAAGGCCTCCATTTCAGTTCTGCTATTTCATATTGCCTTAGGTTGTCTATTTG NM_001272046 RefSeq chr10
+ 114239253 114294500 VWA2 NA von Willebrand factor A domain containing 2 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131084_PI430048170 0.00919001231890367 1.84088412657421 6.1146080093075
6.29980268310178 6.3544897743518 P P P 5.39386542815623 5.58410800193173
5.12387598110464 P P P LNCV6_131084_PI430048170 mRNA
AGTGGACTAAGCTTGCACTCAAGTCAGCGTAAACCTCTTTGCCTTTCTCTCTCTCTCTTT NM_021979RefSeq chr14
+ 64540467 64543236 HSPA2 3306 heat shock 70kDa protein 2
GO:0005515|GO:0006986|GO:0090084|GO:0051861|GO:0000795|GO:0009986|GO:0036128|GO:0007286|GO:0072
562|GO:0005634|GO:0005524|GO:0005829|GO:0005739|GO:0042026|GO:0016020|GO:0070194|GO:0051082|GO:0
031662|GO:0019899|GO:0001673|GO:0007141|GO:0070062|GO:0007140 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_101493_PI430048170 0.0256465646152367 0.4113813186155121.30606737814828
1.19355477097515 1.67281777707864 A A A 3.12179234003149 2.59701649537579
2.19083817359253 P A A LNCV6_101493_PI430048170 mRNA
GCCAAAACACCAAACTATTAGACCCAAAAATGATGTTACCAACCATGTTGTTTTGCCTGT NM_152515RefSeq chr2
- 112736350 112764677 CKAP2L 150468 "cytoskeleton associated protein 2-like, transcript variant 1"
GO:0005813|GO:0005737|GO:0000922 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97129_PI430048170 0.1552473658295891.21562395970419 7.35294533413918 7.36564675828894
7.58925963402787 P P P 6.89080152640271 7.19236548172418 7.35435915044002 P P P
LNCV6_97129_PI430048170 mRNA
AATTCAGATTGTTTGTCTCCTTGTGAAGAACCATCGAAACCTGTTTGTTCCCAGCCCACC NM_004237RefSeq chr5
+ 892853 918049 TRIP13 9319 "thyroid hormone receptor interactor 13, transcript variant 1"
GO:0003712|GO:0005515|GO:0048477|GO:0006366|GO:0007286|GO:0005634|GO:0001556|GO:0007283|GO:0005
524|GO:0042802|GO:0006302|GO:0007144|GO:0001673|GO:0007130|GO:0007141|GO:0007131 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142996_PI430048170 0.4962624345428870.8630889298513960.403648936178701
1.56806332633286 0.366057969923272A A A 1.02350979784231 1.09822785497764
1.19383460043423 A A A LNCV6_142996_PI430048170 mRNA
AACTAGTATGAAAGGGTTATAAAGTAACAGAGGAAAACGCCTCTTGGTCCCTTTAAAAAA NM_001165035 RefSeq

chr3 + 13568739 13638422 FBLN2 2199 "fibulin 2, transcript variant 3"
GO:0031012|GO:0030198|GO:0010811|GO:0005509|GO:0050840|GO:0005578|GO:0005576|GO:0031982|GO:0070
062|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130218_PI430048170 0.00877489715636594 0.571012537463745 9.59126064930995
9.43251771607911 9.67384994799073 P P P 10.2577290869307 10.2345602971998
10.6095036619882 P P P LNCV6_130218_PI430048170 mRNA
AGTGCCCACTGCCTTTCCATCCTGCAATTGTGGCCTGTGTATAATTAAATGATTTTAGCC NM_018233 RefSeq chr16
+ 56451511 56477495 OGFOD1 55239 2-oxoglutarate and iron-dependent oxygenase domain
containing 1
GO:0031543|GO:0031418|GO:0031544|GO:0005506|GO:0008283|GO:0010494|GO:0005634|GO:0006449|GO:0019
511|GO:0005737|GO:0034063|GO:0018126|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142130_PI430048170 0.0514711467492509 0.706841792696355 10.1664020680736
10.1458981472226 10.3622243922857 P P P 10.5593122363098 10.5960409433611
10.9901530222205 P P P LNCV6_142130_PI430048170 mRNA
GGTGTGCAGCCTGATTTAAAACCAAACCCTGAACCCTTTTAAAGAACAATAAAACATATT NM_080391 RefSeq chr1
- 31906420 31938387 PTP4A2 8073 "protein tyrosine phosphatase type IVA, member 2, transcript
variant 1" GO:0005737|GO:0005886|GO:0004727|GO:0035335|GO:0005769|GO:0070062 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_139074_PI430048170 0.0494603731660241 0.605784563529268 8.64472431072272
8.34721932139403 8.48281944984893 P P P 8.81527579688401 9.34293273111222
9.42833801212405 P P P LNCV6_139074_PI430048170 mRNA
GCTCACTACAAATTGTGACTGTAAACATTGTACTGTAAATGTTTTGTAGTTTTCCCCCAA NM_006887 RefSeq chr2
- 43222401 43226606 ZFP36L2 678 ZFP36 ring finger protein-like 2
GO:0030097|GO:0048103|GO:0043488|GO:0006355|GO:0033077|GO:0003700|GO:0008283|GO:0060216|GO:0005
634|GO:0006402|GO:0003677|GO:0035925|GO:2000737|GO:0046872|GO:0005737|GO:1900153|GO:0017091|GO:0
035019|GO:0000288. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127817_PI430048170 0.0534220065237734 0.806168284117571 8.93234582403847
8.84913076732175 8.63138189294173 P P P 9.00287116619266 9.23445098394119
9.11526699692879 P P P LNCV6_127817_PI430048170 mRNA
GCCCACCGGCCACCAACACTCCTGTAATTCCAATAAAGCAGTTTATTTTCTGAGAAAAAA NM_014714 RefSeq chr16
- 1510426 1612108 IFT140 9742 intraflagellar transport 140
GO:0005813|GO:0006996|GO:0060041|GO:0005930|GO:0048705|GO:0072372|GO:0036064|GO:0003674|GO:0042
384|GO:0030991|GO:0032391|GO:0072001|GO:0035721 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130724_PI430048170 0.110210133026519 3.21375086427076 3.18043438742267
2.40562968952069 1.23169792264533 P A A 0.764149377057254 1.04533544030666
0.524284210005342 A A A LNCV6_130724_PI430048170 mRNA
CCAGGGGTGTGGAATGGTGGGGGAATTTGTTTAAAAAGACATTTTATTATAATAAAGTCT NM_004758 RefSeq chr17
- 58301226 58328791 BZRAP1 9256 "benzodiazepine receptor (peripheral) associated protein 1,
transcript variant 1"
GO:0005739|GO:0005515|GO:0008150|GO:0005737|GO:0007268|GO:0030156|GO:0014047|GO:0007269|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134199_PI430048170 0.0405346222617822 0.443095211676529 4.51020377791199
3.68006906801409 4.45362556330136 P P P 5.53551018108226 5.40798404703192
5.35639316076761 P P P LNCV6_134199_PI430048170 mRNA
GTGAGAAATATTTTAGTGGGGTAACAAAAAGAATTGCCAAGGAAGAAAAATCCACCCAGG NM_001031712
RefSeq chr6 + 125986429 126039274 TRMT1160487 tRNA methyltransferase 11 homolog (S. cerevisiae)
GO:0000049|GO:0008168|GO:0032259|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107655_PI430048170 0.0509114420963823 2.16036591139907 5.71088801195253
6.74030328252063 6.16620932180883 P P P 5.43383561177885 4.9668377982549

5.02132647734111 P P P LNCV6_107655_PI430048170 mRNA
CAGTACATTAAGTTTGAAATGCCGGTGCTGGACAGTTTTGTTGAAAAATTAAAAGAAGAG NM_032023 RefSeq chr10
+ 44959770 44994724 RASSF4 83937 Ras association (RalGDS/AF-6) domain family member 4
GO:0005515|GO:0007165|GO:0007049 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145355_PI430048170 0.473084680724631 1.20568849847614 3.22053909438188
3.25064749049989 2.46720908322495 P P A 3.067757617304 2.6498875720498
2.47270117056732 P P P LNCV6_145355_PI430048170 mRNA
CCCAGTCGTTCCTACTTTAAAAACACGGAATAAAATTAAGGAGAGCCAATAAATGAGTAT NM_145028 RefSeq chr6
+ 35737031 35748913 ARMC12 221481 "armadillo repeat containing 12, transcript variant 1"
GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134507_PI430048170 0.402209063591003 1.04985599279537 10.8530001876237
10.8275713576444 10.7129392015433 P P P 10.6029273896048 10.7809332630766
10.7950668006029 P P P LNCV6_134507_PI430048170 mRNA
CCCTCTCCAGTGACAAGGTCATTTACAACTTACATTTACAATTTATAGTGTTTACCAGTA NM_024313 RefSeq chr22
+ 37686336 37693478 NOL12 79159 nucleolar protein 12 GO:0005730|GO:0019843 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136351_PI430048170 0.332548809839663 1.56253394616952 1.62317476085308
1.76429377793795 0.401596792386224 A A A 0.954663853966191 0.247849403313389
0.89949365875508 A A A LNCV6_136351_PI430048170 mRNA
TTTTCTGTTCTGTTTCCTTTCTGTTACAAACACAAAGGGTACATTAAAGAGCCTTTCCCC NM_001123065 RefSeq chr7
+ 47655243 47661648 C7orf65 NA chromosome 7 open reading frame 65 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_131338_PI430048170 0.0428141059180104 0.610310404039391 11.4466018169477
11.4499570538811 11.5771774989921 P P P 11.9962827527354 12.0526637065555
12.5092090214238 P P P LNCV6_131338_PI430048170 mRNA
CGTATTCTTGCCAAGTAACCACCACTTCTGCCTTAGATAATATGATTATAAGGAAATCAA NM_006111 RefSeq chr18
- 49783503 49813881 ACAA2 10449 acetyl-CoA acyltransferase 2
GO:0005739|GO:0005515|GO:0006695|GO:0006631|GO:0005743|GO:0071456|GO:0003988|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136176_PI430048170 0.0595610277079960 .807858184836695 10.2554129814808
10.4293111863937 10.102741338829 P P P 10.5501280571517 10.6814873328083
10.4912356443612 P P P LNCV6_136176_PI430048170 mRNA
CTTTTCTAGAAATAAAATCACCCTGACTGTGGGGTGCATCGGTCTCCGGAGAGCACAGCC NM_001002021 RefSeq
chr21 + 44300033 44327381 PFKL 5211 "phosphofructokinase, liver, transcript variant 1"
GO:0005515|GO:0005975|GO:0070095|GO:0044281|GO:0051259|GO:0005524|GO:0046872|GO:0006096|GO:0042
802|GO:0005829|GO:0009749|GO:0030388|GO:0016020|GO:0051289|GO:0009405|GO:0046835|GO:0006006|GO:0
019900|GO:0046676|GO:0006002|GO:0070061|GO:0070062|GO:0003872|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138005_PI430048170 0.13731718656989 0.833064392618536 7.10980576050253
6.87328576625073 7.17792426836761 P P P 7.1190023081199 7.34468989482086
7.48218046806077 P P P LNCV6_138005_PI430048170 mRNA
GCAAATGAAAAAGTCAGCTACAAAAGTTAATGAATATGCCATCTATGCAGAACAGGCAGA NM_001018024 RefSeq
chrX - 155061624 155071272 CMC4 100272147 C-x(9)-C motif containing 4 GO:0005739|GO:0008283
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127455_PI430048170 0.291020087285825 0.975925236932269 0.283079035762122
0.308786904224641 0.358944783157285 A A A 0.383942383739854 0.320392423457279
0.352283140659135 A A A LNCV6_127455_PI430048170 mRNA
TCTCAGAACTCTGCATCCTGCGGAACTGTTTTAATTACAATTATACTAACAATACACATG NM_152694 RefSeq chrX
- 78656068 78659328 ZCCHC5 203430 "zinc finger, CCHC domain containing 5"

GO:0008270|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_16266_PI430048170 0.4015718749116320.6305133069262890.3799894435508560.380339543127847
0.275633053234708 A A A 0.354816164295436 0.389383801815123 1.79060489515649 A A A
LNCV6_16266_PI430048170 mRNA
AATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACAGTA NM_178135 RefSeq
chr4 - 87303788 87322906 HSD17B13 345275 "hydroxysteroid (17-beta) dehydrogenase 13, transcript variant A"
GO:0005811|GO:0046889|GO:0008150|GO:0003674|GO:0016491|GO:0005576|GO:0005575|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103333_PI430048170 0.788184257200661 1.00753806950558 1.31948055565577
2.96085433421545 1.29550185311354 A P A 1.61434902709619 2.43697821136114
2.05802169152763 A P A LNCV6_103333_PI430048170 mRNA
CAAGACCAAGTCATTCAGAAGGCATTTGGATTTGATCCCAAAGTCGACAGTTATGTTGAG NM_001135147 RefSeq
chr4 - 102251040 102345253 SLC39A8 64116 "solute carrier family 39 (zinc transporter), member 8, transcript variant 3" GO:0005886|GO:0046873|GO:0070574|GO:0031090|GO:0006829|GO:0016021|GO:0055085
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145181_PI430048170 0.9736991461019 0.9982723824030620.279567373062431
0.5469342890362250.371633760004528 A A A 0.5159135830785640.410973117709975
0.282157821757861 A A A LNCV6_145181_PI430048170 mRNA
ACCAAGTGCCATTTCTCACTCTGGAGCCTTAATAAACTGCAATTTGTATCCAGTAAAAAA NM_003737 RefSeq chr11
- 6621323 6655849 DCHS1 8642 dachsous cadherin-related 1
GO:0001658|GO:0043931|GO:0005886|GO:0005509|GO:0045177|GO:0048565|GO:0035329|GO:0016339|GO:0003007|GO:0016020|GO:0090102|GO:0021915|GO:0016021|GO:0007156|GO:0007157|GO:0022008 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144704_PI430048170 0.4128212697628791.08488177984188 9.41281147534278
9.73174600556805 9.41767803807155 P P P 9.32183209987527 9.4880171783966
9.41863966569061 P P P LNCV6_144704_PI430048170 mRNA
GCTTGTCCTTTGGGACAAAGCAGTATTTTACTCATTCTTTGAATGTTCTCATTCTTTTGT NM_031904 RefSeq chr11 +
65386569 65413524 FRMD8 83786 "FERM domain containing 8, transcript variant 1" GO:0005856 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131978_PI430048170 0.5935063452942131.01930932541225 12.2651188760484
12.2837275437582 12.226696418664 P P P 12.1553707199209 12.3087267686927
12.2251627412294 P P P LNCV6_131978_PI430048170 mRNA
TTTTGGGTGTTTTTCTTGTTGTGTCCTGGATTCCGATAAAATTAAAGAAATTGCTTCCTC NM_007260 RefSeq chr1 +
23791155 23795539 LYPLA2 11313 lysophospholipase II
GO:0005737|GO:0016787|GO:0006631|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91164_PI430048170 0.000243059371517431 1.9954914665605 7.2719755838197
7.38157438587649 7.40821550961793 P P P 6.33221379458924 6.34194063266204
6.40002628666784 P P P LNCV6_91164_PI430048170 mRNA
ATGGGCCTCCTGGGGAACCAGTGACCTTCAAGGACGTGGCCGTGGACTTCACCCAAGAAG NM_025027 RefSeq
chr19 - 57977072 58003346 ZNF606 80095 zinc finger protein 606
GO:0006355|GO:0005737|GO:0003700|GO:0005654|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139018_PI430048170 0.461229176190337 0.9675217359245410.437810097939198
0.45912713413678 0.291130007609216 A A A 0.407430889339725 0.486323080638586
0.441859951200025 A A A LNCV6_139018_PI430048170 mRNA
TTTTGGATAACTTCTACTGTGATGTTCCCCAAGTACTGAGACTTGCCTGCACTGACACCT NM_001004707 RefSeq
chr17 + 58169655 58170579 OR4D2 124538 "olfactory receptor, family 4, subfamily D, member 2"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_58593_PI430048170 0.2762778271474740.9571147269967891 4.0219445083675 13.9510527478742
14.0914338711183 P P P 14.1358285706796 14.0845566525336 14.0354208675472 P P P
LNCV6_58593_PI430048170 mRNA
GGCTGGGAGGAGATAAACACCAACCCAGGAATTCTCAATAAATTTTTATTACTTAACCTG NM_001144831 RefSeq
chr12 - 6965351 6970753 PHB2 11331 "prohibitin 2, transcript variant 1"
GO:0005515|GO:0060744|GO:0060762|GO:0030331|GO:0005743|GO:0005634|GO:0006351|GO:0016363|GO:0005
739|GO:0043234|GO:0033147|GO:0033600|GO:0045892|GO:0060749|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_106893_PI430048170 0.0982536362672453 0.6079925666318975.72507122372115
4.79325049537064 5.18461256008655 P P P 6.04805290127887 6.07682051289222
5.87662977932216 P P P LNCV6_106893_PI430048170 mRNA
CCACCTCCTTCCTTCATAATGAGCTACAAACTACCAATGGAGGATCTTAAAGAGACCAGT NM_001042603 RefSeq
chr12 - 280056 389455 KDM5A 5927 lysine (K)-specific demethylase 5A
GO:0005515|GO:0019907|GO:0003700|GO:0006366|GO:0003713|GO:0005730|GO:0006325|GO:0005634|GO:0007
275|GO:0003677|GO:0032922|GO:0005737|GO:0003682|GO:0016706|GO:0005654|GO:0008270|GO:0045893|GO:0
055114|GO:0016568. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131525_PI430048170 0.0127817651931772 0.6321653378274745.92360452758257
6.19462433047723 6.02482226370372 P P P 6.48987206535117 6.88859022582812
6.73486047443974 P P P LNCV6_131525_PI430048170 mRNA
AATATTTAACATAATTAAAGATGGACCCATAAGAGTGACGCCTGTGGAGCGCGTGCTCTT NM_001270764 RefSeq
chr10 - 124007665 124093607 CHST15 51363 "carbohydrate (N-acetylgalactosamine 4-sulfate 6-O)
sulfotransferase 15, transcript variant 3"
GO:0030206|GO:0000139|GO:0005975|GO:0009405|GO:0050659|GO:0044281|GO:0019319|GO:0016021|GO:0050
656|GO:0030204|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140769_PI430048170 0.0736003712215611.02967502740196 0.396442665093816
0.4083356969589050.434584907218475A A A 0.3625927615784330.353298314347614
0.396804592737034A A A LNCV6_140769_PI430048170 mRNA
GGAAATTGATTTTGAACCTGATGAAAATAAAGAATGGAAAGCTTCAGTGCTGCCGATAAA NM_002341RefSeq
chr6_GL000256v2_alt - 2879838 2881705 LTB 4050 "lymphotoxin beta (TNF superfamily, member
3), transcript variant 1"
GO:0005164|GO:0010467|GO:0005102|GO:0007267|GO:0005575|GO:0005125|GO:0005615|GO:0048535|GO:0007
165|GO:0006955|GO:0045084|GO:0043588|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128634_PI430048170 0.9390760693719591.02579403707367 0.273660470239471
0.8707399194696470.333630085424334A A A 0.4277899393306020.665731876709361
0.331179380522281A A A LNCV6_128634_PI430048170 mRNA
CCAAGAACTAAGCCAACTTGATGTGAAAAGCACAGCTGTATATAATGGTGATGTCATAAT NM_002349RefSeq chr2
- 159803355 159904756 LY75 4065 lymphocyte antigen 75
GO:0006955|GO:0006954|GO:0005887|GO:0030246|GO:0004872|GO:0070062|GO:0006897 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137162_PI430048170 0.8689424373118721.09461169777786 5.57403548904761
4.75110910967971 4.43329544038615 P P P 5.04203549903503 5.02121526830616
4.48797108941419 P P P LNCV6_137162_PI430048170 mRNA
CCCTCTCCTAGTTCATTCACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAAAA NM_022357RefSeq chr16
- 67975662 67980549 DPEP3 64180 "dipeptidase 3, transcript variant 1"
GO:0008235|GO:0006508|GO:0031225|GO:0008239|GO:0016805|GO:0046872|GO:0007140 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127124_PI430048170 0.6932025833311030.9368940099587050.464397997727021
1.55523478886668 2.284404416734 A A A 1.43063417205386 2.05449710642916

1.56538571130359 A A A LNCV6_127124_PI430048170 mRNA
CAAATTCACTTCACCTCCCTTAGCTTTAGCCCACCTGTGTGTGAAAATGACTTTGGGAAA NM_001006939 RefSeq
chr10 - 48909483 48914235 LRRC18 474354 leucine rich repeat containing 18 GO:0005737 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134492_PI430048170 0.319329794360053 1.60061160478935 2.04664384297296 2.9939056755368
1.71584520671286 A A A 2.53450444747047 1.25214625894662 0.520770381113667 A A A
LNCV6_134492_PI430048170 mRNA
GACAGTGTAAAAACAAAACAAATCCGCAAGGCTATGCTCAGTCTGCTGCTTACAAAATGA NM_001004752 RefSeq
chr11 - 4768978 4769917 OR51F1 NA "olfactory receptor, family 51, subfamily F, member 1
(gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135253_PI430048170 0.281027777741111 1.02825818970411 0.307367318649759
0.250040116521918 0.344080761924988 A A A 0.269429224610975 0.242670079074555
0.270164709347132 A A A LNCV6_135253_PI430048170 mRNA
ATTGAAATCGCCACTTACCTGAACCTGTCGGAGAAGCAGGTGAAAATCTGGTTTCAGAAC NM_133267 RefSeq chr4
+ 54100080 54101955 GSX2 170825 GS homeobox 2
GO:0030334|GO:0045747|GO:0006355|GO:0048665|GO:0005634|GO:0021978|GO:0048853|GO:0006351|GO:0021
527|GO:0021575|GO:0043565|GO:0002087|GO:0021798|GO:0048714|GO:0021889|GO:0060163 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141144_PI430048170 0.284537018860834 0.781387687614211 0.521533062656304
0.410319212536784 0.525361149839765 A A A 0.447169559348014 0.760063217383062
1.21594485202603 A A A LNCV6_141144_PI430048170 mRNA
TCAAGAGAACAATAGAGTGTGTCTCTTGGGGAAACGTAATAAAAATGAACTTTTCTCACC NM_175064 RefSeq chr7
+ 44000889 44010124 SPDYE1 285955 speedy/RINGO cell cycle regulator family member E1 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_130254_PI430048170 0.0764425991795787 1.42390179638256 6.63838223580626
6.24217717972472 6.15373677941896 P P P 5.86755221828643 5.88099980527234 5.8023978858596
P P P LNCV6_130254_PI430048170 mRNA
GAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGC NM_012196 RefSeq
chrX + 49331625 49338952 GAGE8 NA - NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_139566_PI430048170 0.756880938316438 0.911085803160946 2.04544669865051
2.41353419451956 2.83402411716762 A A A 2.78453699632805 1.99412156110284
2.87404752706242 A A P LNCV6_139566_PI430048170 mRNA
GTGTGTCTCCGTCTTATTTTAATACCAAATTCATCATGTAGTGAAATTATGTCAGGAGGT NM_017649 RefSeq
chr10 + 102918317 103078587 CNNM2 54805 "cyclin and CBS domain divalent metal cation
transport mediator 2, transcript variant 1" GO:0016323|GO:0015693|GO:0010960|GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_81967_PI430048170 0.12161568898067 0.694773352942141 5.39977778701771
4.92664967118826 5.59006736156637 P P P 5.54679699110136 5.77976084639049
6.17364779079675 P P P LNCV6_81967_PI430048170 mRNA
AGTCTGAATTTGAAGGTTTTGAGTATATCAATCCTCTTTTGATGTCTGCAGAAGAATGTG NM_002740 RefSeq chr3
+ 170222431 170305982 PRKCI 5584 "protein kinase C, iota"
GO:0005515|GO:0035089|GO:0043524|GO:0070830|GO:0006612|GO:0046326|GO:0070062|GO:0032869|GO:0034
329|GO:0019904|GO:0045216|GO:0045197|GO:0043234|GO:0010976|GO:0004697|GO:0005923|GO:0042462|GO:0
005886|GO:0005634|GO:0046872|GO:0005829|GO:0035556|GO:0016324|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132395_PI430048170 0.0796480915593891 0.60395251815448 4.41973741696114
4.42832432474209 4.59312744812457 P P P 5.59927761908141 4.85661335207666
5.07040628804591 P P P LNCV6_132395_PI430048170 mRNA

GTAGGCTTATCAGGGAGTTACAGTTACAATTGTTACAGTACTGTTCCCAACTCAGCTGCC NM_000148 RefSeq chr19 - 48748010 48755390 FUT1 2523 "fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)" GO:0042355|GO:0005794|GO:0016020|GO:0005975|GO:0005887|GO:0032580|GO:0008417|GO:0008107|GO:0006486|GO:0036065 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_142040_PI430048170 0.108246822632041 0.400619812930438 0.358831911832609 0.348923096659604 0.325635324285858 A A A 2.26130544235707 1.58605308646033 0.775496734902336 A A A LNCV6_142040_PI430048170 mRNA
GCTTTCTCCTCGTTCTTATTTAATCTCCATTTCTACTGTGTGATCAGGATGTAATAAAGA NM_001523 RefSeq chr19 - 51713111 51723992 HAS1 3036 "hyaluronan synthase 1, transcript variant 1" GO:0005886|GO:0005975|GO:0044281|GO:0006024|GO:0045226|GO:0085029|GO:0036120|GO:0010764|GO:0005887|GO:0009405|GO:0030213|GO:0030212|GO:0050501|GO:0007155|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_139516_PI430048170 0.144091911989106 0.812190465584321 8.99093520089666 8.92668570209683 9.26645518241986 P P P 9.14883041217674 9.34552988308838 9.58059393234201 P P P LNCV6_139516_PI430048170 mRNA
CTTTTAACTGGAAATTTTTATGTGAGTTTTCCTTTTGGTGCATGGAACTGTGGTTGCCAA NM_001040708 RefSeq chr8 - 79764009 79767863 HEY1 23462 "hes-related family bHLH transcription factor with YRPW motif 1, transcript variant 2" GO:0005515|GO:0000988|GO:2001212|GO:0035912|GO:0003700|GO:0000983|GO:0006366|GO:0003184|GO:0005634|GO:2000678|GO:0060317|GO:0061314|GO:0005737|GO:0007219|GO:0009948|GO:0045944|GO:0003222|GO:0060716|GO:0046983|GO:2000820|GO:0045746|GO:0003199|GO:0003198|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135020_PI430048170 0.0433356391996512 0.67910212578604 8.58431408151318 8.51864319019265 8.70805459884036 P P P 8.96425195421707 9.0673037548651 9.42025661946554 P P P LNCV6_135020_PI430048170 mRNA
GTTGTACTCCCTAGTAGATAGGAACTGACCCCAACAATAAACTTTGATAATAAAGACAAT NM_017542 RefSeq chr1 + 166839486 166854472 POGK 57645 pogo transposable element with KRAB domain GO:0005515|GO:0006355|GO:0007275|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_126922_PI430048170 0.263021123609819 1.02041779201771 0.319367473471756 0.255129119561729 0.278433806714213 A A A 0.25597716179001 0.252684907913489 0.257518671284865 A A A LNCV6_126922_PI430048170 mRNA
GACCAACATCCTTAACTTGGAAGGGAAAACATCTCTGATTTGAACTTGTATTTATGTACC NM_005164 RefSeq chr12 - 39551219 39620041 ABCD2 225 "ATP-binding cassette, sub-family D (ALD), member 2" GO:0005515|GO:0000038|GO:0006635|GO:0042626|GO:0055085|GO:0005524|GO:0042803|GO:0043231|GO:0005829|GO:0005739|GO:0032000|GO:0016021|GO:0005778|GO:0042760|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_128373_PI430048170 0.335975422317222 0.971356444895363 0.261802930906398 0.277092757170703 0.365491822354254 A A A 0.380776355644256 0.315564375506936 0.335237373861329 A A A LNCV6_128373_PI430048170 mRNA
GAACAAGTAGCATGTAATGCAACTGTTTGACAGTTTAACTCAAGTCATGCTTCAAACTGT NM_024721 RefSeq chr8 + 76681279 76867285 ZFHX4 79776 zinc finger homeobox 4 GO:0043565|GO:0006355|GO:0008270|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_101244_PI430048170 0.238334458513053 2.44093162298418 2.54141840050745 0.383807679034481 2.00170978231113 A A A 0.39617593307185 0.949467574549894 0.392894019157995 A A A LNCV6_101244_PI430048170 mRNA
TAAAGTAGGAGGAAAAATGACCATGTCCAAGGGCATCAACCATTCCACCGAGATACTTTC NM_013361 RefSeq

chr19 + 44052010 44067994 ZNF223 7766 zinc finger protein 223
GO:0008150|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_127009_PI430048170 0.162009475238741 0.84892455345058 9.01223525197497
9.01716316187105 8.66812355791397 P P P 9.14119318873362 9.19485307191534
9.09561446564862 P P P LNCV6_127009_PI430048170 mRNA
TTGTCCCGGAAAACCCACCAACGTTTGTAACTTTGATTAAACTTCACTTTGTACAAAAAA NM_138466 RefSeq
chr19 - 58367622 58381022 ZNF837 NA "zinc finger protein 837, transcript variant 2" NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_105701_PI430048170 0.388538990921338 0.786656364747455 0.549239542568378
1.91414842902404 0.584987026328384 A A A 1.4571927432035 1.67213715135614
1.39257085684621 A A A LNCV6_105701_PI430048170 mRNA
AAATAAACGGATCAACATCCAAAGCAACAAGATGGGGAAACTGACTCGATGAAGCTCAGG NM_001099408
RefSeq chr5 + 176630681 176646641 EIF4E1B NA eukaryotic translation initiation factor 4E family
member 1B NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144596_PI430048170 0.577036560577213 1.7694936332801 2.97862526180255
0.264442870467989 1.70491164540001 P A A 1.14999841103037 0.318948933513445
1.81115368492543 A A A LNCV6_144596_PI430048170 mRNA
GGTGGAGAGAATAAAGAACCATTGCACATCTTACATCCACAGTAATGAGTCATAATATTA NM_182985 RefSeq
chr15_KI270849v1_alt + 59738 91200 TRIM69 140691 "tripartite motif containing 69, transcript variant a"
GO:0005737|GO:0004842|GO:0016567|GO:0016607|GO:0005886|GO:0016874|GO:0006915|GO:0008270|GO:0005
634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132990_PI430048170 0.934577055393119 1.00257487677404 7.67943517586288
7.66781846096021 7.75342659060044 P P P 7.58261947578397 7.65164563387499
7.84392419099191 P P P LNCV6_132990_PI430048170 mRNA
CTTCCCAAGTTTGAAGGTTCAGACTTAAAACCTGAATTGGAATTACTTCTGTACAAGAAA NM_138421 RefSeq
chr11 -18080342 18106091 SAAL1 113174 serum amyloid A-like 1 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_73510_PI430048170 0.16061496184424 0.7996603585893249.75450699126454 9.69342768614133
10.0187482848856 P P P 9.92658025529392 10.0643351334708 10.418880385235 P P P
LNCV6_73510_PI430048170 mRNA
TCACAACAAAATCACACATGTCATCTTTGTCAAGGGCATAAATATATCATTCATACCCCC NM_007208RefSeq chr3
- 131462200 131503016 MRPL3 11222 mitochondrial ribosomal protein L3
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0003723|GO:0005743|GO:0006
412|GO:0005762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143526_PI430048170 0.276348296704781 1.27911931555442 9.01251136270463
9.41408481586987 9.76514161476067 P P P 9.04512675680467 8.81250368035343
9.32085217215117 P P P LNCV6_143526_PI430048170 mRNA
GCAGGCTGGCTTTGTATAAACTTATCCTCTGGTTTCCTATATGTTGTAAATATTTAGACC NM_014949RefSeq chr1
- 155913042 155934442 KIAA0907 22889 KIAA0907 GO:0003723 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126713_PI430048170 0.267372190095826 1.1539729327606 8.35383073023987
8.24135597913099 8.34794190725008 P P P 8.20699462843571 7.80547744598761
8.27093736784138 P P P LNCV6_126713_PI430048170 mRNA
CTATGTGACCAGTTCTCTGTATGAATGGAAGGGAAAAGAATTAAAAATCTTGCAAAGGGG NM_033625RefSeq chr4
+ 108620592 108630483 RPL34 6164 "ribosomal protein L34, transcript variant 2"
GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0005730|GO:0006415|GO:0006
412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0000184|GO:0016032|GO:0022625|GO:0044267|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_110141_PI430048170 0.0179291224751707 1.17652123295923 6.21219986356569
6.1827011686864 6.11729089017679 P P P 5.96797036879442 5.84470814928921
5.99322539306439 P P P LNCV6_110141_PI430048170 mRNA
AATTCGGATCCTTTTAAGTATAACAATTCAACTGGGATCAGCTATGAGACCCTGGGGCCG NM_020218RefSeq chr17
- 44191804 44198161 ATXN7L3 56970 "ataxin 7-like 3, transcript variant 1"
GO:0005515|GO:0016578|GO:0030374|GO:0000124|GO:0003713|GO:0006325|GO:0071819|GO:0008270|GO:0045
893|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67457_PI430048170 0.00109820158927517 1.52290968142387 10.0309427069765
10.1874833244331 10.08173560474 P P P 9.44308216202678 9.50887434169206
9.53072436476357 P P P LNCV6_67457_PI430048170 mRNA
ACCTTGGCTCCAAGATACTCCTCACCTGCTCCTTGAATGACAGCGCCACAGAGGTCACAG NM_001728RefSeq chr19
+ 572453 583493 BSG682 "basigin (Ok blood group), transcript variant 1"
GO:0005515|GO:0005886|GO:0072661|GO:0043434|GO:0044281|GO:0050900|GO:0051591|GO:0005537|GO:0005
739|GO:0046697|GO:0022617|GO:0006090|GO:0030198|GO:0042475|GO:0002080|GO:0044237|GO:0070062|GO:0
042470|GO:0007566|GO:0042383|GO:0016020|GO:0000139|GO:0007596|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_9546_PI430048170 0.7149562084412350.565001119367153 1.72016717566344 1.25016585127842
1.04985540178205 A A A 1.56549010701283 3.2505239502879 0.297299881238702 A P A
LNCV6_9546_PI430048170 mRNA
CTCCCTTCACTTCCTGGCCATCCAGGCATCTGTGTCTGTGTCCGGGAAGTGGAGGAGGGC NM_001291920 RefSeq
chr9 + 134379294 134440586 RXRA 6256 "retinoid X receptor, alpha, transcript variant 2"
GO:0005515|GO:0010467|GO:0000790|GO:0003700|GO:0006367|GO:0055010|GO:0044212|GO:0055012|GO:0003
707|GO:0035357|GO:0005634|GO:0044281|GO:0003708|GO:0051289|GO:0042809|GO:0045944|GO:0043401|GO:0
043010|GO:0004879|GO:0032526|GO:0060528|GO:0044255|GO:0008203|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143722_PI430048170 0.5035313788261020.798141475140803 2.90628684569012
2.47184500080196 1.95778226815418 A A A 3.13166734561754 2.11708514796518
3.01933339606937 P A P LNCV6_143722_PI430048170 mRNA
GAGAAAAAGAAAAAAGGTATCCTACCCAGAGGCAACCAGATAAACTTTTTTGCCTGTGCA NM_015330RefSeq chr22
+ 24270816 24417740 SPECC1L 23384 "sperm antigen with calponin homology and coiled-coil
domains 1-like, transcript variant 1"
GO:0030835|GO:0007049|GO:0005737|GO:0031941|GO:0030036|GO:0016477|GO:0005815|GO:0007026|GO:0005
819|GO:0005921|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138178_PI430048170 0.3429385359846711.33600615378762 0.367205258027958
1.34345671674947 0.605402196918886 A A A 0.303001068272807 0.29927611809257
0.622339880540307 A A A LNCV6_138178_PI430048170 mRNA
GTGCCTTTAAAAAGACTGTAGGGAAGGCAAAGGCCTCTATAGGATTCATATTTTAATTAT NM_001004733 RefSeq
chr11 - 58439119 58440173 OR5B12 NA "olfactory receptor, family 5, subfamily B, member 12" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133669_PI430048170 0.0111790843277669 0.822257307430979 10.7875765289639
10.7541796175883 10.6415624358451 P P P 11.05191640413 10.976840583642
11.0045985330523 P P P LNCV6_133669_PI430048170 mRNA
TGCTACAGAGGAAATCAGTGGATTTCTTTGAGCTAGGAGAATAAGAGTCTGGAGACTGGG NM_001198903 RefSeq
chr1 - 155659441 155688656 YY1AP1 55249 "YY1 associated protein 1, transcript variant 10"
GO:0005515|GO:0006355|GO:0005737|GO:0051726|GO:0005634|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135994_PI430048170 0.0277368654627874.95045223854961 3.54490541048359
3.44360799958156 3.5205548614134 P P P 1.63662052202729 0.274254742268891
1.35325073109449 A A A LNCV6_135994_PI430048170 mRNA

GGACAAACTGCCCAGACTTGAGCCCAATTAAATTTTATTTTTGCTGGTTTTGAATGAAAA NM_138805 RefSeq chr3 - 58633942 58666834 FAM3D 131177 "family with sequence similarity 3, member D" GO:0005576|GO:0046676|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_145123_PI430048170 0.0982027461723706 0.7634389833042936.91144045638915 6.97173716481119 7.08649523932146 P P P 7.15180978190103 7.32588961143393 7.62547872398467 P P P LNCV6_145123_PI430048170 mRNA
CCCTGGATAGGCAAGGGATAACTCTTCTAACACAAAATAAGTGTTTTATGTTTGGAATAA NM_002421 RefSeq chr11 - 102789909 102798235 MMP1 4312 "matrix metallopeptidase 1, transcript variant 1" GO:0005509|GO:0005578|GO:0005576|GO:0050900|GO:0004175|GO:0022617|GO:0007596|GO:0030198|GO:0030574|GO:0006508|GO:0016032|GO:0008270|GO:0004222|GO:0032461|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_141306_PI430048170 0.0360660630083767 0.6611965910539831 0.679578475051 10.4791129811461 10.8633560724635 P P P 11.1412570425416 11.0949139555847 11.5559389078576 P P P LNCV6_141306_PI430048170 mRNA
ATGTCATGTATTCTCAATAGGCTGTATTCCCAGCAGTCAATAAATGAACACCCGTAAAAA NM_004539 RefSeq chr18 - 57600660 57621945 NARS 4677 asparaginyl-tRNA synthetase GO:0005739|GO:0010467|GO:0005737|GO:0006421|GO:0004816|GO:0003676|GO:0005524|GO:0070062|GO:0006418|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_129825_PI430048170 0.5987238815141471.15088411435152 0.325835733250745 1.08598963516298 0.329109279326457 A A A 0.4948466903438350.420266617253804 0.353644977231339 A A A LNCV6_129825_PI430048170 mRNA
CCTCTGGGTTCCCAAGTTGAAGCCTAGACTTCTGGCTCAAATGAAATAGATGTTTATGAT NM_052968 RefSeq chr11 - 116789369 116792420 APOA5 116519 "apolipoprotein A-V, transcript variant 1" GO:0006695|GO:0010898|GO:0030300|GO:0010902|GO:0005615|GO:0034361|GO:0034364|GO:0034362|GO:0019433|GO:0044255|GO:0042632|GO:0033344|GO:0043691|GO:0060230|GO:0034370|GO:0042157|GO:0006641|GO:0055090|GO:0019899|GO:0008047|GO:0035473|GO:0051006|GO:0050996|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135879_PI430048170 0.1169643677284680.7807969541651714.75591421093462 4.99364711662464 5.25246750949565 P P P 5.17266958773092 5.3824609658039 5.53752572851152 P P P LNCV6_135879_PI430048170 mRNA
GTCTGACATTGTAGCATTCCCTGGGCAGTCATATATCCCATAAAATCGTAAAAGTATGTG NM_001256708 RefSeq chr4 - 144994574 145098541 ANAPC10 10393 "anaphase promoting complex subunit 10, transcript variant 4" GO:0007094|GO:0007067|GO:0070979|GO:0005680|GO:0051437|GO:0005654|GO:0051436|GO:0000278|GO:0031145|GO:0051439|GO:0051301|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135896_PI430048170 0.00314181978748482 0.2778500836577593.06766383992426 2.42050050249271 2.5153049325356 P A A 4.0987635650182 4.70383041045974 4.74548170533446 P P P LNCV6_135896_PI430048170 mRNA
TATGTGCTTATGTACATATCATTGGAATGAAAGTTTCATTAAATAATTACCCTTAAAAAA NM_025136 RefSeq chr19 - 45546280 45584864 OPA3 80207 "optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia), transcript variant 2" GO:0050905|GO:0005739|GO:0070584|GO:0040007|GO:0007601|GO:0050896|GO:0019216 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_138888_PI430048170 0.3097067056417191.03349537987752 0.303925434103303 0.2550533024212210.374875522609231 A A A 0.2749046045661840.244112767370173 0.274547080363178 A A A LNCV6_138888_PI430048170 mRNA
CCCAAAAGAGAAATAAATGCTCACAAGTGCTGTAGAATTAAACTTCAGAAGTTCTAACCT NM_003049 RefSeq chr14 - 69775834 69797289 SLC10A1 6554 "solute carrier family 10 (sodium/bile acid cotransporter), member 1"

GO:0016323|GO:0005886|GO:0005887|GO:0015721|GO:0008508|GO:0006810|GO:0008206|GO:0044281|GO:0006
814|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130496_PI430048170 0.0700360461547003 0.6978497157498242.61196827941376
2.24232669338237 2.7601079043084 A A A 2.76925401076796 3.22887996205614
3.17875131219569 P P P LNCV6_130496_PI430048170 mRNA
GTGTGAGCCAGTGATCTATAAAGAAACATAAGCTTAAAGTTGTTTATCACTGTGGTGTTA NM_153757RefSeq chr4
- 88695914 88697872 NAP1L5 266812 nucleosome assembly protein 1-like 5 GO:0006334|GO:0005634
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135116_PI430048170 0.5235005112067440.8327621337010040.586277959293254
0.4800294798577220.597805742838933A A A 1.30940943731168 0.546441449391798
0.439585019765231A A A LNCV6_135116_PI430048170 mRNA
GCCAAACAACCAAGTCATCATTGATACTGTAGTAAAGGTCATCTTTGCATTTTACACTTT NM_001244752 RefSeq
chr9 + 33524412 33573003 ANKRD18B 441459 ankyrin repeat domain 18B NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_138813_PI430048170 0.4393010052667580.7015590198587980.49783800191159
0.3932981220066041.5273330369395 A A A 0.8708273600312950.85493625168887
2.12308807569326 A A A LNCV6_138813_PI430048170 mRNA
ACACCTTTGTTTTTCATACCAGTACCTGAAGTAGGCTCAATAAAAGAGTCTTTACAGTGA NM_006716RefSeq chr7
+ 87876228 87909541 DBF4 10926 DBF4 zinc finger
GO:0006260|GO:0000082|GO:0008270|GO:0005654|GO:0043085|GO:0008047|GO:0003676|GO:0000278 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133264_PI430048170 0.0049656895786945 0.26902016750438 1.65902906391676
1.85127017872528 2.504049005928 A A A 3.57003169749674 3.98686263591288
4.20997121319547 P P P LNCV6_133264_PI430048170 mRNA
CAGCATTCTAGCAATCCTTCGACTTTTGTGATAGCAAACCATAAAAACAATTTTAGTGGC NM_177925RefSeq chr12
+ 14774335 14778002 H2AFJ 55766 "H2A histone family, member J, transcript variant 1"
GO:0008150|GO:0003674|GO:0046982|GO:0005634|GO:0000786|GO:0003677|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144611_PI430048170 0.0115446887311954 0.5599323689410667.79872894134313
7.78744900749233 8.13537172009535 P P P 8.53530214335596 8.66790595903158 9.013111872393
P P P LNCV6_144611_PI430048170 mRNA
CTTTCGGTATGGTAAAATTGAACCAATCACAGTTAAGATGAGAGATCAACCTGAGTTTTA NM_178012RefSeq chr6
- 3224260 3227734 TUBB2B 347733 "tubulin, beta 2B class IIb"
GO:0005515|GO:0051258|GO:0005874|GO:0003924|GO:0005634|GO:0005525|GO:0055085|GO:0006184|GO:0005
737|GO:0006457|GO:0005200|GO:0051084|GO:0001764|GO:0007017|GO:0044267 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145574_PI430048170 0.0340168465076917 2.12213638388476 3.13709237905537
3.86340658980356 3.35002230537206 P P P 2.87246474085871 2.02037566704586
2.14695282058298 P A A LNCV6_145574_PI430048170 mRNA
AGAACATCTTCTTCATGAGCAAAGTCACCAATCCCAAGCAAGCCTAGAGCTTGCCATCAA NM_001085RefSeq chr14
+ 94612376 94624053 SERPINA3 12 "serpin peptidase inhibitor, clade A (alpha-1 antiproteinase,
antitrypsin), member 3"
GO:0005515|GO:0004867|GO:0072562|GO:0005576|GO:0005634|GO:0006953|GO:0003677|GO:0005615|GO:0019
216|GO:0005622|GO:0010951|GO:0006954|GO:0030277|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_101129_PI430048170 0.2150680833563910.5845131922996080.35550779469809
0.4318016699019680.364888950076477A A A 0.5744911809709450.797547610046443
1.79598618863541 A A A LNCV6_101129_PI430048170 mRNA
GAAAACTTTCAGTTTTGTTTCCTTGCCTGCAAGAAACGAAACTCAACCGAAAGCCTGCAG NM_017523RefSeq chr17

+ 6755836 6775645 XAF1 54739 "XIAP associated factor 1, transcript variant 1"
GO:0005739|GO:0060337|GO:0031333|GO:0035456|GO:0019221|GO:0006915|GO:0008270|GO:0005634|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133750_PI430048170 0.1781397110763 0.8449678778031680.535510543965293
0.5359492546321410.313326750748272A A A 0.5662820497133280.594855527488831
0.934209499148232A A A LNCV6_133750_PI430048170 mRNA
GTCAAAGCACACAGGCAATCCTACTTCAAGTTTCCATGAAGAAAACCTCATCTGCAGCAC NM_000775RefSeq chr1
- 59893307 59926751 CYP2J2 1573 "cytochrome P450, family 2, subfamily J, polypeptide 2"
GO:0019369|GO:0008392|GO:0006805|GO:0070330|GO:0005506|GO:0008395|GO:0019373|GO:0008016|GO:0071
614|GO:0044281|GO:0006690|GO:0043651|GO:0043231|GO:0005737|GO:0019825|GO:0042738|GO:0005789|GO:0
016712|GO:0008405|GO:0008404|GO:0070062|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_131973_PI430048170 0.0485751245093559 1.90483019069391 9.57226321537308
9.63863951210434 9.49719196403792 P P P 8.15610659417566 8.91198507375548
8.75005819976308 P P P LNCV6_131973_PI430048170 mRNA
GAAGTGTTGTTGCTATGGTGACGTCCTTTTGCTGTGAATAAAGGTGCTCTTTGCAGCAAA NM_001040167 RefSeq
chr7 + 2519844 2528429 LFNG 3955 "LFNG O-fucosylpeptide 3-beta-N-
acetylglucosaminyltransferase, transcript variant 1"
GO:0045747|GO:0033829|GO:0007386|GO:0001756|GO:0005576|GO:0014807|GO:0031982|GO:0046872|GO:0032
092|GO:0003674|GO:0001541|GO:0030173|GO:0007219|GO:0008152|GO:0009887|GO:0007143|GO:0008593 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111810_PI430048170 0.1680748214194010.6322723187630632.36600171964925
3.10973233006448 2.39763536772341 A P A 3.80353204393765 3.20761688119661
2.79469897072217 P P P LNCV6_111810_PI430048170 mRNA
AGGACCGGCTTCAGTGTCCCATCTGCCTGGAGGTCTTCAAGGAGTCCCTAATGCTACAGT NM_198924RefSeq chr7
- 72959476 72969466 TRIM73 NA tripartite motif containing 73 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135459_PI430048170 0.0177061040290173 2.40117700680356 9.92537020324737
9.84181546750117 9.81888309366642 P P P 8.94116711661542 8.43818006730299
8.34375956958418 P P P LNCV6_135459_PI430048170 mRNA
CTCACTCTATATTTATGGGAGGAAAAGTGAAGATTAAATTCCCAAGTTGTGCGTGTGTCT NM_198447RefSeq chr1
- 204198159 204214092 GOLT1A 127845 golgi transport 1A
GO:0006629|GO:0000139|GO:0016021|GO:0016192|GO:0015031|GO:0016298 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132584_PI430048170 0.4508537700097651.21471247526666 2.27562224760707
1.64516702311056 2.50059289809445 A A A 1.91771924730366 1.95160345998093
1.83742411458085 A A A LNCV6_132584_PI430048170 mRNA
TCTGAAAACTCATTAGAGATGTTGAGTCTTATCAAATAAAAAGCATGAGACATCATGGCC NM_000864RefSeq chr1
- 23191894 23194729 HTR1D 3352 "5-hydroxytryptamine (serotonin) receptor 1D, G protein-coupled"
GO:0005886|GO:0007268|GO:0009636|GO:0051378|GO:0007193|GO:0014827|GO:0007210|GO:0040012|GO:0004
993|GO:0005887|GO:0007187|GO:0050795|GO:0042310 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137688_PI430048170 0.9036445260008750.9957738351433060.468038456654458
0.43072381416154 0.309007824420017A A A 0.3582099674649160.423852431759643
0.447316992762726A A A LNCV6_137688_PI430048170 mRNA
CATCTTTCATACCATATCACACTACTACCACTTTTTGAAGAATCATCAAAGAGCAATGCA NM_003154RefSeq chr4
+ 69995930 70002456 STATH 6779 "statherin, transcript variant 1"
GO:0005515|GO:0030345|GO:0030197|GO:0001503|GO:0046848|GO:0005576|GO:0030502|GO:0031214|GO:0046
541 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136654_PI430048170 0.0010868054399881 2.60161012345187 6.78086563703428

6.91837812403476 6.86179934901123 P P P 5.37692089203813 5.64617024319414
5.38655478559472 P P P LNCV6_136654_PI430048170 mRNA
ACAAAGGCTTTGATATCAGAATGAACTGTCAAGGGAGGTGCTGGAGAGGGATTAACCTGT NM_178422 RefSeq chr1
- 25861483 25871253 PAQR7 164091 progestin and adipoQ receptor family member VII
GO:0048477|GO:0005886|GO:0043401|GO:0003707|GO:0007275|GO:0016021|GO:0048545|GO:0005496 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140940_PI430048170 0.1571037810527651.07191536801882 0.501880697255163
0.4300829959868080.534001488875374 A A A 0.3056143107628320.38912384005708
0.468038456654458 A A A LNCV6_140940_PI430048170 mRNA
CCACTTGTTAAATCAGGCATGGGAGGAGGAGAGCAGAAAATATAATTGCCTTCTAAAGAT NM_012464 RefSeq chr4
+ 165873257 166104457 TLL1 7092 "tolloid-like 1, transcript variant 1"
GO:0001501|GO:0022617|GO:0030198|GO:0005518|GO:0005509|GO:0006508|GO:0008270|GO:0005576|GO:0004
222|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130306_PI430048170 0.00316048999016481 0.4867531958763957.93400463068649
7.93725443671361 8.30180527814618 P P P 9.02726000179809 8.96597321725094
9.30480096474962 P P P LNCV6_130306_PI430048170 mRNA
CCTGTACTGTTGGTATTGTGTTAGTGTATGGACCAATACTGCCTGTAATAAAGATTTTAT NM_014153 RefSeq chr16
- 11750585 11797258 ZC3H7A 29066 zinc finger CCCH-type containing 7A GO:0005634|GO:0046872
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109382_PI430048170 0.2634601815903040.9077844959065414.88465701460036
4.63889576535757 4.83532493169992 P P P 4.85949428475207 4.83920916406845
5.07808681702946 P P P LNCV6_109382_PI430048170 mRNA
ACAGATCCTTGCAACTATCAGTTAATTCCAGCAGTACCTGGAATATCTCCTAATTCCACC NM_015231 RefSeq chr11
- 47778117 47848505 NUP16023279 nucleoporin 160kDa
GO:0005515|GO:0007077|GO:0010467|GO:0005975|GO:0019083|GO:0019221|GO:0019058|GO:0044281|GO:0005
635|GO:0015031|GO:0055085|GO:0010827|GO:0005829|GO:0008645|GO:0006406|GO:0015758|GO:0005487|GO:0
005643|GO:0031080|GO:0009405|GO:0016032|GO:0000776|GO:0000278 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_133874_PI430048170 0.2191783913950541.01792867643434 0.30697586569377
0.2752576691534650.325629165384509 A A A 0.2861427404722680.271243425224844
0.273972307890771 A A A LNCV6_133874_PI430048170 mRNA
CTTCAGAAGTTTCACCCTTTTTAATCTCTCAGCCACAAACCTCAGTTTCCAAATATTTGT NM_006781 RefSeq
chr6_GL000253v2_alt - 3597690 3676908 C6orf10 10665 "chromosome 6 open reading frame 10,
transcript variant 1" GO:0005634|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136466_PI430048170 0.000446669257353651 0.3423618736815485.39225541990955
5.4700906039736 5.7440532482908 P P P 6.94932506943378 7.06438799686312
7.24095967650484 P P P LNCV6_136466_PI430048170 mRNA
TACCTTGTTACAGTTGGTTTAGTGTAGTGGATTATTGACATGACATCATGAGAAGATGTG NM_012097 RefSeq chr2
- 151800965 151828495 ARL5A 26225 "ADP-ribosylation factor-like 5A, transcript variant 1"
GO:0005622|GO:0007264|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138662_PI430048170 0.1865804812445760.9324059611672840.435630905206805
0.4584534021438360.29566927261953 A A A 0.5670104220483780.485756204935381
0.442437347238778 A A A LNCV6_138662_PI430048170 mRNA
AACCATAGGGAATTTTCTCTTCTAACAAGCACCAGACCTGCTTGCTGCCAAGCGTTTGAA NM_152219 RefSeq chr17
- 40360652 40364693 GJD3 125111 "gap junction protein, delta 3, 31.9kDa"
GO:0005515|GO:0005243|GO:0034220|GO:0007154|GO:0009986|GO:0005887|GO:0005922|GO:0016264|GO:0005
216|GO:0009749 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129303_PI430048170 0.00998394192631676 0.6954588751735537.85935411465781
7.99531576117481 7.74999028923571 P P P 8.28757018051854 8.55962742913812

8.32448900880452 P P P LNCV6_129303_PI430048170 mRNA
TCGCTCTAGACATAGTCTTCCTGCAATAAAAAAGTGGATCCTGCATTCCCCACCAAAAAA NM_145173 RefSeq chr19
- 2714566 2721392 DIRAS1 148252 "DIRAS family, GTP-binding RAS-like 1"
GO:0006184|GO:0005886|GO:0043406|GO:0007264|GO:0003924|GO:0005525|GO:0051019 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_69478_PI430048170 0.1500209380271281.26985495552799 7.16724902697057 7.67517339088818
7.53127487910798 P P P 7.03398235040412 7.2058624710379 7.14093693599032 P P P
LNCV6_69478_PI430048170 mRNA
GTACGAGTCGGCCAAGTTGATGAATGTGACCCAGACAGCGTGGTCCTCTGCCTCTTGGCC NM_015675 RefSeq chr19
+ 2476124 2478259 GADD45B 4616 "growth arrest and DNA-damage-inducible, beta"
GO:0005515|GO:0043065|GO:0006950|GO:0046330|GO:0006915|GO:0005634|GO:0007275|GO:0030154|GO:0000
186|GO:0005737|GO:0000185|GO:1900745|GO:0051726|GO:0006469 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132995_PI430048170 0.0055794814887363 0.3574186858738515.41373561238881
4.87385075780245 5.30477689861028 P P P 6.60870086402343 6.65379861669287
6.82792510621514 P P P LNCV6_132995_PI430048170 mRNA
CTGCCTTGGGATGATTGGAGCTCTTACCATCAAAATCAGTTATTCAAGTGCTTGCCCAGT NM_014797 RefSeq chr6
- 109462515 109483237 ZBTB24 9841 "zinc finger and BTB domain containing 24, transcript variant 1"
GO:0005515|GO:0006355|GO:0002244|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135838_PI430048170 0.3209150574882480.8516885910460925.26715104057393 5.0234237012623
5.42895745182643 P P P 5.20210122388054 5.44644576418421 5.74329333350781 P P P
LNCV6_135838_PI430048170 mRNA
TCCCTATCCAGTGCTTGCCCTTGGAATTGTCTCTAAATGCATCAAGCATACAATAAAAAA NM_001145513 RefSeq
chr7 - 29920102 29990118 SCRN1 9805 "secernin 1, transcript variant 1"
GO:0003674|GO:0031965|GO:0005737|GO:0006508|GO:0005634|GO:0006887|GO:0016805 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137449_PI430048170 0.4244296018550751.36706645926306 1.37349611602571
0.3174732026692550.281359618363819A A A 0.3057814751901090.308549369754648
0.288409240212262A A A LNCV6_137449_PI430048170 mRNA
TCGTGAGGAGCTGTTGGGTGTCTTGCCTCTAGAGGCTTTGAGAAGCTCAGCTGCCTTCCT NM_001146151 RefSeq
chrX + 153905074 153907166 AVPR2 554 "arginine vasopressin receptor 2, transcript variant 2"
GO:0005515|GO:0008284|GO:0005886|GO:0005783|GO:0007249|GO:0021537|GO:0001992|GO:0032870|GO:0007
190|GO:0003084|GO:0045907|GO:0005000|GO:0031398|GO:0006833|GO:0032609|GO:0034097|GO:0042277|GO:0
007588|GO:0005794|GO:0055085|GO:0003091|GO:0007599|GO:0010628|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132434_PI430048170 0.1501891618211570.9383099589369340.244746962777786
0.2888282107084640.295613256051042A A A 0.44693603349247 0.348945223084687
0.305777390173732A A A LNCV6_132434_PI430048170 mRNA
TGCCTAACATGTGGACTTTTACAATAAAAATGCTGCATTCTAATCCATGGTGGCATCTCA NM_198903 RefSeq chr5
+ 162067641 162155539 GABRG2 2566 "gamma-aminobutyric acid (GABA) A receptor, gamma 2,
transcript variant 3"
GO:0005515|GO:0030424|GO:0005230|GO:0030054|GO:0005886|GO:0004890|GO:0034707|GO:0007268|GO:0060
077|GO:0007214|GO:0009791|GO:0055085|GO:0005254|GO:0005737|GO:0034220|GO:0032590|GO:0005887|GO:0
045211|GO:0006810|GO:0008503|GO:0030534|GO:0051932|GO:0071420 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129663_PI430048170 0.0156644642774188 1.14524462876872 9.85564438911563
9.93053000916254 9.8156838659983 P P P 9.66144695235316 9.70289774749184
9.65240702021407 P P P LNCV6_129663_PI430048170 mRNA

CTGCAATAAACGACAGCCTCGGCTGCCTCGTGCTGTGTCTGTCCTGTTGTCTGCAAAAAA NM_178511 RefSeq chr19 + 47274884 47275723 INAFM1 255783 "lnaF-motif containing 1, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144790_PI430048170 0.0033632583185425 0.3338728513927620.61024538881688 0.3107893318892960.48182693744382 A A A 2.3567920789571 1.81153638190195 1.94020597371056 A A A LNCV6_144790_PI430048170 mRNA
CATAGGTAACTCTACTTTCACAAATGAGGATAGTTTAACGGATAGAAGAAACAAGCACAT NM_024672 RefSeq chr4 + 82900683 82920131 THAP9 79725 THAP domain containing 9 GO:0043565|GO:0015074|GO:0006310|GO:0006313|GO:0046872|GO:0016740|GO:0004803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138507_PI430048170 0.0284733053697001 2.05349567408078 5.77563727445871 5.95416039769237 5.58827663933468 P P P 4.33402020106419 5.13190290667109 4.64764933406473 P P P LNCV6_138507_PI430048170 mRNA
ATTTACTTAGCTCAAGTCTGAAGCTGTAGATACTGGAAGACAATGCACCTTGGAGGGTGG NM_001195736 RefSeq chr1_KI270762v1_alt + 137939 142659 FAM213B 127281 "family with sequence similarity 213, member B, transcript variant 1" GO:0019371|GO:0019369|GO:0005737|GO:0001516|GO:0005783|GO:0043209|GO:0047017|GO:0044281|GO:0070062|GO:0055114|GO:0016616|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143921_PI430048170 0.00981742257927001 1.30076098982292 9.06384373012805 9.08934171762871 9.04614173616024 P P P 8.76271610948468 8.68943027160557 8.60513692219724 P P P LNCV6_143921_PI430048170 mRNA
GGATGGGAATTTTCATGTACATGTGTGGCATGTGGAAAATTTCAAATAAAATGGACTTGA NM_024963 RefSeq chr7 - 5475796 5513768 FBXL18 80028 F-box and leucine-rich repeat protein 18 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140639_PI430048170 0.0059235258900131 1.5217210478389 12.2599444738449 12.3156175506691 12.1985075057258 P P P 11.7640010817983 11.6706223203085 11.5137080243753 P P P LNCV6_140639_PI430048170 mRNA
CTGCTTTTCTTAGTCTGATACCAAGCAAGGCCTTTTCTGAATAAATTCATTTGACTTTGANM_007346 RefSeq chr20 + 62804824 62814000 OGFR 11054 opioid growth factor receptor GO:0005737|GO:0016020|GO:0005634|GO:0038003|GO:0005575|GO:0001558|GO:0004985 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137117_PI430048170 0.967369677667437 1.26482069746056 0.376472561173293 3.32418282732049 2.83590875143156 A P A 2.81418996101633 2.40269398472303 1.18196557668038 P A A LNCV6_137117_PI430048170 mRNA
AAATTCCTTTGAACTATCTGTGGTTATTGCTCAACTCTGCTGTTCACATTCTCTCCCTCC NM_005140 RefSeq chrX + 151734745 151745564 CNGA2 NA cyclic nucleotide gated channel alpha 2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_8215_PI430048170 0.0683804649896329 0.64412293765853 11.3981262288331 11.417800135387 11.8781025917661 P P P 11.9253605221996 12.0791114504069 12.5662661999328 P P P LNCV6_8215_PI430048170 mRNA
TGACTTAACTGATCATGCATGATCCCTCATCCCTGAAATTGAGTTTATGTAGTCATTTTA NM_006793 RefSeq chr10 - 119167698 119178865 PRDX3 10935 "peroxiredoxin 3, transcript variant 1" GO:0005515|GO:0042542|GO:0008284|GO:0008785|GO:0008385|GO:0042802|GO:0005829|GO:0005739|GO:0005737|GO:0051092|GO:0018171|GO:0005759|GO:0032496|GO:0030099|GO:0043154|GO:0019900|GO:0042744|GO:0006979|GO:0043027|GO:0070062|GO:0033673|GO:0043066|GO:0019901|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92486_PI430048170 0.543200248938943 0.884400318865522 3.64238433271048 3.11582239639971 3.9163459042282 P P P 3.53506649347812 3.63594627359327 4.08489184737961 P P P LNCV6_92486_PI430048170 mRNA

TAAAACTAAGCAGCAGTGAAGACAGTGATGGGGAACAGGATTGTGATAAGACAATGCCGA NM_014423 RefSeq
chr5 - 132875378 132963662 AFF4 27125 "AF4/FMR2 family, member 4"
GO:0005739|GO:0005515|GO:0006355|GO:0003700|GO:0006366|GO:0007286|GO:0005730|GO:0035327|GO:0005
654|GO:0005634|GO:0008023 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135094_PI430048170 0.8860687860569790.9905413982526620.277467922027731
0.5209153417449190.356640834481372 A A A 0.5078105361795590.400817879980563
0.290102838530929 A A A LNCV6_135094_PI430048170 mRNA
GTCTGCTGTGTAGTTACCTGCTTACATGTACAGCCATTTCAATAAATGTATTCTTTTAACNM_001114734 RefSeq chr4
- 134196333 134201748 PABPC4L 132430 "poly(A) binding protein, cytoplasmic 4-like"
GO:0000166|GO:0003723 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136352_PI430048170 0.7573722345976081.12718397578917 0.275712861411916
0.2844648580893771.19172697635057 A A A 0.4359583406291140.364515096868206
0.623670557089564 A A A LNCV6_136352_PI430048170 mRNA
TGTGTTGAGAGCTTGAAATCTCATGGAAGAATCAGGTTTTACCATGATGGAAAATGTTAG NM_001001325 RefSeq
chr5 + 148169732 148175398 SPINK14 NA "serine peptidase inhibitor, Kazal type 14 (putative)" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131712_PI430048170 0.6045328989221670.9648808686560240.510229755618353
0.5184874679919610.378835268528413 A A A 0.3866191260816240.640683853708131
0.528002963443857 A A A LNCV6_131712_PI430048170 mRNA
GAGAGTTGTTATCCAAGTAGATCAGAGGAAGAATTACTTTACTCTACTTCTGAGAAAGAT NM_001099218 RefSeq
chr2 - 17510718 17518439 RAD51AP2 NA RAD51 associated protein 2 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_145198_PI430048170 0.000586137518856693 0.6838221096279997 12.1027314438431
11.962116804681 12.0182075406664 P P P 12.6452247857505 12.548309257758
12.5354102989162 P P P LNCV6_145198_PI430048170 mRNA
ACTTGGACTCTTGCTCTTTCTACTCTGAACTAATAAATCTGTTGCCAAGCTGGCTAGAAA NM_021975 RefSeq chr11
- 65653595 65662972 RELA 5970 "v-rel avian reticuloendotheliosis viral oncogene homolog A,
transcript variant 1"
GO:0005515|GO:0003700|GO:0006366|GO:0003705|GO:0019221|GO:0033590|GO:0032403|GO:0002756|GO:0002
755|GO:0009887|GO:0001942|GO:0031625|GO:0033256|GO:0032868|GO:0038124|GO:0038123|GO:0019901|GO:0
034134|GO:0007568|GO:0001205|GO:0000122|GO:0000978|GO:0002224|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142577_PI430048170 0.0869263120981060.6175218586243033.44558612553614
3.88386026815083 4.25753468208742 P P P 4.58193086030749 4.55205843870664
4.65043332916127 P P P LNCV6_142577_PI430048170 mRNA
GAGATTTTAGGTTGTCTGCACTCTAGCTTTTTTGTCGTTTTCTTAAGGCTTTTTTAACTG NM_001098577 RefSeq chr2
+ 101002228 101019693 RPL31 6160 "ribosomal protein L31, transcript variant 2"
GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0006415|GO:0006412|GO:0006
413|GO:0005829|GO:0006414|GO:0000184|GO:0016020|GO:0016032|GO:0022625|GO:0044267|GO:0005925|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140998_PI430048170 0.0216963986203559 1.67771841983267 11.352410675739
11.7007929791118 11.8564194979298 P P P 10.9121160250568 10.7592990040566
11.0309936366321 P P P LNCV6_140998_PI430048170 mRNA
GGCAGCAGTTTGACTTATTGCTGTTTCAGCTTTAAGGTTGTTGTGTTTTTGTTTTTGATT NM_033082 RefSeq chr12 -
55757269 55817756 SARNP 84324 "SAP domain containing ribonucleoprotein, transcript variant 1"
GO:0006355|GO:0006406|GO:0016607|GO:0000346|GO:0005654|GO:0005634|GO:0003677|GO:0006417|GO:0006
351|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134265_PI430048170 0.3915695935663311.28475142919017 1.26705112294059
0.4973262250801050.363799613123903 A A A 0.4920510846229790.375796433227643

0.344383114493657 A A A LNCV6_134265_PI430048170 mRNA
CCTCTCTGGGAATAGTCGGGGGAACCTATTTGTGGGCATTGAAAAAGTTTTTTCACTTTC NM_005353 RefSeq chr16
+ 31393311 31426505 ITGAD 3681 "integrin, alpha D"
GO:0008305|GO:0006955|GO:0009986|GO:0005886|GO:0030198|GO:0007229|GO:0050798|GO:0034113|GO:0046
872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136271_PI430048170 0.41246485086317 1.09886229856149 3.97182555123589
4.07594629845857 3.73218868568057 P P P 3.7678240913565 3.99054104700542
3.60917286636737 P P P LNCV6_136271_PI430048170 mRNA
AAGGAGCCCTCTTGATGATTTCTGTGAAATCGAGGCCCCTTGATTGTTTCTGTGAAACAC NM_139239 RefSeq chr19
- 35888240 35900650 NFKBID 84807 "nuclear factor of kappa light polypeptide gene enhancer in B-cells
inhibitor, delta" GO:0006954|GO:0051059|GO:0033085|GO:0070245|GO:0032088|GO:0005634|GO:0043124 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130172_PI430048170 0.350472995102231 1.03999820064748 0.297742089275206
0.268662946915042 0.418018811761076 A A A 0.286579273659296 0.250276999845798
0.281938476527101 A A A LNCV6_130172_PI430048170 mRNA
GACAAAACTGAGCCTGTATAAGGAATAAATGGGAGCGCCGAAAAGCTCCCTAAAAAGCAA NM_001290003
RefSeq chr3 - 184371934 184379688 THPO 7066 "thrombopoietin, transcript variant 5"
GO:0038163|GO:0051897|GO:0008283|GO:0030168|GO:0007275|GO:0005125|GO:0005615|GO:0045654|GO:0005
179|GO:0007596|GO:0001934|GO:0030099|GO:0070374|GO:0008083 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142722_PI430048170 0.000364903670776503 0.274018995823369 10.2806758437046
9.94952457382247 10.1354915616513 P P P 11.9945110167551 11.9035767341738
12.0839165572288 P P P LNCV6_142722_PI430048170 mRNA
GCCCTGTCAAAGGTCCCTATTTGAAATGTGTTATAATACAAACAAGGAAGCACATTGTGT NM_003842 RefSeq chr8
- 23020135 23069187 TNFRSF10B 8795 "tumor necrosis factor receptor superfamily, member 10b,
transcript variant 1"
GO:0005515|GO:0008625|GO:0034976|GO:2001239|GO:0005886|GO:0007250|GO:0045569|GO:0006919|GO:0006
915|GO:0042981|GO:0097190|GO:0070059|GO:0004872|GO:0016021|GO:0071260|GO:0043123|GO:0007166 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113988_PI430048170 0.264692028405017 0.79644804406462 7.16169977724585
6.89824153282296 6.40476997453567 P P P 7.41466747945129 7.15021507283995
6.94552415294523 P P P LNCV6_113988_PI430048170 mRNA
ATTCTGGGTCTCCCTGGCTCGAGAGGTGAACGTGGTCTACCAGGTGTTGCTGGTGCTGTG NM_000089 RefSeq chr7
+ 94394560 94431232 COL1A2 1278 "collagen, type I, alpha 2"
GO:0005515|GO:0046332|GO:0007266|GO:0050900|GO:0005615|GO:0046872|GO:0005584|GO:0042802|GO:0070
208|GO:0071230|GO:0022617|GO:0030198|GO:0030199|GO:0030574|GO:0042476|GO:0007179|GO:0030674|GO:0
070062|GO:0001568|GO:0048407|GO:0030168|GO:0005576|GO:0006898|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143271_PI430048170 0.369517096789927 1.02951626680081 0.547473602403835
0.618969843036608 0.495941729854104 A A A 0.536235464233389 0.500234209384991
0.502383732111698 A A A LNCV6_143271_PI430048170 mRNA
CTTCAGGTCCGTGGGCCGTATCTGTCACAATAAATGGCCAGTGCTGCTTCTTGCAAAAAA NM_001323 RefSeq chr11
+ 66011990 66013505 CST6 1474 cystatin E/M
GO:0010951|GO:0004869|GO:0008544|GO:0009653|GO:0001533|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143927_PI430048170 0.0894670990552813 1.23802071973134 4.63700861147385
4.64194874450743 4.96455111913579 P P P 4.47592340032239 4.54569176428185
4.31300139054404 P P P LNCV6_143927_PI430048170 mRNA
AACAAAACCCACCAGGAAGGAAAATCCAAGAGTTTCAGGTCTAGAGCTTGTGCTGCACTT NM_006049 RefSeq chr15

- 66490327 66497808 SNAPC510302 "small nuclear RNA activating complex, polypeptide 5, 19kDa"
GO:0010467|GO:0006355|GO:0003700|GO:0006366|GO:0005730|GO:0005654|GO:0005634|GO:0006384|GO:0006
383 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133503_PI430048170 0.0100561425661681 0.2232390326463284.90590369517354
4.91710565609162 4.80479229310851 P P P 6.60453272048739 7.00776923914613
7.39946521522478 P P P LNCV6_133503_PI430048170 mRNA
GGCAGCTTTTGAAATTTCTGAGGCTATGATTACATACTCCTCATACTAAAGATTTCTTAG NM_001008394 RefSeq
chr12 + 104303731 104305204 EID3 493861 EP300 interacting inhibitor of differentiation 3
GO:0005515|GO:0006355|GO:0005737|GO:0000781|GO:0006281|GO:0030915|GO:0006310|GO:0005634|GO:0006
351|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138196_PI430048170 0.451193178559448 1.05046191483749 0.29736977333023
0.3052700774028885 0.518421666009288 A A A 0.3152392055665720.27595339140974
0.327373232469123 A A A LNCV6_138196_PI430048170 mRNA
TCTGATGCTTTTACCATGTAGAAGACAAATAAACATAACTGGTGATTCTTGGTCTGAAAG NM_181356 RefSeq chr6
- 44826729 45378051 SUPT3H 8464 "suppressor of Ty 3 homolog (S. cerevisiae), transcript variant 2"
GO:0016578|GO:0006355|GO:0005669|GO:0046982|GO:0006357|GO:0006366|GO:0030914|GO:0003713|GO:0006
325|GO:0005634|GO:0003677|GO:0033276|GO:0043966|GO:0000124|GO:0005654|GO:0045893|GO:0004402 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132926_PI430048170 0.1759507211345030.576923755073043 1.82956931295746
1.36211869903937 2.93037982024102 A A P 2.82887915133808 3.09468564537521 3.0324596498295
P P P LNCV6_132926_PI430048170 mRNA
GTGCTCTTTCATACAGAATGGGAAACATAATCCTCAGGTATCCCAGCATCTCTTGTTGAA NM_001142286 RefSeq
chr2 - 17663811 17753829 SMC6 79677 "structural maintenance of chromosomes 6, transcript
variant 1"
GO:0005622|GO:0005515|GO:0000781|GO:0000724|GO:0030915|GO:0016605|GO:0000722|GO:0005730|GO:0005
654|GO:0005634|GO:0005524|GO:0090398 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134538_PI430048170 0.0130816140879084 0.8166618886343486.93551543900217
7.11138992391714 7.05690175606991 P P P 7.25977966401999 7.36169716435784
7.36208408983338 P P P LNCV6_134538_PI430048170 mRNA
TTGCAGGTTGTATTTTATTTTGGCCCAGGGAGTGTTGCTGTTTTCCCAACATTTTATTAA NM_021784 RefSeq chr20 -
22581003 22584463 FOXA2 3170 "forkhead box A2, transcript variant 1"
GO:0008344|GO:0021533|GO:0003700|GO:0044212|GO:0006366|GO:0000981|GO:2000049|GO:0005634|GO:0010
719|GO:0043433|GO:0045880|GO:0005737|GO:0032525|GO:0045944|GO:0045945|GO:0040019|GO:0000433|GO:0
000432|GO:0021904|GO:0048468|GO:0001705|GO:0006357|GO:0001708|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_49799_PI430048170 0.4173787109114421.2705927203826 1.11257692855966 0.246562838014024
0.281203252797908 A A A 0.2591210425673090.2610535286866720.259234215559695 A A A
LNCV6_49799_PI430048170 mRNA
AATGGAAAAACTTCACGGCAAGATTAGAAAGATACCTGAGCCCAATACCCGCCTGATGTC NM_015515 RefSeq
chr17_JH159146v1_alt - 71963 86911 KRT23 25984 "keratin 23, type I, transcript variant 1"
GO:0005882|GO:0005198 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73715_PI430048170 0.3101604977666141.32065153779105 4.44558910495685 4.84222553494106
4.33041713520085 P P P 4.44513494816357 4.39226795810082 3.41559582691898 P P P
LNCV6_73715_PI430048170 mRNA
TTTAATTTCATCTGGAATTCCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGG NM_001038628 RefSeq
chr3 - 161083882 161105372 B3GALNT1 8706 "beta-1,3-N-acetylgalactosaminyltransferase 1
(globoside blood group), transcript variant 5"
GO:0009312|GO:0000139|GO:0008499|GO:0006486|GO:0016021|GO:0047273 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_130410_PI430048170 0.3599718570911040.9815655947714170.361381530566364
0.3756702320531040.344989058884472A A A 0.4274288194424170.350353083529952
0.383916217736229A A A LNCV6_130410_PI430048170 mRNA
GAAGGACCAATGAATGTTAATTGAAATATGAAAGCTGAAATGCAACAAACAACTTCCGCT NM_002432RefSeq chr1
+ 158831377 158849480 MNDA 4332 myeloid cell nuclear differentiation antigen
GO:0050853|GO:0005515|GO:0006968|GO:0006355|GO:0005737|GO:0043065|GO:0030889|GO:0005634|GO:0003
677|GO:0006974|GO:0006351|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136947_PI430048170 0.16635699463989 0.4682177840992290.43030365227805
1.94273312158404 1.22508496457321 A A A 2.04505818912588 1.61254657517 3.15323311568098 A
A P LNCV6_136947_PI430048170 mRNA
TCAGGCCTTGCTGCTTGTTCTAAACTACACCTTAGGATTTTTTCTTCTTTCCAAAACATT NM_001286807 RefSeq chr13
- 45393318 45418455 SLC25A30 253512 "solute carrier family 25, member 30, transcript variant 3"
GO:0005739|GO:0008150|GO:0003674|GO:0005743|GO:0016021|GO:0006839 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138337_PI430048170 0.0146535478075054 1.45192322832933 6.13098827043499
5.83618693635079 5.89871101496237 P P P 5.37017637271102 5.39173776658728
5.50348925538711 P P P LNCV6_138337_PI430048170 mRNA
CCACCAGAGCTCCCTATGCAGCCTTTTAAAAGAATAAATAGGATCTGTAGCACCAAAAAA NM_001168215 RefSeq
chr17 + 50271405 50281485 TMEM92 162461 "transmembrane protein 92, transcript variant 2"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128065_PI430048170 0.0017788825722775 1.8072024788148 4.62058513978495
4.8837247465344 4.67993446515711 P P P 3.92624538341986 3.98478133237991
3.71118045296759 P P P LNCV6_128065_PI430048170 mRNA
TTAGGGAATTTCCAGACCAATGAGCAAAATGATTGTGCACACCTGGCCTCAGTCTCCTTT NM_152342RefSeq chr16
- 80603778 80804278 CDYL2 124359 "chromodomain protein, Y-like 2"
GO:0005515|GO:0008152|GO:0005634|GO:0035064|GO:0003824 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138206_PI430048170 0.9764158345369071.00264652064027 0.263777182498999
0.2779144451893670.434901107470311A A A 0.3543698018009110.304155337616888
0.312452567525301A A A LNCV6_138206_PI430048170 mRNA
CCTTGTTACTGCTTTGCCAGTTCTACGTTATTTACAATTATTCAGCTCTTGCAATAAATG NM_203487RefSeq chr13 -
66302833 67230336 PCDH9 5101 "protocadherin 9, transcript variant 1"
GO:0005886|GO:0005509|GO:0044291|GO:0030900|GO:0016021|GO:0007156|GO:0030426 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130057_PI430048170 0.5013669945770710.8289653885352770.28104436699553
0.2946815184601650.497169930911539A A A 0.3182199545410951.11735903953884
0.300807658634986A A A LNCV6_130057_PI430048170 mRNA
GCTGTTACATATACGCAGATAGTAGCAAGACAGAAAATGCAAATATGTAAATGTCTTCTG NM_001286264 RefSeq
chr6 + 24402907 24426194 MRS2 57380 "MRS2 magnesium transporter, transcript variant 1"
GO:0015693|GO:0015095|GO:0005743|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138232_PI430048170 0.7379702359242730.8371319803352650.352181764823246
1.28510496840198 0.360837137046485A A A 0.4893274743544910.370552853601986
1.71076258061272 A A A LNCV6_138232_PI430048170 mRNA
GTTGGTCATTCCTTTAAGGCAGTTAAGGATTGCTTTATTTGTGTTCTTTTTTCCCATGAC NM_004745RefSeq
chr8_KI270926v1_alt + 40123 121138 DLGAP2 9228 "discs, large (Drosophila) homolog-associated
protein 2, transcript variant 1" GO:0005515|GO:0030054|GO:0045211|GO:0005883|GO:0014069|GO:0007270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136349_PI430048170 0.3975728929523761.15898099366437 8.14652455205936
8.40999794258543 7.79332194953909 P P P 7.89122119560999 7.79278855937927

8.07802241417428 P P P LNCV6_136349_PI430048170 mRNA
TGGGCACCAGCTCAGGGGCTTCCATTTGCAAAGGGAAATTAAAGAAAGAATGTTGCTTAA NM_178026RefSeq chr20
- 34844719 34872858 GGT7 2686 gamma-glutamyltransferase 7
GO:0019370|GO:0003840|GO:0006750|GO:0006508|GO:0006749|GO:0016021|GO:0031362 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129469_PI430048170 0.1988484166128761.92233009640716 2.01357385963892
2.32081380792885 3.13755204994883 A A P 2.27826463273309 0.350525544374053
1.65601386607879 A A A LNCV6_129469_PI430048170 mRNA
CATGTGAGCACTTTTGAGAAAGAGAAACCTATAGCAACTTCATGAATTAAGCCTTTTTCT NM_021796RefSeq chrX
- 134565842 134658483 PLAC1 10761 placenta-specific 1
GO:0003674|GO:0090214|GO:0005576|GO:0005575|GO:0001890 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131168_PI430048170 0.1084950697627190.4051167493396420.3673889594295412.0593503740141
0.297601731324093A A A 2.19756537518511 3.02946089582906 1.9086252747454 A P A
LNCV6_131168_PI430048170 mRNA
AAACTGTCATTTCTCCCGCTAAATGAAAACCGTGTTGTTATAAAGCTTAATGCAACCTGA NM_006040RefSeq chr16
+ 25692025 26137688 HS3ST4 9951 heparan sulfate (glucosamine) 3-O-sulfotransferase 4
GO:0000139|GO:0016021|GO:0008467|GO:0030201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141397_PI430048170 0.6717811151036331.09642874722161 0.38265738576535
0.3880058930336431.00942684199122 A A A 0.35798036749005 0.339570584574824
0.741253253951264A A A LNCV6_141397_PI430048170 mRNA
GGCACTTACATCATATACTCAGGTGTGTAAAAGCCTGCTATTTGTAACTATAATCCATAA NM_003838RefSeq chr1
+ 74198211 74208702 FPGT 8790 "fucose-1-phosphate guanylyltransferase, transcript variant 1"
GO:0005737|GO:0047341|GO:0006004|GO:0005525|GO:0003824 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142667_PI430048170 0.7049140842604361.01257382913733 0.39617593307185
0.3883203429253240.277029872938707A A A 0.3166472958100090.34565900033523
0.347978234705702A A A LNCV6_142667_PI430048170 mRNA
GTGTGTGAACTGTTTCACCTTTTTTAAAATTCTCTGATTGACAGATCCTTGGATCAGACA NM_001145118 RefSeq
chr7 - 6496777 6551436 GRID2IPNA "glutamate receptor, ionotropic, delta 2 (Grid2) interacting
protein" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137017_PI430048170 0.0163833657012921 1.52365175438253 6.10644258216203
6.47225623932262 6.20308898802989 P P P 5.85003982010358 5.62456480113404
5.48634694951049 P P P LNCV6_137017_PI430048170 mRNA
ACTAACTTCTTGTTGGAGACGGGGGACATTGCCTTCCACATCAAGCCCCGGTTCTCCAGC NM_001291784 RefSeq
chr7 - 2475136 2476383 GRIFIN NA galectin-related inter-fiber protein NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_142906_PI430048170 0.1387951952146360.6820322823880996.11213441033628 6.9240653147179
6.85316659933796 P P P 7.41774226964918 7.21018119062033 7.0215374695909 P P P
LNCV6_142906_PI430048170 mRNA
TGGTCCCTCCCTCTGCTAGCCAGAAATAAACACCTGAGTTGCCTTAGGAACTAGAAAAAA NM_001145054 RefSeq
chr2 - 74414175 74417717 C2orf81 388963 chromosome 2 open reading frame 81 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_11336_PI430048170 0.0026725368621394 2.24034298887968 5.55141516900217
5.96212208150098 5.91359662216283 P P P 4.4364418252475 4.68605962076894
4.82128554038246 P P P LNCV6_11336_PI430048170 mRNA
TAGACCGGGAGTCTGGACTTGGGAGCGTGAACTCTCACCCGAGCCGGTCCCCTTACAACT NM_001270945 RefSeq
chr1 + 111990567 111998841 LOC643355 643355 uncharacterized LOC643355 NA . NA - . NA
NA NA NA NA NA NA NA NA

LNCV6_133167_PI430048170 0.00683127200813686 0.8058168066384330.399185133248276
0.2623172282074780.291971630114803A A A 0.6417987868451890.547451309842871
0.698267085928758A A A LNCV6_133167_PI430048170 mRNA
ATGGGTGGCGAAATTCACGAGTCTACAAATAAGATCTTCCATATGGCACCTAAGACGAAA NM_014477RefSeq chr20
- 45373879 45378317 TP53TG5 27296 TP53 target 5
GO:0035556|GO:0003674|GO:0030308|GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128449_PI430048170 0.2434447746807643.51740052615032 0.424620890823752
2.85628617654161 3.3089683266094 A A P 0.5510971138388511.30904673889578
0.395021657437387A A A LNCV6_128449_PI430048170 mRNA
GTAAACATTGCCTGATTTGTTCCTTCTGGGGCTTTGCCATTAAAATGTATTTACAGATTA NM_000547RefSeq
chr2_KI270774v1_alt + 96658 223095 TPO 7173 "thyroid peroxidase, transcript variant 1"
GO:0005886|GO:0009986|GO:0005509|GO:0044281|GO:0005615|GO:0005739|GO:0034641|GO:0004601|GO:0005
887|GO:0004447|GO:0042446|GO:0006590|GO:0042744|GO:0006979|GO:0035162|GO:0055114|GO:0020037 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142187_PI430048170 0.7056280262742331.03225009777122 1.93612134992376 1.6692838266285
2.29786241456219 A A A 2.68062966872798 1.94054527903666 0.380939041428575P A A
LNCV6_142187_PI430048170 mRNA
AATCTTCACCGTGCAAAGTGGAAACCAGAGGCCCGGTCAGACAGTGACTAATCCAGGGCC NM_138706RefSeq
chr11 + 77034340 77041958 B3GNT6192134 "UDP-GlcNAc:betaGal beta-1,3-N-
acetylglucosaminyltransferase 6"
GO:0009101|GO:0016020|GO:0006493|GO:0000139|GO:0016266|GO:0047223|GO:0016021|GO:0016269|GO:0044
267|GO:0008378|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140892_PI430048170 0.00577582223081284 1.63575440738157 8.71729045337328
8.90648568249564 8.89159715322001 P P P 8.23712923769713 8.20433287612248
7.93268090685875 P P P LNCV6_140892_PI430048170 mRNA
GCAGTGGAATTTTGAGCGACCTTTACTTTATACTTTTCTGTGCTTGACAGATTTTCAGCC NM_013349RefSeq chr1
+ 212432886 212446379 NENF 29937 "neudesin neurotrophic factor, transcript variant 1"
GO:0016020|GO:0005654|GO:0005634|GO:0043410|GO:0008083|GO:0005615|GO:0046872|GO:0020037|GO:0012
505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143587_PI430048170 0.00827141721044449 1.21312633970462 8.99713360194118
9.02532983225358 9.13037274172543 P P P 8.7590429523489 8.84810069045341
8.70951328219781 P P P LNCV6_143587_PI430048170 mRNA
GGGGGAATTTTGTACTTTTTTCCTGTGTAAATATTGGACTTTTTTGAGCTTTATCGTGGT NM_152221RefSeq chr22 -
38290690 38317408 CSNK1E 1454 "casein kinase 1, epsilon, transcript variant 1"
GO:0005515|GO:0008360|GO:0090263|GO:0030178|GO:0032436|GO:0005634|GO:0005829|GO:0005737|GO:0018
105|GO:0000086|GO:0016055|GO:0006996|GO:0005524|GO:0032922|GO:0006897|GO:0007165|GO:0006281|GO:0
004672|GO:0004674|GO:0030529|GO:0007623|GO:0042752|GO:0006468|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145403_PI430048170 0.1456965525916150.5518458878573352.39076869451959
2.78866441452377 3.8319434307379 A A P 3.87821313142032 4.03165015103761
4.06785953235121 P P P LNCV6_145403_PI430048170 mRNA
CATCAAGCCAGTTAACTTCACTTTTCCCTGCAATTTGTATGTCACTAACATTTAAATGCC NM_021994RefSeq chr7
+ 112206587 112343934 ZNF277 11179 zinc finger protein 277
GO:0006355|GO:0070301|GO:0005634|GO:2000772|GO:0000979|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130060_PI430048170 0.000620358566396504 0.3737607796081895.52366743620789
5.69391547417682 5.86222906823121 P P P 6.90101760901582 7.19766475196843 7.2375450765032
P P P LNCV6_130060_PI430048170 mRNA

GAGTTACTACAGTCTCCATGTCAAAGCATAATGTGTAGCATATCAGCAATAACTACATAT NM_003358RefSeq chr9
+ 111896765 111935374 UGCG 7357 UDP-glucose ceramide glucosyltransferase
GO:0008120|GO:0006665|GO:0016020|GO:0008544|GO:0006687|GO:0000139|GO:0006688|GO:0006679|GO:0044
281|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132641_PI430048170 0.0247473436894540.5664729477047686.59864387770038
6.07980436360314 6.46380863383998 P P P 6.85383500621275 7.36186937143419
7.37634740321271 P P P LNCV6_132641_PI430048170 mRNA
AGTGGCTGCCAGTAGCAGACTGTTAAATTGTGGTTTATATACTTTTTGCATTGTAAATAG NM_018490RefSeq chr11
- 27365960 27472787 LGR4 55366 leucine-rich repeat containing G protein-coupled receptor 4
GO:0072202|GO:0005515|GO:0005886|GO:0004930|GO:0034122|GO:0090263|GO:0072282|GO:0007283|GO:0030
282|GO:0050710|GO:0072224|GO:0050673|GO:0001649|GO:0032922|GO:0030539|GO:0061290|GO:0046849|GO:0
007186|GO:0005887|GO:0045087|GO:0045893|GO:0045892|GO:0090190|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132399_PI430048170 0.2655615679561850.5485225381203470.511659981020762
0.5711520540459610.51178697237328 A A A 1.24539789780216 0.438615070721849
2.06382837483915 A A A LNCV6_132399_PI430048170 mRNA
GGACAGGCTGTATGTCAGATTTACCTTTTATTCCGAAGAACTCGGAGCATTTATTTTGTT NM_001303615 RefSeq
chr11 - 19054455 19060017 MRGPRX2 117194 "MAS-related GPR, member X2, transcript variant 1"
GO:0042923|GO:0007186|GO:0005886|GO:0032467|GO:0004930|GO:0030431|GO:0016021|GO:0019233 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108129_PI430048170 0.58137355109431 1.04917732199603 7.99409891546003
7.87816957373177 7.97244644060959 P P P 7.76988202170151 8.10502350641015
7.73500445077445 P P P LNCV6_108129_PI430048170 mRNA
TTGAACTACTCCACCAGAAACTAGAGCTCCCTGACAATGTATCCGGTGAATTTGGATGGT NM_001040199 RefSeq
chr3 - 98515472 98523066 CLDND1 56650 "claudin domain containing 1, transcript variant 6"
GO:0016324|GO:0009986|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136431_PI430048170 0.0543005087537950.7196816175965946.82160788446773
6.56329375811069 6.49952455275264 P P P 6.82600880570553 7.24066287491782
7.22497809810073 P P P LNCV6_136431_PI430048170 mRNA
ATTATCTTAGGAACTCAAGCTTCTAAAACTATCCATGTAGTCAAATCTAGGGGAAAAAGC NM_005707RefSeq chr15
- 65117378 65133836 PDCD7 10081 programmed cell death 7
GO:0008380|GO:2001235|GO:0006915|GO:0070234|GO:0051384|GO:0005689 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139236_PI430048170 0.1167279681270672.22777222502087 1.91065777538965
0.6953059942227091.86930467689515 A A A 0.3802009914482550.470736065160991
0.451227467779392A A A LNCV6_139236_PI430048170 mRNA
ACTAAGTTCAGTCCAGTCAAGAAAAGAACCTAATAGCACCAATACAAATTGAGGACTTAA NM_138715RefSeq chr8
- 16107877 16192791 MSR1 4481 "macrophage scavenger receptor 1, transcript variant SR-AI"
GO:0005515|GO:0005581|GO:0005886|GO:0010744|GO:0030169|GO:0030301|GO:0010886|GO:0006898|GO:0005
829|GO:0030666|GO:0071407|GO:0042953|GO:0005887|GO:0034381|GO:0034362|GO:0005044 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_100267_PI430048170 0.6020096644229581.09996321127127 1.87693238291681
1.79546954133754 2.01903710166233 A A A 2.23485341862643 1.04166750300141
1.77146052287126 A A A LNCV6_100267_PI430048170 mRNA
ACAATGATAGTGACTACAAGAAGGATATGGTGGAAGGGGACAAGTACTGGCACTCCATCA NM_033254RefSeq
chr3 + 113211464 113287463 BOC 91653 "BOC cell adhesion associated, oncogene regulated,
transcript variant 2"
GO:0042692|GO:0005515|GO:0051149|GO:0005886|GO:0007411|GO:0045663|GO:0043025|GO:0016021|GO:0044
295|GO:0007155|GO:0007224 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_142564_PI430048170 0.3496706126099131.02274587515975 0.303254201114307
0.3184317702567550.388909281247311A A A 0.3198520448801670.303677211308987
0.291033783330227A A A LNCV6_142564_PI430048170 mRNA
GGACTGAATCTCTCACCTATTCTTGCAGAAAGACATACTAATTAAACCTTGTCAAAGTAA NM_031226RefSeq chr15
- 51208056 51338598 CYP19A1 1588 "cytochrome P450, family 19, subfamily A, polypeptide 1,
transcript variant 2"
GO:0006694|GO:0060736|GO:0006805|GO:0070330|GO:0005506|GO:0005783|GO:0006703|GO:0008209|GO:0009
055|GO:0044281|GO:0016020|GO:0019825|GO:0005789|GO:0016712|GO:0016125|GO:0008202|GO:0055114|GO:0
020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127929_PI430048170 0.2089807523618011.44487389516443 4.07609613624724
4.16552355119968 4.00546915639463 P P P 3.52448444226862 4.02973998268629
2.88134485499869 P P P LNCV6_127929_PI430048170 mRNA
TTTTTCTCTCCCTCTGGCGAGGACTCTCAGGATGTAGGGACTTGGAAATATTTACTGTCT NM_032642RefSeq chr12
+ 1629245 1647212 WNT5B 81029 "wingless-type MMTV integration site family, member 5B, transcript
variant 1"
GO:0030335|GO:0005886|GO:0009986|GO:0071300|GO:0070307|GO:0005796|GO:0005102|GO:0005578|GO:0005
576|GO:0005615|GO:0005109|GO:0045165|GO:0002062|GO:0030182|GO:0042060|GO:0045600|GO:0045444|GO:0
005788|GO:0016055|GO:0090090|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91369_PI430048170 0.5363057790933231.17749784360436 1.9409217669266 1.35268697222013
1.27079483223791 A A A 2.13067832119377 0.29629257585936 0.904294873268171A A A
LNCV6_91369_PI430048170 mRNA
TACACAGGGACATCAAGGGAGCTAACATCCTCATCAATGATGCTGGGGAGGTCAGATTGGNM_007181RefSeq chr19
- 38587639 38618035 MAP4K1 11184 "mitogen-activated protein kinase kinase kinase kinase 1,
transcript variant 2"
GO:0005515|GO:0008283|GO:0008349|GO:0006950|GO:0007257|GO:0005524|GO:0035556|GO:0005083|GO:0005
737|GO:0046777|GO:0000185|GO:0004672|GO:0018105|GO:0016020|GO:0004674|GO:0006468 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130642_PI430048170 0.0189029049088031 0.5243654091566425.50399212187861
5.33491723990392 5.86188545193644 P P P 6.44187553397189 6.49809536513567
6.60139198636217 P P P LNCV6_130642_PI430048170 mRNA
TCCTGTGGCCTAAGTAATATACATATAGTTGGATTGGATTGTCAGCAGTAACATTGGAAA NM_001271838 RefSeq
chr3 + 158110051 158544835 RSRC1 51319 "arginine/serine-rich coiled-coil 1, transcript variant 1"
GO:0008380|GO:0005515|GO:0005737|GO:0016607|GO:0000398|GO:0000380|GO:0006468|GO:0005634|GO:0046
677|GO:0006913 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83015_PI430048170 0.0168228094149571 1.64040498851264 6.70431390474 6.6263243833631
6.53236293904918 P P P 5.67696945659358 6.10164237296079 5.91619146104931 P P P
LNCV6_83015_PI430048170 mRNA
TTGTCACCGTTGCTGAACAAAAGTATCAGTCTACCTTGTGGGACAAGTCCAAGAAACTGG NM_017803RefSeq chr16
+ 68022943 68079323 DUS2 54920 "dihydrouridine synthase 2, transcript variant 1"
GO:0005739|GO:0005515|GO:0003725|GO:0005737|GO:0005783|GO:0050660|GO:0060548|GO:0017150|GO:0004
860|GO:0006469|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128697_PI430048170 0.3746076731537012.18943427178629 0.290666464560768
2.45560598836384 0.517717967889965A A A 0.3208319035643290.278690355014397
0.328677770533786A A A LNCV6_128697_PI430048170 mRNA
CACTCCTTTCTGACCAAGCAACGCTAACTTTTGTACAGATCGATTTGATAAAATTAAACA NM_014587RefSeq chr16
+ 981807 986979 SOX8 30812 SRY (sex determining region Y)-box 8
GO:0046533|GO:0072034|GO:0090184|GO:0060041|GO:0006366|GO:0048709|GO:0060221|GO:0000981|GO:0001
755|GO:0005634|GO:0007283|GO:0035914|GO:0010817|GO:0045662|GO:0005737|GO:0060009|GO:0072197|GO:0
014015|GO:0045944|GO:0045444|GO:0048469|GO:0033690|GO:0090190|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_131602_PI430048170 0.6836981354743741.05439647853707 3.86781411603516 3.8450504010549
4.2580541573315 P P P 3.8404852224222 3.92782836171868 4.00696654811067 P P P
LNCV6_131602_PI430048170 mRNA
CAGCCTAAAACAAAGGATTGGGTCTATGTACTTCTTTAGTCTATAATGACACTGTGTAAT NM_020243RefSeq chr22
+ 38681948 38684761 TOMM22 56993 translocase of outer mitochondrial membrane 22 homolog
(yeast)
GO:0005739|GO:0005515|GO:0016020|GO:0006626|GO:0005743|GO:0005742|GO:0016021|GO:0008320|GO:0045
040|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130187_PI430048170 0.1586695944253230.3139021008893180.520229289567268
0.5490803094298471.39914711707741 A A A 0.9425914470229942.62376149570506
3.25500154481006 A P P LNCV6_130187_PI430048170 mRNA
CTTTAGCCGTGTAAGGGGTTCACAGATGTTCATACTTTTGTTCTTTATACCTTATATGTA NM_144682RefSeq chr17 -
35435095 35448837 SLFN13 146857 schlafen family member 13 GO:0005622|GO:0005524 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136403_PI430048170 0.3804309486314341.12632850257191 0.458552968437981
0.4869312543231360.896479178931592A A A 0.5286599948007630.413514110985633
0.424950565708832A A A LNCV6_136403_PI430048170 mRNA
CTGGGGGAAGTAGCACCCTTGCATTTCAAAAATAAAATTGATGGCATTACAAATGGAATA NM_001165978 RefSeq
chr2 + 95274452 95291307 PROM2 150696 "prominin 2, transcript variant 1"
GO:0060170|GO:0009986|GO:0031528|GO:0031410|GO:0042995|GO:0044393|GO:0043088|GO:2001287|GO:0005
902|GO:0005929|GO:0016323|GO:0016324|GO:0031346|GO:0005887|GO:0015485|GO:0048550|GO:2000369|GO:0
071914|GO:0001934|GO:0045121|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145545_PI430048170 0.00919417722825716 0.4503575113195135.89388698543542
5.34214254049899 5.74869486484505 P P P 6.51587799617902 6.78193075471932
7.12866389924767 P P P LNCV6_145545_PI430048170 mRNA
CCTAAGTAGCTCTTCAGAGTCTGACCGTAAGTAAAAACACACAGAATTGTGTTGACTGGG NM_003898RefSeq chr6
+ 157981855 158099175 SYNJ2 8871 "synaptojanin 2, transcript variant 1"
GO:0005515|GO:0004439|GO:0016020|GO:0006661|GO:0000166|GO:0003723|GO:0046856|GO:0044281|GO:0006
644|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131258_PI430048170 0.3361347395732671.31051424755371 0.693310236280664
1.40795571968995 0.52574383472731 A A A 0.4354796056514150.603446415972638
0.571021604051632A A A LNCV6_131258_PI430048170 mRNA
AAAGGTCATCGAGGGCTTCTTTGCATTTTACAGTTTTTATTACCATATGTAGTAGGAGAC NM_147195RefSeq chr9
- 38571363 38620363 ANKRD18A 253650 ankyrin repeat domain 18A NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141202_PI430048170 0.1495522904624581.46086815840283 1.14125522256619
1.51060423843444 1.81505789215698 A A A 0.9407201630224181.34242768866317
0.499461032057307A A A LNCV6_141202_PI430048170 mRNA
TAAAAACAAAAACAACAAAAACCAGAGACCCTGGCTTTTGGACAGTTGTTCGTGTGGCTA NM_001030001 RefSeq
chr14 - 49576671 49586416 RPS29 6235 "ribosomal protein S29, transcript variant 2"
GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0015935|GO:0006415|GO:0006412|GO:0006
413|GO:0005829|GO:0006414|GO:0005737|GO:0000184|GO:0022627|GO:0016032|GO:0008270|GO:0044267|GO:0
005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99290_PI430048170 0.0557419917509665 0.837712280310924 5.48753528086881
5.55750010517531 5.43503951777591 P P P 5.60118661075298 5.80007618569753
5.83688647597429 P P P LNCV6_99290_PI430048170 mRNA
ATGGAGCAGTAACTTGTGAAGGCTGCAAAGGATTTTTTAAAAGAAGCATCCGAAAAAATT NM_003297 RefSeq
chr12 - 95020228 95073628 NR2C1 7181 "nuclear receptor subfamily 2, group C, member 1,

transcript variant 1"
GO:0005515|GO:0010467|GO:0003700|GO:0006367|GO:0042826|GO:0003707|GO:0000122|GO:0003677|GO:0042803|GO:0043565|GO:0048386|GO:0016605|GO:0043401|GO:0004872|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97255_PI430048170 0.453817034177188 0.476757701697246 0.386156482057213 0.398734891827825 0.457908990747195 A A A 2.54206295283451 0.330811332300177 0.384682942796552 A A A LNCV6_97255_PI430048170 mRNA
TTTTGGATCCTAGTGGCCTGCTTTCCAAGTGCCATTGCCAGTCATGTGGCAGCAGAGTGT NM_015166 RefSeq chr22 - 50059390 50085929 MLC1 23209 "megalencephalic leukoencephalopathy with subcortical cysts 1, transcript variant 1"
GO:0005515|GO:0005215|GO:0048471|GO:0005886|GO:0005783|GO:0072584|GO:0030136|GO:0015031|GO:0051259|GO:0005764|GO:0032403|GO:0016323|GO:0005737|GO:0016324|GO:0071397|GO:0005911|GO:0006810|GO:0016192|GO:0006811|GO:0032388|GO:0031410|GO:0047484|GO:0005901|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137992_PI430048170 0.163557955607796 0.820448549469384 7.97041520502199 7.52393760897956 7.56000897174546 P P P 7.91879805619151 8.0701198708429 7.96164406649327 P P P LNCV6_137992_PI430048170 mRNA
CTGTGTAGTGTGGAGGCAAAAAGCTCCAAAATCTAGTATAACATAATAAACTGGATATTG NM_024917 RefSeq chrX - 101009344 101052116 TRMT2B 79979 "tRNA methyltransferase 2 homolog B (S. cerevisiae), transcript variant 1" GO:0005739|GO:0001510|GO:0030697|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69307_PI430048170 0.817476813984807 1.02050552001702 5.68970101815208 5.87942000040293 5.92023938077912 P P P 6.0408539012931 5.76821639901655 5.56267582917977 P P P LNCV6_69307_PI430048170 mRNA
ATAACAGAGCACATCATCAAGCCCGACCCTCCAGAAGGCGTGCGCCTAAGCCCCCTCGCT NM_005755 RefSeq chr19 + 4229542 4237527 EBI3 10148 Epstein-Barr virus induced 3
GO:0005515|GO:0004896|GO:0005886|GO:0045078|GO:0006959|GO:0019221|GO:0046641|GO:0045523|GO:0042088|GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132033_PI430048170 0.445452342441932 1.12804639348103 8.01345872378497 8.01573561566784 8.37771686725755 P P P 7.73171761240234 7.80669332046592 8.30789614125889 P P P LNCV6_132033_PI430048170 mRNA
GAAGCTGAGATGATGCTTGTATGGAAAGTTTGATATTTTTATCAGTCACATGGCTTTTGA NM_032358 RefSeq chr12 + 401574 442640 CCDC77 84318 "coiled-coil domain containing 77, transcript variant 1"
GO:0005813|GO:0016020 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129051_PI430048170 0.168151236239289 0.85982688996741 0.432641444999595 0.412916983302135 0.245901032985673 A A A 0.370127631341884 0.700448596237104 0.659774650338425 A A A LNCV6_129051_PI430048170 mRNA
CATTGCTCTTTAGTGTGTGTTAACCTGTGGTTTGAAAGAAATGCTCTTGTACATTAACAA NM_173200 RefSeq chr9 + 99821854 99866891 NR4A3 8013 "nuclear receptor subfamily 4, group A, member 3, transcript variant 3"
GO:0005515|GO:0010467|GO:0042542|GO:0006367|GO:0031100|GO:0003707|GO:0043434|GO:0005634|GO:0048752|GO:0043524|GO:0007411|GO:0045944|GO:0060005|GO:0050885|GO:0043401|GO:0030534|GO:0005667|GO:0001707|GO:0003677|GO:0045787|GO:0043565|GO:0008150|GO:0021766|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143786_PI430048170 0.308703706687329 1.0272839322983 0.340022365553903 0.260453581979555 0.350223184431788 A A A 0.28099615066263 0.269716917621541 0.285100942817785 A A A LNCV6_143786_PI430048170 mRNA
GCATTTAAAAAGGTATTTGCATGTTGCTCATCTGCTCAGAAAGTAGCAACAAGTGATGCT NM_001001964 RefSeq chr1 - 248626177 248627128 OR2T11 NA "olfactory receptor, family 2, subfamily T, member 11

(gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132894_PI430048170 0.471630826455931 1.29879407039371 0.562641662180533
0.506961716390687 1.54579971544385 A A A 0.542642387015158 0.750328514522686
0.422752923183799 A A A LNCV6_132894_PI430048170 mRNA
ATGTGAGATTTTTCCATGGGCCCTGGGAAAAGATTGGTGTTTACGAGTGGGGAAATTCCT NM_001008778 RefSeq
chr11 + 65170235 65173217 SPDYC NA speedy/RINGO cell cycle regulator family member C
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139907_PI430048170 0.267485652805539 0.718219834894533 3.51558806582054
2.56573083828219 3.51060944944891 P A P 3.26651221519458 3.83740355956463
4.01058293145219 P P P LNCV6_139907_PI430048170 mRNA
AAAGGAATGAAGGCTCCAGGGATACAGAGTTGTCCATTACCAAAGCCTGGAAGTTCTCAT NM_013348 RefSeq
chr19 + 48455706 48466110 KCNJ14 3770 "potassium channel, inwardly rectifying subfamily J,
member 14"
GO:0005242|GO:0005886|GO:0008076|GO:0043025|GO:0010107|GO:0007268|GO:0034765|GO:0030425 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_132234_PI430048170 0.00823429996425562 1.48816332369228 9.74785976107631
9.80182786461471 9.7722799840204 P P P 9.07839635195121 9.22930487694306
9.28626014377623 P P P LNCV6_132234_PI430048170 mRNA
ATTGATTATTACTGGCAAAAACGGCCAGGTACAACACCTTTTTCATACAAGGCCCAGGAG NM_002109 RefSeq
chr5 - 140673903 140691727 HARS 3035 "histidyl-tRNA synthetase, transcript variant 1"
GO:0010467|GO:0005737|GO:0006412|GO:0005524|GO:0004821|GO:0006427|GO:0006418|GO:0005829 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_145667_PI430048170 0.258135449494511 0.743455173154037 8.45337442474196
7.62463561454704 7.47117092805648 P P P 8.57869333849484 8.37087786484912
8.0346519808195 P P P LNCV6_145667_PI430048170 mRNA
AGAGAAAAATTACTTAGCCTCTCCCAAGATGAGAAAGTCCTCAAGTGAGGGGAGGAGGAA NM_031479 RefSeq
chr12 + 57455312 57458008 INHBE 83729 "inhibin, beta E"
GO:0005179|GO:0043408|GO:0010862|GO:0042981|GO:0048468|GO:0060395|GO:0040007|GO:0008083|GO:0005
615|GO:0005160|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140989_PI430048170 0.0326790014877799 1.33664365278484 2.30375488900639
2.16782429805316 2.10749293052711 A A A 1.59699737962422 1.76413925429655
1.94779555409964 A A A LNCV6_140989_PI430048170 mRNA
GGTATGGTACTTCAATTTGAGAAACACAAAACTGATACGAATGTGCCTTGTAGTTAATGT NM_001001671 RefSeq
chrX - 19360057 19515261 MAP3K15 389840 mitogen-activated protein kinase kinase kinase 15
GO:0000186|GO:0000165|GO:0006468|GO:0005524|GO:0004709|GO:0046872 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_129335_PI430048170 0.246773531742 0.628876651208816 1.99789784512397
0.314298828327574 0.431963514989534 A A A 1.64850371497184 1.56715478653371
2.12941398023038 A A A LNCV6_129335_PI430048170 mRNA
TACAATTCAAGTTGCTTCTCATGGATGGCACTGCTTTTCTGAGGACTCAAGGGCCAAGAT NM_000483 RefSeq
chr19 + 44945981 44949566 APOC2 344 apolipoprotein C-II
GO:0032375|GO:0007603|GO:0060697|GO:0042627|GO:0070328|GO:0010898|GO:0010902|GO:0044281|GO:0005
615|GO:0042803|GO:0008289|GO:0034361|GO:0034384|GO:0043274|GO:0034382|GO:0034363|GO:0034362|GO:0
055102|GO:0070062|GO:0042632|GO:0033344|GO:0045723|GO:0043691|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139170_PI430048170 0.18213389337298 1.10419045005331 0.628827554330434
0.423843917911807 0.645843508164456 A A A 0.355410385347275 0.414612021844249
0.505930552500348 A A A LNCV6_139170_PI430048170 mRNA
CAGAGACTCAGATGAGCTGTAAAATCCATTAAGGAAAAATAAATGGCATGATTTGGAAGT NM_178450 RefSeq

chr5 - 126867713 127030808 MARCH3 NA "membrane-associated ring finger (C3HC4) 3, E3 ubiquitin protein ligase" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131617_PI430048170 0.366498567851699 1.19936470488006 9.9714760158491 10.4723313897919 9.79965959804457 P P P 9.81646379152781 9.88984156676884 9.83646121734575 P P P LNCV6_131617_PI430048170 mRNA GCATCAGAACTCAGGTGTTTTTTATTTACGCGTCAGGGCTTTTCTTGTTTAATAAAGTTA NM_001517 RefSeq
chr6_GL000253v2_alt + 2218435 2224339 GTF2H4 2968 "general transcription factor IIH, polypeptide 4, 52kDa"
GO:0005515|GO:0010467|GO:0006368|GO:0003700|GO:0006367|GO:0006366|GO:0006363|GO:0006362|GO:0006361|GO:0006360|GO:0004003|GO:0000439|GO:0016032|GO:0032508|GO:0008094|GO:0006355|GO:0006370|GO:0008353|GO:0050434|GO:0006281|GO:0004672|GO:0006283|GO:0045814|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129502_PI430048170 0.0537627987696576 0.438416245216765 1.28442953924459 1.03944316468 0.284959882412155 A A A 2.66214384762407 1.84528289015415 1.63246878270641 P A A LNCV6_129502_PI430048170 mRNA CTTCTCCCAGTGGCATTAAACTTCAAATAATTTGAAAAATATTGTTCCCACACGTTACAC NM_020394 RefSeq chr1 - 246985322 247008093 ZNF695 57116 "zinc finger protein 695, transcript variant 1"
GO:0006355|GO:0005634|GO:0003676|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143275_PI430048170 0.665238047124314 1.13681574076683 4.13799813580477 4.17360158956695 3.30549513616485 P P P 4.13689694518157 3.65248058645321 3.30605432323201 P P P LNCV6_143275_PI430048170 mRNA GGGTCTCACTCGGCCCCCAAAAACTGATAAAAGAATAAAACACTTAAATGAATAACAAAA NM_174895 RefSeq
chr19 - 7631614 7633748 PCP2 126006 "Purkinje cell protein 2, transcript variant 1"
GO:0043547|GO:0005085|GO:0043025|GO:0030695|GO:0016056 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141797_PI430048170 0.0276608302805249 0.391214252647868 9.29656168237122 8.54668813460051 8.26025333369926 P P P 10.2983038752382 10.2249042623606 9.79937372329904 P P P LNCV6_141797_PI430048170 mRNA CCACTCTCCCCACTTTTATCTTTTCCAGTGGTCTTCTGTTAATGTAGTGTCTTTTACAAG NM_206943 RefSeq chr2 + 32947301 33399508 LTBP1 4052 "latent transforming growth factor beta binding protein 1, transcript variant 1"
GO:0005515|GO:0035583|GO:0050431|GO:0005509|GO:0005578|GO:0001527|GO:0005576|GO:0050436|GO:0031012|GO:0043234|GO:0030198|GO:0005024|GO:0007178 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134522_PI430048170 0.759254680932686 0.969118776693511 0.339590308654205 0.531672569602833 0.387649929857087 A A A 0.638734505877662 0.46416924867491 0.276021584923245 A A A LNCV6_134522_PI430048170 mRNA GCCAGAAGGAGATGTGGCAATGTGATTCCTTTTGTAATCTGATTATAATTGAACATTGAT NM_152610 RefSeq chr1 + 223393372 223395470 CCDC185 164127 coiled-coil domain containing 185 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132847_PI430048170 0.34543856348597 1.37976046780323 1.45512535492418 0.556002613799443 0.445317775881179 A A A 0.521664463865845 0.38476010854845 0.376617305300256 A A A LNCV6_132847_PI430048170 mRNA GAAACTTTTGGAAAAACTGAAGTTCCTGGAGGAAAGCCAAACCGTGCTAACACACTAGAG NM_153206 RefSeq chr11 - 118193726 118213359 AMICA1 120425 "adhesion molecule, interacts with CXADR antigen 1, transcript variant 2"
GO:0072672|GO:0060054|GO:0005886|GO:0030593|GO:0046629|GO:0035696|GO:0050900|GO:0042803|GO:0005178|GO:0007596|GO:0050776|GO:0005923|GO:0016021|GO:0050839|GO:0007157 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139999_PI430048170 0.3422105282822740.8570863822880950.255808575955995
0.26480634935239 0.399311299643289A A A 0.3687514034924330.841017310348437
0.323260721796806A A A LNCV6_139999_PI430048170 mRNA
TTTCCTCTACTGGTTAGAGCAACATCAGCAAGATTTTAGGCAGAGATTAATAAACTGTAA NM_001005241 RefSeq
chr15 + 22094430 22095864 OR4N4 283694 "olfactory receptor, family 4, subfamily N, member 4"
GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130617_PI430048170 0.00177711983890995 0.5966766577522651 1.4945514500511
11.5951625887224 11.4572928028959 P P P 12.125798202436 12.2987342461905
12.3514261654169 P P P LNCV6_130617_PI430048170 mRNA
CCAGACCCACGGGGTAACGGGTCTAATCGTGTAGGAATAAAGCTGTATTCCAGTGCTTCC NM_003190RefSeq
chr6_GL000252v2_alt - 4543212 4557902 TAPBP 6892 "TAP binding protein (tapasin), transcript variant 1"
GO:0005515|GO:0002474|GO:0042824|GO:0042825|GO:0042288|GO:0005783|GO:0006890|GO:0042590|GO:0050
823|GO:0042886|GO:0006955|GO:0006461|GO:0015833|GO:0000139|GO:0019885|GO:0042605|GO:0005789|GO:0
071556|GO:0002479|GO:0051082|GO:0015433|GO:0016021|GO:0046978|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_80039_PI430048170 0.0709268177384478 1.47148089148828 7.39994337278498
6.86805999310052 7.10621464512645 P P P 6.55603123471781 6.58945557833455
6.60585250867732 P P P LNCV6_80039_PI430048170 mRNA
GTGACACTAGAAATTGGAAAACAACTAATTAAAGCACAGAAAGGAGCAGCATTTCTTTCT NM_001359RefSeq chr8
+ 90001351 90051999 DECR1 1666 "2,4-dienoyl CoA reductase 1, mitochondrial"
GO:0008670|GO:0006635|GO:0005634|GO:0044281|GO:0070402|GO:0005739|GO:0005737|GO:0051289|GO:0005
759|GO:0016651|GO:0005654|GO:0044255|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118985_PI430048170 0.1582176143547960.7763300457568160.277826428860576
0.2841770307116160.401999375110482A A A 0.3645841979161740.72752261511896
0.917580950286307A A A LNCV6_118985_PI430048170 mRNA
TTAATGAGAGAAATTTAAATATGCTGTTAAATTCCAAAAGTTTCAAGCCTTTGACTGGGG NM_000235RefSeq chr10
- 89213568 89252039 LIPA 3988 "lipase A, lysosomal acid, cholesterol esterase, transcript variant 2"
GO:0016042|GO:0000902|GO:0048873|GO:0048771|GO:0006954|GO:0030324|GO:0008283|GO:0001816|GO:0005
764|GO:0016298|GO:0070062|GO:0004771 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137773_PI430048170 0.0171628549696602 0.5278986946075523.553673421984
3.20993127342661 3.29611253879072 P P P 3.95898399986093 4.56012033155816
4.26583629744966 P P P LNCV6_137773_PI430048170 mRNA
TTACCTCACGGTGACAGTTACACTGCTCCTTTAAAGAGTCATTTACATAATTTGTTATCA NM_004808RefSeq chr10
- 15105771 15168696 NMT2 9397 N-myristoyltransferase 2
GO:0005794|GO:0005886|GO:0007603|GO:0019082|GO:0004379|GO:0022400|GO:0019068|GO:0018008|GO:0005
829|GO:0005737|GO:0016032|GO:0016056|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127583_PI430048170 0.9060688039615131.02448495101795 8.65330889063573
8.58519191106669 9.057520311234 P P P 8.76873587371033 8.69700298480918
8.77084005556802 P P P LNCV6_127583_PI430048170 mRNA
GTAGAGCAGTGTATCTTGCATGTCATCGGAAGAATAGATTTTTGTTTTGGTTTTGTTTTG NM_019006RefSeq chr15
+ 80059567 80138393 ZFAND6 54469 "zinc finger, AN1-type domain 6, transcript variant 1"
GO:0005515|GO:0003674|GO:0043066|GO:0005737|GO:0006625|GO:0071356|GO:0006915|GO:0008270|GO:0005
575|GO:0043122|GO:0003677|GO:0031593 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105980_PI430048170 0.2777820232712731.20111889780685 2.81969900561792
3.10251290283054 2.79977787938667 A P A 2.38393616475029 2.48672539804434
3.00029989911496 A P P LNCV6_105980_PI430048170 mRNA
TGAGAAAGAAGAAATTGGGTCCAGAAAGGGAAGTGAGGAGAATCAGATCCCAGACCTTTG NM_018231RefSeq

chr16 - 58665108 58684777 SLC38A7 55238 "solute carrier family 38, member 7"
GO:0030424|GO:0005290|GO:0005313|GO:0003333|GO:0015180|GO:0015813|GO:0015821|GO:0015803|GO:0015194|GO:0015810|GO:0006867|GO:0015183|GO:0015825|GO:0006868|GO:0015182|GO:0015191|GO:0015190|GO:0043025|GO:0015186|GO:0016021|GO:0006814|GO:0015179|GO:0015817|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125856_PI430048170 0.6442261987628451.1159858502622 5.16150311394183 4.43755789698277 4.5564168462285 P P P 4.82103879070647 4.67646977463445 4.22754624957342 P P P LNCV6_125856_PI430048170 mRNA CAGTGTGGAGGTGCTGGTTCCTCCCAGTATTGAGAACGAGGACTTGGAGGAGGTGATCAA NM_001291815 RefSeq
chr9 + 130265878 130434123 HMCN2 256158 hemicentin 2 GO:0005509|GO:0005578|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130544_PI430048170 0.158516246569978 1.02817663534221 0.380712642818272 0.385339640603122 0.436647276587372 A A A 0.357884025545264 0.338040519826959 0.386764786848466 A A A LNCV6_130544_PI430048170 mRNA TGGCTTATACTGCTGAAATAAAGGTTTTAATGTCTCTTTGTGGCCACATTTTTTGACTACNM_001145029 RefSeq chr18 + 14748239 14852738 ANKRD30B 374860 ankyrin repeat domain 30B
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102828_PI430048170 0.379498744911895 15.6285664189945 5.89223549468086 6.18003338859151 11.3090547956563 P P M 5.90346767157207 5.93675299670461 5.63443218561085 P P P LNCV6_102828_PI430048170 mRNA ACCACGTTATTAGTGCCATTCCAGCTTCAGTGCTCAGTGAGCTGCTCCCTGCTGAGGCTG NM_001122764 RefSeq
chr1 + 161166390 161171220 PPOX 5498 "protoporphyrinogen oxidase, transcript variant 2"
GO:0031966|GO:0042493|GO:0050660|GO:0044281|GO:0006782|GO:0006783|GO:0005758|GO:0004729|GO:0006778|GO:0006779|GO:0031304|GO:0031305|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71001_PI430048170 0.217254544387816 0.671406173635992 3.54704564434878 2.37253830817433 2.80685580064377 P A A 3.33773192614956 3.2636347526229 3.98462489326423 P P P LNCV6_71001_PI430048170 mRNA GGTTAGTAGTGAAATTCATTCTTCAATAAATAAAACACTTTGAAACTCCGGAGGACCACA NM_001282526 RefSeq
chr20 + 18467388 18484648 POLR3F 10621 "polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa, transcript variant 2"
GO:0005515|GO:0032728|GO:0010467|GO:0006386|GO:0006385|GO:0003899|GO:0006359|GO:0003677|GO:0006383|GO:0005829|GO:0051607|GO:0045089|GO:0001056|GO:0045087|GO:0005666|GO:0005654|GO:0032481 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145130_PI430048170 0.245536355691714 0.70138554928322 0.363091626225062 0.391231741303955 0.320423368192987 A A A 1.35268697222013 0.408095889859997 0.680936115875554 A A A LNCV6_145130_PI430048170 mRNA ACACACACATATACACGTGTATGAATATATATATATGGCTATAAGTGGTGCGACTTGCAG NM_003417 RefSeq chr19 + 57191499 57222846 ZNF264 9422 zinc finger protein 264
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143714_PI430048170 0.154139483476062 0.87339797740914 6.6060868901222 6.35678397563521 6.49472019342294 P P P 6.84108327483943 6.63471416556109 6.56386290455303 P P P LNCV6_143714_PI430048170 mRNA AAACAAAATGCTGAAGAATCTGCATCAAATAAACCCTTCCTTCCTTCCTTTTTCCTTCAA NM_001040108 RefSeq
chr14 - 75013763 75051532 MLH3 27030 "mutL homolog 3, transcript variant 1"
GO:0005515|GO:0030983|GO:0000795|GO:0019237|GO:0005634|GO:0005712|GO:0005524|GO:0032300|GO:0008104|GO:0007144|GO:0003697|GO:0003696|GO:0003682|GO:0006298|GO:0001673|GO:0007130|GO:0016887|GO:0007131|GO:0007140. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142872_PI430048170 0.92930127449965 0.998714976167573 6.13247861707266

6.08903250909748 5.80119449016502 P P P 6.35919717540691 5.98625857952147
5.60743004122138 P P P LNCV6_142872_PI430048170 mRNA
GCATGTAATCTGTGGACAATGGCATTCTCTACAATGCAATAAAAACAATTACCCATGAAA NM_001012426 RefSeq
chr6 + 41546425 41602384 FOXP4 116113 "forkhead box P4, transcript variant 1"
GO:0007507|GO:0005515|GO:0001078|GO:0061140|GO:0046982|GO:0048617|GO:0005634|GO:0000122|GO:0000
978|GO:0046872|GO:0042803|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140336_PI430048170 0.0202379557740696 0.1736277486624881.4320912136341
0.4104059647277150.342432543576905A A A 2.19227440046783 3.83430872580928
3.54397742316008 A P P LNCV6_140336_PI430048170 mRNA
ATCTGTTGTTGCAGTGTATCTTTTTGTAAAGTTTGCAACAATCCTCAATCAAGTCTATGG NM_024680RefSeq chr11
- 19224062 19240960 E2F8 79733 "E2F transcription factor 8, transcript variant 1"
GO:0005515|GO:0005667|GO:0032466|GO:0003700|GO:0008283|GO:0003714|GO:0060707|GO:0032877|GO:0001
047|GO:0002040|GO:0005634|GO:0000122|GO:0001890|GO:0000978|GO:0042803|GO:0006351|GO:0001078|GO:0
045944|GO:0033301|GO:0060718|GO:0070365 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91931_PI430048170 0.0915443931191005 0.8180865903365016.60585250867732
6.56310757823152 6.28705642360245 P P P 6.93306666997885 6.75356170652657
6.64381490406091 P P P LNCV6_91931_PI430048170 mRNA
CGCTATTACAGTCTTCCCCCGCATCAGAAGTTCCATTGCCTTCTCTTTCCCCCACAATGC NM_001931RefSeq chr11
+ 112024813 112064278 DLAT 1737 dihydrolipoamide S-acetyltransferase
GO:0005739|GO:0005515|GO:0010510|GO:0004742|GO:0006099|GO:0005967|GO:0006090|GO:0005759|GO:0006
006|GO:0044281|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131640_PI430048170 0.0246696888634418 0.7003011899236894.04463265436314
4.20795322289791 3.81838277461914 P P P 4.40966847265125 4.58707640306244
4.63287619109218 P P P LNCV6_131640_PI430048170 mRNA
TAGCTTCTTCTCATACAGGTGCCAGACACTGTTTGTGCTTTTGATGGATTTTTATTTATA NM_014711RefSeq chr16 +
19523856 19553406 CCP110 9738 "centriolar coiled coil protein 110kDa, transcript variant 2"
GO:0005515|GO:0051298|GO:0043234|GO:0005813|GO:0032465|GO:0006996|GO:0007099|GO:0005814|GO:0000
086|GO:0030030|GO:0000278|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132401_PI430048170 0.3974802521876690.7456178318852811.68584747818921
3.17547693627707 3.61929462022789 A P P 3.32297318926685 3.43683575706569
3.59422866493639 P P P LNCV6_132401_PI430048170 mRNA
CATTGCAGGTACCGTTTGTGTAACATTACTCATTTCTGTATATTCCTTTTATGGGAAGATNM_006380RefSeq chr17 -
60443148 60526240 APPBP2 10513 "amyloid beta precursor protein (cytoplasmic tail) binding protein 2,
transcript variant 1"
GO:0005515|GO:0005737|GO:0005875|GO:0008152|GO:0005874|GO:0046907|GO:0005634|GO:0003777|GO:0006
886|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137609_PI430048170 0.44637991404953 0.9044850152918477.42334355709861
7.88123940696368 7.82363866199013 P P P 8.00578948602708 7.6593999071653
7.91717533039858 P P P LNCV6_137609_PI430048170 mRNA
GGATGAATTGGGGGATAGATCTATAATGTTCACTGTTCAAAACGAAGACTAGCTATTAAA NM_001562RefSeq chr11
- 112143250 112164117 IL18 3606 "interleukin 18, transcript variant 1"
GO:0005515|GO:0042346|GO:0007267|GO:0042088|GO:0032819|GO:0030155|GO:0005615|GO:0045662|GO:0005
829|GO:0042094|GO:0042104|GO:0006955|GO:0042092|GO:0006954|GO:0030101|GO:0000165|GO:0042095|GO:0
031663|GO:0070062|GO:0032729|GO:0032740|GO:0032725|GO:0042253|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_74461_PI430048170 0.150336216911293 1.06096620920492 0.5098910590986540.637819189655887
0.539621226757974A A A 0.4314587585704170.48781508583349 0.51382472493877 A A A
LNCV6_74461_PI430048170 mRNA
AGACATCATGGGTATAAAAGAAAATTCCATGAAAAGCATCATTCACATCGAGGCTATAGA NM_000200RefSeq chr4

+ 70028412 70036538 HTN3 3347 histatin 3
GO:0005515|GO:0050832|GO:0031640|GO:0005576|GO:0031214|GO:0046872|GO:0042742 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131757_PI430048170 0.1251805003414040.53559022929263 0.510971199741945
1.49574521270087 0.486653969904277A A A 1.70573164597302 1.18208818815061
2.32515765317611 A A P LNCV6_131757_PI430048170 mRNA
GCAGGCTCGGCCCTGAGAGGTTCTGTTTGTTCCTCCTTGGGATTTTTGGACTCAGTAGGT NM_001105669 RefSeq
chr1 + 156579726 156586770 TTC24 NA tetratricopeptide repeat domain 24 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_128049_PI430048170 0.5507389265646470.9743233078291970.419211843571016
0.4106665517735860.252798607079976A A A 0.3706543973345910.433577140327381
0.396342737709017A A A LNCV6_128049_PI430048170 mRNA
GCTAATTGTTTTCGCTTTAAAGCGCCAGTCTTTCTGTCAAATGGGACATACAAATAAATT NM_001002916 RefSeq
chrX - 104011146 104013687 H2BFWT NA "H2B histone family, member W, testis-specific" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138580_PI430048170 0.0214508872628387 0.4901175364646794.04292634155149
3.45851337897259 4.12476994784978 P P P 4.54528906380536 5.0369544900204
5.14874738515161 P P P LNCV6_138580_PI430048170 mRNA
GCCTTATGATTTTCTACCAAAAGTAAAAAGGGTTGTATTAAGTCAGAGGAAGATGCCTCT NM_007173RefSeq chr11
+ 86800239 86811231 PRSS23 11098 "protease, serine, 23, transcript variant 1"
GO:0004252|GO:0006508|GO:0005634|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135620_PI430048170 0.2086989023591130.5727912326610293.79944603512995
1.89360626383027 2.89501773850153 P A P 3.93954724548383 3.96003005179376
3.68652517884903 P P P LNCV6_135620_PI430048170 mRNA
CTTCATGACCAGAAGAGAAAGGAACAACAGAAAGATAAACAGACACAGAATGATCTGGTT NM_001031725
RefSeq chr1 - 200644036 200669998 DDX59 83479 DEAD (Asp-Glu-Ala-Asp) box polypeptide 59
GO:0005622|GO:0005737|GO:0003723|GO:0008152|GO:0004386|GO:0005634|GO:0005524|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107662_PI430048170 0.3426191293677610.96917407961454 0.253162146143628
0.2678380482197610.366960566105704A A A 0.3818560908912550.316317542171978
0.327120731671523A A A LNCV6_107662_PI430048170 mRNA
CATAGATGACTGTGAGATGTGTGAGATATTAAAAGATAGTCACATTTCGTGAGAAGAGAA NM_021143RefSeq chr19
- 12131352 12140407 ZNF20 7568 "zinc finger protein 20, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140605_PI430048170 0.0133547618762151 0.6769598848920976.60374840641057
6.69868913442243 6.86119282384636 P P P 7.08003597825063 7.39229638332267
7.37110417359968 P P P LNCV6_140605_PI430048170 mRNA
GCAATGGATTAACCACTGTATCTAAGAATCCACCATTAAAGCATTTGCACAGACAAAAAA NM_194259RefSeq chr16
+ 1309626 1327018 UBE2I 7329 "ubiquitin-conjugating enzyme E2I, transcript variant 2"
GO:0005515|GO:0006511|GO:0010469|GO:0016567|GO:0016874|GO:0045202|GO:0005634|GO:0030425|GO:0051
091|GO:0005737|GO:0007059|GO:0043398|GO:0016032|GO:0071535|GO:0031625|GO:0000795|GO:0016925|GO:0
043425|GO:0000122|GO:0008022|GO:0005524|GO:0007067|GO:0016605|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145651_PI430048170 0.00632905977398922 1.49626165752205 10.1034238743686
10.3544477526514 10.3045833473904 P P P 9.65484731597045 9.75663518213815
9.61522306886505 P P P LNCV6_145651_PI430048170 mRNA
TTCCTATGCAGCTTTAATGTCCCCGTGTCCCCGGGGTGGGAGTTCAAGGCTCAGTAATGG NM_030935RefSeq chr7
- 100466518 100479279 TSC22D4 81628 "TSC22 domain family, member 4, transcript variant 1"

GO:0005515|GO:0005737|GO:0003700|GO:0006970|GO:0005634|GO:0045892|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134352_PI430048170 0.6406126792904560.9329748223891137.34034298787685
7.13204639297494 7.59511982666745 P P P 7.30557949496716 7.31968912914508
7.73701845444578 P P P LNCV6_134352_PI430048170 mRNA
GGCACCTTTCAACATCATTTGCTTCCTTATCTACAGTTGATTCAGAAATCTGCATTTTTT NM_017671RefSeq chr20 -
6074844 6123544 FERMT155612 fermitin family member 1
GO:0090162|GO:0051546|GO:0031941|GO:0030054|GO:0032587|GO:0007155|GO:0043616|GO:0005925|GO:0005
829. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138389_PI430048170 0.7856003603853720.9536954623413770.591734940958421
0.5121151080895180.606519611997087A A A 0.4106974826191880.937509620866977
0.513563341725688A A A LNCV6_138389_PI430048170 mRNA
TGGGTGTGAGTCACAATACTTTGGTTTGTGCACAAGAATAAATTTATGCCCCATACCTTC NM_001114133 RefSeq
chr10 - 73644880 73656105 SYNPO2L 79933 "synaptopodin 2-like, transcript variant 1"
GO:0030018|GO:0005634|GO:0003779|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144094_PI430048170 0.0631196850508183 0.7185236562296469.13233113759593
9.10656368196595 9.36824987469469 P P P 9.44524206451762 9.62355509438726
9.93968170764336 P P P LNCV6_144094_PI430048170 mRNA
CCCATCATGAATTCATTGGAATTTGTGTTGCATGTAAGGCAATCTTTCCTGTTGTAAATC NM_016287RefSeq chr1
- 20742677 20786688 HP1BP3 50809 "heterochromatin protein 1, binding protein 3"
GO:0005515|GO:0097298|GO:0006355|GO:0070828|GO:0005694|GO:0042127|GO:0006334|GO:0071456|GO:0031
491|GO:0005634|GO:0000786|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143465_PI430048170 0.4085697088420451.39751242320671 0.343121756549129
1.40738484088962 0.263016792824323A A A 0.2888548111827290.297227715862341
0.279706267906635A A A LNCV6_143465_PI430048170 mRNA
TTACTTCAGGGCTGGAAAAGTCACACAGACACACAAAATGTCACAATCCTGTCCCTCACT NM_014009RefSeq chrX
- 49250435 49264826 FOXP3 50943 "forkhead box P3, transcript variant 1"
GO:0005515|GO:0032753|GO:0003700|GO:0006366|GO:0032693|GO:0032715|GO:0003705|GO:0000981|GO:0002
513|GO:0032714|GO:0032713|GO:0032792|GO:0001816|GO:0042803|GO:0032914|GO:0042130|GO:0045077|GO:0
002361|GO:0002262|GO:0043029|GO:0032689|GO:0035035|GO:0003714|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140523_PI430048170 0.0117178310128297 1.6907616100309 3.75326435900144
3.57941683595422 3.46153133153313 P P P 3.01070379395218 2.9118007624354
2.57918678701978 P P P LNCV6_140523_PI430048170 mRNA
TACCTGCCCTCAAGGGTGTGTATATTGTATAGGGGCAACTGTATGAAAAATTGGGGAGGA NM_002231RefSeq chr11
+ 44565590 44619765 CD82 3732 "CD82 molecule, transcript variant 1"
GO:0005515|GO:0005886|GO:0005887|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131080_PI430048170 0.00273969294567201 0.4573002507909485.53613902407605
5.17539432418372 5.5588873515528 P P P 6.33520322396917 6.58768184594504
6.73682366206016 P P P LNCV6_131080_PI430048170 mRNA
GGCACCTATTTCTGTAAAATCCCCAAATTGGTGTTGATGATTTTGAGCTTGAATGTTTTC NM_018313RefSeq chr3
- 52545351 52685850 PBRM1 55193 polybromo 1
GO:0007507|GO:0005515|GO:0007067|GO:0006355|GO:0008285|GO:0003682|GO:0000776|GO:0006338|GO:0001
890|GO:0000228|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128429_PI430048170 0.0243641606326863 0.7420869657355869.00617481088154
8.93968538022665 8.69886993355897 P P P 9.40566333495022 9.32199481799004 9.2198904135315
P P P LNCV6_128429_PI430048170 mRNA
TAACCTTTAAAATCTCCAGTTAAAGGGCCTGTTTCTTACTGGCCTGTGAGGTGCACCGTA NM_138384RefSeq chr10
+ 133394116 133420670 MTG1 92170 mitochondrial ribosome-associated GTPase 1

GO:0006184|GO:0070129|GO:0005759|GO:0005761|GO:0005743|GO:0003924|GO:0044065|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71309_PI430048170 0.63302237623713 1.07726985677868 4.50894527219552 4.26265665080578 4.34044654970437 P P P 3.70640401417993 4.41994108219591 4.54217672818371 P P P LNCV6_71309_PI430048170 mRNA CAATGACCAGCAGTTGGTATGAAGAACCTTTGACATTTTGTAAAAGGCCATTTCTTGGGA NM_001161841 RefSeq chr20 - 47657405 47786616 SULF2 55959 "sulfatase 2, transcript variant 3"
GO:0005795|GO:0005886|GO:0009986|GO:0051216|GO:0001822|GO:0005783|GO:0005509|GO:0048706|GO:0035860|GO:0030177|GO:0008449|GO:0032836|GO:0005615|GO:0010575|GO:0060384|GO:0060348|GO:0002063|GO:0003094|GO:0040037|GO:0004065|GO:0030201|GO:0014846 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130709_PI430048170 0.0204586593642864 0.5498302256048073.30410122219738 3.16503783232555 3.39798333309281 P P P 4.2611601900828 4.33052278634387 3.82321810077098 P P P LNCV6_130709_PI430048170 mRNA CCCTCTTGCTCTTCTTTAGTTTGAAAAAACAAAAACGTGGCCTTGGAATTTTCATTTTGA NM_183376RefSeq chr15 + 97960702 97973838 ARRDC4 91947 arrestin domain containing 4
GO:0005886|GO:0051443|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132851_PI430048170 0.4698371238776040.7838429109857152.26466448138999 2.45555321112575 0.294424131997898A A A 2.25140123553599 2.48666701170246 2.11330032468924 A P A LNCV6_132851_PI430048170 mRNA GGTCTCAAAGTTGGATGACCTCATTACTAATATTTGTTGTAAAAGTGAAACTTGTTTGCC NM_015236RefSeq chr4 + 61497120 62072450 ADGRL3 NA adhesion G protein-coupled receptor L3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145710_PI430048170 0.3028875594057551.09693017817228 11.3219243378641 11.6434265483299 11.5140974323961 P P P 11.3243602158581 11.3307277546843 11.439033927167 P P P LNCV6_145710_PI430048170 mRNA GATTCTGACCAGTGACTTACACAAAAGGCGCTCTATACATATTATAATATATTCGCTTAC NM_001276319 RefSeq chr16 + 67170496 67175737 NOL3 8996 "nucleolar protein 3 (apoptosis repressor with CARD domain), transcript variant 7"
GO:0005515|GO:0008380|GO:2001237|GO:0001666|GO:0043066|GO:0003723|GO:0006376|GO:0005730|GO:0051259|GO:0005829|GO:0042802|GO:0005739|GO:0005737|GO:0016528|GO:0014876|GO:0043154|GO:0043027 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63583_PI430048170 0.1384137788095480.7773730332109226.73951022394916 6.78626028196063 6.26670441091223 P P P 6.86072776984893 7.03788734041687 7.03186952457042 P P P LNCV6_63583_PI430048170 mRNA TTAGTGAGCCACAGTTCCACAATGGCGAGTCTGAGGAGAGCCACGAGCAGTTCCTGAAGG NM_004712RefSeq chr17 + 81683931 81702121 HGS 9146 hepatocyte growth factor-regulated tyrosine kinase substrate
GO:0005515|GO:0008285|GO:0046872|GO:0005829|GO:0043231|GO:0005737|GO:0007173|GO:0016197|GO:0061024|GO:0030141|GO:0070062|GO:0042176|GO:0008333|GO:0019904|GO:0032585|GO:0042059|GO:0072657|GO:0046426|GO:0010628|GO:0007165|GO:0031901|GO:0006622|GO:0010324|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145075_PI430048170 0.5946014395819745.70116625355787 5.09991141661842 9.77746831962345 5.34802793795361 P P P 5.57125060192349 5.76679942306349 6.02468554495936 P P P LNCV6_145075_PI430048170 mRNA GGTAAAGCCTACACTCGTTCCAGTCACCTTACTCGCCATGAAAGAAGTCATGATATAGAG NM_024804RefSeq chr1 - 247099961 247104372 ZNF669 79862 "zinc finger protein 669, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_142517_PI430048170 0.3324492820170790.9024930444220245.62606249740501 5.5197175970605
5.8731472990051 P P P 5.65270106670226 5.93662631888143 5.88131850391037 P P P
LNCV6_142517_PI430048170 mRNA
CTTTCCCACTGAAAATCTATTCTCATATTTTGGGAAGGAGCATATGTCCTTTAACTTTCA NM_017902RefSeq chr10
+ 100535883 100553924 HIF1AN 55662 "hypoxia inducible factor 1, alpha subunit inhibitor"
GO:0031406|GO:0005515|GO:0048471|GO:2001214|GO:0036138|GO:0042265|GO:0042264|GO:0036139|GO:0005
112|GO:0061418|GO:0005634|GO:0042803|GO:0005829|GO:0005737|GO:0036140|GO:0071532|GO:0045746|GO:0
048037|GO:0005506|GO:0051059|GO:0071456|GO:0061428|GO:0006351|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_72930_PI430048170 0.16524688577434 1.43841541402884 3.70292308416803 4.08228006689438
4.51325111871888 P P P 3.48961013225734 3.67959532283969 3.66213408486143 P P P
LNCV6_72930_PI430048170 mRNA
TGTACTTGGCTACATCCTGCTGGAAGACCCACAGCTGCATGCCCAGGCCTACGTGAGATT NM_015175RefSeq chr3
+ 46979682 47009704 NBEAL2 23218 neurobeachin-like 2
GO:0035855|GO:0005543|GO:0016020|GO:0007596|GO:0005783|GO:0016197|GO:0070889|GO:0030220|GO:0019
898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127848_PI430048170 0.0808955047146709 0.7354050851191188.08046740178641
8.38782771281086 8.58645376693424 P P P 8.65483738320063 8.70376748547972
9.03955188089893 P P P LNCV6_127848_PI430048170 mRNA
TCTCTCCCTTTCCTGAACCCTATTCTGATCCTGAACCAAATTTATAGCAATATAATTAGTNM_001293285 RefSeq chr12
+ 49366904 49527426 SPATS2 65244 "spermatogenesis associated, serine-rich 2, transcript variant 1"
GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141320_PI430048170 0.3298924549364850.9579660657180621 0.8268377652497
10.6693220983556 10.8011620250086 P P P 10.8737351599536 10.7973058063438
10.8159353426104 P P P LNCV6_141320_PI430048170 mRNA
AGTGGAAGTCCAGGCTTGGATTGCCTAACTACACTGCTAAAAATATTTGTAATCCTTAAT NM_012461RefSeq chr14
- 24239644 24242674 TINF2 26277 "TERF1 (TRF1)-interacting nuclear factor 2, transcript variant 2"
GO:0034502|GO:0005515|GO:0000781|GO:0042162|GO:0010836|GO:0050680|GO:0005634|GO:0010833|GO:0003
677|GO:0016363|GO:0032211|GO:0000723|GO:0005654|GO:0010370|GO:0032206|GO:0070198|GO:0000783|GO:0
032202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129289_PI430048170 0.0139327635344279 0.1859517436445620.55641143018892
0.7470377302177620.588483665975746A A A 2.98757063249058 2.46699543550132
3.53110293890149 P A P LNCV6_129289_PI430048170 mRNA
GTGTAGGAAACTTTTGCAGTTTGACACTAAGATAACTTCTGTGTGCATTTTTCTATGCTT NM_001127208 RefSeq
chr4 + 105146684 105279803 TET2 54790 "tet methylcytosine dioxygenase 2, transcript variant 1"
GO:0005515|GO:0010467|GO:0020027|GO:0001822|GO:0072576|GO:0006211|GO:0080182|GO:0035511|GO:0019
858|GO:0048536|GO:0009791|GO:0003677|GO:0008198|GO:0007049|GO:0006493|GO:0045944|GO:0080111|GO:0
040029|GO:0030099|GO:0008270|GO:0002318|GO:0070579 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131935_PI430048170 0.3203300772359170.8500926730087350.472667122400297
0.3756866332703920.430191945344902A A A 0.9708504647050640.487108132566869
0.466780581745183A A A LNCV6_131935_PI430048170 mRNA
TTGGCTGGAATCCAGGACTGTATTTTCATGGAGAAGAACCTGCAGATTCTTCCATCCTCA NM_020433RefSeq chr20
- 44111696 44187578 JPH2 57158 "junctophilin 2, transcript variant 1"
GO:0005515|GO:0070300|GO:0030018|GO:0060402|GO:0005886|GO:0030314|GO:0080025|GO:0070273|GO:0005
547|GO:0005546|GO:0032266|GO:0055074|GO:0060316|GO:0014701|GO:0060314|GO:0070588|GO:0001786|GO:0
015278|GO:0016021|GO:0055024|GO:0010314 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88565_PI430048170 0.0595850385753705 0.5780766787676226.49865484005074
6.49515666275707 6.67509687388974 P P P 6.99376103707396 7.24650658189908

7.71387609464178 P P P LNCV6_88565_PI430048170 mRNA
GGTGCTGCTCCTGACAAGTGTATGTTAACTGTTTACATTTTCTATCTGTAGAATTATTTC NM_001278547 RefSeq chr10
+ 48306638 48439359 MAPK8 5599 "mitogen-activated protein kinase 8, transcript variant JNK1-b2"
GO:0097300|GO:0005515|GO:0070301|GO:0071732|GO:0051403|GO:0002756|GO:0004705|GO:1900740|GO:0018
105|GO:0018107|GO:0002755|GO:0009411|GO:0035033|GO:0038124|GO:0038123|GO:0034134|GO:0006950|GO:0
002224|GO:0001503|GO:0045087|GO:0005654|GO:0034166|GO:0035666|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133739_PI430048170 0.0124760931017661 0.5585871963583515.10713140948756
4.80959468410441 4.656112954769 P P P 5.55086311962081 5.97839437561115
5.55820195809435 P P P LNCV6_133739_PI430048170 mRNA
TGGGCATTTGCACGCCAAAGGCAAAGAAGAAAAAATGTCCAAATCATTAAAGAACTACAT NM_024537 RefSeq chr13
- 110641409 110706180 CARS2 79587 "cysteinyl-tRNA synthetase 2, mitochondrial (putative)"
GO:0006423|GO:0010467|GO:0004817|GO:0005759|GO:0005524|GO:0046872|GO:0006418|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136406_PI430048170 0.95900103737251 0.9953018376633729.25075681729027
9.17687774040897 9.43907111384623 P P P 9.17658258197329 9.25381798486091
9.45500446168044 P P P LNCV6_136406_PI430048170 mRNA
CTGTGGGAATTCCTCCCAATTTATGGTTTCCCAGAAAATCTTAGTTCCTTTTATTTATAG NM_025010 RefSeq chr3 +
47282839 47346816 KLHL18 23276 kelch-like family member 18 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140546_PI430048170 0.11080080000578 0.4910250275553240.435694549397198
1.89565472005664 1.08447410435866 A A A 2.74689137678174 2.21950083781078
1.71418703924196 P A A LNCV6_140546_PI430048170 mRNA
GACCCTCACTGGGAGGTGAGCTCAGCTGCCCTTTGGAATAAAGCTGCCTGATCCAAAAAA NM_153609 RefSeq chr22
- 37065435 37103653 TMPRSS6 164656 "transmembrane protease, serine 6, transcript variant 2"
GO:0035556|GO:0030514|GO:0005515|GO:0005886|GO:0004252|GO:0030198|GO:0006508|GO:0016021|GO:0001
525|GO:0055072|GO:0042730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143113_PI430048170 0.0261464448843702 0.5298383626098364.47859388373157
4.16093604956667 4.80694558514922 P P P 5.38916937346626 5.3184142229767
5.55025616000603 P P P LNCV6_143113_PI430048170 mRNA
TTAGCTTTTTAGAACTTTGATCTGCTAGGGATTGTCAAAATAATCTCCTTGAGGCATCTT NM_015946 RefSeq chr5
+ 52787939 52802617 PELO 53918 pelota homolog (Drosophila)
GO:0070481|GO:0051276|GO:0007049|GO:0005737|GO:0004519|GO:0090305|GO:0008283|GO:0005634|GO:0071
025|GO:0070966|GO:0046872|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132918_PI430048170 0.4932837107632330.9129747637885430.249946804099587
0.4843963062469760.370868248119767 A A A 0.3818498167684850.76479637848516
0.320911848905478 A A A LNCV6_132918_PI430048170 mRNA
AAAGAGAAGGCTACTGGCAGATGAAAGTCAAATTCTTCCTTCCATACACTCCACATTCCA NM_000808 RefSeq chrX
- 152167161 152451359 GABRA3 2556 "gamma-aminobutyric acid (GABA) A receptor, alpha 3"
GO:0005230|GO:0030054|GO:0005886|GO:0004890|GO:0034707|GO:0007268|GO:0007214|GO:0055085|GO:0005
254|GO:0034220|GO:0005887|GO:0045211|GO:0006810|GO:0008503 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_136795_PI430048170 0.0819780783532634 0.8971077945343111 0.1144825074293
10.1253795876325 9.97412217302185 P P P 10.2329908570168 10.3072041682138
10.1439865068326 P P P LNCV6_136795_PI430048170 mRNA
AATTGGTTTGTACTCACTGGGCTGTGCTCTCCCCTGTTTACCCGATGTATGGAAATAAAG NM_078471 RefSeq chr17
- 29073509 29180389 MYO18A 399687 "myosin XVIIIA, transcript variant 1"
GO:0005515|GO:0005802|GO:0043066|GO:0005793|GO:0042641|GO:0050714|GO:0031032|GO:0006259|GO:0016
459|GO:0003677|GO:0005524|GO:0003774|GO:0051015|GO:0043531|GO:0000139|GO:0016020|GO:0016477|GO:0

007030|GO:0048194|GO:0016887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_46973_PI430048170 0.3779978042533121.99328156452851 0.3637571960277 2.2760348002706
0.439106422810883 A A A 0.3124593444509020.303543118560879 0.355709217426026 A A A
LNCV6_46973_PI430048170 mRNA
ACCTGGTATTGGAGATGTTAAGGTCATTGAAAAAGCAACTAAGTCTATGCTAGACCCAGC NM_001199938 RefSeq
chr10 - 22208813 22209983 EBLN1 NA endogenous Bornavirus-like nucleoprotein 1 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137285_PI430048170 0.28415370280611 0.9601807420448590.296327948133124
0.4073536576399380.314275032812316 A A A 0.4617730041534390.378945383837213
0.353344672629587 A A A LNCV6_137285_PI430048170 mRNA
GGTAGCTGCTTTTAACGATACAGTTTTAATGCAACTTTCATAATCATCCTGAAGACACTT NM_173545 RefSeq chr2
+ 68467558 68580162 APLF 200558 aprataxin and PNKP like factor
GO:0003906|GO:0005515|GO:0000012|GO:0008408|GO:0090305|GO:0045191|GO:0004520|GO:0035861|GO:0005
634|GO:0046872|GO:0006974|GO:0005829|GO:0006302|GO:0000166|GO:0005654|GO:0051106|GO:0000737 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141866_PI430048170 0.1253359420347830.758329281653855 2.6373246386795
2.79182386270505 2.20935479109752 A A A 3.10089379634554 2.94719980014715
2.83654250896988 P P P LNCV6_141866_PI430048170 mRNA
GGCTTTGCTTAGCTTGTTGAAGAAAGTAGCAGAAATTAAATCTTAATAAAAGAAAGCCCC NM_016249 RefSeq chrX
- 142202341 142205290 MAGEC2 51438 melanoma antigen family C2
GO:0005515|GO:0005737|GO:0051443|GO:0005634|GO:0044257|GO:0031625 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135957_PI430048170 0.2616678859661940.938343519562077 9.56134914621754
9.61353932654608 9.49600714792846 P P P 9.76165228404189 9.58420717365187 9.5959605345761
P P P LNCV6_135957_PI430048170 mRNA
GGCGTTGGGTGGCCTCTGGTATTTATTTGGCATTTATAAATATATAAACTCCTTTTTTACNM_015037 RefSeq chr10 +
73785623 73801798 ZSWIM8 23053 "zinc finger, SWIM-type containing 8, transcript variant 1"
GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143446_PI430048170 0.0366254930346888 1.27451853432988 7.87362794957308
8.04567439836159 7.78356600482374 P P P 7.51489377993305 7.70866318063928
7.42732988676439 P P P LNCV6_143446_PI430048170 mRNA
GCCTTCTCTCTAGTGTCTTTAAGTTGCTGATGACTCACAAGGTAAAGCTTGAGAGCAACT NM_052853 RefSeq chr7
+ 140673152 140695108 ADCK2 90956 aarF domain containing kinase 2
GO:0005739|GO:0004674|GO:0006468|GO:0016021|GO:0005524 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138128_PI430048170 0.0114848233568429 0.9481021795994260.383842139574934
0.3605294676084750.338076129127001 A A A 0.4514435950843520.443059702741407
0.418764752120003 A A A LNCV6_138128_PI430048170 mRNA
AGAGCTACAGCAGTATGTACCTGCATTAAAGGATTCCAATCTTAGCTTTGAAGAATTTAA NM_006911 RefSeq chr9
- 5334931 5339873 RLN1 6013 relaxin 1 GO:0007165|GO:0007565|GO:0005179|GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90423_PI430048170 0.1718180700131430.8258597147821648.4158282992336 8.49065683340632
8.80207837419051 P P P 8.80723131085896 8.66559049841566 9.06483090430386 P P P
LNCV6_90423_PI430048170 mRNA
CTTGAACAGGAATATTAAGATAAATGTGAATCTGCAATGGCTGAAAAGAGTTGTGAGCTT NM_001303543 RefSeq
chrX + 155216272 155239841 VBP1 7411 "von Hippel-Lindau binding protein 1, transcript variant 2"
GO:0005515|GO:0005737|GO:0006457|GO:0016272|GO:0051084|GO:0005634|GO:0044267|GO:0043231 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60335_PI430048170 0.0053014788543049 0.3254473472670361.27367313041657

0.7323496726463110.526479687470475 A A A 2.77439090308056 2.16661299605749
2.49268145701024 P A P LNCV6_60335_PI430048170 mRNA
ATACTCCTGAAGTTCTTTTTCTGATGGAAAACAAAATTCAGCTTAATCGTGTACTCAGCA NM_006346 RefSeq chr13
+ 72782091 73016453 PIBF1 10464 progesterone immunomodulatory binding factor 1
GO:0005515|GO:0005813 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139784_PI430048170 0.5605611573167671.20623929315188 1.24320465906514
0.37329537021401 0.327382143454633 A A A 0.505124167268611 0.452174741057436
0.366466767961282 A A A LNCV6_139784_PI430048170 mRNA
GTTGAACATCCTGATAAGTCAATGTTAACCAGAAACCTTTTTGTTCACGTCTGAAATTGA NM_198281 RefSeq chr4
- 89244277 89308010 GPRIN3 285513 GPRIN family member 3 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_95193_PI430048170 0.1439153184764340.87960922251008 8.0237822552968 7.76106404670759
7.98156652083718 P P P 8.00065948773811 8.12083030195451 8.20630589936898 P P P
LNCV6_95193_PI430048170 mRNA
TGGAAGAAAGAACTGGAAAAACACAGGGAGAAATTGTTAAGTGGAAGTGAGAGCTCATCC NM_001040057
RefSeq chr7 - 92560757 92590394 FAM133B 257415 "family with sequence similarity 133, member
B, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56605_PI430048170 0.0117810247759937 0.5513380568998494.31321682342629
3.83754636209661 4.05766196745528 P P P 4.90518416097424 5.067990858515
4.84206055996202 P P P LNCV6_56605_PI430048170 mRNA
CTACTGTGGTGGAGGTTCCATTGAAAGCCTGCAAATCTTAAATTAAAATGTGGAAGCTTC NM_018999 RefSeq chr10
+ 84328588 84518521 CCSER2 54462 "coiled-coil serine-rich protein 2, transcript variant 2"
GO:0008017|GO:0001578|GO:0015630 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131692_PI430048170 0.1089741658580541.03799561966082 0.386659221042444
0.3982511223568390.453134565604787 A A A 0.3490698006064140.339212235850953
0.388761173903515 A A A LNCV6_131692_PI430048170 mRNA
GCTTTCTCTTCACCAGGACATTGACAAAAGAATGGAATTGGTGAAAAAGAAAAAAGTGAT NM_001278298 RefSeq
chr3 + 130345515 130484846 COL6A5256076 "collagen, type VI, alpha 5, transcript variant 1"
GO:0031012|GO:0005515|GO:0005581|GO:0022617|GO:0030198|GO:0030574|GO:0005578|GO:0005576|GO:0007
155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140564_PI430048170 0.1405746247837251.09169422590363 12.019733183985
12.0611580131485 11.9316674232487 P P P 11.7916605270796 11.9813059392133
11.8564194979298 P P P LNCV6_140564_PI430048170 mRNA
AACTGGTAAACGTCTGCTTCGGAGCTTGCTGCTTAATAAATGTTGGTGGAATGAATGAAA NM_001236 RefSeq chr21
+ 36134964 36146562 CBR3 874 carbonyl reductase 3
GO:0005737|GO:0004090|GO:0050890|GO:0005654|GO:0070402|GO:0042376|GO:0005615|GO:0055114|GO:0005
829|GO:0000253 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130624_PI430048170 0.1553072908024081.03956627163489 0.514357954767413
0.4731348894897880.46032388998844 A A A 0.3743120833758940.44829873369568
0.456404731600371 A A A LNCV6_130624_PI430048170 mRNA
GTCATCCTTATCTCGAAGAGCTTAGAAACAAAGAGTGGGAAATTCCACTGGGCCTACCTT NM_000539 RefSeq chr3
+ 129528638 129535344 RHO 6010 rhodopsin
GO:0005515|GO:0060170|GO:0060041|GO:0005886|GO:0007603|GO:0042622|GO:0016918|GO:0046872|GO:0018
298|GO:0009881|GO:0005911|GO:0016056|GO:0006996|GO:0005794|GO:0004930|GO:0030507|GO:0022400|GO:0
001523|GO:0009585|GO:0001917|GO:0007186|GO:0000139|GO:0005887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137133_PI430048170 0.5380560370380320.8325713889825510.273844772757115
1.93471658419785 2.35010290369691 A A A 2.33190505155404 1.66316196511688 1.9877296019398
A A A LNCV6_137133_PI430048170 mRNA

GGTGGAGGTGATATGGCATTCTGAAAGTAGGGAGGGACTAAGTCAGTCATCATACTAAAC NM_020377 RefSeq chr13 + 48653710 48709362 CYSLTR2 57105 cysteinyl leukotriene receptor 2 GO:0005515|GO:0006955|GO:0007186|GO:0005886|GO:0001631|GO:0070374|GO:0016021|GO:0005575|GO:0004974|GO:0010942|GO:0045766 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94697_PI430048170 0.341132151309664 1.14715294802555 6.77549301690134 6.70461923097678 6.8687448477387 P P P 6.21731645448708 6.76990561950889 6.71101721016401 P P P LNCV6_94697_PI430048170 mRNA
ATGTTTGGCACGAAATGCCATGGCTGTGACTTCAAGATCGACGCTGGGGACCGCTTCCTG NM_005451 RefSeq chr5 - 177483393 177497605 PDLIM7 9260 "PDZ and LIM domain 7 (enigma), transcript variant 1" GO:0005515|GO:0001725|GO:0030036|GO:0005634|GO:0007275|GO:0015629|GO:0001726|GO:0006898|GO:0030154|GO:0045669|GO:0005737|GO:0001503|GO:0008270|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144262_PI430048170 0.340212169552488 0.783015344886513 0.426978544385218 0.354827126045232 0.378456688819761 A A A 0.460481780627207 1.19172697635057 0.433077133512407 A A A LNCV6_144262_PI430048170 mRNA
GTGTTTTGGTTATTTTGTATTCCCACCTGTGCTGGTAGATATTATTAACCCATTAGGTAA NM_001291527 RefSeq chrX - 135880751 135888993 CT45A10 NA "cancer/testis antigen family 45, member A10, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132937_PI430048170 0.00636631813587028 1.48394771236188 2.79715097868218 2.7149583168583 2.87642359605983 A A A 2.22149777612402 2.22796672312919 2.23523045449135 A A A LNCV6_132937_PI430048170 mRNA
AAGTGTTAGTGCTTCCAGGCGGCACTGACAGCCTCAGTAACAATAAAAACAATGGTAGCT NM_001207037 RefSeq chr6 - 36366193 36387800 ETV7 51513 "ets variant 7, transcript variant 4" GO:0005515|GO:0000977|GO:0006366|GO:0006357|GO:0000981|GO:0009887|GO:0005654|GO:0005634|GO:0000122|GO:0001227|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134673_PI430048170 0.0515278320852445 1.70326300749842 3.60983214886176 4.01982999019136 4.24491407135691 P P P 3.22492835552862 3.13946128176063 3.27226603224319 P P P LNCV6_134673_PI430048170 mRNA
GTTGGAGAAAAACCTTAGTGATGTGATGGTGCAATAAAGTCTTCACTCAGTCTTCATGAA NM_013398 RefSeq chr19 + 44094328 44108326 ZNF224 7767 zinc finger protein 224 GO:0005515|GO:0031965|GO:0003700|GO:0017053|GO:0005654|GO:0005634|GO:0045892|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135490_PI430048170 0.303644618159627 1.47827228866496 3.04642828360829 2.41001603643696 2.20778230324051 P A A 2.38630338531047 0.984476822444245 2.35113863231552 A A P LNCV6_135490_PI430048170 mRNA
CTCAGTGTTTTATGGAGCTTTGACACCCATGTTGAACCCCCTGATATATAGCCTGAGAAA NM_001004486 RefSeq chrX + 131544073 131545000 OR13H1 NA "olfactory receptor, family 13, subfamily H, member 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131794_PI430048170 0.390971081468015 0.912452609014672 7.39214995738521 7.34099554060557 7.58369206931949 P P P 7.67897354252113 7.35025913560686 7.67184425732805 P P P LNCV6_131794_PI430048170 mRNA
CAGACCATCTGTATGTTAGGTGACATTGATTATGGGTTATAATCAGGGAAACTAATTGTA NM_005113 RefSeq chr14 + 92794230 92839961 GOLGA5 9950 golgin A5 GO:0005801|GO:0017137|GO:0005794|GO:0016020|GO:0000139|GO:0031985|GO:0007030|GO:0048193|GO:0016021|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75963_PI430048170 0.109508043927291 0.554403700167264 2.93747280387238 2.13045197809475 1.69936417659288 A A A 3.05928700066568 2.97635428659865 3.50688950644743 P P P LNCV6_75963_PI430048170 mRNA
GGTTGCCCAAATATAATTTTGCTTTGACTATTGAGATCTAGTGAAAGTGGGGTATATGAA NM_181705 RefSeq chr5

+ 131170913 131205426 LYRM7 90624 "LYR motif containing 7, transcript variant 1" GO:0005759 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130921_PI430048170 0.00114800106321971 0.4927010285338551 1.2375395197619
11.0573517740165 11.2370286662262 P P P 12.1696054107648 12.1850793177998
12.2470851022226 P P P LNCV6_130921_PI430048170 mRNA
ACTGTCCACATGTGAACTTTTTCTAGGTGGCAGGACAAATTGCGCCCATTTAGAGGATGT NM_001142298 RefSeq
chr5 + 179806387 179838077 SQSTM1 8878 "sequestosome 1, transcript variant 2"
GO:0005515|GO:0043130|GO:0006511|GO:0005783|GO:0046578|GO:0051291|GO:0005764|GO:0042803|GO:0030
154|GO:0042802|GO:0005829|GO:0035556|GO:0005737|GO:0008104|GO:0000932|GO:0045944|GO:0005080|GO:0
016197|GO:0043122|GO:0042169|GO:0070530|GO:0070062|GO:0016239|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138239_PI430048170 0.0685282291949432 1.32024634855631 6.00143071433475
6.2990673144098 5.91932963327452 P P P 5.82318268217425 5.74495911224509 5.4514823130079
P P P LNCV6_138239_PI430048170 mRNA
TTACTAAAAAGAAGGTAACCTTTGTTGGATGTTGTCCCTCAGTCTCCATCCCCAGACTAC NM_001099293 RefSeq
chr5 + 155013699 155018125 KIF4B NA kinesin family member 4B NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145512_PI430048170 0.419566467295797 1.02290651402063 0.36689129910311
0.365657080539123 0.271172594587845 A A A 0.296782551009991 0.313357237865232
0.29757201476728 A A A LNCV6_145512_PI430048170 mRNA
TTGGAAAGAAATCTTGTAATAAAACTGCAGCCGTAGGGCTTCAGGCAGCTTCCCAAAAAA NM_203400 RefSeq chr17
- 46978155 46979248 RPRML 388394 reprimo-like GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132818_PI430048170 0.283717578589692 1.65936252614511 1.52340329269542
1.70333256377346 0.318168750790992 A A A 0.462982744653578 0.382126221357755
0.819348003178053 A A A LNCV6_132818_PI430048170 mRNA
ATCAGCACTGGAAAATAACTCCTAAATGTCCAAAAAGAACATGAGATTTATGGTGCTTGA NM_032679 RefSeq chr19
- 51871295 51887976 ZNF577 84765 "zinc finger protein 577, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128159_PI430048170 0.119360760422627 1.06829378887482 0.48761857318413
0.607128904395838 0.536542670102466 A A A 0.385185274905728 0.461540782690627
0.498830722900905 A A A LNCV6_128159_PI430048170 mRNA
CTATAACAGAGAGTGGAAAATCACTCACGGTTTTGAAAGTTCAAACCACAGAGAAAATAT NM_052964 RefSeq chr4
- 10490213 10684762 CLNK NA cytokine-dependent hematopoietic cell linker NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145030_PI430048170 0.0675879116365721 0.252456624724499 2.49074412472025
4.23057732141461 4.58601137942778 A P P 5.63715075787992 6.10835682957291
6.18981576434235 P P P LNCV6_145030_PI430048170 mRNA
GTCTCGCATTTCTTTTACTATTCAAAACTCTTTGGTTGGAAATGACTAATACTGCTCCAA NM_152522 RefSeq chr2
+ 152717892 152761253 ARL6IP6 151188 "ADP-ribosylation factor-like 6 interacting protein 6, transcript
variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136964_PI430048170 0.0883349012354843 0.539262154924254 8.18402310793139
8.37286600305021 8.50110281549592 P P P 8.66027709247453 9.27403831981069
9.64786581335313 P P P LNCV6_136964_PI430048170 mRNA
GGTTGTATGCTCTTCTGTTTTAAAGGTTTGAATCACCAGCATTTTTGTGATCAAAATCCTNM_030919 RefSeq chr20 +
38926311 38953061 FAM83D 81610 "family with sequence similarity 83, member D"
GO:0007067|GO:0005737|GO:0000922|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130575_PI430048170 0.000571954374994518 0.538096308122808 13.3214880339691

13.279893584023 13.1164234318329 P P P 14.0805441378607 14.2195921944417
14.1040293215476 P P P LNCV6_130575_PI430048170 mRNA
ATCCTGGGGCAACCCATCTGGTCTCTTGAATAAAGGTCAAAGCTGGATTCTCGCAAAAAA NM_001008709 RefSeq
chr11 - 67398180 67401905 PPP1CA 5499 "protein phosphatase 1, catalytic subunit, alpha isozyme,
transcript variant 3"
GO:0005515|GO:0005886|GO:0030324|GO:0005634|GO:0044281|GO:0046872|GO:0005829|GO:0016791|GO:0005
737|GO:0006470|GO:0043197|GO:0000164|GO:0043204|GO:0007179|GO:2001241|GO:0004722|GO:0019433|GO:0
043153|GO:0030512|GO:0070062|GO:0005979|GO:0005977|GO:0005730|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_74597_PI430048170 0.124691650947336 1.39100324819272 9.44092296494807 9.15515334905189
9.81172741622054 P P P 8.77848238556897 9.00226300182229 9.23768070215447 P P P
LNCV6_74597_PI430048170 mRNA
ATGGATGATATGGATGATGAAGATGATGATGACCATGTGGACAGCCAGGACTCCATTGAC NM_001251830 RefSeq
chr4 + 87975649 87983411 SPP1 6696 "secreted phosphoprotein 1, transcript variant 5"
GO:0005515|GO:0048471|GO:0007566|GO:0010811|GO:0030593|GO:0050840|GO:0045177|GO:0033280|GO:0005
576|GO:0042995|GO:0048545|GO:0005125|GO:0005615|GO:0031214|GO:0001649|GO:0048685|GO:0046697|GO:0
006954|GO:0022617|GO:0045780|GO:0030198|GO:0007155|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_138745_PI430048170 0.114984342869845 0.838008409627206 11.4877350427941 11.339495129733
11.2270759848544 P P P 11.7603041252864 11.6270036437333 11.424087099417 P P P
LNCV6_138745_PI430048170 mRNA
GGGGCGAGTGGCACGTTTATTTAACTTTTAGTAAAGTCAAGGAGAAATGCGGTGGAAAAA NM_000545 RefSeq chr12
+ 120978567 121002511 HNF1A 6927 HNF1 homeobox A
GO:0005515|GO:0035623|GO:0003700|GO:0046982|GO:0044212|GO:0006357|GO:0005634|GO:0060261|GO:0042
593|GO:0003677|GO:0042803|GO:0006351|GO:0043234|GO:0001077|GO:0005737|GO:0046323|GO:0045944|GO:0
046983|GO:0005654|GO:0045893|GO:0030073|GO:0035565 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_127524_PI430048170 0.292864074876841 1.75100983602221 2.03996691580843
0.508218022274471 1.91791569155902 A A A 0.991558306968604 1.07626639923641
0.289222729179766 A A A LNCV6_127524_PI430048170 mRNA
TTTACAATCTCCATTTTCATTAACGGGGAAACATCCCCGAGCCACTGAGTGCTGTGCTTT NM_014424 RefSeq chr1
- 16014027 16018790 HSPB7 27129 "heat shock 27kDa protein family, member 7 (cardiovascular)"
GO:0006986|GO:0005739|GO:0005515|GO:0005737|GO:0015030|GO:0031005|GO:0008016|GO:0005634|GO:0015
629|GO:0008022 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145305_PI430048170 0.957955415943827 1.00235974724807 0.513220709792323
0.388110717279668 0.504244437683719 A A A 0.42554058611282 0.501496045033255
0.470672386596911 A A A LNCV6_145305_PI430048170 mRNA
ACTGCCTACAGTATGTCTTTTGCATAAAATGCATAAGGGTTTGGGGATGTAAATGGAATT NM_017637 RefSeq chr9
- 16409502 16870788 BNC2 54796 basonuclin 2
GO:0006355|GO:0005737|GO:0003416|GO:0005886|GO:0060021|GO:0060485|GO:0005654|GO:0005634|GO:0043
586|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140512_PI430048170 0.431124972214753 0.881007507350225 7.58580870873339
7.78209256945004 7.96393510390274 P P P 7.79339337849127 7.78473592881159
8.27120870519838 P P P LNCV6_140512_PI430048170 mRNA
CGGTATTTCTGTATGGAATCTGCTTTATTCCTATTTTTCCCAACTCTGATGAGTAGAATA NM_003826 RefSeq chr18 +
10525875 10552769 NAPG 8774 "N-ethylmaleimide-sensitive factor attachment protein, gamma"
GO:0019905|GO:0005739|GO:0005515|GO:0005483|GO:0006461|GO:0050821|GO:0031201|GO:0006891|GO:0061
025|GO:0005765|GO:0006886|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135246_PI430048170 0.000104069546663533 0.573535654986917 10.7377292877522

10.8687770358711 10.8159353426104 P P P 11.6225810614612 11.5476292018009
11.6591398742669 P P P LNCV6_135246_PI430048170 mRNA
ACAATTCCTCAGGATTTGGTAAGGCTTCCAAGTTGTAGCTTTTAGTGTAAGTGCTGGGGT NM_006834RefSeq chr6
+ 146543691 146554950 RAB32 10981 "RAB32, member RAS oncogene family"
GO:0035650|GO:0005515|GO:0005802|GO:0042470|GO:0035651|GO:0035612|GO:0003924|GO:0005525|GO:0006
886|GO:0045335|GO:0005739|GO:0006184|GO:0031905|GO:0030742|GO:0016020|GO:0019882|GO:0035646|GO:0
030670|GO:0032482|GO:0019003|GO:0090382|GO:0005769 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_135539_PI430048170 0.00794560868314027 0.4910564689032474.40802147995136
4.10034415769208 4.04131863177413 P P P 5.22942173920733 5.26678060752128
5.15690872073223 P P P LNCV6_135539_PI430048170 mRNA
GAACATTTTGTTTGCAGCTAATCATTGTCATGAATATCGTTTATGTGTGCCTTGCTGTGA NM_020947RefSeq chr16
- 84476359 84504682 TLDC1 57707 TBC/LysM-associated domain containing 1
GO:0005515|GO:0005765 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130966_PI430048170 0.0417226187616075 0.3601493949216051.42600509096306
1.61930469679861 2.61366554389158 A A A 3.25489565630116 3.63504484339862
3.46153133153313 P P P LNCV6_130966_PI430048170 mRNA
GGCCTTAGCATCAGAATTAAAATAATCTGGATTAAATGGCAATGTGTTCATAGTCAGCAA NM_003616RefSeq chr14
+ 39114283 39136973 GEMIN28487 "gem (nuclear organelle) associated protein 2, transcript variant
alpha"
GO:0005515|GO:0006397|GO:0008380|GO:0000245|GO:0010467|GO:0005730|GO:0005634|GO:0034660|GO:0000
387|GO:0005829|GO:0005737|GO:0032797|GO:0000375|GO:0005654|GO:0005681|GO:0034719 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136179_PI430048170 0.00034299196681646 0.2497157707967772.60361091659683
2.42951272915077 2.83880090283224 A A P 4.53087125413933 4.57591917582775
4.78636756855802 P P P LNCV6_136179_PI430048170 mRNA
GGTGAAAAGCGAATCTGCAGAATAACTGTCAACGTTTTTCATTCTTGTTTTACAAACCTA NM_001293070 RefSeq
chr7 + 29194504 29514335 CHN2 1124 "chimerin 2, transcript variant 4"
GO:0043547|GO:0005515|GO:0051056|GO:0016020|GO:0007264|GO:0005070|GO:0009967|GO:0046872|GO:0005
829|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105984_PI430048170 0.0427971920430913 0.6603834457265415.61398728518542
6.03684374674612 5.66202567386942 P P P 6.61597611189011 6.39057064748251
6.09320460644303 P P P LNCV6_105984_PI430048170 mRNA
TGCCGGCTGCCCCAGAGGACAGTGGGTGGAGTGGTACCTACTTATTAAATGTCTCAGACC NM_000606RefSeq chr9
+ 136945245 136946974 C8G 733 "complement component 8, gamma polypeptide"
GO:0006957|GO:0030449|GO:0005579|GO:0001848|GO:0045087|GO:0019835|GO:0006958|GO:0072562|GO:0005
576|GO:0032403|GO:0019841|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57673_PI430048170 0.7879343012737030.9202822416992184.01255422264392 3.17717818822795
3.73259247605039 P P P 4.10512056274377 3.95288006533014 3.18841144883207 P P P
LNCV6_57673_PI430048170 mRNA
ATTCCAGATCATCCGTGGGAACTTCCCTTACCTCAGCGCCTTTGGGGACCTCGACCAGAA NM_153819RefSeq chr11
- 64726910 64745456 RASGRP2 10235 "RAS guanyl releasing protein 2 (calcium and DAG-regulated),
transcript variant 2"
GO:0043005|GO:0030054|GO:0005886|GO:0005509|GO:0045202|GO:0030168|GO:0007265|GO:0032587|GO:0032
854|GO:0001558|GO:0005829|GO:0008289|GO:0019992|GO:0005085|GO:0007165|GO:0007596|GO:0071277 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134054_PI430048170 0.2950807112061911.3307342149768 0.568016209898558
0.7094428386391271.40559969357435 A A A 0.5148071830306440.534749076737624
0.542164591473112A A A LNCV6_134054_PI430048170 mRNA

CTTAGGAATAAGGATGTCATGGGGGCTCTGAAGAAAATGTTAACTGTGAGATTCGTCCTT NM_001004697 RefSeq chr1_KI270892v1_alt + 139006 139954 OR2T5 401993 "olfactory receptor, family 2, subfamily T, member 5" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135859_PI430048170 0.22115834242581 1.12513499481919 9.78729135175627 10.1175933442169 9.92658025529392 P P P 9.77345857031107 9.84754275767072 9.71631464405904 P P P LNCV6_135859_PI430048170 mRNA
GCACTCTCTTCCTGTACAGTATTTATTGTTCCTGGCACTTTATTTAAAGATATTTGACCC NM_022165 RefSeq chr19 + 49114360 49118460 LIN7B 64130 lin-7 homolog B (C. elegans) GO:0043005|GO:0019904|GO:0097025|GO:0014069|GO:0045202|GO:0006887|GO:0015031|GO:0045199|GO:0007269|GO:0016323|GO:0008105|GO:0005911|GO:0045211|GO:0005923|GO:0097016 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137967_PI430048170 0.0144064526521308 0.3093894478215815.33275834952187 5.14302416658084 5.45192601677507 P P P 6.54161511777722 6.93040098485728 7.4163107074013 P P P LNCV6_137967_PI430048170 mRNA
CCATAAAGTATTTCTCCCATTGAGTCTAATGATGTATACTTTGCCTAGGTCTTTCCAAAA NM_175861 RefSeq chr12 - 29500812 29784759 TMTC1 83857 "transmembrane and tetratricopeptide repeat containing 1, transcript variant 2" GO:0005739|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136248_PI430048170 0.0305032424585387 1.38276983391462 10.269307316486 10.3996206195753 10.0736174203629 P P P 9.82627687067504 9.80202391226063 9.72827025435854 P P P LNCV6_136248_PI430048170 mRNA
CCCTCAGGGACTTGAGATTATTTAAGTACTAGTTCCTAACACGTTCTGGAAAATAAAAAT NM_198527 RefSeq chr15 - 90930917 90932569 HDDC3 374659 "HD domain containing 3, transcript variant 2" GO:0008152|GO:0008893|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140122_PI430048170 0.6841438306682570.9389316813823010.45505949264439 0.4123152721137210.630674165496926A A A 0.3619066344572090.487469713325496 0.879123866488986A A A LNCV6_140122_PI430048170 mRNA
CTGCCCCTACAGTTTGTGTTGCATATTTGTGTTTAAAGCCTATTAAAATAAACTTGAGGG NM_001033602 RefSeq chr13 + 29024610 29505947 MTUS2 23281 "microtubule associated tumor suppressor candidate 2, transcript variant 1" GO:0008017|GO:0005515|GO:0005881|GO:0005813|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127631_PI430048170 0.4260197537644 1.02373155004441 0.363957124729735 0.256327741934793 0.274265140620737 A A A 0.25914657909177 0.279094848240654 0.257013515665958 A A A LNCV6_127631_PI430048170 mRNA
GCTGTTTTTTACTAACAAGGCAGAATGTATGTACTACCTGAATTCTACCTGCATTTCAAT NM_001206572 RefSeq chr10 - 106573662 107164708 SORCS1 114815 "sortilin-related VPS10 domain containing receptor 1, transcript variant 6" GO:0005515|GO:0016020|GO:0007218|GO:0016021|GO:0008188 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139764_PI430048170 0.00586946456607627 1.59263731064928 13.7289298886238 13.8754892359312 13.8715889237898 P P P 13.139723951753 13.0042670569831 13.3066035954038 P P P LNCV6_139764_PI430048170 mRNA
TTTGTGTACCCCACCACCCCATTACCACAGCTGCCTTTGTGTGTTTGTGTCAATAAAAAG NM_006373 RefSeq chr17 - 43014604 43022442 VAT1 10493 vesicle amine transport 1 GO:0010637|GO:0016491|GO:0008270|GO:0005741|GO:0016021|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128202_PI430048170 0.235418007675408 0.855315024430761 14.5896128200302 14.7718454396068 14.2803135736629 P P P 14.7430209227922 14.7072028208648 14.9024756907187 P P P LNCV6_128202_PI430048170 mRNA
CCGCACAGCCTGTCTCTGCTCAGTTGCAATAAACGTGACATCTTGGGAGCGTTCAAAAAA NM_207197 RefSeq

chr1 + 155051271 155062776 ADAM15 8751 "ADAM metallopeptidase domain 15, transcript variant 6"
GO:0005515|GO:0017124|GO:0030308|GO:0005886|GO:0042995|GO:0042246|GO:0060317|GO:0005912|GO:0022617|GO:0030198|GO:0030574|GO:0006508|GO:1900121|GO:0070062|GO:0030336|GO:0001669|GO:0009986|GO:0006915|GO:0001525|GO:0070528|GO:0005178|GO:0007160|GO:0007229|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128012_PI430048170 0.172060645741714 1.08166584469763 0.626934824629621 0.489420650752218 0.445257998490923 A A A 0.384523257357661 0.407633376302021 0.435520498987868 A A A LNCV6_128012_PI430048170 mRNA
AGGGAAGAATGAATAAGAGATACAAGGTCTCACCTTCATCTACTGTGAAGTGATGAGAAC NM_030764 RefSeq
chr1 - 157745732 157777132 FCRL2 79368 "Fc receptor-like 2, transcript variant 1"
GO:0005886|GO:0005070|GO:0007267|GO:0009967|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134017_PI430048170 0.667944270940692 1.06596666140126 2.06537125312477 2.54034044759752 2.18690950625799 A A A 1.92139418176104 2.25128346673424 2.35225894634883 A A A LNCV6_134017_PI430048170 mRNA
GAACAGAGATGAGGTCAATTTCAAATTTTAGCCATCTGTTTGTGATTTCTGTCATAAGCA NM_024576 RefSeq
chr6 + 71288773 71302271 OGFRL1 79627 opioid growth factor receptor-like 1
GO:0016020|GO:0004872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127683_PI430048170 0.696923912531802 0.786715787939685 3.02457000715055 2.61743731439761 2.66509521103679 A A A 2.51403525388124 2.53601351578629 3.87715805646054 A P P LNCV6_127683_PI430048170 mRNA
CGTCCTCATTTCTTCCTCAAATATAAGGAGGAAGATACCAATTAAAAGCTCATAGTATCA NM_175575 RefSeq
chr17 + 50835243 50842348 WFIKKN2 124857 "WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2"
GO:0048747|GO:0032091|GO:0010951|GO:0001501|GO:0004867|GO:0008191|GO:0060021|GO:0007179|GO:0005576|GO:0043392 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136533_PI430048170 0.0105704305227072 2.30585817348832 3.14314960178735 3.66672876009784 3.11177350826743 A P P 2.28641120992288 2.08293405133994 1.99013867512709 A A A LNCV6_136533_PI430048170 mRNA
TATATATCATTGAGGGTGACTAATCTTCAGTGGACCAAATCTCTACCCTTCCCCAACCCT NM_172238 RefSeq chr6 + 50713543 50773033 TFAP2D 83741 transcription factor AP-2 delta (activating enhancer binding protein 2 delta)
GO:0005667|GO:0043524|GO:0000977|GO:0006366|GO:0006357|GO:0061379|GO:0045944|GO:0042127|GO:0000981|GO:0005634|GO:0048856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130481_PI430048170 0.0189640655747633 2.54321704971679 2.03492221398838 1.40741366666627 1.59362196541003 A A A 0.339820383992026 0.376149219057952 0.353435992017207 A A A LNCV6_130481_PI430048170 mRNA
GTATCAATGAAATACATATTGTCATGTCAGTTCTTGCCAGGAACTTCTCAACAAAATGGA NM_205860 RefSeq
chr1 + 200027601 200177422 NR5A2 2494 "nuclear receptor subfamily 5, group A, member 2, transcript variant 1"
GO:0005515|GO:0010467|GO:0003700|GO:0006367|GO:0044212|GO:0003705|GO:0003707|GO:0005634|GO:0009790|GO:0005737|GO:0005543|GO:0045944|GO:0042127|GO:0043401|GO:0008206|GO:0004879|GO:0045070|GO:0042632|GO:0006355|GO:0042592|GO:0000978|GO:0003677|GO:0043565|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64354_PI430048170 0.0795870185379145 1.17025560237195 10.0520879555893 9.84669584382125 9.82982572820947 P P P 9.73884882852502 9.75711861382077 9.55436002312084 P P P LNCV6_64354_PI430048170 mRNA
GCCTCCCAAGGAGGTCATCAACGGAAACATAAAGACAGTGACAGAGTACAAGATAGATGA NM_003755 RefSeq

chr19 - 10115013 10119923 EIF3G 8666 "eukaryotic translation initiation factor 3, subunit G"
GO:0005515|GO:0010467|GO:0048471|GO:0033290|GO:0005852|GO:0016282|GO:0001731|GO:0003743|GO:0005
634|GO:0006412|GO:0006413|GO:0005829|GO:0005737|GO:0000166|GO:0006446|GO:0044267 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139143_PI430048170 0.825159072409505 0.982333293768921 6.31961477324377
5.59180456235079 5.54984898305902 P P P 5.96700325081494 5.99004464711338
5.69986895462737 P P P LNCV6_139143_PI430048170 mRNA
CTCAGCAGCCAATAAAAGCAGAGTGGAAAAAGATTCCAATTCTGCAGAGAGATGCTCAAA NM_001002878 RefSeq
chr22 - 29508166 29553655 THOC5 8563 "THO complex 5, transcript variant 1"
GO:0005515|GO:0006397|GO:0008380|GO:0000347|GO:2000002|GO:0000346|GO:0017145|GO:0001824|GO:0005
634|GO:0060215|GO:0003729|GO:0045650|GO:0046784|GO:2000035|GO:0000902|GO:0005737|GO:0032786|GO:0
006406|GO:0016607|GO:0030224|GO:0000445|GO:0005654|GO:0010793 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134301_PI430048170 0.254540052731249 0.906412923047854 0.389870002828947
0.41385662107428 0.302876794955453 A A A 0.394579991881383 0.679014158103547
0.444373763239395 A A A LNCV6_134301_PI430048170 mRNA
AGTGTCAAGATGAAGGAGATTAGAAAGAGAATACTCAACAGGTTGCAGCCCAGGAAGGTG NM_001004758
RefSeq chr11 - 4848236 4849208 OR51S1 NA "olfactory receptor, family 51, subfamily S, member 1" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137682_PI430048170 0.756467911281668 0.974935769098946 0.630586107711305
0.55707787954874 0.324273404275875 A A A 0.408547205080939 0.651874792582541
0.568295966512318 A A A LNCV6_137682_PI430048170 mRNA
GACACAAAGACTTGACTTTCCTGCTACTTTTATCATTTTCCTTCCCAATTCATTGAGTTA NM_032867 RefSeq chr11
+ 12286899 12359144 MICALCL 84953 MICAL C-terminal like
GO:0008150|GO:0005737|GO:0007275|GO:0007283|GO:0030154|GO:0051019 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_141634_PI430048170 0.0341428822048007 0.717470517714559 9.04093433699856
9.3715191138994 9.22968697164689 P P P 9.55012725531038 9.60515300731574
9.91535228567577 P P P LNCV6_141634_PI430048170 mRNA
ACTGTACAGTTTTCCAACTTGCCATATTCATGATGGGTTTGCATTTTAGCTGCAACAATA NM_002827 RefSeq
chr20 + 50510320 50584762 PTPN1 5770 "protein tyrosine phosphatase, non-receptor type 1,
transcript variant 1"
GO:0008286|GO:0005515|GO:0030948|GO:0005886|GO:0005783|GO:0005158|GO:0019221|GO:0060397|GO:0035
335|GO:0005829|GO:0030968|GO:0060334|GO:0060337|GO:0060338|GO:0030100|GO:0035791|GO:0070373|GO:0
004725|GO:0060333|GO:0030971|GO:0019901|GO:0031532|GO:0046627|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127450_PI430048170 0.501793033445505 1.38310406832895 0.293666144585753
1.57635403541083 0.354354792775285 A A A 0.490980803674391 0.37691230498778
0.336523702748872 A A A LNCV6_127450_PI430048170 mRNA
GTCATAGCCTTGGTTTAGTTTTGGGTGGAGCTGAATAAACCCAAATCTCAGGGCAAAAAA NM_001541 RefSeq
chr11 + 111912735 111914093 HSPB2 3316 heat shock 27kDa protein 2
GO:0006986|GO:0005515|GO:0005737|GO:0005634|GO:0043085|GO:0008047|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126759_PI430048170 0.432153869694614 1.03877254378864 0.286644995547813
0.297601731324093 0.454165889061417 A A A 0.310974049664274 0.278554018613751
0.290218444349193 A A A LNCV6_126759_PI430048170 mRNA
CCTTCACACTATTATCCATGTAAAAACAATTTTGCTTTGCTTCAAACCCAGATTTCAGGA NM_199235 RefSeq chr2
+ 3594831 3644644 COLEC11 78989 "collectin sub-family member 11, transcript variant 2"
GO:0032502|GO:0005581|GO:0007275|GO:0005576|GO:0005537|GO:0006898 . NA - . NA NA

NA NA NA NA NA NA NA
LNCV6_126539_PI430048170 0.298544694548814 0.797015087206598 14.110542034335
13.3142242251336 13.2956200089287 P P P 13.9773485023634 14.1034580254554
13.7584472301592 P P P LNCV6_126539_PI430048170 mRNA
GCCGCCGCCCGACCGCCGGGAGGATGGAGTTCAGCGGGCAGCGGAGCTGTCTCAGTCTTT NM_015112 RefSeq
chr1 + 45803612 46036124 MAST2 23139 microtubule associated serine/threonine kinase 2
GO:0008017|GO:0005515|GO:0005737|GO:0045075|GO:0000287|GO:0005886|GO:0019902|GO:0004674|GO:0015
630|GO:0048515|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_133800_PI430048170 0.700877931676241 0.945728346650591 5.19200802877922
4.91493224586949 5.40637623334219 P P P 5.02121526830616 5.24227208864377
5.49414889411475 P P P LNCV6_133800_PI430048170 mRNA
AAACTCCAAAGTTTGGGACATTCAAACAATGTACATGAAATTATATGTGTGTGGTGTGTG NM_181706 RefSeq
chr11 + 31369829 31432835 DNAJC24 120526 "DnaJ (Hsp40) homolog, subfamily C, member 24"
GO:0005737|GO:0061077|GO:0008270|GO:0032781|GO:0005856|GO:0017183|GO:0008198|GO:0001671|GO:0055
114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131265_PI430048170 0.0354676535485191 0.844222736798295 9.02275331252125
8.97119725600274 9.14854682975957 P P P 9.22189347012073 9.24715427007918
9.4052490938178 P P P LNCV6_131265_PI430048170 mRNA
TAGGAGTACTGATAGGGGTTCATGCTTAATAAACATGTCACAATACAGTAAGTAAAGTGG NM_005038 RefSeq
chr4 - 158709126 158723400 PPID 5481 peptidylprolyl isomerase D
GO:0005515|GO:0000413|GO:0019076|GO:0050714|GO:0051879|GO:0005634|GO:0015031|GO:0005737|GO:0006
457|GO:0031072|GO:0045070|GO:0016018|GO:0043065|GO:0030331|GO:0005730|GO:0003755|GO:0071492|GO:0
006915|GO:0000122|GO:0034389|GO:0006461|GO:0061077|GO:0030544|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_83886_PI430048170 0.156206443785453 1.13136468696253 9.15268243720221
9.25847837032793 9.09862851931944 P P P 9.10490281001279 9.03835199382057
8.82203369683745 P P P LNCV6_83886_PI430048170 mRNA
TTCCAGGTGCGTGACCTGCCCTTTTTCTCATTCCCTTAACTGACATTATTTAGTGTCAGA NM_021646 RefSeq
chr16 - 4750813 4767218 ZNF500 26048 "zinc finger protein 500, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_105765_PI430048170 0.974679474399931 0.9937055209726 9.63824052449297
9.41369928636898 9.59545246990894 P P P 9.27053225166769 9.52381535285641
9.83457844486194 P P P LNCV6_105765_PI430048170 mRNA
TACTCCAGAGGAAGAATGCTTTTCTTGGGAGCCATAGGGTGAATAAAGGAATGTTTAACT NM_001282860 RefSeq
chr1 - 155749657 155857295 GON4L 54856 "gon-4-like (C. elegans), transcript variant 3"
GO:0006355|GO:0003682|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141500_PI430048170 0.416566675104759 0.383534001292208 0.36744916291738
0.353673852636667 0.270426021479999 A A A 0.333610317851114 0.354332937248213
2.8682174443988 A A P LNCV6_141500_PI430048170 mRNA
ATGCCAATAAAAAATTTGAGAATTACTGCATTGCACTACTGCCAAGACAGGTCTGAATTC NM_173598 RefSeq
chr12 - 117453011 117968223 KSR2 283455 kinase suppressor of ras 2
GO:0035556|GO:0005737|GO:0016020|GO:0004674|GO:0006468|GO:0005524|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145381_PI430048170 0.0228720997262267 0.626032794987051 7.06438799686312
6.86099848004117.23239150533132 P P P 7.44330647315924 7.80846346052823
7.91562855311237 P P P LNCV6_145381_PI430048170 mRNA

GTCCTGACAGTGTCTTTAGCTAATCCTTGAAGAAATGAAAGTGGAATTGAATCTTTTTAG NM_005028 RefSeq chr10 - 22534836 22714574 PIP4K2A 5305 "phosphatidylinositol-5-phosphate 4-kinase, type II, alpha" GO:0046854|GO:0035855|GO:0006661|GO:0005886|GO:0005634|GO:0044281|GO:0005575|GO:0006644|GO:0005524|GO:0016309|GO:0016308|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129370_PI430048170 0.482197086280819 1.19314756790642 0.286134576767124 0.438189215150355 1.09111722310199 A A A 0.474442446562873 0.363970576881198 0.34110107837201 A A A LNCV6_129370_PI430048170 mRNA
TCTGACTTGGGAAAGCTGGGCACAAAAATCTTCATGAGCAATATTTCTTTCTTAATAGAA NM_001029888 RefSeq chr10 + 122910700 122913111 FAM24A 118670 "family with sequence similarity 24, member A" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106020_PI430048170 0.402454656600337 1.16757006411307 5.18139718357286 5.42458684206957 5.38155910120359 P P P 5.43754774366739 5.16497160354018 4.60620057424185 P P P LNCV6_106020_PI430048170 mRNA
ATGTCTTCGATTTCACTCAGCCGGCAGGTGTCAGTGGCATGGCCTTCCCGCGCCCCAAGA NM_001272061 RefSeq chrX + 52184822 52192268 MAGED4 NA "melanoma antigen family D4, transcript variant 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129136_PI430048170 0.0621860975273442 1.89522477538012 9.08697368294615 9.10836305931075 9.11283863629118 P P P 8.63735623421143 7.93835970497629 7.82528817395276 P P P LNCV6_129136_PI430048170 mRNA
TTTATCAGTGACATCATCAACTGCGGCATCTACCTCTTTTCTCCTGAAGCCTTGAAGCCT NM_205847RefSeq chr2 + 219498894 219506996 GMPPA 29926 "GDP-mannose pyrophosphorylase A, transcript variant 2" GO:0005737|GO:0016779|GO:0009298|GO:0006488|GO:0044267|GO:0070062|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139959_PI430048170 0.584289656715473 1.59392157625113 2.31083722180002 0.458026886674277 0.404780168197096 A A A 0.421555815857377 0.401121811452616 1.1012374663716 A A A LNCV6_139959_PI430048170 mRNA
AGAAGACAATTGTTGCTTATGAAAGAAAGCTTTAGCTGTCTCTGTTTTGTAAGCTTTCAG NM_001244753 RefSeq chr1 - 161623197 161631462 FCGR3B 2215 "Fc fragment of IgG, low affinity IIIb, receptor (CD16b), transcript variant 1" GO:0006955|GO:0005886|GO:0019864|GO:0031225|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135028_PI430048170 0.0112694992106734 0.365640046860219 6.16901371188535 92305352069173 6.33287080937015 P P P 7.20434681625848 7.51058537735833 7.98507903244372 P P P LNCV6_135028_PI430048170 mRNA
GGTCCGTGCTAAGGACTTGTTAGATCTAGTTCACTCTCCATTTAATAATTATATGCTATT NM_001278209 RefSeq chr6 - 17615034 17706834 NUP1539972 "nucleoporin 153kDa, transcript variant 1" GO:0007077|GO:0005515|GO:0005215|GO:0010467|GO:0019221|GO:0019058|GO:0044281|GO:0051292|GO:0046718|GO:0015031|GO:0042802|GO:0008645|GO:0005737|GO:0015758|GO:0005643|GO:0016032|GO:0017056|GO:0031965|GO:0005975|GO:0019083|GO:0005730|GO:0055085|GO:0003677|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128254_PI430048170 0.288964960486487 1.18089448656459 6.98982773058757 6.80256104004756.89868292369434 P P P 6.30535404074367 6.93963384568314 6.66334646970384 P P P LNCV6_128254_PI430048170 mRNA
ACCTTCCTATAGAAAGTCTTCGTGTGTCCTAGGACTTGGCTATCGTAGAGTGGTACCTTA NM_015492RefSeq chr15 + 75201879 75212169 C15orf39 56905 chromosome 15 open reading frame 39 GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130344_PI430048170 0.266909512185468 0.824724413937727 7.21240494473438 6.73993001237262 6.62653772235736 P P P 7.31138943166735 7.2432844430229 6.8933896574685

P P P LNCV6_130344_PI430048170 mRNA
CCCCTTCAGCCCCCCGGCTGATGCCATCTCTGGTTCTGGACAATTATCAAATATATCAGT NM_001256214 RefSeq
chr19 - 41966581 41994276 ATP1A3 478 "ATPase, Na+/K+ transporting, alpha 3 polypeptide, transcript variant 3"
GO:0008344|GO:0030424|GO:0005886|GO:0005783|GO:0051087|GO:0006883|GO:0045202|GO:0005634|GO:0046872|GO:0034220|GO:0031748|GO:0043209|GO:0007613|GO:0005391|GO:0005794|GO:0030007|GO:0042493|GO:0010107|GO:0086064|GO:0005890|GO:0055085|GO:0005524|GO:0031982|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92915_PI430048170 0.4163040094915721.16795981049659 8.3530421123332 8.89469278494199 8.85271478251656 P P P 8.12338564284201 8.62484936176093 8.67832530548466 P P P
LNCV6_92915_PI430048170 mRNA
CCACATACACTTCTGTGGACTTTTAGCATTTGTGGGTAGACTTAATAAAGCATGTATAAA NM_001206739 RefSeq
chr1 - 63440769 63523273 ITGB3BP 23421 "integrin beta 3 binding protein (beta3-endonexin), transcript variant 1"
GO:0048011|GO:0006355|GO:0043065|GO:0006334|GO:0005634|GO:0008022|GO:0097190|GO:0006351|GO:0005829|GO:0034080|GO:0007165|GO:0005737|GO:0007067|GO:0016020|GO:0000777|GO:0005654|GO:0004871|GO:0000278|GO:0007155|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141463_PI430048170 0.63465716731138 0.7755501503600451.00824352689729 0.8988072385232180.375102282812385A A A 0.2858420924020220.95475652574217 1.8125480599172 A A A LNCV6_141463_PI430048170 mRNA
CCCTGTCAAGTGCCAGTCATGATAGTAGTAATAATAATAATAAACATCTATTGGACCAGG NM_173558RefSeq chr6 + 37005646 37029069 FGD2 221472 "FYVE, RhoGEF and PH domain containing 2"
GO:0030036|GO:0031267|GO:0007264|GO:0008360|GO:0005634|GO:0046872|GO:0005829|GO:0005085|GO:0005737|GO:0007010|GO:0046847|GO:0005856|GO:0005089|GO:0051056|GO:0048011|GO:0005794|GO:0043065|GO:0032587|GO:0001726|GO:0097190|GO:0030027|GO:0043088|GO:0043547|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132479_PI430048170 0.9995416260749261.00045647794249 4.89966973981843 4.68810965845526 4.31788577631837 P P P 4.95725421802713 4.50958310718764 4.43925876118581 P P P LNCV6_132479_PI430048170 mRNA
ATCTTTCATCATTTTACTTCCCTCTTTGCCCTTACCCCTAAATAAAGCAAGCAGTTCTTG NM_130769RefSeq chr11 - 64934470 64935888 GPHA2 170589 glycoprotein hormone alpha 2 GO:0005179|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62742_PI430048170 0.00522047154392297 0.4941183435178336.31728383580188 6.06240450418137 6.22679082445506 P P P 7.21621232609254 7.2257609463901 7.22716569776371 P P P LNCV6_62742_PI430048170 mRNA
GCAGTTGCACCCTGTTTTGCAAAAACCATCAGTGTTTGGGAATGATTCTGATGATGATGA NM_032141RefSeq chr17 + 30116806 30186475 NSRP1 84081 "nuclear speckle splicing regulatory protein 1, transcript variant 1"
GO:0008380|GO:0006397|GO:0005515|GO:0032502|GO:0016607|GO:0000381|GO:0030529|GO:0005634|GO:0003729|GO:0006913 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58275_PI430048170 0.0994049721519344 0.7250468813666430.468218535345242 0.4972272549352320.406342737769874A A A 0.6533439409070371.19105892492304 0.869226029154186A A A LNCV6_58275_PI430048170 mRNA
TGTGGTGGACAGTGGTGCTGGCTTCACAGTCACTCGGCTCAGTGCATACCAGGTGACAAA NM_006760RefSeq chr11 + 118956297 118958559 UPK2 7379 uroplakin 2
GO:0016324|GO:0005887|GO:0030855|GO:0061024|GO:0030176|GO:0007275|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66890_PI430048170 0.4897248311333140.9567390607119034.02378613566429 3.76970192973594 3.94739264525888 P P P 4.05866485947342 3.93732508702868 3.94470651764854 P P P
LNCV6_66890_PI430048170 mRNA

TATTTTCTCGATGGAGGCAAGACTTGCCATGACACTCCCATTTTTTGCTTTTCCATTGAT NM_001305009 RefSeq chr2 - 175923891 176002345 KIAA1715 80856 "KIAA1715, transcript variant 2" GO:0007596|GO:0005789|GO:0060173|GO:0032330|GO:0035115|GO:0016021|GO:0046872|GO:0042733 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75713_PI430048170 0.0122323408405363 0.822831054960628 7.2682009061717 7.39374710048899 7.4310990408322 P P P 7.60046267192739 7.61579979567886 7.72268323208845 P P P LNCV6_75713_PI430048170 mRNA
ACACCATTTTGATCATTAACCAGAGTACCTCTACTCTTAGCAAACTCTAGTTTATGACAA NM_174909 RefSeq chr5 - 83052845 83077453 TMEM167A 153339 transmembrane protein 167A GO:0000139|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127297_PI430048170 0.275193492524245 0.841309100786362 10.7887115364853 10.3356179445891 10.2880370071157 P P P 10.9560631884475 10.6921750710626 10.5349448021506 P P P LNCV6_127297_PI430048170 mRNA
CTTGTGCATAAGCCTGAGATTTGGAAAGAATAAAACACCGAATTGCAGAAGAGCAAAAAANM_006351 RefSeq chr19 - 7926717 7943823 TIMM4410469 translocase of inner mitochondrial membrane 44 homolog (yeast) GO:0005739|GO:0005515|GO:0015450|GO:0005759|GO:0006626|GO:0051087|GO:0005743|GO:0030150|GO:0044267|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136119_PI430048170 0.0433301779514261.76925517002754 2.60746340054415 3.33138505972995 2.82273959595178 A P A 2.32394808818925 1.87312534320884 2.15783815971011 A A A LNCV6_136119_PI430048170 mRNA
TATTAAAGGTAAGGGGTGGACAGACTTTCTGCATTCAGATAATGAGCAGTGGCAACCCCT NM_173527 RefSeq chr14 + 22883222 22887680 REM2 161253 RAS (RAD and GEM)-like GTP binding 2 GO:0006184|GO:0005886|GO:0007264|GO:0003924|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128399_PI430048170 0.37864463340063 1.23201146838058 0.986483872185985 0.2513971551996910.327981582651626 A A A 0.268288060506375 0.244544626981 0.268058349538142 A A A LNCV6_128399_PI430048170 mRNA
CTGAAGTATTGAAACCTATTGATTCAATGGGTAGAGATTTGCTAAGTATGATGTGCTTCC NM_006771 RefSeq chr17 - 41436368 41441344 KRT38 8687 "keratin 38, type I" GO:0005882|GO:0005198|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97082_PI430048170 0.1555142583544981.95025136678535 2.00987073803773 2.50666841240808 2.80207945155711 A A A 2.21277849112567 0.407424906750147 1.37479207775025 A A A LNCV6_97082_PI430048170 mRNA
AAACAGTACCTGGATTTCGGCATCAACAGCAACAATCAGTTGGCAGAGAAGGTCAGATTG NM_001161661 RefSeq chr5 + 168292059 168472303 WWC1 23286 "WW and C2 domain containing 1, transcript variant 1" GO:0046621|GO:0005515|GO:0048471|GO:0032386|GO:0003713|GO:0005634|GO:0030010|GO:0032587|GO:0035329|GO:0000122|GO:0006351|GO:0005829|GO:0035330|GO:0043234|GO:0035331|GO:0032947|GO:0005737|GO:0016477|GO:0043410|GO:0019900|GO:0030674 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138198_PI430048170 0.394835240788142 0.862698079255484 3.7495567928435 3.90505415889347 4.50578086076875 P P P 4.31439587244964 4.19116570757639 4.4010299012438 P P P LNCV6_138198_PI430048170 mRNA
CTACTTGTAATTTCTAACTCCTTATGTTTGAAGAGAAACCTCCGGTGTGAGATATACAAA NM_002847 RefSeq chr7 - 157539051 158587802 PTPRN2 5799 "protein tyrosine phosphatase, receptor type, N polypeptide 2, transcript variant 1" GO:0043235|GO:0006470|GO:0005887|GO:0005001|GO:0043195|GO:0005788|GO:0030141|GO:0035335|GO:0034260|GO:0030658 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132070_PI430048170 0.236636460284671 0.832212495863739 7.86998056630155 7.77473984734712 7.67587307905169 P P P 7.76063889926595 8.28950851278026 8.0235478432644 P P P LNCV6_132070_PI430048170 mRNA

TGCTGAACCTTCTTGTTAATGCTATGACCGTGCCTTGAATAAACAAGTCCTCCCAACCTC NM_020431 RefSeq chr14 + 77181758 77259495 TMEM63C NA transmembrane protein 63C NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143351_PI430048170 0.7498710114969160.9924335647793210.286865892981259 0.3263447266733310.388886969706385 A A A 0.3700874463792450.341620673586296 0.324736479819024 A A A LNCV6_143351_PI430048170 mRNA
ATTCACCCAATAAATTACTATTTGACCCCAGAGTGGGTGGAAGGGTGAGCCATGTGTTTT NM_001145466 RefSeq chr6_GL000256v2_alt - 2888163 2892265 NCR3 259197 "natural cytotoxicity triggering receptor 3, transcript variant 2" GO:0008037|GO:0006955|GO:0006954|GO:0005887|GO:0045954 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144861_PI430048170 0.1649839835483931.11903250892021 7.00758572993151 7.0253093897025 7.14080319120411 P P P 6.77655230346471 6.85352938978144 7.04691481072357 P P P LNCV6_144861_PI430048170 mRNA
TTGTAAAGGTGAAAAAAGCTTTTATGAGCTCATGTAGCAATCAGATTTTCCTGTGGATTG NM_002199 RefSeq chr4 - 184387721 184474572 IRF2 3660 interferon regulatory factor 2 GO:0005515|GO:0006355|GO:0000977|GO:0003700|GO:0008283|GO:0019221|GO:0000122|GO:0001228|GO:0003677|GO:0006351|GO:0005829|GO:0005737|GO:0060337|GO:0007596|GO:0045944|GO:0005654|GO:0005925|GO:0060333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138880_PI430048170 0.0105104637344562 1.32168632341129 11.7373718584916 11.5801390447037 11.5684860591894 P P P 11.2375395197619 11.3347926439784 11.1034585172251 P P P LNCV6_138880_PI430048170 mRNA
GGGGCCGGTCTCCAGGGCGCGTAGATAAATAAATACACTCAGCGTCGTTGTGCTAAAAAA NM_001098784 RefSeq chr11 + 65572348 65574198 FAM89B 23625 "family with sequence similarity 89, member B, transcript variant 3" GO:0001222|GO:0005737|GO:0009986|GO:0060392|GO:0030512 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122423_PI430048170 0.00254304104196276 0.2775414320096782.24835919432753 2.84096841598785 2.79536916840951 A A A 4.33443085937913 4.71327029267789 4.42908899976076 P P P LNCV6_122423_PI430048170 mRNA
AAGAGAGGAAGAAAATAGTTGCATCGTCACATGTTTGATGACCATGACCCAGCTGTGATC NM_003073 RefSeq chr22_KI270879v1_alt + 23324 70880 SMARCB1 6598 "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1, transcript variant 1" GO:0005515|GO:0071565|GO:0000790|GO:0008285|GO:0001835|GO:0006325|GO:0005634|GO:0015074|GO:0071564|GO:0030154|GO:0002039|GO:0051091|GO:0016514|GO:0045944|GO:0006338|GO:0001741|GO:0006357|GO:0043044|GO:0003713|GO:0005730|GO:0031492|GO:0006337|GO:0000978|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133211_PI430048170 0.6156241375266851.10613667372687 3.76107353487959 3.20538888956416 3.74292853635038 P A P 3.129363201081 3.1864287169112 3.89198811609243 P P P LNCV6_133211_PI430048170 mRNA
TCTCATTTTTCTTGTGGTAGATGGTGGTAAAAAGGAGTAGGCAGAGTGTACATAGATAAA NM_138391 RefSeq chr1 + 203007405 203024069 TMEM183A NA transmembrane protein 183A NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143070_PI430048170 0.1349154789575882.76099393296556 8.41685634586835 8.55034001628221 8.4031967704752 P P P 8.10254003631496 5.89364696768336 5.58112654930345 P P P LNCV6_143070_PI430048170 mRNA
CGTGTCAGAACAATCTTTGCTCTGTACAATCGGCCTCTTTACAATAAAACCTCCTGCTCC NM_030630 RefSeq chr17 - 74950743 74972805 HID1 283987 HID1 domain containing GO:0005515|GO:0005881|GO:0031001|GO:0005737|GO:0005794|GO:0000138|GO:0005797|GO:0006886|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138579_PI430048170 0.0769601104016507 0.4839792699090440.405224895877699

0.4378481739009760.386872919421409A A A 1.96115290955891 1.23674506154792
0.990151808903208A A A LNCV6_138579_PI430048170 mRNA
TAACTTGCTAAAGATTCAGGGGATTCTATGAAACCCCGAATTTAGAAACATCTGGTCTAC NM_025191RefSeq chr1
- 184690490 184754907 EDEM3 80267 "ER degradation enhancer, mannosidase alpha-like 3"
GO:0006986|GO:0006457|GO:0005509|GO:0004571|GO:0005789|GO:0006516|GO:0005788|GO:0043161|GO:0044
267|GO:0004569|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141343_PI430048170 3.06420626111467e-05 0.4792354314407979.06619649139706
8.95469796689733 8.9748397827783 P P P 10.0736174203629 9.99037663629521
10.1150051214073 P P P LNCV6_141343_PI430048170 mRNA
CAGCTACTCACGCTGCCATCTGGACTTATTTTATGTCAATCTGTTTATAAATAAAAACCA NM_001172218 RefSeq
chr1 - 41027198 41242143 SCMH1 22955 "sex comb on midleg homolog 1 (Drosophila), transcript
variant 3"
GO:0003700|GO:0010369|GO:0016458|GO:0006338|GO:0005654|GO:0005634|GO:0007283|GO:0009952|GO:0045
892|GO:0009653|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99568_PI430048170 0.00190014828089505 1.82887494705901 10.3679536135078
10.6536445062723 10.4942300811035 P P P 9.8065952945231 9.55213219724419
9.54264727595544 P P P LNCV6_99568_PI430048170 mRNA
AGTGAAATGACCCGCGAAGAGATCAATGCGCTAGTGCAGGAGCTCGGCTTCTACCGCAAG NM_080430RefSeq
chr22 - 31104776 31107565 SELM 140606 selenoprotein M
GO:0048471|GO:0005737|GO:0005794|GO:0005783|GO:0005654 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137305_PI430048170 0.0984699907489185 0.7346392980942271 1.5339420014251
11.5508757405265 11.3533486563279 P P P 11.6599948521674 11.864325196005
12.2037822858932 P P P LNCV6_137305_PI430048170 mRNA
CTGTCTGATGGTGGCATCTTCCTGCAGACATTTCAAACATGTAACTTTTATATGAAAAAA NM_198679RefSeq chr9
- 131576769 131709842 RAPGEF1 2889 "Rap guanine nucleotide exchange factor (GEF) 1, transcript
variant 2"
GO:0051898|GO:0005515|GO:0048011|GO:0017124|GO:2000178|GO:0001568|GO:0032486|GO:0032854|GO:0005
829|GO:0046580|GO:0007165|GO:0000186|GO:0016337|GO:0061028|GO:0010976|GO:0070373|GO:0048008|GO:0
071320|GO:0090090|GO:0007169|GO:0017034|GO:0005769|GO:0005768 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_145721_PI430048170 0.2005658573051531.20138615089053 4.29325876568249
4.39363196618855 4.15112819434592 P P P 3.7049007295615 4.19267024974565
4.11087128236212 P P P LNCV6_145721_PI430048170 mRNA
ACTAATAGGGACTAGAAGGATTTACTGTGGCCTGGGACTGTTGCAGATGATAGAGAGCAT NM_201566RefSeq chr17
+ 7036074 7040121 SLC16A13 201232 "solute carrier family 16, member 13"
GO:0015718|GO:0034220|GO:0005794|GO:0000139|GO:0008028|GO:0016021|GO:0015293 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_123615_PI430048170 0.0214542461029524 1.67713899764711 5.13638144676046
5.54350959679974 5.50790545394646 P P P 4.80030121901413 4.79863423353243
4.33758681902811 P P P LNCV6_123615_PI430048170 mRNA
TAAGAGGCGCTAACGTTACGCTGTTTCCGGTTTTCCAGCGGGCTCTGTTTCCCCTCCCAA NM_013982RefSeq chr5
- 139846778 140043299 NRG2 9542 "neuregulin 2, transcript variant 3"
GO:0048011|GO:0005886|GO:0048015|GO:0005102|GO:0005576|GO:0048513|GO:0009790|GO:0005615|GO:0035
556|GO:0007165|GO:0007173|GO:0008543|GO:0045087|GO:0016021|GO:0008083|GO:0038095 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144165_PI430048170 0.0534420048729027 0.6943300155765216.19535025612314
6.56214708106507 6.56000247336739 P P P 6.7601068616884 6.87740927926946
7.24375824393386 P P P LNCV6_144165_PI430048170 mRNA

GTGTGTTGTGTCCAGCCTGTGGTCGTCTTAACTAATAAATGTGATTTTTCTCCCAAAAAA NM_004396 RefSeq chr17 - 64498255 64506366 DDX5 1655 DEAD (Asp-Glu-Ala-Asp) box helicase 5
GO:0005515|GO:0005516|GO:0003724|GO:0045069|GO:0005634|GO:0050681|GO:0071013|GO:0004004|GO:0000381|GO:0045944|GO:2001014|GO:0036002|GO:0070062|GO:0003713|GO:0030331|GO:0060765|GO:0005730|GO:0000122|GO:0005524|GO:0001701|GO:0006351|GO:0045667|GO:0072332|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68351_PI430048170 0.204570241260882 1.52729123663874 2.91877223730921 2.09594961772696 2.42059692925028 A A A 2.3363007191463 1.97953554191896 1.17770650027904 A A A LNCV6_68351_PI430048170 mRNA
TTCCCTCCGTTTAGAGAATGTACCGGCGCCTAGCCGAGCAGACAGCACTTCAAATGCAGG NM_005263 RefSeq chr1 - 92474760 92486876 GFI1 2672 "growth factor independent 1 transcription repressor, transcript variant 1"
GO:0005515|GO:0044212|GO:0009996|GO:0034121|GO:0005634|GO:0042660|GO:0016363|GO:0000083|GO:0017053|GO:0070105|GO:0016032|GO:0042472|GO:0042491|GO:0032088|GO:0000122|GO:0006351|GO:0001078|GO:0016604|GO:0071222|GO:0045165|GO:0010977|GO:0008270|GO:0007638|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135214_PI430048170 0.5602607280971691 1.14392255922589 0.366299550640252 0.371576332822944 1.05026299888362 A A A 0.608507900799532 0.319552001838502 0.373602370995547 A A A LNCV6_135214_PI430048170 mRNA
GTGAAAGATGCCTCAAAGAAAGCCTTGGATAAAGGTTGTGAAAACTTACAGATATTAACA NM_001004744 RefSeq chr11 - 56417257 56418232 OR5R1 NA "olfactory receptor, family 5, subfamily R, member 1 (gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135333_PI430048170 0.476321205312823 1.0477709715273 0.295160547872964 0.304541608708998 0.518555197255468 A A A 0.318767807694349 0.278192559741242 0.33005728003133 A A A LNCV6_135333_PI430048170 mRNA
ATCCAAAGTGGTCCAACCCAGAACCAAACGATCTGAAGGAAGAAAATGAGGATGAGATCC NM_001199085 RefSeq chr1 + 179591621 179691273 TDRD5 163589 "tudor domain containing 5, transcript variant 1"
GO:0033391|GO:0030719|GO:0007286|GO:0071546|GO:0043046 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130291_PI430048170 0.12344586038129 0.77455484127755 5.41234509488198 4.89102613501354 4.99277092285934 P P P 5.58446648904396 5.34611507171767 5.51534787236697 P P P LNCV6_130291_PI430048170 mRNA
CTCCTTGTCACTAGCCATCTCTTCCCCTAAAGTATAATAAAACTGTCAGGTACTAAAAAA NM_025146 RefSeq chr3 - 113716459 113746299 NAA50 80218 "N(alpha)-acetyltransferase 50, NatE catalytic subunit"
GO:0031415|GO:0005515|GO:0005737|GO:0071962|GO:0043967|GO:0004596|GO:0052858|GO:0010485|GO:0070062|GO:0006474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135732_PI430048170 0.0100112418328429 0.420044109994233 2.64833972903496 2.2656701248967 2.93611205050505 A A P 3.79791031796319 3.77147115783177 4.08999424618852 P P P LNCV6_135732_PI430048170 mRNA
GGTTAGGAAATGTTTAGTTGGAGATTACAAATTGAAACAACCATTGCAATACAGCCAAAG NM_015349 RefSeq chr6 + 42821055 42868558 GLTSCR1L 23506 GLTSCR1-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135692_PI430048170 0.0026191712369680 0.292953945805956 4.86504465390473 4.45001050996939 4.82783621155094 P P P 6.09394603759289 6.7151144224644 6.60971148252394 P P P LNCV6_135692_PI430048170 mRNA
GGCTGAGCTTCATTTCTATGAGCAAAGAGCTCATTTAGCAATGTAGTTATTTCAGTATTT NM_001130528 RefSeq chr17 - 50962173 51120865 SPAG9 9043 "sperm associated antigen 9, transcript variant 1"
GO:0005515|GO:0048471|GO:0030335|GO:0090074|GO:0001669|GO:0030159|GO:0007257|GO:0007283|GO:0005829|GO:0042692|GO:0005737|GO:0051149|GO:0045666|GO:0042147|GO:0051260|GO:0048273|GO:0016021|GO:0

019894|GO:0008432|GO:0051146|GO:0005078|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142614_PI430048170 0.0755385456982042 0.2590788437004522.94088065303977 1.44012788170966 0.384909271690214A A A 3.10292495208673 4.26272692373544 4.118100535898 P P P LNCV6_142614_PI430048170 mRNA GGCTCCTATGTGCCGATGCTGTACAAGACATTTCATTTCTCTTAATGTTTACAACAAGCT NM_014763RefSeq chr2 + 75646782 75662208 MRPL199801 mitochondrial ribosomal protein L19 GO:0070124|GO:0070125|GO:0070126|GO:0031965|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0005840|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132830_PI430048170 0.6931276476150921.44098126235051 2.15769773458354 0.3372426562964830.321686105781331A A A 0.4506954526920891.11685267065471 0.384188081474782A A A LNCV6_132830_PI430048170 mRNA GGGATCAGAAGCCAGAGGTGTAAAAGTGGTCAATTCTTGGTTTACTTCATTTAATCTTTC NM_002364RefSeq chrX + 30215557 30220089 MAGEB2 4113 melanoma antigen family B2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140138_PI430048170 0.4456294722801180.3792254517371940.386736465073342 0.3895295508371150.435237422222342A A A 2.98410533293951 0.325140417829864 0.381107432361602P A A LNCV6_140138_PI430048170 mRNA CATGCACAAGGGTATTTCCAGGTCATTTATCATTGTGAACAGTGTTGCTTATGATAAAAA NM_001135170 RefSeq chr4 + 15339935 15446167 C1QTNF7 114905 "C1q and tumor necrosis factor related protein 7, transcript variant 1" GO:0005581|GO:0051260|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141563_PI430048170 0.0550757837863372 0.62962694591141 7.80712035770248 7.18100843582453 7.27643044134109 P P P 7.94990334126131 8.18427219345501 8.20098334198672 P P P LNCV6_141563_PI430048170 mRNA AGTAAGAGCGAGTCTGCTTTGAGCTGTCTCTCCAAGCAGAAGAAGAAGAAGACAAAGAAG NM_020414RefSeq chr14_KI270847v1_alt - 1165483 1195774 DDX24 57062 DEAD (Asp-Glu-Ala-Asp) box helicase 24 GO:0003724|GO:0016070|GO:0016020|GO:0005730|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136416_PI430048170 0.2648958605645510.6654288425595441.52716769662203 0.4002797879458821.19184423510148 A A A 1.96068882354808 1.00301136625753 1.94525123007406 A A A LNCV6_136416_PI430048170 mRNA GTAAAAGACCGCTTTTAAAATGGGGAAGGCACCATTAAGCCAAAATGAATCTGAAAAAAGNM_052945RefSeq chr22 - 41925031 41926817 TNFRSF13C 115650 "tumor necrosis factor receptor superfamily, member 13C" GO:0001782|GO:0030890|GO:0045078|GO:0031296|GO:0042102|GO:0031295|GO:0002636|GO:0016021|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132247_PI430048170 0.00984669523993597 0.5543201480798669.01025744405637 8.82203369683745 9.16806612581127 P P P 9.7140544910514 9.6988531820629 10.1208924073484 P P P LNCV6_132247_PI430048170 mRNA CATTGGAAGTTTGTGATTTTGCTTTGGCAAAGTTTCATTGACTAGTAGAACTCATTCTGT NM_002572RefSeq chr11 + 117144283 117171046 PAFAH1B2 5049 "platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (30kDa), transcript variant 1" GO:0006629|GO:0005886|GO:0046982|GO:0047179|GO:0005730|GO:0003847|GO:0007283|GO:0042803|GO:0005829|GO:0016042|GO:0005737|GO:0007420|GO:0070062|GO:0016239 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127273_PI430048170 0.1762923850352111.2270597879637 4.34740368936164 4.3737265030801 3.9301214985852 P P P 3.83958795162382 3.90422218925316 4.05473041769736 P P P LNCV6_127273_PI430048170 mRNA CTGGTGGTTCTCTGTTTCCCCCTTTAAATGTGTTTTCTCTGCTTCAAAAATTTAATGCAT NM_001184880 RefSeq chrX

- 100291643 100410273 PCDH19 57526 "protocadherin 19, transcript variant 3"
GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145718_PI430048170 0.56539905931139 0.8698242963400880.470369050659337
0.5425146161471610.470602284872932A A A 1.12746831225739 0.415514231214244
0.424209968006731A A A LNCV6_145718_PI430048170 mRNA
CCACAAAATCAGCTGCAAGTAAATCCTTCTGGATGGTGCCACCAAATGTTCCTACAAGTC NM_001164416 RefSeq
chrX + 104039948 104042454 H2BFM NA "H2B histone family, member M" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_133450_PI430048170 0.2244453152121391.32739627146782 3.99246391023187
4.04440825478607 3.35174299015911 P P P 3.6180919310616 3.15854271935651
3.44680867189327 P P P LNCV6_133450_PI430048170 mRNA
ATGAGGGCCCCTCAGCCCCGCATTGATCTAAATAAAGGACTGCCGAGTTCCATGAAAAAA NM_017422RefSeq chr10
- 5498694 5499570 CALML5 51806 calmodulin-like 5
GO:0007165|GO:0008544|GO:0005509|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73612_PI430048170 0.0343118937114179 0.6189784816760655.31714750738571 4.9744479368045
5.50748017239397 P P P 6.0649739725649 5.8793863026818 5.97444480099569 P P P
LNCV6_73612_PI430048170 mRNA
CAGAGTTTCTCATCCTGTGGTGGAACATCTTTACCACCAACGTTTTACCTCTGCTTCAAC NM_004130RefSeq chr3
+ 148991407 149027669 GYG1 2992 "glycogenin 1, transcript variant 1"
GO:0005515|GO:0005975|GO:0005978|GO:0008466|GO:0044281|GO:0005536|GO:0046872|GO:0005829|GO:0016
020|GO:0009405|GO:0006006|GO:0005980|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100390_PI430048170 0.0381222268671051 1.36576994387787 7.76966442335614
8.10591191238484 7.7613832406609 P P P 7.59117747973531 7.38389865446146 7.3265535265971
P P P LNCV6_100390_PI430048170 mRNA
ATACTTTGAACTGGTGGAGAGATGTGCGGACCAGAGGCCTGAGTCCTCCCTCCTGAACCT NM_000548RefSeq chr16
+ 2047988 2088712 TSC2 7249 "tuberous sclerosis 2, transcript variant 1"
GO:0005515|GO:0050680|GO:0006606|GO:0042803|GO:0007507|GO:0007173|GO:0030100|GO:0046323|GO:0043
025|GO:0051260|GO:0005856|GO:0005794|GO:0046982|GO:0019902|GO:0001843|GO:0014067|GO:0006953|GO:0
014065|GO:0006897|GO:0045792|GO:0033596|GO:0032320|GO:0008543|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132135_PI430048170 0.1665971796213810.9301792997477060.265879298698951
0.3082783865213770.27957200838843 A A A 0.4772910030973630.37807708465857
0.306850505613779A A A LNCV6_132135_PI430048170 mRNA
GTTTGGTATTTGCGGCGTCAGTCTTTTTCTGTTGTAACTTATGTAGATATTTGGCTTAAA NM_003317RefSeq chr14 -
36516398 36519698 NKX2-1 7080 "NK2 homeobox 1, transcript variant 2"
GO:0005515|GO:0003700|GO:0044212|GO:0006366|GO:0048709|GO:0030324|GO:0003705|GO:0021983|GO:0005
634|GO:0030878|GO:0010719|GO:0031128|GO:0060430|GO:0048646|GO:0021795|GO:0021798|GO:0007411|GO:0
045944|GO:0007626|GO:0009725|GO:0021892|GO:0030512|GO:0005667|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135713_PI430048170 0.2614049027622870.7250917078697350.465835193102299
0.4728720057272890.267360906262749A A A 0.4029526949844531.3251733912857
0.723253317090261A A A LNCV6_135713_PI430048170 mRNA
GAAAAAGGAGACCAGAACAACTTAACAACGTGTCTCCTGGATTTTACTTTGAAGCCTATT NM_178821RefSeq chr2
+ 227871610 227924310 DAW1 164781 dynein assembly factor with WDR repeat domains 1 GO:0005929
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141353_PI430048170 0.3164249425319911.07295790596678 13.4410455150573
13.6950421054011 13.5936459452836 P P P 13.4307008855381 13.4611543139903
13.5420483953296 P P P LNCV6_141353_PI430048170 mRNA
CCAGTGAGTGTAAATAATTTTAAATAACCTCTGGCCCTTGGAATAAAGTTCTGTTTTCTG NM_000941RefSeq chr7

+ 75915101 75986855 POR 5447 P450 (cytochrome) oxidoreductase
GO:0050661|GO:0008941|GO:0005515|GO:0046210|GO:0043602|GO:0060192|GO:0010181|GO:0050660|GO:0047
726|GO:0070988|GO:0090346|GO:0043231|GO:0071372|GO:0005739|GO:0045880|GO:0071375|GO:0090031|GO:0
032332|GO:0003420|GO:0043154|GO:0009437|GO:0019395|GO:0005506|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_111619_PI430048170 0.00350973471065944 1.59601080558425 10.2503272399331
10.4945094494628 10.4821163525824 P P P 9.65208124768791 9.72303965265565
9.83534164517187 P P P LNCV6_111619_PI430048170 mRNA
GAATGTATTGGTAATGTGAAGAAATTGCCACTCGTCCATTCCAGCTGGTAACAGGTCGCA NM_000671 RefSeq chr4
- 99070978 99088788 ADH5 128 "alcohol dehydrogenase 5 (class III), chi polypeptide"
GO:0005504|GO:0006069|GO:0006068|GO:0007568|GO:0009055|GO:0005634|GO:0051409|GO:0018119|GO:0045
777|GO:0001523|GO:0042803|GO:0004022|GO:0005739|GO:0003016|GO:0046294|GO:0051903|GO:0032496|GO:0
051775|GO:0008270|GO:0018467|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99961_PI430048170 0.177281626929234 1.23078722786982 6.44179371839282 6.52667254775108
6.0542862343212 P P P 6.01243045330044 5.92092378564416 6.21710037007491 P P P
LNCV6_99961_PI430048170 mRNA
TTTTTGAGTGGGATGCATCTGAGGACACATCCATTGACTACAACCCCCTGTACAAAGAAC NM_004818 RefSeq chr12
- 48829755 48852174 DDX23 9416 DEAD (Asp-Glu-Ala-Asp) box polypeptide 23
GO:0008380|GO:0005515|GO:0008026|GO:0010467|GO:0005886|GO:0005730|GO:0000354|GO:0005634|GO:0071
013|GO:0005524|GO:0004004|GO:0005739|GO:0000398|GO:0000375|GO:0005654|GO:0005682|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145390_PI430048170 0.0590431629896626 1.11433669804312 0.730123282586375
0.8408139365057460.707328943313777 A A A 0.5980565905840630.620495857970155
0.594583740688923 A A A LNCV6_145390_PI430048170 mRNA
ATGATTTCCAAATGTGAATATGTGTAGGGACGTGGTCTATCAGGCCTGGAACAAGATGGG NM_001080506 RefSeq
chr4 - 82484450 82561973 TMEM150C 441027 transmembrane protein 150C
GO:0030262|GO:0016021|GO:0005764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140466_PI430048170 0.255167949571618 1.10116674055216 5.73167093780091
5.46444010538537 5.5737005018525 P P P 5.50707364100522 5.53378348360898
5.31467743459057 P P P LNCV6_140466_PI430048170 mRNA
AGAATTATGATGAGTTCATGAAGCTCCTTGGGATCTCCAGCGATGTAATCGAAAAGGCCC NM_001130958 RefSeq
chr5 + 160187366 160238722 FABP6 2172 "fatty acid binding protein 6, ileal, transcript variant 3"
GO:0006629|GO:0005215|GO:0005737|GO:0008285|GO:0015721|GO:0008206|GO:0044281|GO:0055085|GO:0008
289|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141774_PI430048170 0.0131430410049995 1.57341084568331 7.99757346263188
8.15683116181525 8.09453193769423 P P P 7.47199826063188 7.57523315376599
7.22198515674172 P P P LNCV6_141774_PI430048170 mRNA
GGCCTCCAAGGAAAGTATTTTGACATCTCTCTCTCTTCTGTTTTTATTGACTTGTTAATA NM_001037666 RefSeq chr22
- 30285117 30289627 GATSL3 NA GATS protein-like 3 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_53429_PI430048170 0.0600372371340391 2.2487058017933 9.01437872765358 9.12108652345189
9.32635697601663 P P P 8.69382337287705 8.83767528642821 8.97312347420771 P P P
LNCV6_53429_PI430048170 mRNA
AAGTCTTAAGCAAAATACTCCCAGGTCTCACTCCAGAACATAAAAATGGTGTGTGATCAA NM_199294 RefSeq chr1
+ 10430101 10442815 APITD1 378708 "apoptosis-inducing, TAF9-like domain 1, transcript variant A"
GO:0005515|GO:0071821|GO:0046982|GO:0006334|GO:0003677|GO:0006974|GO:0043240|GO:0005829|GO:0034
080|GO:0007067|GO:0003690|GO:0006281|GO:0000712|GO:0003682|GO:0031398|GO:0000777|GO:0031297|GO:0
005654|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109493_PI430048170 0.225681172311558 1.02742886231493 0.396693823113087

0.3289075634512980.36448652168376 A A A 0.2982499046897490.313507235547182
0.36126033279813 A A A LNCV6_109493_PI430048170 mRNA
ACAGATAAGCCTCAAGTGCACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGGAA NM_001301043 RefSeq
chr11 - 115173624 115504523 CADM1 23705 "cell adhesion molecule 1, transcript variant 3"
GO:0005515|GO:0030424|GO:0008037|GO:0005886|GO:0050715|GO:0007283|GO:0042803|GO:0030154|GO:0030
425|GO:0016323|GO:0051606|GO:0016338|GO:0005911|GO:0042271|GO:0050839|GO:0007156|GO:0007157|GO:0
070062|GO:0034329|GO:0005102|GO:0006915|GO:0030165|GO:0007416|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_56836_PI430048170 0.8604995297407781.02345421917161 6.93326490367392 7.2309791909329
7.36604691010791 P P P 7.10098482895412 6.94244455834747 7.3846420273893 P P P
LNCV6_56836_PI430048170 mRNA
GTCGTCTTAAACCAGAGAGCTACTGAATATAAGAACTCTTGCAGTCTTAGATGTTATAAA NM_145341 RefSeq chr10
+ 110871794 110900006 PDCD4 27250 "programmed cell death 4 (neoplastic transformation inhibitor),
transcript variant 2"
GO:0005515|GO:0005737|GO:0007569|GO:0003723|GO:0006915|GO:0005654|GO:0005634|GO:0045786|GO:0043
508|GO:0045892|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143360_PI430048170 0.00413728444075151 0.61488711481570513.472758649054
13.489196422651 13.4068479794916 P P P 14.0251423025196 14.2407777944125
14.2000393102928 P P P LNCV6_143360_PI430048170 mRNA
GCTTCTCAGATTTCTGAGGAAATTGCTTTGTATTGTATATTACAATGATCACCGACTGAA NM_181353 RefSeq chr20
+ 31605282 31606514 ID1 3397 "inhibitor of DNA binding 1, dominant negative helix-loop-helix protein,
transcript variant 2"
GO:0005515|GO:0060426|GO:0003700|GO:0060425|GO:0048514|GO:0005634|GO:0043433|GO:0007507|GO:0031
648|GO:0043408|GO:0046983|GO:0007179|GO:0046677|GO:0043066|GO:0005794|GO:0045765|GO:0001525|GO:0
000122|GO:0030509|GO:0006351|GO:0043392|GO:0043534|GO:0045668|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138877_PI430048170 0.0305532539678828 1.28503144008754 6.9989781048837
7.12960501115251 6.98647832771287 P P P 6.83410356102982 6.63689102329618 6.5480346897726
P P P LNCV6_138877_PI430048170 mRNA
CAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTCCTGTTT NM_001217 RefSeq chr19
- 48638014 48646194 CA11 770 carbonic anhydrase XI GO:0016323|GO:0005576|GO:0004089 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139809_PI430048170 0.0302145307065505 0.7357420604859139.26330355543542
9.2846983094658 9.47222113391063 P P P 9.60765685609221 9.76415835829334
9.96372187324363 P P P LNCV6_139809_PI430048170 mRNA
CTGGGGACCTCTTGAATTACATGCTGTAACATATGAAGTGATGTGGTTTCTATTAAAAAA NM_002642 RefSeq chr1
- 172441456 172444090 PIGC 5279 "phosphatidylinositol glycan anchor biosynthesis, class C, transcript
variant 2"
GO:0017176|GO:0006501|GO:0016254|GO:0005789|GO:0016021|GO:0003824|GO:0044267|GO:0006506|GO:0000
506|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110988_PI430048170 0.0268385913357147 1.3019716039606 5.93995863337023
5.66211262174631 5.7624748820497 P P P 5.45449100953345 5.33236350726219 5.44622650433 P
P P LNCV6_110988_PI430048170 mRNA
CTCTGTGGACTCAACAGTTTGTGGCAAGACAAGCTCAGAACTGAGAAGCTGTCACCACAG NM_005036 RefSeq chr22
+ 46150595 46243756 PPARA 5465 "peroxisome proliferator-activated receptor alpha, transcript variant
5"
GO:0005515|GO:0010467|GO:0006367|GO:0001190|GO:0003700|GO:0003707|GO:0032403|GO:0007507|GO:0045
820|GO:0004879|GO:0044255|GO:0031624|GO:0001103|GO:0032868|GO:0010745|GO:0019902|GO:0019904|GO:0
046321|GO:0000122|GO:0000978|GO:0032922|GO:0008544|GO:0042060|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_141685_PI430048170 0.1623776904953830.7395537988640036.75505631877519
5.98847599208864 6.32797604194448 P P P 6.69970833609486 6.88699100505339
6.88539820588865 P P P LNCV6_141685_PI430048170 mRNA
TCTACCAACCCTGTGCATGACTGATGTTGGGGAAAAAGAAAAGTAAAAAACTTCCCAACT NM_170665RefSeq chr12
+ 110281226 110351092 ATP2A2 488 "ATPase, Ca++ transporting, cardiac muscle, slow twitch 2, transcript
variant b"
GO:0005515|GO:0006984|GO:0005783|GO:0070296|GO:0046872|GO:0034220|GO:0014704|GO:0007155|GO:0031
095|GO:0045822|GO:0014801|GO:0005509|GO:0032469|GO:0006874|GO:0010882|GO:0033017|GO:0008022|GO:0
055085|GO:0005524|GO:0044548|GO:0005388|GO:0016529|GO:0008544|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131545_PI430048170 0.5634093824280590.9010405613444359.39291838474707
9.26749100965753 9.53696210361472 P P P 9.80451259636918 9.17893983724333
9.60864623430246 P P P LNCV6_131545_PI430048170 mRNA
CTGCCAAACTCCTTCTCATTTAATGCTTATGGCCTTCACATTTCTGTATAATAAAGATCANM_018178RefSeq chr1 -
150646224 150697196 GOLPH3L 55204 golgi phosphoprotein 3-like
GO:0005515|GO:0000139|GO:0032580|GO:0070273|GO:0050714|GO:0007030|GO:0032588 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_50202_PI430048170 0.4175222258680240.8861715866360794.79717003968175 4.37084663203491
4.1646091746338 P P P 4.80371680819713 4.5320998737168 4.5785211363198 P P P
LNCV6_50202_PI430048170 mRNA
GAAGATGAGGATGAAGATGTTCAAGTTGAGGAGGATGAGAAAGTGCAGAAATCATCTGCC NM_001037501
RefSeq chr1 + 120436350 120467844 NBPF8 NA "neuroblastoma breakpoint family, member 8,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129510_PI430048170 0.3818043902403260.7803136814549013.79522995781787
3.62603165896363 3.1394945984563 P P P 4.13957468089595 4.11946007279757
3.30748686329704 P P P LNCV6_129510_PI430048170 mRNA
ATTTTTGCTGCTCCCCCAAAAGCCAGCGCTGTTCTACAATAGTTCAGGTCAGACATCTAA NM_006730RefSeq chrX
- 154401235 154409278 DNASE1L1 1774 "deoxyribonuclease I-like 1, transcript variant 1"
GO:0004536|GO:0005783|GO:0004520|GO:0005634|GO:0006259|GO:0016888|GO:0003677|GO:0000737|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132303_PI430048170 0.0136122216522492 0.63511072692249 9.34835098326872
8.93754900271183 9.10273313856922 P P P 9.7184829873544 9.69217353055456
9.95749548757641 P P P LNCV6_132303_PI430048170 mRNA
TTTCAGTCTAGTTGCCAAATCTGGCTCCTTTACAAAAGAAATACCTTGAGAAATGGGAAA NM_005778RefSeq chr3
+ 50088907 50118964 RBM5 10181 "RNA binding motif protein 5, transcript variant 1"
GO:0008380|GO:0005515|GO:0010467|GO:0000245|GO:0006396|GO:0043065|GO:0008285|GO:0003723|GO:0006
915|GO:0005634|GO:0003729|GO:0003677|GO:0000166|GO:0000381|GO:0000398|GO:0008270|GO:0005654|GO:0
005681 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131444_PI430048170 0.8840020427188881.03267041615636 3.59680887123766
2.63935801727085 2.68643329322633 P A A 3.55956062204004 2.91918633298701 2.2105101230423
P P A LNCV6_131444_PI430048170 mRNA
GGATTGAGAGGGATAATGTGCCCATGTCTCTTAAGGAGTTTGTGCTACTTAAATAAAAAA NM_152706RefSeq chr7
- 88794105 88795717 C7orf62 219557 chromosome 7 open reading frame 62 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_142922_PI430048170 0.5506892548878290.73048617000945 0.360954438638484
0.4422697713323120.382219389876018 A A A 0.24435840020569 0.294036956196521
1.58098665042564 A A A LNCV6_142922_PI430048170 mRNA
ATCTAGAACTCATATTCTAAAGGGAAGTGATTTCTCAGAACAGTGATGTTCTGGAATATG NM_052910RefSeq chr13

- 83877204 83882393 SLITRK1 114798 "SLIT and NTRK-like family, member 1, transcript variant 1"
GO:0035264|GO:0042592|GO:0030534|GO:0016021|GO:0007409 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_102236_PI430048170 0.1033929839633270.8437378708940023.96962573704357
3.94916495180302 4.10503058019834 P P P 4.09749267394334 4.23269733529657
4.41623511520358 P P P LNCV6_102236_PI430048170 mRNA
GGTAGAATCCATTTGGACATATATGCCCCATGTTCATATTTTGGGGAAATTTCGTAATCG NM_030793RefSeq chr5
+ 148383934 148442836 FBXO3881545 "F-box protein 38, transcript variant 1" GO:0005737|GO:0005634
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133628_PI430048170 0.0330374688503244 0.7154451457994455.7538802474471
6.0994898722657 6.09031909408707 P P P 6.2715481241701 6.53978645374145
6.58804362011818 P P P LNCV6_133628_PI430048170 mRNA
CAGGAACCAAATTGGATTTTCTTTCTTTTGTCATTGGACACGGTTTGCAAAGTTGGACAT NM_001302109 RefSeq
chr16 + 3305405 3318576 ZNF75A7627 "zinc finger protein 75a, transcript variant 1"
GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130010_PI430048170 0.1929509374830710.93301065916607 0.263702699726607
0.2785101297440810.367356153994816A A A 0.3924548157640450.495897057589717
0.317962586683436A A A LNCV6_130010_PI430048170 mRNA
AACTCAGGCGCATATGCATATTTTCCCTGCAAGATTAGAATGGTGCTCTTCACGTTTTGA NM_020903RefSeq chr19
+ 57120140 57131925 USP29 57663 ubiquitin specific peptidase 29
GO:0004197|GO:0016579|GO:0004843|GO:0061136|GO:0043161|GO:0005634|GO:0005575 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132872_PI430048170 0.63853695297919 0.9721863920954330.345945131027555
0.2534549164431370.272733031439872A A A 0.4619087403670630.268845783476904
0.255752510558749A A A LNCV6_132872_PI430048170 mRNA
GGTATCTGAAATATTCCCTGGACTAGAAGCAAAACCACAGAAACAAAACTTTACATTTAG NM_153346RefSeq chrX
- 18162930 18220904 BEND2 139105 "BEN domain containing 2, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135887_PI430048170 0.5823366091525281.13465036829527 5.351817050987
5.42964820969341 4.79760463824009 P P P 5.313334082325 5.21316333611123
4.43499711011809 P P P LNCV6_135887_PI430048170 mRNA
TTACGTTGTCTGGGTCCTCTTCATGATCATAGGCCTGTTCTCCATGTATTTCCACATGAC NM_133492RefSeq chr19
- 6306498 6333629 ACER1 125981 alkaline ceramidase 1
GO:0006665|GO:0010446|GO:0005783|GO:0030148|GO:0071633|GO:0044281|GO:0030154|GO:0019216|GO:0017
040|GO:0008544|GO:0030216|GO:0071277|GO:0005789|GO:0046514|GO:0016021|GO:0046512 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137893_PI430048170 0.0347729928314717 1.49030571607798 7.57309133359516
7.86463560107294 7.47041267648028 P P P 7.33284903400964 6.94238317110559
6.89437739123576 P P P LNCV6_137893_PI430048170 mRNA
GCACTCACTCTTGAAGGCACACACATACACATATTTTCAGTGAAATATATTCTGACTTTT NM_145047RefSeq chr1
- 36417905 36450485 OSCP1 127700 "organic solute carrier partner 1, transcript variant 1"
GO:0009925|GO:0006810 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130742_PI430048170 0.0359584881483651 0.2679891070485531.37849747367529
0.5223443932472671.89708201089879 A A A 3.27591507830773 3.35380067553028
3.17793474309877 P P P LNCV6_130742_PI430048170 mRNA
TCACTTGGAGGCTAAAAATCTCCAGTGAAAACAAAACGAAAACCTTTAAGAGAATGTAGA NM_005977RefSeq chr13
- 26212767 26222371 RNF6 6049 "ring finger protein (C3H2C3 type) 6, transcript variant 1"
GO:0005515|GO:0085020|GO:0006511|GO:0030424|GO:0004842|GO:0006355|GO:0031965|GO:0016874|GO:0060

765|GO:0005634|GO:0050681|GO:0044314|GO:0003677|GO:0043231|GO:0005737|GO:0030517|GO:0016605|GO:0
008270|GO:0070936|GO:0045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134261_PI430048170 0.0351685450394470.8018931125891317.09449173560478
7.10132861038163 7.24000005729746 P P P 7.35597150542354 7.41355036268953
7.61371568596671 P P P LNCV6_134261_PI430048170 mRNA
AACTTAGAGTCTGCAGCCCAGAGCCACATGCAAAACACCTTCAATAAACAGCCACTATTT NM_001286697 RefSeq
chr9 + 127424373 127445372 ZNF79 7633 "zinc finger protein 79, transcript variant 3"
GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_52040_PI430048170 0.1787408146393461.1040537776854 8.44042978796118 8.40424265515115
8.25636722291838 P P P 8.1517609145026 8.35770139792419 8.16010378027743 P P P
LNCV6_52040_PI430048170 mRNA
CTACTACCTGGTGCTGGGCTGGTGCTGCGTAGCCATCTTTGTGTTCATGTTTCCCCTTTT NM_001145463 RefSeq
chr19 - 38303559 38315966 YIF1B 90522 "Yip1 interacting factor homolog B (S. cerevisiae), transcript
variant 7" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133583_PI430048170 0.4922485209748420.9607348096023588.79283870862104
8.83934563563579 9.00853077433583 P P P 9.02038005666981 8.91651695095879
8.88262802121023 P P P LNCV6_133583_PI430048170 mRNA
GCAGACTCGCGATTCAATGATCGATATGCTCATAAAAGTGCTCAATTATATTTTCTGTAT NM_017703RefSeq chr19
- 9810266 9819055 FBXL12 54850 F-box and leucine-rich repeat protein 12
GO:0005515|GO:0006511|GO:0005737|GO:0016567|GO:0000151 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_89692_PI430048170 0.5028698700280180.8323666131818710.4824423443172830.569584092886669
0.488367612769097A A A 1.25621953484802 0.4535553306684750.473777561985247A A A
LNCV6_89692_PI430048170 mRNA
AGGAGTCAACTTGCAGGCTGTTAAAGACCTCAAGTCATTAGCATCAGCTGCTGCACTAAA NM_020226RefSeq chr4
+ 80185269 80204328 PRDM8 56978 "PR domain containing 8, transcript variant 1"
GO:0021540|GO:0021957|GO:0003714|GO:0003682|GO:0046974|GO:0006325|GO:0005654|GO:0045892|GO:0003
677|GO:0046872|GO:0006351|GO:0051567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129338_PI430048170 0.0340480221326753 1.35957670397938 9.56251678371635
9.55613709523872 9.42025661946554 P P P 9.26383712773578 9.01503948462322
8.91198507375548 P P P LNCV6_129338_PI430048170 mRNA
TTTGAACTTGGCAGCTCTGGCTGCAACCCGCTGGCTCGGAAAAGATTTTATGAACTCCAC NM_001012974 RefSeq
chr6 - 43506964 43510343 LRRC73 221424 "leucine rich repeat containing 73, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129209_PI430048170 0.1347952321438770.8603610300161436.12687359462059
6.10823954864871 5.91663252988369 P P P 6.29381402315998 6.09662253796013
6.40479977206288 P P P LNCV6_129209_PI430048170 mRNA
GAGGTGTCTCCTTTTATTAGAAAGTAACCATCTTATTCCAATTCTATGCATGTTACTGGT NM_018936RefSeq chr5
+ 141094606 141097381 PCDHB2 56133 protocadherin beta 2
GO:0016339|GO:0005887|GO:0005509|GO:0007268|GO:0016021|GO:0007155|GO:0007416|GO:0007156|GO:0007
399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133024_PI430048170 0.5664336224185811.21178786670517 0.279425602148991
0.3048727605163981.21185211885896 A A A 0.3564998377042910.460030256579446
0.352334419200907A A A LNCV6_133024_PI430048170 mRNA
CTCTTGTTTGAGGTTAGCTTATTTTAATTTAGGACCTGGCTTCTCAAAAAGGCAAATGAA NM_006256RefSeq chr1
+ 88684238 88836255 PKN2 5586 protein kinase N2
GO:0005515|GO:0048471|GO:0030054|GO:0005886|GO:0042826|GO:2000145|GO:0005634|GO:0032154|GO:0043
297|GO:0043296|GO:0005737|GO:0016301|GO:0045111|GO:0070063|GO:0007155|GO:0045070|GO:0006355|GO:0

005813|GO:0032467|GO:0006915|GO:0030496|GO:0005524|GO:0006351|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127202_PI430048170 0.1959966692614920.9677045195424030.456129930040475
0.3671065473094450.411090662589984A A A 0.4518931557294650.481040383845831
0.444593216491437A A A LNCV6_127202_PI430048170 mRNA
CTCAGGAAGGTGGTATTGACAGAGGTCAGGACCCACCTGGATGTCATGCTATGAAACATT NM_001145474 RefSeq
chr1 + 46671832 46673584 TEX38 374973 "testis expressed 38, transcript variant 1" GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131287_PI430048170 0.00119079043493376 2.01238357415056 13.270700966578
13.3530631576056 13.4077627868201 P P P 12.4807926409209 12.2756832396371
12.2397227758601 P P P LNCV6_131287_PI430048170 mRNA
TTCAAGCTCAAACACCACCTCCCTTATTCAGGACCGGCACTTCTTAATGTTTGTGGCTTT NM_007278RefSeq chr17
- 7240418 7242434 GABARAP 11337 GABA(A) receptor-associated protein
GO:0005515|GO:0008017|GO:0008625|GO:0048471|GO:0005886|GO:0007268|GO:0050811|GO:0006605|GO:0015
629|GO:0005764|GO:0005829|GO:0061025|GO:0000045|GO:0005776|GO:0000422|GO:0005875|GO:0005930|GO:0
005874|GO:0000421|GO:0048487|GO:0000226|GO:0000407|GO:0031410|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134046_PI430048170 0.6526171506991570.9081565111514360.314272441485047
2.90310741366616 2.60170455783947 A A A 2.92805477497681 1.9336960048135
2.28058104557766 P A A LNCV6_134046_PI430048170 mRNA
ATCCGTTCTGAATAACCTGCAACTAAAACCCTGGCCCACTGCAGATTATTGCTACGCAAT NM_001080448 RefSeq
chr3 + 96814580 97748942 EPHA6 285220 "EPH receptor A6, transcript variant 1"
GO:0008150|GO:0003674|GO:0005003|GO:0048013|GO:0005886|GO:0007411|GO:0005887|GO:0018108|GO:0005
654|GO:0005575|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143910_PI430048170 0.0207426541427268 1.20855327336206 13.8193192468055
14.0096561704883 13.9480349938162 P P P 13.6680650382135 13.7074306754408
13.5854874093953 P P P LNCV6_143910_PI430048170 mRNA
GGTATTCATTTGCTTTCTCGTTGAAACCTGTTGTTAATAAAGTTTTTCACTCTGGCTGTC NM_016145RefSeq chr19 -
12668066 12669651 WDR83OS 51398 WD repeat domain 83 opposite strand GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_133896_PI430048170 0.00916890246318838 0.46159687527515 0.384063257145996
0.4849473949150170.314937930927685A A A 1.76867103532951 1.42078922457473
1.30409813052193 A A A LNCV6_133896_PI430048170 mRNA
AGTTACTTATTATCCCCCATTCTATACCCCAATAAACTCAGTTTGGGGCTTCTTAAAAAA NM_001024593 RefSeq
chr10 - 73423578 73433561 MSS51 118490 MSS51 mitochondrial translational activator
GO:0035176|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133448_PI430048170 0.2302541165413751.04471896923832 0.33826509860408
0.3206262352226960.439943819005147A A A 0.3014906247818780.281420365465524
0.329079372106064A A A LNCV6_133448_PI430048170 mRNA
AACATCGAAATGATTCTCATTGACTAGTACACCATTTCACACTTCTTGAGTTCTGCCGTT NM_002169RefSeq chr9
- 21304613 21305313 IFNA5 3442 "interferon, alpha 5"
GO:0005132|GO:0019221|GO:0005576|GO:0033141|GO:0045343|GO:0005125|GO:0005615|GO:0005126|GO:0002
250|GO:0051607|GO:0060337|GO:0060338|GO:0042100|GO:0007596|GO:0045087|GO:0006959|GO:0030183|GO:0
043330|GO:0002286|GO:0002323 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132114_PI430048170 0.0183527587878802 0.3878940161179673.76363571659611
3.8258442972267 3.68652517884903 P P P 4.77258880014308 5.05926737080487
5.46238617068054 P P P LNCV6_132114_PI430048170 mRNA
ATTGTTTTCCAGTTGACCGAGTATCTGTTGTGTTTTTGTTTAAAAAGAGGATTCCATGAC NM_014547RefSeq chr15
+ 51829627 51912134 TMOD3 29766 tropomodulin 3 (ubiquitous)

GO:0006936|GO:0048821|GO:0030239|GO:0005865|GO:0007015|GO:0003779|GO:0005523|GO:0051694 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103323_PI430048170 0.207349806005835 1.35236331166667 0.474254142747998 1.13528027980808 0.48571018586717 A A A 0.302651337079793 0.270887463610274 0.318443744706675 A A A LNCV6_103323_PI430048170 mRNA GAGACTCTCCAAAGTCAACAAGTACATCTGTGAAAAAATCATGGATATCAATAAATCCTG NM_001302082 RefSeq chr1 - 48727522 48776969 BEND5 79656 "BEN domain containing 5, transcript variant 2"
GO:0005794 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127356_PI430048170 0.00218624050527921 0.2587666381539725 .8603689995491 5.86611480524623 6.07640278472537 P P P 7.62419644709634 7.82139006242161 8.16598335191227 P P P LNCV6_127356_PI430048170 mRNA CCATGAATAATCCTGGAACAATATTGCTTGTATTCCTGTCATAGAACAGGTTTTGTAATC NM_004586 RefSeq chrX - 20149910 20266632 RPS6KA3 6197 "ribosomal protein S6 kinase, 90kDa, polypeptide 3"
GO:0005515|GO:0034142|GO:0030307|GO:0045597|GO:0007268|GO:0043620|GO:0051403|GO:0005829|GO:0043555|GO:0002756|GO:0007411|GO:0045944|GO:0002755|GO:0032496|GO:0043154|GO:0034138|GO:0043027|GO:0048011|GO:0043066|GO:0038124|GO:0000287|GO:0038123|GO:0019901|GO . NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_137873_PI430048170 0.26671132842282 0.764905208713788 0.302342839743411 0.509237585766769 0.352296155881267 A A A 1.19557091526986 0.441046072000826 0.579098225701306 A A A LNCV6_137873_PI430048170 mRNA TAGTATAGGCTTGGGCATCAACCCAAGATTAAAGTCAAGAACCTCAATCACTTCTCTACA NM_145176 RefSeq chr6 - 133987580 134052651 SLC2A12 154091 "solute carrier family 2 (facilitated glucose transporter), member 12" GO:0048471|GO:0015758|GO:0005886|GO:0022891|GO:0016021|GO:0055085|GO:0012505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144477_PI430048170 0.302441258886599 1.26458808257593 0.977691941110696 0.272541450614948 0.905315403043654 A A A 0.269769949957977 0.66450953983657 0.266526967138712 A A A LNCV6_144477_PI430048170 mRNA GCATCAGATTTAGAAAAGTGTATGTTGGGCGAAGGGAGTTTTCTATTTAGATATTCTAAG NM_001145017 RefSeq chr5 - 151276364 151303773 SLC36A3 285641 "solute carrier family 36, member 3, transcript variant 1"
GO:0015193|GO:0015180|GO:0005774|GO:0015816|GO:0005280|GO:0015078|GO:0035524|GO:0015187|GO:0016021|GO:0015808|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132041_PI430048170 0.786871288116923 0.96286777963626 6.67414981661685 6.65668849304874 7.14836539928074 P P P 6.71846109057278 6.7924899482568 7.14995351850206 P P P LNCV6_132041_PI430048170 mRNA GGCAATGAAGTCTAACTTCAGGTTGAACTTTCTCATGTTTAATCTCAGGCTAAATGTAAA NM_001271904 RefSeq chr14 + 96364735 96387290 GSKIP 51527 "GSK3B interacting protein, transcript variant 1"
GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109822_PI430048170 0.101806352856398 1.12896971954199 9.16497206431054 8.96623697942412 9.11638589842972 P P P 8.91424563997438 8.91044411202631 8.90522943826942 P P P LNCV6_109822_PI430048170 mRNA GTGTCTTCCATAGCAGCCTTCAGTCCATCTCCTGCTTCAGTCCTTACAATGTCAGTAAAA NM_021004RefSeq chr14 + 23953734 23969281 DHRS4 10901 "dehydrogenase/reductase (SDR family) member 4, transcript variant 1"
GO:0031965|GO:0051262|GO:0004090|GO:0006066|GO:0005102|GO:0005634|GO:0043231|GO:0005739|GO:0016655|GO:0005789|GO:0018455|GO:0042180|GO:0005778|GO:0008202|GO:0070062|GO:0055114|GO:0000253|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134753_PI430048170 0.0336274358187625 2.27990312393317 1.95747528650586 1.92716000473758 1.65439207907903 A A A 1.15347299164084 0.315099708618613 0.36032325678292 A A A LNCV6_134753_PI430048170 mRNA

CGATTTTATAAATTGCACTAGACTGCTTGTAACTAACCAAGATGATTGTTGCTGCTTCTA NM_153361 RefSeq chr5 + 43192067 43280850 NIM1K 167359 "NIM1 serine/threonine protein kinase, transcript variant 1" GO:0000287|GO:0004674|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79368_PI430048170 0.536014728244076 1.18777783112547 0.269379511318074 0.287373334232361 1.0756443230434 A A A 0.382494616969595 0.31725078646566 0.341567693994614 A A A
LNCV6_79368_PI430048170 mRNA
ATTGGACAGTATGACAAGGATATGGATTTTTGGGGAAGAGAAAATTTGGAACTTTCACTA NM_145292 RefSeq chr7 + 151956378 152019934 GALNTL5 168391 "polypeptide N-acetylgalactosaminyltransferase-like 5, transcript variant 1" GO:0016757|GO:0031902|GO:0007286|GO:0006486|GO:0016021|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137531_PI430048170 0.0606407435021837 1.04598257527855 0.416138756859026 0.453644174376014 0.461280405760535 A A A 0.348840157303938 0.371476340883376 0.415768670182814 A A A LNCV6_137531_PI430048170 mRNA
TGAGTCTTACATCGGGCTGTGAAAATTGGTATAATGATGCTTTGAAAGATCCTATTATCA NM_198353 RefSeq chr4 - 44173902 44448807 KCTD8 386617 potassium channel tetramerization domain containing 8 GO:0043235|GO:0042734|GO:0030054|GO:0008277|GO:0045211|GO:0051260 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130806_PI430048170 0.00531704479090027 0.430747991770788 10.8755834972203 10.7837020538216 10.7678401546352 P P P 12.2333741640546 11.9611364976645 11.8532016741735 P P P LNCV6_130806_PI430048170 mRNA
CCCCCTTCTCCTCCTGTCTTTCTAGATGAATATGAATATAGGTACTTAATACAGATTTTT NM_014915 RefSeq chr10 - 27004115 27100498 ANKRD26 22852 "ankyrin repeat domain 26, transcript variant 1" GO:0046621|GO:0060259|GO:0005813|GO:0040015|GO:0045599|GO:0046627|GO:0005884|GO:0070373|GO:0042593|GO:0019217 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110400_PI430048170 0.0588278879713371 1.08805897652239 0.683366935817914 0.76129669287894 0.641900185742931 A A A 0.602118726224717 0.565127411164482 0.556192319009973 A A A LNCV6_110400_PI430048170 mRNA
AGAGATCATAATTTGGGGTTCAAGATTCCAGTCTGTGTTTTTCCAGAGGTGCCCTGAGGA NM_152605 RefSeq chr19 - 37667748 37692315 ZNF781 163115 zinc finger protein 781 GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139231_PI430048170 0.15667667475587 0.479842946946181 1.6668446655393 0.546420046394571 2.56202281252842 A A A 2.87967231209636 3.04770542554361 2.66421471841541 P P P LNCV6_139231_PI430048170 mRNA
GATTGAGTTAACTGTGAGGCTTCTCATTAAAATACAATATTGCAGCTATCAGTTGGAGAA NM_018177 RefSeq chr4 + 40056903 40158252 N4BP2 55728 NEDD4 binding protein 2 GO:0005515|GO:0046404|GO:0016310|GO:0004519|GO:0090305|GO:0005524|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127681_PI430048170 0.0626748599153947 0.311050214778302 0.332527935167938 0.270275803190985 0.376522477775029 A A A 2.08340633885645 2.51338015999623 1.10540397108398 A P A LNCV6_127681_PI430048170 mRNA
TCCAGCTAAACGAGCCTGGAATAAACATGCAGTTTATTCAGTCTGCATGTTAGTCACAAA NM_001258394 RefSeq chr11 - 72292425 72434684 CLPB 81570 "ClpB caseinolytic peptidase B homolog (E. coli), transcript variant 4" GO:0034605|GO:0005739|GO:0003674|GO:0005575|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126801_PI430048170 0.0194665035055306 0.636759081405826 9.72720440186005 9.78804986778957 10.0419080429687 P P P 10.3447351231954 10.3906266687104 10.7584114524916 P P P LNCV6_126801_PI430048170 mRNA
GCATTCACTTCCAGATTAATTTTCCGTGTTTGAAGTATGTGCATATGTGCTTTACAGAAT NM_017994 RefSeq chr7

+ 66921215 66958551 TMEM248 55069 transmembrane protein 248 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132669_PI430048170 0.1597250164029431.12853978366529 9.70772680564237
9.81317240578029 9.90939670329395 P P P 9.73637002141506 9.6912287149115 9.4728390268368
P P P LNCV6_132669_PI430048170 mRNA
AGAAGGGAATAAATTATACACCACTGTCATTCTCTCTCTCCCTCTGTCTCTTCCTTTTAC NM_016932 RefSeq chr2 -
45005184 45009403 SIX2 10736 SIX homeobox 2
GO:0072161|GO:0003700|GO:0005886|GO:0008283|GO:0090189|GO:0005634|GO:0006606|GO:0009653|GO:0032
403|GO:0048701|GO:0072038|GO:0005737|GO:0030278|GO:0009948|GO:0002062|GO:0045944|GO:0042474|GO:0
031965|GO:0001822|GO:0072028|GO:0032330|GO:0043565|GO:0007501|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_103109_PI430048170 0.806112269734661 1.04447850664031 11.4378929197764
10.9189969933466 11.3716597722323 P P P 11.2887305628719 11.1564303265523
11.1436957002912 P P P LNCV6_103109_PI430048170 mRNA
ATGCCAAGGACTCTAGGTCAAATGTCAATAAATATGAACCTCGAGAAAGTTCTGAAGGCC NM_003168 RefSeq chr17
- 58345174 58352238 SUPT4H1 6827 "suppressor of Ty 4 homolog 1 (S. cerevisiae), transcript variant
1"
GO:0005515|GO:0010467|GO:0006355|GO:0006368|GO:0032044|GO:0003700|GO:0046982|GO:0006357|GO:0006
366|GO:0005634|GO:0000122|GO:0050434|GO:0032786|GO:0032785|GO:0045944|GO:0016032|GO:0005654|GO:0
006338|GO:0008270|GO:0034244 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133165_PI430048170 0.5190070804321571.66735596308489 0.333800540884392
2.30422500549205 2.53726756912956 A A A 0.537253817005015 1.93630311638903
0.941947137046677 A A A LNCV6_133165_PI430048170 mRNA
CGAGTAACTGACCTGGGCAATGAAAAAGCAGTTGTATTTTTCTTGTGGTTTTTCAAGAAA NM_181644 RefSeq chr1
+ 205568983 205602918 MFSD4 148808 major facilitator superfamily domain containing 4
GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127693_PI430048170 0.918174295124826 1.00570892580887 0.321614188006238
1.39593601482125 0.286066662414845 A A A 1.09719523162036 0.251557299737424
0.80058132458481 A A A LNCV6_127693_PI430048170 mRNA
TGCTGCATTTCAGTTCTGGCTGTCCCACAGCTCCAGGAGTTGTGTCCCCTGAATTTTGCA NM_001012416 RefSeq
chr11_KI270903v1_alt + 170940 171501 KRTAP5-6 NA keratin associated protein 5-6 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137447_PI430048170 0.3893589071496120.9409340432174087.92414077171678
7.91015050638325 7.71256597617984 P P P 8.00034663722022 7.99648328085429
7.81545417453907 P P P LNCV6_137447_PI430048170 mRNA
TAGTGGGAAAGAACAGCTCATCTCCCCCTCATGTGAAAGATTAAATTGTAAAGCAAAAAA NM_001012267 RefSeq
chr9 + 92325467 92615155 CENPP 401541 "centromere protein P, transcript variant 1"
GO:0034080|GO:0006334|GO:0005654|GO:0000278|GO:0000775|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132739_PI430048170 0.000167605898864969 0.4048078452168278.28581015410759
8.15477828674465 8.11097173806707 P P P 9.43858354064775 9.49262596676281
9.53847844455503 P P P LNCV6_132739_PI430048170 mRNA
CTTCTCTTTCAGACTTGAATCTGTAGACATTTCTTTATTGATATGGCAAATTGCTTGCAG NM_014788 RefSeq chr9 -
98084352 98119353 TRIM14 9830 "tripartite motif containing 14, transcript variant 1"
GO:0005622|GO:0003674|GO:0051091|GO:0005737|GO:0051092|GO:0045087|GO:0032897|GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127412_PI430048170 0.8940926737473751.10698669970427 0.423678918580832
2.28450367031124 2.05899940587275 A A A 2.40743211304817 1.15051700163145
0.888954390432558 A A A LNCV6_127412_PI430048170 mRNA

TCGCTGCTGTTTACATTAGAAATCACTTCCAGCTTACATCTTACACGGTGTCTTACAAAT NM_000049 RefSeq chr17 + 3476001 3499406 ASPA 443 "aspartoacylase, transcript variant 1" GO:0005515|GO:0005737|GO:0019807|GO:0022010|GO:0006533|GO:0048714|GO:0016788|GO:0005634|GO:0004046|GO:0046872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137024_PI430048170 0.761262548277831 1.01270794814022 0.418066141674722 0.529747415089416 0.437399097607583 A A A 0.535481513033854 0.393514134191872 0.399534798568806 A A A LNCV6_137024_PI430048170 mRNA
GTGTGATACTATACATTTGTGCTGTGTAAACCCAAAATATTTACCTATACTGACTGGGAA NM_001033017 RefSeq chr8 + 11982320 11984590 DEFB135 NA "defensin, beta 135" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59225_PI430048170 0.493798097103735 0.95715667827724 0.269372189833668 0.437773884903338 0.296256576117349 A A A 0.50530763792045 0.400566346024373 0.284326420643618 A A A LNCV6_59225_PI430048170 mRNA
ATTGGAGAACTGGATTTGCTGTTTATGTCTCTGAGAAATGCCTGCATTTGACCAGAGCAA NM_020525 RefSeq chr12 - 68248244 68253501 IL22 50616 interleukin 22 GO:0006954|GO:0007267|GO:0051384|GO:0005576|GO:0006953|GO:0045518|GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140443_PI430048170 0.94549521114224 0.998335165731158 0.272681819649438 0.276734524458148 0.429659701857072 A A A 0.354709456804803 0.300271257614528 0.336390686103442 A A A LNCV6_140443_PI430048170 mRNA
CAGTGAAAAGGAATGTCAAGAAACCTGCATTCAAGGATGAGCAAGTAAATTGGCCTGTCT NM_001037763 RefSeq chr7 - 7358612 7535829 COL28A1 NA "collagen, type XXVIII, alpha 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117474_PI430048170 0.148196737176697 1.0672132150604 0.480093177722058 0.442630380466106 0.521678449140755 A A A 0.311647610241342 0.386195302029118 0.462171883848162 A A A LNCV6_117474_PI430048170 mRNA
CCAAAGAGAAACGAGCAGTAAACAGTCTCAGCATGGAAAATGCCAACCAAGAAAATGAAG NM_018476 RefSeq chrX - 103062652 103064240 BEX1 55859 "brain expressed, X-linked 1" GO:0005667|GO:0001102|GO:0051091|GO:0005737|GO:0045944|GO:0005634|GO:0030154|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131650_PI430048170 0.260913142142116 1.01638914436848 0.315076554453403 0.329160756574799 0.364878307243979 A A A 0.326067686352711 0.316294928946199 0.296697361808512 A A A LNCV6_131650_PI430048170 mRNA
AGTTATAGCTACAGCCTAGGTTAAATGATTCCTCATCCTGGTGTTTTTATTCTCATGTTT NM_016247 RefSeq chr3 - 101222545 101320575 IMPG2 50939 interphotoreceptor matrix proteoglycan 2 GO:0043235|GO:0005540|GO:0005578|GO:0016021|GO:0008201|GO:0007601|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136083_PI430048170 0.75097013280462 0.674324823576704 1.53743101054831 1.48780977039852 0.546237943436596 A A A 2.85174371196999 0.634871248920146 0.893660815791266 P A A LNCV6_136083_PI430048170 mRNA
CCTTTATTCTTAATGGCCTTCCTCTGTTGCAACCTCAATAAACAGCACAATCTCAAAAAA NM_033448 RefSeq chr12 - 52543908 52553147 KRT71 112802 "keratin 71, type II" GO:0005737|GO:0045109|GO:0005198|GO:0045095|GO:0070062|GO:0031069 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128015_PI430048170 0.462082549792132 0.698260707538268 0.397135572469528 0.258028053545103 0.295141441484579 A A A 0.272263538560696 1.55334968922635 0.278713505946988 A A A LNCV6_128015_PI430048170 mRNA
CCACATCCAAAATTATGTATCTATTACAGCCCCTAGAAGCTTTATAAATACAGTGTGTCT NM_052938 RefSeq chr1 - 157794403 157820150 FCRL1 115350 "Fc receptor-like 1, transcript variant 1" GO:0005886|GO:0016021

. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145327_PI430048170 0.0553369248898384 0.641385769894191 8.33710486221288
8.18182130013191 8.22710455236111 P P P 8.55962742913812 9.12628687392619
8.93064780688568 P P P LNCV6_145327_PI430048170 mRNA
ATGCTGCGTTTGTAACCCCAGATCAGAAGTACTCCATGGACAACACTCCCCACACGCCAA NM_002466 RefSeq chr20
+ 43667018 43716496 MYBL2 4605 "v-myb avian myeloblastosis viral oncogene homolog-like 2,
transcript variant 1"
GO:0005515|GO:0003700|GO:0031523|GO:0000978|GO:0006351|GO:0001077|GO:0000086|GO:0003682|GO:0045
944|GO:0051726|GO:0005654|GO:0090307|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135144_PI430048170 0.38447215609264 1.55315047353769 0.28415051169091
1.69720564280891 0.467957448678054 A A A 0.343209119421846 0.294788486285283
0.341547010173251 A A A LNCV6_135144_PI430048170 mRNA
CAATGACGGTTGGAAATAGAAATTTCCAGAGAAGAGAGTATTGGGTAGATATTTTTTCTG NM_001773 RefSeq chr1
- 207886537 207911338 CD34 947 "CD34 molecule, transcript variant 2"
GO:2001214|GO:0060290|GO:0050900|GO:0005764|GO:0071636|GO:0061042|GO:0016337|GO:0009925|GO:0001
894|GO:1900168|GO:0072089|GO:0032720|GO:0071425|GO:0036053|GO:0005887|GO:0050776|GO:0071971|GO:0
035759|GO:0009897|GO:0008134|GO:0072011|GO:0048471|GO:0071657|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132273_PI430048170 0.840021717825167 0.968475588586447 1.395767701056
1.84824347946839 2.09155863208775 A A A 0.397657042442191 2.29354279091725
2.20652325486058 A A A LNCV6_132273_PI430048170 mRNA
AGTGCCATGGGGGTGAAACCAGTGCTAAATGGAGGTAAAATAAAGTTTGTAAGAGCCCAA NM_024768 RefSeq
chr3 + 129001628 129040742 EFCC1 79825 EF-hand and coiled-coil domain containing 1 GO:0005509
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58138_PI430048170 0.449698234646515 0.893837476926767 7.23037115656223 7.0823341132376
7.39339975359026 P P P 7.19606141924559 7.27738597898593 7.68605212484881 P P P
LNCV6_58138_PI430048170 mRNA
GTTCCATTGCAATTCAGGGAGCCATTGAAAAGGCAGGGATTCCAAAAGAAGAAGTGAAAG NM_000019 RefSeq
chr11 + 108121530 108148164 ACAT1 38 acetyl-CoA acetyltransferase 1
GO:0050662|GO:0014070|GO:0072229|GO:0005743|GO:0009083|GO:0044281|GO:0046872|GO:0042803|GO:0001
889|GO:0005739|GO:0034641|GO:0042594|GO:0046952|GO:0007420|GO:0046951|GO:0005759|GO:0046950|GO:0
003985|GO:0051260|GO:0009725|GO:0019899|GO:0060612|GO:0044255|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_102182_PI430048170 0.376482222145834 1.13370339636051 2.95041487977686
3.17187332731397 2.94660685663825 A P P 3.09906200310132 2.50877559291481
2.86939253352739 P A P LNCV6_102182_PI430048170 mRNA
TCCTTAAGTGGTTCATCGTCTGCATCTTCGTGTGAACCAGTGAGTGATTTTCCAGCATCT NM_001271318 RefSeq
chr2 + 27582968 27623215 ZNF512 84450 "zinc finger protein 512, transcript variant 5"
GO:0006355|GO:0005654|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139004_PI430048170 0.00120229550426422 0.41606457408834 6.66114314850162
6.33462693878035 6.40910531082364 P P P 7.63392967844637 7.60178650880856
7.95766149748846 P P P LNCV6_139004_PI430048170 mRNA
CATAAAGGATTCTTTTTTCCCCCCTCATGAAAATAAACAACAACTTGGGGTAAAAGTGAA NM_013943 RefSeq chr1
+ 24745268 24844324 CLIC4 25932 chloride intracellular channel 4
GO:0005515|GO:0006821|GO:0048471|GO:0005886|GO:0061299|GO:0035088|GO:0015629|GO:0005254|GO:0016
363|GO:0030154|GO:0005829|GO:0005739|GO:0005622|GO:0005737|GO:0035264|GO:0005911|GO:0007035|GO:0
015630|GO:0071277|GO:0034765|GO:0030659|GO:0070062|GO:0005813|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_136776_PI430048170 0.3086540742172811.01019552264309 0.33020252960869
0.3111141592689610.294065686660872A A A 0.3038708766691750.302725921805586
0.28503128264566 A A A LNCV6_136776_PI430048170 mRNA
GGCACAATAAGTGGGAAGGAGCCACAAATATGTTTTTATGGGGTCTTTGTTTTCTGTTTT NM_001252020 RefSeq
chr15 - 31001060 31161273 TRPM1 4308 "transient receptor potential cation channel, subfamily M,
member 1, transcript variant 1"
GO:0005262|GO:0060402|GO:0005886|GO:0046548|GO:0007216|GO:0071482|GO:0055085|GO:0034220|GO:0005
887|GO:0035841|GO:0006810|GO:0070588|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139466_PI430048170 0.0326063615710331 1.5374034348052 9.98013926815009
10.269307316486 10.4843117023936 P P P 9.51001434519313 9.59764684416237
9.79370411830653 P P P LNCV6_139466_PI430048170 mRNA
GAGGGTAAGGGGTTGTGAGTTGTGTCCTGTATGTTTAGGATGGTATTGTTATTTATTAAA NM_013300RefSeq chr12
+ 110468426 110490387 FAM216A 29902 "family with sequence similarity 216, member A" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_145694_PI430048170 0.7976460961133640.9832030238555679.71487332551337 9.4837531785236
9.42584352272064 P P P 9.53762765623322 9.50482805616229 9.66668020701749 P P P
LNCV6_145694_PI430048170 mRNA
ATGCAATAAAGATGTGGTGGCCACTCTTTCATGGTGGTGGCAGCAGTTACCAGTAAAAAA NM_003979RefSeq chr12
+ 12891021 12913666 GPRC5A 9052 "G protein-coupled receptor, class C, group 5, member A"
GO:0007165|GO:0007186|GO:0005886|GO:0005887|GO:0004930|GO:0030659|GO:0070062|GO:0043231 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133498_PI430048170 0.4430432762574270.9248609944422871 0.9166299027404
10.9459542738017 11.2795015720193 P P P 11.2049399216919 11.0271340034869 11.266375747406
P P P LNCV6_133498_PI430048170 mRNA
GCTTGAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGT NM_005776RefSeq chr14
- 54426928 54441430 CNIH1 10175 cornichon family AMPA receptor auxiliary protein 1
GO:0035556|GO:0007165|GO:0006955|GO:0000139|GO:0005789|GO:0016021|GO:0016192 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138059_PI430048170 0.0140768983804294 1.66720259516218 5.30592019353538
5.68642633620053 5.27664517072164 P P P 4.87646103849092 4.48772289884108 4.7036211419949
P P P LNCV6_138059_PI430048170 mRNA
ATTTTCCTGGGTGCATCAAACAAAACAAAAACCAAACACCCAGAGGTCTCATCTCCCAGG NM_018646RefSeq
chr7_KI270803v1_alt - 894244 908785 TRPV6 55503 "transient receptor potential cation channel,
subfamily V, member 6"
GO:0017158|GO:0005515|GO:0005516|GO:0005262|GO:0034220|GO:0005886|GO:0005887|GO:0070588|GO:0006
816|GO:0055085|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145494_PI430048170 0.3539539207706030.7180981538493650.970085239164673
0.4939246435843741.53865097581915 A A A 1.27300068447495 2.09865210498467
1.02509070734823 A A A LNCV6_145494_PI430048170 mRNA
CAGCTTTGAGGCTTCAAATAAGTTTCCATATGCAGGGAGTAACTTTAAACAATGTTTGAA NM_178505RefSeq chr10
- 61406642 61453450 TMEM26 219623 transmembrane protein 26 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133241_PI430048170 0.33252830391113 0.82413874810817611.6217678600968
11.6448909522899 11.881416211615 P P P 11.6988733474842 11.8542073861288 12.361022473419
P P P LNCV6_133241_PI430048170 mRNA
CACTGTTATGCTCAGTCATACACGCGAAAGGTACAATGTCTTTTAGCTAATTCTAATTAA NM_006003RefSeq chr19
- 29207259 29213229 UQCRFS1 7386 "ubiquinol-cytochrome c reductase, Rieske iron-sulfur
polypeptide 1"
GO:0051537|GO:0042493|GO:0005743|GO:0005750|GO:0044281|GO:0032403|GO:0046872|GO:0005739|GO:0022

904|GO:0008121|GO:0009725|GO:0044237|GO:0046677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129788_PI430048170 0.1728320716228131.13970607680401 0.686037595262797
0.3974702184890830.651098545707757A A A 0.28464240658335 0.415542354198697
0.47854268500856 A A A LNCV6_129788_PI430048170 mRNA
AGGGTTACCTGTATCAACCAAAAGCTATGCATTGTCTTAGCCTGAAAAAGAATAGAGAAA NM_001270974 RefSeq
chr16 - 70807383 71230722 HYDIN 54768 "HYDIN, axonemal central pair apparatus protein, transcript
variant 1" GO:0042384|GO:0005929|GO:0021591|GO:0002064|GO:0060438|GO:0003341 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_130958_PI430048170 0.0823149901255781 0.4238902740308032.48496088166179
1.28696500692737 2.79560637392482 A A A 3.05600266311232 3.78099715805505
3.73116368683822 P P P LNCV6_130958_PI430048170 mRNA
TTTCTCCTCTGGAACTTCTTATGTATGCAAGCTCCCATGTTAACCTATCATAAAAATGTTNM_006166RefSeq chr12 -
104117079 104138262 NFYB 4801 "nuclear transcription factor Y, beta"
GO:0005515|GO:0006355|GO:0003700|GO:0046982|GO:0044212|GO:0005634|GO:0044281|GO:0003677|GO:0032
403|GO:0006351|GO:0043565|GO:0016602|GO:0032993|GO:0070491|GO:0005654|GO:0045893|GO:0044255 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137237_PI430048170 0.2170877842368861.13579190417145 7.58996667619234
7.29257931607915 7.27623904068047 P P P 7.28870738051598 7.20145089911047
7.13552341226333 P P P LNCV6_137237_PI430048170 mRNA
AAAGCTCTAAGCTAAGTCAAGAGCTAGGAACTGTTGATACAAATAAAAGTTTTTGAAGGG NM_016506RefSeq chr11
- 47572196 47578969 KBTBD4 55709 "kelch repeat and BTB (POZ) domain containing 4, transcript variant
2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102025_PI430048170 0.2538531414919110.8711802557384058.53316858017535 8.2810174607143
8.60216046767938 P P P 8.45401730813046 8.73111992537082 8.82250725855877 P P P
LNCV6_102025_PI430048170 mRNA
TTTTTAGAATTTGAGAGAGTTGAATCAGCAATTAAAGCGGTTGTTGACTTGAATGGGAGG NM_001145547 RefSeq
chr10 + 6089345 6117459 RBM17 84991 "RNA binding motif protein 17, transcript variant 2"
GO:0005515|GO:0000166|GO:0003723|GO:0000380|GO:0005681|GO:0005654 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127281_PI430048170 0.8486802975295671.07193994150569 1.2724538424282
0.3165307765368920.39874747642511 A A A 0.2857951702686920.3494836099717571.1057126029436
A A A LNCV6_127281_PI430048170 mRNA
GTTAAGGGAAAACCCTTGGCTCTGAGTCTTGTTGTGAATATTTCTTTGATGATTGTTAAT NM_001025290 RefSeq
chr6 - 73353061 73354276 DPPA5 340168 developmental pluripotency associated 5
GO:0005737|GO:0003723|GO:0007275 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139453_PI430048170 0.0591986642634067 1.28364636673788 9.96696844354034
10.26512801076 10.2720909577018 P P P 9.76613538512029 9.88176776796123
9.79351376458299 P P P LNCV6_139453_PI430048170 mRNA
TTTATTTCCTTGTTTGTGCTATGCTGGGCAGGCCTTCTCTTGTCCCTTATAGGTACCTTG NM_001270476 RefSeq chr6
+ 42984498 43012345 PPP2R5D 5528 "protein phosphatase 2, regulatory subunit B', delta, transcript
variant 4"
GO:0005515|GO:0034142|GO:0008601|GO:0000159|GO:0005634|GO:0044281|GO:0051403|GO:0006096|GO:0005
829|GO:0002756|GO:0002755|GO:0006006|GO:0004722|GO:0034138|GO:0048011|GO:0038124|GO:0038123|GO:0
005975|GO:0034134|GO:0002224|GO:0007399|GO:0050790|GO:0006112|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136959_PI430048170 0.1896814218474131.15338017109552 5.096666879392
5.37913758009451 5.35409660321539 P P P 5.19354533550862 5.13275668853823
4.88434450730736 P P P LNCV6_136959_PI430048170 mRNA
GAGATGTACATTCAAGGTACATCAGAACTCTCATTTCTTCCCCTTCCTTTCCTAAACCTT NM_001129883 RefSeq

chr11 + 125788110 125791600 PATE3 NA prostate and testis expressed 3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136064_PI430048170 0.3361971066743610.7382978640201316.01338156191373 7.40821550961793 7.28283421870661 P P P 7.4855881015857 7.45110957000801 7.44525368837472 P P P LNCV6_136064_PI430048170 mRNA
TCCAGACCCCTGCACCTGCTGCCAGTTCTGTGCCCAGTCCCTGTGATGAAGCTTCCCCAA NM_206997RefSeq chr11 - 67451300 67452729 GPR152 NA G protein-coupled receptor 152 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131071_PI430048170 0.6320411059016890.9315146748673189.75929445390268 10.3507541379652 10.4905921910614 P P P 10.2263714483218 10.2590290941189 10.5051729158482 P P P LNCV6_131071_PI430048170 mRNA
CATTTCCGGTTTGTTAATCTTATTCACCAAATGTTCTATCGCTCGTAAGGTAAAACTGTA NM_021824RefSeq chr2 + 200889384 200903932 NIF3L1 60491 "NIF3 NGG1 interacting factor 3-like 1 (S. cerevisiae), transcript variant 2"
GO:0005739|GO:0005515|GO:0005737|GO:0003934|GO:0045893|GO:0005525|GO:0046872|GO:0035998|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143064_PI430048170 0.0981857325832348 0.6579935268524353.81150185701761 3.40402432518312 4.17219932642203 P P P 4.35083772536613 4.49496681002499 4.45096673981686 P P P LNCV6_143064_PI430048170 mRNA
GTTGATTGTCAGTAGTTGCGACTTTTAAATTATATTTCCCCCACTCAAAGAATGGTATCT NM_003328RefSeq chr4 - 48066392 48134256 TXK 7294 TXK tyrosine kinase
GO:0050853|GO:0005515|GO:0050852|GO:0005634|GO:0007202|GO:0001816|GO:0060335|GO:0005737|GO:0046777|GO:0042127|GO:0045944|GO:0032609|GO:0038083|GO:0032729|GO:0006357|GO:0005102|GO:0000978|GO:0005524|GO:0001865|GO:0006351|GO:0031234|GO:0002250|GO:0001077|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127302_PI430048170 0.0243870534105512 0.5378364061581545.95863619116922 5.27400441362623 5.58187232713999 P P P 6.30138842704907 6.72444395631951 6.52380753307673 P P P LNCV6_127302_PI430048170 mRNA
GCATGATTCTTAAAAATGAATAAAACTGTTTACAAGGGAAGGAGAGCTAACTGCAAAGTG NM_052916RefSeq chr17 - 76142452 76240309 RNF157 114804 ring finger protein 157 GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134385_PI430048170 0.1439538759037110.6655664896326584.78808924902295 4.63272470583538 5.40374723420022 P P P 5.21091280353809 5.42049503422427 5.96635886298956 P P P LNCV6_134385_PI430048170 mRNA
GATTCCACTTAATAGACTCTATGTGTGCTGAATGTTCCTGTGTACATATGTGTGTTAAAT NM_015285RefSeq chr18 + 56651384 57029805 WDR7 23335 "WD repeat domain 7, transcript variant 1" GO:0002244 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114912_PI430048170 0.3265481566256940.8809320733838014.68213896278943 4.20318731932713 4.61648336660485 P P P 4.82673744466292 4.62780603145991 4.63198721164089 P P P LNCV6_114912_PI430048170 mRNA
TACAGGTAAACGAGATCAACTTTGAGAACATGAGTAATGACGATGCAGTCCGGGTACTGC NM_004423RefSeq chr3 + 184155495 184173526 DVL3 1857 dishevelled segment polarity protein 3
GO:0005515|GO:0046982|GO:0008013|GO:0038031|GO:0042493|GO:0090263|GO:0090179|GO:0005102|GO:0002020|GO:0005829|GO:0005109|GO:0035556|GO:0003148|GO:0001934|GO:0090103|GO:0043507|GO:0045893|GO:0016055|GO:0090090|GO:0060070|GO:0060071|GO:0035567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128131_PI430048170 0.0277121295194452 1.28453256506361 10.3843704132508 10.5701161241428 10.6340143234261 P P P 10.0182763229066 10.2667927470807 10.2193280714515 P P P LNCV6_128131_PI430048170 mRNA

ATGTAAACGAGCTTGTATCTCCTTCCCTGTGCCACGAGAGAGATTGGCTTTTTATTCCAG NM_053045 RefSeq chr9 - 137204082 137205638 TMEM203 94107 transmembrane protein 203 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127224_PI430048170 0.00714102858824326 1.57683433958997 5.6030223882815 5.28613423168195 5.34493706186756 P P P 4.84460835763469 4.82190805338807 4.604583176041 P P P LNCV6_127224_PI430048170 mRNA
TCCTGGAACGTATGCCCAGGGAGGAGGCTACAGAGATTGAGCAGACAGTCCAGAAAGCAG NM_001174084 RefSeq chr10 - 101578881 101588270 POLL 27343 "polymerase (DNA directed), lambda, transcript variant 1"
GO:0006260|GO:0071897|GO:0003887|GO:0005634|GO:0016446|GO:0006289|GO:0003677|GO:0046872|GO:0016829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133988_PI430048170 0.6926287889262320.9684383054145021 0.9374312031474 10.9578528265136 10.7257478299527 P P P 10.7826874474351 11.053124237007 10.9226189645456 P P P LNCV6_133988_PI430048170 mRNA
CTTGCCCAGATAATCTTCCTTTTTGAGGCAGCTATATAAATGATCATTTGTGCAAGAAAA NM_001258026 RefSeq chr12 + 6868113 6870946 TPI1 7167 "triosephosphate isomerase 1, transcript variant 3"
GO:0005515|GO:0004807|GO:0005975|GO:0019682|GO:0006094|GO:0005634|GO:0007275|GO:0044281|GO:0006098|GO:0005615|GO:0006096|GO:0005829|GO:0009405|GO:0006006|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109101_PI430048170 0.000245620471700865 2.10271645965439 12.1886039895989 12.2893384861646 12.3916925937409 P P P 11.3364797809995 11.1223329943347 11.1928880602513 P P P LNCV6_109101_PI430048170 mRNA
ATAAATTAGTCGACAGAAACTCAGCACTGGGGACAGGATTGCAAAGTCGGGGACATAGAT NM_001010858 RefSeq chr1 + 228487366 228496188 RNF187 149603 ring finger protein 187
GO:0005515|GO:0008284|GO:0005737|GO:0004842|GO:0016874|GO:0043161|GO:0008270|GO:0005654|GO:0005634|GO:0070936|GO:0045893|GO:0051865 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144628_PI430048170 0.000771641804910654 2.49354815631657 3.90844674459221 4.2318822844464 4.11142226761614 P P P 2.59285613267312 2.74418732941336 2.95533673655742 A P P LNCV6_144628_PI430048170 mRNA
ATACCAGGGTACTGGGGGGCAATGCTATGATTAACTTGCTTCAAATAAAAAGTTCCCGCC NM_139278 RefSeq chr8 - 22146829 22156831 LGI3 203190 "leucine-rich repeat LGI family, member 3"
GO:0043005|GO:0030054|GO:0017157|GO:0008152|GO:0005576|GO:0006887|GO:0003824|GO:0008021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139299_PI430048170 0.00641056402358324 1.91387880447266 7.1020843612583 7.00786232083571 6.90578199965557 P P P 5.86247048496309 6.27215924427011 6.04903739981771 P P P LNCV6_139299_PI430048170 mRNA
AGAAGATGAAGTCTATGCCCAGAAGATGAAGTACAAGGCCATTAGCGAGGAACTGGACAA NM_003289 RefSeq chr9 - 35682925 35690056 TPM2 7169 "tropomyosin 2 (beta), transcript variant Tpm2.2"
GO:0005862|GO:0030049|GO:0006936|GO:0043462|GO:0003779|GO:0008307|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130312_PI430048170 0.4932830806517360.7100480851039260.610555659432053 0.7028730820322970.564224012693556 A A A 0.5707783140527271.84365648793924 0.536706276536225 A A A LNCV6_130312_PI430048170 mRNA
GCCTCTGGAAAATGAGGCCAGTACAGTGTGACTACATGTTTAATTTTCAATGTAATTTAT NM_175737 RefSeq chr4 + 39406852 39451533 KLB 152831 klotho beta
GO:0005515|GO:0008286|GO:0048011|GO:0008284|GO:0005886|GO:0005975|GO:0017134|GO:0048015|GO:0005104|GO:0004553|GO:0007173|GO:0008543|GO:0045087|GO:0016021|GO:0090080|GO:0038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136156_PI430048170 0.3582161383689590.8690240121596820.268170973379638

0.2730911944550810.413514110985633A A A 0.3606999766410040.818697886675397
0.334694482126633A A A LNCV6_136156_PI430048170 mRNA
AAATGGTACAGCAGGTGCACTGTTAACAGTGTGATGGAATGACCACCCAAAGAGAAAAAA NM_001303133
RefSeq chr13 + 111316184 111344247 TEX29 121793 "testis expressed 29, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140532_PI430048170 0.00624655014985938 0.3679598423524751 2.6458130200368
12.2164193963538 12.4422072779111 P P P 13.511582394178 13.8762654442255
14.1952524905338 P P P LNCV6_140532_PI430048170 mRNA
CATGTCCTGTAAAGGTTACAAGCCTGCACAATAAAAATGTTTAACGGTTAAACAGTCAAA NM_001172895 RefSeq
chr7 + 116525008 116561185 CAV1 857 "caveolin 1, caveolae protein, 22kDa, transcript variant 2"
GO:0005515|GO:0043627|GO:0019915|GO:0010524|GO:0030879|GO:0006940|GO:0030301|GO:0005113|GO:0042
802|GO:0005622|GO:0016050|GO:0000165|GO:0031397|GO:0032507|GO:0005938|GO:0042632|GO:0005811|GO:0
019901|GO:0000122|GO:0019217|GO:0044325|GO:0016504|GO:0043234|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143164_PI430048170 0.4458151943600390.6855762328986220.430161608102848
0.3512794377561240.387472099143387A A A 1.65910931193367 0.335837826266606
0.393738441427952A A A LNCV6_143164_PI430048170 mRNA
AAAGGAGAGATTATGTTAACTTCCTAGTGGTGAGAATACCATGGGATGGGAGAAGGGCCA NM_001205293
RefSeq chr1 + 181483549 181806784 CACNA1E 777 "calcium channel, voltage-dependent, R type, alpha
1E subunit, transcript variant 1"
GO:0051899|GO:0086010|GO:0005245|GO:0005886|GO:0005509|GO:0007268|GO:0008331|GO:0044281|GO:0005
891|GO:0070509|GO:0006112|GO:0050796|GO:0070588|GO:0006810|GO:0034765 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_100818_PI430048170 0.00885993747973251 0.7575710120325729.20148969880707
9.06575849008497 9.24740784399839 P P P 9.59667753075965 9.52642193469392
9.59816279230845 P P P LNCV6_100818_PI430048170 mRNA
ATCCCAGCCTCCACAAAGAGGCCCTTTTATTTTTTATTCTGATTAGCCATTTTAAACCAA NM_015457RefSeq chr11
+ 57668001 57701187 ZDHHC5 25921 "zinc finger, DHHC-type containing 5"
GO:0018345|GO:0016020|GO:0005886|GO:0016409|GO:0008270|GO:0016021|GO:0030425|GO:0019706 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53540_PI430048170 0.2232343670000771.13083021417069 6.13768985982544 6.23907621649672
5.90078173274388 P P P 5.97556006885209 5.85287090943368 5.93483916118794 P P P
LNCV6_53540_PI430048170 mRNA
TTTGCATATTTCTCCAAAGAACCATCCAGAACCTGAGCAGCCTGTCTTCAGACAGAGAGA NM_181719RefSeq chr1
- 19682212 19799917 TMCO4 255104 transmembrane and coiled-coil domains 4 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70278_PI430048170 0.2292742608538291.15518528572768 0.6972433107188960.293790291914637
0.487578958753887A A A 0.3120148462453260.2745378568632010.29566927261953 A A A
LNCV6_70278_PI430048170 mRNA
ATTGTGAAATCTGTGATGTTCATGTTAATTCAGAAATTCAACTCAAACAGCCGAAGGCAT NM_152520RefSeq chr2
- 179441983 179861505 ZNF385B 151126 "zinc finger protein 385B, transcript variant 1"
GO:0002039|GO:0072332|GO:0008270|GO:0005634|GO:0003676 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144562_PI430048170 0.1267369359653770.7350035752515670.420706238050281
0.4750988081754380.393192667022031A A A 0.5286318257821291.10045876711791
0.935352374610183A A A LNCV6_144562_PI430048170 mRNA
CTTTGAATATGTGACCTTTGCCTGCAAGCACATATGGACTCTTAGAATTGATTTACATAA NM_001278677 RefSeq
chr19 + 24033404 24129967 ZNF254 9534 "zinc finger protein 254, transcript variant 1"
GO:0005634|GO:0000122|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_121256_PI430048170 0.00128375984519482 0.2965802957140943.03610123965899
2.76386060273137 3.04342844381338 P A P 4.54848430271867 4.9860061349999
4.54013113906509 P P P LNCV6_121256_PI430048170 mRNA
ATGTGGCAAGGCTTTTACCCAATCCTCAACCCTTACTACACATAAGAGAATTCATACTGG NM_138330RefSeq chr19
- 23652905 23687215 ZNF675 171392 zinc finger protein 675
GO:0005515|GO:0048471|GO:2000660|GO:0045453|GO:0019221|GO:0007249|GO:0045671|GO:0005634|GO:0032
088|GO:0000122|GO:2000678|GO:0003677|GO:0010804|GO:0006351|GO:0046329|GO:0008270|GO:0043508|GO:0
031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134761_PI430048170 0.0211102201586057 0.4935407651206054.18299388670534
4.47884629157424 4.92255070722734 P P P 5.27046446816945 5.82654937705851
5.58745955717713 P P P LNCV6_134761_PI430048170 mRNA
CCTTTCCATTTCTTAAAGTATTATCAAGTGTCAAGATCAGCAAGTGTCCTTAAGTCAAAC NM_182943RefSeq chr3
- 146069440 146161495 PLOD2 5352 "procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2, transcript
variant 1"
GO:0001666|GO:0031418|GO:0005506|GO:0030198|GO:0005783|GO:0030867|GO:0005789|GO:0008475|GO:0006
464|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128825_PI430048170 0.14178663985463 0.8089907068967189.63985709200627
9.55533574540098 9.90154742541903 P P P 9.88129460497424 9.86771240982021 10.253920700986
P P P LNCV6_128825_PI430048170 mRNA
AGCTGTGCTTAAGAGCCAGTAATGTCTTAATAAACATGTGGCAGCTTTTGTTTGAAAAAA NM_016001RefSeq chr17
+ 51260535 51297931 UTP18 51096 UTP18 small subunit (SSU) processome component homolog
(yeast) GO:0000462|GO:0032040|GO:0005730|GO:0005634|GO:0034388 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_136990_PI430048170 0.0286903659024372 1.33900385164133 9.33003501145613
9.49463338101298 9.62275014306388 P P P 8.93491578617036 9.00404813802086
9.24159969051869 P P P LNCV6_136990_PI430048170 mRNA
AGCCCCACTTAGCCAAGACCTCAAGTATAAATAATTCTGATAATTATGGAGAAATCAACT NM_001017928 RefSeq
chr3 - 122359590 122383231 CCDC58 131076 coiled-coil domain containing 58 GO:0005739 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111264_PI430048170 0.6127776691754780.8618586246641622.22292570772727
2.73361476152866 3.06274728535135 A A P 3.319764137422 2.36505838459799
2.94337236055841 P A P LNCV6_111264_PI430048170 mRNA
ATGCGTACTTTCTAAAAACTGATGGTGAAAAGCTCTTACCGAAGCAACAAAATTCAGCAG NM_001130716 RefSeq
chr4 - 83090057 83109859 PLAC8 51316 "placenta-specific 8, transcript variant 1"
GO:0043066|GO:0008284|GO:0040015|GO:0050873|GO:0045944|GO:0003682|GO:0009409|GO:0042742 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135230_PI430048170 0.90104497350873 0.9755875514246591 0.2279560416419
10.3286571646436 10.0260065109919 P P P 10.1213175070152 10.5214396406013
10.0119308869263 P P P LNCV6_135230_PI430048170 mRNA
GGAGGGGGCAGGTTTTGGTGCCAATTTGAGTGTATAAAGTTTTAGGTAAATACCAAAAAA NM_001130969 RefSeq
chr9 - 137447570 137459334 NSMF 26012 "NMDA receptor synaptonuclear signaling and neuronal
migration factor, transcript variant 1"
GO:0043005|GO:0030054|GO:0045202|GO:0005634|GO:0005635|GO:0030425|GO:0016363|GO:0043523|GO:0005
737|GO:0071257|GO:0071371|GO:0048168|GO:0071230|GO:0045211|GO:0043204|GO:0031965|GO:0005719|GO:2
001224|GO:0035307|GO:0014069|GO:0048814|GO:0016020|GO:0030863|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144426_PI430048170 0.5771008883356180.9778248104403760.33743987041045
0.3153355584250780.279126711383909A A A 0.4326026078296530.305978573213306

0.286575883006748 A A A LNCV6_144426_PI430048170 mRNA
ATGGAAAACATCAACATGTAATATCAGAAGAGTTGTCATCAGTTTCTTTGGAAAGGCTAC NM_001039706 RefSeq
chr7 + 90245173 90311063 CFAP69 79846 "cilia and flagella associated protein 69, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54812_PI430048170 0.0354628887478991 0.887692030078716 14.179965314642
14.0969653262004 14.2454762021735 P P P 14.3088355348141 14.3296272478909
14.4017259620095 P P P LNCV6_54812_PI430048170 mRNA
AACTACCCCTGAGTGTGGTCCCACAGGATATGTAGAGAAAATCACATGCAGCTCATCTAA NM_006694 RefSeq chr1
- 153974268 153977975 JTB 10899 jumping translocation breakpoint
GO:0005813|GO:0019901|GO:0005819|GO:0030496|GO:0005739|GO:0000910|GO:0005737|GO:0007067|GO:0008
637|GO:0016020|GO:0005887|GO:0042127|GO:0045860 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143922_PI430048170 0.191618579382289 1.19922310460394 5.69921674708587
5.94998685220403 5.70658281314113 P P P 5.79439840660177 5.33087476155768
5.41523320787403 P P P LNCV6_143922_PI430048170 mRNA
TCCATGGGCACCTCTGCTGTATTGATATCACTAATAAAGTCTGTCTGCACTGCTAAAAAA NM_001164 RefSeq chr11
- 6395123 6419111 APBB1 322 "amyloid beta (A4) precursor protein-binding, family B, member 1
(Fe65), transcript variant 1"
GO:0005515|GO:0030308|GO:0005886|GO:0045202|GO:0005634|GO:0045739|GO:0007409|GO:0006302|GO:0030
426|GO:0042393|GO:0005737|GO:0001540|GO:0007411|GO:0030198|GO:0045944|GO:0007050|GO:0050760|GO:0
070064|GO:0006355|GO:0043065|GO:0006915|GO:0006974|GO:0006351|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128432_PI430048170 0.00435647298986259 0.359938165147415 9.96959208174606
9.77417452530385 9.94241705171208 P P P 11.0642165318715 11.4751855621213
11.5332306774746 P P P LNCV6_128432_PI430048170 mRNA
ACCTTCCCAGTCTGTCCCATACTGTTACCCATAAAACTATCTCTTTATCTGTGCAAAAAA NM_024111 RefSeq chr15
+ 40953437 40956519 CHAC1 79094 "ChaC glutathione-specific gamma-glutamylcyclotransferase 1,
transcript variant 1"
GO:0006986|GO:0005802|GO:0005515|GO:0045746|GO:0016746|GO:0007219|GO:0070059|GO:0008152|GO:0005
112|GO:0010955|GO:0022008|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127778_PI430048170 0.184142553070471 1.01470435080637 0.31409088228319
0.277209459787119 0.292304687900295 A A A 0.278330833609995 0.271779453571928
0.270542756306477 A A A LNCV6_127778_PI430048170 mRNA
TCCCTATTTGGTCTCGCGACACAGGGACTATTTTCAGCACGCCCACAGTGACTGCCAGGA NM_001024598 RefSeq
chr1 + 6244191 6245578 HES3 NA hes family bHLH transcription factor 3 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134158_PI430048170 0.00137508483559811 1.5305482190353 11.3412655649515
11.2519342422845 11.1429115929086 P P P 10.7072821920461 10.6410264856188
10.5480595891486 P P P LNCV6_134158_PI430048170 mRNA
GAAGCACCCAGGTTGCCCACGGAAAATCCAATAAAAAGACACCAGTGTGAATCCAAAAAA NM_212481 RefSeq
chr2 + 96536726 96552634 ARID5A 10865 AT rich interactive domain 5A (MRF1-like)
GO:0005515|GO:0005667|GO:0006357|GO:0044212|GO:0005730|GO:0005634|GO:0003677|GO:0035066|GO:0006
351|GO:0002062|GO:0045944|GO:0003682|GO:0005654|GO:0045892|GO:0008134 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_90907_PI430048170 0.00501137872430285 3.375528084054 5.14037887409209
4.89873954900463 5.27043413003162 P P P 3.69928380443609 2.96720571986249
3.30902124081358 P P P LNCV6_90907_PI430048170 mRNA
TTCAACATCACAGATGAAATCATGTCTCAGTTCCCATCTAGCAAGGTGGCTTCAGGAGAG NM_001042454 RefSeq
chr16 + 31472154 31477960 TGFB1I1 7041 "transforming growth factor beta 1 induced transcript
1, transcript variant 1"

GO:0005515|GO:0008285|GO:0009408|GO:0006366|GO:0045599|GO:0010718|GO:0050681|GO:0048495|GO:0016363|GO:0005622|GO:0005737|GO:0030855|GO:0016055|GO:0007155|GO:0005856|GO:0030579|GO:0030512|GO:0030511|GO:0003713|GO:0070411|GO:0031012|GO:0045165|GO:0016331|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140606_PI430048170 0.1552432703010370.8208803421652465.61714148285432 5.55171974418442 5.99807256488986 P P P 5.96678805114032 5.95041809936097 6.13779456084916 P P P LNCV6_140606_PI430048170 mRNA ACTTGCCAACATCTGCCTTGCTGGACTTGTATGGGATTGTCTTCTTGATTTGAATTGTAC NM_018079RefSeq chr2 - 45388679 45611294 SRBD1 55133 S1 RNA binding domain 1 GO:0006139|GO:0003723 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135291_PI430048170 0.5233385021761721.09329177863701 12.781294954737 13.0076167901941 13.2402769077531 P P P 13.0925648458333 12.6599456989064 12.8947874542702 P P P LNCV6_135291_PI430048170 mRNA GCTCAGTATATGATAGTTCTGCTGATGTTTTGTTTATTGGGCAGACATATCTTCATTAAG NM_001660RefSeq chr3 - 57571362 57597488 ARF4 378 ADP-ribosylation factor 4
GO:0031584|GO:0005515|GO:0043066|GO:0005154|GO:0005794|GO:0006996|GO:0007264|GO:0003924|GO:0032587|GO:0005525|GO:0015031|GO:0048678|GO:0005829|GO:0006471|GO:0016477|GO:0007173|GO:0016020|GO:0007420|GO:0045944|GO:2000377|GO:0016192|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130610_PI430048170 0.8255056373877970.9838819373792922.01234519041983 1.7262558403767 2.39942916044721 A A A 2.14424861562709 2.03270001918406 2.10882751635518 A A A LNCV6_130610_PI430048170 mRNA TACGAGCAGCTTTGCGAGTTCGTCGAGGCCAACAGGCGCTTCACGCCCACCACCATCTAC NM_001080482 RefSeq chr9 + 136844414 136847345 C9orf172 NA chromosome 9 open reading frame 172 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143107_PI430048170 0.0264239152036299 0.7614856209364241 4.4317719139703 14.2322701388763 14.4759808874956 P P P 14.7794986187732 14.6213326575437 14.9150954036127 P P P LNCV6_143107_PI430048170 mRNA GACTGTGGGTAGATAGGGGAACAATGAGAGTCAACTCAGGCTAACTTGGGTGTGAAAAAA NM_183356RefSeq chr7 - 97852116 97872542 ASNS 440 "asparagine synthetase (glutamine-hydrolyzing), transcript variant 3"
GO:0070981|GO:0031427|GO:0044281|GO:0032870|GO:0042803|GO:0030968|GO:0005829|GO:0034641|GO:0004066|GO:0009416|GO:0042149|GO:0006529|GO:0043200|GO:0032354|GO:0043066|GO:0048037|GO:0009636|GO:0008652|GO:0005524|GO:0009612|GO:0001889|GO:0045931|GO:0006987|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136907_PI430048170 0.00148929973805429 0.7808797047262988.58020127318219 8.52568170857881 8.46224806594526 P P P 8.82140313777439 8.91056333633978 8.9073007035284 P P P LNCV6_136907_PI430048170 mRNA TGTTTGTTGCCCCATTCCTAAGAGGAGTTTATCCATCCTGACTTGTAGCTGTGTGACTTC NM_004623RefSeq chr1 + 54715821 54742655 TTC4 7268 "tetratricopeptide repeat domain 4, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129093_PI430048170 0.0705305315395775 1.04433297137727 0.390399883594097 0.3990779196053310.441218571637336A A A 0.3249190078492240.330993494835913 0.386744005340507A A A LNCV6_129093_PI430048170 mRNA CCCTCCAGGTTGTAATTCACTGTGTCTATGACACAAATGTTGTAGTCAATTAAAGTTTAA NM_001191054 RefSeq chr12 - 133218311 133235836 ANHX 647589 anomalous homeobox
GO:0043565|GO:0006355|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143997_PI430048170 0.0324913942806307 1.43131504597079 11.9445706636569 12.1763162269355 12.066902663955 P P P 11.741800444685 11.5584593791461 11.313005065027

P P P LNCV6_143997_PI430048170 mRNA
ACAGACACCAGATTTGTGAATAAAGTTGGGGAATGGACAGCCTAACTGGGACATTGCAGT NM_032306 RefSeq chr19
+ 6372432 6375250 ALKBH7 84266 "alkB, alkylation repair homolog 7 (E. coli)"
GO:0005759|GO:0006631|GO:0051213|GO:0010883|GO:0046872|GO:0006974|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142039_PI430048170 0.170861415019748 1.40827397787411 6.53088534807577 6.8215610531646
6.84040179842711 P P P 5.67217119781434 6.47062590554348 6.45407532773751 P P P
LNCV6_142039_PI430048170 mRNA
AAGAGCCTTTATACAATTGGACGCATTTTGGTTTTTCCTCATTGAGAATTCAAATCCTCT NM_001199280 RefSeq
chr16 + 69105563 69117667 HAS3 3038 "hyaluronan synthase 3, transcript variant 3"
GO:0005886|GO:0005975|GO:0036117|GO:0044281|GO:0045226|GO:0085029|GO:1900106|GO:0005887|GO:0009
405|GO:0030213|GO:0030212|GO:0050501|GO:0016021|GO:0007155|GO:0045893|GO:0030203 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141545_PI430048170 0.0769679494921273 0.774571088344848 8.16255900398596
8.16784762866494 8.26037645136832 P P P 8.33730426600261 8.61984098430341
8.71513799498911 P P P LNCV6_141545_PI430048170 mRNA
GGGCTGTACTGGTTGCTAAATATTGCACATCATTTTAAAACTATTTGAGATGCACTTTTG NM_032815 RefSeq chr16
+ 28950996 28966446 NFATC2IP 84901 "nuclear factor of activated T-cells, cytoplasmic, calcineurin-
dependent 2 interacting protein" GO:0005737|GO:0045944|GO:0005634|GO:0001816 . NA - . NA
NA NA NA NA NA NA NA NA NA
LNCV6_99805_PI430048170 0.0558664385252405 0.758930445428136 5.0166311428257
4.96101080911212 4.9869809981428 P P P 5.50173986106039 5.45510974469565 5.1819699747655
P P P LNCV6_99805_PI430048170 mRNA
AATTGGTGCTGCCAGCCCAGTCCCAGCTCTGCACACCTTGCTCTGCTCTAAGAGAAATGG NM_001304953 RefSeq
chr17 - 28703196 28711907 PROCA1 147011 "protein interacting with cyclin A1, transcript variant 5"
GO:0016042|GO:0005509|GO:0004623 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143149_PI430048170 0.107932467312417 1.19725827175108 8.49719126531815
8.74965688930183 8.58345370749329 P P P 8.54045348834128 8.29466929736648
8.20639520364317 P P P LNCV6_143149_PI430048170 mRNA
AACCAGCTCTCTCTATAGCGACGAGGAGTCCATCCTCTCCCGCTTCGATGAGGAGGACTT NM_005183 RefSeq chrX
- 49205062 49233371 CACNA1F 778 "calcium channel, voltage-dependent, L type, alpha 1F subunit,
transcript variant 1"
GO:0086010|GO:0060041|GO:0005245|GO:0050856|GO:0006874|GO:0008331|GO:0007409|GO:0005891|GO:0046
872|GO:0048813|GO:0070509|GO:0050908|GO:0070588|GO:0043204|GO:0034765|GO:0016021|GO:0043029|GO:0
007601|GO:0001750. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_46781_PI430048170 0.00901691005146442 1.80079540003729 4.50282703153218
4.87660665689715 4.93046485532652 P P P 3.7209199460753 4.07552293330333
3.98104387824081 P P P LNCV6_46781_PI430048170 mRNA
AAATTGGACATATTGAAAGACAAGGGTCATCTTTGAGAAGGGGGTTCCTGGACTCCTCAC NM_004326 RefSeq chr1
+ 147541500 147626219 BCL9 607 B-cell CLL/lymphoma 9
GO:0005515|GO:0005801|GO:0005794|GO:0008013|GO:0045944|GO:0014908|GO:0005654|GO:0035914|GO:0017
015|GO:0060070|GO:0035019 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131246_PI430048170 0.499766362427359 0.966114377659046 0.274993196766117
0.438358152902603 0.310218068102849 A A A 0.478896412003778 0.369208864787424
0.325476738588775 A A A LNCV6_131246_PI430048170 mRNA
ACACACAAGCCATTAGTTGACACTGATAACTCCGAATACATAAAATGTTTGCTGTTGCAA NM_016427 RefSeq chr18
- 47032571 47035617 TCEB3B 51224 transcription elongation factor B polypeptide 3B (elongin A2)
GO:0006366|GO:0032784|GO:0005634|GO:0016021|GO:0003677 . NA - . NA NA NA NA NA NA NA
NA NA

LNCV6_2347_PI430048170 0.2589023087481041.33022522190737 1.31791094942744 0.622983279994575
0.575514197044449A A A 0.5690498229319030.4126474997429070.419529902731633A A A
LNCV6_2347_PI430048170 mRNA
AACATGACACAAACATTTACTGCCGGATGGACCACAAAGCAGAAGTGGCTTCTTAGCTTC NM_001815RefSeq chr19
+ 41796589 41811553 CEACAM3 1084 "carcinoembryonic antigen-related cell adhesion molecule 3,
transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136678_PI430048170 0.4926060208313081.28609138208038 2.24290142962039
3.32947836473197 2.38268712482175 A P A 2.67772482758309 2.06666225003776
2.31155155324769 P A A LNCV6_136678_PI430048170 mRNA
TTAGGGGCAAGCAGGCGCTGTGCTATCATGATGGAATTTCATATCTACAGATAGAGAGTT NM_005574RefSeq chr11
- 33858575 33892289 LMO2 4005 "LIM domain only 2 (rhombotin-like 1), transcript variant 1"
GO:0005515|GO:0001102|GO:0005667|GO:0097067|GO:0048037|GO:0000977|GO:0001190|GO:0000981|GO:0043
425|GO:0070888|GO:0005634|GO:0007275|GO:0001228|GO:0045647|GO:0045944|GO:0003682|GO:0008270|GO:0
042789|GO:0035162. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144295_PI430048170 0.4669718652525922.27555638043268 1.48329710905517
3.14786399356349 0.310342350582601A P A 0.8968289244693410.776227822858148
1.06627349912532 A A A LNCV6_144295_PI430048170 mRNA
TCTCCTCAAATGAAACTAGAACAGAGGAAGTAAAAGGGAGATTGCTCGGATAATGTCTCA NM_001171192 RefSeq
chrX + 70423030 70433391 GDPD2 54857 "glycerophosphodiester phosphodiesterase domain
containing 2, transcript variant 1"
GO:0006629|GO:0005737|GO:0005886|GO:0047394|GO:0016021|GO:0005856|GO:0008889|GO:0006071|GO:0046
872. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139682_PI430048170 0.3995946712955850.7865333423651785.3638940544199
4.85831082881283 6.03874168598811 P P P 5.36715698709336 5.96133454431305
6.11351760203051 P P P LNCV6_139682_PI430048170 mRNA
TTGTAGGAAAACTTGAAAATTCCAAAATCCTTATTTTCCTATTTGAGAGGCTGGTTCAGC NM_033083RefSeq chr3
+ 15427556 15442613 EAF1 85403 ELL associated factor 1
GO:0005515|GO:0006355|GO:0005737|GO:0015030|GO:0016607|GO:0032783|GO:0005654|GO:0008023|GO:0006
351. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128305_PI430048170 0.5391458605206790.9665876128381630.464902250375948
0.4681064233571640.263100267366527A A A 0.4008224330514010.500218399703708
0.449844999724855A A A LNCV6_128305_PI430048170 mRNA
CCTCAGTAGGATACTTCATAGCAGATAATAACAATACACTCAGTCTTTTAGGTTGGAAAA NM_001172674 RefSeq
chr19 - 53138703 53159060 ZNF347 84671 "zinc finger protein 347, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133365_PI430048170 0.0594616174883219 1.70301025846228 6.9791381235746
7.03605544412031 6.89511435415245 P P P 6.20447111392528 6.52337392300459
5.78928140396397 P P P LNCV6_133365_PI430048170 mRNA
AAGGCTCTGAAGGGCTGAGAACAGTTCTAGAAGCGTCCCAAAGGGTGCTGGGAAAGGTCC NM_173680RefSeq
chr7 + 150379316 150398631 ZNF775 285971 zinc finger protein 775
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128984_PI430048170 0.8814085666371691.00975457542316 7.51833973456914
7.65472767076131 7.92186364323013 P P P 8.09960336091005 7.32345714218323
7.54552903987061 P P P LNCV6_128984_PI430048170 mRNA
CCAAACCATACACTACAGTACTTTGTCACATGGTTGTCCATTATCATGTATTAGAGTCTA NM_004733RefSeq chr3
- 155826510 155854459 SLC33A1 9197 "solute carrier family 33 (acetyl-CoA transporter), member 1,
transcript variant 1"

GO:0015295|GO:0008521|GO:0016020|GO:0000139|GO:0005887|GO:0006810|GO:0005789|GO:0015876|GO:0055085|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130422_PI430048170 0.537685610287696 0.668139223177079 0.358331590557859 0.426396447736243 0.361929460726207 A A A 0.24429169777209 1.79956301298409 0.248352504233957 A A A LNCV6_130422_PI430048170 mRNA GGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTCAGAGGAGAAATATATTCTA NM_001005468 RefSeq chr11 - 124382401 124383343 OR8B2 NA "olfactory receptor, family 8, subfamily B, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127717_PI430048170 0.113095859616423 1.29720631323425 0.716892297732188 0.898402375977452 0.435131876562665 A A A 0.347607947345148 0.309481461586422 0.303984313303419 A A A LNCV6_127717_PI430048170 mRNA AGCCAAAGATTTTATTATGTTCAGAAACCTGTAGTCTGAAATAAAGTGTACACTGTGCTC NM_001426 RefSeq chr2 - 118842170 118848183 EN12019 engrailed homeobox 1 GO:0005634|GO:0009954|GO:0000122|GO:0009953|GO:0042220|GO:0000978|GO:0009653|GO:0001078|GO:0001501|GO:0035264|GO:0016020|GO:0048666|GO:0045944|GO:0043473|GO:0030917|GO:0030901|GO:0035115|GO:0030902 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143555_PI430048170 0.00450197011057721 0.344624376964303 7.51203997838538 7.58629037112476 7.84332564012774 P P P 8.86299181512393 9.15408164042777 9.48859976030327 P P P LNCV6_143555_PI430048170 mRNA CTTCCAATTTGGAATCTTCTCTTTGACAATTCCTAGATAAAAAGATGGCCTTTGCTTATG NM_002228 RefSeq chr1 - 58780790 58784113 JUN 3725 jun proto-oncogene GO:0005515|GO:0042542|GO:0003700|GO:0001190|GO:0006366|GO:0003705|GO:0000981|GO:0002756|GO:0043524|GO:0043525|GO:0003690|GO:0002755|GO:0017053|GO:0032496|GO:0007179|GO:0007612|GO:0001102|GO:0038124|GO:0038123|GO:0005719|GO:0034134|GO:0003713|GO:0007568|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105277_PI430048170 0.106564365592637 0.775448416377738 5.89770793470385 5.42105219700693 5.70999485305775 P P P 6.00911083215589 6.05600045858747 6.10224848385867 P P P LNCV6_105277_PI430048170 mRNA CAAGTTCATACCTGATATCTATATTTACACAGATCACATGAAAGGAGTCAACTCTGGGAA NM_005772 RefSeq chr9 + 4792833 4861077 RCL1 10171 "RNA terminal phosphate cyclase-like 1, transcript variant 1" GO:0008150|GO:0003963|GO:0003723|GO:0005730|GO:0000480|GO:0004521 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130326_PI430048170 0.00324641050176833 2.28559078222488 7.67135848479938 7.67481241718729 7.61800783137924 P P P 6.55741777459601 6.52011586593772 6.29604167020268 P P P LNCV6_130326_PI430048170 mRNA TCATCCTTCTTCAATAAATGCTGAATGACATTCAAGCTGATTTTCTAGACCACTGAGAAA NM_003498 RefSeq chr16 + 11668432 11679161 SNN 8303 stannin GO:0009628|GO:0006950|GO:0005741|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142678_PI430048170 0.0529721246685011 1.88123739606045 4.12167717533085 4.6828203732955 4.25694144968319 P P P 3.93118521302048 3.28723165349453 3.00940671594502 P P P LNCV6_142678_PI430048170 mRNA AACTTCGTTCTGTAGAGAACTATTTTTGTTTGTATTCACTGTCCCCTGCAAGGGGGACGG NM_032536 RefSeq chr9 + 132161946 132242833 NTNG2 84628 netrin G2 GO:0005515|GO:0030424|GO:0003674|GO:0007409|GO:0046658 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127891_PI430048170 0.157790867773466 0.647080553090589 5.63227073633542 4.62018707271975.4944971623929 P P P 5.89847586974258 5.87060173778504 6.04807281514169 P P P LNCV6_127891_PI430048170 mRNA GGAGTGCTTATTTCCCTTTGTGTAAGGACTAAGAAATCATGATATCAAATAAACATGGTG NM_001287219 RefSeq

chr1 + 213051232 213273465 RPS6KC1 26750 "ribosomal protein S6 kinase, 52kDa, polypeptide 1, transcript variant 4"
GO:0005515|GO:0007165|GO:0005737|GO:0016020|GO:0004674|GO:0006468|GO:0035091|GO:0005524|GO:0005769|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137853_PI430048170 0.6912902107627880.9382277616888310.455804614455
10.8096142062376 10.9494877567404 P P P 10.7859990629202 10.5890262490371
11.1109036811783 P P P LNCV6_137853_PI430048170 mRNA
CTCTGGAAGTACCTACCACATTTTAGAGATTTACCGTTTCCATATATTTAACATTCCTGG NM_138701RefSeq chr7 - 40132742 40134652 MPLKIP 136647 M-phase specific PLK1 interacting protein
GO:0005515|GO:0007067|GO:0005813|GO:0005737|GO:0005794|GO:0030496|GO:0005654|GO:0005634|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128307_PI430048170 0.0593651223199847 1.24898724044881 7.57523315376599
7.60301340937469 7.71952526868225 P P P 7.13719900235454 7.47075159397581
7.31240515356909 P P P LNCV6_128307_PI430048170 mRNA
GACAGCTCTGTGATGTAGCTTTTAGGAGGCACTCAGGTGTCACGGCTAGACTGCAGCTAT NM_001282933 RefSeq chr20 + 33731759 33792269 ZNF341 84905 "zinc finger protein 341, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_86077_PI430048170 0.99973591803288 0.8037578251374911.84639623040394 1.99422657972716
1.9562882210848 A A A 0.6412663256771812.06788935418858 3.08855135409214 A A P
LNCV6_86077_PI430048170 mRNA
GCCACTCTTGAATACCATTCTCCACTATTAACATTAATTTACTCAAACCGTTCATAGCAT NM_020156RefSeq chr7 + 7182614 7248649 C1GALT1 56913 "core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase 1"
GO:0060576|GO:0005515|GO:0006493|GO:0000139|GO:0001822|GO:0016266|GO:0016263|GO:0016021|GO:0001525|GO:0044267|GO:0046872|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115274_PI430048170 0.93903340602766 0.9806631541058844.17636094078202
4.02860038667776 4.33616351540051 P P P 4.23509350819604 4.45724723376297
3.89504114148118 P P P LNCV6_115274_PI430048170 mRNA
CACGGTGCTTCCTGGCTGCAGACCACAACCCTCCGCTGGTCGCTGGTCGCTGGTTGGGGA NM_198693RefSeq chr21 - 44550356 44551505 KRTAP10-2 NA "keratin associated protein 10-2, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128970_PI430048170 0.0133601903064758 1.4589710702739 13.0156335890321
13.109682677968 13.3264561956472 P P P 12.6105760761248 12.5246666681054
12.6945057116306 P P P LNCV6_128970_PI430048170 mRNA
GTCTACAAGGTGTTTTGTGGTTTCTGTATTTCTTCTTTTCACTTTACCAGAAAGTGTTCT NM_000421RefSeq chr17 - 40818116 40822611 KRT10 3858 "keratin 10, type I"
GO:0005882|GO:0005737|GO:0016020|GO:0030216|GO:0071277|GO:0005634|GO:0045095|GO:0030280|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143926_PI430048170 0.0613821979883939 1.20814024420796 10.9446996176536
11.1263379456154 10.9817432675965 P P P 10.8748147648873 10.7655911005374
10.5858330835369 P P P LNCV6_143926_PI430048170 mRNA
TCCCGGGGGTATTCTGTGACCATGAATAAAGTTATCATTCTCTTTCTCTTTCACAAAAAA NM_003083RefSeq chr19 + 7920308 7923251 SNAPC26618 "small nuclear RNA activating complex, polypeptide 2, 45kDa, transcript variant 1"
GO:0010467|GO:0006355|GO:0005737|GO:0003700|GO:0009301|GO:0006366|GO:0005654|GO:0005634|GO:0006383 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111754_PI430048170 0.0348346268049222 1.1711345649507 9.37619500749254
9.20506829931908 9.35519822872948 P P P 9.1089815427088 9.11395399750324

9.03440194906256 P P P LNCV6_111754_PI430048170 mRNA
TGCCACTTTGGAAGAGCGAAAGGAAGATCAGTATATGAAAATGACAGTGTGTCTGGAGACNM_001253823 RefSeq
chr7 + 43758672 43807342 BLVRA 644 "biliverdin reductase A, transcript variant 2"
GO:0006778|GO:0004074|GO:0008270|GO:0044281|GO:0042167|GO:0070062|GO:0055114|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144906_PI430048170 0.6207948035817830.9641288632163250.561316441054412
0.5181889849305910.279714844403189A A A 0.4107471333794330.596075628363728
0.520150656838729A A A LNCV6_144906_PI430048170 mRNA
AACGGATGAGACTTTCCACGTGGTACCTAGATTTGCAAATTCTATTGTAATGCCTTTATT NM_194294RefSeq chr8
+ 39934954 40016391 IDO2 169355 "indoleamine 2,3-dioxygenase 2"
GO:0034641|GO:0006569|GO:0005737|GO:0004833|GO:0019441|GO:0033754|GO:0044281|GO:0046872|GO:0055
114|GO:0020037|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137789_PI430048170 0.2877244876069340.9808035657753440.301126134734352
0.3399563902999050.365503113888655A A A 0.38454793884558 0.364390893420842
0.341951012101463A A A LNCV6_137789_PI430048170 mRNA
GATCAAAACACACAGTGTTTATGTTGGAATCTTTTGGAACTCCTTTGATCTCACTGTTAT NM_007115RefSeq chr2
+ 151357591 151380048 TNFAIP6 7130 "tumor necrosis factor, alpha-induced protein 6"
GO:0007165|GO:0030335|GO:0006954|GO:0005540|GO:0007267|GO:0007155|GO:0005615|GO:0030728 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105163_PI430048170 0.266083253781136 1.98931325274044 0.452642170869597
2.02447949693226 2.19494187517208 A A A 0.645782651328932 1.09976199861941
0.408141190816794A A A LNCV6_105163_PI430048170 mRNA
CTAGCAAAGTCCAGTTGTTAAACCTAAAACAGAAAAAGAAAAGCTGAAGGAACTCTTCCC NM_004941RefSeq chr17
+ 43483916 43524318 DHX8 1659 "DEAH (Asp-Glu-Ala-His) box polypeptide 8, transcript variant 1"
GO:0008380|GO:0005515|GO:0004004|GO:0006396|GO:0005737|GO:0000398|GO:0005681|GO:0005654|GO:0005
634|GO:0071013|GO:0005524|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78944_PI430048170 0.0136732707985558 1.27965254301962 9.83894110758731
9.75206642541645 9.80972153841911 P P P 9.38501148442422 9.38474306918843
9.55804988278335 P P P LNCV6_78944_PI430048170 mRNA
GACAGGACTACATGGATGCCATGGCTGAGAAGCAAAAATTGGATGCAGAGTTTCAGAAAA NM_024653RefSeq
chr7 + 102396356 102426682 PRKRIP1 79706 PRKR interacting protein 1 (IL11 inducible)
GO:0042326|GO:0003725|GO:0019901|GO:0005730|GO:0004860|GO:0006469|GO:0070062|GO:0003014 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81475_PI430048170 0.750427653500333 1.04056397134132 9.50638772308834 9.8698117860502
9.59764684416237 P P P 9.85781759444259 9.60984839220464 9.3070362239652 P P P
LNCV6_81475_PI430048170 mRNA
TATGCTGAGGCCTGGGCGTTCCCTGCCCTGTGCTGACTCTGTTGCTCTGTGAATAAACAC NM_206920RefSeq chr9
+ 136852366 136860799 MAMDC4 158056 MAM domain containing 4 GO:0016021|GO:0015031 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143342_PI430048170 0.646390571352867 1.06884678103271 10.4535230664066 10.55167237802
10.9038390511724 P P P 10.3940481907294 10.407180647481 10.8179490954238 P P P
LNCV6_143342_PI430048170 mRNA
CTGTTGTTTTGGGTGACTGAAGTATAAAGTGTTTTCTGTACCTTAGATTCACAAACTTTG NM_024057RefSeq chr12
- 102074194 102118583 NUP37 79023 nucleoporin 37kDa
GO:0007077|GO:0005515|GO:0010467|GO:0019221|GO:0019058|GO:0005634|GO:0005635|GO:0044281|GO:0015
031|GO:0008645|GO:0005829|GO:0007059|GO:0015758|GO:0016032|GO:0005975|GO:0019083|GO:0055085|GO:0
010827|GO:0007067|GO:0031080|GO:0000777|GO:0009405|GO:0000776|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144280_PI430048170 0.0249469070149891.31064743712611 9.9190153729705

10.1525173070791 10.1892427728053 P P P 9.77255442574807 9.75929445390268
9.56333338370961 P P P LNCV6_144280_PI430048170 mRNA
GGCATGAAGAGCCAAGGTGTGAAAAGCAGATTTGATTTTTCAGTTGATTCAGATTTAAAA NM_014908RefSeq chr9
- 128945529 128947733 DOLK 22845 dolichol kinase
GO:0016310|GO:0004168|GO:0005789|GO:0030176|GO:0006488|GO:0044267|GO:0043048|GO:0006489|GO:0043
687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95053_PI430048170 0.0280632942061997 0.840991919340636 10.3031150031275
10.4154755950184 10.5016715142012 P P P 10.6311585594951 10.7305943898524 10.612036358486
P P P LNCV6_95053_PI430048170 mRNA
AAAGCTGACAGCCTTTGTAAACACGTTGAATGGCAAAGATGGAACCGGTTCTCATCTGGT NM_002810RefSeq chr1
+ 151254720 151267478 PSMD4 5710 "proteasome (prosome, macropain) 26S subunit, non-ATPase, 4"
GO:0005515|GO:0002474|GO:0010467|GO:0090263|GO:0044281|GO:0031145|GO:0005829|GO:0042802|GO:0034
641|GO:0005737|GO:0000082|GO:0016032|GO:0090090|GO:0006977|GO:0000209|GO:0000502|GO:0043066|GO:0
006521|GO:0051437|GO:0042590|GO:0006915|GO:0042981|GO:0051436|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136928_PI430048170 0.136462254223083 0.842655014039618 13.4558613886766
13.4077627868201 13.6950421054011 P P P 13.8272947327016 13.5742527193641
13.8953196641586 P P P LNCV6_136928_PI430048170 mRNA
GGCTTGGAGTAGACAAAAGGAAAGGTCTCAGCTTGTATATAGAGATTGTACATTTATTTA NM_001195056 RefSeq
chr12 - 57516587 57520517 DDIT3 1649 "DNA-damage-inducible transcript 3, transcript variant 4"
GO:0005515|GO:0006986|GO:0034976|GO:0003700|GO:0006983|GO:0044212|GO:0005634|GO:0043620|GO:0045
662|GO:0043433|GO:0032757|GO:0005829|GO:0030968|GO:0043525|GO:0042594|GO:0045944|GO:0007050|GO:0
042789|GO:0016055|GO:0090090|GO:0006355|GO:0051209|GO:0046982|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129542_PI430048170 0.517671779659633 1.03946759997155 10.4945094494628
10.5943311361644 10.5537867051467 P P P 10.6353425112915 10.4022078752726
10.4277770790595 P P P LNCV6_129542_PI430048170 mRNA
CAGGCTGATCTGAGGTAAACTTTGAAGTAAAATAAAAGCTGTGTTTGAGCATCATTTGTA NM_005516RefSeq
chr6_GL000255v2_alt + 1744501 1749301 HLA-E 3133 "major histocompatibility complex, class I,
E"
GO:0002474|GO:0002476|GO:0042288|GO:0005886|GO:0019221|GO:0002717|GO:0002715|GO:0060337|GO:0042
605|GO:0030670|GO:0071556|GO:0070062|GO:0042270|GO:0060333|GO:0012507|GO:0030881|GO:0002480|GO:0
009986|GO:0042612|GO:0005102|GO:0042590|GO:0000139|GO:0001916|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93108_PI430048170 0.314554201734382 1.32517649249813 1.15016093075173 0.393020187569503
0.314677782581876 A A A 0.253748756684019 0.283315061104293 0.256956289754779 A A A
LNCV6_93108_PI430048170 mRNA
TGTTTACCTGCTATGGAAAGAAGATGCATTTAAGTTTCCTGCAGTTTCACCCTGGAAATT NM_001129891 RefSeq
chr5 - 169863714 169980740 FAM196B NA "family with sequence similarity 196, member B" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140754_PI430048170 0.413452990600168 1.25901286486696 0.424670781266019
0.431876801790273 1.24424226777723 A A A 0.46064489575133 0.39139490226226
0.412898922975141 A A A LNCV6_140754_PI430048170 mRNA
ACACCTTTCTAACTGGCCAAGTGACATCATGCAATTGCTACCGAGAACAAAACCAGTTCC NM_001101404 RefSeq
chr15 + 78092584 78104051 SH2D7 NA SH2 domain containing 7 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144185_PI430048170 0.00199998419515588 0.454994688237947 4.59083981438865
4.46636674588161 4.86171158696019 P P P 5.59769856520765 5.77509001570701
5.96031052378419 P P P LNCV6_144185_PI430048170 mRNA

TTGATTGACCTGTAGAATGGATGTTAGGAAACTCAAAATTGAACACAGTGAAACAAATGG NM_024573 RefSeq chr6 + 151452257 151470099 ARMT1 NA "acidic residue methyltransferase 1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140454_PI430048170 0.000361715466828946 0.216643641243599 5.61190165984392 5.64712960322199 5.8776834003035 P P P 7.74519698774459 7.82388265401003 8.16653042714459 P P P LNCV6_140454_PI430048170 mRNA
TAATACTAACTATTTAGTATACTGTCAGTACTGTACATCTGCACACTGGTGTTAATAGGG NM_152400 RefSeq chr4 + 112145396 112189081 C4orf32 132720 chromosome 4 open reading frame 32 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78035_PI430048170 0.346419522645977 1.23535255453544 4.14869919339689 4.8211969160899 4.36966829794085 P P P 3.83732416264367 4.54617401260263 4.02850314503133 P P P LNCV6_78035_PI430048170 mRNA
TTTGTGCTGACAGAACGAGAGGGTGCTCTGAAGTATTTCAACAGAAATGATGCCAAGGAG NM_006869 RefSeq chr7 - 897899 954683 ADAP1 11033 "ArfGAP with dual PH domains 1, transcript variant 1" GO:0043547|GO:0005515|GO:0008060|GO:0043533|GO:0005737|GO:0005886|GO:0032312|GO:0005547|GO:0008270|GO:0005634|GO:0043087|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144798_PI430048170 0.372395804163497 0.967185554457299 0.420524261709961 0.445979488263083 0.307626903979653 A A A 0.413262975509572 0.473422577541567 0.434932412416818 A A A LNCV6_144798_PI430048170 mRNA
TGTCTTGAGTTTGGCCTCACTTAATAGCATTTGCAATTGAGTTTGACTTGTTCACATTTT NM_001170700 RefSeq chr4 + 36284021 36344785 DTHD1 401124 "death domain containing 1, transcript variant 1" GO:0007165 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142314_PI430048170 0.275011204124656 0.944829299320191 10.9043676820855 11.0831192734824 10.9308649473615 P P P 11.003308719045 11.1015431695557 11.063948794631 P P P LNCV6_142314_PI430048170 mRNA
CAACCTTGGCTCTAGACTGTTACTCTTAAGCTTTGAGAAATTTTCACATTGATGACTATT NM_001146018 RefSeq chr6 + 43477522 43506556 TJAP1 93643 "tight junction associated protein 1 (peripheral), transcript variant 3" GO:0005802|GO:0005515|GO:0005794|GO:0005886|GO:0007030|GO:0005654|GO:0005923|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143671_PI430048170 0.202168077543718 2.05913569009286 0.273514795620664 1.85838575525478 1.50885886140186 A A A 0.339729053661684 0.298618728876988 0.303966112232691 A A A LNCV6_143671_PI430048170 mRNA
GTCATTTAGATCACCCCAGATGGCCTGATGACAACAAGAGTTTGTGAAGTTATGAAAAAA NM_031498 RefSeq chr17 - 49206233 49209381 GNGT2 2793 "guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2, transcript variant 1" GO:0007186|GO:0005886|GO:0008152|GO:0005834|GO:0003924|GO:0007268|GO:0004871|GO:0007602 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111113_PI430048170 0.0322392915885067 2.94651544820178 3.87864589789356 4.28063642159754 4.19582382432648 P P P 3.14291331126706 1.940876112592 2.36046054665186 P A A LNCV6_111113_PI430048170 mRNA
CTTGCTGGAGAATGACCCAGATGTCCCAGGTGCAGGAGCTCTTCCATGAGGCAGCCCAGC NM_024628 RefSeq chr3 - 125082635 125212765 SLC12A8 84561 "solute carrier family 12, member 8, transcript variant 1" GO:0016021|GO:0055085|GO:0006813|GO:0015293 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145232_PI430048170 0.0686650910997241 0.75025686954193 9.44929497140008 9.43636390720953 9.35684276182644 P P P 9.58387057985679 9.91394370958346 9.96152238201628 P P P LNCV6_145232_PI430048170 mRNA
AACACCAATGTGGATCCTGACAGCTTTCAGTTTTAGCAAAAATACACGTGAAATCTGACT NM_144601 RefSeq chr16

+ 66604324 66613893 CMTM3 123920 "CKLF-like MARVEL transmembrane domain containing 3, transcript variant 1" GO:0031965|GO:0005737|GO:0006935|GO:0016021|GO:0050861|GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142913_PI430048170 0.8867243792576170.9943878586767981 3.4341730788582 13.4686488172849 13.4220139633803 P P P 13.3789397559517 13.5247192659486 13.4422303714197 P P P LNCV6_142913_PI430048170 mRNA
CACCCTTCTCTGCCTTTATTTTTTGATTTGTGCAACTTGTAACTAGGTGTTTATGGAATA NM_005439RefSeq chr12 - 6747991 6752916 MLF2 8079 "myeloid leukemia factor 2, transcript variant 1" GO:0005515|GO:0005737|GO:0016020|GO:0006952|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138696_PI430048170 0.7053879354171340.9752045415802090.592899495559918 0.50127539687954 0.311382633970198A A A 0.4199657941680160.57978548951228 0.52406618393748 A A A LNCV6_138696_PI430048170 mRNA
AACGTTAAGTTTTGTACTTGACGTTTCTGTTTATTAGCTAAATTGTTCCTCAGGTGTGTG NM_002129RefSeq chr4 - 173331375 173334444 HMGB2 3148 "high mobility group box 2, transcript variant 1" GO:0005515|GO:0000793|GO:0048471|GO:0003700|GO:0044212|GO:0007289|GO:0006325|GO:0005634|GO:0005615|GO:0032075|GO:0006921|GO:0045654|GO:0005737|GO:0003690|GO:0050786|GO:0003697|GO:0045944|GO:0006338|GO:0033151|GO:0006357|GO:0008301|GO:0019904|GO:0006334|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109335_PI430048170 0.90307483769762 0.9489217018670420.680864272385851 1.61630107347741 1.25980787991916 A A A 1.86435356186659 0.92852521293024 0.92558907798463 A A A LNCV6_109335_PI430048170 mRNA
AGATCGTGACAGCCCTCGTCAACTGTGCCAAGAGGCCTCATCAGGGGAAGTCTTCCTACT NM_001031853 RefSeq chr11 + 15112423 15247208 INSC NA "inscuteable homolog (Drosophila), transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142663_PI430048170 0.0407429662498959 0.7240141531215166.1892121399155 6.01197599503392 6.24034521209145 P P P 6.36791648742229 6.71331101278018 6.73895324992194 P P P LNCV6_142663_PI430048170 mRNA
TCACTTTTCATGGAAAGAGCTCTATGTAACAGCATAATAAAACTGCCTACCTAGCAGCAT NM_018279RefSeq chr12 + 71686097 71704059 TMEM19 55266 transmembrane protein 19 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126749_PI430048170 0.00148360562923872 1.78444073918474 10.1065504217669 10.0411065830571 9.89456749260868 P P P 9.03514380203487 9.31121343874186 9.18435088661217 P P P LNCV6_126749_PI430048170 mRNA
CCTGGTCTAAGCTGGACTTACCTCTGTGGATTCTGAAATTAAAGAAGTGAGTTGCTAAGG NM_032534RefSeq chr7 + 149715010 149734575 KRBA1 84626 "KRAB-A domain containing 1, transcript variant 1" GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92677_PI430048170 0.0143640116627576 2.13447005172119 5.03127439315291 5.09682743878498 4.54407595868754 P P P 3.89159108804179 3.66652218223072 3.88199882779563 P P P LNCV6_92677_PI430048170 mRNA
TTCCGCCATGCTCAGCTTCTGGACGCAGCAAAAGCAGGTGGTGAGTTCTTGCTGCGGTAT NM_002910RefSeq chrX - 153935268 153944780 RENBP 5973 renin binding protein GO:0010951|GO:0004866|GO:0050121|GO:0006051|GO:0008217|GO:0006044|GO:0019262|GO:0005524|GO:0042803|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126660_PI430048170 0.0592737007473803 0.6606890781240145.08199294501803 5.03691984703942 5.23537700046191 P P P 5.44254164102645 5.64496149582628 6.01005816159914 P P P LNCV6_126660_PI430048170 mRNA
AGTTGTTTACCTATGAAATTCCTTCCTGCAGTCATTCTGAAATAAAGTTGTTACAGCTGA NM_138492RefSeq chr5 - 145756343 145835369 PRELID2 153768 "PRELI domain containing 2, transcript variant 3"

GO:0005758|GO:0015914 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127242_PI430048170 0.00212342907127342 2.217207983468 6.46789740140499
6.77903667908083 6.60663410091919 P P P 5.55008845848948 5.42458684206957 5.4464097010955
P P P LNCV6_127242_PI430048170 mRNA
CCACCCACCTGGATTCCCTGTTCTTTGAAGTGGCACCTAATAAAGAAATAATACCCTGCC NM_002686RefSeq chr17
+ 39668452 39670475 PNMT 5409 "phenylethanolamine N-methyltransferase, transcript variant 1"
GO:0034641|GO:0004603|GO:0042418|GO:0044281|GO:0032259|GO:0042423|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130744_PI430048170 0.0305396758174314 0.48573264646018 0.502140130990949
0.4851379157367420.563261629684661A A A 1.28154751953492 1.42086125013443
1.89958601175569 A A A LNCV6_130744_PI430048170 mRNA
GTGATTTGGGGCCGTTTGTACTCTGCATGTATTCAATAAATTCAATTCAGCAATAGTTAA NM_003958RefSeq chr6
+ 37353971 37394738 RNF8 9025 "ring finger protein 8, E3 ubiquitin protein ligase, transcript variant
1"
GO:0005515|GO:0006511|GO:0004842|GO:0033523|GO:0033522|GO:0007286|GO:0000151|GO:0005634|GO:0045
739|GO:0006303|GO:0042803|GO:0006302|GO:0042393|GO:0070534|GO:0070535|GO:0010212|GO:0034244|GO:0
031625|GO:0000781|GO:0043486|GO:0016881|GO:0045190|GO:0005730|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137716_PI430048170 0.9578640636492040.99892192618313 0.285775426619814
0.29244747633988 0.422866463107589A A A 0.3564603043017580.304127031342955
0.348801338612569A A A LNCV6_137716_PI430048170 mRNA
TTTGCTGTAACATTTGACTTCTAAGGTTTAGATGCCATTTAAGAACTGAGATGGATAGCT NM_016610RefSeq chrX
+ 12906619 12923169 TLR8 51311 "toll-like receptor 8, transcript variant 1"
GO:0003725|GO:0003727|GO:0016064|GO:0003723|GO:0007249|GO:0051607|GO:0006954|GO:0036020|GO:0008
144|GO:0002755|GO:0045078|GO:0004872|GO:0001774|GO:0034158|GO:0045416|GO:0002224|GO:0009615|GO:0
003677|GO:0045359|GO:0000139|GO:0045089|GO:0045087|GO:0045356|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127957_PI430048170 0.8890661510926620.9790895151529631 1.2638428187881
11.1638498617435 11.0939426054302 P P P 11.4031639389648 11.2183162072469
10.9631942471301 P P P LNCV6_127957_PI430048170 mRNA
ATACATACGTGTTGTGTCTGTCAATAAAGTGTAAATAAGGTCTCCCTGCCCCACAAAAAA NM_021008RefSeq
chr11_KI270832v1_alt - 176099 206711 DEAF1 10522 "DEAF1 transcription factor, transcript variant 1"
GO:0005515|GO:0005667|GO:0006357|GO:0006366|GO:0048706|GO:0005730|GO:0001843|GO:0005576|GO:0005
634|GO:0009653|GO:0003677|GO:0007281|GO:0046872|GO:0033599|GO:0005737|GO:0008542|GO:0001662|GO:0
005654|GO:0045893|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144225_PI430048170 0.0275140362383497 1.66898648407815 4.46397789946734
4.98272302975255 4.85583068986973 P P P 3.92171020612459 4.03157178738603
4.17067714409237 P P P LNCV6_144225_PI430048170 mRNA
TGGTAGTCCTTGTGTTTTTCATAGCCCAAGATAGCCATGTGACCTGGAACTTTTAAAAAA NM_170746RefSeq chr11
+ 57741249 57743411 C11orf31 280636 chromosome 11 open reading frame 31
GO:0008430|GO:0045454 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136128_PI430048170 0.0831901833711009 1.05273225437371 0.459266529904938
0.5346657539032650.493110834478511A A A 0.3778139670311630.427218720492314
0.459415530311985A A A LNCV6_136128_PI430048170 mRNA
AGGTTTGGGTACATTACAGCTTGGGTTTTCCAACTGACTTAGGATTTCTGACTTTTTATTNM_025228RefSeq chr1 +
209756031 209782323 TRAF3IP3 80342 "TRAF3 interacting protein 3, transcript variant 1"
GO:0005515|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128410_PI430048170 0.3693049075124920.9182803027008266.25669867336295
6.05213197040299 6.17666355712244 P P P 6.40796620800696 6.34609441160996

6.08820899542604 P P P LNCV6_128410_PI430048170 mRNA
AGGGATGGGAACTTTTATTTCAAAATAAATACTACCGAGGCTGTGATCAGGCTCACCTTG NM_024705 RefSeq chr13
- 51767992 51804162 DHRS1279758 "dehydrogenase/reductase (SDR family) member 12, transcript
variant 2" GO:0016491|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98027_PI430048170 0.6381774807246740.895373966449257 6.56131921117521 5.97826882293343
5.74413785794449 P P P 6.56700285955605 6.39701846568352 5.82427592600357 P P P
LNCV6_98027_PI430048170 mRNA
GCGTCTGTGTCCTTGCTGCCTTCATCCCCTGGGGCCTGTGAATAAAGCTGCAGAACCCCC NM_001297646 RefSeq
chr11 + 1919568 1938706 TNNT3 7140 "troponin T type 3 (skeletal, fast), transcript variant 5"
GO:0005861|GO:0030049|GO:0006942|GO:0003779|GO:0030899|GO:0005829|GO:0030172|GO:0031013|GO:0003
009|GO:0008152|GO:0043462|GO:0005523|GO:0048306 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138328_PI430048170 0.955296103838005 0.991264425878811 11.3028908689138
11.2091027018183 11.2198249667811 P P P 11.0596380628805 11.2950182201757
11.3965889057411 P P P LNCV6_138328_PI430048170 mRNA
TTCATTCTTGGAATAGAAGATGATACTTCATCTGTGACTCCAGTGGAGTTAAAATGTGAA NM_138446 RefSeq chr7
+ 23299320 23309561 MALSU1 115416 mitochondrial assembly of ribosomal large subunit 1
GO:0005739|GO:0090071|GO:0005737|GO:0005759|GO:0043023|GO:0042273|GO:0070130 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131211_PI430048170 0.313250599938811 0.747437820254272 0.3938541963093
0.2573993288882290.291415174234638 A A A 0.564718456491045 1.20575772844793
0.273568852198366 A A A LNCV6_131211_PI430048170 mRNA
CTGGAAGATGGTGAGTGCATGAGTCAAATAATCTAGAGGCACTGCCCTAATGAGAAAAAANM_001145161 RefSeq
chr5 + 6448622 6496721 UBE2QL1 134111 ubiquitin-conjugating enzyme E2Q family-like 1
GO:0016567|GO:0016874|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133647_PI430048170 0.55857271291314 0.90613096218303 9.91976123908638 10.078532562038
10.3331234764634 P P P 10.1283993747677 10.0281971087681 10.5720581490659 P P P
LNCV6_133647_PI430048170 mRNA
GGCCCAAAAGAAAAACTGCTAAAAGACAAAAAAGACCTCACCCTTACTTCATCTATTTTT NM_001136005 RefSeq
chr21_GL383581v2_alt - 108060 115590 GART 2618 "phosphoribosylglycinamide formyltransferase,
phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase, transcript variant 3"
GO:0021987|GO:0009168|GO:0010033|GO:0003360|GO:0008168|GO:0055086|GO:0021549|GO:0044281|GO:0004
637|GO:0032259|GO:0004644|GO:0005524|GO:0046872|GO:0005829|GO:0010035|GO:0004641|GO:0006144|GO:0
006544|GO:0046654|GO:0009113|GO:0070062|GO:0006189 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_95067_PI430048170 0.0169138390584663 0.634789636450694 9.30480096474962
9.04291765283922 9.4707442403112 P P P 9.89524151799384 9.76377367460652 10.133619948409
P P P LNCV6_95067_PI430048170 mRNA
CTTCAACTCCTCTCACTTTTTAAAGCATTGATATTAGTATCTTCTCAGATACAGACCGTT NM_004446 RefSeq chr1 -
219968599 220046658 EPRS 2058 glutamyl-prolyl-tRNA synthetase
GO:0017148|GO:0005515|GO:0035613|GO:0010467|GO:0004818|GO:0004827|GO:0005524|GO:0017101|GO:0005
829|GO:0006418|GO:0005737|GO:0006424|GO:0006433|GO:0006461|GO:0071346|GO:0016020|GO:0030529 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79677_PI430048170 0.0059417804720399 3.69051542336982 2.80969126008517
2.00281573554826 2.35125224848564 A A A 0.293219300365014 0.651461234024354
0.652894254383903 A A A LNCV6_79677_PI430048170 mRNA
TTGTGAAGACAAGCTAGACGGCAGATGAAAGTTCTTGGCACAGAGTGAACACTTGATAAA NM_173174 RefSeq chr8
+ 27311481 27459391 PTK2B 2185 "protein tyrosine kinase 2 beta, transcript variant 1"
GO:0005515|GO:0042542|GO:0030307|GO:0008360|GO:0017146|GO:0001556|GO:0042220|GO:0032403|GO:0030
155|GO:0031175|GO:0007172|GO:0030838|GO:0007173|GO:0000165|GO:0043025|GO:0005856|GO:0004683|GO:0

038083|GO:0005938|GO:0030335|GO:0006950|GO:0014069|GO:0018108|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92819_PI430048170 0.00650823405085289 0.2883697871542644.37345646560516
4.13112917186832 4.90379236976601 P P P 6.10176120672744 6.30241672631058 6.4732717801259
P P P LNCV6_92819_PI430048170 mRNA
TTGTCAACGACAGTGGCAGTGATAAGGACAGTGATGCTGATGACAGTAAGACTGAAACCANM_014575RefSeq chr3
+ 159273246 159897366 SCHIP1 29970 "schwannomin interacting protein 1, transcript variant 1"
GO:0005515|GO:0008150|GO:0005737|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138193_PI430048170 0.7969882955288840.9913892048678440.309908372184305
0.2771801039604960.314418457452189A A A 0.3888331635010390.27366288691972
0.273633985943328A A A LNCV6_138193_PI430048170 mRNA
GTTGCAGTTGAAGTGTTTCTGGTTTATTTTTTGCTCAATGTGTAAAGAAACCTGCTGTGA NM_001258243 RefSeq
chr11 - 125094370 125111708 TMEM218 219854 "transmembrane protein 218, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129640_PI430048170 0.0152614082547725 1.2047515051068 10.4759591721141
10.3728786601149 10.4224334545259 P P P 10.0780748229051 10.1364890283494
10.2472007626271 P P P LNCV6_129640_PI430048170 mRNA
GCTGAGTTCTTCTGTAAAGAGATGAACGCAATGCCAATAAAATTGAACAAGAACAATGAT NM_004637RefSeq chr3
+ 128726135 128814798 RAB7A 7879 "RAB7A, member RAS oncogene family"
GO:0005515|GO:0097208|GO:0045453|GO:0003924|GO:0015031|GO:0005765|GO:0045022|GO:0005764|GO:0043
231|GO:0019886|GO:0007174|GO:0022615|GO:0030670|GO:0042147|GO:0032482|GO:0090383|GO:0090382|GO:0
090385|GO:0070062|GO:0005774|GO:0042470|GO:0005794|GO:0005770|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139713_PI430048170 0.0902543361231806 0.4734655235229890.970638092728032
0.2682232040571991.60980128649883 A A A 2.36570597317726 2.39048839214066
1.44974817557038 A P A LNCV6_139713_PI430048170 mRNA
CAAACTCACTCTCCAGCTCATTTCCTGCAGCCTCAAGTGAAACAATAAAGCAAAAGATCT NM_178348RefSeq chr1
+ 152827472 152828097 LCE1A 353131 late cornified envelope 1A GO:0031424 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_50005_PI430048170 0.1229536330462794.41680658007747 3.29979147587723 0.92237205250388
2.72741591305656 P A A 0.4019420521515280.5209806949536950.487395449151142A A A
LNCV6_50005_PI430048170 mRNA
AATGGGACCCACCACTGCGCAGCAACCTGAACAAACCATACCTGTTCTCTGTGCTGCTGG NM_022119RefSeq chr16
- 2852726 2858170 PRSS22 64063 "protease, serine, 22" GO:0004252|GO:0006508|GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111039_PI430048170 0.00691284022606108 1.56833607870964 4.70181119850049
4.51043410007645 4.37366955350578 P P P 4.03498291165869 3.81479153606575
3.79485129524486 P P P LNCV6_111039_PI430048170 mRNA
ATACGCCTGGAGCCAGGGAAGGCATCAGCCTCCCAGAGAGCAGCTCCCAGGACCAAAACA NM_144719RefSeq
chr3 - 42708381 42773253 CCDC13 152206 coiled-coil domain containing 13 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130105_PI430048170 0.0987387979266516 0.9764944881234310.34565031506063
0.3777615968266710.335670488449824A A A 0.3922318661359960.399791797761882
0.370179535262055A A A LNCV6_130105_PI430048170 mRNA
TTTTGACACAGTAGAGGTGTCTTCTACTCAAATAAAGTGCTAACAATAAGGAAAGGCTCA NM_001163857 RefSeq
chr22 - 36991118 37007836 TEX33 339669 "testis expressed 33, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138661_PI430048170 0.14903311574017 1.07351959393086 12.1666039433987
12.2549678659475 12.3196537296665 P P P 12.1320887118522 12.09279760055

12.2108572994527 P P P LNCV6_138661_PI430048170 mRNA
CTGGCAAGCTGTGCGTGACATTCTTTATGGCTTTTTGTATGTCAAATACTTCATACTAAA NM_001304452 RefSeq
chr1 + 10399117 10420511 PGD 5226 "phosphogluconate dehydrogenase, transcript variant 3"
GO:0050661|GO:0005975|GO:0019521|GO:0005634|GO:0044281|GO:0006098|GO:0009051|GO:0005829|GO:0004
616|GO:0019322|GO:0009405|GO:0055114|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134005_PI430048170 0.2106992436686140.78221930076568 0.35707245285258
0.35967765068608 0.479510655577108A A A 0.9011615464248820.932324028410484
0.361032322375809A A A LNCV6_134005_PI430048170 mRNA
CCTCACTTTCCATTCCCCAAAATGATGTGTATGTTGCTAATTTTCCAATAAACTCATATGNM_024702RefSeq chr17 -
82829433 82840055 ZNF750 79755 zinc finger protein 750
GO:0001077|GO:0008544|GO:0045944|GO:0005730|GO:0005634|GO:0001046|GO:0046872|GO:0030154|GO:0006
351|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133072_PI430048170 0.0519428527510161 1.89145057329539 4.20828912198787
4.08832155495209 3.87049920044285 P P P 2.80254755586161 3.61355294744247
2.86435709491993 P P P LNCV6_133072_PI430048170 mRNA
AAGCTCCCAAGTTGGGTACAAACCAGGATATTGGAGTTACTCTATCCTGGAGTTAACTAG NM_001852RefSeq chr1
- 40300490 40317267 COL9A21298 "collagen, type IX, alpha 2"
GO:0001501|GO:0030020|GO:0022617|GO:0030198|GO:0007411|GO:0030574|GO:0005578|GO:0005788|GO:0005
594|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140862_PI430048170 0.00517098897320026 0.4824969063920867.44694280808254
7.19907060571669 7.67504915459255 P P P 8.33205900752003 8.39567564901506
8.75052443984254 P P P LNCV6_140862_PI430048170 mRNA
GCTGGCATTCAGGGTGACATGATGGTACTAAATGTTTTCCATTAAAGTCTTCTATTTTAA NM_001128626 RefSeq
chr18 - 12446511 12657913 SPIRE1 56907 "spire-type actin nucleation factor 1, transcript variant 1"
GO:0048471|GO:0005794|GO:0030036|GO:0005886|GO:0070649|GO:0046907|GO:0003779|GO:0015031|GO:0032
154|GO:0036089|GO:0045010|GO:0051295|GO:0040038|GO:0048193|GO:0005856|GO:0016192|GO:0005938|GO:0
030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142911_PI430048170 0.1858063440942560.6125048287239210.490258625291479
1.18240659018768 0.266302453413295A A A 1.63803922753515 0.677104524333093
1.70087556815296 A A A LNCV6_142911_PI430048170 mRNA
CTAAGAAGGGAAAATATCCATCCTGAAGGTGTTTTTCATTCACTTTAATAGAAGGGCAAA NM_000882RefSeq chr3
+ 159988835 159996019 IL12A 3592 interleukin 12A
GO:0005515|GO:0050830|GO:0042520|GO:0005615|GO:0032816|GO:0045513|GO:0006955|GO:0005737|GO:0042
102|GO:0051135|GO:0032496|GO:0007050|GO:0045582|GO:0032729|GO:0046982|GO:0005143|GO:0042163|GO:0
050671|GO:0042832|GO:0048662|GO:0097191|GO:0009615|GO:0005125|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142552_PI430048170 0.42113090675585 1.07635331824878 7.22481398675525
7.48194093663103 7.37890388933535 P P P 7.17984491353228 7.13883545481937 7.4410680174817
P P P LNCV6_142552_PI430048170 mRNA
GTATTGCATTTATATCTTTTTACTACAGTGATCTGTGACAGCAGCAGCTTCATGTTGTATNM_005749RefSeq chr17 -
50862225 50866354 TOB1 10140 "transducer of ERBB2, 1, transcript variant 1"
GO:0005515|GO:0017148|GO:0030971|GO:0008285|GO:0060212|GO:0003714|GO:0060213|GO:0046332|GO:0005
634|GO:0009967|GO:0030014|GO:0030514|GO:0005737|GO:0045668|GO:1900153|GO:0005070|GO:0007184 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130222_PI430048170 0.00207914353665489 0.4533159529752195.50206752013883
5.83911188948595 5.51430913547712 P P P 6.53180679788914 6.91407441344836
6.83234381696378 P P P LNCV6_130222_PI430048170 mRNA
CCCTCCCTTTGTATTTGGAGACAATGTGTTGTAATAAAGCTTAAAGTGGATGTTTTCAAA NM_004420RefSeq
chr11_KI270903v1_alt - 30577 48447 DUSP8 1850 dual specificity phosphatase 8

GO:0000188|GO:0005737|GO:0006470|GO:0005634|GO:0008138|GO:0035335|GO:0017017|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140712_PI430048170 0.0560838799716738 1.10931254036358 10.7110779894564 10.7285587229215 10.8211352554186 P P P 10.644356087157 10.5168086973652 10.6491844601967 P P P LNCV6_140712_PI430048170 mRNA ACAAAAAACAGCTGAAGAAATGCTCTGTAGATTGAGTTGCTGGAGGAGTGACAGCCAGGA NM_006649RefSeq chrX + 129906120 129929762 UTP14A10813 "UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast), transcript variant 1" GO:0030490|GO:0005515|GO:0032040|GO:0005730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127028_PI430048170 0.6941806125701561.20226925759319 0.336342922803645 1.45087999593574 0.33219776184919 A A A 0.4804691877801920.360678909894497 0.758614028856236A A A LNCV6_127028_PI430048170 mRNA ACTCTTCCTCATGATACCAGTGAAATGTATTGATTGTGTCCCCAGTTGTTACATAATTTG NM_018159RefSeq chrX - 51490010 51496607 NUDT11 55190 nudix (nucleoside diphosphate linked moiety X)-type motif 11 GO:0052846|GO:0052845|GO:0052844|GO:0052843|GO:0043647|GO:0008486|GO:0052848|GO:0052847|GO:0044281|GO:0046872|GO:0052840|GO:0005829|GO:0005622 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140439_PI430048170 0.0736062451323937 0.7547579323291599.47702837086883 9.39845829506986 9.63629012784441 P P P 9.67349727034926 9.90404884533961 10.1267384966452 P P P LNCV6_140439_PI430048170 mRNA CCTTGTTTCCATGGCCTGTTTGTATATTGTCTCAATAAAACTTGCATCAGCCGGTGGTGG NM_005207RefSeq chr22 + 20917425 20953749 CRKL 1399 v-crk avian sarcoma virus CT10 oncogene homolog-like GO:0005515|GO:0048011|GO:0001568|GO:0007254|GO:0048538|GO:0007265|GO:0009952|GO:0005829|GO:0007507|GO:0035556|GO:0060017|GO:0000186|GO:0005070|GO:0009887|GO:0004871|GO:0070062|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104108_PI430048170 0.000813359219375051 1.48217236357186 9.4494563806145 9.41110191927023 9.510698442548 P P P 8.96456815739423 8.88713611300957 8.81424833503907 P P P LNCV6_104108_PI430048170 mRNA TTTTCTTTGGTCCAGTTTCCCTTATGGGAGTCCTTAAAAGTGGATTTGCCGCTGCAGTCA NM_173471RefSeq chr3 + 66133609 66378927 SLC25A26 115286 "solute carrier family 25 (S-adenosylmethionine carrier), member 26, transcript variant 1" GO:0015805|GO:0005739|GO:0000095|GO:0005743|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136196_PI430048170 0.0263398901101009 0.5908372286726315.78009360854504 5.55673599899785 5.54290768383473 P P P 6.57759149343153 6.4821675577793 6.05899344796652 P P P LNCV6_136196_PI430048170 mRNA ATGCGTTCCCCCTGTTAGCTACATTTGTGATCACATACCCTTCTTTTAAGTGAATTTTTT NM_025081RefSeq chr14 + 24398785 24419288 NYNRIN57523 NYN domain and retroviral integrase containing GO:0008150|GO:0003674|GO:0015074|GO:0016021|GO:0005575|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135292_PI430048170 0.1604481987663540.7726633924166072.94912466372809 2.59518014768926 2.3087438867017 A A A 2.92226347874257 3.07724644612621 3.03693809879397 P P P LNCV6_135292_PI430048170 mRNA GTCACTAAAACACCACATTTGGTTATATAAAAAGTCCCTTTTGCTGTAAAAGGAACACAG NM_002898RefSeq chr12 + 56521824 56596196 RBMS2 5939 "RNA binding motif, single stranded interacting protein 2" GO:0006396|GO:0000166|GO:0003723|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144733_PI430048170 0.4511142457798810.7776266902746360.388990352789538 2.49228088281597 1.15231194139231 A A A 2.25391163484925 1.42334169124007 2.11308013138216 A A A LNCV6_144733_PI430048170 mRNA TGATGACTAAATGGAGTAAGGCAGGGAGGATACACTGTGCTTGGCTCATTAAAGACATTT NM_001304367 RefSeq chr20 + 35968580 35974955 CNBD2 140894 "cyclic nucleotide binding domain containing 2, transcript

variant 3" GO:0030552|GO:0007283|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143225_PI430048170 0.1520956924867910.611399173610249 1.2800041970061
2.50388080576704 2.06116990792089 A A A 2.84307909644728 2.79811184442492
2.57144265131149 P P P LNCV6_143225_PI430048170 mRNA
TTGGGAAGCTGCTGCTCTTGAATGGGTTTTGGAAGTTACACAAAATCTCCCTCTAACCAC NM_001044370 RefSeq
chr22 + 43412013 43506920 MPPED1 758 metallophosphoesterase domain containing 1
GO:0008150|GO:0003674|GO:0016787|GO:0008152|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_98519_PI430048170 0.2515210962758050.7010400295712144.59375632275025 3.55148006772159
4.73185500298537 P P P 4.61002162181671 4.98585559558996 5.04285420450731 P P P
LNCV6_98519_PI430048170 mRNA
CTAGCATTATCATCTTAATGACAAAGGGAATAATGAACTAGAAACCAGCAAGTGAAAGTG NM_152388 RefSeq chr2
- 201620183 201642944 TMEM237 65062 "transmembrane protein 237, transcript variant 2"
GO:0042384|GO:0030111|GO:0016020|GO:0035869|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141256_PI430048170 0.0213184384107021 0.7434792984378119.10129709027942
8.9184001989575 8.81139738680938 P P P 9.42962471602301 9.39965187643519
9.29637281939983 P P P LNCV6_141256_PI430048170 mRNA
TTGGGACAAATAAAGGATTCTCATGGGAAGGGGAGGACCCCTCCTTCCCAACTTATGGCA NM_001288724 RefSeq
chr10 + 102394109 102402529 NFKB2 4791 "nuclear factor of kappa light polypeptide gene enhancer in
B-cells 2 (p49/p100), transcript variant 3"
GO:0005515|GO:0034142|GO:0003700|GO:0007249|GO:0005634|GO:0048536|GO:0005829|GO:0002756|GO:0005
737|GO:0051092|GO:0006954|GO:0030198|GO:0045944|GO:0002755|GO:0032481|GO:0002467|GO:0033257|GO:0
034097|GO:0034138|GO:0006355|GO:0038124|GO:0038123|GO:0002268|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132243_PI430048170 0.6826719693066811.15956421260394 2.67384470806572
2.81489094269866 1.71836447590352 A A A 1.72882694437997 2.12705900362992
2.74985766684299 A A P LNCV6_132243_PI430048170 mRNA
GTGTACTTTCTAACATCCATGAACATTGTGGTCCCCACCTGAAGTTTCACTTTGCATGTT NM_014180 RefSeq chr5
+ 154941072 154969411 MRPL2229093 "mitochondrial ribosomal protein L22, transcript variant 1"
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0015
934 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144281_PI430048170 0.2212384712210550.9182760392723389.67939309533353
9.81454986271269 9.78614299823439 P P P 9.88319989756337 9.76067443463905
9.99888180685401 P P P LNCV6_144281_PI430048170 mRNA
TACGTAGAGGTACGCTTTTTTCCTCAGGCTTAAACCTTTGCCACTGATATTAATAATAAA NM_001039613 RefSeq
chr2 + 9474540 9488462 IAH1 285148 isoamyl acetate-hydrolyzing esterase 1 homolog (S.
cerevisiae) GO:0016042|GO:0016788|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128132_PI430048170 0.0138463273344067 0.7505163529745079.0166638716983
8.91044411202631 8.9998976176176 P P P 9.27076065199142 9.50843855676412 9.3823726767582
P P P LNCV6_128132_PI430048170 mRNA
TAGATGTCGTGTTTTGGATGCTGTGTTTTCAATAAATGCCTCTGGGGCCCTGCTTTTACC NM_001010866 RefSeq
chr1 + 9588873 9604962 TMEM201 199953 "transmembrane protein 201, transcript variant 2"
GO:0010761|GO:0051015|GO:0007097|GO:0005637|GO:0016021|GO:0005521 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127138_PI430048170 0.6360788928775051.22134121367798 2.1964144201181
1.63726794324194 0.745330424734603 A A A 1.12039441098324 2.04738994709431
0.448553182735857 A A A LNCV6_127138_PI430048170 mRNA
ACTTTGTCCAAGTCCATTGTCATCTCTCCAGCTAAGACAGCTTACTTGGCTCATCGTTCA NM_006492 RefSeq chr1

- 110060374 110070700 ALX3 257 ALX homeobox 3
GO:0043565|GO:0007389|GO:0006355|GO:0035116|GO:0048704|GO:0042981|GO:0005634|GO:0035115|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136202_PI430048170 0.7942704861555610.9699130591435882.10890600264358
1.89721073221693 1.48962727877381 A A A 1.80431498588441 2.09342794559236
1.77524218553844 A A A LNCV6_136202_PI430048170 mRNA
TCGGGTGTTACAGGTACAAGTAGGTATGTTGCAGAGGAAAATAAATATCAAACTGTATAC NM_001039771 RefSeq
chr14 - 24426533 24429525 CBLN3 643866 cerebellin 3 precursor
GO:0030054|GO:0005794|GO:0005783|GO:0045202|GO:0005615 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143409_PI430048170 0.00300891303236094 0.2360958280119431.11243169422574
0.4962264404098160.481711745426643A A A 2.93817859744833 2.59588942561456
2.87510412463729 P P P LNCV6_143409_PI430048170 mRNA
TAGCCGTAGTCTATAATTCAGGAATGCTTTATAACCATCAGAAGCCATTATTTGCACTAC NM_001656RefSeq chr5
- 65589679 65624360 TRIM23 373 "tripartite motif containing 23, transcript variant alpha"
GO:0005515|GO:0004842|GO:0016567|GO:0007264|GO:0016874|GO:0003924|GO:0005634|GO:0043085|GO:0005
525|GO:0005765|GO:0042802|GO:0000139|GO:0016032|GO:0008270|GO:0019003|GO:0008047|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132111_PI430048170 0.9124708751435581.01129203695231 3.83392956113056
3.31161025765645 3.48989292741259 P P P 3.85878304324633 3.56616768304358
3.11693828808013 P P P LNCV6_132111_PI430048170 mRNA
CCTGTCTGGGAAGATTTTGAAAACAGGACAAAGAAAACATCATTTTAAAATGTCTTCAGC NM_022550RefSeq chr5
+ 83077497 83353760 XRCC4 7518 "X-ray repair complementing defective repair in Chinese hamster
cells 4, transcript variant 3"
GO:0005515|GO:0051351|GO:0000793|GO:0030054|GO:0010165|GO:0016874|GO:0005634|GO:0048146|GO:0006
303|GO:0006302|GO:0005829|GO:0043524|GO:0050769|GO:0016032|GO:0002328|GO:0005958|GO:0010332|GO:0
071285|GO:0005813|GO:0033077|GO:0033152|GO:0045190|GO:0007417|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106546_PI430048170 0.4969916751619911.01533387075329 0.336319764270885
0.2486947624063010.277951411239521A A A 0.2577014373083450.282867913994843
0.257771544772163A A A LNCV6_106546_PI430048170 mRNA
CTGATGTCTGCCTGAAAGCCCCATGAAGAAAAATAAAACACCTTGTACTTTATTTTCTAT NM_002351RefSeq chrX
+ 124346281 124373161 SH2D1A 4068 "SH2 domain containing 1A, transcript variant 1"
GO:0005515|GO:0006968|GO:0005737|GO:0006959|GO:0005070|GO:0045954|GO:0007267|GO:0009967 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129612_PI430048170 0.1938458412091621.10232500399284 9.21082554767235 9.105244480411
9.31860242179009 P P P 9.0677766408934 8.95773345739439 9.18633622000058 P P P
LNCV6_129612_PI430048170 mRNA
CTGAGACAACAAGTTGTCACCAGCAGAAGATAGATAATATGACCTTTATTAACTTGATGA NM_001293RefSeq chr11
- 77616150 77637806 CLNS1A 1207 "chloride channel, nucleotide-sensitive, 1A"
GO:0005515|GO:0006821|GO:0010467|GO:0005886|GO:0005634|GO:0034660|GO:0000387|GO:0034709|GO:0005
829|GO:0006884|GO:0005737|GO:0034715|GO:0005654|GO:0005856 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_72814_PI430048170 0.3784567464117250.8478028877964060.2747851813025510.484411688721009
0.320961935205374A A A 0.5130547550491810.9325908688098780.280727958099907A A A
LNCV6_72814_PI430048170 mRNA
TAGCCCTGGATGGAAGCAACTGGCAAAGAATAGATCTTTTTAACTTTCAAACAGATGTAG NM_012157RefSeq chr3
+ 33277441 33387265 FBXL2 25827 "F-box and leucine-rich repeat protein 2, transcript variant 1"
GO:0005515|GO:0005516|GO:0004842|GO:0006513|GO:0016567|GO:0019903|GO:0031146|GO:0014066|GO:0005

737|GO:0016020|GO:0006508|GO:0010506|GO:0016032|GO:0006464|GO:0019005 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127118_PI430048170 0.4935732338960291.04930893088236 0.615159031378658
0.36258920832547 0.413551569935702 A A A 0.4599398823664990.379982052670503
0.353458830371009 A A A LNCV6_127118_PI430048170 mRNA
TGTTTATGCTGCTCCTGATATAACACTTTCCAGCCTATAGCAGAAGCACATTTTCAGACT NM_203281 RefSeq chrX
+ 15500776 15556529 BMX 660 "BMX non-receptor tyrosine kinase, transcript variant 1"
GO:0050853|GO:0005515|GO:0050852|GO:0006921|GO:0030154|GO:0046872|GO:0005829|GO:0035556|GO:0046
777|GO:0042127|GO:0004871|GO:0007155|GO:0038083|GO:0005102|GO:0006915|GO:0032587|GO:0005524|GO:0
031234|GO:0002250|GO:0007165|GO:0045087|GO:0006468|GO:0007498|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129041_PI430048170 0.000136703243952181 0.1838156684573674.68635522320056
4.42434536508802 4.54865640316081 P P P 6.79189097812553 7.00575335683736
7.17876277003878 P P P LNCV6_129041_PI430048170 mRNA
GTGTGAGGATTAAGCCCTTAGTCTGCTCTTGCAATTATTCAAATGACAAATTAAATTTGC NM_001130007 RefSeq
chr16 - 11868127 11916662 GSPT1 2935 "G1 to S phase transition 1, transcript variant 3"
GO:0005622|GO:0005515|GO:0000082|GO:0000184|GO:0006479|GO:0003924|GO:0006415|GO:0005525|GO:0003
747 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127481_PI430048170 0.0236760172068034 1.32414355969501 7.8502863483896
7.90624504554427 7.65856056795329 P P P 7.46594522406505 7.50055709590814
7.23022639445049 P P P LNCV6_127481_PI430048170 mRNA
TATTATAAAGCACTGAAATAAGTTAAATAAACAGGTGGGAGGCTGGGCAGTCCCCCAGCC NM_014748 RefSeq chr2
+ 27370495 27377533 SNX17 9784 "sorting nexin 17, transcript variant 1"
GO:0005515|GO:0006707|GO:0005794|GO:0005102|GO:0008022|GO:0006886|GO:0006898|GO:0043231|GO:0005
829|GO:0043234|GO:0007165|GO:0005737|GO:0016020|GO:0030100|GO:0016197|GO:0016023|GO:0035091|GO:0
030659|GO:0005769|GO:0010008|GO:0050750|GO:0005768 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_46891_PI430048170 0.0657643356283132 0.9353451126732210.317595482238187
0.3163132551487170.312180418611957 A A A 0.4597893626490140.403526965980527
0.370654397334591 A A A LNCV6_46891_PI430048170 mRNA
TTAGAGTACCCACGGAAAACTTGTTTACCTTGTCACCATGAGTAAAAGTTAATTCCCACT NM_000564 RefSeq chr3
- 3066323 3110374 IL5RA 3568 "interleukin 5 receptor, alpha, transcript variant 1"
GO:0005515|GO:0002437|GO:0007165|GO:0005886|GO:0008283|GO:0038043|GO:0004914|GO:0032674|GO:0016
021|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133266_PI430048170 0.00768735617424328 0.3914266458939916.69810218542603
6.58804362011818 6.74935957389697 P P P 7.74081830197595 8.05345404446058
8.25897723169936 P P P LNCV6_133266_PI430048170 mRNA
GTCTGCATTCATGTATAATAGCCATTTTATGCACAGATGAGGTGATTCCCACACTTTTTT NM_138635 RefSeq chr7
- 44826888 44848126 H2AFV 94239 "H2A histone family, member V, transcript variant 2"
GO:0008150|GO:0003674|GO:0046982|GO:0005634|GO:0000786|GO:0003677|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130574_PI430048170 0.0499105483226744 1.32811190501199 7.55147436138624
7.47832309338739 7.2090048907145 P P P 7.06224352196708 7.01953420547962
6.94869755340803 P P P LNCV6_130574_PI430048170 mRNA
TTCAGTATCTTTCTCCGTGGTTTTGTGAAATAAACTCAAGTACAAAGCAGACAGCCCAAA NM_001302826 RefSeq
chr11 - 7665094 7674243 CYB5R2 51700 "cytochrome b5 reductase 2, transcript variant 1"
GO:0005739|GO:0016020|GO:0004128|GO:0016126|GO:0005634|GO:0055114 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132585_PI430048170 0.4937603586002021.0455782155467 13.04691688484

12.8959915906616 12.8409638532931 P P P 12.9105310890339 12.9340068244904
12.7473153277223 P P P LNCV6_132585_PI430048170 mRNA
ATCGGCAGTTGGGAGGGGCGCTCTGAGATTAAAGAGTTTTACCTCTGAGATAAATGTGAA NM_032375 RefSeq chr19
- 49869032 49877387 AKT1S1 84335 "AKT1 substrate 1 (proline-rich), transcript variant 1"
GO:0005515|GO:0048011|GO:0032007|GO:0048015|GO:0005829|GO:0034605|GO:0043523|GO:0045792|GO:0005
737|GO:0007173|GO:0031931|GO:0008543|GO:0045087|GO:0005654|GO:0006469|GO:0038095|GO:1900034 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142873_PI430048170 0.1415738280019251.44999194044019 10.4586239752187
10.3640084045463 10.3607622387825 P P P 10.3063297482585 9.61675313453545
9.52138313582019 P P P LNCV6_142873_PI430048170 mRNA
CAAAAGTCTGTAAACTGGTCTGTTTGCCAAAGTGAACACTGGATGACTAAGGAGCTGAAG NM_001017916 RefSeq
chr17 - 63432303 63446184 CYB561 1534 "cytochrome b561, transcript variant 2"
GO:0000293|GO:0022865|GO:0016021|GO:0022900|GO:0055085|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142097_PI430048170 0.2465698033930940.6733129855714053.51616464231478
2.60143187928193 4.05669580104559 P A P 4.25238008172458 4.04315024246651
3.92380285756926 P P P LNCV6_142097_PI430048170 mRNA
GTTCAGACAAATCTTCTAGATCTGCTTCACCCAGCATATTTTCTATTCAGTGATATAAAG NM_032246 RefSeq chr15
- 82041777 82046143 MEX3B 84206 mex-3 RNA binding family member B
GO:0005737|GO:0046777|GO:0000932|GO:0005509|GO:0008270|GO:0006468|GO:0005654 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140363_PI430048170 0.00624041094026817 0.4361039922983026.03684374674612
6.03711238702479 6.54826588540438 P P P 7.47319486531741 7.19523783671172
7.58115977404684 P P P LNCV6_140363_PI430048170 mRNA
GTTTAACTCATATTCTGCACGATCTGTATATAGTACATCAAACTTAGAGGTGTGACCTTA NM_003368 RefSeq chr1
+ 62436711 62451804 USP1 7398 "ubiquitin specific peptidase 1, transcript variant 1"
GO:0005515|GO:0016579|GO:0004843|GO:0005634|GO:0004197|GO:0001501|GO:0006281|GO:0006282|GO:0061
136|GO:0035520|GO:0005654|GO:0043161|GO:0009411 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135636_PI430048170 0.1557581313125460.2801325757409910.439438035222472
0.2850451261459610.338419831622482A A A 2.58382617143194 2.65151741270358
0.511263588172177P P A LNCV6_135636_PI430048170 mRNA
CTCTCTCTGCAGTTATTTAATGCCTGTGTCAGATCTACTGTAAAAAGAGGATTAAGTAAA NM_001678 RefSeq chr17
+ 7650889 7657771 ATP1B2 482 "ATPase, Na+/K+ transporting, beta 2 polypeptide, transcript variant 1"
GO:0005515|GO:0005886|GO:0030007|GO:0050821|GO:0006883|GO:0010107|GO:0032781|GO:0086064|GO:0050
900|GO:0005890|GO:0055085|GO:0005737|GO:0016324|GO:0086009|GO:0034220|GO:0007596|GO:0006810|GO:0
051117|GO:0007155|GO:0001671|GO:0005391 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131574_PI430048170 0.68858357512297 1.0389997254719 10.0593741166689
10.1537816117907 10.3671258556783 P P P 10.0422175289762 10.055636173316
10.3172805114234 P P P LNCV6_131574_PI430048170 mRNA
GTGAAGGTGTATTTTCAGTGCTACCCGCTAGCTGATTTTAACTTTAGGAATAAAATTAGT NM_194271 RefSeq chr12
+ 121400117 121424352 RNF34 80196 "ring finger protein 34, E3 ubiquitin protein ligase, transcript variant
1"
GO:0005515|GO:0016567|GO:0005886|GO:0016874|GO:0005634|GO:0035872|GO:0070417|GO:0005829|GO:0012
505|GO:0002039|GO:0005737|GO:0042787|GO:0016607|GO:2001271|GO:2000374|GO:0043161|GO:0008270|GO:0
070936|GO:0031625. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82296_PI430048170 0.2190073253041141.17188501901288 7.12949356635645 6.70320858292121
6.97241074958242 P P P 6.61941374427098 6.87337174011308 6.64374247687929 P P P
LNCV6_82296_PI430048170 mRNA
AGCACAAGATTGTGATGGAGACCGTTCCGGTGCTGAAGGCCCAGGCGGATATCTACAAGG NM_001099857

RefSeq chrX + 154547346 154565046 IKBKG 8517 "inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma, transcript variant 1"
GO:0005515|GO:0072686|GO:0007249|GO:0051403|GO:0042803|GO:0005622|GO:0002756|GO:0002755|GO:0043123|GO:0070530|GO:0031625|GO:0038124|GO:0038123|GO:0046982|GO:0034134|GO:0019904|GO:0002224|GO:0000922|GO:0051650|GO:0045087|GO:0034166|GO:0035666|GO:0034162|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138922_PI430048170 0.0399377626254874 0.74369357150743910.4277770790595 10.0898695896831 10.1124304709036 P P P 10.7455613070636 10.6105415119238 10.5752943649678 P P P LNCV6_138922_PI430048170 mRNA TGGTAGTCCATTGAAGAAGAGAGTTTGAAAGTTGTATACTGTTAATGACTGTCTGCCCAT NM_020810RefSeq chr14 - 60971448 60981079 TRMT5 57570 tRNA methyltransferase 5
GO:0005759|GO:0030488|GO:0052906|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143503_PI430048170 0.3200535294622820.6268055862317840.282867913994843 0.9684686609901840.510275505632452A A A 1.32684257508745 0.342358428505409 1.83137633103437 A A A LNCV6_143503_PI430048170 mRNA CTCCCGTTAAGTCCTTAACTTTTCTGTACCTCTTCTGTTTTTGTAAAACAGATTAAGGAT NM_001114938 RefSeq chr1 - 45620043 45624059 CCDC17 149483 "coiled-coil domain containing 17, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137498_PI430048170 0.3895930071997160.6727437357829570.511200070853913 0.4022855918699960.272670434581566A A A 0.3705889340618261.66614522920746 0.497936419369248A A A LNCV6_137498_PI430048170 mRNA CTGAGCCTGATATTGATATGGTTTTAAGAAGCAGTTGTACCAAGTGAAATTATTTTGGAG NM_000958RefSeq chr5 + 40679929 40693736 PTGER4 5734 prostaglandin E receptor 4 (subtype EP4)
GO:0005515|GO:0005886|GO:0051492|GO:0007254|GO:0050715|GO:0050710|GO:0004957|GO:0033624|GO:2000420|GO:0009612|GO:0060348|GO:0042093|GO:0006955|GO:0030278|GO:0050728|GO:0050729|GO:0032496|GO:0007188|GO:0016021|GO:0071260|GO:0070371 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130649_PI430048170 0.6994180494039080.96214372437209 10.5937771904833 10.0129056717394 10.2158655052615 P P P 10.3704209630676 10.3539907243545 10.3260007722161 P P P LNCV6_130649_PI430048170 mRNA GTGTGTGTGTGTGTAATTCTAATGTGAAAGGCACTAGCTGTCTAATAGTTTCATGTATCA NM_001277127 RefSeq chr3 - 169839240 169869935 LRRC31 79782 "leucine rich repeat containing 31, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127250_PI430048170 0.9795369466778340.9162525236319472.71195587134589 3.0254848373546 2.47094941991811 A P A 3.50380984044215 2.860902063719 1.79921111826649 P P A LNCV6_127250_PI430048170 mRNA TCCACATCTTGCAACCTTAAGTCTCCCTTAGAGTGGGGCTTCTGCTACCCTAAAAACTTT NM_178466RefSeq chr20 + 33217309 33227806 BPIFA3 128861 "BPI fold containing family A, member 3, transcript variant 1"
GO:0005576|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131937_PI430048170 0.9062613788850240.9378459341175612.43670807799951 0.8898731325347521.85009957097364 A A A 2.04244320983318 2.49043034654824 0.890622049403353A P A LNCV6_131937_PI430048170 mRNA CCAATCTTGACTATTCAGAATGCTGTTTATTTAGTGATGAGGATTAGCACTTGATTGAAG NM_022168RefSeq chr2 - 162267078 162318708 IFIH1 64135 interferon induced with helicase C domain 1
GO:0003725|GO:0005515|GO:0032728|GO:0003727|GO:0034344|GO:0032727|GO:0016925|GO:0004386|GO:0042981|GO:0005634|GO:0009615|GO:0003677|GO:0005524|GO:0005829|GO:0045087|GO:0039528|GO:0043021|GO:0009597|GO:0016032|GO:0008270|GO:0032480 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93049_PI430048170 0.1029196934074331.33703137865132 0.6584287372183041.08532323798007 0.613718185413448A A A 0.28440008318008 0.4089397037227320.450321983872705A A A LNCV6_93049_PI430048170 mRNA

CCTTCCTCTAAGAAAATTAAGCACTGCAAATTAAAGAAGAAGAGTAAAGAAGAAGGAGCC NM_001195190 RefSeq chr1 + 173635521 173637133 LOC730159 NA uncharacterized LOC730159 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77348_PI430048170 0.3194011416361920.8753932241872885.30864076608885 5.63724593306305 5.55527821332739 P P P 5.53182709347048 5.58544126578243 5.94407415757705 P P P LNCV6_77348_PI430048170 mRNA
CATAGAATTTATGGACACTTTCTTCTTCATCCTGCGCAAGAACAACCACCAGATCACGGT NM_001301856 RefSeq chr6 - 53267397 53348945 ELOVL5 60481 "ELOVL fatty acid elongase 5, transcript variant 5" GO:0005515|GO:0006636|GO:0005783|GO:0044281|GO:0035338|GO:0036109|GO:0043651|GO:0033559|GO:0009922|GO:0016020|GO:0043025|GO:0005789|GO:0019432|GO:0034625|GO:0016021|GO:0034626|GO:0042761|GO:0044255 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136971_PI430048170 0.6627004452125790.77797491553216 0.279210289344859 0.28410858971295 1.29244576826331 A A A 1.84460660023553 0.503410309197397 0.338429178593228 A A A LNCV6_136971_PI430048170 mRNA
GACTAGAAGACTGTAAATAAGATACCAAAGGCACTATTTTAGCTATGTTTTTCCCATCAG NM_024829 RefSeq chr12 - 14503662 14567857 PLBD1 79887 phospholipase B domain containing 1 GO:0016042|GO:0016787|GO:0036149|GO:0044281|GO:0006644|GO:0005764|GO:0036151|GO:0046474|GO:0036152|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136908_PI430048170 0.0242033543760990.7683085899189897.04330020747437 6.87853277313845 7.11922508616353 P P P 7.30426886872457 7.32275905826888 7.55174504138519 P P P LNCV6_136908_PI430048170 mRNA
GTTTTGTACATAACTTCAGATACTTGTGAACATGCCTTATATTTGTCCAACAACTGTCAG NM_003316 RefSeq chr21 + 37082946 37203107 TTC3 7267 "tetratricopeptide repeat domain 3, transcript variant 1" GO:0005773|GO:0005739|GO:0005515|GO:0006511|GO:0004842|GO:0045665|GO:0016874|GO:0010771|GO:0008270|GO:0005654|GO:0005634|GO:0070936 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89108_PI430048170 0.1211990855640241.38156519902899 11.559790368077 11.4835791706527 11.3473172227441 P P P 10.6550448236975 11.3371709428643 10.9248100298467 P P P LNCV6_89108_PI430048170 mRNA
ATTCAGCCTCGTCTCTTTACAGAAGTAGTTTTGTTCATGAAATAAAGACTCTTGGACTTG NM_001037 RefSeq chr19 + 35030687 35040449 SCN1B 6324 "sodium channel, voltage gated, type I beta subunit, transcript variant a" GO:0046684|GO:0051899|GO:0021966|GO:0007268|GO:0060307|GO:0086091|GO:0019227|GO:0060048|GO:0040011|GO:0060371|GO:0014704|GO:0010765|GO:0007411|GO:0086002|GO:0001518|GO:0035725|GO:0007155|GO:0061337|GO:0086006|GO:0086047|GO:0005248|GO:0030315|GO:0005576|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138303_PI430048170 0.4876256412923880.7313157901607080.351880514876675 0.3104377125281920.39438124399436 A A A 0.2955058889632030.285175799086306 1.48140202441944 A A A LNCV6_138303_PI430048170 mRNA
GAGGAACAAAGATGTGAAAAATGCTCTTCTGAGAGTCATACATAGAAAACTTTTTCCATG NM_001003750 RefSeq chr11 + 56093307 56094240 OR8I2 NA "olfactory receptor, family 8, subfamily I, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127547_PI430048170 0.64641409590272 0.7097290300169220.330416800546926 0.3219308263873871.54027298937052 A A A 0.2700747035030332.24323416593159 0.757417159448345 A A A LNCV6_127547_PI430048170 mRNA
TGAACCCATGGAATGTTAGAAAAGAGATGCTGTCTTCAAGAAAATATGCCAATAATTCCT NM_198947 RefSeq chr11 + 59107184 59127416 FAM111B 374393 "family with sequence similarity 111, member B, transcript variant 1" GO:0008152|GO:0003824 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131533_PI430048170 0.0231999830097932 1.45895802079902 8.49134385533972 8.77287729944797 8.87839583045702 P P P 8.27289528485444 8.25361186100419

7.99175963023907 P P P LNCV6_131533_PI430048170 mRNA
TAAACAGTGTAGAAGGTCTTTTTAAGGCTCTAAATGTCAGGGTCTCCCATCCCCTGATGC NM_080625 RefSeq chr20
+ 32010441 32032181 CCM2L 140706 cerebral cavernous malformation 2-like
GO:0032091|GO:0008150|GO:0003674|GO:0042060|GO:0003222|GO:0034111|GO:0005575|GO:0090271|GO:0055
017|GO:0003209 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143031_PI430048170 0.466526870313939 1.20832425832263 3.55433229517868
3.95839789168813 3.38974619680143 P P P 3.72588781759254 2.57714809708585 3.5925037409609
P P P LNCV6_143031_PI430048170 mRNA
TCCAGCAAGGAGTTTACAGTCAAACAGGAGAGACATGCCTGTAGTTACATCCAGTGTGAT NM_138788 RefSeq chr11
+ 129815845 129860003 TMEM45B 120224 transmembrane protein 45B GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_78985_PI430048170 0.990860272336125 0.996442478018937 4.42507958053911 3.77090584680116
4.24727916743149 P P P 3.74830271390291 4.30879819222951 4.39646378688386 P P P
LNCV6_78985_PI430048170 mRNA
AGAAGTTAAAGATAAAGAGCATCTCCTGACTTCCACGAGGGAAATACTTCCAAGCCAATC NM_020725 RefSeq chr7
- 105604773 105876585 ATXN7L1 222255 "ataxin 7-like 1, transcript variant 1" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_139512_PI430048170 0.225759586263969 1.08047694542865 0.624392602331705
0.815850826174199 0.623405081854218 A A A 0.545062118155049 0.604117514481154
0.587457966955264 A A A LNCV6_139512_PI430048170 mRNA
CACGTTGTTTCACATCTGGTTAGGGGGCAGATTTTAAAATGTAGTTTTGTAATGTTACAT NM_053277 RefSeq chr21
+ 34669388 34718221 CLIC6 54102 chloride intracellular channel 6
GO:0005737|GO:0031749|GO:0005244|GO:0005886|GO:0034707|GO:0034765|GO:0008022|GO:0005254|GO:0042
803|GO:0031751|GO:0070062|GO:0031750 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136615_PI430048170 0.0183910685686372 0.270711644911605 2.27963229598353
1.56466789800125 2.87284060960931 A A A 3.76182760063454 4.42453035362668
4.38422829011186 P P P LNCV6_136615_PI430048170 mRNA
CTTCTTCTTGATCAAGAGAGCAGGTATAGTGTTTGTTTATTTTGTCTTAGGTATGGAAGA NM_001127892 RefSeq
chr16 - 51135974 51150597 SALL1 6299 "spalt-like transcription factor 1, transcript variant 2"
GO:0035137|GO:0005515|GO:0000792|GO:0008406|GO:0035136|GO:0001657|GO:0001658|GO:0031129|GO:0003
700|GO:0021553|GO:0030325|GO:0008013|GO:0021983|GO:0030177|GO:0045879|GO:0003281|GO:0005634|GO:0
046872|GO:0007507|GO:0005737|GO:0016581|GO:0045944|GO:0042473|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145107_PI430048170 0.187126229574706 1.51284152781002 2.68920051708408
3.25145054710371 3.31191514795083 A P P 1.92857119661934 3.07175623481095
2.29506259311178 A P A LNCV6_145107_PI430048170 mRNA
TTCTGATGTTTGTAACCAGACCCAGCTGTGTCATTAAACAGACCCGTTCTTGCTGTACCT NM_134268 RefSeq chr17
- 76527347 76537905 CYGB 114757 cytoglobin
GO:0043005|GO:0005737|GO:0004601|GO:0019825|GO:0005506|GO:0043025|GO:0005344|GO:0006979|GO:0055
114|GO:0020037|GO:0015671 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132121_PI430048170 0.4627838871015 0.97729980710253 0.389958085140411
0.406168920226759 0.287913527228423 A A A 0.378235635190311 0.42163193199507
0.386007263815568 A A A LNCV6_132121_PI430048170 mRNA
GCAATTGAATGAAGAAGCATTAACGAAAACCAATATTTAAGTACAGTGGACAGCTTAGGA NM_001137671 RefSeq
chr18 - 14511737 14543600 POTEC NA "POTE ankyrin domain family, member C" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_77740_PI430048170 0.0175652071521283 0.764398097672873 3.84639435816639
3.63150392766726 3.83695083761719 P P P 4.11393520691046 4.22246391025696
4.14917941230788 P P P LNCV6_77740_PI430048170 mRNA

GAAAAATCTAATCTCAGCAGCACATCAGTTACTACAAATGGGACAGGAGTAATTACAAGT NM_172105 RefSeq chr6 + 133241356 133532120 EYA4 2070 "EYA transcriptional coactivator and phosphatase 4, transcript variant 4"
GO:0005515|GO:0006355|GO:0007605|GO:0005634|GO:0007275|GO:0009653|GO:0046872|GO:0006351|GO:0035335|GO:0005737|GO:0006281|GO:0007601|GO:0004725|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138025_PI430048170 0.7308854546648260.92014532024073 0.473800762805393 0.6103154811607320.558481368964902 A A A 1.07015172164274 0.412837245254016 0.420010544225642 A A A LNCV6_138025_PI430048170 mRNA
ACTGTTTTCTCTGATCTCAATTACAGGTTGGATCTCACAAATAATAATGTCAGAGACAGA NM_002581 RefSeq chr9 + 116153791 116402321 PAPPA 5069 "pregnancy-associated plasma protein A, pappalysin 1"
GO:0007565|GO:0016020|GO:0006508|GO:0008270|GO:0005576|GO:0004222|GO:0044267|GO:0030154|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136739_PI430048170 0.0503463939445792 1.3676836766016 5.00103356113079 4.9432938193079 4.83394566374659 P P P 4.69129890753809 4.26421550450029 4.44037431792703 P P P LNCV6_136739_PI430048170 mRNA
AGGGAGTCAGTCTTCACTTGCACTGGGGGAACAGATGCTAATAAACTGTTTTTTAATGAA NM_000359 RefSeq chr14 - 24249113 24263210 TGM1 7051 transglutaminase 1
GO:0005515|GO:0031424|GO:0031224|GO:0001533|GO:0046872|GO:0005913|GO:0018149|GO:0030216|GO:0003810|GO:0009887|GO:0043163|GO:0006464|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145398_PI430048170 0.0818304889680838 1.42920660090162 1.61198542792399 1.22537612477497 1.69535492288953 A A A 1.13657574745496 0.651796895905896 1.18334094074706 A A A LNCV6_145398_PI430048170 mRNA
GCTTCCTCTACCACCAGCTATTCAAAGATACATATTATTTAAAGAGTATGATCTCTATGG NM_001290258 RefSeq chr7 + 123601866 123637880 ASB15 NA "ankyrin repeat and SOCS box containing 15, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133711_PI430048170 0.0498665731284944 2.37962175062138 3.90805790472216 5.05601798627398 4.57547793256807 P P P 3.53521856987127 2.71696854982962 3.60168667268797 P P P LNCV6_133711_PI430048170 mRNA
AGGATAGAAAGCTGTTTCCCACCTGTTTGCTTTTACCATTAAAAGGGAAACGTGCCTCTG NM_006018 RefSeq chr12 - 122714755 122716892 HCAR3 8843 hydroxycarboxylic acid receptor 3
GO:0007186|GO:0005886|GO:0005887|GO:0004930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140081_PI430048170 0.2121384679811220.92883648338247416.3463119596693 16.1594173689419 16.1738169686766 P P P 16.3762886647462 16.36401227592 16.2637289873649 P P P LNCV6_140081_PI430048170 mRNA
GTCGCCGTCTGTGAACAAGATTCCTCAAAATATTTTCTGTTAATAAATTGCCTTCATGTA NM_001025071 RefSeq chr5 - 150444228 150449756 RPS14 6208 "ribosomal protein S14, transcript variant 1"
GO:0048027|GO:0010467|GO:0003723|GO:0019058|GO:0045182|GO:0006412|GO:0006413|GO:0006414|GO:0005829|GO:0005739|GO:0030490|GO:0005737|GO:0000184|GO:0016032|GO:0070062|GO:0000028|GO:0003735|GO:0006614|GO:0019083|GO:0005730|GO:0000122|GO:0006415|GO:0006417|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135834_PI430048170 0.9099615252839691.00576985426356 0.354401662548291 0.52004301191144 0.402040500655599 A A A 0.5060177526279790.378692503676975 0.367818157269252 A A A LNCV6_135834_PI430048170 mRNA
CTTGATATTGAAAAGTGTAATAAACTTCATGCTCACCTATTGGAGATTTGGGAAGGTTGA NM_001164685 RefSeq chr6_KI270801v1_alt - 53391 246279 THEMIS NA "thymocyte selection associated, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144236_PI430048170 0.0793781383326043 0.6303490954387514.12361764233879 4.69144948412603 3.9742756866739 P P P 5.17282530758392 5.07540427180601

4.57222706870892 P P P LNCV6_144236_PI430048170 mRNA
ACTTTAATTTCAACATGAGCTACATGGTCATGAACACAATGCAACGCGACCCCACTCCAA NM_022358RefSeq chr20
+ 44745846 44752313 KCNK1560598 "potassium channel, two pore domain subfamily K, member 15"
GO:0005244|GO:0005267|GO:0034765|GO:0016021|GO:0071805 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_99412_PI430048170 0.00434571373420716 1.49214496072065 12.5102315051663
12.6100067570603 12.7651526056108 P P P 11.939917076847 12.0734597688383
12.1439637574733 P P P LNCV6_99412_PI430048170 mRNA
GGCCGTTCATGCAGACTTTTTTAACGATTTTGAAGATCTTTTTGATGATGATGACATCCA NM_138336RefSeq chr2
- 240126562 240136347 MYEOV2 150678 "myeloma overexpressed 2, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_136483_PI430048170 0.0357103839170194 0.7182278863196264.63713780970483
4.33869704863779 4.25630821493045 P P P 4.89485267853013 4.71647196114015
5.06112402979479 P P P LNCV6_136483_PI430048170 mRNA
TGCAACAAGCGCTTCATGCGCAGCGACCACCTGAGCAAACACATTAAGACGCACAACGGG NM_001145250
RefSeq chr2 + 174335092 174337540 SP9 NA Sp9 transcription factor NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145408_PI430048170 0.0273819813494799 0.7632312573946 3.54339155440754
3.78186955054777 3.49306590362719 P P P 4.08719337157085 4.03734297641539
3.87124289323589 P P P LNCV6_145408_PI430048170 mRNA
AATAACAATCATTGACATACTTTAGGGCTATTGTTTCAGGTGGGGGTGTATACATCCCAG NM_007214RefSeq chr6
- 107867755 107958278 SEC63 11231 SEC63 homolog (S. cerevisiae)
GO:0005515|GO:0006807|GO:0005783|GO:0006614|GO:0010259|GO:0031204|GO:0001889|GO:0016020|GO:0006
612|GO:0008565|GO:0005789|GO:0072001|GO:0004872|GO:0006620|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127678_PI430048170 0.6014927194232080.9801829540132240.404295151624992
0.3883887723982390.25154552456371 A A A 0.3551903584682660.405170606132965
0.374893879830519A A A LNCV6_127678_PI430048170 mRNA
CACACTCAGAGTTGGCATCTCACTGCACAGCAGTGAGGAGACTCGCACACTCTGTATCCT NM_170685RefSeq chr17
- 49838308 49848017 TAC4 255061 "tachykinin 4 (hemokinin), transcript variant alpha"
GO:0046878|GO:0008217|GO:0005102|GO:0007217|GO:0005576 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144658_PI430048170 0.0210453187345774 0.6361515508906048.21318848580448
8.24754298080971 8.14120115198363 P P P 8.62632809504008 8.95379568389535
8.95714930816072 P P P LNCV6_144658_PI430048170 mRNA
CCTTTCCCTAAAGACCCTAAATCTGAGGAATCAACAGGGCAGCAGATCTGTATATTTTTT NM_001150RefSeq chr15
- 89784894 89814840 ANPEP 290 alanyl (membrane) aminopeptidase
GO:0005793|GO:0002003|GO:0001525|GO:0009615|GO:0005765|GO:0005615|GO:0030154|GO:0005829|GO:0001
618|GO:0005887|GO:0004177|GO:0006508|GO:0016032|GO:0004872|GO:0008270|GO:0044267|GO:0009897|GO:0
008237|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52350_PI430048170 0.0422785429708702 0.6920406776915595.17655043663703
4.92719262858009 5.14471452213433 P P P 5.83160806159921 5.62738645819054
5.35617973626579 P P P LNCV6_52350_PI430048170 mRNA
TTCTCCAAGGAGAGGCACATCATGGACAGGACCCCCGAGAAACTGAAGAAGGAGCTGGAG NM_001261408
RefSeq chr1 - 93561785 93847150 BCAR3 8412 "breast cancer anti-estrogen resistance 3, transcript
variant 1"
GO:0043547|GO:0005515|GO:0005085|GO:0007165|GO:0033138|GO:0002089|GO:0007264|GO:0042493 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140507_PI430048170 0.9761181123800491.15561214589417 1.85590872610189

1.81621439031908 3.41145329600489 A A P 2.63754258812224 2.16884396450462
2.22274079012498 P A A LNCV6_140507_PI430048170 mRNA
ATATAGTGGACTGCTTCATCTCCAAGCCCTCAGAGAAGAACATTTTCACCCTCTTCATGG NM_005268RefSeq chr1
+ 34755046 34758512 GJB5 2709 "gap junction protein, beta 5, 31.1kDa"
GO:0007154|GO:0060713|GO:0008544|GO:0060708|GO:0005922|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136386_PI430048170 0.2325747022699520.7206660749146175.86912490785587
5.94980115338702 6.05883933449399 P P P 5.88826990234969 6.54384303397098
6.73938260727846 P P P LNCV6_136386_PI430048170 mRNA
CCACTGTTTTCTCAGATGTAAAATAAACCCACATGCAGTTCTTGATTTACACGGAAAAAA NM_005786RefSeq chr18
+ 75210754 75289950 TSHZ1 10194 teashirt zinc finger homeobox 1
GO:0006355|GO:0042474|GO:0005634|GO:0009952|GO:0003677|GO:0046872|GO:0006351|GO:0060023 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144171_PI430048170 0.4977188522696320.7233280975021460.49207330959177
0.4804471280121751.53791567571104 A A A 1.3088183803585 2.01028543111824
0.466428656978599A A A LNCV6_144171_PI430048170 mRNA
CTGAAAAATCAGCTGGGGCATATTTTTACCAATGATGAAGATGTCATTGCCCTGGTGAGC NM_152908RefSeq chr17
- 19678314 19716730 SLC47A2 146802 "solute carrier family 47 (multidrug and toxin extrusion),
member 2, transcript variant 1" GO:0015297|GO:0005886|GO:0006855|GO:0016021|GO:0055085|GO:0015238 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133633_PI430048170 0.00261331228345153 1.52207839407332 8.88922472635316
8.81918320183212 8.79232282007694 P P P 8.13620497507473 8.33194924532205
8.20937562371713 P P P LNCV6_133633_PI430048170 mRNA
CACTGCTCTCCTTTTAATCATGTATTCATCTATTTTAAATTGCCGGCGACGACTTTTGTC NM_032883RefSeq chr20 +
43916141 44069614 TOX2 84969 "TOX high mobility group box family member 2, transcript variant 3"
GO:0006355|GO:0003682|GO:0006338|GO:0005654|GO:0005634|GO:0003677|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137829_PI430048170 0.6839965747202740.8581461558382790.840230235332941
1.98121340387109 0.360080392161138A A A 0.5705723838715011.46852197618465
1.97466054404109 A A A LNCV6_137829_PI430048170 mRNA
AGATTTTGCCAGGAGGAGGAAGAGGTCTGTGTCACTCTAAAGGGAACTGTGACATTTCAA NM_005290RefSeq chr3
+ 98531898 98533150 GPR15 2838 G protein-coupled receptor 15
GO:0007186|GO:0005887|GO:0004930|GO:0072678 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92878_PI430048170 0.98857400151198 1.01631508317352 1.80247945233512 0.296399864839818
0.324403471767668A A A 0.408497931441 0.3270102402883791.71847707365781 A A A
LNCV6_92878_PI430048170 mRNA
ACAAGTTAATGATGGAAAATATTCATTTGAAAACATTCAGCGAGCATGGCGAGAGTACCT NM_001197113 RefSeq
chr3 + 159069251 159897366 IQCJ-SCHIP1 NA "IQCJ-SCHIP1 readthrough, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61937_PI430048170 0.0535780629003278 0.59131080557729 0.547586211588858
0.6329861266690480.55641600827654 A A A 0.9644214292541211.4018517866214
1.57908872948074 A A A LNCV6_61937_PI430048170 mRNA
TCTAAGGAAATTGCAAGACCTAACATGGCTGAAAGAGAAACAGAAACATCAAATTCTGAA NM_017661RefSeq chr15
- 56630175 56734086 ZNF280D 54816 "zinc finger protein 280D, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139282_PI430048170 0.4631580960305080.90691540387645 3.28353939757887
3.33837981867665 3.13271134536747 P P P 3.12632253910787 3.60962500189196
3.40895358049848 P P P LNCV6_139282_PI430048170 mRNA

TTGACAAAAATGCTGATGGCTACATCGACCTGGATGAGCTGAAGATAATGCTGCAGGCTA NM_003280 RefSeq chr3 - 52451090 52454041 TNNC1 7134 troponin C type 1 (slow) GO:0005515|GO:0005861|GO:0030049|GO:0055010|GO:0005509|GO:0015629|GO:0060048|GO:0042803|GO:0005829|GO:0005739|GO:0032972|GO:0006937|GO:0031014|GO:0051015|GO:0002086|GO:0031013|GO:0010038|GO:0043462|GO:0005654|GO:0048306 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141369_PI430048170 0.0204850548137726 0.6312314508646367.63392967844637 7.63392967844637 8.04909306906665 P P P 8.31519553751954 8.38833055301536 8.62698120149535 P P P LNCV6_141369_PI430048170 mRNA
GTGCATGTTTTAGGGATCAATTACCTAACTGTTCCTTGGTCTATTTATGTATAAGAATGC NM_005638 RefSeq chrY + 57067799 57130289 VAMP7 6845 "vesicle-associated membrane protein 7, transcript variant 1" GO:0005515|GO:0005802|GO:0030054|GO:0043312|GO:0045202|GO:0005765|GO:0006887|GO:0006906|GO:0043231|GO:0017156|GO:0030670|GO:0035577|GO:0070062|GO:0019905|GO:0005794|GO:0009986|GO:0008333|GO:0006892|GO:0048280|GO:0043308|GO:0030027|GO:0006897|GO:0006888|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127403_PI430048170 0.0878686016218966 0.7543737415110635.04126313635856 4.72082502780975 5.18595116244277 P P P 5.6224529842461 5.32029415941171 5.23429239413911 P P P LNCV6_127403_PI430048170 mRNA
AACCTCGTGGTGGTTATTGAAACAGATTTATTAGAAGGAGAGGGTAGGTGCAGAGCTGGA NM_017853 RefSeq chr16 - 72084856 72093640 TXNL4B 54957 "thioredoxin-like 4B, transcript variant 1" GO:0000245|GO:0007067|GO:0005681|GO:0005682|GO:0046540 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135367_PI430048170 1.87995457181395e-05 3.14282753356727 7.87009177367798 7.79376228145 7.86740374726863 P P P 6.24953778210847 6.20811409215469 6.11546150721773 P P P LNCV6_135367_PI430048170 mRNA
GTCTTGGTTGAGAGAATAACGTTGCAGTTCCCACAGGGCATGTGACTTTGAAAGAGACTA NM_001197247 RefSeq chr6 + 26365158 26378320 BTN3A211118 "butyrophilin, subfamily 3, member A2, transcript variant 3" GO:0072643|GO:0016020|GO:0005886|GO:0016021|GO:0002456 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127321_PI430048170 0.00133783218822341 0.43570262350771 11.2010627426092 11.2434991087125 11.1100296367271 P P P 12.211421461765 12.4605383617051 12.4671579497256 P P P LNCV6_127321_PI430048170 mRNA
TGCCTGCTCCACTTTTTCTACCTTGGAACTGTATTAGATAAAATCACTTCTGTTTGTTCA NM_005768 RefSeq chr12 - 6976184 7018538 LPCAT3 10162 lysophosphatidylcholine acyltransferase 3 GO:0036150|GO:0047184|GO:0016020|GO:0005789|GO:0044281|GO:0016021|GO:0006644|GO:0036151|GO:0097006|GO:0046474|GO:0036152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80209_PI430048170 0.5238343321604381.10220320411871 12.2026562653747 12.3947724227773 12.7109325348847 P P P 12.1217099582552 12.2323459722447 12.5452207925634 P P P LNCV6_80209_PI430048170 mRNA
TTATGTGCCGAATCACTGTGGGGAAAGGTCAGGAAGGTATAGTCCTTCAATAGGAAATTG NM_014078 RefSeq chr8 - 120395843 120445407 MRPL1328998 mitochondrial ribosomal protein L13 GO:0070124|GO:0005515|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005761|GO:0005743|GO:0006412|GO:0005762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119741_PI430048170 0.0179304885425755 0.7691732806733514.77130009096732 4.53853112809466 4.72878671881745 P P P 5.13283927030727 5.03878637959285 5.01047827621808 P P P LNCV6_119741_PI430048170 mRNA
ATTGGCTTTGCTTTTGGAGCCTTATACTGGAAGAAGAGACAGCCAAGTCTTACAAGGGCA NM_000899 RefSeq chr12 - 88492792 88580473 KITLG 4254 "KIT ligand, transcript variant b" GO:0005515|GO:0033026|GO:0005886|GO:0008283|GO:0001755|GO:0050731|GO:0046579|GO:0005615|GO:0035234|GO:0005737|GO:0007173|GO:0043406|GO:0045636|GO:0007155|GO:0005856|GO:0035162|GO:0048011|GO:0

048015|GO:0045740|GO:0005576|GO:0005125|GO:0097192|GO:0007165|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138456_PI430048170 0.5828019794700460.8294917349353450.412283291845355 0.95475652574217 0.487386873365169A A A 0.3366101141495931.42303290043126 0.75430774288093 A A A LNCV6_138456_PI430048170 mRNA GTGGCTTGCCCTGACATAAATCACTAGTTATTGAAGGCAAAATTCCGTAATGTTGAGAAT NM_080654RefSeq chr11 - 27348871 27363248 CCDC34 91057 "coiled-coil domain containing 34, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118824_PI430048170 0.0913266721652748 0.9212034971062066.89159135130548 6.78193075471932 6.86701544701025 P P P 6.92229063087881 6.92571816843415 7.0465316219617 P P P LNCV6_118824_PI430048170 mRNA CAAGTTGCTATGGCATTGTTCAAGTACCCACTGGACCGTGGTTTTGCAGGAAATGTGAAT NM_004641RefSeq chr10 + 21534171 21743630 MLLT10 8028 "myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10, transcript variant 1"
GO:0005515|GO:0005737|GO:0003700|GO:0045944|GO:0008270|GO:0005654|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130118_PI430048170 0.000558794083174816 0.3301937856395997.32015023077583 6.94338498146508 6.99598411815708 P P P 8.51149591025807 8.85446953564811 8.69859019569115 P P P LNCV6_130118_PI430048170 mRNA GCGTTATATTGCGATTGGCACTTTATGCTGACCATCGGTAACGGACATTTATCACTGGAG NM_145260RefSeq chr2 - 19351484 19358611 OSR1 130497 odd-skipped related transciption factor 1
GO:0008406|GO:0001657|GO:0071300|GO:0048793|GO:0001655|GO:0072239|GO:0072234|GO:0072183|GO:0030154|GO:0072075|GO:0072180|GO:0007507|GO:0002062|GO:0072133|GO:0050679|GO:0030501|GO:0090094|GO:0072190|GO:0072208|GO:0000122|GO:0072207|GO:0072184|GO:0060272|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141485_PI430048170 0.20610420024783 0.8221938556723764.39815344125614 4.71353801144323 4.71980232284712 P P P 4.604583176041 4.96719382065275 5.08733065887006 P P P LNCV6_141485_PI430048170 mRNA GGGTAGATCACTTTAGCTATTAGGAAGAGGATGGGGTAGTGTACAGTATATATTTTTAAA NM_002540RefSeq chr9 + 128456005 128501292 ODF2 4957 "outer dense fiber of sperm tails 2, transcript variant 9"
GO:0005515|GO:0017137|GO:0005813|GO:0006996|GO:0005814|GO:0005874|GO:0007286|GO:0005634|GO:0007275|GO:0072372|GO:0036064|GO:0001520|GO:0005829|GO:0000922|GO:0005198|GO:0000086|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69699_PI430048170 0.59221138886057 0.9129641498706684.20583690013628 3.41739318666365 3.3005392390138 P P P 3.95117590154057 3.63554425860422 3.88868951714566 P P P LNCV6_69699_PI430048170 mRNA ATTTCATACTTTGGTTGCATGAAGGCTGCCCCCATGAAAGAAGCAAACATCCGAGGACAA NM_170735RefSeq chr11 - 27654894 27659649 BDNF 627 "brain-derived neurotrophic factor, transcript variant 1"
GO:0001657|GO:0061193|GO:0010996|GO:0033189|GO:0009642|GO:0005615|GO:0007406|GO:0014076|GO:0007412|GO:0043524|GO:0007411|GO:0071356|GO:0051602|GO:0006120|GO:0072347|GO:0001662|GO:0007612|GO:0030061|GO:0051965|GO:0048839|GO:0005169|GO:0060079|GO:0007214|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129301_PI430048170 0.0349629668672709 1.22977407690976 8.32977152709031 8.55315766128911 8.37246795606143 P P P 8.12189453444391 8.07412772273431 8.17239433711299 P P P LNCV6_129301_PI430048170 mRNA GTAAAAGCTTTGGTTTGTGTTCGTGTTTTGTTTGTTTCACTTGTTTCCCTCCCAGCCCCA NM_000346 RefSeq chr17 + 72121019 72126419 SOX9 6662 SRY (sex determining region Y)-box 9
GO:0005515|GO:0001658|GO:0003700|GO:0003415|GO:0006366|GO:0008013|GO:0003705|GO:0003413|GO:0030879|GO:0007283|GO:0010564|GO:0003188|GO:0030155|GO:0016337|GO:0001894|GO:0007173|GO:0014032|GO:0

030198|GO:0042127|GO:0001942|GO:0035622|GO:0001708|GO:0030916|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131807_PI430048170 0.431681936269829 1.46285125376995 2.20940537897422 3.62232925891863 3.51068303455863 A P P 3.0951102065547 2.2256742691061 2.62034070130074 P A P LNCV6_131807_PI430048170 mRNA TGGTCATCTTTTTCTCTAAAATAGCCACTTACCTTCAATAAAGTATCTACATGCGGTGAA NM_003235 RefSeq chr8 + 132866959 133134899 TG 7038 thyroglobulin GO:0052689|GO:0042403|GO:0007165|GO:0005179|GO:0042446|GO:0031641|GO:0005576|GO:0030878|GO:0015705|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140341_PI430048170 0.00429570314405754 2.20500867562133 5.25056940117878 5.54884101585532 5.46312047111151 P P P 4.29932257451191 4.31125399849915 4.24484584229987 P P P LNCV6_140341_PI430048170 mRNA GGTCAGCCTTGTAAATCTTAGGTAAGGATCAAAGAAATGATTCTTTTGCCACTAAACTTG NM_001865 RefSeq chr6 - 75237674 75243928 COX7A2 1347 "cytochrome c oxidase subunit VIIa polypeptide 2 (liver), transcript variant 1" GO:0005746|GO:0004129|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138659_PI430048170 0.432100926638412 1.22686344634071 0.389051038697489 0.4908644581279491.20111816234858 A A A 0.5320023668081090.481977757928776 0.315276164779392A A A LNCV6_138659_PI430048170 mRNA AAGATTCCGGATGAGGATGAGAGTGAGGTGACATCCTCCGCCAGCGAAAAGCTGGGCAGA NM_153368RefSeq chr10 + 35605409 35608935 GJD4 219770 "gap junction protein, delta 4, 40.1kDa" GO:0007154|GO:0014717|GO:0005922|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137517_PI430048170 5.31660963072919e-05 0.46021855612813610.0106231402047 9.95015333456082 9.86070446355917 P P P 11.063948794631 11.1182158670309 10.999633057017 P P P LNCV6_137517_PI430048170 mRNA TCAAGGACACATTGAATACGTTGTGACCATCCAGAAAATAAATGCTGAGGGGACACAGTC NM_001089RefSeq chr16 - 2275877 2340746 ABCA3 21 "ATP-binding cassette, sub-family A (ABC1), member 3" GO:0005215|GO:0097233|GO:0005886|GO:0097208|GO:0042493|GO:0042626|GO:0005524|GO:0005615|GO:0055085|GO:0016020|GO:0008152|GO:0006810|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138573_PI430048170 0.00475497165737245 0.32873573148981 0.567810533915447 0.51894908858537 0.281480565980783A A A 2.00165358275195 2.37539847288241 1.753521389241 A A A LNCV6_138573_PI430048170 mRNA GCCCAATGCCTACAAGTTGCAAAAACAGGTGAAAAATTTTGCAATAAGTTTTGCCATTTT NM_152317RefSeq chr12 - 100252263 100267079 DEPDC4 120863 DEP domain containing 4 GO:0035556 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133901_PI430048170 0.9046281215775220.9777392680515795.12415647386047 5.4799352208214 5.52756286145447 P P P 5.67770841476412 5.40335311563144 5.12862939675062 P P P LNCV6_133901_PI430048170 mRNA AACATGGTCTTCAGCAACCTGACCCTGGAGCACATCAATGCCATCCTGCTGGGTGCCTAC NM_000229RefSeq chr16 - 67939883 67944112 LCAT 3931 lecithin-cholesterol acyltransferase GO:0042632|GO:0005515|GO:0043691|GO:0005576|GO:0044281|GO:0030301|GO:0005615|GO:0034372|GO:0004607|GO:0034364|GO:0034375|GO:0042157|GO:0034435|GO:0006644|GO:0034186|GO:0090107|GO:0070062|GO:0042158|GO:0006656|GO:0008203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135829_PI430048170 0.00272681366412257 0.49717595462455 7.33354121030909 7.07658902270551 7.24221472476242 P P P 8.09256617816913 8.12947158547271 8.44056897277957 P P P LNCV6_135829_PI430048170 mRNA CCTCAAGATTATCAACTGTGTGTTCGACAGTGAATATTCAATCTGGTACCAGTTGAAATT NM_001247997 RefSeq chr12 - 122271433 122422569 CLIP1 6249 "CAP-GLY domain containing linker protein 1, transcript variant 3"

GO:0005882|GO:0005515|GO:0008017|GO:0005881|GO:0001578|GO:0035371|GO:0042803|GO:0046872|GO:0005829|GO:0005737|GO:0044354|GO:0015631|GO:0051010|GO:0015630|GO:0030659|GO:0005813|GO:0031116|GO:0005874|GO:0003676|GO:0001726|GO:0007067|GO:0000776|GO:0008270|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130081_PI430048170 0.55869596990507 0.79019092798459 0.430519368504204 1.14581394779491 0.955512192590362 A A A 1.33934987691901 1.63839185168538 0.39659747493328 A A A LNCV6_130081_PI430048170 mRNA AGACCATCCAGGTAGACCATCAGCAGGCTGAAGTCTTCATCGTGGAGCAGACTGTCCACG NM_198559 RefSeq chr2 + 218356855 218368094 CATIP NA ciliogenesis associated TTC17 interacting protein NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137489_PI430048170 0.00598961617658434 0.3861264722570564.51949451845562 4.28814123096281 4.67289268060427 P P P 5.48489495002938 6.03444284297115 6.03843537684183 P P P LNCV6_137489_PI430048170 mRNA TTTGGTTCTTGTTGTAGGTATTGACTGTCCTGGGATATCACTGGTCATTTAAATTCACCA NM_153712 RefSeq chr2 + 112482165 112532645 TTL 150465 tubulin tyrosine ligase GO:0030516|GO:0004835|GO:0000226|GO:0005524|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140782_PI430048170 0.0267678530872042 1.5009880554114 9.17843517160739 9.03227559364375 8.8752204966578 P P P 8.17182922040665 8.53366411584339 8.60259847592823 P P P LNCV6_140782_PI430048170 mRNA ATTCAAACTGCTCCAGCAATTTCTGTAGTTTTCACCTCTGAGAATTACAATGTGAGAACC NM_173575 RefSeq chr10 - 132207491 132307973 STK32C 282974 serine/threonine kinase 32C GO:0004674|GO:0006468|GO:0005524|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135385_PI430048170 0.2060738313204090.91022575721502 0.254321824050971 0.2671609283093870.394624073068637 A A A 0.4348466779346960.315384254172722 0.566273686678731 A A A LNCV6_135385_PI430048170 mRNA GTCACTTCCTTCAGCATCTCACTTCTTCTTCTAGAATCCCCACAGGGAAATACTGTATTG NM_004982 RefSeq chr12 - 21764954 21774821 KCNJ8 3764 "potassium channel, inwardly rectifying subfamily J, member 8" GO:0005242|GO:0005886|GO:0008282|GO:0001822|GO:0007268|GO:0010107|GO:0030016|GO:0005524|GO:0042383|GO:0005739|GO:0007507|GO:0051607|GO:0015272|GO:0015467|GO:0042311|GO:0008076|GO:0032496|GO:0034765|GO:0043330|GO:0006813|GO:0017098|GO:0009268 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140916_PI430048170 0.1631171554089281.12107143586895 6.65103286185212 6.53340571354177 6.73510345156307 P P P 6.46205916459945 6.34703933095982 6.61073979691574 P P P LNCV6_140916_PI430048170 mRNA CCTAAAACAAGGAAACAAAAAATATCTGTGCTTTCAGCAAACCATTGACATACCAGATGT NM_153336 RefSeq chr10 + 122980039 122990391 PSTK 118672 phosphoseryl-tRNA kinase GO:0005739|GO:0016310|GO:0000049|GO:0016301|GO:0001514|GO:0097056|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52231_PI430048170 0.3893763227980940.8490532197411526.7230988635484 6.72911313374575 6.86148455929121 P P P 6.64201281126109 6.99376103707396 7.31298805345335 P P P LNCV6_52231_PI430048170 mRNA ACTATAGAAGATCGTATAGTCCTAGAAATAGACCGACTGGAAGACCACGGCGTAGCAGAA NM_054016 RefSeq chr1 - 23964346 23980463 SRSF10 10772 "serine/arginine-rich splicing factor 10, transcript variant 2" GO:0000244|GO:0005515|GO:0006355|GO:0048025|GO:0003723|GO:0006376|GO:0005634|GO:0050733|GO:0005737|GO:0006406|GO:0016607|GO:0000166|GO:0000398|GO:0000375|GO:0016482|GO:0005654|GO:0051082 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104320_PI430048170 0.4948693743191441.11898910015993 4.22176832075978 4.42603088494644 4.02902935037042 P P P 4.25719119530043 4.24177447793384 3.6360884666838

P P P LNCV6_104320_PI430048170 mRNA
CATTAAAGACACCACCACCAGCACAGAGCAGATGCTGTCCCATGGCACCGCTGATGTGGT NM_014738 RefSeq chr17
+ 75456582 75500452 KIAA0195 9772 KIAA0195 GO:0005654|GO:0016021 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_138776_PI430048170 0.0174086095940099 1.50007165263788 13.1701135966533
13.2354227920278 13.3276549950793 P P P 12.699311882908 12.453896060737
12.8069177670029 P P P LNCV6_138776_PI430048170 mRNA
GAGTCAGGAGAAAACCACCTTCATAAACTGCTCTGTGCAAAGAGGAATAAAACATTTTTT NM_001271736 RefSeq
chr12 + 54325089 54351851 COPZ1 22818 "coatomer protein complex, subunit zeta 1, transcript
variant 4" GO:0030126|GO:0006890|GO:0061024|GO:0006891|GO:0006886|GO:0048205|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138006_PI430048170 0.0244380708954992 0.274004761780266 2.8236109595482
1.77126076825372 2.83427666336055 A A A 4.37834711427187 4.26332016139343
4.60413954159945 P P P LNCV6_138006_PI430048170 mRNA
GAGCTAATGGCCATGCTTTTCTTCAAGGAAAGAATAATTTATTTGAATGAAGTGGGATAC NM_152305 RefSeq chr3
+ 119468937 119494707 POGLUT1 56983 "protein O-glucosyltransferase 1, transcript variant 1"
GO:0035251|GO:0007219|GO:0006493|GO:0005788|GO:0030158|GO:0046527|GO:0072358|GO:0008593|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129776_PI430048170 0.873508058192748 0.989631578671721 0.391764970915571
0.49618876637025 0.40530895924416 A A A 0.532503321382567 0.484452507340275
0.314708028505563 A A A LNCV6_129776_PI430048170 mRNA
CTATCAGTGCCAAGGGCTTCCTGTAGTTCTATTCAAGTGTTACAATAAATATTTGTAGAT NM_001001995 RefSeq
chrX - 13770942 13817195 GPM6B 2824 "glycoprotein M6B, transcript variant 1"
GO:0030501|GO:0005886|GO:0015031|GO:0051893|GO:0030154|GO:2000009|GO:0007399|GO:0003674|GO:0085
029|GO:0001503|GO:0032956|GO:0051612|GO:0045121|GO:0016021 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_137502_PI430048170 0.736596527206672 0.923530245146906 3.35531444489745 2.7643509680165
2.96567031109918 P A A 3.5571416967229 2.82603921292289 3.00633213825219 P A P
LNCV6_137502_PI430048170 mRNA
TTAGTCCATATGGTTGGTTAATCAAGAGCCTTCTGGGTTTGGTTTGGTGGCATTAAATGG NM_001254 RefSeq chr17
+ 40287893 40303161 CDC6 990 cell division cycle 6
GO:0005515|GO:0008285|GO:0005634|GO:0000079|GO:0051233|GO:0005829|GO:0005737|GO:0000082|GO:0000
083|GO:0000166|GO:0019900|GO:0005794|GO:0032467|GO:0051984|GO:0005524|GO:0007089|GO:0006260|GO:0
000922|GO:0007067|GO:0003682|GO:0000076|GO:0005654|GO:0008156|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127685_PI430048170 0.427391421993584 1.39515579285152 1.53811754388573
0.457134419167251 0.348929591140376 A A A 0.482850175690414 0.36691059724288
0.368909678796987 A A A LNCV6_127685_PI430048170 mRNA
GAGATGTAATCCTTGCCATACAACAAATGATTAGGGGAAAATCCTTTTGTAAAATTGCAG NM_001004741 RefSeq
chr11 - 56576773 56577721 OR5M10 NA "olfactory receptor, family 5, subfamily M, member 10"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94192_PI430048170 0.857850373362013 1.03690107254585 1.01808006145127 2.60874404400019
2.65902103125564 A A A 2.41562275406615 2.03038593318884 2.17198412725482 P A A
LNCV6_94192_PI430048170 mRNA
AATGTGATGACAAAGAAGTCCACAAAGTGAAAATTTATGCTTACTAGCCTGTCTTCTTTG NM_001080836 RefSeq
chr10 + 14959438 14972851 MEIG1 644890 meiosis/spermiogenesis associated 1
GO:0005634|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137212_PI430048170 0.293437479123693 2.01874206229367 2.39539509308876
1.94916946623901 0.413664843493631 A A A 0.541024606609661 0.408104768959608

1.26118236005654 A A A LNCV6_137212_PI430048170 mRNA
GCGTGAAGCAGGCCCAAGCTAGGGAAGGTGAGAAGCTTTAACCTTAAATTTTCGAGTTTT NM_182610RefSeq chr3
+ 169911571 169939168 SAMD7 344658 "sterile alpha motif domain containing 7, transcript variant 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133770_PI430048170 0.3492501811289453.01597182401192 0.6039199276602663.876959714369
2.72798861348863 A P A 0.8486368937160681.9817721766636 0.865123562917123A A A
LNCV6_133770_PI430048170 mRNA
CAACCTGAGATTTTATTTATAAATTAGCCACTTGTCTTAATTTATTGCCACCCAGTCGCTNM_172138RefSeq chr19 +
39268516 39270092 IFNL2 282616 "interferon, lambda 2"
GO:0051607|GO:0002385|GO:0050778|GO:0007259|GO:0005615|GO:0005125 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128266_PI430048170 0.2577368660069721.02174820100207 0.372115575068115
0.3723041322157630.427198513618757A A A 0.3612115700515660.334066334132115
0.383498234414822A A A LNCV6_128266_PI430048170 mRNA
CAGCATAGAATGCATTACTGTTGGAATAATTGGCCTCTAGCTCTTAAATGTCTCTGATAA NM_001291953 RefSeq
chr4 + 155758972 155807642 GUCY1B3 2983 "guanylate cyclase 1, soluble, beta 3, transcript variant
4"
GO:0007263|GO:0046982|GO:0008015|GO:0051879|GO:0004383|GO:0005525|GO:0046872|GO:0043231|GO:0008
074|GO:0005737|GO:0007596|GO:0006182|GO:0004872|GO:0020037 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140026_PI430048170 0.00542363348950927 0.6094311483407599.6206699176946
9.55656183907895 9.86171661610767 P P P 10.5772623294065 10.2916995521804
10.3137829600594 P P P LNCV6_140026_PI430048170 mRNA
TTGGGCCAACTATTTAGTAAGCCCGGATAGACTTATTGCCAAAAACAAAAAATAGCTTTC NM_001430RefSeq chr2
+ 46297401 46386703 EPAS1 2034 endothelial PAS domain protein 1
GO:0005515|GO:0006366|GO:0030324|GO:0061418|GO:0055072|GO:0005829|GO:0042415|GO:0045944|GO:0048
469|GO:0043129|GO:0004871|GO:0035019|GO:0048625|GO:0035035|GO:0005667|GO:0001666|GO:0046982|GO:0
071456|GO:0001892|GO:0043619|GO:0001525|GO:0003677|GO:0043565|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133049_PI430048170 0.8175977773179861.0079197332702 13.71970557011
13.6472286772654 13.7763473510331 P P P 13.6872025175611 13.6790605353333
13.7448776249275 P P P LNCV6_133049_PI430048170 mRNA
TGGGGGGAAAAAGACCAGGTCTACAGTGATAGAGCAAAGCATCAAAGAATCTTTAAGGGA NM_002567RefSeq
chr12 + 118136064 118145585 PEBP1 5037 phosphatidylethanolamine binding protein 1
GO:0010951|GO:0005515|GO:0005737|GO:0019901|GO:0008429|GO:0004867|GO:0005634|GO:0019899|GO:0005
524|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126865_PI430048170 0.0402479603886026 1.10856953092306 10.6787601851627
10.7601704823118 10.7809332630766 P P P 10.6456123530859 10.6088920794721 10.518312684054
P P P LNCV6_126865_PI430048170 mRNA
TTCTAAGTGCAATACTTGGCCCGCCGGCTTCCCGCTGCCCCCATCGCGCTCACGCAATAA NM_001194RefSeq chr19
+ 589892 617159 HCN2 610 hyperpolarization activated cyclic nucleotide gated potassium channel 2
GO:0005886|GO:0005222|GO:0005248|GO:0007267|GO:0007268|GO:0042802|GO:0030552|GO:0005887|GO:0005
249|GO:0008076|GO:0042391|GO:0034765|GO:0035725|GO:0071320|GO:0071805|GO:0071321 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132184_PI430048170 0.9435657062932470.9909752737801449.53868533295161 9.5287631940316
9.38501148442422 P P P 9.33698444079803 9.66825778959273 9.47217986618649 P P P
LNCV6_132184_PI430048170 mRNA
ACACTTCTTCAAGGTGCTGATCCTGGAGGCAGCAGGTGGGCAAATTGAGCTCCGCACCTA NM_004435RefSeq chr9
+ 128818499 128822676 ENDOG 2021 endonuclease G

GO:0005739|GO:0005515|GO:0004518|GO:0043065|GO:0004519|GO:0006309|GO:0034612|GO:0006310|GO:0003676|GO:0001701|GO:0046872|GO:0046677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132610_PI430048170 0.3919402550763451.09260953071317 0.684354218184951 0.3214717463680470.400444114924184A A A 0.3671741261980990.317027158583143 0.363918449095567A A A LNCV6_132610_PI430048170 mRNA
CCCCACCGTAGTATTTATAGTTAAATTAAGGGTGACAGTACAATAAAGTGATGGCGATGT NM_173849RefSeq chr14 - 94768222 94770162 GSC 145258 goosecoid homeobox
GO:0001103|GO:0005667|GO:0007369|GO:0023019|GO:0030178|GO:0048704|GO:0005634|GO:0000122|GO:0014036|GO:0043565|GO:0048644|GO:0001085|GO:0021904|GO:0042474|GO:0030900 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138327_PI430048170 0.8717315762789061.00889054306431 9.69217353055456 9.68558095379989 9.85376659637617 P P P 9.8102553210433 9.70608640489807 9.6799168298454 P P P LNCV6_138327_PI430048170 mRNA
CCCTGGTCCTGAACTGTGGAAATGCCATTAAACTCTCTCTATAATGTAACTGAAACTGCT NM_032683RefSeq chr19 + 18193229 18196740 MPV17L2 84769 MPV17 mitochondrial membrane protein-like 2
GO:0005743|GO:0070131|GO:0016021|GO:0005762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137037_PI430048170 0.38378575993416 0.8515032018612747.17850949463416 6.53456347144958 6.82721686588428 P P P 6.77826465674798 7.30071374184931 7.17911256884141 P P P LNCV6_137037_PI430048170 mRNA
GGGACACACCCCACTTCGGTAAAAGAAAATAGGGAAAGGCCATAAACAAAGACAGACTTG NM_013286RefSeq chr3 + 51391267 51397905 RBM15B 29890 RNA binding motif protein 15B
GO:0008380|GO:0006397|GO:0005515|GO:0000166|GO:0000381|GO:0003723|GO:0005730|GO:0016032|GO:0005654|GO:0045892|GO:0006351|GO:0006913 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92061_PI430048170 0.2365167958629491.32862668479784 2.42318757307878 2.98164795260467 2.98487139108941 A P P 1.92068851021111 2.72677331919664 2.46851272270391 A P P LNCV6_92061_PI430048170 mRNA
TAAAAAATAGCTTTCCTGGCTAAAAGACCCAGGTAAAAGACCCAACCCCAGCAGAAAGAC NM_004227RefSeq chr7 - 6161780 6272611 CYTH3 9265 cytohesin 3
GO:0090162|GO:0005802|GO:0005886|GO:0005547|GO:0001726|GO:0030155|GO:0005829|GO:0031234|GO:0045785|GO:0043547|GO:0005086|GO:0032012|GO:0048193|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138253_PI430048170 0.4531564895649821.14825614815005 7.15505330822843 7.74224486568411 7.7051617789373 P P P 7.46445371985937 7.20074578812466 7.39751648750783 P P P LNCV6_138253_PI430048170 mRNA
GGGTAATAGAGACAGAACTGTTCAGAGTCCCAAATCCAAATAAACTAGTTTTGTTCTTAA NM_005089RefSeq chrX + 15790450 15823259 ZRSR2 8233 "zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 2" GO:0008380|GO:0005515|GO:0030628|GO:0000245|GO:0000166|GO:0000398|GO:0046872|GO:0005689 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133674_PI430048170 0.7977568034595220.9905961837710330.259569322707208 0.2683484521464430.415915472678936A A A 0.3614749254523390.305350763250137 0.322735893331098A A A LNCV6_133674_PI430048170 mRNA
GCTGTGTTTTATACCATCATCACTCCTATCTTGAATCCAATTATCTATACTCTGAGAAACNM_001004715 RefSeq chr14 + 20117406 20118438 OR4K17390436 "olfactory receptor, family 4, subfamily K, member 17"
GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140142_PI430048170 0.4155656965857081.03036865676509 0.291647934364641 0.3071726743015270.422164991440716A A A 0.31545756522614 0.290219250548771 0.289227835348538A A A LNCV6_140142_PI430048170 mRNA
ATGCCTGCCAAGATAATGGTCTTGTATGTCTTCATTCTCTGCGTAATTTTTGTTTTTGTT NM_015912RefSeq chr8 -

138130022 138496822 FAM135B 51059 "family with sequence similarity 135, member B" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131305_PI430048170 0.0356269581577670.4979875432916788.621973884967
8.20630589936898 8.62883603871444 P P P 9.05795229396943 9.43878104271901 9.8950787482884
P P P LNCV6_131305_PI430048170 mRNA
GAGGAAGAACTGAAAGGCTTTTCAACCACAAAACTCATCTGGAGTTCTCAAAGACCTGGG NM_000214RefSeq chr20
- 10637683 10674046 JAG1 182 jagged 1
GO:0005515|GO:0007220|GO:0005886|GO:0045599|GO:0003184|GO:0005112|GO:0072017|GO:0003215|GO:0061
073|GO:2000737|GO:0061314|GO:0045639|GO:0007219|GO:0045944|GO:0042127|GO:0045445|GO:0045446|GO:0
097150|GO:0045747|GO:0030097|GO:0030334|GO:0042491|GO:0002011|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128053_PI430048170 0.0459332294712627 1.21057253467742 8.65859371058914
8.56898327346608 8.40468716255676 P P P 8.3514086622487 8.25228326474055
8.20918657235179 P P P LNCV6_128053_PI430048170 mRNA
CCTACTGCTTGCTGGCTTCTGTGTTCTCTGCAGTAAACATTGATTTCTGACTCGAAAAAA NM_173832RefSeq chr8
+ 143246927 143262705 ZFP41 286128 "ZFP41 zinc finger protein, transcript variant 1"
GO:0006355|GO:0007275|GO:0005634|GO:0007283|GO:0003677|GO:0046872|GO:0030154|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128013_PI430048170 0.2565698732008 0.9032923818476378.37921473682305
8.54780344423503 8.53207690583133 P P P 8.58112869650387 8.5045065850158
8.80274042588714 P P P LNCV6_128013_PI430048170 mRNA
TAATTCTCTCTTCTCCTCCAGACACAATGGCACTGCTTATCTCCGAAATGGTGTGATCGT NM_058243RefSeq chr19
- 15237489 15280451 BRD4 23476 "bromodomain containing 4, transcript variant long"
GO:0005515|GO:0000790|GO:2000002|GO:0001833|GO:0005634|GO:0002039|GO:0005737|GO:0000083|GO:0007
059|GO:0045944|GO:0016032|GO:0070577|GO:0006338|GO:0044154|GO:0043123|GO:0000794|GO:0008024|GO:0
005694|GO:0050727|GO:0003677|GO:0006351|GO:0006974|GO:0010971|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138038_PI430048170 0.00181862826597505 3.70937942098681 10.7610440670292
10.8966274475143 11.0949139555847 P P P 9.31860242179009 8.73035578130886
8.98922952311904 P P P LNCV6_138038_PI430048170 mRNA
GTTTGCAGTCTTCAGTTGTGTTCTTATGCTTCAGTGTCACATTTCATTTCATTTGAAACT NM_013338RefSeq chr13 -
36949770 36999367 ALG5 29880 "ALG5, dolichyl-phosphate beta-glucosyltransferase, transcript variant
1"
GO:0004581|GO:0004576|GO:0007368|GO:0016020|GO:0005789|GO:0006486|GO:0016021|GO:0006488|GO:0044
267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145382_PI430048170 0.0204251601135094 0.792477423426 9.17454632197694
9.35485296861656 9.28254706717446 P P P 9.54853523502938 9.52444014494609
9.74138479313909 P P P LNCV6_145382_PI430048170 mRNA
GATGAACCTCCTGTAACTTCTATCTGTTCTTTTTTGAGGCTCAGGGAGAAACTAGCATTT NM_030915RefSeq chr2
+ 30231530 30260033 LBH81606 limb bud and heart development
GO:0010468|GO:0005737|GO:0030193|GO:0007275|GO:0005634|GO:0045893|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130356_PI430048170 0.9536360241701911.01849078537024 1.78958459212616
2.32394808818925 2.90675311625083 A A P 1.62510493237352 2.6792243233633
2.62850913518752 A P P LNCV6_130356_PI430048170 mRNA
TTCTGTGTTTTGCCTGAAACGATACCAGGTTCCCCTGAATAGCAACTTTACAAGGTCCAT NM_001287011 RefSeq
chr9 + 36136535 36163913 GLIPR2 152007 "GLI pathogenesis-related 2, transcript variant 3"
GO:0000139|GO:0010718|GO:0070374|GO:0010634|GO:0042803|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_126726_PI430048170 0.0164451966187036 2.45855860113895 5.69693540418469
5.85907147592233 5.50591230753506 P P P 3.94329170918548 4.73790790723016 4.4007743746641
P P P LNCV6_126726_PI430048170 mRNA
GCAGGGATTTTGACTTTGGATGACAAGGCTTTATTTGTAAATATGCTCTTAATATGCAAC NM_001039570 RefSeq
chr22 + 29073077 29146820 KREMEN1 83999 "kringle containing transmembrane protein 1,
transcript variant 3" GO:0005515|GO:0007154|GO:0016020|GO:0016021|GO:0016055|GO:0060828 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_101001_PI430048170 0.370287786780926 1.10981254644359 6.00860617935678
6.30621593331594 6.37654597108807 P P P 6.06280443520581 5.93396319727657
6.25166693123207 P P P LNCV6_101001_PI430048170 mRNA
TTACTTATTTGAACCAAGGTCAGTCATATGAAATTCGGATGCTGGATAATCGGAAAATGG NM_014517 RefSeq chr3
- 33388335 33440378 UBP1 7342 "upstream binding protein 1 (LBP-1a), transcript variant 1"
GO:0043565|GO:0005737|GO:0003700|GO:0006357|GO:0003714|GO:0005654|GO:0005634|GO:0001525|GO:0045
892|GO:0019079|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143658_PI430048170 0.232232217352427 1.04832151856239 11.3458576120514
11.3371709428643 11.2828123697117 P P P 11.2559882763326 11.3227892282133
11.1800967732603 P P P LNCV6_143658_PI430048170 mRNA
ATGGTCATGTATGGCTACAGGAAGCAGTTCGAGGCCCCAACGCTGGCTGAAGGCTTCTCT NM_007254 RefSeq chr19
- 49861202 49867565 PNKP 11284 polynucleotide kinase 3'-phosphatase
GO:0005515|GO:0009314|GO:0090305|GO:0005730|GO:0005634|GO:0019201|GO:0005524|GO:0003684|GO:0046
404|GO:0006261|GO:0003690|GO:0004519|GO:0006281|GO:0016020|GO:0042769|GO:0046403|GO:0016311|GO:0
046939|GO:0017076|GO:0005654|GO:0000718|GO:0006979 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_136716_PI430048170 0.111501321221587 3.42045908439485 4.15789850706181
3.82992269038745 3.77296402817476 P P P 3.24662546327257 1.35311454171023
0.408010538992761 P A A LNCV6_136716_PI430048170 mRNA
GTATTACAAACGGTGTTTACATGGGATGCGATTTACCTCCTGCACTGCAGTCTCTGCAAA NM_018995 RefSeq chr22
+ 50090005 50161687 MOV10L1 54456 "Mov10 RISC complex RNA helicase like 1, transcript variant 1"
GO:0005622|GO:0004004|GO:0010467|GO:0000287|GO:0003723|GO:0034587|GO:0007275|GO:0007283|GO:0007
281|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145085_PI430048170 0.162392619827892 0.833221301552826 6.99841947741303
6.78709231195494 7.23107042200491 P P P 7.17191418128035 7.22076638021975
7.43410623341883 P P P LNCV6_145085_PI430048170 mRNA
TATAATAAAGGCCTTGTTGCTTAAGACACCTTCAGTCTTTGCAGGAGGGCATGGAAGCTC NM_001204814 RefSeq
chr19 + 57769651 57780616 ZNF586 54807 "zinc finger protein 586, transcript variant 3"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135546_PI430048170 0.168177436073617 1.14015889950222 9.9923115691995
10.0422175289762 10.0812418591004 P P P 9.68828455451811 9.82789530065627
10.0146017332603 P P P LNCV6_135546_PI430048170 mRNA
GTGGGGCCTTCAAATTGTTTTTCTCTTTTCATATTAAAAATGGTCTTTCTGTGAACTAGC NM_001500 RefSeq chr6 -
1623799 2245634 GMDS 2762 "GDP-mannose 4,6-dehydratase, transcript variant 1"
GO:0005737|GO:0007219|GO:0008446|GO:0019673|GO:0042351|GO:0070401|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133700_PI430048170 0.0217184638244705 0.490035292059443 5.92936963736984
5.35993370994524 5.71361572398552 P P P 6.27264598847721 6.80209356498526
6.98129646933481 P P P LNCV6_133700_PI430048170 mRNA
CTCCGTGACCATGCTCTGACTTTTGTATTTCAACCTGAGTTTAAACAAATAAACAAGATA NM_015203 RefSeq chr1
+ 150364110 150476565 RPRD2 23248 "regulation of nuclear pre-mRNA domain containing 2, transcript

variant 1" GO:0016591 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137202_PI430048170 0.6695094631909330.7811125090149450.576259454021745
1.41668663880987 1.98038340011226 A A A 0.59654576090247 2.05650977332116
2.23465173396339 A A A LNCV6_137202_PI430048170 mRNA
TTCCATAATCAGGGGAAGAGCTACTGGAATCACTGGAAACTTTGCTAATATTGGGGGAGC NM_199352RefSeq chr11
- 63163823 63229652 SLC22A25 387601 "solute carrier family 22, member 25"
GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131394_PI430048170 0.00358637529102869 0.9468145635165540.354096455072719
0.3600063913426150.328660500604565A A A 0.4418012695178930.421321697659557
0.41624380921173 A A A LNCV6_131394_PI430048170 mRNA
TGTTCCCTGAATTGAAATATTTGCTCTCTACCATAATTTATCACATGGAGCTATTCCTCT NM_033062RefSeq chr17 -
41177445 41178208 KRTAP4-2 85291 keratin associated protein 4-2 GO:0045095 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133992_PI430048170 0.0019921845734065 1.39322325553837 7.96499433716834
8.03012112596067 7.95105648879123 P P P 7.58336124785437 7.49123247040634
7.43356819407849 P P P LNCV6_133992_PI430048170 mRNA
CTCTGTCTGGGGTCGCATTCCGCACAAGCCTTTCATCAACATCTTAAAATAGTAACTGTG NM_004710RefSeq chr17
+ 78168589 78172928 SYNGR29144 synaptogyrin 2
GO:0031594|GO:0030672|GO:0016021|GO:0006605|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143813_PI430048170 0.000245217810665759 0.3660635104370374.8880552176051
5.09078435610364 5.08789855421494 P P P 6.31056697820484 6.50054867767123
6.59955095798036 P P P LNCV6_143813_PI430048170 mRNA
CGTGGATAAAAGTAGTGCCTCTCTTTATACAACTGATGGGGTTTTAAAAAGTGTAAATTG NM_181787RefSeq chr8
+ 94719874 94793848 DPY19L4 286148 dpy-19-like 4 (C. elegans)
GO:0000030|GO:0018406|GO:0005637|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136251_PI430048170 0.122116442934275 1.25136342110227 11.8487954432702 12.259695163248
11.9341363267533 P P P 11.8651876470149 11.7074935875241 11.5110549354389 P P P
LNCV6_136251_PI430048170 mRNA
TCTTGGATGATGTCCTTGCTCCACCACGCAGGCCCTTGCTTCTCCCATCAACGAGTCTTG NM_153266RefSeq chr11
+ 66291901 66296664 TMEM151A 256472 transmembrane protein 151A GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_114529_PI430048170 0.5552091939326480.9029417027170013.41795955719941
3.84915594020517 4.36195722128592 P P P 3.93578612456678 4.21055654046321
4.06637066796976 P P P LNCV6_114529_PI430048170 mRNA
TGGTTGAAATCACCTGTGTGTCTTAATTTCTCAATTCCTTTTTGGCAAGAATATCAAGCA NM_001146321 RefSeq
chr5 + 126423176 126494161 GRAMD3 65983 "GRAM domain containing 3, transcript variant 4"
GO:0005881 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131883_PI430048170 0.7056774876662840.9437900523549192.36449492620853
4.12069338423639 3.09610296003852 A P P 3.15349652846918 3.28393270850681
3.83903124237223 P P P LNCV6_131883_PI430048170 mRNA
GACCTTCGCCTTTCCCTACTTCGAAGGGTCTTTTCAGCCTTTCATCAGATCTTCTTATTT NM_001029865 RefSeq chr11
- 20156213 20160324 DBX1 NA developing brain homeobox 1 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131990_PI430048170 0.0622803295172196 0.8347108802720217.47867660460366
7.32273525229182 7.60301340937469 P P P 7.8335119895786 7.66566623047456
7.69518942464019 P P P LNCV6_131990_PI430048170 mRNA
AGACCAGGAGGACAGAGTTTGCTTTCATATTTTCCCTGTAAGTAAGAGGGCTTATTTATT NM_001282690 RefSeq
chr9 + 89318850 89359663 SECISBP2 79048 "SECIS binding protein 2, transcript variant 4"

GO:0005739|GO:0035368|GO:0030529|GO:0001514|GO:2000623|GO:0043021|GO:0005654|GO:0003730 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121230_PI430048170 0.8136339846298430.9873493719880765.01335163405699
4.84531131295667 4.73220840745895 P P P 4.91513013784747 4.90984053392086
4.83351234798856 P P P LNCV6_121230_PI430048170 mRNA
AACGAGTGGCTGGGGATTAAAAATGAGACTGAGGACCAGTACGCACTCATGGAGGACGAG NM_005027RefSeq
chr19 + 18153177 18170533 PIK3R2 5296 "phosphoinositide-3-kinase, regulatory subunit 2 (beta), transcript variant 1"
GO:0008286|GO:0005515|GO:0050852|GO:0034976|GO:0001678|GO:0007264|GO:0005634|GO:0044281|GO:0050900|GO:0042993|GO:0005829|GO:0007173|GO:0043551|GO:0045944|GO:0016303|GO:0051056|GO:0048010|GO:0030971|GO:0048011|GO:0032869|GO:0006661|GO:0035014|GO:0036092|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142503_PI430048170 0.2848435297190460.4818018101088890.36957629273711
0.3856861438656680.291894817871775A A A 0.2937802589161570.985416634977622
2.24136586662989 A A A LNCV6_142503_PI430048170 mRNA
ACTCTCCTGCCAACCCTTGTTCTACAATCTAAACCAAACATGTGCTAGGAAGAGAAAAAA NM_000119RefSeq chr15
- 43197227 43221125 EPB42 2038 "erythrocyte membrane protein band 4.2, transcript variant 1"
GO:0005515|GO:0020027|GO:0005886|GO:0008360|GO:0048536|GO:0055072|GO:0005524|GO:0000902|GO:0018149|GO:0043249|GO:0003810|GO:0005200|GO:0030863|GO:0005856 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_65849_PI430048170 0.00611028950326367 0.5594151638568475.62126356555325
5.89770793470385 5.69147493541433 P P P 6.46445219504467 6.44042996792038 6.8046179050744
P P P LNCV6_65849_PI430048170 mRNA
ATTGATTTATAAGTTCCTGAATGTTCCAATGTTTCGAAATGTCTCTCTGAAGTGCCTCAC NM_003400RefSeq chr2
- 61477933 61538283 XPO1 7514 exportin 1
GO:0005515|GO:0005215|GO:0010467|GO:0034504|GO:0015030|GO:0003723|GO:0019058|GO:0005634|GO:0005635|GO:0043231|GO:0005829|GO:0005737|GO:0005642|GO:0006611|GO:0008536|GO:0016032|GO:0007179|GO:0046825|GO:0030512|GO:0031965|GO:0042176|GO:0042493|GO:0019904|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_122705_PI430048170 0.4048300283880425.47611067290415 4.15631503524781
0.3129189393398220.435911416335797P A A 0.33705136377708 0.305879210621056
0.299445220086947A A A LNCV6_122705_PI430048170 mRNA
CCAAACTCCTAAATGTTTGTGCACACATTTCTCGGTGACAACGTTGGGAAACACAGCAAC NM_001122757 RefSeq
chr3 - 87259632 87276587 POU1F15449 "POU class 1 homeobox 1, transcript variant beta"
GO:0001102|GO:0008284|GO:0001105|GO:0006355|GO:0008285|GO:0003700|GO:0001708|GO:0006366|GO:0060133|GO:0003714|GO:0000122|GO:0000978|GO:0008340|GO:0001077|GO:0005737|GO:0045944|GO:0043567|GO:0003682|GO:0030183|GO:0032962|GO:0005654|GO:0040018|GO:0045893|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143236_PI430048170 0.00028838685578137 0.9067749394421651 1.0768566731999
11.1021068290267 11.0894562192215 P P P 11.2413147606249 11.2133677375912
11.2372407387178 P P P LNCV6_143236_PI430048170 mRNA
AGCCCCCTCATGCATACTTTTATTAGGCGATAGACTAGTTAAGAAAATTGTTTCTATGTA NM_001163474 RefSeq
chr7 - 149472792 149497807 ZNF746 155061 "zinc finger protein 746, transcript variant 1"
GO:0005515|GO:0003700|GO:0044212|GO:0005634|GO:0000122|GO:0000978|GO:0006351|GO:0046872|GO:0001078|GO:0005737|GO:0045944|GO:0045892|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127811_PI430048170 0.0679894768044186 0.8245363997986190.41564799076875
0.4234621770438050.351078432382355A A A 0.5203214973286920.798464352963357
0.693960585526596A A A LNCV6_127811_PI430048170 mRNA
AATAAGAATGCATGTAATAGCTATACCAACCGCGCATCCGGCTTTCACATGCACTGTCTC NM_004700RefSeq chr1

+ 40784011 40840452 KCNQ4 9132 "potassium channel, voltage gated KQT-like subfamily Q, member 4, transcript variant 1"
GO:0005251|GO:0042472|GO:0009925|GO:0005886|GO:0008076|GO:0007605|GO:0007268|GO:0005267|GO:0034765|GO:0016021|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137923_PI430048170 0.0590439571861289 1.20138594711326 0.986735907045829
0.7934604772966530.773933610103982A A A 0.6034499767908190.592899495559918
0.573250095096455A A A LNCV6_137923_PI430048170 mRNA
CGTCTGTGGTCCTATGGTATCAACCAGTATCTTTATAGCAATAATTTCTTTAATTCCCTT NM_001025616 RefSeq chr4
+ 85475130 86002670 ARHGAP24 83478 "Rho GTPase activating protein 24, transcript variant 1"
GO:0005515|GO:0051056|GO:0035021|GO:0035313|GO:0007264|GO:0001525|GO:0042995|GO:0032863|GO:0030154|GO:0005829|GO:1900028|GO:0005856|GO:0005925|GO:0030675 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58582_PI430048170 0.0713524133510486 1.50355466327586 4.96206009874106
4.94747189880914 4.80850956054033 P P P 3.93758168278503 4.41119368732239
4.54168725706863 P P P LNCV6_58582_PI430048170 mRNA
GGAAGAAAGATGTCAGATGAAGATGATCTAGAAGACTCTGAGCCAGACCAGGATGATTCT NM_001135217
RefSeq chr12 + 6904732 6914242 LRRC23 10233 "leucine rich repeat containing 23, transcript variant 3" GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114312_PI430048170 0.0780314525129773 1.14485727918017 6.69260387872699
6.80036632757225 6.91031977045907 P P P 6.51798279746452 6.69787072976951
6.60453272048739 P P P LNCV6_114312_PI430048170 mRNA
CAAAAAGCATGCCCAGACCTTTTTGGCCCTCTGTGCTACAGATTATACCTTTGCCATGTA NM_001287427 RefSeq
chr6 - 41934932 41941848 CCND3 896 "cyclin D3, transcript variant 6"
GO:0005515|GO:0019901|GO:0045737|GO:0005634|GO:0007165|GO:0005737|GO:0007049|GO:0016020|GO:0042098|GO:0000307|GO:0001934|GO:0004693|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128838_PI430048170 0.866131834516636 1.00593892010912 0.523169154998998
0.5549641900517620.433278011775725A A A 0.5475753541102240.473823443843529
0.465709837344499A A A LNCV6_128838_PI430048170 mRNA
GCAGCTTGTCTTTTTGCATAGCTCAGCCTGATGTGAAACAATAAAACCAGAAATATGCAT NM_178349RefSeq chr1
+ 152811970 152813109 LCE1B 353132 late cornified envelope 1B GO:0031424 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135080_PI430048170 0.000136901068305716 1.43925102045633 11.654690322481
11.6496136628782 11.6283752871679 P P P 11.1516659438423 11.1087870974563
11.0958123642229 P P P LNCV6_135080_PI430048170 mRNA
GGCCCCTAGCTTAGGAAGACTGTTGTGTTATTTGTTCAATTTCAATAAAATGATTTGTAG NM_007275RefSeq chr3
- 50324908 50328238 TUSC2 11334 tumor suppressor candidate 2
GO:0006909|GO:0070945|GO:0032733|GO:0008283|GO:0052567|GO:0007267|GO:0051881|GO:0032700|GO:0005739|GO:0032618|GO:0007049|GO:0006954|GO:0071609|GO:0001779|GO:0048469|GO:2000377 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_13397_PI430048170 0.0575088927073059 0.5939140369175037.92489779622337
7.90018604544156 7.99227389219751 P P P 8.29602745628651 8.89693610020922
8.81099083364985 P P P LNCV6_13397_PI430048170 mRNA
TTTGCCATCTGGATGACAAACGGAAGATCCACTAAAACGTCCACGGGATTAACAGAACGT NM_005434RefSeq chr2
- 110083869 110116566 MALL 7851 "mal, T-cell differentiation protein-like"
GO:0042632|GO:0005515|GO:0005886|GO:0000139|GO:0030136|GO:0016023|GO:0045121|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140280_PI430048170 0.6167281873966741.91956878591807 0.373741928952597
2.79937578169174 0.330657348881821A A A 0.4302925890379780.433493461802313
1.17547531282467 A A A LNCV6_140280_PI430048170 mRNA

CTTCTAATGCTTCAGATAGAATACAGTTGGGTCTCACATAACCCTTTACATTGTGAAATA NM_000261 RefSeq chr1 - 171635416 171652633 MYOC 4653 "myocilin, trabecular meshwork inducible glucocorticoid response" GO:0005515|GO:0051897|GO:0005783|GO:0038031|GO:0035024|GO:0022011|GO:0038133|GO:0005743|GO:0005741|GO:0051894|GO:0005615|GO:0031175|GO:0005109|GO:0005758|GO:1900026|GO:0051901|GO:0043408|GO:0001968|GO:0070062|GO:0032027|GO:0005791|GO:0030971|GO:0005794|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134219_PI430048170 0.4862675679400321.04359426426219 9.04163410272977 8.92884433273499 9.07342502293706 P P P 8.81792048431407 8.98978304555322 9.04583127114736 P P P LNCV6_134219_PI430048170 mRNA
GTCCCGTTTGCAGCACTGGTTTTGTTTCCTTAATAAATTTTTAGTTATGAAACATACCTG NM_017575 RefSeq chr17 - 2059838 2303775 SMG6 23293 "SMG6 nonsense mediated mRNA decay factor, transcript variant 1" GO:0005515|GO:0010467|GO:0035303|GO:0000781|GO:0005697|GO:0042162|GO:0005730|GO:0005634|GO:0004521|GO:0046872|GO:0005829|GO:0005737|GO:0006406|GO:0000184|GO:0000723|GO:0035145 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131007_PI430048170 0.6439667738756690.9585204744416320.294298372533944 0.2844052558033060.405962961062262 A A A 0.2980590230469420.271740496685892 0.580652992199158 A A A LNCV6_131007_PI430048170 mRNA
CAAGACCAAGCAGATTCAGGAAGGTGTAATTAAATTTTTACTTGGAGACAAGGTTAGTTT NM_001005174 RefSeq chr11 + 5820335 5821301 OR52N2 NA "olfactory receptor, family 52, subfamily N, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130883_PI430048170 0.0788564561457791 0.8482580309798156.58263176860634 6.62571955670938 6.7817218501025 P P P 6.87320136660046 7.04492410313242 6.77922872258583 P P P LNCV6_130883_PI430048170 mRNA
GTTTCTGTATAGTTTTGGGTCTTTCTATGCTGGTTGTATTTATATTAAACCCCTGGTTAG NM_194249 RefSeq chr5 - 140670795 140673586 DND1 373863 DND microRNA-mediated repression inhibitor 1 GO:0005737|GO:0035198|GO:0000166|GO:0060965|GO:0017091|GO:0007275|GO:0005634|GO:0007281 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139200_PI430048170 0.0617620327452861.1588436926853 10.4741505627384 10.5643703877369 10.5401152813164 P P P 10.3728786601149 10.3775008480726 10.1833232393054 P P P LNCV6_139200_PI430048170 mRNA
GAACCAGGGGCCCTTTTCTCTTTTAGAATTTTCTTTTAATCAGCCCACCTTTTGACTCCC NM_001002836 RefSeq chr19 - 56087362 56121373 ZNF787 126208 zinc finger protein 787 GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132850_PI430048170 0.0551835374892260.6400281900826927.02415121308039 6.42313524402247 6.50693915381553 P P P 7.1921497709482 7.46213550264815 7.29440478792943 P P P LNCV6_132850_PI430048170 mRNA
TCGAGTGCATTTAACGAGAACAAAACAAAAGGCTCATAACAACAAGAACGTTTCAGAAAA NM_001008701 RefSeq chr19 - 14147736 14206185 ADGRL1 NA "adhesion G protein-coupled receptor L1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138227_PI430048170 0.2634153695717891.38106582517828 10.5934572642521 10.9308649473615 10.8505233751319 P P P 10.8982021789912 9.65631348363643 10.1722146725084 P P P LNCV6_138227_PI430048170 mRNA
GATACTGTAAGGGTGTTTCGTTCCCTTTAAATGAATCAACACTGCCACCTTCTGTACGAG NM_005346 RefSeq chr6_GL000252v2_alt + 3075513 3078033 HSPA1B NA heat shock 70kDa protein 1B NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132257_PI430048170 0.3840758067011980.8039127827855218.27838727308439 8.15269029504065 8.16681200296358 P P P 7.97647008861447 8.73073023473795 8.71768784578476 P P P LNCV6_132257_PI430048170 mRNA

ATGAATCTGCCCTTTAATAAAGCATTATTGAGATTGCTGGCCTATTGGGGAAGCCTGCGG NM_005483 RefSeq chr19 + 4402662 4443397 CHAF1A 10036 "chromatin assembly factor 1, subunit A (p150)" GO:0005515|GO:0000790|GO:0006355|GO:0033186|GO:0070087|GO:0006335|GO:0006351|GO:0042802|GO:0006260|GO:0043234|GO:0007049|GO:0006281|GO:0006461|GO:0031497|GO:0003682|GO:0051082 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140070_PI430048170 0.0222166983793181 1.21919696277912 9.383185073607 9.33309398786775 9.53330948381229 P P P 9.04034310751823 9.17415641449083 9.1805952848203 P P P LNCV6_140070_PI430048170 mRNA
AACTGTTTTCTTAAAGGAAATGAAGCTGTACAGGACGATTCACTGCCATGCCAGTCAGGC NM_024667 RefSeq chr12 - 122865327 122896165 VPS37B 79720 vacuolar protein sorting 37 homolog B (S. cerevisiae) GO:0005515|GO:0000813|GO:0019082|GO:0019058|GO:0030496|GO:0019068|GO:0015031|GO:0016197|GO:0031902|GO:0016032|GO:0061024|GO:0010008|GO:0070062|GO:0048306 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138167_PI430048170 0.490730059211691 1.12944126229951 3.55496627681074 3.87400229776435 3.30923947623292 P P P 3.64050767804519 3.48086047717533 3.09228277386361 P P P LNCV6_138167_PI430048170 mRNA
ATTTATTGAAAATAAACGACGGAAAAGTCTGGCCTTGCCTCTGTGCAAGCTTGGAGGCCT NM_004320 RefSeq chr16 + 28878487 28904509 ATP2A1 487 "ATPase, Ca++ transporting, cardiac muscle, fast twitch 1, transcript variant a" GO:0005515|GO:0048471|GO:0034976|GO:0006200|GO:0006942|GO:0042803|GO:0008637|GO:0034220|GO:0051561|GO:0045988|GO:0006816|GO:0031095|GO:0005793|GO:0090076|GO:0005509|GO:0033017|GO:0034704|GO:0055085|GO:0005524|GO:0005388|GO:0070509|GO:0016529|GO:0016020|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96022_PI430048170 0.0188923578051881 1.2896784551669 13.6965952165261 13.8082434180576 13.8193192468055 P P P 13.3368292844205 13.3300569881074 13.5485357447608 P P P LNCV6_96022_PI430048170 mRNA
CCTGCTAGAAGGTTACAGTGTATTATGTAGCATGCAATGTGTTATGTAGTGCTTAATAAA NM_004541 RefSeq chrX + 119871770 119876666 NDUFA1 4694 "NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa" GO:0022904|GO:0005739|GO:0031966|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0016021|GO:0008137|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141737_PI430048170 0.369511157114519 0.8685440223956528 19684593593038 7.64677781276291 7.60654315205625 P P P 8.1763623371583 8.07541389915427 7.86998056630155 P P P LNCV6_141737_PI430048170 mRNA
CCCAGCTGGGTCCGCCCCGGCCTCAGAGTTGCGCAATAAATGTTACCGACCATGAAAAAA NM_145045 RefSeq chr19 - 11420604 11435159 CCDC151 115948 "coiled-coil domain containing 151, transcript variant 1" GO:0005515|GO:0005929|GO:0005814|GO:0005930|GO:0030030|GO:0003341|GO:0036064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136762_PI430048170 0.00527492817129817 2.43855276553873 5.11794696597638 4.81317115491632 5.37252167378757 P P P 3.49994756825974 3.86799939233008 4.07410477482771 P P P LNCV6_136762_PI430048170 mRNA
GCCACGTACTCAGAGTATAACAATGTGTTCTCATTAAAAAATACATCCCACGGAAACCTC NM_001204375 RefSeq chr5 + 32711331 32791724 NPR3 4883 "natriuretic peptide receptor 3, transcript variant 1" GO:0033688|GO:0048015|GO:0042562|GO:0007200|GO:0008528|GO:0048662|GO:0030157|GO:0007194|GO:0007193|GO:0042803|GO:0001501|GO:0016941|GO:0051000|GO:0005887|GO:0008217|GO:0002158|GO:0017046|GO:0035810|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130886_PI430048170 0.296135994025281 1.07769464644929 8.71636998138348 8.84792729567476 8.67313166528823 P P P 8.5169422151921 8.76904764293327 8.62223061956353 P P P LNCV6_130886_PI430048170 mRNA

GGGCATGACCAGATGCGTCCCAAGATGTTGATTTTTACTGTGTTTTATAAAATAGAGTGT NM_017617 RefSeq chr9 - 136494443 136545786 NOTCH1 4851 notch 1
GO:0005515|GO:0010467|GO:0007386|GO:0007220|GO:0001190|GO:0003700|GO:0006367|GO:0003180|GO:0003181|GO:0003184|GO:0010832|GO:0007409|GO:0007283|GO:0007221|GO:0007507|GO:0001947|GO:0007219|GO:0003241|GO:0009986|GO:0001708|GO:0003273|GO:0005509|GO:0003270|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129179_PI430048170 0.00879132949603709 0.8051774153052778.20132232171012 8.27721718183779 8.32285330205087 P P P 8.66447780334392 8.4938000214734 8.57853484783779 P P P LNCV6_129179_PI430048170 mRNA
GTTGACAGTGTACAATGCCTTTGATGAACTGTTTTGTAAGTGCTGCTATATCTATCCATT NM_001238 RefSeq chr19 + 29811993 29824308 CCNE1 898 cyclin E1
GO:0045859|GO:0005515|GO:0019901|GO:0003713|GO:0005634|GO:0050681|GO:0005829|GO:0000082|GO:0000083|GO:0006270|GO:0016301|GO:0000307|GO:0051726|GO:0016538|GO:0005654|GO:0006468|GO:0045893|GO:0000278|GO:0016055|GO:0030521|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142909_PI430048170 0.0566073599102084 2.38670598454767 4.01463068217427 3.0488350332615 3.99470612796751 P P P 3.11891621802218 1.98640972162795 2.09384189334012 P A A LNCV6_142909_PI430048170 mRNA
CCTCAACCACCTATTCATTGACTTCTTTTGTGTTAGAGTGAATAAAATTTTGTTCATGCC NM_001199215 RefSeq chr3 - 112815708 112845950 CD200R1L NA "CD200 receptor 1-like, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144385_PI430048170 0.1754138759952730.8368405696675720.501230889466871 0.4478650625129060.332290983453796A A A 0.7036965301206080.875705895367963 0.445995550612153A A A LNCV6_144385_PI430048170 mRNA
CAGTAAACTGCTCCACTGTGGCTTGTTTATGTGTTAATACTGCTTGTTTTCTGTTATAAA NM_004066 RefSeq chr18 + 580342 582020 CETN1 1068 "centrin, EF-hand protein, 1"
GO:0034605|GO:0008017|GO:0005515|GO:0007067|GO:0005813|GO:0000922|GO:0032795|GO:0005814|GO:0005509|GO:0032391|GO:0031683|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134828_PI430048170 0.295567412268397 1.08059614256037 8.25153621973528 8.1202317418783 8.01265973293242 P P P 7.98431562929063 8.13537172009535 7.93135547483941 P P P LNCV6_134828_PI430048170 mRNA
TCAAGGCCAACTGTCACATGAAGGAATGAATAAAGAGTTTTTACTGACTTGTGCAAAAAA NM_207327 RefSeq chr22 - 46244012 46250296 CDPF1 150383 "cysteine-rich, DPF motif domain containing 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130587_PI430048170 0.90047207098564 0.9912055575479234.64644821030273 4.58687240613376 4.79011377971525 P P P 4.78707805100795 4.55702893206949 4.71567577874583 P P P LNCV6_130587_PI430048170 mRNA
GCGAATATCTGGACTGCTAATATCTGACAACAGTAGGCGAAATTTACTTTTTCTTCAAAT NM_001113567 RefSeq chr17 - 16442004 16492191 LRRC75A 388341 "leucine rich repeat containing 75A, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53986_PI430048170 0.0492566037721711 0.9325489518490610.362191375669601 0.3272203957094380.311729412511358A A A 0.4828635960293730.433255218485995 0.386109565531233A A A LNCV6_53986_PI430048170 mRNA
ACCACGACACATCCCAGGTCACTTTCTGGGGAACAACACAGTCATCGACATCCTGCGGCA NM_001194986 RefSeq chr1 - 47760527 47996890 TRABD2B 388630 TraB domain containing 2B
GO:0005515|GO:0017147|GO:0031301|GO:0005887|GO:0018158|GO:0008152|GO:0030178|GO:0006508|GO:0016055|GO:0004222|GO:0046872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131784_PI430048170 0.8213448911020250.9875915613355994.66112126673815 4.8408098922302 4.86539510762607 P P P 4.74886916962518 4.77559667398801 4.90079436959111 P P P LNCV6_131784_PI430048170 mRNA

CCTTGTTAAGTGTCTGAAGGACAGGCGTTGAATATCTTAGATACGAATGTGGGCATACTC NM_001271870 RefSeq
chr1 - 144892046 145093246 SRGAP2B 647135 SLIT-ROBO Rho GTPase activating protein 2B
GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99496_PI430048170 0.3305581161672281.25580220707513 2.65020383602485 2.6324753359595
2.50378198750591 A A A 2.15801671589792 2.75819158392981 1.68909739279539 A A A
LNCV6_99496_PI430048170 mRNA
AAATCTAATTTTGATGTTCTGCAAGTTCCCTGGGGGCCATGAAGCACCTGACACTTGGAT NM_001270771 RefSeq
chr4 - 185585443 185956716 SORBS2 8470 "sorbin and SH3 domain containing 2, transcript variant 9"
GO:0005515|GO:0048471|GO:0030018|GO:0005886|GO:0019904|GO:0005634|GO:0015629|GO:0046872|GO:0008
150|GO:0016477|GO:0005200|GO:0007015|GO:0007155|GO:0008307|GO:0008093 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137826_PI430048170 0.65353428539846 1.16739811543861 0.430826561248788
1.31195817270899 0.362358134587329 A A A 0.7939308313349170.397118591633304
0.413591013610153 A A A LNCV6_137826_PI430048170 mRNA
AACCTACAAACTCAAGAGAGTCCTTAGGAATCTGGGCATCACCAAGATCTTCAGCAACGA NM_006220 RefSeq
chr14_KI270847v1_alt - 1478201 1483289 SERPINA2 390502 "serpin peptidase inhibitor, clade A
(alpha-1 antiproteinase, antitrypsin), member 2 (gene/pseudogene), transcript variant 1"
GO:0010951|GO:0005515|GO:0005783|GO:0004867|GO:0005615 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143176_PI430048170 0.00673093994325285 0.4751436462752945.74478379630021
5.93656562578172 6.25161609337783 P P P 6.87611696787342 6.93435854582452
7.34292521458113 P P P LNCV6_143176_PI430048170 mRNA
CTGGTGACTATTTGTGCCTGAAAATTCGTTTTGTATTAAAATTCTGGAGAAGGAATTCAG NM_002618 RefSeq chr2
+ 61017676 61051990 PEX13 5194 peroxisomal biogenesis factor 13
GO:0005515|GO:0016560|GO:0043231|GO:0001967|GO:0021795|GO:0001561|GO:0016020|GO:0007626|GO:0001
764|GO:0005779|GO:0060152|GO:0005778|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144011_PI430048170 0.0711839652707328 0.91704357925073811.752896927476
11.8148206925164 11.6941510164478 P P P 11.8924318212428 11.935521381234
11.8083681560422 P P P LNCV6_144011_PI430048170 mRNA
TTGTCCTCATCAAGAAGGATGTGGATGAAGCTTACATGAACAAGGTAGAGCTGGAGTCTC NM_001256293 RefSeq
chr12 - 52897186 52949866 KRT8 3856 "keratin 8, type II, transcript variant 3"
GO:0005882|GO:0005515|GO:0030018|GO:0097284|GO:0005634|GO:0032403|GO:0016363|GO:0005737|GO:0016
010|GO:0005911|GO:0097110|GO:0016032|GO:0045111|GO:0045095|GO:0070062|GO:0060706|GO:0045214|GO:0
097191|GO:0033209|GO:0042383|GO:0005198|GO:0051599|GO:0043034|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_90714_PI430048170 0.0226691554808318 0.6755084607033867.36088745713377
7.09303490783894 7.25877172594745 P P P 7.96298389430188 7.56624993702005
7.86495021978678 P P P LNCV6_90714_PI430048170 mRNA
CATCCACTCTGAAATCAATGTGAATTTAACTTCAGTTCCATACAGAAACTTCTTTTCCAC NM_001354 RefSeq chr10
- 4987775 5018033 AKR1C2 1646 "aldo-keto reductase family 1, member C2, transcript variant 1"
GO:0044598|GO:0031406|GO:0051897|GO:0008284|GO:0032052|GO:0044597|GO:0006693|GO:0047086|GO:0007
586|GO:0071799|GO:0004032|GO:0005737|GO:0016655|GO:0007186|GO:0071395|GO:0047115|GO:0030855|GO:0
042448|GO:0018636|GO:0008202|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139297_PI430048170 0.15868207673276 0.4904437629924481.81946136876103
0.4585760654364330.296858203103373 A A A 1.38173171054294 2.70695944789447
1.75189549383721 A P A LNCV6_139297_PI430048170 mRNA
TAGGAAACTCTGTGTTCTGTGATTTAGTCAGGCAATAAAATGCTCTCACTCCTTAAAAAA NM_152263 RefSeq chr1
- 154161812 154192135 TPM3 7170 "tropomyosin 3, transcript variant Tpm3.12"
GO:0001725|GO:0005862|GO:0030049|GO:0002102|GO:0006928|GO:0003779|GO:0032154|GO:0005829|GO:0030

426|GO:0003674|GO:0006936|GO:0031941|GO:0030863|GO:0005856|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70817_PI430048170 0.0613044681973399 1.31689115009128 8.9723866518955 8.75662987307845 8.76313267604966 P P P 8.3490530190658 8.66837463368692 8.26144376261976 P P P LNCV6_70817_PI430048170 mRNA
ACTGAAGATGACTTCAATGATTGGTGCCAGCAAGTCAAAAAGCTGTCTCTGCTTGGAGGT NM_178326 RefSeq chr2 + 241637611 241673856 ATG4B 23192 "autophagy related 4B, cysteine peptidase, transcript variant 2"
GO:0005515|GO:0006501|GO:0006995|GO:0045732|GO:0000422|GO:0006914|GO:0051697|GO:0005829|GO:0004197|GO:0005737|GO:0004175|GO:0016485|GO:0006612|GO:0006508|GO:0008234|GO:0000045|GO:0010508 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139393_PI430048170 0.0465780946325744 0.3279063158416031.99992004843447 0.43917949048821 1.4778196042974 A A A 3.09777550614357 2.60344182646068 3.34887549632056 P P P LNCV6_139393_PI430048170 mRNA
CACCAGCATGACAAAATGGTCAAAAAATAAGTCATCAGCACTTAAGAAATGAAAGCAACT NM_001243533 RefSeq chr1 + 26111776 26125548 PDIK1L 149420 "PDLIM1 interacting kinase 1 like, transcript variant 3"
GO:0004674|GO:0006468|GO:0005654|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74110_PI430048170 0.00144323317026692 1.42941137842843 6.22545740207726 6.10210144291977 6.0994898722657 P P P 5.529618424147 5.685953693499 5.66392821208377 P P P LNCV6_74110_PI430048170 mRNA
TGACTCCAGGTATTGAGTTCATCTTCAACTTCTCCCAACAATGAACTGGAGTTTTCTGTG NM_002337 RefSeq chr4 - 3503596 3532497 LRPAP1 4043 "low density lipoprotein receptor-related protein associated protein 1, transcript variant 1"
GO:0032091|GO:0005515|GO:0048237|GO:0005886|GO:0009986|GO:0005783|GO:0005576|GO:0070326|GO:0031982|GO:0006898|GO:1900222|GO:0010916|GO:1900116|GO:0006457|GO:0004873|GO:0051082|GO:0016021|GO:0035473|GO:0016192|GO:0048019|GO:0008201|GO:0050750 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133812_PI430048170 0.0208503374303372 1.23757662941067 11.7353509576675 11.6659947810437 11.5841275749307 P P P 11.2476833854666 11.3417077418445 11.4689203741491 P P P LNCV6_133812_PI430048170 mRNA
GGTACTTGTCCTTTCCCTTTGTAAACTACATTTGACATGGATTAAACCAGTATAAACAGT NM_018150 RefSeq chr1 + 44405287 44651724 RNF220 55182 ring finger protein 220
GO:0005737|GO:0004842|GO:0016567|GO:0016874|GO:0008270|GO:0051865 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136455_PI430048170 0.15904908286953 1.19234215473096 12.1793246905408 12.2032178302837 12.0450517322896 P P P 12.1223253361306 11.8098022198478 11.7058480555889 P P P LNCV6_136455_PI430048170 mRNA
AGGTGCAGTCACTCACACCTGCTTGCGCTCACCATCAATAAAAGTAATTTCACCCGAAAA NM_145040 RefSeq chr11 - 6318945 6320510 PRKCDBP 112464 "protein kinase C, delta binding protein"
GO:0051898|GO:0005515|GO:0043234|GO:0005737|GO:0030866|GO:0005901|GO:0005080|GO:0070374|GO:0032922 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134360_PI430048170 0.5272131135172441.04714794984157 10.9201738101684 10.8083277958858 10.8627691982617 P P P 10.6280083211945 10.9477965386761 10.8005505054529 P P P LNCV6_134360_PI430048170 mRNA
TTCCACCTGGTTTTACTGTAACATTTGGAAAAGGAATAAATGTCGTCCCTTTAGTGGTGC NM_023009 RefSeq chr1 - 32333828 32336239 MARCKSL1 65108 "MARCKS-like 1, transcript variant 1"
GO:0005516|GO:0008284|GO:0005737|GO:0005886|GO:0003779|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140701_PI430048170 0.2827511518717451.27468367247708 1.14504840084515 0.485706064684969 0.495910357110742 A A A 0.3363272298911280.392399676951138

0.448584897614759 A A A LNCV6_140701_PI430048170 mRNA
GATGACAGCTGAAGCTATTCATATGGAGCCATATACTCTATTGTTGAAATAGAATAAGGA NM_152513 RefSeq chr22
+ 41699513 41799455 MEI1 150365 meiosis inhibitor 1 GO:0007286|GO:0007141 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140590_PI430048170 0.142981720229586 0.84124281754749 8.93219004234325
8.78771927325475 8.54123474597995 P P P 8.90261463926375 8.99001870472867
9.13395163311876 P P P LNCV6_140590_PI430048170 mRNA
TGGGCGCAGAGGCTTTTCCAGTGTGTATAAATCCATGAAAATAAACGCCACCTGCACCCC NM_004910 RefSeq chr11
- 67491767 67505372 PITPNM1 9600 "phosphatidylinositol transfer protein, membrane-associated 1, transcript variant 1"
GO:0005811|GO:0006629|GO:0030496|GO:0015031|GO:0032154|GO:0046872|GO:0005737|GO:0008526|GO:0015914|GO:0016020|GO:0007420|GO:0032580|GO:0005789|GO:0007602 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138415_PI430048170 0.681344372629618 1.02036689201843 0.55271708665715
0.399450671511568 0.541035348244721 A A A 0.385370843111202 0.512027601288294
0.509918583269624 A A A LNCV6_138415_PI430048170 mRNA
CATGTGCCCAACACTTTGTACTCTTGGAATAGAGTGTGGAATATTATAAAACTGGATTTT NM_181426 RefSeq chr3
- 180614007 180679495 CCDC39 339829 coiled-coil domain containing 39
GO:0060287|GO:0001947|GO:0035469|GO:0071910|GO:0030324|GO:0060285|GO:0005930|GO:0070286|GO:0005856|GO:0071907 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137540_PI430048170 0.457344616831777 1.13023726459598 2.0912407499753
1.90361227652764 2.20032365475681 A A A 2.28921742622235 1.55648962356552
1.73007660620527 A A A LNCV6_137540_PI430048170 mRNA
TACATGTAGTTCTCACATCTGTGTCATTCTGGCCTTCTACATACCTGGTCTCTTCTCCTA NM_001005178 RefSeq chr11
+ 6199223 6200186 OR52W1 NA "olfactory receptor, family 52, subfamily W, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_8439_PI430048170 0.527772419120721 1.27580235115515 0.535526137481586 0.730876418978501
1.67373467702002 A A A 0.948349163711783 0.518095297536141 0.656230612557878 A A A
LNCV6_8439_PI430048170 mRNA
AATGCAGATGAAGCTCCCAGTGGATTCCCACACTCTATCAATAAACACCTCTGGCTGAAA NM_153324 RefSeq chr20
+ 31440518 31450257 DEFB123 245936 "defensin, beta 123, transcript variant 1"
GO:0009986|GO:0045087|GO:0005576|GO:0042742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139885_PI430048170 0.477948079456821 1.10635444164152 11.488830541898
11.3336485595902 11.7677867843637 P P P 11.2222507211149 11.2585345297971
11.6632287461324 P P P LNCV6_139885_PI430048170 mRNA
GATTCACTATTCTAGAACTTGCATGACCTTTACTGTGTTAGCTCTTTGAATGTTCTTGAA NM_003234 RefSeq chr3 -
196049283 196082090 TFRC 7037 "transferrin receptor, transcript variant 1"
GO:0005515|GO:0003725|GO:0048471|GO:0005886|GO:0072562|GO:0005615|GO:0001558|GO:0042802|GO:0043231|GO:0006879|GO:0033572|GO:0045780|GO:0004998|GO:0042127|GO:0016032|GO:0070062|GO:0042470|GO:0009986|GO:0030316|GO:0005576|GO:0055085|GO:0031982|GO:0035690|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144070_PI430048170 0.00320662485996604 0.499227281884612 7.87936381667368
7.55053325071524 7.9294197841641 P P P 8.71872676353681 8.67941036755993 8.9778652316987
P P P LNCV6_144070_PI430048170 mRNA
CACTTCCAACTCCAAACTTGCTCAACTAATCCTTAAAAATAAACTTGAGCTGGAATTTGA NM_198066 RefSeq chr14
- 52775192 52791668 GNPNAT1 64841 glucosamine-phosphate N-acetyltransferase 1
GO:0005793|GO:0005770|GO:0006041|GO:0006044|GO:0006048|GO:0005829|GO:0001889|GO:0000139|GO:0004343|GO:0048029|GO:0006488|GO:0044267|GO:0010008|GO:0018279|GO:0043687 . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_139490_PI430048170 0.1114507826212741.30916238174944 11.6875443816962
11.6200349702725 11.5002074288465 P P P 10.9077680934091 11.4454635053119
11.2445814717893 P P P LNCV6_139490_PI430048170 mRNA
GTTTTCTCTCACTGTAGACCAAAGAGCCGCTTGTGTGATATTAAAGCCACTTTAGAAAGC NM_025108RefSeq chr16
+ 2460113 2464963 C16orf59 80178 chromosome 16 open reading frame 59 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128277_PI430048170 0.3616723535130090.7027353827796261.14280289662386
0.9672855680927213.27434978598352 A A P 2.51931645013776 3.16144317248837
2.32552428734625 A P A LNCV6_128277_PI430048170 mRNA
ATGCTGTACCAGCATCTGCTCCCTCTACCAGCTGGAGAACTACTGCAACTAGACGCAGCC NM_001185098 RefSeq
chr11 - 2159778 2161209 INS 3630 "insulin, transcript variant 3"
GO:0005515|GO:0030307|GO:0005159|GO:0005158|GO:0046631|GO:0045597|GO:0050731|GO:0002020|GO:0005
615|GO:0042802|GO:0046889|GO:0045922|GO:0015758|GO:0000165|GO:0046326|GO:0045821|GO:0032460|GO:0
030335|GO:0005796|GO:0045740|GO:0014068|GO:0045840|GO:0006953|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130318_PI430048170 0.0228933578178162 0.4449644908990662.17857501191691
2.88489746644391 2.80969126008517 A A A 3.90546129914173 3.65914383852579
3.89850263486129 P P P LNCV6_130318_PI430048170 mRNA
CTACAGACATTTGGCCCCAAATCCCTGACTCAATAAAGTAAGCGTGTACCTAGCAAAAAA NM_001303034 RefSeq
chr11 - 3665586 3671384 CHRNA10 57053 "cholinergic receptor, nicotinic, alpha 10 (neuronal),
transcript variant 2"
GO:0030424|GO:0005262|GO:0030054|GO:0042472|GO:0005102|GO:0007204|GO:0005892|GO:0007271|GO:0016
020|GO:0050910|GO:0042127|GO:0045211|GO:0070588|GO:0043204|GO:0004889 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_111584_PI430048170 0.5505803199095920.8694953440156033.12911972210514
1.83016038554352 2.29992046356891 A A A 2.3585408618181 2.94628644411945
2.80299903953325 A P P LNCV6_111584_PI430048170 mRNA
TCTGCAGGACGAGGATGGCTACAGGATGAAGTTTGCCTGCTACTACCCCCGTGTGGAGTA NM_007293RefSeq
chr6_GL000252v2_alt + 3229829 3250454 C4A NA "complement component 4A (Rodgers blood
group), transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141554_PI430048170 0.0114363883831754 0.4730379397384748.07936086495684
8.04994781071342 8.32641023607873 P P P 8.92492045431931 9.21404695038299
9.51312170787034 P P P LNCV6_141554_PI430048170 mRNA
GAACTTTCCTGTTTTCATGTCTTTGCTTCATCTGGAATTGGCTTAACACCCTTTTATAAA NM_024831RefSeq chr8 +
55773231 55825446 TGS1 96764 trimethylguanosine synthase 1
GO:0005515|GO:0010467|GO:0006355|GO:0015030|GO:0005634|GO:0044281|GO:0034660|GO:0000387|GO:0005
615|GO:0006351|GO:0005829|GO:0005737|GO:0071164|GO:0030532|GO:0022613|GO:0005654|GO:0009452|GO:0
071167|GO:0044255. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145697_PI430048170 0.3728427336976341.27970333888504 1.56500933659331
0.8303710813303750.696941643241921A A A 0.5988507864578510.963087873909702
0.589142659047146A A A LNCV6_145697_PI430048170 mRNA
GGTGTGCTGTGTCCACCGTTGTGTACAGAATTTTTCTTCATTAATTTTGTGTTTAAGTTA NM_000503RefSeq chr8 -
71197432 71362232 EYA1 2138 "EYA transcriptional coactivator and phosphatase 1, transcript variant
EYA1C"
GO:0005515|GO:0001656|GO:0007389|GO:0001658|GO:0007605|GO:0003723|GO:0000132|GO:0035088|GO:0048
704|GO:0005634|GO:0048752|GO:0045739|GO:0009653|GO:0046872|GO:0035335|GO:0006302|GO:0005737|GO:0
045944|GO:0010212|GO:2001240|GO:0090103|GO:0072513|GO:0014706|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106685_PI430048170 0.9957803170524820.9971124827062120.415240904939847

0.4519212815786160.460538746333449A A A 0.3490606450250880.370547088084066
0.606604571542564A A A LNCV6_106685_PI430048170 mRNA
TTACAAGGACACACAGGGTGTGATACTGGTCTATGATGTTGGGCAGAAAGACTCCTTTGA NM_016544RefSeq chr2
- 24943635 24972094 DNAJC27 51277 "DnaJ (Hsp40) homolog, subfamily C, member 27, transcript
variant 1"
GO:0006184|GO:0005739|GO:0003924|GO:0005634|GO:0070374|GO:0032482|GO:0019003|GO:0005525|GO:0006
886|GO:0071701|GO:0012505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141451_PI430048170 0.0117460560101193 2.22561597030087 15.5492315107711
15.5720885637849 15.5590347603982 P P P 14.1469440967067 14.5765374902817
14.4608779858307 P P P LNCV6_141451_PI430048170 mRNA
GAAAGAGTGTTGGTGTTGGCTGGGGTGTCAATAAAGCTGTGCTTGGGGTCGCTGAAAAAA NM_002178RefSeq chr12
+ 53097651 53102344 IGFBP6 3489 insulin-like growth factor binding protein 6
GO:0007165|GO:0008285|GO:0005794|GO:0043567|GO:0031994|GO:0031995|GO:0005576|GO:0044267|GO:0005
615|GO:0001558|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130887_PI430048170 0.00857460667087801 0.5622030477399684.12017220060111
4.25219120451417 3.87537265057894 P P P 4.72814899927789 5.15781377758642
4.84439444132279 P P P LNCV6_130887_PI430048170 mRNA
CACAGGCCCTTTTCCTTGTTTGTTTTGTGTTAGTTTATTGTAAACAGCCATTTGTTGTAA NM_021005RefSeq chr15 +
96330881 96340263 NR2F2 7026 "nuclear receptor subfamily 2, group F, member 2, transcript variant 1"
GO:0005515|GO:0006629|GO:0060674|GO:0003700|GO:0045736|GO:0048514|GO:0003707|GO:0009956|GO:0005
634|GO:0009952|GO:0042803|GO:0043401|GO:0004879|GO:0032355|GO:0006357|GO:0003714|GO:0060707|GO:0
001893|GO:0000122|GO:0006351|GO:0043565|GO:0009566|GO:0007165|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145385_PI430048170 0.2870571641183660.7208825525751121.31154012207835
0.3930112151441530.327805294406716A A A 1.67389580182138 0.86466661624267
0.995698329432919A A A LNCV6_145385_PI430048170 mRNA
CCACTCCCTGAAGTTTATGAGGTTGATAAGAAAACATAACAGATAAAGTTTATTGAGTGC NM_000151RefSeq chr17
+ 42900796 42914433 G6PC 2538 "glucose-6-phosphatase, catalytic subunit, transcript variant 1"
GO:0010468|GO:0006094|GO:0015760|GO:0030176|GO:0044281|GO:0046415|GO:0032094|GO:0008645|GO:0015
758|GO:0035264|GO:0016773|GO:0051156|GO:0008202|GO:0042632|GO:0005975|GO:0005977|GO:0042593|GO:0
055085|GO:0046838|GO:0004346|GO:0042301|GO:0009405|GO:0005789|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127394_PI430048170 0.0425682039131763 0.4705313042931854.50462388791594
4.32324659636997 4.80704015692945 P P P 5.08191513899105 5.68683655661951
6.02015038917219 P P P LNCV6_127394_PI430048170 mRNA
GAGCAGCCTATGAACCTAAAGACATACTGCAGTTTGTTCATAAATGTATTCAGTCTTTTA NM_018015RefSeq chrX
+ 106611929 106679443 CXorf5755086 "chromosome X open reading frame 57, transcript variant 1"
GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134782_PI430048170 0.6602658633979090.7840031572251420.391696426480692
0.7505204693416290.298589649074981A A A 1.56982985219799 0.300371973693948
0.248446101997735A A A LNCV6_134782_PI430048170 mRNA
ATTACTAAATTGCTTCTTTTCGTTTCCCTCATCCCGAGGATGGTAGGGACGAAAAGGGGA NM_005519RefSeq chr10
+ 123148121 123150672 HMX2 3167 H6 family homeobox 2
GO:0048026|GO:0043565|GO:0008284|GO:0006355|GO:0042472|GO:0007420|GO:0005634|GO:0030154|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80419_PI430048170 0.1817761068761531.47686811543423 4.82846267521083 4.74049659377143
3.99033606257166 P P P 3.89217841107909 4.15329341272641 3.95036109455073 P P P
LNCV6_80419_PI430048170 mRNA
AAAGGGTTCAGCATCTGACTCTGGAGAACGAGGCCCTGAAGCAGAGCCTGAGTCTCATGCNM_145754RefSeq chr8

+ 144466336 144474116 KIFC2 90990 kinesin family member C2
GO:0008017|GO:0005871|GO:0005737|GO:0008152|GO:0005874|GO:0003777|GO:0016887|GO:0005524|GO:0007
018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129288_PI430048170 0.9041697382423391.00276994132877 0.35321880727287
0.3322045039538250.267761438101721 A A A 0.3151530506902020.32502903567772
0.302308940592357 A A A LNCV6_129288_PI430048170 mRNA
GAATATGTTCAAAACAGGTCTGACTAGTGACTATGAGAATGGAGCTATTTAGAGTTGATT NM_173518RefSeq chr8
+ 66870748 66922048 MCMDC2 157777 "minichromosome maintenance domain containing 2,
transcript variant 1" GO:0006260|GO:0005524|GO:0003677 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_61217_PI430048170 0.8422589437927041.01931644088371 4.6136266311439 4.73152712619051
4.92903466257972 P P P 4.70875448887196 4.58583166298841 4.89736346898185 P P P
LNCV6_61217_PI430048170 mRNA
AATCTAATTCAGGCTTTGAAAAAGACACCTTATCACCCACACCCACACGTGTTCAATACA NM_005197RefSeq chr14
- 89156171 89417110 FOXN3 1112 "forkhead box N3, transcript variant 2"
GO:0043565|GO:0007095|GO:0005515|GO:0003700|GO:0005634|GO:0008022|GO:0045892|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133658_PI430048170 0.2410270026154670.8483345097193029.92392048799913
9.75588059941678 9.70935546293949 P P P 9.75145116796088 10.1083548473779
10.2109682527423 P P P LNCV6_133658_PI430048170 mRNA
CACCTGCCTTTCTCCTGTGGTCTCTTAATCCAGTAATTGTATTACTGCCATTAAAGGATG NM_015168RefSeq chr19
- 47064189 47113752 ZC3H4 23211 zinc finger CCCH-type containing 4 GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133015_PI430048170 0.0176029305553255 0.697298368661838 5.44327632755059
5.55606174603584 5.6376480151455 P P P 5.9085080717906 6.02960925025986
6.24551271270538 P P P LNCV6_133015_PI430048170 mRNA
GGAAAATTATTATTATGAACCTTCAGCCTACTTTCTTGAGTGCCGTAAAAGTGCTTGTAA NM_005715 RefSeq
chr6 + 148747134 149076990 UST 10090 uronyl-2-sulfotransferase
GO:0030208|GO:0000139|GO:0005975|GO:0009405|GO:0008146|GO:0006477|GO:0044281|GO:0016021|GO:0030
204|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135644_PI430048170 0.0424059374801408 0.612039995220863 5.47913612058124
5.37699536114648 5.72798954802021 P P P 5.96199290595838 6.12533342473484
6.57338321199982 P P P LNCV6_135644_PI430048170 mRNA
GACACATGAAATGAAAGTTTAGCTAGCCCACTATTTGTTGTAAATTGAAAACGAAGTGTG NM_000253 RefSeq
chr4 + 99564077 99623997 MTTP 4547 "microsomal triglyceride transfer protein, transcript variant
1" GO:0043235|GO:0006629|GO:0006869|GO:0042157|GO:0005788|GO:0044281|GO:0005319|GO:0008289 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93081_PI430048170 0.0102892988309326 1.57041158135143 4.56863897949369
4.46046943921726 4.67611702565199 P P P 3.96220627659132 4.06449402322194
3.71054987055704 P P P LNCV6_93081_PI430048170 mRNA
TCCTAAAGCGCTATGCAGAGAAGTACTCTGGGGTCTTGGATTCTCCCTACGAGCGTCCGG NM_001013690 RefSeq
chr12 - 51817891 51831917 FIGNL2 NA fidgetin-like 2 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132817_PI430048170 0.533355346438966 1.12300802744087 3.52829275432292
3.56544672481054 4.10786345347219 P P P 3.73207378739096 3.63470330556185
3.38685919641251 P P P LNCV6_132817_PI430048170 mRNA
TCTGTTTATGTTGAGGGATGTTTTTAAAGCCCACAGGTGAGGTGGATGTGGTAGACTGAT NM_024327 RefSeq
chr19 + 43596391 43600435 ZNF576 79177 "zinc finger protein 576, transcript variant 1"
GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0003677|GO:0046872 . NA - . NA NA

NA NA NA NA NA NA NA
LNCV6_139551_PI430048170 0.361952660550454 0.936920369453381 12.6135463862479
12.4430761513627 12.3248828267281 P P P 12.5142371858257 12.5602638427586
12.6023358261387 P P P LNCV6_139551_PI430048170 mRNA
CCTGGGACCCCACCCCGTGTTAATGAAAAATGAGTTTTGGCAGCGCCTGTGGTCAAAAAA NM_016558 RefSeq
chr20 - 35953616 35955359 SCAND1 51282 "SCAN domain containing 1, transcript variant 1"
GO:0003700|GO:0006366|GO:0006357|GO:0000981|GO:0003713|GO:0005634|GO:0042802 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144797_PI430048170 0.0100875070768094 0.514387066760343 2.2845960080102
2.69281850729289 2.59059243896037 A A A 3.18879361887121 3.50660103248825
3.72984929093914 P P P LNCV6_144797_PI430048170 mRNA
AGTGGTCATATATATCACCAACTATGGATATCAAAAAGTTGGGGTCACATCAGTGCTATT NM_001292003 RefSeq
chr4 - 87160103 87220268 KLHL8 57563 "kelch-like family member 8, transcript variant 1"
GO:0016567|GO:0042787|GO:0031463|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140124_PI430048170 0.0418916550888266 0.82069753358825 9.61396165079071
9.56502278350328 9.62028630649178 P P P 9.75257352268329 9.96244308027378
9.93135328315646 P P P LNCV6_140124_PI430048170 mRNA
CAGTTTGCTCAAGCCCAGGCAAATTTCTGTGATTAAAATGAATTCATCAGTTCCTCCAAA NM_017931 RefSeq chr22
+ 46267963 46294008 TTC38 55020 tetratricopeptide repeat domain 38 GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144982_PI430048170 0.154834354124105 0.459885250019528 0.506056694671817
0.395935466599818 0.487480003671657 A A A 2.23634071283746 1.40950245498292
0.70428296503651 A A A LNCV6_144982_PI430048170 mRNA
GCTCAGCCAGTTCAATGTCTCCTTGTTATCAGAGAAATATTAGTTCAATACTGAAAGAAA NM_152890 RefSeq chr1
- 85729232 86156438 COL24A1 255631 "collagen, type XXIV, alpha 1"
GO:0005581|GO:0030198|GO:0002244|GO:0005578|GO:0005788|GO:0005576|GO:0005201 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141868_PI430048170 0.395429421558401 0.816656981257681 0.260278451811561
0.275566291435411 0.377313504043783 A A A 1.02821880821852 0.329273475668318
0.314376980442214 A A A LNCV6_141868_PI430048170 mRNA
AAGCAGATTGTCGGTGTTTCCTATTACAGTTGAATGTCATCTCTCAGTACATTTTCAATT NM_152601 RefSeq chr19
- 12461183 12484818 ZNF709 163051 zinc finger protein 709
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145262_PI430048170 0.564999384048245 1.23856656213409 0.391703024482385 0.406459934856
1.41294010019078 A A A 0.351682127660055 0.336043032943212 0.799862201043922 A A A
LNCV6_145262_PI430048170 mRNA
GGTTAATGCTGTAGAATAGGACTGTATACCAAATGTAATCTTTCCAATGCTCCAATGAAT NM_022114 RefSeq chr1
+ 3069177 3438621 PRDM16 63976 "PR domain containing 16, transcript variant 1"
GO:0005515|GO:0003713|GO:0046332|GO:0005634|GO:0000122|GO:0043457|GO:0046872|GO:0006351|GO:0043
565|GO:0050872|GO:0050873|GO:0017053|GO:0060021|GO:0030853|GO:0045893|GO:0043586|GO:0045892|GO:0
035019|GO:0030512|GO:0022008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136645_PI430048170 0.0813195502076599 0.614674073707696 2.92545181820328
3.40664695878276 2.57759112587524 A P A 3.3221781403578 3.93110671480593
3.81436652879213 P P P LNCV6_136645_PI430048170 mRNA
ATTTTTCTTTCAGTTTTGCGGCATGTGAGGTACTGGGTGAAAGACAGAAGCCTTCGTCTC NM_001097643 RefSeq
chr12_KI270904v1_alt - 328318 329278 TAS2R30 NA "taste receptor, type 2, member 30" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_132330_PI430048170 0.0338434356096721 0.950891814896373 0.409168234727169

0.3577200793558740.359933604556313A A A 0.452800640886061 0.458246023215184
0.434194431032887 A A A LNCV6_132330_PI430048170 mRNA
AGTACATCCTTAATTCGACATCAGAAAACTCATTTCAGAAAGGAAACCTTAGCAGAGTAA NM_001101338 RefSeq
chr9 - 112997119 113012192 ZNF883 NA zinc finger protein 883 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135002_PI430048170 0.7584566811417560.9468901396458374.50456223854593
4.77160813756674 4.67098268020708 P P P 4.4315858556334 4.68915479061117
5.01549429854067 P P P LNCV6_135002_PI430048170 mRNA
CTACTTTGGAAGCGTCAGTGGATATATTTGAAAGTGGTAATCCTGAATCTCTTTTAAACT NM_018194RefSeq chr1
+ 210328905 210676296 HHAT 55733 "hedgehog acyltransferase, transcript variant 1"
GO:0018345|GO:0016409|GO:0005789|GO:0007275|GO:0016021|GO:0005525|GO:0007224 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135769_PI430048170 0.1285290342533660.6237667645274770.464120705639702
0.3073232871945450.362688883101197A A A 1.23425011974444 0.500780471945191
1.31562786282032 A A A LNCV6_135769_PI430048170 mRNA
GGAACAAAACTCCCTAACTGACTCAGACACTTTGGAAATCATAGTTATTAACCATTCTAA NM_007249RefSeq chr13
- 73686011 74133929 KLF12 11278 Kruppel-like factor 12
GO:0003700|GO:0000977|GO:0006357|GO:0045944|GO:0003714|GO:0005634|GO:0000122|GO:0003677|GO:0001
227|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129889_PI430048170 0.748706614100577 1.04378451133223 0.722598629739044
0.32327597133706 0.319708099822571A A A 0.449087397302182 0.399126422002149
0.368996443536404A A A LNCV6_129889_PI430048170 mRNA
GTAGCCTAGTTATTTGAGCCTGGTTTCAATGTGAGAACCACGTTTACTGTTATTGTATTT NM_080759RefSeq chr13
- 71437965 71867192 DACH1 1602 "dachshund family transcription factor 1, transcript variant 1"
GO:0046545|GO:0005515|GO:0005667|GO:0030336|GO:0007585|GO:0008283|GO:0060244|GO:0048147|GO:0005
730|GO:0005634|GO:0000122|GO:0003677|GO:0043231|GO:0001078|GO:0005737|GO:0010944|GO:0001967|GO:0
001075|GO:0005654|GO:0051123 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129703_PI430048170 0.868164240780352 1.09810056887647 1.78817235947889
0.460138977820903 1.6978623916705 A A A 0.529600257681449 1.61749483369113
1.50610714845238 A A A LNCV6_129703_PI430048170 mRNA
GAAACATGTCCAGAAAGCCAACCCAGAGCCTGCAGAAGGCTAATAAAACATTTTAGAATGNM_144708RefSeq chr2
+ 189675984 189746650 ANKAR 150709 ankyrin and armadillo repeat containing
GO:0042659|GO:0005737|GO:0005913|GO:0045944|GO:0003713|GO:0035257|GO:0005634|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138626_PI430048170 0.0119813507613221 0.568162196718825 4.87189497298346
4.4642155024801 4.42701666137523 P P P 5.50069106407672 5.54171967340739
5.18540135970891 P P P LNCV6_138626_PI430048170 mRNA
AGCCTGCTCCCTAGCCAGAGGCTCTAATGTACAATAAAGCAATGTGGTAGTTCCAAAAAA NM_000106RefSeq
chr22_KI270928v1_alt - 48839 53222 CYP2D61565 "cytochrome P450, family 2, subfamily D,
polypeptide 6, transcript variant 1"
GO:0019369|GO:0006805|GO:0017144|GO:0005783|GO:0070989|GO:0044281|GO:0005739|GO:0004497|GO:0009
820|GO:0009822|GO:0008144|GO:0016712|GO:0008202|GO:0046483|GO:0008392|GO:0033076|GO:0070330|GO:0
005506|GO:0008395|GO:0009804|GO:0016098|GO:0051100|GO:0042737|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140774_PI430048170 0.217870913289826 1.18506307975183 4.90780209087219
4.97495324835189 4.97830639072162 P P P 4.9866006273179 4.57755914308429
4.51649396914567 P P P LNCV6_140774_PI430048170 mRNA
AGAGAGCCCTTACCAGGAATTAAACCTGCTAATCCCTATTTTAATTAGAACAGTGAGAAA NM_001145649 RefSeq
chr19 - 36543614 36605276 ZNF529 57711 "zinc finger protein 529, transcript variant 1"

GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128986_PI430048170 0.30273740244536 1.90831534860916 0.325954553449877 1.10006073501744 2.21656330248257 A A A 0.869553557224914 0.255457899828356 0.256935543795283 A A A LNCV6_128986_PI430048170 mRNA TCTTAGGAACAAGGAAGTGAAGGGAGCTCTGGGTCGAGTCTTTTCTCTCAACTTTTGGAA NM_001005186 RefSeq chr11 + 58030952 58031906 OR6Q1 NA "olfactory receptor, family 6, subfamily Q, member 1 (gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131462_PI430048170 0.315250484265921 0.534687543862038 1.43063417205386 1.06597055441769 0.278038368947801 A A A 2.76856913331131 1.06407829491647 1.21392279317611 P A A LNCV6_131462_PI430048170 mRNA CAACAATCCCAAGGCCCTTTTTATACAAAAATTCTCAGTTCTCTTCACTCAAGGATTTTT NM_000377 RefSeq chrX + 48683796 48691426 WAS 7454 Wiskott-Aldrich syndrome GO:0005515|GO:0050852|GO:0017124|GO:0015629|GO:0005829|GO:0042802|GO:0006955|GO:0005083|GO:0005911|GO:0043274|GO:0016197|GO:0030041|GO:0070062|GO:0012506|GO:0030048|GO:0019901|GO:0006952|GO:0003779|GO:0042110|GO:0050790|GO:0006461|GO:0008544|GO:0008154|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132256_PI430048170 0.450626269364769 0.82425226554143 0.435014762526583 0.445248285534805 1.77778068166437 A A A 1.39779119029895 1.07125068024592 1.44144240078851 A A A LNCV6_132256_PI430048170 mRNA GTGTCTTCACATCTCCTGCTGCGTTTTAAAGCATTTTTATAGTATGCGGTTTTGACTAAT NM_177987 RefSeq chr10 - 46887 49238 TUBB8 347688 "tubulin, beta 8 class VIII" GO:0006184|GO:0008150|GO:0003674|GO:0051258|GO:0005737|GO:0005874|GO:0005200|GO:0003924|GO:0007017|GO:0005525|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129993_PI430048170 0.0950652493947051 1.75400826078376 4.24985980985118 4.36496608492595 4.28421798317836 P P P 2.89572437992227 3.89842862648396 3.50441742631365 P P P LNCV6_129993_PI430048170 mRNA TCAGAAAATGCAGAAAACGCAGGTGAAATGCCGCAAAATCCTGACCAAGATGAAGCAGCA NM_001080503 RefSeq chr19 + 11346504 11354944 CCDC159 126075 coiled-coil domain containing 159 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128824_PI430048170 0.0930240836500212 0.45852608613099 3.48199837400187 3.23328220961623 2.95926496897703 P P P 4.24610717768679 4.92922778865113 3.63165608433548 P P P LNCV6_128824_PI430048170 mRNA TTGAAAATGATTACTGGGATCAAAGTACATTCATGTCGCAATTACAGAGAGAGAGAGAGAAA NM_001029874 RefSeq chr12 + 27696494 27697633 REP15 NA RAB15 effector protein NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111162_PI430048170 0.430427258340816 1.11970005707159 7.04566702746892 7.10461919487517 7.39484736200118 P P P 6.92266911365413 6.77978128520537 7.3220280281139 P P P LNCV6_111162_PI430048170 mRNA ATTGGCAACCAGAACGCCAGGTTCCATTTAATGAAGTTAGATTACCACCACCACCTGATA NM_001013439 RefSeq chr3 + 180912445 180982751 FXR1 8087 "fragile X mental retardation, autosomal homolog 1, transcript variant 3" GO:0017148|GO:0002151|GO:0003723|GO:0005730|GO:0006915|GO:0003729|GO:0030154|GO:0005737|GO:0007517|GO:0016020|GO:0043034|GO:0003730|GO:0005844 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144265_PI430048170 0.122795558284131 0.795685020179297 9.72932566043415 9.82933267908704 10.0306081261464 P P P 10.0170278317128 10.0937443401714 10.4468537822497 P P P LNCV6_144265_PI430048170 mRNA GAAGAGGCCATAGTACCTCCTGTTTGAAGTTGTTTATTCACATCTATCTTATTTGAAGAA NM_017746 RefSeq chr9 - 100302074 100352977 TEX10 54881 "testis expressed 10, transcript variant 1"

GO:0005515|GO:0031965|GO:0005737|GO:0071339|GO:0005730|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105321_PI430048170 0.7475518320819290.9734352618203376.86164561201871 6.85352938978144 7.06491823033902 P P P 6.90949979329083 6.8554681455068 7.12718890303945 P P P LNCV6_105321_PI430048170 mRNA CTTTGGAGGGCAAGTACACAGATCTTAACTCTAATGATGTAACTGGCCTAAGAGAGTCTG NM_004906RefSeq chr6 + 159726997 159756321 WTAP 9589 "Wilms tumor 1 associated protein, transcript variant 1"
GO:0008380|GO:0006397|GO:0031965|GO:0007049|GO:0016607|GO:0000381|GO:0005730|GO:0080009|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139363_PI430048170 0.4214580846836991.27216955262728 0.290079201024618 0.3034018820231591.15606238697464 A A A 0.31301519566397 0.285685994960307 0.288753405931979A A A LNCV6_139363_PI430048170 mRNA GAACCAAGTCCTACATTTCCAGAACTTTCTGGCAAAAATTTGCACTCATATTATTTATCC NM_018593RefSeq chr6 + 111087577 111223403 SLC16A10 117247 "solute carrier family 16 (aromatic amino acid transporter), member 10"
GO:0016323|GO:0005215|GO:0034220|GO:0015801|GO:0005886|GO:0006865|GO:0016021|GO:0055085|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137357_PI430048170 0.1068441778660760.828582656859161 10.311592042956 10.3252269274625 10.3609926262998 P P P 10.7446791346322 10.4170159733009 10.631455531431 P P P LNCV6_137357_PI430048170 mRNA GCTAGACCCTCTTCTGTAATGGGTAATGCGTTTGATTGTTTGAGATTTTCTGTTTTTAAA NM_015397RefSeq chr9 - 34086382 34126773 DCAF1225853 DDB1 and CUL4 associated factor 12
GO:0005813|GO:0005737|GO:0016567|GO:0080008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138260_PI430048170 0.9436156087467481.00134036567343 10.9103747765084 10.8387566828596 10.8025384442717 P P P 11.0394043772539 10.7459991808916 10.7419632488066 P P P LNCV6_138260_PI430048170 mRNA TGGGAGCTTGGAAACCTGGTCTCTTGAATTTCAAACCTGGTTTCTTACAGGTGGTTGTCT NM_012068RefSeq chr19 + 49928701 49933936 ATF5 22809 "activating transcription factor 5, transcript variant 1"
GO:0005515|GO:0005667|GO:0021891|GO:0043066|GO:0000977|GO:0006357|GO:0003714|GO:0001228|GO:0009791|GO:0006351|GO:0048712|GO:0005737|GO:0035264|GO:0045944|GO:0031072|GO:0007623|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134638_PI430048170 0.1402909056050110.9089531268439930.344241227109873 0.31957816705801 0.308650111432698A A A 0.5734758411893180.421264419095216 0.384069521650158A A A LNCV6_134638_PI430048170 mRNA CTTCACAAATGATTGTGTTGTGCTGAAATGGTGCTCTTATAGTACTGGCTTATTAAAAGT NM_001282692 RefSeq chr1 + 171257922 171285978 FMO1 2326 "flavin containing monooxygenase 1, transcript variant 1"
GO:0050661|GO:0006805|GO:0017144|GO:0050660|GO:0006970|GO:0006082|GO:0044281|GO:0070995|GO:0004497|GO:0004499|GO:0005789|GO:0032496|GO:0005788|GO:0009404|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91462_PI430048170 0.2159844205219591.01831592830461 0.3218917000414020.29611000275899 0.271153207706071A A A 0.2703991886769410.2734753484569590.267163985276779A A A LNCV6_91462_PI430048170 mRNA CTGAGATTGAAGACAGCCTTACAGAAGCTTTGGAGCAAATTAAGATAATTAGCTCATCTT NM_024621RefSeq chr3 - 157259742 157499656 VEPH1 79674 "ventricular zone expressed PH domain-containing 1, transcript variant 1" GO:0005886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139343_PI430048170 0.1947958222343381.67275259889825 2.12424585050733 2.50021899469485 3.29881699351807 A A P 2.43820097222577 1.38352422368103 1.94226050609806 A A A LNCV6_139343_PI430048170 mRNA CTTGTACAGAAATCAGGGTTCTTAGCTAGCAGTTTTTCTCCCACGCAGTCACTGTAATGT NM_198179RefSeq chr4

- 121328641 121381026 QRFPR 84109 pyroglutamylated RFamide peptide receptor
GO:0042277|GO:0004983|GO:0007186|GO:0005886|GO:0007218|GO:0005887|GO:0004930|GO:0016021|GO:0032
870 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134514_PI430048170 0.5205935628322411.20013795316312 4.71130482915268
3.96159662861305 4.22840069722555 P P P 3.18554277455795 4.33661164696267
4.40092530585684 P P P LNCV6_134514_PI430048170 mRNA
CTAAGAATCGTTGAGGACCAAAGTTGTCTTTGCTGACACGTGTTGCTTTTCTCTTTGCCT NM_001080421 RefSeq
chr19 - 17601327 17688199 UNC13A 23025 unc-13 homolog A (C. elegans)
GO:0051966|GO:0048786|GO:0043005|GO:0030424|GO:0016081|GO:0030054|GO:0031594|GO:0035249|GO:0050
435|GO:0046872|GO:0007269|GO:0019992|GO:0060384|GO:0035556|GO:0042734|GO:0005737|GO:0047485|GO:0
007528|GO:0016188|GO:0017075|GO:0001956|GO:0048172 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131452_PI430048170 0.0629605198659546 0.78248741798117 6.65905295225367
6.39093787326984 6.30026185417559 P P P 6.81806256458758 6.88254346328831 6.7318099390492
P P P LNCV6_131452_PI430048170 mRNA
CAGGCTGGAGCTGCTGTGTATAGACTGCCAAATGTGAAGTATTTATATTGTATTCAATAA NM_001291586 RefSeq
chr17 + 43211826 43220037 TMEM106A 113277 "transmembrane protein 106A, transcript variant 1"
GO:0008150|GO:0003674|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134106_PI430048170 0.4985858121854521.21270638900963 1.59690279068116
1.28449666207782 0.730009488140756A A A 1.48275588568672 0.848886828299217
0.350344520772488A A A LNCV6_134106_PI430048170 mRNA
ATCCTGTAAGGCAGCCACAGAACTAAAAAACAACAATTATTATTAAACTGCTCTGGATTC NM_001168364 RefSeq
chr2 + 27442365 27446481 KRTCAP3 200634 "keratinocyte associated protein 3, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68061_PI430048170 0.0360314025813882 0.4246170656913732.18758998525737
2.13446158795047 3.0176536783376 A A P 3.57064074720868 3.75989617043871 3.8790046670125
P P P LNCV6_68061_PI430048170 mRNA
GGAGCCAAGTCCTTGCGGGGCACAGACAGAAAACACTATAAATCCACACCTGGCAAAAAG NM_014636 RefSeq
chr9 + 126914773 127223166 RALGPS1 9649 "Ral GEF with PH domain and SH3 binding motif 1,
transcript variant 1"
GO:0043547|GO:0035556|GO:0005085|GO:0005737|GO:0008321|GO:0005886|GO:0032485|GO:0007264|GO:0005
575|GO:0032852 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135148_PI430048170 0.0212539269137201 0.6455333782713913.8496929127047
4.03968909875415 3.63255265434305 P P P 4.56555381718027 4.46096159395694
4.41416846467175 P P P LNCV6_135148_PI430048170 mRNA
ATATTCTCTGTTATAAAGGGGCAACTCCATCTGGTCCTATAGCATCTTTACTACTGATTT NM_021201 RefSeq chr11
+ 60378484 60395953 MS4A7 58475 "membrane-spanning 4-domains, subfamily A, member 7,
transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137696_PI430048170 0.8064672472081191.00516587171264 0.349427219293305
0.3266690139397670.266341337510056A A A 0.3091669498535750.317005656673545
0.295151886341584A A A LNCV6_137696_PI430048170 mRNA
TATTGGAGAATCGATTCCCAAGTCCAGGAAGAGAAATGTAGGGTTTTACAGAGTCGCAGC NM_001098173 RefSeq
chr16 - 90056565 90075930 PRDM7 11105 PR domain containing 7
GO:0006355|GO:0005694|GO:0034968|GO:0005634|GO:0003676|GO:0018024 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132627_PI430048170 0.000436039825062211 0.5036161591149128.84579659107183
8.90699303333828 9.0003718029762 P P P 9.82735064419598 9.85653695578398
10.0335542789777 P P P LNCV6_132627_PI430048170 mRNA
GTATTGGCATAGGCATGATAGATGGGGATTGGTACGTTTTGAATCAGCATTTGCAAAAAA NM_016641 RefSeq chr16

- 19501692 19522128 GDE1 51573 glycerophosphodiester phosphodiesterase 1
GO:0006629|GO:0005737|GO:0047395|GO:0016021|GO:0008889|GO:0006071|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137802_PI430048170 0.8170128955686320.83867795309571 1.98299509532069
0.898598823954002 1.25829197510244 A A A 1.44038173805017 2.44570176668385
0.702033792004351 A A A LNCV6_137802_PI430048170 mRNA
CCAAACAGGGTTGAAGTGCTTTTGACACATTTGTGATAAAAGTTCTGAATAAAAGTCTTG NM_178526 RefSeq chr19
+ 19063993 19113031 SLC25A42 284439 "solute carrier family 25, member 42"
GO:0005743|GO:0005634|GO:0043262|GO:0035349|GO:0005739|GO:0008152|GO:0015866|GO:0015867|GO:0080
122|GO:0015217|GO:0005347|GO:0016021|GO:0080121|GO:0015228 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132967_PI430048170 0.4088182899253821.71426790080647 0.315723726074035
0.58288737536812 2.05763025846356 A A A 0.4346042103170550.343777209169561
0.493273120575223 A A A LNCV6_132967_PI430048170 mRNA
AAGTCCTCTCTTGGATCCTTCTGGAAACAGCAAAAGCCCGTTTTTGCTGAGAAAGTGACT NM_001004326 RefSeq
chr11 + 65213839 65226040 SLC22A20 NA "solute carrier family 22, member 20, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127732_PI430048170 0.97071295109709 0.9987219470156790.294108418491134
0.5294706601203770.381176666352524 A A A 0.5004533171276660.386219770953369
0.32813638820619 A A A LNCV6_127732_PI430048170 mRNA
GCCTATATTGCCAAACAGGAAGAACTTCCTAAACAGAAGGGATTAAAAACTGTAGAATTT NM_030631 RefSeq chr14
- 36677920 37172660 SLC25A21 89874 "solute carrier family 25 (mitochondrial oxoadipate carrier),
member 21, transcript variant 1" GO:0034641|GO:0005743|GO:0044281|GO:0016021|GO:0006554|GO:0055085 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137726_PI430048170 0.5029508400640530.7341538301003430.433760325942094
0.4727208366997220.480473840969428 A A A 0.3356806820747721.59145354935198
0.43832461536383 A A A LNCV6_137726_PI430048170 mRNA
CAAATGGCAAATACGCACTCCTTGAAATGGCTTCTTTTATTTGGTTTTGTTTTCTTAGAC NM_004932 RefSeq chr5 +
31193654 31329146 CDH6 1004 "cadherin 6, type 2, K-cadherin (fetal kidney)"
GO:0005886|GO:0034329|GO:0005509|GO:0016021|GO:0007155|GO:0007156|GO:0045216|GO:0070062|GO:0034
332 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131361_PI430048170 0.9545617564392461.00532845335894 10.205562432303
10.2410676434031 10.515140324142 P P P 10.3741740618088 10.1010835672323
10.4599656994655 P P P LNCV6_131361_PI430048170 mRNA
CTTTCATGTCCTCCCTACTTCCTCAGTGTCAATCAGATTAAAGTGTGTAATCCTAAAAAA NM_014933 RefSeq chr4
- 82818660 82891266 SEC31A 22872 "SEC31 homolog A (S. cerevisiae), transcript variant 1"
GO:0005515|GO:0002474|GO:0030134|GO:0048471|GO:0005783|GO:0048208|GO:0015031|GO:0005829|GO:0030
968|GO:0043231|GO:0019886|GO:0005737|GO:0061024|GO:0018279|GO:0012507|GO:0030127|GO:0030120|GO:0
070971|GO:0006888|GO:0051592|GO:0000139|GO:0005789|GO:0006987|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137186_PI430048170 0.8795968789782 0.9649720976014757.43802123933691
7.30566856034921 7.26810840538692 P P P 7.00861099707707 7.57105153697506
7.52719691097324 P P P LNCV6_137186_PI430048170 mRNA
AGAGCACTCATGGTTCACTCTCTGGTCTAGGACTGATGGGAATAAAAGAGGAAGAAGAAA NM_001199053
RefSeq chr16 + 20806444 20849668 LOC81691 81691 "exonuclease NEF-sp, transcript variant 3"
GO:0004527|GO:0090305|GO:0000166|GO:0003723|GO:0005730|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140506_PI430048170 0.0102672869060172 1.64612404458639 4.27736539578129
4.64326023364942 4.48620292571302 P P P 3.894565976909 3.83089366473669

3.52022941530914 P P P LNCV6_140506_PI430048170 mRNA
AACAACTGAAATGTGGATGTGATTGCCTCAATAAAGCTCGTCCCCATTGCTTAAGCCTTC NM_001110219 RefSeq
chr13 - 20221961 20232395 GJB6 10804 "gap junction protein, beta 6, 30kDa, transcript variant 1"
GO:0042471|GO:0048839|GO:0008285|GO:0007605|GO:0007568|GO:0006915|GO:0005829|GO:0016324|GO:0007
154|GO:0051602|GO:0032496|GO:0005922|GO:0016021|GO:0071333 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_136061_PI430048170 0.9047781387274341.02967563845291 1.00456622965789
1.93006739312509 2.53386776046439 A A A 2.11927095203059 2.02764271294665
1.51177795011618 A A A LNCV6_136061_PI430048170 mRNA
TGTGAACCCATCCAGAGTGTCTTCTTCTTCTCTGGAGACAAGTACTACCGAGTCAATCTT NM_000638RefSeq chr17
- 28367277 28370352 VTN 7448 vitronectin
GO:0005515|GO:0030449|GO:0030949|GO:0033627|GO:0090303|GO:0010811|GO:0050731|GO:0072562|GO:0035
987|GO:0005615|GO:0014911|GO:0032092|GO:0006955|GO:0030198|GO:0007155|GO:0008201|GO:0070062|GO:0
005044|GO:0050840|GO:0005578|GO:0005576|GO:0006898|GO:0010951|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_91998_PI430048170 0.9039830581126 1.0496310915588 1.92750883930225 0.343943334683866
0.289917621807931 A A A 1.48925296316216 0.436326572247518 0.877734828236338 A A A
LNCV6_91998_PI430048170 mRNA
ACTGAACTTTCAGTCCACATTCTCCATGACTACATGTAATCTTCCTGAACACTGGACTGA NM_001113523 RefSeq
chr3 + 122577601 122639047 PARP15 165631 "poly (ADP-ribose) polymerase family, member 15,
transcript variant 1" GO:0006355|GO:0005634|GO:0006351|GO:0003950 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_133676_PI430048170 0.01632363194638 1.25424808370352 7.83427509562002
7.90397209919987 8.02642504634824 P P P 7.48167472899877 7.61758010926806
7.68421737244301 P P P LNCV6_133676_PI430048170 mRNA
ATCCTCATAAAGAAGGCTGGAGATGGATCAAAGAAGATCAAAGGCTGCTGGGATTCCATC NM_001206541 RefSeq
chr1 - 19338772 19485641 CAPZB 832 "capping protein (actin filament) muscle Z-line, beta, transcript
variant 3"
GO:0030036|GO:0005884|GO:0030479|GO:0006928|GO:0051490|GO:0003779|GO:0015629|GO:0030017|GO:0005
829|GO:0010591|GO:0051016|GO:0051015|GO:0007596|GO:0007010|GO:0022604|GO:0071203|GO:0008290|GO:0
005856|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144620_PI430048170 0.16682999615548 1.46984608610202 4.08599818688347
4.33547241773729 4.09630740047564 P P P 4.10222755392808 3.4936635360258
3.08530116864609 P P P LNCV6_144620_PI430048170 mRNA
AAGCCACGGGACTGCTCCGAAGCCGCCATAATAAAATCTGATTGTTCAGCCCCCAAAAAA NM_001010926 RefSeq
chr1_KI270762v1_alt - 79934 81435 HES5 388585 hes family bHLH transcription factor 5
GO:0051216|GO:0048708|GO:0072282|GO:0021861|GO:0007224|GO:0003690|GO:0007219|GO:0002062|GO:0046
983|GO:0045747|GO:0000122|GO:0072049|GO:0072086|GO:0007420|GO:0005654|GO:0045595|GO:0072050|GO:0
045893|GO:0008134|GO:0008284|GO:0042668|GO:0022010|GO:0021781|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137436_PI430048170 0.0102263755125738 0.6283952904308765.2838865315081
5.21760413974989 5.5228575816859 P P P 5.84817272429938 5.96189932457265
6.21798802926972 P P P LNCV6_137436_PI430048170 mRNA
GCCTTGGTTATCAACAGGTGGAATGTAGATATTGTAAAGCTTTTTGTGAATTAAAAGTGC NM_016488RefSeq chr12
+ 42326144 42448620 PPHLN151535 "periphilin 1, transcript variant 1"
GO:0005737|GO:0005794|GO:0031424|GO:0005654|GO:0043231 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128296_PI430048170 0.3928092296147191.08603533591889 0.295524128511876
0.2686277979672030.590931070143272 A A A 0.2869222797776330.255193288011755

0.278218752295894 A A A LNCV6_128296_PI430048170 mRNA
CAAAATATGACTTTCACACTTGGCTTTAGAATCTGTTATTTTGGCCATAGGCTCTCATCA NM_001004754 RefSeq
chr11 + 5453407 5454477 OR51I2 NA "olfactory receptor, family 51, subfamily I, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128676_PI430048170 0.0606283788229818 0.53887458585598 0.343872555826241
0.284471293962368 0.378940114026519 A A A 1.48441443864322 1.34975845466696
0.750025880112066 A A A LNCV6_128676_PI430048170 mRNA
TAAAATAGTATATGAAATAATAAAACTGTAACAGTAAATGGTTATTAGATTGCTTACCTA NM_171846 RefSeq chr15
+ 63121799 63131471 LACTB 114294 "lactamase, beta, transcript variant 2"
GO:0005739|GO:0005737|GO:0016787|GO:0008152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132026_PI430048170 0.320568417062912 0.901266535665861 0.398108623875215
0.261870844015218 0.291236865732626 A A A 0.464082358101633 0.646704449492104
0.269325048160067 A A A LNCV6_132026_PI430048170 mRNA
CTCACATGTTTTTTCTGATTTTTCAGTGACTGTACATAATAGCTTGTAGCGATGTCCATA NM_001812 RefSeq chr4 -
67472270 67545538 CENPC 1060 centromere protein C
GO:0000780|GO:0006334|GO:0019237|GO:0005634|GO:0003677|GO:0005829|GO:0034080|GO:0005737|GO:0007
067|GO:0051382|GO:0005721|GO:0007059|GO:0000777|GO:0000776|GO:0005654|GO:0000278|GO:0051301 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_37464_PI430048170 0.252815214961547 0.71584779607853 2.74342003471695 2.12968268428627
1.80184754923857 A A A 3.13214690374527 2.74720484009271 2.28012315934662 P A A
LNCV6_37464_PI430048170 mRNA
TGATAAAGATTATGCACTGATGTCACTGTGCTCCTGGGTTAATGTCGTGGTGGGTAGAAT NM_015585 RefSeq chr20
+ 20052513 20360702 CFAP61 26074 "cilia and flagella associated protein 61, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72286_PI430048170 0.493667305347023 0.928056561353773 7.96686119110801 8.05585388626693
7.84129187408829 P P P 8.20098334198672 8.13873069280949 7.828568011368 P P P
LNCV6_72286_PI430048170 mRNA
AACTGTCCCCAGCACTGCCTCTGGCCTCCTCAGTCCTGATGCTGCTGATGAGCACCCTGT NM_012265 RefSeq chr22
- 29259854 29267925 RHBDD3 25807 rhomboid domain containing 3
GO:0001889|GO:0045732|GO:0004252|GO:0000165|GO:0032815|GO:0006508|GO:0050708|GO:0016021|GO:0009
410|GO:0002673 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126906_PI430048170 0.888911959400889 1.09919846084204 3.1991338213907
2.83700131532805 4.01999866520647 P A P 3.35794898436247 3.44506416849879
3.08255996458735 P P P LNCV6_126906_PI430048170 mRNA
TCGGACATCCGCAGGCACCAGGGAAAGTCTCCTGGGGCGATCTGTAAATAAACCTTTTTT NM_207581 RefSeq chr15
+ 45114324 45118103 DUOXA2 405753 dual oxidase maturation factor 2
GO:2000609|GO:0050727|GO:0005789|GO:0016021|GO:0015031|GO:0042743 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128976_PI430048170 0.840704561044176 1.10192802705105 9.27950518966508
8.37611757329993 8.08264821974487 P P P 8.80104588723373 7.90741397854834
8.73257798261911 P P P LNCV6_128976_PI430048170 mRNA
CTCCCCTGCTCCTCTGCTGGTGGTGGGCTAATAAAGCTGACTTTCTGGTTGATGCAAAAA NM_005557 RefSeq chr17
- 41609778 41612827 KRT16 3868 "keratin 16, type I"
GO:0005515|GO:0005882|GO:0051546|GO:0030336|GO:0042633|GO:0008283|GO:0045104|GO:0007568|GO:0031
424|GO:0061436|GO:0005634|GO:0006954|GO:0008544|GO:0030216|GO:0045087|GO:0007010|GO:0005200|GO:0
005856|GO:0002009|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136422_PI430048170 0.267881909246262 0.871843467968243 10.1891008477107 9.8422812715566
10.3006770444124 P P P 10.3766232086632 10.377023401791 10.2037257992967 P P P
LNCV6_136422_PI430048170 mRNA

TAAATCGGACTGGAACTCACTTGATGGGATTATTCGTTAAATGCGAGTGTTTGGGGGCCA NM_005098RefSeq chr8
- 71841541 71844496 MSC 9242 musculin
GO:0003700|GO:0006366|GO:0003714|GO:0060539|GO:0046983|GO:0001206|GO:0060021|GO:0005634|GO:0000
980|GO:0014707|GO:0000122 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136899_PI430048170 0.00169227230256048 1.34001951030454 14.3948434820809
14.3026091767007 14.373379617518 P P P 13.8667991775879 14.006845867083
13.9286115170054 P P P LNCV6_136899_PI430048170 mRNA
TTGTGTTTTTATATTGACTCTGCGGCGCGGGCCCTTTAATAAAGCTAGGATACGCCTTTG NM_138689RefSeq chr11
- 64244478 64246941 PPP1R14B 26472 "protein phosphatase 1, regulatory (inhibitor) subunit 14B"
GO:0042325|GO:0005737|GO:0045087|GO:0004864|GO:0043086 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128988_PI430048170 0.506348280685603 1.52642246887405 2.49859145655802
0.661983646392244 2.24102049183105 A A A 0.53434503227095 1.83962372552995
1.48977694358309 A A A LNCV6_128988_PI430048170 mRNA
CAACACTCAGTCAAGCAGAAAATACAAATCCCCCCAAAACTTTGAGACATAGCTTATATA NM_014429RefSeq chr3
- 108958239 109118146 MORC1 27136 MORC family CW-type zinc finger 1
GO:0008270|GO:0007275|GO:0005634|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140487_PI430048170 0.122545198192429 0.541294657313351 0.946714393488152
1.91871264861754 0.731720965313637 A A A 2.68476634635435 1.95740433529552
1.72254311187384 A A A LNCV6_140487_PI430048170 mRNA
GCCCATCCCAGCTTTCTTTACTGCAGTTCAAATAATAAAGGAAATCGTACAACTCCAAAA NM_130899RefSeq chr5
- 157162332 157166268 FAM71B 153745 "family with sequence similarity 71, member B" GO:0005634
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128142_PI430048170 0.0991368914174007 0.400193884172639 0.493479795384493
1.48804551683126 0.943144180531319 A A A 2.73955690664225 2.6346729513336
1.28845749489942 P P A LNCV6_128142_PI430048170 mRNA
GAACACGTTTCTATTCAAGGAGAAAACACCATTCAGTAAGAAGATGGAGTAGATATCAGA NM_006493RefSeq chr13
+ 76991923 77002517 CLN5 1203 "ceroid-lipofuscinosis, neuronal 5"
GO:0005515|GO:0048471|GO:0070085|GO:0005794|GO:0005783|GO:0042551|GO:0005765|GO:0005537|GO:0005
764|GO:0030163|GO:0007420|GO:0007042|GO:0016021|GO:0070062|GO:0006465|GO:0022008 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133838_PI430048170 0.708668871943049 0.931109763284489 3.7939967740599
3.58910799427211 4.0056947549019 P P P 4.25066944367597 3.72070767065772
3.68413088148425 P P P LNCV6_133838_PI430048170 mRNA
TGGATTGGGGGTAACCTTTCATTTGTCAACCTTCATTAAAACTATGACAACGTCCACATG NM_014650RefSeq chr19
- 52033423 52048820 ZNF432 9668 zinc finger protein 432
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143083_PI430048170 0.340830707509695 0.8767156536566 6.97612012984302 6.5099331313971
6.56733557679381 P P P 6.7269260587646 7.08132080672693 6.8376130909428 P P P
LNCV6_143083_PI430048170 mRNA
AGGAGGTGCTGATCCAGGAGTGGTTCACCCTGGTCAACAAGAAGAACGCTCTCATCCGGANM_001099409 RefSeq
chr11 + 65576037 65592645 EHBP1L1 254102 EH domain binding protein 1-like 1
GO:0008150|GO:0003674|GO:0016020 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137149_PI430048170 0.0138219050985438 0.60542903207454 2.76654703575769
2.80104770713005 2.56466379309433 A A A 3.30674502618792 3.67983643635809
3.29456044236588 P P P LNCV6_137149_PI430048170 mRNA
CAGTACTTTCCTCAGTATTTTATGGGCAAAGTAAAAATAACAATGCATAGTGAAAGGGCA NM_005236RefSeq chr16

+ 13920156 13952348 ERCC4 2072 excision repair cross-complementation group 4
GO:0005515|GO:0009650|GO:0010834|GO:0000110|GO:0005634|GO:0000109|GO:0003697|GO:0000723|GO:0006
295|GO:0000724|GO:0006296|GO:0009411|GO:0000784|GO:0000781|GO:0005669|GO:0001094|GO:0004520|GO:0
008022|GO:0003684|GO:0047485|GO:0006281|GO:0006283|GO:0000712|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145400_PI430048170 0.00139618883131302 0.3497160736594949.28787495250232
9.3885324364623 9.01603409360209 P P P 11.0027358011316 10.7032837214814
10.5168086973652 P P P LNCV6_145400_PI430048170 mRNA
GTGGAGTCAGGTTTTCTATTCCTTTCTGTGTTTGCAAATTCAGTGTTAACTAAATAAAGG NM_001287595 RefSeq
chr1 - 53087178 53142632 SLC1A7 6512 "solute carrier family 1 (glutamate transporter), member 7,
transcript variant 1" GO:0005886|GO:0005313|GO:0006835|GO:0017153|GO:0016021|GO:0055085|GO:0006811
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129421_PI430048170 0.6029481387135641.26362503277052 2.84964931512372
4.07989618214538 3.97837565019121 A P P 3.45113447383623 3.36119877072744
3.37130161714262 P P P LNCV6_129421_PI430048170 mRNA
TTACAGAGGATGTTATTTTAGTGAGACCCAGGTCCTAGACCTTCTGATTCCTATTTATTT NM_001039948 RefSeq
chr22 + 24806220 24926846 SGSM1 129049 "small G protein signaling modulator 1, transcript variant 1"
GO:0005794|GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129108_PI430048170 0.1042997022380560.5473605225329940.335595415423345
0.2430919890857820.289266716410882A A A 0.5286491606279171.38775312595118
1.40105580421814 A A A LNCV6_129108_PI430048170 mRNA
AAAGGAAGATACAGAGGTGATTGTACTTCAGAATGATAAACCCATATACCACCTAAAATC NM_001012337 RefSeq
chr3 + 125969143 125983453 ROPN1B 152015 rhophilin associated tail protein 1B
GO:0005515|GO:0046982|GO:0031514|GO:0030159|GO:0007266|GO:0007283|GO:0030317|GO:0042803|GO:0000
910|GO:0005737|GO:0016337|GO:0007342|GO:0007340 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135052_PI430048170 0.00499464658139299 1.38812678566918 12.846942991138
12.8116716116618 12.8052555030516 P P P 12.3156175506691 12.4326788211697
12.2925590424448 P P P LNCV6_135052_PI430048170 mRNA
AATTATCAACATTATGCAGGATCGGCTCAAAGCCTGTCAGCAGAGGGAAGGACAGAACTANM_004548RefSeq chr16
+ 1959515 1961975 NDUFB10 4716 "NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10,
22kDa"
GO:0022904|GO:0005515|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0008137|GO:0044237|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98892_PI430048170 0.58828487759079 0.9204513223460077.30835829628523 7.15717899015816
7.3836582176452 P P P 7.1263912957441 7.36487500468241 7.67342957487929 P P P
LNCV6_98892_PI430048170 mRNA
TTTGGACATTGACCCCAAACTGCAAGAATACCTCGGCAAATTCCGACGTCTTGAAGACTT NM_015315RefSeq chr5
+ 154712901 154817607 LARP1 23367 "La ribonucleoprotein domain family, member 1"
GO:0000339|GO:0005515|GO:0031929|GO:0048027|GO:0008283|GO:0045727|GO:0008494|GO:0006413|GO:0005
737|GO:0031931|GO:0016020|GO:0008190|GO:0005654|GO:0031369|GO:0003730|GO:0016239 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131298_PI430048170 0.1086831598207980.6247323294548091 2.5545161875144
11.7365105240004 11.7164599571709 P P P 12.8554032575411 12.7580010389654
12.5840403668432 P P P LNCV6_131298_PI430048170 mRNA
TACCTCATAGTCCCTCTCTCCCCTCCTTTAAAAGAATTATAAATATTAGGAAAGCTTGTT NM_152990RefSeq chr6
- 36390550 36442889 PXT1 222659 "peroxisomal, testis specific 1"
GO:0008150|GO:0003674|GO:0043065|GO:0005634|GO:0007283|GO:0005777 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129409_PI430048170 0.6927795121149581.01021878531561 0.296148777120032

0.3326245914305190.398302024292383A A A 0.3480198147728370.327581390213953
0.309071115708483A A A LNCV6_129409_PI430048170 mRNA
AACTGCTCATAGACATGCTGACTGAGACCATGGCGCGCATGCACTTGCTGGAGAAGCAGC NM_001164444 RefSeq
chr5 - 179678557 179680974 CBY3 646019 chibby homolog 3 (Drosophila) NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_140064_PI430048170 0.1689025649936791.20949381084227 4.07866448120083
4.17326098055428 4.13599145393352 P P P 4.05104721221746 3.89471285091287
3.58169283739382 P P P LNCV6_140064_PI430048170 mRNA
AGAAGAAATATATCTCTATCTCTCTACTCTGGGCTCTGTGTTTTTCCTCCTGGGTGTCAG NM_022167RefSeq chr17
+ 50346031 50361185 XYLT2 64132 "xylosyltransferase II, transcript variant 1"
GO:0008375|GO:0030206|GO:0000139|GO:0005789|GO:0030158|GO:0016021|GO:0015012|GO:0005575|GO:0006
024|GO:0030210 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144064_PI430048170 0.1978883079901111.0945803039633 0.568397638518668
0.7957370298330850.621807922351712A A A 0.4579815499597070.560183749295998
0.583489077536478A A A LNCV6_144064_PI430048170 mRNA
GGGAAGTCTTTCAGTGGGAGATGAATAAATGTTATACATTGTTATGTCCAGTTATGTCAA NM_014817RefSeq chr7
- 28953357 28958413 TRIL 9865 TLR4 interactor with leucine-rich repeats
GO:0046696|GO:0001530|GO:0034142|GO:0006954|GO:0002718|GO:0045087 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129981_PI430048170 0.6718491377085460.9800194776311490.454612847768627
0.4124305397408820.250287006435599A A A 0.3635858332120070.435994599265
0.412127626348355A A A LNCV6_129981_PI430048170 mRNA
GTTCACTGATTGTTTTCATAGATGATGCTTCTTGGGGAAAAATAGTATAGGATGTGAAAG NM_052954RefSeq chr21
- 26466208 26573262 CYYR1 116159 cysteine/tyrosine-rich 1 GO:0008150|GO:0003674|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119240_PI430048170 0.6689824315856080.9370773328366494.92785964336604
4.27590100293954 3.7563269852793 P P P 4.59632683672638 4.52238588945791
4.35090430310689 P P P LNCV6_119240_PI430048170 mRNA
TATCTCTGGGGACCCTGCTCCCACTGTGATCTGGCAGAAGGCTATCACGCAGGGGAATAA NM_000256RefSeq chr11
- 47331405 47352702 MYBPC3 4607 "myosin binding protein C, cardiac"
GO:0005863|GO:0030049|GO:0055010|GO:0045214|GO:0006942|GO:0003779|GO:0032781|GO:0060048|GO:0030
017|GO:0046872|GO:0042802|GO:0031432|GO:0005829|GO:0032971|GO:0003007|GO:0031034|GO:0002027|GO:0
014705|GO:0017022|GO:0007155|GO:0008307|GO:0031672|GO:0001671|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132563_PI430048170 0.0765845655350286 0.6505096014112096.77698484685908
6.45400185321147 6.434564402953 P P P 6.76447191438037 7.27267425864083
7.43440902696971 P P P LNCV6_132563_PI430048170 mRNA
CCTCTTTGCCTTCCTAGGGGCATTTTCTTTAACTTCCAGAATAGTGATTTTAAAAGTAAA NM_001304940 RefSeq
chr17 - 44395276 44503602 GPATCH8 23131 "G patch domain containing 8, transcript variant 3"
GO:0005515|GO:0008150|GO:0005575|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132448_PI430048170 0.6997233976631410.9770034572226492.26960791499102
0.5192854138435810.548375791827747A A A 1.45221823950769 1.03994212437462
1.63544337940486 A A A LNCV6_132448_PI430048170 mRNA
GAAGACCCTAGTCAAAGTCCCTGTGGAGAGAACGGCCCATTCCAAGGGCAGGAGGATATT NM_138329RefSeq
chr11 + 278569 285388 NLRP6 171389 "NLR family, pyrin domain containing 6, transcript variant 1"
GO:0070255|GO:0031965|GO:0005886|GO:0034122|GO:0050727|GO:0005524|GO:0043409|GO:0009617|GO:0005
737|GO:0050777|GO:0007186|GO:0005000|GO:0042060|GO:0010506|GO:0043124 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144476_PI430048170 0.1674398914020450.8089201730402 9.65468307346148

9.89914465740975 10.1578055476847 P P P 10.1000078753861 10.1113543189262
10.4360585731506 P P P LNCV6_144476_PI430048170 mRNA
CAAGGATATGCTCCCCACTGTTTTCTTTCTACAATTTCCAAAGGTTGCAAGATGTTTTTT NM_006083 RefSeq chr5 +
140647798 140662480 IK 3550 "IK cytokine, down-regulator of HLA II"
GO:0005515|GO:0006955|GO:0007267|GO:0005730|GO:0005654|GO:0005615|GO:0042802 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140947_PI430048170 0.1563067086409550.96473832486045 0.384195911423246
0.40603328082274 0.324141337190817 A A A 0.420706238050281 0.440277011108844
0.409834787947063 A A A LNCV6_140947_PI430048170 mRNA
CCTGTGCTGACCAAAGATTAGTAACCAGTTATACCCAGTATTTTGAGGTTTTATTGTTTT NM_001999 RefSeq chr5
- 128257908 128538042 FBN2 2201 fibrillin 2
GO:0005515|GO:0035583|GO:0030501|GO:0005509|GO:0005578|GO:0001527|GO:0005576|GO:0030326|GO:0009
653|GO:0045669|GO:0031012|GO:0060346|GO:0022617|GO:0030198|GO:0005201 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141111_PI430048170 0.0554378663285971 0.57516399761132511.7797430168987
11.3417077418445 11.5493824730799 P P P 11.9121771665339 12.389935610254
12.6915759291567 P P P LNCV6_141111_PI430048170 mRNA
ATACCAGGAGGTATTTGGGAAGGCCAATGGCGTGGCTCCTTTGAGGAAATAAAACACTAA NM_001376 RefSeq chr14
+ 101964527 102050798 DYNC1H1 1778 "dynein, cytoplasmic 1, heavy chain 1"
GO:0005515|GO:0005813|GO:0033962|GO:0006996|GO:0005874|GO:0030175|GO:0003777|GO:0005524|GO:0005
829|GO:0019886|GO:0034063|GO:0016020|GO:0000086|GO:0008152|GO:0006810|GO:0005868|GO:0051959|GO:0
000278|GO:0007052|GO:0016887|GO:0070062|GO:0007018 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_130051_PI430048170 0.0815841430922462 0.75059194159939 5.92809956526808
5.60437239749718 5.71611989467823 P P P 5.91359662216283 6.16018943445998
6.39535190382277 P P P LNCV6_130051_PI430048170 mRNA
GTGTTTTTGTGTGCGTGTGTGTAGAATGGGTAAATAAAATTGTTGAGTAACTTGAACCTA NM_006212 RefSeq chr1
+ 207053274 207077817 PFKFB2 5208 "6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2, transcript
variant 1"
GO:0005515|GO:0006089|GO:0019901|GO:0005975|GO:0033133|GO:0044281|GO:0005524|GO:0006096|GO:0009
749|GO:0005829|GO:0004331|GO:0016311|GO:0006007|GO:0009405|GO:0046835|GO:0006006|GO:0032024|GO:0
006003|GO:0003873|GO:0006000 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129635_PI430048170 0.0426913203259795 0.1939135083711972.33073808038059
0.8797380436091782.6642921371548 A A A 4.42817422266657 4.52655359429729
4.55741366432612 P P P LNCV6_129635_PI430048170 mRNA
GTTGTAGTTTGACAGAACCATCAGTAAAGACATAAGCAAATAAATGGTCTTGGTGCAAAA NM_002271 RefSeq chr13
+ 97953674 98024296 IPO5 3843 importin 5
GO:0005515|GO:0031965|GO:0005794|GO:0005730|GO:0005634|GO:0043086|GO:0006607|GO:0043231|GO:0005
737|GO:0071230|GO:0006610|GO:0016020|GO:0005643|GO:0008536|GO:0008565|GO:0042307|GO:0016032|GO:0
005654|GO:0005095. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132168_PI430048170 0.0154598554519445 0.7315225384708388.13644493710362
7.9720110608303 7.84168384667576 P P P 8.36488784145175 8.56559654122261
8.37908286593396 P P P LNCV6_132168_PI430048170 mRNA
TCTCCCTTCTCCAGTTCTGGGAATTTACAGGCACAATACACTTCCTTTTCCTGGAAAAAA NM_018664 RefSeq chr1
- 212686416 212699985 BATF3 55509 "basic leucine zipper transcription factor, ATF-like 3"
GO:0001078|GO:0003700|GO:0006366|GO:0003714|GO:0005634|GO:0043011|GO:0000122|GO:0097028|GO:0009
615|GO:0000978 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117001_PI430048170 0.3681394088472052.50626819290612 2.82764788916136
0.4924774023905550.554688220271316 A A A 0.3179868711790350.407330088457473

0.492775271434061 A A A LNCV6_117001_PI430048170 mRNA
ATGGATCACAAAACTTCAATGAAACGTGGGAGAACTACAAATATGGTTTTGGGAGGCTTG NM_014495 RefSeq chr1
+ 62597486 62606305 ANGPTL3 27329 angiopoietin-like 3
GO:0050996|GO:0019915|GO:0070328|GO:0048844|GO:0006071|GO:0005615|GO:0006631|GO:0008203|GO:0004
857|GO:0042632|GO:0004859|GO:0030335|GO:0009986|GO:0055088|GO:0010519|GO:0045766|GO:0051005|GO:0
007165|GO:0005178|GO:0007160|GO:0007229|GO:0055091|GO:0055090|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131911_PI430048170 0.24372726723585 1.1436011179364 8.49254261990678 8.5933159201582
8.62473734487066 P P P 8.30487049956948 8.18488558881606 8.60956155878336 P P P
LNCV6_131911_PI430048170 mRNA
TGATGGTGTTTATTGCAAATGCACAATCTTTTTCCCATTGAAATGTCATCACACTGGAAA NM_025176 RefSeq chr20
- 25452700 25585517 NINL 22981 ninein-like
GO:0006996|GO:0005815|GO:0000086|GO:0005874|GO:0005509|GO:0000278|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_100330_PI430048170 0.0389582974833439 0.5499316656404 4.36874646874793
4.27920122935536 4.20344054133245 P P P 4.80059355887289 5.12394300645622
5.44742910085207 P P P LNCV6_100330_PI430048170 mRNA
CTTGTTCCTCCATCTAGTGGAGTCCTTATTAAATGCTAGCAATGTGGCAATTGAGTGCCA NM_003403 RefSeq chr14
+ 100238764 100279034 YY1 7528 YY1 transcription factor
GO:0005515|GO:0051276|GO:0003700|GO:0044212|GO:0003723|GO:0005634|GO:0048593|GO:0007283|GO:0009
952|GO:0016363|GO:0030154|GO:0034644|GO:0000724|GO:0000400|GO:0031519|GO:0005667|GO:0006357|GO:0
003714|GO:0003713|GO:0000122|GO:0034696|GO:0003677|GO:0006403|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134006_PI430048170 0.35424776917205 0.83367752066576 13.9597918858737
13.2364795385168 13.1679053390379 P P P 13.8544195810319 13.8333290900562
13.5887628417134 P P P LNCV6_134006_PI430048170 mRNA
GTGGCTAGTGTTTGCCGAATGAAACTCAACTCAATAAAAAACAAAAACCAAATTGGGCAG NM_002799 RefSeq chr9
- 124353464 124415473 PSMB7 5695 "proteasome (prosome, macropain) subunit, beta type, 7"
GO:0005515|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0004
298|GO:0034641|GO:0005737|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0
005839|GO:0000502|GO:0043066|GO:0006521|GO:0051437|GO:0042590|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_99142_PI430048170 0.559458679880815 1.02881439132164 0.310323114550215 0.316876599878965
0.479547560509715 A A A 0.338819519815666 0.298415128624715 0.352467169889606 A A A
LNCV6_99142_PI430048170 mRNA
TTCTTTGCCAAAAGTGCCACTATCTACAACCCCGTTATCTATGTCTTTATGAACCGGCAG NM_001048181 RefSeq
chrX + 154219733 154233286 OPN1MW2 NA "opsin 1 (cone pigments), medium-wave-sensitive 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123701_PI430048170 0.0164363839704632 0.486092331714167 3.22558633347454
3.36393395684151 3.80472871747553 P P P 4.18561220165138 4.47123418352298
4.84772303566973 P P P LNCV6_123701_PI430048170 mRNA
GAATAAAAGGTATGTTTACTCATTTTTCCTGAACACTGTGTTGGTAATGTGCATCATGAC NM_001303241 RefSeq
chr5 + 180494398 180578405 CNOT6 57472 "CCR4-NOT transcription complex, subunit 6"
GO:0005515|GO:2000327|GO:0010467|GO:0006355|GO:0008284|GO:0003723|GO:0043928|GO:0004532|GO:0005
634|GO:0070966|GO:0046872|GO:0030014|GO:0006351|GO:0006417|GO:0005829|GO:0004535|GO:0016020|GO:0
010606|GO:0035195|GO:0000289|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130916_PI430048170 0.327367771927051 1.30325953852698 4.79479074505443
4.74981750508002 5.31677056961675 P P P 3.91838861985284 4.66662926180208
5.00035484430977 P P P LNCV6_130916_PI430048170 mRNA

TCTGGGATGCAAGCATTTGTGAGAATAATTCAGACATGAGCATTCTCTAGAAATCACTTT NM_004336RefSeq chr2
- 110637697 110678107 BUB1 699 "BUB1 mitotic checkpoint serine/threonine kinase, transcript variant 1"
GO:0005515|GO:0007094|GO:0007093|GO:0008283|GO:0005829|GO:0005737|GO:0007059|GO:0071173|GO:0016
032|GO:0000780|GO:0051983|GO:0006915|GO:2001244|GO:0005524|GO:0007067|GO:0004672|GO:0016020|GO:0
004674|GO:0000777|GO:0000776|GO:0006468|GO:0005654|GO:0000278|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128839_PI430048170 0.4431690741962040.9741963673207430.338583732386899
0.4170600017567170.328571831005133A A A 0.4660937049582130.358556277446454
0.371951798296545A A A LNCV6_128839_PI430048170 mRNA
CCCCTAGCTTACTCAATGTCATTTGCAGCGTGCATCTGCTGATTAAAGGACTAAAACAAG NM_178351RefSeq chr1
- 152804834 152806631 LCE1C 353133 "late cornified envelope 1C, transcript variant 1" GO:0031424 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142776_PI430048170 0.4728637266988270.9625788674796330.268190869577443
0.4286937728894030.301958446683158A A A 0.48039645820534 0.371800453146416
0.311627190431465A A A LNCV6_142776_PI430048170 mRNA
GTCATACTGTCATAGGATGAGAGAGTTCTTCAAAAATTATGTTTTCCCAAGATCAGTTGC NM_005989RefSeq chr7
+ 138076431 138118304 AKR1D16718 "aldo-keto reductase family 1, member D1, transcript variant 1"
GO:0006707|GO:0006699|GO:0008209|GO:0007586|GO:0044281|GO:0005829|GO:0030573|GO:0047787|GO:0008
206|GO:0008207|GO:0005496|GO:0055114|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140554_PI430048170 0.4215431063615910.3116239643468670.368406116868314
0.3420140696816520.256825530894715A A A 0.3166928583681220.333858194307144
3.25375696455413 A A P LNCV6_140554_PI430048170 mRNA
CTAAAAGCAATCAAACATGTTTCTGCTGGACAGTGACCAAGAATTATAGTACCTTCTTAT NM_003956RefSeq chr10
- 89205936 89207314 CH25H 9023 cholesterol 25-hydroxylase
GO:0006629|GO:0001567|GO:0005506|GO:0006699|GO:0008395|GO:0044281|GO:0005829|GO:0005789|GO:0016
126|GO:0006633|GO:0008206|GO:0016021|GO:0055114|GO:0008203 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145213_PI430048170 0.0101638210281323 0.42167170569506 8.87350404412422
8.21184677287706 8.4731788972675 P P P 9.63524560794104 9.74887665357197
9.96944003078446 P P P LNCV6_145213_PI430048170 mRNA
GCATCACTGTCATACTCACAACTTCGTGAATAAAGTTGTGTGCTTTATTCGTAGAAAAAA NM_001003408 RefSeq
chr10 - 114431109 114684655 ABLIM1 3983 "actin binding LIM protein 1, transcript variant 3"
GO:0005515|GO:0001725|GO:0030032|GO:0003779|GO:0015629|GO:0030027|GO:0042384|GO:0005737|GO:0007
411|GO:0045944|GO:0007010|GO:0009887|GO:0008270|GO:0007601 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133584_PI430048170 0.000234032055775265 0.3455449761068493.72052035360671
3.77760049040488 3.98348130944095 P P P 5.20703007337748 5.3534213379222
5.51707234707849 P P P LNCV6_133584_PI430048170 mRNA
CTATATTTCCGTGAATCTTTGACCTTGCAGTGGGTTGCAATAAAAGAGAAACAAAACAAA NM_001163315 RefSeq
chr5 - 107859032 108382098 FBXL17 64839 F-box and leucine-rich repeat protein 17 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128830_PI430048170 0.0639338438693339 0.5299973268060469.34152745900474
8.5088808764739 8.42052050865547 P P P 9.73477656062581 9.93876513033127
9.50059985023322 P P P LNCV6_128830_PI430048170 mRNA
GCCTCCCCAACCCCTGGCCTCAATTTCCCTTTCTATAAAATGGAAGATGTCCAGAAAAAA NM_080658RefSeq chr11
- 67642554 67650659 ACY3 91703 aspartoacylase (aminocyclase) 3
GO:0008150|GO:0003674|GO:0016324|GO:0006805|GO:0016788|GO:0016032|GO:0044281|GO:0004046|GO:0046
872|GO:0070062|GO:0042802|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144212_PI430048170 0.4215395931215930.9170258043172861 2.7955966437331

12.9698726144795 12.6915759291567 P P P 13.1540088972333 12.8523206780331
12.8149253088919 P P P LNCV6_144212_PI430048170 mRNA
GGCTCACCCTCTCTCTGTCAACACTGGAATAAACTTTGCCTTTTCTGAGTAGTGAAAAAA NM_003312RefSeq chr22
- 37010858 37019453 TST 7263 "thiosulfate sulfurtransferase (rhodanese), transcript variant 1"
GO:0005743|GO:0044281|GO:0005615|GO:0035928|GO:0005739|GO:0034641|GO:0000096|GO:0000098|GO:0005
759|GO:0009440|GO:0030855|GO:0051029|GO:0004792|GO:0008097|GO:0070221|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142886_PI430048170 0.250693954594227 1.67308171562445 1.24860020930654
2.32852122313128 1.14797676129794 A A A 0.3916308113772740.320066471723249
1.67203596921711 A A A LNCV6_142886_PI430048170 mRNA
AGTAGATCACTGGAATGGAATTCCAAATAATAAACTTTGGAAGGTGTAACTCTCCAGTAT NM_138811RefSeq chr7
- 25134696 25180198 C7orf31 136895 chromosome 7 open reading frame 31 GO:0005813|GO:0005737
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132960_PI430048170 0.00554055007598682 0.4858075140278134.10666852920836
3.63029912549865 3.90766415362485 P P P 4.67270150205981 5.12198136534808
4.97804625663127 P P P LNCV6_132960_PI430048170 mRNA
GGGGGGTGTTACAAAGGACTAGCTGTTCAAATATCTTTTGTATTGTATTGATTCCCCTAT NM_133259RefSeq chr2
- 43886223 43996005 LRPPRC 10128 leucine-rich pentatricopeptide repeat containing
GO:0042645|GO:0008017|GO:0000961|GO:0005515|GO:0048471|GO:0006355|GO:0000794|GO:0070129|GO:0003
723|GO:0005874|GO:0048487|GO:0005637|GO:0005634|GO:0006351|GO:0005640|GO:0005739|GO:0051015|GO:0
047497|GO:0016020|GO:0003697|GO:0030529|GO:0005654|GO:0051028|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127705_PI430048170 0.348078943670435 1.18891257746522 1.07955993356978
0.5133755275130370.529553950378097A A A 0.562011818850959 0.409133106325181
0.473081017378972A A A LNCV6_127705_PI430048170 mRNA
TTATTGTGGTGGAGGCAATTATGAGGGTAGCATTTCTTTCGAGACAAAACACCCGTCTGG NM_052970RefSeq chr20
+ 3732669 3753111 HSPA12B 116835 "heat shock 70kD protein 12B, transcript variant 1"
GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135270_PI430048170 0.364252239642394 1.22825459293951 3.42205206927895
3.67139943799818 2.98204177395217 P P P 3.45379419545033 2.71428146093482
3.00232681275434 P P P LNCV6_135270_PI430048170 mRNA
CTCCTTGGGCATTCGTACTTAGGATTCAATAGAAACATGTACAGGGTAAACAATTTTTTA NM_015900RefSeq chr3
+ 119597847 119629811 PLA1A 51365 "phospholipase A1 member A, transcript variant 1"
GO:0016042|GO:0006629|GO:0008970|GO:0006658|GO:0002080|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141188_PI430048170 0.0491524796652966 1.20576566554125 8.26642933577325
8.15978784973717 8.02925473720213 P P P 7.7832284322331 8.01250517058119
7.84990368942652 P P P LNCV6_141188_PI430048170 mRNA
TGCTTCCTTTGAGTTTTTTAATAAAATAATCTCATGCGGCAGGAGAGGAGAGGATCAGGG NM_001082486 RefSeq
chr16 - 67657511 67660815 ACD 65057 "adrenocortical dysplasia homolog (mouse), transcript
variant 1"
GO:0005515|GO:0000781|GO:0016233|GO:0070182|GO:0001655|GO:0005634|GO:0030326|GO:0003677|GO:0006
886|GO:0031848|GO:0051973|GO:0032211|GO:0001501|GO:0005737|GO:0060381|GO:0035282|GO:0000723|GO:0
005654|GO:0070198|GO:0032202|GO:0000783 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71497_PI430048170 0.0103793971156925 1.60347420927733 12.7169475023334
12.7169475023334 12.6257921228191 P P P 12.161899646017 11.987981805235
11.8512506218151 P P P LNCV6_71497_PI430048170 mRNA
TTGCTGTGTGTGAGGGCCCAGGTGGAAGGCGCGGACCTGACAGCATTCCAATAAAGCATANM_001281482 RefSeq
chr20 + 63272784 63289790 ARFGAP1 55738 "ADP-ribosylation factor GTPase activating protein 1,

transcript variant 3"
GO:0005515|GO:0006890|GO:0045202|GO:0015031|GO:0048205|GO:0005829|GO:0030968|GO:0043547|GO:0008
060|GO:0032312|GO:0030660|GO:0061024|GO:0008270|GO:0006987|GO:0044267|GO:0005096 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142139_PI430048170 0.7031267414672771.05109899477339 1.55182490791397
1.50349664411382 2.10835478028823 A A A 1.06094236113649 2.47805711819515
0.94965009501495 A P A LNCV6_142139_PI430048170 mRNA
TGGTGGGTCCAGCTGCTGTAGCCAAACCTGCAATGAGTCCAGCTATTGTCTGCCTTGCTG NM_001190460 RefSeq
chr17 + 41189886 41190639 KRTAP9-1 NA keratin associated protein 9-1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_143541_PI430048170 0.6999617422403480.9865308836358750.398507073398239
0.3719927674573040.24810836038337 A A A 0.3399455999338590.381173897056678
0.360309957888733 A A A LNCV6_143541_PI430048170 mRNA
CCTTGTGCCTTATCAAACAGGACAAATACGTTCTGTTTTATGTCTTGAATTGCATTCTAA NM_001105522 RefSeq
chr11 + 89924063 89933061 TRIM49D2 NA tripartite motif containing 49D2 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_142395_PI430048170 0.6576353935998760.9418514400015636.2713204321632 5.7294947642102
5.99821043710629 P P P 5.96133454431305 6.32525597756021 5.99366387130594 P P P
LNCV6_142395_PI430048170 mRNA
CAGGGACGAATTGTTTACCCCATGATAATGTAGGATATCATAAATTCTTCTTCAAAGGTT NM_024955 RefSeq chr22
- 36487185 36507043 FOXRED2 80020 "FAD-dependent oxidoreductase domain containing 2,
transcript variant 1" GO:0005515|GO:0001948|GO:0050660|GO:0016491|GO:0005788|GO:0030433|GO:0055114
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100408_PI430048170 0.2437656409010041.42076285911437 3.48114904057023
3.17493502754002 2.98038205953649 P P P 3.33903478645616 2.39215125138038
2.13831087914091 P P A LNCV6_100408_PI430048170 mRNA
CCGTCTCTTAAATACTGGAGTTGTCCTATCTCCTTGGGCTGATACCCTGAACTGTCATTT NM_001206945 RefSeq
chr3 - 47562237 47580240 CSPG5 10675 "chondroitin sulfate proteoglycan 5 (neuroglycan C),
transcript variant 5"
GO:0005515|GO:0031103|GO:0005794|GO:0005796|GO:0005975|GO:0050804|GO:0046907|GO:0005576|GO:0044
281|GO:0007399|GO:0030208|GO:0030207|GO:0030206|GO:0016020|GO:0005887|GO:0030660|GO:0005789|GO:0
009405|GO:0016021|GO:0030204|GO:0008083|GO:0030203|GO:0040008|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130168_PI430048170 0.16647859666394 0.8059831524537066.11257826990741
5.97018655270206 6.25082072582788 P P P 6.16620932180883 6.39718528134922
6.67268003059898 P P P LNCV6_130168_PI430048170 mRNA
CAATCCAAAAAAGAAACCAGTTCTTCCCCCAAAGTATTCAATGCTTAGAATACTAAAAGG NM_182922 RefSeq chr16
+ 50065969 50105464 HEATR3 55027 HEAT repeat containing 3 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133043_PI430048170 0.1052521765893091.0402887084378 0.36653353756148
0.3474989289417340.418807021320865 A A A 0.3076250680736250.3020778845239
0.352598882058442 A A A LNCV6_133043_PI430048170 mRNA
GTTGAATTTGTTAATGCACCACACAAGTGCAAAATAAAGACTGATTCACATTACATAGGC NM_152280 RefSeq chr1
+ 155859468 155885199 SYT11 23208 synaptotagmin XI
GO:0005544|GO:0005515|GO:0005215|GO:0030054|GO:0005887|GO:0005509|GO:0006810|GO:0030672|GO:0046
929|GO:0008021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138864_PI430048170 0.0203074943908938 0.4978428477948018.88262802121023
9.19336403903916 9.46489727720843 P P P 9.93710622363411 10.0159020714132
10.5772623294065 P P P LNCV6_138864_PI430048170 mRNA

AGGAAAAAGTACTAACTTGTTCTTTTTGTTCCTGGCTTTCATCAGTTTGTGAGATTTCTC NM_001806 RefSeq chr19 + 33373668 33382686 CEBPG 1054 "CCAAT/enhancer binding protein (C/EBP), gamma, transcript variant 1" GO:0005515|GO:0046982|GO:0006357|GO:0016071|GO:0042267|GO:0005634|GO:0045739|GO:0043353|GO:0003677|GO:0043433|GO:0006351|GO:0043565|GO:0001889|GO:0051091|GO:0001077|GO:0006955|GO:0003690|GO:0045944|GO:0045078|GO:0043388|GO:0030183|GO:0005654|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134357_PI430048170 0.3125523417944820.8026151567978740.291148764356765 0.3121356235652670.28320208200374 A A A 1.00374458036548 0.401279306170681 0.335358814564079 A A A LNCV6_134357_PI430048170 mRNA
CTCCTCAAAGGGGACTTTAGAGGACTTCATACAAAGCTGGGCATTAAGAAAACCACAATG NM_001050 RefSeq chr17 + 73165020 73171923 SSTR2 6752 somatostatin receptor 2 GO:0005515|GO:0043005|GO:0008285|GO:0005886|GO:0007584|GO:0007586|GO:0007267|GO:0007268|GO:0021549|GO:0007283|GO:0030165|GO:0030432|GO:0007193|GO:0071385|GO:0004994|GO:0005737|GO:0006937|GO:0042594|GO:0042923|GO:0005887|GO:0007187|GO:0007218|GO:0071392|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145186_PI430048170 0.0650460163067058 0.6001592118312565.07433502250463 4.29285707164548 4.86230317973613 P P P 5.39789141661472 5.42374320424139 5.70531923384023 P P P LNCV6_145186_PI430048170 mRNA
GTTCTCTATGACTAACAGTTATTAAGTCGGTTGTGTATATGTGTAACTAATGTAACTGCC NM_014862 RefSeq chr15 + 80404349 80597936 ARNT2 9915 aryl-hydrocarbon receptor nuclear translocator 2 GO:0001666|GO:0005667|GO:0043066|GO:0008284|GO:0006355|GO:0003700|GO:0046982|GO:0005634|GO:0007417|GO:0001701|GO:0003677|GO:0006351|GO:0007165|GO:0005737|GO:0007420|GO:0045944|GO:0017162|GO:0004871|GO:0045893|GO:0032355 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130068_PI430048170 0.0672470103256643 0.5191165909541437.1439528661304 7.25154758093406 7.47479267085249 P P P 7.66382325585566 8.34062961933286 8.57625865019447 P P P LNCV6_130068_PI430048170 mRNA
GACACATTTTGCCTACACTTGCTATGTAAATATGTATGCCTGTCATTTTTGTTTCCTTTG NM_001099286 RefSeq chr6 - 136231029 136250311 MTFR2 113115 "mitochondrial fission regulator 2, transcript variant 1" GO:0009060|GO:0005739|GO:0000266|GO:0007005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142167_PI430048170 0.0283494487976239 0.6264110457999586.8460214502816 6.33299140312184 6.43806821707669 P P P 6.98716746909144 7.32926474860249 7.34946789893496 P P P LNCV6_142167_PI430048170 mRNA
ATTCTGTACTCTTGGCAGAGTCAGTAACCAACCACTAATAAAATCAAAGTTGTAGTAAAG NM_052928 RefSeq chr17 - 1779534 1829881 SMYD4 114826 SET and MYND domain containing 4 GO:0008168|GO:0032259|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99418_PI430048170 0.1789811813514831.07888955847739 9.9391842310526 9.76613538512029 9.85681431912013 P P P 9.75754374418234 9.81477961808678 9.6622595688411 P P P LNCV6_99418_PI430048170 mRNA
ATTCTAGGAGATAAGTTTCCATGCACTTTGGTGGCACAGAAAATTGACCTGCCGGAGTAC NM_033453 RefSeq chr20 + 3209359 3223870 ITPA 3704 "inosine triphosphatase (nucleoside triphosphate pyrophosphatase), transcript variant 1" GO:0036220|GO:0051276|GO:0005737|GO:0006193|GO:0000166|GO:0036222|GO:0055086|GO:0009204|GO:0044281|GO:0035870|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128506_PI430048170 0.754268196568816 1.006194334855 0.346310549574949 0.3234305812345360.267404316566882 A A A 0.30647424334453 0.313129173583233 0.291871484680272 A A A LNCV6_128506_PI430048170 mRNA
AGAGAAGTTGGCTGAGAGAACACTCCTTCGTTATTTATTGCGTCTTCATCTCTACATGCG NM_012368 RefSeq chr16 + 3355888 3356924 OR2C1 4993 "olfactory receptor, family 2, subfamily C, member 1" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0005938 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_140505_PI430048170 0.000108800052170342 0.3788155733217973.62436035359115
3.82353861227178 3.79527879909232 P P P 5.27470378388379 5.04857645725997
5.11978990262095 P P P LNCV6_140505_PI430048170 mRNA
CCCTCTAGGACAGATAGTAAAATGTGTACTATGTTGTTACAGTGGTGCAAAAATGTTTTA NM_198568RefSeq chr6
- 87282978 87329278 GJB7 375519 "gap junction protein, beta 7, 25kDa"
GO:0007154|GO:0005922|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139132_PI430048170 0.1889438149533231.18926224923069 10.0553675167459
10.0894220992271 10.2951332587289 P P P 9.69859693804638 9.81433836464651
10.1497824244619 P P P LNCV6_139132_PI430048170 mRNA
CAGCTTCTATCACATGCCGAACTTTCTTGTGACAAATTGTCTGGATTTTTTAAAAAAGGA NM_024065RefSeq chr2
+ 100562955 100576739 PDCL3 79031 phosducin-like 3
GO:0005515|GO:0005737|GO:0001938|GO:0044183|GO:0006457|GO:0050730|GO:0043184|GO:0016032|GO:0006
915|GO:0001525|GO:2000059|GO:0045766 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134063_PI430048170 0.0654903312060317 0.70432937404541 9.23758016912054
9.74856806925707 9.28567974912096 P P P 9.8156838659983 10.1228474462599
9.88922619696408 P P P LNCV6_134063_PI430048170 mRNA
GCAGCACTTGTTTACTGGCTGCTTTCTGGCTCGAAATAAAGGAATCGTGCTTGTGTCGGG NM_001167602 RefSeq
chr2 + 241810931 241817413 NEU4 129807 "sialidase 4, transcript variant 5"
GO:0005515|GO:0006665|GO:0009313|GO:0006687|GO:0006689|GO:0004308|GO:0044281|GO:0005764|GO:0052
794|GO:0005739|GO:0052796|GO:0052795|GO:0019866|GO:0006516|GO:0006488|GO:0044267|GO:0043687|GO:0
018279|GO:0043202. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141814_PI430048170 0.3808886891195781.68703130698561 0.506511053704028
2.04664384297296 0.55180456879272 A A A 0.4084211191752170.48547817932978
0.518704156877157 A A A LNCV6_141814_PI430048170 mRNA
CCAGTGATAACTCTCTTGTCTTGTAAAAAGGGTTTGTACATAACTTGTACATGGTTTCAT NM_001014797 RefSeq
chr10 - 76869600 77637819 KCNMA1 3778 "potassium channel, calcium activated large
conductance subfamily M alpha, member 1, transcript variant 1"
GO:0005515|GO:0005886|GO:0007268|GO:0046872|GO:0016324|GO:0008076|GO:0005249|GO:0042391|GO:0034
765|GO:0006813|GO:0071805|GO:0034465|GO:0070062|GO:0060072|GO:0001666|GO:0043065|GO:0030007|GO:0
006970|GO:0003779|GO:0060073|GO:0045794|GO:0060083|GO:0051592|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_39450_PI430048170 0.303359244300697 1.14802298073674 4.2799407266093 4.18473956123296
4.07008945088319 P P P 4.01529387020664 4.20548843921923 3.67509026199059 P P P
LNCV6_39450_PI430048170 mRNA
TCTTCCTGACTGGCCTCTGTTTCGCCATCCTGCTGGAGGCCATCGAGCGCTTCATCGAGC NM_021194RefSeq chr1
- 211575038 211578757 SLC30A1 7779 "solute carrier family 30 (zinc transporter), member 1"
GO:0005515|GO:0071577|GO:0031965|GO:0005794|GO:0005886|GO:0005783|GO:0071585|GO:0006874|GO:0006
882|GO:0030315|GO:0071584|GO:0055085|GO:0001701|GO:0090281|GO:0046929|GO:0070509|GO:0005737|GO:0
005385|GO:0019855|GO:0070574|GO:0006829|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_135543_PI430048170 0.00254761597421539 0.3545447758505944.06930818973657
3.55881796989595 3.67449398411982 P P P 5.21115811746122 5.15434948609762
5.45758192572085 P P P LNCV6_135543_PI430048170 mRNA
GTCTGCCATTCACCAGGAAAAATTTCTATGGCAATTTTGTACCATGAAGTAAACTGTTAC NM_020147RefSeq chr15
- 70881341 70892433 THAP10 56906 THAP domain containing 10 GO:0003677|GO:0046872 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_73843_PI430048170 0.00423110967176683 0.5640195123851937.57447911629602
7.55590662736022 7.24769479682376 P P P 8.14837734846345 8.2777422636778

8.43857536278608 P P P LNCV6_73843_PI430048170 mRNA
TCAAATTTCTGCGTCCACACTATGGCAAACTGAAGGAAATCTATGAGAACATGGCCCCTG NM_002808 RefSeq
chr3 + 184299097 184309054 PSMD2 5708 "proteasome (prosome, macropain) 26S subunit, non-ATPase, 2, transcript variant 1"
GO:0005515|GO:0002474|GO:0010467|GO:0090263|GO:0044281|GO:0031145|GO:0005829|GO:0034641|GO:0000082|GO:0016032|GO:0030234|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0000502|GO:0043066|GO:0005838|GO:0042176|GO:0006521|GO:0051437|GO:0042590|GO:0006915|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128524_PI430048170 0.440567506158486 0.954767642910515 9.97931491081189 9.72558950470966 9.85127110856219 P P P 9.89163213634631 9.92196551907115 9.95340357991306 P P P LNCV6_128524_PI430048170 mRNA
GAAGCTGTCTTGAATGCCTTGGATAAAATTGTGGAAGAAGGCAAAGTCCGCAAAGAGCCA NM_001199662 RefSeq
chr1 + 156212987 156243332 PMF1-BGLAP NA "PMF1-BGLAP readthrough, transcript variant 2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92498_PI430048170 0.19051853079076 1.1433364053246 7.25766692532612 7.32170506103986 7.0072819289287 P P P 7.0072819289287 7.00535484667162 7.01301916602893 P P P LNCV6_92498_PI430048170 mRNA
AAACCTGGATGAAGATGGTGCCTCGGCCCTCTTCGACATGATCGAGTACTACGAGTCGGC NM_019121 RefSeq
chr19 + 45093172 45147285 PPP1R37 284352 "protein phosphatase 1, regulatory subunit 37"
GO:0005515|GO:0019902|GO:0010923|GO:0004864 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127508_PI430048170 0.401951363230328 0.897067235580977 8.83065717195843 8.93824584390837 9.20167812796743 P P P 9.04855871178684 8.9976512676454 9.3881425646913 P P P LNCV6_127508_PI430048170 mRNA
GGTGTCTTACAAGTGAGCTGACACCATTTTTTATTCTGTGTATTTAGAATGAAGTCTTGA NM_030938 RefSeq
chr17 + 59707501 59840591 VMP1 81671 vacuole membrane protein 1
GO:0005515|GO:0005886|GO:0005783|GO:0007566|GO:0034329|GO:0000421|GO:0006914|GO:0000407|GO:0006887|GO:0016337|GO:0016020|GO:0033116|GO:0007030|GO:0010506|GO:0016021|GO:0007029 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56451_PI430048170 0.109701519293905 1.11970221356233 0.430411246784925 0.552390843774149 0.338438145162373 A A A 0.261590106434356 0.322366126776969 0.254986014645931 A A A LNCV6_56451_PI430048170 mRNA
ACATTGGAGAAGCTCAAGTCCTCCAGATGCATTCAAGCCAGAACACAGAGAAGAAGACAT NM_152710 RefSeq
chr10 - 70771238 70785401 TBATA 219793 "thymus, brain and testes associated"
GO:0007275|GO:0005634|GO:0007283|GO:0030154|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144428_PI430048170 0.070925649079981 2.09491128868486 11.9678115893785 11.9163646137632 11.8870636929015 P P P 11.4272119113217 10.4828993614833 10.4307245123781 P P P LNCV6_144428_PI430048170 mRNA
GGAGGGCTGTATTCACTGATCCTTAGTAACATGTTAACATTTATGAAGCACTATATATTG NM_018116 RefSeq
chr1 + 155610169 155614967 MSTO1 55154 "misato 1, mitochondrial distribution and morphology regulator, transcript variant 1" GO:0048311|GO:0003674|GO:0005737|GO:0005741|GO:0007005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116132_PI430048170 0.925863810240878 0.97968882657902 6.258522567876 6.24850808136609 6.72215557027634 P P P 6.09991881349417 6.46610295220938 6.73502056764486 P P P LNCV6_116132_PI430048170 mRNA
GTGAGTCTTGCGAGGTGGAAGTAATGATTAAATACTCATGTGTTCAGAAAACATAAACTT NM_003384 RefSeq
chr14 + 96797346 96881614 VRK1 7443 vaccinia related kinase 1
GO:0005515|GO:0007077|GO:0008360|GO:0005634|GO:0090166|GO:0005829|GO:0005737|GO:0046777|GO:0016

055|GO:0005795|GO:0007084|GO:0005819|GO:0005730|GO:0031493|GO:0005524|GO:0006897|GO:0035175|GO:0
072354|GO:0007067|GO:0072355|GO:0004672|GO:0004674|GO:0043987|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134750_PI430048170 0.236267262065656 0.745132363182473 4.43910945998162
4.57907945451007 4.7448869259067 P P P 4.55584396184094 5.00280264156143
5.37823860669015 P P P LNCV6_134750_PI430048170 mRNA
TGGAACACATGAAATCTTTGGTTCACAGACTATTTACAATCTTGCATTTAGAAGAGTCTC NM_017918RefSeq chr4
+ 109560198 109687716 CCDC109B 55013 coiled-coil domain containing 109B
GO:0005739|GO:0006851|GO:0019855|GO:0051560|GO:0031305|GO:0031224|GO:0034704|GO:0005216 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93284_PI430048170 0.3189985073207391.28759970084903 1.49362820720962 0.808229479719729
1.36668655511465 A A A 0.558641363680355 0.589097584687131 1.36318182602184 A A A
LNCV6_93284_PI430048170 mRNA
AGCCAGGGAAAGACTGGCAAGAAAAGAGTTAAGGCAAAAAAGGATGCAACAATTCTCCCG NM_000266RefSeq
chrX - 43948775 43973675 NDP 4693 Norrie disease (pseudoglioma)
GO:0005515|GO:0009986|GO:0008283|GO:0007605|GO:0007267|GO:0061299|GO:0001890|GO:0035426|GO:0005
125|GO:0005615|GO:0042803|GO:0007399|GO:0031012|GO:0005109|GO:0007165|GO:0051091|GO:0007033|GO:0
045893|GO:0016055|GO:0060070|GO:0007601|GO:0008083 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131033_PI430048170 0.249600573907175 1.9794773882461 0.24912733666033
1.63590488178487 1.94577542108766 A A A 0.67807085314712 0.347400845023106
0.315400021967301 A A A LNCV6_131033_PI430048170 mRNA
CAATTGGAGAAGCATCCTTCTCAACGCTTTACAAAAGAGTAGTTTGGGGGCCTTTTGTTT NM_001039500 RefSeq
chr1 + 20290918 20354894 VWA5B1 127731 von Willebrand factor A domain containing 5B1
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93791_PI430048170 0.687352722410397 1.05286938902633 3.81069895472531 3.78708118625113
3.94895151182842 P P P 3.52305399617182 4.23582341496741 3.42899175479009 P P P
LNCV6_93791_PI430048170 mRNA
ACATGCTCTAAAGCCCTTCACAGCAAGACCCAGGAAGCCGCGGGCAAACTCAGACTCGAA NM_024599RefSeq
chr17 - 76470892 76501427 RHBDF2 79651 "rhomboid 5 homolog 2 (Drosophila), transcript variant
1" GO:0019838|GO:0005886|GO:0004252|GO:0050709|GO:0006508|GO:0005789|GO:0016021|GO:0015031 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140638_PI430048170 0.0738712625052904 0.790369722645515 6.32935628088688
6.26098368337068 6.62885377509486 P P P 6.89852315176216 6.63757892431831 6.7158241757043
P P P LNCV6_140638_PI430048170 mRNA
TACCCAGTGGGTCAACTTCTGCAAAATTCCGTAATGGTGTATTAGTATTAGAATAGTGAA NM_001153585 RefSeq
chr4 + 140343460 140382556 SCOC 60592 "short coiled-coil protein, transcript variant 5"
GO:0005802|GO:0005515|GO:0000139|GO:0016239|GO:0005829|GO:0005768 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_104219_PI430048170 0.325129992802464 0.967096583941424 0.249451631687725
0.263525259421793 0.364931333911188 A A A 0.38428434083222 0.318541831185348
0.321701670178355 A A A LNCV6_104219_PI430048170 mRNA
AGTAGCTCATTTCGACAGTCGGATCCATAGCAGCCATGTGCTGGAAATGAAACTGACAAA NM_181744RefSeq chr6
+ 47782038 47826380 OPN5 221391 "opsin 5, transcript variant 1"
GO:0005502|GO:0018298|GO:0009881|GO:0007186|GO:0004930|GO:0016021|GO:0007602|GO:0007601 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135332_PI430048170 0.144821378657338 0.560701829231338 2.92352516418386
4.09259549365066 2.76719811969334 A P A 4.08524872783466 4.33276091501665
4.24605813931869 P P P LNCV6_135332_PI430048170 mRNA

GACCTTCCACTTTCTCTTCAGAATAAGTAGCTGTGGTGGATATTATTATTTGAAGAAAGA NM_001146071 RefSeq chr13 + 60396456 60573879 TDRD3 81550 "tudor domain containing 3, transcript variant 3" GO:0005737|GO:0003682|GO:0003713|GO:0005634|GO:0035064|GO:0035145|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137860_PI430048170 0.00689343437153983 0.6046282073179563.29016444269922 3.22353867654824 3.56198983124471 P P P 4.00456386272373 4.21260656000646 4.050491974967 P P P LNCV6_137860_PI430048170 mRNA
AAGATCTCCTTTCTGGTTATATCTTCCTTGGGGCAGAGGGAGTTTCAGACAAGACTTCTG NM_001039887 RefSeq chr19 + 35758142 35769175 PROSER3 148137 proline and serine rich 3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144950_PI430048170 0.50685901031614 1.2009930802374 4.26319119021278 3.605789531459 3.53759888528787 P P P 4.08124658675773 3.51645482454464 2.8922280294077 P P P LNCV6_144950_PI430048170 mRNA
CGGGTGGAGGGGGTGGGCAGGGTATTTATTTAAATTAAAAAACAAAACAGAAGAGATGTC NM_173564RefSeq chr7 + 100483926 100494801 NYAP1 222950 neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 1 GO:0048812|GO:0014065 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133917_PI430048170 0.0193056334883453 0.3853419441436451.98174344262027 1.54060371944437 2.15415359412559 A A A 3.37749562214753 3.63059513504637 2.71635143218296 P P P LNCV6_133917_PI430048170 mRNA
ACTCACCTTCCCCAGCTACAAAAATCTGTATTATCCTCTTAAAGTAAAACTGGAGTTACA NM_000025RefSeq chr8 - 37962995 37966666 ADRB3 155 adrenoceptor beta 3 GO:0005515|GO:0005886|GO:0009409|GO:0002024|GO:0002025|GO:0031699|GO:0051379|GO:0005634|GO:0006091|GO:0015052|GO:0042803|GO:0051380|GO:0007190|GO:0031649|GO:0040015|GO:0046677|GO:0005975|GO:0007568|GO:0004939|GO:0006898|GO:0002032|GO:0043235|GO:0006112|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145738_PI430048170 0.4548873303446331.02456582051111 0.526703023920184 0.5963932549896260.468836646088203 A A A 0.5150611059511530.485804626399878 0.488679526452747 A A A LNCV6_145738_PI430048170 mRNA
CTCTGACACTTGCAACCATGTTCAGTATAGAATGTGCCAAACAGACGAAACAGATGGTTG NM_001040433 RefSeq chr5 + 148335558 148339849 SPINK9 NA "serine peptidase inhibitor, Kazal type 9" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140350_PI430048170 0.0165885165776585 0.42677150509321811.8561316812251 11.7562430096398 11.706244610935 P P P 12.6386726857083 13.0658575264447 13.2393296147899 P P P LNCV6_140350_PI430048170 mRNA
CTGCTTGCTTCCTGTCCCCGAAATGTTCGTTTCTTCTGAAGTAAATATACATATATAAAT NM_001127392 RefSeq chr11 + 61752636 61788518 MYRF 745 "myelin regulatory factor, transcript variant 2" GO:0003700|GO:0048709|GO:0022010|GO:0005634|GO:0003677|GO:0006351|GO:0032286|GO:0014003|GO:0005789|GO:0006508|GO:0008233|GO:0016021|GO:0045893|GO:0031643 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142572_PI430048170 0.0414723487718098 1.16401205677675 12.7715525722729 12.6661279309116 12.7697972517675 P P P 12.4367051665769 12.4804986964338 12.6283964393678 P P P LNCV6_142572_PI430048170 mRNA
CACAGTAAGGTTTGCCTGTGTACAGACCTCCGTTCAATAAATTATTGGCATGAAAACCTG NM_019884RefSeq chr19 - 42230185 42242584 GSK3A 2931 glycogen synthase kinase 3 alpha GO:0005515|GO:0030877|GO:0050321|GO:0010905|GO:0044027|GO:0030968|GO:0007173|GO:0046325|GO:0016055|GO:0045823|GO:2000467|GO:0071285|GO:0010800|GO:2000466|GO:0032869|GO:0005977|GO:0051348|GO:0003073|GO:0061052|GO:0008543|GO:0045087|GO:2000077|GO:0006987|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140333_PI430048170 0.7161714586408220.9952432505569740.356513509811821

0.3574246852680870.374952102199233A A A 0.3887145256646840.339013999755387
0.381376226278971A A A LNCV6_140333_PI430048170 mRNA
GCTGTTTATCAGATGTTCTTAACAACTGTTAGGTGTCTGATATGGTTGGTAAAGAAATCT NM_004609RefSeq chr20
- 603992 610266 TCF15 6939 transcription factor 15 (basic helix-loop-helix)
GO:0048339|GO:0003700|GO:0006357|GO:0001756|GO:0060231|GO:0016265|GO:0048705|GO:0005634|GO:0003
677|GO:0006351|GO:0045198|GO:0043583|GO:0048644|GO:0003016|GO:0050884|GO:0046983|GO:0007498|GO:0
042755|GO:0043588. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143802_PI430048170 0.4414034826457170.90911212126539 11.3657524011342
11.4770008044922 11.7044858388192 P P P 11.6966855502966 11.4210502994206
11.8328263411858 P P P LNCV6_143802_PI430048170 mRNA
GTTGGTTTTAATGTGCATGTGAATGGCCTAGAGAACCTATTTTTGTGTCTAAAGTTTACA NM_014315RefSeq chr14
+ 49768068 49783138 KLHDC2 23588 kelch domain containing 2 GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126722_PI430048170 0.00233175634901192 0.4556336241661851 0.8998965108032
10.900543573878 10.6602648494371 P P P 11.9046632821222 11.991382482751
11.9783617775874 P P P LNCV6_126722_PI430048170 mRNA
CTCTCGAATTTTCTTCCCTCTGAAATCCTATTTAAGAACTTTTGGAAGCTTAGCCATTTT NM_001130100 RefSeq chr16
- 57758216 57802527 KIFC3 3801 "kinesin family member C3, transcript variant 2"
GO:0090136|GO:0008017|GO:0005813|GO:0005871|GO:0005794|GO:0005874|GO:0045218|GO:0003777|GO:0005
524|GO:0005915|GO:0008152|GO:0007030|GO:0007601|GO:0016887|GO:0030659|GO:0070062|GO:0007018 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128755_PI430048170 0.000239494947969848 0.2375192572564895.09810544441973
4.758694307122 5.12319741545231 P P P 6.93256085881497 6.96547347543692
7.30186501439581 P P P LNCV6_128755_PI430048170 mRNA
TGGGGGTATACTTGGACTGCAGGGGTTATTGTCAATGTGTGATTTGTGTTTTTATTTTAT NM_152230RefSeq chr10
- 58191516 58267934 IPMK 253430 inositol polyphosphate multikinase
GO:0016310|GO:0000824|GO:0008440|GO:0043647|GO:0032958|GO:0005730|GO:0005654|GO:0005634|GO:0044
281|GO:0005524|GO:0000823|GO:0001841 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77444_PI430048170 0.0651373244849433 0.7753903269489564.5585810208188
4.85178534774351 4.50948831029314 P P P 5.06899569571482 4.8146859367806
5.14142740915229 P P P LNCV6_77444_PI430048170 mRNA
AGAGGAAAGTACAACAGAAACGACACTGTAGTACCTATCAGCCTACTCCTCCTCTATCTC NM_015571RefSeq chr6
+ 75601508 75718285 SENP6 26054 "SUMO1/sentrin specific peptidase 6, transcript variant 1"
GO:0005515|GO:0005737|GO:0016926|GO:0016925|GO:0006508|GO:0070646|GO:0016929|GO:0005654|GO:0090
234|GO:0090169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135768_PI430048170 0.5321311085353451.01841641875746 0.332310778661464
0.2649139243410120.368974752840741A A A 0.2824099721961690.265908695397205
0.339776021010937A A A LNCV6_135768_PI430048170 mRNA
AAGTACATTCTGGACAGCTGGAAGAAACACGACTCAGAAGAGAAATAAAGAGTGCAGCCC NM_019612RefSeq
chr19 + 43716061 43720017 IRGC 56269 "immunity-related GTPase family, cinema"
GO:0016787|GO:0016020|GO:0008152|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133116_PI430048170 0.1757290755400090.9393413625647450.245437471120935
0.3136040136997750.287713236394634A A A 0.4566838609708810.353506529087681
0.303988870838954A A A LNCV6_133116_PI430048170 mRNA
ACACCGAGTGCCTTTCTTTGATCAGGAGGACCCGGATTCCTACCTGGAGGAGGAGGACAA NM_175734RefSeq chr17
+ 7425615 7427567 C17orf74 201243 chromosome 17 open reading frame 74 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136488_PI430048170 0.0135388961246350.9529386810594390.356526148883887
0.36435148227273 0.329683856084335A A A 0.4396179961462740.422453694610534

0.397034780062363 A A A LNCV6_136488_PI430048170 mRNA
CATAATTACTCCAGGTGTTATACTTGCCAAGTCAGCAATTCTGTGAGCAGCAAGAATGGC NM_001256030 RefSeq
chr1 - 160680421 160711851 CD48 962 "CD48 molecule, transcript variant 2"
GO:0005515|GO:0016020|GO:0005886|GO:0007596|GO:0005887|GO:0045121|GO:0006952|GO:0004872|GO:0031
225|GO:0050900|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124885_PI430048170 0.398709185199363 1.65483840429186 1.58849302060352 2.2855302061296
0.366153021372112 A A A 0.242355801513441 1.66699225069279 0.24355826497829 A A A
LNCV6_124885_PI430048170 mRNA
GCAGGGTGGAGATCGCTGCATCCCTGCAGCTCAACGAGACCCAAGTGAAGATCTGGTTCC NM_005522 RefSeq chr7
- 27092994 27096006 HOXA1 3198 "homeobox A1, transcript variant 1"
GO:0005515|GO:0060876|GO:0007634|GO:0071300|GO:0007605|GO:0005634|GO:0048844|GO:0021599|GO:0009
952|GO:0048702|GO:0009653|GO:0050905|GO:0045944|GO:0090102|GO:0090103|GO:0042473|GO:0048839|GO:0
021569|GO:0021953|GO:0007275|GO:0060840|GO:0006351|GO:0043565|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135329_PI430048170 0.00304643444042167 3.3182232317663 5.08692972351989
5.59546830282213 5.43604793024109 P P P 3.2362612073557 3.75238822939386
3.90311091736562 P P P LNCV6_135329_PI430048170 mRNA
TGGTCGAGCAGGGCAGTACTGGACCAGGTCTACGTCAGCATTCAGGTTCAATGGGGACAC NM_001197237 RefSeq
chr6 + 26383210 26394872 BTN2A2 10385 "butyrophilin, subfamily 2, member A2, transcript variant 3"
GO:0031324|GO:0046007|GO:0016021|GO:0050710|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130785_PI430048170 0.0611069367821251 1.46444148584041 4.59744397027758
4.32707090186245 4.56383395567422 P P P 4.26706006473301 3.81140098345048
3.71083654978746 P P P LNCV6_130785_PI430048170 mRNA
CACATGAGGAGAGGCAGGGCGTGTCAGCAGCAAACCTAAGTGTGTGCTCATTTCTGTGGG NM_173627 RefSeq chr17
+ 80415166 80438084 ENDOV 284131 "endonuclease V, transcript variant 1"
GO:0005737|GO:0003727|GO:0006281|GO:0000287|GO:0016891|GO:0043566|GO:0005730|GO:0016888|GO:0000
737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135271_PI430048170 0.869576298118437 0.968570305178116 3.19673696682276 2.6669041103236
3.06330979346821 P A P 3.34190066270446 2.97007756767499 2.73941882986701 P P P
LNCV6_135271_PI430048170 mRNA
GCTTGGGGGGATTTGCCCCCTCTGGTAGATACCAGAACTATGGATATGCCTTTATATATT NM_001145402 RefSeq
chr19 - 55354907 55363252 FAM71E2 284418 "family with sequence similarity 71, member E2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135440_PI430048170 0.304736403962102 1.72669117339487 0.392448221199695
1.69880306991506 1.957030452697 A A A 0.715818708598359 0.930746041008355
0.422432164981772 A A A LNCV6_135440_PI430048170 mRNA
AAGAAAAATCAAGGGGCTGTGTTCAAGAACTGGCTCCCTTGGTGATTGTATTACGAAGCC NM_001145454 RefSeq
chr1 - 25884185 25906502 STMN1 3925 "stathmin 1, transcript variant 4"
GO:0043005|GO:0031115|GO:0005874|GO:0007409|GO:0009615|GO:0031175|GO:0005829|GO:0035556|GO:0005
622|GO:0007165|GO:0005737|GO:0051493|GO:0015631|GO:0016020|GO:0007420|GO:0004871|GO:0007052|GO:0
051272|GO:0007019|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141877_PI430048170 0.141674698969744 0.803672487717559 10.0645688271181
10.3914115180935 10.561082967973 P P P 10.7280270648802 10.5582559929927
10.7139396281664 P P P LNCV6_141877_PI430048170 mRNA
CCAGCGCCTTTTAAAAGTTGTTATGTGGTTTTCTTTTAAAAAGCTCCTGTTTTTGGAAAG NM_016304 RefSeq chr15
- 55181313 55197033 RSL24D1 51187 ribosomal L24 domain containing 1
GO:0042254|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135821_PI430048170 0.0170715137973912 0.273387289459612 4.63687022028055

3.46580816418811 4.38196948173092 P P P 5.72748930560819 6.23019129065289
6.31519271412195 P P P LNCV6_135821_PI430048170 mRNA
AGGCTCTTATGTGCTAGTTTTGTTGGTAGCACGTTATTTAATGCATAAAGGCAGAATTCT NM_022458RefSeq chr7
- 156680875 156893208 LMBR1 64327 limb development membrane protein 1 GO:0016021|GO:0042733
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130005_PI430048170 0.4704469938118380.9081913824264821.63972231840204 1.8662238789842
1.42655487498758 A A A 1.56062325484156 1.97866985908534 1.81313252941372 A A A
LNCV6_130005_PI430048170 mRNA
CCTTGAAGAGAATAGTAATGATGGGAATTTAGAGGTTTATGACTGAATTCCCTTTGACAT NM_004665RefSeq chr6
- 132743869 132758008 VNN2 8875 "vanin 2, transcript variant 1"
GO:0017159|GO:0015939|GO:0005886|GO:0006928|GO:0031225 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128290_PI430048170 0.0365484194722686 0.84967921651752615.9094090814459
15.713118911649 15.7743628315801 P P P 16.0938937759806 16.0093614106096
16.0039342167785 P P P LNCV6_128290_PI430048170 mRNA
CTCCCCGAGTTGGTGGAAAACGCTAAACTGGCAGATTAGATTTTTAAATAAAGATTGGAT NM_000986RefSeq chr3
- 101681089 101686719 RPL24 6152 ribosomal protein L24
GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0006415|GO:0006412|GO:0006
413|GO:0005829|GO:0006414|GO:0000184|GO:0016020|GO:0016032|GO:0022625|GO:0044267|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124221_PI430048170 0.1536132395160231.19939370958168 14.1579250450377
14.2611655713564 14.5448237011958 P P P 14.1149042034996 13.8965179957739
14.1789301194394 P P P LNCV6_124221_PI430048170 mRNA
CGGAGGCGGAGGCTTGGGGCGTTCAAGATTCAACTTCACCCGTAACCCACCGCCATGGCCNM_001016RefSeq chr6
+ 132814568 132817564 RPS12 6206 ribosomal protein S12
GO:0010467|GO:0003735|GO:0006614|GO:0019083|GO:0019058|GO:0006415|GO:0006412|GO:0006413|GO:0005
829|GO:0006414|GO:0000184|GO:0016020|GO:0022627|GO:0016032|GO:0044267 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_106332_PI430048170 0.0367110422597721 1.23026809992443 12.36953782343
12.1607343520863 12.1395622770207 P P P 11.9623653173708 11.9699664808913
11.8487954432702 P P P LNCV6_106332_PI430048170 mRNA
TATTAAGGGAGATGGCGAGGTCCTAGAGGAAATCGTAACCAAAGAACGACACAGAGAGAT NM_001278380
RefSeq chr12 + 122980059 122982913 ARL6IP4 51329 "ADP-ribosylation factor-like 6 interacting
protein 4, transcript variant 7" GO:0008380|GO:0006397|GO:0005515|GO:0016607|GO:0005730|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128259_PI430048170 0.000289479767123311 0.4467840113381676.26477620345255
6.16112351658881 6.40175619750299 P P P 7.34795526455797 7.39331279652777
7.57357208461558 P P P LNCV6_128259_PI430048170 mRNA
GGCAGTCTCGTTTTGCTTTTCAAAGACATTTTGTAGAGATTTTTCACTAATGTGAATCTG NM_018360RefSeq chrX
+ 16786431 16844519 TXLNG 55787 "taxilin gamma, transcript variant 1"
GO:0019905|GO:0031965|GO:0030500|GO:0007049|GO:0006355|GO:0046982|GO:0051726|GO:0010564|GO:0006
351|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129378_PI430048170 0.0911085659337966 0.6175657988472873.41670273791525
2.70898037145713 3.52060145846558 P A P 3.68181279815041 3.83116010568741 4.2777554347615
P P P LNCV6_129378_PI430048170 mRNA
CCCAATTGTCAAACATCCTAGGTAAGTGGTTGACATTTCTTACAGCAATTACAGATTATT NM_018284RefSeq chr1
- 89006676 89022866 GBP3 2635 guanylate binding protein 3
GO:0005515|GO:0051607|GO:0005737|GO:0016020|GO:0008152|GO:0003924|GO:0005525 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_138678_PI430048170 0.8547119468212920.99303990555972 0.429417253585741
0.4829804165273720.38769909365426 A A A 0.5218735588965630.397206415092316
0.409529971294127A A A LNCV6_138678_PI430048170 mRNA
GGTGTAAAGAGACAAGCATTCCTCTGTAAGCCATCAAGAAATAAACTGCTGGCTTTTCCT NM_173489RefSeq chr5
- 40998019 41071342 MROH2B 133558 maestro heat-like repeat family member 2B NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129470_PI430048170 0.0513652285103548 0.6637478286868637.27039734340501
7.53543933938111 7.62929869252487 P P P 7.94986006692214 7.84111687253378
8.38300055506252 P P P LNCV6_129470_PI430048170 mRNA
AAATCCCAAGAATGGATGTTCTTTGTGTGGTATGAGAGGTTGGTTTGTATCTCAAAAGCA NM_001201329 RefSeq
chr8 - 9136253 9151642 PPP1R3B 79660 "protein phosphatase 1, regulatory subunit 3B,
transcript variant 1"
GO:0042587|GO:0005979|GO:0050790|GO:0019888|GO:0016311|GO:0000164|GO:0005977|GO:0004721|GO:0019
899|GO:0043231|GO:0005981 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138931_PI430048170 0.0180155557058014 0.4803067293249738.64120117306648
8.89307507115325 9.07041303269329 P P P 9.69645478590419 9.71205252967732
10.3128612920122 P P P LNCV6_138931_PI430048170 mRNA
GGCTTTTGTTGAACTAGAACCCTCAGCACATACTGTGTTGTACTTTTGTAAATGATTTTTNM_001242581 RefSeq chr20
+ 19886520 20002459 RIN2 54453 "Ras and Rab interactor 2, transcript variant 1"
GO:0017112|GO:0050790|GO:0005737|GO:0005083|GO:0007264|GO:0032851|GO:0005575|GO:0006897|GO:0005
096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138039_PI430048170 0.4236298670923821.09579919842124 0.349660656338651
0.3492996716027660.714925832977562A A A 0.3552744560791660.320762792415411
0.373074823891452A A A LNCV6_138039_PI430048170 mRNA
GAACCCAATAATCTATACTTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAAACTGAA NM_001005501 RefSeq
chr14 + 19876267 19877212 OR4K2 NA "olfactory receptor, family 4, subfamily K, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131646_PI430048170 0.1382072700095751.50972553061083 9.63739931736368 9.5368620840036
9.40945942716616 P P P 9.43382642654979 8.63774650188914 8.5700890782415 P P P
LNCV6_131646_PI430048170 mRNA
CTTGGCAGAGCCAGAGTGTACACATTCCTAAACCATTAAACAGATTTCTATAACAAGCCA NM_001204890 RefSeq
chr3 - 129087568 129161230 ISY1-RAB43 NA ISY1-RAB43 readthrough NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_126683_PI430048170 0.0817102305651272 1.87269145970833 3.68558961429536
3.8494900910367 3.35871366871187 P P P 3.18742806468608 2.06405563942748
2.75586610111408 P A P LNCV6_126683_PI430048170 mRNA
GGATCCAGTCCTGTCAGCATGATGCCTCCATGAATAAGAGTGAACTTCTTGTAAAGTGAA NM_013442RefSeq chr9
- 35099775 35103195 STOML2 30968 "stomatin (EPB72)-like 2, transcript variant 1"
GO:0001772|GO:0005515|GO:0050852|GO:1900210|GO:0006851|GO:0034982|GO:0005102|GO:0005743|GO:0006
874|GO:0015629|GO:0090297|GO:0051259|GO:0010876|GO:0035710|GO:0005758|GO:0010918|GO:0008180|GO:0
042776|GO:0042101|GO:0032623|GO:0045121|GO:0007005|GO:0005856|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131754_PI430048170 0.2887088024194531.087124990428 9.79095360660682
9.94783651522274 9.81689045285655 P P P 9.87400944180824 9.72898764841154
9.58124393118342 P P P LNCV6_131754_PI430048170 mRNA
TGATTAAAGTATTTTCATACATTTTGCTTCTTGCCCAGCAGGGACAGGTGGCAGAGCCGA NM_006816RefSeq chr5
- 177331561 177351884 LMAN2 10960 "lectin, mannose-binding 2"
GO:0005793|GO:0005794|GO:0009986|GO:0006890|GO:0015031|GO:0005537|GO:0005615|GO:0046872|GO:0050
766|GO:0001948|GO:0000139|GO:0005887|GO:0033116|GO:0031072|GO:0005789|GO:0030246|GO:0070062 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82738_PI430048170 0.0390677706974426 1.15905091612253 4.88820803354799
4.73214200369963 4.88005733135464 P P P 4.54925525541223 4.71393147976894
4.59869114071475 P P P LNCV6_82738_PI430048170 mRNA
ACCTTTCACTGTGATTCGGGCTACCAGCTGCAGGGAGAGGAGACCCTCATCTGCCTCAAT NM_001243332 RefSeq
chr16 - 29871158 29899264 SEZ6L2 26470 "seizure related 6 homolog (mouse)-like 2, transcript variant
5" GO:0005886|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109333_PI430048170 0.1080417070076880 0.7991367466599756 0.03316542260563
6.18252880002694 6.4547971482977 P P P 6.52730908587368 6.60971148252394 6.5345274182426
P P P LNCV6_109333_PI430048170 mRNA
TCAATGAAACCCTGAAACTTCCTCCCAGGAGCATCAAGTGGAATGTGGATTCTGTTCATG NM_018222 RefSeq chr11
+ 12377478 12535356 PARVA 55742 "parvin, alpha"
GO:0005515|GO:0070252|GO:0030018|GO:0031532|GO:0005886|GO:0034329|GO:0008360|GO:0071670|GO:0002
040|GO:0003779|GO:0005634|GO:0015629|GO:0030027|GO:0005829|GO:0005737|GO:0007163|GO:0060271|GO:0
003148|GO:0034446|GO:0034113|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132502_PI430048170 0.0396997070421201 0.2448189927806911.45468215169648
0.5041812039338352.04577599636518 A A A 3.54893872671445 3.51694328906121
3.41995665078767 P P P LNCV6_132502_PI430048170 mRNA
CCAGTTACTGGGTTTAACTGGTGTACATTAATTAGATGTCCATACTGTATTTTGTTTGCA NM_001949 RefSeq chr6
+ 20401905 20493714 E2F3 1871 "E2F transcription factor 3, transcript variant 1"
GO:0005515|GO:0005667|GO:0008284|GO:0003700|GO:0005794|GO:0006367|GO:0001047|GO:0005634|GO:0043
231|GO:0005737|GO:0007219|GO:0005654|GO:0045893|GO:0000278 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144504_PI430048170 0.2261661616001421.1749730569317 6.00203434296836
6.10441501336241 5.80103161261186 P P P 5.82651204871812 5.90171000491075
5.46017375989655 P P P LNCV6_144504_PI430048170 mRNA
ATCTTAGGTATCTACTTTAGAGTCTTCTCCAATGTCCAAAAGGCTAGGGGGTTGGAGGTG NM_139025 RefSeq chr9
+ 133421999 133459403 ADAMTS13 11093 "ADAM metallopeptidase with thrombospondin type 1 motif,
13, transcript variant 1"
GO:0005515|GO:0036066|GO:0005615|GO:0009100|GO:0006493|GO:0016485|GO:0006508|GO:0070670|GO:0034
341|GO:0043171|GO:0009986|GO:0005509|GO:0005578|GO:0009636|GO:0030168|GO:0005178|GO:0007160|GO:0
007229|GO:0005788|GO:0008270|GO:0034612|GO:0004222|GO:0044267|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131916_PI430048170 0.0178557693706920.7144495364159896.59848185677127
6.70258187009384 6.92486320483688 P P P 7.15094903390384 7.18042140452037
7.36031423087426 P P P LNCV6_131916_PI430048170 mRNA
GTATATGGCTTTGTTTTAACATTCCCCTAAATAAAATGGCTTCATTCTCCCCTTGGAAAA NM_001203 RefSeq chr4
+ 94757976 95158450 BMPR1B 658 "bone morphogenetic protein receptor, type IB, transcript variant 2"
GO:0005515|GO:0031290|GO:0060041|GO:0005886|GO:0001654|GO:0045597|GO:0046332|GO:0042698|GO:0009
953|GO:0046872|GO:0006954|GO:0004702|GO:0002063|GO:0060350|GO:0035108|GO:0005025|GO:0023014|GO:0
030501|GO:0030509|GO:0005524|GO:0030166|GO:0045669|GO:0043235|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145546_PI430048170 0.0916891494202595 0.4355565722252622.73120525843695
1.19417721773871 2.35353704452369 A A A 3.20681255985601 3.28130667895269
3.73084443642836 P P P LNCV6_145546_PI430048170 mRNA
CACAGACATTCTGTACATATCCTGTGAAACGTGCTGTCATATGAAATAAATATATCTGTC NM_203446 RefSeq chr21
- 32628758 32728040 SYNJ1 8867 "synaptojanin 1, transcript variant 2"
GO:0016082|GO:0043647|GO:0006661|GO:0003723|GO:0046488|GO:0034595|GO:0048489|GO:0048488|GO:0044
281|GO:0004445|GO:0006796|GO:0030117|GO:0005829|GO:0004439|GO:0000166|GO:0046855|GO:0046856|GO:0

006836|GO:0006644|GO:0016191 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130664_PI430048170 0.0646233221987151 0.6372919886705943.41323724564656
4.0585422057292 3.60224035594616 P P P 4.05773777164638 4.6553482982037
4.32667012596321 P P P LNCV6_130664_PI430048170 mRNA
CATCTGGGAATGCAAATCTTCAATCACATTTCTATTCTCAAACACTTGGAGAAGTCTATA NM_030790RefSeq chr16
- 47154387 47461274 ITFG1 81533 "integrin alpha FG-GAP repeat containing 1, transcript variant 1"
GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127834_PI430048170 0.5173668378501610.9506233804637339.36634225153779
9.26314499882207 9.03277529533599 P P P 9.23144540914491 9.35822305360031
9.30884957191822 P P P LNCV6_127834_PI430048170 mRNA
AACAAAGCAGTCGCCCATCTACTTCCCGTTGGAAGGAATGCTGGGCAGTAATAAATTAGA NM_001271977 RefSeq
chr2 - 241494706 241508695 STK25 10494 "serine/threonine kinase 25, transcript variant 1"
GO:0005515|GO:0023014|GO:0042542|GO:0005794|GO:0006915|GO:0032874|GO:0051683|GO:0005524|GO:0090
168|GO:0046872|GO:0042803|GO:0035556|GO:0007165|GO:0005737|GO:0046777|GO:0004672|GO:0007163|GO:0
004702|GO:0045595|GO:0006468|GO:0050772|GO:0051645|GO:0006979|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144437_PI430048170 0.6959319743535581.01297274439658 0.399131162750448
0.39173912967952 0.280381139760309A A A 0.31808940549568 0.348361742232388
0.351816709484514A A A LNCV6_144437_PI430048170 mRNA
GCTGAGCCGGCAGCTGAAAATCTAACTCATAATTTATGTTGTAGAGAAATAGAATTACCT NM_173576RefSeq chr10
- 27672873 27745849 MKX 283078 "mohawk homeobox, transcript variant 1"
GO:0006366|GO:0005634|GO:0000122|GO:0000978|GO:0045662|GO:0001078|GO:0002932|GO:0001077|GO:0007
517|GO:0032967|GO:0035990|GO:0045944|GO:0030199|GO:0001085 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_118260_PI430048170 0.3747866256128371.2289589590854 3.36495929349055
2.91221095444849 2.72769588477848 P A A 2.62216094263745 3.14729310221104
2.28743343462071 P P A LNCV6_118260_PI430048170 mRNA
ATACGGGAGAGAAACCATATGAATGTGCCGAATGTGGGAAAAGCTTCAGTAAGAGCTCCA NM_145238RefSeq
chr1 + 33472630 33496395 ZSCAN20 7579 zinc finger and SCAN domain containing 20
GO:0006355|GO:0003700|GO:0003682|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_91324_PI430048170 0.6027842705304420.9888403557998210.2934876726652540.333813227887578
0.38074662334228 A A A 0.3768124970306060.3498370772248590.330923224764058A A A
LNCV6_91324_PI430048170 mRNA
ATAATTGCAGTGCTGCTTTGCTTCCAAAACTGGGCAGTGAGTTCAACAACAACGACAACA NM_001172813 RefSeq
chr8 + 116950950 117176714 SLC30A8 169026 "solute carrier family 30 (zinc transporter), member 8,
transcript variant 4"
GO:0071577|GO:0005794|GO:0005886|GO:0061088|GO:0032119|GO:0006882|GO:0042593|GO:0055085|GO:0042
803|GO:0009749|GO:0005385|GO:0016023|GO:0032024|GO:0006829|GO:0008270|GO:0060627|GO:0034341|GO:0
016021|GO:0030141|GO:0044267|GO:0030073|GO:0070555|GO:0030658|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141031_PI430048170 0.6785906048069851.02509121072858 0.272195864046429
0.2853315275394990.480895495482245A A A 0.3372927307760530.291556626460402
0.311562151216983A A A LNCV6_141031_PI430048170 mRNA
CCCATATGTCTAAGGAAAGGATGCTATTTGGTAATGAGGAACTGTTATTTGTATGTGAAT NM_000372RefSeq chr11
+ 89177871 89295759 TYR 7299 tyrosinase
GO:0005515|GO:0033162|GO:0042470|GO:0048471|GO:0006726|GO:0046982|GO:0005507|GO:0008283|GO:0005
798|GO:0048538|GO:0005764|GO:0042803|GO:0004503|GO:0005737|GO:0006583|GO:0016021|GO:0007601|GO:0
055114 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_134748_PI430048170 0.4663172422754421.04214091302954 0.282976196068442
0.2976652315394830.480330274552877A A A 0.315879350230436 0.279571295262323
0.295135141220011A A A LNCV6_134748_PI430048170 mRNA
GACTTGGGAACAGGACTTTATACCTCTTTTACTGTAACAAGTACTCATTAAAGGAAATTG NM_006475RefSeq chr13
- 37562581 37598844 POSTN 10631 "periostin, osteoblast specific factor, transcript variant 1"
GO:0031012|GO:0005802|GO:0005515|GO:0001501|GO:0030198|GO:0009888|GO:0005578|GO:0007155|GO:0050
839|GO:0008201|GO:0005615|GO:0008593 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_37664_PI430048170 0.0243944906690373 0.5234262170714893.02596122321822
3.06845155250565 2.49716209446387 P P A 3.78151761441326 3.72271610636691
3.94676142274654 P P P LNCV6_37664_PI430048170 mRNA
GCAGGGATATTTTGTGTTTATGTGTCCAAAAAAGGAATAAATTGGCATTCTTGTGCCAAA NM_017629RefSeq chr1
+ 35808226 35857889 AGO4 192670 argonaute RISC catalytic component 4
GO:0005515|GO:0010467|GO:0048011|GO:0048015|GO:0006402|GO:0016441|GO:0005829|GO:0016442|GO:0035
068|GO:0035278|GO:0035198|GO:0007173|GO:0007219|GO:0016020|GO:0000932|GO:0008543|GO:0045087|GO:0
038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130766_PI430048170 0.5733788938758060.9722016272795270.319919832017308
0.2939658237727790.2993932576978 A A A 0.2934599116519620.457254567610423
0.27777763876705 A A A LNCV6_130766_PI430048170 mRNA
ATGATGGTGGCAATGAGAAGACGATGCTCTCAGTTTGTGAATTACAGTAAAATCTTTTAA NM_001005326 RefSeq
chr15 + 101805719 101806658 OR4F6 NA "olfactory receptor, family 4, subfamily F, member 6" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133635_PI430048170 0.4406477104413760.8809466017178659.27104046803787
9.36306551893296 9.54152713264075 P P P 9.28523227602406 9.52332089869068
9.86874164843159 P P P LNCV6_133635_PI430048170 mRNA
TTTTAAAATTGAATTCATTCTGATGCTTGGCCCCCATACCCCCAACCTTGTCCAGTGGAG NM_001126103 RefSeq
chr12 - 49989161 50025524 RACGAP1 29127 "Rac GTPase activating protein 1, transcript variant 2"
GO:0051256|GO:0005515|GO:0008017|GO:0072686|GO:0007264|GO:0005634|GO:0007283|GO:0009790|GO:0051
233|GO:0007108|GO:0032154|GO:0046872|GO:0005829|GO:0007405|GO:0019886|GO:0000915|GO:0070062|GO:0
007018|GO:0051056|GO:0043015|GO:0001669|GO:0019901|GO:0051988|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_85666_PI430048170 0.0874121395469588 1.40720253248691 5.4327466608635
6.01162425880144 5.82134077896991 P P P 5.44075385810999 5.06695784760757
5.31366802746798 P P P LNCV6_85666_PI430048170 mRNA
AATGAGTTGAAACTGATGGAAGAATTTGTCAAGCAATATAAGAGCGAGGCCCTCGGCGTG NM_001278235 RefSeq
chr3 + 8501806 8551274 LMCD1 29995 "LIM and cysteine-rich domains 1, transcript variant 4"
GO:0031012|GO:0005737|GO:0003714|GO:0008270|GO:0005634|GO:0000122|GO:0070886|GO:0010611|GO:0005
615|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74969_PI430048170 0.0352248158419436 0.4831017660915593.47091680501107
2.85486323151065 3.38751557089765 P A P 4.73672284030333 3.86774774016025 4.1959749659875
P P P LNCV6_74969_PI430048170 mRNA
CTACCTGCATTTGGAAAAAGTTTTGAATGCACAAGAACTGCAAAGTGAAACAAAAGGAAA NM_005651RefSeq
chr4_GL383527v1_alt + 68315 85029 TDO2 6999 "tryptophan 2,3-dioxygenase"
GO:0034641|GO:0006569|GO:0004833|GO:0019825|GO:0019441|GO:0044281|GO:0019442|GO:0016597|GO:0046
872|GO:0055114|GO:0020037|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143942_PI430048170 0.67618033291014 1.0478942107609 8.85753495515161
9.25170647054689 9.11789673024684 P P P 9.15224486549294 8.92720610308659
8.96232247548705 P P P LNCV6_143942_PI430048170 mRNA
GGTTTTTCTGGCATAGGAGCCCACTTGCATTTTCATAGTTTTATTTGATAAAATTCCATC NM_033450RefSeq chr6 +
43431750 43450425 ABCC1089845 "ATP-binding cassette, sub-family C (CFTR/MRP), member 10, transcript

variant MRP7A" GO:0005886|GO:0008152|GO:0042626|GO:0016021|GO:0005765|GO:0055085|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138220_PI430048170 0.0051345770848981 7.91214110197281 3.41375184598829
2.86836285999259 3.58862443871645 P A P 0.355654920528431 0.303526002964086
0.352370845164314 A A A LNCV6_138220_PI430048170 mRNA
AAGCGAATTGCACTTTGATGTTCAGAAACCCACTTTGTTCTCAGCCACGCAAAACTCCCT NM_019060 RefSeq chr1
+ 152514501 152516005 CRCT1 54544 cysteine-rich C-terminal 1 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135956_PI430048170 0.0711797766813362 0.518249154551872 7.0558669882085
6.71788695208307 7.20074578812466 P P P 7.34868493173833 7.99738989391058
8.34509782344669 P P P LNCV6_135956_PI430048170 mRNA
CAGTGCCTCCTTTATTAAGGGGTTCTTTGAGAATAAAAGAGAAAAGACCTACTTTATTTG NM_006938 RefSeq chr18
+ 21612268 21630245 SNRPD1 6632 "small nuclear ribonucleoprotein D1 polypeptide 16kDa,
transcript variant 1"
GO:0005515|GO:0008380|GO:0000245|GO:0010467|GO:0003723|GO:0005634|GO:0034660|GO:0071013|GO:0000
387|GO:0034709|GO:0005829|GO:0000398|GO:0030532|GO:0034715|GO:0005654|GO:0005687|GO:0034719|GO:0
005685|GO:0005689. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135797_PI430048170 0.0691927469551424 1.17128819574961 8.87285250677274
8.7489037329505 8.91943945501016 P P P 8.48118590361638 8.63662866830044 8.73330004644 P
P P LNCV6_135797_PI430048170 mRNA
GCATCACTCTGCCAGAGTATGACTTTTTACAGATTATTAAATAAAGCTGCATATGTCTCA NM_032013 RefSeq chr20
- 36651765 36746138 NDRG3 57446 "NDRG family member 3, transcript variant 1"
GO:0003674|GO:0030308|GO:0005737|GO:0007283|GO:0030154|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130373_PI430048170 0.271439704024335 1.03534048577017 0.383404411111214
0.285605829184445 0.282489524985905 A A A 0.257460178048596 0.29261495618844
0.253081968401963 A A A LNCV6_130373_PI430048170 mRNA
GCATGGCATGAACAGTTTAGCTTAAGTACTGTTTAAATAATGAGTCAAGACTGCATTTTG NM_004770 RefSeq chr8
+ 72537390 72938349 KCNB2 9312 "potassium channel, voltage gated Shab related subfamily B,
member 2"
GO:0005251|GO:0005886|GO:0008076|GO:0007268|GO:0051260|GO:0034765|GO:0016021|GO:0006940|GO:0006
813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137229_PI430048170 0.638337471539488 1.0725793539603 6.39357033439072
6.35197392750347 5.93590254636237 P P P 6.34795795076407 6.12165355562461 5.919556041444
P P P LNCV6_137229_PI430048170 mRNA
ACCGGCGCGCTCTTCGCGCCCGCCCCTGCAGCACGGACAATAAACCTCCGCCAATGCAAA NM_000490 RefSeq chr20
- 3082555 3084724 AVP 551 arginine vasopressin
GO:0030307|GO:0006091|GO:0051970|GO:0005615|GO:0003084|GO:0006833|GO:0070371|GO:0005184|GO:0005
185|GO:0043027|GO:0031394|GO:0042538|GO:0043084|GO:0002125|GO:0035176|GO:0007623|GO:0035813|GO:0
007621|GO:0008284|GO:0045471|GO:0030819|GO:0007267|GO:0031894|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_112119_PI430048170 0.00408825888597222 0.34983519802518 0.434057218819116
0.445592878880913 0.881989662153561 A A A 2.4650177036159 1.97267182513569 1.8385363400205
A A A LNCV6_112119_PI430048170 mRNA
GTTACAAACATCAAGTTGGGAAGAAAAGCATTTATTGATGCCAATGGGATGAAAATTCTG NM_001286715 RefSeq
chr9 - 85546538 85742029 AGTPBP1 23287 "ATP/GTP binding protein 1, transcript variant 1"
GO:0001754|GO:0035610|GO:0005634|GO:0035609|GO:0005829|GO:0050905|GO:0005739|GO:0005737|GO:0015
631|GO:0021772|GO:0021702|GO:0006508|GO:0008270|GO:0007005|GO:0004181 . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_127112_PI430048170 0.0581732840563478 0.8649001450089651 2.0919344909775
12.0943362608545 12.1763162269355 P P P 12.389935610254 12.3880952497802
12.2067872283715 P P P LNCV6_127112_PI430048170 mRNA
TTCTGTTCGGCCCGACCTCCACCCCGGCTCCCAATAAAATTTAACTGATCTTTGTTTCTC NM_013292 RefSeq chr16
+ 30374801 30377989 MYLPF 29895 "myosin light chain, phosphorylatable, fast skeletal muscle"
GO:0006955|GO:0007519|GO:0005509|GO:0005859|GO:0008307|GO:0005765 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141119_PI430048170 0.929981959839951 1.00695042511622 0.495512512009381
0.366694853591725 1.76073539821715 A A A 1.52751462250735 0.313556109132184
0.941293147892929 A A A LNCV6_141119_PI430048170 mRNA
AATGTAGGTACCAGCCTTCTAGTTGACCATCAGAACACACAACGCCAAGATCTTACTCCA NM_181727 RefSeq chr3
+ 57060440 57075432 SPATA12 353324 spermatogenesis associated 12 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_145634_PI430048170 0.416150324690474 1.04749864323086 0.709618697568119
0.530988120434062 0.569642255925067 A A A 0.438627134798631 0.595437300733476
0.576500209111705 A A A LNCV6_145634_PI430048170 mRNA
AAATGAGGTTTCTTAAAGCTTATTTTTATAAAGCTTTTTCATAAAACTGGTTGTAGTTGC NM_003823 RefSeq chr20 +
63696650 63698698 TNFRSF6B 8771 "tumor necrosis factor receptor superfamily, member 6b, decoy"
GO:0005515|GO:0043066|GO:0006915|GO:0004872|GO:0005615 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135299_PI430048170 0.759818509159169 0.924336995593933 10.4163790114696
10.2249042623606 10.0061818485688 P P P 9.90404884533961 10.3021227129111
10.7013915192489 P P P LNCV6_135299_PI430048170 mRNA
TCCCCAACCCTTGGAGCTAAATGCGTTGTAAAATATTGCCAAAATGAAAAGTGTTTTGTA NM_139215 RefSeq
chr17_KI270857v1_alt + 43986 81774 TAF15 8148 "TAF15 RNA polymerase II, TATA box binding
protein (TBP)-associated factor, 68kDa, transcript variant 1"
GO:0005515|GO:0005737|GO:0000166|GO:0005730|GO:0008270|GO:0005654|GO:0005634|GO:0045893|GO:0003
677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142490_PI430048170 9.70630911107375e-05 3.25751641131174 8.71837418515733
8.87972914536456 8.67974861519019 P P P 6.96060298771804 7.20841938867808
6.99260675664497 P P P LNCV6_142490_PI430048170 mRNA
TTCCTGGCTCTAAGGCTCGTCTGTGTAACCCATAAAACCTGCTTTGATTCCAAAATGAGG NM_001271082 RefSeq
chr5_KI270792v1_alt + 27468 57319 NKD2 85409 "naked cuticle homolog 2 (Drosophila), transcript
variant 2"
GO:0005515|GO:0072661|GO:0005509|GO:0032436|GO:0031410|GO:0006887|GO:0016328|GO:0071944|GO:0016
323|GO:0010954|GO:0019838|GO:0048210|GO:0016023|GO:0016055|GO:0090090|GO:0031625|GO:0090004 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141408_PI430048170 0.00607092319612239 0.578503649245467 8.79532495430903
8.50100044450058 8.79299537988654 P P P 9.32409295444023 9.43382642654979
9.69418339502431 P P P LNCV6_141408_PI430048170 mRNA
GACAGGTTACTGTTTTGCCTTATTGCTTAACTTAATGTAGTGAAATAAAGCAGACAAAGC NM_001135644 RefSeq
chr5 - 150708746 150758520 DCTN4 51164 "dynactin 4 (p62), transcript variant 3"
GO:0019886|GO:0005813|GO:0005737|GO:0047485|GO:0007097|GO:0005634|GO:0005868|GO:0005869|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139840_PI430048170 0.448891005357841 1.29722174415594 2.15394759932833
3.15304396498428 3.1484589290758 A P P 2.72167917682204 2.31093288055406
2.47636647848274 P A P LNCV6_139840_PI430048170 mRNA
TCTACAAGGGAAATCATGATTTCCGTTCATAAACAGCATGCTCATCCCCCTAACACCATT NM_030810 RefSeq chr6
- 7881249 7910814 TXNDC5 81567 "thioredoxin domain containing 5 (endoplasmic reticulum),

transcript variant 1"
GO:0005515|GO:0034976|GO:0043066|GO:0005783|GO:0006892|GO:0003756|GO:0043277|GO:0006457|GO:0005
788|GO:0061024|GO:0045454|GO:0043202|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141586_PI430048170 0.00975670736290106 0.159000510076228 1.29778578818277
1.78968947152807 2.38289740164909 A A A 4.39937073259013 4.55865606638613
4.66343077616576 P P P LNCV6_141586_PI430048170 mRNA
GTAATTCCCGAATAGCAAAACATTAATATTCCATGATTAGCTCTACTGTGTTGTCTCACT NM_001177665 RefSeq
chr2 + 151410089 151477346 RIF1 55183 "replication timing regulatory factor 1, transcript variant 4"
GO:0007049|GO:0005737|GO:0000781|GO:0001939|GO:0005886|GO:0019827|GO:0005819|GO:0005634|GO:0001
940|GO:0006974 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128989_PI430048170 0.385802302877778 1.10035463735304 9.24124155762804
9.21333666887711 9.43298059252951 P P P 8.95128335484979 9.11134458065593
9.38703408748359 P P P LNCV6_128989_PI430048170 mRNA
GGGACATTTGTGTTTTTGGAGGAAAAGATACCCTGATTCTTTGAATCTTCCTTAAGTTTA NM_014941 RefSeq chr22
- 30926610 30968497 MORC2 22880 "MORC family CW-type zinc finger 2, transcript variant 3"
GO:0005737|GO:0006631|GO:0008270|GO:0005654|GO:0005634|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_99603_PI430048170 0.270623995855776 0.956986017745105 16.625927732223 16.7712456725755
16.6989250526366 P P P 16.7777793187243 16.7948016706969 16.7162895195057 P P P
LNCV6_99603_PI430048170 mRNA
GTCTGAAGAGTCAGATGATGACATGGGATTTGGCCTTTTTGATTAAATTCCTGCTCCCCT NM_001004 RefSeq chr11
+ 809935 812876 RPLP2 6181 "ribosomal protein, large, P2"
GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0006415|GO:0006412|GO:0006
413|GO:0005829|GO:0006414|GO:0000184|GO:0016020|GO:0016032|GO:0022625|GO:0044267|GO:0005925|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144227_PI430048170 0.00103693061744562 1.35887592576757 12.1900557256515
12.1666039433987 12.1588923934001 P P P 11.7044858388192 11.7779330034554
11.7048273779861 P P P LNCV6_144227_PI430048170 mRNA
GGTCAGCTTCTTTTACCTCAATTTTGTTTGCAATAAATGCTCTATAGCCAAAGCCAAAAA NM_020892 RefSeq
chr7_KI270809v1_alt + 1314 5014 DTX2 113878 "deltex 2, E3 ubiquitin ligase, transcript variant 1"
GO:0005515|GO:0031965|GO:0005737|GO:0016567|GO:0007219|GO:0016874|GO:0008270|GO:0005654 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67702_PI430048170 0.0231932443672228 2.37285399518779 1.56616325759798
2.03184973123611 1.3389642131062 A A A 0.351857114555587 0.435568680518599
0.494413220838514 A A A LNCV6_67702_PI430048170 mRNA
ACAAATAGGCTCTGCCATCAGGAAATGGGAAGCAAGAAAACGGTAACTCAAGAGGACAGA NM_172312 RefSeq
chr9 - 35807784 35812262 SPAG8 26206 "sperm associated antigen 8, transcript variant 2"
GO:0008017|GO:0008150|GO:0003674|GO:0016020|GO:0001669|GO:0045944|GO:0005634|GO:0032092 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140473_PI430048170 0.227844634749528 0.417269817464173 1.88098089001662
0.302338257506105 1.54068686534148 A A A 3.23571554784125 1.13310469242067
2.83619985723966 P A P LNCV6_140473_PI430048170 mRNA
AGGGACATCCTGTTTTTAAATGGGTTTGTTTGAGGGTATTATCTTCTGGTAATATAGATG NM_152281 RefSeq chr1
+ 170532121 170553833 GORAB 92344 "golgin, RAB6-interacting, transcript variant 1"
GO:0005515|GO:0005737|GO:0005794|GO:0005730|GO:0005654|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127468_PI430048170 0.00688296658538209 0.491984163506481 5.94142718724285
5.69921674708587 6.02627056834254 P P P 6.72061440275624 6.79535119198218
7.19430542869925 P P P LNCV6_127468_PI430048170 mRNA

GCCTCATCAATATTGCCGTCATCTGTTTAACACTCCCAGTATATTTTCTCAATGTCTGTT NM_152682 RefSeq chr4 - 183639634 183659219 RWDD4 201965 RWD domain containing 4 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131177_PI430048170 0.9230523863991241.10913088136585 0.242685158123517 0.2851217218155631.77594503714819 A A A 1.45790750276376 0.33918513182305 0.311409529072069 A A A LNCV6_131177_PI430048170 mRNA
GATGTCCTGAAAATGGTATTTCAATGAGGCATATGTTCAGGATTTCAGAAACAAGAAGTT NM_004334 RefSeq chr4 + 15702949 15732173 BST1 683 bone marrow stromal cell antigen 1
GO:0003953|GO:0016849|GO:0005886|GO:0030890|GO:0050135|GO:0006959|GO:0008152|GO:0007275|GO:0031225|GO:0016740|GO:0070062|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138824_PI430048170 0.5459876209897061.06220502624537 12.789060242431 12.9271977679732 13.0992610367667 P P P 12.6898537602056 12.8280009771824 13.032533461192 P P P LNCV6_138824_PI430048170 mRNA
CTGGATTTGGTGTACAAGCAGGCCTTTAATTTATATTGAACTGTAAATATGTCACTAGAG NM_021074 RefSeq chr18 + 9102629 9134345 NDUFV2 4729 "NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa"
GO:0051537|GO:0005743|GO:0009055|GO:0044281|GO:0046872|GO:0007399|GO:0005739|GO:0022904|GO:0048738|GO:0005747|GO:0006120|GO:0008137|GO:0044237|GO:0045272 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116638_PI430048170 0.4750635308087390.8054663546751770.509002742751697 0.6197721723009890.334729001550885 A A A 0.3952582540841941.3192350528626 0.515739528932777 A A A LNCV6_116638_PI430048170 mRNA
TCATCATGGGCCTGAAGCAGACGCTCAGCAACTGCGTCGAGTACCTGGTCCCGTGAGTGC NM_001012302 RefSeq chr11 - 417929 442011 ANO9 338440 anoctamin 9
GO:0005622|GO:0006821|GO:0034220|GO:0005886|GO:0017128|GO:0006869|GO:0005229|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142407_PI430048170 0.367682885202392 1.12479934354938 7.83402516251 7.73297497312883 7.4569066066239 P P P 7.6702138728347 7.5823175161296 7.25611258429952 P P P LNCV6_142407_PI430048170 mRNA
TGCGGCCTCGCGCATGCTCCGTCAGTAAAGGTGGAAGCCGCGCAGTGTGCGCTGAAAAAA NM_001024678 RefSeq chr8 - 144522376 144527032 LRRC24 NA leucine rich repeat containing 24 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142841_PI430048170 0.9946204810451221.00138849628885 7.3760818219058 7.72862348365442 7.66110587090111 P P P 7.48859373549049 7.52478877050628 7.75537878084556 P P P LNCV6_142841_PI430048170 mRNA
GGCTTTTAGTGTATCTTCTTTGTCCCAATTAAACAGTTGCTTGCTGTGATGTAATCTTAA NM_006859 RefSeq chr4 + 39459023 39477651 LIAS 11019 "lipoic acid synthetase, transcript variant 1"
GO:0005739|GO:0051539|GO:0006954|GO:0009249|GO:0032496|GO:0009107|GO:0001843|GO:0016992|GO:0006979|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2965_PI430048170 0.4746016183558380.88696780214279 7.3599632770905 6.89770589799955 7.32075332306383 P P P 7.21642705606969 7.19579722201784 7.67640094316301 P P P LNCV6_2965_PI430048170 mRNA
CGATTGTTCTCCATGGTTCCAACAAATTGCAAATAAAACTGTATGGAAACGATGAGCAAG NM_015909 RefSeq chr2 - 15166907 15561348 NBAS 51594 "neuroblastoma amplified sequence, transcript variant 1"
GO:0031965|GO:0005737|GO:0005794|GO:0016020|GO:0006890|GO:2000623|GO:0005730|GO:0000956 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129449_PI430048170 0.9080731925149450.9872255097056391.51579586759724 0.2463894795528340.543860924046135 A A A 0.8821421760791871.33745535140982 0.268701687608217 A A A LNCV6_129449_PI430048170 mRNA
ATAGATGAAGACATAAAAGACACTGGTAAACACCAAGGTAAAAGGGCCCCCAAGGTGGTC NM_001559 RefSeq

chr1 + 67307363 67396900 IL12RB23595 "interleukin 12 receptor, beta 2, transcript variant 1"
GO:0032729|GO:0008284|GO:0004896|GO:0019901|GO:0005887|GO:0019221|GO:0032496|GO:0018108|GO:0032
609|GO:0009897|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143911_PI430048170 0.0225271475295017 0.749116555774275 12.6332574642856
12.858981213559 12.9201007215573 P P P 13.3686871053729 13.1411965741849
13.1568472904284 P P P LNCV6_143911_PI430048170 mRNA
TAACTGGGCAACTCAAGATTCTGGCTTCTACTGAAGAACCATAAAGAAAAGATGAAAAAA NM_001568 RefSeq chr8
- 108201742 108248730 EIF3E 3646 "eukaryotic translation initiation factor 3, subunit E"
GO:0005515|GO:0010467|GO:0033290|GO:0016282|GO:0005852|GO:0001731|GO:0003743|GO:0005634|GO:0006
412|GO:0006413|GO:0005829|GO:0005737|GO:0047485|GO:0016020|GO:0000184|GO:0016605|GO:0006446|GO:0
045947|GO:0005654|GO:0044267|GO:0000785|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_127539_PI430048170 0.581446201995128 0.966364895868096 6.14583445181246
6.20248586464606 6.03962454877292 P P P 6.14849088618507 6.08411115586849
6.29957946835434 P P P LNCV6_127539_PI430048170 mRNA
CCTTAAGTTAAAGTGTTAGAGAAGACCTTCTTCCCATAAAAAGGTTGGTGGATCGTTTTC NM_024097 RefSeq chr1
+ 42767244 42775742 C1orf50 79078 "chromosome 1 open reading frame 50, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72969_PI430048170 0.0283827707053322 2.0220272270623 6.55708222570227
6.50853035915841 6.50976970058233 P P P 5.1782707841896 5.80629642867327
5.47553614108793 P P P LNCV6_72969_PI430048170 mRNA
AGATGATGGTGAGCTCAGGAGATAAGATGGAAGATGCAACAGCCAATGGTCAAGAAGACT NM_001040454
RefSeq chr3 - 48625722 48633846 SLC26A6 65010 "solute carrier family 26 (anion exchanger),
member 6, transcript variant 4"
GO:0005515|GO:0015562|GO:0019531|GO:0019532|GO:0015660|GO:0031526|GO:0005254|GO:0015797|GO:0015
659|GO:0070633|GO:0030165|GO:0038166|GO:0015499|GO:0071346|GO:0005887|GO:0008272|GO:0051454|GO:0
015701|GO:0008271|GO:0051453|GO:0048240|GO:2001150|GO:0006820|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133410_PI430048170 0.890196940069327 0.987355463994112 0.450761866349579
0.499914242108435 0.515649214304296 A A A 0.433806252216133 0.401400010137027
0.671627622279617 A A A LNCV6_133410_PI430048170 mRNA
TGGAATGTGCCTCTTATAAAAGTACATTTACAAATCTTCCCGTGACTGTGGCTTTGAGCA NM_001010879 RefSeq
chr19 + 57584259 57592390 ZIK1 284307 zinc finger protein interacting with K protein 1
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_92780_PI430048170 0.697070479292781 1.30694746928557 2.21473771689087 0.50964450016032
0.590923886431384 A A A 0.349030931459857 0.396951511457891 1.67948467858878 A A A
LNCV6_92780_PI430048170 mRNA
CTCTAGCCCAAAAAGCAAAAGAAGAGATGAGAAGAGGCACAAGAAACAATCTCGAAGCCG NM_194286 RefSeq
chr12 + 118981494 119163051 SRRM4 84530 serine/arginine repetitive matrix 4
GO:0008380|GO:0006397|GO:0000381|GO:0007605|GO:0043484|GO:0005634|GO:0003729|GO:0030154|GO:0007
399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145268_PI430048170 0.982918754192939 1.00675540253424 0.358736751820369
0.947974671676342 1.18990898371406 A A A 1.114218083157 1.01744769992265
0.341280086369232 A A A LNCV6_145268_PI430048170 mRNA
ATCAATGAGAACTTCAGGGACCCGTGTCCTACAGAGTCGGAAAGAGAAGCTAAAGTTCTA NM_001024661 RefSeq
chr1 - 13341891 13347134 PRAMEF14 NA PRAME family member 14 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_135322_PI430048170 0.535793235737792 0.959051648285412 0.311572865355436

0.2841264407653440.319697609688865A A A 0.2916521774485930.279844852300501
0.512949275412004A A A LNCV6_135322_PI430048170 mRNA
AAGGTCCTCTTGAAATGTTAATGGTTAATGTTCCCAAACCAGAGAATGCTTTGAAAATGT NM_013243RefSeq chr15
+ 51681352 51721026 SCG3 29106 "secretogranin III, transcript variant 1"
GO:0007596|GO:0002576|GO:0030168|GO:0005576|GO:0034774|GO:0030658 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126826_PI430048170 0.9065426499704410.9890507877512188.47156291009724
8.30577342550838 8.42713821543041 P P P 8.33002492431326 8.32804640662599
8.58383432805599 P P P LNCV6_126826_PI430048170 mRNA
AATAATGAAGAGCAAGCCTTTCAGGTAAGCAAATTAAAGTTCAGTTTGCTCATCGACAAA NM_003846RefSeq chr1
- 145911347 145918924 PEX11B 8799 "peroxisomal biogenesis factor 11 beta, transcript variant 1"
GO:0005515|GO:0042803|GO:0044375|GO:0005739|GO:0007165|GO:0043234|GO:0016020|GO:0007031|GO:0051
260|GO:0005779|GO:0005778|GO:0070062|GO:0005777|GO:0016559 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140806_PI430048170 0.0163681912391479 0.5103999295749244.7470089514135
4.97758285765153 4.88351247976529 P P P 5.52443473159177 6.07955070361729
5.87079857261954 P P P LNCV6_140806_PI430048170 mRNA
TCTCATCTAAATATTTCCATATTCTGTATTAGGAGAAAATTACCCTCCCAGCACCAGCCC NM_004415RefSeq chr6
+ 7541636 7586713 DSP1832 "desmoplakin, transcript variant 1"
GO:0005882|GO:0005515|GO:0030057|GO:0045109|GO:0005886|GO:0005634|GO:0086091|GO:0001533|GO:0006
921|GO:0005916|GO:0005739|GO:0016323|GO:0086069|GO:0016337|GO:0003223|GO:0014704|GO:0097110|GO:0
005080|GO:0030674|GO:0050839|GO:0086005|GO:0070062|GO:0006915|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_53409_PI430048170 0.2045288177340321.08416087024491 4.92255070722734 4.80896889275486
5.01783685772714 P P P 4.73331411453341 4.78508692821124 4.88465701460036 P P P
LNCV6_53409_PI430048170 mRNA
AATGGTGAGCTGCAGGTGTGTCATTTAGTGTGATTTTCCTGTTGACTGACTCATAGGAGC NM_001201483 RefSeq
chr1 - 8860999 8871576 ENO1 2023 "enolase 1, (alpha), transcript variant 2"
GO:0005515|GO:0030308|GO:0003700|GO:0005886|GO:0006094|GO:0005634|GO:0044281|GO:0005615|GO:0004
634|GO:0006096|GO:0005829|GO:0005737|GO:0006006|GO:0070062|GO:0000287|GO:0005975|GO:0003714|GO:0
000122|GO:0009615|GO:0003677|GO:0031430|GO:0006351|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144104_PI430048170 0.8897182318658631.01898798264137 3.39304563965612
2.66840293725733 2.74143753894203 P A A 3.46494752256081 2.40954626359945
2.75614227913324 P A P LNCV6_144104_PI430048170 mRNA
TGCCTTAGGTTCTCCAGAGTGATGTGGAATTTTAAAGTGTCTCTCTCTGATTGCCTCCAA NM_018368RefSeq chr6
- 69675748 69797157 LMBRD1 55788 LMBR1 domain containing 1
GO:0051898|GO:0009235|GO:0005886|GO:0031419|GO:0046627|GO:0005158|GO:0006767|GO:0038016|GO:0044
281|GO:0005765|GO:0045334|GO:0016020|GO:0006766|GO:0046325|GO:0016032|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134656_PI430048170 0.00186761073692469 0.4170071266387827.52235881661164
7.84561351108504 7.80972151162725 P P P 9.08426760793584 8.97911856921158
8.91609412428822 P P P LNCV6_134656_PI430048170 mRNA
CAAAATCCTTCAAAGGCTTTCCACTTTCTTTAGTGGCATTCAGACCCCCTCTAGTTTGAC NM_005610RefSeq chr1
+ 32651147 32686211 RBBP4 5928 "retinoblastoma binding protein 4, transcript variant 1"
GO:0005515|GO:0010467|GO:0000790|GO:0008285|GO:0033186|GO:0042826|GO:0006325|GO:0005634|GO:0042
393|GO:0016581|GO:0031497|GO:0016580|GO:0000086|GO:0051726|GO:0006338|GO:0016589|GO:0008094|GO:0
006355|GO:0043044|GO:0006334|GO:0031492|GO:0006335|GO:0006336|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_129601_PI430048170 0.0530038828329244 1.02940595772027 0.422084058059144
0.450083335502435 0.430577886451142 A A A 0.377000441338751 0.383971313205542
0.416176958599635 A A A LNCV6_129601_PI430048170 mRNA
GTCATGGCCTTCTGGATATAGGATCCAGAAAATTGTACTTCATAAAAATTGGCAATAAAC NM_001014342 RefSeq
chr1 - 152348736 152360006 FLG2 NA filaggrin family member 2 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_53470_PI430048170 0.763354393431621 1.00733086945518 15.9877954489902 16.0433524516053
15.9565702536551 P P P 15.9540193182131 15.981602844932 16.0210384083512 P P P
LNCV6_53470_PI430048170 mRNA
GGCAAATGTTTGTGTGGCCTCCTTAAACTAGCTGTTATGATTTTATTCTTTGTGAGTTAANM_016139RefSeq chr7 -
56101572 56106494 CHCHD2 51142 coiled-coil-helix-coiled-coil-helix domain containing 2
GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132921_PI430048170 0.00806990553481614 0.620998740312972 5.59066898119016
5.30831287631401 5.6064182422388 P P P 6.03700766134969 6.1476669204845
6.38025913859012 P P P LNCV6_132921_PI430048170 mRNA
GTCCCTGCAATGTTTTCATATCTAGTAGTCATTTTAGGGAAAGTGATAATCTGTAGAATG NM_020782RefSeq chr12
+ 27780253 27803040 KLHL42 57542 kelch-like family member 42
GO:0005515|GO:0000209|GO:0007067|GO:0005737|GO:0004842|GO:0031463|GO:0005819|GO:0032886|GO:0043
161|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131673_PI430048170 0.526640411661152 0.890285721608349 0.504652254215322
0.459553849075436 0.396886134931231 A A A 0.3722151511745 0.969249236441151
0.448864222726937 A A A LNCV6_131673_PI430048170 mRNA
TGTGTTTGAACTGGAGGCTCTGACAGCCACTGTCCTATTCATTCTCTTTCCTTTCTTGCT NM_207186RefSeq chr11 +
6876624 6877619 OR10A4283297 "olfactory receptor, family 10, subfamily A, member 4"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0007411|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144097_PI430048170 0.00483233237264194 0.649164001238648 7.18182593713075
6.94380732742439 6.94600190216452 P P P 7.58552018490774 7.74364791897113
7.62088364245257 P P P LNCV6_144097_PI430048170 mRNA
TTCTAATAAATCATTCTTCTATCACATGGCAGCACGCTGGAGCCTGTCACCTTGAAAAAA NM_001112726 RefSeq
chr14 + 104865312 104896770 CEP170B 283638 "centrosomal protein 170B, transcript variant 1"
GO:0005737|GO:0005874 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139676_PI430048170 0.0772055782595742 0.791144350021723 7.07020969545112
7.15887371637375 7.3881372896131 P P P 7.52184106511432 7.37071617324934
7.73428645793647 P P P LNCV6_139676_PI430048170 mRNA
CTTCAGGAGGGAAATGAACCACTTAATATACCCATACTACCTTGAACAATGAAATTGAAT NM_006768RefSeq chr12
- 111642145 111685996 BRAP 8315 BRCA1 associated protein
GO:0005515|GO:0004842|GO:0031965|GO:0016567|GO:0016874|GO:0000151|GO:0007265|GO:0005737|GO:0000
166|GO:0000165|GO:0008139|GO:0008270|GO:0009968 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126757_PI430048170 0.0580645505650767 0.468805633843781 9.20584097196624
8.9998976176176 9.25343442831369 P P P 9.66914127323007 10.2752599836627
10.6439966954183 P P P LNCV6_126757_PI430048170 mRNA
CATCATCCTTCTCTTTTGTTTCCATAGCCTTTTATAATGCATATATGATGCTGTGAACAG NM_005737RefSeq chr2 -
234493040 234497049 ARL4C 10123 "ADP-ribosylation factor-like 4C, transcript variant 2"
GO:0005515|GO:0005737|GO:0005886|GO:0043014|GO:0007264|GO:0032456|GO:0008152|GO:0003924|GO:0005
634|GO:0030175|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134904_PI430048170 0.114287308262174 1.61604809607806 13.9840274979025
13.9767884456502 14.1469440967067 P P P 13.8484966143257 12.9238794719118
13.0879379153406 P P P LNCV6_134904_PI430048170 mRNA

TGGCTAGTGTGGAAGCATAGTGAACACACTGATTAGGTTATGGTTTAATGTTACAACAAC NM_006408RefSeq chr7 - 16792639 16805114 AGR2 10551 anterior gradient 2
GO:0070254|GO:0005739|GO:0005515|GO:0002162|GO:0005783|GO:0005576|GO:0060480 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132106_PI430048170 0.9845396704677 1.00084959184146 8.45429367227403 8.09372055355072 8.31593901603239 P P P 8.20465338367332 8.4345187009656 8.23273093938314 P P P LNCV6_132106_PI430048170 mRNA
TTTTACATGAGGAAGAAAAACGGAGGCGAAAGGAACAGAGTGACCTGACCACCCTAACAT NM_004489RefSeq chr17 - 7312658 7315339 GPS2 2874 G protein pathway suppressor 2
GO:0005515|GO:0000188|GO:0007049|GO:0046329|GO:0017053|GO:0003714|GO:0007254|GO:0006325|GO:0005654|GO:0000122|GO:0005095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142124_PI430048170 0.628806182112555 1.01701096540414 0.51684874350766 0.46162058029584 0.390487199833623 A A A 0.3785382573778630.460859092851752 0.457828724978686 A A A LNCV6_142124_PI430048170 mRNA
GAATTGCGCAACACCTTTAGGGAGATTCTCTGTGGCTGCAACGGCATGAACTTGGGATAG NM_019888RefSeq chr20 + 56248731 56249815 MC3R 4159 melanocortin 3 receptor
GO:0005515|GO:0005886|GO:0030819|GO:0007200|GO:0055078|GO:0032922|GO:0004977|GO:0042923|GO:0002027|GO:0005887|GO:0007187|GO:0004980|GO:0008217|GO:0007188|GO:0017046|GO:0042309 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62022_PI430048170 0.2219449812348990.648903610283832 1.42584186005949 1.7058685991132 0.362549934946647 A A A 2.19539873224026 1.87440321147822 1.53724271579681 A A A LNCV6_62022_PI430048170 mRNA
AGAAGATGTGGCAGTTGGAGCTGAACACACACTTGCTTTGGCATCAAATGGAGATGTGTA NM_003922RefSeq chr15 - 63608617 63833948 HERC1 8925 HECT and RLD domain containing E3 ubiquitin protein ligase family member 1
GO:0004842|GO:0005794|GO:0016567|GO:0016874|GO:0031175|GO:0005829|GO:0043547|GO:0005086|GO:0005737|GO:0016020|GO:0021702|GO:0050885|GO:0006810|GO:0010507 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56117_PI430048170 0.00730439478010982 0.5170366156994257.71598177499797 7.45022163339098 7.68996955971192 P P P 8.33906402467272 8.53670873950424 8.81081715047736 P P P LNCV6_56117_PI430048170 mRNA
TTGAGCTGCATTTAAGTAGACTTTGGACCGTTAAGCTGGGCAAAGGAAATGACAAGGGGA NM_100264RefSeq chr10 + 28532587 28623112 WAC 51322 "WW domain containing adaptor with coiled-coil, transcript variant 2"
GO:0005515|GO:0000993|GO:0005634|GO:0032435|GO:0006351|GO:0006974|GO:0016607|GO:0003682|GO:0071894|GO:0005654|GO:0005681|GO:0045893|GO:0010390|GO:0016239 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132988_PI430048170 0.5122034346795650.863679224706503 0.574310972364087 0.3573423458554280.529942602435555 A A A 1.10492323653551 0.514303916765595 0.37832665049357 A A A LNCV6_132988_PI430048170 mRNA
CATGACTATATTGTGATATTCTTTTCAAAATAAAGTTTATTTGGGAGATAACTGAAAAAA NM_017946RefSeq chr7 - 30010582 30026801 FKBP14 55033 "FK506 binding protein 14, 22 kDa, transcript variant 1"
GO:0000413|GO:0061077|GO:0005509|GO:0005789|GO:0003755|GO:0005788|GO:0005528|GO:0006987|GO:0044267|GO:0030968 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134829_PI430048170 0.0357135209867357 0.5290644281773842.82276484697686 3.50102447263768 2.99017250797585 A P P 3.99555672719839 3.66810229011965 4.40110285175269 P P P LNCV6_134829_PI430048170 mRNA
GGGGGTTGGTACAGAAACTTGAAGCTGTTTGTGATATGTACAACTCAGATGTTTCTCATT NM_182914RefSeq chr14 + 63852964 64226451 SYNE2 23224 "spectrin repeat containing, nuclear envelope 2, transcript variant

5"
GO:0005515|GO:0030018|GO:0034504|GO:0007097|GO:0031527|GO:0034993|GO:0005634|GO:0090286|GO:0005
635|GO:0005739|GO:0005640|GO:0010761|GO:0051642|GO:0005737|GO:0051015|GO:0031022|GO:0006998|GO:0
045111|GO:0070062|GO:0031965|GO:0030335|GO:0016235|GO:0031258|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134338_PI430048170 0.4652880192642640.90568646190268 0.268285574911983
0.2843292045280420.451731069839085A A A 0.3469404796633420.300662034987013
0.749311714347372A A A LNCV6_134338_PI430048170 mRNA
GGGAGCAGTGAATCAAGGCAGACTTATGAAATCTGTATTATATTTGTAACAGAATATAGG NM_000885RefSeq chr2
+ 181456891 181537741 ITGA4 3676 "integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4
receptor)"
GO:0005515|GO:0060710|GO:0005886|GO:0050900|GO:0035987|GO:0050901|GO:0046872|GO:0007507|GO:0034
669|GO:0005911|GO:0030198|GO:0030183|GO:0007159|GO:0034446|GO:0034113|GO:0001968|GO:0050839|GO:0
007157|GO:0070062|GO:0003366|GO:0090074|GO:0009986|GO:0072678|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130495_PI430048170 0.0105506212286769 1.2752612195973 13.6971022294222
13.6826409601292 13.5457207883392 P P P 13.2875650007235 13.2631404105165
13.3264561956472 P P P LNCV6_130495_PI430048170 mRNA
GAGGGCCGCTGACCCTGCCGGAGATAAAGGATACAGAGAGCCCCTCCCCACGTGAAAAAA NM_174894RefSeq
chr19 + 7680820 7682862 TRAPPC5 126003 "trafficking protein particle complex 5, transcript
variant 1" GO:0005794|GO:0030008|GO:0005783|GO:0016192 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139998_PI430048170 0.0841358333960865 1.1218695472269 0.571938226732099
0.7192605574266540.722298720436615A A A 0.6106435310643570.445926887230886
0.45837377916084 A A A LNCV6_139998_PI430048170 mRNA
GAATCAAATAGCCTTCCAGAGGCTAAGAAATTTCTGTTAGTAAAAGATGTTCTTTTTCCC NM_001017436 RefSeq
chrX - 135760158 135768191 CT45A4 NA - NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141933_PI430048170 0.00360531472248071 2.4679711737205 1.65786527058592
2.10689723881641 1.90434940796373 A A A 0.398174492400301 0.898598823954002
0.442219866403437 A A A LNCV6_141933_PI430048170 mRNA
GTGGCTGCCACCAGCGAATGAAACTTTTGTATGATACATAAAGTGCTTGAGTCTATTTTT NM_145008 RefSeq
chr11 - 57645086 57649944 YPEL4 219539 yippee-like 4 (Drosophila) GO:0005730 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134440_PI430048170 0.124622660095152 0.770988702467721 4.69293346976447
4.22685207946635 4.63523219515795 P P P 4.66635335717959 4.91799314509717
5.10610553252329 P P P LNCV6_134440_PI430048170 mRNA
CACCTAAATCAGAAGACGTTCTAAAGTCAGTAAGAAAGTGTGAAATGCTAGTATAAAGGT NM_001272069 RefSeq
chr3 + 111978875 111993368 ABHD10 55347 "abhydrolase domain containing 10, transcript variant
2" GO:0005739|GO:0019391|GO:0004553|GO:0005829 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145648_PI430048170 0.0324713036734726 0.719571538717561 11.2401055909928
11.4159821974284 11.2685227993263 P P P 11.9951252607984 11.6735877812084
11.6610743897043 P P P LNCV6_145648_PI430048170 mRNA
GGGAACTCAGGAAAATTCACAGGACTTGGGAGATTCTAAATCTTAAGTGCAATTATTTTT NM_000152 RefSeq
chr17 + 80101555 80119880 GAA 2548 "glucosidase, alpha; acid, transcript variant 1"
GO:0000023|GO:0005765|GO:0060048|GO:0005764|GO:0046716|GO:0003007|GO:0032450|GO:0002086|GO:0016
020|GO:0002026|GO:0050884|GO:0050885|GO:0009888|GO:0030246|GO:0006006|GO:0007626|GO:0005985|GO:0
043181|GO:0007040|GO:0005980|GO:0070062|GO:0004558 . NA - . NA NA NA NA NA
NA NA NA NA

LNCV6_144953_PI430048170 0.00682761082746918 0.376528672838679 7.81094645112888 7.09185283913345 7.46823126146072 P P P 8.5924491883877 9.02017723098188 9.03277529533599 P P P LNCV6_144953_PI430048170 mRNA TGATTTAGACCTTTTGAGAATAGGACACTTGGCAGGAGGGAAAAGGAAGAGGACAAAGGA NM_015106 RefSeq chr3 + 51541579 51663596 RAD54L2 23132 RAD54-like 2 (S. cerevisiae) GO:0003712|GO:0019901|GO:0008152|GO:0004386|GO:0005634|GO:0005524|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79020_PI430048170 0.0417700415178549 0.797162898208171 4.85515319653288 4.97991246147058 5.13165107685114 P P P 5.45026686814073 5.18491533458766 5.31380937006208 P P P LNCV6_79020_PI430048170 mRNA GAACAGTAAAAATGAGTTGGAGCCATGCATTTTATGACAGTCAAACATGGGAAAACATTC NM_015723 RefSeq chr7 - 108470421 108526318 PNPLA8 50640 "patatin-like phospholipase domain containing 8, transcript variant 1" GO:0019369|GO:0008219|GO:0048471|GO:0044281|GO:0005524|GO:0043651|GO:0005622|GO:0000139|GO:0001516|GO:0016020|GO:0047499|GO:0004622|GO:0005789|GO:0006631|GO:0034638|GO:0016021|GO:0006644|GO:0046338|GO:0036151|GO:0005778|GO:0050482|GO:0046474|GO:0036152|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129845_PI430048170 0.694641482297109 1.05823564579684 6.71101721016401 6.61645709648411 6.3431098062938 P P P 6.76793699388157 6.54470749302654 6.046472106726 P P P LNCV6_129845_PI430048170 mRNA TTCGTCTTGTAAATAAGCCCTTTTATGTGGTTCCTGCCCCTGAGAATAAAGAAGCCCCAG NM_001207020 RefSeq chr22 - 41909553 41914667 SHISA8 440829 shisa family member 8 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93005_PI430048170 0.29628707028366 1.3884742930242 4.13495018181741 3.69594557404332 3.22144985329698 P P P 3.82231495228248 2.81610247640715 2.90999565044256 P P P LNCV6_93005_PI430048170 mRNA TCCCAGCTGGAGCCCCTTCTGACCTTGGAGAACATTGAGCAGCTGGAGGCAACATTTGTG NM_178516 RefSeq chr16 - 67184378 67190204 EXOC3L1 283849 exocyst complex component 3-like 1 GO:0030133|GO:0003674|GO:0000145|GO:0051601|GO:0000149|GO:0030141|GO:0030072|GO:0006887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104800_PI430048170 0.237488553202857 0.829177329583084 11.2395846073936 11.2758426256218 11.5176019755013 P P P 11.424087099417 11.4732761913717 11.9111352861386 P P P LNCV6_104800_PI430048170 mRNA GTCCAATGTGAACATTTATTCATATTGTTTTGATTACCCTCGTGTTACTACAAGATGGCA NM_001304464 RefSeq chr1 + 203861584 203871152 SNRPE 6635 "small nuclear ribonucleoprotein polypeptide E, transcript variant 2" GO:0005515|GO:0008380|GO:0006369|GO:0010467|GO:0006366|GO:0003723|GO:0031124|GO:0005634|GO:0071013|GO:0071011|GO:0005829|GO:0005683|GO:0030532|GO:0005681|GO:0005682|GO:0046540|GO:0005687|GO:0005685|GO:0070062|GO:0005686|GO:0000245|GO:0042633|GO:0008334|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140964_PI430048170 0.725954796851837 1.08972175044563 10.231411247063 10.50653470462 11.0068935999369 P P P 10.6039959341601 10.0928270720615 10.7125808783904 P P P LNCV6_140964_PI430048170 mRNA CAGTTCATCACACTTCTTCATGATGTTGCCCCTAAATTTTGCACACTATATTCTTGTATA NM_012257 RefSeq chr7 + 107169014 107202529 HBP1 26959 "HMG-box transcription factor 1, transcript variant 2" GO:0005515|GO:0006355|GO:0003723|GO:0043268|GO:0007050|GO:0005654|GO:0016055|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138688_PI430048170 2.89030953574832e-06 0.178401143412689 0.295342790503997 0.270615411790557 0.418769248902366 A A A 2.76016998098872 2.79973468075631

2.8867193459889 P P P LNCV6_138688_PI430048170 mRNA
CAAATAGAAATCATTTCTGAAGACAAAAGCAGAGGAATATTGTCAGTGCCAAGTAATGGA NM_001244766 RefSeq
chr4 + 70902339 70988174 MOB1B 92597 "MOB kinase activator 1B, transcript variant 1"
GO:0005515|GO:0019209|GO:0005737|GO:0046777|GO:0005634|GO:0035329|GO:0019900|GO:0046872|GO:0070062|GO:0042327|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93915_PI430048170 0.0567598073211005 1.38393223795058 10.3432814106749
10.7243633513725 10.3356179445891 P P P 9.92128965780522 10.0286171270499
10.0778071980923 P P P LNCV6_93915_PI430048170 mRNA
TTTATTTGTAGGGTTTGCTTTTAAGGATCGGCTCCCTGTCGCGCCCGAGGAGGGCCTGGA NM_020533 RefSeq chr19
+ 7522609 7534009 MCOLN1 57192 mucolipin 1
GO:0051209|GO:0005261|GO:0005886|GO:0005765|GO:0055085|GO:0006879|GO:0043235|GO:0033572|GO:0005737|GO:0034220|GO:0072345|GO:0005887|GO:0031902|GO:0070588|GO:0016021|GO:0006812|GO:0010008 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138682_PI430048170 0.275917500995914 1.66459348472996 1.50401624065033
0.274133932978503 1.65361183606782 A A A 0.290697149286694 0.259715638993495
0.925976765535191 A A A LNCV6_138682_PI430048170 mRNA
GACTTATGGAACATTACAATATATTCTCGGTCCAAGTGAGTAAGTTCTTTGCTTTATGTG NM_052858 RefSeq chr16
+ 71626152 71636205 MARVELD3 91862 "MARVEL domain containing 3, transcript variant 2"
GO:0005515|GO:0046329|GO:0070830|GO:0050680|GO:0031435|GO:0006970|GO:0031410|GO:0016021|GO:0005923|GO:0045216|GO:0010633 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116883_PI430048170 0.241741674131928 0.690191629641044 2.62130476408488
1.76781353539029 3.07185886864024 A A P 3.04914912107286 2.93277739470355
3.33897661715717 P P P LNCV6_116883_PI430048170 mRNA
TTCCTTCCCATCTTAATAATAAGTCCTGCAGAGTGACATCTCTGTGTTACAGTGAAGATG NM_001198956 RefSeq
chr1 + 167936558 168075843 DCAF6 55827 "DDB1 and CUL4 associated factor 6, transcript variant 3"
GO:0005737|GO:0030374|GO:0016567|GO:0045944|GO:0005654|GO:0005634|GO:0080008|GO:0005925 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131756_PI430048170 0.170017811484372 0.885961349264242 10.4775786771671
10.5960409433611 10.4892621019635 P P P 10.5315213366666 10.8186696472029
10.7250327434718 P P P LNCV6_131756_PI430048170 mRNA
CTCTGTGCTGCCTGTACTGTATTGACCTGTTTTATAGGTGCCTTTTTATTAAAAAGAAAA NM_182557 RefSeq chr11
- 118896140 118910904 BCL9L 283149 B-cell CLL/lymphoma 9-like
GO:0008013|GO:0003713|GO:0005730|GO:0010718|GO:0005634|GO:0035914|GO:0006351|GO:0045944|GO:0022604|GO:0005654|GO:0035019|GO:0060070|GO:0030512 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83667_PI430048170 0.383940691487866 0.850477482640905 4.37034948892873 3.71775171995898
4.51864067258663 P P P 4.40034596733099 4.53941805924493 4.48343552193793 P P P
LNCV6_83667_PI430048170 mRNA
TATGTGTAAAATAGGGAAGAAAGTTAGTATTGGATCAGTGTGAGTCCTGAAGCACTTTCA NM_023011 RefSeq chr13
+ 114281583 114305816 UPF3A 65110 "UPF3 regulator of nonsense transcripts homolog A (yeast), transcript variant 1"
GO:0005515|GO:0010467|GO:0005886|GO:0003723|GO:0045727|GO:0005634|GO:0043231|GO:0005829|GO:0006913|GO:0005737|GO:0000166|GO:0000184|GO:0005487|GO:0005654|GO:0051028|GO:0035145 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136008_PI430048170 0.00311362168378529 0.410331864703544 6.44774001965106
6.31652411042313 6.59094904423234 P P P 7.51757740437171 7.68158759192274
7.98502569658085 P P P LNCV6_136008_PI430048170 mRNA
AGTGCTTAAAAACGCCTTCTTGCATGAGGGGATTGAACTATACAATGTTTGTTAACTTTG NM_016485 RefSeq chr6
+ 142147161 142220948 VTA1 51534 "vesicle (multivesicular body) trafficking 1, transcript variant 1"
GO:0005515|GO:0016197|GO:0019058|GO:0061024|GO:0016032|GO:0015031|GO:0010008|GO:0070062|GO:0005

829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113651_PI430048170 0.4593263029198731.09210320361163 4.80260321501024
4.80713901689496 4.71883787893211 P P P 4.50269296988879 4.44536110631839
4.94699818304261 P P P LNCV6_113651_PI430048170 mRNA
TCCTCAGGGACAGAATTCAACGCCGTCAAATCTCTCATATTGGGAAAGGTTTTAGAGGCT NM_033655 RefSeq chr9
- 39072766 39288303 CNTNAP3 79937 contactin associated protein-like 3
GO:0008037|GO:0005886|GO:0005576|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135432_PI430048170 0.0585139446692205 0.7370553168197055.88597065249581
6.28875222246779 6.09739055533966 P P P 6.51476756664629 6.53626734527244
6.56905114487436 P P P LNCV6_135432_PI430048170 mRNA
CCATGTTTGATTCCTAACCTTTTGCTACCTGAATAAAGCAGAGTCTATTTCAACACAAAA NM_001099220 RefSeq
chr7 + 149838419 149867479 ZNF862 643641 zinc finger protein 862
GO:0008150|GO:0003674|GO:0006355|GO:0046983|GO:0005634|GO:0005575|GO:0003676|GO:0046872|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143969_PI430048170 0.1671690437928481.23678825508849 10.9526227161607
10.9782182765053 11.0150195928841 P P P 10.3646661723292 10.742594493893
10.8725996016854 P P P LNCV6_143969_PI430048170 mRNA
ACCAGCGTGTGACTTTCCTAGATAACACTGCTTTCTCATAATAAAGACTATTTGCATTTG NM_019013 RefSeq chr17
+ 6444414 6451065 FAM64A 54478 "family with sequence similarity 64, member A, transcript
variant 1" GO:0005515|GO:0007067|GO:0005737|GO:0005730|GO:0005634|GO:0051301 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_135854_PI430048170 0.6909430779637660.8174145678374162.73585790059052
1.69765329344927 2.2735895890968 A A A 1.69540355292473 3.190429336345 2.5022308708497
A P P LNCV6_135854_PI430048170 mRNA
TTAACTATTGTGTGGGCAAAGAACATTTAAAGGGCATAGTAGAGGTAAGGAGAGACACAT NM_173084 RefSeq chr3
- 160435502 160449838 TRIM59 286827 tripartite motif containing 59
GO:0005622|GO:0008270|GO:0016021|GO:0043124 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130196_PI430048170 0.9235470212048460.9971848952235380.270314849488899
0.2749108844975030.427959026779175 A A A 0.3555382208513010.300560363008218
0.334399217216576 A A A LNCV6_130196_PI430048170 mRNA
CTGTAGAGTAGACACAGTGAGTATGTGGACCTCTTTTATAAGGAAAAATACATTTTGGAT NM_001099660 RefSeq
chr7 + 111091005 111125453 LRRN3 54674 "leucine rich repeat neuronal 3, transcript variant 1"
GO:0030131|GO:0005886|GO:0001934|GO:0016021|GO:0032403 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130201_PI430048170 0.0703826852509323 1.12711369806161 10.0323336171433
10.0006478931987 9.94345671437426 P P P 9.70954102443612 9.8943362036825 9.8496854283246
P P P LNCV6_130201_PI430048170 mRNA
TTGTATGTTCTTTTGGCCTTTTGTTCCTACCTAAATGAAGAAACCATGCCTGGAGGGGCC NM_031488 RefSeq chr22
+ 41205308 41231271 L3MBTL2 83746 l(3)mbt-like 2 (Drosophila)
GO:0005515|GO:0042393|GO:0006355|GO:0008270|GO:0005634|GO:0035064|GO:0006351|GO:0016568 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127315_PI430048170 0.5232171628170760.9027594979660357.84263382556645
7.78221524027572 7.58860845931298 P P P 7.5639783384672 8.13416479734643
7.91381731120808 P P P LNCV6_127315_PI430048170 mRNA
TGGTTCCACTGGTCTCAAAAGTCACCTGCCTACAAATGTACAAAAGGCGAAGGTTCTGAT NM_001282166 RefSeq
chrX + 48695553 48709015 SUV39H1 6839 "suppressor of variegation 3-9 homolog 1 (Drosophila),
transcript variant 1"
GO:0005515|GO:0000792|GO:0010467|GO:0006364|GO:0006325|GO:0005634|GO:0030154|GO:0042054|GO:0036

123|GO:0000183|GO:0036124|GO:0016032|GO:0000976|GO:0000794|GO:0071456|GO:0033553|GO:0008757|GO:0
000122|GO:0006351|GO:0006974|GO:0018024|GO:0007049|GO:0047485|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129869_PI430048170 0.1374971989481660.2980987673193350.381386471210164
0.4043231307952070.303827907098398A A A 0.64649264166886 2.71798708878461
2.26466448138999 A P A LNCV6_129869_PI430048170 mRNA
CCTTTAAATGGCTGTCACACTTGATTGTAGGTAAGATAATATACTGGAGAAAACTACTAG NM_001001411 RefSeq
chr19_GL383576v1_alt + 111922 129773 ZNF676 163223 zinc finger protein 676
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131445_PI430048170 0.1691282703195081.21291765190623 4.15878927973616
3.96947593448356 4.04548112292351 P P P 3.86707046582941 3.95020865588978
3.48623350179958 P P P LNCV6_131445_PI430048170 mRNA
GCAGAACTTGTTTTCCGTTCCCCTGCCAGTTTTATATTTTTGGTTTTACAAGAAAAAACA NM_147193RefSeq chr1
- 53506232 53734204 GLIS1 148979 GLIS family zinc finger 1
GO:0000977|GO:0006366|GO:0045944|GO:0005634|GO:0000122|GO:0001228|GO:0001227|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142582_PI430048170 0.61953664079355 0.9685945617522481 4.314383446159
14.2169696202195 14.0219445083675 P P P 14.1901537750788 14.2627727850364
14.2526018696907 P P P LNCV6_142582_PI430048170 mRNA
ATGGAGTTACTGAAGGTCTCCAAGGACAAACGGGCCCTCAAATTTATCAAGAAAAGGGTG NM_015414RefSeq chr19
+ 5690334 5691667 RPL36 25873 "ribosomal protein L36, transcript variant 2"
GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0005730|GO:0006415|GO:0006412|GO:0006
413|GO:0005829|GO:0006414|GO:0005737|GO:0000184|GO:0016020|GO:0016032|GO:0022625|GO:0044267 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116546_PI430048170 0.000781719094885881 1.5699453280886 13.5048731621478
13.6409895564352 13.5718197844502 P P P 12.8184672073067 12.9612050944083
12.9835808567941 P P P LNCV6_116546_PI430048170 mRNA
TTAGTTGGTTTTAGTTGCTCTGGGGGGAGGAGAGAAGGTAGAGCTGTTCTTAAATTTATT NM_006442RefSeq chr11
+ 65919256 65921577 DRAP1 10589 DR1-associated protein 1 (negative cofactor 2 alpha)
GO:0043565|GO:0005515|GO:0003700|GO:0046982|GO:0003714|GO:0005634|GO:0000122|GO:0003677|GO:0006
351|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143724_PI430048170 0.0945027805343074 0.9314205873426650.279617786385106
0.2835282509723590.30465923655532 A A A 0.4572638497997110.377244454656238
0.33834977020255 A A A LNCV6_143724_PI430048170 mRNA
CGTAACTACTGCTTCTACTACCCAAAAATAAGAATTTCAACACTACTTCCAAGAGACTTT NM_012390RefSeq chr4
+ 70360775 70367106 SMR3A 26952 submaxillary gland androgen regulated protein 3A GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59165_PI430048170 0.9310226034167040.9768735853679226.13169582923429 6.09735624495681
6.16545323768898 P P P 5.90721672804718 6.08207582227895 6.45256630619212 P P P
LNCV6_59165_PI430048170 mRNA
ATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTCCAA NM_153377RefSeq chr12
- 58872154 58920538 LRIG3 121227 "leucine-rich repeats and immunoglobulin-like domains 3,
transcript variant 2" GO:0005886|GO:0032474|GO:0016021|GO:0005615|GO:0030659 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_138118_PI430048170 0.4178183463529920.7878041951075841.96942448231077
0.3319289019102250.449391982807483A A A 1.70726473485974 1.20604155888418
1.44861537848022 A A A LNCV6_138118_PI430048170 mRNA
GTGTGCCCCGTTAGTTTTCAGCATTTTGTAAGCAAAATGAACTTAACACATAGTAATTCT NM_018702RefSeq chr10

- 1177312 1737476 ADARB2 105 "adenosine deaminase, RNA-specific, B2 (non-functional)"
GO:0006397|GO:0003725|GO:0003727|GO:0004000|GO:0005634|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131803_PI430048170 0.0877395486087617 0.7281526564158466.28224539999608
6.01016075814928 6.58992786277483 P P P 6.60686280481583 6.81019230709855 6.8827317071761
P P P LNCV6_131803_PI430048170 mRNA
TCCTTTGTTGTTGTCAATTGTGGTTTATTTTCAGAGGTGTAAATAAAGTGCTCTTGCCTG NM_001356 RefSeq chrX +
41333307 41350287 DDX3X 1654 "DEAD (Asp-Glu-Ala-Asp) box helicase 3, X-linked, transcript variant 1"
GO:0005515|GO:0017148|GO:0048027|GO:0030308|GO:0030307|GO:0043273|GO:0032508|GO:0043024|GO:0045
070|GO:0070062|GO:0032728|GO:0005852|GO:0042256|GO:0071470|GO:2001243|GO:0043280|GO:0034063|GO:0
010501|GO:0045087|GO:0071243|GO:0008134|GO:0008625|GO:0035613|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142037_PI430048170 0.0818536189691988 0.8676587200859091 1.729684607026
11.7216079880007 11.7712790611312 P P P 11.8382682661806 11.9292994077212
12.0611580131485 P P P LNCV6_142037_PI430048170 mRNA
ACTTAATGACTTCCTTGGCACCAATCATGTATTTCACCGTTTGCACTTTTTGTATTTCAA NM_004308 RefSeq chr11 -
46677074 46700665 ARHGAP1 392 Rho GTPase activating protein 1
GO:0005515|GO:0051056|GO:0017124|GO:0005886|GO:0007264|GO:0009967|GO:0007266|GO:0001726|GO:0032
855|GO:0005100|GO:0005829|GO:0005070|GO:0030675|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133063_PI430048170 0.768317183522585 1.03291971410928 7.74765123402967
7.77673897637384 8.06419333144098 P P P 8.02054081513047 7.60796360417163
7.81210348385728 P P P LNCV6_133063_PI430048170 mRNA
GATGTTCAACATCAGTTTACTTGCAGCTGGAAGCATTTGTTTTTGAAGTTGTACATAGTA NM_003115 RefSeq chr1
+ 162561505 162599843 UAP1 6675 UDP-N-acetylglucosamine pyrophosphorylase 1
GO:0005737|GO:0003977|GO:0005886|GO:0030246|GO:0005654|GO:0006488|GO:0006048|GO:0044267|GO:0043
687|GO:0018279|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63213_PI430048170 0.00155516453347183 0.469774295756761 5.75325941086271
5.49108190332921 5.42140032853653 P P P 6.77782960449265 6.61974872486081
6.55012828166714 P P P LNCV6_63213_PI430048170 mRNA
CCATGGTGGCACATTTCTGCTATAATGAAGATTAAATAGAATAACAGTTCCAGGATAACA NM_005486 RefSeq chr17
+ 54900690 54961967 TOM1L1 10040 target of myb1 (chicken)-like 1
GO:0005515|GO:0043130|GO:0017124|GO:0005795|GO:0019901|GO:0030295|GO:0005764|GO:0006886|GO:0005
829|GO:0032147|GO:0045839|GO:0007165|GO:0005737|GO:0030276|GO:0043162|GO:2000278|GO:0010008|GO:0
070062|GO:0031954|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143264_PI430048170 0.200639697648067 1.04008689994345 0.370941879836233
0.376923507490746 0.465480860864374 A A A 0.342542419560095 0.324454387510085
0.377684425958335 A A A LNCV6_143264_PI430048170 mRNA
AGGATGTGTACTCAAGCTGATAGTAATTCTGAGCCCTGTCTAATAAAAAAGGAAGGATGT NM_001291911 RefSeq
chr18 - 13882043 13915707 MC2R 4158 "melanocortin 2 receptor (adrenocorticotropic hormone),
transcript variant 2"
GO:0005515|GO:0005737|GO:0007186|GO:0005886|GO:0007218|GO:0007187|GO:0005887|GO:0030819|GO:0004
978|GO:0001890|GO:0004977 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142596_PI430048170 0.827236996114763 0.837042752112371 4.51204205966629
2.79525815432983 3.26446416933366 P A P 3.01094053696153 4.8901536813646
3.21995006225099 P P P LNCV6_142596_PI430048170 mRNA
GTGTGAAAACATGGTTATGGTAATAGGAACAGCTTTTAAAATGCTTTTGTATTTGGGCCT NM_001242638 RefSeq
chr5 + 55851378 55922854 IL31RA 133396 "interleukin 31 receptor A, transcript variant 4"
GO:0043066|GO:0008284|GO:0004896|GO:0005886|GO:0019901|GO:0043031|GO:0042517|GO:0003713|GO:0019

221|GO:0042523|GO:0042592|GO:0006952|GO:0007259|GO:0019955|GO:0000165|GO:0030225|GO:0030224|GO:0
016021|GO:0045893|GO:0007169 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144738_PI430048170 0.8043389902792670.9977945386085260.327539810886891
0.3570980590026150.353640856158623A A A 0.3571770334665260.356759510485594
0.333956630961174A A A LNCV6_144738_PI430048170 mRNA
TGCAAACGTTTGTGCCTCTGAAATGCTCCGTTGTTATTGTTTCAAGACCCTAACTTTTTT NM_001029871 RefSeq chr20
- 958452 1002264 RSPO4 NA "R-spondin 4, transcript variant 1" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142699_PI430048170 0.0223547106223365 0.4464869480923633.087917275186
3.43187983193856 3.86686331554231 P P P 4.4999032749158 4.6644677648054
4.80244820842195 P P P LNCV6_142699_PI430048170 mRNA
GGTATGCCTATATAGGTCTTTAAAAATGGGTATGTATGCTGTTTAATGTGCACTGAACAT NM_024546RefSeq chr13
- 78614285 78659179 RNF219 79596 ring finger protein 219 GO:0048026|GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139571_PI430048170 0.0256515097672841 0.4845980066823363.81355461687172
3.36729548061441 3.43467835138444 P P P 4.17413193199281 4.55467049976738
4.95737673705623 P P P LNCV6_139571_PI430048170 mRNA
GGAAATTTTGTTACAACCTGGTTGAGATCAACCTCTTTACAATGACACAAATTGTGACAT NM_032167RefSeq chr16
+ 11976733 12574289 SNX29 92017 sorting nexin 29GO:0035091|GO:0070062 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_126949_PI430048170 0.6633231973223271.17782868937128 0.424223586683309
1.36358237584649 0.312503606673442A A A 0.2679795345755160.315932267505089
0.948161618287839A A A LNCV6_126949_PI430048170 mRNA
TTGCATTACATACTGTACCCATGGAATTTTTGTTTTACTTTTTGGGGCTGGTTTTGAAAG NM_139057RefSeq chr15 -
99971437 100341978 ADAMTS17 170691 "ADAM metallopeptidase with thrombospondin type 1 motif, 17"
GO:0006508|GO:0005578|GO:0008270|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141336_PI430048170 0.8046070676861291.05081519040742 1.84944521956261
2.39124741655679 2.69919524549779 A A A 2.69770703480803 1.45389592702151
2.42624918693208 A A A LNCV6_141336_PI430048170 mRNA
TATTCTATTGGGCTGTCGTTCAAATGTGGCTTTTAAACTTCAGTTACTTGTTCTTTCTAC NM_001130913 RefSeq chr16
+ 31713228 31761565 ZNF720 124411 zinc finger protein 720 GO:0005622|GO:0006355|GO:0003676 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136473_PI430048170 0.1562951997193970.91531528348409 12.1395622770207
12.0508228901586 11.9561615885089 P P P 12.1768806588687 12.2643611286636
12.0887666555374 P P P LNCV6_136473_PI430048170 mRNA
CTGATGTGCTCAGATGGGCTCATCGTTGGTTCGTTTTTACTGTATATTTATAGTAATAAA NM_001142290 RefSeq
chr16 + 4624823 4690974 MGRN1 23295 "mahogunin ring finger 1, E3 ubiquitin protein ligase,
transcript variant 3"
GO:0005515|GO:0004842|GO:0045744|GO:0006513|GO:0005886|GO:0016874|GO:0008333|GO:0005634|GO:0005
829|GO:0005737|GO:0016020|GO:0008270|GO:0005769|GO:0043951|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140952_PI430048170 0.3810132901081460.69972394000602 0.4097821193633
0.4147725600764860.263557087717729A A A 0.3764637630774440.434924941979929
1.52071649896941 A A A LNCV6_140952_PI430048170 mRNA
ATTACTGAAACCTGATTTATTGCTTTGTCACTTTAACCACATCTCTCAACTCTCTGCAAT NM_001114132 RefSeq chr2
+ 203014878 203217994 NBEAL1 65065 neurobeachin-like 1 NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142965_PI430048170 0.2471269477019910.8930954827190950.527132573963142
0.5846490812563160.45241761259092 A A A 0.7929495859306290.761436060449773

0.482412053506451 A A A LNCV6_142965_PI430048170 mRNA
AGATGGATCTGCCAAAAAGAACTAACACCTGTGAGAAATAAAGTGTATCCTGACTCTTGA NM_002258 RefSeq chr12
- 9595273 9607901 KLRB1 3820 "killer cell lectin-like receptor subfamily B, member 1"
GO:0005886|GO:0030246|GO:0016021|GO:0007166|GO:0004888 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131472_PI430048170 0.517409134375343 1.03266875830095 13.0149106307849
13.0795129785503 12.9584922998008 P P P 13.0716586080252 12.8781623493341 12.959946496122
P P P LNCV6_131472_PI430048170 mRNA
CGCTAGGGATAAAGCAGATGTGGATGCCCTTTAAGAGATATTAAATGCTTTTATTTTCAA NM_002018 RefSeq chr17
- 18244816 18258916 FLII 2314 "flightless I homolog (Drosophila), transcript variant 1"
GO:0051014|GO:0005515|GO:0006355|GO:0005737|GO:0030036|GO:0006936|GO:0005815|GO:0007275|GO:0005
654|GO:0003779|GO:0005925|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129559_PI430048170 0.297049063775296 1.00789339401606 0.330327225243226
0.341701125979206 0.336776857527691 A A A 0.333510216502405 0.332550219001583
0.308600372443101 A A A LNCV6_129559_PI430048170 mRNA
CTGCCGTAGATATACTTTAGGTTAGTATTTCTACATTCGTGGCAAGCATTTTGGTAACAC NM_005575 RefSeq chr5
+ 96935641 97029411 LNPEP 4012 "leucyl/cystinyl aminopeptidase, transcript variant 1"
GO:0000209|GO:0002474|GO:0048471|GO:0002480|GO:0007565|GO:0005886|GO:0042590|GO:0007267|GO:0005
576|GO:0005765|GO:0060395|GO:0005829|GO:0005622|GO:0030163|GO:0031905|GO:0016020|GO:0005887|GO:0
004177|GO:0006508|GO:0061024|GO:0008270|GO:0030659|GO:0008237 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_136415_PI430048170 0.389515663827542 1.05289981582819 0.31131886267224
0.313781010762913 0.508973680382448 A A A 0.311657258210365 0.277203259298981
0.330646135019685 A A A LNCV6_136415_PI430048170 mRNA
TGTCCTGGAGGAATTCATAGCCTCATGGGGCAAAAGTAAATAAACAGCTTATTACAATTC NM_001136022 RefSeq
chr14 + 24366910 24379606 NFATC4 4776 "nuclear factor of activated T-cells, cytoplasmic, calcineurin-
dependent 4, transcript variant 1"
GO:0005515|GO:0006366|GO:2001235|GO:0005634|GO:0042975|GO:0005829|GO:0007507|GO:0005737|GO:0034
644|GO:0006954|GO:0048167|GO:0045944|GO:0045111|GO:0071285|GO:0005667|GO:0001569|GO:0008630|GO:0
032760|GO:0003713|GO:0000122|GO:0000978|GO:0001078|GO:0045333|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143859_PI430048170 0.0745174670407294 0.955170151475224 6.61728430210873
6.68296980140803 6.67467875870612 P P P 6.71578384673261 6.72227750091279
6.73619004987637 P P P LNCV6_143859_PI430048170 mRNA
AATAACAATGAATGGTGCTTTCTTCTGAAAGACTCAGCCTAATTAAAGGATTAAGAGGCA NM_017884 RefSeq chr8
- 10764960 10839899 PINX1 54984 "PIN2/TERF1 interacting, telomerase inhibitor 1, transcript variant 1"
GO:0051974|GO:0005515|GO:0000781|GO:0010521|GO:0008285|GO:0005730|GO:0005819|GO:0005634|GO:0000
228|GO:0051972|GO:0043231|GO:0005739|GO:0005737|GO:0000777|GO:0000776|GO:0005654|GO:0007080|GO:0
007004|GO:0070034. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131474_PI430048170 0.443166918931397 0.876084268970574 6.31827941755718
6.10608095836086 6.64111573815937 P P P 6.23316772129542 6.63360940493236
6.76977162907295 P P P LNCV6_131474_PI430048170 mRNA
CCCCAGATGCAGCATGTCCTGAATGAATGATCTGTAAAATACAATAATAAAAGCTTATAG NM_018246 RefSeq chr8
- 27733315 27772653 CCDC25 55246 "coiled-coil domain containing 25, transcript variant 1"
GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131759_PI430048170 0.117248473976277 1.11032177875253 11.1727887622571
11.0920840785627 11.1133467161942 P P P 10.8510135843556 11.0502092915251
11.0174763310341 P P P LNCV6_131759_PI430048170 mRNA
TTCCCAGGCTATGCCCCACCCTCTTTGTATTAAAAGCCTCCTCTTTTGGGCCTTAAAAAA NM_004704 RefSeq chr3

- 51933425 51941941 RRP9 9136 "ribosomal RNA processing 9, small subunit (SSU) processome component, homolog (yeast)" GO:0006364|GO:0030532|GO:0005730|GO:0005732|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71465_PI430048170 0.6242462181143640.9595135262838275.21760413974989 4.95995565693079 5.00443442446228 P P P 5.17842490468618 5.22030821883291 4.96244213552726 P P P LNCV6_71465_PI430048170 mRNA
TCACAGACCCTACCTGTGACACAGACAGCGGCCAGTGCAGTGCAGACCCAACGTGACTGG NM_005560RefSeq chr20 - 62309059 62367312 LAMA5 3911 "laminin, alpha 5"
GO:0001658|GO:0008037|GO:0030324|GO:0008283|GO:0001755|GO:0005634|GO:0009790|GO:0005615|GO:0030155|GO:0001738|GO:0030154|GO:0022617|GO:0030198|GO:0048041|GO:0042127|GO:0007010|GO:0042475|GO:0034446|GO:0045446|GO:0001942|GO:0070062|GO:0030334|GO:0005605|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134169_PI430048170 0.26394701137665 1.23004412187128 4.03585305132417 4.26162308058898 4.49229524131693 P P P 3.63699309144647 3.90170409270178 4.31031769952205 P P P LNCV6_134169_PI430048170 mRNA
GGCAATCAGTTTGTAGCTGTGCCCTTATTTTTATAGATAGTTTGCCATTTCTTGGGTTTA NM_001258345 RefSeq chr4 + 20700412 20728357 PACRGL133015 "PARK2 co-regulated-like, transcript variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_29809_PI430048170 0.00113716944662233 1.48236124553131 2.76484067140484 2.61032926296255 2.61751614816032 A A A 2.17637144681797 2.06921236447736 2.04533905196879 A A A LNCV6_29809_PI430048170 mRNA
AGCTCCTCAGGAACGACTGGGGAAGCTGTGGCTTCATGGTCCCCGAGGCTGCCCGAGGAA NM_001145249 RefSeq chr9 + 138216186 138243722 FAM157B NA "family with sequence similarity 157, member B" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135655_PI430048170 0.0576260346607213 1.49420471301226 7.07566561368253 7.61699279472849 7.30585427286215 P P P 7.02319231804493 6.74667014841977 6.49331610197962 P P P LNCV6_135655_PI430048170 mRNA
AAAGATGCCTTAGAAGAGTCGCTTCTGCTGAAGGACTGCAAGTGCCGCTCCCGCCTCTTC NM_172139RefSeq chr19 - 39243631 39244971 IFNL3 282617 "interferon, lambda 3"
GO:0051607|GO:0050778|GO:0007259|GO:0005615|GO:0005125|GO:0045071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127752_PI430048170 0.0223073779645617 1.21112976253653 0.734818421067432 0.8507348930435880.911861052637992A A A 0.6659763410934680.486021129452031 0.515393208039915A A A LNCV6_127752_PI430048170 mRNA
GTGTCAGCTGTAACTCCTAGGATATTTTATGTGGAACCTAACATGCAGATGAAAGCTGGC NM_173689RefSeq chr9 + 123356166 123378755 CRB2 286204 "crumbs family member 2, transcript variant 1"
GO:0001707|GO:0005886|GO:0001756|GO:0005509|GO:0010718|GO:0045199|GO:0014028|GO:0010951|GO:0019828|GO:0030513|GO:0043234|GO:0045121|GO:0016021|GO:0072358|GO:0019899|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108496_PI430048170 0.6810080624070681.055254326414 8.14551035372015 7.85971139830177 7.73754852805602 P P P 7.64329463167771 8.09372055355072 7.76551109905377 P P P LNCV6_108496_PI430048170 mRNA
ACATCAACGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAA NM_000660RefSeq chr19 - 41330530 41353933 TGFB1 7040 "transforming growth factor, beta 1"
GO:0005515|GO:0001657|GO:0002513|GO:0006796|GO:0005615|GO:0007406|GO:0005114|GO:0006754|GO:0010763|GO:0001948|GO:0007173|GO:0000165|GO:0002062|GO:0006611|GO:0007179|GO:0000060|GO:0010800|GO:0007565|GO:0009986|GO:0002460|GO:0005796|GO:0010742|GO:0007568|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138713_PI430048170 0.5071632011003081.02125586804024 0.373341405933662

0.25046058445503 0.284461482205868A A A 0.2672156030911940.284763404989181
0.267989429114866A A A LNCV6_138713_PI430048170 mRNA
AACCAACCATCCAGTGAGTCTACTAAGTGTTTACCTATATGGTTTGATGAGGGTATTAAA NM_001008536 RefSeq
chr1 - 152084143 152089064 TCHHL1NA trichohyalin-like 1 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_127036_PI430048170 0.0450711224224931 0.65018277807968 7.79286890575602
7.75242034451373 7.8168435054917 P P P 8.13810767947606 8.44240646184788 8.6070587655903
P P P LNCV6_127036_PI430048170 mRNA
GACACCCTTCAAGTGACCATGTCATTGTTTTCTTGCTATGTCTTTAGCTTAATGATTAAGNM_001105570 RefSeq chr19
+ 32691960 32713796 NUDT19 390916 nudix (nucleoside diphosphate linked moiety X)-type motif 19
GO:0005739|GO:0008150|GO:0016787|GO:0008152|GO:0005102|GO:0005575|GO:0046872|GO:0005777 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128547_PI430048170 0.00558065189864124 1.57841724751699 9.23144540914491
9.30191301494694 9.16525909564914 P P P 8.72802292537128 8.51952480329491
8.46534546033435 P P P LNCV6_128547_PI430048170 mRNA
TATGCCCATGCCTCCATACATGGACTGGTTCTGTTTTATTAAAACTAATATTTCATACAG NM_032709RefSeq chr10
- 98383564 98415221 PYROXD2 84795 pyridine nucleotide-disulphide oxidoreductase domain 2
GO:0016491|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137310_PI430048170 0.8788768365080580.9932747206877480.341638472167244
0.4888011887827150.37174461216005 A A A 0.4936551895376160.372835117895746
0.36550143416186 A A A LNCV6_137310_PI430048170 mRNA
AATCCTCAACATCGACTTTAGCAATGCAGACATTGACGTGTTGGAGGACCTTTTGGTGCT NM_182519RefSeq chr20
+ 33081511 33111751 BPIFB4 149954 "BPI fold containing family B, member 4"
GO:0005737|GO:0005576|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137016_PI430048170 0.5190823719899120.9410800672639199.90375872950232
10.2508042398117 9.92458950192209 P P P 10.2103081893944 9.99483790773622
10.1551416034715 P P P LNCV6_137016_PI430048170 mRNA
GTTAGCTAAGGTTATTGCTTTTTGTGGCAAATCTAATTAAATGACAGGAATCTCTTCACG NM_001206710 RefSeq
chr12 - 49002271 49018748 PRKAG15571 "protein kinase, AMP-activated, gamma 1 non-catalytic
subunit, transcript variant 4"
GO:0005515|GO:0008286|GO:0004679|GO:0008603|GO:0005634|GO:0007283|GO:0051291|GO:0005829|GO:0045
860|GO:0061024|GO:0007050|GO:0006633|GO:0070062|GO:0006996|GO:0016208|GO:0019901|GO:0031588|GO:0
005524|GO:0010628|GO:0006110|GO:0007165|GO:0004672|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138768_PI430048170 0.0113445159745926 1.62809714802453 9.55146503663197
9.45614287278244 9.30955202987039 P P P 8.95369884387917 8.68023045763585
8.55462268043335 P P P LNCV6_138768_PI430048170 mRNA
TTTTCGACAACTGCAGCTGAATCTCATGGAAAAGCTGGATTCCTCTGCCTTACGCAGAAA NM_207446RefSeq chr15
- 92617448 92655801 FAM174B 400451 "family with sequence similarity 174, member B" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129003_PI430048170 0.9883588420144771.21100520020928 0.603113796803684
1.37745927440425 2.77230962910136 A A A 1.85617613300475 1.56549010701283
1.29929546290321 A A A LNCV6_129003_PI430048170 mRNA
TATAGTCAGACCTGGTTACACACATACACACACACAATATCACCATGACAAATACACATT NM_003807RefSeq chr19
- 6663136 6670588 TNFSF14 8740 "tumor necrosis factor (ligand) superfamily, member 14,
transcript variant 1"
GO:0005515|GO:0005164|GO:0005886|GO:0031295|GO:0010820|GO:0005102|GO:0006915|GO:0005125|GO:0005
615|GO:0007165|GO:0042110|GO:0005737|GO:0006955|GO:0008588|GO:0042098|GO:0045663|GO:0016021|GO:0
071260|GO:0043154|GO:0043029|GO:0043027 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139936_PI430048170 0.0690738080176269 0.8460311655707377.54578861288611
7.5398771357477 7.30802572953436 P P P 7.73792568123231 7.61250350885514
7.77446466797799 P P P LNCV6_139936_PI430048170 mRNA
TTCCTGAAGACTATCTTCCCATCTCAAAATGGACATGATGGATCCACGGATGTACAGCAG NM_001282511 RefSeq
chr16_KI270853v1_alt + 2040291 2055014 NPIPA8 NA "nuclear pore complex interacting protein
family, member A8" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144859_PI430048170 0.0284936313441232 0.6572139201675289.39075641408987
9.06525343240787 8.92677276154912 P P P 9.63066498699525 9.87486698252361
9.72337183610064 P P P LNCV6_144859_PI430048170 mRNA
TGGTCTTGTGCCCGAGACGGGCGGAGGCTGGAACTTGAGACCTCAATAAAGGAAGTAGAG NM_032259RefSeq
chr16 - 684621 690424 WDR24 84219 WD repeat domain 24 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_115958_PI430048170 0.2077222417919640.8705830216522077.12299153410603
6.90848199203755 6.75226495868093 P P P 7.07283664800691 7.28784163923437
7.03386473631643 P P P LNCV6_115958_PI430048170 mRNA
AATGCAGCAGGAAGGAACAAAGACAGGCAAACGGCAACGTAGCCTGGGCTCACTGTGCTG NM_002204RefSeq
chr17 + 50055975 50090485 ITGA3 3675 "integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3
receptor), transcript variant a"
GO:0005515|GO:0030111|GO:0005518|GO:0097205|GO:0031527|GO:0002020|GO:0050900|GO:0007507|GO:0001
948|GO:0030198|GO:0071438|GO:0007613|GO:0017015|GO:0035640|GO:0070062|GO:0008305|GO:0009986|GO:0
046982|GO:0019904|GO:0060135|GO:0060076|GO:0043235|GO:0097062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137621_PI430048170 0.00548197539278957 2.68390992371548 4.00000616149691
4.56216415525591 4.58071352422243 P P P 3.29691324656083 2.70591683919789
2.87312573703773 P P P LNCV6_137621_PI430048170 mRNA
GCTTTGTACGAGGCTTAGTATTTAGACATGATGTACATTTTTTACAGTGCATACTACTCA NM_172341RefSeq chr19
+ 35745576 35747155 PSENEN55851 "presenilin enhancer gamma secretase subunit, transcript variant 1"
GO:0042987|GO:0005515|GO:0048011|GO:0043065|GO:0005794|GO:0007220|GO:0070765|GO:0048013|GO:0005
886|GO:0005783|GO:0031293|GO:0043085|GO:0097190|GO:0007219|GO:0005887|GO:0007411|GO:0016485|GO:0
032580|GO:0005789|GO:0006509 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142868_PI430048170 0.0109025264621305 0.5294776246019760.326242892489859
0.2426608527323770.298543149497956A A A 0.9990394465260381.22521054811542
1.37227636106028 A A A LNCV6_142868_PI430048170 mRNA
CTGCAGTGTCCCAGTCATTTATTTGCATGAATCTGCTTAAATAAGTTTTTTGTTGCTGTT NM_032438RefSeq chr6 +
130018582 130141449 L3MBTL3 84456 "l(3)mbt-like 3 (Drosophila), transcript variant 1"
GO:0003674|GO:0006355|GO:0043249|GO:0030225|GO:0005634|GO:0030851|GO:0006351|GO:0016568 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130166_PI430048170 0.00873216109980935 0.4103338307570135.20207104651681
4.5496720454362 5.10820326456548 P P P 6.03044713836396 6.13971986161636
6.56942653258463 P P P LNCV6_130166_PI430048170 mRNA
GAATGCCTGAAGTCTAATCCTGACCTTACTTTGTTGCCCATAAATATCTTTCAAATTGAA NM_018072RefSeq chr1
- 236549004 236604541 HEATR1 55127 HEAT repeat containing 1
GO:0005739|GO:0005515|GO:0000462|GO:0030515|GO:0016020|GO:0045943|GO:0032040|GO:0005730|GO:0005
634|GO:0034455|GO:0030686 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135875_PI430048170 0.3300997894066180.8970473159772540.605539530951703
0.7320588770838570.57275339398248 A A A 0.5546725051009170.884405288318387
0.919176065487116A A A LNCV6_135875_PI430048170 mRNA
GAGTTTGAAGAAGACTCTGGACTGCTTCCAATACGTAGGAATTATATTTCTAAAGTTTAG NM_207321RefSeq chr10
+ 95194199 95228929 ACSM6 NA acyl-CoA synthetase medium-chain family member 6NA . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_143218_PI430048170 0.00555880519700355 0.4700191952959864.84210121865729
4.56311836013094 4.73558129553294 P P P 5.51806890488346 5.88957530799991
5.97476155973691 P P P LNCV6_143218_PI430048170 mRNA
GTGGGATGGTAAAAAATGTCACAAAAGACTCCTCACCAATACTTTATGTTGATATCACTT NM_003607RefSeq chr1
- 226989864 227318125 CDC42BPA 8476 "CDC42 binding protein kinase alpha (DMPK-like), transcript variant B"
GO:0005515|GO:0000287|GO:0042641|GO:0031532|GO:0007097|GO:0000226|GO:0031032|GO:0005524|GO:0042802|GO:0035556|GO:0050790|GO:0005083|GO:0005737|GO:0016477|GO:0004674|GO:0005911|GO:0006468|GO:0031252|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137038_PI430048170 0.150379484407905 1.09325842437971 0.509573226643991
0.5852688004505010.608164537188823A A A 0.3284258426643750.445959189434281
0.537000621939392A A A LNCV6_137038_PI430048170 mRNA
TGTGATTCTCACAGACACCAAGAAGTCCCAGGCCAAAATTGTCATTGGGCTAGACAATGT NM_001256041 RefSeq
chr12 - 57028516 57050765 MYO1A 4640 "myosin IA, transcript variant 1"
GO:0005516|GO:0030033|GO:0007605|GO:0003779|GO:0016459|GO:0005524|GO:0016328|GO:0005903|GO:0005902|GO:0016323|GO:0003774|GO:0005737|GO:0016324|GO:0031941|GO:0009925|GO:0008152|GO:0051648|GO:0030864 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141355_PI430048170 0.00323644095246021 0.7457972798753451 3.6069796160837
13.5457207883392 13.4366571971717 P P P 13.882523329234 13.9782808514066
14.0004155602977 P P P LNCV6_141355_PI430048170 mRNA
GCAGATGTTCAATAAAGGAGACAAGTGCTTTCCCAGCTCTTTTCCTGCACCACCAAAAAA NM_001747RefSeq chr2
- 85394747 85410697 CAPG 822 "capping protein (actin filament), gelsolin-like, transcript variant 1"
GO:0042470|GO:0051016|GO:0006461|GO:0030031|GO:0008290|GO:0005634|GO:0003779|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139094_PI430048170 0.17727513957535 1.05840065630272 0.482980416527372
0.3988619182678780.484585782832269A A A 0.3036988153818520.3722034476229
0.443153262828614A A A LNCV6_139094_PI430048170 mRNA
CACTTTTCTCAATGTAGAGAAAATACCTACCATTTTTTGGCTTCATGCTCCAGAAGGAAC NM_181612RefSeq chr21
- 30541534 30541864 KRTAP19-6 NA "keratin associated protein 19-6, transcript variant KRTAP19-6-V1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112131_PI430048170 0.00385250083821322 0.5007290964748586.9344714264906
6.99064392535502 7.32232523219988 P P P 7.89533342451501 8.06490107983304 8.2854417537135
P P P LNCV6_112131_PI430048170 mRNA
CTCTATCCTGAGTAACTAATGGACATCTTCTCATGCAAGGTTTATATGAAGCCTTTTTAA NM_001256394 RefSeq
chr9 - 92297357 92325594 NOL8 55035 "nucleolar protein 8, transcript variant 2"
GO:0006260|GO:0005515|GO:0005737|GO:0000166|GO:0030307|GO:0006364|GO:0005730|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145690_PI430048170 0.890211841178431 1.00488033625707 0.281901414726504
0.31846895628718 0.409473127810327A A A 0.3568570728759640.324712327872201
0.309809667853623A A A LNCV6_145690_PI430048170 mRNA
TTCCTGCCTTTTCTGGACTGAGGAAAATTTCCCATGAAGACAGTAACCAGGAAAAATTCA NM_002551RefSeq chr17
- 3277889 3278974 OR3A2 4995 "olfactory receptor, family 3, subfamily A, member 2"
GO:0050911|GO:0007165|GO:0004984|GO:0007186|GO:0005886|GO:0005887|GO:0004930|GO:0007606|GO:0004872|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134986_PI430048170 0.3923646564776740.7457478555185730.37740920510302
0.3554326004453370.258034105764866A A A 0.3316854034273721.32135561610659
0.382392243050927A A A LNCV6_134986_PI430048170 mRNA
CTACCAGATCATTAAACCTGCTGTCAAAGGGCCACAACAGTAGCAGCCAAAACTAAAAAA NM_001004432 RefSeq

chr1 - 151800264 151805442 LINGO4 339398 leucine rich repeat and Ig domain containing 4
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129957_PI430048170 0.3317947547294460.9056278229478621 3.197780788403
13.0530651934257 12.9668059820685 P P P 13.0156335890321 13.36537142091
13.2533960798542 P P P LNCV6_129957_PI430048170 mRNA
TTCCCACTCCCATCTTTCTTCCGGACAATGAAATAAAGAGTTACCACCCAGCAGAAAAAA NM_003254RefSeq chrX
+ 47582290 47586791 TIMP1 7076 TIMP metallopeptidase inhibitor 1
GO:0005515|GO:0008284|GO:2001044|GO:0051045|GO:0043434|GO:0002020|GO:0005615|GO:0046872|GO:0022
617|GO:0030198|GO:0031093|GO:0009725|GO:0034097|GO:0070062|GO:0043066|GO:0007568|GO:0005578|GO:0
030168|GO:0005576|GO:0005125|GO:0005604|GO:0010951|GO:0048553|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134972_PI430048170 0.0321319904926979 0.6591440498088739.25941165676389
9.0346967279432 9.32018743302499 P P P 9.64984702847638 9.66041238300643
10.0803854536785 P P P LNCV6_134972_PI430048170 mRNA
CAACTTGTACTGCGCCTGAATAGTCATGTGATAATTTACTGAAGAAATCTAGTGTACTTT NM_014613RefSeq chr5
+ 176448354 176510074 FAF2 23197 Fas associated factor family member 2
GO:0006986|GO:0005811|GO:0005515|GO:0043130|GO:0005783|GO:0034098|GO:0035473|GO:0043086|GO:0034
389|GO:0055102|GO:0031625|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135726_PI430048170 0.6539727952322320.9850125253512960.393633659238366
0.4479621012617070.355834536898676A A A 0.4899727344532410.377504344544204
0.394229397890978A A A LNCV6_135726_PI430048170 mRNA
GCACATTCTCCTTTGGCCATCAGAGACTTTACACTGGAGAGAAAAATGTGAGAGTGTTTA NM_030613RefSeq chr5
+ 178895914 178933209 ZFP2 80108 ZFP2 zinc finger protein
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139322_PI430048170 0.0189207557619013 1.58443761492723 9.79899035446971
10.1745705186539 10.113260102113 P P P 9.37365738183752 9.45187710534706
9.29238751513824 P P P LNCV6_139322_PI430048170 mRNA
TGGAAATGATGAGCAGTAGCATCATTTCTCCCTGTTGGGTTTTAGCCAGTTTGCCAGCAA NM_017825RefSeq chr1
+ 36088851 36093932 ADPRHL2 54936 ADP-ribosylhydrolase like 2
GO:0071451|GO:0005759|GO:0008152|GO:0004649|GO:0005654|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_89139_PI430048170 0.0562182876081575 1.15189904706058 8.26612718458349
8.34295461399209 8.17297539534856 P P P 8.1634703027792 8.04039850133695 7.964109016687
P P P LNCV6_89139_PI430048170 mRNA
AAGGACCCGAAGTGAGCTTCTGCCTTTCCTTACAGATACCATCTATGATGAAGATGAGGT NM_014225RefSeq chr19
+ 52189801 52226425 PPP2R1A 5518 "protein phosphatase 2, regulatory subunit A, alpha, transcript variant 1"
GO:0005515|GO:0008380|GO:0010467|GO:0030308|GO:0030111|GO:0006672|GO:0008601|GO:0000159|GO:0005
634|GO:0030155|GO:0003823|GO:0005829|GO:0005739|GO:0000188|GO:0006470|GO:0007059|GO:0000184|GO:0
000086|GO:0015630|GO:2001241|GO:0004722|GO:0006275|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_108246_PI430048170 0.0735734191919961 1.21081090491429 12.2549678659475
12.5213773527075 12.3934917285786 P P P 12.2771239590614 12.0685614320578
11.9933332888871 P P P LNCV6_108246_PI430048170 mRNA
GTGTGTGCCACTTCCCCTACCCCAACGTGAAAACCTCAATAAACTGCCCGAAGCAGCTTG NM_001143993 RefSeq
chr11_KI270832v1_alt + 90626 93681 RASSF7 8045 "Ras association (RalGDS/AF-6) domain family (N-terminal) member 7, transcript variant 2" GO:0007165|GO:0005737|GO:0005815|GO:0006915 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_134645_PI430048170 0.0646396545342533 1.25651009360972 10.8362965708372
10.6027597878309 10.4914449429192 P P P 10.4132449928663 10.3436089845746
10.1988949693566 P P P LNCV6_134645_PI430048170 mRNA
GTGCCATAAAATGAGACTTTTTACGCCTTTATAAGGCCTTAGATGTAAATAAACTCACCC NM_203290RefSeq chr6
+ 43517038 43521508 POLR1C9533 "polymerase (RNA) I polypeptide C, 30kDa"
GO:0010467|GO:0006386|GO:0006385|GO:0003899|GO:0006363|GO:0006362|GO:0006361|GO:0006360|GO:0003
677|GO:0006383|GO:0005829|GO:0001056|GO:0005736|GO:0045814|GO:0045087|GO:0001054|GO:0046983|GO:0
040029|GO:0005666|GO:0032481|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131604_PI430048170 0.6102106843412310.97728489029481 0.480798320817764
0.4959483794240390.350273300802839A A A 0.3994261525185780.529319392716155
0.498944045741059A A A LNCV6_131604_PI430048170 mRNA
CTTTTACACAGTAAGAATAGGATCAGCTGTGCTAAACTAACAAATACCCAGATATCCAGG NM_002121RefSeq
chr6_GL000256v2_alt + 4524908 4538679 HLA-DPB1 3115 "major histocompatibility complex,
class II, DP beta 1"
GO:0032729|GO:0050852|GO:0012507|GO:0005886|GO:0009986|GO:0019221|GO:0031295|GO:0042613|GO:0005
765|GO:0032588|GO:0030666|GO:0019886|GO:0000139|GO:0016020|GO:0050870|GO:0042605|GO:0042102|GO:0
071556|GO:0030669|GO:0010008|GO:0060333|GO:0030658 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_140653_PI430048170 0.73143546267498 1.03885641674781 3.10762719785856
2.98852145988247 3.02847220313289 A P P 2.95844318051218 3.33548054041454
2.56657655188612 P P P LNCV6_140653_PI430048170 mRNA
TCACCTTCCTGGGGTCTGTGACTGACTGGAGATAAAAATAAAAGCAATTGTGACACCTGA NM_012306RefSeq chr12
- 49866895 49903977 FAIM2 23017 Fas apoptotic inhibitory molecule 2
GO:0043066|GO:0030054|GO:2001234|GO:0006915|GO:0021549|GO:0043523|GO:0043524|GO:0021680|GO:0021
702|GO:0002931|GO:0021681|GO:0045211|GO:0045121|GO:0016021 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145745_PI430048170 0.2464363082077530.750315902226669 8.76772127551769
8.64694841617565 8.80614830738606 P P P 8.67086169314555 9.21743123818805
9.46943153606554 P P P LNCV6_145745_PI430048170 mRNA
TAAACAGACATGTGACTGGGAACATCTTGCTGCCAAAAGAATCCTAGGCAGTGGCTCATT NM_001256295 RefSeq
chr21 + 38805306 38824954 ETS2 2114 "v-ets avian erythroblastosis virus E26 oncogene homolog
2, transcript variant 2"
GO:0005515|GO:0003700|GO:0006357|GO:0006366|GO:0000981|GO:0005634|GO:0035259|GO:0000122|GO:0000
978|GO:0003677|GO:0030154|GO:0001078|GO:0001501|GO:0045944|GO:0005654|GO:0045893 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138331_PI430048170 0.2957888886959340.799490325439653 8.43196185240429
7.64593673823965 7.82441634218684 P P P 8.42917112044447 8.50223524748182
8.01521905557351 P P P LNCV6_138331_PI430048170 mRNA
GCGCGGGCGCCGCCCACCGCCATACTAAACGATCGAGGAATAAAGACACTTGGTTTTTCT NM_007046RefSeq chr2
+ 27078566 27086397 EMILIN1 11117 elastin microfibril interfacer 1
GO:0031012|GO:0005515|GO:0005581|GO:0030198|GO:0010811|GO:0005578|GO:0030023|GO:0005576|GO:0007
155|GO:0070062|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139097_PI430048170 0.13589994413491 0.6820407273301649.56870592986826
8.79160035287457 8.80039039196988 P P P 9.77775782809148 9.69278475055028
9.47455741873878 P P P LNCV6_139097_PI430048170 mRNA
GGAGATGGCTGCTGCTGCCCATCATGCTACAGAAGATATAGATTCACTGGCTTCTACTAA NM_181608RefSeq chr21
- 30487189 30487348 KRTAP19-2 NA keratin associated protein 19-2 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_103497_PI430048170 0.1134771504017090.900965039284479 7.54695309229143

7.50072823837045 7.34843840600995 P P P 7.53708752293914 7.64810935119097
7.66632639352539 P P P LNCV6_103497_PI430048170 mRNA
ACCCCCACAGCAGGACTACACGAAGGCTTGGGAGGAGTACTACAAGAAGCAAGCGCAAGT NM_003685 RefSeq
chr19 - 6413107 6424811 KHSRP 8570 KH-type splicing regulatory protein
GO:0006397|GO:0008380|GO:0010467|GO:0006355|GO:0010494|GO:0003729|GO:0006402|GO:0003677|GO:0006
351|GO:0005829|GO:2000628|GO:0016020|GO:0000375|GO:0005654|GO:0051028 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145119_PI430048170 0.529821300551682 0.930565089911615 8.35971340099805 8.0766872627286
7.92778507185558 P P P 8.34206199712419 8.30529440318212 8.04419910554219 P P P
LNCV6_145119_PI430048170 mRNA
GGCCCTCTCTTCTCACCTTTGTTTTTTGTTGGAGTGTTTCTAATAAACTTGGATTCTCTA NM_004994 RefSeq chr20 +
46008907 46016561 MMP9 4318 matrix metallopeptidase 9
GO:0005515|GO:0051549|GO:0005518|GO:0035987|GO:0050900|GO:2001258|GO:0005615|GO:0042802|GO:0022
617|GO:0007411|GO:0030198|GO:0030574|GO:0006508|GO:0030225|GO:1900122|GO:0070062|GO:0043065|GO:0
048013|GO:0007566|GO:0005578|GO:0005576|GO:0001501|GO:0004175|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133028_PI430048170 0.167467613600637 0.388796749079781 1.86255692390591
1.78590384147727 2.06418167763189 A A A 1.97804134338365 3.4770172148163
3.79745142822235 A P P LNCV6_133028_PI430048170 mRNA
GCCTGTGTGGTAAATAGTAAATACAATGGCATAAAAGTAACTTTCTCTGAAGATGTGATG NM_001174116 RefSeq
chr15 - 51447723 51622770 DMXL2 23312 "Dmx-like 2, transcript variant 1"
GO:0017137|GO:0030054|GO:0030672|GO:0005615|GO:0008021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139853_PI430048170 0.920867247669473 1.64286681481444 3.12336292716523
0.317137616214157 0.326876353146426 P A A 1.03202488509603 1.58808999704104
0.827546038180709 A A A LNCV6_139853_PI430048170 mRNA
TTTGCCAGAGAAGGACCCCTGGGGTCCATAGCTCATGAAGTCCAAACATATCTATACATT NM_021173 RefSeq chr11
- 67350764 67353596 POLD4 57804 "polymerase (DNA-directed), delta 4, accessory subunit, transcript
variant 1"
GO:0005515|GO:0003887|GO:0005634|GO:0006260|GO:0006271|GO:0006281|GO:0071897|GO:0000723|GO:0006
283|GO:0006284|GO:0000722|GO:0006297|GO:0005654|GO:0006298|GO:0006289|GO:0000278|GO:0032201 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135857_PI430048170 0.482148187957955 1.03446512593743 12.2925590424448
12.4198319618431 12.4754484604218 P P P 12.3606726337001 12.3131926043303
12.3726792712436 P P P LNCV6_135857_PI430048170 mRNA
CCGCTCAAGAGCTGGTTTGTTAATTATTGTTAGACTTTGCCATTGTTTTCTTTTGTACCT NM_080916 RefSeq chr2 +
73926825 73958961 DGUOK 1716 "deoxyguanosine kinase, transcript variant 1"
GO:0009157|GO:0046070|GO:0004138|GO:0055086|GO:0005634|GO:0044281|GO:0019206|GO:0005524|GO:0009
165|GO:0005829|GO:0005739|GO:0046122|GO:0006144|GO:0005759|GO:0043101|GO:0010977|GO:0006468|GO:0
008617 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139161_PI430048170 0.00449253088539696 1.22469255915583 11.8746488672373
11.8796814552081 11.7893920854613 P P P 11.5071506013237 11.6302698556773
11.5277784320189 P P P LNCV6_139161_PI430048170 mRNA
AGTGACTGCTGAATGTACCCTGTGTGGCGACTTGGAATCAATAAACCATTTGTGGATCCT NM_025078 RefSeq chr18
- 79902419 79951653 PQLC1 80148 "PQ loop repeat containing 1, transcript variant 1" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133862_PI430048170 0.258393722499862 0.614256577733494 0.290295227921337
0.325684786409247 0.362335502146286 A A A 1.65559958448591 0.361807934751978
0.755604183258647 A A A LNCV6_133862_PI430048170 mRNA

TCAGTAATAAAACATCTTTCCAGTCCTTGGTCAGTTTGGTTGTGTAAGAGAATGTTGAAT NM_000756RefSeq chr8
- 66176376 66178611 CRH 1392 corticotropin releasing hormone
GO:0005515|GO:0043627|GO:0032811|GO:0006704|GO:0033685|GO:2000310|GO:2000854|GO:0060291|GO:0005
615|GO:0051602|GO:0060548|GO:0007611|GO:0005184|GO:0010942|GO:0035641|GO:0008306|GO:0014062|GO:0
051412|GO:0007565|GO:0007616|GO:0007567|GO:0071314|GO:0050801|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145672_PI430048170 0.0429823027474220.6510376712113947.78645195448079
7.56129329200616 7.73500445077445 P P P 8.09852860403173 8.19618185810192
8.60394081081293 P P P LNCV6_145672_PI430048170 mRNA
CTTTGAATTAAAGGACAAACTCCTGGAACCTTTCCATATACCAGAGTAAACTAGAATATC NM_001267809 RefSeq
chr1 - 153661787 153671028 ILF2 3608 "interleukin enhancer binding factor 2, transcript variant 2"
GO:0003725|GO:0005515|GO:0005730|GO:0005634|GO:0003677|GO:0005524|GO:0006351|GO:0005737|GO:0006
955|GO:0016020|GO:0030529|GO:0005654|GO:0045893|GO:0016740 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138288_PI430048170 0.22903941203075 0.8681741937026214.90081368685065
5.16009892162477 4.81072542833112 P P P 5.05184269914109 5.35987100217241
5.07404088993039 P P P LNCV6_138288_PI430048170 mRNA
GCAGGGCGTATATTTTGTTGAGCCCTTCCTCCTTTGCAAAATTTATATTAAAGCATTGGT NM_148959RefSeq chr6
- 655938 656964 HUS1B 135458 HUS1 checkpoint homolog b (S. pombe)
GO:0030896|GO:0006281|GO:0005730|GO:0000077 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131093_PI430048170 0.5143889461474381.02285031952354 0.388059821971236
0.2546755677126360.289689952412111A A A 0.270028502044125 0.294597440142437
0.273226605566989A A A LNCV6_131093_PI430048170 mRNA
AACACCGTGTGCTTCGTGACGGTCAAGAACAACACCATGAAGTACTTCAAGAAGATGATG NM_144773RefSeq chr20
- 5302039 5314369 PROKR2128674 prokineticin receptor 2
GO:0004983|GO:0005886|GO:0007218|GO:0007623|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131675_PI430048170 0.9647963566619561.00070624287537 0.473081017378972
0.4468577127321480.481684194403383A A A 0.490952402538998 0.505593046798739
0.399997273045461A A A LNCV6_131675_PI430048170 mRNA
TGCCTCGTACAATTAATAGTGATATTTTGGACAAGGAGTTCTGGTGACAAGCTATACCTA NM_001042357 RefSeq
chr10 + 46932376 47002320 PTPN20 NA "protein tyrosine phosphatase, non-receptor type 20B,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142558_PI430048170 0.5162273430861481.67880646187771 2.54922902616422
0.5039875863176150.853937113410095A A A 0.400717708786527 1.36602242896045
0.594660330199825A A A LNCV6_142558_PI430048170 mRNA
CAGCTTAACAAACATATTAGACAGACAAAGGTCTCAAATTAAAGGGAAAGATTCAGAGGGNM_020741RefSeq chr3
- 128970938 128994143 KIAA1257 57501 KIAA1257 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130208_PI430048170 0.3339321384328710.5833817192783491.02034478742343
0.8940809844191790.542534261241582A A A 0.483868218410207 2.16895726977247
1.70655795851068 A A A LNCV6_130208_PI430048170 mRNA
TGGGGTCCAAGTTTTGTGTATTCTTCAACCTCATTGACAAGAACTGAAACCACCAAAAAA NM_000799RefSeq chr7
+ 100720799 100723701 EPO 2056 erythropoietin
GO:0005515|GO:0042541|GO:0008284|GO:0043627|GO:0009651|GO:0010523|GO:0008015|GO:0033189|GO:0061
418|GO:0042523|GO:0046579|GO:2001258|GO:0048678|GO:0005615|GO:0043249|GO:0018105|GO:0051602|GO:0
045860|GO:0032496|GO:0070555|GO:0005128|GO:0071474|GO:0009986|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143335_PI430048170 0.3525001696250650.9186875617723674.19103222802472

4.10723367804259 4.13901810471558 P P P 4.28795722451541 4.08295289359628
4.41537390104735 P P P LNCV6_143335_PI430048170 mRNA
GTAGTGATGAGATATCAAATCCCTTAGTGTTTCCATTTTGGGAAATGAGGCACTATTTTT NM_001301268 RefSeq
chr15 + 40324055 40326715 INAFM2 100505573 InaF-motif containing 2 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126983_PI430048170 0.3837371182196410.7732948529239576.78131096709597
6.85012377241483 6.88358287906514 P P P 6.58496828651779 7.38695389286034
7.49787285531497 P P P LNCV6_126983_PI430048170 mRNA
GAGGGAAGGGTTTCTCTATTAAAATGCATTCGTTGTGTTTTTTAAGATAGTGTAACTTGC NM_005573 RefSeq chr5
+ 126776622 126837020 LMNB1 4001 "lamin B1, transcript variant 1"
GO:0031965|GO:0016020|GO:0043274|GO:0005198|GO:0006915|GO:0005637|GO:0005654|GO:0005635|GO:0006921|GO:0005638 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_26217_PI430048170 0.1111646280172140.6838419812826967.27877698947762 7.22920287711652
7.43724299998496 P P P 7.58282041266095 7.69444309397176 8.23397431566975 P P P
LNCV6_26217_PI430048170 mRNA
CACGAAAGTATGATGCAAAATTCACAGACTTCAGCTTACCTCCCAGTAGAAAACAGAAAA NM_012345 RefSeq chr13
- 44939248 44989478 NUFIP1 26747 nuclear fragile X mental retardation protein interacting protein 1
GO:0005515|GO:0048786|GO:0006396|GO:0003723|GO:0070761|GO:0005730|GO:0000492|GO:0005634|GO:0003677|GO:0008023|GO:0046872|GO:0016363|GO:0042802|GO:0005726|GO:0043234|GO:0030515|GO:0022626|GO:0045944|GO:0005654|GO:0030674 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135306_PI430048170 0.38403761015194 1.01705723450789 0.308844760382051
0.3309422071965050.381235374173592A A A 0.33122668436744 0.3182069753820330.2991628187306
A A A LNCV6_135306_PI430048170 mRNA
GGGAACTTTTTTCGAAAGGATACATGACCACCTTCTTAAATAGTATGACTTTACATAGAC NM_031461 RefSeq chr8
+ 74984472 75034561 CRISPLD1 83690 "cysteine-rich secretory protein LCCL domain containing 1, transcript variant 1" GO:0003674|GO:0060325|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_135297_PI430048170 0.0591898171501016 1.39383735710605 3.90938046104724
3.99436007512665 4.35511660455055 P P P 3.80856009939136 3.40086757597124
3.62330949646808 P P P LNCV6_135297_PI430048170 mRNA
GTAAGATTCTGATATCTAGCCATGTAAATGAAAGATGGAGAAACACAAAGTTTTCAGCCT NM_005645 RefSeq chr1
- 109064375 109076002 TAF13 6884 "TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa"
GO:0003712|GO:0005515|GO:0010467|GO:0006352|GO:0006368|GO:0003700|GO:0005669|GO:0006367|GO:0046982|GO:0006357|GO:0006366|GO:0005730|GO:0005634|GO:0008022|GO:0003677|GO:0016032|GO:0005654 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132088_PI430048170 0.1616028907363440.5925594979966143.06298755272308
1.98017029386084 3.26392564589489 A A P 3.45039098830848 3.75384963527916
3.64970943235303 P P P LNCV6_132088_PI430048170 mRNA
AAGAAACTGGGTTTTGAACCTAGAGTTCCATGGACTCTTAGGAATTAGACTACTACTACT NM_001290043 RefSeq
chr6_GL000251v2_alt - 4237609 4251022 TAP2 6891 "transporter 2, ATP-binding cassette, sub-family B (MDR/TAP), transcript variant 1, A allele"
GO:0005515|GO:0005215|GO:0002474|GO:0042825|GO:0030176|GO:0002591|GO:0046968|GO:0046967|GO:0019885|GO:0002489|GO:0015197|GO:0002481|GO:0019060|GO:0046980|GO:0002485|GO:0042590|GO:0055085|GO:0005524|GO:0016020|GO:0008152|GO:0005789|GO:0002479|GO:0015433|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143356_PI430048170 0.21072153523261 1.01666955296527 0.30948456600019
0.2651626639102870.297266802628031A A A 0.2712232622583340.261815555185506
0.267669544530729A A A LNCV6_143356_PI430048170 mRNA

CATTTCCGTGTAGATGGAGATCACTGTGTGTAATAAACCACAAGTGCGTGTCTGAAAAAA NM_173465 RefSeq chr5 - 178237615 178590555 COL23A1 91522 "collagen, type XXIII, alpha 1" GO:0005581|GO:0022617|GO:0005886|GO:0030198|GO:0030574|GO:0005788|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134076_PI430048170 0.4062094217540290.7279251270091513.47026903820458 1.02178185628544 2.65029215996771 P A A 2.81833365252099 3.24967881831421 3.33258552012863 P P P LNCV6_134076_PI430048170 mRNA
GGGCTAGATCGATGATATGACCAGAAATCAAAAAGGGAATGCATTATTTATTGCTGTGTA NM_000849 RefSeq chr1 - 109733931 109741038 GSTM3 2947 "glutathione S-transferase mu 3 (brain), transcript variant 1" GO:0043627|GO:0006805|GO:0070458|GO:0042178|GO:0006749|GO:0005634|GO:0044281|GO:0004364|GO:0042803|GO:0005829|GO:0042802|GO:0043295|GO:0005737|GO:0008065|GO:0018916|GO:0035686|GO:0019899|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145073_PI430048170 0.00767629206034993 1.29202613378085 12.7740977308324 12.8069177670029 12.8004301119095 P P P 12.3648972592646 12.4076537061361 12.4970313577252 P P P LNCV6_145073_PI430048170 mRNA
TGTACCATCCAGAGCCCACCAGAAGCTATTGATCATTAAAATTATGAGAATTTCAACTCC NM_003876 RefSeq chr17 - 21197949 21214595 TMEM11 8834 "transmembrane protein 11, transcript variant 1" GO:0005515|GO:0003674|GO:0005887|GO:0031305|GO:0007005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145036_PI430048170 0.0767388709225832 0.3767475481977323.18666667563981 2.10409932255129 3.74186189820352 P A P 4.55461790992341 4.34696610558312 4.7676255803657 P P P LNCV6_145036_PI430048170 mRNA
GCTGCTTGGTGAACAATCATTAATTCTTCGATATTTCTGTAGCTTGAATGTAACTGCTTTNM_000341 RefSeq chr2 + 44275457 44320823 SLC3A1 6519 "solute carrier family 3 (amino acid transporter heavy chain), member 1" GO:0005515|GO:0005774|GO:0006520|GO:0046982|GO:0005886|GO:0043169|GO:0005975|GO:0005743|GO:0006865|GO:0031526|GO:0003824|GO:0055085|GO:0003333|GO:0015802|GO:0016020|GO:0015184|GO:0015171|GO:0005887|GO:0015811|GO:0015174|GO:0070062|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59_PI430053867 0.25789761437989 0.9561079081168110.5646417239391020.620801743006731 0.507595925658562 A A A 0.5565391206845120.6715855056343580.658668197223474 A A A LNCV6_59_PI430053867 mRNA
GGACTCATTCTGAACACGTGAAAGAGGCTGGAAGCTGGATTCAGTTGCTACTAGAACATA NM_033403 RefSeq chr3 - 36712421 36739861 DCLK3 85443 doublecortin-like kinase 3 GO:0005737|GO:0004674|GO:0006468|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143030_PI430048170 0.1758621096570041.09474923783256 0.569369079907506 0.4621912576900510.618607036218581 A A A 0.2990020973705050.438438533353711 0.516945872645217 A A A LNCV6_143030_PI430048170 mRNA
CTAGGAGGCTGGAAAGCCATTTATCCTAGGACATAAACTCAGATTTTGGGGGTCAAAAAA NM_173483 RefSeq chr19 + 15508524 15552317 CYP4F22 126410 "cytochrome P450, family 4, subfamily F, polypeptide 22" GO:0004497|GO:0006805|GO:0005506|GO:0005789|GO:0044281|GO:0016705|GO:0006690|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144494_PI430048170 0.4329927066572230.9204246297070714.78838955540414 4.67195747460512 4.63318928774175 P P P 4.58744350485706 4.88951637494642 4.95411160773995 P P P LNCV6_144494_PI430048170 mRNA
GAAGCTGTTCTAGAATTCAGGTTGGTATCATCATAAATGAGTTCAGAAAAAGAACTTCTG NM_024110 RefSeq chr17 + 80178507 80209331 CARD14 79092 "caspase recruitment domain family, member 14, transcript variant 1" GO:0050700|GO:0043066|GO:0005737|GO:0051092|GO:0007250|GO:0005886|GO:0001934|GO:0006915|GO:0033

209. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132592_PI430048170 0.3356224797377070.8463967658880978.67384582670299
8.80666061904293 9.19415215806725 P P P 9.05299309870017 8.91189437171867 9.4321213488212
P P P LNCV6_132592_PI430048170 mRNA
GGGATTCATTTGAAGCACTCTATTTCTGTTTTAATGGTTTTATCCAATTTTGCCTTCCCA NM_015497RefSeq chr15 -
42210451 42273584 TMEM87A 25963 "transmembrane protein 87A, transcript variant 1" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58681_PI430048170 0.00185356449246213 1.88183251038717 6.30444992432239
6.18279950923632 6.46218652879488 P P P 5.52366743620789 5.22205566731935
5.46361270328329 P P P LNCV6_58681_PI430048170 mRNA
AAGACTTTACTTTCACCATACCAGATGTAGAGGACTCAAGTCAGAGACCAGATCAGGGAC NM_007244RefSeq
chr12_KI270904v1_alt - 44554 48182 PRR4 11272 "proline rich 4 (lacrimal), transcript variant 2"
GO:0001895|GO:0007601|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133210_PI430048170 0.3582130597578340.92810671301239 10.2856961418874 10.189626833528
10.0326643317885 P P P 10.2111825881419 10.4227134124905 10.1969712666141 P P P
LNCV6_133210_PI430048170 mRNA
GCTGGCATCTTAATGTTCTGTAGGTGGAATATTTCCAATAAACACAAGGTGCCGTAATTG NM_207309RefSeq chr9
+ 137077500 137084538 UAP1L1 91373 UDP-N-acetylglucosamine pyrophosphorylase 1 like 1
GO:0008152|GO:0070569 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145126_PI430048170 0.00062826589521206 0.3512995196298973.67278229411151
3.96673914813162 4.04463265436314 P P P 5.31947174024643 5.58036425446839
5.32218000351475 P P P LNCV6_145126_PI430048170 mRNA
GGGTGTTCCTGTAATTCACAACTGTAGACACATGGGCAAAATTAGGATTTTTAAGAATAA NM_012243RefSeq chr1
+ 99969788 100026978 SLC35A3 23443 "solute carrier family 35 (UDP-N-acetylglucosamine (UDP-
GlcNAc) transporter), member A3, transcript variant 1"
GO:0005515|GO:0005794|GO:0000139|GO:0005462|GO:0008643|GO:0005351|GO:0016021|GO:0006047|GO:0015
788|GO:0055085|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144134_PI430048170 0.116121698953195 1.15847564797551 0.461793430869418
0.7402352171217710.565868305558346 A A A 0.3413630629260880.385349489255255
0.417312277724833 A A A LNCV6_144134_PI430048170 mRNA
AAATGGATGATAACCAAAAAACCTCCAACTGTCTCAGAGTCTCAGGAAACACCAGCTGGC NM_194251RefSeq chr5
- 146514853 146516113 GPR151 NA G protein-coupled receptor 151 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_53160_PI430048170 0.00134999805321684 0.4438395497266096.03452497578786
5.70238775155318 5.92036865698321 P P P 6.84500668805 7.20024064165226 7.12349876751888 P
P P LNCV6_53160_PI430048170 mRNA
TTCATGAACAACTACTTGTGGCATGCATTGGCACTCGGAATAAAGCGCACTATTGTCACT NM_012426RefSeq chr16
+ 70523787 70577668 SF3B3 23450 "splicing factor 3b, subunit 3, 130kDa"
GO:0005515|GO:0006397|GO:0008380|GO:0010467|GO:0003723|GO:0071013|GO:0006461|GO:0000398|GO:0000
375|GO:0030532|GO:0005654|GO:0005681|GO:0005689 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141909_PI430048170 0.0264048640888359 0.6065065466646635.47546642662739
5.24836228127401 5.51993299032864 P P P 5.94668224710998 5.99090964314571
6.43309206566873 P P P LNCV6_141909_PI430048170 mRNA
TGTCACATTTCATTAGCTTTGACAACCATACTGTAACATTAAACCTAGCATTCCACAAGA NM_003972RefSeq chr10
+ 91923978 92030323 BTAF1 9044 "BTAF1 RNA polymerase II, B-TFIID transcription factor-associated,
170kDa"
GO:0003700|GO:0008152|GO:0004386|GO:0005634|GO:0045892|GO:0005524|GO:0003677|GO:0035562 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116650_PI430048170 0.805112701922658 0.985649396124017 5.3630298735008

5.32179986966751 5.20461554923013 P P P 5.2019842340871 5.39832026827652
5.3491860266046 P P P LNCV6_116650_PI430048170 mRNA
ATATGACACTTGGAATGTGACAGGGCAGGATGTGATCTTTGGCTGTGAAGTGTTTGCCTA NM_030929 RefSeq
chr10 + 101061241 101065594 KAZALD1 81621 Kazal-type serine peptidase inhibitor domain 1
GO:0001503|GO:0030198|GO:0007275|GO:0005614|GO:0001558|GO:0030154|GO:0005520 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140770_PI430048170 0.373766904390052 1.22663279303745 0.377763354867906
0.300639292165344 1.01633026610126 A A A 0.292099517059779 0.297601731324093
0.3321698572227 A A A LNCV6_140770_PI430048170 mRNA
GTCCTTAACGTCAGACTTTCTCCAAGACAAAAACTCTAAGAACTTATTTCCATTCTTACA NM_001243722 RefSeq
chr16 + 32253323 32255928 TP53TG3D NA "TP53 target 3D, transcript variant 1" NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_138336_PI430048170 0.7721274420608 0.958749926466361 7.00999456672916
7.4551153902683 7.49582172329316 P P P 7.30505182939695 7.1999184979896
7.64786539373487 P P P LNCV6_138336_PI430048170 mRNA
CTTAGAATATATTCTGTGCGGATGCTTATATTTTGTTAACTTCACGACTTATGGCATGTC NM_020448 RefSeq chr1
+ 24415754 24472983 NIPAL3 57185 NIPA-like domain containing 3
GO:0015693|GO:0015095|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_145656_PI430048170 0.00653126152759656 0.571228927091736 7.17876277003878
7.16328755227014 7.4745767851441 P P P 8.07802241417428 7.87914710793217
8.27739155871973 P P P LNCV6_145656_PI430048170 mRNA
CGTGACCTGATAATGAATCTATTCATCCTGAGTAAGCTATACTTCTGTGCTTTATATTGA NM_001168479 RefSeq
chrX + 102599167 102604157 ARMCX5 64860 "armadillo repeat containing, X-linked 5, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128323_PI430048170 0.0151255768654948 0.460397901014056 3.21084979027043
2.72388688921792 3.42076733330088 P A P 4.48920048184882 4.10280438086933
4.17636094078202 P P P LNCV6_128323_PI430048170 mRNA
ATGATGAACTCTAGCACTGGTGTATATGAGAAGGAAGGCGAAAGCATGACAGGAAACCTG NM_020121 RefSeq
chr13 - 95801580 96053482 UGGT2 55757 UDP-glucose glycoprotein glucosyltransferase 2
GO:0005793|GO:0006457|GO:0005788|GO:0003980|GO:0044267|GO:0043687|GO:0018279 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_112199_PI430048170 0.00268774441033189 0.468599199181416 11.5504869967373
11.1323240678681 11.2662026697391 P P P 12.4267117706234 12.5723267556906
12.2441160302725 P P P LNCV6_112199_PI430048170 mRNA
GCACCGCCCAACCCCCACCTCCCGGTGTATGCAGTGGTGATGCCTAAAGGAATGTCACGC NM_007327 RefSeq
chr9 + 137139156 137168762 GRIN1 2902 "glutamate receptor, ionotropic, N-methyl D-aspartate 1,
transcript variant GluN1-1a"
GO:0005515|GO:0005516|GO:0030054|GO:0017146|GO:0018964|GO:0045202|GO:0043524|GO:0034220|GO:0007
411|GO:0060992|GO:0045211|GO:0048169|GO:0042165|GO:0001661|GO:0051963|GO:0005262|GO:2000463|GO:0
046982|GO:0009986|GO:0007616|GO:0071287|GO:0060134|GO:0005509|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141965_PI430048170 0.375989524846384 1.06880007356462 8.77576532305331
8.80564107982628 8.9446242718554 P P P 8.75690580711606 8.59512343296747
8.87784075353244 P P P LNCV6_141965_PI430048170 mRNA
GTACAGATAATTCAAAACTGCTGTTGGTTTTAATTTTGTAACCTGTGGCCTGATCTGTAA NM_001010983 RefSeq
chr3 - 52694483 52706083 GLT8D1 55830 "glycosyltransferase 8 domain containing 1, transcript
variant 3" GO:0016020|GO:0016757|GO:0008152|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_135638_PI430048170 0.768069840932377 0.968992149062713 4.5493502477189 4.33214017095892 4.00044536334445 P P P 4.51443717738449 4.29738965732466 4.24413584036616 P P P LNCV6_135638_PI430048170 mRNA AAACCCTAAATCACTCCTCTCTCCACTTGACATATCAAATAAATGTGTTCAGAAGTCAAA NM_001039888 RefSeq chr1 - 145959440 145964582 ANKRD34A 284615 ankyrin repeat domain 34A GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61444_PI430048170 0.441289422651524 1.53714214417751 1.17286723441546 0.260194241642176 1.97794020610992 A A A 0.787700193619695 0.253556886937008 0.918507726135288 A A A LNCV6_61444_PI430048170 mRNA AGGATAGACACCAAGGCAGGACCCCCAGAGATGCTGAAGCCTCTTTGGAAAGCAGCAGTG NM_138790 RefSeq chr14 + 104924815 104933236 PLD4 122618 "phospholipase D family, member 4" GO:0006909|GO:0043647|GO:0004630|GO:0005634|GO:0044281|GO:0032588|GO:0045335|GO:0016042|GO:0002244|GO:0004435|GO:0070290|GO:0005789|GO:0016021|GO:0006644|GO:0006655|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138376_PI430048170 0.186536585464566 1.43138187600274 3.24916961991504 4.09835540698831 3.5749781644636 P P P 3.29530905957102 3.06008797691614 3.13382247305534 P P P LNCV6_138376_PI430048170 mRNA GATAACAATTGTGGTTTTATTGTGTCCAACCAATGCATCAATAAATGAACTTGAAGCCCA NM_001242704 RefSeq chr17 - 42025575 42038026 ZNF385C NA zinc finger protein 385C NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134633_PI430048170 0.105777608659887 1.09921801193587 6.75754964433926 6.79109239126004 6.73655806543219 P P P 6.52915102035789 6.6341282670339 6.70746741067875 P P P LNCV6_134633_PI430048170 mRNA GCTCCACGACAAAAGGACAAGATTTGACTTAAATTAAGTTTTTCCCTTGAGGATATTTTC NM_001080436 RefSeq chr19 + 34481974 34501180 WTIP NA Wilms tumor 1 interacting protein NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_36513_PI430048170 0.0387157695801689 0.782503611614768 13.6139095306175 13.4574673680657 13.6921452415932 P P P 13.7742654431356 14.0805441378607 13.9636031151919 P P P LNCV6_36513_PI430048170 mRNA GAGACCACCTTCAACTCCATCATGAAGTGTGACGTGGACATCCGCAAAGACCTGTACGCC NM_001199954 RefSeq chr17 - 81509970 81512866 ACTG1 71 "actin gamma 1, transcript variant 1" GO:0005515|GO:0005886|GO:0006928|GO:0072562|GO:0005634|GO:0030016|GO:0005615|GO:0005829|GO:0042802|GO:0007411|GO:0001895|GO:0061024|GO:0005856|GO:0031625|GO:0070062|GO:0048010|GO:0048013|GO:0034329|GO:0045214|GO:0005524|GO:0045216|GO:0070527|GO:0031941|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127316_PI430048170 0.0312355224529439 0.700420456178577 10.9170223041296 10.8901569703698 10.9958920801273 P P P 11.6491097446243 11.3197421091496 11.3542355133434 P P P LNCV6_127316_PI430048170 mRNA GGGCTTCAAGTTCATTTATTGATGCATTGGTTGGACACAATAAAACCACAATTGTTATCA NM_001144927 RefSeq chr17 + 42020068 42025638 NKIRAS2 28511 "NFKB inhibitor interacting Ras-like 2, transcript variant 3" GO:0006184|GO:0005737|GO:0016020|GO:0007264|GO:0007249|GO:0003924|GO:0005575|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140319_PI430048170 0.414296663706953 1.33221779741225 0.281362249703099 0.559295851155619 1.3811560811263 A A A 0.513452424808105 0.406823076512134 0.287289873189206 A A A LNCV6_140319_PI430048170 mRNA AATCTCTAGCTATCTGGTAAGTGGGTATGAAAGTGGTAGATGGGAGAGGTCAGCTGATAC NM_001005161 RefSeq chr11 - 4367262 4368386 OR52B4 NA "olfactory receptor, family 52, subfamily B, member 4 (gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67607_PI430048170 0.0547690639111353 0.734358275036118 4.04698529036952

4.02104377339187 3.64073361008622 P P P 4.23177043649084 4.4607727015184
4.37801584285714 P P P LNCV6_67607_PI430048170 mRNA
TTCCCAGCTGACAGCCTCTCTGAGGACAATGACATATGAATGAGGATCAAAACGAGCTTT NM_015506 RefSeq chr1
+ 45500183 45511067 MMACHC 25974 "methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria"
GO:0009236|GO:0005739|GO:0005515|GO:0009235|GO:0031419|GO:0006766|GO:0006767|GO:0044281|GO:0005
829. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134586_PI430048170 0.3205570232116060.8211617066815415.14806509483985 4.8278096267493
5.33227613448249 P P P 5.03652479963896 5.40290024056818 5.69204781955422 P P P
LNCV6_134586_PI430048170 mRNA
TCAGGTGAGTAGTTGCCGCGTAATATCATTGGAGTACATTCTTTATACTGTTTGTGAAAT NM_020738 RefSeq chr2
- 8728856 8837625 KIDINS220 57498 "kinase D-interacting substrate, 220kDa"
GO:0048011|GO:0005770|GO:0030165|GO:0001701|GO:0005829|GO:0043234|GO:0048813|GO:0000186|GO:0016
020|GO:0010976|GO:0016482|GO:0005654|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128578_PI430048170 0.0903943913701679 0.6283410352046756.24884080461231
5.56220965151704 5.55360098366805 P P P 6.4605085927956 6.52583799748121 6.5040530008673
P P P LNCV6_128578_PI430048170 mRNA
AGCCCACCTCAGGCCTCCTGCAAAAATACATAGAATAAACAACAACAGTTACTAAATGAA NM_014834 RefSeq
chr17_KI270908v1_alt + 1032390 1075355 LRRC37A NA leucine rich repeat containing 37A NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135553_PI430048170 0.0338346106214083 3.37256172522814 5.2576359397611
5.67896805130426 5.23170676630451 P P P 4.22971865144277 3.57018339190154 2.8148120398852
P P P LNCV6_135553_PI430048170 mRNA
GCACGCAGTGATGGGCAAACCAATTGCTGCCCATCTGGCCTGTGTGCCCATCTTTTTCTG NM_152891 RefSeq chr16
- 2783952 2786707 PRSS33 260429 "protease, serine, 33" GO:0004252|GO:0006508|GO:0005615 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131322_PI430048170 0.8745007607166581.02114804671511 0.988233495710902
0.6450281822457340.551650539848941 A A A 0.5847455992625080.507569371940583
0.991341704858554 A A A LNCV6_131322_PI430048170 mRNA
AGCTCATTTTTCTATTAGTAACTCTGCTGAGGATCCATTTATTGCAATTCATGCTGAATCNM_020978 RefSeq chr1 +
103554643 103579534 AMY2B NA "amylase, alpha 2B (pancreatic)" NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_64477_PI430048170 0.2852027566200950.8824635158259935.50387109805235 5.25783529164184
5.11932961394053 P P P 5.28868031474024 5.60504915171591 5.53622379558662 P P P
LNCV6_64477_PI430048170 mRNA
AGCAGATCATTCCAAAGAACCTACTGGACTCCAAGTCCCTGAAACTCATCATCAGCATGA NM_001130065 RefSeq
chr19 + 17075780 17213295 MYO9B 4650 "myosin IXB, transcript variant 2"
GO:0005515|GO:0005516|GO:0048471|GO:0043008|GO:0006200|GO:0007264|GO:0030010|GO:0007266|GO:0016
459|GO:0015629|GO:0032433|GO:0030898|GO:0042803|GO:0005829|GO:0005737|GO:0000146|GO:0051015|GO:0
032011|GO:0005938|GO:0016887|GO:0030048|GO:0072673|GO:0051056|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93696_PI430048170 0.9524310204745810.99920570886991 8.59122822995602 8.64926504087182
9.18028260846892 P P P 8.62402404586408 8.77454829247993 9.06593961973 P P P
LNCV6_93696_PI430048170 mRNA
AGAAGTTGGAGATGGCACAAACTTTGTTCTGGTATTTGCTGGAGCTCTCCTGGAATTAGC NM_001282907 RefSeq
chr21 - 29056321 29073797 CCT8 10694 "chaperonin containing TCP1, subunit 8 (theta), transcript variant 2"
GO:0005515|GO:0005813|GO:0016235|GO:0042623|GO:0005832|GO:0005874|GO:0007339|GO:0005524|GO:0044
297|GO:0005829|GO:0046931|GO:0005737|GO:0006457|GO:0051084|GO:0002199|GO:0051082|GO:0045111|GO:0

044267|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126659_PI430048170 0.33884949343383 1.04094814098651 0.301636691548199
0.2689347684599940.418601419484671A A A 0.2858991306199550.250141590721792
0.283488582775526A A A LNCV6_126659_PI430048170 mRNA
GTTCATACTTTCTTGTGTACAGATGGTGCTAGTCAAGATGAAAACAACAAAACAAACAAG NM_018012RefSeq
chr1_KI270759v1_alt + 61135 401151 KIF26B 55083 kinesin family member 26B
GO:0008017|GO:0072092|GO:0005871|GO:0005737|GO:0022409|GO:0008152|GO:0005874|GO:0030010|GO:0003
777|GO:0016887|GO:0005524|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130672_PI430048170 0.4565034178911940.7682733913389880.45273616571808
0.3902865113475630.324234082140313A A A 1.34888175029706 0.351125371014736
0.372216637332989A A A LNCV6_130672_PI430048170 mRNA
GTCAGGGTAAAACCTGGAGCCACATGTTATTCAAGTTATTTTTGTTATCTAATGATTGAC NM_001145065 RefSeq
chr4 + 90127532 91602219 CCSER1 401145 "coiled-coil serine-rich protein 1, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144355_PI430048170 0.2245212000953750.7019549742221781.06255636655418
1.28767845004086 2.15656920325826 A A A 2.15362571747049 1.75048938382747
2.31926983817696 A A A LNCV6_144355_PI430048170 mRNA
GTGCACACATGGAGAGAACATGAGTCTCTCTTAATTTTTATCTGGTTGCTAAAGAATTAT NM_016184RefSeq chr12
+ 8123631 8138607 CLEC4A 50856 "C-type lectin domain family 4, member A, transcript variant 1"
GO:0005887|GO:0045087|GO:0030246|GO:0007155|GO:0007166|GO:0004888 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138317_PI430048170 0.3514514667170350.8208465231421294.2756507512478
4.37858352501288 5.02401265712499 P P P 4.75985126395594 4.64981000860308 5.1850295526516
P P P LNCV6_138317_PI430048170 mRNA
GAATCTGATGTGTCTCAAGCTGAGAAAGATTTGCTACATTCTGAAGGTAGTGAAAACGAA NM_174907RefSeq chr3
+ 72996967 73065860 PPP4R2 151987 "protein phosphatase 4, regulatory subunit 2"
GO:0005515|GO:0006397|GO:0008380|GO:0005813|GO:0005634|GO:0010569|GO:0030289|GO:0050790|GO:0005
737|GO:0030362|GO:0002244|GO:0005654|GO:0030674|GO:0006464 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130350_PI430048170 0.0350490258809599 0.6026177853755818.42195890857149
8.18204940624667 7.81534614713887 P P P 8.89469278494199 9.12820480071598
8.60483333984246 P P P LNCV6_130350_PI430048170 mRNA
TGCCCTGCAAAGACCCCCGCCATGTTGAGTCACCAGCAGTAAACTCTAGGCCTGCCCGAA NM_001135914 RefSeq
chr7 - 128876864 128910719 KCP375616 "kielin/chordin-like protein, transcript variant 1" GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76252_PI430048170 0.42800662318446 1.16302063335356 1.81376511843609 1.44844719712435
2.10763553859157 A A A 1.68411509322648 1.72946713791673 1.34803464426606 A A A
LNCV6_76252_PI430048170 mRNA
ATGTGACCAGTTTTGGGCCCGTGTCAGATGTGGAGATGGAGTATACGATGGATGTTTTTT NM_000811RefSeq chr5
+ 161685651 161702592 GABRA6 2559 "gamma-aminobutyric acid (GABA) A receptor, alpha 6"
GO:0005230|GO:0030054|GO:0005886|GO:0004890|GO:0034707|GO:0007268|GO:0007214|GO:0055085|GO:0005
254|GO:0007165|GO:0034220|GO:0005887|GO:0045211|GO:0006810|GO:0008503 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_81223_PI430048170 0.7071615328097261.04407051088455 5.53718697028543 5.37889201455767
5.27470378388379 P P P 4.99542346309324 5.57306928691534 5.38902283062586 P P P
LNCV6_81223_PI430048170 mRNA
TTTTGCAAATTGCTTTCCAAACTCACTTGAATGATGACATTGCTGTGGACCTGGGTTCTG NM_153045RefSeq chr9
+ 114611425 114646423 C9orf91 203197 chromosome 9 open reading frame 91
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_136078_PI430048170 0.2503909830982515.48213781043463 0.29055848294647
4.18554811318923 3.66586040375697 A P P 0.30018437995446 0.268686618580196
1.77459205202406 A A A LNCV6_136078_PI430048170 mRNA
TTTCTCCTGAATTTTTAATGCAGAAGTTTGAATGAAGCAAGGGAAGGCATGTAGGGACAG NM_014391 RefSeq chr10
- 90912099 90921275 ANKRD1 27063 ankyrin repeat domain 1 (cardiac muscle)
GO:0005515|GO:0042826|GO:0050714|GO:0071560|GO:0005634|GO:0044281|GO:0035914|GO:0030017|GO:0005
829|GO:0002039|GO:0005737|GO:0045944|GO:0071356|GO:0001085|GO:0055008|GO:0044255|GO:0005667|GO:0
001105|GO:0043065|GO:0003714|GO:0045214|GO:0005730|GO:0071456|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_102506_PI430048170 0.0732012041831965 1.1958042645343 8.23073171760897
8.35522708539922 8.16324343371748 P P P 8.14886311334646 7.96152821808957
7.85611693215297 P P P LNCV6_102506_PI430048170 mRNA
GCTAGCTCCTCCCTTTCTTTCTTTTTCCACCTGAGACTTGTTTATAAAAAACAAAACAAT NM_022370 RefSeq chr11 +
124865408 124881474 ROBO3 64221 "roundabout, axon guidance receptor, homolog 3 (Drosophila)"
GO:0030424|GO:0016199|GO:0007411|GO:0071679|GO:0016021|GO:0001764 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93518_PI430048170 0.1105078950163050.64982534626136 4.04972601497763 3.81021771869747
3.33426203276349 P P P 4.62546591416166 3.91938457995048 4.5096681868468 P P P
LNCV6_93518_PI430048170 mRNA
CAGAGCTACAGGATTTAGATGAAGAATTTCGTGAAAACAACATAGAAATTGTGACCAGAT NM_014846 RefSeq chr8
- 125024260 125091819 KIAA0196 9897 KIAA0196
GO:0005515|GO:0005783|GO:0016197|GO:0071203|GO:0005769|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143177_PI430048170 0.1712887274238120.8116074881896186.00090144028825
5.86599401480291 6.17305109151398 P P P 6.08582416921444 6.25720647289638
6.57377378063772 P P P LNCV6_143177_PI430048170 mRNA
GTTCTTTCTGCTTGCTGCTAAGAGTTTGCTAAAGTGTCATGAATTATTCTGGTTATTACT NM_000286 RefSeq chr17 -
35574794 35578637 PEX12 5193 peroxisomal biogenesis factor 12
GO:0005515|GO:0006625|GO:0007031|GO:0008270|GO:0016558|GO:0008022|GO:0005779|GO:0005778|GO:0005
777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124642_PI430048170 0.0801909220500906 1.11160083579826 12.5914207403609
12.6586293068361 12.7640464690612 P P P 12.498650909576 12.503235382399
12.5587830556001 P P P LNCV6_124642_PI430048170 mRNA
TGTTGTCCTTGGAGCTGTGGTCACTGGAGCTGTGGTCGCTGCTGTGATGTGGAGGAAGAA NM_001098479 RefSeq
chr6_GL000256v2_alt + 1029598 1033525 HLA-F 3134 "major histocompatibility complex, class I,
F, transcript variant 1"
GO:0002474|GO:0012507|GO:0002480|GO:0005886|GO:0009986|GO:0005783|GO:0042612|GO:0019221|GO:0042
590|GO:0005102|GO:0060337|GO:0000139|GO:0016020|GO:0031901|GO:0001916|GO:0050776|GO:0042605|GO:0
030670|GO:0071556|GO:0002479|GO:0046978|GO:0046979|GO:0060333 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_133545_PI430048170 0.6560970898862821.04799796493339 6.85236887157057
6.83907851808905 7.13800004781176 P P P 6.84330664740858 6.71246596690093
7.06829407449278 P P P LNCV6_133545_PI430048170 mRNA
CGCGTGCTTTCTCAGCAGCATTTTTCCTTCAAAATCATCTTTTTAATCAACAGTCATTAA NM_000027 RefSeq chr4 -
177430774 177442503 AGA 175 "aspartylglucosaminidase, transcript variant 1"
GO:0051604|GO:0005783|GO:0006517|GO:0006508|GO:0003948|GO:0008233|GO:0043621|GO:0005764|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136780_PI430048170 0.2765454240103861.31258774483803 5.47640118477413
5.07609064769702 5.65319987414309 P P P 5.22490515845779 5.28655418855577

4.42817422266657 P P P LNCV6_136780_PI430048170 mRNA
ATCAAGTGTCTGGAGTCACAGATCAACTACTGCTCGGTGCTCGTGTCCTCCGTGGCTGAC NM_014555 RefSeq chr11
- 2404515 2423045 TRPM5 29850 "transient receptor potential cation channel, subfamily M, member
5"
GO:0005244|GO:0005886|GO:0005272|GO:0005267|GO:0055085|GO:0034220|GO:0050909|GO:0070588|GO:0034
765|GO:0035725|GO:0005227|GO:0016021|GO:0005216|GO:0071805 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_27500_PI430048170 0.0859858984547691 1.48673340970792 3.60571358976929
3.61929462022789 3.19702574990382 P P P 3.16439402026045 3.01023529463054
2.48540011988984 P P P LNCV6_27500_PI430048170 mRNA
AAGCTGTGTGTAAACAAGGGTGTAATTTGCTCCACGGGGGATGCACCGTGCCTGGGGAGT NM_002226 RefSeq chr14
- 105140980 105168824 JAG2 3714 "jagged 2, transcript variant 1"
GO:0030334|GO:0005515|GO:0007220|GO:0005886|GO:0042492|GO:0005509|GO:0005112|GO:0007283|GO:0030
155|GO:0001701|GO:0030154|GO:0001501|GO:0003016|GO:0007049|GO:0009912|GO:0030217|GO:0016331|GO:0
007219|GO:0005887|GO:0045061|GO:0042127|GO:0042475|GO:0008083 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_136710_PI430048170 0.5586976677537460.9141797605974720.293953918996431
0.3098287749476230.413358487969997 A A A 0.7706875528113120.293573983442322
0.289321159943211 A A A LNCV6_136710_PI430048170 mRNA
TACCATCTACTTCTGTTGTTTTCCCAGGCTTCCATAAACAATGGAGATACATGCAAAAAA NM_001127510 RefSeq
chr5 + 112737858 112846239 APC 324 "adenomatous polyposis coli, transcript variant 2"
GO:0005515|GO:0008017|GO:0009798|GO:0060041|GO:0051171|GO:0008013|GO:0030877|GO:0048538|GO:0031
122|GO:0035371|GO:0007409|GO:0070830|GO:0051010|GO:0031274|GO:0051781|GO:0001942|GO:0005813|GO:0
033077|GO:0045296|GO:0030335|GO:0045295|GO:0019901|GO:0000281|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135886_PI430048170 0.4901701464378430.8429032946673231.30635761896037
2.50611883045201 2.36717934595297 A A A 2.18275140231374 2.63887920398632
2.32941153235741 A A A LNCV6_135886_PI430048170 mRNA
ATGGGAAACACCTGTGCCCTCCAGGAAAACCAAGTACCTCTGAGAAGATTAACAAGACAT NM_173358 RefSeq chrX
- 52644060 52654900 SSX7 280658 "synovial sarcoma, X breakpoint 7"
GO:0006355|GO:0005634|GO:0003676|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140589_PI430048170 0.1021715716245521.73569572247956 4.70562805639016
4.47602615489034 4.73320102352081 P P P 3.22966331107146 3.80806990939922 4.306803829307
P P P LNCV6_140589_PI430048170 mRNA
GTGTCGCCTCCAATTCTGTTAAACCTTTTAAATAAGTGCCAAGTTATTAATTGAAGACAC NM_003030 RefSeq chr3
- 158096010 158106163 SHOX2 6474 "short stature homeobox 2, transcript variant 1"
GO:0031965|GO:0060415|GO:0003170|GO:0002053|GO:0032330|GO:0000122|GO:0001649|GO:0003209|GO:0007
399|GO:0043565|GO:0005739|GO:0007507|GO:0045880|GO:0001501|GO:0048743|GO:0048557|GO:0002063|GO:0
060351|GO:0060272|GO:0045944|GO:2000172|GO:0005654|GO:0050772|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139188_PI430048170 0.0642046397116962 1.80342950384846 8.5430495476323
8.66790595903158 8.24063982135533 P P P 8.1211622194944 7.20879246644287
7.44059125771422 P P P LNCV6_139188_PI430048170 mRNA
GCTGCGGTGGGGAGCTATAAAAATGACAATTAAAAGAGACACTAGTCTTTTATTTCTAAA NM_000050 RefSeq chr9
+ 130444706 130501274 ASS1 445 "argininosuccinate synthase 1, transcript variant 1"
GO:0005515|GO:0006531|GO:0005783|GO:0005741|GO:0005634|GO:0044281|GO:0005764|GO:0010043|GO:0045
429|GO:0005829|GO:0071418|GO:0070852|GO:0034641|GO:0005737|GO:0071230|GO:0071377|GO:0071356|GO:0
006526|GO:0043204|GO:0032355|GO:0070062|GO:0071499|GO:0060416|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_134328_PI430048170 0.1639345911649211.11890772510622 10.7359567638804
10.6186392364196 10.7091079434484 P P P 10.6660313346624 10.5123306041507
10.3882094524453 P P P LNCV6_134328_PI430048170 mRNA
GGAGCTGGTGGTTTCATGAGTTAATGATACATCTTGCAAGGTGTACACATAGAGAAAAAA NM_001302643 RefSeq
chr20 + 62952646 62968597 SLC17A9 63910 "solute carrier family 17 (vesicular nucleotide
transporter), member 9, transcript variant 2" GO:0005215|GO:0016021|GO:0006887|GO:0055085 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140668_PI430048170 0.2312394654368331.29466191373709 6.3646469287632
6.46103886348986 6.35567578007104 P P P 5.78294768368723 6.4663287299333
5.68562698873012 P P P LNCV6_140668_PI430048170 mRNA
GGGGTGGTGGACTGTTTTTGCCTACTTTTTGTTTTTGAAAAACATGCACTCCCCACTCTG NM_198540RefSeq chr19
- 41425358 41428730 B3GNT8374907 "UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8"
GO:0006493|GO:0000139|GO:0030311|GO:0016262|GO:0016266|GO:0016021|GO:0044267|GO:0008378|GO:0070
062|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116984_PI430048170 0.6280268165667060.91568909808805 4.56308662449839
3.57583805607901 3.72704913033868 P P P 4.36764643754755 4.15643625942279
3.88970878064023 P P P LNCV6_116984_PI430048170 mRNA
CTTTTCTTTAATTTCTGCCCAGCTTTGAGAAAGGGAACAACCTATGAAGAGGAAATTAAT NM_001105659 RefSeq
chr1 - 74026017 74198187 LRRIQ3 127255 leucine-rich repeats and IQ motif containing 3 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128351_PI430048170 0.0315933058270844 0.9636108423065410.351266894000378
0.3759346673663440.332914273200169A A A 0.4207753938188150.413462659757982
0.386406677764513A A A LNCV6_128351_PI430048170 mRNA
CCTGAGGATCTAACTTGCAGTTGGACACTATGTTACATACTCTAATATAGTAGTGAAAGT NM_001207006 RefSeq
chr4 - 122612627 122621057 IL21 59067 "interleukin 21, transcript variant 2"
GO:0008284|GO:0032740|GO:0005134|GO:0032733|GO:0030890|GO:0042517|GO:0002729|GO:0042511|GO:0032
825|GO:0005125|GO:0005615|GO:0005126|GO:0007165|GO:0006955|GO:0045078|GO:0034105|GO:0050729|GO:0
045954|GO:0042102|GO:0048469 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138935_PI430048170 0.00130550289927299 2.0845804245521 8.59615558337654
8.2901113362378 8.41107394693589 P P P 7.28598318737208 7.47532636603846
7.36705954898676 P P P LNCV6_138935_PI430048170 mRNA
GGAGTGGCTGTTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTTA NM_206967RefSeq chr16
- 85707517 85751083 C16orf74 404550 chromosome 16 open reading frame 74 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144392_PI430048170 0.3207217511237830.8375548159749946.40448689571235
5.90236365730123 5.87600775931138 P P P 6.35974256275864 6.56579108081646
6.04038295657563 P P P LNCV6_144392_PI430048170 mRNA
CGCTCCCTCTGTGGCTATGGCTATGGATGCGGCTCTGGCTCTGGCTACTATTATTGAGGA NM_181602RefSeq chr21
- 30613685 30613904 KRTAP6-1 NA keratin associated protein 6-1 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_142427_PI430048170 0.5016345548896211.09340812634197 0.777769812621249
0.4002072740811350.686444050869996A A A 0.2794671354467960.427376431674078
0.755545506000459A A A LNCV6_142427_PI430048170 mRNA
CCTGGAAGTTTGACTTTGAGTGTGGGAGAAGTCCTAATAAACCATTTTGGAAATTAAAAA NM_001159677 RefSeq
chr6 - 85607783 85643325 SYNCRIP 10492 "synaptotagmin binding, cytoplasmic RNA interacting
protein, transcript variant 6"
GO:0017148|GO:0005515|GO:0008380|GO:0006396|GO:0070934|GO:0005783|GO:0003723|GO:0005634|GO:0071
013|GO:0001649|GO:0071346|GO:0000166|GO:0016020|GO:0000398|GO:0030529|GO:0008143|GO:0016032|GO:0
005654|GO:0071204|GO:0070937 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_141221_PI430048170 0.6236272358880990.9920352511088050.399607528517061
0.4016379294088250.365439469540007A A A 0.4309303711864650.369593042541019
0.400405676476621A A A LNCV6_141221_PI430048170 mRNA
CCAACAGACCAACTCAGATTGGATTATGACTTCATGAAATTAAAAAATGGAGGAAGAGTT NM_173550RefSeq chr9
+ 15553098 15971899 CCDC171 203238 coiled-coil domain containing 171 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_138216_PI430048170 0.65557438759388 1.05049382634424 6.03895691210839
6.04468980510712 6.08536601583036 P P P 5.729180492967 6.32108552538371
5.83464991411908 P P P LNCV6_138216_PI430048170 mRNA
TGTGTGCTGTCTAATGATGGGATGACCACACTTTTCCATGTTCTAAAAGTGCTCCTCTCC NM_004327RefSeq chr22
+ 23180364 23318037 BCR613 "breakpoint cluster region, transcript variant 1"
GO:0005515|GO:0043314|GO:0030036|GO:0030054|GO:0007264|GO:0032855|GO:0005829|GO:0050766|GO:0046
777|GO:0016301|GO:0045211|GO:0051726|GO:0050885|GO:0032496|GO:0005089|GO:0030675|GO:0070062|GO:0
051056|GO:0030336|GO:0042472|GO:0014069|GO:0018108|GO:0005524|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145557_PI430048170 0.8517943128510110.9675444908446480.535931509757512
0.3796011863155880.497873759895912A A A 0.4205715095009970.797489230761282
0.294081218523472A A A LNCV6_145557_PI430048170 mRNA
TCAACTTAGTAGTGTACAGCAGTGAAGAAAAACATTATTACATGCCCAGTGTGTCAAACA NM_001004686 RefSeq
chr1 + 248038171 248039305 OR2L2 NA "olfactory receptor, family 2, subfamily L, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125436_PI430048170 0.0110612222995421 0.5445633074371666.67800486425907
6.77949191989654 7.14313691858845 P P P 7.72716840123589 7.63898296035096
7.89554195990567 P P P LNCV6_125436_PI430048170 mRNA
TTGAGTATTTTAAATCGGTTTGTGTAGTTAGGTTTCCCAACATCTGTGGTTACCTAATGTNM_002865RefSeq chr8 +
60516909 60623644 RAB2A 5862 "RAB2A, member RAS oncogene family, transcript variant 1"
GO:0005515|GO:0042470|GO:0003924|GO:0005634|GO:0005525|GO:0005765|GO:0006886|GO:0006184|GO:0006
888|GO:0000139|GO:0033116|GO:0005789|GO:0007030|GO:0032482|GO:0000278|GO:0019003|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141940_PI430048170 0.00489230963509992 0.4120468490354097.35077303006942
7.22546614268162 7.30864907764796 P P P 8.38324707863971 8.52788506031873 8.7849214477692
P P P LNCV6_141940_PI430048170 mRNA
GCTCTGTCTTGGCATGCTTCTAGACTGTAAGATTTGGGTTTTGTTTTGTATTTTATGTTT NM_014631RefSeq chr10 -
103594026 103855406 SH3PXD2A 9644 SH3 and PX domains 2A
GO:0005515|GO:0005737|GO:0030054|GO:0006801|GO:0002102|GO:0042995|GO:0035091 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135622_PI430048170 0.00502928092307529 0.36359155517251210.0155571311049
9.68240553848125 9.95313729098035 P P P 10.9954034874917 11.3769050552844
11.6129370528499 P P P LNCV6_135622_PI430048170 mRNA
GCTCTTGTTGATCTTGTATTCAGTCAGGTTAAAACAACGGACAATAAAAGAATGAACACA NM_001677RefSeq chr1
+ 169106708 169132722 ATP1B1 481 "ATPase, Na+/K+ transporting, beta 1 polypeptide"
GO:0010468|GO:0005515|GO:0005886|GO:0006883|GO:0050900|GO:0060048|GO:0016323|GO:0016324|GO:0086
009|GO:0034220|GO:0014704|GO:0051117|GO:0007155|GO:0070062|GO:0005391|GO:0001666|GO:0030007|GO:0
006874|GO:0010882|GO:0050821|GO:0010107|GO:0032781|GO:0086064|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131390_PI430048170 0.0829208933158759 0.9362462149556320.286928300677219
0.29583054196022 0.313042466799014A A A 0.4509423553085850.381090815709382
0.347059162316165A A A LNCV6_131390_PI430048170 mRNA
TACAGCAATGTTTCTGTATCTTATTTTTGCTGCTTCTGAATAAAACTCCACTTTTGTCGC NM_030976RefSeq chr17 -

41139432 41140487 KRTAP4-6 81871 keratin associated protein 4-6 GO:0045095 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138455_PI430048170 0.0351200509818169 1.35071814444474 4.14565232328346
4.17240443867551 3.9234117961735 P P P 3.78648432216466 3.71149710923626
3.43125354772789 P P P LNCV6_138455_PI430048170 mRNA
GAATTTCATGCTTTCCTAAAGTCTCTGCTGCTAAGGCTCTATTTCCTCCCCCAGTTAAAC NM_000697 RefSeq chr17
+ 6996064 7010736 ALOX12 2239 arachidonate 12-lipoxygenase
GO:0005515|GO:0019369|GO:0008284|GO:0030307|GO:0061436|GO:0006928|GO:0044281|GO:0005829|GO:2001
306|GO:0071396|GO:0005737|GO:0051901|GO:0045909|GO:2001300|GO:2001303|GO:0070062|GO:0042554|GO:0
019395|GO:0043066|GO:0030335|GO:0005506|GO:0072593|GO:0007568|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_61708_PI430048170 0.00188500800420758 1.63494756902151 11.1546214124384
11.3134412488646 11.30035637395 P P P 10.4574699759083 10.4917704395585
10.6860823067821 P P P LNCV6_61708_PI430048170 mRNA
CTGCTGCTAAATCAAGAACTGTTGCAGCATCTCCTTTCAATAAATTAAATGGTTGAGAAC NM_016454 RefSeq chr15
+ 34224996 34230165 EMC4 51234 "ER membrane protein complex subunit 4, transcript variant 1"
GO:0072546|GO:0006915|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141568_PI430048170 0.283964258463075 0.731291272811809 0.358541743251408
0.537040890880168 0.402328801482221 A A A 1.15313365112989 1.07538236400077
0.279074438021669 A A A LNCV6_141568_PI430048170 mRNA
TAGGTGAATTGGTGGCATTCACAAAGCTAATAGGGACGTTTATATCAAGAAACATTTCTG NM_005222 RefSeq chr7
+ 97005977 97011040 DLX6 1750 distal-less homeobox 6
GO:0050679|GO:0006355|GO:0003700|GO:0042472|GO:0005634|GO:0030326|GO:0007399|GO:0043565|GO:0001
501|GO:0048646|GO:0030855|GO:0060021|GO:0060322 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135666_PI430048170 0.00815120352418005 1.75039014473734 6.88882964568514
7.08512505516383 6.96253652999979 P P P 6.37478012851498 6.13451842386104
5.98383526237674 P P P LNCV6_135666_PI430048170 mRNA
TGGCCAAGAGTATTTTCAAAAAAGTCTAAAGGTGTAGTTTCCACTGTAACTGTTGAGTAC NM_020422 RefSeq chr16
+ 21158376 21180616 TMEM159 57146 "transmembrane protein 159, transcript variant 2"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129778_PI430048170 0.691636867761634 1.01545485908812 0.533410848036463
0.403923195129408 0.532002366808109 A A A 0.432064658950103 0.510708961445364
0.46288749605951 A A A LNCV6_129778_PI430048170 mRNA
CTTGCAAGAATCAGTGCAAAGATTTGCTTTAATTGTTAAGATATGATGTCCCTATGGAAG NM_006273 RefSeq chr17
+ 34270215 34272242 CCL7 6354 chemokine (C-C motif) ligand 7
GO:0008009|GO:0030335|GO:0008360|GO:0006874|GO:0007267|GO:0005576|GO:0005615|GO:0002548|GO:0031
726|GO:0007165|GO:0071361|GO:0006955|GO:0006954|GO:0006935|GO:0031727|GO:0007010|GO:0048245|GO:0
010332|GO:0008201|GO:2000503 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137437_PI430048170 0.434047962345417 0.802253966876526 0.52727355998629
0.572982288893741 0.442814896793871 A A A 0.538021912566018 1.32286265850794
0.476543187783604 A A A LNCV6_137437_PI430048170 mRNA
TATCACTGGCTGTGAAAAACCACCAGTTGAAAATTATTCATTCCTTAATGCAGCTAATCA NM_005708 RefSeq chr13
+ 93226824 94408019 GPC6 10082 glypican 6
GO:0005886|GO:0007603|GO:0005796|GO:0005975|GO:0005578|GO:0006027|GO:0043395|GO:0005634|GO:0044
281|GO:0031225|GO:0001523|GO:0005615|GO:0006024|GO:0016477|GO:0005887|GO:0009405|GO:0030204|GO:0
030203|GO:0043202. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126838_PI430048170 0.750042209612542 0.961957958530146 2.27129244675603
3.10368041985201 1.21283201927513 A A A 2.84928327030778 2.01624289297346
2.35399408720068 A A A LNCV6_126838_PI430048170 mRNA

CAGTACTGATTGCAGGGAGCACTGTAGAAGAGGAATGAAGGCCAAACAATTAAAAGCGGA NM_001036645 RefSeq chr1 + 70354809 70368022 HHLA3 11147 "HERV-H LTR-associating 3, transcript variant 2" GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131603_PI430048170 0.0901223927596786 0.7322517519965318.42681998757898 8.15212704154788 8.72956846119532 P P P 8.80450767571624 8.8123690636903 9.08073995124637 P P P LNCV6_131603_PI430048170 mRNA
TTCTCCCAGAAATGTAATTGCCAAACACTATTCATCCCCATCTTAAGTTTTACAAGGTGA NM_014765 RefSeq chr1 - 235109342 235128941 TOMM20 9804 translocase of outer mitochondrial membrane 20 homolog (yeast)
GO:0005739|GO:0005515|GO:0015450|GO:0006626|GO:0005742|GO:0044233|GO:0051082|GO:0016021|GO:0071806|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105870_PI430048170 0.71336128274435 0.9365520261450038.71393902691591 8.52384765717789 8.99914065491005 P P P 8.49236355975636 8.94834625297187 9.05963391726583 P P P LNCV6_105870_PI430048170 mRNA
TCTGACAAATCAGAAGATGGAAGGCTAATTTATACTGGCAATATGGCCCGAGCAGTGTTT NM_001040613 RefSeq chr8 + 73976141 73982783 TMEM70 54968 "transmembrane protein 70, transcript variant 2" GO:0005739|GO:0003674|GO:0033615|GO:0032592|GO:0005743|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2949_PI430048170 0.0861487304201207 1.23034636115575 8.72412788909923 8.84270175453467 8.79898630568082 P P P 8.39954596349207 8.6889837695174 8.35971340099805 P P P LNCV6_2949_PI430048170 mRNA
TAGAAGTTGTCATTTAAAGCAGCCTTCTAATAAAGTTGTTTCAAAGCTGATCATGGAGCC NM_001265614 RefSeq chr9 + 128091463 128109258 SLC25A25 114789 "solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25, transcript variant 5"
GO:0014823|GO:0046034|GO:0005509|GO:0005743|GO:0002021|GO:0032094|GO:0043231|GO:0005739|GO:0045333|GO:0035264|GO:0070588|GO:0043010|GO:0016021|GO:0060612|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130239_PI430048170 0.0545312305751091 0.6468209276441770.392161145251974 0.3873306460403180.896309183347066 A A A 1.16157546765794 1.28907239901494 1.16862513556243 A A A LNCV6_130239_PI430048170 mRNA
GTGGACGATTTGTTCTAGCACCTTTGAGAATTTACTTTATGGAGCGTATGTAAGTTATTT NM_001130914 RefSeq chr21_KI270873v1_alt - 447 9256 BTG3 10950 "BTG family, member 3, transcript variant 1" GO:0005515|GO:0005737|GO:0008285|GO:0045930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107448_PI430048170 0.2350514437107 0.8403205925075134.32252765052701 3.79935692251674 4.18814122350817 P P P 4.19633583138146 4.44324405364352 4.45838375414894 P P P LNCV6_107448_PI430048170 mRNA
TTTTCATTGATGAGCAAGACATACTTAATGCATTTTTGGTTTGTGTATCCATGCACCTAC NM_003147 RefSeq chrX + 52751202 52761536 SSX2 6757 "synovial sarcoma, X breakpoint 2, transcript variant 1" GO:0005515|GO:0006355|GO:0005634|GO:0003676|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132985_PI430048170 0.000377683353911754 0.4769726375656517.54091328137834 7.60263676439649 7.66368807729912 P P P 8.58562809081099 8.63628595828057 8.7845232859135 P P P LNCV6_132985_PI430048170 mRNA
GGCAGTTTTGCTTGATCTTTTGTGACTTTGAGCCTTTTAAGTAGTTTGAATGATAAGACT NM_001177718 RefSeq chr2 + 10044244 10054836 KLF11 8462 "Kruppel-like factor 11, transcript variant 3" GO:0043065|GO:0008285|GO:0003700|GO:0000083|GO:0044212|GO:0006366|GO:0000981|GO:0006915|GO:0005634|GO:0000122|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138180_PI430048170 0.3817603821140191.04088910541276 11.2697729607349 11.3566484795605 11.4366119587396 P P P 11.2419123633745 11.3094503002084

11.3412655649515 P P P LNCV6_138180_PI430048170 mRNA
TTCTGAGATAGAATATCTGGCAGAAGTGTGAAACTGTATTGCATGCTGCGGCCTGTGCAA NM_001272051 RefSeq
chr16 - 1419743 1420800 C16orf91 NA chromosome 16 open reading frame 91 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_144745_PI430048170 0.628595483697932 1.0895242644839 8.46139390623575
8.75415611754704 9.05988245285033 P P P 8.64753565594276 8.39894843323899
8.87987548572784 P P P LNCV6_144745_PI430048170 mRNA
TTAGGTCATCATAGTTGAGGTATGTGTCTGCTATTTGCAAAGAAGTTGGTCGTATTTTTT NM_024045 RefSeq chr10
+ 68901277 68946847 DDX50 79009 DEAD (Asp-Glu-Ala-Asp) box polypeptide 50
GO:0016020|GO:0005886|GO:0008152|GO:0005730|GO:0004386|GO:0005524 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_109846_PI430048170 0.641501861747317 1.03815270641847 4.06113058390213
4.17096950848266 4.22421023068687 P P P 4.26603839367753 3.9030797373557 4.1071012716682
P P P LNCV6_109846_PI430048170 mRNA
ACTCAGTAGTAGTTGTTGGAAAAGGCGTATTTGGAAGTTTAAGTTCAGCACCAGCAACCT NM_015091 RefSeq chr14
+ 44962189 45074431 FAM179B 23116 "family with sequence similarity 179, member B" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_108045_PI430048170 0.442797182696641 0.762542000361401 1.93334306027408
1.74086173653019 0.410047252675001 A A A 2.30757142750216 1.84249523845761
1.37720150538082 A A A LNCV6_108045_PI430048170 mRNA
TTCTGTGGTGCCAGAGGAAGACAGCACCGTACCGCAACGTCAACGTGCAGAACTTCCACA NM_001258371 RefSeq
chr11 + 66546394 66563329 ACTN3 89 "actinin, alpha 3 (gene/pseudogene), transcript variant 2"
GO:0005515|GO:0030049|GO:0005884|GO:0005509|GO:0003779|GO:0042981|GO:0042803|GO:0005829|GO:0031
143|GO:0005178|GO:0048041|GO:0008307|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140401_PI430048170 0.0238589013208893 0.651869361598491 2.3718948678987
12.4487053028473 12.5932305809648 P P P 12.8562799094593 13.089343328836
13.2956200089287 P P P LNCV6_140401_PI430048170 mRNA
CTAACCATGTAGACTTATTGCGGCCTGGTTTCTCTGTTACAATAAAATTACTGTAGACCC NM_002080 RefSeq chr16
- 58707130 58734357 GOT2 2806 "glutamic-oxaloacetic transaminase 2, mitochondrial, transcript
variant 1"
GO:0006531|GO:0006532|GO:0005886|GO:0006533|GO:0045471|GO:0006094|GO:0005743|GO:0044281|GO:0019
551|GO:0019550|GO:0005739|GO:0034641|GO:0097052|GO:0005759|GO:0006103|GO:0006006|GO:0004069|GO:0
080130|GO:0070062|GO:0006536|GO:0005975|GO:0006107|GO:0008652|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131169_PI430048170 0.10940702598142 1.2637243909748 5.71011602445495
5.53666234124564 5.96720335232729 P P P 5.29106415318402 5.6055528547389
5.31541515676244 P P P LNCV6_131169_PI430048170 mRNA
CAGTTGTACGTGGTTATTCCATTCCTAAAGGCACAACAGTAATTACAAATCTTTATTCTG NM_024514 RefSeq chr11
- 14878009 14892205 CYP2R1 120227 "cytochrome P450, family 2, subfamily R, polypeptide 1"
GO:0006805|GO:0005506|GO:0030343|GO:0042359|GO:0008395|GO:0044281|GO:0006082|GO:0043231|GO:0005
737|GO:0019825|GO:0042738|GO:0006766|GO:0005789|GO:0016712|GO:0008202|GO:0055114|GO:0020037 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129792_PI430048170 0.00911234374804025 0.35651896820496 4.33675730437736
3.78553573064808 4.54168725706863 P P P 5.49897846834344 5.90870752728078
5.79146676693594 P P P LNCV6_129792_PI430048170 mRNA
CGGTATCATGTGAAGTGCTGTTTATGTAAATCTCAACATATCCCTTACTCAGGGAAAAAA NM_000108 RefSeq chr7
+ 107891106 107921198 DLD 1738 "dihydrolipoamide dehydrogenase, transcript variant 1"
GO:0050661|GO:0007369|GO:0006099|GO:0050660|GO:0009083|GO:0044281|GO:0005739|GO:0034641|GO:0006

090|GO:0050787|GO:0005759|GO:0042391|GO:0006508|GO:0006120|GO:0006554|GO:0004148|GO:0016152|GO:0
044237|GO:0010510|GO:0043159|GO:0045340|GO:0005929|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131119_PI430048170 0.1191469690364450.8228641751769868.44310572082514 8.1444057915955
8.4230705866048 P P P 8.52700261112554 8.50036302579978 8.82317635429983 P P P
LNCV6_131119_PI430048170 mRNA
TGTACTTCTCTATTGCGCCGCCATTAAAAGCAGCATTAGTGCATTTTGTCATTCAAAAAA NM_001098832 RefSeq
chr17 - 73207352 73232394 FAM104A 84923 "family with sequence similarity 104, member A,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144022_PI430048170 0.6094840862726951.08898463773185 0.366696438688657
0.3556549205284310.872038097031343A A A 0.4507646811655390.430756280177814
0.406026112900814A A A LNCV6_144022_PI430048170 mRNA
CGGGAATCAGTTCACTCCAAGGTATCCCCACTAAATAAACAGTTTCCCATCCAAATCAAG NM_001271539 RefSeq
chr20 - 13849397 13990619 SEL1L2 NA "sel-1 suppressor of lin-12-like 2 (C. elegans), transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143175_PI430048170 0.3194046529819181.72545723429684 2.90879670694528
1.56131750021887 3.21024901995169 A A P 1.03779792537863 1.67023198601471
2.63015676844044 A A P LNCV6_143175_PI430048170 mRNA
ATGGATCTCATACATGTTTTTAGAACATTGTTCTTCTGATTGAAGAAGTCTGATGCTCCT NM_001168214 RefSeq
chr3 + 160225635 160228213 C3orf80 401097 chromosome 3 open reading frame 80 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122324_PI430048170 0.9070742856428170.9928733378266020.70118942879391
0.5368952213659760.304400625660616A A A 0.4126957287160880.630711592310724
0.548974637284755A A A LNCV6_122324_PI430048170 mRNA
GACCCGAGGAAAGCCGTGTTGACCAAAAGCAAGACAAATGACTCACAGAGAAAAAAGATG NM_001243428
RefSeq chr21 - 38380027 38660667 ERG2078 "v-ets avian erythroblastosis virus E26 oncogene
homolog, transcript variant 5"
GO:0005515|GO:0006357|GO:0006366|GO:0008283|GO:0000981|GO:0005634|GO:0007275|GO:0003677|GO:0030
154|GO:0043565|GO:0007165|GO:0005737|GO:0030529|GO:0006468|GO:0004871 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139628_PI430048170 0.1795103622530940.5631493399602423.80395147462843
2.32399049147659 3.43645154214934 P A P 3.49797238774233 4.30189610064925
4.45254645673807 P P P LNCV6_139628_PI430048170 mRNA
GAAGTGACTGATTCTCAACTGAACATTATGTCGTTACTTTGATAAGCATTCCACTTTTGT NM_014937RefSeq chr10
+ 119726046 119829150 INPP5F 22876 "inositol polyphosphate-5-phosphatase F, transcript variant 1"
GO:0031161|GO:0042578|GO:0048015|GO:0014898|GO:0051896 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131244_PI430048170 0.2927630940591690.6854581221711740.254191592290718
0.2957700362396890.286089991079257A A A 1.38984522870987 0.540038349059956
0.30465923655532 A A A LNCV6_131244_PI430048170 mRNA
TTTTGGATGGTAAGGACATTTAATTCTAAATCGATGAGAATGTGTCTTTGGGGTAGGTTT NM_176889RefSeq
chr12_KI270904v1_alt - 194656 196570 TAS2R20 259295 "taste receptor, type 2, member 20"
GO:0050909|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134432_PI430048170 0.9301292107544361.00413904645883 0.328981664484614
0.3321035027810170.46737304824329 A A A 0.3429728540630080.410079282547601
0.361062557357222A A A LNCV6_134432_PI430048170 mRNA
TCCTTGCTTACATTTGGAGGACAGGGACAAGGACTGAGCAAAAACAAAATGAAAAAATCANM_024082RefSeq chrX
+ 151695257 151701591 PRRG3 79057 "proline rich Gla (G-carboxyglutamic acid) 3 (transmembrane),

transcript variant 1" GO:0008150|GO:0005509|GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130648_PI430048170 0.9076156394303861.00698509837206 3.45362672650056 3.27041905416937 3.28723165349453 P P P 3.50550196769598 3.26070196778254 3.20404480526298 P P P LNCV6_130648_PI430048170 mRNA ATGGACAAAGGGCTCCACATTTCCCACAACCCTTTATCCAAGCCTCTGCCGGAGCTGGTG NM_001105581 RefSeq chr18 + 7231138 7232044 LRRC30 NA leucine rich repeat containing 30 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142856_PI430048170 0.0018678428587394 0.6301483728986347.16238041828195 6.93968755439155 7.11510678565967 P P P 7.63877328778421 7.7642035954428 7.81658242788012 P P P LNCV6_142856_PI430048170 mRNA TGCTGCTCTGTTTCCTTTGATGACGCTTTGAAATAAAGGCAGGAGTACAAGCCTAAAAAA NM_014764RefSeq chr12 + 51238723 51243933 DAZAP2 9802 "DAZ associated protein 2, transcript variant 1" GO:0005515|GO:0005737|GO:0050699|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139078_PI430048170 0.7431564598622250.9896754778797350.453800076590708 0.4719770623474790.375839702307737A A A 0.5094762754979220.411919895615711 0.424979042644866A A A LNCV6_139078_PI430048170 mRNA ATAAATGTGACTGGAGCCCAACATGATTCAGCTGAGGCAAGGGTCAAAAGGACATTTTGG NM_001001955 RefSeq chr11 + 49952390 49953419 OR4C13NA "olfactory receptor, family 4, subfamily C, member 13" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123031_PI430048170 0.0875194497973568 0.8584256920414190.292128757430122 0.3540160325192650.281398810973313A A A 0.5041454324082470.410934777923984 0.662912011688955A A A LNCV6_123031_PI430048170 mRNA TTCCACTGGCTTATCCTTAATGAAGGAAATCCCCTGATAATTACTTTGATTCTGAAAATG NM_000809RefSeq chr4 - 46918899 46994407 GABRA4 2557 "gamma-aminobutyric acid (GABA) A receptor, alpha 4, transcript variant 1" GO:0005230|GO:0030054|GO:0005886|GO:0004890|GO:0034707|GO:0007268|GO:0007214|GO:0007417|GO:0055085|GO:0005254|GO:0034220|GO:0005887|GO:0045211|GO:0006810|GO:0008503|GO:2001023 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135904_PI430048170 0.21816260343391 0.8100858859179274.10160399673666 3.48623350179958 3.96446825449914 P P P 4.08747981403333 4.26832222451744 4.1719557677624 P P P LNCV6_135904_PI430048170 mRNA GCCTGCTGCAAACTTTTAAAATATTATGATAGATTCTGTACTACATGTGGGAAACAAGCA NM_014035RefSeq chr5 + 122845464 123009207 SNX24 28966 sorting nexin 24GO:0035091|GO:0015031|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132279_PI430048170 0.00237259246902837 1.20428403827918 10.7485435552014 10.650631591632 10.6954288452314 P P P 10.3974789093741 10.4833611693942 10.4093944721506 P P P LNCV6_132279_PI430048170 mRNA GGCCGTTTACATGGCGAGTCTCCGTGCTGGTGTTTAAGTCATTAAAAAGATACTCAAAGA NM_018708RefSeq chr19 + 4791715 4795559 FEM1A 55527 fem-1 homolog a (C. elegans) GO:0005737|GO:0004842|GO:0016567|GO:0050728|GO:0051438|GO:0031867 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129985_PI430048170 0.00289964340864694 0.4039771818684643.94881885488281 4.23076892135534 3.76822209024455 P P P 5.44644576418421 5.21036314633785 5.24035325867466 P P P LNCV6_129985_PI430048170 mRNA CTTGTGCAGTGTAGTAAACATGCAAGTTGTTACGATTGAGCTGTATTACCATAAGTAGAA NM_022900RefSeq chr7 + 94509857 94557016 CASD1 64921 CAS1 domain containing 1 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139558_PI430048170 0.4249269414154530.6194185184084290.479615676948052

0.4240554945447180.308267978010424A A A 0.4724654160150311.91414842902404
0.333155035378083A A A LNCV6_139558_PI430048170 mRNA
GAGTTGATGCAACCATTGTGGTATTCACTTTCCTCATGTTTATGATGAATATTTTGCACTNM_182971RefSeq
chr14_KI270847v1_alt + 461752 462916 COX8C NA cytochrome c oxidase subunit VIIIC NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140728_PI430048170 0.2589596277676021.70383066823378 0.332637976151203
1.77277014615646 1.38391907390759 A A A 0.761035723699655 0.388542244687834
0.347745715623618A A A LNCV6_140728_PI430048170 mRNA
TGCACCACTGGTCATAGCATCTATCTCCTTTGCCTTAATTTACTGAAATACATCATTTTA NM_001393RefSeq chr9 -
92495311 92536092 ECM2 1842 "extracellular matrix protein 2, female organ and adipocyte specific,
transcript variant 1"
GO:0005178|GO:0007160|GO:0030198|GO:0010811|GO:0005578|GO:0005614|GO:0008201|GO:0070052 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143631_PI430048170 0.00290852279481085 0.4313824255312227.0740512580348
6.79257493118854 6.82792510621514 P P P 8.08488809251093 8.09453193769423
8.16912436744052 P P P LNCV6_143631_PI430048170 mRNA
GGGGCCCAGGGAGGACCTGGGAGCCACCCCGCATTAAAGCACATTTGACCTTTCAAAAAA NM_001134316
RefSeq chr19 - 5782959 5784765 PRR22 163154 proline rich 22 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128717_PI430048170 0.3328782431070820.921423252298354 0.416441279721828
0.4356762386468680.281440040211929A A A 0.394335600369805 0.666503321769488
0.415572279336525A A A LNCV6_128717_PI430048170 mRNA
TTCAACCAAATATGAAAAAGTTTAAGTGGATAGATAAGACTGAAGAATAAAAGGGTCTAT NM_020890RefSeq chr3
- 108549870 108589644 KIAA1524 57650 KIAA1524
GO:0005515|GO:2000179|GO:0005737|GO:0005886|GO:0016021|GO:0007283 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_61253_PI430048170 0.2602818988295752.05641433765684 0.325660516029181 1.51877078510415
2.23005264792738 A A A 0.763844247270719 0.384271260990381 0.357329207151042A A A
LNCV6_61253_PI430048170 mRNA
ATGTGTGTTAACCAAAATGGCGGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGA NM_006329RefSeq chr14
- 91869410 91947702 FBLN5 10516 fibulin 5
GO:0005515|GO:0005509|GO:0005578|GO:0005576|GO:0071953|GO:0008022|GO:0001558|GO:0005615|GO:2000
121|GO:0046903|GO:0042803|GO:0031012|GO:0005178|GO:0007160|GO:0030198|GO:0034394|GO:0070062|GO:0
048251 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136895_PI430048170 0.00100405479377952 0.4085806115240414.11479024781651
3.82383986552689 3.86190244451164 P P P 5.2828791200546 5.13168619301466
5.27265534972585 P P P LNCV6_136895_PI430048170 mRNA
GAAGTTCCAAGGTTTTGATTTTGGTCTGGTCTTTAAGTGAAAAATTAAAGCAACCAGTAG NM_015932RefSeq chr13
+ 28659003 28678956 POMP 51371 proteasome maturation protein
GO:0043248|GO:0005515|GO:0005737|GO:0005783|GO:0031090|GO:0005654|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128481_PI430048170 0.00937392540941055 4.2718763643821 6.82417424410419
6.65893041326829 6.798213902051 P P P 4.9345569166103 4.79011377971525
4.16867305402445 P P P LNCV6_128481_PI430048170 mRNA
GGAACTCTGGTTATTATGGTGTTAGTTATCGAATAAAAACGACTTCAGAATGCAGCTAAA NM_001100876 RefSeq
chr9 + 128920894 128942041 PHYHD1 254295 "phytanoyl-CoA dioxygenase domain containing 1,
transcript variant 1" GO:0051213|GO:0046872|GO:0055114 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_136974_PI430048170 0.7497906586341051.01309607783742 6.24831559682878

6.34499009890035 6.24860086707104 P P P 6.2668914289305 6.33897471021949
6.17736292542542 P P P LNCV6_136974_PI430048170 mRNA
TGAAAACAAACACAAACCAAAGTTTCTGGCCATCTGTGGCTGGAGGGTTCTGAATGTCCT NM_173542RefSeq chr12
+ 113358565 113389653 PLBD2 196463 "phospholipase B domain containing 2, transcript variant 1"
GO:0016042|GO:0016787|GO:0070062|GO:0043202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130182_PI430048170 0.3435171947572050.8362727643110586.93069431228643
6.94333049196124 6.7406699581679 P P P 6.77837190434618 7.43984237841013
7.10354677078774 P P P LNCV6_130182_PI430048170 mRNA
CTGTTTTTAACGTGCCCGTTTGTACTGATGTATGAACTTGTCAATAAACACAATTGTTTG NM_001128608 RefSeq
chr15 + 41774433 41827855 MAPKBP1 23005 "mitogen-activated protein kinase binding protein 1,
transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127386_PI430048170 0.56851539359751 1.21495934513408 1.56024457551951
0.4690284376963160.83208174357812 A A A 1.23468913051345 0.412538030247969
0.430282417919835A A A LNCV6_127386_PI430048170 mRNA
CCCCTAGGGTCTATAATTCCTTAAAATTTTCATTCTGAATCTGAAGGAGAGAGTCTTTTA NM_001190811 RefSeq
chr3 - 16586793 16604790 DAZL 1618 "deleted in azoospermia-like, transcript variant 1"
GO:0005515|GO:0003723|GO:0005634|GO:0007275|GO:0008494|GO:0001556|GO:0007283|GO:0007281|GO:0042
802|GO:0007147|GO:0045836|GO:0005737|GO:0000166|GO:0045948|GO:0003730|GO:0005844 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136272_PI430048170 0.00868293501348086 1.24805721825426 10.0400122986694
10.0589730576397 9.89953242755524 P P P 9.67895878776177 9.74594790877348 9.6168678248367
P P P LNCV6_136272_PI430048170 mRNA
AGCCACTGGGGAAGGGAAGTTTCAGTAACATGACACTAAAATGGCAGAGACGTTAAAAAA NM_004556RefSeq
chr6 - 44258165 44265788 NFKBIE 4794 "nuclear factor of kappa light polypeptide gene enhancer in
B-cells inhibitor, epsilon"
GO:0005515|GO:0048471|GO:0005737|GO:0005794|GO:0042942|GO:0042994|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137102_PI430048170 0.184909703758836 1.04450790334409 0.397812999553978
0.3077866965631130.295129703177926A A A 0.2585304823055290.302467178559208
0.252937641272832A A A LNCV6_137102_PI430048170 mRNA
CTATGTGTGACTTTAAACTGTAAAATTAAACACTGCTTTTGTGGGTTCAGTGGGCATAAT NM_007038RefSeq chr21
- 26917911 26967120 ADAMTS5 11096 "ADAM metallopeptidase with thrombospondin type 1 motif, 5"
GO:0005515|GO:0005578|GO:0005576|GO:0036066|GO:0005178|GO:0006493|GO:0022617|GO:0030198|GO:0006
508|GO:0005788|GO:0008270|GO:0004222|GO:0044267|GO:0042742|GO:0008237|GO:0043687 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128743_PI430048170 0.4688728934493750.83444637087757 6.31914690543315
6.36478587350909 5.75362004559617 P P P 6.07673099208314 6.85465787360693
6.24560233221015 P P P LNCV6_128743_PI430048170 mRNA
AAAGTGAAACTGGCGGGACGTTCCCCTTTGAAAATTTTAAACGGCTCTTTTCAGAGCCAC NM_005320RefSeq chr6
- 26234211 26234988 HIST1H1D 3007 "histone cluster 1, H1d"
GO:0000790|GO:0005719|GO:0006334|GO:0016584|GO:0000786|GO:0031490 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128618_PI430048170 0.9109124062663130.9920405001032121 3.7595943518679
14.0219445083675 14.2352457611523 P P P 14.0960133992678 13.8544195810319
14.1249799187536 P P P LNCV6_128618_PI430048170 mRNA
TATCCCGCTAAGAGAGAGACATGTCAAAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGG NM_033378RefSeq chr19
+ 49031872 49033238 CGB2 114336 "chorionic gonadotropin, beta polypeptide 2"
GO:0005179|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75523_PI430048170 0.00816179556032932 0.7440419204078753.86353180942245

3.94812719077339 3.91678792087736 P P P 4.22403384095301 4.40776288417039
4.37106858824722 P P P LNCV6_75523_PI430048170 mRNA
TAATGGGCATACATTTCACCGTATAATTAAGGGCTTTATGATTCAGACTGGAGATCCAAC NM_001278926 RefSeq
chr5 + 65563238 65587543 PPWD1 23398 "peptidylprolyl isomerase domain and WD repeat
containing 1, transcript variant 2"
GO:0000413|GO:0006457|GO:0000398|GO:0003755|GO:0005654|GO:0005634|GO:0071013 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_124202_PI430048170 0.0309275733231559 0.8499441992271375.1721349727775
5.20610138233918 5.10771374107873 P P P 5.28948948508965 5.46793083978137
5.42792016389036 P P P LNCV6_124202_PI430048170 mRNA
CTTCTCCCATGTGCTTGAAGGAAAAATAAAGTGTCACTACCGTATTTCTTGTTTTCATCA NM_021648RefSeq chr6
- 116249967 116254098 TSPYL4 23270 TSPY-like 4 GO:0006334|GO:0005634 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_142574_PI430048170 0.6206023461404150.95521289245313 0.299892054550108
0.2730527604941050.364539189231012A A A 0.5736495301353360.266137629184049
0.275912481698107A A A LNCV6_142574_PI430048170 mRNA
TCTCAAAGCTGTGCAGTCTTTTGTTACTGGGACACTTTTAAACTCTGAATAGGCATTAAA NM_001242957 RefSeq
chr6 - 10762722 10838555 MAK 4117 "male germ cell-associated kinase, transcript variant 3"
GO:0005515|GO:0072686|GO:0005813|GO:0006355|GO:0003713|GO:0030496|GO:0007275|GO:0005634|GO:0007
283|GO:0045494|GO:0005524|GO:0030154|GO:0006351|GO:0001917|GO:0005737|GO:0046777|GO:0004672|GO:0
051726|GO:0006468|GO:0001750|GO:0004693 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105282_PI430048170 0.402464224762451 1.14573031817359 3.04729457457001
3.55455187319042 3.13811074869585 A P P 2.80985960098131 3.11621122372159
3.24352079804876 P P P LNCV6_105282_PI430048170 mRNA
TGAAATCGAGCTGTCGGTAGGAAATGACCGCCTGTGGTTTGTGAATCCTATTTTCATCGA NM_024832RefSeq chr14
+ 92513780 92688989 RIN3 79890 Ras and Rab interactor 3
GO:0005515|GO:0017112|GO:0007165|GO:0017137|GO:0032851|GO:0016023|GO:0031410|GO:0005769|GO:0006
897|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128324_PI430048170 0.00607076585884531 3.98807815782523 3.15621559415415
2.80891582908209 2.36328660026004 A A A 0.4164293890142961.32543083854378
0.528086338475905A A A LNCV6_128324_PI430048170 mRNA
TGGCAGGCCCAAGTATTTTCTGTGATATCCCAGGTTAATAAAGATTAGATTCTAAGTTAC NM_001162499 RefSeq
chr3 + 12796671 12834814 CAND2 23066 "cullin-associated and neddylation-dissociated 2 (putative),
transcript variant 1"
GO:0005622|GO:0005515|GO:0016567|GO:0017025|GO:0005634|GO:0045893|GO:0010265|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131619_PI430048170 0.3861080123633430.7260145058109310.334007563569862
0.3364538919628420.319521038406788A A A 0.3266003735920760.403058075427327
1.38838372066892 A A A LNCV6_131619_PI430048170 mRNA
TTTCTGCTTTTTTCTAGTCATTCAATTTATCACTGCTGAATTGCATCAGATCATGGATGC NM_022444RefSeq chr7 -
123113533 123199971 SLC13A1 6561 "solute carrier family 13 (sodium/sulfate symporter), member 1"
GO:0005886|GO:0035725|GO:0016021|GO:0055085|GO:0015382 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136564_PI430048170 0.0443521193830991 0.4364079307266893.83239232509336
3.00324565626164 3.85467642661463 P P P 4.72531380976522 4.85172955553326
4.84987094194358 P P P LNCV6_136564_PI430048170 mRNA
CTGGTTTTTGGCCAGTCTAAATATTGTAAGAGAGAGAGAAGAAAAGTGTACGGAATATAA NM_006208RefSeq chr6
+ 131808015 131895155 ENPP1 5167 ectonucleotide pyrophosphatase/phosphodiesterase 1
GO:0005515|GO:0030308|GO:0090305|GO:0050427|GO:0005886|GO:0006200|GO:0045599|GO:0005158|GO:0004

551|GO:0006767|GO:0009143|GO:0044281|GO:0006091|GO:0006796|GO:0005765|GO:0005615|GO:0042803|GO:0
031953|GO:0006771|GO:0016323|GO:0030279|GO:0006955|GO:0030730|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143011_PI430048170 0.5281416438433541.08496854612625 7.09816335872624
6.99283530036966 7.43386665060619 P P P 7.20563834376432 6.9220553918818
7.06785451419298 P P P LNCV6_143011_PI430048170 mRNA
GCCTTTAAAGCAAAATCCTCAGAAATGGTCTAAATAAAACACTTGATATGCCTAGAGAAC NM_017917RefSeq chr14
- 35085467 35122542 PPP2R3C 55012 "protein phosphatase 2, regulatory subunit B", gamma"
GO:0005813|GO:0001782|GO:0045579|GO:0005819|GO:0000226|GO:0005634|GO:0048536|GO:0046872|GO:0032
147|GO:0002759|GO:0005737|GO:0051900|GO:0030865|GO:0043029 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_131669_PI430048170 0.0291691450639484 1.47843844653606 9.64911762063664
10.0182763229066 9.83927316494033 P P P 9.28938789480009 9.31683134836812
9.23043932904114 P P P LNCV6_131669_PI430048170 mRNA
CTGCTACTGTGTGTTTGCTGGTTCCAATGATACATAATTTGTGCTTTTCGTAATTAAAGTNM_001287682 RefSeq chr20
+ 2206927 2213151 LOC388780 NA uncharacterized LOC388780 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142787_PI430048170 0.4158977557840120.9703018383335670.31554113219173
0.4154956625330060.321723063735593A A A 0.4645837588406110.3564299914959280.3618248685462
A A A LNCV6_142787_PI430048170 mRNA
GGAAGGTATCTATACTGAATTACCCCAACCTTACTTTTAAGATGTGTGGTATAGATAGTA NM_198992RefSeq chr12
- 33375412 33439819 SYT10 341359 synaptotagmin X
GO:0017158|GO:0005215|GO:0030054|GO:0046982|GO:0006810|GO:0030672|GO:0016021|GO:0046872|GO:0042
803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136299_PI430048170 0.3079673355410380.96673644917024 0.422967081069393
0.4448640415124580.327265836392258A A A 0.4189804020200590.478990437027955
0.445606473753607A A A LNCV6_136299_PI430048170 mRNA
GTTCCTTAATTTGACTGTAACACATTTGTTTCAAGTCTTTGGATTCAAACAACCGGATTG NM_001009931 RefSeq
chr1 - 152212075 152224196 HRNR NA hornerin NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131003_PI430048170 0.0457611475455135 0.7086151650969248.31558773980556
8.13630880969748 8.33031764693991 P P P 8.58253637104845 8.65810053857038
9.00440490035036 P P P LNCV6_131003_PI430048170 mRNA
TAGGTCAGTGTAAAGAAATATGATTTGAGGTGGTGCATGCAAGTAACTAGGGTTTATTCT NM_001114RefSeq chr16
+ 50287911 50318134 ADCY7 113 "adenylate cyclase 7, transcript variant 1"
GO:0005886|GO:0030819|GO:0007268|GO:0007202|GO:0044281|GO:0007193|GO:0046872|GO:0035556|GO:0007
173|GO:0071377|GO:0006171|GO:0006833|GO:0034199|GO:0048011|GO:0060135|GO:0005524|GO:0055085|GO:0
003091|GO:0007165|GO:0071361|GO:0006112|GO:0004016|GO:0008543|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127182_PI430048170 0.00655138306413798 0.7053682388196243.7103884162432
3.90292463090102 3.94645763910045 P P P 4.44140557053035 4.26967303832148
4.36500190863511 P P P LNCV6_127182_PI430048170 mRNA
ACCCCACATTGGTCATCTTCCCTATCACACAAATGATGTTATTTTGGACTAGCTTAATTT NM_005073RefSeq chr13
- 98683800 98752675 SLC15A1 6564 "solute carrier family 15 (oligopeptide transporter), member 1"
GO:0005427|GO:0035672|GO:0016020|GO:0005886|GO:0005887|GO:0007586|GO:0006810|GO:0015031|GO:0055
085|GO:0015333|GO:0015992|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132748_PI430048170 0.8402793745723981.0946963568247 1.33020834387783
0.4760323566668740.291568236714695A A A 0.4083991073593150.988642276215845
0.458421903467127A A A LNCV6_132748_PI430048170 mRNA

ACTTCGGCTAGGGAGGAAGGTAGAGTAAGAGGTTGAAGATAACAGAGTGCAAAGTTTCCT NM_033130 RefSeq chr19 - 51410020 51417803 SIGLEC10 89790 "sialic acid binding Ig-like lectin 10, transcript variant 1" GO:0005886|GO:0030246|GO:0005576|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139040_PI430048170 0.89656807553548 0.9888171389015320.433309173893806 0.3798094648493770.460667085671439 A A A 0.5960756283637280.341860518520026 0.372101269727039 A A A LNCV6_139040_PI430048170 mRNA
ATAGAAAAAACTCGTTTGATTTTTGGGGGGAAACAAGGGCTACCTTTACTGGAAAATCTG NM_001511 RefSeq chr4 + 73869391 73871302 CXCL1 2919 "chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha), transcript variant 1"
GO:0008009|GO:0070098|GO:0030036|GO:0008285|GO:0008283|GO:0005102|GO:0005576|GO:0045236|GO:0043085|GO:0005615|GO:0002690|GO:0007399|GO:0035556|GO:0007165|GO:0006955|GO:0006954|GO:0006935|GO:0007186|GO:0060326|GO:0032496|GO:0008047|GO:0008083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132672_PI430048170 0.8187539308184740.9368840241886944.32578478949813 4.18054241018771 4.04049751990958 P P P 3.78359442149156 4.53773495986232 4.41445557007093 P P P LNCV6_132672_PI430048170 mRNA
TGTTACGTTGGTGGAGAAGCAAAACATTTGGTGAGTTGTATTCTGGTTTTCCGGAGTTGG NM_001284194 RefSeq chr10 + 73772290 73776218 FUT11 170384 "fucosyltransferase 11 (alpha (1,3) fucosyltransferase), transcript variant 2" GO:0046920|GO:0032580|GO:0006486|GO:0016021|GO:0036065|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136599_PI430048170 0.0673525691293287 1.80210997972182 1.1608094224583 1.91115690278262 1.50111511280003 A A A 0.34901362028871 0.43147730122075 1.18659447344314 A A A LNCV6_136599_PI430048170 mRNA
AGGAATAAAGATGTCCACGTTGCCCTGAAGAAAACGCTAGGGAAAAGAACATTCTTATGA NM_001005198 RefSeq chr11 + 124264826 124265867 OR8G5 NA "olfactory receptor, family 8, subfamily G, member 5" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116517_PI430048170 0.2470861824677361.15279124422115 8.7594425484949 8.94205909506362 9.15451367671744 P P P 8.61640138117017 8.69800919307158 8.93419580479849 P P P LNCV6_116517_PI430048170 mRNA
TTTAGAATGAGAAGAGATACTGTGTCTTTATTGTGTGTGTGTGAGTGCAGGTGTGTGTCT NM_001286117 RefSeq chr11 - 83259092 83286407 CCDC90B 60492 "coiled-coil domain containing 90B, transcript variant 3" GO:0005739|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126661_PI430048170 0.0516825066162534 1.19991293555319 11.4673438510831 11.4452005179482 11.6297520015633 P P P 11.1683757565456 11.3977286394241 11.1829102336325 P P P LNCV6_126661_PI430048170 mRNA
TTTATCATTAAAAATCAACTTCCAGCCCTGTCTGCTGTCTACGTGGTGGGTTGTGGGGAT NM_013237 RefSeq chr5 + 177303761 177306959 PRELID1 27166 "PRELI domain containing 1, transcript variant 1"
GO:0005515|GO:0043066|GO:0051881|GO:0006915|GO:0097035|GO:0070234|GO:0007275|GO:0005739|GO:0005758|GO:0043234|GO:0006955|GO:0010917|GO:0090201|GO:0015914|GO:0010950|GO:0045580|GO:0005654|GO:2001140 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139328_PI430048170 0.0172863621421379 0.3387069982418796.95601305872144 6.72874770275888 7.11756258870822 P P P 7.96115581966192 8.54012467971801 8.87109728700424 P P P LNCV6_139328_PI430048170 mRNA
GTCTGTAAGGTATGGCTGTGGAAAGATATTGTAGTAGTTTTGACACTATTGTTATTACCT NM_001171689 RefSeq chrX - 110194185 110440233 AMMECR1 9949 "Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1, transcript variant 3"
GO:0005515|GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63515_PI430048170 0.4165555385621861.07205972259711 11.9962827527354 12.1725660103056

11.9699664808913 P P P 12.1080154815958 11.9341363267533 11.7859881003707 P P P
LNCV6_63515_PI430048170 mRNA
CCCCAATGAACTCTGCCCTGCCTGGGACTCTATTTATTCTGATTAAAGGGGTTTTGCAAA NM_001127198 RefSeq
chr17 - 78112917 78128780 TMC6 11322 "transmembrane channel-like 6, transcript variant 1"
GO:0005515|GO:0008150|GO:0031965|GO:0005737|GO:0005794|GO:0005783|GO:0005789|GO:0016021|GO:0070
062|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130444_PI430048170 0.00106681459424028 0.6543881699603726.41348698084658
6.55309399283389 6.57960175775738 P P P 7.04989246478215 7.10921758536498
7.22251446559838 P P P LNCV6_130444_PI430048170 mRNA
AATGAGTACATCCTTGTATTTGTATTTGTTTTCAACATCGCCAAGGTGCTATGGGAAATT NM_052879RefSeq chr12
+ 50400808 50480005 LARP4 113251 "La ribonucleoprotein domain family, member 4, transcript variant
1" GO:0016020|GO:0022604|GO:0007010 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_22874_PI430048170 0.471195187982106 1.7614155357282 2.38645983876298
0.54234126548428 0.546912070431918 A A A 0.437419162113212 0.818047340696028
0.592159118638503 A A A LNCV6_22874_PI430048170 mRNA
TTTGTTCTGGCAAGAGCAGAAAACTGAGAAGCCGTGTTACCTACCACTACCTGGGATTAA NM_001304732 RefSeq
chr10 - 59736989 59753445 MRLN NA "myoregulin, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_61944_PI430048170 0.456834564009547 1.1103484408601 5.99747122780351
6.41779967134538 6.29661228381165 P P P 6.35763824118934 5.98821541270926
5.90329368456712 P P P LNCV6_61944_PI430048170 mRNA
TATATTTGATCTCTAAATCTGAACAGTTTATGGTCACAGTCCAGCCTCCTCCGTGCAGCC NM_207037 RefSeq
chr15 + 56918634 57288516 TCF12 6938 "transcription factor 12, transcript variant 2"
GO:0005515|GO:0000790|GO:0003700|GO:0046982|GO:0044212|GO:0006357|GO:0043425|GO:0070888|GO:0046
332|GO:0005634|GO:0000978|GO:0006351|GO:0035326|GO:0001077|GO:0005737|GO:0006955|GO:0007517|GO:0
045666|GO:0045944|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127499_PI430048170 0.831840998691453 0.971828061672122 0.634054034947989
0.773775544942455 0.60457570418394 A A A 0.954155107669176 0.585307263638401
0.5685336764549 A A A LNCV6_127499_PI430048170 mRNA
GAAGGGAAACCTTACATTATGCTATGAAGAGTAGTAATAATAGCAGCTCTTATTTCCTGA NM_000764 RefSeq
chr19 - 40875438 40882752 CYP2A7 1549 "cytochrome P450, family 2, subfamily A, polypeptide 7,
transcript variant 1"
GO:0008392|GO:0006805|GO:0070330|GO:0005506|GO:0008395|GO:0019373|GO:0009804|GO:0043231|GO:0005
737|GO:0019825|GO:0042738|GO:0005789|GO:0016712|GO:0055114|GO:0020037 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_46971_PI430048170 0.86634838743998 0.996057728818453 0.369703214182638
0.346385861430054 0.25971067834116 A A A 0.324203526324535 0.344166863949019
0.326756918665993 A A A LNCV6_46971_PI430048170 mRNA
GAACATTGTTAGAAGTTGCACCCTGGAAAGATGTAACCAGTGGAAATGCTAAAATTTACC NM_018324 RefSeq
chr10 + 15043895 15073852 OLAH 55301 "oleoyl-ACP hydrolase, transcript variant 1"
GO:0016295|GO:0004320|GO:0006633|GO:0016296 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144197_PI430048170 0.00321400370359087 1.77968090516231 6.87566493196735
6.96867767815865 6.86689359891429 P P P 5.91932963327452 6.17020957168825
6.11712940531606 P P P LNCV6_144197_PI430048170 mRNA
ATCCTTTTCTATGAAGTGTTGACTTTGTAAATCTGCCCACACCCAGCTGGCCATATCCAC NM_001199281 RefSeq
chr22 + 24011369 24178628 CABIN1 23523 "calcineurin binding protein 1, transcript variant 1"
GO:0005737|GO:0016235|GO:0004864|GO:0006336|GO:0005654|GO:0043086|GO:0007166|GO:0016568 . NA
- . NA NA NA NA NA NA NA NA NA

LNCV6_74699_PI430048170 0.00555977586366789 0.516564055744689 1.3683581538562
1.50790785296733 1.76429377793795 A A A 2.53151404719596 2.39821413066576
2.59132659800269 A A P LNCV6_74699_PI430048170 mRNA
TACATGTCAAATGGATCTCTTTCTCCACCCATCCCGAGAACATCAAATAAAGTGCCCGTG NM_016269 RefSeq
chr4 - 108047544 108168956 LEF1 51176 "lymphoid enhancer-binding factor 1, transcript variant 1"
GO:0005515|GO:0003700|GO:0008013|GO:0006366|GO:0030307|GO:0032714|GO:0003705|GO:0001756|GO:0001
755|GO:0032713|GO:0030879|GO:0021861|GO:0032993|GO:0016202|GO:0016055|GO:0043027|GO:0021542|GO:0
022407|GO:0022408|GO:0000977|GO:0022409|GO:0030335|GO:0033153|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132116_PI430048170 0.79930817558973 1.02331416064653 5.17251698463426
4.91238608113231 5.06348208980489 P P P 5.10242711091169 5.15735939992464
4.77118976277061 P P P LNCV6_132116_PI430048170 mRNA
AACCAACAGAAAATGAAGAAGGCCACATCTTTAAGGCCACCTCTGCCTCTATCAGATGAG NM_003275 RefSeq
chr9 + 97501638 97601743 TMOD1 7111 "tropomodulin 1, transcript variant 1"
GO:0008344|GO:0030049|GO:0051694|GO:0005829|GO:0006936|GO:0051015|GO:0008180|GO:0016020|GO:0030
239|GO:0005865|GO:0007015|GO:0030863|GO:0005523 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_64651_PI430048170 0.309401984387867 0.831554015360353 4.37267773695771
4.92752111777895 4.37764863818642 P P P 5.09182033574276 4.58463525235863
4.82833445894582 P P P LNCV6_64651_PI430048170 mRNA
GAAAATGAGCAACTCAGAAATGATAACAAGAGACAAGTAGCTCCAGGTGCTCCTTCAGCT NM_001114093 RefSeq
chr19_GL383574v1_alt + 20187 77263 LSM14A 26065 "LSM14A, SCD6 homolog A (S. cerevisiae),
transcript variant 1"
GO:0003725|GO:0039529|GO:0005737|GO:0003727|GO:0033962|GO:0003690|GO:0010494|GO:0000932|GO:0060
340|GO:0007275|GO:0006417|GO:0043231 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_133081_PI430048170 0.0151440434277779 1.12944818348371 10.9265085035784
10.9420422044327 10.9081591585146 P P P 10.7778519989631 10.6944598967525
10.7761780296002 P P P LNCV6_133081_PI430048170 mRNA
AGTGCTCGGAACCCCGTCACCTAATTAAAGTTTCTCGGCTTCCTCAGAGAAATGAAAAAA NM_007277 RefSeq
chr5 + 443218 467294 EXOC3 11336 exocyst complex component 3
GO:0005515|GO:0006996|GO:0000145|GO:0051601|GO:0000149|GO:0061024|GO:0015031|GO:0006887|GO:0044
267|GO:0030667|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_4702_PI430048170 0.238075178884526 1.2521373051824 0.267404975802113
0.870331311147323 0.729171771802264 A A A 0.348609892055089 0.301706998099725
0.309397271218486 A A A LNCV6_4702_PI430048170 mRNA
CTTCTGTGACATGTACATCCTGCTGTGGCTGGCATGTTCCAACACCCACATCATTCACAC NM_014566 RefSeq
chr17 - 3062668 3063607 OR1D5 8386 "olfactory receptor, family 1, subfamily D, member 5"
GO:0050911|GO:0007608|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135060_PI430048170 0.930913208861983 1.02414857544906 1.9724325778906
0.494738164532366 1.65644473312172 A A A 2.155865189704 0.540248683795163
1.24797398266177 A A A LNCV6_135060_PI430048170 mRNA
ACACGTGGGGCCGCAGACATAGCCTGATGGTTAATAAATGTGCCAAGTGAGTTCATGGCA NM_153330 RefSeq
chr3 - 128462431 128467248 DNAJB8 165721 "DnaJ (Hsp40) homolog, subfamily B, member 8"
GO:0090084|GO:0061077|GO:0044183|GO:0051087|GO:0005634|GO:0051082|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_58057_PI430048170 0.179187675155313 0.719310580415224 3.81994504811552
3.43815232393135 2.92322671809574 P P P 3.85740678774246 4.0260163952772

3.85421512765133 P P P LNCV6_58057_PI430048170 mRNA
TGATCCTCCCTGTCTGACCTATCTTTACTTCTCAGCAGTTGATCCAATTAAGGACACCAG NM_001098672 RefSeq
chr11 + 94021211 94114208 HEPHL1 NA hephaestin-like 1 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_139960_PI430048170 0.0131888031207575 0.721726074247813 7.7238006285216
7.62843533278303 7.90980499969988 P P P 8.23777027580624 8.09464250965457
8.34453633705409 P P P LNCV6_139960_PI430048170 mRNA
TAATACAGAAAGGAAACATGGCGTCGGGGAGAGGGATAAAACCTGAATGCCATATTTTAA NM_001289125 RefSeq
chr21 + 33229894 33264513 IFNAR2 3455 "interferon (alpha, beta and omega) receptor 2, transcript variant 4"
GO:0005515|GO:0005886|GO:0006357|GO:0019901|GO:0008283|GO:0035455|GO:0019221|GO:0005576|GO:0009615|GO:0005615|GO:0007259|GO:0060337|GO:0060338|GO:0004905|GO:0019962|GO:0005887|GO:0007166 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138192_PI430048170 0.162490021776182 1.03481269969991 0.387196533117361
0.327662897546709 0.406271616630131 A A A 0.345848246865919 0.322337031350845
0.305715121420726 A A A LNCV6_138192_PI430048170 mRNA
AATCACCCCAAAAATGAATGTTTGCCTTTATTCCGTGTTTGGTACTTGATTCACTTTCTT NM_014406 RefSeq chr22
- 16590757 16592810 CCT8L2 150160 "chaperonin containing TCP1, subunit 8 (theta)-like 2"
GO:0006820|GO:0005737|GO:0006810|GO:0044267|GO:0015269|GO:0005524|GO:0071805|GO:0005253 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_127779_PI430048170 0.0512343536612723 0.530008436640014 5.25029898645599
5.17290229470953 5.65300602015489 P P P 5.79568102723548 6.27404328332959
6.67072766813092 P P P LNCV6_127779_PI430048170 mRNA
CCAGGTTGATAAGTAGGAACTGAAAGTCTTCCAGATTCACAGTAGAAAATTTTATAGACA NM_032436 RefSeq
chr13 + 114314489 114327328 CHAMP1 283489 "chromosome alignment maintaining phosphoprotein 1, transcript variant 1"
GO:0005515|GO:0000793|GO:0034501|GO:0005819|GO:0035372|GO:0005634|GO:0031134|GO:0003676|GO:0046872|GO:0005737|GO:0051315|GO:0000777|GO:0005654 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132183_PI430048170 0.347143545162888 0.758995111434546 0.341499550119173
0.349238517186543 0.326584967411658 A A A 1.23890320784296 0.413358487969997
0.387431475305315 A A A LNCV6_132183_PI430048170 mRNA
CATTGTGATAACAGTTGAGTGCACACAGTTTGCTGTTTGAATCCAATGCACAAAATTAAA NM_001166247 RefSeq
chr6 + 101398984 102070083 GRIK2 2898 "glutamate receptor, ionotropic, kainate 2, transcript variant 3"
GO:0030054|GO:0005886|GO:0005234|GO:0007268|GO:0032839|GO:0051402|GO:0006886|GO:0019228|GO:0030425|GO:0042803|GO:0046328|GO:0043524|GO:0043525|GO:0034220|GO:0045211|GO:0043195|GO:0048169|GO:0015277|GO:0006810|GO:0043204|GO:0001662|GO:0031625|GO:0031624|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_126760_PI430048170 0.760880690016991 0.962780760838214 0.532958734809247
0.327574511504782 0.291155003451325 A A A 0.678620475762849 0.319820798926694
0.2967566541815 A A A LNCV6_126760_PI430048170 mRNA
GGTTTCCTGTCAGATTTAATTCTACCCAGTGGCAAAGAATTTTTTCAATTGTGGCTTTAA NM_130386 RefSeq
chr18 - 319354 500729 COLEC12 81035 collectin sub-family member 12
GO:0005581|GO:0005886|GO:0030169|GO:0006952|GO:0006910|GO:0046872|GO:0006898|GO:0030666|GO:0002221|GO:0009756|GO:0005534|GO:0045087|GO:0051260|GO:0016021|GO:0070062|GO:0005044|GO:0008329 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139749_PI430048170 0.2429350021748860.5707162417481723.00018855994139
0.7842497614351372.2283556200821 A A A 2.80299903953325 3.05178074942568

3.31851841887467 A P P LNCV6_139749_PI430048170 mRNA
CCTAATCCCTCTATTTTAAGATTTCTGAAAAAACACTCCATGTTATATTCTGGGGAAAGC NM_006901 RefSeq chr15
- 71826019 72118099 MYO9A 4649 myosin IXA
GO:0005515|GO:0051056|GO:0007264|GO:0003779|GO:0005524|GO:0046872|GO:0005829|GO:0043547|GO:0003
774|GO:0016461|GO:0008152|GO:0016021|GO:0007601|GO:0005096 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_81765_PI430048170 0.3299254569256930.7257006708535960.4751016623978431.33229212934877
1.45847317596173 A A A 1.995597518026 1.01361721092766 1.66236108049258 A A A
LNCV6_81765_PI430048170 mRNA
AATGTGACCTGGCCAGTGAGGTTATTTTCTTTTGTAGGTGAAAGGTGTAGCAGTCACTCG NM_014138 RefSeq chrX
- 52947255 52995472 FAM156A 29057 "family with sequence similarity 156, member A, transcript
variant 1" GO:0035064|GO:0016021|GO:0005635 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_23359_PI430048170 0.274320376004064 1.12003988374401 5.75176545617917 5.71211448085975
5.8436600552953 P P P 5.70261128111465 5.36600035534298 5.72426126274261 P P P
LNCV6_23359_PI430048170 mRNA
GTGTACATATTTGAACTGGCCAAGAGCAATCAGATGTACCCAGTGCTTATCCCAACGTAG NM_017580 RefSeq chr10
+ 124942122 124987436 ZRANB1 54764 "zinc finger, RAN-binding domain containing 1"
GO:0005515|GO:0004843|GO:0030177|GO:0005634|GO:0005737|GO:0071947|GO:0070536|GO:0016477|GO:0035
523|GO:0007010|GO:0022604|GO:0005654|GO:0008270|GO:0016055|GO:0070530 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_113238_PI430048170 0.699574125309871 1.06335503086729 6.12868970685096
5.81237264721276 6.36397976677714 P P P 6.06997227436227 6.05473891800023
5.96468795858516 P P P LNCV6_113238_PI430048170 mRNA
ATTACAAAAAGGCTGCTGCAGTACACGTTCGTGGGGGACATATTTATGGTTCCCGATGAT NM_153029 RefSeq chr16
- 48538725 48610209 N4BP1 9683 NEDD4 binding protein 1
GO:0005515|GO:0034644|GO:0016605|GO:0005730|GO:0032435|GO:0031397 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133246_PI430048170 0.163038404576435 1.10277050414056 10.5989711888234
10.5665023522895 10.4945094494628 P P P 10.2719264017552 10.4614751839966
10.4952639403619 P P P LNCV6_133246_PI430048170 mRNA
GTCACATGACACCAGCATGCATTGCAGGATTATTAGTGTATTTTGAGTCTGTAAAAATAA NM_020312 RefSeq chr16
+ 57447424 57461275 COQ9 57017 coenzyme Q9 GO:0005739|GO:0006744|GO:0006120 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_129204_PI430048170 0.414407970596677 0.710192722662809 3.40198913903486
0.313775052530969 0.323571628735274 P A A 1.69244230048041 2.21059796941249
3.39721727853741 A A P LNCV6_129204_PI430048170 mRNA
TGATAATCAGTTGATCTCAGGTTTTTCACTGTACATTACTTTGCAGATATGGACAGCCTT NM_018938 RefSeq chr5
+ 141121749 141125621 PCDHB4 56131 protocadherin beta 4
GO:0016339|GO:0005737|GO:0005886|GO:0005887|GO:0005509|GO:0007268|GO:0045111|GO:0016021|GO:0007
155|GO:0007416|GO:0007156|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135128_PI430048170 0.0209030086881206 0.601940333533386 4.52609552799505
4.47050270073243 4.04027335303471 P P P 4.93525456563626 5.27891098485167
5.04524869944673 P P P LNCV6_135128_PI430048170 mRNA
ATGCCTAGCCTGCACGTAGCTTTTCCGTCTTCACCCCAAATAAAGTCCTAATGCATCAGC NM_020321 RefSeq chr7
+ 151048291 151052756 ASIC3 9311 "acid sensing (proton gated) ion channel 3, transcript variant 2"
GO:0005261|GO:0005886|GO:0009408|GO:0005272|GO:0010447|GO:0050915|GO:0030165|GO:0055085|GO:0007
165|GO:0005737|GO:0015280|GO:0034220|GO:0005887|GO:0042931|GO:0042930|GO:0050968|GO:0006810|GO:0
050966|GO:0035725|GO:0050965|GO:0007600 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145324_PI430048170 0.193960322649837 0.951187085129671 0.259953941091526

0.3489506036060460.296484895405726A A A 0.4463858460249430.34591792617302
0.328235886347725A A A LNCV6_145324_PI430048170 mRNA
GTGCTGATCTTTTGCCAACTATACGGACGTGGAGTTTTTCCTTTTCAGAATATGATTATT NM_001146110 RefSeq
chr1 + 66924894 66988619 MIER1 57708 "mesoderm induction early response 1, transcriptional
regulator, transcript variant 10"
GO:0005515|GO:0007165|GO:0005737|GO:0017053|GO:0003682|GO:0005654|GO:0004871|GO:0043123|GO:0003
677|GO:0031937|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142152_PI430048170 0.1156385951098271.21822700491942 8.86442347839303
9.14385438340612 9.20115945961457 P P P 8.77680810632881 8.80284121765205
8.79730086104884 P P P LNCV6_142152_PI430048170 mRNA
CCCATCTGTGAGTTTGTCTTATTGGCGCCTTTTTCCTCAGCTGTCTTCCAAGTATTATTT NM_018660RefSeq chr8 -
28345584 28386460 ZNF395 55893 zinc finger protein 395
GO:0006355|GO:0005737|GO:0005634|GO:0000978|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138805_PI430048170 0.2019314552244450.5747851297350132.0457205556732
0.3217250068397351.60724752780666 A A A 2.28596542583927 2.48431926250555
2.06543427360833 A P A LNCV6_138805_PI430048170 mRNA
CATCCATTAATATACTTCAGTAAGTATGTGAGTGGATTATGAGGTCTTAAAATGCTGGGT NM_022160RefSeq chr9
+ 22446840 22452473 DMRTA1 63951 DMRT-like family A1
GO:0000987|GO:0006355|GO:0001541|GO:0003700|GO:0007548|GO:0005634|GO:0060179|GO:0046872|GO:0042
803|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136922_PI430048170 0.6906541379267310.8384772859522311.45105844738396
0.6024408849876810.572072960808121A A A 0.3496274641585681.71123571219786
1.19908452151906 A A A LNCV6_136922_PI430048170 mRNA
CCTGCCTTAATTCTATCAGCCAGTTTCTCTTGTGATTCTTTGGCTGGTGTCTTTTAGTTT NM_144648RefSeq chr7 +
134127351 134264181 LRGUK 136332 leucine-rich repeats and guanylate kinase domain containing
GO:0016310|GO:0005737|GO:0016301|GO:0005654|GO:0005524 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_126201_PI430048170 0.00522216668408676 6.81776125762309 6.30347501053028
6.25429581265798 6.23727734072953 P P P 3.07379538856695 3.53697414822707
3.78865404474534 P P P LNCV6_126201_PI430048170 mRNA
GGTGAGTTCTTCTGTCCAGCGTCAGTATTTTGATGGTGGCTTTAGACTTGCCAGATAACA NM_001288747 RefSeq
chrX + 154762741 154777689 DKC1 1736 "dyskeratosis congenita 1, dyskerin, transcript variant 3"
GO:0009982|GO:0005515|GO:0006396|GO:0005697|GO:0015030|GO:0008283|GO:0003720|GO:0003723|GO:0006
364|GO:0005730|GO:0005634|GO:0001522|GO:0005737|GO:0000723|GO:0005654|GO:0007004 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137470_PI430048170 0.0511804136619452 0.79282819962251812.6811900136141
12.4480551160795 12.6883401104614 P P P 12.9853308327035 12.7644833305418
13.0684033390069 P P P LNCV6_137470_PI430048170 mRNA
AGCCAAGATCGAAGATTTATCCCAGCAAGCACAACTAGCAGCTGCTGAGAAATTCAAAGT NM_001113203 RefSeq
chr12 - 56712426 56725542 NACA 4666 "nascent polypeptide-associated complex alpha subunit,
transcript variant 1"
GO:0005515|GO:0006355|GO:0003713|GO:0048742|GO:0061384|GO:0005634|GO:0015031|GO:0003677|GO:0006
412|GO:2000138|GO:0006351|GO:0005737|GO:0048633|GO:0017025|GO:0016032|GO:0043403|GO:0003231|GO:0
005854|GO:0070062|GO:0010664 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142658_PI430048170 0.1559929296286820.5327544620494440.563867342143686
0.3906748384921761.97864039208858 A A A 1.67281777707864 2.36717934595297
2.09950399001692 A A A LNCV6_142658_PI430048170 mRNA
GAGAGAGGCAGCACTGTAAACTGAAGTCAAATAAATTCAGCTCTTAATGAATCCTTAAAA NM_014927RefSeq chrX

+ 21374417 21654695 CNKSR2 22866 "connector enhancer of kinase suppressor of Ras 2, transcript variant 1"
GO:0043005|GO:0005794|GO:0005886|GO:0045211|GO:0043025|GO:0009966|GO:0070062|GO:0042802 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125756_PI430048170 0.7794346491745360.9912764988282380.269891304701975
0.2949055008254720.401326824321968A A A 0.36966311044575 0.324835751977121
0.312316935187427A A A LNCV6_125756_PI430048170 mRNA
TGCTTCTGTGTGCCCGGATAAAAGTAAAGGAAGTTACCGGCAGCATTTTTTCAAGCACGG NM_006378RefSeq chr9
- 89377236 89479696 SEMA4D 10507 "sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D, transcript variant 1"
GO:0005515|GO:1900220|GO:0043931|GO:0005886|GO:0008360|GO:0050732|GO:0050731|GO:0005615|GO:0010693|GO:0048672|GO:0006955|GO:0007411|GO:0004872|GO:0007155|GO:0043066|GO:0030335|GO:0005102|GO:0014068|GO:0000122|GO:0048814|GO:0007162|GO:0031344|GO:0045668|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134985_PI430048170 0.5335564672247491.0244349821027 0.325805326444803
0.3290538667386990.459528844263275A A A 0.3453279957413720.307049634412006
0.361065178316478A A A LNCV6_134985_PI430048170 mRNA
GTATACCTGTGCAGGCACTAGTCCTTTACAGATGACCATTCTGATGTCTCTGTTCATCTT NM_002171RefSeq chr9
- 21206180 21207143 IFNA10 3446 "interferon, alpha 10"
GO:0005132|GO:0019221|GO:0005576|GO:0033141|GO:0045343|GO:0005125|GO:0005615|GO:0002250|GO:0051607|GO:0060337|GO:0060338|GO:0007596|GO:0042100|GO:0045087|GO:0006959|GO:0030183|GO:0043330|GO:0002286|GO:0002323. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135949_PI430048170 0.2071253902367830.6901585189656591.59886594831248
2.68336925663382 2.02782940456559 A A A 2.40753055019438 2.58369734379689
3.05389776747837 A P P LNCV6_135949_PI430048170 mRNA
CCCCGGTACTTCTGTATTTTTTGCATTTTTCTTGCACTAGTAATTACCACAAACCTATAA NM_182521RefSeq chr2 -
186827479 186849170 ZSWIM2 151112 "zinc finger, SWIM-type containing 2"
GO:0000209|GO:0004842|GO:0016874|GO:0006915|GO:0008270|GO:0043621 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140030_PI430048170 0.37716439043265 1.36877746515889 0.442877517297881
1.13374949472417 1.61884067109425 A A A 1.04012044949185 0.521911572919192
0.430542026649401A A A LNCV6_140030_PI430048170 mRNA
CTTCCTATTTTCAGCTCCATTTAAACCAGGAGTTATTTATAAAGACCTCTTCCTCTCATG NM_013305RefSeq chr18 -
46679117 46757169 ST8SIA529906 "ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5"
GO:0003828|GO:0030173|GO:0008373|GO:0000139|GO:0005975|GO:0006688|GO:0006488|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135018_PI430048170 0.0256322795538550.41679559515915 4.75998855270022
4.17657344040453 4.94105590340316 P P P 5.95916411456438 5.82038837206286
5.98586652236615 P P P LNCV6_135018_PI430048170 mRNA
GCAGCAGTATTTGGTTTGCATTTAAAGTGAAAATAACGGCTGTTATTTTTCTGGCATTAC NM_005633RefSeq chr2
- 38981548 39120463 SOS1 6654 son of sevenless homolog 1 (Drosophila)
GO:0005515|GO:0008286|GO:0017124|GO:0005886|GO:0007264|GO:0007265|GO:0050900|GO:0005829|GO:0007173|GO:0007411|GO:0043025|GO:0005089|GO:0005088|GO:0051056|GO:0048011|GO:0043065|GO:0046982|GO:0045742|GO:0051057|GO:0014069|GO:0030168|GO:0097190|GO:0003677|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139183_PI430048170 0.00430053591583115 0.61961341243687912.8826293266279
12.9327635644832 13.1389953397832 P P P 13.5059310293904 13.7215115115088
13.7961136485061 P P P LNCV6_139183_PI430048170 mRNA
GCTGGGTGTTTCAGTTTGAAAATATTTTGTTGCCTTCATCTTCACTGCAATTTTGTGTAA NM_000903RefSeq chr16 -

69709400 69726630 NQO1 1728 "NAD(P)H dehydrogenase, quinone 1, transcript variant 1"
GO:0005515|GO:0006805|GO:0004128|GO:0007584|GO:0045471|GO:0006521|GO:0007568|GO:0009636|GO:0044
281|GO:0043086|GO:0007271|GO:0042802|GO:0005829|GO:0006809|GO:0034641|GO:0005737|GO:0043525|GO:0
019430|GO:0003955|GO:0043025|GO:0032355|GO:0070062|GO:0055114|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_79428_PI430048170 0.6327857947864561.03957046024972 7.64741837102409 7.41085127911549
7.54440153673274 P P P 7.39519078959778 7.37843705896298 7.65393813950008 P P P
LNCV6_79428_PI430048170 mRNA
CCAGCAGCCCCTCAGGATCAATGGTGTTAAGGTATACACTGAAAATGTAGACAAAAGGCA NM_020728 RefSeq chr7
- 158730997 158829628 ESYT2 57488 extended synaptotagmin-like protein 2
GO:0005515|GO:0008429|GO:0005509|GO:0031210|GO:0031227|GO:0006897|GO:0031234|GO:0042802|GO:0005
544|GO:0016020|GO:0005887|GO:0006869|GO:0044232|GO:0035091 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_135909_PI430048170 0.0708490938357047 1.16376177844504 12.542243698853
12.5602638427586 12.4583829013694 P P P 12.1886039895989 12.4303713106628
12.2771239590614 P P P LNCV6_135909_PI430048170 mRNA
AGCTGTTCGGGCCCTTTACCAGGAATTACTATGTTCGGGCCGTCCTGCATCTCCTGCTCT NM_000101 RefSeq chr16
- 88643288 88651084 CYBA 1535 "cytochrome b-245, alpha polypeptide"
GO:0045730|GO:0005515|GO:0002474|GO:0017124|GO:0005886|GO:0030307|GO:0051279|GO:0006801|GO:0071
480|GO:0050665|GO:0046872|GO:0030425|GO:0070257|GO:0005739|GO:0016324|GO:0006954|GO:0071230|GO:0
016175|GO:0071356|GO:0043025|GO:0030670|GO:0031667|GO:0071333|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137570_PI430048170 0.4824501441235820.7983200511417580.469217424774048
1.88723163292424 2.12941398023038 A A A 2.33535466951086 1.90955122752422
1.60642430290945 A A A LNCV6_137570_PI430048170 mRNA
TTTCTGCTTCTGTTCCAAAAATAAAAGCTGGCACTTGGCTTCCGCTTGTCTCTTAAAAAA NM_000420 RefSeq
chr7_KI270803v1_alt - 964180 985483 KEL 3792 "Kell blood group, metallo-endopeptidase"
GO:0005515|GO:0008361|GO:0005886|GO:0042552|GO:0006874|GO:0031133|GO:0048741|GO:0046872|GO:0010
961|GO:0042310|GO:0006508|GO:0016021|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142935_PI430048170 0.0843683092309033 0.4134552188130160.58692931607405
0.3881638155252341.30530372218869 A A A 1.53757993901198 1.550094072803
2.79579752300854 A A P LNCV6_142935_PI430048170 mRNA
TTTGATGTTTTGTCATTTGAGAGCATGTATTCTAAATTATGTGCCCATGGGACAAGAGAT NM_015652 RefSeq chr10
+ 96981283 96985828 C10orf12 26148 chromosome 10 open reading frame 12 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134957_PI430048170 0.2624008764039341.03672881263068 0.387508126567571
0.2885409474828850.285188220490209 A A A 0.2581807989803890.295387120548281
0.25354804258562 A A A LNCV6_134957_PI430048170 mRNA
AATGATATCCCTGTTCTAATTCCACTCTGGCTAAACTGAAAGTAAAGATCCTTAAGCTTA NM_001286389 RefSeq
chr14_KI270845v1_alt - 148686 162583 TMEM179 388021 "transmembrane protein 179, transcript variant
1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108437_PI430048170 0.2619582457440040.5955236595296671.5724118430605
2.88331201131216 3.22000185408764 A A P 4.05654090002855 2.91771425153085
3.14311530790257 P P P LNCV6_108437_PI430048170 mRNA
CCCCAGGACACAATTGAATTAAACAGATTGAATTTAGAATCTTCCAATTCAAAGTACTCC NM_001114091 RefSeq
chr17 - 47117696 47189312 CDC27 996 "cell division cycle 27, transcript variant 1"
GO:0005515|GO:0007094|GO:0005813|GO:0008283|GO:0019903|GO:0051437|GO:0005819|GO:0005634|GO:0051
436|GO:0031145|GO:0051439|GO:0005829|GO:0005737|GO:0070979|GO:0005680|GO:0005654|GO:0005876|GO:0
000278|GO:0007091. NA - . NA NA NA NA NA NA NA NA NA

LNCV6_138644_PI430048170 0.0039492814303798 0.4825083206140537.27072437196265
7.28553954579636 7.41160434000126 P P P 8.25079060328292 8.27766571405814
8.57482175467691 P P P LNCV6_138644_PI430048170 mRNA
TTTCTGAATTGTAAAACCCCCTTTGGGAGTCCCTGGTTTCTTATTGAGCCAATTTCTGGG NM_019010RefSeq chr17
- 40875888 40885243 KRT20 54474 "keratin 20, type I"
GO:0005882|GO:0005515|GO:0005737|GO:0045109|GO:0005200|GO:0050708|GO:0006915|GO:0033554 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134562_PI430048170 0.8131260889499730.9507074297096974.17588755783395
4.48760339635563 4.49566883661 P P P 4.81501065555231 4.2799407266093 4.22978965010727 P
P P LNCV6_134562_PI430048170 mRNA
CCAGCCTTCTTGCTCTCAGAGCTATTGTTCAAGCAGAAAACAAGCTGCTTTTATTACAGT NM_001048205 RefSeq
chr14 + 24172024 24180257 REC8 9985 "REC8 meiotic recombination protein, transcript variant 2"
GO:0007286|GO:0005634|GO:0000800|GO:0001556|GO:0007283|GO:0030999|GO:0009566|GO:0007126|GO:0000
724|GO:0072520|GO:0007062|GO:0034991|GO:0000778|GO:0001673|GO:0007141|GO:0007131 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_115385_PI430048170 0.0688037556708722 0.3696165856167230.388290306413553
0.3938078039661640.426357263157659A A A 2.14179009600661 2.1085146436307
1.00426382986719 A A A LNCV6_115385_PI430048170 mRNA
TGCCCTGAAGGTGTTCCCCATGTATCGCTACTTCGTGACAGTGTGGCTGAGGCACTACAA NM_001287395 RefSeq
chr2 + 233775678 233833423 MROH2A 339766 maestro heat-like repeat family member 2A NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134552_PI430048170 0.000352729897729739 1.27968921518137 10.434868483069
10.5014300221274 10.5068845767814 P P P 10.0889450410338 10.1327092747008
10.1544864198026 P P P LNCV6_134552_PI430048170 mRNA
TTTTTGTATGATCTAGTAACTTGCAAACAGACCAAATGGATGAGAGGCGGGGACCGTGCA NM_018270RefSeq chr20
+ 62796452 62800593 MRGBP 55257 MRG/MORF4L binding protein
GO:0006355|GO:0006325|GO:0043189|GO:0005654|GO:0005634|GO:0040008|GO:0006351|GO:0016568 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137029_PI430048170 0.0153247292108888 1.6363481420766 5.49238577991198
5.54398840051587 5.19421821338497 P P P 4.92232750431104 4.70233543112214
4.46202155319302 P P P LNCV6_137029_PI430048170 mRNA
AAACAAGAATAAAAGAAGCTGTTCGCTAGACCCCATAATGGGCAGGTTTTAAACAAAAAA NM_138439RefSeq chr16
+ 2883194 2899382 FLYWCH2 114984 "FLYWCH family member 2, transcript variant 1"
GO:0008150|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127234_PI430048170 0.6758053485378430.92709796413768 8.84258757756915
8.50393787701227 8.77421673100199 P P P 9.14061882456225 8.54195990842628
8.72063542332783 P P P LNCV6_127234_PI430048170 mRNA
CCTCCCTCTGGTTTAAAGAGATATATAAACTAATTTCACATAATTTGTGTGTGCAGGTGA NM_003324RefSeq chr12
+ 2890866 2941140 TULP3 7289 "tubby like protein 3, transcript variant 1"
GO:0005515|GO:0005886|GO:0005634|GO:0045879|GO:0060831|GO:0009952|GO:0048702|GO:0032403|GO:0031
076|GO:0060434|GO:0006355|GO:0005930|GO:0005730|GO:0005546|GO:0001843|GO:0021953|GO:0005576|GO:0
072372|GO:0005929|GO:0060348|GO:0008277|GO:0007186|GO:0007420|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142356_PI430048170 0.0146443165832932 0.95318622119581 0.369538511909839
0.3713819183406430.332254562617808A A A 0.4414480668986170.432043450495705
0.407315221544339A A A LNCV6_142356_PI430048170 mRNA
TCCTCTGTATCTTTAGAATTTCCCAGGTGAGCACTCATAACGCAAGTAATAAAATACTGA NM_052956RefSeq chr16
- 20623236 20691256 ACSM1 116285 acyl-CoA synthetase medium-chain family member 1
GO:0042632|GO:0019395|GO:0006805|GO:0072562|GO:0018874|GO:0044281|GO:0005525|GO:0005524|GO:0047

760|GO:0046872|GO:0015645|GO:0005759|GO:0006633|GO:0003996|GO:0019605|GO:0015980|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139509_PI430048170 0.9843886642912830.8812143421095793.13641111581233 2.49709054232088 3.38621620642726 A A P 1.94387857940046 3.17421339108897 3.94261083818206 A P P LNCV6_139509_PI430048170 mRNA
TTTCTTGAGATGCATTGTCCTGCTAACCCACAAACCTGTTTGGAAATAAACATGGAAGAA NM_014345RefSeq chr6 - 43336069 43369443 ZNF318 24149 zinc finger protein 318
GO:0051321|GO:0006355|GO:0005737|GO:0008270|GO:0005654|GO:0003676|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139278_PI430048170 0.0901641349473201 0.82585883131071 7.05463904532178 6.95969597875237 6.7208260992083 P P P 7.26730247733729 7.13560002186244 7.17737020146032 P P P LNCV6_139278_PI430048170 mRNA
TTTCTTTGATAATTGATGTGATAAGGAAAAAAGTCCTATTTTTATACTCCCAACAAAAAA NM_018056RefSeq chr1 + 32072901 32102866 TMEM39B 55116 transmembrane protein 39B GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111071_PI430048170 0.8141890208745030.9559891914454987.41930909818602 7.05265951821161 7.08644322405629 P P P 7.57924867310592 7.13269164778429 7.00575335683736 P P P LNCV6_111071_PI430048170 mRNA
AGCCAATACCAGCCGCCATCCTTCTCCAGAATTCTTGTAAATAAAATAAATCCCTCTTTG NM_001282714 RefSeq chr3 - 58564111 58627610 FAM107A 11170 "family with sequence similarity 107, member A, transcript variant 4" GO:0043005|GO:0003674|GO:0005634|GO:0001558 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129354_PI430048170 0.7984543442509690.9712817836485855.37099143037846 5.04378762279586 4.48949776508526 P P P 4.86740782476276 5.23647208119697 5.03591725721981 P P P LNCV6_129354_PI430048170 mRNA
AATGCTTTGTAAGCTTTCTCTCCCCACATAAGAATGCCCTGTAAGCATTTTGTTAAATAT NM_033480RefSeq chr6 + 53065458 53100872 FBXO9 26268 "F-box protein 9, transcript variant 2" GO:0005515|GO:0032006|GO:0005737|GO:0004842|GO:0016567|GO:0045087|GO:0045444|GO:0000151|GO:0031146|GO:0019005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143691_PI430048170 0.0307881523151553 0.5117059527788042.60244864505384 2.08615024046947 2.88384951810285 A A A 3.4359398777015 3.29049945626464 3.8057313203815 P P P LNCV6_143691_PI430048170 mRNA
GCACTGTATGCCATAATGAATGTGAGAAAGCTGTCATTTAAATCTCATCCATTATTGCTA NM_144689RefSeq chr19 + 37078479 37129749 ZNF420 147923 zinc finger protein 420
GO:0005515|GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137938_PI430048170 0.00948564598292997 0.4236390690064015.89403008738101 5.25160100892747 5.61367357774058 P P P 6.70760786623707 6.79718705512991 7.02404018463403 P P P LNCV6_137938_PI430048170 mRNA
TGGCCTGGAAGAGTGATATGCTTGCTGCTTAATCAAAGGATTAAAGATTTAAAGATGTCT NM_001136223 RefSeq chr1 + 211259365 211316383 RCOR3 55758 "REST corepressor 3, transcript variant 1" GO:0005515|GO:0006355|GO:0003682|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139785_PI430048170 0.0283311373809691.09230196140611 0.35651891852189 0.4489400566345520.389611229933886A A A 0.2577151332682670.294055822272422 0.262436966325191A A A LNCV6_139785_PI430048170 mRNA
ATCCAGTACCCAAACTACTGTTCCTTCAAAAGCCAGCAGTGTCTGATGAGAAACCGCAAT NM_032489RefSeq chr12 - 6638075 6647414 ACRBP 84519 acrosin binding protein
GO:0008150|GO:0003674|GO:0001669|GO:0005634|GO:0005576 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_51410_PI430048170 0.0466888262227846 0.363292576822135 1.69471366981553
0.604174776380276 0.476672616853828 A A A 2.26062499784579 2.59607192999542
2.60566879316082 A A P LNCV6_51410_PI430048170 mRNA
CCTAGGGGTTCATAGAAAAAGGAAGTTTGCAGATGCAATAAATGTGAGGAAGTATTTAAT NM_001265588 RefSeq
chr16 + 31873757 31917308 ZNF267 10308 "zinc finger protein 267, transcript variant 2"
GO:0006355|GO:0003700|GO:0007275|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127484_PI430048170 0.0341615798765514 0.651822257257934 3.35563328200169
3.41559582691898 3.43338438311897 P P P 3.91162320002169 3.86328912458246
4.25141916261941 P P P LNCV6_127484_PI430048170 mRNA
ATGCCATGTCTGATACCTTTAAGTCCATAAGCATTCAATTTTCTCATTTCCACCTTCATC NM_001145427 RefSeq chr5
+ 54517758 54546586 SNX18 112574 "sorting nexin 18, transcript variant 3"
GO:0005515|GO:0000281|GO:0030136|GO:0005546|GO:0006886|GO:0036089|GO:0031234|GO:0006897|GO:0030
426|GO:0043547|GO:0016050|GO:0007067|GO:0016197|GO:0043025|GO:0016023|GO:0030659|GO:0010008|GO:0
070062|GO:0005768. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118229_PI430048170 0.622801681560508 1.11248919932174 5.77931904337521
6.38467468959219 6.45444445386345 P P P 6.02086844393787 5.88617983408704
6.30793547419999 P P P LNCV6_118229_PI430048170 mRNA
AAAGGATTACCTGATATGGATTCTTCGATCCTTATACACCACAATGGAGGTATCCCAGCC NM_018202 RefSeq chr1
+ 25430857 25500207 TMEM57 55219 "transmembrane protein 57, transcript variant 1"
GO:0044306|GO:0030424|GO:0008150|GO:0003674|GO:0031965|GO:0007420|GO:0045202|GO:0005634|GO:0016
021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93124_PI430048170 0.200884271975608 1.20823638922099 9.50424344967769 9.43616569212744
9.3659159436708 P P P 8.92699843945839 9.44971281663008 9.06199935171577 P P P
LNCV6_93124_PI430048170 mRNA
TTGAGAACCTCAAGGAGGAGCTGGCCTACCTGAAGAAGAACCACGAGGAGATGAACGCCC NM_000422 RefSeq
chr17 - 41619439 41624630 KRT17 3872 "keratin 17, type I"
GO:0005515|GO:0005882|GO:0042289|GO:0045109|GO:0030307|GO:0031424|GO:0045727|GO:0071944|GO:0031
069|GO:0007165|GO:0051798|GO:0005737|GO:0008544|GO:0005200|GO:0032395|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126706_PI430048170 0.594872745766217 1.10379701084426 2.84052725151707
2.85219008476859 2.54809580425414 A A A 1.99911000348347 3.30419550294512
2.15524434137504 A P A LNCV6_126706_PI430048170 mRNA
TGACTTCAAATTCCAGGTGTGGAGGAAGATGTTCCGGGCTCTGATGCCAGCGCTGGAGGA NM_001008274 RefSeq
chr16 + 31214020 31225189 TRIM72 493829 "tripartite motif containing 72, E3 ubiquitin protein ligase"
GO:0042383|GO:0007517|GO:0001786|GO:0001778|GO:0051260|GO:0008270|GO:0006887|GO:0003012|GO:0030
659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142382_PI430048170 0.232407951578451 1.3487954798574 8.10067057294247
7.65481918785931 7.43282150419764 P P P 7.65183503175186 7.3814176381971
6.82253868926915 P P P LNCV6_142382_PI430048170 mRNA
GTGGAGGCTTTGAATCTCTCAGAAAAAAGGAAAGACAGGAAAGCTCAGAAACAAAGAGAC NM_001293171
RefSeq chr11_KI270721v1_random + 47588 51476 HOTS 103344718 H19 Opposite Tumor Suppressor
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139772_PI430048170 0.674986230126704 0.987101458649432 0.437707491976673
0.457878618075363 0.36681354456237 A A A 0.499864081398754 0.401688438971629
0.416662320939434 A A A LNCV6_139772_PI430048170 mRNA
TTCCTCTTCGGTGAATGCAGGTTATTTAAACTTTGGGAAATGTACTTTTAGTCTGTCATA NM_021192 RefSeq chr2
+ 176107355 176109588 HOXD11 3237 homeobox D11

GO:0001656|GO:0001658|GO:0006355|GO:0010720|GO:0009954|GO:0001759|GO:0009953|GO:0009952|GO:0006351|GO:0043565|GO:0007338|GO:0048589|GO:0060351|GO:0060272|GO:0005654|GO:0032332|GO:0035115|GO:0042733 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134240_PI430048170 0.57383416048972 0.8630802441492865.33820011282471 5.31677056961675 5.58166744235008 P P P 5.16949860869484 5.54079335286398 6.0443367018678 P P P LNCV6_134240_PI430048170 mRNA
CTAATTAAAAAGTAGCCAAGCTAAGATGCCTGGCTGGGCTTCTGAGGAATTAATACACTC NM_006784RefSeq chr1 + 117929748 117960426 WDR3 10885 WD repeat domain 3
GO:0000462|GO:0031965|GO:0030515|GO:0032040|GO:0005730|GO:0005634|GO:0034388 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142018_PI430048170 0.1995756788674271.2570651743563 4.4510671099408 4.95938795111417 4.95273278412718 P P P 4.26085481669789 4.49343865493922 4.64899906862788 P P P LNCV6_142018_PI430048170 mRNA
ATCCAAAACCAGCCTGGATTTCATACATGGACTTCTGATTAAAAGTGGCAGGTTGTGCAT NM_018530RefSeq chr17 - 39904594 39917540 GSDMB 55876 "gasdermin B, transcript variant 2" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131185_PI430048170 0.9714194730505150.9918548055857730.501089204056517 1.07808147841077 0.554192700765078A A A 0.3908617192123190.71151267408266 1.06155277852896 A A A LNCV6_131185_PI430048170 mRNA
AGTACCTTTGGCAGCTCACCTCTAACCAGTAAAATAAGAGGATTCCATGGTTTCAAAAAA NM_019114RefSeq chr9 - 109171973 109320964 EPB41L4B 54566 "erythrocyte membrane protein band 4.1 like 4B, transcript variant 2" GO:0008092|GO:0005737|GO:0005200|GO:0045177|GO:0031032|GO:0005856|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132189_PI430048170 0.00111319674306632 2.13303811301136 4.52856621400492 4.77834290271843 4.51639216575836 P P P 3.34137733471651 3.67390499549093 3.52558871008274 P P P LNCV6_132189_PI430048170 mRNA
AGGCTGGGCCCAGGGCAGGACACCAGTCCTGATGTCCACCTTGATGTCTACCTTAACCCT NM_080669RefSeq chr17 - 28394641 28406212 SLC46A1 113235 "solute carrier family 46 (folate transporter), member 1, transcript variant 1"
GO:0015886|GO:0005886|GO:0009986|GO:0015232|GO:0015884|GO:0006767|GO:0044281|GO:0031526|GO:0008517|GO:0055085|GO:0006879|GO:0016324|GO:0005542|GO:0005737|GO:0006766|GO:0046655|GO:0016021|GO:0015350|GO:0051958. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140265_PI430048170 0.00850318323244928 1.7440149764228 4.25061373905056 4.21335220736848 3.8790046670125 P P P 3.20243579759752 3.3175063662985 3.43466813330833 P P P LNCV6_140265_PI430048170 mRNA
AGCCATGCGGTTAATTCCTGACTTAGTTTATTTTTGCAAAACGTCGATCTCCTCCTCCCC NM_020971RefSeq chr19 + 40467218 40576459 SPTBN4 57731 "spectrin, beta, non-erythrocytic 4, transcript variant sigma1"
GO:0005515|GO:0008091|GO:0005886|GO:0007605|GO:0007409|GO:0019226|GO:0016363|GO:0005829|GO:0070852|GO:0043194|GO:0005737|GO:0005543|GO:0005912|GO:0007411|GO:0033135|GO:0043203|GO:0043025|GO:0007628|GO:0040018|GO:0061337|GO:0016192|GO:0007016|GO:0070062|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145100_PI430048170 0.0689325097986529 1.52012545283012 2.98904291534858 3.23646001387031 2.93805790398478 P P P 2.70362846874935 2.04668772501633 2.54065124377943 P A P LNCV6_145100_PI430048170 mRNA
TTGAGAGAGGAACAACAGAACAGTGTCGTGCTAGAAGACTTGTTGGAAAACATGGAGGCA NM_001166136 RefSeq chr4 - 5562418 5709548 EVC2 132884 "Ellis van Creveld syndrome 2, transcript variant 2"
GO:0005929|GO:0060170|GO:0005737|GO:0005634|GO:0016021|GO:0005856|GO:0007224 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91058_PI430048170 0.1368933610046491.2754384357303 8.77654406798391 9.01776744453043

8.66372750568651 P P P 8.70762417706108 8.4972598713306 8.17379446240198 P P P
LNCV6_91058_PI430048170 mRNA
AATTCAAGAGAAGCTTCAAAGTGCGCGTGTCCACAGAGACCTCCAGCCCCCTGTCTCCAC NM_004292 RefSeq chr11
- 66332070 66336529 RIN1 9610 Ras and Rab interactor 1
GO:0005515|GO:0008306|GO:0005886|GO:0030425|GO:0006897|GO:0043547|GO:0007165|GO:0005737|GO:0031
914|GO:0043025|GO:0007613|GO:0005856|GO:0017016|GO:0005096 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140764_PI430048170 0.0330335173978424 0.80727142712444211.8177005274504
11.670992175032 11.7074935875241 P P P 12.1860389037135 11.9724525557687
11.9568409467399 P P P LNCV6_140764_PI430048170 mRNA
AGCTCAACCCCCTCCTTTCTCCCAGTGGTGACAAGATATCAATAAACTTATTTTTAATAC NM_001012643 RefSeq
chr19 - 45890022 45902604 MYPOP 339344 "Myb-related transcription factor, partner of profilin"
GO:0001078|GO:0003682|GO:0005634|GO:0000122|GO:0000978|GO:0042803|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143682_PI430048170 0.41807716371032 0.2510736222094060.393664225309559
0.3778330270931010.255053302421221 A A A 0.3483532809684533.65560132076403
0.362423130739513 A P A LNCV6_143682_PI430048170 mRNA
CCCGAATACTCTGTCTATAGTGACACACTGTAGGTGTCATAAATTTTAAGAAACCTGCTT NM_001199563 RefSeq
chr6 - 105096823 105137174 BVES 11149 "blood vessel epicardial substance, transcript variant C"
GO:0090136|GO:0005886|GO:0008360|GO:0060931|GO:0016328|GO:0043088|GO:0007517|GO:0030552|GO:0032
314|GO:0002027|GO:0002244|GO:0005198|GO:0042391|GO:0001921|GO:0034446|GO:0040017|GO:0005923|GO:0
016021|GO:0016192. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130705_PI430048170 0.0159330187474429 0.78511099594473810.9824343982541
11.1720601205427 11.0506718529076 P P P 11.397474987501 11.4572928028959
11.4031639389648 P P P LNCV6_130705_PI430048170 mRNA
GCCTGGGACTCAGCATTTCTGATATGCCTTAAGAATTCATTCTGTTTTGTACAATTATTT NM_001025604 RefSeq chr19
+ 18001131 18014102 ARRDC2 27106 "arrestin domain containing 2, transcript variant 2"
GO:0007165|GO:0005886|GO:0031410 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131136_PI430048170 0.4388243566150980.9114454622098878.01265973293242
8.19107879588835 7.95248345099462 P P P 8.42494013857692 8.08069221328926
8.02988663770832 P P P LNCV6_131136_PI430048170 mRNA
TCTGTTGGGTTCCTGGGATGGAATCAGTGCATCATAAAGGGCATTCTTTAAGCAGAGAAG NM_006227 RefSeq chr20
- 45898619 45912364 PLTP 5360 "phospholipid transfer protein, transcript variant 1"
GO:0006629|GO:0006869|GO:0005576|GO:0030317|GO:0010189|GO:0005615|GO:0008289 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132302_PI430048170 0.0196132703630903 0.3303111552811326.7705926069908
6.70646472911131 6.98073059014585 P P P 7.90091690907247 8.41737892102552
8.80797120977205 P P P LNCV6_132302_PI430048170 mRNA
CAGTACTTGGAATTGTGTTCTTTATGGTTGTAGTGTTGGTAAAGCACTAATATGCAGAAA NM_001663 RefSeq chr14
+ 49893017 49897054 ARF6 382 ADP-ribosylation factor 6
GO:0090162|GO:0005515|GO:0035020|GO:0005886|GO:0007264|GO:0033028|GO:0097284|GO:0003924|GO:0031
527|GO:0006928|GO:0031996|GO:0030139|GO:0015031|GO:0032154|GO:0031529|GO:0051489|GO:0030838|GO:0
060998|GO:0007155|GO:0016192|GO:0005938|GO:0070062|GO:0005794|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_110473_PI430048170 0.3657874550120560.7096483500998120.437272489468272
0.2759242284646151.97447797903715 A A A 1.89610357301758 0.946051080248515
1.80871446788639 A A A LNCV6_110473_PI430048170 mRNA
AGACGTTGTCCCGACTGCACAGAGGCTGCTCTGCAGCTCCTTAAAGGCGCTAGGCGTGAC NM_173632 RefSeq chr19
+ 57746795 57758159 ZNF776 284309 zinc finger protein 776

GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132003_PI430048170 0.4043353078016791.02684933661034 0.507179635676929
0.4835210397567730.541446610084592A A A 0.4876914540346050.5248269584772510.4028485799128
A A A LNCV6_132003_PI430048170 mRNA
TGACAATGAATACAAATCAAATAGCACCCAAAATTGTGAAGGATACGGAACCTCATTGAT NM_001102651 RefSeq
chr19 + 2819873 2836735 ZNF554 115196 zinc finger protein 554
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_124137_PI430048170 0.3751256321295440.9381473445079314.0402486180174
13.9636031151919 14.0731396151734 P P P 14.0511031314665 14.0241035224678
14.2677402397011 P P P LNCV6_124137_PI430048170 mRNA
AATAAAATCAGGTACAACTCCAAAAGGAGACATTGGAGAAGAACCAAGCTGGGTCTATAA NM_001000RefSeq
chrX - 119786503 119791659 RPL39 6170 ribosomal protein L39
GO:0010467|GO:0003735|GO:0050830|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0006415|GO:0005
615|GO:0006412|GO:0006413|GO:0002227|GO:0005829|GO:0006414|GO:0000184|GO:0019731|GO:0016032|GO:0
022625|GO:0044267. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99973_PI430048170 0.5547533829757391.09813627203533 0.3764871010667230.826977952444558
0.299303454774518A A A 0.3742243391652780.4073710623275260.373807434880525A A A
LNCV6_99973_PI430048170 mRNA
AACCATACTATGGAGTGTGTCAGTATTGTGCACTGTGAGGTCAGTGAATGGAATCCTTGG NM_032784RefSeq chr6
+ 127118902 127199481 RSPO3 84870 R-spondin 3
GO:0005109|GO:0001664|GO:0090263|GO:0060670|GO:0005102|GO:0005576|GO:0060070|GO:0008201|GO:0005
615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143435_PI430048170 0.2161262808456770.78669985066027 7.73618655396631 7.2040860889603
7.02145585256437 P P P 7.78175727423898 7.59671939267396 7.71403138751191 P P P
LNCV6_143435_PI430048170 mRNA
TTTTAGGCCTCCTCTCTGCCACCACCCCATAATCTCATTCAAAGAATACTAGAATGGTAG NM_020999RefSeq chr10
- 69572034 69573454 NEUROG3 50674 neurogenin 3
GO:0021510|GO:0060290|GO:0005634|GO:0005737|GO:0051091|GO:0003690|GO:0045944|GO:0030855|GO:0046
983|GO:0003713|GO:0001047|GO:0000122|GO:0007417|GO:0000978|GO:0006351|GO:0031490|GO:0007399|GO:0
048814|GO:0001078|GO:0001077|GO:0045666|GO:0031018|GO:0007422|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142217_PI430048170 0.4834972696400290.9768851188566290.405735010740768
0.4104140155007260.397567512340438A A A 0.3944599964322250.513758204708836
0.403665113269489A A A LNCV6_142217_PI430048170 mRNA
GGTGTGTGAGGAAGTCACTACTCCTAGCCTTTGTTAAGATGTAATTTTAAATATTCAGTT NM_015225RefSeq chr9
- 76611375 76906087 PRUNE2158471 prune homolog 2 (Drosophila)
GO:0016462|GO:0005737|GO:0008152|GO:0006915|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129141_PI430048170 0.000413783216746176 0.30317362671861511.9457958710045
11.689768347474 11.5513334422212 P P P 13.4670855232404 13.257545481516
13.6315056271022 P P P LNCV6_129141_PI430048170 mRNA
GTGCACCAATGAGACCACGATGGGAAAGGGCCTATTTAACTCCTAATAAAAAACTGGCAT NM_002960RefSeq chr1
- 153547332 153549258 S100A3 6274 S100 calcium binding protein A3
GO:0005737|GO:0005509|GO:0005730|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133432_PI430048170 0.14684452183894 1.07514190497517 0.481432250331226
0.5240615020347840.554101158796295A A A 0.3289051131325410.41716750804498
0.496025614490926A A A LNCV6_133432_PI430048170 mRNA

CATGAGTGTCATGATTTTGAAAAACCAATTGGTTTCTGCACAAAACTAAATGCCAACTGT NM_001166478 RefSeq chr6 - 49946100 49949444 DEFB133 NA "defensin, beta 133" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136512_PI430048170 0.00374629510856159 0.3175662322472290.45360449387049 0.4491364488061490.511807209006419A A A 1.93133050226193 2.10018321812965 2.32179728460683 A A A LNCV6_136512_PI430048170 mRNA
CCAAAGCATCCTTTGATATTATGTATGGATTAAATTAACACTGCTTTCCAAATGTGGTCC NM_145207RefSeq chr4 + 122923069 123319449 SPATA5 166378 spermatogenesis associated 5
GO:0005739|GO:0005737|GO:0007275|GO:0007283|GO:0005524|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128641_PI430048170 0.4022756114822870.7104054692041410.459789362649014 0.4250071608289220.300158134022109A A A 1.53195630284277 0.41738789790083 0.413370765105509A A A LNCV6_128641_PI430048170 mRNA
AATATTAAAGATTAATTGAAAATGAAAGATTAAATTTATTTGCTTTCTACACTTAAAAAA NM_033109RefSeq chr2 - 55634062 55693910 PNPT1 87178 polyribonucleotide nucleotidyltransferase 1
GO:0097222|GO:0005515|GO:0000962|GO:0000965|GO:0035458|GO:0000964|GO:0043457|GO:0035928|GO:0035927|GO:0005739|GO:0070207|GO:0005758|GO:0008266|GO:0005737|GO:0051260|GO:2000772|GO:0045926|GO:0000957|GO:0043631|GO:0000958|GO:0006402|GO:0006401|GO:0071850|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111399_PI430048170 0.2227182116482970.8418010871762355.35861896972209 5.66861159069391 5.24121636778671 P P P 5.8405226105849 5.44622650433 5.73324346758993 P P P LNCV6_111399_PI430048170 mRNA
TCCACACCTGGATTAGGCAGTGTCTAAAATATGATGCACAAGACAAAGCCCTATATACCC NM_001286748 RefSeq chr5 - 72219408 72320257 MRPS27 23107 "mitochondrial ribosomal protein S27, transcript variant 1"
GO:0070124|GO:0005515|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0005743|GO:0005840 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144150_PI430048170 0.1482520662134411.13958059803074 4.21098440913421 4.07424609672822 3.94669109659672 P P P 3.9731858733718 3.74550877568128 3.94916495180302 P P P LNCV6_144150_PI430048170 mRNA
TTCGTGGGGAGAGGGCGTGAATTGTTTTGAGTACAAACCTTAAATCCAAAGGCTCTTCTC NM_003532RefSeq chr6 + 26225154 26225616 HIST1H3E 8353 "histone cluster 1, H3e"
GO:0005515|GO:0010467|GO:0046982|GO:0006325|GO:0006335|GO:0005576|GO:0005634|GO:0000228|GO:0003677|GO:0032776|GO:0043234|GO:0060968|GO:0016020|GO:0000183|GO:0007596|GO:0045814|GO:0040029|GO:0005654|GO:0000786|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134452_PI430048170 0.00219464965958402 0.2717820097282185.78356067936442 5.63832638327322 5.82912447920934 P P P 7.41533586960436 7.54473845080788 7.8930084109886 P P P LNCV6_134452_PI430048170 mRNA
CTCACGCATGTATGCTTAGTATAAATGTGTCACTTCTAAAGTTTTGTCTCTGACTTTTAG NM_001008390 RefSeq chr3 - 88051949 88058996 CGGBP1 8545 "CGG triplet repeat binding protein 1, transcript variant 1"
GO:0003690|GO:0000977|GO:0005654|GO:0005634|GO:0000122|GO:0001227|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145377_PI430048170 0.0197905459548750.6992237989808495.91881776980533 5.64800743354022 5.99849084321363 P P P 6.27207552189937 6.33146589383717 6.52131197656409 P P P LNCV6_145377_PI430048170 mRNA
GTAATTCATTCTTAAGCTTTAACTTGAAGGTATCGTAATTGCCGGCATTTGATGTTTAGC NM_015884RefSeq chrX + 21839537 21885423 MBTPS251360 "membrane-bound transcription factor peptidase, site 2"
GO:0051091|GO:0005737|GO:0000139|GO:0031293|GO:0044281|GO:0016021|GO:0006987|GO:0004222|GO:0044267|GO:0046872|GO:0030968|GO:0008203 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139727_PI430048170 0.9179481074959840.9764098728727048.80519925273618
8.69859019569115 9.11117419376516 P P P 8.64465065550406 8.81006135313297
9.23111911622882 P P P LNCV6_139727_PI430048170 mRNA
GGTTTCTTTAAGATGTGCATTCCTTTCTGCTTGCTCTCTAGTAAATGTTTTACTACCGGG NM_007372RefSeq chr17 +
63774188 63819317 DDX42 11325 "DEAD (Asp-Glu-Ala-Asp) box helicase 42, transcript variant 1"
GO:0005515|GO:0005737|GO:0015030|GO:0008104|GO:0016607|GO:0016020|GO:0008152|GO:0004386|GO:0005
654|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139974_PI430048170 0.245043614307837 1.04642100978246 0.336908210892027
0.3226872143889140.449673000336626A A A 0.3031962664750690.281836663063312
0.330811332300177A A A LNCV6_139974_PI430048170 mRNA
TCCTGTGGAGACACTGAGTCAGAATTCTTCATCCTAAATTATTTTGTTAGTGGAAAATGG NM_003039RefSeq chr1
- 9036945 9069828 SLC2A5 6518 "solute carrier family 2 (facilitated glucose/fructose transporter),
member 5, transcript variant 1"
GO:0005886|GO:0005975|GO:0044281|GO:0055085|GO:0008645|GO:0015755|GO:0016324|GO:0015758|GO:0005
353|GO:0009405|GO:0016021|GO:0071332|GO:0005355|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_80026_PI430048170 0.36924051317414 0.8081911262798623.9904517953706 2.83519139384414
3.40189043679255 P A P 3.79259007055252 3.81717741973639 3.7678814593876 P P P
LNCV6_80026_PI430048170 mRNA
AAAGCAGATGCTTTATTAGGAAAAGCAACGATAGATTTGAAACAAGCTCTGTTGATACAC NM_007013RefSeq chr8
+ 86342764 86467949 WWP1 11059 WW domain containing E3 ubiquitin protein ligase 1
GO:0005515|GO:0004842|GO:0016567|GO:0005886|GO:0016874|GO:0000151|GO:0005634|GO:0046718|GO:0007
417|GO:0055085|GO:0005829|GO:0007165|GO:0005737|GO:0034220|GO:0042787|GO:0043161|GO:0045892|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126835_PI430048170 0.9666455878176920.99396096976881 0.372038844760503
0.4143332922583980.334579335141635A A A 0.2896790745213790.546585664387348
0.296899384360689A A A LNCV6_126835_PI430048170 mRNA
CTTTTGTCTAAGTACATTCTTAGAAGCTGGAAATTTTGACATCTTTTGGATTCTGACCAG NM_001144933 RefSeq
chr17 + 62370217 62416478 EFCAB3 146779 "EF-hand calcium binding domain 3, transcript variant 1"
GO:0005509 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134317_PI430048170 0.0470423747209169 0.5895561410669256.90733449667123
7.47739980763548 7.52878031636355 P P P 8.02720612895828 8.01911188170117
8.22313008428273 P P P LNCV6_134317_PI430048170 mRNA
ATCTGCATTGATTACAATTTGGATATTTCCTCTCCTCCTGTAGCCATACTTTGATTTTGC NM_032490RefSeq
chr14_KI270847v1_alt - 317453 321676 C14orf142 84520 chromosome 14 open reading frame 142
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115712_PI430048170 0.00102943634626031 0.5051466989795644.61037259602737
4.49678199694807 4.3602682809826 P P P 5.62092348863124 5.47187205771696
5.32608140057271 P P P LNCV6_115712_PI430048170 mRNA
ACTATGTGAATGGGAAGTGGTTAAAGCCTGAACACAGAAATTCAGTGCCTTGCCAGGATC NM_153329RefSeq chr19
+ 49453215 49471048 ALDH16A1 126133 "aldehyde dehydrogenase 16 family, member A1, transcript
variant 1" GO:0016020|GO:0004029|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131329_PI430048170 0.5768222432610281.14680478003387 3.14250844348458
3.16618303832462 3.75769570719783 P P P 3.30844800942148 2.47478342506352
3.56762593989636 P P P LNCV6_131329_PI430048170 mRNA
AGAAAAGCAAAACTGCAAGTGACTGTGAATAAAGGGTGAATGTAGTCTCAAATCCTCAAA NM_000301RefSeq chr6
+ 160702192 160754053 PLG5340 "plasminogen, transcript variant 1"
GO:0005515|GO:0008285|GO:0048771|GO:0005886|GO:0004252|GO:0010812|GO:0072562|GO:2000048|GO:0071

674|GO:0042246|GO:0005615|GO:0046716|GO:0022617|GO:0030198|GO:0051603|GO:0060716|GO:0031093|GO:0
045445|GO:0070062|GO:0009986|GO:0060707|GO:0019904|GO:0051919|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_107973_PI430048170 0.3462076914113191.13869553602155 7.25141029379084
6.88929710905757 7.01848915261851 P P P 7.12020918734399 6.61796868795856
6.83832746801552 P P P LNCV6_107973_PI430048170 mRNA
ATGCTCCTGAAGCCTAGTGTTTTAGTGAACATTAGTGATTGTTAGCAGTGGTTCAAAAAA NM_182838RefSeq chr1
- 1727384 1745999 SLC35E2 9906 "solute carrier family 35, member E2, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137293_PI430048170 0.00305585884266936 2.4756504484755 9.60650049466956
9.29310228695673 9.08391503964484 P P P 7.93904258475913 8.26832147586261
7.86885557436919 P P P LNCV6_137293_PI430048170 mRNA
ACCTGCCAGGGAGACAGAGCTCACAATAAAAATGGCTCAGATGCCACTTCAAAGAAAAAA NM_001771RefSeq
chr19 + 35329168 35347361 CD22 933 "CD22 molecule, transcript variant 1"
GO:0005515|GO:0005887|GO:0030246|GO:0007155|GO:0009897|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141047_PI430048170 8.37684808751087e-06 6.94283084636503 9.82414713550137
9.6330644533219 9.81701041362962 P P P 6.83974789860809 7.08143479264151
6.96436884531085 P P P LNCV6_141047_PI430048170 mRNA
GGGCTTAAGATTCCAGACTCTGATTCATTAAACTATAGTCACCCGTGTCCTGTGAAAAAA NM_006744RefSeq chr10
- 93591835 93601236 RBP4 5950 "retinol binding protein 4, plasma"
GO:0005515|GO:0060044|GO:0060065|GO:0007603|GO:0030324|GO:0001654|GO:0045471|GO:0060068|GO:0048
706|GO:0016918|GO:0006094|GO:0007283|GO:0019841|GO:0005615|GO:0005829|GO:0007507|GO:0030277|GO:0
050908|GO:0042574|GO:0042572|GO:0048807|GO:0032024|GO:0032526|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128600_PI430048170 0.3325581154186371.11466249934246 10.5184833397192
10.8823239859156 10.7865021611094 P P P 10.4586239752187 10.5253134597994
10.7422601663227 P P P LNCV6_128600_PI430048170 mRNA
CGGCCTAATTTTTCTGACTCTTACGAAAACGATTGCCAACACATACTTCTACTTTTAAAT NM_001100879 RefSeq
chr15 - 79898839 79915256 ST20 NA "suppressor of tumorigenicity 20, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131704_PI430048170 0.0701746418548132 0.5172809179099310.2939372404075
10.2462951149432 10.1605765380205 P P P 10.6232215514411 11.3607911306634 11.441126286925
P P P LNCV6_131704_PI430048170 mRNA
CAACTGACCTTATAACCCTCTGCACCTTCAAAAAGATTCATGGTTTTTAATTGCTGCTTT NM_015651RefSeq chr9
- 120855650 120877328 PHF19 26147 "PHD finger protein 19, transcript variant 1"
GO:0005515|GO:0010467|GO:0006355|GO:0035098|GO:0061087|GO:0045814|GO:0040029|GO:0008270|GO:0005
654|GO:0035064|GO:0006351|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130511_PI430048170 0.6060014550514910.9414235324038010.7768162745186
10.8025384442717 10.8396008945743 P P P 10.6377424572674 10.9560631884475
11.0549494065991 P P P LNCV6_130511_PI430048170 mRNA
TGAAAATGCTGTGCACTCATTCCATGGAATAAATGTTGGAAAGCTGATCTTTTCTGATAT NM_001284341 RefSeq
chr7 + 32957403 33006931 FKBP9 11328 "FK506 binding protein 9, 63 kDa, transcript variant 2"
GO:0000413|GO:0061077|GO:0006457|GO:0005783|GO:0005509|GO:0005789|GO:0003755|GO:0005528 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140583_PI430048170 0.3442435834800070.734158579229101 3.07593027302031 2.11581343716
2.36997442017043 P A A 3.46063659628406 3.00804498787086 2.42673287243141 P P P
LNCV6_140583_PI430048170 mRNA
TGAGATGCAACTAACAGCCCCTTCCTGGATGAAGGAGTCAAAGAATAAAGCTTGCCTAGA NM_003420RefSeq chr3

+ 44648740 44660791 ZNF35 7584 zinc finger protein 35
GO:0043565|GO:0048471|GO:0006355|GO:0003700|GO:0071300|GO:0005623|GO:0005634|GO:0007283|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137479_PI430048170 0.6045198161714630.828330379597188 0.929377315347648
1.66196062336367 0.347127658444843 A A A 1.91836409768594 0.75269564880762
1.13106799619418 A A A LNCV6_137479_PI430048170 mRNA
TTTGTCATCCAGTTCACCTCTCAGTTCCTCAAGCTGGACTACTTCCAGAAGCTTTACATG NM_001080830 RefSeq
chr1 + 12774847 12777905 PRAMEF12 NA PRAME family member 12 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_95837_PI430048170 0.2982607102741731.57959327148347 0.5778008493544791.83544720561927
0.748370918612638 A A A 0.6139859203203390.4459198265436580.459507161417972 A A A
LNCV6_95837_PI430048170 mRNA
TTTGACATTTTGGACAATTTCAACCTCCTTCCAGACACCCAGGAGCGTTTCTATGCCTCT NM_001300935 RefSeq
chr7 + 34658238 34849978 NPSR1 387129 "neuropeptide S receptor 1, transcript variant 5"
GO:0005737|GO:0005886|GO:0007218|GO:0005887|GO:0005000|GO:0051281|GO:0008188 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137201_PI430048170 0.0383647665643821 1.32146375823001 12.3167706450262
12.5045148775676 12.4574536447505 P P P 12.2243948133289 11.9043076515096
11.9276142177653 P P P LNCV6_137201_PI430048170 mRNA
GAAGTGTCAAGAGAGCAATCATCAATGATAATGTATTGTGTGAGACCTTTGCATCTTGTA NM_080820RefSeq chr20
+ 18587911 18763916 DTD1 92675 D-tyrosyl-tRNA deacylase 1
GO:0006260|GO:0006399|GO:0005737|GO:0002161|GO:0051500|GO:0005634|GO:0006450|GO:0019478|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129012_PI430048170 0.2862476129737111.18545389065529 9.34899568444799 9.8665657115446
9.7447542460672 P P P 9.62666231978581 9.33495364630468 9.28772065097731 P P P
LNCV6_129012_PI430048170 mRNA
AGATTCTTTATACACTTTGTAAGATTTACGCCAAACCCCAGCTCTCGATCTCTTCTTCTC NM_004218RefSeq chr19 +
8390320 8404433 RAB11B 9230 "RAB11B, member RAS oncogene family"
GO:0005515|GO:2001135|GO:0030054|GO:0003924|GO:0071468|GO:0006886|GO:2000008|GO:0032402|GO:0005739|GO:0045054|GO:0033572|GO:0045055|GO:0044070|GO:0001881|GO:0030670|GO:0035773|GO:0030672|GO:0032482|GO:0070062|GO:0090150|GO:0005525|GO:0008021|GO:0006184|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_62036_PI430048170 0.81543332091804 0.9769472493234976.72155321292903 6.35567578007104
6.20954333630474 P P P 6.42306054097777 6.64516251156907 6.35227079516039 P P P
LNCV6_62036_PI430048170 mRNA
ATTCTCAAACAAGAAACTGTTCCTGTGCCACCCAAGAGCACTGCAAAGGAATTGGAAGCA NM_139242RefSeq chr15
- 65001511 65029639 MTFMT 123263 mitochondrial methionyl-tRNA formyltransferase
GO:0070124|GO:0005739|GO:0032543|GO:0006996|GO:0071951|GO:0004479 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140072_PI430048170 0.5788037532222 0.77770951015692 2.408883470854
2.23137168044078 0.678620475762849 A A A 1.50339860524524 2.12308807569326
2.95108387006552 A A P LNCV6_140072_PI430048170 mRNA
ATCCACATGCCGCCATAGCAAAAGAGAAACTGAAAAACAAGAATATTTAGCTCTTATCTT NM_021204RefSeq chr4
+ 82430479 82461175 ENOPH1 58478 "enolase-phosphatase 1, transcript variant 1"
GO:0034641|GO:0000287|GO:0000096|GO:0019509|GO:0016311|GO:0006595|GO:0005634|GO:0044281|GO:0070062|GO:0043874|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138498_PI430048170 0.0213524428337158 1.18723663632239 13.5094356474255
13.3628973529158 13.3864206450753 P P P 13.1821349988315 13.197780788403 13.139723951753
P P P LNCV6_138498_PI430048170 mRNA

GAGGGAAACGCTGTCTGCTGCCTTCATACAGATGCTGATTAAAGTGATAGCGATTCAGAT NM_004092RefSeq chr10
- 133362482 133373404 ECHS1 1892 "enoyl CoA hydratase, short chain, 1, mitochondrial"
GO:0005739|GO:0005515|GO:0006635|GO:0005759|GO:0044281|GO:0004300|GO:0044255|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136555_PI430048170 0.1203013926448591.04906163492505 0.425136819759497
0.4480909473513660.458352428954531A A A 0.32892391156525 0.367965542270667
0.425937617269582A A A LNCV6_136555_PI430048170 mRNA
CTCCACTTGAAGCACTTAAGTCTTCCTTAAATGACTTTTCTTAAGTAATGATACTGTGTG NM_004482RefSeq chr2
- 165747802 165794293 GALNT3 2591 polypeptide N-acetylgalactosaminyltransferase 3
GO:0048471|GO:0005794|GO:0030145|GO:0005975|GO:0005509|GO:0016266|GO:0004653|GO:0000139|GO:0006
493|GO:0016020|GO:0018242|GO:0032580|GO:0030246|GO:0018243|GO:0016021|GO:0044267|GO:0070062|GO:0
043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128649_PI430048170 0.7607417175534270.97030988656845 0.302318075989869
0.2721804332552580.425836490308108A A A 0.28757150531185 0.251742135152184
0.574021396518369A A A LNCV6_128649_PI430048170 mRNA
GTGCTGAAGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGA NM_172201RefSeq chr21
+ 34364023 34371141 KCNE2 9992 "potassium channel, voltage gated subfamily E regulatory beta
subunit 2"
GO:0005251|GO:0005242|GO:0005886|GO:0009986|GO:0007568|GO:0060306|GO:0010107|GO:0015459|GO:0060
307|GO:0086091|GO:0005764|GO:0035690|GO:0042803|GO:0044325|GO:0071435|GO:0086009|GO:0008076|GO:0
086002|GO:0086011|GO:0034613|GO:0043586|GO:0071805|GO:0086005 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144746_PI430048170 0.7290379186477850.9871598076408287.15707016066 7.03244251684165
7.16223001317251 P P P 7.16474321087643 7.07831219548847 7.16657536581213 P P P
LNCV6_144746_PI430048170 mRNA
GTGTGTGCAAGTGCACATGTGTGTGTGTAATAACACATTGTAAAGAACAGAAATTACTTT NM_019556RefSeq chrX
- 134887625 134915344 MOSPD1 56180 motile sperm domain containing 1
GO:0048471|GO:0005737|GO:0045944|GO:0005634|GO:0016021|GO:0000122 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127836_PI430048170 0.0617261153908668 0.53043575103465 7.30881044587515
7.22539415965628 7.80207115581354 P P P 7.88760315061417 8.28354247189361
8.82452655655863 P P P LNCV6_127836_PI430048170 mRNA
CGTCCTGTAATCTGTTTCTAGGTGAAGCATACTCCAGTGTTTTAGGGGTTTTGAAAATAA NM_016542RefSeq chrX
+ 132023216 132075943 STK26 51765 "serine/threonine protein kinase 26, transcript variant 1"
GO:0005515|GO:0042542|GO:0048471|GO:0030033|GO:0005634|GO:0006921|GO:0042803|GO:0071944|GO:0005
829|GO:0042802|GO:0005737|GO:0016324|GO:0046777|GO:0070062|GO:0005813|GO:0005794|GO:0000287|GO:0
005798|GO:0006915|GO:0042981|GO:0005524|GO:0004672|GO:0000139|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145703_PI430048170 0.00202820850070114 0.5268020105114387.02314665808129
6.75478185650581 6.86822185713472 P P P 7.73443381107901 7.84979352068607
7.84561351108504 P P P LNCV6_145703_PI430048170 mRNA
AAACCAGATACCTTAGGTCTCAATACTCGGCTCTACAAGTGGATACCCCAGAATGACCTT NM_001074RefSeq chr4
+ 69096474 69112987 UGT2B77364 "UDP glucuronosyltransferase 2 family, polypeptide B7"
GO:0006629|GO:0052696|GO:0052695|GO:0008209|GO:0015020|GO:0032870|GO:0043231|GO:0016020|GO:0009
813|GO:0001972|GO:0005789|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143539_PI430048170 0.3407768931339044.44753243498943 2.09898441064835
1.11693415838246 4.75571530033782 A A P 1.60743637383103 1.16706841758555
1.15867299206522 A A A LNCV6_143539_PI430048170 mRNA
TCACAAAATATCATCGACTTGACCAACAAAGATCCCTGCTACTCCAAGCATTACAGGAGC NM_001001676 RefSeq

chr9 + 135663321 135665909 LCN9 NA lipocalin 9 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144247_PI430048170 0.00944984035708502 0.56998868399778 9.70089225226874 9.28828484276519 9.481641533673 P P P 10.1508835772726 10.2006915423996 10.548466969525 P P P LNCV6_144247_PI430048170 mRNA
CGGACTTGGTGCCCCTGTGCATTTGGAAATCAATAAACTATTACTGGAAATGCCAAAAAA NM_017583 RefSeq chr11 + 35662751 35811053 TRIM44 54765 tripartite motif containing 44
GO:0005622|GO:0005515|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129803_PI430048170 0.0245480610616911 0.8869745478952885.86346540142669 5.81168654526152 5.89797796413121 P P P 5.99361134246465 5.99124665905689 6.10569263801294 P P P LNCV6_129803_PI430048170 mRNA
AGAGACGAAAAATGAATATTCTGTCATTTCAGACTAAACTACTCACCCAGCTCACACTAA NM_015332 RefSeq chr7 - 44382365 44490786 NUDCD3 23386 NudC domain containing 3 GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140713_PI430048170 0.0034486207206809 0.242173964692343 3.94841629406355 3.17090116193163 3.32710454040679 P P P 5.26778702435644 5.76543392214792 5.62802513181046 P P P LNCV6_140713_PI430048170 mRNA
GGGATGTCAAAGTATTAACGAAGGGTACTGAAAACATACTTTTACTTGGGTCAAATTACT NM_001099678 RefSeq chr3 - 120324728 120349339 LRRC58 116064 leucine rich repeat containing 58 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133295_PI430048170 0.177333415593435 0.863766977873501 3.53860346831281 3.84018389972626 3.78687546501896 P P P 3.75381113521129 4.01323206532996 4.03357291656101 P P P LNCV6_133295_PI430048170 mRNA
GAAACAGCTTTCTCTGTACATATGCAACTCCTAATAAAAGGCATATTTCTTCCTGTTCAA NM_019619 RefSeq chr10 - 34109559 34815325 PARD3 56288 "par-3 family cell polarity regulator, transcript variant 1"
GO:0090162|GO:0044319|GO:0005515|GO:0030054|GO:0005886|GO:0022011|GO:0007409|GO:0007205|GO:0005829|GO:0051642|GO:0032970|GO:0005913|GO:0070830|GO:0005911|GO:0006612|GO:0005080|GO:0043025|GO:0007179|GO:0005938|GO:0031643|GO:0008356|GO:0003383|GO:0034329|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130963_PI430048170 0.377776037353469 1.01364130706391 0.321008285620137 0.297554309746928 0.269296748451044 A A A 0.301662442403112 0.266581166245305 0.261101904499475 A A A LNCV6_130963_PI430048170 mRNA
CAAAACCTTCATAATGGGGGTACAAAAACGCCTGTAAGCTACAAAAGCAATTAATTCAAT NM_198451 RefSeq chrX + 55623399 55626188 FOXR2 NA forkhead box R2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136250_PI430048170 0.242254483499606 0.635974318093356 1.35010200766071 0.493529495405954 1.99013867512709 A A A 1.93006739312509 2.50726236194111 1.57183599512401 A A A LNCV6_136250_PI430048170 mRNA
CACCCTTTTAATAATGCTCAGTTCTGTAGGCTCTCTATCCTAGAGGAATTGAGCAAAACA NM_006656 RefSeq chr11 + 74988904 75007698 NEU3 10825 sialidase 3 (membrane sialidase)
GO:0006665|GO:0009313|GO:0005886|GO:0006687|GO:0005975|GO:0006689|GO:0004308|GO:0044281|GO:0052794|GO:0005887|GO:0052796|GO:0052795|GO:0016997|GO:0006488|GO:0044267|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142836_PI430048170 0.390036341847444 0.75880082508105 2.47201013001825 1.42140823964052 2.63381293346221 A A A 2.15651726763177 3.01572627295282 2.69490399614262 A P P LNCV6_142836_PI430048170 mRNA
ATGTGGTCCTGAATTGGCTACTAGTTTAAGCAAATAAACTGTAAGTCATTTATGGGTTAG NM_003666 RefSeq chr1 + 169367955 169396542 BLZF1 8548 basic leucine zipper nuclear factor 1
GO:0003700|GO:0006357|GO:0043001|GO:0005796|GO:0008283|GO:0005634|GO:0001558|GO:0003677|GO:0005

737|GO:0000139|GO:0007030|GO:0005654|GO:0000278|GO:0019899|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131886_PI430048170 0.359501496878603 1.2527590641299 0.315555777649275 1.11758201605024 0.922333229520723 A A A 0.794361658123438 0.296259650375707 0.351603096794099 A A A LNCV6_131886_PI430048170 mRNA TTGGGTTTTGTCACACTCTGCTCATTTTGACTGAATAAAAGTCCTGTTGCCAAAGTGAAA NM_004884 RefSeq chr15 - 65327126 65378040 IGDCC3 9543 "immunoglobulin superfamily, DCC subclass, member 3" GO:0005887|GO:0050885 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94387_PI430048170 0.542440895813967 1.03525593986035 0.540397156362668 0.721175401105143 0.577943735465004 A A A 0.50565113795118 0.521233031098238 0.66372458150085 A A A LNCV6_94387_PI430048170 mRNA CTGGGAAGAAAACCCTGAGTTCTACTTTAATTCTTGGGCATTGACTTCAAACTAAGATGA NM_001261424 RefSeq chr2 + 181985823 182131382 PPP1R1C 151242 "protein phosphatase 1, regulatory (inhibitor) subunit 1C, transcript variant 1" GO:0035556|GO:0007049|GO:0005737|GO:1900087|GO:0030307|GO:0004864|GO:0004865|GO:0006469|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127571_PI430048170 0.00883228881749891 0.806717271179825 10.1651248644035 10.2815031037432 10.2095991102702 P P P 10.625150832208 10.4821163525824 10.4759591721141 P P P LNCV6_127571_PI430048170 mRNA CCCACCTCCAGCCCACAGTGCTCAGTTGTACTTTTTATTAAGCTGTAATATCTATTTTTG NM_001290184 RefSeq chr1 + 160343272 160358952 NCSTN 23385 "nicastrin, transcript variant 2" GO:0005515|GO:0007220|GO:0005886|GO:0005783|GO:0031293|GO:0005765|GO:0007219|GO:0022617|GO:0042098|GO:0007411|GO:0016485|GO:0030198|GO:0006508|GO:0006509|GO:0002262|GO:0070062|GO:0042987|GO:0042470|GO:0048011|GO:0005794|GO:0043065|GO:0048013|GO:0043085|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141440_PI430048170 0.00800677234042348 2.1933139280432 7.58637494890771 7.58073404765942 7.20138277248701 P P P 6.65727218731189 6.19644383733074 6.08190406406943 P P P LNCV6_141440_PI430048170 mRNA CTGAGCGAGTCTGTTGTGGAGAAGAACTTTTTGTAGTAATTTACTAGGAAAAATTCTGAA NM_031308 RefSeq chr8 - 143857318 143878464 EPPK1 83481 epiplakin 1 GO:0008150|GO:0005737|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137759_PI430048170 0.894373685556327 1.07912335171669 0.515460998614662 1.80980034612874 0.574396800327905 A A A 1.62915717434926 0.495198148730455 0.536604335496254 A A A LNCV6_137759_PI430048170 mRNA AAACAACCTGATATAGCAGAACTGACTGTATAAATTATGTGAGCACAGTGCAAGTAATTC NM_001243328 RefSeq chr6 - 149883374 149896059 RAET1E 135250 "retinoic acid early transcript 1E, transcript variant 4" GO:0002474|GO:0005886|GO:0001913|GO:0046703|GO:0042267|GO:0050776|GO:0042605|GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140844_PI430048170 0.152170677210939 0.868196362672807 5.95465952727698 6.01177053097293 6.17952777015026 P P P 6.39169005754766 6.08423059187053 6.27479024193723 P P P LNCV6_140844_PI430048170 mRNA TCCTGGGTGGGTCGTCTTGACCCAAACTCTTGTGTTGTTACATTTTGAGAGGTTTTCATA NM_020141 RefSeq chr1 + 109090780 109096932 TMEM167B 56900 transmembrane protein 167B GO:0000139|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128019_PI430048170 0.0386419824446832 0.846572742216564 12.7461744612078 12.8119911393046 12.607931542589 P P P 13.020652871286 12.9454375873684 12.9266194713857 P P P LNCV6_128019_PI430048170 mRNA TAGTCATCAACTATGACCTTCCCACCAACAGGGAAAACTATATCCACAGAATCGGTCGAG NM_001416 RefSeq chr17 + 7572705 7579006 EIF4A1 1973 "eukaryotic translation initiation factor 4A1, transcript variant 1"

GO:0000339|GO:0003725|GO:0005515|GO:0010467|GO:0016281|GO:0031100|GO:0019221|GO:0004386|GO:0003743|GO:0003729|GO:0005524|GO:0006412|GO:0006413|GO:0005829|GO:0016020|GO:0016032|GO:0044267|GO:0000289|GO:0008135|GO:0070062|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143858_PI430048170 0.42252495849798 1.1140719385637 0.798533890465517 0.330716734054177 0.441398841823911 A A A 0.283738841593877 0.478560114565062 0.376609897124296 A A A LNCV6_143858_PI430048170 mRNA GGTTCTACCAGCTTCCAATCATAAAACCAAGGGGCAATAATACATAAAATTGGAACTTAT NM_001278501 RefSeq chr1 - 15168473 15171624 C1orf195 NA "chromosome 1 open reading frame 195, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128071_PI430048170 0.000626261581300139 3.62298710271658 6.59191566343608 6.85201607142049 7.00747738108161 P P P 5.23455867263031 4.85418428601005 4.77880948654187 P P P LNCV6_128071_PI430048170 mRNA CCCACAGGCAATGGGTTTATAGACATTATGTGAGTTTCCTGCTATATTAACATCATCTTA NM_001772 RefSeq chr19 + 51225078 51240019 CD33 945 "CD33 molecule, transcript variant 1" GO:0005515|GO:0007165|GO:0008285|GO:0005886|GO:0005887|GO:0007267|GO:0030246|GO:0004872|GO:0007155|GO:0009897|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55562_PI430048170 0.0162203683664325 0.709787870710926 3.67524159865344 3.51519961729322 3.36695459976531 P P P 4.00193161709983 3.9509938538727 4.1005476896854 P P P LNCV6_55562_PI430048170 mRNA CACCTGCGGAAAAAGGAAGAGATTTAGAGTCACGACTCATAGAAGCATACGTTATTCAAT NM_144695 RefSeq chr1 + 222712552 222735196 BROX 148362 "BRO1 domain and CAAX motif containing, transcript variant 1" GO:0016020|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137999_PI430048170 0.131276664581801 0.774129391284725 7.86639503722682 7.77337980070992 8.17879272529651 P P P 8.07084251413178 8.26729459527578 8.57515636817432 P P P LNCV6_137999_PI430048170 mRNA GGAGGGCTGTTTTAACATCTTTGAAGTATGGCTTGCTGAATATCTTTACCAACATCTTGA NM_016048 RefSeq chr5 + 129094748 129114026 ISOC1 51015 isochorismatase domain containing 1 GO:0008150|GO:0003674|GO:0008152|GO:0003824|GO:0070062|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133977_PI430048170 0.345670084326222 0.903508767385184 10.1280323325031 9.9701864376381 9.7186937468613 P P P 10.1032709112939 10.2082154149669 9.96336446785582 P P P LNCV6_133977_PI430048170 mRNA CTCAAGCTGCCACTTGGGCCTGGTTTTAGATGTTTTTAATTTTGTAAAAGAAAACAAGTA NM_130459 RefSeq chr9 - 127731523 127735349 TOR2A 27433 "torsin family 2, member A, transcript variant 2" GO:0005179|GO:0051085|GO:0005788|GO:0051260|GO:0005576|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67497_PI430048170 0.00242880121671002 1.85088294867395 10.527335108005 10.6445384532355 10.4632675534211 P P P 9.48733382965619 9.79403085260408 9.67855116820481 P P P LNCV6_67497_PI430048170 mRNA TGTCCACTCTGGATGAGAATTGGCCACCTGATGGTTATTTATACGTCCAGAAGAACATCA NM_007059 RefSeq chr19 - 47475140 47484264 KPTN 11133 "kaptin (actin binding protein), transcript variant 1" GO:0048471|GO:0005815|GO:0007605|GO:0032420|GO:0006928|GO:0007015|GO:0005634|GO:0003779|GO:0015629|GO:0030426 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144567_PI430048170 0.149122945527861 0.763937885216147 9.02834081238841 8.89945566736141 9.02418663508379 P P P 9.02294759518318 9.49483358897294 9.54775342417594 P P P LNCV6_144567_PI430048170 mRNA GCAGAGGTTAGAAGTCAAAGAACATATTCTTGAAAGTTATGATGCATTCTTTTGGGTGGT NM_001286524 RefSeq chr6 + 126339788 126348875 CENPW 387103 "centromere protein W, transcript variant 1"

GO:0005515|GO:0051276|GO:0046982|GO:0005730|GO:0006334|GO:0003677|GO:0016363|GO:0034080|GO:0007067|GO:0051382|GO:0007059|GO:0000777|GO:0000776|GO:0005654|GO:0000278|GO:0000775|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126834_PI430048170 0.706558282435023 0.992897503314967 0.420990833202814 0.426468730650385 0.369563823312371 A A A 0.448903593441318 0.387581281528049 0.411405274067179 A A A LNCV6_126834_PI430048170 mRNA AGCATTTCTTATGGTTTCTCTGAATCAGTTCATCCCACACATCATCCTGAGGCACCTGCA NM_001005405 RefSeq chr11 - 71581854 71582875 KRTAP5-11 NA keratin associated protein 5-11 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131144_PI430048170 0.84046322669355 0.956008077783968 0.561897968287316 0.717606313009084 0.69730855988914 A A A 0.60596488322504 0.443153262828614 1.05574043835618 A A A LNCV6_131144_PI430048170 mRNA CACAATTTAGGAAGATGACTTTCTAGAGAAAACACAGAAACCATAAGAAATGGGTAACAC NM_152763 RefSeq chr1 - 108815897 108857104 AKNAD1 254268 "AKNA domain containing 1, transcript variant 1" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133846_PI430048170 0.299805131898801 0.54384576005475 2.78453699632805 2.80042328760013 2.82906716081815 A A P 2.4988322968902 3.90143781708555 4.1658883626681 A P P LNCV6_133846_PI430048170 mRNA CTAGTTGTTTCTATGGACACCTGCTCTGAATTGTACATTGACTTCATTACTAAAGAACAA NM_001251962 RefSeq chr3_KI270777v1_alt - 24215 164217 ARHGEF26 26084 "Rho guanine nucleotide exchange factor (GEF) 26, transcript variant 1" GO:0032321|GO:0001886|GO:0097178|GO:0005089|GO:0001726 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138577_PI430048170 0.085965892170181 2.49272044711155 2.95533673655742 3.15257079043742 3.2070485343466 A P P 2.36191163942825 0.770868362900058 1.82239235803027 A A A LNCV6_138577_PI430048170 mRNA CAAGGAGGTAAAGGAAGGCTTTAAAAGGTTGGTTGCAAGAGTCTTCTTAATCAAGAAATA NM_012367 RefSeq chr6 + 27957240 27958182 OR2B6 26212 "olfactory receptor, family 2, subfamily B, member 6" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136498_PI430048170 0.602653475804516 0.888164745483709 1.95971415233758 1.60646370651858 2.50322744530084 A A A 1.86083503806372 2.19555065333383 2.57983379163434 A A P LNCV6_136498_PI430048170 mRNA GTGCCTTCAGGGAAACTAGGATTGGATTTACTAAATTCTCATTTTTTAGATCTCAGATAC NM_033092 RefSeq chr11 - 5663194 5685109 TRIM5 85363 "tripartite motif containing 5, transcript variant gamma" GO:0005515|GO:0004842|GO:0016874|GO:0019221|GO:0002218|GO:0042803|GO:0005829|GO:0042802|GO:0005737|GO:0002221|GO:0051091|GO:0051607|GO:0070206|GO:0070534|GO:0051092|GO:0000932|GO:0016032|GO:0031664|GO:0043123|GO:0060333|GO:0046597|GO:0045087|GO:0008270|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133505_PI430048170 0.400321877342914 1.04121607669161 0.290205643412586 0.282997499743038 0.44583721393567 A A A 0.298708105278097 0.264804968466052 0.286451685008916 A A A LNCV6_133505_PI430048170 mRNA AAATGCATTTCCTTTTCTGGTTCGTTTTTCTTGTTAACACGCGCACACAGACACACACAC NM_022062RefSeq chr11 + 125164662 125433389 PKNOX2 63876 PBX/knotted 1 homeobox 2 GO:0043565|GO:0003785|GO:0005737|GO:0051015|GO:0006357|GO:0015630|GO:0005634|GO:0015629|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136314_PI430048170 0.182157953294906 1.98791462075998 0.380425438487377 1.20926900081811 1.87216447451804 A A A 0.278858270134846 0.291864001480854 0.28927954535741 A A A LNCV6_136314_PI430048170 mRNA CCCATTTGCTACATTCCTTTTCCTGTGAAATATGTGAGTGATAATTAAACACTTTAGACC NM_001301272 RefSeq

chr16 + 56657942 56659303 MT1F 4494 "metallothionein 1F, transcript variant 2"
GO:0071294|GO:0048471|GO:0005737|GO:0008270|GO:0005634|GO:0071276|GO:0045926 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137429_PI430048170 0.8107975632077251.02585739723685 3.64802313282789
1.67077025351575 2.98696208813466 P A P 3.10949704894999 2.66100404516069
3.01728386417626 P A P LNCV6_137429_PI430048170 mRNA
GTCTTCCTCTCTGCATCAGTTGCTTTATAAATGATTGTCAAACCAATAAATACACACAAG NM_005074RefSeq chr6
- 25782897 25832059 SLC17A1 6568 "solute carrier family 17 (organic anion transporter), member 1"
GO:0044341|GO:0015321|GO:0016020|GO:0005886|GO:0005887|GO:0035435|GO:0006817|GO:0046415|GO:0006
814|GO:0055085|GO:0015293|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135562_PI430048170 0.0219693676524776 1.25026429237605 11.2620460889729
11.2162352679906 11.3452067377406 P P P 10.8494525383788 10.9240654830205
11.0768566731999 P P P LNCV6_135562_PI430048170 mRNA
TGTTCAGCGTTCTAGCAACACGTGTGTGTGTGTGTGTGTAAAGGCTATGCAGCCAAAATA NM_020137RefSeq chrX
- 48973719 49002264 GRIPAP1 56850 GRIP1 associated protein 1
GO:0008150|GO:0003674|GO:0072562|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129700_PI430048170 0.3677114414625611.05243637853639 0.302421515462671
0.2917264097548820.481830897543955A A A 0.2985067464287420.262446407833416
0.301514271159881A A A LNCV6_129700_PI430048170 mRNA
GCGAGCAATTTCTTGGGACCAAAGTCAATACTCCGGAGGGTCAAGAGATTTCGAGCACGC NM_022363RefSeq chr12
- 113462888 113472072 LHX5 64211 LIM homeobox 5
GO:0043565|GO:0021846|GO:0021766|GO:0021702|GO:0021937|GO:0021879|GO:0008270|GO:0005634|GO:0045
893|GO:0021527|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118293_PI430048170 0.1807299541886150.53205805742412 2.54447054870651
1.01584281100309 1.35024508344414 A A A 3.16838354023688 1.89455729495058
2.77584185711049 P A P LNCV6_118293_PI430048170 mRNA
ATGCGTCTAGAGCAGGATTTGAAGAATCAAGCTTTGGACAACCGAGAAATAGATAAAAAA NM_003629RefSeq chr1
- 46040139 46132708 PIK3R3 8503 "phosphoinositide-3-kinase, regulatory subunit 3 (gamma),
transcript variant 1"
GO:0008286|GO:0005515|GO:0006661|GO:0043551|GO:0036092|GO:0035014|GO:0016303|GO:0044281|GO:0006
644|GO:0005942|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140930_PI430048170 0.2337335122396 0.7670174593912 0.293854224896521
0.2741031424888070.424011497046375A A A 0.2908089729793531.01793603802764
0.744737914707576A A A LNCV6_140930_PI430048170 mRNA
GCAGAGAAATGTGATCGCTGAGATGTAAAAAGTTTTTAATGCTAGTTTCCACCATCTTTC NM_006552RefSeq chr11
+ 62190237 62193537 SCGB1D1 10648 "secretoglobin, family 1D, member 1"
GO:0046982|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134323_PI430048170 0.0130397998303705 4.05888740202831 6.85556434428656
6.82226387309273 6.90262970181729 P P P 4.88328983489647 5.17317401642379
4.34305255340001 P P P LNCV6_134323_PI430048170 mRNA
AGAATGAGTTTAATATCAAAGTGTAAGCTTACTTTCCATCCCCAAGCCAGCCTGCCCCCT NM_001288708 RefSeq
chr16 - 90004864 90020131 DBNDD1 79007 "dysbindin (dystrobrevin binding protein 1) domain
containing 1, transcript variant 3" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139257_PI430048170 0.4614634879731030.868550765250538 4.85077017495685
4.17757461314207 3.96830429812576 P P P 4.78111662078999 4.53334541171329
4.42130140802069 P P P LNCV6_139257_PI430048170 mRNA
CTCCAGTGCCCACCAGCCTTGTCCTAATAAAATTAAGTTGTATCATTTCATCTGAAAAAA NM_001317RefSeq chr17
- 63894907 63896661 CSH1 1442 chorionic somatomammotropin hormone 1 (placental lactogen)
GO:0005179|GO:0005576|GO:0060397|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_141891_PI430048170 0.3092385363452330.9427731655371333.82436410675644 3.8507474259713
3.88910698133613 P P P 4.03947533442134 3.9454610042492 3.82725724630506 P P P
LNCV6_141891_PI430048170 mRNA
GCTTGGAGATAGAAAGGAATTCAACAATATATCAAATACTTTCCTTCCCACCTTTTTCCT NM_007207RefSeq chr1
- 221701419 221742176 DUSP1011221 "dual specificity phosphatase 10, transcript variant 1"
GO:0033549|GO:0005794|GO:0048709|GO:0006950|GO:0007254|GO:0005634|GO:0090335|GO:0060266|GO:0035
335|GO:0000188|GO:0002819|GO:0016791|GO:0005737|GO:0046329|GO:0006470|GO:0044387|GO:0048715|GO:0
032496|GO:0004721|GO:0005654|GO:0008138|GO:0043508|GO:0017017|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131647_PI430048170 0.0221634954472741 0.52525573836717 6.85839838352899
6.55080500496838 6.73782194014417 P P P 7.31844805794282 7.61156831912943
7.95075106199283 P P P LNCV6_131647_PI430048170 mRNA
CAGAGAATGGCTTCCTGTTGTTTTGTTTATTTTCTTAACGTGTACAGATGGAAACTTCAT NM_006031RefSeq chr21
+ 46324121 46445769 PCNT 5116 pericentrin
GO:0005515|GO:0005516|GO:0021696|GO:0034451|GO:0036064|GO:0005829|GO:0061351|GO:0005737|GO:0021
772|GO:0035264|GO:0000086|GO:0007051|GO:0000242|GO:0035108|GO:0005813|GO:0043066|GO:0006996|GO:0
005814|GO:0031514|GO:0005874|GO:0000226|GO:0090316|GO:0001701|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131017_PI430048170 0.9984640354292431.04795961865736 0.288961582105909
0.3071202898597211.22759887322679 A A A 0.7406199252280250.4990473217178
0.581964192027754A A A LNCV6_131017_PI430048170 mRNA
TTAAGCAGAGAGTGGGCAGGATATTCCTGATAGGAGGAACTACATGAATAAAGGGGTAAG NM_007053RefSeq
chr1 + 145719445 145739288 CD160 11126 "CD160 molecule, transcript variant 1"
GO:0050829|GO:0006968|GO:0005886|GO:0008283|GO:0050776|GO:0005102|GO:0004872|GO:0046658|GO:0007
166|GO:0032393 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138515_PI430048170 0.0364644154806795 0.3594313116041424.09675267724693
3.03882917004466 4.17969946943849 P P P 5.04015263336573 5.31255651238218
5.59223152067725 P P P LNCV6_138515_PI430048170 mRNA
CGCACACTTTGTTAATGACAAACTTCACTCTACACTATACAGTACCTTGTTGATATATTC NM_013231RefSeq chr14
+ 85530143 85627926 FLRT2 23768 fibronectin leucine rich transmembrane protein 2
GO:2001222|GO:0005578|GO:0050919|GO:0005615|GO:0035556|GO:0008150|GO:0045499|GO:0005887|GO:0007
411|GO:0005057|GO:0007155|GO:0030674|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_131094_PI430048170 0.1631867514526451.03278261607061 0.358869730334897
0.3273095125279430.40438008671512 A A A 0.3006898529724090.312632648665886
0.338411083639762A A A LNCV6_131094_PI430048170 mRNA
AAGAGCTAACACCATGCTGATCTTGCTTTGCTATATGTGTAACTAATAAACTGCCTAAAT NM_001302695 RefSeq
chr8 - 11993176 12000752 DEFB134 NA "defensin, beta 134" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140813_PI430048170 0.1258105441495371.2588773085585 9.33474929985699
9.57554053889373 9.11608741598636 P P P 9.14961617882791 8.82084844736218
9.07589678868976 P P P LNCV6_140813_PI430048170 mRNA
TTTCAGACCCCATGTTGTTGGTCAATGAAATAAAGCATCTTACAGAAGGTGTTAACTGTT NM_032775RefSeq chr22
- 20441518 20495883 KLHL22 84861 "kelch-like family member 22, transcript variant 1"
GO:0005515|GO:0072686|GO:0007094|GO:0005827|GO:0005813|GO:0005737|GO:0000070|GO:0006513|GO:0031
463|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132720_PI430048170 0.6382222221476751.47052125206836 1.54990586335633
2.73464101946165 0.408884104731078A A A 0.3748011642023922.04195480720976
1.00397275665089 A A A LNCV6_132720_PI430048170 mRNA

TCATTGATACTCTTGAAAAGGAATTGGCGGAGAGAATGAAGAACAGGAATGCAGAGGAGG NM_138451 RefSeq chr12 - 113195440 113221094 IQCD 115811 IQ motif containing D NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135283_PI430048170 0.9355588438830290.9962154540461339.7041988574786 9.2799416007696 9.46698289690206 P P P 9.35599620028387 9.59413167177867 9.53826121052464 P P P LNCV6_135283_PI430048170 mRNA
AAGCATAAGAACATCGGAACTGCGACTCAGCATGCAGAAGTCAATGCAAAATCATGCTGCNM_004168 RefSeq chr5 + 218222 257082 SDHA 6389 "succinate dehydrogenase complex, subunit A, flavoprotein (Fp), transcript variant 1"
GO:0005515|GO:0006099|GO:0050660|GO:0005743|GO:0008177|GO:0044281|GO:0007399|GO:0005739|GO:0022904|GO:0005749|GO:0006105|GO:0000104|GO:0044237|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132172_PI430048170 0.6853271117252150.9661290775581650.332985171747105 0.2690865431424440.373741928952597 A A A 0.5535151689932170.267124573877082 0.28822748805959 A A A LNCV6_132172_PI430048170 mRNA
ATCATTACTGTTCCAGATTCCTATGATGGATGGCAGACTCTTTAATAAATTGCTTACTGA NM_020386 RefSeq chr3 + 193241127 193270855 HRASLS 57110 HRAS-like suppressor
GO:0016042|GO:0005641|GO:0046485|GO:0007031|GO:0016021|GO:0004620|GO:0016740|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132774_PI430048170 0.8103758847767 0.9627242069911 4.56935953968568 3.9046417661392 3.66720409872876 P P P 3.84005781233456 4.46366675574983 4.08981908597297 P P P LNCV6_132774_PI430048170 mRNA
TACTTTGAGTTCAGAGCATGAGACTTTTAGTTCAGAGCAGAGCCTGATGCCTGAGATCCT NM_001105519 RefSeq chr2 + 26562612 26579527 C2orf70 339778 chromosome 2 open reading frame 70 GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141051_PI430048170 0.0808911846262283 0.8554320968399275.93936403788418 5.75533119623641 5.75744814938867 P P P 5.90696284877582 6.05786659353788 6.15983064480594 P P P LNCV6_141051_PI430048170 mRNA
AATCTGTTTCCTACCTGTTCAGCCATGTTCCTTTATAACAGAATAACTTCTAGGTTATGCNM_175886 RefSeq chr7 - 18026775 18027863 PRPS1L1 221823 phosphoribosyl pyrophosphate synthetase 1-like 1
GO:0016310|GO:0000287|GO:0016301|GO:0004749|GO:0006015|GO:0005575|GO:0005524|GO:0042803|GO:0009165|GO:0009156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111583_PI430048170 0.0149675225383475 1.44398656959491 8.48477463582607 8.43057165620908 8.48948520110365 P P P 8.0679106986468 7.92881621033336 7.80682830667231 P P P LNCV6_111583_PI430048170 mRNA
TTTCCTACCATGAAGATGTTTGAATATGTCAGGAATGACCGTGACGGCTGGAATCCCTCT NM_005510 RefSeq chr6 - 31969810 31972255 DXO 1797 decapping exoribonuclease
GO:0000287|GO:0008409|GO:0005886|GO:0090305|GO:0071028|GO:0003729|GO:0006402|GO:0005737|GO:0050779|GO:0000166|GO:0008152|GO:0005654|GO:0034353 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143700_PI430048170 0.00329084788826079 0.4942744786424323.66901164284084 3.76519772455633 4.06559141069085 P P P 4.69113509809941 4.95544470964147 4.91932776592484 P P P LNCV6_143700_PI430048170 mRNA
GTGTCTTGAAAACTAAGTATTGGAGTGGATTTTCTTCTGCTTTCATTGATACTTGTCAGA NM_004713 RefSeq chr14 - 49783813 49853073 NEMF 9147 "nuclear export mediator factor, transcript variant 1"
GO:0005634|GO:0051168 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145756_PI430048170 0.431914557229527 0.694232533873863 1.95309876220955 1.72572407233454 2.77345693616714 A A A 3.13018608118139 1.75064930629723 3.01256882248023 P A P LNCV6_145756_PI430048170 mRNA
TTTAGCACCTCATAGGAATTCCTGTTTCTCTCTTAACTCTCACCACATCCCTGTAGGATG NM_015510 RefSeq chr17

+ 21126927 21191972 DHRS7B 25979 dehydrogenase/reductase (SDR family) member 7B
GO:0008150|GO:0003674|GO:0016020|GO:0016491|GO:0005789|GO:0016021|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141268_PI430048170 0.00883879416804718 0.4981346186108796.78595704798636
6.6847138644335 6.90299439068603 P P P 7.51780545036303 7.86781668947998 7.9740635773599
P P P LNCV6_141268_PI430048170 mRNA
TTTGGTTTTCCAGAAGCTGCCAGTGGGTTCCCGTGAATTGCGTTAAGATATCGATGATTT NM_018984RefSeq chr12
- 108782689 108857583 SSH1 54434 "slingshot protein phosphatase 1, transcript variant 1"
GO:0005515|GO:0030036|GO:0005886|GO:0032268|GO:0030496|GO:0003779|GO:0032154|GO:0003677|GO:0071
318|GO:0035335|GO:0030027|GO:0010591|GO:0000902|GO:0005737|GO:0006470|GO:0008064|GO:0004721|GO:0
005654|GO:0008138|GO:0005856|GO:0050770|GO:0004725 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_132037_PI430048170 0.0851137802391763 0.5807231818212828.61120005012646
8.44392147459708 8.69932460885864 P P P 8.84364342221299 9.48894657974869
9.66332967424336 P P P LNCV6_132037_PI430048170 mRNA
ATCTGTCTCCCAAATTGCAATTCCTAAGACCTCAATAAAAACACCTTGTCTTGCTGCAAA NM_001100624 RefSeq
chr16 + 81006497 81031485 CENPN 55839 "centromere protein N, transcript variant 2"
GO:0034080|GO:0007067|GO:0007059|GO:0006334|GO:0000777|GO:0005654|GO:0005634|GO:0000278|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98646_PI430048170 0.2104671479462471.13921761503877 9.22455206913444 8.9546232868684
9.28611745489702 P P P 8.86036517113645 9.0522668465855 9.00280582882576 P P P
LNCV6_98646_PI430048170 mRNA
TGTGTCGAAGTGGAAACTGATGTGGTGTCCAACACTAGTGGGTCCGCCAGGGTCAAGCTG NM_015004RefSeq chr3
+ 44976248 45011470 EXOSC723016 "exosome component 7, transcript variant 1"
GO:0005515|GO:0010467|GO:0003723|GO:0006364|GO:0005730|GO:0004532|GO:0043928|GO:0005634|GO:0000
178|GO:0005829|GO:0006401|GO:0000175|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144066_PI430048170 0.4764757151453910.9678642447605120.435532233383428
0.4543642034963360.281917602188216A A A 0.4023141558428520.480663919537998
0.435257516814132A A A LNCV6_144066_PI430048170 mRNA
GCCACTGAGGTAATTAATGGAATAATTGATTTTGAACTTGGGTCTGTCTGATTTCATGTG NM_006226RefSeq chr2
+ 197804701 198149884 PLCL1 5334 phospholipase C-like 1
GO:0006629|GO:0005886|GO:0007214|GO:0050811|GO:0035556|GO:0004629|GO:0070679|GO:0005737|GO:0004
435|GO:0032228|GO:0033135|GO:0004871|GO:1900122 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103514_PI430048170 0.0739603541948707 0.6900482472218576.21940456091748
6.14994694940731 6.51085387129363 P P P 6.50885111987429 6.83516531486893
7.10637885695291 P P P LNCV6_103514_PI430048170 mRNA
TACGGGAAATGGAAAGTCTGGGCCAGCATCAATAAAATGACACCAAAAATAAGTAGATGA NM_016224RefSeq
chr6 + 157823170 157945077 SNX9 51429 sorting nexin 9
GO:0005802|GO:0005515|GO:0051044|GO:0005886|GO:0097320|GO:0030136|GO:0006886|GO:0042803|GO:0036
089|GO:0005545|GO:0016050|GO:0005737|GO:0016197|GO:0045860|GO:0032461|GO:0030659|GO:0031625|GO:0
070062|GO:0000281|GO:0071933|GO:0001726|GO:0006898|GO:0006897|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143771_PI430048170 0.0221923512855734 0.5826770901115158.24433846186012
8.03974953407167 8.32555371670911 P P P 8.67265970194557 9.03094231626374
9.20814516784211 P P P LNCV6_143771_PI430048170 mRNA
TCATTGGATTGTGCCAGTTATCAGTGGCTCTTGGGTTCAAAGTAATAAAGAATTCCAAAA NM_005530RefSeq chr15
+ 78149376 78170542 IDH3A 3419 isocitrate dehydrogenase 3 (NAD+) alpha
GO:0005739|GO:0051287|GO:0006099|GO:0000287|GO:0004449|GO:0005975|GO:0005759|GO:0005634|GO:0044
281|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_144338_PI430048170 0.4512400435317871.03262084942802 10.4313779841056
10.4574699759083 10.5569160053706 P P P 10.3557814546056 10.4639188807539
10.4868283191315 P P P LNCV6_144338_PI430048170 mRNA
TAAAAAATCTCCAAAGATCTCTTTAAGGGCTGGGCATGGTGGCTCACTTTGGGAGATGGA NM_017846RefSeq chr1
+ 28553016 28578545 TRNAU1AP 54952 "tRNA selenocysteine 1 associated protein 1, transcript variant
1" GO:0005737|GO:0000166|GO:0001514|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139511_PI430048170 0.1978355177591460.4551528036562970.606604571542564
2.76676839486943 2.81750360776978 A A A 3.55190740963461 2.74337881360908
3.94126550581486 P P P LNCV6_139511_PI430048170 mRNA
GGTTTGCAACAACCACATCATTTCCATTAACTTAGATTTAGGTTTTACTGGATTCATTGC NM_007256RefSeq chr11
+ 75150986 75206400 SLCO2B1 11309 "solute carrier organic anion transporter family, member 2B1,
transcript variant 1" GO:0005886|GO:0015347|GO:0043252|GO:0008514|GO:0016021|GO:0055085 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139477_PI430048170 0.17461217487057 1.08370250378877 12.7974755034614
12.9822435204721 12.846942991138 P P P 12.7614196096045 12.7694195446549
12.7542730640536 P P P LNCV6_139477_PI430048170 mRNA
CGCCTCCTGGAACGGAAGCATTTTCCTTTTTGTATAGGTTGAATTTTTGTTTTCTTAATA NM_016199RefSeq chr19 -
2321520 2328615 LSM7 51690 "LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)"
GO:0008380|GO:0006397|GO:0005515|GO:0010467|GO:0043928|GO:0005681|GO:0017070|GO:0005829|GO:0000
288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135481_PI430048170 0.1910640042952370.8085432818522556.77441843357245
6.32921277505707 6.21603026566 P P P 6.87133013901925 6.82115674844082 6.59431343061598 P
P P LNCV6_135481_PI430048170 mRNA
GGCTCTGGCCAAAGCTTGCTCCCTGCTCCCACACAGGCTCAATAAAGCAAGTCAAAGCCA NM_002722RefSeq chr17
- 43940803 43942465 PPY 5539 pancreatic polypeptide
GO:0007631|GO:0009306|GO:0001664|GO:0005179|GO:0007218|GO:0007586|GO:0007267|GO:0005102|GO:0032
098|GO:0005576|GO:0005184|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138203_PI430048170 0.4256535346852220.8271084970988170.573895405613186
0.50630285179042 0.588572732364186A A A 0.6113913256554671.25775984032062
0.501943692326537A A A LNCV6_138203_PI430048170 mRNA
GTCTTGAAATTGTCACTCGCTTACTGGATCCAAGCGTCTCGAGGATAAATAAAGATCATG NM_024025RefSeq chr8
- 33591329 33600106 DUSP2678986 dual specificity phosphatase 26 (putative)
GO:0005515|GO:0001102|GO:0005794|GO:0005634|GO:0000122|GO:0035335|GO:0004647|GO:0045785|GO:0005
739|GO:0002039|GO:0005737|GO:0006470|GO:0044387|GO:0070373|GO:0004721|GO:0008138|GO:0004725|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91271_PI430048170 0.0118885379249682 0.5972474366460838.36488784145175
7.98892606240267 8.28581015410759 P P P 8.87490329558709 8.96833439751582
9.04855871178684 P P P LNCV6_91271_PI430048170 mRNA
CAACGCAGAAGGTATTCATTTTTCCTAGGTATTTGGAAAACAGAAATTTTCAAGGTCAAG NM_014473RefSeq chr5
- 62388523 62403901 DIMT1 27292 DIM1 dimethyladenosine transferase 1 homolog (S. cerevisiae)
GO:0031167|GO:0005737|GO:0005730|GO:0052909|GO:0005634|GO:0000179 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136395_PI430048170 0.0891448945398631 0.6171255416771893.6384284030266
4.34531972485822 4.3455213969203 P P P 4.82097482113061 4.87337094028444
4.83204262494605 P P P LNCV6_136395_PI430048170 mRNA
GAAATGCAGAAGAAAGGCTTGTTTTGGTTGTTTTTCTTTTTTAGGAAAACGCTGCCTAAA NM_173083RefSeq chr1
- 226231148 226309503 LIN9 286826 "lin-9 DREAM MuvB core complex component, transcript variant 1"
GO:0005515|GO:0071897|GO:0017053|GO:0000086|GO:0051726|GO:0005654|GO:0000278|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_131101_PI430048170 0.6451310762901560.9539024031200020.271699925436352
0.2842007651179660.479679134432317A A A 0.62012451771727 0.291790620860003
0.313600376413612A A A LNCV6_131101_PI430048170 mRNA
CTCAGCCACTCTGTCTGAGAGATGATTTTCTAATATTTATCCACTAATAAAGAAGAGTGT NM_024059RefSeq chr20
+ 63553019 63556682 C20orf195 79025 chromosome 20 open reading frame 195 GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128969_PI430048170 0.7917162543535451.01506347742173 12.1502353963352
12.1270849367144 12.0114245873243 P P P 11.9568409467399 12.2026562653747
12.0577066969219 P P P LNCV6_128969_PI430048170 mRNA
CAGGGCTGGCCCGTTTGGGACAGCTGACCAATAAACACTGATGGTGTGTTTGTCAAAAAA NM_003863RefSeq chr9
- 127935094 127938484 DPM2 8818 "dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit"
GO:0005515|GO:0006501|GO:0004582|GO:0048471|GO:0033185|GO:0019348|GO:0016254|GO:0030176|GO:0035269|GO:0000506|GO:0050790|GO:0031647|GO:0005789|GO:0030234|GO:0006488|GO:0044267|GO:0006506|GO:0043687|GO:0018279. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143327_PI430048170 0.00856429932333302 0.31846219523481 2.31062455945569
1.46334702122834 2.06820892529565 A A A 3.87986861566826 3.37024794698513
3.62560174120102 P P P LNCV6_143327_PI430048170 mRNA
GTGGCTGCTGATAACCCAACATTCCATCTCTACCCTCATACTTCAAAATTAAATCAAGTA NM_005213RefSeq chr3
+ 122325163 122341968 CSTA 1475 cystatin A (stefin A)
GO:0004869|GO:0010466|GO:0005634|GO:0002020|GO:0005615|GO:0001533|GO:0045861|GO:0010951|GO:0005737|GO:0016337|GO:0018149|GO:0005198|GO:0030216|GO:0005654|GO:0030674|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_37976_PI430048170 0.2364600236574311.04718351112277 13.0530651934257 12.9891730460733
12.9170972586879 P P P 12.9189975211431 12.959946496122 12.883025195763 P P P
LNCV6_37976_PI430048170 mRNA
AACACCTTCTCGCCGGGCTGGGAACAATAAATGCAGCCATGTCTCTGCAGCTGGTGCTGA NM_017914RefSeq chr19
+ 1275520 1279244 C19orf24 55009 chromosome 19 open reading frame 24
GO:0005737|GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113183_PI430048170 0.1862172481797891.17227250186992 4.76135602326413
4.63833850012567 4.69220296850667 P P P 4.70549323688975 4.34256078987902 4.3258136859823
P P P LNCV6_113183_PI430048170 mRNA
TACTTGTAAATCCTTAGAAGAAAAGCTGGATCTGGTCACGAACAAGCAGCACAGCCCCAT NM_001173543 RefSeq
chr16 + 87970017 88077318 BANP 54971 "BTG3 associated nuclear protein, transcript variant 7"
GO:0005515|GO:0002039|GO:0034504|GO:0007049|GO:0006355|GO:0042177|GO:0007275|GO:0005654|GO:0003677|GO:0006351|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131798_PI430048170 0.00999141077432379 0.463321235170815 0.588966189687049
1.19394643294086 1.0642226146796 A A A 1.87436832247341 2.31477163084012
2.01997198681578 A A A LNCV6_131798_PI430048170 mRNA
CGATGCTGTGCAAAGGATTTTAAAATATGAGAGTCACTGAAAGAGTTTAAACATCTGTTC NM_019001RefSeq chr3
- 142306606 142448062 XRN1 54464 "5'-3' exoribonuclease 1, transcript variant 1"
GO:0005515|GO:0010467|GO:0016075|GO:0005794|GO:0090305|GO:0005886|GO:0071028|GO:0000956|GO:0043928|GO:0003677|GO:0005829|GO:0004527|GO:0005737|GO:0016020|GO:0000932|GO:0071044|GO:0045111|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133068_PI430048170 0.541093335729288 1.53521573739941 2.28504413944328
0.6767528894524760.559064284667048A A A 0.5790824522836830.525640113932547
1.16486038434835 A A A LNCV6_133068_PI430048170 mRNA
ACAGTAACAACAACATTTTGAAGACTTTTCCCTGGTGGCATCCTAGAGGGACCGACTTTC NM_175922RefSeq chr6
- 166305679 166308383 PRR18 285800 proline rich 18 NA . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_140610_PI430048170 0.4596236507335851.24403159599294 0.255752510558749
1.16833459580838 0.401993733904453A A A 0.369192296682127 0.370438282861152
0.315165980047547A A A LNCV6_140610_PI430048170 mRNA
CCGATCAAGTCAACTCAGTACTCACGGGAGAAAAATAGACTTTATTTACAAGTAATAACA NM_005699RefSeq chr11
+ 71999062 72002919 IL18BP 10068 "interleukin 18 binding protein, transcript variant C"
GO:0070301|GO:1900116|GO:0071356|GO:0032496|GO:0042088|GO:0005576|GO:0048019|GO:0005615|GO:0070
062|GO:0042007 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134697_PI430048170 0.000269286752791908 0.5537510921477097.24334395436087
7.1116347442115 7.20113065966362 P P P 7.99742452065411 8.06031890855491 8.058669422713
P P P LNCV6_134697_PI430048170 mRNA
CTCAAGACTTCCAGAGCCTCAAATGAGAAAATGTCTTTATTAAATGTAGAAAGTGATCCA NM_005308RefSeq chr10
+ 119207684 119455619 GRK5 2869 G protein-coupled receptor kinase 5
GO:0005515|GO:0043066|GO:0031965|GO:0005886|GO:0038032|GO:0007217|GO:0006915|GO:0005634|GO:0005
524|GO:0005737|GO:0046777|GO:0008277|GO:0004703|GO:0005543|GO:0004674|GO:0005080|GO:0005654|GO:0
007188|GO:0016055|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94479_PI430048170 0.00109935410294008 1.62815134876191 4.36038370901376 4.3686913008796
4.18024992376561 P P P 3.50431033854197 3.60188983337871 3.69487629361814 P P P
LNCV6_94479_PI430048170 mRNA
AAACTTCATACAAGTATAGCTGGACGCAACCTTTATATCCGTTTCCAGTCCAGGTCAGGG NM_000859RefSeq chr5
+ 75337167 75362101 HMGCR 3156 "3-hydroxy-3-methylglutaryl-CoA reductase, transcript variant 1"
GO:0005515|GO:0050662|GO:0006695|GO:0005783|GO:0045471|GO:0032874|GO:0015936|GO:0044281|GO:0070
402|GO:0042803|GO:0061045|GO:0043407|GO:0045908|GO:0010666|GO:0045445|GO:0070374|GO:0005778|GO:0
044255|GO:0010664|GO:0051262|GO:0007584|GO:0004420|GO:0007568|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_104487_PI430048170 0.1349507067444480.86950936177265 8.07847614482426
7.95190926185852 7.77406377409756 P P P 8.15333820820499 8.23073171760897
8.03495390529699 P P P LNCV6_104487_PI430048170 mRNA
AGGTCTTCCAGCTCCTCTTCCTCAAACCATTCTGATAACTTTTTCAGGATGGGTAGCAGT NM_001077525 RefSeq
chr3 + 9649432 9702394 MTMR14 64419 "myotubularin related protein 14, transcript variant 2"
GO:0048471|GO:0006661|GO:0004438|GO:0044281|GO:0006644|GO:0001726|GO:0035335|GO:0004725|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132609_PI430048170 0.1191336208159611.1702211210193 7.01135000975549
7.16870921910887 7.08170871261438 P P P 6.68572831529544 6.86747055082124
7.01390112445427 P P P LNCV6_132609_PI430048170 mRNA
TCTGCCTGGTGTGTGCACACAAGTCTTACTTGGAATAAATTTACTGGTACAAATTCTTAA NM_020905RefSeq chr2
- 18554722 18560693 RDH14 57665 retinol dehydrogenase 14 (all-trans/9-cis/11-cis)
GO:0005739|GO:0016020|GO:0005783|GO:0016491|GO:0005789|GO:0005634|GO:0005765|GO:0001649|GO:0055
114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135354_PI430048170 0.3552684710532071.12883578473752 11.1128253250671
11.2375395197619 11.4994601703284 P P P 10.9388537667266 11.0299258290606
11.3507533093585 P P P LNCV6_135354_PI430048170 mRNA
CAGCATCAAATACCTTGTAACGTCTTCTCTGCCTTGTTAGTGCATATTTTTACTTTTCTG NM_022748RefSeq chr7 -
47275153 47582144 TNS3 64759 tensin 3
GO:0005515|GO:0008284|GO:0005737|GO:0048286|GO:0016477|GO:0005925 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130110_PI430048170 0.1818865997075743.12199208337304 0.470445931876383
2.54109430187159 2.51868019849426 A A A 0.5517286226040880.416493345453759
0.425589639159592A A A LNCV6_130110_PI430048170 mRNA

TATCCGTTGGATGCCACCAGAGTCCATTTTTTATAACCGCTACACTACAGAGTCTGATGT NM_005592RefSeq chr9
+ 110668770 110800998 MUSK 4593 "muscle, skeletal, receptor tyrosine kinase, transcript variant 1"
GO:0005515|GO:0006355|GO:0031594|GO:0030054|GO:0018108|GO:0007275|GO:0005524|GO:2000541|GO:0030
154|GO:0043235|GO:0010628|GO:0046777|GO:0043525|GO:0030198|GO:0005887|GO:0007528|GO:0045211|GO:0
001934|GO:0007613|GO:0004713|GO:0004714|GO:0008582|GO:0007169|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132055_PI430048170 0.1932124264771161.21928732945786 6.49113501657033
6.54125444465402 6.92476308699105 P P P 6.24381998843895 6.26376295816872
6.60264779920421 P P P LNCV6_132055_PI430048170 mRNA
CTCTCACATGACAGGTTTTCTACTTAGTACCTTTTATGGCATCAATGTAAATTTAAGCTG NM_001145268 RefSeq
chr7 + 102748951 102809225 FAM185A 222234 "family with sequence similarity 185, member A,
transcript variant 1" GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131076_PI430048170 0.7237272204261270.9893434960641020.450666511214712
0.4664995708526050.372739484328034A A A 0.50220600071716 0.41011384505877
0.423971799577665A A A LNCV6_131076_PI430048170 mRNA
GCATCAGTTCTTGCACTCTTTGTACAGAATTGGTATAAAAAGGATAATTCCACACTGAAA NM_004799RefSeq chr1
+ 52142093 52346686 ZFYVE9 9372 "zinc finger, FYVE domain containing 9, transcript variant 3"
GO:0005515|GO:0007183|GO:0005545|GO:0031901|GO:0007184|GO:0006508|GO:0008236|GO:0007179|GO:0046
872|GO:0030512|GO:0005769|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105759_PI430048170 0.156824671972218 1.20706493021318 6.31596376438649
6.60453272048739 6.68708029004152 P P P 6.05671035828528 6.41434255592103
6.32423744304849 P P P LNCV6_105759_PI430048170 mRNA
TTGACAAAGATGGTGATGGAGAATAAACCAAGAGGAGTTCATTGCTATTATGACTGGTGA NM_001297765 RefSeq
chr5 - 90393334 90409786 CETN3 1070 "centrin, EF-hand protein, 3, transcript variant 1"
GO:0007067|GO:0005813|GO:0007098|GO:0005814|GO:0005509|GO:0005730|GO:0051301 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135783_PI430048170 0.0245935735343826 1.09281216230462 0.455247512284364
0.3852491587182090.396245361222276A A A 0.2609221172644250.339558955222464
0.251480466511393A A A LNCV6_135783_PI430048170 mRNA
GGCAAACAAAGCCATCATTCTGGGGCTTAATTAATAAAGCTCCTAGTTTCATAGAAAAAA NM_152376RefSeq chr1
+ 20186077 20196048 UBXN10 127733 UBX domain protein 10 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134247_PI430048170 0.5026650318759291.27208879089723 4.56602683353317
5.42098176366485 4.39593130924719 P P P 3.69173477342392 4.83949758916899
4.77065851961784 P P P LNCV6_134247_PI430048170 mRNA
TGCCCTACTCAGCTTCCATCACCCCTAGCAATATGTATTAAAGTCTGAAGTGTTGCCATG NM_019858RefSeq chr12
+ 6821796 6827418 GPR162 27239 "G protein-coupled receptor 162, transcript variant A-2"
GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132623_PI430048170 0.2808427609132610.91595643853298 4.96989176708006
5.27832034556336 5.12084396709813 P P P 5.33175483157322 5.18319065356472
5.24668132210138 P P P LNCV6_132623_PI430048170 mRNA
AGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAGGCCT NM_145202RefSeq
chr10 + 133347339 133352683 PRAP1 118471 "proline-rich acidic protein 1, transcript variant 1"
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127756_PI430048170 0.0898561949204275 0.5121427012783542.22765205967137
2.87336801988072 2.93004183823725 A A P 2.94449960105281 3.9344710529885
3.93988241285588 P P P LNCV6_127756_PI430048170 mRNA
CTTGTGTGACCTCCAGTGCATATTAGACCATTCACTGTATGAAAGAAAACATGTTGAATA NM_005568RefSeq
chr17_KI270857v1_alt + 1173836 1180980 LHX1 3975 LIM homeobox 1

GO:0010468|GO:0001657|GO:0007389|GO:0001658|GO:0003700|GO:0006366|GO:0001655|GO:0048793|GO:0048703|GO:0009791|GO:0072077|GO:0009653|GO:0009880|GO:0072278|GO:0035846|GO:0035847|GO:0048646|GO:0072177|GO:0072178|GO:0009887|GO:0035849|GO:0001705|GO:0001706|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135058_PI430048170 0.0458210494211301 0.7468613186400266.74949600982139 6.45817420474947 6.36228962827891 P P P 6.9893318799858 7.06311460489693 6.796526375423 P P P LNCV6_135058_PI430048170 mRNA
CCGTCTATGCCTAAAAGATAATAAAACTGAAATATGTCTTCACAGGTCTCCCACAAAAAA NM_001627RefSeq chr3 + 105366712 105576913 ALCAM 214 "activated leukocyte cell adhesion molecule, transcript variant 1"
GO:0005515|GO:0030424|GO:0007165|GO:0008045|GO:0007411|GO:0043025|GO:0005102|GO:0016021|GO:0007155|GO:0005925|GO:0009897|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139118_PI430048170 0.2586893468032320.6346712560317615.05556378783457 3.37988250306125 4.20174493395764 P P P 5.37120761305647 5.11279749053134 4.44644956895293 P P P LNCV6_139118_PI430048170 mRNA
CCCACCCCTTTTCTACTGAATTTGTGGGGATCCTATAATAAAAGTGAATGACTAAAAATT NM_138817RefSeq chr8 - 86214058 86230375 SLC7A13 157724 "solute carrier family 7 (anionic amino acid transporter), member 13" GO:0015171|GO:0016021|GO:0003333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126779_PI430048170 0.1580393232572950.7391504855532361 1.3977286394241 10.7669746783177 10.7113558042273 P P P 11.5155275389363 11.4831254121628 11.2795015720193 P P P LNCV6_126779_PI430048170 mRNA
TCCTGGTGCCTGCCTCTCTCCTCCACCCCAGGCTTAGAGGACAGAAAAATGTGAAGAGAC NM_001300804 RefSeq chr6 + 41637176 41654244 MDFI 4188 "MyoD family inhibitor, transcript variant 1"
GO:0005515|GO:0060707|GO:0030178|GO:0005634|GO:0042994|GO:0048704|GO:0000122|GO:0007257|GO:0009790|GO:0009950|GO:0043392|GO:0005737|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144936_PI430048170 0.0134362099613844 1.38535132637898 10.0190626396168 9.84290646482576 9.88810947033604 P P P 9.28337705612039 9.56779256704815 9.47949981376537 P P P LNCV6_144936_PI430048170 mRNA
ACAACTGTCGTAGTCATGGCTTTGGGATGGGTTCTGTTTATTAAAATCCTATTGCTCCTA NM_173595RefSeq chr12 - 56237806 56258359 ANKRD52 283373 ankyrin repeat domain 52 GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140648_PI430048170 0.9628493349659460.9959055839089171 4.327898774518 14.351007416131 14.2407777944125 P P P 14.046839657508 14.5471081119277 14.3026091767007 P P P LNCV6_140648_PI430048170 mRNA
TCTGGGCCCTCCTTCAGCCCCCATCATGGGAATAAATTAATTTTCTCAATGTACAAAAAA NM_001916RefSeq chr8 + 144095034 144097527 CYC1 1537 cytochrome c-1
GO:0005506|GO:0070469|GO:0005743|GO:0005634|GO:0044281|GO:0005739|GO:0022904|GO:0045155|GO:0016020|GO:0033762|GO:0016021|GO:0044237|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131771_PI430048170 0.2314992473047180.9553023616440710.269462718275423 0.3663145664845610.299435245876138A A A 0.4493730526539880.347420481239331 0.335299372408818A A A LNCV6_131771_PI430048170 mRNA
TTTTGTGTTTATACTGGGCCAGGTCCTGGTAGAACCTTTCAACAAACAACCAAACAAAAA NM_006237RefSeq chr13 - 78599094 78603560 POU4F15457 POU class 4 homeobox 1
GO:0043005|GO:0000790|GO:0021986|GO:0021535|GO:0006366|GO:0051355|GO:0003705|GO:0021559|GO:0007409|GO:0043524|GO:0001967|GO:0050767|GO:0003223|GO:0045944|GO:0043065|GO:0001205|GO:0021953|GO:0048665|GO:0000122|GO:0007416|GO:0060384|GO:0001077|GO:0048880|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144213_PI430048170 0.6197045109869470.9255485618871223.09799874965061 2.67606749658919 3.0386082552717 P A P 3.33726073260374 2.95623233073809 2.84125692580374 P P P LNCV6_144213_PI430048170 mRNA

GTAGGAGAAAAATCCCCAGCCTTTTTAAATTTAGATTATTTCCTTTCCATTAGGGTCAGA NM_152786RefSeq chr9
+ 113410707 113429684 C9orf43 257169 "chromosome 9 open reading frame 43, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129388_PI430048170 0.9656465760574780.937309939426367 8.61548735269729
8.38316483677678 8.41726076202335 P P P 9.14306636455818 8.05525405137217
8.26680067091804 P P P LNCV6_129388_PI430048170 mRNA
CCTAGTCTGTAACTCTTTCTGAGGAGCTGTTACTGAATATTAAAAAGATAGACTTCAACT NM_005347RefSeq chr9
- 125234847 125241387 HSPA5 3309 "heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)"
GO:0005515|GO:0006983|GO:0035437|GO:0030968|GO:0051787|GO:0001948|GO:0031398|GO:0071353|GO:0031
625|GO:0070062|GO:0042470|GO:0005793|GO:0030335|GO:0009986|GO:0019904|GO:0005509|GO:0030168|GO:0
030496|GO:0030433|GO:0021589|GO:0005790|GO:0005789|GO:0005788|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143876_PI430048170 0.0239378465770509 1.80361115772226 10.5366211992585
10.7069345445128 10.6804364476153 P P P 9.45478456627947 9.96869659706634
9.90154742541903 P P P LNCV6_143876_PI430048170 mRNA
TCTGTGACTCCTAATAGGCCAGTTTGTGATAAGCTTACTCTATGAGTCTTCATTTTTCTA NM_001032291 RefSeq chr1
- 109279553 109283168 PSRC1 84722 "proline/serine-rich coiled-coil 1, transcript variant 3"
GO:0005515|GO:0008017|GO:0031116|GO:0030308|GO:0060236|GO:0001578|GO:0005819|GO:0045737|GO:0030
496|GO:0005829|GO:0000922|GO:0005737|GO:0015630|GO:0005654|GO:0005876|GO:0007080|GO:0045893|GO:0
051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135997_PI430048170 0.2018952451700121.22651563978745 6.74501396696339
6.68834158949529 6.71460390271652 P P P 6.17381469581772 6.7304518634974
6.29990055949164 P P P LNCV6_135997_PI430048170 mRNA
TGCCAACTGGAGAAAGGCCTAATTACCAGGATCTAGACCTTCATCTCTCTCTCTCTCTTT NM_001291088 RefSeq
chr19 - 37884822 37906706 WDR87 83889 "WD repeat domain 87, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_137484_PI430048170 0.4743856663949120.8664095974721870.39118792302706
0.2831293759258090.326978027615477 A A A 0.2882893741767650.916987007049428
0.329496859099865 A A A LNCV6_137484_PI430048170 mRNA
TTGGATTGCTTATTCAGGCATTATAAGGTACTCTGGAGGAAGGAATCACTTCTCTTTTTT NM_001017992 RefSeq
chr5 - 57480015 57482809 ACTBL2 345651 "actin, beta-like 2"
GO:0008150|GO:0003674|GO:0005737|GO:0005856|GO:0005615|GO:0005524|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144214_PI430048170 0.3952830794235840.9775196114908620.2766965844072860.293498855396
0.370654397334591 A A A 0.3778330270931010.3155538551999340.346948410418986 A A A
LNCV6_144214_PI430048170 mRNA
GTATGAATCATATTGCCAGGGTTGATTCCAGTCAATTCAGCAGGCCTAGATTTATTTTCC NM_001032377 RefSeq
chr2 - 37167819 37188547 SULT6B1 NA "sulfotransferase family, cytosolic, 6B, member 1"NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140115_PI430048170 0.0159507636462511 0.5236529114465792.08158056785713
2.24787167753398 2.67449176197315 A A A 3.53372208161751 3.26707969651862
3.02447852176677 P P P LNCV6_140115_PI430048170 mRNA
AATGCCCTGAATCACCTCTCTCATGGAAGAACCAATTAACACCAATGAATCAACCATTAA NM_003159RefSeq chrX
+ 18425604 18653629 CDKL5 6792 "cyclin-dependent kinase-like 5, transcript variant I"
GO:0045773|GO:0005634|GO:0032587|GO:0032839|GO:0044294|GO:0005524|GO:0032855|GO:0048365|GO:0005
737|GO:0046777|GO:0004672|GO:0004674|GO:0016301|GO:0050775|GO:0051726|GO:0050773|GO:0005654|GO:0
006468|GO:0001764|GO:0004693 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145361_PI430048170 0.3906111876626951.67101782632906 1.88400633056136
0.322080416206338 0.414429094713927 A A A 0.3468675789470870.319056295151246

0.304769340923277 A A A LNCV6_145361_PI430048170 mRNA
AGGAACAAAGACATGAAGCAGGGTTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA NM_001005236
RefSeq chr9 + 122661715 122662648 OR1L1 NA "olfactory receptor, family 1, subfamily L, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126880_PI430048170 0.844321224451815 1.01990184244313 5.1917692390186
5.06259860167216 4.8547617715321 P P P 5.09172684034546 4.94993897111364
4.99839373220373 P P P LNCV6_126880_PI430048170 mRNA
ACACTTGAAGATGTGCTCCCTCCACGATCATCTCAGCAACCTGCCACTTGAGGGGTCCAC NM_021733 RefSeq chr19
- 49739753 49763258 TSKS 60385 testis-specific serine kinase substrate
GO:0005515|GO:0019901|GO:0001669|GO:0005814|GO:0010923 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141620_PI430048170 0.769420045933373 1.00584067431086 0.346914040345383
0.324291101287777 0.267669544530729 A A A 0.307584152990219 0.314314211566388
0.292838052492776 A A A LNCV6_141620_PI430048170 mRNA
TTGTTTCCAGGCTTTTGCTACTCTTCACTCAGCTACAATAAACATCCTGAATGTTTTCTT NM_016523 RefSeq chr12 +
9827480 9845004 KLRF1 51348 "killer cell lectin-like receptor subfamily F, member 1, transcript variant
1" GO:0016020|GO:0005887|GO:0030246|GO:0007166|GO:0032393|GO:0004888 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_65917_PI430048170 0.876828654920741 0.976507866110644 1.47461506564511 1.96133000603834
0.372174652766399 A A A 0.696651781341033 1.55057458528583 1.85168208881992 A A A
LNCV6_65917_PI430048170 mRNA
AGTAAGTCAAGGAACACCTTATAATCCTGATGGACAGCCCATGGGAGGTTTCGTAATGGA NM_002398 RefSeq chr2
+ 66435399 66572759 MEIS1 4211 Meis homeobox 1
GO:0005515|GO:0005667|GO:0046982|GO:0006366|GO:0003705|GO:0060216|GO:0005634|GO:0001525|GO:0000
978|GO:0001077|GO:0035855|GO:0002089|GO:0045665|GO:0045638|GO:0045944|GO:0003682 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129119_PI430048170 0.83860122612139 1.03050130039565 4.39846404560278
4.25341272834233 3.93792060171723 P P P 4.11123125539781 4.10582402159647 4.2739376708773
P P P LNCV6_129119_PI430048170 mRNA
CTGAGCCTCACCCCGGCTTTTTATTTAACAGCTCACCCATAAAAGGCCCTTTTCAGGGCC NM_003540 RefSeq chr6
+ 26240425 26240793 HIST1H4F 8361 "histone cluster 1, H4f"
GO:0005515|GO:0010467|GO:0006325|GO:0005634|GO:0045653|GO:0000723|GO:0000183|GO:0000786|GO:0070
062|GO:0035574|GO:0035575|GO:0046982|GO:0006334|GO:0006335|GO:0005576|GO:0006336|GO:0000228|GO:0
003677|GO:0032776|GO:0034080|GO:0043234|GO:0016020|GO:0045814|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138980_PI430048170 0.566227587988574 0.918703725788415 3.90107605401104
4.01504909576712 3.79105137661978 P P P 4.27604187455218 4.01529387020664
3.74236809719061 P P P LNCV6_138980_PI430048170 mRNA
ATGGTATAAACACCTGGTCATTTCAATCCAACATGGGACGGACACTGACAGACAGTACTC NM_006943 RefSeq chr20
+ 325570 330228 SOX12 6666 SRY (sex determining region Y)-box 12
GO:0000976|GO:0001105|GO:0006357|GO:0021510|GO:0005634|GO:0005575|GO:0003677|GO:0065004|GO:0006
351|GO:0001077|GO:0045165|GO:0032993|GO:0045944 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129396_PI430048170 0.646129874985 1.16154471595732 1.56376486234134
2.44625755346239 2.54003090741098 A A A 2.01668802466588 2.44418710452379
1.46233472074688 A A A LNCV6_129396_PI430048170 mRNA
ATCACACACCGTATGTGTTTGCTAACTGGCTTTACCCAAAAGAAAATTAAACTTTCTTTG NM_005127 RefSeq chr12
- 9852368 9869859 CLEC2B 9976 "C-type lectin domain family 2, member B"
GO:0005887|GO:0030246 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134331_PI430048170 0.0173245312620514 0.563396101234572 0.442718484206965

0.40559796912883 0.259721744388339 A A A 0.915564878856922 1.38382592295255
1.25867891378522 A A A LNCV6_134331_PI430048170 mRNA
GCTACTGGGAGGGTAAAGCCATTTGAAGAATAAAGTCATCCAGAGCCTCAGGACAAAAAA NM_012202 RefSeq
chr11 + 62707593 62709206 GNG3 2785 "guanine nucleotide binding protein (G protein), gamma 3"
GO:0000187|GO:0006112|GO:0007186|GO:0005886|GO:0071377|GO:0005834|GO:0003924|GO:0007268|GO:0044
281|GO:0004871|GO:0031702|GO:0007204 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138494_PI430048170 0.476294454204846 1.22791140036305 1.40217665241909
0.616300916622466 0.523816684239908 A A A 0.818047340696028 0.479298520132485
0.500453317127666 A A A LNCV6_138494_PI430048170 mRNA
GGTAAACTCTTAGTCCAAAACCCAAACATGCAATAAATAAAACTCCCTTATTTGACAGCT NM_004590 RefSeq
chr17_KI270857v1_alt - 211056 216060 CCL16 6360 chemokine (C-C motif) ligand 16
GO:0008009|GO:0006955|GO:0007154|GO:0006954|GO:0006935|GO:0060326|GO:0007267|GO:0005576|GO:0042
056|GO:0005615|GO:0050918 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111035_PI430048170 0.40983210070605 1.02723952001907 0.294430621626011
0.311917302851065 0.411736988295592 A A A 0.318216001020612 0.296041655514527
0.29015449752316 A A A LNCV6_111035_PI430048170 mRNA
TTCAGAGTCCTGAGAGCTCTAAAAACTATTTCAGTTATCCCAGGCTGAAGACCATCGTGG NM_001099404 RefSeq
chr3 - 38548061 38649672 SCN5A 6331 "sodium channel, voltage gated, type V alpha subunit,
transcript variant 3"
GO:0005515|GO:0005516|GO:0086010|GO:0086070|GO:0060307|GO:0060048|GO:0019228|GO:0060371|GO:0086
067|GO:0086069|GO:0060373|GO:0060372|GO:0010765|GO:0007411|GO:0086002|GO:0001518|GO:0045760|GO:0
086006|GO:0031625|GO:0086004|GO:0086005|GO:0050679|GO:0019901|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_121971_PI430048170 0.478201645411218 0.865907526143997 0.596146412510523
0.638595662352182 0.55915942888559 A A A 0.590408321799812 0.551181954549966
1.18541379567953 A A A LNCV6_121971_PI430048170 mRNA
TTGTGATGCCAATTGCCCTCTTGACAATAATGTTTGCATTGCCATTCCAGTCCCTATTAA NM_000867 RefSeq chr2
- 231108235 231125110 HTR2B 3357 "5-hydroxytryptamine (serotonin) receptor 2B, G protein-coupled"
GO:0019722|GO:0030054|GO:0001755|GO:0045202|GO:0001819|GO:0048598|GO:0004993|GO:0014033|GO:0060
548|GO:0007610|GO:0051781|GO:0070374|GO:0043123|GO:0070371|GO:0051209|GO:0010513|GO:0014065|GO:0
007210|GO:0002031|GO:0016310|GO:0007186|GO:0032320|GO:0005887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145322_PI430048170 0.29397525297706 0.853593196170366 0.424300637300591
0.425937617269582 0.337667453867575 A A A 0.329148688918438 0.851027255224871
0.647417056611461 A A A LNCV6_145322_PI430048170 mRNA
AACTGACTGCAAGATGCCTTAAGGGTGTAGAACAAGAGAAAAAGGAACTGAGGCACCTCA NM_001161498
RefSeq chr14 + 69484753 69528498 PLEKHD1 NA "pleckstrin homology domain containing, family D
(with coiled-coil domains) member 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143404_PI430048170 0.00483786699894131 1.47613475615845 7.79912174499769
7.75952327556282 7.93501610587994 P P P 7.19098121556555 7.41615431022515
7.19529624602231 P P P LNCV6_143404_PI430048170 mRNA
TTTGGGGTACAAGCTGTGATCACTGATCAATAAATTATCTCTAGATTGGTCCTTGTGAGG NM_003449 RefSeq chr6
- 30184454 30213494 TRIM26 7726 "tripartite motif containing 26, transcript variant 1"
GO:0051091|GO:0046597|GO:0045087|GO:0019221|GO:0008270|GO:0005575|GO:0003677|GO:0046872|GO:0060
333|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64410_PI430048170 0.0843484301741864 0.677692129810432 5.83028951305204
5.88029251771503 5.26550384568761 P P P 6.29357863038421 6.32930484889041
6.10397010300718 P P P LNCV6_64410_PI430048170 mRNA
GCACCCAGTCCGGTCACCGCAGCGGAGAGCTCGCCGCTCGCTGCAGCGAGGCCCGGAGCG NM_002229 RefSeq

chr19 + 12791495 12793311 JUNB 3726 jun B proto-oncogene
GO:0005515|GO:0010467|GO:0003700|GO:0006367|GO:0033687|GO:0045597|GO:0043434|GO:0051591|GO:0032
870|GO:0046697|GO:0003690|GO:0045944|GO:0071277|GO:0060716|GO:0051726|GO:0007179|GO:0009416|GO:0
034097|GO:0000785|GO:0051412|GO:0000977|GO:0006357|GO:0003714|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130909_PI430048170 0.8923937292721881.13666110286948 1.97270950066328
0.44751448760245 0.357234830197798A A A 0.4918907127766320.3821697622458691.6183507303194
A A A LNCV6_130909_PI430048170 mRNA
CAGAACCTTGGTTATTGTTTTTTAGCCATAGAATCTTCTAGTAAAAAATATCTGCCGCCA NM_139245RefSeq chr3
+ 160756207 161071029 PPM1L 151742 "protein phosphatase, Mg2+/Mn2+ dependent, 1L"
GO:0006665|GO:0006470|GO:0000165|GO:0030148|GO:0005789|GO:0007178|GO:0044281|GO:0016021|GO:0004
722|GO:0046872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121800_PI430048170 0.3326688286751670.7961315773820690.705320192389092
0.80675491096584 0.669342490629167A A A 1.06315465163248 0.599204627371661
1.39970121532749 A A A LNCV6_121800_PI430048170 mRNA
TATTTGTAATGCTGGTACAAGGCAGCTGGCAACGTTCCCTTCAAGACACAGAGGAGAAAT NM_002054RefSeq chr2
- 162142868 162152404 GCG 2641 glucagon
GO:0005515|GO:0007631|GO:0005886|GO:0008283|GO:0030819|GO:0035948|GO:0044281|GO:0010737|GO:0090
280|GO:0005615|GO:0032092|GO:0042802|GO:0033138|GO:0042594|GO:0071377|GO:0045860|GO:0031769|GO:0
070374|GO:0010800|GO:0043066|GO:0035774|GO:0005102|GO:0005576|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_54997_PI430048170 0.180092433010035 1.27991594932688 10.4983394705934 11.0302346766994
10.5383688938809 P P P 10.5140186712636 10.3934961081936 10.1275849621135 P P P
LNCV6_54997_PI430048170 mRNA
CGGTTCTGGAATAAGAATATAGGTTCAAACCGTCCTCTGTCTCCCCACATTACTATCTAC NM_003001RefSeq chr1
+ 161314375 161364745 SDHC 6391 "succinate dehydrogenase complex, subunit C, integral membrane
protein, 15kDa, transcript variant 1"
GO:0006099|GO:0005743|GO:0009055|GO:0044281|GO:0046872|GO:0005739|GO:0009060|GO:0022904|GO:0005
749|GO:0000104|GO:0016021|GO:0044237|GO:0055114|GO:0020037|GO:0045273 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136981_PI430048170 0.6335024461767061.33622397066217 1.75815554530028
0.4513176859614830.265027454232358A A A 0.3959000145049520.479217969480178
0.802642812688592A A A LNCV6_136981_PI430048170 mRNA
GTAGATTTTGAAGGGCAAGAGAACAGGAACGAACCATGTCTGAGAAGCCAATATAGAAAA NM_001145024
RefSeq chr11 - 112248152 112260860 PLET1 NA placenta expressed transcript 1 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140696_PI430048170 0.0890940663741590.7075041017132773.73177591393987
3.73549401630768 4.28486412891527 P P P 4.20062414409737 4.52836596399586
4.56631945949065 P P P LNCV6_140696_PI430048170 mRNA
GGAGTATGGCATCTGAAGGTAAATGGCTCATCAATAAACTCGATATCAACAATTAATTGT NM_032861RefSeq chr6
- 158109503 158168280 SERAC1 84947 "serine active site containing 1, transcript variant 1"
GO:0031012|GO:0005739|GO:0005737|GO:0030198|GO:0005783|GO:0016788|GO:0005654|GO:0016021|GO:0008
654|GO:0006886|GO:0006505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136621_PI430048170 0.0803446293369019 1.08928445877051 12.1553707199209
12.2499909142113 12.2829111411346 P P P 12.038595649491 12.1642632464433
12.1155170448771 P P P LNCV6_136621_PI430048170 mRNA
TGGGACGCGCTCTAAATAATTGCAATAAAACAAACCTTTCTCTGCAAACCATTTCCTCCC NM_001130012 RefSeq
chr16 + 2026867 2039026 SLC9A3R2 9351 "solute carrier family 9, subfamily A (NHE3, cation
proton antiporter 3), member 3 regulator 2, transcript variant 1"

GO:0005515|GO:0005886|GO:0008013|GO:0019902|GO:0005102|GO:0005634|GO:0014067|GO:0008022|GO:0012505|GO:0005737|GO:0016324|GO:0006461|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133192_PI430048170 0.1970591979802070.6609778883343444.36422805864359 4.36832322832952 4.5026301772403 P P P 4.45525805696994 4.95674437141655 5.44989295828304 P P P LNCV6_133192_PI430048170 mRNA
CACAAACAAACCCATACGATCTGTATTTGTATATACACGTGTCCGTACAAGTATAACTAA NM_001962RefSeq chr5 - 107376888 107670895 EFNA5 1946 ephrin-A5
GO:0031290|GO:0022407|GO:0048013|GO:0005886|GO:0050919|GO:0050731|GO:0006915|GO:0005576|GO:0051893|GO:0031362|GO:0007399|GO:0070507|GO:0045499|GO:0032314|GO:0046875|GO:0007411|GO:0005901|GO:0032956|GO:0032319|GO:0061178 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114314_PI430048170 0.00525902150231579 0.7880475178257111 6.4701826152276 16.4258005408198 16.5675448485282 P P P 16.8216623879831 16.7576247876299 16.9145147726627 P P P LNCV6_114314_PI430048170 mRNA
GAATGTTTTGTGGACCACTTTGGTTTTCTTTTTTGCGTGTGGCAGTTTTAAGTTATTAGT NM_001402RefSeq chr6 - 73515749 73521032 EEF1A1 1915 eukaryotic translation elongation factor 1 alpha 1
GO:0005515|GO:0010467|GO:0005853|GO:0006355|GO:0019901|GO:0005886|GO:0003924|GO:0005730|GO:0005634|GO:0003746|GO:0005525|GO:0006412|GO:0005615|GO:0006351|GO:0006414|GO:0005829|GO:0005737|GO:0016020|GO:0071364|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127674_PI430048170 0.0441254606247259 1.37754960106086 5.62279343282007 5.97079610947324 5.79424247258069 P P P 5.36095720021309 5.33401578987591 5.3273003543517 P P P LNCV6_127674_PI430048170 mRNA
TATTTGACCATGGAGACCTGTGAGGATGGCAACGATCTTGTCTTCTTCTATCAGGTTTGC NM_002441RefSeq chr6_GL000251v2_alt + 3217227 3239935 MSH5 NA "mutS homolog 5, transcript variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90110_PI430048170 0.140145482268924 0.749273773331281 5.23936201447754 5.17532997981914 4.64080985103252 P P P 5.36653396884948 5.48637044253136 5.51892282691527 P P P LNCV6_90110_PI430048170 mRNA
AGGTACTGACACTAGGAGGGTCTACCTTACATAAGGTACAGGTAGAAGCTTGATTGCTAG NM_018044 RefSeq chr7 - 73302515 73308867 NSUN5 55695 "NOP2/Sun domain family, member 5, transcript variant 2" GO:0006364|GO:0008168|GO:0005730|GO:0005634|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112662_PI430048170 0.885153275469237 1.02546806937253 4.45968854848798 4.78648824283075 4.28989986193674 P P P 4.63291718532714 4.48574206023811 4.33835226634172 P P P LNCV6_112662_PI430048170 mRNA
AGAAATACTCGCCTAGTGAGCCCTAACTAGAGTTAAAAAAGTCCTACCTCCATCTCCGTG NM_001077238RefSeq chr19 + 2328629 2355102 SPPL2B 56928 "signal peptide peptidase like 2B, transcript variant 3"
GO:0005515|GO:0005886|GO:0031293|GO:0030660|GO:0050776|GO:0071556|GO:0071458|GO:0006509|GO:0005765|GO:0042803|GO:0042500|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138400_PI430048170 0.0060427956519555 1.56436856988505 5.926345378687 5.88854714267489 5.66473099556353 P P P 5.25574814797935 5.1871521112143 5.10990390564063 P P P LNCV6_138400_PI430048170 mRNA
CTCCCTGGAGTGGGTGAGGGTGGGAGAAAGTTACATATTTAAAGAAAAATAAATTTAATA NM_024787RefSeq chr8 - 33547753 33567128 RNF122 79845 ring finger protein 122
GO:0005794|GO:0005783|GO:0008270|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136427_PI430048170 0.0121605642853265 1.17527081329414 8.62269899518645 8.71636998138348 8.73135789840319 P P P 8.382146147012 8.46818366695178 8.52014936005438 P P P LNCV6_136427_PI430048170 mRNA
TGGGCTGAGGCATATGAATGCTATAGTTGTGCATTAAAATAAATGTTTTTTATCTCCTGG NM_015540RefSeq chr15

- 41517175 41544277 RPAP1 26015 RNA polymerase II associated protein 1
GO:0006366|GO:0003899|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142608_PI430048170 0.6397073875627020.9269318098642132.57941800260069
3.48324935589459 2.6754529916537 A P A 3.26019145094806 3.06957237093278
2.89305561358192 P P P LNCV6_142608_PI430048170 mRNA
AATTATTTTTACTAATTTACACTACCACCTCACCTGGTCCTCAGTCAGAAACAGCGCGAG NM_001301011 RefSeq
chr1 + 32200385 32205390 CCDC28B 79140 "coiled-coil domain containing 28B, transcript variant
1" GO:0005515|GO:0042384|GO:0005813|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143717_PI430048170 0.00697179570002808 0.3167722948970096.75359466460255
6.4293278985342 6.7227748410938 P P P 8.03339390872961 8.07866533503604
8.69276083899794 P P P LNCV6_143717_PI430048170 mRNA
GATGATGATTTTACCTGTCAATACCAGCACTGTATTACTAACATGCAAAATACTGCAGAT NM_007146RefSeq chr17
- 57971548 57988254 VEZF1 7716 vascular endothelial zinc finger 1
GO:0006968|GO:0005737|GO:0006366|GO:0006357|GO:0001885|GO:0005654|GO:0005634|GO:0001525|GO:0003
677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145657_PI430048170 0.9703074353550921.01587487852764 4.07239339591352
3.05059729350426 3.63767973641069 P A P 3.25462996887684 3.87381205023843
3.67405419603546 P P P LNCV6_145657_PI430048170 mRNA
TTTATTGTAGCGGATACACTTTCTGACCTATCATGAGTATACACATCTGCGAAGGGAAAC NM_005026RefSeq chr1
+ 9651731 9729114 PIK3CD 5293 "phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit
delta"
GO:0050853|GO:0005515|GO:0050852|GO:0001782|GO:0005886|GO:0044281|GO:0001816|GO:0042629|GO:0010
818|GO:0005829|GO:0002679|GO:0006954|GO:0007173|GO:0030101|GO:0060374|GO:0016303|GO:0001779|GO:0
035747|GO:0072672|GO:0048011|GO:0043303|GO:0006661|GO:0036092|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138242_PI430048170 0.2293566467843231.09386928784841 8.92379632226415
8.90833562243479 9.04556178339377 P P P 8.89850716956489 8.91037135337128
8.67218952928298 P P P LNCV6_138242_PI430048170 mRNA
ACAGTTTTAAGAGCAGTCTTTTGGCTCTGACCATTTCTTGTTCTGTTTCCAATGAAATCANM_024757RefSeq chr9 +
137618991 137836126 EHMT1 79813 "euchromatic histone-lysine N-methyltransferase 1, transcript variant 1"
GO:0005515|GO:0005886|GO:0008168|GO:0006325|GO:0005634|GO:0009790|GO:0002039|GO:0005737|GO:0051
567|GO:0070734|GO:0005694|GO:0016571|GO:0018027|GO:0000122|GO:0016279|GO:0018026|GO:0018024|GO:0
006306|GO:0046974|GO:0008270|GO:0005654|GO:0070742|GO:0045892|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127308_PI430048170 0.0185310293201978 0.5821748350654863.8671984985078
3.48755945124838 3.59582702123892 P P P 4.12300643803175 4.51260974206178
4.63523219515795 P P P LNCV6_127308_PI430048170 mRNA
GGTGTTTTGCCTTTGCCTGTGGGGAAAAAGTAGGGATGATATTTTAAAATTTTAAGAAAC NM_001164211 RefSeq
chr13 + 46553160 46744901 LRCH1 23143 "leucine-rich repeats and calponin homology (CH) domain
containing 1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140275_PI430048170 0.1079034802922830.8558062028494496.24690502073584
6.21182724430394 6.27839909078977 P P P 6.58303062639574 6.50674389110548
6.30830814308845 P P P LNCV6_140275_PI430048170 mRNA
AAAGGAAAGACCAAAGTGTGCCCTCATCCTGGCTGTGGCAAGAAGTTCTATTTATCCAAC NM_138783RefSeq chr19
- 11483426 11505923 ZNF653 115950 zinc finger protein 653
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142386_PI430048170 0.6062260188681790.8947845441985052.08809873158652
2.79820670320201 1.79349564472044 A A A 2.6291745861428 2.60352040005577

2.04797972637403 A P A LNCV6_142386_PI430048170 mRNA
ACATAAAATCTGGGAGCCCAGAGCTGCTGAGGTGTGGTCAGCTCCCCTAAAATGGGCACGNM_014460RefSeq chr22
+ 41561009 41576666 CSDC2 27254 "cold shock domain containing C2, RNA binding"
GO:0006397|GO:0006355|GO:0005737|GO:0003723|GO:0005634|GO:0003677 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138512_PI430048170 0.1528403525707410.5252320616371082.68539540114517
1.05016163292701 2.01751569950854 A A A 3.06285896430077 2.41151261501525
3.35357545842794 P A P LNCV6_138512_PI430048170 mRNA
CTTATTGACGTTAACACCAGGAATCTCCATGTTTATTATTTTTCGTGGAAACTCCATGTTNM_001080398 RefSeq chr9
- 111360692 111484745 KIAA0368 23392 KIAA0368
GO:0005802|GO:0030134|GO:0000502|GO:0005793|GO:0005813|GO:0005770|GO:0005783|GO:0005771|GO:0030
139|GO:0005634|GO:0030433|GO:0003674|GO:0016020|GO:0016023|GO:0005769 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_63549_PI430048170 0.0751564536824693 1.57497398000653 4.61119963200472
4.36274362649523 4.44516949779922 P P P 4.08961226928853 3.91193999800197
3.36934910431554 P P P LNCV6_63549_PI430048170 mRNA
TACTCCTTCGAGGTGACTGGATACCAGCCTTTCATCCTAACAGGGGAGACAGCTGAGGGG NM_001166347 RefSeq
chr17 + 80220400 80253509 SLC26A11 284129 "solute carrier family 26 (anion exchanger), member 11,
transcript variant 1"
GO:0008509|GO:0005794|GO:0005886|GO:0015301|GO:0005783|GO:0008272|GO:0008271|GO:0016021|GO:0005
765|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49969_PI430048170 0.1884218890791620.8812212526216289.69278475055028 9.61760034139794
9.84654299080538 P P P 9.8683281219892 9.76178817176894 10.06683232791 P P P
LNCV6_49969_PI430048170 mRNA
GCACTGCATTATTTGACCAGAGTTGAAGTGACAGAATTTGAAGATATTAAATCAGGTTAC NM_003011RefSeq chr9
+ 128689229 128696396 SET 6418 "SET nuclear proto-oncogene, transcript variant 2"
GO:0005515|GO:0010467|GO:0048471|GO:0005783|GO:0008601|GO:0004864|GO:0006334|GO:0005634|GO:0006
337|GO:0035067|GO:0043086|GO:0003677|GO:0005829|GO:0006913|GO:0006260|GO:0043234|GO:0042393|GO:0
050790|GO:0043524|GO:0005737|GO:0005654|GO:0000278|GO:0045892 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_14599_PI430048170 0.2828778195371890.84540312062114 0.4450080015026870.458979328429111
0.273770151620632A A A 0.9322821962619970.4871923608491560.439605231184963A A A
LNCV6_14599_PI430048170 mRNA
CTTCCTTGATGACCCAGCTACTTTACATCTCTGGATGGAATCCTCCTCTTTGCTCTAATG NM_001257177 RefSeq
chr3 + 17962571 18268918 LOC339862 NA uncharacterized LOC339862 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_101591_PI430048170 0.0497663230014651 1.35024319275542 5.72879868866923
6.07720400376017 6.05712187366423 P P P 5.56721752053153 5.31907986979117
5.67974571860713 P P P LNCV6_101591_PI430048170 mRNA
CCAATTATAGTGCTGCAAAGTTGGGTCTTCTGGGCCTTGCAAATTCTCTTGCAATTGAAG NM_001199291 RefSeq
chr5 + 119452496 119542335 HSD17B4 3295 "hydroxysteroid (17-beta) dehydrogenase 4, transcript
variant 1"
GO:0000038|GO:0005782|GO:0006699|GO:0044281|GO:0042803|GO:0043231|GO:0005739|GO:0060009|GO:0008
206|GO:0044255|GO:0005778|GO:0005777|GO:0044594|GO:0006635|GO:0008209|GO:0005102|GO:0003857|GO:0
036109|GO:0033989|GO:0001649|GO:0033559|GO:0008210|GO:0036112|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141944_PI430048170 0.7950417200701921.02785348913184 6.92144186515743
6.69318052069154 6.63256079696073 P P P 6.37600608971091 7.07083383990762
6.60939878930949 P P P LNCV6_141944_PI430048170 mRNA

GCTCAGAGAGCGAGCTTTGTGGTATTGATAAATGAATAAATTAGTATGTTCATGTTGGAA NM_001271909 RefSeq chr16 + 89658046 89670458 SPATA33 124045 "spermatogenesis associated 33, transcript variant 4" GO:0005634|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135457_PI430048170 0.0550975277484821 0.807234183697041 10.0139703332331 10.080611565859 10.2662436518773 P P P 10.3798405980703 10.310033372147 10.5943311361644 P P P LNCV6_135457_PI430048170 mRNA
CAGTCATGGAGGCCAAGAACTTGCAATACCAATGTTCTAAAGTTTTGCAACAATAAAGTA NM_145740 RefSeq chr6 - 52791379 52803866 GSTA1 2938 glutathione S-transferase alpha 1 GO:0006805|GO:0030855|GO:0008152|GO:0006749|GO:0044281|GO:0004364|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_144933_PI430048170 0.2891877737690190.810987309986956 0.336517856748816 0.3223102430404850.294272382054271 A A A 0.9641711348697620.313858581602001 0.50266955024758 A A A LNCV6_144933_PI430048170 mRNA
GACGCATTAAAAGAAACTTACTGCACAAGCTGCTAATAAATTTGTAAGCTTTGCATACCT NM_001845 RefSeq chr13 - 110148957 110307157 COL4A11282 "collagen, type IV, alpha 1, transcript variant 1" GO:0005515|GO:0001569|GO:0048407|GO:0048514|GO:0005587|GO:0005576|GO:0030023|GO:0006898|GO:0005604|GO:0061333|GO:0031012|GO:0061304|GO:0071230|GO:0022617|GO:0030198|GO:0007411|GO:0007420|GO:0007528|GO:0030855|GO:0030574|GO:0005788|GO:0071711|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_135204_PI430048170 0.740727339323591 1.06459357410117 8.38273453890604 8.35323645804774 7.82477570123364 P P P 8.30775599376415 8.19392965270546 7.80712035770248 P P P LNCV6_135204_PI430048170 mRNA
TGAGACGTATCTTGACATCTTCCGCGACTTCTCCCTCATGGCGTCAGACGACCCGGAGAA NM_014716 RefSeq chr17 + 7336528 7351474 ACAP1 9744 "ArfGAP with coiled-coil, ankyrin repeat and PH domains 1" GO:0043547|GO:0008060|GO:0016020|GO:0032312|GO:0008270|GO:0015031|GO:0055038 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_141391_PI430048170 0.52561730574238 0.379309316578741 0.996625560406852 0.3827448952210550.288826527865073 A A A 0.3521708394658830.311562151216983 3.23280780698711 A A P LNCV6_141391_PI430048170 mRNA
ATTCTGAATCAGTCAAGAAAGCCGAGTCAGAAGATATCCAAGGAAGCAGCTCCTCATTGG NM_032137 RefSeq chr3 + 14675098 14773036 C3orf20 84077 "chromosome 3 open reading frame 20, transcript variant 1" GO:0005737|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_137244_PI430048170 0.0217326337659908 0.2650669385409930.568964567747299 1.00154021629536 1.69791812631455 A A A 2.9398684060171 3.20128555986402 3.09056833454868 P P P LNCV6_137244_PI430048170 mRNA
GTAGTCCTGTGGGGGCAAATGTGTAGATATTTTTAAACATTTTGCCATAATTGCACAATT NM_032505 RefSeq chr3 + 66998302 67011208 KBTBD8 84541 kelch repeat and BTB (POZ) domain containing 8 GO:0005794|GO:0005819 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_115789_PI430048170 0.2191476355233340.856873433993777 5.50190669791279 5.22842872541651 5.39386542815623 P P P 5.36769139598804 5.78342212321056 5.62456480113404 P P P LNCV6_115789_PI430048170 mRNA
ACACAGGGATCTTCGAGACAGTCAGTGTAGGCGACCTGACTGAGGTCAAAGGGCAGACCA NM_138353 RefSeq chr19 + 13952506 13961444 DCAF1590379 DDB1 and CUL4 associated factor 15 GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_137359_PI430048170 0.5131878260554631.299376479131 1.56584710761841 0.7310685166822360.318073917803349 A A A 0.4836921461664050.358017607978272 0.876013286466267 A A A LNCV6_137359_PI430048170 mRNA
AGCCAACAGAAGAGTTAAAAATTAGTGATATGACTATATTCAGGGGGAAGGAGAGCTGAG NM_001163438 RefSeq chrX + 134990937 134992473 SMIM10 644538 small integral membrane protein 10

GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140544_PI430048170 0.0438165546477066 2.37087046543053 2.38735941572867
3.31295043674963 3.22162867286128 A P P 1.57702447434438 1.88495335778101
1.87031013453329 A A A LNCV6_140544_PI430048170 mRNA
GCATTTGGTGCTTGACGTATTATTGTCCTTTGATTCCAAATAATATGTTTCCTTCCCTCA NM_024022 RefSeq chr21 -
42371886 42396091 TMPRSS3 64699 "transmembrane protease, serine 3, transcript variant A"
GO:0004252|GO:0005783|GO:0007605|GO:0043025|GO:0006883|GO:0006508|GO:0005789|GO:0016021|GO:0006
898|GO:0017080|GO:0005044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142976_PI430048170 0.3663043399489421.95729094119732 2.45823167184051
0.7207010684643650.589378557192945 A A A 0.5861266064352370.547242845387855
0.541866673395087 A A A LNCV6_142976_PI430048170 mRNA
AGAGTGTGGCGAGGGGAACCTTCTCAGGAAAGAAAATAGAGGTCCTGTTTTAGGAAAAAA NM_001242668
RefSeq chr8 - 93134094 93166850 C8orf87 NA chromosome 8 open reading frame 87 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_130645_PI430048170 0.000967862372901627 1.48261676678233 6.33672026666191
6.50239385828001 6.40321076226015 P P P 5.81138385650778 5.93090666691216
5.79663923854782 P P P LNCV6_130645_PI430048170 mRNA
TCATTATTCCATGGAACCTTGGCTCTTACTGATATTGAGCATCCTTCTCTCTGGAACCGT NM_032340 RefSeq chr6
- 33696760 33711751 UQCC2 84300 ubiquinol-cytochrome c reductase complex assembly factor 2
GO:0042645|GO:0005739|GO:0005515|GO:0005758|GO:0034551|GO:0050796|GO:0005759|GO:0005743|GO:0070
131|GO:0005634|GO:2001014|GO:0002082 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140729_PI430048170 0.0563001323492038 1.49695544969691 7.34365905796254
7.1766502277819 7.13686212647352 P P P 6.306556360125 6.67452088971318
6.88100184529805 P P P LNCV6_140729_PI430048170 mRNA
GTATTAAATAGCCATTCATTCTGGAACTCAAGGACAGGACTGTAATAAAATGGAATGGAA NM_001080414 RefSeq
chr14 - 91271322 91417844 CCDC88C 440193 coiled-coil domain containing 88C
GO:0031648|GO:0005737|GO:0051260|GO:0001932|GO:0043621|GO:0030165|GO:0016055|GO:0031098 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112467_PI430048170 0.0181997291595260.5486682632558957.31795868429661
7.11696163173617 7.20293777385732 P P P 7.77446466797799 8.16388335607712
8.26015898865535 P P P LNCV6_112467_PI430048170 mRNA
ATTACAAGCATAACATGGAGCTCTTGTTGCACTAAAAAGTGGATTACAAATCTCCTCGAC NM_001286167 RefSeq
chr16 - 89737550 89816657 FANCA 2175 "Fanconi anemia, complementation group A, transcript
variant 3"
GO:0005515|GO:0008585|GO:0005737|GO:0006461|GO:0006281|GO:0042127|GO:0005730|GO:0005654|GO:0005
634|GO:0008584|GO:0043240|GO:0007140 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107476_PI430048170 0.3346716810760630.8265515214942275.34280479663563 5.6474508951594
5.90966731382526 P P P 5.53546663445507 6.07946273878037 6.09735624495681 P P P
LNCV6_107476_PI430048170 mRNA
GTAAAGGAAGTAGAACTCATACCTACTTTGGAATGGCTATCAGAAAGAAGACATTACTAT NM_001373 RefSeq chr1
+ 224929653 225399294 DNAH14 127602 "dynein, axonemal, heavy chain 14, transcript variant 1"
GO:0005929|GO:0005737|GO:0030286|GO:0008152|GO:0005874|GO:0003777|GO:0005524|GO:0007018 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94948_PI430048170 0.1629671057944421.17934661164632 8.40936526442401 8.41891558341361
8.7489037329505 P P P 8.34520385416876 8.17608079039264 8.36127372237618 P P P
LNCV6_94948_PI430048170 mRNA
ATGACAGCAGAGGAGAAGCAAACATTACTAAAGAGGAGATTGCTTGCAGAGAAACTCAAA NM_001282761
RefSeq chr2 + 55519594 55545080 CFAP36 112942 "cilia and flagella associated protein 36, transcript
variant 1" GO:0005737|GO:0005634|GO:0042995 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_68104_PI430048170 0.0221652129024809 1.92898709949731 4.15062005838124
4.10834142501473 3.94167695177862 P P P 2.74813795008432 3.23585335393953
3.31835037125114 P P P LNCV6_68104_PI430048170 mRNA
AGACTACTTTCAGCATCCTCACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTCCC NM_005090 RefSeq chr15
+ 41828084 41848148 JMJD7-PLA2G4B 8681 "JMJD7-PLA2G4B readthrough, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49988_PI430048170 0.0775554029553904 1.35261449963 6.75611783226794 7.21678061177489
6.97774286654071 P P P 6.49209542202742 6.60531742337184 6.58032622463569 P P P
LNCV6_49988_PI430048170 mRNA
TGGTTATCCAGGAGCTAATCAATACAGTTAGGCAGTGTACCAGTAAGCTCAGTTCCTACC NM_001005360 RefSeq
chr19 + 10718052 10831910 DNM2 1785 "dynamin 2, transcript variant 1"
GO:0005515|GO:0008017|GO:0017124|GO:0005886|GO:0050999|GO:0003924|GO:0044281|GO:0005829|GO:0030
426|GO:0031623|GO:0033572|GO:0019886|GO:0005737|GO:0030516|GO:0045211|GO:0000086|GO:0061024|GO:0
046209|GO:0070062|GO:0006355|GO:0043065|GO:0005794|GO:0005874|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130551_PI430048170 0.37525502479824 0.8809620766963090.457669405644958
0.4526421708695970.384891962190691 A A A 0.4054184339958430.502319568001897
0.890323593016573 A A A LNCV6_130551_PI430048170 mRNA
CCAGCCACTTGGGAACAGCAGGTAATACTGAAGAAAAATAAAAATAGATTTTGAAAACGT NM_177980 RefSeq chr20
+ 59958415 60013113 CDH26 60437 "cadherin 26, transcript variant a"
GO:0005886|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133479_PI430048170 0.2958371525604690.4978671006547221.28415923952369
0.4033149932360180.430572891109308 A A A 0.9632741057206232.67772482758309
0.93129122611879 A P A LNCV6_133479_PI430048170 mRNA
GCCATGTGTAACAAAGAGAAATGTGCAAATATTTTTTAAGGCAGTATTAAGTGCAAGAGG NM_012425 RefSeq chr10
- 16590617 16817454 RSU1 6251 "Ras suppressor protein 1, transcript variant 1"
GO:0043547|GO:0005515|GO:0007165|GO:2000179|GO:0034329|GO:0010810|GO:0010811|GO:0007265|GO:0005
925|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136265_PI430048170 0.32264311119933 1.37243290684876 0.621167281257491
0.5331692733692581.47648434469398 A A A 0.4234105415028870.498614857399818
0.534806669589246 A A A LNCV6_136265_PI430048170 mRNA
TTCTTTTATAAAGACTTGTCTAGACTCCACTGGGAAGAGTCCTTTGCTTTGGGGCCCAGT NM_198681 RefSeq chr1
- 6466091 6520061 PLEKHG5 57449 "pleckstrin homology domain containing, family G (with
RhoGef domain) member 5, transcript variant 2"
GO:0051056|GO:0048471|GO:0048011|GO:0035767|GO:0043065|GO:0005886|GO:0007264|GO:0030139|GO:0097
190|GO:0030027|GO:0005829|GO:0005737|GO:0005911|GO:0032321|GO:0004871|GO:0005089|GO:0043123 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134149_PI430048170 0.64028819168025 0.8977784298120082.32777372212119
2.32429736192584 2.09998260734423 A A A 2.75784704765193 1.98333731713409
2.38615165248528 P A P LNCV6_134149_PI430048170 mRNA
AAACTGTGAACCTGCAGATTTCACCTATTTTGATTTACTATAAGAGCTGGGATTTGATTC NM_016644 RefSeq chr5
+ 120464277 120687330 PRR16 51334 "proline rich 16, transcript variant 2" GO:0045793|GO:0045727 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68627_PI430048170 0.0808382028957426 1.98833770472145 4.71548817326261
4.75890586221083 4.63296990433312 P P P 3.00446804357162 3.86678436977734
4.06140035681321 P P P LNCV6_68627_PI430048170 mRNA
GACGCAACAAGTTTGGTCAGCTAGGTCTTAATGATGAAAATGATAGGTATGTTCCTAATT NM_022079 RefSeq chr10
- 67921898 68075346 HERC4 26091 "HECT and RLD domain containing E3 ubiquitin protein ligase 4,
transcript variant 1"

GO:0005737|GO:0004842|GO:0042787|GO:0016874|GO:0005634|GO:0007283|GO:0030154|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65798_PI430048170 0.3374764062122630.8785059306969291 1.1790341909158 10.9734763896252 11.3507533093585 P P P 11.2813766946254 11.1732960104574 11.5991788362251 P P P LNCV6_65798_PI430048170 mRNA
ATATAGATTATATATGTATAGTGTTTCACAAAGCTTAGACCTTTACCTTCCAGCCACCCC NM_020532 RefSeq chr2 - 54972190 55050598 RTN4 57142 "reticulon 4, transcript variant 1"
GO:0005515|GO:0030334|GO:0048011|GO:0030308|GO:0005886|GO:0005783|GO:0071786|GO:0006915|GO:0021801|GO:0042981|GO:0030176|GO:0042995|GO:0001525|GO:0005635|GO:0005622|GO:0060317|GO:0007413|GO:0030517|GO:0043025|GO:2000172|GO:0050771|GO:0050770|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106564_PI430048170 0.1330767387439990.77418890520792 10.8791317624528 10.6144120121664 10.5788473785014 P P P 10.7416555974594 11.1856256218773 11.2239207515337 P P P LNCV6_106564_PI430048170 mRNA
GCCCGGCGAGGGTATGTCAGTGTCACTGGATGTCAAACAGTAATAAATTAAACCAACAAC NM_001128844 RefSeq chr19 + 10960921 11062282 SMARCA4 6597 "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4, transcript variant 2"
GO:0005515|GO:0000792|GO:0071565|GO:0000790|GO:0030308|GO:0070307|GO:0007070|GO:0006325|GO:0010424|GO:0050681|GO:0035887|GO:0071564|GO:0005615|GO:0030198|GO:0070577|GO:0008094|GO:0001105|GO:0003407|GO:0070182|GO:0005719|GO:0003714|GO:0043044|GO:0003713|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72771_PI430048170 0.6837553354996151.02340262301755 0.36470838472354 0.561764072437397 0.441559436858031 A A A 0.5173380196490230.3840358035569440.368726264051952 A A A LNCV6_72771_PI430048170 mRNA
AGGAAAGAAATAATGAAGAGACACATGTGTTAGCTGCAGCCTTTTGAAACACGCAAGAAG NM_052953 RefSeq chr3 + 26622808 26710774 LRRC3B 116135 leucine rich repeat containing 3B GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128204_PI430048170 0.0233726795063618 0.7126476926783329.27744704489819 9.31037064606319 9.34963626468947 P P P 9.89891855903159 9.63011456447557 9.86114114824084 P P P LNCV6_128204_PI430048170 mRNA
TGCCTTTCTGTTAGCTTTCTCTGACTCAAGCTGTGGGGCTCCTCTATACATGCTATACAT NM_022337 RefSeq chr11 - 88113246 88175467 RAB38 23682 "RAB38, member RAS oncogene family"
GO:0005802|GO:0005515|GO:0005886|GO:0007264|GO:0005783|GO:0035612|GO:0003924|GO:0015031|GO:0006886|GO:0005829|GO:0030670|GO:0032482|GO:0090383|GO:0035650|GO:0042470|GO:0035651|GO:0072657|GO:0005525|GO:0006184|GO:0045335|GO:0030742|GO:0031905|GO:0016020|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127188_PI430048170 0.57485113982423 0.9668066399319230.487707144371357 0.4701029718439320.2541451414626 A A A 0.3995440950823580.509745324215842 0.458181440904889 A A A LNCV6_127188_PI430048170 mRNA
GGCTATACTGTAATCGTGATTGAAGCTTGGACTAAGAATTTTTTCCCTTTAGATGTAAAG NM_005084 RefSeq chr6 - 46704315 46735414 PLA2G7 7941 "phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma), transcript variant 1"
GO:0034440|GO:0034441|GO:0005576|GO:0003847|GO:0016042|GO:0005737|GO:0005543|GO:0034374|GO:0047499|GO:0034362|GO:0050729|GO:0090026|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141677_PI430048170 0.9593939647535020.9947953967359248.30612702326941 8.40766921246931 8.62080747724316 P P P 8.18713123899703 8.31134030719996 8.8013715021625 P P P LNCV6_141677_PI430048170 mRNA
AAATTTTTTGTCCCTACATAGCAATTTTCTGTGGCACTGAGAAACCATGTATGACCACAA NM_007259 RefSeq chr1 + 150067292 150145327 VPS45 11311 "vacuolar protein sorting 45 homolog (S. cerevisiae), transcript

variant 1"
GO:0003674|GO:0005794|GO:0000139|GO:0007596|GO:0016021|GO:0005575|GO:0006886|GO:0010008|GO:0006904 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76301_PI430048170 0.3453322257475231.53102365250836 1.60140485820195 1.40519166861762 0.244700653317263 A A A 0.36726108857905 0.4423439176664540.877368118786056 A A A
LNCV6_76301_PI430048170 mRNA
TTAGGAGGGAAAGACAAAATGAGGCTTGTTCATGATCAAATTCTGTGTACTCTAGTTGCT NM_001144954 RefSeq chr5 + 173989158 174006140 C5orf47 133491 chromosome 5 open reading frame 47 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128673_PI430048170 0.96552153963018 1.00092338848273 0.455605593856759 0.49825784692058 0.429121547233122 A A A 0.4212644190952160.515187966532541 0.441682482698597 A A A LNCV6_128673_PI430048170 mRNA
TCTGGTGTATTTTGCACAGACAAGCATCTGCCTTAAAATATATACACTTGTACAAAAAGG NM_173567 RefSeq chr1 + 92029975 92063536 EPHX4 253152 epoxide hydrolase 4 GO:0016787|GO:0008152|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126650_PI430048170 0.3115289196655421.18180914037307 1.07489996567241 0.5340366107677710.632341434293041 A A A 0.43987468972817 0.562197478608791 0.571756404743007 A A A LNCV6_126650_PI430048170 mRNA
TCCCCAAGGGCACAACCATAATGGCATTACTGACTTCCGTGCTACATGATGACAAAGAAT NM_001198855 RefSeq chr10 - 95036771 95069497 CYP2C8 1558 "cytochrome P450, family 2, subfamily C, polypeptide 8, transcript variant 4"
GO:0019369|GO:0034875|GO:0008392|GO:0006805|GO:0070330|GO:0005506|GO:0017144|GO:0008395|GO:0019373|GO:0070989|GO:0044281|GO:0006082|GO:0043231|GO:0004497|GO:0005737|GO:0019825|GO:0042738|GO:0097267|GO:0005789|GO:0016712|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127506_PI430048170 0.5778587976717950.9676361423574020.483547523885288 0.4596384775317530.25026104980463 A A A 0.3948092542134430.499785351073182 0.450554962338803 A A A LNCV6_127506_PI430048170 mRNA
GTGTAGCAATGATTGTTGCTAGGCTACAGAGTTGTATATGTAATGTATAGCTGAAATCAT NM_017993 RefSeq chr13 - 43213529 43786980 ENOX1 55068 "ecto-NOX disulfide-thiol exchanger 1, transcript variant 1"
GO:0005886|GO:0000166|GO:0016491|GO:0048511|GO:0003676|GO:0005615|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54768_PI430048170 0.0381972308461898 0.67451937455508 5.24241685401224 5.25363718198984 5.35510755775776 P P P 5.69908007742602 5.73486611818533 6.09076385894238 P P P LNCV6_54768_PI430048170 mRNA
GGGAACATTTTTTCTGAGGGGCCAAAAGAATAAAGGACCAAATTTCTTAGCTCATATCAT NM_144618 RefSeq chr1 + 151070603 151118531 GABPB2 126626 "GA binding protein transcription factor, beta subunit 2"
GO:0046982|GO:0044212|GO:0045944|GO:0005634|GO:0042803|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128572_PI430048170 0.1324631858751552.33603946708147 0.729964765191503 2.06265001604312 2.09280122083338 A A A 0.4457256441021350.544769907560139 0.588398432128653 A A A LNCV6_128572_PI430048170 mRNA
TCCAGTTAGGGCTGTTGATTTATGCTTTAACTTCAGAGTGAGTGTAGGGGTGGTGATGCT NM_003742 RefSeq chr2_GL383522v1_alt - 109565 123061 ABCB11 8647 "ATP-binding cassette, sub-family B (MDR/TAP), member 11"
GO:0005215|GO:0005886|GO:0006699|GO:0045177|GO:0042626|GO:0015126|GO:0044281|GO:0055085|GO:0005524|GO:0046581|GO:0016020|GO:0005887|GO:0015721|GO:0008554|GO:0015722|GO:0006810|GO:0015432|GO:0035725|GO:0008206|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145533_PI430048170 0.53033464304633 1.01866013622077 0.294191466408763

0.3252745141405720.407904704153503A A A 0.3358478091457540.314112330976008
0.299567806395608A A A LNCV6_145533_PI430048170 mRNA
GAGGCCTCAGTTATGAGTGACAGAGCTTTCTGTGTATAATTTGTCTAAATAATTTGTCTA NM_001510RefSeq chr4
+ 92304398 93774555 GRID2 2895 "glutamate receptor, ionotropic, delta 2, transcript variant 1"
GO:0030054|GO:0008328|GO:0005886|GO:0005234|GO:0045202|GO:0030425|GO:0021707|GO:0043523|GO:0034
220|GO:0043197|GO:0045211|GO:0004970|GO:0097110|GO:0006810|GO:0007157|GO:0060134|GO:0035249|GO:0
060079|GO:0007215|GO:0030165|GO:0035235|GO:0005887|GO:0010975|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132262_PI430048170 0.1482861882595240.8295591383385441 1.5015973791076
11.6880795801183 11.4568867278379 P P P 11.689768347474 12.0513415104754
11.6941510164478 P P P LNCV6_132262_PI430048170 mRNA
GCCTGACGTTTTACGGTTTTGTTTTTTACTGGTTTGTGTTTATATTTTCGGGGATACTTA NM_001197181 RefSeq chr16
+ 89922008 89936097 TUBB3 10381 "tubulin, beta 3 class III, transcript variant 2"
GO:0005515|GO:0042277|GO:0030424|GO:0051258|GO:0005874|GO:0003924|GO:0005634|GO:0005525|GO:0055
085|GO:0030425|GO:0071944|GO:0006184|GO:0005737|GO:0007067|GO:0006457|GO:0007411|GO:0043025|GO:0
005200|GO:0051084|GO:0007017|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_130857_PI430048170 0.0589257445968091.4623343356169 9.99704351016895
9.80820595768145 9.65181076055945 P P P 9.44683283419656 9.40740285565117 8.921989710428
P P P LNCV6_130857_PI430048170 mRNA
CTGCTAGGTTGCTGTTATTTTGTGCTAATAAAAGAGTAATTAATTCCACCAGAGGCAAAA NM_025124RefSeq chr11
- 67464347 67469277 TMEM134 80194 "transmembrane protein 134, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141532_PI430048170 0.3270971829068970.2633577867149080.9980133641972331.8969001417979
0.378698976482456A A A 4.4203168830956 1.40929072475713 1.37516976629333 P A A
LNCV6_141532_PI430048170 mRNA
CCAGTATTTCACAACTTCCTGGTCGCTGAGAATATTTATTCAAAAACAGGGATTGAAAAA NM_080865RefSeq chr3
+ 51955313 51957504 GPR62 118442 G protein-coupled receptor 62
GO:0043235|GO:0008150|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0005575 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130588_PI430048170 0.5081774313593871.02042285501379 0.5918281144015940.6425107399807
0.539058532561275A A A 0.5759025207406320.5108071798268760.599582263546727A A A
LNCV6_130588_PI430048170 mRNA
CTGGCCGCGGTAACAGACTTTTACATGGAATTGTTTAATTATTTGTACTTTTCATGCCAG NM_001420RefSeq chr19
- 11451327 11480988 ELAVL3 1995 "ELAV like neuron-specific RNA binding protein 3, transcript variant
1" GO:0000166|GO:0017091|GO:0030154|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133323_PI430048170 0.0113940298801864 0.6809718334440651 0.4463124117304
10.3742708032185 10.401096037694 P P P 10.8308081792681 10.9651414208128
11.0789839092631 P P P LNCV6_133323_PI430048170 mRNA
CATCTTGTTGACATCGAATATGACTTTGATAATAAATACCGGTTCCTGAAAACGGCAAAA NM_005968RefSeq chr19
+ 8444918 8489118 HNRNPM 4670 "heterogeneous nuclear ribonucleoprotein M, transcript variant
1"
GO:0005515|GO:0008380|GO:0010467|GO:0003723|GO:0019904|GO:0005730|GO:0071013|GO:0016363|GO:0031
012|GO:0042382|GO:0000166|GO:0016020|GO:0000398|GO:0005887|GO:0000380|GO:0005654|GO:0005681|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128265_PI430048170 0.7988522138911360.9706351092458114.48258737857712
5.07386092631304 4.73679760058182 P P P 4.93046485532652 4.92395779504123
4.60591967970117 P P P LNCV6_128265_PI430048170 mRNA
AGAAGCTGAGTCTTCTGCATCAGATTATTGCAACATTTAACCTGAATTTAAAAGCACACG NM_012467RefSeq chr16

- 1221650 1225254 TPSG1 25823 tryptase gamma 1
GO:0004252|GO:0005887|GO:0006508|GO:0008236 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141754_PI430048170 0.600395246193398 0.946933674329707 6.57077962429463
6.26369586510375 6.69332472068884 P P P 6.52491967186521 6.51550893791715 6.7447332601017
P P P LNCV6_141754_PI430048170 mRNA
AATGTCCTAAACCCTTGCTGCCTCTTATCAAAACCATGTTGCACATCTCATCATATAGTA NM_014413 RefSeq chr7
- 6022246 6059229 EIF2AK1 27102 "eukaryotic translation initiation factor 2-alpha kinase 1,
transcript variant 1"
GO:0008285|GO:0006950|GO:0010999|GO:0005524|GO:0042803|GO:0005737|GO:0009605|GO:0045993|GO:0046
777|GO:0046501|GO:0046986|GO:0004694|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131703_PI430048170 0.200334294268368 1.33823786242722 5.59280294360248
5.85868260442965 5.261817558114 P P P 5.52378524287898 5.12821310239064
4.76098015791144 P P P LNCV6_131703_PI430048170 mRNA
GTTTTTAGTAATTTCAATGTAGTTTTCCCTCCTTCAAATAAACATGTCTGCCCTCATGGT NM_014513 RefSeq
chr19_GL000209v2_alt - 29857 44878 KIR2DS5 NA - NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_119018_PI430048170 0.346108863635444 1.2077515220646 0.388581000517661
0.372188585833245 0.97910392423045 A A A 0.312155919980108 0.320107458062883
0.376028792416853 A A A LNCV6_119018_PI430048170 mRNA
TCACCAACCACCAGATCTATGAATTGGAAAAGCGCTTTCTATACCAGAAGTACCTGTCCC NM_006562 RefSeq chr10
- 101226975 101228960 LBX1 10660 ladybird homeobox 1
GO:0005667|GO:0003700|GO:0008285|GO:0021522|GO:0048664|GO:0005634|GO:0009653|GO:0006351|GO:0021
920|GO:0001947|GO:0043565|GO:0007517|GO:0045665 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58589_PI430048170 0.0558569671440131 1.33197077574776 5.64124418370689
5.66052769531774 5.31278386867514 P P P 5.17290229470953 5.17262092182973
5.05069170798277 P P P LNCV6_58589_PI430048170 mRNA
AAGTACCCGCTGAACTGCTCCGATCCCACTAGTGAGAGGTGGTACCATGGCCACATGTCT NM_080549 RefSeq chr12
+ 6951270 6961316 PTPN6 5777 "protein tyrosine phosphatase, non-receptor type 6, transcript
variant 3"
GO:0005515|GO:0042267|GO:0019221|GO:0050732|GO:0050900|GO:2000045|GO:0030154|GO:0035335|GO:0042
130|GO:0060334|GO:0060337|GO:0060338|GO:0005001|GO:0042169|GO:0070372|GO:0060333|GO:0070062|GO:0
019901|GO:0018108|GO:0014068|GO:0035855|GO:0007186|GO:0001784|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129945_PI430048170 0.0186920042673470 0.77923986168234 4.83359853245774
4.69975409014227 4.61037259602737 P P P 4.96244213552726 5.06321256207926
5.19682825191459 P P P LNCV6_129945_PI430048170 mRNA
CAAATAAAGGGTCCTAGAAGACTAGAAAGCCAAGGTCTTTTATTAAAGGTCCCGACTGGT NM_024585 RefSeq chr17
+ 75109951 75130265 ARMC7 79637 "armadillo repeat containing 7, transcript variant 1"
GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135618_PI430048170 0.00332464293445165 1.38935289174526 9.65690615806088
9.76909947850732 9.64638112983625 P P P 9.14329251651702 9.32539488516707
9.17712145819636 P P P LNCV6_135618_PI430048170 mRNA
AACTGCGTCTGGACTCTTAGATTCATAAAATATTCGAGGGTTTGGGAGTCACAGACCCTC NM_022749 RefSeq chr8
+ 22089202 22104380 FAM160B2 64760 "family with sequence similarity 160, member B2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132073_PI430048170 0.202451312949968 0.690192214022037 0.372304132215763
0.378678633281723 0.466469639532141 A A A 1.1128431164785 1.20440858818992
0.371833900955101 A A A LNCV6_132073_PI430048170 mRNA
GCAATGGATGCCCCTCAAGAAGTTTACAATGACATTGTTTCTATGATATCAGAAGATAAA NM_001198829 RefSeq

chr10 + 88664388 88678815 LIPF 8513 "lipase, gastric, transcript variant 1"
GO:0016042|GO:0005739|GO:0004806|GO:0016615|GO:0006641|GO:0006108|GO:0005576|GO:0005575|GO:0055
114|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109481_PI430048170 0.207409503682664 1.11434842196668 0.659647863137782
0.390844664370235 0.628423978231851 A A A 0.342469846216714 0.41114400672226
0.46862953811294 A A A LNCV6_109481_PI430048170 mRNA
AACTATTTTAAACCATGTCCTTCATGTAGTGAAAAACCTAGGTCAAAGCAATATGGACTC NM_000051 RefSeq chr11
+ 108222831 108369099 ATM 472 ATM serine/threonine kinase
GO:0005515|GO:0002331|GO:0001756|GO:0004677|GO:0051402|GO:0032403|GO:0048599|GO:0007507|GO:0034
605|GO:0043525|GO:0046777|GO:0018105|GO:0016303|GO:0046983|GO:0007131|GO:0006977|GO:0000781|GO:0
033151|GO:0036092|GO:0005819|GO:0030889|GO:0035174|GO:0006281|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135404_PI430048170 0.276316640824233 1.32655344982528 3.44287015422285
3.43683575706569 3.0431024895775 P P P 2.50397402193798 3.47428663902593
2.53308311745945 A P P LNCV6_135404_PI430048170 mRNA
AATAGAAGCATGGCCGTGCCCTTGCAGCCTGCTTAGACTCCAGTCAGCCACTTGTACCTG NM_001080524 RefSeq
chr16 - 3493483 3495421 C16orf90 NA chromosome 16 open reading frame 90 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_52641_PI430048170 0.483141975205204 1.07499655958707 5.33023916006933 5.4573024008949
5.10487882673302 P P P 5.27752720160895 5.27501760437227 5.03555998402201 P P P
LNCV6_52641_PI430048170 mRNA
TATCATAAGGTGTTAAGAGTCCCTTGTTAAAGGGGCAGTGGGAGTTATGGGGTCATCAAG NM_147161 RefSeq chr1
+ 54548133 54610332 ACOT11 26027 "acyl-CoA thioesterase 11, transcript variant 2"
GO:0052689|GO:0047617|GO:0035556|GO:0009266|GO:0005737|GO:0009409|GO:0006631|GO:0070062|GO:0008
289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130014_PI430048170 0.285731724097304 1.30443499590925 4.24836772136854
4.06474793742908 3.62582121550068 P P P 3.9393862935988 3.72474539334572
3.05312712490324 P P P LNCV6_130014_PI430048170 mRNA
CTGCGGAGTGCTTCTCACCCCTCATTAAAATCATCCGTTTGCATGTCTGCCTTTAAAAAA NM_001142854 RefSeq
chr21_KI270872v1_alt - 20584 45829 SPATC1L 84221 "spermatogenesis and centriole associated 1-
like, transcript variant 1" GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_112366_PI430048170 0.623407558016407 0.780667771828581 0.450357179406951
0.584768365027121 1.71220389228033 A A A 0.373424934738642 1.36369141903326
1.99992004843447 A A A LNCV6_112366_PI430048170 mRNA
TCTGTTCACTAATTTCCTGGGTCCTGGAATCTATAGAGACAAGCAGGACTGAACCTGTGT NM_001145348 RefSeq
chr16 + 27203974 27221768 KDM8 79831 "lysine (K)-specific demethylase 8, transcript variant 1"
GO:0070544|GO:0003682|GO:0000086|GO:0005634|GO:0045893|GO:0051864|GO:0046872|GO:0006351|GO:0055
114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136216_PI430048170 0.574627599263247 0.944417949984602 6.4877825659958
6.37872604636498 6.75818962919489 P P P 6.63440657914051 6.47897703452343 6.7709440254784
P P P LNCV6_136216_PI430048170 mRNA
CTCACTCTGTCATTCAGCATTATCATGATCGTGAACAAAATTGTACTGAGAAAGTTTGTA NM_152416 RefSeq chr8
+ 95024985 95058716 NDUFAF6 137682 "NADH dehydrogenase (ubiquinone) complex I, assembly factor
6" GO:0032981|GO:0005737|GO:0009058|GO:0005743|GO:0005634|GO:0016740 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132695_PI430048170 0.0225596324888633 0.435520106148491 3.17920052956254
3.37992858314265 2.5183354642282 P P A 3.90067556275779 4.33267499829103
4.50912563884217 P P P LNCV6_132695_PI430048170 mRNA

GGCAGGATGTCTTTCCTAGAGGCTGGAAGAAAAGTGTATCGTACATTTTAAATTTATTTT NM_020718 RefSeq chr16 - 23061406 23149270 USP31 57478 ubiquitin specific peptidase 31 GO:0004197|GO:0016579|GO:0004843|GO:0061136|GO:0043161|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128623_PI430048170 0.000850871990731576 3.72969864806016 6.57020776011161 6.74394494428221 6.36251211577632 P P P 4.92744368419541 4.62811118742715 4.40038251727299 P P P LNCV6_128623_PI430048170 mRNA
CTCCACACAGAAAATCTTCTTGATTCTATAGAGACTTAATCATGCCTATGGCTTTGAATA NM_024693 RefSeq chr10 + 11742356 11764066 ECHDC3 79746 enoyl CoA hydratase domain containing 3 GO:0005739|GO:0008152|GO:0003824 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2146_PI430048170 0.5161682195592020.8878853073395740.3756262165653130.473765095718831 0.438362766471273 A A A 0.28147214834702 0.92553502381211 0.522721351803289 A A A LNCV6_2146_PI430048170 mRNA
TCCAATTGTTTCTTTAAACATGTATGATTATTTTATTTATAACCAGGTAGAGTATTTATA NM_001300977 RefSeq chr11 + 83193738 83215200 ANKRD42 338699 "ankyrin repeat domain 42, transcript variant 6" GO:1900017|GO:0051092|GO:0051059|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98190_PI430048170 0.4703481350071281.47365010054353 0.31194722899798 1.76264774255483 0.440272935287387 A A A 0.2987247210152620.2605086219401130.71172454486603 A A A LNCV6_98190_PI430048170 mRNA
TGAAATTGCACGCAATGCATACAGGAACAAAGAGAGGGTCAAGATGGTTATCTTTCCTCC NM_001206673 RefSeq chr14 + 50872159 50904970 ABHD12B 145447 "abhydrolase domain containing 12B, transcript variant 1" GO:0016787|GO:0008152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137223_PI430048170 0.8737937740347731.07887835848119 1.30645376962257 0.4595071614179720.327408473657969 A A A 0.9635010047089820.492282207564606 0.457703371901611 A A A LNCV6_137223_PI430048170 mRNA
AAGAATGCAATGAAGAAACTGTGGGGCAGAAATGTTTTCTTGGAGGCTAAAGGGAAATAG NM_001004059 RefSeq chr11 + 55650903 55651839 OR4S2 NA "olfactory receptor, family 4, subfamily S, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102161_PI430048170 0.3699212309116230.9581897859596414.7331670071898 14.6029247999653 14.5883612374088 P P P 14.7537683115909 14.6234457243636 14.7331670071898 P P P LNCV6_102161_PI430048170 mRNA
AGACGCATCTGTAGCAGAGTGGAACTTGTACTAACTTATGATAGAATGTATCAGAATAAA NM_019059 RefSeq chr7 - 22812632 22822852 TOMM7 54543 translocase of outer mitochondrial membrane 7 homolog (yeast) GO:0005739|GO:0005515|GO:0006626|GO:0005742|GO:0016021|GO:0008320|GO:0030150|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141604_PI430048170 0.8826324663611520.8753211261671851.25511324322221 0.477823920726525 2.35669331038372 A A A 2.6088818486153 1.4448859455541 0.42935833143062 A A A LNCV6_141604_PI430048170 mRNA
TCTCACTAGAAAAGTCCACAACTTCCAGGCCAAGCCCGCAGTGCCTACGTCTAAGCTGGG NM_001172357 RefSeq chr8 + 22161670 22164478 SFTPC 6440 "surfactant protein C, transcript variant 3" GO:0005515|GO:0071732|GO:0007585|GO:0097208|GO:0005771|GO:0033189|GO:0051384|GO:0070848|GO:0005615|GO:0051591|GO:0042803|GO:0009749|GO:0055093|GO:0032496|GO:0070741|GO:0007623|GO:0051260|GO:0032526|GO:0071260. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127314_PI430048170 0.2091971095105960.4757910527725962.28380830743504 2.66868620240639 0.398474967989294 A A A 2.33254091024404 3.20362747941152 3.59926561607761 A P P LNCV6_127314_PI430048170 mRNA
GGATAAATTGTTTACATGATTGGACCCTCAGATTCTGTTAACCAAAATTGCAGAATGGGG NM_001193424 RefSeq chr10 + 14878782 14904305 SUV39H2 79723 "suppressor of variegation 3-9 homolog 2 (Drosophila), transcript variant 1"

GO:0005515|GO:0000976|GO:0006325|GO:0071456|GO:0000122|GO:0030154|GO:0006351|GO:0006333|GO:0005720|GO:0036123|GO:0003682|GO:0036124|GO:0046974|GO:0008270|GO:0005654|GO:0006338|GO:0048511|GO:0042754|GO:0045892|GO:0000785|GO:0000775|GO:0007140 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131523_PI430048170 0.62563242751603 1.43280927337258 1.20720152476831 0.3632251012281372.42515544384212 A A A 0.3098262823106271.68937923348034 0.842328282688291 A A A LNCV6_131523_PI430048170 mRNA AAATACTTCCTAACTTCAGAGAGCACCAGAAGACACAAGAAAGCAACCGATAGCCTCCCA NM_181538 RefSeq chr7 - 99923268 99929620 GJC3 349149 "gap junction protein, gamma 3, 30.2kDa" GO:0007154|GO:0043209|GO:0042552|GO:0007605|GO:0005922|GO:0016021|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_43770_PI430048170 0.50401822022223 1.13611185868565 3.287351622216 3.7202534714381 3.65314560529697 A P P 3.54397742316008 3.62977248377348 2.85306244919181 P P P LNCV6_43770_PI430048170 mRNA TACATGACGCAGAGGGCATTTGATAAATAACTGGAAAAGTCAATAAATCTTTGCTACCCT NM_014186 RefSeq chr11 - 36272291 36289449 COMMD9 29099 "COMM domain containing 9, transcript variant 1" GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136525_PI430048170 0.000872838355688669 3.87218960459621 5.25205378932142 5.24159170649471 4.86173763703072 P P P 3.11936929238952 3.30632393068567 3.09399455869988 P P P LNCV6_136525_PI430048170 mRNA CCCAGAGCAGCTCCACGTGAGAGCATTAAAGATGTAATGAAGATGTTTACATGGAAAAAA NM_016210 RefSeq chr3 - 50558024 50567792 C3orf18 51161 "chromosome 3 open reading frame 18, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114985_PI430048170 0.5823539867643640.8856810633608471.39216664181799 0.2809046014894322.54284858763888 A A A 2.21747052494822 1.6838497348506 1.60938880584571 A A A LNCV6_114985_PI430048170 mRNA CCAAAGAAGATGTTAAAGAACCAGATGTGTCAGAAGAATTGGATACAAAACTCCCTCTTG NM_017554 RefSeq chr3 + 122680824 122730840 PARP14 54625 "poly (ADP-ribose) polymerase family, member 14" GO:0006355|GO:0005737|GO:0016020|GO:0005886|GO:0005634|GO:0006351|GO:0003950 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139360_PI430048170 0.7114142061592340.9325150649185288.85915529784529 8.44435074974589 8.40280196154545 P P P 9.00390618585647 8.59401015047986 8.38660763650886 P P P LNCV6_139360_PI430048170 mRNA CATCCCATCTCCATCACAGATAAAATCTTAGGAGATAAACACATTCAAAAAGGAATGAGA NM_024105 RefSeq chr22 - 49903205 49918458 ALG12 79087 "ALG12, alpha-1,6-mannosyltransferase" GO:0000030|GO:0005783|GO:0016020|GO:0006457|GO:0000009|GO:0005789|GO:0006487|GO:0016021|GO:0006488|GO:0044267|GO:0018279|GO:0043687|GO:0052917 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136215_PI430048170 0.1388743388661290.7178980474925693.80390860738158 4.19743597264493 4.50510798752745 P P P 4.91238608113231 4.34684286352035 4.71031879612304 P P P LNCV6_136215_PI430048170 mRNA GGCACTGATTGTTTTAATAAAAATGGGAAACAGACTAAATGGCTATTCACAGGAAACTGA NM_144736 RefSeq chr2 + 37231630 37249161 NDUFAF7 55471 "NADH dehydrogenase (ubiquinone) complex I, assembly factor 7, transcript variant 1" GO:0005739|GO:0032981|GO:0008168|GO:0019899|GO:0032259|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137505_PI430048170 0.0454445217439972 0.3313963797138493.19375324314493 2.85166859799533 3.36877051382958 P A P 3.97588494942752 4.6438283935825 5.31573213940299 P P P LNCV6_137505_PI430048170 mRNA GCTGACAGATTTCCCATTTAGTAGTCATAGAATACAGAAATAGTTTAGGGACATGTATTC NM_001134420 RefSeq chr1 + 91501107 91525764 CDC7 8317 "cell division cycle 7, transcript variant 3"

GO:0005515|GO:0006909|GO:0008284|GO:0008360|GO:0005634|GO:0005524|GO:0046872|GO:0045171|GO:0006260|GO:0010971|GO:0000082|GO:0005737|GO:0004672|GO:0018105|GO:0016301|GO:0004674|GO:0006270|GO:0010571|GO:0015630|GO:0000727|GO:0005654|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133682_PI430048170 0.9247857798431930.9972661577386720.272326471616519 0.2764146277075190.427291319844465A A A 0.35557614458369 0.300801802739776 0.336436067391003A A A LNCV6_133682_PI430048170 mRNA CAGGAAACGCTAATTCTCTTTAGACTCCTTGTTCTTTTATGACTACAATGAACATATGTC NM_080818RefSeq chr13 - 96985718 96994350 OXGR1 27199 oxoglutarate (alpha-ketoglutarate) receptor 1
GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136508_PI430048170 0.0558677567873227 0.8477624720004281 1.0502092915251 10.9385396685009 10.9505042584787 P P P 11.0864200023503 11.2389762900239 11.3215084688439 P P P LNCV6_136508_PI430048170 mRNA CTAGAGCACACACCAAAATCCAACCTTCTAATAAACATGATGGCGCAGTCCCACAAAAAA NM_030912RefSeq chr10 + 102644494 102658319 TRIM8 81603 tripartite motif containing 8
GO:0016567|GO:0016874|GO:0019221|GO:0032897|GO:0042803|GO:0005829|GO:0042802|GO:0043231|GO:0051091|GO:0005737|GO:0051092|GO:0046597|GO:0045087|GO:0016605|GO:0005654|GO:0008270|GO:0043123|GO:0060333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130305_PI430048170 0.00119277060654041 0.140113666281062 2.32012181648869 1.73803719064074 2.50963559116334 A A A 5.12857152417572 4.77216701389483 5.23971683573345 P P P LNCV6_130305_PI430048170 mRNA CCCAATGTGTACCTCAAGATAAACACAGTATGTTATGTCTAAAAATTTCCTTGTCTGTTG NM_001242409 RefSeq chr18 - 32263520 32470484 GAREM 64762 "GRB2 associated, regulator of MAPK1, transcript variant 1"
GO:0005515|GO:0008284|GO:0007173|GO:0005886|GO:0071364|GO:0051781|GO:0070374|GO:0070064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140021_PI430048170 0.00546797153395781 0.241897139736074 1.97808150335187 1.6586320218134 2.42619344578027 A A A 3.93678271158365 4.12124228975316 4.23577670586732 P P P LNCV6_140021_PI430048170 mRNA TGGTAACCAGCATCATTTTCCTTCATGTGATGTCTTCTTATGCCTTTGAAAGAAAGTTAC NM_001304RefSeq chr17 + 30378923 30469657 CPD 1362 "carboxypeptidase D, transcript variant 1"
GO:0004185|GO:0016020|GO:0006508|GO:0008270|GO:0016021|GO:0070062|GO:0004181 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143007_PI430048170 0.399608769538924 0.702742490377346 3.51284913844507 2.50590172450282 4.07260591096945 P A P 3.18063955216025 4.3183368484959 4.26692168553664 P P P LNCV6_143007_PI430048170 mRNA GCATTGATAAGTGTCTCATAATATTTGCTGTGATTGGAGAAAAAATGTAGTCGTAGCCAA NM_007166RefSeq chr11 - 85957170 86069097 PICALM 8301 "phosphatidylinositol binding clathrin assembly protein, transcript variant 1"
GO:0072583|GO:0005515|GO:0048471|GO:0030132|GO:0035459|GO:0035615|GO:0032050|GO:0008283|GO:0005634|GO:0007409|GO:0055072|GO:0043231|GO:0031623|GO:0032880|GO:0005545|GO:0030100|GO:0030276|GO:0045211|GO:0016197|GO:0043025|GO:0016192|GO:0030097|GO:0005794|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116907_PI430048170 0.785114815536898 0.968437609509183 6.71819138355967 6.75416033867269 7.22043927513378 P P P 6.95106336816665 6.77151376731773 7.14150874678008 P P P LNCV6_116907_PI430048170 mRNA GCACTGTACTCCTGGCAATTATTACATATGTTAGAACATGGATTTTGCACTGTAGACAAC NM_013330RefSeq chr1 - 169132529 169367963 NME7 29922 "NME/NM23 family member 7, transcript variant 1"
GO:0006241|GO:0005813|GO:0007368|GO:0003351|GO:0060830|GO:0004550|GO:0005524|GO:0036064|GO:0046872|GO:0006165|GO:0006228|GO:0006183|GO:0042073|GO:0060972|GO:0007420 . NA - . NA NA NA

NA NA NA NA NA NA
LNCV6_127675_PI430048170 0.9835501588928241.00782549487983 2.80357254601279
0.421812153252888 1.68287386495563 A A A 2.85187074728217 1.48717091827036
0.505546809311726 P A A LNCV6_127675_PI430048170 mRNA
CCTAGAGTTCCTGTAGTGTCCTACATTAAAAATATAATGTCTCTCTCTATTCCTCAACAA NM_013251 RefSeq chr12
- 57009996 57016560 TAC3 6866 "tachykinin 3, transcript variant 1"
GO:0005515|GO:0007565|GO:0007218|GO:0005102|GO:0007217|GO:0005576|GO:0005615|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58061_PI430048170 0.2671047665869530.8451818042814234.50247286541348 4.51093608130587
4.33174904025058 P P P 4.38027103098534 4.77359552081886 4.87978123137248 P P P
LNCV6_58061_PI430048170 mRNA
ATGGGTGATCGGCCTGTCCAGTTTGAAATTCTCAGTGATCAGTCAGTCAACTTTGGTTTT NM_005590 RefSeq chr11
- 94417300 94493874 MRE11A 4361 "MRE11 meiotic recombination 11 homolog A (S. cerevisiae),
transcript variant 2"
GO:0007095|GO:0005515|GO:0008408|GO:0030870|GO:0090305|GO:0008283|GO:0031573|GO:0032876|GO:0005
634|GO:0006303|GO:0005829|GO:0006302|GO:0004003|GO:0003690|GO:0000723|GO:0000724|GO:0032481|GO:0
032508|GO:0000785|GO:0031954|GO:0007131|GO:0033674|GO:0000781|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142876_PI430048170 0.0917735487121187 0.8140465499947756.55351569120749
6.7238733999503 6.90003388908428 P P P 7.13042349736758 6.84500668805 7.09672727571102 P
P P LNCV6_142876_PI430048170 mRNA
CTTACTACAATTACAGATTTTCAGGAGTTGTTTGCTAGTCTCTTTCAGTCAGGTACTAAA NM_017748 RefSeq chr17
- 38800433 38825350 CWC25 54883 "CWC25 spliceosome-associated protein homolog (S. cerevisiae),
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140829_PI430048170 0.15174890269676 0.96977299070162 0.361134632001836
0.3874869881369480.31773312720849 A A A 0.3773936564266740.399977501308442
0.422334918822204 A A A LNCV6_140829_PI430048170 mRNA
GAGGGTTTGAGGACATGATTTAGCGAGCCTCTGTTTTTTAAATATATTTTCCAATCTTGA NM_173663 RefSeq chr5
- 177723363 177780504 FAM153A 285596 "family with sequence similarity 153, member A" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134991_PI430048170 0.3450871364862680.7452770090458151.28156833988419
0.4563244697195172.00904075515595 A A A 1.62382816477628 2.01896454622966
1.75228795425212 A A A LNCV6_134991_PI430048170 mRNA
CAGGCTCCAAAGACAGCCTAACCTCTCAACTACATTTGAAATAAACCCAACCATAATGGT NM_015052 RefSeq chr7
+ 43112598 43563339 HECW1 23072 "HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1,
transcript variant 1" GO:0004842|GO:0042787|GO:0016874|GO:0090090|GO:0005829 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_90741_PI430048170 0.9571939759961970.9989899904374464.2714462197089 4.39482004428309
4.11479024781651 P P P 4.21144797424785 4.25618666848409 4.32894043656359 P P P
LNCV6_90741_PI430048170 mRNA
TGGGCTCTGTCTACTGTCGCAAAAGCTTTTAAAGATATTCATTAAACACGGACCTTCCTG NM_001144956 RefSeq
chr1 + 151721536 151729606 RIIAD1 284485 regulatory subunit of type II PKA R-subunit (RIIa) domain
containing 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113513_PI430048170 0.0096062818884995 0.5901059867434399.62237196580744
9.26100983155348 9.55949821828569 P P P 10.3838394488145 10.0055587048486
10.3331234764634 P P P LNCV6_113513_PI430048170 mRNA
CGCTGACTTTGAAGGTTGTGTTGTAGCATGAGGAACACAAATAAAACAATTCTAAATCAA NM_001415 RefSeq chrX
+ 24054947 24078811 EIF2S3 1968 "eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa"
GO:0005515|GO:0010467|GO:0003924|GO:0003743|GO:0005525|GO:0044267|GO:0006412|GO:0008135|GO:0006

413|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134329_PI430048170 0.0940881775612988 2.10434482723468 2.25163649184813
2.05940148603858 1.20974769738018 A A A 1.50423858910199 0.306084667829489
0.344620199964499 A A A LNCV6_134329_PI430048170 mRNA
ATTTCAGGAATCCTACAGTAGTAAAAAGCTGTGCACACTGGCCATCCACGCCATGGATAT NM_000537 RefSeq chr1
- 204154815 204166337 REN 5972 renin
GO:0005886|GO:0002003|GO:0005159|GO:0070305|GO:0005615|GO:0051591|GO:0005737|GO:0002018|GO:0043
408|GO:0006508|GO:0032496|GO:0048469|GO:0035902|GO:0001822|GO:0001823|GO:0005102|GO:0005576|GO:0
035690|GO:0050435|GO:0009755|GO:0042756|GO:0008217|GO:0008233|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128412_PI430048170 0.0224055283787767 0.58389009452017 5.68355348755873
5.20406655289748 5.67199683091504 P P P 6.0136311226637 6.39403295186893
6.48808474879974 P P P LNCV6_128412_PI430048170 mRNA
GAGCTTTCTGGCATGTGATTATTTACTTCAAAACTAGAGTTCCAAGCACCTACATTAATT NM_133646 RefSeq chr2
+ 173075836 173227145 ZAK 51776 "sterile alpha motif and leucine zipper containing kinase AZK,
transcript variant 2"
GO:0009314|GO:0005515|GO:0008219|GO:0043065|GO:0000287|GO:0008283|GO:0006950|GO:0005634|GO:0007
257|GO:0005524|GO:0030154|GO:0035556|GO:0000186|GO:0005737|GO:0004674|GO:0007010|GO:0000075|GO:0
007050|GO:0006468|GO:0000077|GO:0004709 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132084_PI430048170 0.137622240169364 1.42172155275536 7.51489377993305
7.53452311254758 7.46882589071435 P P P 7.40289935968142 6.83410356102982
6.64850115523168 P P P LNCV6_132084_PI430048170 mRNA
AAGATGTGAGGGTGTTAATCTAGGAAACTTCCCCCGTGAAAAGATTGGTCTAGTATTAAA NM_001199877 RefSeq
chr15 + 43777095 43796089 SERF2 10169 "small EDRK-rich factor 2, transcript variant 4"
GO:0008150|GO:0003674|GO:0005634|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143840_PI430048170 0.915824771495666 0.981491549207663 0.371852296919342
1.31736504776243 0.462665050401317 A A A 1.23514496353097 0.325750208878329
0.726152424083728 A A A LNCV6_143840_PI430048170 mRNA
GAGGTTGGTTTCAAGATCCAAGAAGATCAAGACATCCAATCAAATGCTGGTTTTTAATGT NM_153035 RefSeq chr1
+ 54053571 54101648 TCEANC2 127428 "transcription elongation factor A (SII) N-terminal and central
domain containing 2, transcript variant 1" GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_131442_PI430048170 0.197553404652924 0.854220350363354 5.12569455982585
4.79156518045922 4.79118485990587 P P P 4.93705604405987 5.22159736750476
5.23876138805151 P P P LNCV6_131442_PI430048170 mRNA
AACACCAATTTCTTCACCACTGCTCATGTGAGGTGAAGCAGCAGCTAACCCTAGAAAAAA NM_024650 RefSeq chr11
+ 66744735 66843516 C11orf80 79703 "chromosome 11 open reading frame 80, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108124_PI430048170 0.0598530358085075 0.828895256951514 5.34854363088133
5.40406969738121 5.51612170577019 P P P 5.84826596746575 5.57777115682745
5.64610052698013 P P P LNCV6_108124_PI430048170 mRNA
TTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCAC NM_021626 RefSeq chr17
+ 56978106 57006768 SCPEP1 59342 serine carboxypeptidase 1
GO:0004185|GO:0045909|GO:0042573|GO:0006508|GO:0045776|GO:0070062|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133926_PI430048170 0.0258232931573628 0.471025681176523 3.01339305642803
3.14311530790257 3.12924149421016 A P P 3.78435513407192 4.29723715744342
4.39470676738868 P P P LNCV6_133926_PI430048170 mRNA
GTGGTCCACCATTGTTTTTCTATCAATTTATATTGTGGCAATCCTAGAGTACTTTGCACT NM_080660 RefSeq chr7 -

139025705 139036029 ZC3HAV1L 92092 "zinc finger CCCH-type, antiviral 1-like" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136470_PI430048170 0.0406444809642561 0.5579632699869461.74115925055047 1.9714090340893 1.24101408297659 A A A 2.78068671858555 2.16198853317557 2.56287843364421 P A P LNCV6_136470_PI430048170 mRNA TTAATTTCAACCTAAGAAGGGAGTGAGAAACAACGAGAACCATGAGGGGAGAGTTAACGG NM_015990RefSeq chr4 + 39062231 39126233 KLHL5 51088 "kelch-like family member 5, transcript variant 1" GO:0008150|GO:0003674|GO:0005737|GO:0003779|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128364_PI430048170 0.3084733016363231.17083600625899 0.399713609235853 0.88912785137501 0.44904063390265 A A A 0.35382674434462 0.353895851235093 0.398977262811677A A A LNCV6_128364_PI430048170 mRNA GGCAAATGCTCTTTATGGGCAATAGGGTCTCATTAAATGATTGCTGAATAAATAACACAA NM_052818RefSeq chr13 - 32400722 32428178 N4BP2L1 90634 "NEDD4 binding protein 2-like 1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128001_PI430048170 0.00225333334570673 1.51274889666534 9.1305252606977 9.29270649188752 9.10671154237581 P P P 8.45436126407875 8.64828968535566 8.63494871965799 P P P LNCV6_128001_PI430048170 mRNA TTTGTTGGAACAATTACACTGGCCATGCCATAATGTTGAATAAAACTCTCTTCTTATGAG NM_016445RefSeq chr14 - 67386982 67412111 PLEK2 26499 pleckstrin 2 GO:0035556|GO:0005737|GO:0030036|GO:0031258|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127199_PI430048170 0.9712656429735661.01011752644914 0.716824563472373 0.3328640083339452.06405563942748 A A A 0.4242323670776780.5196225832101822.0834766892585 A A A LNCV6_127199_PI430048170 mRNA GTTTCATCTCTTTGCTAAGCTGGCTGCTTCTACCATCTAATAAATAATTGGCCAAGTTCT NM_032126RefSeq chr1 + 178513076 178522654 TEX35 84066 "testis expressed 35, transcript variant 1" GO:0015630|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142578_PI430048170 0.0444354239425289 0.8749691407291071 0.7815960447746 10.9446996176536 10.7957008034822 P P P 11.0958123642229 11.0388453898543 10.9683300770678 P P P LNCV6_142578_PI430048170 mRNA TTTATTTGGTCCTGGTGAGGGTGTTTGTGCCTTGTGAGACTCCGTACATTAAAGACCTGT NM_030818RefSeq chr19 + 13747938 13763292 CCDC130 81576 coiled-coil domain containing 130 GO:0005515|GO:0005575|GO:0009615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136161_PI430048170 0.3130927555594480.83657613332955 8.52007384327895 8.32759964785434 8.7711543974079 P P P 8.52148200955571 8.73810673154734 9.10490281001279 P P P LNCV6_136161_PI430048170 mRNA ATGCTAACTCTTGCATGTCAAGAAACATTAGTCTTAGGAATTCTTCAAAAAATGGCATCC NM_004939RefSeq chr2 + 15591620 15631111 DDX1 1653 DEAD (Asp-Glu-Ala-Asp) box helicase 1 GO:0005515|GO:0003725|GO:0006388|GO:0003724|GO:0090305|GO:0010494|GO:0005634|GO:0071920|GO:0072669|GO:0006302|GO:0005737|GO:0004527|GO:0008143|GO:0032508|GO:0003712|GO:0008026|GO:0000245|GO:0006355|GO:0033677|GO:0007275|GO:0009615|GO:0005524|GO:0003677|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138029_PI430048170 0.000805461776702982 0.7239385401476461 2.3736981409363 12.2524007662669 12.2834759914632 P P P 12.8052555030516 12.6973470528509 12.8052555030516 P P P LNCV6_138029_PI430048170 mRNA AGCCATGCTGCCTCCTTACATCCTTTTTGGAACAGAGCACGGTATAAATAATAAACTAAT NM_001048226 RefSeq chr20 + 45407988 45410610 DBNDD2 55861 "dysbindin (dystrobrevin binding protein 1) domain containing 2, transcript variant 6" GO:0005515|GO:0005737|GO:0006469 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_139033_PI430048170 0.2453069706244541.18851558267157 6.97235142852923
7.05755280242226 7.06041132706712 P P P 6.43525509391912 6.89628347558423
6.95858598644657 P P P LNCV6_139033_PI430048170 mRNA
AGACTACCTACTTTTTCTGGTCATTCTTGACTTGGAAAACGGTATGGAAAAGTATTTAGT NM_002493RefSeq chr9
- 32553525 32573184 NDUFB6 4712 "NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6,
17kDa, transcript variant 1"
GO:0022904|GO:0005739|GO:0031966|GO:0005747|GO:0006120|GO:0005743|GO:0005654|GO:0044281|GO:0016
021|GO:0008137|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54676_PI430048170 0.0184400341441529 0.5073690167815699.25221505209906
9.33003501145613 9.37262241452446 P P P 10.0689619614005 10.2105532246348
10.5678654685339 P P P LNCV6_54676_PI430048170 mRNA
TTCCTGATCTGTCCACTTCTGGTGTCAAAGATTTTACTCATCTTCTTAGTACATTCTATG NM_153713RefSeq chr1 -
145933423 145958019 LIX1L 128077 Lix1 homolog (chicken) like
GO:0008150|GO:0003674|GO:0005737|GO:0006914|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_106264_PI430048170 0.0346115818597408 1.57578541465679 4.873453709943
4.91827753523902 5.32205540710715 P P P 4.47906442351283 4.39642668083092
4.30859520333381 P P P LNCV6_106264_PI430048170 mRNA
ATGAAGATCAAAGAGCTTTACCGACGACGCTTTCCCCGGAAGACCCTGGGGCCCTCTGAT NM_006099RefSeq chr1
- 145848521 145859081 PIAS3 10401 "protein inhibitor of activated STAT, 3"
GO:0005515|GO:0006355|GO:0016874|GO:0016925|GO:0045202|GO:0015459|GO:0005634|GO:0008022|GO:0030
425|GO:0006351|GO:0045838|GO:0010628|GO:0005737|GO:0047485|GO:0019789|GO:0033235|GO:0008270|GO:0
009725|GO:0019899. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129467_PI430048170 0.00438123206788207 2.16376290565952 10.1773520113043
10.2987051820798 10.1859107205649 P P P 9.29810175715529 9.06969773659926
8.93294752973771 P P P LNCV6_129467_PI430048170 mRNA
TTGCTGTTTGTCTTCCTAGTTAAGGCTCTTTATAAAGAGCTTGTTCTTCATGTTTTAAGC NM_015470RefSeq chr2 -
73073381 73113018 RAB11FIP5 26056 RAB11 family interacting protein 5 (class I)
GO:0005515|GO:0017137|GO:0005794|GO:0005815|GO:0043015|GO:0005741|GO:0071468|GO:0015031|GO:2000
008|GO:0043231|GO:0045055|GO:0000139|GO:0031901|GO:0035773|GO:0055037|GO:0030141|GO:0055038|GO:0
005769|GO:0030658. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140777_PI430048170 0.0367953564638768 1.32947430262584 10.8131914358847
11.0048163153789 10.8148354427167 P P P 10.6484504628126 10.4507406134872
10.2868309891817 P P P LNCV6_140777_PI430048170 mRNA
GACTAACAGACCCTTGGAGGCAGGGGCTGTGGAAATAAATCTCTGCCTGCTGGCAAAAAA NM_153219RefSeq
chr19 + 55600339 55603138 ZNF524 147807 zinc finger protein 524
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143994_PI430048170 0.0343967307893710.5828340913781628.84692878751556
8.93583785565398 9.39937096759381 P P P 9.56892765071966 9.77361700314922
10.1725829379532 P P P LNCV6_143994_PI430048170 mRNA
GATGGGGAGGATCCTTGGACTTTGTGTTTTTGATTGTATGTTGATATTCTAAAAACATCT NM_001303096 RefSeq
chr2 + 189441432 189475562 WDR75 84128 "WD repeat domain 75, transcript variant 2"
GO:0005730|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103471_PI430048170 0.7821320951972920.8179456234647150.478157110078506
1.48385583903288 0.423919106893632A A A 0.5556718783435950.386908961811414
1.99465635215567 A A A LNCV6_103471_PI430048170 mRNA
GTGAAATTACTCCTGCTCGGGGCTGGAGAATCAGGAAAAAGCACCATTGTGAAGCAGATGNM_138736RefSeq chr16

+ 56191338 56348199 GNAO1 2775 "guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O, transcript variant 2"
GO:0042542|GO:0043005|GO:0005886|GO:0031852|GO:0008016|GO:0003924|GO:0031175|GO:0046872|GO:0006936|GO:0051926|GO:0007626|GO:0004871|GO:0034097|GO:0051430|GO:0042493|GO:0007568|GO:0005834|GO:0043278|GO:0007212|GO:0005525|GO:0031683|GO:0006184|GO:0032794|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88989_PI430048170 0.5451582451158610.9332454944150248.31714636146077 8.36452683669264 8.64181898917927 P P P 8.37642634452375 8.49497442114246 8.74761453731051 P P P LNCV6_88989_PI430048170 mRNA
GACCTTTTTAACTCTATCATTACAAGATATGGCAAGTCGTGTGCAGTTGTCTGGACCTCA NM_003653RefSeq chr17 - 17246623 17281303 COPS3 8533 "COP9 signalosome subunit 3, transcript variant 1"
GO:0005515|GO:0007165|GO:0006511|GO:0005737|GO:0008180|GO:0010388|GO:0009416|GO:0005654|GO:0005634|GO:0001701 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132482_PI430048170 0.00142965900039847 1.39429208378852 13.9515550431602 14.1022660841903 14.0572896309628 P P P 13.5217404495913 13.6239283448425 13.5286882122629 P P P LNCV6_132482_PI430048170 mRNA
TGTTGGCCAGATTTCTGCAATAAACACTTGTGGTTTGCGGCCATCTCCTTGGTTAAAAAA NM_012094RefSeq chr11 + 64318087 64321823 PRDX5 25824 "peroxiredoxin 5, transcript variant 1"
GO:0048471|GO:2001057|GO:0001016|GO:0051354|GO:0005782|GO:0005634|GO:0005615|GO:0072541|GO:0005829|GO:0043231|GO:0005739|GO:0005737|GO:0006954|GO:0004601|GO:0005759|GO:0046983|GO:0016480|GO:0051920|GO:0042744|GO:0043154|GO:0006979|GO:0043027|GO:0070062|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142606_PI430048170 0.8614854989254660.9399676238809371.43886733085617 0.4936551895376160.359779213219767A A A 1.5312689935052 0.527887064145224 0.500932042690372A A A LNCV6_142606_PI430048170 mRNA
CACCTTCCTATGTTTTCATGGTTGTAAAACATAATAAAACCTCCCACGTGGAAGACTTGG NM_001030059 RefSeq chr10 + 120456953 120589855 PPAPDC1A 196051 phosphatidic acid phosphatase type 2 domain containing 1A GO:0005886|GO:0046839|GO:0045087|GO:0016021|GO:0008195|GO:0038096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138775_PI430048170 0.8635097129304741.05198986128949 6.434564402953 5.66777279431868 6.16046544337049 P P P 5.95822251555707 6.23876056021906 5.92712588642705 P P P LNCV6_138775_PI430048170 mRNA
ATTCTAGGTATTTGATAGGGTATTGAGTGTATTTTGTGTGTGTGTGGATGTGTGTTTTGG NM_007212RefSeq chr1 + 185045418 185102608 RNF2 6045 ring finger protein 2
GO:0035102|GO:0031519|GO:0005515|GO:0035518|GO:0004842|GO:0000791|GO:0016874|GO:0000151|GO:0005634|GO:0000122|GO:0001739|GO:0001702|GO:0006351|GO:0016604|GO:0009948|GO:0071339|GO:0003682|GO:0005654|GO:0008270|GO:0071535|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54912_PI430048170 0.7045739406327881.01243553607452 0.5192402842029360.414285298429398 0.524971679205988A A A 0.4520902009239750.5103759479911830.444302195178265A A A LNCV6_54912_PI430048170 mRNA
AACATTTAACTTGAGGAACTTCCTCCTTTTCCAGCTTTGGGAGTCAAGCTTCTCACCTGG NM_006365RefSeq chr1 - 156404262 156429392 C1orf61 10485 chromosome 1 open reading frame 61 GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134457_PI430048170 0.00412490771465617 0.5482597313163896.9336056445681 6.98743172450602 7.24813014091809 P P P 7.82331999870669 7.80465216921225 8.13756773317987 P P P LNCV6_134457_PI430048170 mRNA
GAGCCTTTGTACTTTGCCATCACTGCTAGTAATTTCTTGGTCCTTTTCAATACTCCATTT NM_173834RefSeq chrX + 68498781 68537285 YIPF6 286451 "Yip1 domain family, member 6, transcript variant A"
GO:0060576|GO:0005802|GO:0030134|GO:0005801|GO:0005783|GO:0016021|GO:0042802 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_139446_PI430048170 0.0256133098773039 0.6431691212887844.86765278276192
4.54387651003277 5.0051121236979 P P P 5.38468015720147 5.27043413003162
5.67848267658362 P P P LNCV6_139446_PI430048170 mRNA
AAGCTGTGAAATTGTTCAACCTACTTTGTAACCAAAGAAGCAAAGCTGTGTAATGGAGTT NM_014779RefSeq chr3
+ 150408334 150460118 TSC22D2 9819 "TSC22 domain family, member 2, transcript variant 1"
GO:0006355|GO:0003700|GO:0006970 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95074_PI430048170 0.0198270815087182 2.05491127261161 5.98436160438766
5.78537068315044 5.77254296743439 P P P 4.4595698702876 5.10810259846933
4.79487502953322 P P P LNCV6_95074_PI430048170 mRNA
AGTTGTCAGCAAGAAAGCCCCAGGGCTGAAGTCCAAGTCCGTCGGGAACATGCCAGCTAA NM_007137RefSeq
chrX + 47836901 47922256 ZNF81 347344 zinc finger protein 81
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138033_PI430048170 0.0181130845143796 0.274947923013272 0.312009984727148
0.304551956528408 0.298623831222138 A A A 1.63007947690803 2.38381131862242
2.36907138098391 A A P LNCV6_138033_PI430048170 mRNA
CATATGTTTATCTCACACACATTATGAGCTTGAATTCTTAATTCATCCTAGCAAATTCTA NM_006785 RefSeq chr18
+ 58671385 58750139 MALT1 10892 "MALT1 paracaspase, transcript variant 1"
GO:0005515|GO:0050852|GO:0048471|GO:0004842|GO:0016567|GO:0005886|GO:0050856|GO:0002237|GO:0009
620|GO:0005634|GO:0043621|GO:0002020|GO:0051259|GO:0005829|GO:0005737|GO:0051092|GO:0042098|GO:0
006508|GO:0031398|GO:0001923|GO:0004871|GO:0043123|GO:0051168|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130628_PI430048170 0.0952681677242828 0.833005816780938 12.339029348035
12.4727220160771 12.3167706450262 P P P 12.4641511589323 12.7943407240265
12.6469488060689 P P P LNCV6_130628_PI430048170 mRNA
GGTCCAAGCCTGTGGCTGGAGCTGGTGTGTGTTTATCTAATAAAGTCCCACAGGTGCCTC NM_031921 RefSeq
chr1 + 1471783 1496202 ATAD3B 83858 "ATPase family, AAA domain containing 3B"
GO:0005743|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134326_PI430048170 0.0167715151928813 0.5580178983091058.81268502128351
8.64664720713602 9.02258262912315 P P P 9.39538771644226 9.63264665515887
9.94952457382247 P P P LNCV6_134326_PI430048170 mRNA
GTCTGGCATTGCATAAACTTCTCTGGTGTGAAAGGATAAATATGCCTTTCTAAAGTTGTA NM_019042RefSeq chr7
- 105456510 105522238 PUS7 54517 pseudouridylate synthase 7 (putative)
GO:0009982|GO:0019899|GO:0001522|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93403_PI430048170 0.5729023059704190.8851720692369440.6932201945546980.59761094433446
0.293979944632183 A A A 0.406840306237361 1.10020004192071 0.537627894349485 A A A
LNCV6_93403_PI430048170 mRNA
CAAGAAGTGAGAAACCAAGATAGATTCATCTCGACACTGAAATTACAGGCATTTGGATAC NM_025244RefSeq chr2
- 98997260 99154724 TSGA10 80705 "testis specific, 10, transcript variant 1"
GO:0043005|GO:0003674|GO:0031965|GO:0005737|GO:0031514|GO:0030031|GO:0007283|GO:0005575 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100264_PI430048170 0.63821296470239 0.9639513123366 0.296092602915302
0.2775719584842740.392499511461233 A A A 0.2924504016617240.540975276689346
0.278930726053313 A A A LNCV6_100264_PI430048170 mRNA
TTGCTGCATATGGGTTCACCTGAGCCACCAGGCACGGGCCATGCTGATGATACCAGCTTT NM_001272068 RefSeq
chr3 - 48467797 48504050 SHISA5 51246 "shisa family member 5, transcript variant 5"
GO:0005515|GO:0042771|GO:0031965|GO:0050699|GO:0005789|GO:0016021|GO:0004871|GO:0043123|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133355_PI430048170 0.7858373933206750.8992822690879260.264910432357311
0.3469247314543641.02082989452049 A A A 1.3095021834218 0.342392072819895
0.333820754184863A A A LNCV6_133355_PI430048170 mRNA
GCGAGCCAATCTCAGTTGTTGTTCTTGTTCTTCTTGTTCTTTGTAAATATTGAGAAAGTT NM_138344RefSeq
chr14_KI270847v1_alt + 1033455 1044170 FAM181A 90050 "family with sequence similarity 181,
member A, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128448_PI430048170 0.0735642899046847 0.6964673650510222.74467603143681
2.96919200367637 2.38973975043043 A P A 3.32538802181118 2.96398101275138
3.40123390302663 P P P LNCV6_128448_PI430048170 mRNA
CCTAGAACACTGGATACAAATAGAGCTATGTTGGTTTATCATAATATGTACGCAGAAACT NM_001256695 RefSeq
chr11 + 45147342 45235124 PRDM11 56981 "PR domain containing 11, transcript variant 1"
GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136877_PI430048170 0.0883259415348564 0.6328881835266574.31337090896552
3.65926145875085 4.44090946563759 P P P 5.12253330125829 4.6076963419315
4.72667066650621 P P P LNCV6_136877_PI430048170 mRNA
GCCTTGGATTTATTGTGCACAGTTTGTTGAGTTGTATGTTTTTGTGAATTATCAGGAGTA NM_015046RefSeq chr9
- 132261439 132354985 SETX 23064 senataxin
GO:0005515|GO:0006369|GO:0030424|GO:0070301|GO:0071300|GO:0005634|GO:2000144|GO:0033120|GO:0006
302|GO:0030426|GO:0005737|GO:0000165|GO:0045944|GO:0032508|GO:0001147|GO:0006396|GO:0043066|GO:0
060566|GO:0006376|GO:0005730|GO:0000228|GO:2000806|GO:0005524|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128542_PI430048170 0.1164260385688751.02833591671737 0.387305276765637
0.3943242578422960.434846677934696A A A 0.3601880144251330.344512906074615
0.390911598883669A A A LNCV6_128542_PI430048170 mRNA
CCCTGACATTTTTGATATTTCATATAATAGAGAACACTGGTGTCATACATGGGAAGTATG NM_001184727 RefSeq
chrX + 102651400 102659082 GPRASP1 9737 "G protein-coupled receptor associated sorting protein
1, transcript variant 4" GO:0005515|GO:0005737|GO:0008333 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128010_PI430048170 0.2210398128183671.04292102699511 0.338325540787269
0.3154000219673010.429367616293578A A A 0.2990296542256560.279809301335175
0.324550453315707A A A LNCV6_128010_PI430048170 mRNA
GAAAATATTCACTGGGACAGTCTTGGATCAAGAGGGAGTTTTGAGGTGGAGGCTCATTCT NM_144499RefSeq chr3
+ 50191609 50197696 GNAT1 2779 "guanine nucleotide binding protein (G protein), alpha transducing
activity polypeptide 1, transcript variant 1"
GO:0000035|GO:0060041|GO:0005886|GO:0007603|GO:0042622|GO:0008283|GO:0003924|GO:0009642|GO:0046
872|GO:0005829|GO:0071257|GO:0016324|GO:0050908|GO:0043025|GO:0009416|GO:0004871|GO:0001580|GO:0
016056|GO:0001664|GO:0019901|GO:0051343|GO:0051344|GO:0005834|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135799_PI430048170 0.11220762390618 0.6981903791880767.30956517898095
7.19678619619259 7.57579259435968 P P P 7.50533706008826 7.88257529408423 8.1942993540082
P P P LNCV6_135799_PI430048170 mRNA
CACAAAAGCAGATACTTGAGGAAAACACTATTTCCAAAAGCACATGTATTGACAACAGTT NM_004817RefSeq chr9
+ 69174054 69255208 TJP2 9414 "tight junction protein 2, transcript variant 1"
GO:0005515|GO:0030054|GO:0010033|GO:0005886|GO:0019904|GO:0004385|GO:0006915|GO:0035329|GO:0008
022|GO:0006921|GO:0005829|GO:0050892|GO:0005737|GO:0005912|GO:0046939|GO:0005654|GO:0005923|GO:0
030674 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80698_PI430048170 0.0274002448998385 0.7671784935833166.4250884228822
6.16505725403399 6.38073833604643 P P P 6.56012978527914 6.72682309004547
6.83134153445558 P P P LNCV6_80698_PI430048170 mRNA

GACCAAATGTGCAGGCTATTAGCTCCAGATTGTGAAATCATACAGGAAGTGGGAAAACTC NM_016042RefSeq chr9
- 37779713 37785092 EXOSC351010 "exosome component 3, transcript variant 1"
GO:0005515|GO:0034475|GO:0010467|GO:0034427|GO:0003723|GO:0006364|GO:0071038|GO:0071035|GO:0004
532|GO:0005634|GO:0071034|GO:0000178|GO:0005829|GO:0071051|GO:0005737|GO:0000288|GO:0045190|GO:0
005730|GO:0035327|GO:0043928|GO:0045006|GO:0000175|GO:0000177|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133986_PI430048170 0.00122083476676137 3.09393439469752 2.13112678417195
2.41562275406615 2.52018251283154 A A A 0.5006239567406390.6581714105072771.0011451654688
A A A LNCV6_133986_PI430048170 mRNA
TCTTCCTCATCATAAAGAGCTACAGAAAATATCGAAGGGAGAGGCTTCCCATTTCCCCAG NM_174896RefSeq chr1
+ 111473868 111478512 C1orf162 128346 "chromosome 1 open reading frame 162, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142150_PI430048170 0.00125006032215712 0.3636363167347647.73391512902206
8.03444198090026 7.98447950738846 P P P 9.22195846071162 9.26209010686891
9.62890506966649 P P P LNCV6_142150_PI430048170 mRNA
CTATGGGTGTTATCACCTAGCTGAATGTTTTTCTAAAGGAGTTTATGTTCCATTAAACGA NM_005904RefSeq chr18
- 48919852 48950711 SMAD7 4092 "SMAD family member 7, transcript variant 1"
GO:0005515|GO:0010467|GO:0001657|GO:0006367|GO:0003700|GO:0008013|GO:0044212|GO:0055010|GO:0005
518|GO:0071560|GO:0016342|GO:0048844|GO:0060373|GO:0010944|GO:0031398|GO:0051444|GO:0007179|GO:0
031397|GO:0017015|GO:0031625|GO:0030336|GO:0022409|GO:0030509|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138314_PI430048170 0.1299980096414430.4142397457914350.279535836603023
0.4459021746744040.746450937455965A A A 0.8359395652944281.55945910032574
2.46886253249473 A A P LNCV6_138314_PI430048170 mRNA
GCATCTTGTTCCCATGGTGATAACACTAATTGAATATATCTATGAGGGCATGTATTAGTT NM_001148RefSeq chr4
+ 113049628 113383740 ANK2 287 "ankyrin 2, neuronal, transcript variant 1"
GO:0005515|GO:0030018|GO:0003283|GO:0051928|GO:0086070|GO:0015459|GO:0043268|GO:0060307|GO:2001
259|GO:0060048|GO:0005622|GO:0086066|GO:0007411|GO:0045211|GO:0051924|GO:0051117|GO:0030674|GO:0
005856|GO:0086004|GO:0086005|GO:0030913|GO:0019901|GO:0030507|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_66103_PI430048170 0.2094234499319521.15649832136782 8.59068728036884 8.3828852369948
8.773141295191 P P P 8.3409840467201 8.35383073023987 8.44660259229303 P P P
LNCV6_66103_PI430048170 mRNA
TTACATTCAGATTTGGAAGAGGCGAGATAATGATGAAACCAACCAGCAGGGGGCTTGAAG NM_006590RefSeq
chr2 + 85616091 85649284 USP39 10713 "ubiquitin specific peptidase 39, transcript variant 1"
GO:0008380|GO:0006397|GO:0006511|GO:0000245|GO:0007049|GO:0008270|GO:0005681|GO:0051301 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135755_PI430048170 0.9147040235606561.13465986868437 0.312411634217843
3.05896472560848 2.03658843353251 A P A 1.22971680594353 2.56195644201663
1.92776778714591 A P A LNCV6_135755_PI430048170 mRNA
GCCAACACAATCACCTTTACTTTGTACTCTGTGTGTATGTTTTGGTTTTCTGTGTTTTAA NM_015557RefSeq chr1 -
6101786 6180134 CHD5 26038 chromodomain helicase DNA binding protein 5
GO:0000792|GO:0008026|GO:0060850|GO:0008285|GO:0006366|GO:0005634|GO:0003677|GO:0005524|GO:0016
020|GO:0016581|GO:0043967|GO:0008270|GO:0021895|GO:0035093 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139035_PI430048170 0.3727932624415650.7446703875372722.71725329841347
3.33457559304411 1.8706807461581 A P A 3.14755733034565 3.55981410961822
2.73005522443941 P P P LNCV6_139035_PI430048170 mRNA
TCCAGGTGCAGAAGTGACCGCGGAGACTCTGCTTCACGAGTTTCAGGAGCTGCTGAAAGA NM_001014980 RefSeq

chr1 - 1242445 1246722 FAM132A 388581 "family with sequence similarity 132, member A"
GO:0045721|GO:0051897|GO:0046324|GO:0005179|GO:0035774|GO:0050728|GO:0046326|GO:0046628|GO:0005
576|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130974_PI430048170 0.1054988488497320.7965104053795775.8281438907503
5.86524332079663 6.13937746817756 P P P 6.09647537928988 6.2136920355793
6.49775259421083 P P P LNCV6_130974_PI430048170 mRNA
CTATTTGGTGCTTAGTGAAAAGATTTTGAATTACTGTACGTACCAGTTGTTGCCATTTCT NM_025205RefSeq chr4
+ 17614627 17625628 MED28 80306 mediator complex subunit 28
GO:0005515|GO:0006355|GO:0016020|GO:0051151|GO:0019827|GO:0016592|GO:0003779|GO:0030864|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142567_PI430048170 0.1407933554522611.34509887294756 7.6707648159485
8.03656432389918 7.7379823358107 P P P 7.72197878215784 7.34998723379098
7.03490183173055 P P P LNCV6_142567_PI430048170 mRNA
TGGAGGGGAGCTCTGTCTGTCCGTGTTATTTATTGCTACTTCCTGCCTGGTCTCCTGCCC NM_080600RefSeq chr19
+ 35292085 35313806 MAG 4099 "myelin associated glycoprotein, transcript variant 2"
GO:0043220|GO:0048011|GO:0005886|GO:0021762|GO:0007596|GO:0033270|GO:0030246|GO:0050771|GO:0016
021|GO:0050900|GO:0007155|GO:0050770 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144059_PI430048170 0.4070572755018191.04912136042405 0.558695072213985
0.3545727656712370.529232423437649A A A 0.4366472765873720.382734936562251
0.423347787489672A A A LNCV6_144059_PI430048170 mRNA
GGAAAGGCTGTGTGGAAATTCATTGATGATACTTTAAAATGTCATCTTTGCTTGTACTAG NM_001385RefSeq chr8
- 104379423 104467049 DPYS 1807 dihydropyrimidinase
GO:0051219|GO:0006210|GO:0006212|GO:0055086|GO:0044281|GO:0002059|GO:0002058|GO:0005829|GO:0019
482|GO:0046135|GO:0051289|GO:0008270|GO:0004157|GO:0006206|GO:0016597|GO:0070062|GO:0006208 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135371_PI430048170 0.0777463682128725 1.16648434071376 7.84034835501797
7.8360032115177 7.83283802136712 P P P 7.48588765920415 7.71417784681167 7.6334183740715
P P P LNCV6_135371_PI430048170 mRNA
TCGCGTGGGTGTTAAAATGTTTATCATGCCTAAGGGAGACATTTATGATTAAACCATTTA NM_005679RefSeq chr16
- 84177846 84187070 TAF1C 9013 "TATA box binding protein (TBP)-associated factor, RNA polymerase
I, C, 110kDa, transcript variant 1"
GO:0005515|GO:0010467|GO:0006366|GO:0000183|GO:0045814|GO:0006363|GO:0006362|GO:0040029|GO:0006
361|GO:0006360|GO:0005654|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137840_PI430048170 0.0202032470461898 0.5191464555079937.43528701912444
7.23887011653173 7.24525352001968 P P P 7.91236304566577 8.32186031668449
8.47450269794421 P P P LNCV6_137840_PI430048170 mRNA
TTTTTCTGACAATGTGACCAGACTGAATTTCCTCATAAAGAAAAAATGGCGTGCCTTGTG NM_022754RefSeq chr5
+ 175478510 175528618 SFXN1 94081 sideroflexin 1
GO:0005739|GO:0034220|GO:0015075|GO:0030218|GO:0005743|GO:0006826|GO:0016021|GO:0055072 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127959_PI430048170 0.4732320499073231.2337452738271 1.5419867397995
2.02051446900915 1.55749096607461 A A A 0.3233103038329941.9993249613813 1.4778196042974
A A A LNCV6_127959_PI430048170 mRNA
GCCATACTTAGGCTTGAAAAGGCTAATGTTGGAAAAAACATGTTCTTCTAATTGGTCAAA NM_018988RefSeq chr6
- 13363354 13487637 GFOD1 54438 "glucose-fructose oxidoreductase domain containing 1, transcript
variant 1" GO:0016491|GO:0005576|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63642_PI430048170 0.00443696258068388 1.24069132123008 8.59270344548052
8.64515907625379 8.50702466712367 P P P 8.31631351584644 8.2854417537135
8.21103588766144 P P P LNCV6_63642_PI430048170 mRNA

AAACAGGAAAAACTGGGAGATTTTCTGCAGAAATTGAGTTCCAGCCTCTCTCGAACCTGG NM_001193653 RefSeq chr17 - 82442585 82450831 C17orf62 79415 "chromosome 17 open reading frame 62, transcript variant 4" GO:0005515|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129756_PI430048170 0.211055447977842 1.41991820110742 4.45254645673807 5.14802122034191 4.3203149816842 P P P 4.12017220060111 4.13001997715134 4.29001405330535 P P P LNCV6_129756_PI430048170 mRNA
CCCCCAACCTGACTATCATGGACAAGAGATTTGATGGATAGAATAAAAGGCTGCAGCGAG NM_033506 RefSeq chr7 + 100586332 100601117 FBXO24 26261 "F-box protein 24, transcript variant 1" GO:0005515|GO:0004842|GO:0016567|GO:0000151 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140733_PI430048170 0.988045296026879 0.998458123333087 0.297676362373747 0.264154584213825 0.405579998468598 A A A 0.284214902898246 0.249119304724998 0.437532441431941 A A A LNCV6_140733_PI430048170 mRNA
CAGAGACAGGCACTATATGTTCTTTTGTTTTTAATGTATCATATGTTTGCATAGGCACAG NM_006036 RefSeq chr2 - 44317608 44360674 PREPL 9581 "prolyl endopeptidase-like, transcript variant 1" GO:0005794|GO:0004252|GO:0006508|GO:0005856|GO:0070008|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125346_PI430048170 0.94373378471791 0.9991149539824220 .380391450397408 0.3786989764824560 .377691088354376 A A A 0.397439276573981 0.351793185656616 0.390961110087224 A A A LNCV6_125346_PI430048170 mRNA
TTTGCATATTTCCAGTCACATAAGCAGCCTTGGCGTGAAAACAGTGTCAGACTCGATTCC NM_000237 RefSeq chr8 + 19939070 19967259 LPL 4023 lipoprotein lipase GO:0005515|GO:0004806|GO:0007603|GO:0005886|GO:0009409|GO:0042627|GO:0070328|GO:0044281|GO:0031225|GO:0005615|GO:0034361|GO:0019432|GO:0006633|GO:0019433|GO:0008201|GO:0070062|GO:0009986|GO:0010744|GO:0042493|GO:0005102|GO:0005576|GO:0004620|GO:0010886|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134550_PI430048170 0.0236179339830191 0.796876624277312 7.71403138751191 7.53852781724273 7.77244566706885 P P P 8.03695383085939 7.923144821631 8.05427888920496 P P P LNCV6_134550_PI430048170 mRNA
GATCTCTCCATTCAGAAGTGTGCAGTCTTAAATGTACAGCGATAAGAAACTGTTATTTTA NM_015094 RefSeq chr22 + 21417403 21451461 HIC2 23119 hypermethylated in cancer 2 GO:0005886|GO:0005654|GO:0005634|GO:0008022|GO:0045892|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135842_PI430048170 0.952823428776007 1.00330275414978 0.512659082369922 0.453815174333844 0.344744318397932 A A A 0.379374115519251 0.465883591438674 0.455159819605902 A A A LNCV6_135842_PI430048170 mRNA
CTCGGATCTGGAGAATCAGACACAGACATAAAAATGAAGCCAGAATGAAAAATGAAAGCC NM_033180 RefSeq chr11 - 5323297 5324352 OR51B2 79345 "olfactory receptor, family 51, subfamily B, member 2 (gene/pseudogene)" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131423_PI430048170 0.0457956676169407 1.35459116879827 8.41170693548478 8.51164441464082 8.80236772594846 P P P 8.01925192858783 8.16927672840628 8.24370422325681 P P P LNCV6_131423_PI430048170 mRNA
CTTTGCACACACACTAGCCTTCTTTTGTACTTTTCATTCTGGATGGGCTTGGCCAAAACA NM_006052 RefSeq chr21 - 37223424 37267532 DSCR3 10311 Down syndrome critical region 3 GO:0008150|GO:0003674|GO:0008565|GO:0005634|GO:0006886|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92416_PI430048170 0.402979462515235 1.28751748276346 2.25500167074324 2.91842952100927 1.9268305005121 A A A 2.2068494350421 2.00822732919259 1.96085522981771 A A A LNCV6_92416_PI430048170 mRNA

TATCAGTTACATTATAAAAATTTACCTCGTGCCTGAGGCCCCAGAGCCCAAGGGTGCAAA NM_000149RefSeq chr19 - 5842887 5851474 FUT3 2525 "fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group), transcript variant 1" GO:0017060|GO:0046920|GO:0009312|GO:0016020|GO:0032580|GO:0009988|GO:0008417|GO:0006486|GO:0043413|GO:0016021|GO:0036065|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142995_PI430048170 0.9385095777442010.9971396220320280.4826103090905191.688105069356 0.572671590806327A A A 0.3529103747297731.80583482623663 0.433970008424362A A A LNCV6_142995_PI430048170 mRNA
GTTCTCAATTGTATTTCTCTCAAATGGACAGGTTCCTTCTTTACTGGAGGATTTTTGTTT NM_001099640 RefSeq chr17 - 55719626 55732121 TMEM100 55273 "transmembrane protein 100, transcript variant 1" GO:0071773|GO:0048471|GO:2001214|GO:0005886|GO:0005783|GO:0060842|GO:0001525|GO:0030509|GO:0001701|GO:0003674|GO:0007219|GO:0043491|GO:0043204|GO:0016021|GO:0001570|GO:0045603 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139874_PI430048170 0.1100289991574232.5829061530253 0.716465943162724 2.16031044111517 1.95581165852319 A A A 0.3731255079745460.340751368839645 0.386449721768869A A A LNCV6_139874_PI430048170 mRNA
TGTTAATCTAGAAGAAAGTGGTTGCATAGAGAAGAGTAAGAATGTAGACCAGCTTATTGA NM_152462RefSeq chr17 - 35192519 35194393 SLC35G3 146861 "solute carrier family 35, member G3" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137198_PI430048170 0.0432612732991802 1.27891497169962 10.0799868174536 9.99418207128545 9.79618552083117 P P P 9.65648865389726 9.58753842223166 9.57471287979353 P P P LNCV6_137198_PI430048170 mRNA
ATCTTCATTAGCATGATCCTCTTCATTCGAATCATGCCTAAACTCAAATAAAGACCCCCG NM_018467RefSeq chr19 + 17215345 17219829 USE1 55850 unconventional SNARE in the ER 1 homolog (S. cerevisiae) GO:0006888|GO:0005515|GO:0030163|GO:0060628|GO:0005783|GO:0071786|GO:0005789|GO:0007041|GO:0016021|GO:0015031|GO:0032940|GO:0005764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132264_PI430048170 0.3599461051209841.27346153620877 0.331937813455943 1.06992472818727 0.276653194771431A A A 0.2506251277266680.270667095618245 0.253494551760973A A A LNCV6_132264_PI430048170 mRNA
CGTGTGTCTTCATCTCTCTAGCCATGTGCATAAATGACGTAAGTTACTTTGTATGGTTAA NM_001303530 RefSeq chr18 + 12308058 12326616 TUBB6 84617 "tubulin, beta 6 class V, transcript variant 8" GO:0051258|GO:0005874|GO:0003924|GO:0005634|GO:0005525|GO:0055085|GO:0006184|GO:0003674|GO:0005737|GO:0006457|GO:0005200|GO:0051084|GO:0007017|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133924_PI430048170 0.1653022140259021.07409102376112 0.515069182288812 0.4128743605675990.536235464233389A A A 0.3012421192729240.387691742164952 0.464283148450872A A A LNCV6_133924_PI430048170 mRNA
AACAAGGATGTGAAAGAGGCAGTAAAACACCTACTGAACAGAAGGTTCTTTAGCAAGTGA NM_001004481 RefSeq chr9 - 104604670 104605627 OR13C2NA "olfactory receptor, family 13, subfamily C, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138810_PI430048170 0.8383712328987530.996042899664825 1.09816900261434 2.32362413973064 1.95813176019017 A A A 1.96861789239563 1.97021122987466 1.69774676506344 A A A LNCV6_138810_PI430048170 mRNA
AAGGAGCTGAAGAATGCCATAAATAAAAACTTTTGCAGAAGGTTCTGCCCTCTAAGCTCC NM_013938RefSeq chr19 + 15741392 15742343 OR10H3 26532 "olfactory receptor, family 10, subfamily H, member 3" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143890_PI430048170 0.1406449339684790.7005618046974063.84630074319067 3.05280758531241 3.19380884830017 P P P 3.92062804793621 4.08654728809395

3.73383949630898 P P P LNCV6_143890_PI430048170 mRNA
CAGGGATGGGAGGGGGCCATTTGCTGTTCCTCTGAGTAAAGCTTGTTCTGCATGAAAAAA NM_172168RefSeq chr16
- 1978916 1981549 NOXO1 124056 "NADPH oxidase organizer 1, transcript variant c"
GO:0005515|GO:0005543|GO:0022617|GO:0016176|GO:0006801|GO:0060263|GO:0010310|GO:0043020|GO:0043
085|GO:0035091|GO:0019899|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131313_PI430048170 0.4803569677690960.7924627034128363.18414876881027 3.0994317516828
3.66775231362567 A A P 3.86841597122787 2.97292061856566 3.98782062861721 P P P
LNCV6_131313_PI430048170 mRNA
ATGGCATGTGAAACTGATCTGTTGGTAACTGGAAGAAAACTCAGCATCTGTATTTATACA NM_003369RefSeq chr11
+ 75815166 76144238 UVRAG 7405 UV radiation resistance associated
GO:0005515|GO:0035493|GO:0017124|GO:0005770|GO:0046718|GO:0005764|GO:0045335|GO:0043234|GO:0005
737|GO:0006281|GO:0000149|GO:0060627|GO:0005769|GO:0010508 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130757_PI430048170 0.0033071084302695 0.3872239662164614.92597648078825
4.56890726889414 4.68495653115988 P P P 5.82704124978642 6.05992088283047
6.37058828894555 P P P LNCV6_130757_PI430048170 mRNA
CCATCTTTGAACTTCTGACTACTTGTTGTATCTGCTGGATATTTAGTTCAACTGTATAGT NM_002890RefSeq chr5 +
87268252 87391926 RASA1 5921 "RAS p21 protein activator (GTPase activating protein) 1, transcript
variant 1"
GO:0005515|GO:0051252|GO:0008360|GO:0048514|GO:0009790|GO:0005829|GO:0035556|GO:0046580|GO:0005
737|GO:0043524|GO:0001948|GO:0030833|GO:0007411|GO:0048010|GO:0048013|GO:0000281|GO:0005102|GO:0
031235|GO:0001726|GO:0005099|GO:0007165|GO:0007162|GO:0051020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138843_PI430048170 0.6839052889945211.03769934670165 4.95441960058068
4.85363709057794 4.63769360700053 P P P 4.63552485335298 4.81964434272986
4.83967285022319 P P P LNCV6_138843_PI430048170 mRNA
ACTCTTATATTGGCTTTTTAAGGAAGCAGTCTTAACAAAGGCTCTTTTCAGAGCCACCCA NM_021065RefSeq chr6
- 26198783 26199293 HIST1H2AD 3013 "histone cluster 1, H2ad"
GO:0008150|GO:0003674|GO:0046982|GO:0005634|GO:0000786|GO:0003677|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128224_PI430048170 0.0270700331017774 0.6241038559353617.45624091178809
7.21500824382069 7.7474934762706 P P P 7.9661667405086 8.12934810850279
8.38233985430788 P P P LNCV6_128224_PI430048170 mRNA
CACCAAATTTAGTGACAGTGTCTAGCCATGTTAGCAATAATGTTAACAGAAGCTTTTGTT NM_016470RefSeq chr20
- 44195940 44210906 OSER1 51526 oxidative stress responsive serine-rich 1 GO:0070301 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134949_PI430048170 0.25216630708765 0.7807159784116096.54060938628696
6.78718825942511 6.73578015871955 P P P 6.59917050610152 7.20066242662127
7.25900344766923 P P P LNCV6_134949_PI430048170 mRNA
GCCTTAGGTGAAAGCAACATGTATCCCTTTAGACTACTAACGGTATATGTTGTTCTTATG NM_170743RefSeq chr1
- 24154156 24187275 IFNLR1 163702 "interferon, lambda receptor 1, transcript variant 1"
GO:0005515|GO:0051607|GO:0002385|GO:0008285|GO:0004896|GO:0032002|GO:0019221|GO:0034342|GO:0016
021|GO:0050691 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141194_PI430048170 0.0386452925988021.21064493361733 9.14287199353717
9.08697368294615 9.22811857310133 P P P 8.75052443984254 8.99627306519267 8.8768989543739
P P P LNCV6_141194_PI430048170 mRNA
GTAAAGGAATATTTGAGTAAAGTGAGTTGCCGTTCTTGAAGCCCGTCTCCTAAGGATTCT NM_001029RefSeq chr12
+ 56041901 56044223 RPS26 6231 ribosomal protein S26
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0019058|GO:0015935|GO:0005730|GO:0003

729|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0000184|GO:0
033119|GO:0022627|GO:0016032|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_145730_PI430048170 0.00149899591226704 0.1809042062448347.44757382445033
7.86954829725884 7.72594640062284 P P P 10.5084461499628 9.78438905939527
10.0894220992271 P P P LNCV6_145730_PI430048170 mRNA
AGGTCACCGCGAGGCCTGACTGGCCTTATTGTTGAATAAATGTATCTGAATATCCCCAAA NM_003122RefSeq chr5
- 147824579 147839231 SPINK1 6690 "serine peptidase inhibitor, Kazal type 1"
GO:0010751|GO:0005515|GO:0060046|GO:0004866|GO:0004867|GO:0050732|GO:1900004|GO:2001256|GO:0005
615|GO:0090281|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142600_PI430048170 0.0097708751420059 0.2805896167049665.501837078773
4.74859585321339 5.62074264508295 P P P 6.96972685648903 7.1024829973183
7.40850934989638 P P P LNCV6_142600_PI430048170 mRNA
AAGATTGACTGGATTCGATCCAAAAGATAAAACTTGAAGCTATTCTGGAACTAACATGGA NM_005126RefSeq chr3
+ 23945259 23980618 NR1D2 9975 "nuclear receptor subfamily 1, group D, member 2, transcript
variant 1"
GO:0005515|GO:0010467|GO:0006355|GO:0006367|GO:0055088|GO:0050727|GO:0003707|GO:0005634|GO:0019
216|GO:0043401|GO:0042752|GO:0005654|GO:0008270|GO:2001014|GO:0048511|GO:0001046|GO:0004879|GO:0
045893|GO:2000505|GO:0045892|GO:0030522 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_3703_PI430048170 0.0158416183698729 0.48199592519394 7.35071587425156
6.75681588420927 6.79211965663951 P P P 8.23692577642842 7.95516088712397
7.92529391532453 P P P LNCV6_3703_PI430048170 mRNA
GTGTTAAACAACTACAGAATACTAAATAAAAAGTTTGGCCAAAACCAACCATGAAGCTGC NM_002139RefSeq chrX
- 136873445 136880780 RBMX 27316 "RNA binding motif protein, X-linked, transcript variant 1"
GO:0005515|GO:0008380|GO:0048026|GO:0010467|GO:0048025|GO:0006366|GO:0003723|GO:0005634|GO:0071
013|GO:0003729|GO:0005615|GO:0000166|GO:0044530|GO:0000381|GO:0045944|GO:0051260|GO:0006509|GO:0
070062|GO:0005719|GO:0001047|GO:0001649|GO:0016020|GO:0000398|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127874_PI430048170 0.1305828417294370.9455582878137320.252298144604059
0.2663044526212040.323139526902904A A A 0.4267161469732930.34334708095207
0.312511061026131A A A LNCV6_127874_PI430048170 mRNA
TCAGTAAGCTGTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAA NM_212557RefSeq chr4
+ 70518571 70532743 AMTN NA "amelotin, transcript variant 1" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128232_PI430048170 0.00812035379300253 0.5718339822415533.45643441246957
3.05163590458297 3.3281257101827 P A P 4.04125174493025 4.00528679552195
4.22776687102049 P P P LNCV6_128232_PI430048170 mRNA
GACAGGTTGAGTAATAAGGAATTAAGTCGTCGTCATTTCATTAAAACTGAGAGATGATGT NM_001162501 RefSeq
chr22 + 40177924 40335808 TNRC6B 23112 "trinucleotide repeat containing 6B, transcript variant 1"
GO:0005515|GO:0010467|GO:0048011|GO:0048015|GO:0060213|GO:0031047|GO:0006417|GO:0016441|GO:0005
829|GO:0000166|GO:0007173|GO:0007219|GO:1900153|GO:0000932|GO:0008543|GO:0045087|GO:0038095 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109302_PI430048170 0.5883621254113211.11112407945395 4.62963969084921 4.274954758793
3.96419421281874 P P P 4.40389495831609 3.95081193872294 4.09729376776277 P P P
LNCV6_109302_PI430048170 mRNA
TGGTCACTTCTCCACCTTCGACCACCACGTGTACGACTTCTCGGGGACGTGCAACTACAT NM_005961RefSeq
chr11_KI270927v1_alt - 82414 111099 MUC6 4588 "mucin 6, oligomeric mucus/gel-forming"
GO:0030277|GO:0006493|GO:0005796|GO:0016266|GO:0005576|GO:0044267|GO:0043687|GO:0005201 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_52008_PI430048170 0.2575116734476541.0378894526693 0.3301357785902160.282125293850912
0.399449304292446 A A A 0.2888701827463260.2683099016095020.295847073350546 A A A
LNCV6_52008_PI430048170 mRNA
AGGCTGCATGCACGGAGGCAGCTATATGCTGCCTGTGCCGTTTGCTTTGTCTTCATGGCT NM_003459 RefSeq chr2
- 27254571 27263092 SLC30A3 7781 "solute carrier family 30 (zinc transporter), member 3"
GO:0071577|GO:0043005|GO:0030054|GO:0061088|GO:0005770|GO:0015633|GO:0055085|GO:0008021|GO:0005
737|GO:0016020|GO:0005887|GO:0006810|GO:0030672|GO:0051050|GO:0005768 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140111_PI430048170 0.7161957654193280.8756997485306151.80536503571432
1.81324905280624 0.728576287113119 A A A 1.76690564519251 0.994090476538038
2.17044064604165 A A A LNCV6_140111_PI430048170 mRNA
CCCCAAACCTCGGACCAATATCCCTCTAAACATCAATCTATCCTCCTGTTAAAGAAAAAA NM_001206609 RefSeq
chr12 - 108621903 108632078 SELPLG 6404 "selectin P ligand, transcript variant 1"
GO:0005515|GO:0016020|GO:0005886|GO:0007596|GO:0005887|GO:0005102|GO:0071354|GO:0016021|GO:0050
900|GO:0007155|GO:0050901|GO:0050902 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71725_PI430048170 0.884787988255057 1.02740475359289 3.08697563725688 2.75762506199733
3.32807365967205 A A P 3.28940208359455 2.89528352101043 2.88961988136705 P P P
LNCV6_71725_PI430048170 mRNA
TCGTGAAGAAGGGACTCAATTTCGGTACCAGGACCACACATTTTTAAAGATGCTCCTCAC NM_014825 RefSeq chr21
- 32311018 32393003 URB1 9875 URB1 ribosome biogenesis 1 homolog (S. cerevisiae)
GO:0008150|GO:0005730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140743_PI430048170 0.378164691502091 1.1378187718891 9.23590249634339
9.24702693217882 9.64017927824346 P P P 9.11933105797574 9.00019967170643
9.44507994161507 P P P LNCV6_140743_PI430048170 mRNA
TGGGACTGAGCTGTACAGTATGGTTGCCCCTATCCAAGTGTCGCTATTTAAGTTAAATTT NM_001136015 RefSeq
chr15 - 60347150 60397986 ANXA2 302 "annexin A2, transcript variant 4"
GO:0008092|GO:0005515|GO:0006900|GO:0005765|GO:0005615|GO:0035749|GO:0044354|GO:0030199|GO:0005
938|GO:0070062|GO:0005811|GO:0042470|GO:0017137|GO:0009986|GO:0005509|GO:0005546|GO:0030496|GO:0
043086|GO:0005604|GO:0043234|GO:0045121|GO:0042730|GO:0019897|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143690_PI430048170 0.4090960811700751.15126051148959 12.6655813795102
12.6335477988506 12.8300711461412 P P P 12.0488862617725 12.5607260583313
12.8156288613192 P P P LNCV6_143690_PI430048170 mRNA
AAGATGGGAAACTGAATAAAGCAGTTGATCAGCATCATTGGAACATGGGGACGAGTGACG NM_014220 RefSeq
chr3 - 149369017 149377781 TM4SF1 4071 transmembrane 4 L six family member 1
GO:0008150|GO:0003674|GO:0005887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138369_PI430048170 0.00126879323274798 0.1711104093453391.60582577270288
1.0880388990231 1.80765098765887 A A A 3.60634878947871 4.37511428731625
4.14895904379664 P P P LNCV6_138369_PI430048170 mRNA
CAGAGGTTTGTTTTAGAACTGAAGGCAATTTAATCAAAATTCCTGTCAAGAAAAGCTGCT NM_175061 RefSeq chr7
- 27830573 28180818 JAZF1 221895 JAZF zinc finger 1
GO:0017053|GO:0003714|GO:0005634|GO:0000122|GO:0003676|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144210_PI430048170 0.131446980540897 1.0441024778216 0.359777995261259
0.3908084450852580.302816915407594 A A A 0.2829974997430380.301971865405208
0.282936888184507 A A A LNCV6_144210_PI430048170 mRNA
TTCGTGGGGGTCAAGTTCCGCACACACCTGAAACATGTTCTCCGGCAGTTCTGGTTCTGC NM_005283 RefSeq chr3
- 46020798 46027487 XCR1 2829 "chemokine (C motif) receptor 1, transcript variant 1"
GO:0070098|GO:0051209|GO:0006954|GO:0007186|GO:0006935|GO:0005886|GO:0007187|GO:0005887|GO:0004

950|GO:0007204 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127826_PI430048170 0.0522737516434081 0.5191486023708828.13786910362042
7.97364284273747 8.5305731299263 P P P 8.62899754106286 9.24687108821717
9.52278113439431 P P P LNCV6_127826_PI430048170 mRNA
GTGGCAAGATGAGAGTAAAACCAGAGAGCAAACCTCTATAAGTGTTGAGTATATGTATAC NM_001237RefSeq chr4
- 121816443 121823933 CCNA2 890 cyclin A2
GO:0005515|GO:0007095|GO:0019901|GO:0010389|GO:0031100|GO:0005634|GO:0007265|GO:0048146|GO:0000
079|GO:0005737|GO:0007067|GO:0001939|GO:0033762|GO:0000086|GO:0005654|GO:0001940|GO:0045893|GO:0
000278|GO:0032355|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129560_PI430048170 0.143512915222653 0.905427031555089 12.8149253088919 13.023725711615
12.8576751543746 P P P 13.023725711615 13.0700523868743 13.0406881596988 P P P
LNCV6_129560_PI430048170 mRNA
CCCAGACGGGCTTCTGCATCCATTCCCTCTTTTTGTTTTTAAAATAAATTGTATTTTTGA NM_146388RefSeq chr19 +
10251963 10260060 MRPL4 51073 "mitochondrial ribosomal protein L4, transcript variant 3"
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0022626|GO:0005743|GO:0006
412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72988_PI430048170 0.104119793683253 1.35031128353116 4.49172752296312 4.54770039523679
4.20877643989995 P P P 3.96904255527533 4.26671546591575 3.67430339435276 P P P
LNCV6_72988_PI430048170 mRNA
CCTTGCTGGAGAATTTGGCCACAAAGAGTTGCCAAGATAGCTGGGCCAGGAAGAAAGCGC NM_001199161
RefSeq chr3 - 49108045 49120938 USP19 10869 "ubiquitin specific peptidase 19, transcript variant
2"
GO:0005515|GO:0016579|GO:0034976|GO:0004843|GO:0030433|GO:0048642|GO:0046872|GO:0005829|GO:0090
068|GO:0004197|GO:1900037|GO:0031647|GO:0061136|GO:0005789|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128118_PI430048170 0.422630884732613 1.07490661418349 0.298624251529459
0.628890685504193 0.401536358880571 A A A 0.365471198745126 0.312761466173213
0.357665520312115 A A A LNCV6_128118_PI430048170 mRNA
CTCCAAGTCTTCAGCGAGACCCTTGCATTAGAAACTGAAAACTGTAAATACAAAATAAAA NM_001048RefSeq chr3
- 187668905 187670413 SST 6750 somatostatin
GO:0030334|GO:0008285|GO:0009408|GO:0007584|GO:0042493|GO:0007586|GO:0007267|GO:0007268|GO:0005
576|GO:0048545|GO:0006972|GO:0005615|GO:0005179|GO:0007186|GO:0043025|GO:0043200|GO:0007166|GO:0
008628 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115026_PI430048170 0.598716376550385 1.02693927814729 0.303327410178202
0.311126834165853 0.479662408138067 A A A 0.338942997654598 0.296632566102021
0.349910073311402 A A A LNCV6_115026_PI430048170 mRNA
CAGATGATGAGGTGAAGGTGACAGTGGTGGGAAATGAAAACAATTCTCTGTTGATAGAGT NM_021082RefSeq chr3
+ 121894323 121944187 SLC15A2 6565 "solute carrier family 15 (oligopeptide transporter), member 2,
transcript variant 1"
GO:0005515|GO:0005886|GO:0015031|GO:0055085|GO:0005887|GO:0006810|GO:0042891|GO:0015893|GO:0042
895|GO:0015333|GO:0042936|GO:0015334|GO:0070062|GO:0042938|GO:0006811|GO:0015992 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127048_PI430048170 0.0175081300290688 0.638423752241644 7.45185056489883
7.63675909665301 7.76102680281244 P P P 8.00752453008929 8.36988752815923
8.39912522541658 P P P LNCV6_127048_PI430048170 mRNA
TGATGGGGCTGTTTTCTCACAATATAAACGAATAAAGTGTCTTCTGGCCTACTTCTGAAA NM_007033RefSeq chr1
+ 2391774 2405446 RER1 11079 retention in endoplasmic reticulum sorting receptor 1
GO:0003674|GO:0030173|GO:0005793|GO:0005794|GO:0009986|GO:0006890|GO:0033130|GO:0071340|GO:0090
004 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137399_PI430048170 0.1600021951508871.14003731284757 7.36673645598165
7.42099377405561 7.45936836272368 P P P 7.32537756929819 7.30017193565357
7.03871674181946 P P P LNCV6_137399_PI430048170 mRNA
TTGCTACAGAATCTGACTCTGCAAGAGATTACCTTCTCCTTCTGCCGTCTGTTTGAGAAG NM_006369RefSeq chr1
- 46278399 46303366 LRRC41 10489 leucine rich repeat containing 41
GO:0005737|GO:0016567|GO:0016020|GO:0005634|GO:0042803 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129540_PI430048170 0.0279364632690527 0.5283675538423226.35242158971632
6.17034008390139 6.30276776680733 P P P 6.8494547694635 7.22161901969698
7.45774598726104 P P P LNCV6_129540_PI430048170 mRNA
GAGAGAATAATGCATTCTCCCCTTGCTGTGTATGACATGGAACAGTATGACCATTGCACT NM_031490RefSeq chr16
+ 48244166 48353979 LONP2 83752 "lon peptidase 2, peroxisomal, transcript variant 1"
GO:0005515|GO:0014070|GO:0031998|GO:0004252|GO:0005782|GO:0006625|GO:0005102|GO:0005634|GO:0002
020|GO:0005524|GO:0016020|GO:0016485|GO:0004176|GO:0007031|GO:0006515|GO:0008233|GO:0019899|GO:0
016558|GO:0005777. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130602_PI430048170 0.2461443285863931 1.3917320607393 2.57888446513025 6.3651611791784
1.62009706227393 A P A 1.12722220164025 2.2157792245717 0.264106030339907A A A
LNCV6_130602_PI430048170 mRNA
CAATCTCAGACTTACCAAAGTTAAAGTTGAGAAAGCTTGAACTAAGAGTCTCAGGGGGCC NM_012403RefSeq chr4
- 164197006 164197711 ANP32C 23520 "acidic (leucine-rich) nuclear phosphoprotein 32 family,
member C" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108499_PI430048170 0.0783975790837949 0.9319147753717570.301648220965065
0.3037280261453770.307175705952788A A A 0.4618245068569820.395386044016288
0.358634872085733A A A LNCV6_108499_PI430048170 mRNA
TTGTTCAACATGAGAGAACTCATACAGCTGAAAAACACTTTGAATGTAAAGAATGTGGGA NM_181845RefSeq chr19
+ 43827320 43848898 ZNF283 284349 "zinc finger protein 283, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138042_PI430048170 0.3548815294836021.02787431594356 0.297767009942423
0.3046018936916040.398927843590817A A A 0.3098071945818410.288787654620467
0.285823217225429A A A LNCV6_138042_PI430048170 mRNA
GTGAACTGAAACATTGTCTAATGTCTTTGTGGCTTTAGAGCTTTTGTTATATTGTGCCTANM_020927RefSeq chr16 +
77788563 77980107 VAT1L 57687 vesicle amine transport 1-like GO:0016491|GO:0008270|GO:0055114
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143477_PI430048170 0.1194133400375640.8149043356837235.03614422707523
5.05018633645537 5.0468006103864 P P P 5.1182628120454 5.39599098438331
5.48044323951224 P P P LNCV6_143477_PI430048170 mRNA
GCTTTGAGAGTGTCCTGATCCCTGCAAAGCCTCTAATAAATTGGTCATTTGGGCAAAAAA NM_001142964 RefSeq
chr22 + 41690542 41698136 C22orf46 79640 chromosome 22 open reading frame 46 GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64933_PI430048170 0.4364992042944221.13939835122232 5.01277365154464 4.72952775554737
4.4429380788227 P P P 4.45855830527729 4.79965005810784 4.38335754325636 P P P
LNCV6_64933_PI430048170 mRNA
TCTTTAAGAAAGCTGGCCACCCCTTCATGTGGAACCAGCACCTGGGCTACGTGCTCACCT NM_001824RefSeq chr19
- 45306412 45322977 CKM 1158 "creatine kinase, muscle"
GO:0004111|GO:0034641|GO:0016310|GO:0046314|GO:0006600|GO:0044281|GO:0005524|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139185_PI430048170 0.7631970716057390.9851292663721010.503636566944958
0.5092859012426260.386439236809198A A A 0.3868514038920640.550538386178096

0.524807906399268 A A A LNCV6_139185_PI430048170 mRNA
CACCTGAGTCTAACAGCAGTTTGACTTTGTTGTACAATACAGCAAGTGATCATCAAAAAA NM_001012980 RefSeq
chrX - 85092285 85108968 SATL1 NA spermidine/spermine N1-acetyl transferase-like 1 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139348_PI430048170 0.295591997351386 1.01857216773093 0.329478977068689
0.311581874469948 0.266278462702291 A A A 0.276018487093278 0.281583898077301
0.270805554504066 A A A LNCV6_139348_PI430048170 mRNA
GCGTGCTGTATGAATCTAGAAAGCCTTAATTTACTACCAAGAAATAAAGCAATATGTTCG NM_012304 RefSeq chr5
+ 15500195 15939796 FBXL7 23194 "F-box and leucine-rich repeat protein 7, transcript variant 1"
GO:0006511|GO:0007067|GO:0005813|GO:0005737|GO:0004842|GO:0016567|GO:0008283|GO:0000086|GO:0000
151|GO:0031146|GO:0019005|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129653_PI430048170 0.91996721052597 0.986613372548417 11.8796814552081
11.8066574240366 11.7959380432023 P P P 11.7019835321246 12.0458011195021
11.7708985423168 P P P LNCV6_129653_PI430048170 mRNA
GTAAATCAGCTGTGTGGTGCCCGCGTGGCTGGAAGGAAATAGACCCTTTTGTAGCTCCCT NM_002969 RefSeq chr22
- 50252901 50261759 MAPK12 6300 "mitogen-activated protein kinase 12, transcript variant 1"
GO:0005515|GO:0007265|GO:0005829|GO:0005739|GO:0042692|GO:0005737|GO:0018105|GO:0000165|GO:0007
050|GO:0045445|GO:0004707|GO:0048010|GO:0006355|GO:0048011|GO:0000287|GO:0006996|GO:0005524|GO:0
006351|GO:0006975|GO:0007165|GO:0010952|GO:0051149|GO:0007517|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140604_PI430048170 0.325411513541223 1.28675884311861 1.1029341036688
0.301503764958094 0.439803075394284 A A A 0.312821186047572 0.283166099918448
0.28943070976582 A A A LNCV6_140604_PI430048170 mRNA
ATCTATAGTTTGAGGAACAAGGAACTGAAAGATGCCCTAAGGAAAGCATTGAGAAAATTC NM_001005324 RefSeq
chr11 - 59712915 59713845 OR10V1 NA "olfactory receptor, family 10, subfamily V, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102803_PI430048170 0.39466907083255 1.25624076111226 0.97618293618148
1.51312341376825 1.23389634092562 A A A 1.56406634363254 0.286476417034221
0.617114293913604 A A A LNCV6_102803_PI430048170 mRNA
CGACAAAGCCTTCCATGACCTCGTTAGAGTAATTAGGCAACAGATTCCGGAAAAAAGCCA NM_012219 RefSeq chr3
+ 138347647 138405535 MRAS 22808 "muscle RAS oncogene homolog, transcript variant 1"
GO:0006184|GO:0030742|GO:0030036|GO:0007517|GO:0005886|GO:0003924|GO:0007275|GO:0007265|GO:0005
525|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111043_PI430048170 0.5147619820401 1.46821894673439 0.55031920211349 1.879664405818
0.324131349804012 A A A 0.459302557235535 0.611805830432871 0.539428668088697 A A A
LNCV6_111043_PI430048170 mRNA
TGATCCTCATAAAATACAGGAGGCTCCGAATTATGACCAACATCTACCTGCTCAACCTGG NM_001837 RefSeq chr3
+ 46242380 46266706 CCR3 1232 "chemokine (C-C motif) receptor 3, transcript variant 1"
GO:0005515|GO:0070098|GO:0005886|GO:0007204|GO:0045766|GO:0006968|GO:0006954|GO:0001938|GO:0006
935|GO:0005887|GO:0004950|GO:0016032|GO:0007188|GO:0016493|GO:0007155 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_94920_PI430048170 0.38322383760526 1.06895887748329 11.6163720951523 11.7805984090859
11.5323923737409 P P P 11.6152481474056 11.6090144782996 11.4191385555158 P P P
LNCV6_94920_PI430048170 mRNA
AAATGGCTGCACTGGCCGATTCTGGTCTCCAGAGGACCTTGGTGTTTGCTCTCCCTTGAC NM_006634 RefSeq chr2
+ 85584407 85593388 VAMP5 10791 vesicle-associated membrane protein 5
GO:0005802|GO:0048471|GO:0005886|GO:0009986|GO:0043001|GO:0005770|GO:0031201|GO:0006887|GO:0006
906|GO:0030154|GO:0007269|GO:0008021|GO:0005484|GO:0007517|GO:0014704|GO:0031301|GO:0005887|GO:0
007519|GO:0000149|GO:0030659|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_101437_PI430048170 0.000416921939729736 0.6439686097909267.24707176684834
7.2315799294789 7.12990101068923 P P P 7.78517616355753 7.80391325569883 7.923144821631
P P P LNCV6_101437_PI430048170 mRNA
CAGCAGTTTTCCATTTCTCCACAGTATCCTTTTCATTTAGAGGAGCTTAATAAATGCTTT NM_207396RefSeq chr1 +
6206128 6221299 RNF207 388591 ring finger protein 207 GO:0005622|GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136965_PI430048170 0.3009494356543191.1173680994489 6.76219500502629
6.94002096591073 6.8507955275703 P P P 6.54920321238035 6.57161399150953
6.92564981530512 P P P LNCV6_136965_PI430048170 mRNA
AATCCCATACTCCAAACTGTCTCAGTCGAAGCACCTAAAGGCCAGGACGGGCGGTAGCCA NM_001039999 RefSeq
chr17 - 18971067 19004747 FAM83G NA "family with sequence similarity 83, member G" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136443_PI430048170 0.3763641675249731.10929918443413 0.441485427255047
0.4359078614028990.8087296361536 A A A 0.3836418146509560.464922981249718
0.419942430132578A A A LNCV6_136443_PI430048170 mRNA
TTTTGGGAACATAAGGAGGTATACAGAACTGCAGACCTCTAAACATAAGTAGGAAAAAGA NM_014950RefSeq chr14
+ 64504573 64533690 ZBTB1 22890 "zinc finger and BTB domain containing 1, transcript variant 2"
GO:2000176|GO:0033077|GO:0046982|GO:0048538|GO:0005634|GO:0000122|GO:0032825|GO:0002711|GO:0003
677|GO:0046872|GO:0042803|GO:0016604|GO:0045087|GO:0030183|GO:0051260|GO:0005654|GO:0042789|GO:0
045582 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131378_PI430048170 0.0489465531535147 1.36511137144729 12.1434609698831
12.1345202827299 11.9982765541976 P P P 11.4287373738342 11.8481595710602
11.6262939442092 P P P LNCV6_131378_PI430048170 mRNA
CGAACCCGTGGAGCAATGCCCTGTCTGGCCTCCAAAACCAAAATAAAACTGGGTCACTTT NM_133467RefSeq chr1
- 40861055 40862346 CITED4 163732 "Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-
terminal domain, 4" GO:0043627|GO:0005737|GO:0003713|GO:0005634|GO:0045893|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_94765_PI430048170 0.0429457996534375 1.26703133283332 5.91663252988369
6.12073332927152 6.22266531607119 P P P 5.81001574197811 5.64161432813748
5.79473456710441 P P P LNCV6_94765_PI430048170 mRNA
AGGACTATTAAGATTGATAGAAGATTGACGGGTGCCAATATAATTGATGAACCTCTCCAG NM_015132RefSeq chr7
- 17790760 17940508 SNX13 23161 sorting nexin 13
GO:0043547|GO:0031901|GO:0038032|GO:0032266|GO:0035091|GO:0006886|GO:0005769 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_106492_PI430048170 0.00822349593588623 1.51881417885124 11.2798193872467
11.3704602879555 11.4977207146902 P P P 10.822582780335 10.5972108377194
10.9099411977971 P P P LNCV6_106492_PI430048170 mRNA
ACACTGTATGAAGTATATGTTGATACTATGACATGTTGCCAACACCTTGAGAAGCATTAT NM_006754RefSeq chr7
- 106090367 106112647 SYPL1 6856 "synaptophysin-like 1, transcript variant 1"
GO:0042470|GO:0005215|GO:0030285|GO:0005887|GO:0006810|GO:0007268|GO:0016021|GO:0030141|GO:0030
659|GO:0070062|GO:0008021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130435_PI430048170 0.0221332913792257 1.08884470266993 0.410013412432553
0.4815719185428330.491200893518434A A A 0.3113849785919670.339358087073087
0.364515096868206A A A LNCV6_130435_PI430048170 mRNA
ACCACAGTGATCTCTATTTTCTCCCTTTGCCAAGGTTAATGAACTGTTCTTTTCAAATTC NM_005478RefSeq chr1 -
66797740 66801259 INSL5 10022 insulin-like 5 GO:0008150|GO:0005179|GO:0005576|GO:0005575 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62137_PI430048170 0.3399583564196181.18747079628427 3.82725724630506 4.36184729850078
3.87232643696114 P P P 4.04275157258716 3.73207378739096 3.56462404398556 P P P

LNCV6_62137_PI430048170 mRNA
CGGCGCGCAGGGGCAGCCTTCCACCACGGGGAGCCCAGCTGTCAGCCGCCTCACAGGAAG NM_001024736
RefSeq chr15 + 73684280 73714518 CD276 80381 "CD276 molecule, transcript variant 1"
GO:0005515|GO:0030501|GO:0008283|GO:0005102|GO:0042130|GO:0045669|GO:0045085|GO:0006955|GO:0042
110|GO:0045077|GO:0050728|GO:0045078|GO:0050776|GO:0042102|GO:0016021|GO:1900042|GO:0009897|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145219_PI430048170 0.3662914837333070.9687561873194080.249865719499288
0.26202833637899 0.370265851625154A A A 0.3848775988312940.321848244316081
0.314851883705731A A A LNCV6_145219_PI430048170 mRNA
GATGTGATTCCTCATTTTGCAGTGGTGCCTATAAAATAAAAGCCTTTTGCAGTGTTTAAA NM_015009RefSeq chr3
- 73382429 73624921 PDZRN3 23024 "PDZ domain containing ring finger 3, transcript variant 1"
GO:0004842|GO:0031594|GO:0016567|GO:0007528|GO:0016874|GO:0008270 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138019_PI430048170 0.5851997487408091.08780181314095 7.64316365018574
7.82927506025099 7.96871862561886 P P P 8.10111679957175 7.33966549829534
7.54353209985463 P P P LNCV6_138019_PI430048170 mRNA
AGGGGCTTTTCTGGATGGGATACATTGATATTTTATGGCCTTGAAACACTATCCTGATTA NM_001164407 RefSeq
chr17_KI270861v1_alt - 132817 140396 TLCD2 727910 TLC domain containing 2 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138254_PI430048170 0.0205724887961901 2.15894866540449 1.41614326183388
1.48686871555523 1.9584410769644 A A A 0.5934525768677170.497723229822082
0.499422421843653A A A LNCV6_138254_PI430048170 mRNA
TTCCCAATCTAAGCACTACAATCTGCCTTCAGCTTGCTTAGATTCTAGGTGTGCTTTTTT NM_001129890 RefSeq chr8
+ 91102618 91219236 LRRC69 NA leucine rich repeat containing 69 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145387_PI430048170 0.2317373744701921.0697647008567 11.4272119113217
11.5097289917143 11.5722611781201 P P P 11.3513985577994 11.3492099862723
11.5140974323961 P P P LNCV6_145387_PI430048170 mRNA
TTAGGATGACACAATGAATAACACCTAGTCATAGAAATCAGTCTCTCTGGTTTGTTTTGT NM_001171203 RefSeq
chr9 + 34179004 34252523 UBAP1 51271 "ubiquitin associated protein 1, transcript variant 2"
GO:0043130|GO:0005737|GO:0005794|GO:0000813|GO:0005886|GO:0015031|GO:0043162|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135197_PI430048170 0.0104450449582220.428370791827 4.08869341604796
3.43621848504202 3.81582080960034 P P P 4.62481972290142 5.14582361915318
5.23979389837582 P P P LNCV6_135197_PI430048170 mRNA
GTGGTTCCCTGATCCCTCAAAAATCCATTTGTTTTTGGATTTCCAAAAACGAACATTAAA NM_023070RefSeq chr1
+ 40450664 40463718 ZFP69B 65243 ZFP69 zinc finger protein B
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140376_PI430048170 0.00732002174000524 0.2058918257132081.28057431519267
0.55670832179215 1.33172116993153 A A A 3.60609580549238 2.63269781869008
3.67687179013484 P P P LNCV6_140376_PI430048170 mRNA
TGAAAAGACTTTACCATAGACAATAACATGCAGTTTTATCAGCACCAAAGAATGTTGTCC NM_022902RefSeq chr5
+ 69093948 69131072 SLC30A5 64924 "solute carrier family 30 (zinc transporter), member 5, transcript
variant 1"
GO:0071577|GO:0005794|GO:0005730|GO:0006882|GO:0005634|GO:0055085|GO:0010043|GO:0016324|GO:0005
385|GO:0016020|GO:0005887|GO:0006829|GO:0008270|GO:0010155|GO:0030141|GO:0044267|GO:0030667|GO:0
006824 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127463_PI430048170 0.00705901860573329 0.4531565391717863.60640244884062

4.1176135979089 4.05275206645809 P P P 4.98102096167078 4.84952278461478
5.37137868872016 P P P LNCV6_127463_PI430048170 mRNA
GCTCCTAGATACTTGGTGGTCAATAGAACTGATTTGATTAACTTTCATTTAACTGTGGTT NM_001287036 RefSeq
chr9 + 112486967 112665311 KIAA1958 158405 "KIAA1958, transcript variant 1" NA . NA -
NA NA NA NA NA NA NA NA NA NA
LNCV6_137431_PI430048170 0.2702553280727280.9633352044068080.24820774365819
0.2631922220279780.360658779160412A A A 0.3872277874143760.327867718521395
0.320301915442436A A A LNCV6_137431_PI430048170 mRNA
GTTGAATCATAGCTGGAAACAGAATTTATTTCCTCTATTTGCTTCATTCTGTCCTTCCAC NM_194455 RefSeq chr7 -
92198968 92246100 KRIT1 889 "KRIT1, ankyrin repeat containing, transcript variant 4"
GO:0005515|GO:0008017|GO:0005886|GO:0007264|GO:0005874|GO:2000114|GO:0005546|GO:0001525|GO:0032
403|GO:0005615|GO:0032092|GO:0010596|GO:0050790|GO:0005083|GO:0005737|GO:0001937|GO:0005911|GO:0
016525|GO:0045454|GO:2000352 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127005_PI430048170 0.1346966435225680.5582563759852291.17837587477238
0.7381476868766862.09064491321239 A A A 2.01652395405211 2.7114235410387
2.02717670404488 A P A LNCV6_127005_PI430048170 mRNA
CGTTGTTAACCTCGAAAACATACTTTGTTGGCTGCAAAAATAAACAAAGGGAAACTCAAA NM_022121 RefSeq chr6
- 138088504 138107523 PERP 64065 "PERP, TP53 apoptosis effector"
GO:0030057|GO:0005739|GO:0005794|GO:0002934|GO:0072332|GO:0097186|GO:0005887|GO:0034113|GO:0097
202|GO:0045862 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138740_PI430048170 0.8253660357869251.06430393008501 7.16911810225375
7.74370591988043 7.00130120109959 P P P 7.39751648750783 7.1059692523467
7.23476299479197 P P P LNCV6_138740_PI430048170 mRNA
GGAGGATTTGGGGTGGGGGTGGGGTGATTGAATATTTGTATAAAAAGCAAAAAGAAAAAA NM_006266 RefSeq
chr9 - 133097719 133121250 RALGDS 5900 "ral guanine nucleotide dissociation stimulator,
transcript variant 1"
GO:0043547|GO:0005903|GO:0005515|GO:0005085|GO:0051056|GO:0050790|GO:0048011|GO:0005083|GO:0007
265|GO:0005634|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127745_PI430048170 0.1085656823655490.82592886328754 10.0612664353795
10.4203909914158 10.3565728316772 P P P 10.4481977150374 10.6234486775356
10.6125609168079 P P P LNCV6_127745_PI430048170 mRNA
TATATGAAGAAATAGAAGAGGGGCTTGAAGTCCTCCTCGCGAGTGCCTTCTTGCAATTAC NM_001300887 RefSeq
chr19 - 10572670 10587315 AP1M2 10053 "adaptor-related protein complex 1, mu 2 subunit,
transcript variant 1"
GO:0030131|GO:0006892|GO:0006605|GO:0005765|GO:0032588|GO:0006903|GO:0050690|GO:0005829|GO:0043
231|GO:0019886|GO:0030665|GO:0000139|GO:0061024|GO:0016032|GO:0030659 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143039_PI430048170 0.9235372406024811.11986470357562 1.67073377610971
0.3501419609026240.332527935167938A A A 1.1395800559465 0.681417629878099
0.377173180374516A A A LNCV6_143039_PI430048170 mRNA
CATGTGTTCTGGATGTGAAATGTTACTGATCATTCTAGTTTACAAGGCTAAGAAAAGATG NM_001010893 RefSeq
chr8 - 81693655 81694972 SLC10A5 NA "solute carrier family 10, member 5" NA . NA -
NA NA NA NA NA NA NA NA NA NA
LNCV6_109704_PI430048170 0.0573798959202961.79482396674302 3.6847413280443
3.87457141448311 3.14298024739128 P P P 2.72727380081187 2.67003886778243
2.86235828349168 P P P LNCV6_109704_PI430048170 mRNA
ATGCAGCTGGACCCCCACAAGCTGGAGGTGGGTGCAAAGCTGGACCTGTTCGGCAGACCC NM_001142641
RefSeq chr12 + 132490570 132585187 FBRSL1 57666 fibrosin-like 1 NA . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_139259_PI430048170 0.2743850499938320.6258753607326821.71085932007086
0.3457797656471882.21107487509409 A A A 1.99259587702318 2.04420821831155
2.71255854794354 A A P LNCV6_139259_PI430048170 mRNA
TAGGTTGGGGTTGCAACATCTTTTAACTTCTCAGTTATTTGTATGTCAGGAGACAGATTG NM_019080RefSeq chr13
+ 79481123 79556077 NDFIP2 54602 "Nedd4 family interacting protein 2, transcript variant 1"
GO:0005515|GO:0048471|GO:0005794|GO:0005783|GO:0050699|GO:0032410|GO:0032585|GO:0051224|GO:0043
231|GO:0005739|GO:0007165|GO:0005737|GO:0000139|GO:0010629|GO:0031398|GO:0004871|GO:0016021|GO:0
043123 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141137_PI430048170 0.7074460222334551.12374184773948 1.13486699539065
0.2774437294264870.363380432637163A A A 0.3956792416507150.691598928413197
0.31834050278593 A A A LNCV6_141137_PI430048170 mRNA
CAACCCTTTGATGAGTGATATTTCCCTATACCTATGTACCCAGATAGATATATGCATAGA NM_173798RefSeq chrX
+ 118823823 118826968 ZCCHC12 170261 "zinc finger, CCHC domain containing 12"
GO:0030374|GO:0016607|GO:0008270|GO:0030509|GO:0003676|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126740_PI430048170 0.00838639099850188 0.5748025155817193.29621145523744
3.67390499549093 3.66194432466093 P P P 4.21559900547726 4.33081914192265
4.49905263844402 P P P LNCV6_126740_PI430048170 mRNA
CTCAGCCAAAAACACTTGGAAAGCATATTTTGGTATCTGCATTGCTTTGCATATCTAAAT NM_024725RefSeq chr11
- 96352764 96389919 CCDC82 79780 coiled-coil domain containing 82 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_130453_PI430048170 0.4883322081316640.9550909187143150.2956043719506
0.4398553683892460.305592540805535A A A 0.52278863155944 0.427329227413946
0.284433053399802A A A LNCV6_130453_PI430048170 mRNA
ACTTTCCCATAGCAAATAGCATACCTGACTCTCTGTGCTAATATTGCACATTTGTTAAAC NM_004525RefSeq chr2
- 169127108 169362612 LRP2 4036 low density lipoprotein receptor-related protein 2
GO:0006629|GO:0005515|GO:0017124|GO:0005886|GO:0007603|GO:0005783|GO:0008283|GO:0030139|GO:0044
281|GO:0031526|GO:0005765|GO:0005764|GO:0016324|GO:0008202|GO:0070062|GO:0005794|GO:0042359|GO:0
005509|GO:0001523|GO:0006898|GO:0006897|GO:0043235|GO:0005905|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_54985_PI430048170 0.1076071371332681.2449977930332 8.37302854178085 8.23241852867859
8.281510097169 P P P 8.13569022103063 8.04715109306889 7.7281818626454 P P P
LNCV6_54985_PI430048170 mRNA
ACCCTTAAGCCCCAGGCTCCCCGTTTACCTCAGAGACGTCTATTTTTGTGTCTTTTTAAT NM_001014443 RefSeq
chr1 + 161159463 161165726 USP21 27005 "ubiquitin specific peptidase 21, transcript variant 3"
GO:0016578|GO:0006355|GO:0004843|GO:0005886|GO:0003713|GO:0005575|GO:0046872|GO:0006351|GO:0004
197|GO:0019784|GO:0005737|GO:0061136|GO:0005654|GO:0043161|GO:0008234|GO:0045893 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138839_PI430048170 0.7810300510659930.8173647438689071.03956833018487
0.4153431379131831.21213298860848 A A A 1.95452092678641 0.300142472159409
0.906018687904543A A A LNCV6_138839_PI430048170 mRNA
TAAAGTGTCATGATTCTGTCATAGACCCTGACTTAACATTGTAAGGACTATGAGTCCTCC NM_198859RefSeq chr3
- 64093849 64225455 PRICKLE2 166336 prickle homolog 2 (Drosophila)
GO:0031965|GO:0005737|GO:0008270|GO:0016328|GO:0031175|GO:0016327|GO:0045197 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137161_PI430048170 0.7999396864501790.9908350565364780.424003521796098
0.4742082745853540.379398977678416A A A 0.5144557567204250.394119894126049
0.407402970376107A A A LNCV6_137161_PI430048170 mRNA
CCCTGTTGTGCAGGCACAAATATTTCCTGAAATAAATGTTTTGGACATAGAAACAGAAAA NM_022355RefSeq chr16

- 67987389 67999518 DPEP2 64174 dipeptidase 2
GO:0008235|GO:0006508|GO:0031225|GO:0008239|GO:0016805|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136418_PI430048170 0.00625745402685924 0.5024283512783456.62135342021412
6.2621929327669 6.58977439602687 P P P 7.25583477405164 7.44122395085033 7.7401431222062
P P P LNCV6_136418_PI430048170 mRNA
GTTGAGGCTCCTCAGTTTTAGTGCTGAAATAATAAACAGTGACAGGTCAACAGTAAAAAA NM_004555RefSeq chr16
+ 68085365 68229259 NFATC34775 "nuclear factor of activated T-cells, cytoplasmic, calcineurin-
dependent 3, transcript variant 2"
GO:0071285|GO:0005515|GO:0001569|GO:0006357|GO:0006366|GO:0005730|GO:0005634|GO:0000978|GO:0005
829|GO:0007507|GO:0045333|GO:0001077|GO:0005737|GO:0006954|GO:0045944|GO:0045087|GO:0003682|GO:0
071277|GO:0005654|GO:0055001|GO:0038095|GO:0051145 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_74692_PI430048170 0.8014596508424870.9503250037146460.8637431713411020.895087752362115
0.919351397652862A A A 0.6748001933285961.28140023541963 0.875630282320721A A A
LNCV6_74692_PI430048170 mRNA
AGATTGGTTTCATTCCAGATATGTATTTCCACTACACAAAATTTTCCACCTCTGGGATAC NM_001290768 RefSeq
chr4 - 106044316 106316266 TBCK 93627 "TBC1 domain containing kinase, transcript variant 5"
GO:0004672|GO:0032851|GO:0006468|GO:0005524|GO:0005097 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143085_PI430048170 0.0266701781857421 0.69508693031192211.3405597655816
11.3949710139256 11.4792100106548 P P P 11.7842060898739 11.8556779841971
12.1290610137529 P P P LNCV6_143085_PI430048170 mRNA
GCCTTCAGTGAATATTGGTTTCTCTTTGGTATGTCAATAAAAGTTTATCCGTATGTCAGA NM_004577RefSeq chr7
- 56011050 56051575 PSPH 5723 phosphoserine phosphatase
GO:0043005|GO:0000287|GO:0005509|GO:0008652|GO:0044281|GO:0033574|GO:0042803|GO:0004647|GO:0005
829|GO:0009612|GO:0034641|GO:0005737|GO:0016311|GO:0031667|GO:0006564|GO:0006563 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126769_PI430048170 0.000770178300759273 1.57880570760632 9.79796772834341
9.82711099690339 9.69242054308365 P P P 9.0439980524944 9.2158485219184
9.07882831047169 P P P LNCV6_126769_PI430048170 mRNA
TCGTGTTTTCGACTTGACCTTGTGGTATTTTTCTTGGCCTAGTTGTGTGCCATGGATATT NM_013337RefSeq
chr17_KI270910v1_alt + 36363 41397 TIMM2229928 translocase of inner mitochondrial membrane 22
homolog (yeast) GO:0045039|GO:0006626|GO:0005743|GO:0016021|GO:0044267|GO:0015266 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127500_PI430048170 0.4603540649078951.82684752093313 2.32226367481168
0.51801050352024 0.348150120187381A A A 0.3933080080162170.559590192107922
0.517005188781203A A A LNCV6_127500_PI430048170 mRNA
GAAACCCTTACATTATGCTATGAAGAGTAGTAATAATAGCAGCTCTTATTTCCTGAGCAA NM_000762RefSeq chr19
- 40843537 40850447 CYP2A6 1548 "cytochrome P450, family 2, subfamily A, polypeptide 6"
GO:0005881|GO:0008392|GO:0006805|GO:0005506|GO:0017144|GO:0008395|GO:0019373|GO:0009804|GO:0044
281|GO:0008389|GO:0043231|GO:0046226|GO:0019825|GO:0042738|GO:0005789|GO:0016712|GO:0019899|GO:0
008202|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53195_PI430048170 0.3231543608989270.5330632621849470.2902390514555460.285020113024711
0.437424133805981A A A 0.3169708939317830.7030404383562012.0862532993372 A A A
LNCV6_53195_PI430048170 mRNA
GGGAATGTGAATTTTTACCGTTTGTACTTAAGATACATTTGTTGTCTAAAATGGCTCTGG NM_198581RefSeq chr2
+ 112275600 112340063 ZC3H6 376940 zinc finger CCCH-type containing 6
GO:0008150|GO:0003674|GO:0005575|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_128407_PI430048170 0.8412077304196741.06484723581663 1.7226331633963
0.6317093344084251.61817583981847 A A A 1.87675993733675 1.16549018704539
0.60574906263995 A A A LNCV6_128407_PI430048170 mRNA
GCCCTCCTGAAACTTACACACAAAACGTTAAGTGATGAACATTAAATAGCAAAGAAAGAA NM_002507RefSeq chr17
+ 49495292 49515020 NGFR 4804 nerve growth factor receptor
GO:0005515|GO:0005886|GO:0031293|GO:2001235|GO:0021675|GO:0048146|GO:0006886|GO:0005829|GO:0031
069|GO:0007411|GO:0004872|GO:0004871|GO:0031625|GO:0048011|GO:0043066|GO:0017137|GO:0043065|GO:0
048406|GO:0009986|GO:0005576|GO:0042593|GO:0045786|GO:0007417|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138373_PI430048170 0.0742745868470015 0.7197402118926419.47188195200174
9.54286285130348 9.28207788113559 P P P 9.63089082305558 10.1589613154242
9.89456749260868 P P P LNCV6_138373_PI430048170 mRNA
AGTAAACATTCCAAGTAAGCGTCTTAACACCTAACCCCAAAGGCTCTTTTAAGAGCCACC NM_003526RefSeq chr6
- 26123466 26123904 HIST1H2BC 8347 "histone cluster 1, H2bc"
GO:0046982|GO:0050830|GO:0019731|GO:0006334|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0005
615|GO:0003677|GO:0070062|GO:0002227 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142972_PI430048170 0.1547208485712350.7350482190277351 0.0881656302762 10.013722156927
10.0825477459227 P P P 10.1035144030327 10.6541031233881 10.6890188131323 P P P
LNCV6_142972_PI430048170 mRNA
GACTTGTATTGGCCACCAACTGTAGATGTATATATGGTGCCCTTCTGATGCTAAGACTCC NM_000304RefSeq chr17
- 15229776 15265357 PMP22 5376 "peripheral myelin protein 22, transcript variant 1"
GO:0005515|GO:0008219|GO:0008285|GO:0005886|GO:0043218|GO:0007422|GO:0032060|GO:0010977|GO:0007
268|GO:0016021|GO:0005923|GO:0032288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131161_PI430048170 0.0664350198322401 0.6904849958519173.99344898908464
3.94373601723907 4.06436625888023 P P P 4.29566927751684 4.46227714961896 4.802173050096
P P P LNCV6_131161_PI430048170 mRNA
ATGCACCTGCTCTGGGAACTACTTGTCTTTAGTTAGTAGAACTGTTTTATTTCAACTAAT NM_024942RefSeq chr10
- 122930902 122954403 C10orf88 80007 chromosome 10 open reading frame 88 GO:0042802 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81674_PI430048170 0.1010195771628710.4612053247287440.3792216059116891.05534225367649
1.98320857535688 A A A 1.93987843329807 2.37221988829935 2.783371892227 A A P
LNCV6_81674_PI430048170 mRNA
CTTTTTGTCACTAATGAGAGTAATTCACGAAAGACCTACATAGTACATTGCCAAGATTGT NM_001291415 RefSeq
chrX + 44873174 45112612 KDM6A 7403 "lysine (K)-specific demethylase 6A, transcript variant 1"
GO:0010468|GO:0006325|GO:0001843|GO:0051213|GO:0005634|GO:0000978|GO:0001701|GO:0048570|GO:0046
872|GO:0042802|GO:0003007|GO:0003016|GO:0035097|GO:0032525|GO:0035264|GO:0071557|GO:0005654|GO:0
048333|GO:0060070|GO:0051568|GO:0071558|GO:0055114 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_128381_PI430048170 0.2250619789868620.9085839625060630.316176662373798
0.3520471887924950.334595104281632A A A 0.4168147061636820.621226840520576
0.367174965088549A A A LNCV6_128381_PI430048170 mRNA
TAGGAACAAAGAAGTGAAAAGTGCTCTCTGGAAAATACTCAACAAACTTTACCCCCAATA NM_001005218 RefSeq
chr11 - 58507175 58508105 OR5B21 NA "olfactory receptor, family 5, subfamily B, member 21" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136546_PI430048170 0.9110185858775110.9985538544269580.402357728457308
0.4036120371917580.377702192279407A A A 0.4181528791591710.369693165091061
0.40181657061397 A A A LNCV6_136546_PI430048170 mRNA
TATTGGACTCTTGATCCGAACTGCGAGAAAATGTTTGACAATGGGAACTTCCGTCGGAAG NM_001135649 RefSeq
chr2 - 88448206 88452535 FOXI3 344167 forkhead box I3

GO:0043565|GO:0006355|GO:0003700|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144003_PI430048170 0.0158791935648556 1.0760082510528 0.393590279929833 0.386727085661625 0.339769732186733 A A A 0.252832004759747 0.30660876383172 0.243361622566465 A A A LNCV6_144003_PI430048170 mRNA AGTAAATATCAGAATTTTATGGTTTGACCAGCGCTTATCACATTCCCAATTCAGTGAGAA NM_024763 RefSeq chr1 - 66812885 66924887 WDR78 79819 "WD repeat domain 78, transcript variant 1" GO:0002244 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127694_PI430048170 0.263766632020332 1.01913158330248 0.304568573238343 0.260769019600867 0.320268618618531 A A A 0.275104277099946 0.258994980747957 0.27009597920602 A A A LNCV6_127694_PI430048170 mRNA CAATGTGAAGATGGCATTTCAGTGTTTATTTCTGGATCTATGAGTTACTTTAGCAGAGTT NM_032511 RefSeq chr6 - 99272916 99349655 FAXC 84553 failed axon connections homolog (Drosophila) GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143606_PI430048170 0.885510918215769 1.01659569911101 5.16497160354018 5.05336081711708 5.49665195236669 P P P 5.21438518209148 4.8703373451101 5.52328975236924 P P P LNCV6_143606_PI430048170 mRNA TGAACTATATTGTATGTAATTTGGAAGTCGTGTTAATAAAACCCTGCAGTTTCCACTCTG NM_053043 RefSeq chr7 + 155644508 155781485 RBM33 155435 RNA binding motif protein 33 GO:0000166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131060_PI430048170 0.0388581303646604 0.316839922266601 0.354142223380399 0.514738351955616 1.70892116436571 A A A 1.86363878264121 2.82171007899553 3.02722563585925 A P P LNCV6_131060_PI430048170 mRNA CGTCCTGTTTTCTTTGCCTAGTATTAGCACCACAGGTACATATTTGTAAAATAAGCATTA NM_031844 RefSeq chr1 - 244850299 244864525 HNRNPU 3192 "heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A), transcript variant 1"
GO:0005515|GO:0008380|GO:0006396|GO:0010467|GO:0070934|GO:0009986|GO:0003723|GO:0001047|GO:0005634|GO:0071013|GO:0003677|GO:0005524|GO:0032922|GO:0001649|GO:0016020|GO:0000398|GO:0030529|GO:0005654|GO:0070937. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138451_PI430048170 0.0944533131348252 0.794229869470271 5.63476551231145 5.5145577915147 5.7998912566895 P P P 5.74170116938279 6.06856784946366 6.12177903951679 P P P LNCV6_138451_PI430048170 mRNA TTGTCGTTATTTCTGAGTATTATTTGGATGGTTCATTTTGACTTAAGGATAGCCCTGTGA NM_033204 RefSeq chr19 + 19668787 19683506 ZNF101 94039 "zinc finger protein 101, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136068_PI430048170 0.335545481361852 0.683537965241306 2.9936894859696 1.40288077000374 3.19964693224276 P A P 3.59881093621628 3.17730753333018 2.96351299606757 P P P LNCV6_136068_PI430048170 mRNA AGAGATAGGAAAACTTGCCGCCTCTTCTTTTTTGTCCCTTAATCAAACTCAAATAAGCTT NM_024915 RefSeq chr8 + 101492439 101669724 GRHL2 79977 grainyhead-like 2 (Drosophila)
GO:0003700|GO:0008283|GO:0005634|GO:0048701|GO:0051973|GO:0035264|GO:0070830|GO:0005911|GO:0044030|GO:0043010|GO:0007155|GO:0003382|GO:0006357|GO:0034329|GO:0001843|GO:0090132|GO:0003208|GO:0001701|GO:0006351|GO:0043565|GO:0007420|GO:0060324|GO:0060463|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106683_PI430048170 0.279796027647089 1.85442038477671 0.369306966410995 2.03158646067883 0.901776581950557 A A A 0.409114455331142 0.348832831677547 0.386748419137146 A A A LNCV6_106683_PI430048170 mRNA TTTTTCCTGAGTAGGGCTTAGTTTTATTCTGGAAAGACATCTCCAAGGTGGACCCGGTCT NM_080538 RefSeq

chr3 - 15450132 15498872 COLQ 8292 "collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase, transcript variant II"
GO:0005515|GO:0005581|GO:0030054|GO:0008105|GO:0005605|GO:0001507|GO:0045202|GO:0005615 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_129657_PI430048170 0.0329133826441445 0.376397694698136 4.407032494407
4.34898209341287 4.64614287566056 P P P 5.38785632614959 5.71367148565363
6.36946921734701 P P P LNCV6_129657_PI430048170 mRNA
GAGAAGAATTTGAAGGATATGAACATTTTCAAGAACTCTGCTGAGGTCACTTAGAGCGCC NM_182643 RefSeq
chr8 - 13083362 13514920 DLC1 10395 "DLC1 Rho GTPase activating protein, transcript variant 1"
GO:0005515|GO:0008285|GO:0030036|GO:0007264|GO:0008360|GO:0035024|GO:0005634|GO:0021575|GO:0005
829|GO:0008289|GO:0005737|GO:0048041|GO:0032956|GO:0030675|GO:0042169|GO:0051056|GO:0030336|GO:0
006919|GO:0035307|GO:0006915|GO:0001843|GO:0005100|GO:0051497|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131117_PI430048170 0.731573044424348 0.890606396869122 1.75588550186368
0.504129326455496 1.97079298871996 A A A 1.86472636684546 0.92193758151505
2.08722944523324 A A A LNCV6_131117_PI430048170 mRNA
TCTTATGAAGAATGAGTTCTTTCTGTGGTGTGTGACTTTAGTGGGAGGGCAGCTCTTGCT NM_199133 RefSeq chr5
- 10225507 10249909 FAM173B 134145 "family with sequence similarity 173, member B, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103864_PI430048170 0.384975788330151 1.55100253363642 1.69341291119279
0.323615983647624 0.413321475385085 A A A 0.34440710034982 0.318244099709104
0.303701737458844 A A A LNCV6_103864_PI430048170 mRNA
CACACACCCCAAAGGAGTTTCTAAGGAATGGATCCTTGACTTCAGACTGTGAGATCTTTT NM_001136534 RefSeq
chr12 + 119593458 119641558 TMEM233 387890 transmembrane protein 233 GO:0009607|GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77579_PI430048170 0.335088672745377 0.946534661190253 8.65902271107532 8.67739178320939
8.61267999493499 P P P 8.61452035526941 8.82485380861682 8.7405803104643 P P P
LNCV6_77579_PI430048170 mRNA
CACTATTAGAGGGCATTCATGAAAGAACAACTCTTGCACCTCTCAGAGAAGATAACTGCC NM_144578 RefSeq chr14
+ 55051643 55070194 MAPK1IP1L 93487 mitogen-activated protein kinase 1 interacting protein 1-like
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144725_PI430048170 0.0830024774022604 1.51169651653425 5.82640416819873
6.35812978796704 6.14386377717137 P P P 5.82250803397825 5.56475860939904
5.11496906345851 P P P LNCV6_144725_PI430048170 mRNA
TCTCAGTGTGGAGGAACTGGCTGCACGTGGGACCTGAAGGTGCCCTCTGTGTTTATGTTG NM_002246 RefSeq chr2
+ 26692712 26731198 KCNK3 3777 "potassium channel, two pore domain subfamily K, member 3"
GO:0071294|GO:0046982|GO:0005886|GO:0042493|GO:0051481|GO:0071456|GO:0005267|GO:0007268|GO:0008
022|GO:0022841|GO:0042803|GO:0005252|GO:0044548|GO:0034220|GO:0005887|GO:0007420|GO:0090102|GO:0
034765|GO:0005216|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49695_PI430048170 0.18353809023961 0.801997545740125 4.19352667465494 3.78593741554026
3.63330520638627 P P P 4.26984331246429 4.34206755453918 3.9922117560448 P P P
LNCV6_49695_PI430048170 mRNA
CTCTGATGCCCCCACTCAGATTGGTCTCCACTGTGCCAAAAAACATGGAGTCAATCTATG NM_001102597 RefSeq
chr19 - 44506158 44529525 CEACAM20 125931 "carcinoembryonic antigen-related cell adhesion molecule 20, transcript variant 5L" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134652_PI430048170 0.350545099239675 1.19493583197925 2.72403741451871
2.14659852973704 2.24740389730689 A A A 2.43730685055973 1.94813339090225
1.97579194393303 A A A LNCV6_134652_PI430048170 mRNA
CTGTGGCAAGAGATTTCATAATTTCTACTGCACTTACATTCAACACTTGATGATTCACTA NM_025057 RefSeq chr14

+ 74019355 74066092 CCDC176 80127 coiled-coil domain containing 176
GO:0044458|GO:0005737|GO:0036064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137661_PI430048170 0.0514863947753551.19669419049314 10.7641463298395 10.866369174159
10.9887384081759 P P P 10.4807282786362 10.6529523497238 10.7075952476522 P P P
LNCV6_137661_PI430048170 mRNA
ACTCACCAAGCTGGGAAAACCATTTAAATACATCGTGACCTGTGTAATTATGCAGAAGAA NM_006519RefSeq chr6
- 158636474 158644786 DYNLT16993 "dynein, light chain, Tctex-type 1, transcript variant 1"
GO:0005515|GO:0005794|GO:0019060|GO:0005874|GO:0000132|GO:0005819|GO:0046718|GO:0042802|GO:0003
774|GO:0007067|GO:0008277|GO:0032314|GO:0051493|GO:0050768|GO:0048812|GO:0008152|GO:0005868|GO:0
051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126635_PI430048170 0.0551349589078823 0.94021378444801 0.436815684444569
0.4291365482900520.37329537021401 A A A 0.55167071710026 0.486191252986961
0.467676666946689A A A LNCV6_126635_PI430048170 mRNA
GTTTGCTTTCTTACTGGTATCATTCTGTTTCCTTGACTTGAAACAAGAGAACATTGAACC NM_080615RefSeq chr20
- 56491491 56525925 GCNT7 NA glucosaminyl (N-acetyl) transferase family member 7 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145556_PI430048170 0.1519278729293982.18000194254564 5.15376136563034
5.32502937878173 4.95309820332182 P P P 4.71891430218119 4.02120253276975
2.66794672186157 P P P LNCV6_145556_PI430048170 mRNA
TTGCTTTGGATCTTGCCTGGAAGGTGTTTTAAGTTTTGTAATAAACAAGATGATGTCTGA NM_152672RefSeq chr3
+ 196216511 196233430 SLC51A 200931 "solute carrier family 51, alpha subunit"
GO:0043234|GO:0005215|GO:0046982|GO:0005886|GO:0015721|GO:0006810|GO:0005789|GO:0016021|GO:0042
803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141141_PI430048170 0.0676189655455591 0.7104909317968371 0.0883577506039
10.0857363205492 9.90489837669693 P P P 10.2109682527423 10.636063564081
10.6746148317305 P P P LNCV6_141141_PI430048170 mRNA
AAACAACTTTGCATTGCATTGGCTTGACCCATAAACTAAGTTATATCCGTGGGCAAAAAA NM_002541RefSeq chr7
+ 44606521 44709070 OGDH 4967 "oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide),
transcript variant 1"
GO:0006099|GO:0021695|GO:0051087|GO:0006091|GO:0044281|GO:0004591|GO:0021860|GO:0046872|GO:0006
096|GO:0005829|GO:0005739|GO:0021794|GO:0022028|GO:0034641|GO:0006104|GO:0005759|GO:0031072|GO:0
006103|GO:0006554|GO:0045252|GO:0034602|GO:0044237|GO:0031966|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145225_PI430048170 0.31135060951856 0.7165323889819570.544306171641805
0.4187958695668610.565996786023456A A A 0.7745096138676281.51729072907954
0.479074968057047A A A LNCV6_145225_PI430048170 mRNA
GTGCTTTCTAAATTCAAAGACTAGAAGGAAAATGGATAAAAATCACAAGTGCCGTTTCTC NM_017431RefSeq chr2
- 218822382 218831789 PRKAG353632 "protein kinase, AMP-activated, gamma 3 non-catalytic subunit"
GO:0008286|GO:0006996|GO:0031588|GO:0004679|GO:0019901|GO:0005978|GO:0005524|GO:0005615|GO:0005
829|GO:0035556|GO:0015758|GO:0061024|GO:0006468|GO:0006633|GO:0007050|GO:0007005 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137913_PI430048170 0.7043273336433390.94580744811038 1.70254917098348 2.3507696361377
1.44411353889258 A A A 2.05610931472397 2.08379611635782 1.72835461321634 A A A
LNCV6_137913_PI430048170 mRNA
GGCAGGAACGTATGCTGAATTAAAGTAATTTTACTACGAAGTTTGCTTATTAAGTATGCC NM_002396RefSeq chr18
+ 50879061 50949792 ME2 4200 "malic enzyme 2, NAD(+)-dependent, mitochondrial, transcript
variant 1"
GO:0005739|GO:0051287|GO:0005759|GO:0009055|GO:0006108|GO:0004471|GO:0008948|GO:0046872|GO:0055
114|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_138290_PI430048170 0.0286054724173113 0.5559122805126678.78166324867287
8.68382936184465 8.78934002284696 P P P 9.47491857800191 9.383185073607
9.88864582311133 P P P LNCV6_138290_PI430048170 mRNA
GGTGCTTTCACCTGCTGGTAAAAGATACATCTGTATATCTGAAATGCAAGATATTGATTT NM_017735RefSeq chr2
+ 32628019 32821051 TTC27 55622 "tetratricopeptide repeat domain 27, transcript variant 1"
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75716_PI430048170 0.478222725981 0.2366995450784960.3907362788877180.844271684565366
0.252120174228911 A A A 0.3239808007785483.96656043813512 0.34507697129988 A P A
LNCV6_75716_PI430048170 mRNA
GTAAAGAGTCATTTTCATAAAGATCAATTCATTGATTTGTTTTTTGTAAAGCTATCATTC NM_001884RefSeq chr5 -
83638197 83721077 HAPLN1 1404 hyaluronan and proteoglycan link protein 1
GO:0031012|GO:0001501|GO:0005540|GO:0030198|GO:0005578|GO:0005576|GO:0007417|GO:0007155|GO:0005
201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_4953_PI430048170 0.1475114877445940.7570590108240831 0.7063620452457 10.0522924815082
10.253920700986 P P P 10.9292018094905 10.7105164595838 10.6410264856188 P P P
LNCV6_4953_PI430048170 mRNA
TATGGCAGTGGCAGATTTTAATTAGGAAACAAAGCTTAGCAGGAGAGGAGAGCCAGAGAA NM_031157RefSeq
chr12 + 54280703 54285246 HNRNPA1 3178 "heterogeneous nuclear ribonucleoprotein A1,
transcript variant 2"
GO:0005515|GO:0006397|GO:0008380|GO:0010467|GO:0003727|GO:0051170|GO:0003723|GO:0071013|GO:0006
405|GO:0005737|GO:0016020|GO:0000166|GO:0003697|GO:0000398|GO:0030529|GO:0016032|GO:0005654|GO:0
005681|GO:0051028|GO:0045111|GO:0051168|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_127706_PI430048170 0.0367063895159408 0.58412817449074 5.33971350441522
5.31664279015471 5.76764473535138 P P P 5.90578538858057 6.24850808136609 6.5673805046032
P P P LNCV6_127706_PI430048170 mRNA
GTTTTGATGTTATTCATGGAATACCTTCTGTGTTAAATACAGTCACTTAATTCCTTGGCC NM_001017963 RefSeq chr14
- 102080737 102139749 HSP90AA1 3320 "heat shock protein 90kDa alpha (cytosolic), class A member 1,
transcript variant 1"
GO:0005515|GO:0006986|GO:0005886|GO:0050999|GO:0005634|GO:0044281|GO:0045040|GO:0042803|GO:0045
429|GO:0042802|GO:0005829|GO:0005739|GO:0034605|GO:0042026|GO:0005737|GO:0000166|GO:0007411|GO:0
071682|GO:0000086|GO:0046209|GO:0030235|GO:0051131|GO:0006839|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145401_PI430048170 0.31427163670326 0.8969299258209345.55220623385279
5.61548118529785 5.95888987518508 P P P 5.89304551447701 5.85193397765378
5.88606481845838 P P P LNCV6_145401_PI430048170 mRNA
TGTTTTCTGGCACTCACTATAATCAGCCTTGCACTAGAGCTGTTTGTGGACTTGGCTTCA NM_001080485 RefSeq
chrX + 153334154 153352926 ZNF275 10838 zinc finger protein 275
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138321_PI430048170 0.1960601589001442.43563797323579 0.287552928545089
2.18736838570812 1.69060452568691 A A A 0.3197404077992280.291710223941208
0.291908458186464 A A A LNCV6_138321_PI430048170 mRNA
GATTGGTACACAAAAGCTAAAGCAGTGGCTGGGGCTTTGTTTTTAAATTTTGGGTTTTTT NM_058237RefSeq
chr14_KI270847v1_alt + 1288873 1394297 PPP4R4 57718 "protein phosphatase 4, regulatory subunit
4, transcript variant 1" GO:0005515|GO:0008287|GO:0005737|GO:0019888|GO:0080163|GO:0032515 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_137031_PI430048170 0.0133964839351814 0.6713362613135872.6356977501675
2.48411831925706 2.55152627128767 A A A 3.1211863861201 2.96889533331046

3.29183215325708 P P P LNCV6_137031_PI430048170 mRNA
TGTTTCCTGTTATCCACAGGAGAATGTAATGCCTCAGTTCATTTTCAGTTATCTTTGATT NM_152356 RefSeq chr19 +
11798575 11808491 ZNF491 126069 zinc finger protein 491
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144687_PI430048170 0.0585288260063343 1.4483963746549 8.53891135993188
8.82879514867822 9.06593961973 P P P 8.34785312597816 8.03144868316738 8.46480050526568 P
P P LNCV6_144687_PI430048170 mRNA
CCCACTGTTTAAAAATGTTACCTGTGTATTTCCATGCAGTGTATATATTGAGATGCTGTA NM_001270879 RefSeq
chr6 - 166364919 166383013 MPC1 51660 "mitochondrial pyruvate carrier 1, transcript variant 2"
GO:0005739|GO:0008150|GO:0003674|GO:0006850|GO:0006090|GO:0050833|GO:0005743|GO:0044281|GO:0016
021|GO:0005575|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96670_PI430048170 0.353493817999005 1.17355049878502 5.51119997595543 5.64776583285453
5.57197092071556 P P P 5.72191598322507 5.25132598985477 4.96576504859997 P P P
LNCV6_96670_PI430048170 mRNA
GGAAACATTTTCAGACCTATGGAAACACTTCCTGAAAACAACGTTCTTCCCCCTTGCCGT NM_001276696 RefSeq
chr17 - 7668401 7687550 TP53 7157 "tumor protein p53, transcript variant 3"
GO:0005515|GO:0000790|GO:0009651|GO:0003700|GO:0006983|GO:0006366|GO:0009303|GO:0000981|GO:0001
756|GO:0005657|GO:0002020|GO:0007406|GO:0007219|GO:0005759|GO:0010666|GO:0007179|GO:0002360|GO:0
002326|GO:0006978|GO:0010332|GO:0000785|GO:0000060|GO:0006977|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143611_PI430048170 0.810319750045273 0.975724233290198 6.89329837543578
6.40501750236093 6.16321588829438 P P P 6.64805437745041 6.64020740396842
6.35919717540691 P P P LNCV6_143611_PI430048170 mRNA
CTGTGCTGTCTCTCCTATGCATTGAAACCTCCACCGGTCCCCAAGCATGAATATGAGTAG NM_001037500 RefSeq
chr20 - 31465505 31473013 DEFB124 NA "defensin, beta 124" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141269_PI430048170 0.0220195065515071 0.430903191014328 3.6318556310483
3.45787833360207 4.05061009140276 P P P 4.54124708672728 4.78458843430387
5.38820859842596 P P P LNCV6_141269_PI430048170 mRNA
CTGTTTTTAAATGTGAACTTGTGCGCAAATGTGCAGATTCAATGTTCTTGTTACAGATTG NM_001282129 RefSeq
chr17 - 29625938 29930228 SSH2 85464 "slingshot protein phosphatase 2, transcript variant 1"
GO:0030036|GO:0003779|GO:0003677|GO:0005615|GO:0035335|GO:0010591|GO:0005737|GO:0006470|GO:0008
064|GO:0004721|GO:0008138|GO:0005856|GO:0050770|GO:0004725 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128675_PI430048170 0.557374207211962 0.703210362665744 0.290454248351811
0.644378389332014 0.424337369285895 A A A 0.321961988204724 0.296957846417596
1.76201154492918 A A A LNCV6_128675_PI430048170 mRNA
CTCTGCGTCTTGTTACTTAGCATGTCAATAAAGAGGCAGATTCCTGTGTCAGTGAAAAAA NM_182688 RefSeq chr21
- 44768579 44801836 UBE2G2 7327 "ubiquitin-conjugating enzyme E2G 2, transcript variant 2"
GO:0005515|GO:0006511|GO:0004842|GO:0005783|GO:0016874|GO:0030433|GO:0005524|GO:0005829|GO:0042
802|GO:0019787|GO:0070936|GO:0044257|GO:0031625|GO:0018279 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_67338_PI430048170 0.615841905918513 0.933511620471522 5.02908767486821 5.55124529465193
5.51163697002019 P P P 5.26942245197383 5.51472062826359 5.63777261659154 P P P
LNCV6_67338_PI430048170 mRNA
TCATACAAGTCACCTGTCACCACTTTAGATAAGAGCACTGGCATTGGGATCTCTACAGAA NM_145658 RefSeq chr15
+ 68930499 68946811 SPESP1 246777 sperm equatorial segment protein 1
GO:0001669|GO:0007342|GO:0007275|GO:0007340 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_132700_PI430048170 0.00565775486477632 0.6605146099864776.66936743250145
6.95197833393151 6.78989201915569 P P P 7.26352038821841 7.43637119528566
7.50942560157466 P P P LNCV6_132700_PI430048170 mRNA
AAACGTTGTAAGTTTTCTAAAACACATAAGCTCTCAATAAACGTTAGCTTATCATTGTCA NM_001031727 RefSeq
chr19 + 13764522 13774282 MRI1 84245 "methylthioribose-1-phosphate isomerase 1, transcript
variant 1"
GO:0034641|GO:0005737|GO:0000096|GO:0019509|GO:0006595|GO:0005730|GO:0019284|GO:0044281|GO:0042
995|GO:0046523|GO:0042802|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132987_PI430048170 0.00291093999231671 0.5624472051967299.14913193800372
9.0364024104234 9.03094231626374 P P P 9.80324084260387 9.83817019523745 10.055636173316
P P P LNCV6_132987_PI430048170 mRNA
GCCTTGGCTTGCTCGGATAAAACTTTGTATGTATTTTGTATGGCATAGATTCTATATTGTNM_015995RefSeq chr15 +
31326854 31377899 KLF13 51621 "Kruppel-like factor 13, transcript variant 1"
GO:0005515|GO:0008285|GO:0045647|GO:0006366|GO:0045944|GO:0005634|GO:0003677|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130346_PI430048170 0.0362249896244099 2.08338163502144 8.05038941332599
8.15491082664872 8.02932091246876 P P P 6.56515875659272 7.32785080766731
7.06717582672017 P P P LNCV6_130346_PI430048170 mRNA
TTTTCTTTTTTGGGGTGGGGGGATTGGTTTGTAAAAATTCTCTACTCTTTTGGAATGTGANM_080627RefSeq chr20 -
36783774 36863684 SOGA1 140710 "suppressor of glucose, autophagy associated 1, transcript variant 1"
GO:0045721|GO:0008286|GO:0003674|GO:0010506|GO:0005615|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141627_PI430048170 0.3343323903716880.9277307902417547.85816391145853
8.01438430728236 8.0053314895431 P P P 7.91147737848076 8.17622884412447
8.10721568041871 P P P LNCV6_141627_PI430048170 mRNA
CAGAAGTAACTTATTTTGTACTAGTGTCCGCATAAGAAAAAGAATCGGCAGTATTTTCTG NM_001145661 RefSeq
chr3 - 128479421 128488530 GATA2 2624 "GATA binding protein 2, transcript variant 1"
GO:0006909|GO:0005515|GO:0021514|GO:0021533|GO:0003700|GO:0045599|GO:0001655|GO:0021983|GO:0070
345|GO:0035065|GO:0060872|GO:0050766|GO:0045654|GO:0048873|GO:0045944|GO:0048469|GO:0021902|GO:0
035019|GO:0097154|GO:0045746|GO:2000178|GO:0042472|GO:0001709|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132550_PI430048170 0.5447581564742841.14561510164889 0.568156824786151
1.12572107486154 0.384523257357661 A A A 0.4081198089424350.677439234802316
0.497912411577423 A A A LNCV6_132550_PI430048170 mRNA
CACTTGTTAATGTATTTGGGTCAAATGAGAGGCCTCAATAAAGACATCTGGGGCAGCATG NM_001231RefSeq chr1
+ 160190494 160201886 CASQ1 844 "calsequestrin 1 (fast-twitch, skeletal muscle)"
GO:0051258|GO:0005794|GO:0010033|GO:0009408|GO:0005783|GO:0014804|GO:0005509|GO:0045214|GO:0033
018|GO:0033017|GO:0030315|GO:0014894|GO:0055085|GO:0014809|GO:0005790|GO:0005739|GO:0034220|GO:0
016529|GO:0007519|GO:0005759|GO:0007029|GO:0051282|GO:0031674 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140955_PI430048170 0.0541611785986325 0.5830896028032884.16069824491081
3.91688439497853 4.6562740189738 P P P 5.17199798665345 4.93025533384095
5.05663605341655 P P P LNCV6_140955_PI430048170 mRNA
AAGTGGTAGGCAGTGTCCCTTCTGCTTGAAACCTATTGAAACCAATTTAAAACTGTGTAC NM_018398RefSeq chr3
+ 54122665 55074557 CACNA2D3 55799 "calcium channel, voltage-dependent, alpha 2/delta subunit 3"
GO:0005245|GO:0070588|GO:0034765|GO:0016021|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143114_PI430048170 0.00978894708639625 0.4973029408545456.59472623811046
6.25879078630685 6.82226387309273 P P P 7.45271636252293 7.41281694317986

7.84736454529049 P P P LNCV6_143114_PI430048170 mRNA
AGCCAAGGAATCGACATATATTAGGTGCGTGTACTGTTTCTAAAAACCACAAACTAAGAA NM_016626RefSeq chr18
- 51174549 51197681 MEX3C 51320 mex-3 RNA binding family member C
GO:0097009|GO:0005515|GO:0005737|GO:0003415|GO:0045598|GO:0016874|GO:0008152|GO:0008270|GO:0005
634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141556_PI430048170 0.9477899208220720.9677022694206780.976649213422218
0.5379223830236591.31623303525594 A A A 0.3793154243362071.23963297213794
1.28986927825744 A A A LNCV6_141556_PI430048170 mRNA
CTCCGAGGACTTGAGTAAGTGGAAAAAACAAAACACAGACTGCAATGTTTGTTTCTAAGT NM_138328RefSeq chr17
+ 32266175 32324661 RHBDL3162494 "rhomboid, veinlet-like 3 (Drosophila)"
GO:0004252|GO:0005509|GO:0006508|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132511_PI430048170 0.00754468189840598 0.4920182590944783.97486837939066
4.03202823627173 4.46844842457907 P P P 4.98642921534154 5.19759094241185
5.38554740299756 P P P LNCV6_132511_PI430048170 mRNA
CGAAGGGATTGTGTATCTGTGCTTCTAATATTAGTTGGCTTTCATAAATCATGTTGTTGT NM_001278RefSeq chr10
- 100188366 100229587 CHUK 1147 conserved helix-loop-helix ubiquitous kinase
GO:0005515|GO:0035631|GO:0007249|GO:0009653|GO:0042803|GO:0043231|GO:0002756|GO:0007173|GO:0002
755|GO:0071356|GO:0032496|GO:0043123|GO:0033194|GO:0038124|GO:0046982|GO:0038123|GO:0034134|GO:0
009636|GO:0002224|GO:0033598|GO:0008543|GO:0045087|GO:0009898|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136002_PI430048170 0.6866080120474860.8632203608178471.33128749858774
0.33419282292174 0.294647527023417A A A 1.52645723507029 0.711373906083511
0.354128434725361A A A LNCV6_136002_PI430048170 mRNA
TCTTCGTTGGCAGAGATTTCCAAGAAAAGTTTTTCCAGTCTTTGACTTCTGCCCTGGCGA NM_001506RefSeq chr19
+ 50770463 50771732 GPR32 2854 G protein-coupled receptor 32
GO:0007186|GO:0005887|GO:0004930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142448_PI430048170 0.2403161844618181.01978158790682 0.305624932981997
0.2565691101185480.310575993602931A A A 0.2690401903017960.252468543962809
0.267039453568343A A A LNCV6_142448_PI430048170 mRNA
CGAATGGATTGTTGCTTCTGAGAAATTGTTCCTTGTTTTTTGGATAATAAACGATCTTCC NM_001110822 RefSeq
chr19 + 32719772 32790808 TDRD12 91646 tudor domain containing 12
GO:0010467|GO:0004386|GO:0007275|GO:0005575|GO:0007283|GO:0031047|GO:0003676|GO:0005524|GO:0030
154|GO:0009566|GO:0003674|GO:0008150|GO:0034587|GO:0043046|GO:0007140 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127399_PI430048170 0.1105606649743261.26216775523239 6.99355196219342
7.19801540224647 7.02432346576251 P P P 6.99334942444127 6.54415369496517
6.63947039763984 P P P LNCV6_127399_PI430048170 mRNA
TCTAGTGATTTGATGGTGAACTTTTCTAAATAAATAGCCCTTTCCCCTCCGGTGTCGGTA NM_153612RefSeq chr6
- 114055585 114062877 HS3ST5 222537 heparan sulfate (glucosamine) 3-O-sulfotransferase 5
GO:0005515|GO:0005975|GO:0008467|GO:0044281|GO:0050656|GO:0006024|GO:0015015|GO:0050819|GO:0000
139|GO:0046596|GO:0009405|GO:0006477|GO:0016021|GO:0030203 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128571_PI430048170 1.68956218083023e-05 0.1180357235041832.49580468221284
2.63645456099904 2.32646472260828 A A A 5.54515214475091 5.70687654236409
5.46048877040548 P P P LNCV6_128571_PI430048170 mRNA
GCGGGTTCAACATGTCCTCTTTCAAGTTAAAAGAATAAAAGACTTCCAGCCGAGAAAAAA NM_006498RefSeq chr22
- 37570245 37580017 LGALS2 3957 "lectin, galactoside-binding, soluble, 2" GO:0030246|GO:0016936
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139975_PI430048170 0.5618174333063721.21190183150502 2.78587954075942

1.91188162804993 1.82890984498387 A A A 1.77977520173399 2.61494583794399
1.11603387932175 A P A LNCV6_139975_PI430048170 mRNA
TAAATGCTCAATAAATTGTAGCTGCCAGTGCCGGGCATTGCTCTTGGCATTTGCAAAAAA NM_001042RefSeq chr17
+ 7281734 7288048 SLC2A4 6517 "solute carrier family 2 (facilitated glucose transporter), member 4"
GO:0010021|GO:0005515|GO:0048471|GO:0005886|GO:0045471|GO:0030136|GO:0044281|GO:0055056|GO:0008
645|GO:0005829|GO:0015758|GO:0046323|GO:0061024|GO:0030140|GO:0005355|GO:0070062|GO:0012506|GO:0
032869|GO:0071470|GO:0005975|GO:0005771|GO:0071456|GO:0030315|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130360_PI430048170 0.0186907310721632 1.25455576977242 9.91633188000486
9.94590237274623 9.81266280276349 P P P 9.45937208574574 9.68316119188245
9.54532020219409 P P P LNCV6_130360_PI430048170 mRNA
AGGTGGGCATTTTTGGGCTACCTGGTTCGTTTTTATAAGATTTTGCTGGGTTGGTTTTTT NM_016270RefSeq chr19 +
16324839 16327528 KLF2 10365 Kruppel-like factor 2
GO:0051247|GO:0005515|GO:0071499|GO:0070301|GO:0003700|GO:0032715|GO:0005634|GO:0071409|GO:0001
701|GO:0046872|GO:0006351|GO:0060509|GO:0043565|GO:0000902|GO:0043249|GO:0035264|GO:0045944|GO:0
071356|GO:0071347|GO:0040029|GO:0036003 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141270_PI430048170 0.0237451507417095 0.8181109441921398.91376147404705
9.03293265887283 8.84002543875215 P P P 9.1777857300707 9.33427160905326
9.14287199353717 P P P LNCV6_141270_PI430048170 mRNA
GCTAGTCAGTTTTTCATAGCCTTACAGTATCTGGCTTTGTACTGAGAAATAAAACACATT NM_017857RefSeq chr11
+ 67303447 67312607 SSH3 54961 slingshot protein phosphatase 3
GO:0010591|GO:0005737|GO:0006470|GO:0008064|GO:0005634|GO:0003779|GO:0008138|GO:0005856|GO:0050
770|GO:0003677|GO:0035335|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129465_PI430048170 0.47478588107121 1.34798532598216 1.55250995556811
2.28153362265003 0.919682423645001A A A 0.5775744900787590.84644089592235
1.96192646611394 A A A LNCV6_129465_PI430048170 mRNA
TCTTGCCAAAGGGCCTGGAGTAGAAGGACAACAGGGCAGCAACTTGGAGGGAGTTCTCTG NM_001039933
RefSeq chr17 - 63928737 63932344 CD79B 974 "CD79b molecule, immunoglobulin-associated beta,
transcript variant 3"
GO:0050853|GO:0019815|GO:0007165|GO:0006955|GO:0005737|GO:0005794|GO:0005886|GO:0005887|GO:0005
654|GO:0009897|GO:0070062|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136881_PI430048170 0.00276799281198155 0.5309547544718485.78080032031108
5.53870462679703 5.58335976845199 P P P 6.53828359509605 6.72421391417976 6.3703131002057
P P P LNCV6_136881_PI430048170 mRNA
GCTGTCAGTGTGACTGTAACAAAGGCTTCAAATCTGTCAAGAAGTAAGGAAAAGTTTTGT NM_001048199 RefSeq
chr1 + 28505942 28539196 RCC1 1104 "regulator of chromosome condensation 1, transcript
variant 4"
GO:0005515|GO:0031965|GO:0000790|GO:0000794|GO:0007088|GO:0031492|GO:0005634|GO:0051225|GO:0032
853|GO:0042393|GO:0000082|GO:0005737|GO:0007067|GO:0007059|GO:0003682|GO:0016032|GO:0005654|GO:0
007052|GO:0005087|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135936_PI430048170 0.48670537517181 0.9648479817057290.524396052616733
0.5553355037979160.436786907279305A A A 0.5512971461368390.464318005039712
0.652248454501024A A A LNCV6_135936_PI430048170 mRNA
CCCTTGATTTACAGTTTGAGGAACAAAGAAATTAAAGATGCCTTAAAGAGGTTGCAAAAG NM_001004729 RefSeq
chr11 + 59364458 59365394 OR5AN1 NA "olfactory receptor, family 5, subfamily AN, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145207_PI430048170 0.8681914784042270.9913751939912870.299795856227646
0.50468801317666 0.366822588171555A A A 0.4941481259006430.378547690178917
0.339190187732246A A A LNCV6_145207_PI430048170 mRNA

GTTCCCTGATATGGATTCCTATAACATGCTTTCATCCCCTTTTGTAATGGATATCATATT NM_152430RefSeq chr11 + 4643925 4655486 OR51E1 143503 "olfactory receptor, family 51, subfamily E, member 1" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141499_PI430048170 0.0416563078667218 0.4980304099852997.81950512181457 7.88413052002477 8.10786490031403 P P P 8.46824504388554 8.9812265696702 9.28152037473878 P P P LNCV6_141499_PI430048170 mRNA
CCTCAGTGGAGCTTCTGAGTTTTATACTGCTCAAGATCGTCATAAATAAAATTTTTTCTC NM_016359RefSeq chr15 + 41332693 41381050 NUSAP1 51203 "nucleolar and spindle associated protein 1, transcript variant 1" GO:0008017|GO:0007076|GO:0005737|GO:0000070|GO:0005694|GO:0000281|GO:0040001|GO:0005730|GO:0045840|GO:0005876|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130504_PI430048170 0.3801531807146791.12156638353405 5.59433266657059 5.41264882064216 5.85895270432498 P P P 5.27948844395168 5.51073558401263 5.59604605109386 P P P LNCV6_130504_PI430048170 mRNA
TATCCCTTACGATGAGCGCCCTATTTTGTTCCTTCTGTCTATCTCTGTTGCTGAGATCAG NM_020778RefSeq chr15 + 84816679 84873482 ALPK3 57538 alpha-kinase 3 GO:0007507|GO:0004674|GO:0006468|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132660_PI430048170 0.3329194851524810.9510872896755487.79663582120452 7.71358447451595 7.86639503722682 P P P 7.89726785911228 7.76918757542045 7.92645760315929 P P P LNCV6_132660_PI430048170 mRNA
CAATCAGAATTATATCTTGGGTCATTTATGTGCCGTCTGTTCTTGATTCTCTATGCTCTA NM_018463RefSeq chr12 + 2812620 2825071 ITFG2 55846 "integrin alpha FG-GAP repeat containing 2, transcript variant 1" GO:0005654|GO:0005829|GO:0002314 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139284_PI430048170 0.2835761252859060.72428323710019 0.434536248031253 0.4886109797764590.481667491339353A A A 0.3513359539866021.32302057072946 0.966021621174318A A A LNCV6_139284_PI430048170 mRNA
CCTTGGTTCTGTCAATTGCTGACATCTGAGAACACAGAATAATCCATCATTTTTAATTTC NM_001608RefSeq chr2 - 210187991 210225491 ACADL 33 "acyl-CoA dehydrogenase, long chain" GO:0090181|GO:0001659|GO:0006635|GO:0016401|GO:0031966|GO:0044242|GO:0050660|GO:0045717|GO:0046322|GO:0044281|GO:0019254|GO:0033539|GO:0004466|GO:0005739|GO:0005737|GO:0051289|GO:0005759|GO:0042758|GO:0003995|GO:0000062|GO:0044255|GO:0055114|GO:0042413 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138797_PI430048170 0.1130647829718050.8751761896260159.14037976886791 9.38172192511223 9.16628185839272 P P P 9.38089867753741 9.42747411243168 9.46812048807758 P P P LNCV6_138797_PI430048170 mRNA
GGATGCACCCGTCTTTAGAACCAAAAATATTCTCTCACAGATTTCATTCCTGTTTTTATA NM_016463RefSeq chr5 + 139648715 139683095 CXXC5 51523 CXXC finger protein 5 GO:0007165|GO:0005737|GO:0008270|GO:0005654|GO:0004871|GO:0043123|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110342_PI430048170 0.7215056581107311.04760287149089 4.38695093351086 4.07837713695456 3.94416113084665 P P P 3.93310189165248 4.18561220165138 4.11422555282653 P P P LNCV6_110342_PI430048170 mRNA
CCAGGAGCTGATCGAAAACATCAACAAGAGCCGGCAAAAGGACCATGCACTCATGACCAA NM_001105578 RefSeq chr19 - 12899079 12919272 SYCE2 256126 synaptonemal complex central element protein 2 GO:0000801|GO:0007130|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132432_PI430048170 0.4424928527688970.8604332408153042.17623377178304 2.21494624431902 3.07998922466117 A A P 2.79637202978322 2.78427810355682 2.73127326235475 P P P LNCV6_132432_PI430048170 mRNA

TAGAAGCTGTATGTATTATAAAGGAAAGAAATGCCCTTGGTGGCTTCCAGGGTGTTTTTT NM_003927 RefSeq chr18 - 54151600 54224788 MBD2 8932 "methyl-CpG binding domain protein 2, transcript variant 1" GO:0005515|GO:0000792|GO:0010467|GO:0000790|GO:0008327|GO:0030177|GO:0005634|GO:0003729|GO:0043623|GO:0005737|GO:0003696|GO:0042127|GO:0042711|GO:0043044|GO:0019904|GO:0031492|GO:0000122|GO:0000978|GO:0006351|GO:0043234|GO:0000118|GO:0035197|GO:0045814|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61275_PI430048170 0.000119388555831504 1.35909717453049 12.0836191024188 12.0420681880299 12.0592078918498 P P P 11.6425756806583 11.5818600184321 11.6320889127772 P P P LNCV6_61275_PI430048170 mRNA
AACCTCCAAAACCCCCACTCAAGTCAGAGAAACATGAGGAATAAAGGTCACATGCAGATG NM_032036 RefSeq chr14_KI270847v1_alt - 1242342 1244182 IFI27L2 83982 "interferon, alpha-inducible protein 27-like 2" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137370_PI430048170 0.000300115342512422 1.38507631841172 8.45253764382237 8.50531661338627 8.53011139498437 P P P 8.03964097895438 7.97004825837302 8.06771991350767 P P P LNCV6_137370_PI430048170 mRNA
CCTCCCTCAACCGGACTAATTAAAGAAAGACACTTGTGTTCCCAAGTGGTGGTTTTATTT NM_017772 RefSeq chr6 + 37257703 37332970 TBC1D22B 55633 "TBC1 domain family, member 22B, transcript variant 1" GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140472_PI430048170 0.769071221353774 0.978622561648562 5.24822994149261 5.15548345142485 5.28672753299167 P P P 5.31494456571601 5.10395209958218 5.35576024985509 P P P LNCV6_140472_PI430048170 mRNA
TCTGTAAATGATGGCTTGATGTACAGAAAATGTATTTTTGCTTAAAAGATGCCTGGGTAC NM_198463 RefSeq chr3 - 58742009 59049989 C3orf67 NA chromosome 3 open reading frame 67 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109869_PI430048170 0.145318766782626 1.0706026523857 0.474598194013951 0.495111451624430 0.537538939661539 A A A 0.323875303378447 0.404575463860548 0.480021032568426 A A A LNCV6_109869_PI430048170 mRNA
ATCTTGTTCTGGACAGGTATGTACCCTCTGGTCACAGCGACCCAGGATGCTGACAGCAGC NM_001291712 RefSeq chr14 - 64226711 64338550 ESR2 2100 "estrogen receptor 2 (ER beta), transcript variant k" GO:0005515|GO:0010467|GO:0060065|GO:0030308|GO:0003700|GO:0006367|GO:0060068|GO:0050680|GO:0003707|GO:0007267|GO:0030284|GO:0005634|GO:0034056|GO:0005739|GO:0051091|GO:0001541|GO:0043401|GO:0004879|GO:0001046|GO:0048019|GO:0005496|GO:0006355|GO:0060743|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145731_PI430048170 0.26199298302646 0.636238285716622 1.55349665586327 2.42263085331418 2.45742982452749 A A A 2.13235512985153 2.75590956555023 3.3969528125668 A P P LNCV6_145731_PI430048170 mRNA
CCCCTTAAAAAGCTTGGGAATGTTTTGTATGTACAAGTTTATTAAAACTGGGTATGCTTC NM_032834 RefSeq chr12 + 34022280 34028301 ALG10 84920 "ALG10, alpha-1,2-glucosyltransferase" GO:0016758|GO:0005789|GO:0016021|GO:0006488|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131829_PI430048170 0.00020633701409253 0.561252274540309 10.2235451104127 10.2586971659651 10.1369888271706 P P P 11.0625867658907 11.1050457319613 10.9497052654432 P P P LNCV6_131829_PI430048170 mRNA
AAGGTGAAGCATCCCAACTGACTAGAGACTCAGGCCCTGCAGGGCCCTATAGAACCTGTG NM_001258373 RefSeq chr17 + 50547088 50555852 SPATA20 64847 "spermatogenesis associated 20, transcript variant 3" GO:0008152|GO:0007275|GO:0005576|GO:0007283|GO:0003824|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142199_PI430048170 0.1474423064552 1.13735732685584 9.38606976865699 9.58470953728559 9.47785161031221 P P P 9.46270872715011 9.2085714356105

9.21216691295576 P P P LNCV6_142199_PI430048170 mRNA
CCCCAGAGAGGGCCTGGAAATTATAAATCTCTATCACATAAGGATTATATATTTGAACTT NM_006405 RefSeq chr14
- 24189142 24195736 TM9SF1 10548 "transmembrane 9 superfamily member 1, transcript variant 1"
GO:0000421|GO:0006914|GO:0031410|GO:0016021|GO:0005765 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141883_PI430048170 0.00672077720797083 1.43947671055974 8.75005819976308
8.6596259277644 8.80723131085896 P P P 8.09676469275541 8.18855736238721
8.34754829083653 P P P LNCV6_141883_PI430048170 mRNA
CTTGCCCGGGCAGTAGTGGCTGACCAATAAAGACCTTTACCTGTTTTGTATGGCAAAAAA NM_030923 RefSeq chr2
- 134455758 134719001 TMEM163 81615 transmembrane protein 163
GO:0030054|GO:0030285|GO:0031901|GO:0030672|GO:0008270 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142879_PI430048170 0.3511075091099030.91976035041268 9.68474824061122 9.7359970855247
9.59050945541028 P P P 9.97309823531887 9.71422917275472 9.67082812316034 P P P
LNCV6_142879_PI430048170 mRNA
GTCGGAAGGGTTTTTGTTTTTGTTTCTGTTGCCATTTGTGTAAATACTAGTCTTTTTGGA NM_004429 RefSeq chrX +
68828996 68842163 EFNB1 1947 ephrin-B1
GO:0005515|GO:0048013|GO:0005886|GO:0001755|GO:0007267|GO:0045202|GO:0005634|GO:0009880|GO:0005
737|GO:0046875|GO:0005887|GO:0007411|GO:0042102|GO:0045121|GO:0007155|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129898_PI430048170 0.157833404842981 0.433790599735011 0.498023763496332
0.325842773725795 0.418918624046305 A A A 0.671501872521937 2.32226367481168
1.39678276823245 A A A LNCV6_129898_PI430048170 mRNA
GATGACGAATATTATGAAATGTGCCTTTTCTGAAGAGATTGTGTTAGCTCCAAAGCTTTT NM_001143676 RefSeq
chr6 - 134169245 134318058 SGK1 6446 "serum/glucocorticoid regulated kinase 1, transcript variant
2"
GO:0005515|GO:0005886|GO:0015459|GO:0032411|GO:0070294|GO:0001558|GO:0005829|GO:0005739|GO:0051
090|GO:0005737|GO:0034220|GO:0060453|GO:0042127|GO:0006814|GO:0030334|GO:0007616|GO:0005246|GO:0
006950|GO:0006915|GO:0042981|GO:0055085|GO:0005524|GO:0006974|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136036_PI430048170 0.0342220601073218 0.642629393328897 8.21773568421547
8.08752091916476 7.68871049916587 P P P 8.63871682298986 8.82871788898704
8.46893454019278 P P P LNCV6_136036_PI430048170 mRNA
GGAGTGTCCCCCTCCCAGAAGCATATCCCAGATGAGTGGTACATTATATAAGGATTTTTT NM_182904 RefSeq chr11
- 74266648 74311676 P4HA3 283208 "prolyl 4-hydroxylase, alpha polypeptide III, transcript variant 1"
GO:0031418|GO:0005506|GO:0005788|GO:0004656|GO:0019511|GO:0016702|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127279_PI430048170 0.106886845650925 1.04050850214588 0.335636934719542
0.354321708419237 0.283144620892842 A A A 0.260847266196196 0.27915582948058
0.262101832947219 A A A LNCV6_127279_PI430048170 mRNA
GCTGGTCAACACCCTATTCCATCTGTCATCGAGAAAGAAAATGTTAAAATAGACTTAAAA NM_207410 RefSeq chr6
+ 55327468 55402493 GFRAL 389400 GDNF family receptor alpha like
GO:0043524|GO:0005886|GO:2001240|GO:0016021|GO:0031098 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135652_PI430048170 0.507672725911499 1.1704961780578 4.01766436691501
4.73311775900371 4.62335888011499 P P P 3.81244808096901 4.54058477126209
4.34299165491589 P P P LNCV6_135652_PI430048170 mRNA
GATGCTGGCATCTGAGTCTCATTTTTGTACCGTGTTATTTGAGCAAATAAATACATTAAC NM_001010903 RefSeq
chr6 - 36315757 36336885 C6orf222 NA chromosome 6 open reading frame 222 NA . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_134529_PI430048170 0.00679174347557301 0.3758323066837334.89140703471403
4.57398299468704 4.53483926164327 P P P 5.77685892377872 5.9751003809498
6.43110514340219 P P P LNCV6_134529_PI430048170 mRNA
GAACCTAATCCTCATATCTATTGCCTACAAAAATAGACCAAGAATGTTGCTGCTCTTTTA NM_020840RefSeq chr4
+ 158769029 158906802 FNIP2 57600 folliculin interacting protein 2
GO:0005515|GO:0033138|GO:0005737|GO:0008630|GO:0005886|GO:0005815|GO:0006468|GO:0005654|GO:0001
932|GO:0000122 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136717_PI430048170 0.3112574122840621.03542254169209 0.309926294777455
0.2578189448188740.384840032446007A A A 0.2778841418409180.248385802577195
0.278285867307549A A A LNCV6_136717_PI430048170 mRNA
GACTAGTATAGTATACGGTCAGTTATGTCAATGTTTCATGGTCAATAAAAAGGAAGTTGC NM_033035RefSeq chr5
+ 111071691 111078024 TSLP 85480 "thymic stromal lymphopoietin, transcript variant 1"
GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139529_PI430048170 0.0078762819033811 0.4376221654539915.08074875262097
4.88078697394217 5.334763174586 P P P 5.97662735717892 6.26252339215683 6.6018522108031
P P P LNCV6_139529_PI430048170 mRNA
CTGCTCAAAGGATACCAAATAATGGTTTAACTGGACAACCTGAAAATTAGCATAGAAAAC NM_017943RefSeq chr14
+ 55271302 55353611 FBXO3455030 "F-box protein 34, transcript variant 1" GO:0005737|GO:0005654
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66825_PI430048170 0.7272807149104 1.06659100740071 11.1160132515672 11.4861213729025
11.729684607026 P P P 11.1981469560034 11.2041850494046 11.6642870502766 P P P
LNCV6_66825_PI430048170 mRNA
GTGGACCTAATTCGGTTTTCCTTTTAAAAGCCCCGCAAACAAAAGTCGTTTAAAACCTAT NM_014168RefSeq chr2
- 169811757 169824931 METTL5 29081 "methyltransferase like 5, transcript variant 1"
GO:0008168|GO:0003676|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128686_PI430048170 0.00447459866831996 0.5349907828095036.01502169361344
5.93936403788418 6.28992939399409 P P P 6.8264657576923 6.91837812403476 7.203466937821
P P P LNCV6_128686_PI430048170 mRNA
GTATTACTCTCCAAATCTACTGTACTGTCAGCTTCACTCCACCTGAGAAAAAAGAAAAAA NM_001001484 RefSeq
chr10 + 16436942 16513745 PTER 9317 "phosphotriesterase related, transcript variant 1"
GO:0003674|GO:0030855|GO:0016788|GO:0009056|GO:0008270|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136139_PI430048170 0.1341088653539510.6534034005484584.62727919865665
5.07725083345179 5.32325758682881 P P P 5.12177696777449 5.87291307841066
5.84159227363351 P P P LNCV6_136139_PI430048170 mRNA
TCACCAAAGCTCAAATGAGAATCAGCTTCCATGTTCTTTCCTTTACCAGAAATTTGCAAT NM_152450RefSeq chr15
+ 59438172 59523552 FAM81A 145773 "family with sequence similarity 81, member A" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_101109_PI430048170 0.3308793153982630.8527833995732263.8841548860108 3.849323275533
4.27757171052757 P P P 4.26243052661986 4.47803417993433 3.95241728623023 P P P
LNCV6_101109_PI430048170 mRNA
AGAGAACTGGTTTCCAGCAGTCCATTGTGTGGCCTTCCCCAAGGTCACCAGCTCTGTACG NM_181808RefSeq chr4
- 2071957 2242164 POLN 353497 polymerase (DNA directed) nu
GO:0005515|GO:0006261|GO:0000724|GO:0030332|GO:0003887|GO:0005730|GO:0005654|GO:0005634|GO:0019
985|GO:0003677|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133805_PI430048170 0.3698183335578581.027883015276 0.526964373796928
0.4630130972798630.54795120563286 A A A 0.4720993612741820.524983209447962
0.421305358238238A A A LNCV6_133805_PI430048170 mRNA

AAATGTCCTAAGTTTCTCAAAGTCAGAAATTATTTCTATGTAGTCCAGACCTGACTCCAG NM_144625 RefSeq chr1 + 241652277 241802132 WDR64 128025 WD repeat domain 64 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76324_PI430048170 0.0991450170593554 1.35498646207902 4.90477300939688 5.19638783525526 5.43388534033064 P P P 4.71707335788632 4.7011790023809 4.84580163942286 P P P LNCV6_76324_PI430048170 mRNA
TATAGAAAAAGCACCTGGATCCCAGTCTTTCAATGGCTTCAAGACAACCAGAAGTGCCTG NM_020444 RefSeq chr5 - 176346060 176361807 KIAA1191 57179 "KIAA1191, transcript variant 1" GO:0008150|GO:0003674|GO:0005737|GO:0016491|GO:0005575|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136212_PI430048170 0.4037444623481270 0.9086058495868449 4.24263481632179 9.21714547382405 9.44015490868031 P P P 9.30866841548796 9.31848865584197 9.66825778959273 P P P LNCV6_136212_PI430048170 mRNA
CATTCCATGGATGGCTGCCTTATAATTTTGTCTCTTTCCACTTTAATTGTGAATGGTTAA NM_018375 RefSeq chr14 + 69398667 69462391 SLC39A9 55334 "solute carrier family 39, member 9, transcript variant 1" GO:0046873|GO:0006829|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136445_PI430048170 0.00889221670004539 0.49970133727372 5.97854008997376 5.64883239772528 5.93976118025788 P P P 6.56214708106507 6.88115082057805 7.09864343145549 P P P LNCV6_136445_PI430048170 mRNA
ATCTTCCGTTAGGCCAATAAAAGAAGGGCCTCACAAGACAAAACAGGAGCCAGAAGTAAG NM_020861 RefSeq chr6 - 151364114 151391700 ZBTB2 57621 zinc finger and BTB domain containing 2 GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73429_PI430048170 0.0104601042069797 0.3339441275867491 .31730030530814 2.18523019232944 1.55857467416215 A A A 3.01806023385316 3.52552057941226 3.36256101575823 P P P LNCV6_73429_PI430048170 mRNA
GGAGAAATGAATTCAGAAGAAAACTCATCAGGTGCTTCTTTTTAAAACTAGAACTTGGCT NM_022757 RefSeq chr3 - 123913426 123961408 CCDC14 64770 coiled-coil domain containing 14 GO:0005813|GO:0021762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136944_PI430048170 0.0374572785309481 .28985554877314 9.37262241452446 9.3798796850837 9.43616569212744 P P P 8.95302238276145 8.93531957720094 9.18576291394081 P P P LNCV6_136944_PI430048170 mRNA
CCTGTTGGACATTTCCTTTTGGATTCATGCTTTCTGGAAGGTTTAAATTCATTAACGTTA NM_032315 RefSeq chr1 + 9539468 9582773 SLC25A33 84275 "solute carrier family 25 (pyrimidine nucleotide carrier), member 33" GO:0071156|GO:0008284|GO:0032869|GO:0031966|GO:0030307|GO:0051881|GO:0005743|GO:0006864|GO:0006390|GO:0034551|GO:0031930|GO:0007005|GO:0015218|GO:0016021|GO:0006264|GO:0002082 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99971_PI430048170 0.00273484419284004 0.2385872660449093.15780060298567 2.36533214499767 2.60669142092494 P A A 4.85721948235297 5.09476431372743 4.417891436192 P P P LNCV6_99971_PI430048170 mRNA
TTGTACCTCCCAAGTATTTGGGGGATATATTTATTCTGTATTGACAAAAGCAAATCCACT NM_024007 RefSeq chr5 - 158695914 159099780 EBF1 1879 "early B-cell factor 1, transcript variant 2" GO:0003700|GO:0046983|GO:0070742|GO:0007275|GO:0005634|GO:0045893|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126662_PI430048170 0.99980549473215 0.8087093884843183.97866409385073 4.31665901961844 4.16888962989732 P P P 2.9025399270756 5.32185517683279 4.24039816605399 P P P LNCV6_126662_PI430048170 mRNA
GACGTCTGAACCTTTGTACAAATGTGTAGATGACATCTTGCTACAGCTTTTATTTGTGAA NM_015656 RefSeq chr14 + 104138722 104180898 KIF26A 26153 kinesin family member 26A

GO:0008017|GO:0005871|GO:0005874|GO:0003777|GO:0005524|GO:0048484|GO:0005829|GO:0019886|GO:0001560|GO:0007596|GO:0008152|GO:0009968|GO:0016887|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132159_PI430048170 0.4255733216165560.6382601297254250.339933783630575 0.3219098206344410.284896047453716A A A 0.3103504947932230.313587452365195 1.75167116239873 A A A LNCV6_132159_PI430048170 mRNA
AATGTGGTAACCACAGAATTAATAACTGTACTACCCTGACAAGCTATATACATGTCTTCA NM_001638RefSeq chr12 - 56360570 56362799 APOF 319 apolipoprotein F
GO:0006629|GO:0033344|GO:0034364|GO:0015485|GO:0034362|GO:0006869|GO:0005102|GO:0006641|GO:0005576|GO:0005319|GO:0008203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141054_PI430048170 0.6718081348521880.9496243370450329.87400944180824 9.90280208099129 10.2586971659651 P P P 9.90154742541903 10.0713075595096 10.2922948840216 P P P LNCV6_141054_PI430048170 mRNA
CGTTCTGTGTTCTTGGCTTCCTAAATTTATCTGCCCATATGATTCTCATGCATTTGATAT NM_018158RefSeq chr2 + 27663470 27694980 SLC4A1AP 22950 "solute carrier family 4 (anion exchanger), member 1, adaptor protein" GO:0005515|GO:0005737|GO:0005886|GO:0005654|GO:0005634|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127786_PI430048170 0.000666548664617637 2.96887713354466 9.60425724701994 9.52829781847626 9.34109008360833 P P P 7.69011522201439 8.06075410660678 7.99893637182695 P P P LNCV6_127786_PI430048170 mRNA
GCCTGGCTCTGTTATTTACCGTGTATCATATGTAAATATCGACAGAAACTTCAATAAACT NM_031896RefSeq chr19 + 53912736 53943715 CACNG7 59284 "calcium channel, voltage-dependent, gamma subunit 7" GO:0005245|GO:0032281|GO:2000311|GO:0070588|GO:0006816|GO:0005891 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132438_PI430048170 0.2762228626005880.6476974708863081.20766529175036 1.04186722052586 0.363495752119744A A A 1.53836458282063 0.769650028756867 2.04317754579056 A A A LNCV6_132438_PI430048170 mRNA
GCACCCTTATCCCAGTTATAAGACAGTCAAAATGACTATTTCCTAAATATTGTGAGTGTA NM_025107RefSeq chr6 + 152697894 152724580 MYCT1 80177 myc target 1 GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132119_PI430048170 0.0526463112214315 0.8745421637680079.73299424337882 9.57581487042827 9.5575068764968 P P P 9.76531646366028 9.8950787482884 9.78931923531797 P P P LNCV6_132119_PI430048170 mRNA
AATCTTGAGTTGAGGAAATATATGCACAGGAGTCAAAGAGATGTCTTTATATCTGACTGT NM_023079RefSeq chr17 + 48908368 48929060 UBE2Z 65264 ubiquitin-conjugating enzyme E2Z
GO:0005515|GO:0000209|GO:0005737|GO:0019787|GO:0016874|GO:0006915|GO:0005654|GO:0005524|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133946_PI430048170 0.00266387090204746 0.4322923505971017.30802572953436 6.96997855960443 7.41579725007792 P P P 8.32285330205087 8.38365260217484 8.63436692209831 P P P LNCV6_133946_PI430048170 mRNA
GGAAGGTTACTTCTTGTCAAACTTGCCTGGCAGTGTTTGTTCAAAACTTGTATTTAATAA NM_004788RefSeq chr11 + 118359580 118399211 UBE4A 9354 "ubiquitination factor E4A, transcript variant 1" GO:0005515|GO:0000209|GO:0006511|GO:0005737|GO:0016874|GO:0034450|GO:0000151 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141828_PI430048170 0.2517839329396610.7913450371943410.555401934169092 0.50209293382222 0.578174707432864A A A 1.08390365394787 0.466280118095312 1.02294442067699 A A A LNCV6_141828_PI430048170 mRNA
TACAAGTCTACCACTGCCGATTGACTAAAAAATACATTATCCCATGCATAAAATGTCCTA NM_178445RefSeq chr3 + 132600136 132602641 ACKR4 51554 "atypical chemokine receptor 4, transcript variant 1"

GO:0005515|GO:0070098|GO:0005886|GO:0006898|GO:0019956|GO:0006955|GO:0006935|GO:0007186|GO:0005887|GO:0004950|GO:0055037|GO:0005769|GO:0005044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115998_PI430048170 0.5743768185938380.9331089260345021 2.4558139878125 12.361844877401 12.4406839320128 P P P 12.2898000830561 12.488767164726 12.7449321997173 P P P
LNCV6_115998_PI430048170 mRNA
AAGGGCGCTGTCCCGCCCAACCCCGCCTTTAAACGCCACAAATAAAGAGCATTGTTACCG NM_012138 RefSeq
chr17_KI270857v1_alt + 1185239 1293236 AATF 26574 apoptosis antagonizing transcription factor
GO:0005515|GO:0048011|GO:0043066|GO:0005813|GO:0043065|GO:0003700|GO:0005794|GO:0042254|GO:0048156|GO:0005730|GO:0032929|GO:0005634|GO:0097190|GO:0042985|GO:0006974|GO:0043522|GO:0007346|GO:0005737|GO:0040016|GO:0045944|GO:2000378|GO:0007155|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136962_PI430048170 0.75017669450599 0.8481711021660240.65280815423785 1.41058587521952 0.59464265605819 A A A 0.93756737112259 0.40784525926343 1.81820322029116 A A A LNCV6_136962_PI430048170 mRNA
GAAGCTAAAATGGAATTCATCTTCATACTAACTGGCTACAGATTATTCTCTTGCTGGATT NM_001142749 RefSeq
chr7 - 86876905 87059698 KIAA1324L 222223 "KIAA1324-like, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136548_PI430048170 0.0792565595011903 1.37708605691179 4.38435505743037 3.9531127964303 4.04230069344833 P P P 3.74276312166819 3.86789152324775 3.37717054223287 P P P LNCV6_136548_PI430048170 mRNA
TTGGGGCCTGAGGACAGCTTAATAAAGTAGACAAATGAAGAAAAACAACAATTTGCATTA NM_016946 RefSeq chr1 - 160995210 161021343 F11R 50848 F11 receptor
GO:0005515|GO:0030054|GO:0005886|GO:0034259|GO:0031032|GO:0032854|GO:0045777|GO:0050900|GO:2000249|GO:0006954|GO:0070830|GO:0005911|GO:0030198|GO:0015630|GO:0016032|GO:0007179|GO:0007155|GO:0070062|GO:0009314|GO:0034329|GO:0031410|GO:0030165|GO:0045216|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143549_PI430048170 0.2989348464536910.9424638932013530.484947394915017 0.4333692703636360.490207443011435 A A A 0.4801701458138690.505883817835466 0.672012955137487 A A A LNCV6_143549_PI430048170 mRNA
GGAGGTGGTAAGAACACCTGACAACTTCTGAATATTGGACATTTTAAACACTTACAAATA NM_018965 RefSeq chr6 - 41158505 41163186 TREM2 54209 "triggering receptor expressed on myeloid cells 2, transcript variant 1"
GO:0070891|GO:0005886|GO:0042834|GO:0050731|GO:0005576|GO:0097028|GO:0050850|GO:0043231|GO:0001530|GO:2000350|GO:0071223|GO:0070392|GO:0002588|GO:0007411|GO:0006959|GO:0045087|GO:0097110|GO:0032497|GO:0004872|GO:0070374|GO:0016021|GO:0032499|GO:0071224 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129060_PI430048170 0.15883909707528 1.06138539611736 0.4749589443598040.4264447560258 0.500324984201702 A A A 0.3097748573755490.3787651823680090.452770951044023 A A A
LNCV6_129060_PI430048170 mRNA
CGGTGGCAATATTATGTAACCTTTTTTCCTATGAAGTTTTTTGTAGGTCCTTGTTGTAAC NM_000840 RefSeq chr7 + 86643913 86864876 GRM3 2913 "glutamate receptor, metabotropic 3"
GO:0051966|GO:0030424|GO:0005886|GO:0004930|GO:0005246|GO:0001641|GO:0001642|GO:0007268|GO:0014069|GO:0007196|GO:0007194|GO:0042734|GO:0043197|GO:0005887|GO:0045211|GO:0008066 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143552_PI430048170 0.0595196278629415 0.767479729328675 6.98647832771287 6.6397772681428 6.64330179983489 P P P 7.0459896735136 7.17177393895703 7.21983016875708 P P P LNCV6_143552_PI430048170 mRNA
ATTCAGCCTGACACGCTTTGCCAGGAACAAACCTCATGTGAAAGAAAACAAAATGAATTT NM_013975 RefSeq chr17 + 34980497 35005069 LIG3 3980 "ligase III, DNA, ATP-dependent, transcript variant alpha"

GO:0005515|GO:0003909|GO:0070421|GO:0005634|GO:0006303|GO:0006302|GO:0006273|GO:0005739|GO:0043504|GO:0000795|GO:0033151|GO:0005694|GO:0003910|GO:0005524|GO:0003677|GO:0007049|GO:0006281|GO:0071897|GO:0006284|GO:0005654|GO:0006288|GO:0008270|GO:0006289|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130308_PI430048170 0.9533408918023540.9958985191931339.72827025435854 10.3232726685449 9.66104712524488 P P P 9.72179415871201 9.78016035741227 10.261410088065 P P P LNCV6_130308_PI430048170 mRNA
CTGCATTTCTCAGCTGGGCAGTAATCAATTTAATGGTCCTTTAAAATGTCTGTGTATTAA NM_017590RefSeq chr22 + 41301502 41360147 ZC3H7B23264 zinc finger CCCH-type containing 7B
GO:0005515|GO:0016032|GO:0005634|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130608_PI430048170 0.42020088912872 0.8326756774627423.91561586628597 3.79634181286144 4.39589201938894 P P P 4.13233431681981 4.02239193172856 4.71721304136614 P P P LNCV6_130608_PI430048170 mRNA
TTGTCCTTTTCTGCTATCACCTTCCTCTTGTCAGAATGAATATAGACACTGTATCTAAGT NM_001159RefSeq chr2 + 200586007 200671494 AOX1 316 aldehyde oxidase 1
GO:0008762|GO:0005506|GO:0051537|GO:0004854|GO:0072593|GO:0050660|GO:0042816|GO:0006767|GO:0009055|GO:0044281|GO:0005829|GO:0004031|GO:0043546|GO:0005737|GO:0051287|GO:0006954|GO:0006766|GO:0070062|GO:0055114. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138311_PI430048170 0.00612219644015174 0.65233155538378 5.9060274054202 5.66669406427822 5.80066292480691 P P P 6.24619793228497 6.42313524402247 6.54720199631699 P P P LNCV6_138311_PI430048170 mRNA
AGTCATACAGAGCGGTCCACCTAAAAGGCACTCCTGATAATAATAAATGATTTTAAACAA NM_004949RefSeq chr18 - 31065973 31102432 DSC2 1824 "desmocollin 2, transcript variant Dsc2b"
GO:0005515|GO:0030057|GO:0086042|GO:0005886|GO:0005509|GO:0031410|GO:0086091|GO:0086069|GO:0005913|GO:0014704|GO:0016021|GO:0007155|GO:0007156|GO:0009267|GO:0070062|GO:0086005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135423_PI430048170 0.5822785341366390.9786416952729410.25980283925453 0.2679599250154850.413674951936667A A A 0.3621023299237980.353325719179905 0.324436682899796A A A LNCV6_135423_PI430048170 mRNA
CATGGGGCAAATGTTTTTACTGTCAATGTATATTGCAAGGTGAATTCAAATGCATCCTTT NM_152512RefSeq chr22 - 39743043 39893790 ENTHD1 150350 ENTH domain containing 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132481_PI430048170 0.1310785952683710.6127802926480390.537693157429294 0.4797686254339250.263967127203307A A A 0.9260325748507191.62077531684889 0.703800166215123A A A LNCV6_132481_PI430048170 mRNA
GGGTGAAACTTGTTTTTCTGAAAAATGAAGTAACTGAAAATGCTGCTTCAGAATGTCTTG NM_004239RefSeq chr14 - 91967898 92040059 TRIP11 9321 thyroid hormone receptor interactor 11
GO:0005515|GO:0005801|GO:0005794|GO:0006996|GO:0006366|GO:0003713|GO:0003281|GO:0005634|GO:0002079|GO:0000139|GO:0002081|GO:0005856|GO:0000042 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99635_PI430048170 0.0194396474075855 0.8438563762378598.28701833402513 8.13850757897603 8.24825532548195 P P P 8.37883866352929 8.53608969264027 8.4931821678726 P P P LNCV6_99635_PI430048170 mRNA
ACGGACAGTTTGCTTTCGGCATCTTCGATGACAGCTTCGAGATCCCCACGTTCCCTCCTG NM_194460RefSeq chr19 - 647525 663233 RNF126 55658 ring finger protein 126
GO:0005515|GO:0005154|GO:0006513|GO:0016874|GO:0042059|GO:0005634|GO:0071629|GO:0070534|GO:0005737|GO:0042787|GO:0042127|GO:0042147|GO:0008270|GO:0043161|GO:0070936|GO:0043162 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141295_PI430048170 0.7386900516086820.9706154991397731 1.7164599571709 11.7477201916884 11.9253605221996 P P P 11.7898990271024 11.7083012787224

12.0119843434887 P P P LNCV6_141295_PI430048170 mRNA
GAATCACATTTCGACTCGGTCTGCTGATCTGAGGTTTTTAGATTTTAAATATTTATGTGG NM_015622 RefSeq chr7
+ 5898709 5925972 CCZ1 51622 CCZ1 vacuolar protein trafficking and biogenesis associated
homolog (S. cerevisiae) GO:0031988|GO:0016192|GO:0005765|GO:0043231 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_71295_PI430048170 0.2179797575282320.8436416473465540.4313815543970960.46418624270878
0.493277391015467 A A A 0.8619465002416430.7932731807182260.434787799229497 A A A
LNCV6_71295_PI430048170 mRNA
AAAGGATGAAAGTCTGAGAATGCCCAACTCTTCATTTTGAGTCTCAGGCCCTGAAGGTTC NM_030777 RefSeq chr20
+ 46709639 46736346 SLC2A10 81031 "solute carrier family 2 (facilitated glucose transporter), member
10"
GO:0048471|GO:0005737|GO:0015758|GO:0005886|GO:0005351|GO:0016021|GO:0055085|GO:0015992|GO:0012
505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59719_PI430048170 0.3087117301427330.8430912318706686.82860158446175 6.64256088584376
6.91792116386993 P P P 6.73789990998413 7.02145585256437 7.32275905826888 P P P
LNCV6_59719_PI430048170 mRNA
GTCCTCATTGTGAAATGCATGCCATACGAAATTTGAACGTAGCTTTGGAAAAAGGGACTA NM_001516 RefSeq chr12
+ 123633738 123662604 GTF2H3 2967 "general transcription factor IIH, polypeptide 3, 34kDa, transcript
variant 1"
GO:0010467|GO:0006368|GO:0003700|GO:0006367|GO:0006366|GO:0006363|GO:0006362|GO:0006361|GO:0006
360|GO:0006412|GO:0046872|GO:0000439|GO:0016032|GO:0008094|GO:0006355|GO:0006370|GO:0008353|GO:0
050434|GO:0003684|GO:0047485|GO:0006281|GO:0004672|GO:0006283|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_110749_PI430048170 0.2827766643919241.16984125268661 8.64000784229305
8.79343017548626 8.38984920578751 P P P 8.65194681744074 8.30789614125889
8.16927672840628 P P P LNCV6_110749_PI430048170 mRNA
TACATTGGCAAATACAAGTGTGACTGTCCCCCAGGCTTCTCCGGGCGGCACTGCGAGATA NM_001080437 RefSeq
chr2 + 240998837 241094228 SNED1 25992 "sushi, nidogen and EGF-like domains 1"
GO:0007160|GO:0005509|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130715_PI430048170 0.0131090484934697 0.5979314033548682.3562448704788
2.71972145700139 2.29663698052425 A A A 3.04176140871973 3.31086365700886
3.26885663997872 P P P LNCV6_130715_PI430048170 mRNA
AAACTACTAGGATCCTGTGTGTGTTCAAACTCAGTGCCATTAACAAACCCAAAGTGAAGC NM_014930 RefSeq chr9
- 96755864 96778046 ZNF510 22869 zinc finger protein 510
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138772_PI430048170 0.6364079851685121.03308750261598 0.490478226304626
0.3825565911632660.647066555014541 A A A 0.4184041544868190.493479795384493
0.478560114565062 A A A LNCV6_138772_PI430048170 mRNA
AATAACTTGCTCTGGTGTCAATTCGCTATTCGCCAGCAGACATCAGAACACACCGAGTTT NM_001256819 RefSeq
chr3 - 150926566 150972999 CLRN1 7401 "clarin 1, transcript variant 6"
GO:0005886|GO:0007605|GO:0060088|GO:0045494|GO:0030027|GO:0005902|GO:0010592|GO:0048870|GO:0007
015|GO:0050957|GO:0016021|GO:0007601|GO:0050896|GO:0050953 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140643_PI430048170 0.3247250206937830.7782153849215370.29687335261893
0.2715085161244740.384751268767106 A A A 0.2882322531683530.508336864795731
1.11359060392911 A A A LNCV6_140643_PI430048170 mRNA
GCTGACTAAGCCTGGGAGAGGGTTTGTCACAATAAAAGAATACTTACTAACCTCAAAAAA NM_001099434 RefSeq
chr1 + 32209093 32216196 DCDC2B NA doublecortin domain containing 2B NA . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_140165_PI430048170 0.0144275051619608 0.3220468617854553.61232290924186
2.76515531718085 3.56616768304358 P A P 4.39824193153818 5.09875654814594
5.34021353997625 P P P LNCV6_140165_PI430048170 mRNA
GGGCCTATCATTAACATTAGCTTAGGGATTCTGATTTCAAAGACATAAAGAATTGGCAAA NM_017666RefSeq chrX
- 130202698 130268948 ZNF280C 55609 zinc finger protein 280C
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138627_PI430048170 0.0533873238707223 1.39252348196154 5.4770274936116
5.58223729237454 5.8448958727853 P P P 5.40676867683842 5.10942763564155 4.9411207910486
P P P LNCV6_138627_PI430048170 mRNA
GGAGCAAAACTGGCTATTTCTGTGAATGATATAAAACAGGGTTCTCTGTAATGGTATTGT NM_052920RefSeq chr2
+ 23385426 23708613 KLHL29 114818 kelch-like family member 29 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130049_PI430048170 0.00644154545013395 0.2658225357670841.35663918196177
1.31747918423837 2.03899347358648 A A A 3.34550817377424 3.49982123086887
3.69959623485918 P P P LNCV6_130049_PI430048170 mRNA
GGATGGTCCTCTTATCTTTACCAGTGCACATGGTGAAAAAATTCAAACAGTATAATAAAG NM_001291999 RefSeq
chr3 + 136862207 136951610 NCK1 4690 "NCK adaptor protein 1, transcript variant 3"
GO:0005515|GO:0060734|GO:0050852|GO:0005886|GO:0005783|GO:0030032|GO:0030159|GO:0005634|GO:0005
829|GO:0006930|GO:0005737|GO:0007172|GO:0071074|GO:0030838|GO:0033137|GO:0005911|GO:0007411|GO:1
900102|GO:0045944|GO:0000164|GO:0042102|GO:0060548|GO:0007015|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139531_PI430048170 0.0547274690596022 1.96786528702702 4.88241619422196
4.72561338382488 5.10192841173891 P P P 4.10909264127224 3.31952451146948
4.22071108870872 P P P LNCV6_139531_PI430048170 mRNA
ACGAAGCACAAGTCTGTTAAGCAGAAGGCTCCAAGCTGTATTCTATACTTGGGAATCCTT NM_058229RefSeq chr8
- 123497886 123541253 FBXO32 114907 "F-box protein 32, transcript variant 1"
GO:0005515|GO:0030018|GO:0016567|GO:0005730|GO:0014894|GO:0071549 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141124_PI430048170 0.1772333831278081.12236755190681 0.640683853708131
0.3727394843280340.591562298915066A A A 0.2832599952712240.405164432587811
0.42667965439161 A A A LNCV6_141124_PI430048170 mRNA
TGTCAGCACTGGAGTCTTCTTGCTGAACTGCGAATAAAGAGATGTGCTGTTTAACAACCC NM_174927RefSeq chr11
- 133840621 133845538 SPATA19 219938 "spermatogenesis associated 19, transcript variant 1"
GO:0007275|GO:0005741|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129416_PI430048170 0.00557918818809222 0.5730477631447151 0.7272840312552
10.4970244945202 10.3795632050451 P P P 11.328835809892 11.4452005179482
11.2551922706065 P P P LNCV6_129416_PI430048170 mRNA
CACTTCTGGGGGGCCCTTTCAGAGGCACTTTTAAAGCAAATAAAACATTTATTGTTCAGA NM_017842RefSeq chr12
+ 47773183 47782753 SLC48A1 55652 "solute carrier family 48 (heme transporter), member 1"
GO:0015886|GO:0015232|GO:0016021|GO:0005765|GO:0010008 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_97145_PI430048170 0.0587897564091156 0.6603023167403655.75263879756599
6.14487858959982 6.31645330218142 P P P 6.67935855612546 6.62147719018081
6.76239125243859 P P P LNCV6_97145_PI430048170 mRNA
ACATGGACACAAGCAACACCAGCATCAGTAAAATGAAAAGATCCAGACCCACATCTGAGG NM_001267039
RefSeq chr4 + 112636963 112657592 LARP7 51574 "La ribonucleoprotein domain family, member 7,
transcript variant 3"

GO:0005515|GO:0006396|GO:0005737|GO:0005794|GO:0000166|GO:0030529|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140735_PI430048170 0.5835666228178060.9518113988777651 0.0114326244743 10.2834159133609 10.2872624193665 P P P 10.3679536135078 10.1079823642132 10.3237078233781 P P P LNCV6_140735_PI430048170 mRNA
CCCAGGAAGCTTACAATTTTCTTCTCTCTCTTTTGTGCAATTTGTCTGATTTAGGACTTG NM_153450RefSeq chr11 - 57703714 57712201 MED19 219541 mediator complex subunit 19
GO:0005515|GO:0001104|GO:0006366|GO:0006357|GO:0016592|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132665_PI430048170 0.1013215167751840.3173247666449720.325372952897431 2.62911477108907 1.9336960048135 A A A 3.31122592321416 3.58906713472139 3.75736129408772 P P P LNCV6_132665_PI430048170 mRNA
GGCACTACAATGAAATGGCAGGATGCCAATATGAGATATTTCAGGAATAATAAGAAATAC NM_024594RefSeq chr5 - 168555622 168579609 PANK3 79646 pantothenate kinase 3
GO:0004594|GO:0016310|GO:0005737|GO:0015937|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133117_PI430048170 0.3527271026413850.7971023579799418.12083030195451 8.09291778373127 8.36922188411307 P P P 8.03867385659177 8.55147666853263 8.87170901573717 P P P LNCV6_133117_PI430048170 mRNA
GAGATAGACTCGTGTTACCTTGATGGATATTGGATTTGTCTAAGTCTCTTCTAGAAAAAA NM_001294314 RefSeq chr12 - 111931282 112013219 TMEM116 89894 "transmembrane protein 116, transcript variant 4"
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135321_PI430048170 0.0997426111733433 0.6995064517144038.91957700594094 8.70339779193027 8.50724725026646 P P P 8.83592128542855 9.41931271532663 9.38089867753741 P P P LNCV6_135321_PI430048170 mRNA
TCTGTACTAGTTTGTGGCAGCTCAAGTAAAATCGAGTCCAAACCAACGGCTCTTTTCAGG NM_021064RefSeq chr6 + 27133037 27133535 HIST1H2AG 8969 "histone cluster 1, H2ag"
GO:0005515|GO:0008150|GO:0046982|GO:0005634|GO:0019899|GO:0000786|GO:0003677|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142788_PI430048170 0.0063925960966697 6 0.7092526949062179.51178407650894 9.43298059252951 9.34611747317738 P P P 10.013722156927 9.97309823531887 9.78558757655725 P P P LNCV6_142788_PI430048170 mRNA
ATGGAACCCCAGGATGACTCAGCAATAAAATATTTTTGGTTTTTTGGTTTTGTATGTTGG NM_017807RefSeq chr14 - 20447047 20455108 OSGEP 55644 O-sialoglycoprotein endopeptidase
GO:0070526|GO:0016747|GO:0005737|GO:0000408|GO:0005634|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138926_PI430048170 0.3379568869534970.92251521212177 15.6844536894455 15.678121251824 15.4821726681129 P P P 15.8666865458845 15.7372068450151 15.5852330491591 P P P LNCV6_138926_PI430048170 mRNA
GGAGCAAGTTTTGTATTTGTGACCTCAGCTTTGGGAATAAAGGATCTTTTGAAGGCCAAA NM_001025195 RefSeq chr16_GL383556v1_alt - 26724 57068 CES1 1066 "carboxylesterase 1, transcript variant 1"
GO:0052689|GO:0030855|GO:0008152|GO:0009636|GO:0005788|GO:0047374|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131880_PI430048170 0.7847361738120761.05447617288168 1.94013304021137 1.07205044750418 1.95517056064004 A A A 0.6451018326076932.23797944785551 1.59886594831248 A A A LNCV6_131880_PI430048170 mRNA
CTCAGTCTGGAAGACAATGTGGTGACTTAATTTGTTGAGAACTATGTTACAAATAATGTG NM_003953RefSeq chr1 + 167721949 167791919 MPZL1 9019 "myelin protein zero-like 1, transcript variant 1"
GO:0005515|GO:0009986|GO:0005887|GO:0005198|GO:0007267|GO:0007169|GO:0005925 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_134373_PI430048170 0.0793143519746745 1.11236875358389 9.92458950192209
9.98122890098232 9.9701864376381 P P P 9.83323835975764 9.70474028993689
9.87245895999176 P P P LNCV6_134373_PI430048170 mRNA
TGCTATGGCCTCATCATCAAGACTTTCAATCCTATCCCAAGTGAAATAAATGGAATGAAA NM_004633 RefSeq chr2
+ 101991843 102028422 IL1R2 7850 "interleukin 1 receptor, type II, transcript variant 1"
GO:0005515|GO:0006955|GO:0004910|GO:0005886|GO:0019221|GO:0004908|GO:0005576|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135963_PI430048170 0.3882835274814190.90087682075632 0.393047653830852
0.2834286833117710.32669549136864 A A A 0.2883252680897450.415851310380794
0.718502500097888 A A A LNCV6_135963_PI430048170 mRNA
GCACACATACAGCAAAGTGTATAGAACAAAGTACGTACAACTCTGAATTCTTATGAAGTA NM_152539 RefSeq chr3
+ 119146149 119151455 C3orf30 152405 chromosome 3 open reading frame 30 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_134453_PI430048170 0.3634610002577471.02778353139808 0.353367710052427
0.3544039759045560.451768340658214 A A A 0.3517824834597880.318699735056465
0.372174652766399 A A A LNCV6_134453_PI430048170 mRNA
TTCTAATCTGTCTGCTCCTTGTTCTACGGATTCCAAACCAAAAGAGGCAAGCAAGTCTGC NM_001291470 RefSeq
chr17_KI270909v1_alt + 165199 167015 CCL4L2 9560 "chemokine (C-C motif) ligand 4-like 2, transcript
variant CCL4L2b2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130514_PI430048170 0.0315199933856246 1.52613516008454 13.342294213992
13.3875072276162 13.4266223916217 P P P 13.001280750702 12.6915759291567
12.6043726106387 P P P LNCV6_130514_PI430048170 mRNA
TTCGAGGTGGAGCTGCTCAAAATAGAGCGACGAACTGAGCTGTAACCAGACTGGGGAGGG NM_004470 RefSeq
chr11 + 64240940 64244135 FKBP2 2286 "FK506 binding protein 2, 13kDa, transcript variant 1"
GO:0005515|GO:0000413|GO:0061077|GO:0005783|GO:0005789|GO:0003755|GO:0005528|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90938_PI430048170 0.0415800086510411 1.49076318995935 6.33673701556185
6.79147050043428 6.68169538612289 P P P 6.2730605309426 6.01310861474023
5.79355137674181 P P P LNCV6_90938_PI430048170 mRNA
AGCCTGCTTAAAAAGCTGGGGAGCAACACGTACCCCTTTCTCCTGACGTTTCCTGACTAC NM_000541 RefSeq chr2
+ 233307662 233347055 SAG 6295 S-antigen; retina and pineal gland (arrestin)
GO:0051219|GO:0001917|GO:0007603|GO:0004864|GO:0022400|GO:0002046|GO:0043086|GO:0007601|GO:0007
166|GO:0016056|GO:0005829|GO:0001750 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142077_PI430048170 0.0154653389819759 0.5457573760249957.18612744870615
7.16476482845904 6.74325993725935 P P P 8.08556425406775 8.03365764983451
7.58767739600537 P P P LNCV6_142077_PI430048170 mRNA
TGGGAGCCCTGATGCTGCCGTGTGATGTTTCAATAAAGGTGGATCTCACTGTTGAAAAAA NM_001098537 RefSeq
chr9 - 137459951 137550569 PNPLA7 375775 "patatin-like phospholipase domain containing 7, transcript
variant 1"
GO:0006629|GO:0032502|GO:0031965|GO:0031966|GO:0005783|GO:0004622|GO:0016021|GO:0005765 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132081_PI430048170 0.5093369054403521.03563253570344 0.280891242661341
0.3023323980708130.470956402535095 A A A 0.3241988977630030.28902072094021
0.296793864822413 A A A LNCV6_132081_PI430048170 mRNA
CAGGTCTACAAGGAGATACTTTGTTTCTAAAAAAGGAGTTAAATCGTGTCACCTGAATTT NM_153207 RefSeq
chr12 + 19439673 19522239 AEBP2 121536 "AE binding protein 2, transcript variant 1"
GO:0010467|GO:0001078|GO:0035098|GO:0045814|GO:0003714|GO:0040029|GO:0005654|GO:0000122|GO:0000
978|GO:0046872|GO:0006351|GO:0016568 . NA - . NA NA NA NA NA NA NA NA

NA
LNCV6_126496_PI430048170 0.385948158056575 1.04803400982556 0.324201913051662
0.328800224101968 0.504195274954388 A A A 0.322786339285362 0.291006869254031
0.34719346724085 A A A LNCV6_126496_PI430048170 mRNA
AGGGTCTGAGAACTGTCAGCCTTTTGCCATTCAAAAACATTTATGTCCAACCTGAAAAAA NM_001146312 RefSeq
chr17 + 12665889 12768948 MYOCD 93649 "myocardin, transcript variant 1"
GO:0005515|GO:0006366|GO:0055012|GO:0010832|GO:0045661|GO:1900222|GO:0001560|GO:0051152|GO:0061
049|GO:2001015|GO:0010667|GO:0055007|GO:0035035|GO:0048286|GO:0051150|GO:2000721|GO:0003713|GO:2
000724|GO:0000122|GO:2000727|GO:0043388|GO:0045893|GO:0003231|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143807_PI430048170 0.821062643761578 0.981809815693824 10.1241523802857
9.94241705171208 9.71462637895501 P P P 9.83086148616967 10.0371800564565
10.0129056717394 P P P LNCV6_143807_PI430048170 mRNA
ATTCCTGCTGCCTGTATTCTCTATTCCAATAAAGCAGAGTTTGACACCGTCTGCAAAAAA NM_007184 RefSeq
chr3 + 52455507 52493072 NISCH 11188 "nischarin, transcript variant 1"
GO:0005515|GO:0030336|GO:0030036|GO:0005886|GO:0006915|GO:0042802|GO:0005829|GO:0016601|GO:0005
178|GO:0007186|GO:0016020|GO:0032228|GO:0008217|GO:0006006|GO:0055037|GO:0035091|GO:0008227|GO:0
048243|GO:0005769. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131270_PI430048170 0.49496675393308 0.9769959871728170.359046884725154
0.34484423023946 0.275716377001623A A A 0.3272445248710690.430486005075717
0.321341183358064A A A LNCV6_131270_PI430048170 mRNA
AGTGTAAGGAAACTGTCTGGGGTGATTCCTAGAAGATCATTAAACTGTGGTACATTTTTT NM_001290271 RefSeq
chr19_KI270938v1_alt + 555577 570141 LILRA2 11027 "leukocyte immunoglobulin-like receptor,
subfamily A (with TM domain), member 2, transcript variant 4"
GO:0007165|GO:0006952|GO:0005576|GO:0004872|GO:0016021|GO:0003823|GO:0002376 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128441_PI430048170 0.1031470800062853.36114142923148 2.98076087496701
1.18451252476399 2.79195770852104 P A A 0.4770627346395010.860873300992056
0.908663315624939A A A LNCV6_128441_PI430048170 mRNA
GGGCCTCTTTACCATAGCTTAAGAAGTATCCCTGATTTATTCTGGTGTCTAATAAACACA NM_000798RefSeq chr4
+ 9781633 9784009 DRD5 1816 dopamine receptor D5
GO:0005886|GO:0007268|GO:0060292|GO:0031526|GO:0045776|GO:0019226|GO:0042220|GO:0001992|GO:0007
191|GO:0007190|GO:0001963|GO:0033861|GO:0045924|GO:0008306|GO:0001588|GO:0072593|GO:0006874|GO:0
004952|GO:0010579|GO:0035240|GO:0046960|GO:0045762|GO:0001975|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133359_PI430048170 0.8002043400757630.9754650352531364.41045847485942
4.51475381398982 3.95068023027803 P P P 4.33538666234276 4.47169959776414
4.22584894205666 P P P LNCV6_133359_PI430048170 mRNA
GTAGCGGTCCAAGCCTGCAACTCATCTTTCATTAAAGGCTTCTCTCTCACCAGCAAAAAA NM_006271RefSeq chr1
+ 153628396 153632037 S100A1 6271 S100 calcium binding protein A1
GO:0005515|GO:0043005|GO:0030018|GO:0005509|GO:0008016|GO:0005634|GO:0000122|GO:0031430|GO:0042
803|GO:0042802|GO:0035556|GO:0044548|GO:0043234|GO:0016529|GO:0021762|GO:0051117|GO:0048306 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141663_PI430048170 0.8382310876085471.0440381074122 8.08357266734629
8.58622987494994 8.72543187218508 P P P 8.13688160318511 8.38878235680237
8.70290141155703 P P P LNCV6_141663_PI430048170 mRNA
GGACTTTACAGAGTTCTTTTTCCTCTTGGCATTTCCTAATAACAAAACTTTCTGTGTTCT NM_138443RefSeq chr18 +
46104331 46128333 HAUS1 115106 "HAUS augmin-like complex, subunit 1, transcript variant 1"
GO:0051297|GO:0005515|GO:0003674|GO:0007067|GO:0005813|GO:0005737|GO:0000922|GO:0005874|GO:0070

652|GO:0051225|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130450_PI430048170 0.00805200360044614 0.4741209337427676.53274892903458
6.28489071129955 6.30020937441612 P P P 7.17893817785776 7.43176633907123
7.70315723839138 P P P LNCV6_130450_PI430048170 mRNA
GGTCAGCCCTTGTCCACTTATTCACTTCCCTCCTTTTGTAAAATAAGTGCTTTAATTATA NM_002336RefSeq chr12 -
12116025 12266877 LRP6 4040 low density lipoprotein receptor-related protein 6
GO:0005515|GO:0017147|GO:0019534|GO:0045599|GO:0045598|GO:0045202|GO:0014029|GO:0042803|GO:0021
861|GO:0042802|GO:0009880|GO:0001947|GO:0005041|GO:0005109|GO:0021794|GO:0016337|GO:0042074|GO:0
021795|GO:0046849|GO:0014033|GO:0043025|GO:0016055|GO:0005794|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106213_PI430048170 0.454254972608892 1.04179378940969 0.284115659072061
0.2976206388739030.474138690663884A A A 0.3140022410660720.278877712301691
0.293466484095599A A A LNCV6_106213_PI430048170 mRNA
GTGTAATGAACACCGAGTGGATAATAGAAAGTTGAGACTAAACTGGTTTGTTGCAGCCAA NM_000879RefSeq chr5
- 132541443 132543522 IL5 3567 interleukin 5
GO:0005515|GO:0071803|GO:0005137|GO:0030890|GO:0019221|GO:0050731|GO:0005576|GO:0005125|GO:0005
615|GO:0046427|GO:0051091|GO:0006955|GO:0006954|GO:0045645|GO:0051024|GO:0045893|GO:0008083 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131928_PI430048170 0.1001753337508191.29336140167797 5.55613728049261
5.62236751786774 5.6703455612356 P P P 5.46489775356622 5.24332957664651
4.99073095308465 P P P LNCV6_131928_PI430048170 mRNA
TGTCCTCACAGGACACTCTCCGCTCCACGAAGTCTGGCCCCAAGCTTCTCTCTGGCCTGT NM_001162914 RefSeq
chr8_KI270816v1_alt - 183740 185156 CCDC166 100130274 coiled-coil domain containing 166 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129387_PI430048170 0.196134779181777 1.40693740904628 4.94415652260558
5.11759773780753 5.56582242705741 P P P 5.12232428770847 4.75376541504621
4.20268035018845 P P P LNCV6_129387_PI430048170 mRNA
ACATTTGTATTTTTATATCCGACTCTTTGTTTACTGGCTCTGCTCATGGTTCCTGCCCTC NM_033259RefSeq chr3 -
184259214 184261463 CAMK2N2 94032 calcium/calmodulin-dependent protein kinase II inhibitor 2
GO:0005813|GO:0019901|GO:0008427|GO:0005634|GO:0006469|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139047_PI430048170 0.566832641870032 0.9202405218686867.9257909878519
8.26723785877033 7.89195428549418 P P P 8.40333362845234 8.1155080824404
7.91433051302949 P P P LNCV6_139047_PI430048170 mRNA
CAGCCCTAATGATGCTGTGTCCATGATGCTTTTAATAAAAACAACCCCCACTGCAAAAAA NM_006647RefSeq chr9
+ 137423394 137434406 NOXA1 10811 "NADPH oxidase activator 1, transcript variant 1"
GO:0005515|GO:0048365|GO:0017124|GO:0005737|GO:0016176|GO:0006801|GO:0060263|GO:0010310|GO:0043
020|GO:0043085|GO:0019899 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129495_PI430048170 0.362912356802296 1.13444924902301 0.41632002594176
0.8452852991714940.414802140453323A A A 0.3847630551301950.378484618709203
0.410941107675854A A A LNCV6_129495_PI430048170 mRNA
ATCTCGTGAAAACTCAGAAATGACAATAAAGCGTGGCATTTGCCTCTGTATTATAAATGA NM_003476RefSeq chr11
- 19182029 19210571 CSRP3 8048 cysteine and glycine-rich protein 3 (cardiac LIM protein)
GO:0005515|GO:0030018|GO:0033365|GO:0042805|GO:0006874|GO:0031433|GO:0005634|GO:0035995|GO:0060
048|GO:0048738|GO:0003300|GO:0002026|GO:0007519|GO:0045944|GO:0055003|GO:0008270|GO:0005856|GO:0
008307 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137287_PI430048170 0.0107829411889203 0.595574752430522 8.47425384255427
8.35188225881657 8.3331777175022 P P P 8.92465605473509 9.17324230536595
9.28523227602406 P P P LNCV6_137287_PI430048170 mRNA

TTCGTTGAATGCTCCTTCCCCTAGGCAGCTGGTAATAGAGGGGTAAAGCTCTGGGCCCCT NM_003893 RefSeq chr10 - 102107565 102114966 LDB1 8861 "LIM domain binding 1, transcript variant 3" GO:0000790|GO:0006366|GO:0005634|GO:0043621|GO:0042803|GO:0009948|GO:0010669|GO:0022607|GO:0021702|GO:0032784|GO:0045944|GO:0030182|GO:0030274|GO:0046985|GO:0043973|GO:0016055|GO:0001942|GO:0035019|GO:0005667|GO:0001102|GO:0006355|GO:0003714|GO:0000972|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140585_PI430048170 0.1938421820926581.0368138008539 0.424236846850136 0.3828950044538960.406675980691408A A A 0.3087781785266460.342392072819895 0.404814040603712A A A LNCV6_140585_PI430048170 mRNA
GTGTTAATTACAATATAGACCTCCTCAAGTTGGTTTTACAAATCTAGAACCATAGTGCAC NM_005795 RefSeq chr2 - 187341962 187448294 CALCRL 10203 "calcitonin receptor-like, transcript variant 1" GO:0004948|GO:0005515|GO:0005886|GO:0004930|GO:0005783|GO:0030819|GO:0001525|GO:0015031|GO:0048661|GO:0005764|GO:0031623|GO:0007507|GO:0006937|GO:0007187|GO:0001605|GO:0005887|GO:0050728|GO:0071329|GO:0008565|GO:0006171|GO:0006816|GO:0007189|GO:0001635|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89044_PI430048170 0.0632248804316356 0.8481059448655888.65342044275675 8.50186020150854 8.59289426458227 P P P 8.67641081673156 8.85871516286896 8.919194164688 P P P LNCV6_89044_PI430048170 mRNA
TCATTTTTCACTACTTAAGGAATAAATCCAAGAGCTTTCCAGAGACTGGCTGCTGCAGCC NM_001291641 RefSeq chr17 - 75236591 75261661 GGA3 23163 "golgi-associated, gamma adaptin ear containing, ARF binding protein 3, transcript variant 3" GO:0005802|GO:0005515|GO:0045732|GO:0030131|GO:0030306|GO:0016192|GO:0006886|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135259_PI430048170 0.2451821941774810.7642650375753673.262669102266 3.45404212616239 3.87597742099524 P P P 3.69550058536354 3.704004316401 4.33056174623808 P P P LNCV6_135259_PI430048170 mRNA
GTGCCAGATCTATTTTTTACAAGAACTGTGCAAATATCAGTAACTTTTGGGTAGGTATTG NM_014241 RefSeq chr10 - 17589958 17617374 HACD1 NA 3-hydroxyacyl-CoA dehydratase 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134743_PI430048170 0.1087331235205111.38567241531466 3.88495374839426 4.373605758034 4.39477855236615 P P P 3.67973962051854 3.52067189593648 4.04532952764671 P P P LNCV6_134743_PI430048170 mRNA
CCAGCAATGAAAGTAAGACACACAGCATATGACATAAGACACAGTGTGAAATAAATGAGT NM_182597 RefSeq chr7 + 112481010 112490888 LSMEM1 286006 "leucine-rich single-pass membrane protein 1, transcript variant 1" GO:0005737|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133069_PI430048170 0.0500522730594569 0.6780762498055387.75636339433412 7.27072437196265 7.745384131343 P P P 8.31730406836192 8.1444057915955 8.02867108534315 P P P LNCV6_133069_PI430048170 mRNA
TTTAAGGAGGCTTTCAACATGATTGACCAGAACCGTGATGGCTTCATTGACAAGGAGGAC NM_006097 RefSeq chr20 + 36541483 36549823 MYL9 10398 "myosin, light chain 9, regulatory, transcript variant 1" GO:0070527|GO:0030018|GO:0006937|GO:0001725|GO:0006936|GO:0048013|GO:0007411|GO:0005509|GO:0005859|GO:0008307|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137362_PI430048170 0.1068991462595260.6916287038674845.67903042466623 5.07116463967252 4.99212661194921 P P P 5.99290160053881 5.60347467477948 5.81748188011299 P P P LNCV6_137362_PI430048170 mRNA
GAAAGCTGTCCCCTGGCTGCCTCTAACAAACATTTTATCAAAAATCAGCAAATAAATAAA NM_001048249 RefSeq chr5 - 61157708 61162475 SMIM15 643155 small integral membrane protein 15 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100541_PI430048170 0.00334856138303174 1.42665242533009 9.49586368569569

9.65208124768791 9.69740090698213 P P P 9.11723837147803 9.0077717895374
9.18459950233331 P P P LNCV6_100541_PI430048170 mRNA
AATATGCCTCCTGTACCTCATGGAATGATGCCGCAGATGATGCCCCCTATGGGAGGGCCA NM_017892RefSeq chr2
- 152651592 152717461 PRPF40A 55660 PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)
GO:0005515|GO:0006397|GO:0008380|GO:0032465|GO:0008360|GO:0016363|GO:0005737|GO:0007049|GO:0016
020|GO:0016477|GO:0016607|GO:0007010|GO:0005654|GO:0070064|GO:0051301 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_68354_PI430048170 0.1737928405647390.82337948094812 6.23145317750545 5.91471176718112
6.12341478709025 P P P 6.1099256992918 6.42597210396971 6.55676348155969 P P P
LNCV6_68354_PI430048170 mRNA
TTAACCCTCGAGGAATACCTCAATACCTCAGACAAGGCCCTTCCAATATGTTTACGTTTT NM_133263RefSeq chr5
+ 149730251 149855022 PPARGC1B 133522 "peroxisome proliferator-activated receptor gamma,
coactivator 1 beta, transcript variant 1"
GO:0006366|GO:0003723|GO:0050682|GO:0005634|GO:0044281|GO:2000273|GO:0051591|GO:0005739|GO:0051
091|GO:0030374|GO:0000166|GO:0045780|GO:0045944|GO:0007015|GO:0044255|GO:0006355|GO:0006996|GO:0
001104|GO:0030331|GO:0045672|GO:0051384|GO:0006390|GO:0060346|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145646_PI430048170 0.0383740663794268 1.51297568538858 6.35206249970936
6.35168385888504 6.44994942499369 P P P 5.57958571832877 6.03062991441862
5.71582662331406 P P P LNCV6_145646_PI430048170 mRNA
ACTGATTCTGAAACAAAATGAAACTGCAAACCTCGTGTGTCTTAACTCCCCCCAGGGATG NM_012398RefSeq chr19
- 3630180 3700479 PIP5K1C 23396 "phosphatidylinositol-4-phosphate 5-kinase, type I, gamma,
transcript variant 2"
GO:0006909|GO:0005515|GO:0072583|GO:0030036|GO:0034333|GO:0005634|GO:0044281|GO:0005829|GO:0016
337|GO:0007411|GO:0007016|GO:0006661|GO:0030593|GO:0001891|GO:0032587|GO:0048488|GO:0005524|GO:0
016079|GO:0012505|GO:0016308|GO:0070527|GO:0046854|GO:0001931|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126652_PI430048170 0.4279835833870281.48161202442735 1.57216231830617
0.2510598310552550.292944303339474A A A 0.2715386050917430.286370497110193
0.275486872454034A A A LNCV6_126652_PI430048170 mRNA
GAGGAATGTATATGTTGGCTGTTTTTCCCCAACATCTCAATAAAACTTTGAAAGCAGAAA NM_003284RefSeq chr2
- 216859458 216860059 TNP1 7141 transition protein 1 (during histone to protamine replacement)
GO:0000012|GO:0006342|GO:0007289|GO:0035042|GO:0007286|GO:0007290|GO:0007275|GO:0006337|GO:0030
317|GO:0003677|GO:0019953|GO:0006338|GO:0000786|GO:0001673|GO:0045892 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_106632_PI430048170 0.0670970554713178 1.41968220960657 7.05984429217366
6.93306666997885 6.58496828651779 P P P 6.38759782359281 6.58489657606655
6.08646516269613 P P P LNCV6_106632_PI430048170 mRNA
TGAGCCTGAAGGACCAACAGACGTTCGCGCGCTCTGTGGGTCTCAAATGGCGCAAGGTGG NM_003789RefSeq
chr16 - 67154185 67159909 TRADD 8717 TNFRSF1A-associated via death domain
GO:0008625|GO:0005515|GO:2001239|GO:0031264|GO:0005634|GO:0032403|GO:0051291|GO:0005829|GO:0042
802|GO:0070513|GO:0005737|GO:0051092|GO:0060090|GO:0004871|GO:0019900|GO:0005856|GO:0043123|GO:0
005164|GO:0043065|GO:0006919|GO:0006915|GO:0097191|GO:0033209|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140876_PI430048170 0.00188160381509058 4.32662606013113 9.12108652345189
9.47785161031221 9.27248088152281 P P P 7.53482720308402 6.99541121393644
6.94723860660824 P P P LNCV6_140876_PI430048170 mRNA
TCGCTGGCTTTTCCCCTTGTGTTCTGAGAATACACCATCGGCTCATTCCCACCAGCGGCT NM_002282RefSeq chr12
- 52314300 52321398 KRT83 3889 "keratin 83, type II"

GO:0042633|GO:0008544|GO:0005198|GO:0007568|GO:0045095|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116450_PI430048170 0.00787858906218628 1.41674214536276 9.76138085805099 10.0246565524207 9.88844937892026 P P P 9.50135388403358 9.3918364084712 9.27686022476048 P P P LNCV6_116450_PI430048170 mRNA GGAATTTGTATTTTTTGCCTTTGTTCAGAATACATGACATTGGTAAATATGCCACATGCC NM_018009 RefSeq chr12 + 6452010 6462322 TAPBPL 55080 TAP binding protein-like
GO:0005886|GO:0000139|GO:0005789|GO:0016021|GO:0002590|GO:0032403|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141390_PI430048170 0.938607746951751 1.05196379966666 2.08615024046947 0.496963869289494 0.263324939366367 A A A 1.78695601508209 0.549253673865755 0.68228847554023 A A A LNCV6_141390_PI430048170 mRNA CAGGGGCATTTAGGGAGCAGATGACTGAGAACATTAAAAAAGAACTTAAATGACACAGCA NM_001243168 RefSeq chr6 + 42915988 42925837 PTCRA 171558 "pre T-cell antigen receptor alpha, transcript variant 1" GO:0005515|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117869_PI430048170 0.936745171053225 1.05640213265063 1.58579898122572 0.527151261660061 1.44621211010055 A A A 0.77366317314377 1.35091783038557 1.33611063502654 A A A LNCV6_117869_PI430048170 mRNA AAACTAAATTACTTCCTAGTATTGAGGAGGCATGGAGCCTACCAATCCCCGCAGAGCTTA NM_001258249 RefSeq chrY - 13248378 13480670 UTY 7404 "ubiquitously transcribed tetratricopeptide repeat containing, Y-linked, transcript variant 4"
GO:0010468|GO:0071557|GO:0051213|GO:0005634|GO:0046872|GO:0071558|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127958_PI430048170 0.394267738914783 1.1013479107797 0.297527644206778 0.26088724076193 0.637587835554581 A A A 0.282169883591666 0.249957176937869 0.276512070186277 A A A LNCV6_127958_PI430048170 mRNA AATTGCCTGCTTCAGAGGCTAATATAACAAAACCAATAAAACCGAGTGATGGTGAAAAAA NM_001278635 RefSeq chr5 - 1877426 1886984 IRX4 50805 "iroquois homeobox 4, transcript variant 4"
GO:0043565|GO:0007507|GO:0006355|GO:0005634|GO:0048561 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142594_PI430048170 0.0430751427021782 0.434298808822425 0.37362093001278 0.376688977438296 0.441744090198324 A A A 1.83527195266231 1.05579977489135 1.78782505651547 A A A LNCV6_142594_PI430048170 mRNA TGTGCACGTGTATAGCTCAAAGAGCTTAGACTTCAAATATATCTGGTGAATGACTCTTTG NM_005822 RefSeq chr6 - 46220729 46325892 RCAN2 10231 "regulator of calcineurin 2, transcript variant 1"
GO:0000166|GO:0031987|GO:0007614|GO:0033173|GO:0005575|GO:0006979 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139826_PI430048170 0.185960115116929 0.271040896579144 1.55514519493998 0.329631966994371 0.402503718962173 A A A 1.3368582563294 3.87323492194942 1.6668446655393 A P A LNCV6_139826_PI430048170 mRNA AAACTGAGTCTGATACGTAGTGAGGCAGAGACAAAAGGGCTAGGGTGGAAAAATTTTTAA NM_001136030 RefSeq chr12 - 54948302 54984746 TESPA1 9840 "thymocyte expressed, positive selection associated 1, transcript variant 1"
GO:0033089|GO:0005737|GO:0010387|GO:0008180|GO:0005789|GO:0005102|GO:0050862 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136624_PI430048170 0.715911936718622 1.05599556877168 5.51136277039693 5.25198293146981 5.76301229037488 P P P 5.26684193662275 5.4196512465655 5.62646420354925 P P P LNCV6_136624_PI430048170 mRNA ATCCTTCTCTTTGTAGAGAATAGAGACGTTTGTCTTGTCTGTCTTCAACCTACTTTTCCT NM_001258329 RefSeq chr20

+ 36092709 36232799 EPB41L1 2036 "erythrocyte membrane protein band 4.1-like 1, transcript variant 3"
GO:0005886|GO:0030866|GO:0005198|GO:0007268|GO:0003779|GO:0005856|GO:0019898|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124443_PI430048170 0.4396721047192010.9524634433403631 0.1937589941142
10.2312294223731 10.3743813051315 P P P 10.2781204002696 10.4563256636039
10.2744889478157 P P P LNCV6_124443_PI430048170 mRNA
AAAGATTTTCAACGACGAATTCTTGTGGCTACCAACCTATTTGGCCGAGGCATGGACATC NM_004640RefSeq
chr6_GL000255v2_alt - 2786080 2798331 DDX39B 7919 "DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B, transcript variant 1"
GO:0008380|GO:0005515|GO:0000245|GO:0043008|GO:2000002|GO:0000346|GO:0030621|GO:0005634|GO:0005524|GO:0046784|GO:0008186|GO:0004004|GO:0005737|GO:0032786|GO:0006406|GO:0016607|GO:0000398|GO:0010501|GO:0005654|GO:0005681|GO:0017070|GO:0005687|GO:0005688 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144329_PI430048170 0.0543955654145937 0.6365332647676319.24986767715967
8.70230234312699 9.27693852258216 P P P 9.73299424337882 9.88383184041135
9.62507662760027 P P P LNCV6_144329_PI430048170 mRNA
CAATCAATCAGTCACTGTGTCCCAGACATATTCAATAAACACAGATTGGTACCACCCAGC NM_004599RefSeq chr22
+ 41833078 41907308 SREBF2 6721 "sterol regulatory element binding transcription factor 2, transcript variant 1"
GO:0005515|GO:0006629|GO:2000188|GO:0005783|GO:0005634|GO:0044281|GO:0005829|GO:0005737|GO:0045944|GO:0032937|GO:0046983|GO:0044255|GO:0072368|GO:0008203|GO:0071499|GO:0012507|GO:0000247|GO:0005730|GO:0070888|GO:0000122|GO:0000978|GO:0008022|GO:0010886|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_62439_PI430048170 0.1639785428747821.19171807859821 4.35611762826618 4.45455362974958
4.48444344140987 P P P 4.25630821493045 4.3300680967897 3.9205902577276 P P P
LNCV6_62439_PI430048170 mRNA
TCTGTACCAAAATCTACGTGGATGCGGTCTTCATTGACACAAGTAACCTGGACATCACTC NM_013272RefSeq chr15
+ 91853707 92165907 SLCO3A1 28232 "solute carrier organic anion transporter family, member 3A1, transcript variant 1" GO:0005215|GO:0005886|GO:0043252|GO:0016021|GO:0055085 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_137324_PI430048170 0.3634267979251160.9669749875590390.421981763254124
0.4471305822071730.311280610167416A A A 0.41467696080885 0.475868292334102
0.438124438601617A A A LNCV6_137324_PI430048170 mRNA
CTCCATTACAGGGGTCTTCTAGGTATTCCCCACACATTATTTGTGGGCATAAGCAAACAC NM_052907RefSeq chr12
+ 125326615 125662377 TMEM132B 114795 "transmembrane protein 132B, transcript variant 1"
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131522_PI430048170 0.1375176890344041.33064827560881 5.14877571654295
5.44106162482249 5.22946647541587 P P P 4.55498425963807 5.20213734444049
4.76469160192073 P P P LNCV6_131522_PI430048170 mRNA
CTCCCTAATTCAGACCCAGCCTCAAGAGGAAAGGGAGTAAAATAAAACTAACTTGTTTAT NM_020435RefSeq chr1
+ 228149713 228159826 GJC2 57165 "gap junction protein, gamma 2, 47kDa"
GO:0005243|GO:0043209|GO:0007267|GO:0009636|GO:0005922|GO:0016021|GO:0055085 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126654_PI430048170 0.03926972328688 1.25454089307536 11.0987264980044
11.2968040056445 11.3164309796681 P P P 11.0197365425252 10.7485435552014
10.9582997987304 P P P LNCV6_126654_PI430048170 mRNA
GGAAAGAGAACCTTCCCTTCTGTACTGTTAACTTAAAAATAAATAGCTCCTGATTCAAAG NM_004751RefSeq chr15
+ 59611782 59620011 GCNT3 9245 "glucosaminyl (N-acetyl) transferase 3, mucin type"

GO:0003829|GO:0005975|GO:0002426|GO:0016266|GO:0008109|GO:0050892|GO:0000139|GO:0006493|GO:0016020|GO:0060993|GO:0048729|GO:0016021|GO:0044267|GO:0047225|GO:0070062|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137269_PI430048170 0.0315176095476171 0.2668532409081591.66775000539076 1.94147664280221 1.99362871643964 A A A 2.95312683051453 4.0449837550942 4.08510224610212 P P P LNCV6_137269_PI430048170 mRNA
GAGGTGGGTCTGAAATTCATACATGAAGTCAGGAAAAGAAAAGAAACTTAGTTCTACCTT NM_025214RefSeq chr18 - 54901508 54959508 CCDC68 80323 "coiled-coil domain containing 68, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145755_PI430048170 0.2043380424157491.27246997252118 4.707511907007 4.4926108999304 4.34852787419624 P P P 4.51475381398982 4.1121212707627 3.81572143286876 P P P LNCV6_145755_PI430048170 mRNA
CCTCTCAAATACCCTTATTTTATTTATGTTTCTCCCAATAAAAACCCAGCCTGTGTGCCANM_031948RefSeq chr16 - 2712421 2720551 PRSS27 83886 "protease, serine 27"
GO:0005886|GO:0004252|GO:0006508|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129483_PI430048170 0.0170087375754254 1.27884961495094 14.4774865552133 14.711181459121 14.6149777943139 P P P 14.1828460301979 14.327898774518 14.2341057605247 P P P LNCV6_129483_PI430048170 mRNA
TGTCAACACCCTTGGCTCCTGTGTTTAGAGGGGTGGCCTGAAGGACCTTTTCTGCTGGGA NM_033362RefSeq chr19 + 38930707 38933019 MRPS12 6183 "mitochondrial ribosomal protein S12, transcript variant 2"
GO:0070124|GO:0005515|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0015935|GO:0005761|GO:0005743 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136283_PI430048170 0.1413193603875790.9578488279525530.41908039220265 0.3786925036769750.376566558532728A A A 0.4891407608880690.47153588531736 0.398873863466874A A A LNCV6_136283_PI430048170 mRNA
TGAAAAACTAAATATCGTTCTGTCAGGGCCTTTGCATAAAGCCATTTGTGTGTACATGCA NM_031947RefSeq chr5 - 141302628 141304063 SLC25A2 83884 solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 2 GO:0034641|GO:0006810|GO:0005743|GO:0000050|GO:0044281|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140581_PI430048170 0.2642273727305140.8645193022270141 0.9009399972429 10.805042772334 10.9482726793933 P P P 10.8373653860872 11.1308292208865 11.284650137529 P P P LNCV6_140581_PI430048170 mRNA
TCCTGACAGAGGTACTTAACAATGGCTCTGCTGGAAATTTCTATAAATAAAATGTCCAAA NM_133443RefSeq chr16 + 46884379 46931297 GPT2 84706 "glutamic pyruvate transaminase (alanine aminotransferase) 2, transcript variant 1"
GO:0034641|GO:0004021|GO:0042851|GO:0005759|GO:0042853|GO:0030170|GO:0006103|GO:0008652|GO:0044281 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135573_PI430048170 0.18894124657535 2.50605202436542 1.27586118404662 0.8982398314936992.77703452458015 A A A 0.8610319025862790.393633659238366 0.395130452831819A A A LNCV6_135573_PI430048170 mRNA
TATAGCCTGAGAAACAAGGATGTGAAGGCAGCTCTGAGGAAAGTAGCCACAAGGAATTTC NM_003700RefSeq chr11 - 6891573 6892500 OR2D2 NA "olfactory receptor, family 2, subfamily D, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132557_PI430048170 0.00291894613868358 1.17910568161747 13.6706348593095 13.5827059388279 13.6110386338303 P P P 13.4167395688686 13.4019779124999 13.332591862276 P P P LNCV6_132557_PI430048170 mRNA
GGGCAGGAGCCCACCCCCAGCACCCCCATCTGTTAATAAATATCTCAACTCCAGGGTGTT NM_007263RefSeq chr19 - 18899513 18919390 COPE 11316 "coatomer protein complex, subunit epsilon, transcript variant 1"
GO:0006888|GO:0030126|GO:0005794|GO:0005198|GO:0006890|GO:0061024|GO:0006891|GO:0005654|GO:0015

031|GO:0048205|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_42975_PI430048170 0.8831531767159630.9154153801818422.55567040605782 0.450679354616754
1.57594083118619 A A A 0.5785951618743113.05424381304551 0.456794936985008 A P A
LNCV6_42975_PI430048170 mRNA
CAAAATGATCAACGTTCAGGGTCCCTTCATCTCAGAGGGTCTCGAGTCACCTCATTTAAA NM_001272086 RefSeq
chr17 - 81375898 81385360 LOC100130370 100130370 uncharacterized LOC100130370 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_136321_PI430048170 0.6443410668286830.9714135957896460.2948618125873
0.2865822503302540.403495517446592 A A A 0.5021401309909490.319518533557495
0.282043427058309 A A A LNCV6_136321_PI430048170 mRNA
TGGCCCTTTCCAATGTTGTCTTCACATTGGAGTATAAGAATTCTCTATAGGACTCTTTAA NM_199040 RefSeq chr12
+ 93377922 93403248 NUDT4 11163 "nudix (nucleoside diphosphate linked moiety X)-type motif 4,
transcript variant 2"
GO:0052846|GO:0052845|GO:0052844|GO:0052843|GO:0009187|GO:0019722|GO:0043647|GO:0008486|GO:0052
848|GO:0052847|GO:0019935|GO:0046907|GO:0044281|GO:0050072|GO:0052840|GO:0046872|GO:0005829|GO:0
005622|GO:0035556|GO:0030515|GO:0046831 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128227_PI430048170 0.00500957320713383 0.56609184085807 6.34922062218742
6.46373418227326 6.72283102385846 P P P 7.23022639445049 7.26580223701078 7.5116166782928
P P P LNCV6_128227_PI430048170 mRNA
CCTCCAACATGATGGATCTACTTATGGTCTTGTTTGTTGACATGACAAATTAACATTCTT NM_004768 RefSeq chr1
+ 70205681 70252018 SRSF11 9295 "serine/arginine-rich splicing factor 11, transcript variant 1"
GO:0008380|GO:0006397|GO:0005515|GO:0010467|GO:0006369|GO:0006406|GO:0006366|GO:0000166|GO:0000
398|GO:0031124|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135364_PI430048170 0.0557748504204591 0.7417808522008335.12759496966642
5.01230242671073 5.35194711045246 P P P 5.45202758354642 5.48720945035624
5.83454314606417 P P P LNCV6_135364_PI430048170 mRNA
ACCATGCATTTTGAGAAGCACTGGAGATTACTGGAAAGTATGAAAGCACAGTATGTTGCT NM_001286756 RefSeq
chr4 + 25377225 25418498 ANAPC4 29945 "anaphase promoting complex subunit 4, transcript
variant 1"
GO:0005515|GO:0007094|GO:0004842|GO:0019903|GO:0051437|GO:0005634|GO:0051436|GO:0031145|GO:0051
439|GO:0005829|GO:0007067|GO:0070979|GO:0005680|GO:0005654|GO:0000278|GO:0051301 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135882_PI430048170 0.1970708341199131.14377303302337 4.65206959238208
4.34828731257125 4.49010990920848 P P P 4.40067522499341 4.38415759032934
4.12392204412947 P P P LNCV6_135882_PI430048170 mRNA
TCTCGAGAGATGTCTTCAATGTGTATGTGAATAGCTCCATTCCTATCCCCTCCTCCAACT NM_176882 RefSeq chr7
+ 143222078 143223050 TAS2R40 259286 "taste receptor, type 2, member 40"
GO:0033038|GO:0007186|GO:0005886|GO:0016021|GO:0001580 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_104593_PI430048170 0.8539888895751441.00372065994198 0.304561934364888
0.3411179722400020.384213045044591 A A A 0.3544981432827480.339400049353168
0.320826840659397 A A A LNCV6_104593_PI430048170 mRNA
ATTGCTAGCCCAAAAATCCCAGGGGCAAAATAAAGTTCAACAAAAGTGCAAAATATGACA NM_006204 RefSeq chr10
+ 93612587 93665672 PDE6C 5146 "phosphodiesterase 6C, cGMP-specific, cone, alpha prime"
GO:0046549|GO:0030553|GO:0007603|GO:0005886|GO:0008152|GO:0047555|GO:0007601|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136764_PI430048170 0.0214805829801024 0.6689832063558745.44495291421544
5.16607461807609 5.04582291837445 P P P 5.94627035455264 5.85848957984504
5.59934665921369 P P P LNCV6_136764_PI430048170 mRNA

CCTCCTCCGGGGGCCAAGGACAGGGTGGCCTTACTCAGTAAAGGTGTTTCCTGCAAAAAA NM_030943 RefSeq chr14
+ 102922655 102930842 AMN 81693 amnion associated transmembrane protein
GO:0007588|GO:0015889|GO:0009235|GO:0005886|GO:0043001|GO:0005102|GO:0006767|GO:0030139|GO:0007
275|GO:0044281|GO:0005615|GO:0006898|GO:0016324|GO:0006766|GO:0042157|GO:0016021|GO:0010008|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126953_PI430048170 0.3492527226925731.0354008249284 0.409574865201553
0.2799107529566860.298832288622772 A A A 0.2665839546008440.307741590049036
0.266459362817667 A A A LNCV6_126953_PI430048170 mRNA
CCTAGGAACAAGGAAAAACAGAAAGCATATAATACGGTGGTCGTTTCATTGTGTTTTTCT NM_133638 RefSeq chr5
+ 129460409 129738683 ADAMTS19 171019 "ADAM metallopeptidase with thrombospondin type 1 motif,
19" GO:0006508|GO:0005578|GO:0008270|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135196_PI430048170 0.9729708574323051.00281560260815 0.274030911008455
0.2781383886190910.439796516478087 A A A 0.3512313260638250.298317492365091
0.336005944740358 A A A LNCV6_135196_PI430048170 mRNA
GAAATCACTTTCAACAAGACGAGCAGAGCTGTAATTTTCCACTGAAATAAACAAGTTCTA NM_001293083 RefSeq
chr2 + 96642736 96704885 FER1L5 90342 fer-1-like family member 5
GO:0005886|GO:0007520|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140863_PI430048170 0.4448454687631190.9399151888746837.19295128940055
7.10959841173346 7.07178822823744 P P P 7.27259588454909 7.32084491567788
7.03595742109896 P P P LNCV6_140863_PI430048170 mRNA
AGAATACAGTCTCCATCCTGCTGTCTCTGTCCTGTCCCCAAGTTTTCAAATAAAACTTTC NM_014450 RefSeq chr9
- 35649300 35650950 SIT1 27240 signaling threshold regulating transmembrane adaptor 1
GO:0005515|GO:0007165|GO:0050863|GO:0005886|GO:0005887|GO:0019900|GO:0042169|GO:0070062|GO:0002
376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144178_PI430048170 0.2194976406985660.56315477356706 2.24272083306264
0.2717344220255240.330143257153075 A A A 2.20257538283634 2.06705841330425
1.99529594616141 A A A LNCV6_144178_PI430048170 mRNA
CAGCATCATTTCCTCTTCACCTTGCATGAATACATGAAATCATAATATCGTTCATGTTGT NM_001018116 RefSeq
chr9 + 100578078 100588387 MURC NA muscle-related coiled-coil protein NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_133178_PI430048170 0.4464260199915180.8628373958403310.268578236695333
0.2821562893045420.462416830347278 A A A 0.3444051875563420.919314400398201
0.312047055810501 A A A LNCV6_133178_PI430048170 mRNA
GCTTCCCTTCATGTTATATGCACATTGCCAAGAATTACTGTCAAGAGAAATGATAAGTAA NM_015460 RefSeq chr3
+ 39809659 40260320 MYRIP 25924 "myosin VIIA and Rab interacting protein, transcript variant 1"
GO:0005515|GO:0030133|GO:0042470|GO:0048471|GO:0017137|GO:0031045|GO:0045202|GO:0003779|GO:0015
629|GO:0006886|GO:0000145|GO:0008270|GO:0032024|GO:0051018|GO:0001750 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138120_PI430048170 0.0741267637160419 1.1552546007002 5.40162483531235
5.47777180977276 5.49835305480747 P P P 5.13199349156123 5.24447420361083
5.36871294928195 P P P LNCV6_138120_PI430048170 mRNA
CTTTAGGACTGACCTGTTAGGGGATAAACATCACAATAATCTGAATTCCAAGTTATTTTG NM_014065 RefSeq chr3
- 131013872 131026854 ASTE1 28990 "asteroid homolog 1 (Drosophila), transcript variant 2"
GO:0004518|GO:0006281|GO:0090305 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72096_PI430048170 0.5393940607258350.9380382205155285.1625096937142 5.59604605109386
5.40904742067198 P P P 5.34287725596907 5.55857367420406 5.56462017265647 P P P
LNCV6_72096_PI430048170 mRNA
ATAACAAGAAATCTCAAGCTTCCGTCAGTGATCCTATGAATGCACTCCAGAGCCTGACTG NM_001293237 RefSeq
chr22 + 20508047 20587632 MED15 51586 "mediator complex subunit 15, transcript variant 6"

GO:0005515|GO:0010467|GO:0005737|GO:0006367|GO:0001104|GO:0016020|GO:0006357|GO:0019827|GO:0016
592|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141449_PI430048170 0.156823490356553 1.17992584902293 13.0735522642843
13.2460961398435 13.3831114616756 P P P 13.2009047337214 12.9123342820059 12.866791644938
P P P LNCV6_141449_PI430048170 mRNA
TGGAAGGAGACTTAGGAACCTACCAGTTGGCCATGATGTCTTTTCTTCTTTTTCTTTTTT NM_001552 RefSeq chr17 +
40443423 40457730 IGFBP4 3487 insulin-like growth factor binding protein 4
GO:0008283|GO:0031994|GO:0031995|GO:0005576|GO:0006259|GO:0001558|GO:0005615|GO:0010906|GO:0007
165|GO:0001501|GO:0044342|GO:0006954|GO:0043568|GO:0043567|GO:0043410|GO:0044267 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136950_PI430048170 0.46899164075911 1.11748275146363 4.0569341889588 4.5654203820783
4.11842659275374 P P P 4.14171670229218 4.11374674933301 4.05839298699755 P P P
LNCV6_136950_PI430048170 mRNA
ATTAGAAATCTAATTCCTCTCAAATATTTGCCTTGGGAATGCTCCCGGGCAGGTGCAACC NM_201520 RefSeq chr17
- 8287763 8294852 SLC25A35 399512 "solute carrier family 25, member 35"
GO:0006810|GO:0005743|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134537_PI430048170 0.127830170203147 0.854843636788316 8.89021760530965
9.19390271983897 8.91689751838057 P P P 9.27744704489819 9.1106345532272
9.30421885461375 P P P LNCV6_134537_PI430048170 mRNA
ACTGAAGTCTGATTCTTTCCCGGGAAGCGGGGTACTGGCTGTGTTTAATCATTAAAGGTA NM_004497 RefSeq chr19
+ 45864259 45873797 FOXA3 3171 forkhead box A3
GO:0003700|GO:0044212|GO:0001678|GO:0006366|GO:0000981|GO:0019904|GO:0005634|GO:0007283|GO:0030
154|GO:0043565|GO:0045944|GO:0031018|GO:0008134|GO:0009267|GO:0016568 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139135_PI430048170 0.00180842898165738 0.2204478715623043 14520452148216
3.18457657990544 3.59258097913246 P P P 5.05962711302462 5.61586196970563
5.74707897226993 P P P LNCV6_139135_PI430048170 mRNA
GATGATGTGATCCAATAACTGTGGAGGTAGCTTTAACTTGGTTCTGTGTAAATAGTATGT NM_001173489 RefSeq
chrX + 37349329 37457295 PRRG1 5638 "proline rich Gla (G-carboxyglutamic acid) 1, transcript
variant 3" GO:0005887|GO:0005509|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140618_PI430048170 0.00284696987072386 0.3571771373992268 0.00471261249465
7.50580798190544 7.77083510128743 P P P 8.93017897355505 9.28254706717446
9.50940402502799 P P P LNCV6_140618_PI430048170 mRNA
CGTTTGCATGATACGCTTTGTTAGAAACATTAATTGTAGTTTGGAAGCAAGTGTGTATGA NM_002737 RefSeq chr17
+ 66302807 66810744 PRKCA 5578 "protein kinase C, alpha"
GO:0005515|GO:0007077|GO:0010467|GO:0007603|GO:0050730|GO:0006937|GO:0007173|GO:0002062|GO:0030
198|GO:0046325|GO:0043025|GO:0031666|GO:0002159|GO:0070062|GO:0016056|GO:0031966|GO:0030335|GO:0
030593|GO:0030168|GO:0022400|GO:0045651|GO:0045785|GO:0050930|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128757_PI430048170 0.0332193411161158 0.7508972816147 8.4009042635128
8.06581776240762 8.32092191514981 P P P 8.69088881376735 8.54668813460051
8.79971285433774 P P P LNCV6_128757_PI430048170 mRNA
CGGTGTGGGGAAAAGTCCATGAAAACTCACAGCATGATTGACAGTAGTTTATCAAAAATT NM_001657 RefSeq chr4
+ 74445097 74455009 AREG 374 amphiregulin
GO:0005515|GO:0042542|GO:0008284|GO:0005154|GO:0008283|GO:0060750|GO:0007267|GO:0043434|GO:0005
634|GO:0005615|GO:0051591|GO:0060598|GO:0031175|GO:0014009|GO:0005737|GO:0007173|GO:0032355|GO:0
060744|GO:0009986|GO:0045740|GO:0051384|GO:0005125|GO:0045668|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129606_PI430048170 0.505737401928005 1.41676275146659 1.75696000272031

0.5046805564047840.355213441626516A A A 0.4242077280805090.584202320792976
0.534958856348214A A A LNCV6_129606_PI430048170 mRNA
GTCCAACTTGCTATCAGAAAAGTGTTGGGCAAGAAAGGTTCTCTAAAACTATATAATTGA NM_001004472 RefSeq
chr1 + 158479877 158480885 OR10R2 343406 "olfactory receptor, family 10, subfamily R, member 2"
GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133242_PI430048170 0.00678465511233233 0.4952406332803727.37521845347917
7.19559826318303 7.27340088228188 P P P 8.09453193769423 8.25234792576977
8.51309788300502 P P P LNCV6_133242_PI430048170 mRNA
TGCCTCTTGGCTATATAACTTCTGAGTGCAAATCATTGAACACTTTAACGAAGTATTGTA NM_001199140 RefSeq
chr2 - 127861630 127885940 AMMECR1L 83607 "AMMECR1-like, transcript variant 2" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131813_PI430048170 0.00924160539919247 1.13746779528485 13.352344461771
13.265436456506 13.3205788589555 P P P 13.1811506000228 13.0799191158735
13.1193406127831 P P P LNCV6_131813_PI430048170 mRNA
TGCTGCGGCGTGTTAGGAATGACCTGGAATTGTCAATAAACAGATGCTGCTGTCAAAAAA NM_014188RefSeq chr1
- 1541672 1574882 SSU72 29101 SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)
GO:0005515|GO:0006378|GO:0005737|GO:0070940|GO:0005634|GO:0008420 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_116659_PI430048170 0.8961951697506911.01262908640307 0.444092595198072
0.6354654364491550.336677956230178A A A 0.4139090508834440.497742983532499
0.465042569928302A A A LNCV6_116659_PI430048170 mRNA
AACAACAACATCAAGTCAATTTCAAGACATACTTTCCGGGGACTAAAGTCATTAATTCAC NM_005097RefSeq chr10
+ 93757808 93798174 LGI1 9211 "leucine-rich, glioma inactivated 1"
GO:0005515|GO:0030054|GO:0008283|GO:0030307|GO:0005102|GO:0045202|GO:0005576|GO:0005615|GO:0031
175|GO:0007399|GO:0007411|GO:0050806|GO:0051260 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142007_PI430048170 0.21964078810967 1.02350907917396 0.326407357838371
0.2692601485328680.270028502044125A A A 0.2523927483561160.25920080503533
0.254269954512429A A A LNCV6_142007_PI430048170 mRNA
CTTTGTTTGTGTTGTTGGAAAAAGTCACATTGCCATTAAACTTTCCTTGTCTGTCTAGTT NM_000633RefSeq chr18 -
63123345 63319380 BCL2 596 "B-cell CLL/lymphoma 2, transcript variant alpha"
GO:0016248|GO:0005515|GO:0001656|GO:0030308|GO:0001658|GO:0033689|GO:0030307|GO:0010523|GO:0007
409|GO:0002020|GO:0009791|GO:0006808|GO:0031069|GO:0018105|GO:0018107|GO:0010039|GO:0014031|GO:0
001662|GO:0002326|GO:0033033|GO:0010332|GO:0031625|GO:0000209|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140352_PI430048170 0.0224194592049633 1.36177413777338 6.18718039134945
6.16929695846038 6.03513955793481 P P P 5.85713054940269 5.63752229200463 5.5474211403027
P P P LNCV6_140352_PI430048170 mRNA
CGACTGCTTTGTTCACACACATTTGATTAAAAATAAACAAACAGCATCTCCCCACAAAAA NM_014808RefSeq chr2
+ 241356248 241494842 FARP2 9855 "FERM, RhoGEF and pleckstrin domain protein 2, transcript variant
1"
GO:0008092|GO:0071800|GO:0031532|GO:0030316|GO:0032855|GO:0033623|GO:0005829|GO:0016322|GO:0005
737|GO:0016601|GO:0007411|GO:0071526|GO:0005089|GO:0005856|GO:0007155|GO:0030676|GO:0019898 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58933_PI430048170 0.1335378569189790.6324123260093942.83290344550868 3.64203528330708
2.6202218590889 A P A 3.90920202432792 3.88429688042899 3.45132770985569 P P P
LNCV6_58933_PI430048170 mRNA
TATGTTTGCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGA NM_015270RefSeq chr12
- 48766191 48784094 ADCY6 112 "adenylate cyclase 6, transcript variant 1"

GO:0005515|GO:0005886|GO:0007268|GO:0007202|GO:0044281|GO:0071380|GO:0007193|GO:0046872|GO:0035556|GO:0007173|GO:0071377|GO:0006171|GO:0006833|GO:0034199|GO:0048011|GO:0019901|GO:0007212|GO:0055085|GO:0005524|GO:0003091|GO:0007165|GO:0005929|GO:0006112|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140797_PI430048170 0.2800482201787280.8951153042998027.50773928298079 7.87411342105363 7.78546227681669 P P P 7.7605346719064 7.9459250446441 7.95690386299869 P P P LNCV6_140797_PI430048170 mRNA
TGAACTGAAATGAATTTCATTATTTCCTCCAATGTGTACTTTTGTGCCCCCCTCTCACTT NM_001039661 RefSeq chr11 + 126283086 126294933 TIRAP 114609 "toll-interleukin 1 receptor (TIR) domain containing adaptor protein, transcript variant 3"
GO:0005515|GO:0050830|GO:0007249|GO:0046330|GO:0032757|GO:0042803|GO:0032648|GO:0002755|GO:0005080|GO:0032496|GO:0030099|GO:0070374|GO:0030674|GO:0043123|GO:0044130|GO:0045410|GO:0038124|GO:0032760|GO:0038123|GO:0046982|GO:0034134|GO:0005546|GO:0002224|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140278_PI430048170 0.0135144279945761 0.5688511105797324.84622618120352 4.41758149899488 4.80244820842195 P P P 5.24812201105848 5.54230293979405 5.71653172798789 P P P LNCV6_140278_PI430048170 mRNA
CATTCCTGCAAAATCACCAGAGAAATGCAGATTGGACATGATTCCGGACCTCAAAGCCAT NM_013451 RefSeq chr10 - 93306428 93482317 MYOF 26509 "myoferlin, transcript variant 1"
GO:0005515|GO:0031965|GO:0030947|GO:0005886|GO:0008015|GO:0007520|GO:0005635|GO:0031410|GO:0043231|GO:0034605|GO:0005543|GO:0006936|GO:0005901|GO:0001778|GO:0016021|GO:0030659|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133822_PI430048170 0.0375387796197949 1.48324598582765 6.26695216007331 6.65793405867686 6.48843319843429 P P P 6.17928143090532 5.80059532757309 5.70949196109228 P P P LNCV6_133822_PI430048170 mRNA
CTCCCAACTCTAAAGCCAAGCACTTTATATTTTCCTCTTAGATATTCACTAAGGACTTAA NM_006084 RefSeq chr14 + 24161212 24166566 IRF9 10379 interferon regulatory factor 9
GO:0005515|GO:0000975|GO:0006355|GO:0003700|GO:0006366|GO:0019221|GO:0045351|GO:0005634|GO:0005829|GO:0005737|GO:0051607|GO:0060337|GO:0005654|GO:0007166|GO:0060333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91652_PI430048170 0.18837712137398 1.08668081492152 8.35798980492574 8.28308024797292 8.49451334956897 P P P 8.23952358830476 8.22424491748704 8.31827171874498 P P P LNCV6_91652_PI430048170 mRNA
GCAAGAACTCTGGAGTTCTTATGGTAGTAAAATGCCGGAAAGAAAATTCTGCATTGAAAG NM_182523 RefSeq chr3 + 28241632 28319772 CMC1 152100 C-x(9)-C motif containing 1 GO:0005739|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136233_PI430048170 0.00209235196896077 1.59392595020641 11.959488834317 12.1545680413324 12.1827330531416 P P P 11.527346593958 11.4129869120256 11.342740473338 P P P LNCV6_136233_PI430048170 mRNA
GGGGGAAAATGTGATTTGTGCCTGATCTTTCATCTGTGATTCTTATAAGAGCTTTGTCTT NM_015987 RefSeq chr12 - 12974864 13000309 HEBP1 50865 heme binding protein 1
GO:0005739|GO:0007623|GO:0005576|GO:0070062|GO:0020037|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138421_PI430048170 0.5794933877366480.9450450517933512.0319476033367 12.0102673528999 12.4367051665769 P P P 12.158021067222 12.2683514412486 12.3329460604721 P P P LNCV6_138421_PI430048170 mRNA
ACGATTATATTTCACCTGGGACATGCTGCTATGCTGGGACTCATGTATGTCTACTGGACT NM_002951 RefSeq chr20 + 37179052 37241622 RPN2 6185 "ribophorin II, transcript variant 1"
GO:0005791|GO:0010467|GO:0005783|GO:0042493|GO:0006614|GO:0000421|GO:0007568|GO:0005634|GO:0006

412|GO:0016020|GO:0004579|GO:0005789|GO:0043022|GO:0016021|GO:0008250|GO:0044267|GO:0006464|GO:0043687|GO:0018279. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82980_PI430048170 0.8534410110547830.958405931939347 1.14671484446298 0.465956708148142 0.260217119107368 A A A 0.3995315174320730.513909091755163 1.17248858227626 A A A
LNCV6_82980_PI430048170 mRNA
CCACTCCAAAGTCTATACACAGGGGTGGTCTCTTCAATAAAGAAGTGTTGATTAGACCTG NM_173815 RefSeq chr16 + 66988588 67009756 CES4A 283848 "carboxylesterase 4A, transcript variant 1"
GO:0052689|GO:0008152|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130180_PI430048170 0.00727244543983173 0.3604392776242123.66635155804013 3.262669102266 4.03108960289066 P P P 4.88741852685559 5.05114338133198 5.47433934115353 P P P LNCV6_130180_PI430048170 mRNA
GGAAGTTTGTCAAAAAATTCAATGCATAGTCTGTAGTATGTCCTGACAAGAAGTTAGCAT NM_001123355 RefSeq chr9 - 125146572 125189939 PPP6C 5537 "protein phosphatase 6, catalytic subunit, transcript variant 1" GO:0005515|GO:0000082|GO:0006470|GO:0004722|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142719_PI430048170 0.5284351639296910.8860713588901052.85016126175487 3.03431826655288 2.26553246242841 A P A 2.71611564996498 2.80645299013457 3.20849223664339 A P P LNCV6_142719_PI430048170 mRNA
GCAGGTCTTTACCAAAGTTCTTGGTTTATTGCTTTCAAACTTCTTTGCAACCTTCAGTAA NM_152667 RefSeq chr20 - 25612935 25624012 NANP 140838 N-acetylneuraminic acid phosphatase
GO:0050124|GO:0046380|GO:0016311|GO:0006045|GO:0005575|GO:0006488|GO:0044267|GO:0043687|GO:0018279|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133481_PI430048170 0.0417638862297843 0.3477966337121380.304910463124053 0.2826531835428140.451561932608196 A A A 1.32852945684499 1.66137192966634 2.40783039765819 A A P LNCV6_133481_PI430048170 mRNA
GAATAGGATTGCTCTCACATTAAAGATAGTTACTTCAATTTGAAGGCTGGATTTAGGGAT NM_004612 RefSeq chr9 + 99105088 99154191 TGFBR1 7046 "transforming growth factor, beta receptor 1, transcript variant 1"
GO:0005515|GO:0010468|GO:0030307|GO:0051491|GO:0048705|GO:0048844|GO:0048538|GO:0046332|GO:0009791|GO:0048701|GO:0005114|GO:0007507|GO:0004702|GO:0018105|GO:0018107|GO:0030199|GO:0007179|GO:0031396|GO:0023014|GO:0043393|GO:0032924|GO:0001701|GO:0043235|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140438_PI430048170 0.21546636879556 1.55306959934642 1.19265436526183 2.30464970714888 1.65062311599772 A A A 1.12820672230869 1.00795959244424 1.30889864478846 A A A LNCV6_140438_PI430048170 mRNA
GCACCATTAACTCCTCCTGAGCTCTGATAAAAGAATCAAAATTTCTCAATAATTTCATCC NM_001256497 RefSeq chr7 - 99684678 99735200 CYP3A7-CYP3A51P NA CYP3A7-CYP3A51P readthrough NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80304_PI430048170 0.2826704491185591.17168831610961 4.19691452294923 4.53263333247732 4.36318264386985 P P P 4.322639408608 4.24325346441625 3.8096502435195 P P P
LNCV6_80304_PI430048170 mRNA
TTTTGATTGAGCCTCCACCTCTGGGATTTTTCTTCCATTTTTCTCCTCTCTTAGGAGGGA NM_003033 RefSeq chr8 - 133454847 133571940 ST3GAL1 6482 "ST3 beta-galactoside alpha-2,3-sialyltransferase 1, transcript variant 1"
GO:0005975|GO:0006054|GO:0016266|GO:0044281|GO:0003836|GO:0042339|GO:0030173|GO:0000139|GO:0006493|GO:0016020|GO:0018146|GO:0032580|GO:0009405|GO:0006468|GO:0006487|GO:0006488|GO:0044267|GO:0030203|GO:0006464|GO:0070062|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127115_PI430048170 2.04492313429972e-05 1.64524271533709 8.25361186100419 8.28992327866452 8.22695103548754 P P P 7.51635888636454 7.54295626695486

7.55667222006898 P P P LNCV6_127115_PI430048170 mRNA
GTGTGGCCTTTCTCTTCCCTTCTTTTATTAAACACAGATAGGTTTATGCTGGATAAAAAA NM_001142405 RefSeq
chr18 + 12407895 12432237 SLMO1 10650 "slowmo homolog 1 (Drosophila), transcript variant 1"
GO:0005758|GO:0015914 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107206_PI430048170 0.871630057921756 1.02633480805367 8.0420721905734
7.55460266464914 7.85474664748442 P P P 7.60635178541365 7.89142333880107 7.8655638898513
P P P LNCV6_107206_PI430048170 mRNA
TATCCAGACCCAATGGAACATCAGCAATGCTTCTGTGACCTTGGGAAAGGTGTTGAAAGT NM_004269 RefSeq chr9
- 131860109 132079887 MED27 9442 "mediator complex subunit 27, transcript variant 1"
GO:0005515|GO:0010467|GO:0005667|GO:0005737|GO:0006367|GO:0006357|GO:0019827|GO:0016592|GO:0003
713|GO:0005730|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91717_PI430048170 0.0533816303127603 1.35026680262194 9.39007865055465
9.79290200260793 9.47346402891453 P P P 9.30540461596382 9.04533479770655
9.02038005666981 P P P LNCV6_91717_PI430048170 mRNA
AAATTAAATGGTCGTTATTGAAATGAAGGCTGTGGATTCAAGGCTCCCTGCCCCCCAGAT NM_016429 RefSeq chr17
- 48026166 48037806 COPZ2 51226 "coatomer protein complex, subunit zeta 2"
GO:0005801|GO:0030126|GO:0033116|GO:0016192|GO:0006886 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134734_PI430048170 0.0828079372227460 0.935276582765477 0.288210829745765
0.296449145195833 0.311713420508103 A A A 0.452884261062615 0.382915472684678
0.348302474567761 A A A LNCV6_134734_PI430048170 mRNA
GACAAACTGCTTTTGAACAGTGTCTTCAATGTATCAAGCACAAATAACTCTTTCTTCAAC NM_004440 RefSeq chr6
- 93240020 93419582 EPHA7 2045 "EPH receptor A7, transcript variant 1"
GO:0005515|GO:0031290|GO:0031594|GO:0005886|GO:0050730|GO:0030425|GO:0031952|GO:0005004|GO:0043
525|GO:0007411|GO:0045211|GO:0043025|GO:0070372|GO:0022407|GO:0048013|GO:0050919|GO:0018108|GO:0
005524|GO:0016310|GO:0045499|GO:0043281|GO:0046875|GO:0007420|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132732_PI430048170 0.314789507645409 1.22458702904494 0.446242817616442
0.60680684355784 1.11079496266159 A A A 0.5563128342765 0.403571138197094
0.407610355491992 A A A LNCV6_132732_PI430048170 mRNA
GCATCACTGGGTGTTGATCTTACAAGATATTGATGATAACACTTAAAATTGTAACCTGCA NM_024426 RefSeq chr11
- 32387775 32435535 WT1 7490 "Wilms tumor 1, transcript variant D"
GO:0008406|GO:0005515|GO:0017148|GO:0001657|GO:0001658|GO:0030308|GO:0003700|GO:0044212|GO:0007
281|GO:0072075|GO:0007507|GO:0030539|GO:0072302|GO:0009888|GO:0035802|GO:2000195|GO:0060231|GO:0
072207|GO:0000122|GO:0060923|GO:0072284|GO:0060539|GO:0070742|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_115732_PI430048170 0.88857223262092 0.964923659297965 9.84525739761085
9.70851167714192 9.51420719752472 P P P 9.99551716570193 9.8220190067673
9.34921424433438 P P P LNCV6_115732_PI430048170 mRNA
GTGAGCTCAGCCTACCGCTGGCCCTGCCGTTTCCCCTCCTTGGCTTTATGCAAATACAAT NM_006533 RefSeq chr19
+ 40775376 40777493 MIA8190 "melanoma inhibitory activity, transcript variant 1"
GO:0008283|GO:0008083|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136585_PI430048170 0.678905182525564 0.99462851851165 0.358867536626351
0.359673528070613 0.372961938655251 A A A 0.391154554241556 0.34071639512233
0.382483918773861 A A A LNCV6_136585_PI430048170 mRNA
CTTACAGATGGAATGAATGTGGCAAAATCTTTAGTTAGAATTCACACCTAGCACAACATT NM_001161425 RefSeq
chr19 + 52336244 52367123 ZNF610 162963 "zinc finger protein 610, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA

LNCV6_141847_PI430048170 0.853632927354411 0.609481748310438 3.04631354993859
0.332350817052487 0.260119704163446 P A A 3.91713573861522 0.319539593424193
0.298640174244521 P A A LNCV6_141847_PI430048170 mRNA
AACTCATGGGATTAGAGTATTCTCTGCTAGAGATCTGAAAAATAAACACAACTTTGCACC NM_015370 RefSeq chr22
- 29058671 29061919 C22orf31 25770 chromosome 22 open reading frame 31 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135254_PI430048170 0.402621385878504 1.93551786624311 0.331070537563083
0.306555182669238 2.19589721922526 A A A 0.288860971636974 0.290330285489236
0.276797123857004 A A A LNCV6_135254_PI430048170 mRNA
ATCAGCTTGAGAAAGCAACACAATTTCAAATCCTATCTTCTAGATGCAAGCAGTGTTAAA NM_152565 RefSeq chr8
+ 86098909 86154225 ATP6V0D2 245972 "ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2"
GO:0005515|GO:0008286|GO:0051701|GO:0015078|GO:0055085|GO:0006879|GO:0033572|GO:0016324|GO:0016
020|GO:0015991|GO:0030670|GO:0090382|GO:0005769|GO:0010008|GO:0016471|GO:0033179|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138097_PI430048170 0.160625499058318 1.08098206060216 0.50734237690235
0.489081487156671 0.571105604841924 A A A 0.313269093407783 0.409742661913606
0.502575273860849 A A A LNCV6_138097_PI430048170 mRNA
CTTCCAAGGCTGAAAACTCAGCTTTTGAAAGTGAAATGTTTGTTCATCGGGGCCAGAGCA NM_014248 RefSeq chr22
+ 40951346 40973015 RBX1 9978 "ring-box 1, E3 ubiquitin protein ligase"
GO:0005515|GO:0031461|GO:0004842|GO:0016567|GO:0006513|GO:0030891|GO:0016874|GO:0034450|GO:0061
418|GO:0031146|GO:0032403|GO:0005829|GO:0007219|GO:0019788|GO:0016032|GO:0090090|GO:0031625|GO:0
045116|GO:0071456|GO:0006281|GO:0031463|GO:0031462|GO:0043161|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134663_PI430048170 0.729853457388691 0.690579321475121 1.24070398248039
0.760341893541747 1.6272005852449 A A A 2.76295879322966 0.793785899297127
0.869143757054487 A A A LNCV6_134663_PI430048170 mRNA
TTTTAGAACCCCACTCGTGGTCACTTCAGGATCTACTTCTGTTTTAGAACCTCCACATTC NM_006950 RefSeq chrX
- 47571900 47619857 SYN1 6853 "synapsin I, transcript variant Ia"
GO:0005515|GO:0005215|GO:0005794|GO:0030054|GO:0019901|GO:2000300|GO:0046928|GO:0007268|GO:0003
779|GO:0003824|GO:0005524|GO:0030425|GO:0007269|GO:0005829|GO:0008021|GO:0008152|GO:0048306 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112277_PI430048170 0.42637734413212 0.812306796629189 3.94077017519247
0.909315490231745 0.317670388428865 P A A 2.14485512923144 3.26584542176094 3.1226597438965
A P P LNCV6_112277_PI430048170 mRNA
TAAAGACATGGTAGATCCTAAAAAAGAGGCTGACCATGAAATACCTACTGTTAGTGGCAG NM_007231 RefSeq chrX
+ 116436578 116461458 SLC6A14 11254 "solute carrier family 6 (amino acid transporter), member 14"
GO:0006520|GO:0005886|GO:0005328|GO:0006865|GO:0009636|GO:0031526|GO:0055085|GO:0003333|GO:0031
982|GO:0015171|GO:0006810|GO:0006836|GO:0016021|GO:0070062|GO:0006811 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141267_PI430048170 0.16163095324277 1.20599573403497 6.111925449127
6.05101344997105 5.71923839402986 P P P 5.84153411502508 5.71564091342606
5.52724115110526 P P P LNCV6_141267_PI430048170 mRNA
TGAAAAATTAAACAAGGAATAGCATGCCCCCATTTCCCTACCATAGGCCACATTTAAAAA NM_024577 RefSeq chr5
- 148982149 149063174 SH3TC2 79628 SH3 domain and tetratricopeptide repeats 2
GO:0005886|GO:0033157|GO:0031410|GO:0055037|GO:0032287 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131466_PI430048170 0.0863671122584314 1.0591191854339 0.463155606533146
0.548487590800085 0.509172543147845 A A A 0.373982783137732 0.431400098039737
0.466590579134473 A A A LNCV6_131466_PI430048170 mRNA

GAAGTATATTTACATTATCTGGAGAGTTTTGTTGCAGCTACGAGTTTGTATGGCAAATTC NM_000824 RefSeq chr4 + 157076124 157172090 GLRB 2743 "glycine receptor, beta, transcript variant 1" GO:0005515|GO:0030054|GO:0005886|GO:0034707|GO:0007268|GO:0055085|GO:0051291|GO:0016933|GO:0016934|GO:0007399|GO:0001964|GO:0034220|GO:0005887|GO:0007218|GO:0045211|GO:0008144|GO:0042391|GO:0007628|GO:0016594|GO:0007340|GO:0060012|GO:0007601|GO:0060013|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140548_PI430048170 0.3241413043660280.8729499019649570.268902499814699 0.4434731606484780.298715044815126 A A A 0.5044470043604880.77433881906619 0.284667248601053 A A A LNCV6_140548_PI430048170 mRNA
AGGGCTCCTACATGAAGCAGGGATAACTGATGGCAGTAAATGTGGTCTCAAATTGCAGAT NM_001290094 RefSeq chr11 + 118077011 118119841 TMPRSS4 56649 "transmembrane protease, serine 4, transcript variant 6" GO:0004252|GO:0006508|GO:0016021|GO:0006898|GO:0005044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130507_PI430048170 0.2538107752599230.66771985787703 0.472687915269573 0.33800552788774 0.407610355491992 A A A 0.93143168226387 0.35040794809804 1.47289322876399 A A A LNCV6_130507_PI430048170 mRNA
CTGAGGAGGAAAGACAAGAATGAGGAGGCATAATCACAGTGGTATCTCATATTTAAACCA NM_014939 RefSeq chr18 - 31829172 31943128 TRAPPC8 22878 trafficking protein particle complex 8 GO:0006888|GO:0005515|GO:0031410|GO:0000407|GO:0032258|GO:0000045|GO:0034497|GO:0030242 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134971_PI430048170 0.0212329619982002 0.5849886299304914.77170047710558 4.51446915978476 4.98794088232974 P P P 5.58107180089155 5.45813807812448 5.59039372954985 P P P LNCV6_134971_PI430048170 mRNA
CAGCAATTTGAAATTAGAACTAGTGGTTTTAGAGAACTCAGGTATTCTTTCCTGACATTG NM_016125 RefSeq chr17 - 59952361 59964756 RNFT1 51136 "ring finger protein, transmembrane 1" GO:0008270|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139140_PI430048170 0.2860214867180791.04133895651474 0.320809110726785 0.2828191162225240.417329202584701 A A A 0.2899487944751090.263758356885783 0.295089000496743 A A A LNCV6_139140_PI430048170 mRNA
GGTCATAAAACTTTGTTAAGGAACTCTTTTGGAATAAAGAGCAGGATGCTGCAAAGTTAA NM_004951 RefSeq chr13 - 99294534 99307495 GPR183 1880 G protein-coupled receptor 183 GO:0006955|GO:0008142|GO:0007186|GO:0005886|GO:0030890|GO:0005887|GO:0004930|GO:0006959|GO:0070374|GO:0002313 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61762_PI430048170 0.1035426094861210.6268485146023782.71942430772315 2.40157431214593 2.64274904484413 A A A 2.74457948823373 3.47146599895944 3.47308588933668 P P P LNCV6_61762_PI430048170 mRNA
ACTTAAGAAGATCGATAACTGCCTCACTGAGATGGAAACAGAAACTAAGAATTTGGAGGA NM_170589 RefSeq chr15 + 40594248 40662683 CASC5 57082 "cancer susceptibility candidate 5, transcript variant 1" GO:0005515|GO:0001675|GO:0001669|GO:0034501|GO:0006334|GO:0005634|GO:0005829|GO:0034080|GO:0005737|GO:0007067|GO:0010923|GO:0071173|GO:0000777|GO:0005654|GO:0000278|GO:0008608|GO:0070062|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144696_PI430048170 0.0130816161516236 0.2715439323242016.73493293845496 6.15764359640016 6.54543276591792 P P P 7.75221392549299 8.3595653139856 8.82999486617562 P P P LNCV6_144696_PI430048170 mRNA
CCTGAAGACTTACCAGTATTCTAGTGTATTATGAAGCTTTCAACATTACTATGCACAAAC NM_001621 RefSeq chr7 + 17298651 17346151 AHR 196 aryl hydrocarbon receptor GO:0005515|GO:0010468|GO:0003700|GO:0006805|GO:0044212|GO:0006366|GO:0045899|GO:0003705|GO:0051879|GO:0005634|GO:0005737|GO:0045944|GO:0046983|GO:0030850|GO:0004879|GO:0004871|GO:0009410|GO:0005667|GO:0006355|GO:0001568|GO:0046982|GO:0006357|GO:0006915|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_139310_PI430048170 0.5088933116163611.04328279116891 0.294036956196521
0.3042135550702230.514488580330533A A A 0.3236766584210980.281857904460673
0.334188426566111A A A LNCV6_139310_PI430048170 mRNA
CACCAGTCTATTTTTACTGAGAGCTGGACAACAGCAAACACTTGACAAATAAACTTATTT NM_147197RefSeq chr20
- 45648562 45670239 WFDC11 259239 WAP four-disulfide core domain 11 GO:0005576 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_126849_PI430048170 0.5171760874800370.9660744489896742.97511954645589
3.15382184322561 3.0648119334269 P P P 3.09640200517595 3.20538888956416
3.04205225574396 P P P LNCV6_126849_PI430048170 mRNA
ATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATGATTA NM_032020RefSeq chr6
- 143494811 143511883 FUCA2 2519 "fucosidase, alpha-L- 2, plasma"
GO:0009617|GO:0004560|GO:2000535|GO:0016139|GO:0042806|GO:0006004|GO:0005764|GO:0005615|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131131_PI430048170 0.0298686926528216 0.42828087018528 1.52272377861521
2.12580068591064 1.48602379046902 A A A 3.4513124321821 2.51732483220381 2.7605670098048
P P P LNCV6_131131_PI430048170 mRNA
CTTGTTAATACAAACTGGATTGGTTGGTGTAGCTAATCTGACAAAAGATGCAATTGGATA NM_001281731 RefSeq
chr12 - 50129305 50167533 CERS5 91012 "ceramide synthase 5, transcript variant 2"
GO:0006665|GO:0031965|GO:0005783|GO:0030148|GO:0005789|GO:0050291|GO:0044281|GO:0016021|GO:0046
513|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145366_PI430048170 0.786228403439385 1.05419221965708 1.92592924365655
2.17555163972529 2.85430453974519 A A A 2.76047737913322 2.5084319064098
1.19119340237815 P P A LNCV6_145366_PI430048170 mRNA
CATATGCATGCCCTTCCTTTCTATATCCTTGACACCTTACTTTCCCATTGTAACAATAAA NM_130463RefSeq
chr6_GL000256v2_alt - 2843734 2846132 ATP6V1G2 534 "ATPase, H+ transporting, lysosomal
13kDa, V1 subunit G2, transcript variant 1"
GO:0008286|GO:0006879|GO:0042470|GO:0033572|GO:0051701|GO:0008553|GO:0006200|GO:0030285|GO:0090
382|GO:0055085|GO:0016471|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144096_PI430048170 0.0353165523375614 1.31883200398353 10.8083277958858
11.1256838159324 11.0687665241372 P P P 10.5377703895299 10.7534098200105
10.5214396406013 P P P LNCV6_144096_PI430048170 mRNA
GACCTAATTATTACCAGAGTAGCAGCAAGAGAGGAAACGTTGTGAATTAAGTATTCAATT NM_144636RefSeq chr3
- 14112076 14124871 CHCHD4 131474 "coiled-coil-helix-coiled-coil-helix domain containing 4,
transcript variant 2"
GO:0005739|GO:0005758|GO:0006626|GO:0015035|GO:0051084|GO:0044267|GO:0055114|GO:0045041|GO:0022
417 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134815_PI430048170 0.0381782983132424 1.05947648721413 0.346039568377069
0.3755434638126520.303583914622755A A A 0.2457474482272060.280591536997534
0.249424203653493A A A LNCV6_134815_PI430048170 mRNA
GTTTCTCAGTTGTCTAAATCATGTTGTACTTGGTGTTTGTGAAGCCAGTTACTTTTCAAA NM_000842RefSeq chr11 -
88504575 89063678 GRM5 2915 "glutamate receptor, metabotropic 5, transcript variant b"
GO:0051966|GO:0006355|GO:0005886|GO:0004930|GO:0031687|GO:0007216|GO:0014069|GO:0007268|GO:0007
205|GO:0007206|GO:0005737|GO:0000185|GO:0050890|GO:0043197|GO:0043198|GO:0005887|GO:0040013|GO:0
002029|GO:0008066|GO:0007626|GO:0006468|GO:0007612|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144690_PI430048170 0.0532441530027921.19132204849259 7.88548579973235
7.85493745231977 7.81789629496303 P P P 7.66462742499227 7.46297375540013
7.66457895520301 P P P LNCV6_144690_PI430048170 mRNA

TTGCAAATTTGGATTTACACCCATTGTTTTGGAAGCACATCAGCTGAATAAAGTTGAGGT NM_004287RefSeq chr17 + 46923119 46941367 GOSR2 9570 "golgi SNAP receptor complex member 2, transcript variant A" GO:0005215|GO:0012507|GO:0005794|GO:0005795|GO:0031201|GO:0006891|GO:0048280|GO:0006896|GO:0030968|GO:0006888|GO:0005484|GO:0016020|GO:0000139|GO:0031902|GO:0000149|GO:0005789|GO:0042147|GO:0006623|GO:0061025|GO:0016021|GO:0006987|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141034_PI430048170 0.2193240309011150.7598128068338543.00844873188538 3.63155231379228 3.6454119416443 A P P 3.84665895479124 3.51484224943362 4.13375078228678 P P P LNCV6_141034_PI430048170 mRNA
TTAAGTTACATGACCAGGAAGGTTATGCCACTTTGTGGTCATTCCATGCAAGTCATGGCG NM_017429RefSeq chr16 + 81238690 81291142 BCO1 53630 beta-carotene oxygenase 1 GO:0035238|GO:0004497|GO:0007603|GO:0042574|GO:0042572|GO:0001523|GO:0046872|GO:0055114|GO:0005829|GO:0003834 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78065_PI430048170 0.46014574786405 1.02759537873923 8.63372217585724 8.62208550635845 8.56117731202464 P P P 8.51233257965242 8.53576332166341 8.64841960308014 P P P LNCV6_78065_PI430048170 mRNA
AATGACGTAAAAGACCCTGTCTCAATTGAAGAAAGAGCGAGATGGACAGAGACGTATGTG NM_001037283 RefSeq chr7 + 2354838 2380742 EIF3B 8662 "eukaryotic translation initiation factor 3, subunit B, transcript variant 2" GO:0005515|GO:0010467|GO:0033290|GO:0005852|GO:0016282|GO:0001731|GO:0003743|GO:0006412|GO:0006413|GO:0005829|GO:0032947|GO:0005737|GO:0000166|GO:0071541|GO:0006446|GO:0031369|GO:0005654|GO:0044267|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137569_PI430048170 0.3637390105433690.7694009383207982.52927719994222 3.51638670242199 3.9294277538324 A P P 3.78855295289959 3.9521327120907 3.68724101394989 P P P LNCV6_137569_PI430048170 mRNA
GGAAGTGTCATTTACGTGATGATCTTCCTTTATTGATGTCTTCATCATGTTCAGTGTTTT NM_020772RefSeq chr17 - 29255835 29294148 NUFIP2 57532 nuclear fragile X mental retardation protein interacting protein 2 GO:0005515|GO:0005737|GO:0016020|GO:0042788|GO:0003723|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138915_PI430048170 0.0704739139922081.8307715334185 6.10484682511536 6.11761432511461 5.85035376171597 P P P 5.56760887445376 5.14432718365595 4.59937344113421 P P P LNCV6_138915_PI430048170 mRNA
CCGATCCCTGAGGGCGGTGAGGGGGAATATCAATAATTAAAGTCTGTGGGTACCAAAAAA NM_014312RefSeq chr11 - 124747473 124752213 VSIG2 23584 V-set and immunoglobulin domain containing 2 GO:0016020|GO:0005887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127469_PI430048170 0.3720078232756290.6508581187108550.473904988752577 0.5852688004505010.531636308930813A A A 0.7849130723995771.84681280970565 0.422253097787419A A A LNCV6_127469_PI430048170 mRNA
ACTGTACGAAGAAAACTTCCAGTGGAACTAATATGAAATCTATTTGCAAATTATGGGGGG NM_177964RefSeq chr2 + 149038466 149215258 LYPD6B 130576 LY6/PLAUR domain containing 6B GO:0005886|GO:0031225 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141905_PI430048170 0.0292500939090770.7899990039582 10.0064911221872 9.90205827472009 9.73299424337882 P P P 10.1175933442169 10.2930410943603 10.2583196947639 P P P LNCV6_141905_PI430048170 mRNA
TATGTACCTCCCACTGGTGTCCCTGCAAAGCCTGGCGCTTTTGACATCAATAATAAAAGT NM_001015072 RefSeq chr7 - 100888722 100889718 UFSP1 NA UFM1-specific peptidase 1 (non-functional) NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134260_PI430048170 0.7437804513638910.7504732020206852.31802128155145 2.8195080681578 2.04384444985736 A A A 3.52593589058472 2.84616198124827 1.50357805541194 P P A

LNCV6_134260_PI430048170 mRNA
AAAGGATGGATCATTTATCTACCTGATTACTGAGAGCTTTATTTGTCTCCCTCTGATAGC NM_054112RefSeq chr20
+ 31368617 31373902 DEFB118 117285 "defensin, beta 118"
GO:0009986|GO:0007160|GO:0045087|GO:0005576|GO:0007283|GO:0042742 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144174_PI430048170 0.85181380552466 1.00822455606373 0.298152267025148
0.2677297024268690.415621041559619A A A 0.2858901766367570.380672843958651
0.281561683339643A A A LNCV6_144174_PI430048170 mRNA
GTAATTCCTGCTTCTTTTATCTTTCTCTGTGTATTAAATGCTGCTCTCACGAGATTTAAG NM_001166246 RefSeq chr10
- 98457076 99235875 HPSE2 60495 "heparanase 2 (inactive), transcript variant 4"
GO:0005622|GO:0008150|GO:0005886|GO:0005975|GO:0030305|GO:0009405|GO:0005578|GO:0006027|GO:0043
395|GO:0044281|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128731_PI430048170 0.1477434543786920.7290218042734353.49489156576996
3.88568563696426 4.22913745882097 P P P 4.32889305769508 4.3918064350523
4.34874266961736 P P P LNCV6_128731_PI430048170 mRNA
TATTCTTAGGGCTTTTGTGTATGTCTGACTTGTTTTTAAATAACTTCCTCAGCAATGCAG NM_001270393 RefSeq chr6
+ 122471916 122726373 PKIB 5570 "protein kinase (cAMP-dependent, catalytic) inhibitor beta,
transcript variant 4" GO:2000480|GO:0005737|GO:0005634|GO:0004862 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142154_PI430048170 0.0010609041800152 0.5257893007203468.13023359431961
7.86384668955805 7.98830512474563 P P P 8.76687168048618 8.98565449777949
9.01218114111672 P P P LNCV6_142154_PI430048170 mRNA
AAATGCTGGGTTTAAGAAAGGCAACCAATAAAAGCCAGATGCTAGAGCCTCTGCCTGACA NM_001286270 RefSeq
chr16 + 4495818 4510347 HMOX2 3163 "heme oxygenase (decycling) 2, transcript variant 8"
GO:0005515|GO:0001666|GO:0005886|GO:0004392|GO:0006788|GO:0044281|GO:0055085|GO:0046872|GO:0006
879|GO:0006778|GO:0016020|GO:0005789|GO:0042167 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55068_PI430048170 0.1489734028173670.4306253372808370.4519798167440610.515831855920876
0.476904402384877A A A 2.46134358335425 1.10956705786653 1.04526530236547 A A A
LNCV6_55068_PI430048170 mRNA
TAAAAGCTACTGCAAACTGAGGGCAAATTGCAATCTTCTATTCCTTTTTGTTGCAAGGGG NM_001198783 RefSeq
chr1 + 167329043 167427345 POU2F1 5451 "POU class 2 homeobox 1, transcript variant 2"
GO:0005515|GO:0005667|GO:0010467|GO:0030910|GO:0003700|GO:0060235|GO:0005634|GO:0006383|GO:0043
231|GO:0043565|GO:0001077|GO:0045944|GO:0005654|GO:0045892 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130492_PI430048170 0.000116995333103787 4.05249233305885 6.08463546658847
6.07859026675983 5.93408594054028 P P P 4.01245827718669 3.98267801004397
4.04993565293673 P P P LNCV6_130492_PI430048170 mRNA
AGATGGGACTTCAGGGAGACCTGGCTTGGGCTAAAATCGAAATACAATATATATAGGCTG NM_001672 RefSeq
chr20 + 34260364 34269342 ASIP 434 agouti signaling protein
GO:0008343|GO:0032438|GO:0005102|GO:0007267|GO:0006091|GO:0005615|GO:0032402|GO:0040030|GO:0007
165|GO:0009755|GO:0042438|GO:0071514|GO:0031781|GO:0031782 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136802_PI430048170 0.0012209128387192 0.419410273713689 6.7149532264225
6.36506182675978 6.65095491013113 P P P 7.69562154197097 7.88172324188894
7.92752534490086 P P P LNCV6_136802_PI430048170 mRNA
GATAAGTTGGGAAGATATATTGATTATGCTGTTCTGTTGAGGGAAAGGTCATGTATTTAG NM_007006 RefSeq
chr16 - 56429135 56451349 NUDT21 11051 nudix (nucleoside diphosphate linked moiety X)-type
motif 21
GO:0005515|GO:0006397|GO:0008380|GO:0010467|GO:0006369|GO:0006378|GO:0005813|GO:0051262|GO:0042

826|GO:0006366|GO:0003723|GO:0031124|GO:0005634|GO:0003729|GO:0042803|GO:0042382|GO:0016787|GO:0000398|GO:0017091|GO:0005654|GO:0005849 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103332_PI430048170 0.568030760524581 0.921617598232932 6.93806728499279 6.74239796582692 6.68806957329935 P P P 6.65312913502943 7.16438907211012 6.87053353790752 P P P LNCV6_103332_PI430048170 mRNA TTTCATCCATTCCTAGATGAGATTCTCATTGGGAAGATCAAAGGCTGCAGCCCAGAAGGA NM_001018050 RefSeq chr22 - 41525800 41544489 POLR3H 171568 "polymerase (RNA) III (DNA directed) polypeptide H (22.9kD), transcript variant 3" GO:0010467|GO:0005813|GO:0006386|GO:0006385|GO:0003899|GO:0006384|GO:0003677|GO:0006383|GO:0043231|GO:0005829|GO:0051607|GO:0006139|GO:0001056|GO:0045087|GO:0005666|GO:0032481|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113444_PI430048170 0.0977276725897331.33556546127984 9.43878104271901 9.67770111607292 9.93106050348696 P P P 9.01437872765358 9.34872295432394 9.44015490868031 P P P LNCV6_113444_PI430048170 mRNA TAGAAGATATTAGTCTTGGGGCAGGATGATTTTGGCCTCATTACTTTACCACCCCCACAC NM_002444RefSeq chrX + 65667643 65741931 MSN 4478 moesin GO:0005515|GO:0003725|GO:0005886|GO:0006928|GO:0031528|GO:0072562|GO:0030175|GO:0050900|GO:0005615|GO:0071944|GO:0016323|GO:0005737|GO:0016324|GO:0061028|GO:0007159|GO:0022614|GO:0005856|GO:0050839|GO:0070062|GO:0019901|GO:0005102|GO:0045177|GO:0003779|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129376_PI430048170 0.0728924120176215 0.8162450114793439.00595851969852 8.86422654574155 8.76904764293327 P P P 8.98581936211142 9.23043932904114 9.29367464646359 P P P LNCV6_129376_PI430048170 mRNA GCCCGCATTATAAACACAGGAGAATAATCAATAGAATAAAAGTGACCGACTGTCAAAAAA NM_017436RefSeq chr22 - 42692120 42720870 A4GALT53947 "alpha 1,4-galactosyltransferase" GO:0007009|GO:0030173|GO:0050512|GO:0016020|GO:0001576|GO:0015643|GO:0006688|GO:0006486|GO:0008378|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136924_PI430048170 0.0974891897124592 1.28624699613318 4.83920916406845 4.88941269884593 4.73762439468401 P P P 4.68055156529619 4.45011391672999 4.21231849250196 P P P LNCV6_136924_PI430048170 mRNA TTATAATATACGTGACAGGTGTGACTTTCCTCTTGCTCCCCATTTCTGCCATTGTGGCCT NM_001004490 RefSeq chr11 - 6768006 6768957 OR2AG2 NA "olfactory receptor, family 2, subfamily AG, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145692_PI430048170 0.1638225280582430.7025353944169860.255218974738914 0.3235792855069350.30277570779071 A A A 0.4335961898665640.686473633976461 1.18652749699721 A A A LNCV6_145692_PI430048170 mRNA CTACCTACCAAACTATCCACAATTTAAATAAAGAACTGCTGTGTCTGACTTACTCTCAAT NM_020711RefSeq chr2 - 157318612 157325948 ERMN 57471 "ermin, ERM-like protein, transcript variant 2" GO:0008360|GO:0033270|GO:0030175|GO:0005737|GO:0031344|GO:0033269|GO:0051015|GO:0043209|GO:0043025|GO:0007015|GO:0005856|GO:0005938|GO:0070062|GO:0001763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88704_PI430048170 0.2803875929010091.61575192705122 5.62577151675855 6.05736795390219 5.24893135580032 P P P 5.74703259054809 4.86984213094712 3.62822971212685 P P P LNCV6_88704_PI430048170 mRNA ATCAAAAGACATCCGGGGATCATCCCGATGATCGGCTTAATCTGCCTGGGCATGGGCAGC NM_020142RefSeq chr12 - 57234902 57240692 NDUFA4L2 56901 "NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131109_PI430048170 0.7195460853231050.9268219971973225.04541967123451

4.62131891023844 4.79474422622918 P P P 4.6546758363382 5.3049902786488
4.77679726284834 P P P LNCV6_131109_PI430048170 mRNA
AAACAATTCCTCTCACCCACAAAACAATGTAATCCCAGCGATGGACTGGATTCTGAAGGC NM_015016RefSeq chr19
+ 18097792 18151689 MAST3 23031 microtubule associated serine/threonine kinase 3
GO:0005515|GO:0000287|GO:0004674|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133237_PI430048170 0.9635991697275180.9982858235521661 3.2781775478896
13.2114476741016 13.2476722360681 P P P 13.0141163328667 13.3478416174073
13.3577463714061 P P P LNCV6_133237_PI430048170 mRNA
GAAAGCATGTCTGCTGGGTGTGACCATGTTTCCTCTCAATAAAGTTCCCCTGTGACACTC NM_006142RefSeq chr1
+ 26863141 26864456 SFN2810 stratifin
GO:0005515|GO:0010839|GO:0051219|GO:0071901|GO:0030307|GO:0031424|GO:0061436|GO:0005634|GO:0001
836|GO:0000079|GO:0003334|GO:0005615|GO:0005829|GO:0046827|GO:0005737|GO:1900740|GO:0061024|GO:0
043154|GO:0030659|GO:0070062|GO:0008630|GO:0010482|GO:0019901|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130843_PI430048170 0.0790579933563274 1.37340544179814 5.43472062387478
5.53686610434308 5.15542219337086 P P P 5.20989721850834 4.83118257436113
4.68757164568239 P P P LNCV6_130843_PI430048170 mRNA
GCGTCCAGCACACAAATAAAAGACCCTTGGGCCCTGGCTCTGAGCCCATCCTGCAAAAAA NM_003834RefSeq chr16
- 268300 275943 RGS11 8786 "regulator of G-protein signaling 11, transcript variant 2"
GO:0031681|GO:0005886|GO:0005834|GO:0038032|GO:0044292|GO:0035556|GO:0043547|GO:0043234|GO:0005
737|GO:0008277|GO:0007186|GO:0004871|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143307_PI430048170 0.00220242173875621 0.3169664342311733.85878304324633
3.32434251549319 3.36772526530754 P P P 5.00575186001039 5.39977778701771
5.15358628105917 P P P LNCV6_143307_PI430048170 mRNA
GCACTTGTTAAACTGTGATGAACTTGTGATTTTGTGTTTTACTTGACCAAAACCAAGTGT NM_005664RefSeq chr15
+ 23565306 23568019 MKRN3 7681 makorin ring finger protein 3
GO:0005515|GO:0016567|GO:0030529|GO:0016874|GO:0008270 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145217_PI430048170 0.38742250836129 1.06962514101381 10.7177285384839
10.9759426402701 10.964465178751 P P P 10.750584035123 10.795286960793
10.8341910693995 P P P LNCV6_145217_PI430048170 mRNA
TGTGTGTTTTGTGTACTCCTGTGGGACTCCCATGGTTGTAAATAAAGGTTTCTCTTTTTT NM_030768RefSeq chr2 -
238170401 238203683 ILKAP 80895 integrin-linked kinase-associated serine/threonine phosphatase
GO:0005515|GO:0005737|GO:0033262|GO:0006470|GO:0004722|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142884_PI430048170 0.2056278810332150.5145714376068951.16241426398476
0.4086000999096581.53309632781238 A A A 1.2239131475857 1.71758898601522
2.79265666451592 A A P LNCV6_142884_PI430048170 mRNA
AGCTACCTTTTATTGAGTGCTATGTGCAAGTCAGTGTGCTAGGACTTCTATTGTTTATAG NM_001271562 RefSeq
chr11 - 114398533 114400550 C11orf71 54494 "chromosome 11 open reading frame 71, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132857_PI430048170 0.0113673184316719 0.5387430281768988.3223123866765
8.10922794754077 8.52700261112554 P P P 9.0394038288851 9.07006421972409
9.50726687664546 P P P LNCV6_132857_PI430048170 mRNA
CTTACTTGGAGGTTAAAGCAAACCCAAATGTGTATTATTTTGTTACAGAGCTCTGCTTTA NM_001017368 RefSeq
chr17 - 35009111 35063740 RFFL 117584 "ring finger and FYVE-like domain containing E3 ubiquitin
protein ligase, transcript variant 2"
GO:0005515|GO:0006511|GO:0032006|GO:0005886|GO:0016874|GO:0002020|GO:0006886|GO:0005764|GO:0005

829|GO:0002039|GO:0010762|GO:0005737|GO:0042787|GO:0031625|GO:0019901|GO:0010804|GO:0000139|GO:0
016020|GO:2001271|GO:0016023|GO:0008270|GO:0043161|GO:0070936|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130547_PI430048170 0.0888014141172565 0.4758876706620549.18476114568848
10.3103205779247 10.3139682921518 P P P 11.0373071712073 11.1909553383947
11.0542422987522 P P P LNCV6_130547_PI430048170 mRNA
CCGCTGAGATGCCCCCACCCCAGGTTTCCCCCATCAGAGTTAAGAGGAAAGAAGGCTGTT NM_021248RefSeq chr20
- 46173732 46308498 CDH22 64405 "cadherin 22, type 2"
GO:0016339|GO:0005886|GO:0007420|GO:0005509|GO:0016021|GO:0007156 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135422_PI430048170 0.0559927038122321 1.16361110548493 13.6174892754458
13.5718197844502 13.420021780664 P P P 13.2104958914577 13.3462671685898
13.3976447324539 P P P LNCV6_135422_PI430048170 mRNA
TGAGGCTTTGTCCCTTCCCAATAAAGCCTGCTACCTGGCAGTACCCCTGAAGAGAAAAAA NM_052850RefSeq chr19
- 12954155 12957254 GADD45GIP1 90480 "growth arrest and DNA-damage-inducible, gamma
interacting protein 1"
GO:0070124|GO:0005739|GO:0005515|GO:0070125|GO:0070126|GO:0007049|GO:0032543|GO:0006996|GO:0005
759|GO:0016032|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140995_PI430048170 0.5756962968767740.9728459925360830.440517109836196
0.4167935425116940.24419701805485 A A A 0.3717807557407250.446577557731927
0.409177831512976A A A LNCV6_140995_PI430048170 mRNA
TCAACTGCATTCATGTACTTAAAACCCTCCACAATCAGTTCCTTGACCCAGGAGAATGTG NM_001005194 RefSeq
chr11 + 124570068 124571049 OR8A1 NA "olfactory receptor, family 8, subfamily A, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81275_PI430048170 0.0187227867797551 0.3132568523023461.55857467416215
1.05096551420208 0.456550172976567A A A 2.52002251319367 2.7125174993704
3.01923944262986 P P P LNCV6_81275_PI430048170 mRNA
TGTGTTTGGAAATCATAGAGGGTATTTACCTTGAGGGCTCTTTTGTTGACCTTATTTATTNM_173690RefSeq chr9 -
124942608 125143559 SCAI 286205 "suppressor of cancer cell invasion, transcript variant 1"
GO:0005515|GO:0031965|GO:0030336|GO:0006355|GO:0005737|GO:0035024|GO:0003714|GO:0005634|GO:0016
021|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141340_PI430048170 0.3378910482504450.9682193152897131 5.38348582894
15.3937606927222 15.2913510129397 P P P 15.3968197624887 15.4540917456046
15.3580350098784 P P P LNCV6_141340_PI430048170 mRNA
GCTACATGTTACCTCCTTCAATTGATAATAAACCTTTCTGAGATGCAGAGGGTCCAGGTC NM_025029RefSeq chr2
+ 130181927 130190727 MZT2B 80097 mitotic spindle organizing protein 2B
GO:0005515|GO:0005813|GO:0005819|GO:0008274 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133375_PI430048170 0.3385393139297630.7161398697095161.43216437015148
2.18965000198331 3.32985315709112 A A P 3.1901673657318 2.86399776880826
2.95819856065515 P P P LNCV6_133375_PI430048170 mRNA
TTTACATCCTTATGGCAGCCTTCGAATACCTTTTAACTCCCAGTTCCCTTAACTGGGGGT NM_014171RefSeq chr2
+ 46617171 46630176 CRIPT 9419 cysteine-rich PDZ-binding protein
GO:0005515|GO:0008017|GO:0030054|GO:0005730|GO:0014069|GO:0035372|GO:0005634|GO:0031122|GO:0030
165|GO:0032403|GO:0030425|GO:0045184|GO:0005737|GO:0043197|GO:0043198|GO:0043025 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130367_PI430048170 0.4646484081419671.03435223774429 0.306890003134975
0.2820453452464540.445380641010925A A A 0.34097778510938 0.25786909828504
0.293504623296922A A A LNCV6_130367_PI430048170 mRNA
CTAGATTTTCCTAGGACTCCAATAGCATGCTTTCCAAGTGTTATTATTCCCTTAATGTTA NM_001178036 RefSeq chr2

+ 114461602 115844750 DPP10 57628 "dipeptidyl-peptidase 10 (non-functional), transcript variant 5"
GO:0016020|GO:0006508|GO:0008236|GO:0016021|GO:0008239 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134503_PI430048170 0.9315798737699860.95966312040366 3.70799368628946
4.00319623419434 3.82793924419498 P P P 3.49329656513636 3.80307924563402
4.31508010587808 P P P LNCV6_134503_PI430048170 mRNA
TGCGTGAAACTCAAAGTTGCTAACATCATCTTCCTTATTTTCAGCCAGTGCTGTTACTGC NM_021818RefSeq chr14
- 50633579 50668353 SAV1 60485 salvador family WW domain containing protein 1
GO:0005515|GO:0060044|GO:0043065|GO:0060412|GO:0050680|GO:0005634|GO:0035329|GO:2000036|GO:0005
829|GO:0060575|GO:0005737|GO:0030216|GO:0060487|GO:0001942 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130758_PI430048170 0.0158308879471052 0.5154779725232413.88331044707947
3.46304608759267 4.05758341567234 P P P 4.8978350516264 4.58418944992472
4.83410845025874 P P P LNCV6_130758_PI430048170 mRNA
CTGTTCTATAGGCTTATGATCTGAGCAAAATGTGAACTTCAGTATGTTTACTATTGCTCT NM_018191RefSeq chr13
- 49531945 49585583 RCBTB1 55213 regulator of chromosome condensation (RCC1) and BTB (POZ)
domain containing protein 1 GO:0007049|GO:0006355|GO:0005737|GO:0005634|GO:0006351|GO:0016568 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141506_PI430048170 0.00752837547298647 0.4484034410099819.1694541284658
8.94834625297187 9.02038005666981 P P P 9.96005670805377 10.148516642361
10.4643544673982 P P P LNCV6_141506_PI430048170 mRNA
GCCAGGAAGTTGTCTTTGTGGACTCTGCCTGCATGGCTTAGTAGTAGAAGGAAATTTTTT NM_015100RefSeq chr1
- 151402723 151459465 POGZ 23126 "pogo transposable element with ZNF domain, transcript variant 1"
GO:0005515|GO:0005737|GO:0000790|GO:0051382|GO:0005654|GO:0005634|GO:0003677|GO:0046872|GO:0051
301|GO:0007064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143126_PI430048170 0.0231077595159557 0.6594264139934636.62642239277107
6.84763551962145 7.07393302867258 P P P 7.43737437726466 7.33335798440611
7.60133574810072 P P P LNCV6_143126_PI430048170 mRNA
CCGAAGTAGGATACTGTAACTGTGTAAGGATTTTGTTTGTAATCTTGTAACATTGAACCA NM_207435RefSeq chr12
- 110041176 110067695 C12orf76 400073 chromosome 12 open reading frame 76 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133120_PI430048170 0.8275769327440211.0113593691171 11.934459678329
11.8743311049312 11.8136509420353 P P P 11.9071247014726 11.9445706636569
11.7139324704058 P P P LNCV6_133120_PI430048170 mRNA
TTGAGTGGGCAGCCAAGCCCAGGCTCGCAGTATCAATAAAGCAGTTCTCTGAGGAATGAC NM_007024RefSeq chr3
- 50354748 50359508 TMEM115 11070 transmembrane protein 115
GO:0005515|GO:0003674|GO:0008285|GO:0005794|GO:0032580|GO:0006890|GO:0017119|GO:0006486|GO:0005
634|GO:0016021|GO:0015031|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121197_PI430048170 0.7391099521669330.9714081182479438.59630363881615
8.59413646273126 8.65260056035716 P P P 8.46534546033435 8.71872676353681
8.76742511083057 P P P LNCV6_121197_PI430048170 mRNA
TAGAAGCTGAGAAGGGTCGTGATGCCTTCCCCGTGGCTGGACAGAAACTCATCTATGCCG NM_005053RefSeq chr19
+ 12945813 12953643 RAD23A 5886 "RAD23 homolog A (S. cerevisiae), transcript variant 1"
GO:0005515|GO:0003684|GO:0005737|GO:0000502|GO:0003697|GO:0016032|GO:0043161|GO:0032434|GO:0005
654|GO:0006289|GO:0045070|GO:0031593 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140345_PI430048170 0.0561701551056780.3847331517409664.23770175584799
2.92269639292721 3.38734535266196 P A P 4.85060125726559 5.12797204218927
5.00550583539485 P P P LNCV6_140345_PI430048170 mRNA
GTGCCAAGAACTGGAAAGTCTACTTTTTGGAGGGAAATGATACTTAGAATTTGTAAACAT NM_025054RefSeq chr8

- 66630252 66667217 VCPIP1 80124 valosin containing protein (p97)/p47 complex interacting protein 1
GO:0071108|GO:0007067|GO:0005737|GO:0016567|GO:0004843|GO:0005795|GO:0005783|GO:0016320|GO:0006
508|GO:0090168|GO:0035871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63828_PI430048170 0.2354082327928381.127852163703 3.43651991397281 3.52424423127334
3.77456288646287 P P P 3.50117561427524 3.39387796380066 3.3363259300761 P P P
LNCV6_63828_PI430048170 mRNA
AAGATAATCACAGCTGGCTTATCAATATTGCTGTTTGATGCGATCCTGACCAGTGCAACC NM_032933 RefSeq chr18
- 23296014 23437961 TMEM241 85019 transmembrane protein 241 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128170_PI430048170 0.4145821263066531.02651727429855 0.294728093661225
0.3133551673546720.410855382391717 A A A 0.3196057382890920.297845368356513
0.290773042528714 A A A LNCV6_128170_PI430048170 mRNA
GCTCTCTTATGAAGGCAGAGTCAGATAAAATGATATTCTGCAATTATCTAGATCATAAGC NM_001030311 RefSeq
chr2 - 181536673 181657107 CERKL NA "ceramide kinase-like, transcript variant 2" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127974_PI430048170 0.6799314217645180.9769166261168460.511050840547091
0.4513127619177660.26564844380444 A A A 0.3889670325635160.491450709975806
0.457984000629351 A A A LNCV6_127974_PI430048170 mRNA
CTTCAGATGGACTTATACATTCTGTGCTTTGGAAGCACAAGAAGAACAAAATATGTGTAT NM_182540 RefSeq chrX
+ 135520629 135582535 DDX26B 203522 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133870_PI430048170 0.7447304331993651.01512552738235 0.539583841947858
0.3974457570890160.531338537750749 A A A 0.3883563491733940.50893093060094
0.507191647351178 A A A LNCV6_133870_PI430048170 mRNA
AGTGTTTTGATCGCATTGGTTGTTTTCCGTATGATGATTGTGAGGTGCACCTTACAGCAA NM_001276254 RefSeq
chr19 - 39246313 39248856 IFNL4 NA - NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138371_PI430048170 0.1562333063675521.0593436435272 0.448814281147429
0.3212082124640590.34779127017258 A A A 0.2687462750421060.329968332789061
0.271924596552891 A A A LNCV6_138371_PI430048170 mRNA
CTATATAGAAAACTGTTCAACTCCAAATACGTACATCTGCATGCAAAGGACTGTGTAAAG NM_007360 RefSeq chr12
- 10372352 10390054 KLRK1 22914 "killer cell lectin-like receptor subfamily K, member 1"
GO:0005515|GO:0005886|GO:0009986|GO:0031295|GO:0030154|GO:0007165|GO:0030101|GO:0005887|GO:0045
087|GO:0050776|GO:0045954|GO:0030246|GO:0004872|GO:0016021 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139305_PI430048170 0.0704417475542204 1.04457368778368 0.395444359265396
0.4080250363113420.443155473532344 A A A 0.3275112794940910.3373983173308
0.392542557237646 A A A LNCV6_139305_PI430048170 mRNA
TACAATGTCAACGAAGATGCCAAGGCAGCAATGACTGAACTCAAGTCCTGTATAGATGGC NM_145651 RefSeq chr11
+ 193079 194573 SCGB1C1 147199 "secretoglobin, family 1C, member 1" GO:0005576 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143909_PI430048170 0.2290781212449231.60029865463822 0.285017646223975
1.46722834605868 1.18904806144188 A A A 0.5584923079442070.271878673363385
0.303055463716985 A A A LNCV6_143909_PI430048170 mRNA
TGATACACACACACCCCTTATATGGGACTAATTTTACACTTTTCTGTGTTATGTGTGTATNM_001010892 RefSeq chr6
+ 116616478 116632985 RSPH4A 345895 "radial spoke head 4 homolog A (Chlamydomonas), transcript
variant 1"
GO:0003674|GO:0035082|GO:0031514|GO:0005930|GO:0005730|GO:0005654|GO:0005634|GO:0003341|GO:0005
856|GO:0001534 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135235_PI430048170 0.0529230077147741 0.4280449254452221.89893335598497

3.02774496586549 2.51671761720151 A A A 3.64990902625559 3.79055415778065
3.88207906544996 P P P LNCV6_135235_PI430048170 mRNA
GTCCAGGAAACCACCAGAAGATGGATTTTTAGTGTTTTTGAAATCTTGTATTTCCTTTTG NM_032410RefSeq chr8
+ 42896889 43030539 HOOK3 84376 hook microtubule-tethering protein 3
GO:0008017|GO:0005515|GO:0005801|GO:0030897|GO:0034451|GO:0031122|GO:0015031|GO:0045022|GO:0042
802|GO:0005737|GO:0050768|GO:0022027|GO:0071539|GO:0007032|GO:0000242|GO:0051645|GO:0070695|GO:0
097150|GO:0005813|GO:0005794|GO:0005815|GO:0008333|GO:0005874|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145111_PI430048170 0.4592722826864670.7413915654023490.336221374451737
0.3211814705457412.49043034654824 A A A 1.11544336917768 2.52978730407026
1.59744830080295 A P A LNCV6_145111_PI430048170 mRNA
CTTTTGGTGAAAGCTGAGAACTCCTGACTGTAACATATTCTGTATGAACTTTATCTAAAG NM_001275RefSeq
chr14_KI270847v1_alt + 37661 49856 CHGA 1113 "chromogranin A (parathyroid secretory protein 1),
transcript variant 1" GO:0048471|GO:0008217|GO:0005576|GO:0030141|GO:0030658 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_143652_PI430048170 0.2863506848727520.8742301312349120.403217177128565
0.4288368547516330.305041431640668A A A 0.8174075533622090.453438736948818
0.415942866948207A A A LNCV6_143652_PI430048170 mRNA
GACAACTACTGGAGAGTCATGTTTGTTGAAATTCTCATTAATGTTTATGGGTGTTTTCTG NM_000601RefSeq chr7
- 81702127 81770136 HGF 3082 "hepatocyte growth factor (hepapoietin A; scatter factor), transcript
variant 1"
GO:0005515|GO:0004252|GO:2000573|GO:0031100|GO:0050731|GO:0001837|GO:0005615|GO:0042802|GO:0000
187|GO:0090201|GO:0060665|GO:0070572|GO:0045944|GO:0035729|GO:0006508|GO:0031093|GO:0043154|GO:0
031643|GO:0048012|GO:0030335|GO:0046982|GO:0030168|GO:0014068|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_109619_PI430048170 0.00350519548044082 1.27288996710945 13.133871832866
13.1540088972333 13.0395227857652 P P P 12.6831552032711 12.7708188965425
12.8280009771824 P P P LNCV6_109619_PI430048170 mRNA
GAAAGCACGTTCCAGCCACCAGGAGGCCACCTATTGTTTCAAAATAAAGACTGGGTTCCT NM_001199629 RefSeq
chr12 + 56152419 56157987 MYL6B 140465 "myosin, light chain 6B, alkali, smooth muscle and non-
muscle, transcript variant 1"
GO:0005515|GO:0030049|GO:0005509|GO:0016459|GO:0005829|GO:0003774|GO:0006936|GO:0016461|GO:0007
519|GO:0008152|GO:0005859|GO:0008307|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144954_PI430048170 0.0169800772322497 2.32532533398684 4.85257103928132
4.88767643711621 5.47640118477413 P P P 4.02731081278024 3.75106517892656 3.8610963377773
P P P LNCV6_144954_PI430048170 mRNA
TTCCAATGAATGAAAGTCATGCACTTTATTTATAGGCTCTATGTTTTGGCTTCTGCAGTA NM_198827RefSeq chr12
+ 130953906 131141463 ADGRD1 NA adhesion G protein-coupled receptor D1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_145241_PI430048170 0.8085233292151140.8562236769853161.97512333824503
1.73792719054814 1.43586297962164 A A A 0.9960467739381672.09925727066725
2.42432872391497 A A P LNCV6_145241_PI430048170 mRNA
CCACCTGTAAGGCAAATCTGCCTTAAGTGTATTATGTGTTACTTAAAGGCAAATTTGTGA NM_032852RefSeq chr1
+ 62784105 62865271 ATG4C 84938 "autophagy related 4C, cysteine peptidase, transcript variant 1"
GO:0006501|GO:0006995|GO:0000422|GO:0006914|GO:0005576|GO:0051697|GO:0005829|GO:0004197|GO:0005
737|GO:0016485|GO:0006612|GO:0006508|GO:0008233|GO:0000045 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_121776_PI430048170 0.0730055120829910.5046716566695690.306853848949788
0.34542938118125 0.363602839592023A A A 1.5112541408862 1.58370087347441

0.739972065480265 A A A LNCV6_121776_PI430048170 mRNA
CATGTAAAAACATTCAAACAAACACACTCAGCGGATTTATTTATTGTGCAATGGGGCAAT NM_014795 RefSeq chr2
- 144384374 144520391 ZEB2 9839 "zinc finger E-box binding homeobox 2, transcript variant 1"
GO:0021846|GO:0048023|GO:0001756|GO:0001755|GO:0001843|GO:0030177|GO:0070412|GO:0005634|GO:0000
122|GO:0003677|GO:0046872|GO:0006351|GO:0007399|GO:0021766|GO:0019208|GO:0045944|GO:0045636|GO:0
043507|GO:0048066. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62929_PI430048170 0.0377857574632348 0.680011201631941 5.94446727253437
5.64188773278574 5.82502948970379 P P P 6.07410905751295 6.47171921253327
6.51144624287015 P P P LNCV6_62929_PI430048170 mRNA
CCATGGAAGTGTCACCATTGCACCTGTAAATGAAAATATGCAAGTCAACAAAATAAAGAA NM_001067 RefSeq chr17
- 40388520 40417950 TOP2A 7153 topoisomerase (DNA) II alpha 170kDa
GO:0005515|GO:0043130|GO:0000793|GO:0042826|GO:0000819|GO:0005634|GO:0042803|GO:0007059|GO:0040
016|GO:0002244|GO:0045944|GO:0019035|GO:0008144|GO:0005080|GO:0045070|GO:0008094|GO:0043065|GO:0
009330|GO:0003918|GO:0000287|GO:0046982|GO:0008301|GO:0005814|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143749_PI430048170 0.266265509622015 0.518042195181065 0.29834065310098
0.259475780965124 0.383383581141474 A A A 2.01424577731573 0.965272795157974
0.275387225046888 A A A LNCV6_143749_PI430048170 mRNA
GTTCTTCATACCCATTTTGACAAAGTGGAACAGTGGAGCTGTTTTTTGCTTTTGTTTTTA NM_139164 RefSeq chr5 -
111496034 111512597 STARD4 134429 StAR-related lipid transfer (START) domain containing 4
GO:0006869|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109039_PI430048170 0.102477734856426 4.80274305029925 4.24044536182149
1.74521689111561 2.59496935384696 P A A 1.32818072749416 0.339579762575943
1.08091161898441 A A A LNCV6_109039_PI430048170 mRNA
CTTTACGAAGATGGCGACCGTAACACTCCTTAGAAACTGGCAGTCGTATGTTAGTTTCAC NM_052886 RefSeq chr8
+ 119208370 119245673 MAL2 114569 "mal, T-cell differentiation protein 2 (gene/pseudogene)"
GO:0005515|GO:0048471|GO:0016324|GO:0045121|GO:0016021|GO:0070062|GO:0012505 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139364_PI430048170 0.00754765619385837 1.32515144195766 7.76282870391229
7.88280585279389 7.7291032743765 P P P 7.34365905796254 7.50533706008826
7.30384740280059 P P P LNCV6_139364_PI430048170 mRNA
AGATTTAGGACCATAATGAGGTCTCATGTTCTCTGCTCCCACACCTAAGCCAAGACCTTT NM_001300980 RefSeq
chr5 + 140639426 140645408 TMCO6 55374 "transmembrane and coiled-coil domains 6, transcript
variant 1" GO:0005737|GO:0008565|GO:0005634|GO:0016021|GO:0006606 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144498_PI430048170 0.221210633815417 0.928204611598636 10.6193859561439
10.7382085377315 10.521733743821 P P P 10.6746148317305 10.735417106704
10.7973058063438 P P P LNCV6_144498_PI430048170 mRNA
GGCCTTTTTCACTTAGAAGCTGCACATTATGGAGCATTAAACACTTTTGTCATAGAAAAA NM_014550 RefSeq chr22
- 37490361 37519203 CARD10 29775 "caspase recruitment domain family, member 10"
GO:0005515|GO:0005737|GO:0006461|GO:0032449|GO:0007250|GO:0030159|GO:0042981 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140802_PI430048170 0.786330206115206 0.950247419170571 0.674019157899962
0.537776139975305 0.772207455818577 A A A 1.06066111927035 0.529465162794209
0.560530082044956 A A A LNCV6_140802_PI430048170 mRNA
GATGCTATGAAGAAATTGCTGGGCAAAATAACATTGCATCAAACACACGAACATCTCTGA NM_205859 RefSeq chr9
- 111327482 111328433 OR2K2 NA "olfactory receptor, family 2, subfamily K, member 2" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133148_PI430048170 0.456744596799353 1.32134362771485 2.52630368968216

1.32643619870979 1.84562299021269 A A A 2.05397356703931 1.51620690508601
0.974531270338419 A A A LNCV6_133148_PI430048170 mRNA
AATACAAGTGTGGGATGAAAAACCATCATCCTGAACAGCAAAGCTCCCTGCTAAACCTCT NM_201402 RefSeq chr8
- 12137167 12138760 USP17L2 NA ubiquitin specific peptidase 17-like family member 2 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134379_PI430048170 0.349429739530901 1.40829564421512 1.65695591566481
0.658968684619797 0.620267183746043 A A A 0.605832645599028 0.621854642542609
0.476339862199066 A A A LNCV6_134379_PI430048170 mRNA
GTGAGGCTGAGCTGAAGGAATGTGGGCCCAGGTTTCTTAATAAAATGATTTACTCTTCAA NM_001372 RefSeq chr17
+ 11598430 11969748 DNAH9 1770 "dynein, axonemal, heavy chain 9, transcript variant 2"
GO:0005930|GO:0005874|GO:0006928|GO:0007283|GO:0003777|GO:0005524|GO:0003774|GO:0030286|GO:0008
152|GO:0030030|GO:0005856|GO:0016887|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127822_PI430048170 0.0273469204841429 3.50493787212233 2.74629642582277
3.85306847261782 3.50792744658312 A P P 1.7751760824556 1.48958318120346
1.60985974126414 A A A LNCV6_127822_PI430048170 mRNA
GAAAGAATTCACACTGGGGAGGAACCCTATGAATATAAGGGTATGAATGTTACCATTTAG NM_001199814 RefSeq
chr19 - 9690137 9700817 ZNF812 729648 zinc finger protein 812
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127282_PI430048170 0.154698127214777 1.10463109474444 0.576893264697315
0.359220980666906 0.531826584135442 A A A 0.280647120454863 0.386814808365819
0.376457280235644 A A A LNCV6_127282_PI430048170 mRNA
GTGAAGACCAAGCAGATCAGAGATAAGGTTATACTTTTGTTTTCTAAGGGTACAGGATGA NM_001005289 RefSeq
chr11 - 5544560 5545523 OR52H1 NA "olfactory receptor, family 52, subfamily H, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143623_PI430048170 0.942475842853988 1.0008704723235 10.3532867130745
10.4759591721141 10.6216790445675 P P P 10.1687447942056 10.5418832667296 10.698986899293
P P P LNCV6_143623_PI430048170 mRNA
CTTGAGCATGACACTTCTTTCAGTATATTGCTTGATGCTTCAAATAAAGTTTTGTCTTGGNM_004126 RefSeq chr7 +
93921703 93926514 GNG11 2791 "guanine nucleotide binding protein (G protein), gamma 11"
GO:0007165|GO:0006112|GO:0007186|GO:0005886|GO:0071377|GO:0005834|GO:0003924|GO:0044281|GO:0004
871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137805_PI430048170 0.213888597227565 0.754254941615745 0.297547579825846
0.261016709011189 0.384177303711508 A A A 0.969303642307764 0.831938297779669
0.27573448115986 A A A LNCV6_137805_PI430048170 mRNA
TCCCCATGACTGTCCTTCAGTCACAATTCCAGAATAAAAGAATCTACTTTGTGTAAAAAA NM_002269 RefSeq chr6
+ 116681203 116741867 KPNA5 3841 karyopherin alpha 5 (importin alpha 6)
GO:0005515|GO:0005737|GO:0019221|GO:0008565|GO:0005654|GO:0006607|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133644_PI430048170 0.18208627864218 0.282313085230544 0.483977994768484
0.567810533915447 0.564245641040227 A A A 0.613383761238439 2.3626709309296
3.13240399405033 A A P LNCV6_133644_PI430048170 mRNA
GTCGGATGTTAAGATATTATATTTCAGTACTAGGAGCTTCTTTGCAGTCATTAACATGAC NM_032021 RefSeq chr11
+ 100992079 100993935 TMEM133 83935 transmembrane protein 133 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135302_PI430048170 0.0294922612715656 1.30735962477502 6.21225003396445
6.09196021497783 6.12623867470583 P P P 5.63326113243238 5.91632157823515
5.70847985708685 P P P LNCV6_135302_PI430048170 mRNA
TTAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGAC NM_033102 RefSeq chr1

- 205657852 205680502 SLC45A3 85414 "solute carrier family 45, member 3" GO:0016021|GO:0055085
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139011_PI430048170 0.00507503144940398 0.72973705303483912.0420681880299
11.8564194979298 12.00648878459 P P P 12.3797452671529 12.3502842415709
12.5380971638978 P P P LNCV6_139011_PI430048170 mRNA
CAGGCACTGTTTTGCTTCAGCTAGAAAATACAATGCAGATGTCATTAAAAGACTTACTTT NM_000169RefSeq chrX
- 101397790 101408013 GLA 2717 "galactosidase, alpha"
GO:0005515|GO:0006665|GO:0005794|GO:0009311|GO:0006687|GO:0046477|GO:0052692|GO:0046479|GO:0005
102|GO:0016936|GO:0005576|GO:0016139|GO:0044281|GO:0003824|GO:0005764|GO:0042803|GO:0005737|GO:0
051001|GO:0016787|GO:0045019|GO:0004557|GO:0070062|GO:0043202 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_53650_PI430048170 0.00206767628571159 1.83614269406781 7.18578231958461
7.35924207574252 7.09615061431693 P P P 6.51572369905389 6.27427262743736
6.21583398078296 P P P LNCV6_53650_PI430048170 mRNA
TGTTTGAACCTGGGCATCCTAGAGGTGACAGTCTACGCATTCAGCATTGAGAACTTCAAA NM_024887RefSeq chr1
+ 26432281 26471304 DHDDS 79947 "dehydrodolichyl diphosphate synthase, transcript variant 2"
GO:0005515|GO:0005789|GO:0016765|GO:0006488|GO:0044267|GO:0006489|GO:0043687|GO:0018279 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128188_PI430048170 0.00201644071780933 0.59264907714003910.6363472919537
10.7786118792058 10.5067003136398 P P P 11.5259489538904 11.3458576120514
11.3179810246252 P P P LNCV6_128188_PI430048170 mRNA
TTTCCATGAGCTCTTGGAGGCACCAAGAAATAAACTCGTAACCCTGTCCTTCAGAAAAAA NM_001258289 RefSeq
chr1 - 151364301 151372734 SELENBP1 8991 "selenium binding protein 1, transcript variant 3"
GO:0005515|GO:0008430|GO:0016020|GO:0005730|GO:0015031|GO:0005615|GO:0070062|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143471_PI430048170 0.8001001731288070.9739537666815730.330189887317627
0.3323126980086890.499629408134627A A A 0.6256481438939350.2894086745503
0.344961211263586A A A LNCV6_143471_PI430048170 mRNA
CTTAGGCAACTAGATTCGGTTCTTGCTTATTCTGCCAATAAAATACTTTATTGAGATGCT NM_130759RefSeq chr7
+ 150716556 150724280 GIMAP1170575 "GTPase, IMAP family member 1"
GO:0030217|GO:0000139|GO:0030183|GO:0005789|GO:0016021|GO:0005525 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137730_PI430048170 0.32772875931011 1.03021202656272 0.355931316405018
0.3570899679588670.454027930377182A A A 0.3477839014297450.319359717233316
0.372800022041218A A A LNCV6_137730_PI430048170 mRNA
TCCCATGCTTAACAAATCATTAAAACACCCTAGAACACTCCTAGGATAGATTAATGTAGT NM_004185RefSeq chr1
+ 112466540 112521288 WNT2B 7482 "wingless-type MMTV integration site family, member 2B, transcript
variant WNT-2B1"
GO:0090263|GO:0005578|GO:0061072|GO:0005576|GO:0005615|GO:0021871|GO:0061303|GO:0005109|GO:0071
425|GO:0045165|GO:0060638|GO:0002062|GO:0002088|GO:0030182|GO:0060492|GO:0016055|GO:0060070|GO:0
090190|GO:0008584|GO:0009267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139881_PI430048170 0.0544553813492701 0.87972032211408910.6059089599487
10.4344112163611 10.4527139948508 P P P 10.7359567638804 10.6916560011586
10.6240967810985 P P P LNCV6_139881_PI430048170 mRNA
CCAGCGTCACCTTTGAAGTATACGTGAGAGAAATATATTTACAAATGCTTTATTCTCTTC NM_014603RefSeq chr17
+ 74987631 75005797 CDR2L 30850 cerebellar degeneration-related protein 2-like NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145753_PI430048170 0.8913229019090740.9815860714797489.67868255550412
9.61132846310697 9.32376226947861 P P P 9.77697000876681 9.56369945903716

9.34541319390149 P P P LNCV6_145753_PI430048170 mRNA
TTATGATTTGGATGCCCCGCTCTCAGTTGAGAGCGAAGGAGAAATAAACCTGACATGTTG NM_032301 RefSeq chr19
- 12688915 12696641 FBXW9 84261 F-box and WD repeat domain containing 9
GO:0005515|GO:0031146 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130071_PI430048170 0.000139015829758103 0.2692944133706558.8492772206304
8.86683932530421 9.14554071022865 P P P 10.9606783385459 10.6999113268122
10.8864899423261 P P P LNCV6_130071_PI430048170 mRNA
ACTGTGGCTTATGTTACACATGTTCATGTTCACCTCTCATTCACCTGTTTTATATGGTTT NM_014637 RefSeq chr8 +
65644652 65710563 MTFR1 9650 "mitochondrial fission regulator 1, transcript variant 1"
GO:0009060|GO:0005739|GO:0005737|GO:0005886|GO:0000266|GO:0007005 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130741_PI430048170 0.0625928232898322 0.8556807304234791 1.7603041252864
11.6328082615409 11.5301180619276 P P P 11.863916968686 11.7704307195813
11.9660483939029 P P P LNCV6_130741_PI430048170 mRNA
AAGTGCTTCCGCCCCCTCACTACCTCCTTTAATACAAATTCAATAAAAAAGGTGAAATAT NM_006913 RefSeq
chr6_GL000256v2_alt + 3494591 3497000 RNF5 6048 "ring finger protein 5, E3 ubiquitin protein
ligase"
GO:0005515|GO:0004842|GO:0031966|GO:0016874|GO:0031648|GO:0009617|GO:0070534|GO:2000785|GO:0005
789|GO:0010507|GO:0008270|GO:0016021|GO:0044257|GO:0070936|GO:0071712 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_126719_PI430048170 0.0832559411884012 0.6805005306071121 0.0979000712022
9.9599080186415 10.0368609731205 P P P 10.2223133003861 10.7493395599747
10.7327724504042 P P P LNCV6_126719_PI430048170 mRNA
GTCACTTTTTAAACCACTGTATAGAAGGTTTTTGTAGCCTGAATGTCTTACTGTGATCAA NM_000527 RefSeq chr19
+ 11089361 11133829 LDLR 3949 "low density lipoprotein receptor, transcript variant 1"
GO:0006629|GO:0005515|GO:2000188|GO:0032050|GO:0005886|GO:0007603|GO:0010899|GO:0044281|GO:0030
301|GO:0005764|GO:0030299|GO:0005041|GO:0001948|GO:0034383|GO:0015914|GO:0030229|GO:0034362|GO:0
016032|GO:0008203|GO:0042632|GO:0005794|GO:0010867|GO:0009986|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128595_PI430048170 0.590593683245585 1.60135645203394 0.313514994290987
2.19236515292133 0.324971316263476 A A A 0.469729545624028 0.35928519983731
0.803073940041711 A A A LNCV6_128595_PI430048170 mRNA
GTTTCTTACTTATCACTAATTTTTACTGCAGGTCTGTGCTGTTTCTTAGAAAGTACATGC NM_001270623 RefSeq chr12
+ 59596039 59789854 SLC16A7 9194 "solute carrier family 16 (monocarboxylate transporter),
member 7, transcript variant 1"
GO:0035873|GO:0035879|GO:0005886|GO:0005887|GO:0050833|GO:0005477|GO:0015355|GO:0015129|GO:0055
085|GO:0015293 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132510_PI430048170 0.984948127030523 0.878709752485211 2.70725884403277
3.23972568128303 2.47686362879987 A P A 3.81764167477738 2.82021460803283
1.74617694745909 P P A LNCV6_132510_PI430048170 mRNA
GATTAGAAAATAGAAGCAGAAAGAAGACTCATTGGCCATCCCACTCTCTGGGGTGAATAC NM_020379 RefSeq chr1
+ 25617467 25786207 MAN1C1 57134 "mannosidase, alpha, class 1C, member 1, transcript variant 1"
GO:0030173|GO:0000139|GO:0005509|GO:0004571|GO:0006487|GO:0044267|GO:0070062|GO:0043687|GO:0018
279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57228_PI430048170 0.151446150960972 0.797698761508112 4.5111244242372 4.68874769960648
4.65266421558702 P P P 4.64242326694493 5.0946002874718 5.05764016398847 P P P
LNCV6_57228_PI430048170 mRNA
TGGGAGGTTTTCCTTGAAGTTCTTGATGGGGTAGAGAAGATGAAGTCCATGTCACAGCTT NM_001282659 RefSeq
chr11 + 11841422 11959325 USP47 55031 "ubiquitin specific peptidase 47, transcript variant 1"

GO:0005515|GO:0043066|GO:0004843|GO:0030307|GO:0042493|GO:0005634|GO:0006974|GO:0004197|GO:0005
737|GO:0034644|GO:0010972|GO:0071987|GO:0061136|GO:0006284|GO:0035520|GO:0043161|GO:0043154|GO:0
045892|GO:0019005. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131515_PI430048170 0.37461620500123 0.9344248666885435.28037232717228
5.40503319310964 5.58238875269063 P P P 5.59408658626891 5.44760977580576
5.53195753968777 P P P LNCV6_131515_PI430048170 mRNA
CTTCCTAAGTTCCCTTCTATATCCTCAAGGTAGAAATGTCTATGTTTTCTACTCCAATTC NM_000396RefSeq chr1 -
150796207 150808441 CTSK 1513 cathepsin K
GO:0045453|GO:0005518|GO:0043394|GO:0005576|GO:0002224|GO:0005615|GO:0004197|GO:0001957|GO:0022
617|GO:0030198|GO:0051603|GO:0045087|GO:0036021|GO:0030574|GO:0006508|GO:0008234|GO:0001968 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130181_PI430048170 0.5749014868666851.01593366346222 0.361354952159043
0.2481051615413050.293419730808159A A A 0.2696865612662240.295028306884093
0.271866943398473A A A LNCV6_130181_PI430048170 mRNA
CTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTTTTTATTATGTAAGC NM_001201397 RefSeq
chr13 - 77895480 77919768 EDNRB 1910 "endothelin receptor type B, transcript variant 4"
GO:0005515|GO:0014070|GO:0008284|GO:0005886|GO:0060406|GO:0001755|GO:0007200|GO:0019934|GO:0007
194|GO:0031702|GO:0007204|GO:0006885|GO:0042045|GO:0031620|GO:0042311|GO:0042310|GO:0050678|GO:0
043066|GO:0031965|GO:0014826|GO:0007568|GO:0014043|GO:0030318|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141867_PI430048170 0.0873888061095111 2.05301524332934 2.37505899160974
3.39951456477341 3.44549656348417 A P P 1.71508212976891 2.29097970901279
2.26190525557937 A A A LNCV6_141867_PI430048170 mRNA
CTAAAGATACATACCTGGTTTGCTTGGCTTACGTAAGAAAGTAGAAGAAAGTAAACTGTA NM_005462RefSeq chrX
+ 141903855 141909401 MAGEC1 9947 melanoma antigen family C1 GO:0005515 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_57256_PI430048170 0.0104230171030663 0.1815268287743072.65006394680009
1.51812686314434 2.17572626091184 A A A 4.85603370149302 4.53313211562932
4.53185625000312 P P P LNCV6_57256_PI430048170 mRNA
GACACATGGTAATGGTGATGCTGTGCCTTGTTATCTAAGAACATGATTGTATAATTTGTT NM_000728RefSeq chr11
+ 15073599 15078631 CALCB NA calcitonin-related polypeptide beta NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132962_PI430048170 0.000218239735333553 0.2525643315224456.82463288051969
6.88674863836209 7.08110577139402 P P P 8.80151609453128 8.80699586744315
9.12764209192732 P P P LNCV6_132962_PI430048170 mRNA
GGGGCAACCACATCCAGTACAAGCTTTTACAAATGTTATTAGTGTCCTTTTTTATTTCTA NM_033049RefSeq chr3
- 124905441 124934751 MUC13 56667 "mucin 13, cell surface associated"
GO:0016324|GO:0030277|GO:0006493|GO:0005796|GO:0016266|GO:0016021|GO:0044267|GO:0005615|GO:0042
803|GO:0070062|GO:0043687|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144803_PI430048170 0.00422669140127079 0.7106306748483399.73932824130828
9.56747310041091 9.5436730259532 P P P 10.1857512084954 10.1035144030327
10.0441837337621 P P P LNCV6_144803_PI430048170 mRNA
CTTTGGCTCAGCTGCCCTTCCCCACAAATAAAAACCAACAAAGAGGACAAATCAGGACAA NM_017706RefSeq chr5
+ 140664798 140670968 WDR55 54853 WD repeat domain 55
GO:0008150|GO:0003674|GO:0005737|GO:0016070|GO:0006364|GO:0005730|GO:0042273|GO:0005634|GO:0005
575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145639_PI430048170 0.000465238196701025 2.23604929695365 6.28538137978338
6.39124066751048 6.56057365819476 P P P 5.37327194572926 5.21926540692945
5.16720409255301 P P P LNCV6_145639_PI430048170 mRNA

ACATAAAAAATGAAGGGCTCGCATCATCCAGGAAAGAATTCAGCAGAAGTTCACTTTTTT NM_016608 RefSeq chrX
+ 101550530 101554692 ARMCX1 51309 "armadillo repeat containing, X-linked 1" GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135153_PI430048170 0.0756867050151227 0.72633443985620510.7605687406669
10.7450354588186 10.8737351599536 P P P 10.9619690868699 11.4011679642215
11.3638222014413 P P P LNCV6_135153_PI430048170 mRNA
CCTCAGATGTGTACATATACGGCTATTTCCTATTTTACTGTTCTTCAGATTTAGTACTTG NM_032242 RefSeq chr3 +
126988593 127037392 PLXNA1 5361 plexin A1
GO:0005886|GO:0014910|GO:0005634|GO:0007275|GO:0002116|GO:0005737|GO:0017154|GO:0007411|GO:0060
666|GO:0071526|GO:0004872|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108412_PI430048170 0.0345914904434970.7898856850524214.5673892928718 14.687696623324
14.859161139127 P P P 15.1391448843491 15.0612041653303 14.9430007739855 P P P
LNCV6_108412_PI430048170 mRNA
AAGGTCAAATCATTTTGGACAGCTTCTTTTGAATAAAGACCTGATTATACAGGCAGTGAG NM_000968 RefSeq chr15
- 66499314 66504855 RPL4 6124 ribosomal protein L4
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0006614|GO:0003723|GO:0019058|GO:0005730|GO:0005
634|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0000184|GO:0
030529|GO:0016032|GO:0022625|GO:0044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_64257_PI430048170 0.484594539093096 1.05072356698565 12.7165822429334 12.6805185320972
12.4980863639174 P P P 12.6854225168321 12.5107405595382 12.4859461330942 P P P
LNCV6_64257_PI430048170 mRNA
CCTGCACATAGACCTGCAGTTAGTAAATCATAAGCCCAAATAAACAGGTTGTTTGAATAT NM_025241 RefSeq chr19
- 4445005 4457794 UBXN6 80700 "UBX domain protein 6, transcript variant 1"
GO:0005515|GO:0008150|GO:0003674|GO:0005737|GO:0005815|GO:0005730|GO:0005634|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139253_PI430048170 0.31484380729983 0.6640620100734422.05967011168481
2.14114244604253 3.60794285312156 A A P 3.07747397118868 2.89807584941474
3.94350833231578 P P P LNCV6_139253_PI430048170 mRNA
AGGGGCCTTAATAACCATTTAGTCCTGAATCTTATGTATCATTGGTATCTGTATGCAGAA NM_006259 RefSeq chr4
- 81087369 81215117 PRKG2 5593 "protein kinase, cGMP-dependent, type II, transcript variant 1"
GO:0031965|GO:0072661|GO:0050999|GO:0044281|GO:0005524|GO:0032922|GO:0042803|GO:0005829|GO:0007
165|GO:0016324|GO:0004672|GO:0030553|GO:0007596|GO:0046209|GO:0006468|GO:0004692 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_102351_PI430048170 0.176244662767394 1.02622996830112 0.326790411162335
0.317883538687419 0.26796298029033 A A A 0.264053530250768 0.273633985943328
0.263558990582906 A A A LNCV6_102351_PI430048170 mRNA
CAGATTAACTGGATACATGAAGACACTTTTCAAAGCCATCATCAATTAAGCACACTTGTG NM_005582 RefSeq chr5
- 67182275 67196789 CD180 4064 CD180 molecule
GO:0071222|GO:0006954|GO:0002322|GO:0005886|GO:0045087|GO:0031666|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134600_PI430048170 0.0254716181966949 1.31931435103719 11.4628974003636
11.4448727944747 11.3351873916379 P P P 10.9166299027404 11.1794765275873
10.9356029002904 P P P LNCV6_134600_PI430048170 mRNA
TTGAGGAGAGGCTGTGATGTTTATGATCCCTGAATAAAGCTACTCCTTGGAGAGAAAAAA NM_015386 RefSeq chr16
- 70480568 70523554 COG4 25839 "component of oligomeric golgi complex 4, transcript variant 1"
GO:0048213|GO:0005515|GO:0000139|GO:0006890|GO:0007030|GO:0017119|GO:0015031 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_41217_PI430048170 0.167349259029953 1.24652040155752 10.1661974650033 9.95340357991306

10.4679162666119 P P P 9.87740193730367 9.79602213626434 9.99972777834049 P P P
LNCV6_41217_PI430048170 mRNA
ATTCGTCGCAGAAGCCTAAGGACACGTGCTATCAAAATGTTGGTTTTGGATGAAGCTGAT NM_014740 RefSeq chr17
- 80135213 80147183 EIF4A3 9775 eukaryotic translation initiation factor 4A3
GO:0017148|GO:0005515|GO:0010467|GO:0006364|GO:0019221|GO:0045727|GO:0071013|GO:0003729|GO:0048
701|GO:0005524|GO:0005829|GO:0004004|GO:0005737|GO:0016607|GO:0016020|GO:0000184|GO:0000398|GO:0
008143|GO:0005654|GO:0051028|GO:0035145|GO:0000289|GO:0000288 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_135173_PI430048170 0.0412393170551406 2.04226761410629 3.49713924501341
4.16076062369497 3.43729504180147 P P P 2.79797206846879 2.74167586992502
2.57235411498773 A P P LNCV6_135173_PI430048170 mRNA
TGAATTGTCTTTATTAACAAACAGGATATCCAAGGCCACTACATTGAGGAGGGGTGGGGG NM_000080 RefSeq chr17
- 4897768 4903074 CHRNE 1145 "cholinergic receptor, nicotinic, epsilon (muscle)"
GO:0030054|GO:0005886|GO:0008324|GO:0007268|GO:0005892|GO:0007271|GO:0007165|GO:0006936|GO:0005
887|GO:0045211|GO:0015464|GO:0042391|GO:0006810|GO:0004889 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_51699_PI430048170 0.52861616114112 6.97602594601548 0.4803302745528771.93562500392893
5.82887318681349 A A P 1.23200126374829 1.45904291297706 1.92534885688349 A A A
LNCV6_51699_PI430048170 mRNA
CATTAGGGTCAATTCAGCATTGACTTGAGTTTGTATTGACTTAACATTGAGTTCAAGCAT NM_001008401 RefSeq
chr19 + 53431973 53458261 ZNF761 388561 "zinc finger protein 761, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143186_PI430048170 0.8939806639975961.04966572884476 0.576863281456785
1.97694969937797 2.66977918274351 A A A 2.12921755832498 1.21153796987644
2.18362921537565 A A A LNCV6_143186_PI430048170 mRNA
GGCTTGTCCCTCCAACTGCAGGAAAACCCTTAATAAAATCTTCTGATGAGTTCTAAAAAA NM_006953 RefSeq chr22
+ 45284986 45295874 UPK3A 7380 "uroplakin 3A, transcript variant 1"
GO:0000902|GO:0016324|GO:0001822|GO:0030855|GO:0060157|GO:0055075|GO:0005789|GO:0055078|GO:0016
021|GO:0006833|GO:0015840|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75983_PI430048170 0.0724510275339371 1.17567400111682 13.7015089882626
13.9494362927154 13.8992806003224 P P P 13.5457207883392 13.6013078804374
13.7096187630425 P P P LNCV6_75983_PI430048170 mRNA
TCTGCATTGTAGTGTCTCAAAGACACAATAAACTTCCTATGGTCTGCACTGTTGTGATAT NM_014402 RefSeq chr5
+ 132866626 132868844 UQCRQ 27089 "ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa"
GO:0070469|GO:0005743|GO:0044281|GO:0021548|GO:0021854|GO:0021860|GO:0021539|GO:0005739|GO:0021
794|GO:0022904|GO:0021766|GO:0008121|GO:0021680|GO:0030901|GO:0044237 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_65361_PI430048170 0.9134674448763271.00409457041602 14.4877428085405 14.3788805044533
14.450306675094 P P P 14.4458894215816 14.3405912437658 14.5098384960243 P P P
LNCV6_65361_PI430048170 mRNA
CTCACGGGCAAGGATGTTAATTTTGAATTCCCAGAGTTTCAATTGTAAACAAAAATGACT NM_001011 RefSeq chr2
+ 3575262 3580919 RPS7 6201 ribosomal protein S7
GO:0005515|GO:0010467|GO:0006364|GO:0003723|GO:0019058|GO:0005634|GO:0006412|GO:0006413|GO:0005
829|GO:0006414|GO:0005737|GO:0002181|GO:0000184|GO:0016032|GO:0042274|GO:0070062|GO:0003735|GO:0
005815|GO:0006614|GO:0019083|GO:0032040|GO:0005730|GO:0006415|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132803_PI430048170 0.4662327536935190.9181025268404754.99166658071471
4.90206513541874 5.30786746031328 P P P 5.07160101193783 5.38808923168592

5.12354066968287 P P P LNCV6_132803_PI430048170 mRNA
CTGCTTCATGGTTGTTAAGTCTACTGTCTGGCTTCTTTTGCATTTTTAAAAATAAGACGANM_152434RefSeq chr11 -
107326345 107457846 CWF19L2 143884 "CWF19-like 2, cell cycle control (S. pombe)"
GO:0008152|GO:0003824 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144460_PI430048170 0.0919862292896991.27407645844723 4.74494566164839
4.68635522320056 4.83855785373704 P P P 4.37654495820368 4.62626886527142
4.18930404075247 P P P LNCV6_144460_PI430048170 mRNA
CTGCCCTGTGTTTTGTACCTTGAACCTAAGATATATTAAACATCTCTCAGATGGAAAAAA NM_004594RefSeq chr16
+ 67248951 67272191 SLC9A5 6553 "solute carrier family 9, subfamily A (NHE5, cation proton antiporter
5), member 5"
GO:0015385|GO:0005886|GO:0006810|GO:0035725|GO:0016021|GO:0055085|GO:0006885|GO:0006811 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131222_PI430048170 0.8708636923760160.98775176051628 0.284464858089377
0.5292824064223240.358398775229757A A A 0.52522448786339 0.425668048960285
0.27466811345812 A A A LNCV6_131222_PI430048170 mRNA
CTGTCCACGATTCACTCATCTGTGTATTTTCTATAGATGTTTACTAGGCGTTTGTTATAT NM_021635RefSeq chr6 -
138215985 138218490 PBOV1 59351 prostate and breast cancer overexpressed 1 GO:0005737|GO:0005634
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136783_PI430048170 0.4209587072845 1.11603592125807 4.67219590692904
4.52547831715269 4.96993135662723 P P P 4.34672079269103 4.64032534886277
4.71573297068714 P P P LNCV6_136783_PI430048170 mRNA
GTATTGCTACAAAAATCTCTTGTTGGGGGCAATGCAGGTAATAAAGTAGTATGTTGTTAT NM_003329RefSeq chr9
- 110243811 110256640 TXN 7295 "thioredoxin, transcript variant 1"
GO:0005515|GO:0051897|GO:0008283|GO:0007267|GO:0015035|GO:0006928|GO:0005634|GO:0015037|GO:0044
281|GO:0035872|GO:0005829|GO:0005739|GO:0046826|GO:0005737|GO:0033138|GO:0032148|GO:0033158|GO:0
070062|GO:0009314|GO:0015949|GO:0006662|GO:0055086|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145047_PI430048170 0.0202881535902745 0.7680574397849155.6885132928403
5.92598688192478 5.82566577943094 P P P 6.26797674142763 6.2684946855207
6.04425607306949 P P P LNCV6_145047_PI430048170 mRNA
TAAGTATTCTACGCACCTGCATCTAGCAGATGATTGTATGAAGCACTTCAAGGGCTCGGT NM_001272034 RefSeq
chr19 + 7637100 7647874 STXBP2 6813 "syntaxin binding protein 2, transcript variant 3"
GO:0005515|GO:0043304|GO:0005886|GO:0043312|GO:0042581|GO:0031201|GO:0042582|GO:0015031|GO:0005
829|GO:0006904|GO:0030348|GO:0001909|GO:0044194|GO:0070820|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127875_PI430048170 0.3050904736462731.04696095485509 0.469927468351057
0.3068116970797350.371135238168567A A A 0.2795817940277430.340072020723175
0.333533238901096A A A LNCV6_127875_PI430048170 mRNA
TAAAAAGCCTGATGATTTAATATTTTTCATAAAGAAAACTTTTGACAATTTGTTTTTAAG NM_198484RefSeq chr3
+ 40524877 40539794 ZNF621 285268 "zinc finger protein 621, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134232_PI430048170 0.2891282885899721.13211479577834 0.290964576095067
0.69374713024545 0.424026461722863A A A 0.3179316662773620.292725944311813
0.290436711350219A A A LNCV6_134232_PI430048170 mRNA
TTATCAAGTTCCTAGGTCTTAAAAAGGCCAGTAAATGAGTCCTGGGGCTAAAACTCCCCC NM_001004756 RefSeq
chr11 + 5389376 5390434 OR51M1 NA "olfactory receptor, family 51, subfamily M, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145025_PI430048170 0.3365963102144530.6262907512477630.569572265575258

0.3918798763388242.03633558101643 A A A 2.59578044489477 1.24734140711353
1.37584109208537 A A A LNCV6_145025_PI430048170 mRNA
AGTATCAACATGGCCCTAGAGATCAACGGGGTGGTCTACACTGGTGTCCTCTTTGCCCGC NM_001017363 RefSeq
chr9 - 34621457 34628014 ARID3C NA AT rich interactive domain 3C (BRIGHT-like) NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132589_PI430048170 0.8575699228849311.02617925341677 0.699880731999252
0.3496002909128090.286964060952518A A A 0.5046015800460050.418797848110152
0.331167568653491A A A LNCV6_132589_PI430048170 mRNA
CTTCAATGGGGAGAAATAATTAGAATGAGCAATAGAAATGCACAGATGCCTATACATACA NM_002288RefSeq
chr19_KI270938v1_alt + 485126 493014 LAIR2 3904 "leukocyte-associated immunoglobulin-like
receptor 2, transcript variant 1" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139366_PI430048170 0.3002200952642180.8826463129587570.431479262448675
0.4449060828473520.268989864954784A A A 0.3943968850645480.46998805505584
0.795611672420042A A A LNCV6_139366_PI430048170 mRNA
GGAATTTATAAACGGACTTGGATTAAACATGTCTGCCTTTCTAAGGTTGCAAATGTTACA NM_002285RefSeq chr2
- 99547253 100142575 AFF3 3899 "AF4/FMR2 family, member 3, transcript variant 1"
GO:0006355|GO:0005737|GO:0003690|GO:0035116|GO:0034612|GO:0005654|GO:0005634|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145308_PI430048170 0.7839192309521371.03748939749665 16.6884428605501
16.8613383619205 17.1390499964478 P P P 16.7427074540463 16.877903179683 16.938209663077
P P P LNCV6_145308_PI430048170 mRNA
CAATATCCTAGAATCTTTGTGCTCTTGCTGCAGTTCCCTTTGGGTTCCATGTTTTCCTTG NM_001164262 RefSeq chr1
+ 144592867 144593652 PPIAL4FNA peptidylprolyl isomerase A (cyclophilin A)-like 4F NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139672_PI430048170 0.0155929485820564 1.06288117933511 0.400959473758463
0.45254957556387 0.404997192093183A A A 0.3081263099331390.334492611325112
0.352178750939823A A A LNCV6_139672_PI430048170 mRNA
CCTGCTAAACCCATTTATTTACAGCTTGAGAAATAAAAAAGTCATGCATGCATTGAGAAG NM_054106RefSeq chr3
+ 98087172 98088102 OR5AC2 NA "olfactory receptor, family 5, subfamily AC, member 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107290_PI430048170 0.9398904994192191.02291129281777 3.6208629982301
3.41171669897482 4.22117888795046 P P P 3.7197595271111 3.32982350442446
4.12380481497736 P P P LNCV6_107290_PI430048170 mRNA
ACACCTCTTACAAAGGCAGCAGATATCAGCTTAGACAATTTGGTGGAAGGGAAGCGGAAA NM_005657RefSeq
chr15 - 43407213 43510509 TP53BP1 7158 "tumor protein p53 binding protein 1, transcript variant
3"
GO:0005515|GO:0001102|GO:0000781|GO:0001104|GO:0006366|GO:0005657|GO:0042162|GO:0005634|GO:0035
064|GO:0006974|GO:0006302|GO:0003684|GO:0002039|GO:0051091|GO:0005737|GO:0006281|GO:0000724|GO:0
045944|GO:0000777|GO:0005654|GO:0045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139123_PI430048170 0.000500637667577362 3.24711501177395 4.47040953095304
4.76572470638352 4.84622618120352 P P P 2.90375224032016 2.93887100143884
3.15566604975906 P P P LNCV6_139123_PI430048170 mRNA
ATCTCAACCCGGGCTTTGAAATGTGTTTGTTCACATAATTGTCCATTACCCATCCTTCCTNM_001256272 RefSeq chr20
- 25070885 25082379 VSX1 30813 "visual system homeobox 1, transcript variant 4"
GO:0043565|GO:0006355|GO:0003700|GO:0060040|GO:0042551|GO:0005634|GO:0005575|GO:0007601|GO:0050
896|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137404_PI430048170 0.9031193430297751.00430080500869 0.430057564362556
0.5122479599072410.419439832042292A A A 0.5358837467676050.397921675905866
0.406997177953862A A A LNCV6_137404_PI430048170 mRNA

CAAAAGTGATATCCAGTGACATCTAACTTTCATGGATGTATGTGACAGTGTTCAAGTTAA NM_173571 RefSeq chrX
- 120982465 120985784 CT47A11 255313 "cancer/testis antigen family 47, member A11" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_142376_PI430048170 0.4804677217423050.8818008412164561.00893334443961
0.8685076682936471.61026098268903 A A A 1.11795652129963 1.50751863099284
1.48614430364225 A A A LNCV6_142376_PI430048170 mRNA
GGTCATCCCTTACTAATCATTATAAAATTCACATTGAAGAGGACTCCTTAAAAGCCGATT NM_058230 RefSeq chr5
+ 178859952 178884423 ZNF354B 117608 zinc finger protein 354B
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142924_PI430048170 0.8777754056176140.9947798555053130.260301016772299
0.2738344907029220.420637797519575 A A A 0.36044481423281 0.307705981714323
0.314242273451943 A A A LNCV6_142924_PI430048170 mRNA
CTAACAGCTTTGTAGGAAGCACTTTTAATGTTTTCTCTCTCACACACAAAGATTCAAAAG NM_014926 RefSeq chr3
- 165186719 165196681 SLITRK3 22865 "SLIT and NTRK-like family, member 3" GO:0016021|GO:0007409
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141149_PI430048170 0.0153599202631054 1.07550693157443 0.397315776125603
0.4648463277938540.430759847827356 A A A 0.3035538924180690.328820402288493
0.345972184025084 A A A LNCV6_141149_PI430048170 mRNA
CTGTCTTCACTTCAAGGCAAGGATTTCCAGCATAAAAATAAATTCATTCACTGGAGAAAA NM_001256268 RefSeq
chr10 + 68109432 68212016 MYPN 84665 "myopalladin, transcript variant 5"
GO:0008092|GO:0005515|GO:0051371|GO:0030018|GO:0017124|GO:0045214|GO:0005634|GO:0003779|GO:0031
674 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140536_PI430048170 0.0142152860975123 1.8241171038377 3.49150481977189
3.74919903006095 3.99122431977666 P P P 2.76654703575769 3.173423432833
2.68462700118719 P P P LNCV6_140536_PI430048170 mRNA
TAAAGAAGGATGTCTTAGGCATTTAGTAAAAATTCAGTGGTTCCCCGCTATCCTCGGGGG NM_022549 RefSeq chr11
- 125488199 125496310 FEZ1 9638 "fasciculation and elongation protein zeta 1 (zygin I), transcript
variant 2"
GO:0005515|GO:0030424|GO:0005813|GO:0043015|GO:0005886|GO:0005874|GO:0030425|GO:0007399|GO:0005
739|GO:0051654|GO:0005737|GO:0047485|GO:0071363|GO:0007411|GO:0005080|GO:0010976|GO:0015630|GO:0
006810|GO:0007155. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141136_PI430048170 0.5286707497779280.8479535121495280.468772014911516
0.51269110421178 0.536617430764772 A A A 1.20265739331358 0.410146778199547
0.480090333357794 A A A LNCV6_141136_PI430048170 mRNA
GCTTCTGCCCCACGGGCAAATCTAGTTATTAAATAGTCATTCTGAGCACCAATCAAAAAA NM_203303 RefSeq chrX
+ 74304189 74305034 ZCCHC13 389874 "zinc finger, CCHC domain containing 13"
GO:0008270|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142265_PI430048170 0.0393072166353296 1.2045852782764 10.1432108924211
10.3246941761485 10.3167619540592 P P P 10.1228474462599 9.94590237274623
9.90828079881733 P P P LNCV6_142265_PI430048170 mRNA
GAAGAGGTAGGAAGAAAGGTGATGAAAACTCCTGGTCATTCCTTGAATAAACTTGATTTT NM_013979 RefSeq chr5
+ 173144441 173164387 BNIP1 662 "BCL2/adenovirus E1B 19kDa interacting protein 1, transcript variant
BNIP1-b"
GO:0005515|GO:0043066|GO:0005783|GO:0006914|GO:0097194|GO:0006915|GO:0031201|GO:0030176|GO:0005
635|GO:0043231|GO:0005739|GO:0005484|GO:0005737|GO:0016320|GO:0016192|GO:0007029 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138739_PI430048170 0.1301139392343271.63402849977175 4.2316294624422
3.46974701686964 3.32556769964344 P P P 3.21084979027043 2.81978077470737

3.01667715058829 P P P LNCV6_138739_PI430048170 mRNA
AATGGATTTGTGTGTCAGGAGAGAAAAAAGTTGAGTGTTGACAAACTGTATGCAAACTAA NM_001013646 RefSeq
chr20 + 56533245 56536518 FAM209B 388799 "family with sequence similarity 209, member B"
GO:0005634|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127971_PI430048170 0.32049668678667 0.8058358274712623.84018389972626 3.5299450171307
3.33864235961281 P P P 4.22361561718727 3.87959517502569 3.4931372712742 P P P
LNCV6_127971_PI430048170 mRNA
GCTGCATGTTCTGTGCTCTCCAGTTTGTCCCTTCCAATATTAATAAACTTCCCTTTTAAA NM_148962RefSeq chr2 -
42762498 42764261 OXER1 165140 oxoeicosanoid (OXE) receptor 1
GO:0007186|GO:0005886|GO:0004930|GO:0030817|GO:0050646|GO:0016021|GO:0050647|GO:0050648 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138610_PI430048170 0.7392582735669320.91793694996324 6.03486585586607
5.87513948745224 5.52634591733641 P P P 6.37583037918148 5.67132965644728
5.68847613298012 P P P LNCV6_138610_PI430048170 mRNA
CACAAGATCTGAGTGAAATGAGCAAAAGTCACCTGCCCAATAAAGCTTGACAAGACACTC NM_001286359 RefSeq
chr16 - 11275635 11276480 PRM2 5620 "protamine 2, transcript variant 5"
GO:0030261|GO:0007275|GO:0006323|GO:0005654|GO:0005634|GO:0007283|GO:0000786|GO:0003677|GO:0030
154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128222_PI430048170 0.87982357144588 0.9669839145669111.17851037105036
2.47962274707767 2.11092427514024 A A A 1.66463650726747 1.74292817716423
2.59892580036058 A A P LNCV6_128222_PI430048170 mRNA
GAGTAGTACAAGCGAGGAAAAAATACGGAGGATAACCACTATTTTTGTGCAAATAATATG NM_001012761 RefSeq
chr5 + 98769294 98796494 RGMB 285704 repulsive guidance molecule family member b
GO:0007165|GO:0005793|GO:0005886|GO:0007411|GO:0045121|GO:0030509|GO:0045893|GO:0015026|GO:0007
155|GO:0046658|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137901_PI430048170 0.000107111876788225 2.59154663513265 2.59990185584904
2.65464607127338 2.45044428466206 A A A 1.11459512821282 1.26343640087779
1.20926900081811 A A A LNCV6_137901_PI430048170 mRNA
GCAGGTACACGTCTCAGGTGTGCAAGAAATATCACAAGAATGTAACTTCTGTTTTGAGCC NM_001042590 RefSeq
chr9 + 35829497 35854847 TMEM8B 51754 "transmembrane protein 8B, transcript variant 1"
GO:0005739|GO:0005515|GO:0007346|GO:0009986|GO:0007160|GO:0005886|GO:0005783|GO:0005634|GO:0016
021|GO:0040008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74557_PI430048170 0.0586654425058048 0.6908311649793831 1.9508098104132
11.8451461284322 11.9395000010325 P P P 12.1737417750877 12.4679440240947
12.6564342488098 P P P LNCV6_74557_PI430048170 mRNA
CCAGTGTGACAGTGTCATGATGTAGTAGTGTCTTACTGGTTTTTTAATAAATCCTTTTGTNM_031370RefSeq chr4 -
82353313 82373996 HNRNPD 3184 "heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa), transcript variant 1"
GO:0005515|GO:0008380|GO:0043488|GO:0006396|GO:0010467|GO:0006355|GO:0003723|GO:0042162|GO:0045
727|GO:0005634|GO:0006351|GO:0005829|GO:0006401|GO:0000166|GO:0000398|GO:0030529|GO:0042752|GO:0
005654|GO:0097167|GO:0045893|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134461_PI430048170 0.453571462435086 0.9399799618291056.77101577840154 7.0251236860845
6.99690683945681 P P P 6.95629979234668 6.94061934267494 7.16606263040816 P P P
LNCV6_134461_PI430048170 mRNA
TACCCTCCTGTATAAATCCAACCTCTGGGTCCGTTCTCGAATATTTAATAAAACTGATAT NM_153693RefSeq chr12
+ 54016851 54030823 HOXC6 3223 "homeobox C6, transcript variant 2"
GO:0043565|GO:0005737|GO:0003700|GO:0006357|GO:0003714|GO:0048706|GO:0007275|GO:0005654|GO:0009
952|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133935_PI430048170 0.9738727433954530.9650328705586042.8485233607832

3.47239748105587 2.94705351246215 A P P 3.76674691410052 2.8927884490348 2.5650518380511
P P P LNCV6_133935_PI430048170 mRNA
GGGTGTTCTAAACTCTTTTCATGTCATGTTTTGATTATAGGCTTTGGTCTTTTCATCTGC NM_005467 RefSeq chr11 +
90134649 90192611 NAALAD2 10003 "N-acetylated alpha-linked acidic dipeptidase 2, transcript variant 1"
GO:0006508|GO:0004180|GO:0008236|GO:0016021|GO:0042135|GO:0008239|GO:0050129|GO:0016805|GO:0046
872|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130636_PI430048170 0.1153262555186981.03300182102739 0.334041269667103
0.3027283390191740.270498563238869 A A A 0.2487747391289860.267357290343233
0.251236669652013 A A A LNCV6_130636_PI430048170 mRNA
CACAGTTCTGCAAGTATATTGTGAATGTATTGTTCTAGTGGGATACACAAATAAGTCAGT NM_005864 RefSeq chr14
- 23356399 23365633 EFS 10278 "embryonal Fyn-associated substrate, transcript variant 1"
GO:0035556|GO:0017124|GO:0005737|GO:0019904|GO:0007155 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128393_PI430048170 0.8693606689356720.9896105478056660.401180259475712
0.4218514614727260.449793067577254 A A A 0.56273217548894 0.347039937069658
0.399809476165244 A A A LNCV6_128393_PI430048170 mRNA
TGCTTTTACGCCATGCAAAACCAGGTTTCCTGGAAATTTACCCAATAAAGTGTGTTCTCC NM_003771 RefSeq chr17
- 41486135 41489864 KRT36 8689 "keratin 36, type I"
GO:0005882|GO:0045616|GO:0008150|GO:0030280|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_64481_PI430048170 0.1974138183068591.21844026784968 2.87763242857134 3.30840907879234
3.31636910614622 A P P 2.84052725151707 2.8967611259219 2.95005934371775 P P P
LNCV6_64481_PI430048170 mRNA
CCCGAGCCGAGGGGAGGAGCGGCGCATGCCCACAAGCCCCCCGCGGGAAGTAGGAAATCG NM_152363 RefSeq
chr19 + 17281644 17287646 ANKLE1 126549 "ankyrin repeat and LEM domain containing 1, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128301_PI430048170 0.1496769352361581.06848797472647 0.483301409127132
0.4468632694127040.526248469446536 A A A 0.3117375004648880.388959871158611
0.465977597955959 A A A LNCV6_128301_PI430048170 mRNA
GCTCATGTTCTAAACATGGAAACTAGGAGCCTAATAAACTTCCTAATTCAGTATGGAAAA NM_001282428 RefSeq
chr2 + 17877846 17932958 KCNS3 3790 "potassium voltage-gated channel, modifier subfamily S,
member 3, transcript variant 2"
GO:0005251|GO:0005794|GO:0005886|GO:0007268|GO:0015459|GO:0044281|GO:0005737|GO:0006112|GO:0050
796|GO:0008076|GO:0051260|GO:0034765|GO:0016021|GO:0006813|GO:0071805 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_107913_PI430048170 0.0586019296019406 1.46481956586687 4.55476769384974
4.79466487222016 5.09394477033375 P P P 4.16184550240807 4.38895948095283
4.28224839674437 P P P LNCV6_107913_PI430048170 mRNA
TCTGAAGGAGTCTGAGAAGACGGCGCTGTCAGAGAAGTTGATGGGTACACGGCACAGCCT NM_014675 RefSeq
chr1 + 16921949 16972979 CROCC 9696 "ciliary rootlet coiled-coil, rootletin"
GO:0005515|GO:0005813|GO:0010457|GO:0005886|GO:0033365|GO:0005814|GO:0015629|GO:0051297|GO:0005
737|GO:0007049|GO:0008104|GO:0005198|GO:0035253|GO:0030030|GO:0019894|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134164_PI430048170 0.6971964238929311.07189941344517 3.23148993384418
3.03590289176527 3.52098209833949 P A P 2.44196398804373 3.4852742626906
3.39103106468766 A P P LNCV6_134164_PI430048170 mRNA
GCATTGGAGAACTTTAACTTGAACATTCTCATCGATACTTCCTGGACATATTTTGTGTTT NM_001290268 RefSeq
chr20 - 50586109 50691530 FAM65C 140876 "family with sequence similarity 65, member C,
transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_138858_PI430048170 0.0642963026519791 1.28155967199392 10.3901644768867
10.3910160131026 10.2711433857439 P P P 10.1432108924211 10.0368609731205
9.77775782809148 P P P LNCV6_138858_PI430048170 mRNA
TTTTAGAAAAAGTGAAGAGCTGGAATGTGGGGGAAAATAAAAAGCTTTTTTGCCCAGTGG NM_001083613 RefSeq
chr16 + 29962029 29973052 TMEM219 124446 "transmembrane protein 219, transcript variant 1"
GO:0005886|GO:0006915|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130406_PI430048170 0.0295777197598002 0.56747320452857 10.063382834059
9.53305976147759 9.45100826151933 P P P 10.6901999811577 10.6280083211945
10.2163737403701 P P P LNCV6_130406_PI430048170 mRNA
TCCCCCTCCTTCTCCATCCCTGTAAAATAAATGTAATTTATCTTTGCCAAAACCAAAAAA NM_020061 RefSeq chrX
+ 154144223 154159032 OPN1LW NA "opsin 1 (cone pigments), long-wave-sensitive" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129564_PI430048170 0.0505174773965232 0.5658138325277884.14741199322141
3.56156296097849 4.26991498114866 P P P 4.7269991039863 4.85292228928086
4.94959368234701 P P P LNCV6_129564_PI430048170 mRNA
GTCTGCATTACTAACTTGTTGAATTCATGATATTCTGCCTATGGCACAAATTGTAAACCT NM_019022 RefSeq chr18
- 68673687 68715116 TMX3 54495 thioredoxin-related transmembrane protein 3
GO:0034976|GO:0009986|GO:0006457|GO:0005783|GO:0005789|GO:0003756|GO:0045454|GO:0016021 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_133930_PI430048170 0.0379784485294404 1.48989882153779 8.51931223249137
8.58540106594531 8.65130940335583 P P P 7.74256578013306 8.08169912718112
8.17428031902747 P P P LNCV6_133930_PI430048170 mRNA
CAACCTGTTTACTGTACTGTTGTAAATATCATGCCCTTTATATCCTGTATATTGGCTTCT NM_001136265 RefSeq
chr1 - 18904279 18956332 IFFO2 126917 intermediate filament family orphan 2
GO:0005882|GO:0005198 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132506_PI430048170 0.558815978890384 1.27640886262988 2.57966221323599
2.08439921016519 1.26367245690099 A A A 1.92341823021293 1.93682347139442
1.17971698320964 A A A LNCV6_132506_PI430048170 mRNA
TTAGGAACCTAGTGCTGACCTCTGTTGTTGGATGAGGACTCTCGTTCCTTCATCAAAATC NM_001101362 RefSeq
chr15 + 65076815 65079938 KBTBD13 NA kelch repeat and BTB (POZ) domain containing 13 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127160_PI430048170 0.412474994775745 0.892719087225645 5.59440711949097
5.11839489024702 5.09855879865249 P P P 5.49059986540233 5.58493760399816
5.26500893257103 P P P LNCV6_127160_PI430048170 mRNA
CCCTCATACAGGGGAAAGCAACCTGGTCTAGCAAATTGAAAATAAAGATGATAAAACTCT NM_005306 RefSeq
chr19 + 35449714 35451767 FFAR2 2867 free fatty acid receptor 2
GO:0005515|GO:0002879|GO:0005886|GO:0004930|GO:0019915|GO:0090276|GO:0042995|GO:0042593|GO:0032
722|GO:0002673|GO:0002720|GO:0008289|GO:0071398|GO:0002232|GO:0002385|GO:0007186|GO:0002752|GO:0
005887|GO:0045444|GO:2000484 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132078_PI430048170 0.0204166724732049 1.79845433332468 9.33677863410009
9.48563341484196 9.21266510519034 P P P 8.81507353413659 8.31787595048851
8.31543995939194 P P P LNCV6_132078_PI430048170 mRNA
CCTCCCTTGCAGGTCGGTTTGGTTTGTTGTAAATAAAAGTATTTAATTAGTTTGGCAAAA NM_005357 RefSeq
chr19 - 42401506 42427426 LIPE 3991 "lipase, hormone-sensitive"
GO:0046340|GO:0005515|GO:0005811|GO:0004806|GO:0019901|GO:0044281|GO:0005829|GO:0016042|GO:0005
901|GO:0042758|GO:0006468|GO:0019433|GO:0033878|GO:0008203 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_51529_PI430048170 0.0131089508593291 1.54464127147382 6.41180830931992
6.539136782693 6.49610038407071 P P P 5.98257880202799 5.90346767157207

5.66324749702478 P P P LNCV6_51529_PI430048170 mRNA
CATTGACTACATGTTCTTTGAGAAGCGAGGAGGCGCTGGGCCCTCTGCCGTCACCAGTTA NM_020360 RefSeq chr17
- 7389727 7394843 PLSCR3 57048 "phospholipid scramblase 3, transcript variant 1"
GO:0005515|GO:0042632|GO:0017121|GO:0017124|GO:0031966|GO:0005886|GO:0017128|GO:0005509|GO:0006
915|GO:0042593|GO:0071222|GO:0016021|GO:0048306 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128149_PI430048170 0.1839976301772641.07053435253828 15.2215981342581
15.2056854020796 15.3067090808037 P P P 15.2294394668169 15.0546324379179
15.1516824050963 P P P LNCV6_128149_PI430048170 mRNA
GTTTCTGTCTGTAAGTTAAGACCTTGGATGTGGTTTAATTGTTTGTCCTCAAAAGGAATA NM_004181 RefSeq chr4
+ 41256880 41268429 UCHL1 7345 ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
GO:0005515|GO:0030424|GO:0043130|GO:0016579|GO:0004843|GO:0005886|GO:0008283|GO:0016874|GO:0031
694|GO:0005829|GO:0050905|GO:0048747|GO:0007412|GO:0005737|GO:0043407|GO:0007628|GO:0043025|GO:0
008242|GO:0070062|GO:0019233|GO:0004197|GO:0002931|GO:0005789|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136723_PI430048170 0.3750881446532111.65138977373701 0.415989904578746
1.88595161526202 0.447186666629343 A A A 0.3286310340285330.358678687066472
0.415273180329477 A A A LNCV6_136723_PI430048170 mRNA
TCAGTCTCAACTTCAAAAGAACAAACGCGCACTCAAAACAAAGGAAGACCGTCCTCGACT NM_001129778 RefSeq
chr17 + 19127468 19158835 GRAPL 400581 GRB2-related adaptor protein-like NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_47234_PI430048170 0.4807718177958551.12990772821245 5.89029520823336 5.92604667711809
5.70031181200712 P P P 6.04260125872015 5.64329578628262 5.18684043202518 P P P
LNCV6_47234_PI430048170 mRNA
TAGAAACTGCGCATTCGGAACTCCCCCAGCAAGACTCTCTGCTTGTTTCTCTCCCATCTG NM_001257357 RefSeq
chr6 + 36697850 36733183 RAB44 NA "RAB44, member RAS oncogene family" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142398_PI430048170 0.0678346084320521 1.04248821737559 0.422470559261987
0.4421319091880590.381320108608442 A A A 0.3249778618801490.361580104437902
0.379404707929438 A A A LNCV6_142398_PI430048170 mRNA
GCCTATCTTCTTACCCTGAAACAGAAAATAAATATTGTGCTTTATGTGGTAGTGTTGTAC NM_199131 RefSeq chr10
- 117128520 117138301 VAX1 NA "ventral anterior homeobox 1, transcript variant 2" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141972_PI430048170 0.5268567669564910.852050808400841 0.472801404399258
0.4680669648173170.526365836005974 A A A 1.16703993452772 0.393586802207272
0.468267896620963 A A A LNCV6_141972_PI430048170 mRNA
TTTAAAGGAAGATACAGAGATGATTGTACTTCAGAATGACTGAAACCCATATACCACCCA NM_017578 RefSeq chr3
- 123969031 123991352 ROPN1 54763 rhophilin associated tail protein 1 GO:0005737|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51876_PI430048170 0.9391394853707110.9971795666324470.53365038902015 0.476605138927558
0.591457459052797 A A A 0.3061005570388440.4113065585417440.841459264338937 A A A
LNCV6_51876_PI430048170 mRNA
GTCACAATCTTTTGATGAGGACGAAATGAATCAGCATGAACTTGCTGTGCATAAAAAGAA NM_002873 RefSeq
chr5_GL339449v2_alt + 153900 198224 RAD17 5884 "RAD17 homolog (S. pombe), transcript variant 8"
GO:0005515|GO:0000781|GO:0007093|GO:0005634|GO:0005524|GO:0006974|GO:0006260|GO:0042325|GO:0006
281|GO:0000076|GO:0005654|GO:0000077|GO:0008156 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140670_PI430048170 0.6375432924544330.9346574320341246.28966207765291
5.86148931524626 6.34883129291367 P P P 6.37986322752293 6.01260353374272 6.4139686355898
P P P LNCV6_140670_PI430048170 mRNA
AACTAATAAACTAGTTTGGGACTTGGCTGGCATGTGCTGCCAGACCCAAAGGGATTGTAT NM_015149 RefSeq chr1

+ 183636046 183928551 RGL1 23179 "ral guanine nucleotide dissociation stimulator-like 1, transcript variant 1" GO:0008321|GO:0007264|GO:0044281|GO:0005575|GO:0044255|GO:0032852|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63143_PI430048170 0.0223362032648356 0.7466323182496121 1.9385146749093 1.9874584903643 12.1936118559564 P P P 12.3131926043303 12.4599039863532 12.6088326853556 P P P LNCV6_63143_PI430048170 mRNA
GGAGGTGTCTACTGAAAAGGGAACCTGCTTCTTTACTCCAGAACTCTGTTCTTTAAAGAC NM_006937 RefSeq chr17 - 75167729 75183003 SUMO2 6613 "small ubiquitin-like modifier 2, transcript variant 1" GO:0005515|GO:0016925|GO:0016605|GO:0032436|GO:0005654|GO:0005634|GO:0044267|GO:0031625|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133044_PI430048170 0.0564496481291557 0.3315294761077183 .13376946551276 1.87250919755778 1.80383760677808 P A A 4.06066740170577 3.97168471274281 3.97040136112016 P P P LNCV6_133044_PI430048170 mRNA
CGACGATGTGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAAATAAAAAA NM_144962 RefSeq chr8 - 22713251 22927908 PEBP4 157310 phosphatidylethanolamine-binding protein 4 GO:0005515|GO:0005764|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_43621_PI430048170 0.0626866369301496 0.8604389973065738.29424547685571 8.32603887287929 8.49639224083809 P P P 8.62857920120541 8.56734833014602 8.5788714310288 P P P LNCV6_43621_PI430048170 mRNA
CAACAGAAAGATCATTTGAAACCAGTTTTTATCCCTTCTCTTTCCTTCCCTTTCCCTAAA NM_006320 RefSeq chr4 - 128269236 128288829 PGRMC2 10424 progesterone receptor membrane component 2 GO:0016020|GO:0043401|GO:0003707|GO:0016021|GO:0005496|GO:0020037|GO:0012505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127416_PI430048170 0.4988488160392120.8464548243072010.415855636018687 0.3655695548465810.393107162269975 A A A 0.3057073400693041.07104228586105 0.392483391861236 A A A LNCV6_127416_PI430048170 mRNA
CATGTACACCTTCAACCACAACAAGATTATCTCTGTGCTCTACACTATCATTGTACCATT NM_001160325 RefSeq chr1 - 158562650 158563604 OR6P1 NA "olfactory receptor, family 6, subfamily P, member 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142916_PI430048170 0.3146711636296321.04189726229184 0.349002708669525 0.3525759830081870.481631329404173 A A A 0.3351949853712950.309292681272959 0.364549834565485 A A A LNCV6_142916_PI430048170 mRNA
GCTGGATATGCAGGGAGATGAGACTCTTTTAATCTCAAAATAAACAGATTCTTTCAAGAA NM_024652 RefSeq chr15 + 100919214 101070112 LRRK1 79705 leucine-rich repeat kinase 1 GO:0005515|GO:0007264|GO:0045453|GO:0050732|GO:0050731|GO:0005525|GO:0005524|GO:0046872|GO:0042802|GO:0005739|GO:0005737|GO:0036035|GO:0004674|GO:0006468 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79583_PI430048170 0.5468620593824531.1236253681972 0.42174232916218 0.900550241533003 0.244394835564375 A A A 0.3513396293026090.4075991168528680.38470403026747 A A A LNCV6_79583_PI430048170 mRNA
CTGAAGGGCTTCATGATATGGCAATCTAGATGGTGACCCAAAAGAAATCTCTCCAGTTAT NM_004686 RefSeq chr8 - 17296796 17413531 MTMR7 9108 myotubularin related protein 7 GO:0006470|GO:0016020|GO:0006661|GO:0046855|GO:0046856|GO:0044281|GO:0006644|GO:0035335|GO:0004725|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135673_PI430048170 0.0183340178202638 1.54864169125314 7.50871162268051 7.54653849976801 7.39422987243495 P P P 6.81092199465208 7.05448276561344 6.66875387147674 P P P LNCV6_135673_PI430048170 mRNA
TTAAACCTTTGTGTCGTGTTGCAGCAGAGTGACGATGGGGGTTGGGGGGTTATTTATTTT NM_014284 RefSeq chr1 + 35557791 35566779 NCDN 23154 "neurochondrin, transcript variant 3"

GO:0030424|GO:0048168|GO:0016020|GO:0045453|GO:0043025|GO:0005634|GO:0031175|GO:0030425|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110982_PI430048170 0.3638505667806561.03317493754473 10.8320464817746 10.831159957866 10.8275713576444 P P P 10.7044309371938 10.8458500263966 10.7957008034822 P P P
LNCV6_110982_PI430048170 mRNA
ATCTCCTCTCCATGTAGTTCCCAGTGGGCAAGAGCCTTTGAAAATGCAGGATTCTAAACA NM_001003828 RefSeq chr22 + 43999210 44169232 PARVB 29780 "parvin, beta, transcript variant 1"
GO:0005515|GO:0030018|GO:0005886|GO:0031532|GO:0034329|GO:0030032|GO:0003779|GO:0030027|GO:0005829|GO:0030031|GO:0071963|GO:0005856|GO:0007155|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139456_PI430048170 0.65692088659935 1.20440692701408 1.46570087050829 0.2873610005862050.48686571293987 A A A 0.3341691625505110.289299890415996 0.990859161476516A A A LNCV6_139456_PI430048170 mRNA
AAACCAGCTTCACATTAGGACTTCTCCATACAAATGCTTTATCATTGGTTCTTAAATTGG NM_018420RefSeq chr1 + 115976497 116070054 SLC22A15 55356 "solute carrier family 22, member 15"
GO:0022857|GO:0016021|GO:0055085|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95686_PI430048170 0.9347156606779071.00642250294262 0.5895105538230530.40700116753232 0.634838575441692A A A 0.4799556074997980.6217626070087820.507920788588187A A A
LNCV6_95686_PI430048170 mRNA
ATGCTTACACGCCATTATGATCCAAGCAAAATAAAACTGCAGTTGTCAACATTAGAACAT NM_139173RefSeq chr4 - 102900927 103019739 SLC9B1 150159 "solute carrier family 9, subfamily B (NHA1, cation proton antiporter 1), member 1, transcript variant 1" GO:0034220|GO:0005886|GO:0015299|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136744_PI430048170 0.1267768807514991.3175480877576 4.45290474814503 4.72395758638584 4.22584894205666 P P P 4.35729405583613 3.85778547182679 3.98982960346946 P P P LNCV6_136744_PI430048170 mRNA
CACCTATGCACTCCCACTCCAACCCTTCTGAGTGAATAAAGCACAAAGAAACGCAAAAAA NM_001243212 RefSeq chr19 - 38908979 38912158 CCER2 643669 coiled-coil glutamate-rich protein 2 GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133799_PI430048170 0.0588941689460689 1.43151176983267 7.37823083105993 7.54135853593365 7.79062924238178 P P P 7.10904707770071 6.75327461184749 7.27699844467812 P P P LNCV6_133799_PI430048170 mRNA
CATATTCACGGTAGTAAATCAGTACCCCTGTTAAAGGATTTATCCCATTGCTTCATATTA NM_001015882 RefSeq chr9 + 111631351 111654351 DNAJC25 548645 "DnaJ (Hsp40) homolog, subfamily C, member 25, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65801_PI430048170 0.72241955784998 1.27730589820393 0.9924442108566960.357359257068807 2.15511240906915 A A A 0.4405397886837140.7445398788967961.59219229463474 A A A
LNCV6_65801_PI430048170 mRNA
GGCTTTAGCTCAGATTGTCTACAGTGAATGTGGCCTGCACAAGAAAGCTATTCTTTGCTT NM_152385RefSeq chr2 - 55172550 55232313 CLHC1 130162 "clathrin heavy chain linker domain containing 1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143122_PI430048170 0.2855290794038320.7920513677238630.41225293703656 0.3524873775846070.361657018735158A A A 0.4757559087364970.461959452678537 1.10185107132702 A A A LNCV6_143122_PI430048170 mRNA
TTGGAGAGAAGACTGAGAATCCAAAGAAGTTCAAGATCAACTATACGGTGGCGAACGAGG NM_001018049 RefSeq chr9 + 135561757 135566776 PAEP 5047 "progestagen-associated endometrial protein, transcript variant 1" GO:0036094|GO:0006810|GO:0007275|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51743_PI430048170 0.0780062617979020.7490831100058339.61980623642497 9.44753628807536

9.83186502555366 P P P 9.89633697067086 9.92985758218286 10.311329142315 P P P
LNCV6_51743_PI430048170 mRNA
GGTATCCCTACTCTTGATCCTGGAACCAGACAAGCAAGAAGCTTTGATTGAAAGCCTATG NM_006360 RefSeq chr11
+ 32583766 32602873 EIF3M 10480 "eukaryotic translation initiation factor 3, subunit M"
GO:0005515|GO:0033290|GO:0016282|GO:0005852|GO:0001731|GO:0071541|GO:0006446|GO:0003743|GO:0031
369|GO:0002183|GO:0006413 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135019_PI430048170 0.00904479887061896 0.767100297585335 7.36789928143941
7.46965497575205 7.4609844122362 P P P 7.70060478630311 7.88938004501013
7.85145016648733 P P P LNCV6_135019_PI430048170 mRNA
AGAATTTTAGTGGGAGCTGTTGATTTATTTCTCAGGGCATACATGTGCCAATCTGTCTCA NM_014478 RefSeq chr7
+ 66114817 66154566 CRCP 27297 "CGRP receptor component, transcript variant 1"
GO:0010467|GO:0009360|GO:0006386|GO:0006385|GO:0001669|GO:0005886|GO:0003899|GO:0006384|GO:0006
383|GO:0005829|GO:0051607|GO:0000166|GO:0007218|GO:0001056|GO:0045087|GO:0005666|GO:0032481|GO:0
005654|GO:0001635. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139114_PI430048170 0.229800574076954 1.20934367843943 6.5110878859436
6.07351849799715 6.02379951361315 P P P 5.79984688746464 6.04594538447146 5.9802212804309
P P P LNCV6_139114_PI430048170 mRNA
TTTTTAAAGGAGAATTCTGTACATTTAGAACTCTTGTAAATTAAAAACCGATCCTTTTTT NM_015711 RefSeq chr19 +
47608195 47703277 GLTSCR1 29998 glioma tumor suppressor candidate region gene 1 GO:0005515
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56384_PI430048170 0.0257732291038827 0.722461116483332 7.30677412431191
7.29103221851497 7.26049007102827 P P P 7.63980169440053 7.70583763284592
7.90651514548668 P P P LNCV6_56384_PI430048170 mRNA
CTGTTCATTTCACCCAGTATAAGCAAGTGCAGTGTACAAAGAAGTATATTCTGAATACAT NM_005436 RefSeq chr10
- 59788747 59906656 CCDC6 8030 coiled-coil domain containing 6
GO:0005515|GO:0008150|GO:0017124|GO:0005737|GO:0005200|GO:0005856 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133099_PI430048170 0.494339164661601 1.44331758471481 0.25740506189384
0.271581292301626 1.62625759101655 A A A 0.379921630803594 0.315000150802964
0.331309342919153 A A A LNCV6_133099_PI430048170 mRNA
GCAAACATGTTTCCTCATCTTTCTGGCTTATCCAGTATGTAGCTATTTGTGACATAATAA NM_000345 RefSeq chr4
- 89724098 89837199 SNCA 6622 "synuclein, alpha (non A4 component of amyloid precursor),
transcript variant 1"
GO:0005515|GO:0008017|GO:0030054|GO:0043030|GO:0032410|GO:0010040|GO:0005764|GO:0042802|GO:0031
623|GO:0032496|GO:0032026|GO:0005938|GO:0043027|GO:0005791|GO:0006638|GO:0005504|GO:0005794|GO:0
000287|GO:0005507|GO:0005509|GO:0007568|GO:0019904|GO:0010517|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135402_PI430048170 0.727157673888598 1.28861063198307 1.49420189990033
3.45884001424684 3.36888563603468 A P P 3.36617589714748 1.60755733909335
2.42685361196488 P A P LNCV6_135402_PI430048170 mRNA
TTGTTGATGTTAATCAAAGCTCCCTAATATACACCATCCCTAATTGCTCTTTCTCACCTC NM_020358 RefSeq chr11 -
89797654 89808575 TRIM49 57093 tripartite motif containing 49 GO:0005622|GO:0008270 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_68652_PI430048170 0.0141282854475807 0.535921665385044 9.90091897142952
9.96327848083854 9.74490014165707 P P P 10.512667717277 11.0165058377684 10.744140347708
P P P LNCV6_68652_PI430048170 mRNA
CTGGCCGTGTCTAATAAAAAGTATTTGAACCTTGGGAGCACCCAAGCTTGCTCATGTGGC NM_182687 RefSeq chr16
- 2972790 2980539 PKMYT1 9088 "protein kinase, membrane associated tyrosine/threonine 1,
transcript variant 2"

GO:0005515|GO:0007088|GO:0005794|GO:0005783|GO:0000079|GO:0005524|GO:0046872|GO:0005829|GO:0007067|GO:0000082|GO:0004672|GO:0016020|GO:0000139|GO:0016301|GO:0004674|GO:0010923|GO:0000086|GO:0051726|GO:0005789|GO:0006468|GO:0005654|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132139_PI430048170 0.90163407917636 1.00594777409787 4.3663438982265 4.04214015229555 4.26298606472132 P P P 4.18992402894452 4.54184685404562 3.850140987454 P P P LNCV6_132139_PI430048170 mRNA AACGAGAGCGAGAAAAACGCTTCAGCTTCTTTAAGAAGAACAAGTAGTTGGGGGCAAGGT NM_006946 RefSeq chr11 - 66685248 66721399 SPTBN2 6712 "spectrin, beta, non-erythrocytic 2"
GO:0008091|GO:0030054|GO:0003779|GO:0005615|GO:0007416|GO:0051693|GO:0005829|GO:0019886|GO:0005737|GO:0016324|GO:0005543|GO:0035264|GO:0007411|GO:0043025|GO:0005200|GO:0021692|GO:0030534|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139367_PI430048170 0.3750329810247820.5864552612461430.471106108652529 0.4835277468223040.363269122838291 A A A 2.03546508724209 0.518604964068103 0.494693284334323 A A A LNCV6_139367_PI430048170 mRNA AAGCACCCCTTTGCCATTGAGAACATTATTGGCCGGGACTACAAGGGCGTGCTGCAGGCT NM_001013735 RefSeq chr9 + 77019654 77020953 FOXB2 NA forkhead box B2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137560_PI430048170 0.1286819041878250.9505313730347940.245723681076266 0.2786496219494810.321694484411473 A A A 0.4148365900057670.329926477866744 0.319997709130167 A A A LNCV6_137560_PI430048170 mRNA CCATGATGAAGAGAAATCTTCTGAGTGTAATAAATGTGGCATGTTTTTCAGACATTGTTC NM_001039886 RefSeq chr19 + 52527655 52556050 ZNF808 388558 zinc finger protein 808
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141835_PI430048170 0.00783236052903602 0.6358995101045075.12058985372065 4.96094804516921 4.83131509862963 P P P 5.44386298995226 5.63837180887695 5.78449072152088 P P P LNCV6_141835_PI430048170 mRNA GGAGAGAAACACAGCGATCACAAAGGGCCATGTTTGCCAAGAAATAAAATATACTTGGAA NM_012241 RefSeq chr6 + 13574626 13615158 SIRT5 23408 "sirtuin 5, transcript variant 1"
GO:0006342|GO:0070403|GO:0005634|GO:0036049|GO:0003950|GO:0005829|GO:0036054|GO:0005739|GO:0006471|GO:0036055|GO:0005758|GO:0005759|GO:0036047|GO:0036048|GO:0008270|GO:2000378|GO:0006476 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135475_PI430048170 0.1600938789870791.13242815154595 8.31901444228973 8.42509453693901 8.2711539125523 P P P 8.1912053278277 8.28559402598074 7.98879657649739 P P P LNCV6_135475_PI430048170 mRNA TTTAATCAAAATGCAATGCTTTGCAAGTCTTTACTGCTTGGAGGTGGCTGAGTTGGGGGC NM_022489 RefSeq chr14 + 104689605 104719610 INF2 64423 "inverted formin, FH2 and WH2 domain containing, transcript variant 1"
GO:0048471|GO:0005737|GO:0030036|GO:0032535|GO:0005783|GO:0017048|GO:0005634|GO:0003779|GO:0090140 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95276_PI430048170 0.0180912078415009 0.7475732426590576.0431626034104 6.08414992935189 6.23145317750545 P P P 6.50944362797112 6.40937113430517 6.69164254442979 P P P LNCV6_95276_PI430048170 mRNA GCCTGTGCTGAGTTACACCAGAATGTAAATGTGAAGAACATAATCATTGCTTTAATTGAT NM_018206 RefSeq chr16 - 46659676 46689232 VPS35 55737 vacuolar protein sorting 35 homolog (S. cerevisiae)
GO:0005515|GO:0045056|GO:0005770|GO:0008565|GO:0042147|GO:0005765|GO:0006886|GO:0005769|GO:0070062|GO:0030904|GO:0005829|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129603_PI430048170 0.1091570540078010.7620443753425421 1.5160704831443 11.600719097637

11.5114860764092 P P P 11.7677867843637 11.794050136879 12.202051870989 P P P
LNCV6_129603_PI430048170 mRNA
AGCAGAAATCCTCATTTCTGTGCTACGGATTTACCAAAAATTGTCAAGTCTTTTTCAGTT NM_001184970 RefSeq
chr22 - 42869765 43015178 PACSIN2 11252 "protein kinase C and casein kinase substrate in
neurons 2, transcript variant 1"
GO:0008092|GO:0005515|GO:0005215|GO:0070300|GO:0030036|GO:0097320|GO:0072584|GO:0070836|GO:0005
829|GO:0042802|GO:0043231|GO:0005737|GO:0005911|GO:0030100|GO:0045806|GO:0005856|GO:0030659|GO:0
070062|GO:0031988|GO:0032587|GO:0048858|GO:0005901|GO:0036010|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_100833_PI430048170 0.00490842958194028 1.79569862515604 4.13443891593759
4.05669580104559 4.1991545828612 P P P 3.34670245163132 3.09736751795663 3.3984958092239
P P P LNCV6_100833_PI430048170 mRNA
TCACTCCAGCTCCTAAAAAGCCACCATGGGAAGAGCTGCCTCCAATTAAAGTTCTTGATT NM_001199233 RefSeq
chr9 - 114666433 114682089 LOC100505478 100505478 uncharacterized LOC100505478 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_118796_PI430048170 0.00926529237308131 0.1570190134228440.315927757201625
1.34864016190172 0.344940585503791A A A 3.47128320324696 3.57753380608788
3.20268014125381 P P P LNCV6_118796_PI430048170 mRNA
GACGAAGGGCATGCTTTTGGTTTGCTGTAAGATTGTATTCTGTATATATGTTTTCATGTA NM_001029880 RefSeq
chr10 - 7158623 7411486 SFMBT257713 "Scm-like with four mbt domains 2, transcript variant 1"
GO:0005515|GO:0042393|GO:0006355|GO:0016235|GO:0010629|GO:0005654|GO:0005634|GO:0043231 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141459_PI430048170 0.0271521649230983 0.7336526870265871 1.7103486324987
11.692181029616 11.5847005031751 P P P 11.9822714524846 12.0446914624085
12.2858197654711 P P P LNCV6_141459_PI430048170 mRNA
GAGCTGTGCGTTTGTATCGCCACTGTATTTGTGTACTTTAACAATCGTGTAAATAATAAA NM_139062RefSeq chr17
- 82242660 82273718 CSNK1D 1453 "casein kinase 1, delta, transcript variant 2"
GO:0051219|GO:0005515|GO:0048471|GO:0005886|GO:0008360|GO:0090263|GO:0050321|GO:0032436|GO:0005
634|GO:0005829|GO:0001948|GO:0018105|GO:0000086|GO:0005876|GO:0016055|GO:0042277|GO:0005813|GO:0
005794|GO:0006996|GO:0005819|GO:0051225|GO:0005524|GO:0032922|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134762_PI430048170 0.00238275755365665 0.7988015976527971 4.2231512568441
14.3042109577406 14.2542474396853 P P P 14.515627570329 14.6205015505044
14.6164867200236 P P P LNCV6_134762_PI430048170 mRNA
GTGATAAATTATTAATGTTCCGCAGTCTCACTCTGAATAAAGGACAGTTTGTAAGTCTTG NM_001084RefSeq chr7
- 101205976 101217730 PLOD3 8985 "procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3"
GO:0005515|GO:0031418|GO:0005506|GO:0005783|GO:0060425|GO:0008475|GO:0033823|GO:0001701|GO:0032
870|GO:0048730|GO:0008104|GO:0070831|GO:0001886|GO:0030198|GO:0050211|GO:0042311|GO:0030199|GO:0
030867|GO:0005789|GO:0021915|GO:0006464|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140367_PI430048170 0.0222768537560208 0.7891300970362871 3.2001159114995
13.0353272408692 12.9612050944083 P P P 13.3111983316819 13.5217404495913
13.3912969196387 P P P LNCV6_140367_PI430048170 mRNA
CTTCCTTGTCCTTCTCTGGAAAATGCCAAAATACACGATGTGAATAAAAGTACAACGGCT NM_001098536 RefSeq
chr12 + 6852120 6866631 USP5 8078 "ubiquitin specific peptidase 5 (isopeptidase T), transcript
variant 1"
GO:0071108|GO:0005515|GO:0004197|GO:0006511|GO:0004843|GO:0032436|GO:0008270|GO:0008242|GO:0005
764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144731_PI430048170 0.4739349528648450.7670357316288640.4592938128205

1.99073834915976 1.35331736226698 A A A 1.18766620172314 1.62705175287654
2.30401297295094 A A A LNCV6_144731_PI430048170 mRNA
TAATGGGAGGCCTGTCCTAGTACAACTCCTTTACTCTTTTCACCTTCATCTTGACCTTCT NM_182758 RefSeq chr15 -
53513740 53759662 WDR72 256764 "WD repeat domain 72, transcript variant 1" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_81635_PI430048170 0.8768717560652110.9857641452511779.17893983724333 8.90356767146155
9.04729512540152 P P P 8.96833439751582 8.98159839012538 9.23864417339221 P P P
LNCV6_81635_PI430048170 mRNA
GGCTGCTTGATTTTGTAGAGAAATTAGAACCCATAACCATACACAGGCTATCAACATGTT NM_006307 RefSeq chrX
- 38149334 38220924 SRPX 8406 "sushi-repeat containing protein, X-linked, transcript variant 1"
GO:0034976|GO:0005776|GO:0016020|GO:0009986|GO:0005783|GO:0060244|GO:0006914|GO:2001241|GO:0001
845|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78879_PI430048170 0.0426182881275567 1.22191370943198 11.6853802090356
11.6345109111642 11.6152481474056 P P P 11.3949710139256 11.4466018169477
11.2171426457909 P P P LNCV6_78879_PI430048170 mRNA
TTGCTGTGGGCAGCGGCTCTCGTGTGATCTCCATCTGTTATTTCGAGCAGGAGAATGACT NM_005720 RefSeq chr7
+ 99374674 99394781 ARPC1B 10095 "actin related protein 2/3 complex, subunit 1B, 41kDa"
GO:0034314|GO:0005737|GO:0051015|GO:0005885|GO:0005200|GO:0006928|GO:0015629|GO:0005925|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129279_PI430048170 0.00129617683921 0.69417355763632413.65689108652
13.4952286240612 13.5363983183413 P P P 14.1554610091337 14.1004990465995
14.0138653850526 P P P LNCV6_129279_PI430048170 mRNA
GGCGCTGTTAGGCCGGAATTAAAGTGGCTTTTTGAGGTTTGGTTTTTCACAATCAAAAAA NM_004596 RefSeq chr19
+ 40750853 40765392 SNRPA 6626 small nuclear ribonucleoprotein polypeptide A
GO:0008380|GO:0005515|GO:0010467|GO:0005737|GO:0000166|GO:0000398|GO:0003723|GO:0005730|GO:0017
069|GO:0005681|GO:0005654|GO:0005685 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143082_PI430048170 0.0036064123450295 0.4218025309301935.23693122793875
5.12277251144182 5.62734175552632 P P P 6.53525769604494 6.4069729058915
6.80209356498526 P P P LNCV6_143082_PI430048170 mRNA
GTTGGGTTCTTCCTGTAATGCGCTATTATGTCTTGGGCTTAATAAAAATATTTGTGATCA NM_001128429 RefSeq
chr4 + 94207844 94291292 SMARCAD1 56916 "SWI/SNF-related, matrix-associated actin-dependent
regulator of chromatin, subfamily a, containing DEAD/H box 1, transcript variant 1"
GO:0000792|GO:0005515|GO:0070932|GO:0070933|GO:0043044|GO:0035861|GO:0004386|GO:0003676|GO:0003
677|GO:0005524|GO:0016363|GO:0051304|GO:0051260|GO:0005654|GO:0006338|GO:0045893|GO:0000018|GO:0
043596|GO:0000729|GO:0009117|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130204_PI430048170 0.3522378452667780.9491408832698641 0.9602348785742
11.0911376041423 10.9087741363902 P P P 10.9922431313591 11.1521127355106
11.0432348982258 P P P LNCV6_130204_PI430048170 mRNA
TTCCCACTGCCCAGTTGTTTGTCCACATCAGGAGTTGCTGATTGAATTCTTGCTACTCTT NM_139179 RefSeq chr7
- 6409115 6448012 DAGLB 221955 "diacylglycerol lipase, beta, transcript variant 1"
GO:0019369|GO:0016042|GO:0005886|GO:0007596|GO:0030168|GO:0042136|GO:0016021|GO:0005765|GO:0046
872|GO:0016298|GO:0007405 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142940_PI430048170 0.4699669058427810.8935256157998061 0.3265985781502
10.1600954163237 10.4787713044725 P P P 10.2025722591962 10.4599656994655
10.7547635152308 P P P LNCV6_142940_PI430048170 mRNA
TTGTGTACTGTTGCTTGGATGCGGCACAGTGGTTGGTAATGGAATAAAGGATGCATGGAT NM_021214 RefSeq chr15
+ 80695310 80755621 ABHD17C 58489 abhydrolase domain containing 17C GO:0016787|GO:0008152
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142216_PI430048170 0.0136397811423741 0.5830089487677346.86004721187601

6.67854490661766 7.14920787073148 P P P 7.79087638364391 7.53435658123021
7.72510138442765 P P P LNCV6_142216_PI430048170 mRNA
TAAAAAGTATCATATAAAGCTGAATACAAATTGGTTTGGGGGGAGATCCTTTCCTACCCA NM_006353 RefSeq chr6
+ 26538343 26546936 HMGN4 10473 high mobility group nucleosomal binding domain 4
GO:0031492|GO:0005634|GO:0000785 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143523_PI430048170 0.0452002790178335 0.4668333567047092.56691839127863
2.51829819526167 2.69208337134532 A A A 3.1716164510894 3.99281253258144
3.79463558983487 P P P LNCV6_143523_PI430048170 mRNA
GAGCAGACAATAAGAGGAAGAATGAAGCCAACTAAAATTCTGAATGCTTTTTGTTGGATT NM_176825 RefSeq chr2
+ 108288638 108309915 SULT1C2 6819 "sulfotransferase family, cytosolic, 1C, member 2, transcript variant 2"
GO:0005737|GO:0006805|GO:0050427|GO:0008146|GO:0051923|GO:0009308|GO:0044281|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126883_PI430048170 0.6076064500933290.9664053335632190.531122407213803
0.4858549349234580.260267189274741 A A A 0.4085354302832460.540502136094516
0.487386873365169 A A A LNCV6_126883_PI430048170 mRNA
CAGGACCACTTCAAAACTGGTAGAATATTTATTCATATGACAAGGATACCTGAGTAAAAC NM_001526 RefSeq chr6
+ 55174272 55282620 HCRTR2 3062 hypocretin (orexin) receptor 2
GO:0007631|GO:0042277|GO:0005886|GO:0022410|GO:0045187|GO:0007200|GO:0007268|GO:0008188|GO:0032870|GO:0016499|GO:0005887|GO:0007218|GO:0017046 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104481_PI430048170 0.0455196575102778 0.8399658446214415.85185013061774
6.07506798744209 6.01162425880144 P P P 6.32029542319982 6.12751669568217 6.2480573817899
P P P LNCV6_104481_PI430048170 mRNA
GTTTATAATCTGCACCAGAAGAATGGCTTCACATGTATGCTCATCGGGGAGATCTTTGAG NM_001077198 RefSeq
chr2 - 219219379 219229688 ATG9A 79065 "autophagy related 9A, transcript variant 1"
GO:0005515|GO:0005802|GO:0005776|GO:0000422|GO:0005770|GO:0000421|GO:0031410|GO:0000407|GO:0015031|GO:0034497|GO:0016020|GO:0045087|GO:0034067|GO:0031902|GO:0005789|GO:0034727|GO:0016021|GO:0055037|GO:0000045|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49790_PI430048170 0.0261703579885721 0.4427716688589043.81266969562135
4.09098917060559 4.28043351427816 P P P 4.79371297702703 5.16660411913023
5.65706258301727 P P P LNCV6_49790_PI430048170 mRNA
CTGAACTGTTTAAAAATCTAGCATGTAGAGCAAGCCTGTTTTGTGGAAAATCCTTATTCA NM_016396 RefSeq chr15
+ 44427380 44527231 CTDSPL2 51496 "CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2"GO:0016311|GO:0004721 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134775_PI430048170 0.2316256348150551.02614477093203 0.371998155605031
0.29911739291911 0.354038532473611 A A A 0.2919105891671030.294245998934573
0.32800654190864 A A A LNCV6_134775_PI430048170 mRNA
TTAATCATTTCCAGCATCCTCAAGATTCACTCCTCTGAGGGGAGAAGCAAAGCTTTCTCT NM_001001956 RefSeq
chr9 - 104617247 104618204 OR13C9NA "olfactory receptor, family 13, subfamily C, member 9" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111084_PI430048170 0.6992015498833060.9835852677270630.433396602300254
0.3976073954471340.248474844036966 A A A 0.3520590946809980.41178398250842
0.393214637446161 A A A LNCV6_111084_PI430048170 mRNA
CATCTTCTCAGGTTCAGTTCAAGTCTTTACCATAGGTAGTGTCTTAATATCTTATCTCTA NM_001004737 RefSeq chr3
+ 98497680 98498631 OR5K2 NA "olfactory receptor, family 5, subfamily K, member 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132561_PI430048170 0.3245237881207450.7601163254990972.85883027690604
3.60135051735708 3.36452987449891 A P P 3.16014510674383 4.03711626831981

3.77663340563531 P P P LNCV6_132561_PI430048170 mRNA
GTGACTTTTAAAGGATTAATGTTGAATCACATTGTCAGAATTTTTTCCTCCTCGCTGTTC NM_001143935 RefSeq chr7
+ 87345634 87399796 CROT 54677 "carnitine O-octanoyltransferase, transcript variant 1"
GO:0006635|GO:0005782|GO:0005102|GO:0044281|GO:0006091|GO:0008458|GO:0015936|GO:0043231|GO:0005
739|GO:0006631|GO:0051791|GO:0015908|GO:0033540|GO:0009437|GO:0044255|GO:0005777 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134897_PI430048170 0.1078249189286911.42722874320231 9.00963629185432
9.29917095820533 9.25241920725329 P P P 9.06273353710671 8.39340104074425
8.48730317637742 P P P LNCV6_134897_PI430048170 mRNA
CAGGACACGAAGGCTGCCCCTGTAAGGTTTCAATGCATACAATAAAAGAGCTTTATCCCT NM_002615 RefSeq chr17
+ 1761964 1777565 SERPINF1 5176 "serpin peptidase inhibitor, clade F (alpha-2 antiplasmin,
pigment epithelium derived factor), member 1"
GO:0060770|GO:0046685|GO:0048471|GO:0060041|GO:0071300|GO:0008283|GO:0004867|GO:0010447|GO:0042
698|GO:0005615|GO:0050769|GO:0071279|GO:0043203|GO:0071333|GO:0070062|GO:0042470|GO:0001822|GO:0
007614|GO:0007568|GO:0007275|GO:0005576|GO:0005604|GO:0010951|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128782_PI430048170 0.3627872123947540.7986514972247130.355236449227802
0.4376695010667330.341474462646544A A A 0.4771075620560360.3651339002409241.1401944804868
A A A LNCV6_128782_PI430048170 mRNA
CCACCCAGACCTCATTATTTCTTGCTCTATCATTCTGTTTCAATAAAGACATTTGGAATANM_016609RefSeq chr14 -
23346310 23352912 SLC22A17 51310 "solute carrier family 22, member 17, transcript variant 2"
GO:0006879|GO:0007165|GO:0005774|GO:0031301|GO:0005887|GO:0022857|GO:0015891|GO:0055085|GO:0006
811|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143258_PI430048170 0.4031663353373040.86632229424685 0.275570343712429
0.2797108631720990.443718385294047A A A 0.3500182116681680.87238317862561
0.337128017068905A A A LNCV6_143258_PI430048170 mRNA
TGCTTCTGCTCCATTATAGCAGTAAAGAACGAATATCCAATGCAACAGGACAATTAAAAA NM_014335 RefSeq chr15
+ 48878092 48880183 EID1 23741 EP300 interacting inhibitor of differentiation 1
GO:0005515|GO:0035035|GO:0035034|GO:0016235|GO:0003714|GO:0005634|GO:0035065|GO:0000122|GO:0006
351|GO:0030154|GO:0005737|GO:0007049|GO:0005654|GO:0045892 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_137170_PI430048170 0.3429780408139530.1621125247915782.62781649613034
2.57546220019804 0.265223306561768A A A 2.30677858313751 6.19119170437566
2.10169724638668 A P A LNCV6_137170_PI430048170 mRNA
CGGGTAGGACTCCTTATGTCTCTCCAGAATTATAAAACATATACATTTATTTACAAGTGC NM_001164496 RefSeq
chr3 - 113286929 113441514 CFAP44 55779 "cilia and flagella associated protein 44, transcript variant 1"
GO:0042995 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54502_PI430048170 0.1179025179530880.438823440925552 0.391154554241556 1.96742748226439
0.257834107678569A A A 2.01746492282827 2.31053852601454 2.48946000055767 A A P
LNCV6_54502_PI430048170 mRNA
CAAGAAGCAAGAGATTGGCTGTTCCTCTTGAGGAAAAACCTTAATAAACCTTCCCATTTT NM_001010935 RefSeq
chr1 + 111619782 111716695 RAP1A 5906 "RAP1A, member of RAS oncogene family, transcript variant
1"
GO:0005515|GO:0043005|GO:0048471|GO:0030054|GO:2001214|GO:0005886|GO:0030033|GO:0003924|GO:0044
281|GO:0015031|GO:0032854|GO:0032403|GO:0005829|GO:0005737|GO:0000186|GO:0061028|GO:0045860|GO:0
070374|GO:0017016|GO:0017034|GO:0070062|GO:0032045|GO:2000301|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132195_PI430048170 0.8116832295876870.9857792929949868.1877885275948
8.41866404862844 8.34181307707894 P P P 8.24228285602838 8.42322168289069 8.3485374049458

P P P LNCV6_132195_PI430048170 mRNA
CCTTGGGTGACAAATTCCTCTTTGATGAATGTACCCTGTGGGGATGTTTCATACTGACAG NM_002309RefSeq chr22
- 30240446 30246851 LIF 3976 "leukemia inhibitory factor, transcript variant 1"
GO:0060426|GO:0008284|GO:0008285|GO:0042503|GO:0006366|GO:0050731|GO:0033141|GO:1900182|GO:0005
615|GO:0046888|GO:0048644|GO:0046697|GO:0006955|GO:0005737|GO:0033138|GO:0048666|GO:0045944|GO:0
072307|GO:0070373|GO:0005146|GO:0048286|GO:0007566|GO:0060708|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_103002_PI430048170 0.0904696457492704 0.80617086327333810.8809387765694
10.5509179750377 10.5502773522313 P P P 10.8173629072898 11.1057249962151
11.0027358011316 P P P LNCV6_103002_PI430048170 mRNA
CAGGATGAGATGCTGCGGCGGGTGGATGCTGAGAACAGGCTGCAGACCATGAAGGAGGAA NM_170707RefSeq
chr1 + 156114669 156140089 LMNA 4000 "lamin A/C, transcript variant 1"
GO:0005882|GO:0005515|GO:0007077|GO:2001237|GO:0034504|GO:0048471|GO:0005634|GO:0090343|GO:0005
635|GO:0006921|GO:0005638|GO:0005829|GO:0030968|GO:0005737|GO:1900180|GO:0090201|GO:0035105|GO:0
030334|GO:0007084|GO:0030951|GO:0071456|GO:0006915|GO:0007517|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129933_PI430048170 0.0443557540437269 0.5808984871323925.21338195525418
4.55963099780631 5.20450019777238 P P P 5.54128359200202 5.95597190398389
5.88985221650307 P P P LNCV6_129933_PI430048170 mRNA
CAAACCTCCCCAAAAGAATATGCAATTGTTTGATTCATTTCTCTGTTATCAGACACCAAT NM_001076785 RefSeq
chr16 + 68264515 68301823 SLC7A6 9057 "solute carrier family 7 (amino acid transporter light chain,
y+L system), member 6, transcript variant 1"
GO:0006520|GO:0005886|GO:0006865|GO:0050900|GO:0055085|GO:0003333|GO:0016323|GO:0006461|GO:0015
297|GO:0015171|GO:0005887|GO:0007596|GO:0006810|GO:0006811 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_137528_PI430048170 0.2868094017562121.99991815633362 1.61796379679233
2.38099198883211 0.405904525002127A A A 0.4559017068183870.400989976064928
1.07709541712845 A A A LNCV6_137528_PI430048170 mRNA
TTACCGCTGCAATGACACCATCCCAGAGGACTATGAGACCCATCAGCTGCGGCAAGCCTA NM_000095RefSeq chr19
- 18782772 18791305 COMP 1311 cartilage oligomeric matrix protein
GO:0005515|GO:0043066|GO:0003417|GO:0005509|GO:0005518|GO:0005578|GO:0006915|GO:0043395|GO:0005
576|GO:0002020|GO:0005615|GO:0031012|GO:0001501|GO:0030198|GO:0009887|GO:0060173|GO:0007155|GO:0
008201|GO:0070062|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140058_PI430048170 0.0347546073997880.3650285250097820.555197561015697
1.42794642633664 1.18595416127269 A A A 2.14257757662424 2.09881647113634
3.15867132266713 A A P LNCV6_140058_PI430048170 mRNA
GGAAATGCGAAGTAGTTGCTATAGCAAGAATTGGGAACTGGGATATAAGTCATAATATTA NM_024408RefSeq chr1
- 119911552 120069703 NOTCH2 4853 "notch 2, transcript variant 1"
GO:0005515|GO:0010467|GO:0007220|GO:0006367|GO:0060674|GO:0003184|GO:0046579|GO:0007219|GO:0046
849|GO:0009887|GO:0042742|GO:0009986|GO:0001709|GO:0005509|GO:0007275|GO:0000122|GO:0001701|GO:0
043235|GO:0005929|GO:0005887|GO:0005789|GO:0016049|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134642_PI430048170 0.0158051426027560.3736869323838755.78744687432983
6.32788023151586 6.43099331458621 P P P 7.59260366643676 7.58580870873339
7.70414434849528 P P P LNCV6_134642_PI430048170 mRNA
GTACTTGAAACATGGTCATTTTTAGCCCTTTTCCTTAGGAACCATGTCTTTATTTTCTCA NM_001461RefSeq chr1 -
147186260 147225638 FMO5 2330 "flavin containing monooxygenase 5, transcript variant 1"
GO:0050661|GO:0008150|GO:0004499|GO:0050660|GO:0005789|GO:0016021|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_97240_PI430048170 0.3636335147928441.02319229785582 0.3646771989665670.269203595893258
0.330200339688746 A A A 0.2843481387483770.2850718753985190.297009338821483 A A A
LNCV6_97240_PI430048170 mRNA
ATAAAGTCCTGGGTACTTGCTGGCTGTAAGCAGCACCTGCAAGGCCTTATATACTATACA NM_001195442 RefSeq
chr3 + 46612434 46626543 LOC100132146 NA uncharacterized LOC100132146 NA . NA -
NA NA NA NA NA NA NA NA NA
LNCV6_68798_PI430048170 0.1373178321885620.9508580430095691 4.492707564912 14.5528548853659
14.5280271159928 P P P 14.5352774019662 14.6414840316846 14.6134662335807 P P P
LNCV6_68798_PI430048170 mRNA
GGGGCTGTCCCTCAAGTTATCTCCTCTGCTAAGACAAAAAGTAAAGCACTGTGGTCTTTG NM_144779RefSeq chr19
+ 35154768 35169885 FXYD5 53827 "FXYD domain containing ion transport regulator 5, transcript
variant 1" GO:0045296|GO:0034220|GO:0030033|GO:0046588|GO:0003779|GO:0016021|GO:0005216 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138432_PI430048170 0.8024923731571411.01124859914098 7.23458290926105
7.26318029600246 7.33176029450059 P P P 7.21955964112908 7.18137707278711
7.37457279758378 P P P LNCV6_138432_PI430048170 mRNA
GGAGAGAGATTGGGTGCAATTTGCCTCTTTCTTTGAATAAAAAGCTCTTTGCTCACCCTC NM_016598RefSeq chr3
- 44915260 44976182 ZDHHC3 51304 "zinc finger, DHHC-type containing 3, transcript variant 2"
GO:0018345|GO:0005794|GO:0016020|GO:0000139|GO:0016409|GO:0008270|GO:0016021|GO:0006605|GO:0019
706 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137845_PI430048170 0.7529900661944741.26247143031352 0.473991030081599
1.88452759155552 0.344943964778807 A A A 1.12956812027215 0.522791141937383
0.49183873342755 A A A LNCV6_137845_PI430048170 mRNA
GATGACCAGTTACACAATTCCTGTTTTTATTTTGTCCTGTTGTGCTCATCTTCTATGAAA NM_019087RefSeq chr5 -
53884783 54310573 ARL15 54622 ADP-ribosylation factor-like 15
GO:0005622|GO:0008150|GO:0003674|GO:0007264|GO:0005525|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_53675_PI430048170 0.494890974255105 1.09201632313084 0.446622372073466 0.428607488203639
0.848932484747569 A A A 0.414948590457418 0.490444851843288 0.476949321102111 A A A
LNCV6_53675_PI430048170 mRNA
ATGTGGTTAACATGGATTAATGTGGGAACTTGGCTTCAAGAACACAACCTTAGGACCTTG NM_001105556 RefSeq
chr1 + 27872542 27886685 THEMIS2 9473 "thymocyte selection associated family member 2,
transcript variant 3" GO:0050852|GO:0005737|GO:0006954|GO:0005634|GO:0007155 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_133791_PI430048170 0.318270020063515 0.866681046972569 0.396809706380743
0.410705441325992 0.280891242661341 A A A 0.847004445259 0.427482456824697
0.390815138844395 A A A LNCV6_133791_PI430048170 mRNA
TGCCCTTTACAACTCATATTCAGTTCTGCCTCCAAAATGCATGTGTCCACTTACATGAGA NM_006065RefSeq chr20
- 1564382 1620043 SIRPB1 10326 "signal-regulatory protein beta 1, transcript variant 1"
GO:0005515|GO:0007165|GO:0005886|GO:0005887|GO:0045087|GO:0016021|GO:0007166|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99577_PI430048170 0.4957480881756271.10814080222912 3.89610244249965 4.27291041260015
4.05482909046991 P P P 3.60983214886176 4.24264493004052 3.88160181406471 P P P
LNCV6_99577_PI430048170 mRNA
ACATCCTGATCCTGGAGGCCATCGAGAACCACAACCTCGCAGACACGGTGCTCAAGATCA NM_002446RefSeq chr19
+ 40191743 40215575 MAP3K10 4294 mitogen-activated protein kinase kinase kinase 10
GO:0043065|GO:0003714|GO:0046330|GO:0007254|GO:0043425|GO:0006915|GO:0007256|GO:0007257|GO:0005
524|GO:0043433|GO:0042803|GO:0007224|GO:0004706|GO:0007165|GO:0005737|GO:0046777|GO:0004672|GO:0
018105|GO:0004674|GO:0018107|GO:0043507|GO:0045892 . NA - . NA NA NA NA NA NA NA NA

NA
LNCV6_60498_PI430048170 0.759329790996245 1.28474046586904 0.4825039566177630.597882002625856
2.08764822979529 A A A 1.17705946547992 0.9220748905187450.503914167589849 A A A
LNCV6_60498_PI430048170 mRNA
AAAGTCACCTGAAGAGAATCTACAAGGTGCTGTAAAATCTTTCTGCACAAGTGCCTCAGG NM_017693 RefSeq chr13
+ 102799048 102841538 BIVM 54841 "basic, immunoglobulin-like variable motif containing, transcript
variant 1" GO:0005737|GO:0005634|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126945_PI430048170 0.0138368452733524 1.55941862483745 7.36031423087426
7.39760675659599 7.22314014254542 P P P 6.7886687033449 6.78839882205103
6.46290667493933 P P P LNCV6_126945_PI430048170 mRNA
AAGAATCTTAGCAGAGATTGGGATGCCTTACTCAATAAAGCTAAGATGACTATGCTGAAA NM_001979 RefSeq chr8
+ 27491001 27544922 EPHX2 2053 "epoxide hydrolase 2, cytoplasmic, transcript variant 1"
GO:0019369|GO:0090181|GO:0006805|GO:0017144|GO:0044281|GO:0042803|GO:0005829|GO:0016791|GO:0005
737|GO:0042577|GO:0006954|GO:0045909|GO:0033885|GO:0070062|GO:0005777|GO:0042632|GO:0000287|GO:0
019373|GO:0072593|GO:0006874|GO:0005102|GO:0009636|GO:0010628|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130045_PI430048170 0.6942260504198511.0534121019633 3.28715239133001
2.70566891444003 3.00816107211225 P A P 3.53263821519731 3.1394945984563
1.43958227169945 P P A LNCV6_130045_PI430048170 mRNA
GTGTCCTAAGTAAGGATCTGTGCAGAGGACAAATAAATCAGTTTTTGATTTGTCTTGAAA NM_003708 RefSeq chr12
- 56951430 56957634 RDH16 8608 retinol dehydrogenase 16 (all-trans)
GO:0006629|GO:0005789|GO:0009055|GO:0016021|GO:0004745|GO:0055114|GO:0043231 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145056_PI430048170 0.4370566308929440.7483325609047043.21763262402919
1.09473163662505 1.33557881880316 P A A 2.80399702613825 3.00362064501569
1.86938753209494 P P A LNCV6_145056_PI430048170 mRNA
GTCCCTGCTAAATAATTCCCTTCTTGCAATCCAGAAGGATAAATAAATGTAATTTCTGGA NM_001257964 RefSeq
chr18 + 57147061 57150408 BOD1L2 284257 biorientation of chromosomes in cell division 1-like 2
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134277_PI430048170 0.2173289983043920.3662011514793610.493306258859967
0.4957698534125760.278218752295894 A A A 2.78083874535819 0.533333927342805
1.42561291191958 P A A LNCV6_134277_PI430048170 mRNA
GAAAGAGTGTTATCATATTGGTGCTGAGTGCTATGTGTGCTTATACAATTTGTTCTTGTA NM_000793 RefSeq chr14
- 80197524 80231054 DIO2 1734 "deiodinase, iodothyronine, type II, transcript variant 2"
GO:0005886|GO:0004800|GO:0044281|GO:0034641|GO:0042403|GO:0008430|GO:0016020|GO:0001514|GO:0042
446|GO:0006590|GO:0016021|GO:0031625|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131571_PI430048170 0.0466061592319548 0.3036578073068271.34869180611899
0.4548132059733560.337694947933217 A A A 2.17473898202155 1.68954614965965
3.22062039959454 A A P LNCV6_131571_PI430048170 mRNA
ATCTACGGCTGAAATATAATATGCGTGGACAAGCTTTTGCTGAAGTGTAGTGTGTCCTTT NM_001282187 RefSeq
chrX - 78271471 78327691 CYSLTR1 10800 "cysteinyl leukotriene receptor 1, transcript variant 1"
GO:0005515|GO:0005886|GO:0007585|GO:0006952|GO:0004974|GO:0007204|GO:0045766|GO:0006954|GO:0045
907|GO:0006935|GO:0007186|GO:0016020|GO:0005887|GO:0006816 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128488_PI430048170 0.1586608635710792.35279873309666 1.64838038210402
1.50256746671913 3.13198492018392 A A P 0.56375022177531 1.62054308985282
0.77366317314377 A A A LNCV6_128488_PI430048170 mRNA
TGAATGTTTAATGCTCATGAAAATTGGGGGAGGGGGTTCTATTAACACAAAGCTTCTGAG NM_015551 RefSeq chr3
- 33150044 33219215 SUSD5 26032 sushi domain containing 5 GO:0005540|GO:0016021|GO:0007155

. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136358_PI430048170 0.4170512617381670.7312456981975370.402010475483744
0.3725777284674080.248908232906021A A A 0.333604059335187 1.41095846913843
0.359772654969509A A A LNCV6_136358_PI430048170 mRNA
ACAGCAACAACAGTGACAATGATGACAACAGAAAAACTGACTTTTGAACTTGAGTATATC NM_207645RefSeq chr11
+ 109422119 109429167 C11orf87 399947 chromosome 11 open reading frame 87 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125674_PI430048170 0.0377331233195872 1.23336547550455 9.90165532108086
10.0249554523062 10.1636764668781 P P P 9.73200168856532 9.80372174230965
9.65484731597045 P P P LNCV6_125674_PI430048170 mRNA
CTAAATACAACAGGGACACTCTGGACAATGACATCATGCTGATCAAACTCTCCTCACCTG NM_001197097 RefSeq
chr9 + 33750465 33799231 PRSS3 5646 "protease, serine, 3, transcript variant 3"
GO:0005515|GO:0009235|GO:0004252|GO:0005509|GO:0007586|GO:0006767|GO:0005576|GO:0044281|GO:0005
615|GO:0006766|GO:0043542|GO:0045087|GO:0006508|GO:0008236|GO:0031638|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138635_PI430048170 0.2809023169195361.12455131431353 0.470788116395369
0.8155050684398440.498134255605332A A A 0.391263824972336 0.441398841823911
0.468695739448654A A A LNCV6_138635_PI430048170 mRNA
AGGTAGGACAGAGATTATGGCACATCTCACATTAAATGCTATATTTTCGTTGGAAATACA NM_001270930 RefSeq
chr10 + 89392545 89406487 IFIT1 3434 "interferon-induced protein with tetratricopeptide repeats
1, transcript variant 5"
GO:0005515|GO:0032091|GO:0019060|GO:0050689|GO:0003723|GO:0019221|GO:0051097|GO:0009615|GO:0005
829|GO:0071360|GO:0005737|GO:0051607|GO:0060337|GO:0071357|GO:0045070|GO:0045071 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_89881_PI430048170 0.0510285015325046 0.7705778725504178.44916467523128
8.23199593113148 8.44042978796118 P P P 8.84146800760259 8.53443284562122 8.8612652410371
P P P LNCV6_89881_PI430048170 mRNA
GCTTTTCTCAAGTTAGTTATAGGATGTACTTAAGCAGTAAGCGTATTTAGGTAAAAGCAG NM_001257293 RefSeq
chr5 - 179614177 179623710 HNRNPH1 3187 "heterogeneous nuclear ribonucleoprotein H1 (H),
transcript variant 1"
GO:0005515|GO:0008380|GO:0006396|GO:0010467|GO:0003723|GO:0005634|GO:0071013|GO:0008266|GO:0000
166|GO:0016020|GO:0000398|GO:0005654|GO:0043484 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132925_PI430048170 0.00267204156032672 0.2308278013477854.18175813609924
3.83120859028301 4.61794325273384 P P P 6.05925193788327 6.4902040889253 6.4931722384242
P P P LNCV6_132925_PI430048170 mRNA
GCTTTAGATATGTGTCGTAATGGGAGTCTGAAAACTGTAATAAACTGTATTCATATCCTG NM_173491RefSeq chr5
+ 157743694 157760709 LSM11 134353 "LSM11, U7 small nuclear RNA associated"
GO:0005515|GO:0006369|GO:0010467|GO:0006398|GO:0006366|GO:0008334|GO:1900087|GO:0031124|GO:0005
634|GO:0005683|GO:0005654|GO:0071204|GO:0071209 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142542_PI430048170 0.0251883756655182 0.6065282528062636.71344629517731
6.87931500387859 6.9631419845909 P P P 7.50258467207595 7.33679335945688
7.84445438879332 P P P LNCV6_142542_PI430048170 mRNA
AATGTGGGTAAAGTGGCTGACATAGTATCTGATGCATAGGAGCTCAGTAAGTCATGGAAG NM_001166419 RefSeq
chrX - 72473415 72573103 HDAC8 55869 "histone deacetylase 8, transcript variant 3"
GO:0032041|GO:0070932|GO:0070933|GO:0005886|GO:0006325|GO:0046970|GO:0005634|GO:0071922|GO:0000
122|GO:0000228|GO:0046872|GO:0006351|GO:0005829|GO:0006333|GO:0005737|GO:0000118|GO:0007062|GO:0
005654|GO:0004407|GO:0000278|GO:0046969|GO:0016568|GO:0008134 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_141542_PI430048170 0.0143795307435812 0.4357278458905784.01558008168456

3.82220701243332 3.82840326552653 P P P 5.11239036482355 4.73672284030333
5.35505480325176 P P P LNCV6_141542_PI430048170 mRNA
GTCAAATTTACAGTTTAGTACCAAGCCAGTAGATGTCAGTATGATGCCTTAAATTAAGTC NM_018237 RefSeq chr10
+ 68721143 68792377 CCAR1 55749 "cell division cycle and apoptosis regulator 1, transcript variant 1"
GO:0008380|GO:0005515|GO:0010467|GO:0048471|GO:0007049|GO:0006355|GO:0030374|GO:0000398|GO:0006
915|GO:0005654|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130129_PI430048170 0.0454236610929611 1.22260226112663 11.3280636717867
11.3333937294473 11.2779429159737 P P P 11.075383434617 11.1038194310091
10.8809387765694 P P P LNCV6_130129_PI430048170 mRNA
GGATGAGCTTGAATTTGAATGAATTGAGTTTGTATTTCTAGAACCCTGGGTTTTTACATG NM_017907 RefSeq chr11
- 72097291 72103387 LAMTOR1 55004 "late endosomal/lysosomal adaptor, MAPK and MTOR activator
1"
GO:0005515|GO:0032418|GO:0032008|GO:0005886|GO:0032439|GO:0010872|GO:0005765|GO:0005764|GO:0010
874|GO:0043231|GO:0005085|GO:0071986|GO:0071230|GO:0007032|GO:0060620|GO:0070062|GO:0042632|GO:0
005794|GO:0043547|GO:0032947|GO:0001919|GO:0031902|GO:0016049|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128342_PI430048170 0.488963582584446 1.13329844636145 4.76774147738389
4.52847838664772 4.92639515626972 P P P 4.07242798354972 4.6603856943655
4.86400657057675 P P P LNCV6_128342_PI430048170 mRNA
CTTGGATGTGATTTTGAATTTCAAGAAAGCATCCATTCTCTATCACACCTTTCATATGAC NM_001098802 RefSeq
chr9 + 78236074 78267067 CEP78 84131 "centrosomal protein 78kDa, transcript variant 1"
GO:0005813|GO:0006996|GO:0000086|GO:0000278|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133908_PI430048170 0.460712681505863 0.779258889698148 0.55310143398154
0.467120853550701 2.313536683725 A A A 1.09068047729873 1.84417605662718
2.10959641992655 A A A LNCV6_133908_PI430048170 mRNA
CATGAGAGCAGTTCAAAGCTGCTTCATACTTATGGTCTCAAATATAGTATGTGTTGAATT NM_024754 RefSeq chr5
+ 72320366 72359353 PTCD2 79810 "pentatricopeptide repeat domain 2, transcript variant 1"
GO:0048747|GO:0006397|GO:0005739|GO:0001889|GO:0055010|GO:0001822|GO:0007005|GO:0050684 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129218_PI430048170 0.1069205173253 0.802036033538274 7.31348002277786 7.4159946578172
7.4539734936216 P P P 7.53755984326382 7.6426268506545 7.93221337375343 P P P
LNCV6_129218_PI430048170 mRNA
TCTCATTTTTTAAAATGCTCTTTTAGAACGGGAAACGGCTCAGATCCTGCTGTGGCACGG NM_015695 RefSeq chr6
+ 36196772 36232790 BRPF3 27154 "bromodomain and PHD finger containing, 3"
GO:0005515|GO:0070776|GO:0043966|GO:0007596|GO:0002576|GO:0030168|GO:0008270|GO:0005576|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69171_PI430048170 0.159936323066866 1.4433416189949 5.70803623450029 6.18994151783966
6.0450716261715 P P P 5.87890489075351 5.42353262385601 4.94399717775877 P P P
LNCV6_69171_PI430048170 mRNA
TTTCCTTCTTGGTCATCACAAAATGCCTTGATGTTCCTGACCCTTTTGTGCCTGACCCTA NM_005050 RefSeq chr14 -
74285276 74303064 ABCD4 5826 "ATP-binding cassette, sub-family D (ALD), member 4, transcript variant
1"
GO:0009235|GO:0006767|GO:0042626|GO:0044281|GO:0005765|GO:0005524|GO:0055085|GO:0006766|GO:0005
789|GO:0016021|GO:0043190|GO:0005778|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131607_PI430048170 0.434415075019164 1.09500955543759 6.64156185182798
6.30070209027593 6.24543110594453 P P P 6.23059787864288 6.30116554900865 6.2947365580427
P P P LNCV6_131607_PI430048170 mRNA
CCATAATTGATGATAGACCTAATACATTTCCTCTGTGTGTGTGTGTGTAACATTCCAAATAC NM_053025 RefSeq chr3

- 123612295 123884302 MYLK 4638 "myosin light chain kinase, transcript variant 1"
GO:0005515|GO:0005516|GO:0051928|GO:0090303|GO:0032154|GO:0046872|GO:0005829|GO:0006939|GO:0005
737|GO:0006936|GO:0005911|GO:0004687|GO:0007015|GO:0004683|GO:0070062|GO:0001725|GO:0030335|GO:0
071476|GO:0014820|GO:0060414|GO:0032060|GO:0003779|GO:0005524|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127761_PI430048170 0.0419830702716158 0.5877898960676038.97312347420771
8.3587953533172 8.54961257371247 P P P 9.32612608476888 9.44085795813823 9.4799988743609
P P P LNCV6_127761_PI430048170 mRNA
TCACCCCACTCCCCCAACACAGGACGCTTCATATAGATGTGTACAGTATATGTATTTTTT NM_001135243 RefSeq
chr5 + 150357638 150400308 TCOF1 6949 "Treacher Collins-Franceschetti syndrome 1, transcript
variant 4"
GO:0005515|GO:0005215|GO:0005737|GO:0001501|GO:0006810|GO:0005730|GO:0005634|GO:0042790 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142854_PI430048170 0.9406595779690991.12741066509064 1.78107737233833
0.3425704845723810.374869959768785A A A 1.10401979129446 0.321019911487248
0.944540143426904A A A LNCV6_142854_PI430048170 mRNA
GACGCCACCATAATAATCATCACCACACCGTGAGCAGATCTGAAAGGCACACTTTGATTT NM_002591RefSeq chr20
+ 57561080 57566457 PCK1 5105 phosphoenolpyruvate carboxykinase 1 (soluble)
GO:0031406|GO:0032868|GO:0014823|GO:0030145|GO:0000287|GO:0017144|GO:0005975|GO:0006094|GO:0006
107|GO:0044281|GO:0042593|GO:0005525|GO:0005829|GO:0046327|GO:0005737|GO:0004613|GO:0009405|GO:0
006006|GO:0019003|GO:0006475|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63479_PI430048170 0.2006926008303091.59971583306833 3.21484985721965 2.86198311310174
2.07103753626969 P A A 2.39385735313051 1.97808150335187 1.91836409768594 A A A
LNCV6_63479_PI430048170 mRNA
AGGAGGGCTGCCTTGTGGCCTTCATCATCGGCTCGCTCTGGGACAAGGAGAGACTCATGC NM_001166579 RefSeq
chr17 + 76453350 76470117 AANAT 15 "aralkylamine N-acetyltransferase, transcript variant 1"
GO:0051412|GO:0032868|GO:0048471|GO:0030187|GO:0044281|GO:0010043|GO:0005829|GO:0071889|GO:0051
592|GO:0034641|GO:0046219|GO:0034695|GO:0004060|GO:0007623|GO:0009416|GO:0004059|GO:0071320|GO:0
046688|GO:0034097|GO:0006474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143102_PI430048170 0.3591412217085091.16571112862809 2.27379808527789 1.941767457275
1.93744414685719 A A A 2.04708818883348 1.43422334893302 1.96156011253647 A A A
LNCV6_143102_PI430048170 mRNA
TAGAAATTAAGAAAATGTGGGCTCCTGTTTGTAACTAAACGGACGTGGGGAGGTGCACCT NM_001103176 RefSeq
chr7 - 155501257 155533844 CNPY1 NA canopy FGF signaling regulator 1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_32721_PI430048170 0.9788481469265061.00285810633791 11.7742252845763 11.5841275749307
11.4133960990619 P P P 11.6259004287666 11.5972886779614 11.5580071228688 P P P
LNCV6_32721_PI430048170 mRNA
TTCTTGGTTGGAAGCTGCAGCTGGCCCAAGAAAGAAAATAAAAAACAACACTTTTGCATG NM_003827RefSeq chr19
- 47487633 47515258 NAPA 8775 "N-ethylmaleimide-sensitive factor attachment protein, alpha,
transcript variant 1"
GO:0035494|GO:0005515|GO:0019905|GO:0005774|GO:0035249|GO:0006892|GO:0010807|GO:0006891|GO:0031
201|GO:0045176|GO:0006886|GO:0005829|GO:0005483|GO:0016020|GO:0007420|GO:0030182|GO:0061024|GO:0
061025|GO:0070062|GO:0070044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132160_PI430048170 0.6104093652963050.9059431995581657.82202423995591
7.47818190738151 7.83118751573303 P P P 7.4736770712895 7.90602161112519
8.13118680471981 P P P LNCV6_132160_PI430048170 mRNA
GTAGATTTTAACTGGACAACTTTGAGTACTGACATCATTGATAAATAAACTGGCTTGTGG NM_004811RefSeq chr11
- 58526870 58575917 LPXN 9404 "leupaxin, transcript variant 2"

GO:0003712|GO:0005515|GO:0033628|GO:0048471|GO:0006355|GO:0005886|GO:0050859|GO:0002102|GO:0005634|GO:0042995|GO:0006351|GO:0007165|GO:0005737|GO:0007162|GO:0006461|GO:0016020|GO:0008270|GO:0007155|GO:0005925. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127748_PI430048170 0.00368052832568742 0.4212169010150236.3703131002057 6.37459273510232 6.49577373812305 P P P 7.45377339730731 7.67152290391321 7.83576831270514 P P P LNCV6_127748_PI430048170 mRNA
TTAAAGAAGGTGTCTTGAAGAGCCCAGAGGACACTCACGTGCTAAGGTGTCCATTTTATG NM_004096RefSeq chr10 + 70404104 70428618 EIF4EBP2 1979 eukaryotic translation initiation factor 4E binding protein 2
GO:0008286|GO:0005515|GO:0019933|GO:0008190|GO:0045947|GO:0006412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144921_PI430048170 0.0489265061877629 0.9556382745082170.42030794407929 0.3653227187216780.371559048466385A A A 0.4458940547420220.464826292696529 0.443395093732485A A A LNCV6_144921_PI430048170 mRNA
CATTCTAAATAATCATGACCACAAATAAATTGCCCTGAGTAGGTCTGTAACCTGGAAAAA NM_173611RefSeq chr15 + 38454126 38487710 FAM98B 283742 "family with sequence similarity 98, member B"
GO:0005737|GO:0005634|GO:0072669 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136058_PI430048170 0.000508981503647879 0.7257239092085067.59888176489416 7.70330619017948 7.61379707535168 P P P 8.09783786769109 8.14594666183175 8.06068017182419 P P P LNCV6_136058_PI430048170 mRNA
TCAAATCAAGGGCTCCCTGGCTACCAAATTCTGTCTAGTAAAAATTATTCGAGCAGCGTG NM_020745RefSeq chr6 - 44298725 44313326 AARS2 57505 "alanyl-tRNA synthetase 2, mitochondrial"
GO:0005739|GO:0010467|GO:0000049|GO:0033108|GO:0070143|GO:0004813|GO:0008270|GO:0005524|GO:0006418 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143983_PI430048170 0.00124136547410623 1.71081811721758 12.7077202999144 12.7660103037339 12.5401023624513 P P P 11.8616250368752 11.9908064032766 11.8421952741753 P P P LNCV6_143983_PI430048170 mRNA
AACCTCCAGCCTCCCTTTTCAGAGCACAGCATTAAAGTTTGGGGAATTCTGTAGAAAAAA NM_001040197 RefSeq chr1 + 11736084 11750771 AGTRAP 57085 "angiotensin II receptor-associated protein, transcript variant 5"
GO:0005515|GO:0001666|GO:0004945|GO:0005886|GO:0038166|GO:0043231|GO:0005737|GO:0000139|GO:0005789|GO:0008217|GO:0005654|GO:0016021|GO:0005938|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78242_PI430048170 0.80653743923118 0.8635996614251330.5240615020347841.68507830956013 2.04963558831592 A A A 2.52259724422035 1.36641454377392 0.893780136970937A A A LNCV6_78242_PI430048170 mRNA
CAAGTTACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGA NM_138771RefSeq chr7 + 23597378 23644708 CCDC126 90693 coiled-coil domain containing 126
GO:0030144|GO:0016020|GO:0005576|GO:0006487 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130805_PI430048170 0.848124042302575 1.00922280669285 11.6386670675908 11.7652497649524 11.7000195211537 P P P 11.8102762643751 11.6425756806583 11.6057922378572 P P P LNCV6_130805_PI430048170 mRNA
AACCAGGCTCCTGTGATAGAGTTCTTTTAAGCCCAAGATTTTTTATTTGAGGGTTTTTTG NM_001641RefSeq chr14 + 20455130 20457772 APEX1 328 "APEX nuclease (multifunctional DNA repair enzyme) 1, transcript variant 1"
GO:0005515|GO:0004844|GO:0003906|GO:0008408|GO:0070301|GO:0008311|GO:0032403|GO:0004528|GO:0004523|GO:0080111|GO:0006297|GO:0006298|GO:0043488|GO:0005813|GO:0008081|GO:0003714|GO:0003713|GO:0007568|GO:0004520|GO:0031490|GO:0004519|GO:0006281|GO:0006283|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131818_PI430048170 0.198148248649302 1.05533025474422 0.3744474920865

0.27392537595444 0.411139305284776 A A A 0.2906235323690620.258663317640914
0.280430930737569 A A A LNCV6_131818_PI430048170 mRNA
GGAGGGACAAAGTGAGGAAAAGGTGCTCATTAAAGCTACCGGGCACCTTAGCTCAAAAAA NM_019609 RefSeq
chr20 - 2794068 2800646 CPXM1 56265 "carboxypeptidase X (M14 family), member 1, transcript
variant 1" GO:0006508|GO:0008270|GO:0005615|GO:0004181 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143651_PI430048170 0.0994816210705245 1.13201914617279 12.1805853502556
12.066902663955 11.9991853188895 P P P 11.8367839462588 12.0309815134227
11.8393415935415 P P P LNCV6_143651_PI430048170 mRNA
AGTGTTTCTCAGGGATGTGACTGAGGCCCAGGAGGGACCTGTGAGGGTCTGTTTACAGAG NM_001173988 RefSeq
chr9 + 136807921 136841187 RABL6 55684 "RAB, member RAS oncogene family-like 6, transcript
variant 3" GO:0005515|GO:0005813|GO:0005737|GO:0007264|GO:0005730|GO:0005634|GO:0005525 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131343_PI430048170 0.2299776144329510.8156351702895876.05893971029134
5.76488158454299 6.05736795390219 P P P 6.48500184580826 5.92853602207135
6.31421950559676 P P P LNCV6_131343_PI430048170 mRNA
TCAAGGAAAATCTGGGCTAAGAGTAGGATATGAGGGATGATGGATAAGGCATGAGACATG NM_001034173
RefSeq chr12 - 105019783 105084563 ALDH1L2 160428 "aldehyde dehydrogenase 1 family, member
L2, transcript variant 1"
GO:0005739|GO:0016155|GO:0009058|GO:0008168|GO:0004029|GO:0016742|GO:0032259|GO:0006730|GO:0070
062|GO:0055114|GO:0009258 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135485_PI430048170 0.0070398147680206 2.28426144804764 5.35432491297042
5.52937979537629 5.12826665821607 P P P 4.17493579963458 4.18737411351898
4.10079015244493 P P P LNCV6_135485_PI430048170 mRNA
GTTTGCCGCTTCATCATTGTCTGTTGATTTTCTTCAAAAGAACAGGTTTTGAGCATTGGA NM_001291516 RefSeq
chr9 - 136280941 136306901 MGC50722 399693 "uncharacterized MGC50722, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80558_PI430048170 0.5035262537446750.7824690239698681.40226657923062 0.613076141992158
0.524923384872357 A A A 1.48033268755187 0.4751641079111781.58080789444861 A A A
LNCV6_80558_PI430048170 mRNA
TGCCCTGAAAGAAGTTTCATGCATTCAAATAATGGCACCATTTCTGTGGTATCTGTATTG NM_017794 RefSeq chr9
+ 20658308 20995955 FOCAD 54914 focadhesin GO:0005515|GO:0016021|GO:0005925 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127643_PI430048170 0.1534433163050790.7558393748212694.45708013234593
4.80006380029458 5.03966738747466 P P P 4.91224722399429 5.14874738515161
5.45443019623174 P P P LNCV6_127643_PI430048170 mRNA
GTTGTACTATGGAAAATCAGCTGCTCAGCAACCTTTCACCTTTGTGTATTTTTCAATAAT NM_002742 RefSeq chr14
- 29576480 29927693 PRKD1 5587 protein kinase D1
GO:0005515|GO:0005802|GO:0010837|GO:0038033|GO:0042802|GO:0046777|GO:0018105|GO:0007030|GO:0060
548|GO:0043123|GO:0005938|GO:0010595|GO:0043536|GO:0007229|GO:0005887|GO:0045087|GO:0010976|GO:0
004697|GO:0035924|GO:2001044|GO:0005886|GO:0008283|GO:0005634|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134428_PI430048170 0.4352788137498861.71654580544995 1.98320857535688
0.3356431844229370.263094076069674 A A A 0.3159513033414540.328526010179852
0.306850505613779 A A A LNCV6_134428_PI430048170 mRNA
GCTACTCGGAGCATTGAGAGGGAGGCCTAAGAATAATAACAATCCAGTGCTTAAGAGTCA NM_015991 RefSeq chr1
+ 22636624 22639682 C1QA 712 "complement component 1, q subcomponent, A chain"
GO:0005515|GO:0006956|GO:0005581|GO:0045087|GO:0006958|GO:0007267|GO:0005576|GO:0005602|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_140588_PI430048170 0.9359478679060070.9994932964484525.62551476622245
5.98187616537492 6.02939998747146 P P P 5.89706661392396 5.87101912722441
5.90346767157207 P P P LNCV6_140588_PI430048170 mRNA
GATTAGGAGAAAATTGTGTTTAGTGTGTATCAATAAACAGCCCGTGGACCCAATCTGAAA NM_018947RefSeq chr7
- 25118650 25125361 CYCS 54205 "cytochrome c, somatic"
GO:0005515|GO:0070469|GO:0005743|GO:0000159|GO:0005634|GO:0044281|GO:0005829|GO:0005739|GO:0005
758|GO:0045155|GO:0006123|GO:0006122|GO:0004722|GO:0044237|GO:0006996|GO:0008635|GO:0005506|GO:0
006915|GO:0055085|GO:0097193|GO:0022904|GO:0045333|GO:0006309|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139158_PI430048170 0.9670028957432281.00064275010755 0.643870193466624
0.4034438894651220.294913928642028A A A 0.4731139298400930.365102536992756
0.519312088320521A A A LNCV6_139158_PI430048170 mRNA
TGTAACCTTCTGTAACTATTGGATGACGCTTTCTCCAGCTTAGCCCTAAATAAAGCACAG NM_020180RefSeq chr18
- 37243044 37566037 CELF4 56853 "CUGBP, Elav-like family member 4, transcript variant 1"
GO:0048026|GO:0017148|GO:0048025|GO:0042835|GO:0006376|GO:0005634|GO:0009790|GO:0003729|GO:0007
281|GO:0005737|GO:0090394|GO:0000166|GO:0000381|GO:0000380|GO:0000900 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137189_PI430048170 0.2797275514788031.07994120965928 15.708873323373
15.6946290835367 15.735272049113 P P P 15.4540917456046 15.7251301211759
15.6142012151984 P P P LNCV6_137189_PI430048170 mRNA
GATGATGTTTGCCGTCAGCATTCACCAAATAAACTTGCTCTCTGGGCCCTCGGTAAAAAA NM_021019RefSeq chr12
+ 56158260 56161582 MYL6 4637 "myosin, light chain 6, alkali, smooth muscle and non-muscle,
transcript variant 1"
GO:0005515|GO:0030049|GO:0048013|GO:0005509|GO:0016459|GO:0031982|GO:0030898|GO:0005829|GO:0003
774|GO:0006936|GO:0016461|GO:0016020|GO:0007411|GO:0007519|GO:0008152|GO:0008307|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129759_PI430048170 0.0231428178081859 0.7310141103852568.21901383395975
8.21541133420962 8.46007761283191 P P P 8.56977315721886 8.78658699653934 8.8898533519294
P P P LNCV6_129759_PI430048170 mRNA
CCTGTGTAAGTTGGTATTTGGGCACTTTATATTTTTCTAAAAACGTGTTTTGGATCCTGT NM_033624RefSeq chr12 -
117143779 117190495 FBXO21 23014 "F-box protein 21, transcript variant 1"
GO:0006511|GO:0004842|GO:0016567|GO:0000151|GO:0003677 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_84323_PI430048170 0.0655870133269578 0.620940401425 3.8194452569481
4.11199529163423 4.48955545898257 P P P 4.82761742268627 4.8844888437819
4.84937123696591 P P P LNCV6_84323_PI430048170 mRNA
TTTCCTACATGATTGCAGGCGAGAACACGATCTTCTTCCACATCTCCAGCAAGTTCTCAA NM_152245RefSeq chr22
- 50568860 50578667 CPT1B 1375 "carnitine palmitoyltransferase 1B (muscle), transcript variant 2"
GO:0005739|GO:0006635|GO:0004095|GO:0006853|GO:0005741|GO:0044281|GO:0016021|GO:0044255 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126975_PI430048170 0.372079893456615 1.18856226011542 5.43874966595086
4.81669509804972 5.36843568550358 P P P 5.14698737625132 4.95897657834359
4.82909461911556 P P P LNCV6_126975_PI430048170 mRNA
TCTACCTTCGAGGATTTCTTTTCCATTGTGTCGGTGTCTTTTTTACATGCCCTGGTCCAC NM_130901 RefSeq
chr15_KI270905v1_alt - 3768956 3940487 OTUD7A 161725 OTU deubiquitinase 7A
GO:0005737|GO:0004843|GO:0006508|GO:0008270|GO:0005634|GO:0003677|GO:0035871 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135433_PI430048170 0.0200549209239755 1.23859361840801 10.8030756443362
10.7726483321066 10.6901999811577 P P P 10.3334649187054 10.5461891735334

10.4546500702585 P P P LNCV6_135433_PI430048170 mRNA
TTCCATCCTCAACAAGTACGACGACAACGTCAAGGCCTACTTCAAGCGGGGCAAGGCCCA NM_003977 RefSeq
chr11 + 67483028 67491108 AIP 9049 "aryl hydrocarbon receptor interacting protein, transcript variant 1"
GO:0005515|GO:0006805|GO:0005886|GO:0051344|GO:0003713|GO:0006626|GO:0010738|GO:0005829|GO:0022417|GO:0007165|GO:0005737|GO:0005654|GO:0051082|GO:0004871|GO:0036004|GO:0008134 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132938_PI430048170 0.00245448646897678 0.725784325744654 7.03038151136567
6.93216556856828 7.09904196696883 P P P 7.42817226810946 7.48716072221234
7.53624877010619 P P P LNCV6_132938_PI430048170 mRNA
ATTTGGTGCTAGTTAGAGGCTGTTCACTCTCTCCTGCTCCTCTTCGGAGTAGAAATAAAG NM_001987 RefSeq
chr12 + 11649853 11895391 ETV6 2120 ets variant 6
GO:0005515|GO:0000977|GO:0003700|GO:0006357|GO:0006366|GO:0000981|GO:0019904|GO:0005730|GO:0000122|GO:0000978|GO:0001227|GO:0030154|GO:0001077|GO:0005737|GO:0045944 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_143803_PI430048170 0.00611009463800632 1.51339281454402 8.46436209197203
8.51149591025807 8.50378553009433 P P P 7.79527624449217 7.89269175843224
7.99204903729938 P P P LNCV6_143803_PI430048170 mRNA
TGATTCAGTATAACCTAGACCAGTCCTGTTTGCCTCATGATATCAGGTGGGAGCTGAATG NM_057161 RefSeq
chr6 + 43014102 43021298 KLHDC3 116138 "kelch domain containing 3, transcript variant 1"
GO:0005515|GO:0005737|GO:0000790|GO:0003682|GO:0006987|GO:0044267|GO:0030968|GO:0007131|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127369_PI430048170 0.114282221220045 1.05607812893648 0.438586861677998
0.4754821748241 0.486822731960755 A A A 0.333565858902428 0.385921700155225
0.443593744954895 A A A LNCV6_127369_PI430048170 mRNA
CAAAACTCCTTACCCAATGTGATGTTTTTCACTTGCATTGTCATTAGATGTCCAGAAAAA NM_002578 RefSeq chrX
+ 111096146 111220945 PAK3 5063 "p21 protein (Cdc42/Rac)-activated kinase 3, transcript variant 2"
GO:0005515|GO:0050852|GO:0017124|GO:0005886|GO:2000573|GO:0031295|GO:0007409|GO:0046872|GO:0005829|GO:0000187|GO:0005737|GO:0030833|GO:0043525|GO:0004702|GO:0000165|GO:0007411|GO:0060997|GO:0061003|GO:0004708|GO:0023014|GO:0048010|GO:0048013|GO:0005524|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_67758_PI430048170 0.567424287356068 0.933269214349856 9.08154899145976
9.11734362343461 9.03704391340522 P P P 9.42511940563301 9.03791954486887
9.03726401523171 P P P LNCV6_67758_PI430048170 mRNA
CTGGCAAGAGATACTATGGGGGAGCAGAGGTGGTGGATGAAATTGAGCTGCTGTGCCAGC NM_001166357
RefSeq chr12 + 57230359 57234935 SHMT2 6472 "serine hydroxymethyltransferase 2 (mitochondrial), transcript variant 3"
GO:0042645|GO:0008284|GO:0005743|GO:0004372|GO:0008732|GO:0042802|GO:0035999|GO:0019264|GO:0005739|GO:0005758|GO:0051289|GO:0003682|GO:0005759|GO:0030170|GO:0015630|GO:0006564|GO:0006730|GO:0016597|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91910_PI430048170 0.0105665803288933 1.20029072559916 7.14681150154482
7.04509689767438 7.09121638684388 P P P 6.84112500968537 6.8239739573335
6.82962092901326 P P P LNCV6_91910_PI430048170 mRNA
TGCTAGATGACAAGCATTTGCTGAAGCCATGGGATGCTAAGAAGCTATCCTCATCCTCTT NM_181715 RefSeq chr1
- 153947671 153958656 CRTC2 200186 CREB regulated transcription coactivator 2
GO:0005515|GO:0006094|GO:0042593|GO:0006351|GO:0032793|GO:0005737|GO:0008140|GO:0051289|GO:0045944|GO:0016032|GO:0005654|GO:0043970|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132025_PI430048170 0.0603310080322001 1.47634430266828 7.51063614241714

7.06339400263761 7.51473758936801 P P P 6.8846991559823 6.76836736337078
6.79189097812553 P P P LNCV6_132025_PI430048170 mRNA
TAGCAGAACACAAGAGAGCAAGAAAATGTCACATCTATACCAAATTAAGGATGTTGAGTT NM_006451 RefSeq chr5
- 43526267 43557093 PAIP1 10605 "poly(A) binding protein interacting protein 1, transcript variant 1"
GO:0005515|GO:0010467|GO:0005737|GO:0003723|GO:0045727|GO:0008494|GO:0048255|GO:0006413|GO:0000
289|GO:0005829|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133209_PI430048170 0.3150074931500551.07169915279763 0.361403990810544
0.2769392227470790.523796280881615 A A A 0.2867903852246880.284566683658239
0.302017464722727 A A A LNCV6_133209_PI430048170 mRNA
GGGATAATGTTTCTCCAACTGGAGACCTTCAATAAAACACTTCAATAGGTGCTTTAAAAA NM_001195597 RefSeq
chr6 + 130827404 130837136 SMLR1 100507203 small leucine-rich protein 1 GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_145009_PI430048170 0.0870439767320003 0.7267231715220467.15025366713513
7.16880129894184 7.65286062451545 P P P 7.62862124112685 7.73677228262218
8.01786003182519 P P P LNCV6_145009_PI430048170 mRNA
CATAGTAGGAAATAACATGTTAGTTGTCATTTGGCATGAGTGTGCATTCCAGTAATTCTT NM_001130042 RefSeq
chr1 - 74705487 74733408 CRYZ 1429 "crystallin, zeta (quinone reductase), transcript variant 1"
GO:0005794|GO:0042178|GO:0070404|GO:0003960|GO:0070402|GO:0005829|GO:0043231|GO:0005737|GO:0051
289|GO:0008270|GO:0003730|GO:0007601|GO:0055114|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132848_PI430048170 0.6663323071519670.9698049563213930.58912539669268
0.5069764371306880.296899384360689 A A A 0.41824177067222 0.59195238947437
0.525722122456627 A A A LNCV6_132848_PI430048170 mRNA
TTTTTGACAACTTCAGGCTCGATGAGAAGACAGAATTTGTGTGGCTCGACTGTCCCTTAG NM_152481 RefSeq chr19
- 35224800 35228725 FAM187B 148109 "family with sequence similarity 187, member B" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130508_PI430048170 0.3128917770466471.22704106266838 8.06746098246971
8.48443960126222 8.00874896751738 P P P 8.30659050470907 7.73030879087112
7.58073404765942 P P P LNCV6_130508_PI430048170 mRNA
TCTCTGGTTTTGGTCCCTGCACTTTGTGGTGTGACTCCGGTGCCTCCTGGTGAACCACAT NM_001039380 RefSeq
chr10 - 44997697 45000910 C10orf25 220979 "chromosome 10 open reading frame 25, transcript
variant 1" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136477_PI430048170 0.5242829715687081.18821017396125 1.18907969883191
0.4166734891974930.391815918947056 A A A 0.6071787858208390.375686633270392
0.40687059378187 A A A LNCV6_136477_PI430048170 mRNA
GGAGGAAAAAGCAAAGCAAAAGAAGCAGTGGATATTTTAAGACTAAAAAGGAAAACAAAA NM_001030288
RefSeq chr16 + 29662949 29670502 SPN6693 "sialophorin, transcript variant 1"
GO:0050688|GO:0005515|GO:0005886|GO:0031295|GO:0050900|GO:0005615|GO:0042130|GO:0006955|GO:0006
935|GO:0001562|GO:0042102|GO:0042742|GO:0070062|GO:0009986|GO:0042535|GO:0001808|GO:0097190|GO:0
005604|GO:0007165|GO:0006968|GO:0007162|GO:0007163|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143946_PI430048170 0.3015562647143120.6917506329258920.484966808918257
0.4469767797741640.458383754148936 A A A 1.53838883737918 0.800538391593655
0.415376673077775 A A A LNCV6_143946_PI430048170 mRNA
AGACTCACTTCTCCTATAACCACCACAAGTTGAATCAAAATTTTCAAATGTTTTCAGGAG NM_002172 RefSeq chr9
- 21239201 21239979 IFNA14 NA "interferon, alpha 14" NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138799_PI430048170 0.4527988357194441.02772647971072 0.315786375701894
0.2717643967406930.40595679090681 A A A 0.3331835698952010.257005467151773

0.287186939134488 A A A LNCV6_138799_PI430048170 mRNA
GTTTCCATAACAGAGACAGCCTAACAATGATGAGTTGTATTTAATGGATTACCATTGTAC NM_004752 RefSeq chr6
- 10873222 10881865 GCM2 9247 glial cells missing homolog 2 (Drosophila)
GO:0006355|GO:0043066|GO:0071310|GO:0006874|GO:0005634|GO:0007275|GO:0003677|GO:0006351|GO:0030
154|GO:0046872|GO:0043565|GO:0060017|GO:0030643 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141239_PI430048170 0.00750739565692187 0.4315713645381424.82918893430204
4.65646014064342 4.32126093464303 P P P 5.92791991392064 5.7251861355923
5.82895931046384 P P P LNCV6_141239_PI430048170 mRNA
GAAGGCTTATCTTAAACTGTGTAGTACCTTAGACTTGGCATTTATTTTTGATAGAGCAGA NM_172069 RefSeq chr2
+ 43637299 43767987 PLEKHH2 130271 "pleckstrin homology domain containing, family H (with MyTH4
domain) member 2" GO:0030835|GO:0005737|GO:0005886|GO:0003779|GO:0030864|GO:0030027|GO:0042802
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129329_PI430048170 0.0919498087535847 2.28948067010857 3.29456044236588
2.51983021349391 2.83869768507524 P A A 1.88796925355352 0.670617087529884
2.20865646598161 A A A LNCV6_129329_PI430048170 mRNA
TGTGACCTAAGGGTCCGCATTACTGCCCTTCTTCGGAGGAACTGGTTTGTTTTTAAAAAA NM_022377 RefSeq chr19
+ 10286966 10288584 ICAM4 3386 "intercellular adhesion molecule 4 (Landsteiner-Wiener blood
group), transcript variant 2"
GO:0016337|GO:0005737|GO:0005178|GO:0005886|GO:0030198|GO:0005887|GO:0050776|GO:0016021|GO:0007
155|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130335_PI430048170 0.2815840120520052.96733997040406 0.382516382019487
0.9075053732881862.92244075139931 A A P 0.2653594981450390.290454248351811
0.264734281330296 A A A LNCV6_130335_PI430048170 mRNA
GTGAAGTGTTTCCTTAGAAGAAGAAAGCCTTTTGTTCCATAGAGACCCCTAAAGAGTATC NM_023917 RefSeq
chr12_KI270904v1_alt - 7799 8874 TAS2R9 50835 "taste receptor, type 2, member 9"
GO:0050912|GO:0008150|GO:0007186|GO:0005886|GO:0008527|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126972_PI430048170 0.24599324778633 0.8496023020446436.77731450146671
6.82047370596872 6.59464575601479 P P P 6.84677274733889 7.2315799294789
6.78797756452772 P P P LNCV6_126972_PI430048170 mRNA
AGAGAGCCTCCTGTTCTTTCTATGCTTGGTCTGACTGAGCCTAAAGTTGAGAAAATGGGT NM_014002 RefSeq chr1
+ 206470242 206496890 IKBKE 9641 "inhibitor of kappa light polypeptide gene enhancer in B-cells,
kinase epsilon, transcript variant 1"
GO:0005515|GO:0034142|GO:0031966|GO:0008630|GO:0008384|GO:0007252|GO:0005634|GO:0002224|GO:0005
524|GO:0038061|GO:0005829|GO:0002756|GO:0004704|GO:0005737|GO:0006955|GO:0045087|GO:0016605|GO:0
035666|GO:0005654|GO:0006468|GO:0043123|GO:0034138|GO:0032480|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132321_PI430048170 0.0506546198531511 1.55076830452327 8.40033533522307
8.94848832721966 8.76579793463961 P P P 8.08111731415409 8.18098217202408
8.00065948773811 P P P LNCV6_132321_PI430048170 mRNA
GAGATTGGGAACGAAAAGGACGCTGTATTGATTTTTAAGTCGCATATTCTTTAACTTCAA NM_145267 RefSeq chr6
+ 70566921 70588903 SDHAF4 NA succinate dehydrogenase complex assembly factor 4 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_131125_PI430048170 0.1982636227945954.92710374562142 0.268113599314953
2.90754946822814 3.34291556374211 A A P 0.36759062190729 0.309801704873244
0.375061494562617 A A A LNCV6_131125_PI430048170 mRNA
TTTCTGTGAGGTACAAGCTTTATTGAAGCTGGCCTGTGCAGACACTTCCCTTTTTGACAC NM_001258283 RefSeq
chr5 - 181124356 181125304 OR2V1 NA "olfactory receptor, family 2, subfamily V, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_144475_PI430048170 0.0326902333226124 0.5471763111714380.954155107669176
0.3953604503727241.09851612948621 A A A 1.93334306027408 1.73168570731944
1.44224959720723 A A A LNCV6_144475_PI430048170 mRNA
AAGTGCCAATTTGCTCAGAAGATTCGGGAATTCAAGCTGCTGCCTGGAAGCAAGATCTAA NM_001129885 RefSeq
chr17 - 73248448 73261880 CPSF4L NA cleavage and polyadenylation specific factor 4-like NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134512_PI430048170 0.1585960144819250.933109846363045 0.253220995465151
0.2925759689457150.287480411856535 A A A 0.4623446683861460.361608737246651
0.30485380178589 A A A LNCV6_134512_PI430048170 mRNA
GGAAGAACTAGAGTGATGTCATGAACATTAAGCTTAACTTATTGTATCTCATCCAAAGAC NM_001136508 RefSeq
chr1 + 51102233 51148082 C1orf185 NA chromosome 1 open reading frame 185 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127713_PI430048170 0.1071694720161780.42364077970205 2.89054721411889
1.44625570046009 3.10251290283054 A A P 3.56841117802992 4.02579897148685
4.00534174576469 P P P LNCV6_127713_PI430048170 mRNA
TAAGCCATCCAGAGTAAAATCTGTTTAGATTATCTTGGAGTAAGGGGGAAAAAATCTGTA NM_001127223 RefSeq
chr11 - 33703009 33722727 CD59 966 "CD59 molecule, complement regulatory protein, transcript variant 5"
GO:0005515|GO:0030449|GO:0043066|GO:0001848|GO:0005886|GO:0009986|GO:0005576|GO:0031982|GO:0031
362|GO:0005615|GO:0042383|GO:0016020|GO:0007596|GO:0045087|GO:0043218|GO:0001971|GO:0042102|GO:0
005925|GO:0001775|GO:0007166|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123420_PI430048170 0.5309951460337611.02311314383951 0.408431083261293
0.2665120452864840.30893663053264 A A A 0.2794523171214340.308425592885766
0.300649209250978 A A A LNCV6_123420_PI430048170 mRNA
GAATGTTTTCCCAAACATGAAGTGATAAGCTTATTCATTTTGGTGGGATTTATAGGAGAG NM_000587 RefSeq chr5
+ 40909496 40982941 C7 730 complement component 7
GO:0006957|GO:0030449|GO:0006956|GO:0005579|GO:0045087|GO:0019835|GO:0006958|GO:0006883|GO:0005
576|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145679_PI430048170 0.0164744256285704 0.4278841540359611.78753882383142
1.70954628333941 2.28009103107547 A A A 3.19380884830017 3.09795187952367
3.22511350724728 P P P LNCV6_145679_PI430048170 mRNA
GAAAGCATCATGCAAATGGCTAATTAAATTGGGTGATGACTGAAAGGTTATAAATCCTTC NM_033110 RefSeq chr13
- 100530163 100533802 GGACT 87769 "gamma-glutamylamine cyclotransferase, transcript variant 1"
GO:0003839|GO:0042219|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141389_PI430048170 0.6173471631036530.9820339347252050.356429991495928
0.4443520281295470.345230426583029 A A A 0.4800055170102530.36645706932657
0.377329331252829 A A A LNCV6_141389_PI430048170 mRNA
GCGCAAAATGCAGCTTTATACTTTTTACTTTCAATTGCCTAGCACAATAGTGAGTACATT NM_033014 RefSeq chr9
- 92383966 92404655 OGN 4969 "osteoglycin, transcript variant 1"
GO:0005515|GO:0005796|GO:0005975|GO:0005578|GO:0048662|GO:0005576|GO:0044281|GO:0005615|GO:0031
982|GO:0042339|GO:0031012|GO:0018146|GO:0042340|GO:0009405|GO:0008083|GO:0030203|GO:0070062|GO:0
043202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130107_PI430048170 0.0392597889226568 1.33849598426063 9.45955402393274
9.74272576154664 9.74817392108268 P P P 9.20393907277711 9.06558945412202
9.41582192752259 P P P LNCV6_130107_PI430048170 mRNA
GTCTAAAACCAAGCTCAGGTTTCTAAGCCACATGACCTTGATTGTTAAATGTAGTTATAT NM_001011667 RefSeq
chr8 + 56211755 56218617 CHCHD7 79145 "coiled-coil-helix-coiled-coil-helix domain containing 7, transcript variant 1" GO:0005758 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144376_PI430048170 0.4186854889860430.5783512000289260.482941878851944

0.3290112770338690.389808709047463A A A 0.46789764588009 0.347199780493318
2.06994975419226 A A A LNCV6_144376_PI430048170 mRNA
TGTGTAAATAACTGAGTAATGCATATGAAATGGAACTTTTGGGTGCCAAATGGGACTTTT NM_001001346 RefSeq
chr6 + 155264012 155276548 CLDN20 NA claudin 20 NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140537_PI430048170 0.0820965712624705 1.3200002668027 8.57403381077189
8.6820778944931 8.78702078807614 P P P 8.0082402657043 8.31330473825746
8.48769502027879 P P P LNCV6_140537_PI430048170 mRNA
GCACCTGGGGGGTTCTGGTTTTTACTTTTTTAATGTAAGTCTCAGTCTTTGTAATTAATT NM_006035 RefSeq chr14 -
102932378 103057405 CDC42BPB 9578 CDC42 binding protein kinase beta (DMPK-like)
GO:0000287|GO:0042641|GO:0031532|GO:0005886|GO:0031032|GO:0005524|GO:0035556|GO:0007165|GO:0050
790|GO:0005083|GO:0005737|GO:0004672|GO:0007163|GO:0016477|GO:0004674|GO:0005911|GO:0007010|GO:0
017048|GO:0006468|GO:0005856|GO:0031252|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_94935_PI430048170 0.3930111869539750.8955413242385861 1.2883712521691 11.31703700437
11.6139910011222 P P P 11.3873771717344 11.4961200960834 11.8035340108416 P P P
LNCV6_94935_PI430048170 mRNA
GGAATGTGGGGATTCTGAAACAGAAATGAAACTGTCCTTTTGACAACTCTCTTATATAAT NM_032359 RefSeq chr3
+ 99817833 100178632 CMSS1 84319 "cms1 ribosomal small subunit homolog (yeast), transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66200_PI430048170 0.3111017239077591.66156362522563 1.94376320576163 1.29787987131107
0.368611175686928A A A 0.4960692598525310.3749905758828260.899112712649234A A A
LNCV6_66200_PI430048170 mRNA
AATGACCCAACATTTAGAAAGGATGAAAGACATGTACAGAGAGCTGTGGGAGACGTGCCT NM_001136486
RefSeq chr11 + 89968503 89974072 TRIM64 120146 tripartite motif containing 64
GO:0005622|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133045_PI430048170 0.00242569852895883 0.4054232949316255.31065373695632
5.39718328435425 5.66866396678014 P P P 6.66610254496353 6.56781926316966
7.03217432820669 P P P LNCV6_133045_PI430048170 mRNA
CATTTGGTTGTGGAATTGTGTGTGGTTTTAGAGGGTTTCTGTTTGTGAAATGTATGTATT NM_016217 RefSeq chr6
+ 139135111 139180809 HECA 51696 headcase homolog (Drosophila)
GO:0003674|GO:0016020|GO:0030323 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136933_PI430048170 0.8875585292203770.9883438964948687.8896213819933
7.94825401160014 7.71209177624656 P P P 7.9932962990995 7.88423148249969
7.72055870360023 P P P LNCV6_136933_PI430048170 mRNA
TCTCTTCTCATATGCAATATCAGTCATTCACAGGGGCGGCCGGTCTCCAAAATGCAAAAT NM_020959 RefSeq chr19
- 17323222 17334829 ANO8 57719 anoctamin 8
GO:0005622|GO:0006821|GO:0034220|GO:0005886|GO:0005229|GO:0016021|GO:0055085 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_101526_PI430048170 0.94657027984807 0.9999925269983169.22399560264265
9.15351517221558 9.13458932014966 P P P 9.38754714856059 9.00936676909214
9.08863629951684 P P P LNCV6_101526_PI430048170 mRNA
CCACCCAGAGTTAGACATTGTTTTTGTAGAAAACAGGCATTTATTATGTCTAGGGTTTTG NM_139265 RefSeq chr15
- 41899440 41972557 EHD4 30844 EH-domain containing 4
GO:0005515|GO:0048471|GO:0006907|GO:0005886|GO:0005783|GO:0005509|GO:0032456|GO:0050731|GO:0005
634|GO:0003676|GO:0005525|GO:0005524|GO:0071363|GO:0016020|GO:0030100|GO:0031901|GO:0051260|GO:0
055038|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73378_PI430048170 0.7834436834122940.9502699090998490.4527040148982671.40226657923062
0.377393656426674A A A 1.19797596857979 0.9629539201408440.427835966682637A A A

LNCV6_73378_PI430048170 mRNA
CTCTGCTCTTCTGTGATCTTAAAACAAAATGAAATAAACGTGAAAAGGAGATGTGTCTTC NM_002338 RefSeq chr3
- 115802362 116445538 LSAMP 4045 limbic system-associated membrane protein
GO:0005515|GO:0043005|GO:0016337|GO:0050767|GO:0009986|GO:0005886|GO:0005911|GO:0043025|GO:0031
225|GO:0035641|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133903_PI430048170 0.2093750621743271.29380075107455 1.31680803255431
0.8417231911098250.685847777135093 A A A 0.5844311705174120.62430150850547
0.597504159442087 A A A LNCV6_133903_PI430048170 mRNA
AGGATCGTCCAACTTTTCACTTACCTTGGGTTTTCTTTTCAATTCACTCTTACACTAGTC NM_134260 RefSeq chr15 -
60488283 60627530 RORA 6095 "RAR-related orphan receptor A, transcript variant 2"
GO:0005515|GO:0010467|GO:2000188|GO:0060850|GO:0006367|GO:0003700|GO:0006805|GO:0008013|GO:0045
599|GO:0043030|GO:0003707|GO:0070328|GO:0005634|GO:0046068|GO:0010906|GO:0006809|GO:0042692|GO:0
001222|GO:0008142|GO:0021702|GO:0045944|GO:0043401|GO:0004879|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140518_PI430048170 0.1696531054993 1.04920897635193 0.506158446963821
0.6127610668650960.516993090503857 A A A 0.4519124923096580.480287701692622
0.49783800191159 A A A LNCV6_140518_PI430048170 mRNA
CTGTGCCATACACTAAAAAACAACTGTTGCCTTCATACTATATTTGTTAGAGCAGAATAC NM_080676 RefSeq chr20
+ 13995499 16053196 MACROD2 140733 "MACRO domain containing 2, transcript variant 1"
GO:0042278|GO:0007420|GO:0016798|GO:0019213|GO:0051725|GO:0005634|GO:0006974 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141789_PI430048170 0.3969044614446141.042415555448 0.290584196396064
0.2819747463322450.448517062163481 A A A 0.2977051378232230.262753654108065
0.286771975791069 A A A LNCV6_141789_PI430048170 mRNA
GGTGATTTCCTCTAAAGAAACTTGGCTGGAATTTCTGCTGTGGTCTATAAAATAAACTTC NM_002652 RefSeq chr7
+ 143132080 143139741 PIP 5304 prolactin-induced protein
GO:0005515|GO:0070233|GO:0002682|GO:0003779|GO:0005634|GO:0005615|GO:0010628|GO:0016324|GO:0001
948|GO:0001895|GO:0019864|GO:0046983|GO:0006508|GO:0004190|GO:0001580|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134421_PI430048170 0.00548237422419483 1.663026470805 7.562651002733
7.85683062989928 7.86974887386474 P P P 7.16850063906099 7.01033172375359
6.91818743671128 P P P LNCV6_134421_PI430048170 mRNA
ACAGTCCAATTGCAGGTTTTCTGCAGAAAAACAAGGCTGGAGGAATGCATCACATCTGCA NM_032601 RefSeq chr2
- 71109675 71130264 MCEE 84693 methylmalonyl CoA epimerase
GO:0006635|GO:0004493|GO:0005759|GO:0019626|GO:0044281|GO:0046872|GO:0046491|GO:0044255 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81129_PI430048170 0.0347383292090652 0.6490167290849348.27962319345601 8.2299111983736
8.35650655170186 P P P 8.75662987307845 8.78435456691619 9.16231751358826 P P P
LNCV6_81129_PI430048170 mRNA
CCCTTAAGTGGCAAAGAAGCTGTTATAGTCTTCTGAAAATTATCACTATGAGTGCTATAA NM_001198807 RefSeq
chr9 + 100427212 100451734 MSANTD3 91283 "Myb/SANT-like DNA-binding domain containing 3,
transcript variant 4" GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103196_PI430048170 0.0192727734028812 0.5976888226549798.41249836300559
8.73635085258262 8.25005265713009 P P P 9.26084369317716 9.31439087211031
9.08450024341618 P P P LNCV6_103196_PI430048170 mRNA
TGGAGGTGGGGCGAGGCAGGCCGACTGTACTAAAGTAACGCAATAAACGCATTATCAGCC NM_004636 RefSeq
chr3 + 50267557 50277171 SEMA3B 7869 "sema domain, immunoglobulin domain (Ig), short
basic domain, secreted, (semaphorin) 3B, transcript variant 1"
GO:0016020|GO:0007411|GO:0005783|GO:0007267|GO:0004872|GO:0070062 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_136076_PI430048170 0.7910019487701070.9840761560942020.28241414368652
0.2907572587929490.499660700108797A A A 0.3320246336735 0.483981003399932
0.331554978096309A A A LNCV6_136076_PI430048170 mRNA
GCACTCTAATGGATAACAATCCAAGAATAAATGATTGTAAAAGATGATGCCGAAGAGTTG NM_014668RefSeq chr2
+ 11534115 11642786 GREB1 9687 "growth regulation by estrogen in breast cancer 1, transcript variant
a" GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131417_PI430048170 0.6590827388250350.8571278276971620.273933549380261
1.18999761920348 0.658572539851421A A A 1.41142931913368 0.294659514291056
1.01970440491273 A A A LNCV6_131417_PI430048170 mRNA
AAATTATCCCCTATGCAGCAAGTTTGATCAGGAAAGAAAAGCTTGGCGCCCATCTCAGCA NM_001278063 RefSeq
chr18 - 47212088 47249183 SKOR2 NA "SKI family transcriptional corepressor 2, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138683_PI430048170 0.1490687737298460.5847202191899153.78542831677822
4.08710297125449 3.99501846969368 P P P 4.93003008599182 4.02924901230066
5.04897119673395 P P P LNCV6_138683_PI430048170 mRNA
CTTCCCAAATCAGCTTCCAATTGGTTTAACCAGTATGCAACATTAAAGATTTTACTCAGA NM_001038603 RefSeq
chr5_GL339449v2_alt + 198534 225032 MARVELD2 153562 "MARVEL domain containing 2, transcript
variant 1"
GO:0005515|GO:0043220|GO:0007605|GO:0031410|GO:0045216|GO:0016323|GO:0005737|GO:0016324|GO:0033
010|GO:0070830|GO:0061028|GO:0005923|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144138_PI430048170 0.4896362072873991.02167013467057 0.502963965184989
0.45868507127924 0.394940832690102A A A 0.3712058818645830.445974545965852
0.447352085338846A A A LNCV6_144138_PI430048170 mRNA
CTCTAAAGACTGAAATATTTCCTAAAATGTATGGGCACTGTTTACCAGAAAGTACCTTAG NM_021915RefSeq chr19
+ 11887854 11914550 ZNF69 7620 zinc finger protein 69
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132646_PI430048170 0.0132453743131429 0.6928157731357779.89240094339573
9.76240031107073 9.56448255463867 P P P 10.1439865068326 10.3152998068558
10.3583079751856 P P P LNCV6_132646_PI430048170 mRNA
GGGCTCAGCACGAAAGGGCTTTCAATGAATTAAGTGAAAACTTTTTCCTTTTTTACAAAA NM_001080419 RefSeq
chr17 + 75784838 75825805 UNK 85451 "unkempt family zinc finger, transcript variant 1"
GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142793_PI430048170 0.5355778162784621.88241780243446 3.06881237927521 0.3250445160657
1.22683607893238 A A A 0.3671373077478270.3347406222372371.93182284485266 A A A
LNCV6_142793_PI430048170 mRNA
GCGGGTGAGAATGGGTCTGTAATTTCTCTAAGATGAATAAAGGGGCAGTAAATGAAAAAA NM_032266RefSeq chr2
+ 27576521 27582722 C2orf16 84226 chromosome 2 open reading frame 16 GO:0005634|GO:0070062
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136855_PI430048170 0.0257749698983094 0.6128744366133282.83387378230243
2.4988322968902 2.30633554909727 A A A 3.16249743469751 3.51735525974193
3.09122760211761 P P P LNCV6_136855_PI430048170 mRNA
CAGCTGGGTGGTGTAAAAAATGAACTTCAAATTATGGAGTGGAAAAAGCGTAATGTTAAT NM_025047RefSeq chr3
+ 160677159 160678447 ARL14 80117 ADP-ribosylation factor-like 14
GO:0005515|GO:0007264|GO:0016023|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119776_PI430048170 0.3767937144525260.8256444045074334.31208050903083
4.11123125539781 4.32789965751221 P P P 4.44311086087547 4.14982460301673
4.89778391583534 P P P LNCV6_119776_PI430048170 mRNA

ACGCAAAATGCCCTTCAATGGCGAGAAGCAGTGTGTGGGAGAGGACCAGCCAAGCGATTC NM_152772 RefSeq
chr12 + 106302790 106347014 TCP11L2 255394 "t-complex 11, testis-specific-like 2, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144880_PI430048170 0.6389342415941951.04997679446516 4.49516919077248
4.47031125688903 4.56351652196121 P P P 4.15017905056625 4.41979347551125
4.69772341625859 P P P LNCV6_144880_PI430048170 mRNA
CTGAAGTACTGTGGGGCTGTCCTCTGTATACTGACATTAAATAAACGTGTGTGAGTGAAC NM_001242415 RefSeq
chr14 + 102139851 102215004 WDR20 91833 "WD repeat domain 20, transcript variant 5" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_128025_PI430048170 0.0223377231976499 0.6434425679497010 3.3772472300588
10.1305944144799 10.4117418854803 P P P 10.7172021576476 10.9121160250568
11.1773844461028 P P P LNCV6_128025_PI430048170 mRNA
AGGCTGGGCCCAGGAGGTCAGGTTCATTTTGTTACATATGCAATAAACTCACGACTTTAC NM_020429 RefSeq chr7
- 99027434 99144120 SMURF1 57154 "SMAD specific E3 ubiquitin protein ligase 1, transcript variant
1"
GO:0005515|GO:0030424|GO:0004842|GO:0016567|GO:0005886|GO:0016874|GO:0005634|GO:0030154|GO:0005
829|GO:0030514|GO:0005737|GO:0030279|GO:0042787|GO:0048185|GO:0006611|GO:0043025|GO:0007179|GO:0
030579|GO:0030512|GO:0070062|GO:0000209|GO:0070411|GO:0070412|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138201_PI430048170 0.0172987937589372 1.41259322141486 11.7522691992836
12.0161423729687 11.7905977494611 P P P 11.4049161574359 11.3690272800692
11.3024865170335 P P P LNCV6_138201_PI430048170 mRNA
AAGTGGACTAAAGTATTAAACCCTCTAGCTCCCATTGGCTGAAGACACTGAAGTAGCCCA NM_017823 RefSeq chr1
+ 159780968 159782543 DUSP2354935 dual specificity phosphatase 23
GO:0005634|GO:0008138|GO:0035335|GO:0004725|GO:0070062|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_67258_PI430048170 0.6468615326853151.02949964019381 0.2768004978755470.285754203375239
0.495621661749105 A A A 0.3331988389702160.2861727130998330.323346470739596 A A A
LNCV6_67258_PI430048170 mRNA
GTGTTATAATACGGGAAAATTTTGTACTGACAACAGCAAAATGTTCACTGTTACACAGGA NM_001256134 RefSeq
chr13 + 113158653 113172384 PROZ 8858 "protein Z, vitamin K-dependent plasma glycoprotein,
transcript variant 1"
GO:0017187|GO:0004252|GO:0007596|GO:0005796|GO:0005509|GO:0006508|GO:0005788|GO:0044267|GO:0070
062|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128092_PI430048170 0.00623523275818171 2.90033567794696 3.24386433116638
3.57064074720868 3.36717811092339 P P P 1.49516940401435 2.17067233760738
1.84770920715114 A A A LNCV6_128092_PI430048170 mRNA
ACTATGTTGAGCTAACACAGACCTGCTGAATCAGCTTCTTTCTGAGCTGCCAGAAGTACA NM_001006114 RefSeq
chr21 + 46286352 46292197 YBEY 54059 "ybeY metallopeptidase (putative), transcript variant 2"
GO:0005739|GO:0006364|GO:0006508|GO:0005654|GO:0005634|GO:0004222|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140538_PI430048170 0.1503377507871381.28287675677988 3.74498610273084
3.49400260596748 3.51359410134223 P P P 3.48100104060005 3.25951274041986
2.88633471869529 P P P LNCV6_140538_PI430048170 mRNA
AGAGCCGCGTGGTCAAGTGCAGCGCCAACCCCATCTTCAACGAGGATTTCTTTTTCGACG NM_001136003 RefSeq
chr1 - 151837862 151840557 C2CD4D NA C2 calcium-dependent domain containing 4D NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130111_PI430048170 0.9732195372606140.9898684969830791 2.5092090214238
12.4339184761024 12.5325229393128 P P P 12.3050491115185 12.4591975117857

12.7255974213845 P P P LNCV6_130111_PI430048170 mRNA
GTTCCTCTGGATTCACCATCTGTTGAGTTGTAAATGTGAGAGAAAAAGTTATATGTGAAT NM_001184986 RefSeq
chr4 - 139289916 139301210 NDUFC1 4717 "NADH dehydrogenase (ubiquinone) 1, subcomplex
unknown, 1, 6kDa, transcript variant 1"
GO:0022904|GO:0005739|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0016021|GO:0008137|GO:0044
237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128124_PI430048170 0.4204659677570840.8169572049300662.18267333686206 2.438327321464
2.44603177849568 A A A 2.46617185868282 2.26764755391672 3.09095431962236 A A P
LNCV6_128124_PI430048170 mRNA
GCACATTACTTTTGCACCAACCGACCTAATATGACTTTCTTTTAGTGTTCTTAGGATTTT NM_018225 RefSeq chr9 -
33041851 33076716 SMU1 55234 smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)
GO:0005515|GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68632_PI430048170 0.0181725352856896 0.4180023805870310.323215250881207
0.2452153109909570.290647652397759 A A A 1.20773092970243 1.81389013943269
1.55054716926501 A A A LNCV6_68632_PI430048170 mRNA
TGTTCGAGAACGTCCAGTGCTGGACCAGCAATGACAACATGGGCTTCTGGTGGATCCTGC NM_000160 RefSeq chr17
+ 81804131 81814013 GCGR 2642 glucagon receptor
GO:0005886|GO:0007584|GO:0044281|GO:0042593|GO:0006091|GO:0070873|GO:0006887|GO:0004967|GO:0043
547|GO:0005085|GO:0042594|GO:0006112|GO:0009755|GO:0071377|GO:0005887|GO:0008217|GO:0007188|GO:0
016021|GO:0007189|GO:0017046|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88844_PI430048170 0.196715618668068 0.8965413464642181 1.6667463118177 11.9382663694635
11.7898990271024 P P P 11.8628730740512 11.9264934930833 12.0821546976656 P P P
LNCV6_88844_PI430048170 mRNA
TAAGTCTGGAATGAATGTGGCTCGTCTGAACTTCTCTCATGGAACTCATGATACCATGCG NM_001206796 RefSeq
chr15 - 72199028 72231386 PKM 5315 "pyruvate kinase, muscle, transcript variant 4"
GO:0005515|GO:0000287|GO:0005886|GO:0005975|GO:0005634|GO:0044281|GO:0030955|GO:0012501|GO:0031
982|GO:0005524|GO:0006096|GO:0005829|GO:0031012|GO:0005739|GO:0016310|GO:0005929|GO:0005737|GO:0
023026|GO:0009405|GO:0006006|GO:0004743|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_65294_PI430048170 0.0166202648347408 1.32298354828249 8.24353604020968
8.16221297410492 8.30803331630923 P P P 7.68079458153237 7.91965044382947
7.89393672295695 P P P LNCV6_65294_PI430048170 mRNA
CCTATTGGACCCCAGAGGTCATCCCAGCTCCAGACGTGGACACATTTTCTTCCAATGATG NM_014480 RefSeq chr19
+ 58228703 58263642 ZNF544 27300 zinc finger protein 544
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136482_PI430048170 0.4098768628654280.7782100937565124.12399320447437
3.60895959440995 3.51043319278687 P P P 3.49165033533892 4.29328402880562
4.45102786418484 P P P LNCV6_136482_PI430048170 mRNA
CCCGGCACAATGATTGTGAAAGAACTGACATTTAACTTTGAAGGTATTTTTAACTTGTAC NM_198566 RefSeq chr5
- 43486700 43515171 C5orf34 375444 chromosome 5 open reading frame 34 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_140482_PI430048170 0.11439508353565 1.07134729887226 0.478262057419331
0.58965915543167 0.539909355043713 A A A 0.3669154450441860.44751448760245
0.494406393505327 A A A LNCV6_140482_PI430048170 mRNA
TGCAGGCTGCATGGCAGAATCATCAAATCTCATCATCTCCATCCTTTTTGTTATATGGGA NM_001079935 RefSeq
chr19 + 9251043 9252063 OR7E24 26648 "olfactory receptor, family 7, subfamily E, member 24"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_64340_PI430048170 0.4845941751148711.09735089754601 4.70000832482506 4.93633452894288
4.99717157573766 P P P 5.00086776049116 4.44259930846089 4.75106455388587 P P P
LNCV6_64340_PI430048170 mRNA
AATGACAAGAGGCTACAGTGGATGGAAACTCTGTGACTGTAAGAATTGTGGAGAGGTCTT NM_152289 RefSeq chr19
- 9607325 9621240 ZNF561 93134 zinc finger protein 561
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_92986_PI430048170 0.3051062573081721.5344464587083 2.94064916593757 2.60556122031557
2.54034044759752 A A A 1.89408551282621 2.89555209809771 0.680663421603688 A P A
LNCV6_92986_PI430048170 mRNA
AATGACAGTCGAGCTTTGGCTAAGGCTCCGGGGAAAGGGTCTAGCCATGCTGCATGTGAC NM_018273 RefSeq chr19
- 48332355 48364237 TMEM143 55260 "transmembrane protein 143, transcript variant 1"
GO:0005739|GO:0008150|GO:0003674|GO:0002244|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_69517_PI430048170 0.2022261809155981.24746012446842 9.4077996998029 9.72478730261088
9.55989317518131 P P P 9.45040277009557 9.37097657062376 8.86455141603781 P P P
LNCV6_69517_PI430048170 mRNA
GACGGGGCCGCCCCGATGGGACGCCGCGCTCCGGCCCCTGCGCGCCGCTGAGCCGAGCGC NM_005892 RefSeq
chr17 + 45221924 45247316 FMNL1 752 formin-like 1
GO:0005515|GO:0005886|GO:0006929|GO:0008360|GO:0005829|GO:0051014|GO:0032794|GO:0045335|GO:0048
365|GO:0003674|GO:0051015|GO:0032059|GO:0016020|GO:0030866|GO:0005522|GO:0005938|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145538_PI430048170 0.86867797997645 0.8852646124837682.53713074622342
0.3331652277051770.881499264334258 A A A 0.4351565075379091.10342781123778 2.7136990770312
A A P LNCV6_145538_PI430048170 mRNA
CCCTACCCTCTAGAGAAATAAGATCTTTTTTGTCAGTTTGTTTGTATGAAACTAAAGCCT NM_000429 RefSeq chr10
- 80271819 80289678 MAT1A 4143 "methionine adenosyltransferase I, alpha"
GO:0034641|GO:0006520|GO:0006805|GO:0000096|GO:0006556|GO:0044281|GO:0032259|GO:0006730|GO:0005
524|GO:0004478|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142931_PI430048170 0.4055863138751471.27852716359582 0.335910562533111
0.3395536155701251.18734346814644 A A A 0.32456769571144 0.297124040302514
0.352923949106615 A A A LNCV6_142931_PI430048170 mRNA
TTTGCCTTGAAACAGAAATCCATGTTGGGAGATGTTTAAATAGCCAACCCTGCTGCCTGC NM_001002035 RefSeq
chr11 + 71833199 71837562 DEFB108B NA "defensin, beta 108B" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139559_PI430048170 0.0978868768181142 0.5861882378335152.41157163783446
2.84577672151035 2.66911027759315 A A A 3.01858827325198 3.18985623194675
3.90321152455496 P P P LNCV6_139559_PI430048170 mRNA
TACTGATCACAATTCTAATCCCCATCAAGCAATGTACAGATAACTCTTCCAAGAAATGTT NM_001142645 RefSeq
chr2 - 190506892 190534742 TMEM194B NA transmembrane protein 194B NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_130358_PI430048170 0.0414957093940411 1.21769106441053 7.01384804353633
7.05654234507758 6.82896218680352 P P P 6.81325456485486 6.62215346362777
6.61248134367528 P P P LNCV6_130358_PI430048170 mRNA
TGTGGCTGATATTAACTGTCAATGGTTATGGGTCCTATAAAAATGCCCCTCCCAGATAAA NM_006563 RefSeq chr19
- 12884422 12887203 KLF1 10661 Kruppel-like factor 1 (erythroid)
GO:0000987|GO:0000790|GO:0003700|GO:0044212|GO:0005634|GO:0001701|GO:0046872|GO:0006351|GO:0001
889|GO:0043249|GO:0030218|GO:0006338|GO:0045893|GO:0035162 . NA - . NA NA NA NA NA NA
NA NA NA

LNCV6_131963_PI430048170 0.1146453247534121.26082821336035 6.44548929101336
6.45829655270037 6.65799472891779 P P P 6.38021829381631 5.91215091844089
6.23727734072953 P P P LNCV6_131963_PI430048170 mRNA
CAGTTTGTGATATAGCAGAGGTTTAAATGTACCCTCCCCTTTTATGCACTTCAAATAATT NM_006618RefSeq chr1
- 202727403 202808421 KDM5B 10765 lysine (K)-specific demethylase 5B
GO:0005515|GO:0003700|GO:0003714|GO:0006325|GO:0005634|GO:0003677|GO:0006351|GO:0034720|GO:0005
737|GO:0034721|GO:0034648|GO:0034647|GO:0016706|GO:0005654|GO:0008270|GO:0048511|GO:0045892|GO:0
055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134573_PI430048170 0.2333501514141210.5952377974132590.371394557936898
2.14899417490689 0.385185274905728A A A 2.33608030115018 1.86510362980573
1.64443992073176 A A A LNCV6_134573_PI430048170 mRNA
CTTCAAGGCCTGATTCAGATTTTAACTTTTTAAAGGCTATCTGAATCATTCAAGGAGAAG NM_004707RefSeq chr5
- 115828196 115841851 ATG12 9140 "autophagy related 12, transcript variant 1"
GO:0006995|GO:0006501|GO:0005515|GO:0034045|GO:0000422|GO:0045087|GO:0019776|GO:0034274|GO:0000
045|GO:0032480 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54120_PI430048170 0.3652274892430261.4350055976892 0.3743187613636641.50281846214161
0.448600050033001A A A 0.3203975456560120.3656031474247140.369706005584543A A A
LNCV6_54120_PI430048170 mRNA
TTACACACTGACCTTTATAAATTTCTAACAAAGAGAGGTGAGAAGATGACTCGAGAAGAA NM_032437RefSeq chr1
+ 63523300 63572693 EFCAB7 84455 EF-hand calcium binding domain 7 GO:0005509|GO:0072372 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57116_PI430048170 0.0270004514454687 1.49677740020304 7.45141060215354
7.71318910110885 7.30735732983559 P P P 7.03994661200654 7.02183114164336
6.66404947373553 P P P LNCV6_57116_PI430048170 mRNA
TTTTTATTCCACGCTGTGCTGTTTGGATGGGAGCCCCACAGAGGCAGGTCCTGGAACCAC NM_020896RefSeq chr11
- 3087115 3165352 OSBPL5 114879 "oxysterol binding protein-like 5, transcript variant 1"
GO:0016020|GO:0008142|GO:0015485|GO:0005789|GO:0030301|GO:0016021|GO:0006893|GO:0008203|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132079_PI430048170 0.0311753554861278 0.7673685647069561 0.5656614308602
10.5214396406013 10.5755676088436 P P P 10.8300516637629 10.8911257348839
11.0765308147852 P P P LNCV6_132079_PI430048170 mRNA
CATCTTACCTAGCCCACCCAACCTTATAAACATGATAATTGACTACTTTCCTGAGCTAAA NM_006833RefSeq chr7
+ 100088959 100092199 COPS6 10980 COP9 signalosome subunit 6
GO:0005515|GO:0005737|GO:0008180|GO:0010388|GO:0016032|GO:0005654|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140066_PI430048170 0.4985065667168560.4844023969604670.410352502836878
0.4215752043113670.742749291351364A A A 2.66509521103679 0.372676344129406
0.406738194440847A A A LNCV6_140066_PI430048170 mRNA
GTCAAGACCAAGCAAATCCGTGAGAGCATCTTGGGAGTATTCCCAAGAAAGGATATGTAG NM_001005172 RefSeq
chr11 + 4449294 4450361 OR52K2 119774 "olfactory receptor, family 52, subfamily K, member 2"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134879_PI430048170 0.5567575245749230.5286282903793620.567639871961855
0.7202791949726670.723820792876233A A A 2.65836821853041 0.443255659069947
0.455846310791132A A A LNCV6_134879_PI430048170 mRNA
CATTTTGGGAAGATATATTGGGTTCACATTCTGGAGTTCTCTTTATTTTCCACCACAAAA NM_144633RefSeq chr3
+ 19148524 19535643 KCNH8 131096 "potassium channel, voltage gated eag related subfamily H,
member 8"
GO:0023014|GO:0000160|GO:0005886|GO:0005887|GO:0005249|GO:0042391|GO:0007268|GO:0034765|GO:0000

155|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128615_PI430048170 0.000691526422955734 6.77481469630972 5.58365155748147
5.46542089001087 5.7305857972333 P P P 2.90444096894425 2.51297408741011 3.0431024895775
P P P LNCV6_128615_PI430048170 mRNA
TGTCGCTGGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAACTGAGCTACGA NM_139250 RefSeq chrX
- 154617608 154619271 CTAG1A 246100 cancer/testis antigen 1A GO:0005515|GO:0005737 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_135331_PI430048170 0.389600919352933 1.23703953758372 0.370852535814967
0.375352549098659 1.10072776071991 A A A 0.347699743938257 0.326834772665141
0.379420050102387 A A A LNCV6_135331_PI430048170 mRNA
CCTGCTGTGTCCACAACCTTAGAAATCTGTAGCTAGATTTTTGTTGTTATAGATAGAATT NM_198795 RefSeq chr10
+ 114179269 114232304 TDRD1 56165 tudor domain containing 1
GO:0010467|GO:0051321|GO:0007275|GO:0007283|GO:0031047|GO:0007281|GO:0046872|GO:0033391|GO:0005
737|GO:0034587|GO:0071546|GO:0043186|GO:0043046 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134244_PI430048170 0.000422075466228538 0.463366772405842 9.94783651522274
10.0227643609402 9.9714760158491 P P P 11.0304777068715 11.0492174591976 11.18756600761
P P P LNCV6_134244_PI430048170 mRNA
TGTGGGAACACCTTGTACCTGAGCTTACAGGTACCAATAAAGAGGCTTTATTTTTAGCAA NM_033027 RefSeq chr3
- 39141850 39153611 CSRNP1 64651 cysteine-serine-rich nuclear protein 1
GO:0003700|GO:0006915|GO:0048705|GO:0005634|GO:0001228|GO:0009791|GO:0006351|GO:0043565|GO:0003
674|GO:0060325|GO:0045944|GO:0060021|GO:0048008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128486_PI430048170 0.910994694576909 0.996429878718554 0.447845054620478
0.413997662855812 0.280944172580961 A A A 0.350078918030589 0.409327750368884
0.403464795384438 A A A LNCV6_128486_PI430048170 mRNA
GTCTGTTGAGTGATTAAATCACATCCTCAGGTCTGCAGCAAATAAATGAAAGTTTCTTTA NM_145282 RefSeq chr5
+ 135834675 135888637 SLC25A48 153328 "solute carrier family 25, member 48"
GO:0005743|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136664_PI430048170 0.0157890984962182 0.587716554316704 7.7368807206255
7.31282518583575 7.76685009747924 P P P 8.26579661227379 8.27537517280155
8.59413646273126 P P P LNCV6_136664_PI430048170 mRNA
GTATCCCCTTCCCACTTATATATTGTGTGATATGATTTTGCTTGCCTATAGGAGTTAAAA NM_003931 RefSeq chr6
- 110099818 110180004 WASF1 8936 "WAS protein family, member 1, transcript variant 1"
GO:0005515|GO:0031209|GO:0030054|GO:0006928|GO:0045202|GO:0003779|GO:0015629|GO:0032403|GO:0048
365|GO:0016601|GO:0006461|GO:0030041|GO:2000601|GO:0005856 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_54761_PI430048170 0.126766982764222 1.44118052412162 3.75845758087898 3.72093982250054
3.60173672282533 P P P 3.52464403142738 2.7376076669649 3.13514489430369 P P P
LNCV6_54761_PI430048170 mRNA
AGAAGAAAAGAAAAACCACAAACTTCCTTTGAAAACCAGCTTGTAGTCAGGGCCCGGAGC NM_018379 RefSeq
chr1 - 150996824 151008378 FAM63A 55793 "family with sequence similarity 63, member A,
transcript variant 1" GO:0008150|GO:0005654|GO:0005634|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_130165_PI430048170 0.434273326829751 1.03288138837841 0.444731550300367
0.287349356424142 0.341824480764045 A A A 0.280887541749307 0.327590376556188
0.329332439394262 A A A LNCV6_130165_PI430048170 mRNA
CCACCTCATTCATATATTTGAGCTTCAGAAATACATGTACCTAGTATAATGCTTAACAGC NM_001166417 RefSeq
chr1 - 84643706 84690468 SSX2IP 117178 "synovial sarcoma, X breakpoint 2 interacting protein,
transcript variant 1"
GO:0005515|GO:0035020|GO:0034451|GO:0019904|GO:2000145|GO:0005634|GO:0036064|GO:0051297|GO:0042

384|GO:0043234|GO:0005913|GO:0035735|GO:0007155|GO:0031252 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127476_PI430048170 0.6886099298622140.8598803107138450.286848105357369
0.3123090441278242.25870051899008 A A A 0.3263480251368672.11990465105583
1.49964998608536 A A A LNCV6_127476_PI430048170 mRNA
GTTCACACTATTTCTGTTTTACAGCAGTTTTGAAAAACACATACTATGCCACCAATTGTC NM_001199835 RefSeq
chr7 + 26291894 26374329 SNX10 29887 "sorting nexin 10, transcript variant 1"
GO:0005813|GO:0005783|GO:0030316|GO:0005634|GO:0015031|GO:0006897|GO:0005545|GO:0016050|GO:0042
384|GO:0031313|GO:0071539|GO:0051117|GO:0007032 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90809_PI430048170 0.00961031893839328 0.6443883783489915.57137904897138
5.34968225962206 5.32647137410856 P P P 5.92384183113775 5.96580128912742
6.25042283018306 P P P LNCV6_90809_PI430048170 mRNA
AATTGCGAATATTCTGGCCCACCAAAACCATTGCCAAAGGATGGATATGACTTAGTGCAG NM_000271 RefSeq chr18
- 23531498 23586617 NPC1 4864 "Niemann-Pick disease, type C1"
GO:0031579|GO:0005515|GO:0015248|GO:0048471|GO:0005783|GO:0016242|GO:0005635|GO:0030301|GO:0005
765|GO:0005764|GO:0015485|GO:0060548|GO:0007628|GO:0004872|GO:0008206|GO:0070062|GO:0008203|GO:0
042632|GO:0033344|GO:0005794|GO:0090150|GO:0042493|GO:0006914|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_108389_PI430048170 0.0839581424126856 0.7460314571341443.79612321456075
4.04108860396733 4.13783546936082 P P P 4.47157475055216 4.13393267320105 4.6171414338657
P P P LNCV6_108389_PI430048170 mRNA
GCTGCCAAAAAGCTTGAGCAGTCAAAAGAGGCAGATATAGATTCCAGTGATGAGAGTGAT NM_017437 RefSeq
chr14 + 92121953 92164199 CPSF2 53981 "cleavage and polyadenylation specific factor 2, 100kDa"
GO:0005515|GO:0006379|GO:0008380|GO:0006369|GO:0006378|GO:0010467|GO:0006398|GO:0006366|GO:0003
723|GO:0031124|GO:0006406|GO:0016020|GO:0000398|GO:0005847|GO:0005654 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140788_PI430048170 0.1625726590133141.13392024932696 12.9390276306254
12.6868707101339 12.9066619942408 P P P 12.542243698853 12.6679864909956 12.781294954737
P P P LNCV6_140788_PI430048170 mRNA
ATTGAGATGGAACTCTCCAAGTACCTGCGGGATTACTCAAGGACTATTCCAGGAAAACAG NM_001166285 RefSeq
chr2 + 73234235 73253022 CCT7 10574 "chaperonin containing TCP1, subunit 7 (eta), transcript
variant 4"
GO:0005515|GO:0005832|GO:0005874|GO:0007339|GO:0005524|GO:0044297|GO:0005829|GO:0042802|GO:0005
739|GO:0005737|GO:0006457|GO:0051084|GO:0002199|GO:0051082|GO:0044267|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136072_PI430048170 0.3242277242897091.28523266000054 1.48565369030237
0.8333582150579650.673496423512982A A A 0.5825402673562920.620218691393531
0.825133656035473A A A LNCV6_136072_PI430048170 mRNA
CAGGGTGGAGAGGAATAAGAGACTAAGTATATGCTTCAAGTTTTAAATTAATACCTCAAG NM_006495 RefSeq chr17
- 31303769 31314112 EVI2B 2124 ecotropic viral integration site 2B GO:0005887 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142607_PI430048170 0.1413865288738271.17549792672842 9.65043335908071
9.60012418029114 9.60373373955927 P P P 9.29350260992936 9.25662566897064 9.582369927661
P P P LNCV6_142607_PI430048170 mRNA
TGCTGGTGTGTTTTCCAATGGCCAGTGATAAGAAATTAAATAAGTATTTGTGAGATTTGC NM_015439 RefSeq chr6
+ 138773519 138793319 CCDC28A 25901 coiled-coil domain containing 28A NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_22030_PI430048170 0.0567270203522106 1.04764666874 0.3466819547484960.340463598413954
0.28478894560674 A A A 0.2455666701451120.2772473069889450.248250964844848A A A

LNCV6_22030_PI430048170 mRNA
AACTATAAAGGAAAATCGGGTGAGCAGGTGGGATAGTCAAGTGATTCTATTTGCATGAAT NM_001100111 RefSeq
chr9 - 88647178 88652160 LOC286238 NA uncharacterized LOC286238 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_142339_PI430048170 0.0590853845794414 1.292166627172 4.88232211590665
4.92927995272206 5.08747083262721 P P P 4.80169922047187 4.41542787580384
4.55383456499395 P P P LNCV6_142339_PI430048170 mRNA
GGCTAGAAAAGAATGTAATCTGATATGGAAGGATAGCAGCTTCTAATTTTCAATCATCTG NM_018423 RefSeq chr12
- 10618938 10674292 STYK1 55359 serine/threonine/tyrosine kinase 1
GO:0005515|GO:0005886|GO:0045087|GO:0042127|GO:0005102|GO:0016021|GO:0038083|GO:0007169|GO:0005
524|GO:0004715|GO:0030154|GO:0031234 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145054_PI430048170 0.3526375697214520.9192484058641487.54373430228068
7.31240515356909 7.29750646720075 P P P 7.34117972689787 7.61101003820331
7.56512759907656 P P P LNCV6_145054_PI430048170 mRNA
GGAATCGTCAGAGTCCAATGTGTGCCTCTACAGTAATGTCGGAAATAAATACCATTCTTG NM_005993 RefSeq
chr17_KI270860v1_alt - 158238 177991 TBCD 6904 tubulin folding cofactor D
GO:0005515|GO:0031115|GO:0005874|GO:0034333|GO:0051087|GO:0048487|GO:0010812|GO:0055085|GO:0016
328|GO:0043547|GO:0005737|GO:0070830|GO:0005912|GO:0006457|GO:0051084|GO:0005923|GO:0007023|GO:0
044267|GO:0005096. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143594_PI430048170 0.0480715612435718 1.25831271439779 9.18711181023885
9.34872295432394 9.09032510223718 P P P 8.86815793906562 8.89046929034753 8.8848586757042
P P P LNCV6_143594_PI430048170 mRNA
GGGGCTTGCCCCACCTTCTACATTCCAATTTTTATATCTTTGAATTATGTGATTAGATAT NM_001037335 RefSeq chr20
- 63558085 63574239 HELZ2 85441 "helicase with zinc finger 2, transcriptional coactivator, transcript
variant 1"
GO:0005515|GO:0030374|GO:0016020|GO:0045944|GO:0004386|GO:0005654|GO:0044281|GO:0005524|GO:0003
677|GO:0046872|GO:0044255|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88175_PI430048170 0.7211194985523381.13146561610644 2.3338665883923 3.35131583853352
2.59419750678517 A P A 2.11208700997841 2.87073380500656 2.84300235707663 A P P
LNCV6_88175_PI430048170 mRNA
AGATCGTGGCTGTGAGCTGCCGGGAGAAGTTCGTCCGCATCTTCAACCCGTCGCAGGAGA NM_173573 RefSeq
chr11_KI270832v1_alt - 84489 90434 LMNTD2 256329 lamin tail domain containing 2 GO:0048026
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110372_PI430048170 0.2577150308151211.13964041153099 6.25465598684217 6.2206007895164
6.45694177874457 P P P 5.87237996069739 6.24884080461231 6.22670439524612 P P P
LNCV6_110372_PI430048170 mRNA
GTGTCCTCTCAAGGGAGCAAGTGGATGCCCTGGGGCTGAGAGGAGTCTTCTGGTGCAGTC NM_173531 RefSeq
chr19_GL383575v2_alt - 85230 128818 ZNF100 163227 zinc finger protein 100
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_104586_PI430048170 0.18112341266589 0.7616530348897574.19854051400934
3.46530814676512 3.71852072941058 P P P 4.06229803628406 4.17980017071926
4.39651447791834 P P P LNCV6_104586_PI430048170 mRNA
GGCTCTATCAAAGAAAGCAAGAGATGGAAAATTGTTGCCTGAAGAATACCAAGGAGGATC NM_003477 RefSeq
chr11 + 34916129 34996128 PDHX 8050 "pyruvate dehydrogenase complex, component X,
transcript variant 1" GO:0010510|GO:0016746|GO:0006090|GO:0005759|GO:0044281|GO:0044237 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142121_PI430048170 0.0967210511032263 1.0393029461274 0.460094406598706
0.4356047711646460.446815375415646A A A 0.3513067207551080.410092492400935

0.413526928374396 A A A LNCV6_142121_PI430048170 mRNA
CTCACTTTGTAAATAAAAACACACCTTAAAACATGAACAAGCCAAAACTGTGTGCAGACA NM_080685 RefSeq chr4
+ 86594314 86815175 PTPN13 5783 "protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95
(Fas)-associated phosphatase), transcript variant 4"
GO:0005515|GO:0043005|GO:0005886|GO:0005634|GO:0014066|GO:0030027|GO:0035335|GO:0044297|GO:0005
737|GO:0006470|GO:0005856|GO:0004725|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143048_PI430048170 0.0827890372292460.528446512258957 2.72932548140591
2.30656537024231 3.42099175362303 A A P 3.56128130486953 3.50986967684575
4.24662558993903 P P P LNCV6_143048_PI430048170 mRNA
CTCAGTTTACAGAATGGGATCTGAAACTACAGCTTTTTGCTATTAAACCAAATACTTGTG NM_001142684 RefSeq
chr13 - 19823483 19863636 ZMYM5 9205 "zinc finger, MYM-type 5, transcript variant 3"
GO:0008270|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133810_PI430048170 0.5129055561388180.7529891797425270.36596813635054
0.41661728676363 0.339985132553691 A A A 0.28267366179444 0.304551956528408
1.44023129036479 A A A LNCV6_133810_PI430048170 mRNA
ATTATCCTTGATGAAACTCAGAATTTCCACAGTGGGAATGAATAAGAAGGCAAAACTCAT NM_018042 RefSeq chr17
- 35410921 35432524 SLFN12 55106 "schlafen family member 12, transcript variant 1" GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126734_PI430048170 0.4970432909942911.10939518139981 4.31657853416581
3.77247091652838 4.03077055786698 P P P 4.06191700466218 3.88705664368137
3.75654173427389 P P P LNCV6_126734_PI430048170 mRNA
TGTATCTCTAATCCCTGTGGCCTACGTGCTCGGTGTGGGCCTTGCAACACATTTGGGTAC NM_004138 RefSeq
chr17_GL383564v2_alt + 89448 94168 KRT33A 3883 "keratin 33A, type I"
GO:0005882|GO:0005198|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96904_PI430048170 0.0912520820529544 0.7504707762902976.17017033892481
5.70903003366835 5.71048732981833 P P P 6.19801412492698 6.42622815563693
6.24831559682878 P P P LNCV6_96904_PI430048170 mRNA
CATCCACACACTTCTGCCCCCACTGCATTGAATTTTTTGCTTATGTTGTTTATAATAAAA NM_018326 RefSeq chr7 +
150567369 150573953 GIMAP455303 "GTPase, IMAP family member 4" GO:0005525|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145115_PI430048170 0.0905663555928509 1.09965991045876 0.583778845057228
0.6905032151137020.675364613875192 A A A 0.6104112422742930.457623532420791
0.467614939796436 A A A LNCV6_145115_PI430048170 mRNA
GGAGTGAAGACCAAGCAAATTCGTGACCATATTGTGAAAGTGTTTTTCTTCAAAAAAGTA NM_001005160 RefSeq
chr11 - 5131691 5132642 OR52A5 NA "olfactory receptor, family 52, subfamily A, member 5" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135592_PI430048170 0.1841740670197660.7875550273278660.387728683019897
0.3998756315670150.333968563087524 A A A 0.6444937585538430.446703175517841
1.00787123259736 A A A LNCV6_135592_PI430048170 mRNA
CAAGTATAATAATTGCCTTTATTACAGCTCTGGCTGAGTGTTCAGCCTGAGGATATTTTT NM_024503 RefSeq chr1
- 41506364 41918707 HIVEP3 59269 "human immunodeficiency virus type I enhancer binding protein 3,
transcript variant 1" GO:0005737|GO:0005634|GO:0045893|GO:0035914|GO:0003677|GO:0046872|GO:0006351
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133885_PI430048170 0.0229929279694907 0.3882112141358232.35920764349005
2.70703769971568 1.88583092913208 A A A 3.61315951768879 3.79550791533913
3.74784978289354 P P P LNCV6_133885_PI430048170 mRNA
TCTCCGAACTGTAGTATTTCCTTCTCACTACCTTGTACCTTTATACTTAGATTGGAATTC NM_025114 RefSeq chr12 -
88049012 88142216 CEP290 80184 centrosomal protein 290kDa
GO:0005515|GO:0060041|GO:0034451|GO:0048793|GO:0036038|GO:0005634|GO:0015031|GO:0036064|GO:0005

829|GO:0005737|GO:0000086|GO:0070201|GO:0000930|GO:0051011|GO:0030814|GO:0005813|GO:0006996|GO:0030916|GO:0090316|GO:0042384|GO:0043234|GO:0007163|GO:0016020|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133790_PI430048170 0.3836442822292390.7926450643304371.06521199493107 1.60718549442522 2.22653031392831 A A A 1.67489696466879 2.32338395307261 2.06687173714201 A A A LNCV6_133790_PI430048170 mRNA
AGTCGTCCTCAGTCCTGAGTTGTGACATCTCCAGAAATAACAAATACATCGTGACAGGCT NM_001300846 RefSeq chr19 - 2997637 3029201 TLE2 7089 "transducin-like enhancer of split 2, transcript variant 4"
GO:0005515|GO:0007165|GO:0007219|GO:0003714|GO:0009887|GO:0005654|GO:0005634|GO:0016055|GO:0090090|GO:0045892|GO:0005615|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137791_PI430048170 0.6846564269290050.9621209056891566.5324921939498 6.64776508947915 6.66038788129564 P P P 6.46499367520897 6.72248460451485 6.8025610400475 P P P LNCV6_137791_PI430048170 mRNA
GTGAGTTAGTGATATGTTTGGTTGGTGTTAATTTGAGTCCTAAATAAAATCGAGAACTGG NM_001199107 RefSeq chr16 + 2475145 2505733 TBC1D24 57465 "TBC1 domain family, member 24, transcript variant 1"
GO:0005515|GO:0005737|GO:0031594|GO:0043195|GO:0032851|GO:0031175|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140633_PI430048170 0.0445729187436937 0.9327654771619670.362724786774237 0.3266784469390130.312553114470903A A A 0.4811034341664340.433027087678126 0.388029871907263A A A LNCV6_140633_PI430048170 mRNA
AGAGTGTACCCAGCCAGACTGTCTTTATCTCCATGGATTTTCATCAGGGCAAAGATCACA NM_000497RefSeq chr8 - 142872356 142879820 CYP11B1 1584 "cytochrome P450, family 11, subfamily B, polypeptide 1, transcript variant 1"
GO:0006805|GO:0005506|GO:0006704|GO:0005743|GO:0044281|GO:0042593|GO:0004507|GO:0032870|GO:0034651|GO:0005739|GO:0006955|GO:0035865|GO:0006700|GO:0008217|GO:0032342|GO:0016125|GO:0008202|GO:0055114|GO:0020037. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135650_PI430048170 0.1933489018710320.6875161345924261.36542285808962 0.4099850004930270.406371312240492A A A 1.27221663064422 1.6151624064264 1.09023874304106 A A A LNCV6_135650_PI430048170 mRNA
AAATGACCAAAACACACACACACATTTACAATGGACTGCTGGTGCAGAAGAATAAACAAC NM_001039362 RefSeq chr2 + 10721648 10785110 ATP6V1C2 245973 "ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2, transcript variant 1"
GO:0008286|GO:0051701|GO:0030177|GO:0033180|GO:0005765|GO:0055085|GO:0005829|GO:0006879|GO:0033572|GO:0008553|GO:0015991|GO:0046983|GO:0090382|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127262_PI430048170 0.2354666480882392.00619949836401 0.540347887650018 2.24950728512666 1.225977080364 A A A 0.5456033672046340.486697213308778 0.485695074808213A A A LNCV6_127262_PI430048170 mRNA
TCTAGGAAATTGTATCAGCCTCCCAAGCATATAACCCCCTAAGGAATCCATCGGACAAGA NM_145762RefSeq chr20 - 3659291 3663399 GFRA4 64096 "GDNF family receptor alpha 4, transcript variant 2"
GO:0030279|GO:0016167|GO:0005886|GO:0035860|GO:0031225|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139349_PI430048170 0.3594454511355680.5220309985863990.284858666822245 0.2951991909948120.509489281517851A A A 0.3271207316715232.20757825569723 0.620801743006731A A A LNCV6_139349_PI430048170 mRNA
TGCAGAGTACTGTGTTGTTGGTGCTGTCCATGCTGTAGCTCAAAATAAAGAAGCTATTTT NM_001001850 RefSeq chr3 - 94014370 94028610 STX19 NA syntaxin 19 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133497_PI430048170 0.1503114483586742.424273795019 0.684801984543088

2.04668772501633 2.2849355486894 A A A 0.6481846999318230.479079108225116
0.502368964434481 A A A LNCV6_133497_PI430048170 mRNA
ATTTGTAATTTTTAAGTTATAGATTGTTTTTATTAAACACTTATGAATACTGTTAAAAAA NM_001114182 RefSeq chr12
+ 43758943 43789543 IRAK4 51135 "interleukin-1 receptor-associated kinase 4, transcript variant 1"
GO:0005515|GO:0034142|GO:0005886|GO:0019221|GO:0005634|GO:0001816|GO:0005615|GO:0005829|GO:0005
737|GO:0002755|GO:0043123|GO:0005149|GO:0000287|GO:0038124|GO:0038123|GO:0034134|GO:0007254|GO:0
002224|GO:0048661|GO:0005524|GO:0004672|GO:0004674|GO:0045087|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_104046_PI430048170 0.8107495933161470.7211437390614420.400604598041397
1.81611674779161 2.30471365711769 A A A 3.14143085621683 0.34997487806266
1.79333075966236 P A A LNCV6_104046_PI430048170 mRNA
TTGGGAACCCTTTCCTCCGGAAGAAAGTGTCAGAGGCACATCTGCCCTCTGGCATCCACA NM_003323 RefSeq chr19
- 48880964 48898739 TULP2 7288 tubby like protein 2
GO:0005737|GO:0005576|GO:0032403|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143221_PI430048170 0.3983720758191491.0523304880879 0.311236591402342
0.3150944516120410.511684435735892 A A A 0.3138742306746710.278912751141603
0.333183569895201 A A A LNCV6_143221_PI430048170 mRNA
CTCAACAACAACTCACCAAACATCAGATATTCTGAGAACGCCGTGAGGATTGAGCCAAAC NM_053285 RefSeq chr17
- 6799980 6831741 TEKT1 83659 tektin 1 GO:0005929|GO:0005737|GO:0005874|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130193_PI430048170 0.3754634886812140.888923495844961 0.272260691476814
0.2781893079450290.400045653434312 A A A 0.3658089781982330.307406355122352
0.749458466087178 A A A LNCV6_130193_PI430048170 mRNA
ACTGGACATCTCATCCATTCTCATATGTATTCTCAATGACAAATTCACTGATGCCCAATT NM_002195 RefSeq chr9
+ 5231418 5233967 INSL4 3641 insulin-like 4 (placenta)
GO:0007165|GO:0007565|GO:0005179|GO:0008283|GO:0005159|GO:0007267|GO:0005102|GO:0007275|GO:0005
615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141614_PI430048170 0.1246860134274440.7117602799772657.06206611128345
7.18125961622273 7.40828019924822 P P P 7.33787429580017 7.7045040524402
8.02207915266357 P P P LNCV6_141614_PI430048170 mRNA
GCTGTCTGTCATTTACCTACTTCTTTCCCACTAAATAAAAGAATTCTTCAGTTTCCCTGT NM_002497 RefSeq chr1 -
211662771 211675630 NEK2 4751 "NIMA-related kinase 2, transcript variant 1"
GO:0005515|GO:0005634|GO:0031145|GO:0046872|GO:0005829|GO:0005737|GO:0046777|GO:0007059|GO:0000
086|GO:0090307|GO:0051321|GO:0000794|GO:0005813|GO:0007088|GO:0006996|GO:0051988|GO:0019903|GO:0
001824|GO:0005874|GO:0046602|GO:0005730|GO:0030496|GO:0051225|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_104621_PI430048170 0.2891766212915480.9156434738807317.24221472476242
7.27524316143727 7.51315395637072 P P P 7.40575302484553 7.42051819281668
7.59352470985629 P P P LNCV6_104621_PI430048170 mRNA
TGTTACTACTTTTACCAAGCGGAAGATGGACAGCATATGTTCCTGCACCCTGTGAATGTG NM_014868 RefSeq chr12
+ 120534328 120577594 RNF10 9921 ring finger protein 10
GO:0005515|GO:0010626|GO:0005737|GO:0004842|GO:0044212|GO:0045944|GO:0008270|GO:0005634|GO:0045
893|GO:0006351|GO:0051865|GO:0031643 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68206_PI430048170 0.0973547012117039 0.5325615673111837.26318029600246
8.21609532684496 8.37663239644728 P P P 8.90833562243479 8.78098631321747 9.1047015250001
P P P LNCV6_68206_PI430048170 mRNA
ACAGCTACTGGTTCCAAGTAGACGATGAAGGAAGATATAGTCCCTTATGTATATAGCTTT NM_184234 RefSeq chr20
- 35703608 35742336 RBM39 9584 "RNA binding motif protein 39, transcript variant 1"
GO:0008380|GO:0006397|GO:0005515|GO:0006396|GO:0006355|GO:0016607|GO:0005815|GO:0000166|GO:0015

630|GO:0005654|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135605_PI430048170 0.0157475065280252 1.74015786510494 4.17757461314207
4.63653491450532 4.37155526167782 P P P 3.84854649538699 3.34100436191517
3.59090425076971 P P P LNCV6_135605_PI430048170 mRNA
GACAGAAAAGAAACCAGGGAGTTTGTAGAGACTGTGCATTTTTAGTATAACATTTTCACC NM_152834RefSeq chr2
- 667972 677439 TMEM18 129787 transmembrane protein 18
GO:0031965|GO:0005737|GO:0016477|GO:0016021|GO:0003677|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126992_PI430048170 0.5999018007982211.02284334242445 0.29464580194645
0.2742689679111040.4313369773579 A A A 0.2906388654413330.33256751880991
0.283915373481747A A A LNCV6_126992_PI430048170 mRNA
TTGTTACATGCTCATGGAAGACCGTGCAGTATTGAAAGTATTTGTTAATTATCTGCTTAG NM_004274RefSeq chr14
+ 32329272 32833062 AKAP6 9472 A kinase (PRKA) anchor protein 6
GO:0005515|GO:0034237|GO:0048471|GO:0030307|GO:0030818|GO:0060306|GO:0010738|GO:0006605|GO:0005
635|GO:0061051|GO:0060316|GO:0035556|GO:0014701|GO:0005737|GO:0014704|GO:0010880|GO:0051018|GO:0
051281|GO:0031965|GO:0008179|GO:0051533|GO:0030315|GO:0034704|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137835_PI430048170 0.7723853373296930.9594139376668216.29515708057217 6.4656360823724
6.51327222980237 P P P 6.66404947373553 6.55893333380756 6.19940792465779 P P P
LNCV6_137835_PI430048170 mRNA
TAACAAGCACACCGGCCTGCTGTTCTGTCCTTCCATCCCTCTTTTGGGCTCTTCTGGAGG NM_000312RefSeq chr2
+ 127418419 127429246 PROC 5624 protein C (inactivator of coagulation factors Va and VIIIa)
GO:0005515|GO:0043066|GO:0004252|GO:0005796|GO:0005509|GO:0005576|GO:0050900|GO:0017187|GO:0007
596|GO:0030195|GO:0006508|GO:0005788|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139665_PI430048170 0.00253940630565327 0.27263959657503 7.20244580200386
7.23066640062164 7.49699953713592 P P P 9.03825906596452 8.94784618051871
9.51980000450579 P P P LNCV6_139665_PI430048170 mRNA
GCCTTTTCAAGGTTCCCATGGTCCAGAATGATGTTTGATTCTTAATTTTTCTGTCCCTTT NM_004661RefSeq chr5 -
138187647 138213343 CDC23 8697 cell division cycle 23
GO:0006511|GO:0007094|GO:0004842|GO:0007096|GO:0051437|GO:0051436|GO:0031145|GO:0051439|GO:0005
829|GO:0005622|GO:0007067|GO:0070979|GO:0005680|GO:0005654|GO:0007080|GO:0030071|GO:0000278|GO:0
007091|GO:0051301. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141831_PI430048170 0.3734343705021860.91662105377405 4.83606037286194
5.17068875969831 4.94067082245443 P P P 5.2686801618028 5.01128153254124
5.05132148758738 P P P LNCV6_141831_PI430048170 mRNA
AAGGTCAGCTTCCTGAGCGCTCTCGAGGAGTACACTAAGAAGCTCAACACCCAGTGAGGCNM_000039RefSeq chr11
- 116835752 116837622 APOA1 335 apolipoprotein A-I
GO:0005515|GO:0006695|GO:0043627|GO:0007603|GO:0019915|GO:0010898|GO:0018206|GO:0030300|GO:0010
903|GO:0030301|GO:0005615|GO:0042802|GO:0034361|GO:0034365|GO:0034364|GO:0034115|GO:0007179|GO:0
006656|GO:0042632|GO:0033344|GO:0009986|GO:0043691|GO:0034366|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134375_PI430048170 0.3283234658007071.08948547146404 11.0673416963331
11.2862190908781 11.3764644026777 P P P 11.0915924080588 11.2076784539021
11.0733576710807 P P P LNCV6_134375_PI430048170 mRNA
TAAAAAACTCTTGTACAAAACTGATCTAATTCTTCACTCCTGCTCCAAGGGCTGGGCTGT NM_015343RefSeq chr17
- 7243586 7251940 CTDNEP1 23399 "CTD nuclear envelope phosphatase 1, transcript variant 1"
GO:0005515|GO:0007077|GO:0034504|GO:0031965|GO:0010867|GO:0007276|GO:0090263|GO:0071595|GO:0005
635|GO:0005737|GO:0006470|GO:0005789|GO:0006998|GO:0007498|GO:0004722|GO:0016021|GO:0000278 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145658_PI430048170 0.0888973145039643 1.03780319883543 0.3908941778709
0.4048302954440640.451321554841184A A A 0.3505648541499750.344194101843013
0.391917809612734A A A LNCV6_145658_PI430048170 mRNA
GAGGACCAGTTGTAAATGTTACTGCTTCCTACTAATAAATGCTGACCTGATCAAATGGAA NM_014213RefSeq chr2
+ 176122684 176124917 HOXD9 3235 homeobox D9
GO:0035137|GO:0008344|GO:0000977|GO:0048704|GO:0005634|GO:0009954|GO:0030879|GO:0000122|GO:0009
952|GO:0001227|GO:0006351|GO:0007338|GO:0007519|GO:0045944|GO:0048935|GO:0035115 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136312_PI430048170 0.00943552334727116 2.3625470428945 2.48987180316894
2.67976990431083 3.08465990567742 A A P 1.41862678402522 1.68929453793972 1.4762770354521
A A A LNCV6_136312_PI430048170 mRNA
TTCATGATAGACACGATGAAATCCACCCTCAAAGAGCAGTTCCAGTTTGTGGAAGTCCCA NM_014509RefSeq chr22
+ 42553861 42574382 SERHL2 253190 "serine hydrolase-like 2, transcript variant 1"
GO:0005739|GO:0008150|GO:0003674|GO:0048471|GO:0016787|GO:0008152|GO:0016023|GO:0005575|GO:0005
777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139194_PI430048170 0.3645054952067980.9353820052781999.36345806432746
9.27053225166769 9.24974595024404 P P P 9.23709230120842 9.50168318971653
9.42397601692551 P P P LNCV6_139194_PI430048170 mRNA
GAGACCACTCATCCTCTGGAATCAACCTCTTTCTAATACCCTCTTGGAAAAAGAGCTTGC NM_018052RefSeq chr16
- 70687438 70801158 VAC14 55697 Vac14 homolog (S. cerevisiae)
GO:0005515|GO:0006661|GO:0005783|GO:0043550|GO:0044281|GO:0070772|GO:0007165|GO:0000139|GO:0031
901|GO:0031902|GO:0016032|GO:0004872|GO:0006644|GO:0010008 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128762_PI430048170 0.313165301708369 0.791364024067552 8.25334649177063
9.05012372409018 9.20072699134352 P P P 9.16742199301338 9.20303046907856
9.30980009966298 P P P LNCV6_128762_PI430048170 mRNA
TGATGATGATAATGAAGATCAGGGGGACAACCAGCTGGAGTTGATCAAGGATGATGAAAA NM_001302551
RefSeq chr1_KI270766v1_alt - 110147 111075 HNRNPCL4 NA heterogeneous nuclear
ribonucleoprotein C-like 4 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143153_PI430048170 0.735601565256137 1.12358691234614 3.09332551068478
3.25281598204189 4.01486095109673 P P P 3.3891237482544 3.39062910037941
3.24833376472198 P P P LNCV6_143153_PI430048170 mRNA
AGCAAAACCAGGCAGCTGCTAATTAAATGCTTAGAACCAATGAAAGCTGGCTGTGGTCCT NM_001040694 RefSeq
chr11 + 62123972 62153163 INCENP 3619 "inner centromere protein antigens 135/155kDa,
transcript variant 1"
GO:0005515|GO:0010369|GO:0005874|GO:0005819|GO:0030496|GO:0000801|GO:0000800|GO:0005829|GO:0043
234|GO:0000910|GO:0007067|GO:0005721|GO:0007059|GO:0000777|GO:0000776|GO:0000278|GO:0000775 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126784_PI430048170 0.928161834620794 1.20524764621533 2.66661617788104
2.46418728848894 0.301750538064071 A A A 0.797547610046443 2.27868505284356
2.09720186272111 A A A LNCV6_126784_PI430048170 mRNA
TTTCCTCATTTTTATCCGCATTCTTGGCATTCTCCTGTCCAAGCTGAGGACACGGCAAAT NM_000164 RefSeq
chr19 + 45668243 45683724 GIPR 2696 gastric inhibitory polypeptide receptor
GO:0005886|GO:0007584|GO:0006091|GO:0048678|GO:0007204|GO:0009749|GO:0051592|GO:0007190|GO:0016
519|GO:0070542|GO:0002029|GO:0031018|GO:0032024|GO:0016021|GO:0017046|GO:0007166|GO:0004888 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55529_PI430048170 0.0222087079506167 0.516682822895109 7.39472748595149
7.28226619174001 7.36789928143941 P P P 8.03197646120816 8.25554912115945

8.56723987234575 P P P LNCV6_55529_PI430048170 mRNA
ATTAGTCAATGTTTCGTGTTCCGCATTATTTGAACCATTTGCCCTTACAGAAAGAGAAAT NM_014827 RefSeq chr1
+ 203795622 203854128 ZC3H11A 9877 zinc finger CCCH-type containing 11A
GO:0005515|GO:0016973|GO:0000346|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134978_PI430048170 0.226481339737854 0.890349061148469 9.78982443689977
9.56667142901137 9.71612775056662 P P P 9.75541052344752 10.0392396744471
9.77156074963996 P P P LNCV6_134978_PI430048170 mRNA
CAACCACCCTTGCACTGTGGAGGAGGAGATGTCTGTGCCCTTGAAAGAACTGATTGAGAA NM_007103 RefSeq
chr11 + 67606851 67612541 NDUFV1 4723 "NADH dehydrogenase (ubiquinone) flavoprotein 1,
51kDa, transcript variant 1"
GO:0022904|GO:0051539|GO:0051287|GO:0005747|GO:0010181|GO:0006120|GO:0005743|GO:0044281|GO:0008
137|GO:0046872|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_39363_PI430048170 0.0783414899047197 0.50584919005737 0.404645760460952
0.680676622513589 0.25677352992573 A A A 1.38782020404844 0.839504408540536
1.90355450055292 A A A LNCV6_39363_PI430048170 mRNA
CATTGAGCTTCTTAGGAGAGATTACATGCAGCTACTTAGGACCACCTCAGCAAAATGGAG NM_004544 RefSeq
chr2 - 239957371 240025402 NDUFA10 4705 "NADH dehydrogenase (ubiquinone) 1 alpha
subcomplex, 10, 42kDa"
GO:0022904|GO:0005747|GO:0042493|GO:0005759|GO:0006120|GO:0005743|GO:0044281|GO:0019206|GO:0008
137|GO:0005524|GO:0044237|GO:0009165 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_142783_PI430048170 0.00278035384259021 0.785838823964883 9.5575068764968
9.42980898009236 9.49145202479736 P P P 9.83715991426749 9.77665147645513
9.90787532462349 P P P LNCV6_142783_PI430048170 mRNA
GGCCTCATTCTCTTTCTAATCTTGCTGGTTTCAAGATTAGAAAATGGCATTATTTGATCT NM_022766 RefSeq chr22
- 46684409 46738255 CERK 64781 ceramide kinase
GO:0006665|GO:0000287|GO:0005886|GO:0006687|GO:0006672|GO:0044281|GO:0055085|GO:0005524|GO:0001
729|GO:0007205|GO:0005739|GO:0003951|GO:0004143|GO:0046834|GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_102224_PI430048170 0.00469087768626636 1.46866522271984 8.605759078729
8.5736453573016 8.64444198535314 P P P 7.96513367487783 8.15322503444215
8.03656432389918 P P P LNCV6_102224_PI430048170 mRNA
TTTTCCGTGTAGAGGTTACAGCCTTTTATGCTGTTGAGCTCCCAGGTACCAAAAAGCTTG NM_001130524 RefSeq
chr19 + 16197853 16235345 AP1M1 8907 "adaptor-related protein complex 1, mu 1 subunit,
transcript variant 1"
GO:0005515|GO:0030131|GO:0032438|GO:0006892|GO:0005765|GO:0032588|GO:0006886|GO:0050690|GO:0005
829|GO:0019886|GO:0030665|GO:0000139|GO:0016020|GO:0035646|GO:0061024|GO:0016032|GO:0030659|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135700_PI430048170 0.000107221040767605 0.650885282680162 12.5082702993847
12.4716693724813 12.567220878714 P P P 13.1584225285719 13.0770436996048
13.1701135966533 P P P LNCV6_135700_PI430048170 mRNA
CTGGGCTTTTTTCGGTGTTAGATTCAACACTGCGCTAAAGCGGGGATGTTCCATTGAATA NM_004630RefSeq chr11
- 64764603 64778844 SF1 7536 "splicing factor 1, transcript variant 1"
GO:0000245|GO:0006355|GO:0003714|GO:0003723|GO:0050810|GO:0048662|GO:0005634|GO:0000389|GO:0006
351|GO:0000398|GO:0030238|GO:0033327|GO:0005840|GO:0005654|GO:0005681|GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128747_PI430048170 0.0470825202291320 0.562196746508496 3.94953399923351
3.27504967195095 3.7911729624175 P P P 4.29560157055808 4.91619858833483

4.28482329840591 P P P LNCV6_128747_PI430048170 mRNA
AAAGTAAATTCAGTTAGAAGTTTCTTCTAGTAACCCAACGGCTCTTTTAAGAGCCACCTA NM_005325 RefSeq chr6
- 26017031 26017812 HIST1H1A 3024 "histone cluster 1, H1a"
GO:0005515|GO:0000790|GO:0005719|GO:0006334|GO:0007283|GO:0000786|GO:0031490 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_7542_PI430048170 0.0490122259179991 0.741244763938193 4.88881661953982
5.11550544680152 4.69022729396357 P P P 5.22269091239829 5.4714502177004
5.31677056961675 P P P LNCV6_7542_PI430048170 mRNA
CTGGAGGTGCACCAGTTCTGGCCGCTGGTGGAGATCCAGTGCTCGCCCGATCTCAAGTTC NM_031866 RefSeq chr10
- 35638248 35641434 FZD8 8325 frizzled class receptor 8
GO:0042813|GO:0005515|GO:0017147|GO:0033077|GO:0005794|GO:0005886|GO:0004930|GO:0005102|GO:0000
122|GO:0001525|GO:0030165|GO:0007186|GO:0045944|GO:0030182|GO:0043507|GO:0016021|GO:0060070|GO:0
031625|GO:0035567. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_8756_PI430048170 0.204686592774571 0.886070292027536 7.17610913874588 7.41452274290748
7.38315993956524 P P P 7.63552635277103 7.33953025910944 7.51841199794279 P P P
LNCV6_8756_PI430048170 mRNA
GAAGGCTGCCCCTTTGCTCTCTGGGGTAGCCTTCAGATCTTGGTGTTTTGAATTCTTACT NM_005082 RefSeq chr17
- 56887908 56914048 TRIM25 7706 tripartite motif containing 25
GO:0005515|GO:0043627|GO:0003700|GO:0016567|GO:0016881|GO:0019221|GO:0033280|GO:0005829|GO:0051
607|GO:0051091|GO:0005737|GO:0051092|GO:0046596|GO:0046597|GO:0045087|GO:0016032|GO:0005654|GO:0
008270|GO:0043123|GO:0032480|GO:0060333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142321_PI430048170 0.838078775836652 0.987591437186998 1.1192173794479
0.316479010771973 0.296559956216733 A A A 0.737200734294471 0.742304063936946
0.448244631057685 A A A LNCV6_142321_PI430048170 mRNA
GTTATATTAATGATGCTGGCGACCAGGGAAATTCCAAACTGCTGGACTTCCTATGCAGGA NM_153347 RefSeq chr11
+ 18698734 18704785 TMEM86A 144110 transmembrane protein 86A GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134270_PI430048170 0.884284613459728 0.991175215107724 0.416183445587192
0.453773567380386 0.461015964190484 A A A 0.574250736331821 0.371794692612199
0.415744066461327 A A A LNCV6_134270_PI430048170 mRNA
GCGGTATGGGAATACCAAAAGCCAATCATTAACAAAATCACTAGTAAACTCCATCAAAAA NM_001037729 RefSeq
chr6 - 49968676 49969625 DEFB113 NA "defensin, beta 113" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128609_PI430048170 0.49372205182441 0.830318422450199 0.965000230425237
0.282373614478114 0.459535314081408 A A A 1.08131576415135 1.09111722310199
0.293335421953069 A A A LNCV6_128609_PI430048170 mRNA
TGAATTTAGATTGCCTGCCAGCTACCTACCTTAGTTCGTATACATCCCTGATCCCTCTTA NM_000745 RefSeq chr15
+ 78565519 78595269 CHRNA5 1138 "cholinergic receptor, nicotinic, alpha 5 (neuronal)"
GO:0030054|GO:0005886|GO:0007268|GO:0005892|GO:0035095|GO:0007165|GO:0034220|GO:0015464|GO:0045
211|GO:0006810|GO:0004889|GO:0006812|GO:0015276 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126792_PI430048170 0.951675751627588 1.00417567092931 0.321895374192781
0.529109791179159 0.395061702410666 A A A 0.501262316599201 0.380485654550334
0.34949110214167 A A A LNCV6_126792_PI430048170 mRNA
ATTGGTGGGCTGCTTTAGGTATATCAAAATTGCTTGTTTAGATTCTCTAATGCACAGAAA NM_001010876 RefSeq
chr6 - 129831243 129861271 TMEM244 NA transmembrane protein 244 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_137708_PI430048170 0.514733820501529 0.982250700451353 0.402126387393854
0.42174232916218 0.348045053156883 A A A 0.470844156125013 0.377460662622599
0.400476905207422 A A A LNCV6_137708_PI430048170 mRNA

CAAATTCCCAAATCAATCTCTGGAATAAATAGAGAGGTAATTAAATTGCTGGAGCCAACT NM_016562 RefSeq chrX
+ 12867082 12890361 TLR7 51284 toll-like receptor 7
GO:0003725|GO:0032755|GO:0042346|GO:0003727|GO:0005886|GO:0005783|GO:0032009|GO:0005764|GO:0032
757|GO:0051607|GO:0005737|GO:0006954|GO:0036020|GO:0045078|GO:0002755|GO:0008144|GO:0001774|GO:0
034154|GO:0007252|GO:0045416|GO:0032722|GO:0002224|GO:0043235|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_107941_PI430048170 0.1843392080080091.27010025064132 5.26933124519357
5.69012949636166 5.8402514300193 P P P 5.1500082710818 5.25265080045257
5.40915572938572 P P P LNCV6_107941_PI430048170 mRNA
CCTGGACAAAAAGGGAAGCTGACTCTCACTGCATTCCTTAAACTGATATGTATATTTTTT NM_001242359 RefSeq
chr10 - 60869439 60944275 RHOBTB1 9886 "Rho-related BTB domain containing 1, transcript
variant 4" GO:0051056|GO:0005886|GO:0007264|GO:0005525|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143809_PI430048170 0.0159977798605112 1.70951692535243 6.20983575910519
6.3544897743518 6.13335141156571 P P P 5.49618445126616 5.65978168951738
5.19125448965009 P P P LNCV6_143809_PI430048170 mRNA
AACTTGTTACAATGACGATGATGATGATTCTTGGCGGTTACACAATCCTTCCTCCTGGGG NM_001001479 RefSeq
chr22 + 30635805 30647875 SLC35E4 339665 "solute carrier family 35, member E4" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69048_PI430048170 0.1774416077962620.8741832312386215.86904094324384 5.5925733451954
5.91040196642288 P P P 5.95295071149378 6.02923402804587 5.99102808967824 P P P
LNCV6_69048_PI430048170 mRNA
ACATCAGTCTCAACATCGATCCAGCCGTGAAGGCCGTCATGGGCATCTTCAGCCTGGTGA NM_018161 RefSeq chr11
+ 71453170 71501535 NADSYN1 55191 NAD synthetase 1
GO:0005737|GO:0003952|GO:0016810|GO:0006766|GO:0019674|GO:0006767|GO:0044281|GO:0009435|GO:0005
524|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88854_PI430048170 0.2423108124945261.1307867645397 11.0110801125971 11.1550379767388
11.3033415381974 P P P 10.8687770358711 10.8872336915785 11.1753419364768 P P P
LNCV6_88854_PI430048170 mRNA
CAAAGAGAATGTACGGATTGATCATGACATTCCTTACCTTCTTAGGCTTGTTTAAAAGAA NM_001303247 RefSeq
chr15 - 78283235 78299726 WDR61 80349 "WD repeat domain 61, transcript variant 1"
GO:0005515|GO:0080182|GO:0035327|GO:0005634|GO:0055087|GO:0006351|GO:0005737|GO:0051571|GO:0045
638|GO:0045944|GO:0032968|GO:2001162|GO:0016593|GO:0005654|GO:0016055 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_50509_PI430048170 0.3536461879246630.7222892225669630.4315951484564910.340211792557878
0.380282091979511 A A A 1.4255752277623 0.5129290547923640.38830472769144 A A A
LNCV6_50509_PI430048170 mRNA
GGGCTGCACAGGCTGAAGGTTAGTTGAGTAAATTAAGTAGCTATGCTAGCTTTTAAAAAA NM_001190766 RefSeq
chr6 + 17102257 17131372 STMND1 401236 stathmin domain containing 1
GO:0005737|GO:0051493|GO:0031110|GO:0015631|GO:0007019 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_126859_PI430048170 0.42455254650886 0.9726083619238520.253963325715673
0.2675436082761990.376601655483841 A A A 0.3834829355498410.324190024711407
0.312799176125455 A A A LNCV6_126859_PI430048170 mRNA
ATTCATTTACACTTTGCGGAACAAGGAGGTGAAGCATGCTCTGCAAAGGCTTTTGTGCAG NM_001004474 RefSeq
chr11 - 123976695 123977691 OR10S1 NA "olfactory receptor, family 10, subfamily S, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145330_PI430048170 0.00629341606007972 2.52224701222312 9.37592103823793
9.25891969617932 9.10396147712237 P P P 7.94856240080899 8.15683116181525

7.58531423998957 P P P LNCV6_145330_PI430048170 mRNA
CTGACTCATGCCTTGAGTACATACCATACAGCAAATAAATGGTAGCAAAACATTCTAAAA NM_005165 RefSeq chr17
- 28573114 28576933 ALDOC 230 "aldolase C, fructose-bisphosphate"
GO:0005515|GO:0008092|GO:0014070|GO:0030424|GO:0031100|GO:0006094|GO:0051290|GO:0044281|GO:0006
096|GO:0005829|GO:0005739|GO:0004332|GO:0051289|GO:0030855|GO:0006006|GO:0005856|GO:0006000|GO:0
070062|GO:0001666|GO:0005975|GO:0007568|GO:0006915|GO:0010243|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135456_PI430048170 0.0266089416701735 0.36378335248148 1.32992735782733
0.53636047656595 0.319606537866198 A A A 1.60126023531469 2.53002615686427
2.46410706623444 A A A LNCV6_135456_PI430048170 mRNA
GCCTCCCGCAGATGCAAAAGCTTTAGAAGAAGCCAGAAAGATTTTCAGGTTTTAATAAAG NM_000847 RefSeq chr6
- 52896640 52909698 GSTA3 2940 glutathione S-transferase alpha 3
GO:0006805|GO:0006749|GO:0044281|GO:0004364|GO:0070062|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131969_PI430048170 0.0247103188774605 1.18783368073236 9.49181535867416
9.54532020219409 9.46180683028884 P P P 9.1694541284658 9.34650254170908
9.23363353647107 P P P LNCV6_131969_PI430048170 mRNA
GCTGTTGGGGCTGCACTGAGCTGCAATTTTTAACATGGATTTATAACTTAATGTTTCTGT NM_007368 RefSeq chr13
- 113977782 114132620 RASA3 22821 RAS p21 protein activator 3
GO:0035556|GO:0005099|GO:0046580|GO:0007165|GO:0005737|GO:0032320|GO:0070588|GO:0031235|GO:0015
278|GO:0046872|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127686_PI430048170 0.976219761239703 0.999832909621506 0.413755275439726
0.39148307482989 0.264345239970397 A A A 0.331360751282856 0.372890452482384
0.370141026080697 A A A LNCV6_127686_PI430048170 mRNA
TTGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCTTGAAGAATGTCCTGAGATGA NM_001005245 RefSeq
chr11 - 56542339 56543257 OR5M11 NA "olfactory receptor, family 5, subfamily M, member 11"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73517_PI430048170 0.984755573214569 1.1708968341667 2.39156340616294 0.511907966350393
0.599416509387467 A A A 1.3518626349554 1.58849302060352 0.519458873001207 A A A
LNCV6_73517_PI430048170 mRNA
CCAAGATCATTGATCACTCAGGAGATCCTGCAGAAGGAGTATATAAAACTTATATTTGTG NM_153240 RefSeq chr3
- 132680608 132722459 NPHP3 27031 nephronophthisis 3 (adolescent)
GO:0005515|GO:0007368|GO:0003283|GO:0030324|GO:2000167|GO:2000095|GO:0048496|GO:0045494|GO:0005
829|GO:0001947|GO:0060287|GO:0060027|GO:0060993|GO:0016055|GO:0071909|GO:0090090|GO:0071908|GO:0
035469|GO:0006996|GO:0001822|GO:0071910|GO:0072372|GO:0005929|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142942_PI430048170 0.941975117370572 1.05765077376859 1.85791804581891
0.349188912255939 1.64963691731612 A A A 1.04985540178205 1.36426817364874 1.5623825445791
A A A LNCV6_142942_PI430048170 mRNA
CTCTAAATAAGTGCTTATGTAAGCACTTCCAAACCCAAAGGCTCTTTTCAGAGCCACCTA NM_021062 RefSeq chr6
- 26043226 26043657 HIST1H2BB 3018 "histone cluster 1, H2bb"
GO:0005515|GO:0046982|GO:0006334|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0003677 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145680_PI430048170 0.855913709446301 0.96784442933577 0.515420291008939
0.660797216231935 0.556472742656827 A A A 0.423367151876373 0.494665297496458
0.910629444123935 A A A LNCV6_145680_PI430048170 mRNA
GTTGTTGTTGTTGATGTTGTTAATTGCTTGTATTTTCTGCTTATGGGAAGGATCTCACAT NM_024884 RefSeq chr14 -
50242433 50312229 L2HGDH 79944 L-2-hydroxyglutarate dehydrogenase
GO:0005739|GO:0006103|GO:0005743|GO:0031305|GO:0047545|GO:0044281|GO:0016021|GO:0044267|GO:0044

237|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130109_PI430048170 0.0243191145304296 0.6164099685342886.50863366948133
6.62984018189838 6.97552271607852 P P P 7.35175993651639 7.36560739309766
7.52572098464112 P P P LNCV6_130109_PI430048170 mRNA
AAGCAGATGGTTTCTGGGCAAAATCAAATGATTTCTGTCTCTATTTTCTTGAGTACCAAT NM_004549RefSeq chr11
- 78068346 78080219 NDUFC2 4718 "NADH dehydrogenase (ubiquinone) 1, subcomplex unknown,
2, 14.5kDa, transcript variant 1"
GO:0022904|GO:0005737|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0016021|GO:0008137|GO:0044
237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136646_PI430048170 0.00890817041225908 0.5507234001275432.69746151313798
2.2718641751925 2.49967392246455 A A A 3.53024053697295 3.0934863719275
3.42331865076992 P P P LNCV6_136646_PI430048170 mRNA
ACTTTTCTTTCAGTTTTGCGGCAAGTGAGGTACTGGGTGAAAGGAGAGAAGCCTTCATCT NM_176885RefSeq
chr12_KI270904v1_alt - 229391 230412 TAS2R31 259290 "taste receptor, type 2, member 31"
GO:0033038|GO:0007186|GO:0005886|GO:0016021|GO:0001580 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_76008_PI430048170 0.0545843548146238 1.49432237503081 6.40405649472984 6.4876476348646
6.91005470055249 P P P 6.3096650325231 5.83115499528232 5.92956851774702 P P P
LNCV6_76008_PI430048170 mRNA
GAGTTTACAACTTTTATGTGTCATGTTTCCAACAGCTGTGTTTGGGGTGGTCACTGGCAG NM_024715RefSeq chr5
+ 134873769 134901633 TXNDC15 79770 thioredoxin domain containing 15 GO:0045454|GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135263_PI430048170 0.443328993543881 0.673310173084672 0.449853977635425
1.40892983369986 0.254964081719378 A A A 0.93759599430549 2.12010499983057
0.567687244033955 A A A LNCV6_135263_PI430048170 mRNA
GGTGCCTAAAATGCCAGCTATTGCCAAGAAGAAAATAGTTGATGTCTGTCAATAACTGTG NM_001178007 RefSeq
chr4 + 122732701 122744943 BBS12 166379 "Bardet-Biedl syndrome 12, transcript variant 1"
GO:0005515|GO:0005929|GO:0042073|GO:0045599|GO:0042755|GO:0051131|GO:0045494|GO:0044267|GO:0005
524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137248_PI430048170 0.1222694509863 0.755721079988232 0.598301677062735
0.548547103778319 0.304618685039441 A A A 0.577189033703293 0.912300229233401
1.13686192828809 A A A LNCV6_137248_PI430048170 mRNA
GCCATTGGTATCCTATCTTCCTTTTGTGGACTTCTGCAAAACAAAAATACATTTGTTAGT NM_032439RefSeq chr10
+ 59176587 59247774 PHYHIPL 84457 "phytanoyl-CoA 2-hydroxylase interacting protein-like,
transcript variant 1" GO:0005739|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130550_PI430048170 0.343703156074791 1.09268658355794 0.441500477362227
0.298428287066619 0.638378489844031 A A A 0.33075369081702 0.32862542401441
0.355428540859052 A A A LNCV6_130550_PI430048170 mRNA
AGAAAAGCCTTGATAAAACGTCATCTCCATGTAATTTAGAGAAGGATAACCTTGACTGTA NM_001141919 RefSeq
chrX + 2752051 2816501 XG 7499 "Xg blood group, transcript variant 2"
GO:0008150|GO:0003674|GO:0005887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125321_PI430048170 0.0807953790097649 0.791143547047784 7.62073314051914
7.36745130051439 7.61552284844993 P P P 7.7997548860321 7.71768864537166
8.08777433074172 P P P LNCV6_125321_PI430048170 mRNA
TGACAGTGAGGTTGACAAAAAGTTAAAGAGGAAAAAGCAAGTTGCTCCAGAAAAACCTGT NM_006713RefSeq
chr5 + 32585498 32604079 SUB1 10923 SUB1 homolog (S. cerevisiae)
GO:0005515|GO:0005667|GO:0006357|GO:0003697|GO:0045944|GO:0003713|GO:0005730|GO:0001205|GO:0005
634|GO:0060395|GO:0006351|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137869_PI430048170 0.00549467298094739 1.37142096935288 11.3704602879555

11.4538306586828 11.2690008957558 P P P 10.7868685839119 10.9432193086246
10.9941200408418 P P P LNCV6_137869_PI430048170 mRNA
CAGGCATGCTTCGCTTTGTAGACAAGGTTCATTTACATTAATTATCAAAACTTTGTGCTA NM_001256964 RefSeq
chr3 - 48432169 48440119 CCDC51 79714 "coiled-coil domain containing 51, transcript variant 1"
GO:0005739|GO:0005654|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132286_PI430048170 0.0133099928302409 0.7608124194876127.46423532819786
7.6239220823827 7.38990906134565 P P P 7.91433051302949 7.94272786376738
7.81085339866128 P P P LNCV6_132286_PI430048170 mRNA
GTGTAAGAAAAACTGAAGAGCAAGTGCCTGAAATAAAATCCCCCACATGTATCAGCCTGC NM_022764RefSeq chr16
- 86530175 86555235 MTHFSD 64779 "methenyltetrahydrofolate synthetase domain containing,
transcript variant 3" GO:0000166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134545_PI430048170 0.2714639531651140.9297966847629740.476200377930003
0.4691210236135450.257388224896778A A A 0.5673588522105810.504989810616824
0.453683151509149A A A LNCV6_134545_PI430048170 mRNA
TGCCTGCCTATTTGGGTGGATATATCAAACTCTTTTTTCTGAACACTTGAAAACTAAAAC NM_001099852 RefSeq
chr1 + 13410449 13421328 PRAMEF20 NA PRAME family member 20 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_6791_PI430048170 0.0513245251280139 1.12927490298218 8.08587093233068 8.2154924726715
8.23365666232126 P P P 8.01126807528685 8.02916656015505 7.97226529568597 P P P
LNCV6_6791_PI430048170 mRNA
CTGTACATTCTGGGGTACATGGATTTCTACTGAGTTGGATAATATGCATTTGTAATAAAC NM_016371RefSeq chr1
+ 162790701 162812818 HSD17B7 51478 "hydroxysteroid (17-beta) dehydrogenase 7, transcript variant
1"
GO:0006695|GO:0004303|GO:0005148|GO:0005886|GO:0006703|GO:0005789|GO:0044281|GO:0016021|GO:0055
114|GO:0000253 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127174_PI430048170 0.00527540781249381 1.29953471115336 13.5008995015777
13.6376931813947 13.5048731621478 P P P 13.1249377676701 13.270700966578
13.1126688329724 P P P LNCV6_127174_PI430048170 mRNA
CCAGGACTAACACGGCTCCTCAAATTCCTTCCCTGTCAAATAAACAGCTCCCTTGGTTGG NM_183241RefSeq chr9
+ 136992417 136993976 C9orf142 286257 chromosome 9 open reading frame 142 GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133706_PI430048170 0.4366622828229580.8593186080098397.58695222249179
7.17992932076906 6.97660522949536 P P P 7.727429605235 7.55396585150355
7.12095787856839 P P P LNCV6_133706_PI430048170 mRNA
TGGAAGGACCAGACTCTCCCAAATAAATCCCCACACGAACAAAATCCAAAACCAAATCCC NM_020862RefSeq chr19
- 39306816 39315336 LRFN1 57622 leucine rich repeat and fibronectin type III domain containing 1
GO:0030054|GO:0045211|GO:0014069|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126651_PI430048170 0.1354452598921120.6179575304518721.89124632529219
2.09234513717315 2.92831567803399 A A P 2.63050499505715 3.16964445012988
3.32645144348536 P P P LNCV6_126651_PI430048170 mRNA
CCCTTCATCCAACTGGATCACTTTGAGATTCAGTTTTACATCATTTTAGCATTTTGTTTG NM_001300860 RefSeq chr5
+ 134758733 134831136 DDX46 9879 "DEAD (Asp-Glu-Ala-Asp) box polypeptide 46, transcript variant 1"
GO:0008380|GO:0006397|GO:0015030|GO:0016607|GO:0004386|GO:0005524 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132356_PI430048170 0.0152697608832962 1.84452324335377 12.058352520572
12.1290610137529 12.2432601815297 P P P 10.9850621635295 11.2832145543736
11.4767872906342 P P P LNCV6_132356_PI430048170 mRNA
ACTCAGTGTAAGTTTCTGTCAGCAGTAGTTTCACCCATTTGCATGGAAAAATTTAAAGCT NM_206915RefSeq chrX
+ 103376322 103378164 NGFRAP1 27018 "nerve growth factor receptor (TNFRSF16) associated protein 1,

transcript variant 2"
GO:0005515|GO:0008625|GO:0048011|GO:0006919|GO:0005634|GO:0007275|GO:0005123|GO:0008656|GO:0097190|GO:0046872|GO:0005829|GO:0005737|GO:0043281 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129669_PI430048170 0.912854114415069 1.02105642070393 11.1560810743003 11.6143448304479 11.6842840083314 P P P 11.3965889057411 11.2592847487947 11.7233927425798 P P P LNCV6_129669_PI430048170 mRNA
AATGTCTGGAACATTTCATTTCCTGTTTTGTTACCTGTGCCTCTGTAAATCTACTTTTGC NM_016093 RefSeq chr5 + 172959435 172969771 RPL26L1 51121 ribosomal protein L26-like 1
GO:0010467|GO:0003735|GO:0006614|GO:0019083|GO:0019058|GO:0015934|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0000184|GO:0016032|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136823_PI430048170 0.0122648921020022 8.08957548148933 9.28006111593015 9.67292133045739 9.66847725601234 P P P 8.5058280909069 8.5232024789645 8.4354460789182 P P P LNCV6_136823_PI430048170 mRNA
AGAAGGTAAAGAAGAGGCATGTCCAGTATGCTTTGCAGGGTGTGTTTGCTCTTTTCCATG NM_017836 RefSeq chr3 - 126006356 126084291 SLC41A3 54946 "solute carrier family 41, member 3, transcript variant 2"
GO:0005886|GO:0008324|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144151_PI430048170 0.206556921053226 6.93509838486973 0.407524613337677 4.23224374742934 3.37049987041504 A P P 0.48572151905752 0.382788786268494 0.755735913555275 A A A LNCV6_144151_PI430048170 mRNA
GCTGCCTCAGATGACAAATGAGGCTAATGGACATAATCTACAGTGTCCTTTTTCACTTGC NM_015345 RefSeq chr6 + 39792996 39904877 DAAM2 23500 "dishevelled associated activator of morphogenesis 2, transcript variant 2" GO:0007368|GO:0030036|GO:0017048|GO:0003779|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142524_PI430048170 0.313043723430168 1.37353011144489 0.305002720383324 1.26411191695847 0.476592524265963 A A A 0.297570821397047 0.262566175318515 0.301520572893232 A A A LNCV6_142524_PI430048170 mRNA
GCTGAAAAATAATCCTAACAAACCCAAACTTTGTCACCATCCAATTGTAGAAGAACCTTA NM_003551 RefSeq chr5 - 138115171 138139443 NME5 8382 NME/NM23 family member 5
GO:0006241|GO:0003351|GO:0007286|GO:0004550|GO:0036126|GO:0005575|GO:0007283|GO:0005524|GO:0005622|GO:0006165|GO:0006228|GO:0042384|GO:0006183|GO:0021591|GO:0009116 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145446_PI430048170 0.639540888763704 0.789991615707375 1.93248132911245 0.269507631280984 0.396041086749272 A A A 0.284231370473228 1.36928276738931 2.0779928117428 A A A LNCV6_145446_PI430048170 mRNA
ATGGGTCAGGGAAGGTGAACATGAAACACTGCACAGTAGGTTGTATCAATGCTATAAAAC NM_001288653 RefSeq chr17 + 59619688 59696956 CLTC 1213 "clathrin, heavy chain (Hc), transcript variant 2"
GO:0005515|GO:0003725|GO:0030132|GO:0005886|GO:0032051|GO:0030136|GO:0006886|GO:0043231|GO:0005829|GO:0030118|GO:1900126|GO:0031623|GO:0033572|GO:0019886|GO:0005737|GO:0071439|GO:0061024|GO:0070062|GO:0042470|GO:0019901|GO:0006892|GO:0005819|GO:0031982|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132568_PI430048170 0.397036501537435 3.52982705636156 3.43932313217186 0.264262608218332 0.595611070926527 P A A 0.419285206568904 0.337508291937148 0.311126834165853 A A A LNCV6_132568_PI430048170 mRNA
CTCAGCTCTTCAACTAAGTCATTTTAAGAAAAATAGAAACGTGTGTCTTAATGGTGAAGC NM_001080487 RefSeq chr16 - 88863339 88866660 PABPN1L NA "poly(A) binding protein, nuclear 1-like (cytoplasmic), transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138814_PI430048170 0.228740390514023 0.867181564852537 13.1679053390379 12.8364435305825 12.7620923839681 P P P 13.1150133768812 13.265436456506

13.0256303573894 P P P LNCV6_138814_PI430048170 mRNA
AGGCCAGATGACCTGATTCCAGCAAAAATAAAACTCAGATTTGGGCAAAATGAGAAAAAA NM_016034RefSeq
chr9 + 135500630 135504673 MRPS2 51116 "mitochondrial ribosomal protein S2, transcript variant 1"
GO:0005739|GO:0003735|GO:0006412|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136511_PI430048170 0.0482567322352709 1.35472413139243 9.25528336047692
9.54441644581402 9.65226159407305 P P P 9.03893480582424 8.95469796689733
9.16512503193861 P P P LNCV6_136511_PI430048170 mRNA
TCTTTTGTACCGGATTTAATGACTTTGAACTGTGCTGTAAATAAATAATACAGCTGGACC NM_199418RefSeq chr11
- 82824366 82900515 PRCP 5547 "prolylcarboxypeptidase (angiotensinase C), transcript variant 2"
GO:0005515|GO:0002155|GO:0005886|GO:0060055|GO:0045178|GO:0042593|GO:0005764|GO:0097009|GO:0043
535|GO:0004185|GO:0007596|GO:0007597|GO:0002353|GO:0006508|GO:2000377|GO:0003085|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54899_PI430048170 0.00671802406540188 1.62621491971919 8.12544842882948
8.11273696408903 8.20368569359198 P P P 7.38050276879897 7.34653811029525
7.59877050436193 P P P LNCV6_54899_PI430048170 mRNA
TATCTCCTAATCCATTGTTAAATCACCTGCCCCAATTCAGTAAATGAATTGTGGAACAAA NM_001304821 RefSeq
chr1 + 156338591 156346994 TSACC 128229 "TSSK6 activating co-chaperone, transcript variant 1"
GO:0005737|GO:0051087 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130379_PI430048170 0.1179343762388820.61558083389414 0.43624731797388
0.4730394426706240.431009204671209A A A 1.49146687257708 1.18501811803285
0.639291290149003A A A LNCV6_130379_PI430048170 mRNA
TACGTGGGAGAGGCAGAAAGGGTAGGTTCAGTAATCATTTCTGATATTTGCTGGAGTGCT NM_000674RefSeq chr1
+ 203127707 203167405 ADORA1 134 "adenosine A1 receptor, transcript variant 1"
GO:0006909|GO:0005515|GO:0001659|GO:0043268|GO:0060087|GO:0046888|GO:0048167|GO:0006612|GO:0045
211|GO:0043025|GO:0030673|GO:0048786|GO:0046982|GO:0051967|GO:0045741|GO:0060079|GO:0014069|GO:0
002674|GO:0031683|GO:0016042|GO:0001609|GO:0042734|GO:0005887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144560_PI430048170 0.2522286531526880.2760404231124250.330945896603026
0.35502122735267 0.342337035320155A A A 3.27768988186264 0.338874767711769
1.49577744164388 P A A LNCV6_144560_PI430048170 mRNA
AGGACACTGAAATATAAGATGCATAAGAGTCTAAGTGAAGAGGTTCTTTGTGGTTAACTT NM_033468RefSeq chr19
+ 22052463 22091101 ZNF257 113835 zinc finger protein 257
GO:0006355|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141133_PI430048170 0.0632548082447795 1.64104350644841 3.05982205308947
3.62567759772567 3.7581109044873 P P P 2.4771483719321 3.01958998708856
2.84209608817995 P P P LNCV6_141133_PI430048170 mRNA
AATGCAGATAGAACACATCTAGGCTCTTTTCCCCAGGAGAGTGATGATGGAGCATATAGA NM_023938RefSeq chr1
- 207018520 207032756 C1orf116 79098 "chromosome 1 open reading frame 116, transcript variant 1"
GO:0008150|GO:0003674|GO:0005737|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127649_PI430048170 0.0439227233209389 0.76139782903346 15.7035727016612
15.4318454061865 15.4233018609932 P P P 15.9094090814459 15.9565702536551
15.8897203767856 P P P LNCV6_127649_PI430048170 mRNA
CCCCTCCCAGAGATGGCAATAAAACTGACTCTCAACATCTATCTCTGTTAACTTAAAAAA NM_001014763 RefSeq
chr19 - 51345154 51354842 ETFB 2109 "electron-transfer-flavoprotein, beta polypeptide, transcript
variant 2"
GO:0022904|GO:0005739|GO:0005759|GO:0009055|GO:0044281|GO:0044237|GO:0070062|GO:0043231 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129826_PI430048170 0.4921374263029470.92795710372925 12.929662245069

12.6567789758239 12.4348250993377 P P P 12.857018132269 12.8144094282509
12.7123689014612 P P P LNCV6_129826_PI430048170 mRNA
GGAGGCTGCTTACTCAACTTGTGTCTTAATTAAAAGTGACAGAGGAAACCACGGAAAAAA NM_001256399 RefSeq
chr1 - 43363396 43367738 ELOVL1 64834 "ELOVL fatty acid elongase 1, transcript variant 2"
GO:0005515|GO:0005783|GO:0019367|GO:0030148|GO:0030176|GO:0044281|GO:0035338|GO:0009922|GO:0016
020|GO:0005789|GO:0019432|GO:0034625|GO:0042761|GO:0044255 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134447_PI430048170 0.0229617877491658 0.7115411361823283.81554486007135
3.66763557285374 3.98059400737493 P P P 4.30817166173864 4.37197952925028
4.27178371566229 P P P LNCV6_134447_PI430048170 mRNA
GTCCTCTACAAAGAGCTGCAAGACAAAAATTAAAATAAATGCTCCCCACCCTAGAAAAAA NM_001897 RefSeq chr15
- 75674321 75712848 CSPG4 1464 chondroitin sulfate proteoglycan 4
GO:0048771|GO:0008347|GO:0008283|GO:0050731|GO:0044281|GO:0030208|GO:0035556|GO:0000187|GO:0030
207|GO:0016324|GO:0030206|GO:0004871|GO:0030204|GO:0030203|GO:0070062|GO:0043202|GO:0009986|GO:0
019901|GO:0031258|GO:0005975|GO:0005796|GO:0005576|GO:0001525|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142736_PI430048170 0.6349000909541871.07493990745461 4.29237035074022
4.04861024025953 4.07094268422841 P P P 4.16652625957711 4.31425555423271
3.51174763660549 P P P LNCV6_142736_PI430048170 mRNA
TTTAATTTTGGTGGTAGCCCTCACCCAATTCTGTGTGGCTTTCTTTGTAGAGGATTCCATNM_198505 RefSeq chr3 -
193275041 193378725 ATP13A5 344905 ATPase type 13A5
GO:0008152|GO:0016021|GO:0016887|GO:0005524|GO:0046872|GO:0006812 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140180_PI430048170 0.000591853588778867 0.1922745303667842.38430478936142
2.34921395087873 1.93752430973816 A A A 4.75827083731512 4.24244397605264
4.78581608501819 P P P LNCV6_140180_PI430048170 mRNA
GCCTTAAATTCCCAGTAAAGAATGTGAAAGCAAGCATGTAAAATAAACTGGTCTTCATGA NM_032385 RefSeq chr5
- 154818491 154850653 FAXDC2 10826 fatty acid hydroxylase domain containing 2
GO:0005506|GO:0016491|GO:0006633|GO:0016021|GO:0055114 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140435_PI430048170 0.1581832547462821.14925792664357 6.62307096389663
6.91201784888418 6.70863340996372 P P P 6.65882659199886 6.58466075554864
6.40157224726824 P P P LNCV6_140435_PI430048170 mRNA
GTTGTGTACAACTCCACGAGGTGAAAAATATTCAGTAACTTGTTTACATAGCATTTGTGT NM_001853 RefSeq chr20
+ 62817061 62841159 COL9A31299 "collagen, type IX, alpha 3"
GO:0008585|GO:0030020|GO:0022617|GO:0030198|GO:0007411|GO:0030574|GO:0005578|GO:0005788|GO:0005
594|GO:0005576|GO:0008584 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140366_PI430048170 0.2001607815463632.15967499732174 0.423726242426508
2.09937847534727 1.94432486225277 A A A 0.2625928735934030.288333065003795
0.975608788407743 A A A LNCV6_140366_PI430048170 mRNA
TAATACATTTTGGTGTTACCCAGATGCTTTCTAGAACGGGTTCTTTCCTCATCCCTGCCA NM_003363 RefSeq chr3
- 49277143 49340103 USP4 7375 "ubiquitin specific peptidase 4 (proto-oncogene), transcript variant
1"
GO:0000244|GO:0005515|GO:0016579|GO:0004843|GO:0005886|GO:0005634|GO:0005764|GO:0046872|GO:0031
685|GO:0042802|GO:0004197|GO:0005737|GO:0031647|GO:0061136|GO:0034394|GO:0043161|GO:0031397 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131335_PI430048170 0.0104349166550696 0.7247496012917671 1.8373346342038
11.9180718108042 11.7204065915423 P P P 12.1395622770207 12.3988000628098
12.3253836036397 P P P LNCV6_131335_PI430048170 mRNA

CAAGGCAAATCCATGGATGAGAAGTGCAATGGGCATAGTAAAAGTGCATGAATTTATCTT NM_001607 RefSeq chr3 - 38122709 38137242 ACAA1 30 "acetyl-CoA acyltransferase 1, transcript variant 1" GO:0005515|GO:0000038|GO:0006635|GO:0016401|GO:0005782|GO:0044281|GO:0036109|GO:0033559|GO:0043231|GO:0016020|GO:0008206|GO:0033540|GO:0003988|GO:0044255|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_41868_PI430048170 0.1760688819376140.9562953469033040.2843081969270870.31372605094335 0.35248199140466 A A A 0.3881579362309360.3225435519469670.431945424176774 A A A LNCV6_41868_PI430048170 mRNA
TTCTGTCACTAAATACCCACTCTGGTGAGCATATTCCATTTCAATAAAGATCATCGCTTC NM_001278577 RefSeq chr19 + 31588188 31593550 THEG5 100507527 "testis highly expressed protein 5, transcript variant 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141060_PI430048170 0.00932297431636947 2.65475215683623 1.76188237162288 1.88538420502373 1.4071261989571 A A A 0.32991136541635 0.2660170780479250.273479287254 A A A LNCV6_141060_PI430048170 mRNA
TCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCT NM_024164 RefSeq chr16 - 1228335 1230184 TPSB2 NA tryptase beta 2 (gene/pseudogene) NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136617_PI430048170 0.0312879381664083 1.29064532293151 5.66651688011794 5.47423722362379 5.46450735963664 P P P 5.14432718365595 5.32580769090869 5.0238667710344 P P P LNCV6_136617_PI430048170 mRNA
TACCTGACTAAGAATGGCTCAGAGATACCCTCCACCATGCAAGATGCCAAAGACTTGATT NM_206919 RefSeq chr4 + 56505208 56523892 ARL9 132946 ADP-ribosylation factor-like 9 GO:0005622|GO:0007264|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75892_PI430048170 0.5193986404207571.18420962586021 1.04966828660052 0.269774836254187 0.304472316318064 A A A 0.3811635583052190.3689765216221280.281146167130315 A A A LNCV6_75892_PI430048170 mRNA
ACAAAAAGACAAATGATTGTAGGATCCATGGAAGTGCACTTAGGCTTGCTGTGGTGGAGG NM_173800 RefSeq chr5 + 115962453 116027602 LVRN NA laeverin NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139616_PI430048170 0.00413000603719689 0.35403649021714 7.16973313028092 6.8924997704184 7.43709468327285 P P P 8.30434736646382 8.7181508466512 8.94980127981349 P P P LNCV6_139616_PI430048170 mRNA
GACTTACCATAAGATGCACTGTTGATAATGCTTTCTGATGTGTGTTTGATAAGAGTGATA NM_175866 RefSeq chr1 + 162497804 162529629 UHMK1 127933 "U2AF homology motif (UHM) kinase 1, transcript variant 1" GO:0005515|GO:0030424|GO:0071598|GO:0003723|GO:0005634|GO:0032839|GO:0005524|GO:0031175|GO:0046777|GO:0018105|GO:0004674|GO:0043021|GO:0045948|GO:0007050|GO:0019899|GO:0046825|GO:0016740 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63614_PI430048170 0.00890443088588115 1.50858911423101 9.27403831981069 9.28907068171052 9.14213357030408 P P P 8.78126249227629 8.65483738320063 8.47805459888847 P P P LNCV6_63614_PI430048170 mRNA
TCCATTACCTGTTGCTGAAGGCGGGTGCTAGGCTGGCTGGGTGTCAAGGAGCAGGCTCCA NM_002917 RefSeq chr17 - 82047901 82051774 RFNG 5986 RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase GO:0045747|GO:0007389|GO:0033829|GO:0005576|GO:0030154|GO:0046872|GO:0007399|GO:0032092|GO:0003674|GO:0030173|GO:0008152|GO:0009887|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129422_PI430048170 0.00191476253186047 0.1353943932901250.497075635177742 0.4790280453218780.422604931196773 A A A 3.07837796249301 3.37611575535568 3.55931696200204 P P P LNCV6_129422_PI430048170 mRNA
GGAGAGCGAGAACCATTTTGGAAACTGTAATGTAACTTATTTTTTCCTTTAACCTCGTCA NM_018896 RefSeq chr17 + 50561067 50627471 CACNA1G 8913 "calcium channel, voltage-dependent, T type, alpha 1G subunit, transcript variant 1"

GO:0086010|GO:0005886|GO:0008332|GO:0007268|GO:0005891|GO:0010045|GO:0060371|GO:0070509|GO:0002027|GO:0007411|GO:0045956|GO:0097110|GO:0042391|GO:0070588|GO:0006810|GO:0034765 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74951_PI430048170 0.140593827418974 1.78332668038851 3.48330416116646 3.59811977223854 2.59708667702346 P P A 2.59938294363688 1.73321230590001 2.82166028780773 P A P LNCV6_74951_PI430048170 mRNA
ATAAAAATGAAACCAGTTCCAGACTTGGTTCCCGGAAATTTTAAGAGCCAGCTTCAGAAG NM_000508 RefSeq chr4 - 154583127 154590745 FGA 2243 "fibrinogen alpha chain, transcript variant alpha-E"
GO:0005515|GO:0051258|GO:0005886|GO:0050714|GO:0072562|GO:0005615|GO:0043623|GO:0045921|GO:1900026|GO:0045907|GO:0030198|GO:0031091|GO:0034116|GO:0031093|GO:0070374|GO:0030674|GO:0050839|GO:0005938|GO:0070062|GO:0009986|GO:0090277|GO:0005102|GO:0005577|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134259_PI430048170 0.295857614070588 0.649207009643438 0.496952112922971 2.49056700717064 1.21427880897412 A A A 2.39484230997682 2.55172042083265 1.71453780097171 A A A LNCV6_134259_PI430048170 mRNA
ATTGTGTTTTGAGGTTTCCTTCAGACAGATTCCAGGCGATGTGCAAGTGTATGCACGTGT NM_001145808 RefSeq chr16 + 31259966 31332892 ITGAM 3684 "integrin, alpha M (complement component 3 receptor 3 subunit), transcript variant 1"
GO:0005515|GO:0034142|GO:0005886|GO:0005634|GO:0014005|GO:0050900|GO:0046872|GO:0001948|GO:0030198|GO:0010668|GO:0007155|GO:0008201|GO:0070062|GO:0008305|GO:0009986|GO:0046982|GO:0002523|GO:0030593|GO:0001846|GO:0043395|GO:0002224|GO:0007596|GO:0007229|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131312_PI430048170 0.00111029010367369 2.06816753635736 10.9772758682998 11.1398683992484 11.1301356081291 P P P 9.88193614921652 10.1751998849795 10.0359002302926 P P P LNCV6_131312_PI430048170 mRNA
GGTCCAGCTACTTCCTTTTGGAACCTTAAATAGAATGGGTGTTGGTTGATTAATTTTATT NM_006397 RefSeq chr19 + 12806613 12813648 RNASEH2A 10535 "ribonuclease H2, subunit A"
GO:0032299|GO:0006260|GO:0004523|GO:0003723|GO:0005634|GO:0004540|GO:0006298|GO:0046872|GO:0006401 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132227_PI430048170 0.177250412568269 0.706173603332399 0.351166012227491 0.321936308607747 0.310583244656429 A A A 1.17673179742802 0.818781314233532 0.387513824700219 A A A LNCV6_132227_PI430048170 mRNA
GAGGTCCAAAGAAATGACTCCTTTTTAAGGGATGGGCATAAAAAAGTGATCAAAACATTG NM_181847 RefSeq chr12 - 47075706 47079951 AMIGO2 347902 "adhesion molecule with Ig-like domain 2, transcript variant 2"
GO:0005515|GO:0043069|GO:0043066|GO:0005886|GO:0007420|GO:0005634|GO:0016021|GO:0007156|GO:0007157 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141073_PI430048170 0.626423896570022 1.00728159869631 0.436482757947742 0.453348124479095 0.396624599194828 A A A 0.432079451216928 0.400885446076228 0.422499264598338 A A A LNCV6_141073_PI430048170 mRNA
CTTATGAGCTACCAAAACTAAATTCTTTCTCTGCTATTAACTGGCTAGAAGACATTCATC NM_001081455 RefSeq chr3 - 151212116 151249210 P2RY14 9934 "purinergic receptor P2Y, G-protein coupled, 14, transcript variant 1" GO:0045029|GO:0007186|GO:0005886|GO:0045028|GO:0005887|GO:0035589|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133589_PI430048170 0.697139624223669 0.96906849053586 10.6392559836344 10.432434894798 10.2823309323147 P P P 10.4775786771671 10.6109199428984 10.4170159733009 P P P LNCV6_133589_PI430048170 mRNA
ACTAGTATGATGCAGTGTCCAGTGTGAACAGCAGAAATTAAACATGTTGCAACCAAAAAA NM_024544 RefSeq chr1 - 20499447 20508181 MUL1 79594 mitochondrial E3 ubiquitin protein ligase 1
GO:0051898|GO:0005515|GO:0004842|GO:0030308|GO:0016567|GO:0050689|GO:0016874|GO:0071650|GO:0090

141|GO:0042802|GO:0005739|GO:0005737|GO:0060339|GO:0019789|GO:0033235|GO:0004871|GO:0043123|GO:0051646|GO:0031625|GO:0005777|GO:0045824|GO:0000266|GO:0006919|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65531_PI430048170 0.591047692519954 1.07569045267441 3.41963971934001 3.88871467878952 3.77283685210994 P P P 3.5102324145611 3.75079745814619 3.53218294997413 P P P LNCV6_65531_PI430048170 mRNA CGGGCTTTGTCACCGGGACCCGCAGGAGCCAGAACCACTCGGCGCCGCCTGGTGCATGGG NM_004881 RefSeq chr2 - 24077432 24085215 TP53I3 9540 "tumor protein p53 inducible protein 3, transcript variant 1" GO:0048038|GO:0008270|GO:0006739|GO:0003960|GO:0070402|GO:0042803|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144905_PI430048170 0.151506831346442 1.04903137081466 0.385453310208185 0.360658779160412 0.283427260866834 A A A 0.268900703765 0.286443286472643 0.268902499814699 A A A LNCV6_144905_PI430048170 mRNA TTCCTGTCATTACCCATTGTAACAGAGCCACAAACTAATACTATGCAATGTTTTACCAAT NM_002164 RefSeq chr8 + 39913808 39928791 IDO1 3620 "indoleamine 2,3-dioxygenase 1" GO:0006569|GO:0070233|GO:0032693|GO:0046006|GO:0070234|GO:0002534|GO:0032735|GO:0044281|GO:0046872|GO:0030485|GO:0005829|GO:0042130|GO:0034641|GO:0002678|GO:0032496|GO:0007565|GO:0004833|GO:0009055|GO:0032421|GO:0033555|GO:0002666|GO:0019441|GO:0033754|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98337_PI430048170 0.0295143199932943 1.45946418130554 4.9762709819166 5.40041081152992 5.11293528121555 P P P 4.78963475505926 4.62554160249306 4.45128508584151 P P P LNCV6_98337_PI430048170 mRNA TTGGCCAAGTGCATAAGACTAAGGAGCAGTTTGGCCAGGACGGCCCCATCTCTGTCCACT NM_002850 RefSeq chr19 - 5205507 5340803 PTPRS 5802 "protein tyrosine phosphatase, receptor type, S, transcript variant 1" GO:0005515|GO:0022038|GO:0021766|GO:0021987|GO:0021510|GO:0030198|GO:0005887|GO:0005001|GO:0021549|GO:0007155|GO:0035335|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137719_PI430048170 0.108828713973897 0.676327426049338 3.15566604975906 3.62871584348031 3.30830016938873 P P P 4.00636296017466 4.22421023068687 3.50478782852556 P P P LNCV6_137719_PI430048170 mRNA ATATTTTCTCATTGGCAGTCGGCCACGTAGGTGACCAGGTGGCAGAGGATACTGCTGGCC NM_001278651 RefSeq chr22 - 41244776 41286017 RANGAP1 5905 "Ran GTPase activating protein 1, transcript variant 1" GO:0005515|GO:0048471|GO:0031965|GO:0005829|GO:0032853|GO:0005098|GO:0007165|GO:0046826|GO:0000922|GO:0005737|GO:0005643|GO:0000777|GO:0000776|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111740_PI430048170 0.582148866426743 1.10590632643561 10.3425393751016 10.7626389379236 10.9748188271803 P P P 10.5048011151816 10.4423683414906 10.7485435552014 P P P LNCV6_111740_PI430048170 mRNA AAGGCATTTGTTAGAAGAGACTGGGACAATTCAGGACCTTTTTGTGGAACTATAAGTAGC NM_016447 RefSeq chr7 + 24573345 24693703 MPP6 51678 "membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6), transcript variant 1" GO:0005515|GO:0006461|GO:0016020|GO:0005886|GO:0030165|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142415_PI430048170 0.617508938470664 1.23918605513873 1.64985799537159 1.64318185119042 0.428076446888541 A A A 1.00395345359112 1.53496914538612 0.304979384136128 A A A LNCV6_142415_PI430048170 mRNA AAAGTTAAAAGAGGAAGAGTTGTCCCTGTTTTACCAAATATAGGTAGTGGTGGCAGTTCA NM_144644 RefSeq chr4 - 176184573 176195671 SPATA4 132851 spermatogenesis associated 4 GO:0003674|GO:0005737|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90498_PI430048170 0.63998408039117 1.04379450781024 12.6203948814384 12.3648972592646 12.2978494135479 P P P 12.4583829013694 12.3477332847365 12.3076913502227 P P P

LNCV6_90498_PI430048170 mRNA
AAGAAGATTCCCACCCCTGCCTCCCATGCCTGGTCCCAAGACAGTGAGACAGTCTGGAAA NM_005556RefSeq chr12
+ 52233169 52248925 KRT7 3855 "keratin 7, type II"
GO:0005882|GO:0005515|GO:0005737|GO:0005198|GO:0016032|GO:0005634|GO:0045095|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127671_PI430048170 0.00726316248355345 1.25904192673835 13.3392690787362
13.4336007190675 13.5066860384613 P P P 13.0084485815484 13.1519945520734
13.1230439785529 P P P LNCV6_127671_PI430048170 mRNA
ATGGACGGGGCATTCCAGCTGAGACACTGTGATTTTAAATTAAATCTTTGTGGTCTTTGC NM_006012RefSeq chr19
+ 6361451 6368904 CLPP 8192 caseinolytic mitochondrial matrix peptidase proteolytic subunit
GO:0005739|GO:0005515|GO:0004252|GO:0051603|GO:0005759|GO:0051260|GO:0009368|GO:0008233|GO:0042
802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135192_PI430048170 0.447304171432755 0.927282124803015 9.87811967290989
9.93330145833758 9.74311604175887 P P P 10.1600954163237 9.88810947033604
9.81646379152781 P P P LNCV6_135192_PI430048170 mRNA
GAGTTTTTCTTTGTTCATGGAATGTTTTTTCCTGATTAAATGTTGGGGAAATGCCATCCANM_017514RefSeq chrX +
154458280 154473646 PLXNA355558 plexin A3
GO:0005515|GO:0005886|GO:0050919|GO:0048843|GO:0007275|GO:0021860|GO:0021785|GO:0002116|GO:0005
622|GO:0021766|GO:0016020|GO:0017154|GO:0007411|GO:0051495|GO:0021637|GO:0071526|GO:0016021|GO:0
021612|GO:0004888. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82067_PI430048170 0.164224034104826 0.587556678354957 2.55648275677903 1.35983542557052
1.25336184480563 A A A 2.68924286823582 2.61453737777114 2.55182646614128 A P P
LNCV6_82067_PI430048170 mRNA
AAGCCTTTTGAAAAGAATTGCCAAAATATTACTGTGGAGGTTGAAGAGTTTGTTCCAGAA NM_144658RefSeq chrX
+ 118495908 118686160 DOCK11 139818 dedicator of cytokinesis 11
GO:0032321|GO:0007596|GO:0007264|GO:0017048|GO:0005089|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145502_PI430048170 0.258576033578803 1.05698985173625 0.492021507787363
0.61095954124664 0.562114423249529 A A A 0.572870755655743 0.420685760121647
0.428994746353847 A A A LNCV6_145502_PI430048170 mRNA
GTTTCTCTTGAGCTTTTGTTTCTGTTTGCTCAGACCCTGTTTTCATGTTGTTGAATAAAC NM_001003811 RefSeq chrX
- 70528939 70908717 TEX11 56159 "testis expressed 11, transcript variant 1"
GO:0009566|GO:0005515|GO:0043066|GO:0000795|GO:0051026|GO:0000712|GO:0000801|GO:0007060|GO:0006
311|GO:0007130|GO:0008584|GO:0007131 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72198_PI430048170 0.415649599104205 0.510715132384558 0.388975479303096 0.375362002751838
0.258174486010439 A A A 0.347269092140135 2.29029960279055 0.358279690038671 A A A
LNCV6_72198_PI430048170 mRNA
TTTACTGAGGTGCACGAGGGCCGTGCTGACATCATGATCGACTTCGCCAGGTACTGGCAT NM_005940RefSeq
chr22_KI270879v1_alt + 9210 20678 MMP11 4320 matrix metallopeptidase 11
GO:0005796|GO:0045599|GO:0005509|GO:0005578|GO:0005576|GO:0007275|GO:0022617|GO:0030198|GO:0030
199|GO:0030574|GO:0006508|GO:0071711|GO:0008270|GO:0004222 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138075_PI430048170 0.00153506591965178 2.67300973615821 7.33828772192669
7.30445962906402 7.24426297377176 P P P 6.03279119772856 5.75342625630487
5.83241646250228 P P P LNCV6_138075_PI430048170 mRNA
TCCTTACAGGACTGACACCCTAATGCCAATAAAAGTTGCTCATTATGGACTGCTACAAAG NM_032211RefSeq chr10
- 98247685 98268250 LOXL4 84171 lysyl oxidase-like 4
GO:0043235|GO:0005515|GO:0016020|GO:0005507|GO:0004720|GO:0005615|GO:0006898|GO:0070062|GO:0055
114|GO:0005044 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_131811_PI430048170 0.0174670816109247 1.16780453046591 9.49800817032899
9.55388734974896 9.53173084934248 P P P 9.27941960186051 9.25051595075766
9.37963720579834 P P P LNCV6_131811_PI430048170 mRNA
CAACTGTATCAGTAGCACAGTATTTTTGTATGAAAAGTGGGAGACTTCTGAACAGTAATT NM_014338 RefSeq chr22
- 31618490 31630824 PISD 23761 phosphatidylserine decarboxylase
GO:0005739|GO:0006646|GO:0005634|GO:0044281|GO:0004609|GO:0006644|GO:0046474 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144948_PI430048170 0.8271253043005620.989221965855275 1.83411283369127
0.45017644122228 0.993226178202197 A A A 0.915365118244798 1.5400443023515
1.13992870933721 A A A LNCV6_144948_PI430048170 mRNA
CACAGAGGGACAGGAAATGTGATTTATTGACCATAAAAGCTTTAATTTAAAATTGCTGGC NM_138796 RefSeq chr1
+ 217631323 217868153 SPATA17 128153 spermatogenesis associated 17 GO:0005516|GO:0005737 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141312_PI430048170 0.9334742534946671.01179958745715 8.28962800647359
8.37937800603642 8.72489852051081 P P P 8.23656516587679 8.41654710101267
8.69088881376735 P P P LNCV6_141312_PI430048170 mRNA
CCTTATTCTGTGTGTAGACATTGTATTCCACAATTTTGAATGGCTGTGTTTTACCTCTAA NM_020755 RefSeq chr6 -
122443347 122471807 SERINC1 57515 serine incorporator 1
GO:0006665|GO:0005515|GO:0015194|GO:0005886|GO:0015825|GO:0005789|GO:0051347|GO:0016021|GO:0008
654|GO:0006658|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139532_PI430048170 0.000490051911661607 0.3397088444856315.86070474286447
5.48727720600799 5.71532145845613 P P P 7.09303490783894 7.20244580200386
7.44256397844619 P P P LNCV6_139532_PI430048170 mRNA
CTGCCCTTCAGTTCTTTATCCTGATACCATTTAACACTGTCTGAATTAACTAGACTGCAA NM_001244944 RefSeq
chr7 + 90211685 90237678 STEAP2 261729 "STEAP family member 2, metalloreductase, transcript
variant 4"
GO:0052851|GO:0005215|GO:0005886|GO:0006893|GO:0008823|GO:0055072|GO:0046872|GO:0005829|GO:0006
897|GO:0043231|GO:0045055|GO:0030173|GO:0015677|GO:0009725|GO:0030140|GO:0005769|GO:0010008|GO:0
055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128221_PI430048170 0.4448483680963010.7144146289815440.312747024626582
0.2718991657217960.286941416494238 A A A 0.2701988439009041.44745726978108
0.266821474726406 A A A LNCV6_128221_PI430048170 mRNA
GTACGTTACTTATTAAAGGGCGACTCTGTGTAAGTAACCTAAGAAACGAAGAAAAATTCT NM_199047 RefSeq chr14
- 55414210 55440545 TBPL2 NA TATA box binding protein like 2 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_98175_PI430048170 0.2142280447312170.8026803295924499.18391616074142 8.72024505645888
8.54278155091048 P P P 9.26833683880579 9.22273820001567 8.96719704913021 P P P
LNCV6_98175_PI430048170 mRNA
CAGCGGCCTCTCCTCCAACTTCAATGAATGGCATGAAGAGCAAAAATATCCCTTCCGGAG NM_007129 RefSeq chr13
+ 99981771 99986765 ZIC2 7546 Zic family member 2
GO:0031290|GO:0003700|GO:0001843|GO:0005634|GO:0003677|GO:0006351|GO:0031490|GO:0046872|GO:0051
091|GO:0005737|GO:0007420|GO:0045893|GO:0007601|GO:0045892|GO:0048066 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130541_PI430048170 0.0111493565263835 0.48515661853237 0.434639791388782
0.4471027155514190.267404316566882 A A A 1.13022505024015 1.62323462755736
1.48914324484966 A A A LNCV6_130541_PI430048170 mRNA
ATTCCTTCACCCTATTTACCTTCCTCAAGTACTGGAGAATAAAATTGAACTGAATGTTTG NM_178499 RefSeq chr12
+ 119334711 119541047 CCDC60 160777 coiled-coil domain containing 60 NA . NA - . NA
NA NA NA NA NA NA NA NA

LNCV6_140635_PI430048170 0.8476967777297591.01060776222415 0.565673695149735
0.5071796356769290.595487269764452A A A 0.3944953010076230.714751498867465
0.496036184973107A A A LNCV6_140635_PI430048170 mRNA
CCATCCAACTCCTCTAGTCAGCACTAGATCATGGGATCCTAAAATAAACCTTGGAAAAAT NM_000498RefSeq chr8
- 142910558 142917843 CYP11B2 1585 "cytochrome P450, family 11, subfamily B, polypeptide 2"
GO:0006705|GO:0006805|GO:0005506|GO:0055075|GO:0005743|GO:0055078|GO:0047783|GO:0044281|GO:0004
507|GO:0032870|GO:0034651|GO:0003091|GO:0005739|GO:0035865|GO:0002017|GO:0006700|GO:0032342|GO:0
016125|GO:0008202|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129473_PI430048170 0.0330150485068861 0.4704418177403772.26130544235707
2.29540790866564 1.49223665260689 A A A 3.19814378346175 2.89262031686293 3.3221781403578
P P P LNCV6_129473_PI430048170 mRNA
GTGGGGAATGGTGTGTACCGATATATAGTATTTCTTTAGACAACTTGCAGATAATTTCTT NM_007218RefSeq chr8
+ 124474766 124488618 RNF139 11236 ring finger protein 139
GO:0005515|GO:0017148|GO:0004842|GO:0008285|GO:0016567|GO:0060628|GO:0005783|GO:0016874|GO:0070
613|GO:0002020|GO:0031648|GO:2000060|GO:0019787|GO:0005789|GO:0031396|GO:0004872|GO:0008270|GO:0
016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53692_PI430048170 0.2122997731571750.9569445101044151 0.9482726793933 11.0421490919885
10.9299269490301 P P P 11.0106215784944 11.0846261574471 11.0169362817376 P P P
LNCV6_53692_PI430048170 mRNA
CCCCAGGGCCAGCCTTAAGGTATCTAATAAAGTCTGAACTCTCCCTTCCAAAAAGTAGAA NM_001024732 RefSeq
chr1 - 29192656 29230958 MECR 51102 "mitochondrial trans-2-enoyl-CoA reductase, transcript
variant 2" GO:0005739|GO:0019166|GO:0006631|GO:0008270|GO:0006633|GO:0005634|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128833_PI430048170 0.4557888852956680.5787139085943030.402010475483744
0.4250621419365540.451924269917864A A A 2.12660756728136 0.355749645160983
0.400926239168038A A A LNCV6_128833_PI430048170 mRNA
CATGACACTGAAAAGATGATGCTATCAGATGCTGTTTAGAAAGCATTTATCTTGCATTTC NM_152538RefSeq chr3
- 118900630 119146051 IGSF11 152404 "immunoglobulin superfamily, member 11, transcript variant 1"
GO:0005886|GO:0016021|GO:0007155|GO:0040008|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_68430_PI430048170 0.79823254120869 0.93135517152874 3.83427501133285 4.23814891694138
3.86309712848283 P P P 3.73791529619554 3.90842448681801 4.51371212291581 P P P
LNCV6_68430_PI430048170 mRNA
ACATTCATGCCCAATAGTATAAGGGAACTCAAGGGAAAAGGAAACACACGCAAAAACTAT NM_170677RefSeq
chr15 - 36891020 37100140 MEIS2 4212 "Meis homeobox 2, transcript variant a"
GO:0003712|GO:0005515|GO:0003700|GO:0006366|GO:0001654|GO:0003714|GO:0005634|GO:0000122|GO:0070
848|GO:0000978|GO:0009612|GO:0043565|GO:0001077|GO:0031016|GO:0045638|GO:0045944|GO:0008134 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127010_PI430048170 0.2840755316513631.30393490194191 2.91960050051349
2.78873376485063 3.35981397144842 A A P 3.15905372592092 2.27196972173234
2.38215182023823 P A A LNCV6_127010_PI430048170 mRNA
GTCTTAAAACAAAATTCAATGTGGAAAAGCCTTTAGATGTTCTCCTAACTTCTGGGTTCA NM_001102657 RefSeq
chr19 - 52154871 52171643 ZNF836 NA zinc finger protein 836 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139996_PI430048170 0.7145842896488850.9852204064523840.424629758371341
0.3910474755640390.24811915136156 A A A 0.3468544957523270.402063246581908
0.384793993875176A A A LNCV6_139996_PI430048170 mRNA
CTTGATCTACAGTTTGCGGAACAAGGATGTGAAAGCTGCTTTCAAAAAGCTAATTGGAAA NM_001004730 RefSeq
chr11 + 56663685 56664618 OR5AR1 NA "olfactory receptor, family 5, subfamily AR, member 1

(gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129551_PI430048170 0.817421106576992 1.01866295892871 11.3501699441956
11.1068285550791 11.1177781448293 P P P 11.1282347501147 11.083319203674
11.2883712521691 P P P LNCV6_129551_PI430048170 mRNA
GCAGCCTGGAGAAAACCAGAGATCCAGTACAGAAAGGAAAGGATATTTATTGATTAACAG NM_032940 RefSeq
chr16 + 57462638 57472009 POLR2C 5432 "polymerase (RNA) II (DNA directed) polypeptide C, 33kDa"
GO:0008380|GO:0010467|GO:0006368|GO:0006367|GO:0006366|GO:0006370|GO:0005634|GO:0003677|GO:0050
434|GO:0005737|GO:0006281|GO:0000398|GO:0006283|GO:0001055|GO:0034587|GO:0015630|GO:0046983|GO:0
005665|GO:0016032|GO:0005654|GO:0006289|GO:0035019 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_21341_PI430048170 0.0480793280181834 0.612772169852568 2.84383775875618
3.38481793411536 3.22013931149607 A P P 4.20096175374007 3.78129623354629
3.56427938386588 P P P LNCV6_21341_PI430048170 mRNA
TTACTTGACTCCTTATGTGCATGGCAATGTATTAAAATGTGGGATTTCTATTACCGTGTA NM_001101676 RefSeq
chr8 - 118189455 118621945 SAMD12 401474 "sterile alpha motif domain containing 12, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119586_PI430048170 0.444382438612359 0.848343828329925 3.68696528958982 3.7839107646558
3.60698536728805 P P P 4.13278314263195 3.46312257511834 4.10520551005886 P P P
LNCV6_119586_PI430048170 mRNA
TTGTTCTCAGGGTGTGTGGAATCAACTTTCCGGAAGCAACCAGCCCACCAGAGGAGTCCC NM_002820 RefSeq chr12
- 27962320 27971983 PTHLH 5744 "parathyroid hormone-like hormone, transcript variant 2"
GO:0010468|GO:0008284|GO:0008285|GO:0030819|GO:0007267|GO:0051428|GO:0005615|GO:0043433|GO:0005
737|GO:0016485|GO:0060649|GO:0030855|GO:0043129|GO:0032331|GO:0007565|GO:0005794|GO:0048286|GO:0
046058|GO:0005576|GO:0060659|GO:0001958|GO:0001501|GO:0007492|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140975_PI430048170 0.26299117239183 0.730528194834034 0.41476354154827
0.379765298266903 0.402832575532474 A A A 0.354434575804642 1.26511539448687
0.793885480960978 A A A LNCV6_140975_PI430048170 mRNA
CTGCATTAATGTTATAGCTGTATTGATGTAATACCAGAGTTGTTACGTTCGGGTTATATG NM_080282 RefSeq chr17
- 69148006 69244815 ABCA10 10349 "ATP-binding cassette, sub-family A (ABC1), member 10"
GO:0005215|GO:0008152|GO:0006810|GO:0016021|GO:0016887|GO:0005524 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143739_PI430048170 0.36134388743302 1.60845629147689 0.684019013089289
2.02437275672389 0.643241124348438 A A A 0.590923886431384 0.591171145184407
0.571833892182613 A A A LNCV6_143739_PI430048170 mRNA
TCAAATTTGTTAGGAATCAGTTGGCCCCAAAAAACCTCATCTGAGCAAGCAGCCACGACA NM_181536 RefSeq chr16
- 71929537 71999978 PKD1L3 342372 polycystic kidney disease 1-like 3
GO:0005515|GO:0005262|GO:0005261|GO:0005886|GO:0009986|GO:0034703|GO:0001822|GO:0008324|GO:0071
468|GO:0050915|GO:0043235|GO:0070588|GO:0030246|GO:0033040|GO:0006812|GO:0070062|GO:0001581 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131699_PI430048170 0.515025022744824 1.16629811047011 5.15505789709929 4.6822385210491
4.84309762722057 P P P 5.32331445961425 4.45169423758841 3.93099589579848 P P P
LNCV6_131699_PI430048170 mRNA
CGTGGGGAGAGCTTTGCCTGTTAATAAAACGCACAAACCATTTCACACACAGTGAAAAAA NM_003857 RefSeq chr17
+ 76074800 76077541 GALR2 8811 galanin receptor 2
GO:0005515|GO:0007631|GO:0005886|GO:0007586|GO:0004966|GO:0007268|GO:0007275|GO:0007194|GO:0007
204|GO:0031175|GO:0006936|GO:0007218|GO:0045944|GO:0007611|GO:0007188|GO:0016021|GO:0017046|GO:0
007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110165_PI430048170 0.0121687112724868 2.02056383441044 9.76464831502011

9.79796772834341 10.055636173316 P P P 9.17997305636834 8.63138189294173
8.71837418515733 P P P LNCV6_110165_PI430048170 mRNA
ACTTTGGTCTTCATTCAATGTGTGATCAATGCTGTGTTTGCCAAGATCTGGTGGATCGTA NM_005827 RefSeq chr17
- 49700933 49707951 SLC35B1 10237 "solute carrier family 35, member B1, transcript variant 1"
GO:0072334|GO:0006810|GO:0005789|GO:0016021|GO:0005459|GO:0043231 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145504_PI430048170 0.2008480348665640.5106431322256540.274947669242378
0.3007896419214562.41602504663514 A A A 2.78858893614477 1.90782708157552
2.19259740059192 P A A LNCV6_145504_PI430048170 mRNA
GTAGATCTTCACCCCATTGTGGTGTCATCAATGAATCCAAAGCAGGTGCCATTATTTTTT NM_001301036 RefSeq
chr12 - 94567123 94616151 TMCC3 57458 "transmembrane and coiled-coil domain family 3, transcript
variant 2" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134671_PI430048170 0.0602280098796852 0.8393566797354444.30964344970784
4.10503058019834 4.31693833084808 P P P 4.48210609787611 4.53059714910604
4.48620292571302 P P P LNCV6_134671_PI430048170 mRNA
GGTGATAAATCCTATAAAAGTAATAGGGGTGGTAAGAACATCAGAGAATCCACACAGGAA NM_001032372
RefSeq chr19 + 44165163 44177685 ZNF226 7769 "zinc finger protein 226, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137800_PI430048170 0.13447726625662 0.9395168205882390.247641942930031
0.2733217468790180.305784996075896 A A A 0.4389952180545780.346999916732833
0.308225527596675 A A A LNCV6_137800_PI430048170 mRNA
TTAATTTAACTCAGCCTCTGTGTGAGTGGATGATTCAGGTTGCCAGAGACAGAACCCTCA NM_001007532 RefSeq
chr17_KI270908v1_alt + 701368 701813 STH246744 saitohin GO:0005737|GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140107_PI430048170 0.0366532418165147 0.78845325623783811.1089006540543
11.0489335317065 10.8362965708372 P P P 11.3735178062761 11.3873771717344
11.2732720708577 P P P LNCV6_140107_PI430048170 mRNA
CGGGAGGGTGGGCTCTATATTTTCATTCCAAATAAAATTCTCTTTCTAAAAGCCAAAAAA NM_001018070 RefSeq
chr11 - 67438046 67443821 CORO1B 57175 "coronin, actin binding protein, 1B, transcript variant 2"
GO:0005515|GO:0090135|GO:0001725|GO:0035767|GO:0030036|GO:0005886|GO:2000394|GO:0005884|GO:0034
316|GO:0071933|GO:0015629|GO:0030027|GO:0031529|GO:0042802|GO:0005737|GO:0051015|GO:0016477|GO:0
042060|GO:0051017|GO:0005925|GO:0031252|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_137645_PI430048170 0.0236716604164292 0.6040049522735984.94931438769519
4.72012429952193 4.78695429054956 P P P 5.27678727217388 5.54723079235833
5.78045927831749 P P P LNCV6_137645_PI430048170 mRNA
ATTTCAGGAAATCAGGAGGTGTTTCACAATACAGAATGATGGCCTTTAACTGTGAAAAAA NM_005257 RefSeq chr18
+ 22169436 22202528 GATA6 2627 GATA binding protein 6
GO:0005515|GO:0060045|GO:0071773|GO:0043627|GO:0003700|GO:0006366|GO:0044212|GO:0000981|GO:0003
705|GO:0003310|GO:0032911|GO:0032912|GO:0071158|GO:0060575|GO:0048645|GO:0003309|GO:0060430|GO:0
055007|GO:0001103|GO:0019901|GO:0000122|GO:0070848|GO:0000979|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136122_PI430048170 0.4973026689653480.9361713822947684.77704546932255
4.71928357851866 5.01114262974383 P P P 4.7486391436878 5.01931606200145
5.02490642312231 P P P LNCV6_136122_PI430048170 mRNA
AATAAAATGGTAGAGTGAACCTCCATGTACCCAGCATCCAGCTCCAGTAACCATCAACGT NM_000262 RefSeq chr22
- 42058333 42070842 NAGA 4668 "N-acetylgalactosaminidase, alpha-"
GO:0005737|GO:0016052|GO:0009311|GO:0046477|GO:0019377|GO:0016139|GO:0004557|GO:0008456|GO:0005

764|GO:0042803|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51385_PI430048170 0.0217297600675767 0.2989429748296061.40614442442178
1.52956869225285 2.27379808527789 A A A 3.56310106836643 3.51220300998741
3.51983358849707 P P P LNCV6_51385_PI430048170 mRNA
GATGTAGTCTTTATGTTTGGACAGTTCACCAGATTCTCAAGAAGGCTTTCAAACAACTAT NM_134442RefSeq chr2
+ 207529891 207605560 CREB1 1385 "cAMP responsive element binding protein 1, transcript variant B"
GO:0005515|GO:0008361|GO:0001190|GO:0003700|GO:0006366|GO:0003705|GO:0046889|GO:0002756|GO:0010
944|GO:0007219|GO:0007173|GO:0007411|GO:0002755|GO:0046887|GO:0007613|GO:0033363|GO:0003712|GO:0
001102|GO:0006996|GO:0038124|GO:0038123|GO:0005719|GO:0034134|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130397_PI430048170 2.69379279217846e-05 0.1749934677103982.10395994420897
1.97364298813639 1.89542342259425 A A A 4.38398888711205 4.47186008425489 4.6553732017141
P P P LNCV6_130397_PI430048170 mRNA
GACTATTTGCGTTGTGTGGCCTTAGTTTGTTTATTGACATTAACGAGTGTTTTAAAAAGG NM_018364RefSeq chr1
- 113761831 113812476 RSBN1 54665 "round spermatid basic protein 1, transcript variant 1"
GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128294_PI430048170 0.5441072710474651.02921674346509 15.0493510486308 14.981479652642
14.9854626283704 P P P 14.8671745531053 15.0690015129575 14.9493197091177 P P P
LNCV6_128294_PI430048170 mRNA
CAGTCTGCCCTTGTCACTGGTCTGAGGTCATTAAAATTACATTGAGGTTCCTACAAAAAA NM_005567RefSeq chr17
- 78971252 78979979 LGALS3BP 3959 "lectin, galactoside-binding, soluble, 3 binding protein"
GO:0031012|GO:0007165|GO:0006968|GO:0016020|GO:0005578|GO:0072562|GO:0007155|GO:0005615|GO:0006
898|GO:0070062|GO:0005044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128564_PI430048170 0.0100949072420117 0.9468167867508490.378647008281908
0.3568518344163840.334496920943045 A A A 0.4528456136842280.439300966178575
0.414452909026343 A A A LNCV6_128564_PI430048170 mRNA
AGATGGTGCGTTACTGCCATCTAATGGGAAAAGAGAAAACTGCAGTTGGGAAAAGCAGCT NM_001010846
RefSeq chr1 - 154479477 154502050 SHE126669 Src homology 2 domain containing E GO:0005515
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144939_PI430048170 0.7695764332521421.02913128797127 9.43251771607911
9.70474028993689 9.74785976107631 P P P 9.52869178911244 9.51001434519313
9.73133925690199 P P P LNCV6_144939_PI430048170 mRNA
AAGCTTCTCAAGGAGAAATATGGCATCAACACAGATCCACCAAAATAAATGTTTTCTACA NM_016047RefSeq chr2
- 24067583 24076444 SF3B6 51639 "splicing factor 3b, subunit 6, 14kDa"
GO:0008380|GO:0010467|GO:0000166|GO:0000398|GO:0005654|GO:0005689 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137291_PI430048170 0.0156812806550745 0.4733241165723831 1.5832989047735
11.5450329125049 11.5504869967373 P P P 12.3535601531943 12.7955966437331
12.7291067591613 P P P LNCV6_137291_PI430048170 mRNA
AACACACCCACACCAGGCCTCAGGATTTTGTGTTGATCAAGTTCCAAGGAAAAGGAACAT NM_178448RefSeq chr9
- 137062126 137070576 SAPCD2 89958 suppressor APC domain containing 2
GO:0005737|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96218_PI430048170 0.0734284857209938 0.7197888907197910.2015745439814
10.2259647635122 10.4243708486119 P P P 10.5425403628771 10.6553452687244
11.0394043772539 P P P LNCV6_96218_PI430048170 mRNA
CACTGTATTAACCAATGGAGAAGCAGCAATGCAGTCTTCCAATTCAGAATCAAAAAAGAA NM_006773RefSeq chr2
+ 117814678 117832377 DDX18 8886 DEAD (Asp-Glu-Ala-Asp) box polypeptide 18
GO:0005515|GO:0004004|GO:0016020|GO:0008152|GO:0005730|GO:0005524 . NA - . NA NA
NA NA NA NA NA NA NA

LNCV6_59094_PI430048170 0.00410601674389066 2.02495735337599 1.88572702037069 1.91658129176599 1.72492437957519 A A A 0.663607248700813 0.748555978317202 1.0409551856398 A A A LNCV6_59094_PI430048170 mRNA TAGCAAAACAAGCCAGAAGACCATGGATGATTTAAATTTGAGCACCTCTGAGGCTCTGCG NM_201444 RefSeq chr12 + 55932027 55954023 DGKA 1606 "diacylglycerol kinase, alpha 80kDa, transcript variant 1" GO:0005886|GO:0005509|GO:0030168|GO:0005524|GO:0007205|GO:0005829|GO:0035556|GO:0016310|GO:0003951|GO:0005543|GO:0016020|GO:0007596|GO:0004143 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142720_PI430048170 0.179365613207865 1.0483510666901 0.367246548610209 0.372495636466372 0.473070104134 A A A 0.327362960813237 0.314243801207245 0.368761459145969 A A A LNCV6_142720_PI430048170 mRNA GAATAAGTCATGTTCCTTCAAGATCATGTACCCCAATTTACTTGCCATTACTCAATTGAT NM_001171171 RefSeq chr3 - 39263493 39281273 CX3CR1 1524 "chemokine (C-X3-C motif) receptor 1, transcript variant 2" GO:0005515|GO:0043005|GO:0048471|GO:0030336|GO:0070098|GO:0005886|GO:0009611|GO:0071560|GO:0045766|GO:0032809|GO:0006968|GO:0071222|GO:0021795|GO:0006935|GO:0007186|GO:0016495|GO:0005887|GO:0016525|GO:2001240|GO:0004950|GO:0016032|GO:0002282|GO:0048246|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142451_PI430048170 0.0144515419050072 0.290629532133388 2.34474642008267 1.80477383151511 1.95816554756506 A A A 3.17830992345744 3.98537397642885 4.16819165787375 P P P LNCV6_142451_PI430048170 mRNA CCTCATTCTTTGTGTAGTATCTACACATTGTTATAAGCCAAAAAACAAAGTCTGTCTGGA NM_002895 RefSeq chr20 - 36996350 37096000 RBL1 5933 "retinoblastoma-like 1, transcript variant 1" GO:0005515|GO:0005667|GO:0010467|GO:0006367|GO:0043550|GO:0005634|GO:0000122|GO:0006351|GO:0045944|GO:0051726|GO:0016032|GO:0005654|GO:0007179|GO:0000278|GO:0008134|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88501_PI430048170 0.0134279201303937 0.633866006206011 4.86317280641625 4.80862779636847 4.59860083103554 P P P 5.43685559626801 5.40150583399218 5.41838045028809 P P P LNCV6_88501_PI430048170 mRNA TCCGTAGCACTGAGGACCCCCGGAGAAGATGGGGAGGAAAAAGATTCAGATCCAGCGAAT NM_005920 RefSeq chr1 - 156463720 156500842 MEF2D 4209 "myocyte enhancer factor 2D, transcript variant 1" GO:0005515|GO:0000977|GO:0003700|GO:0042826|GO:0006366|GO:0000981|GO:0006915|GO:0005634|GO:0035914|GO:0001649|GO:0043231|GO:0007399|GO:0007512|GO:0001958|GO:0007517|GO:0002062|GO:0045944|GO:0046983|GO:0005654|GO:0033613 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61788_PI430048170 0.760509056541103 1.08186375135607 0.493127234744841 0.329822370915269 1.09868399168577 A A A 0.321157990367105 0.883165520080209 0.43138868659555 A A A LNCV6_61788_PI430048170 mRNA GACCATTGGGAAGGAGGTGACTATGGATGTTCCTGCTCCAAATGTACCCGTTGTGGGCAT NM_178034 RefSeq chr15 - 42067682 42094554 PLA2G4D 283748 "phospholipase A2, group IVD (cytosolic)" GO:0036149|GO:0036148|GO:0044281|GO:0046872|GO:0005829|GO:0036150|GO:0004623|GO:0006644|GO:0006654|GO:0009395|GO:0030659|GO:0036151|GO:0036152|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139451_PI430048170 0.0422126657455281 0.603431942280421 7.31108693766189 7.63705808890239 7.99494576315142 P P P 8.19618185810192 8.3520549790836 8.62847731614042 P P P LNCV6_139451_PI430048170 mRNA GAAAGATCTTCATTGGGGGATTGAGCAGCATTTAATAAAGTCTATGTTTGTATTTTGCCT NM_006243 RefSeq chr1 + 212285536 212361863 PPP2R5A 5525 "protein phosphatase 2, regulatory subunit B', alpha, transcript variant 1" GO:0005515|GO:0030018|GO:0008601|GO:0035307|GO:0090219|GO:0000159|GO:0005634|GO:0031430|GO:0007165|GO:0005737|GO:0016020|GO:0090005|GO:0019900|GO:0000775 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_139312_PI430048170 0.0181497649487044 0.681477304592621 5.96140705443621
5.80859536399255 5.85273256998017 P P P 6.40164272448045 6.26051676133301
6.60391005947443 P P P LNCV6_139312_PI430048170 mRNA
CCTGTGGTTCTGGGTAGCAAAGGAAATACAGTATAACTTAATTTGTTATGGATTAGTCTT NM_017634 RefSeq
chr8 - 25427847 25458468 KCTD9 54793 potassium channel tetramerization domain containing 9
GO:0051260 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137757_PI430048170 0.143772428777719 1.08960369535058 0.508025791100788
0.661124630991778 0.593452576867717 A A A 0.366033809626514 0.481134096987661
0.542563645841482 A A A LNCV6_137757_PI430048170 mRNA
GGTGGCACAGCTATTCATAACCTATATTCTAGAGTAGACAATCTGGACTATGTAATAAAT NM_004288 RefSeq
chr2 - 157414618 157444092 CYTIP 9595 cytohesin 1 interacting protein
GO:0005515|GO:0005737|GO:0005654|GO:0030155|GO:0005938|GO:0005769 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_128876_PI430048170 0.00546054347982436 1.64328747956672 4.1959749659875
4.532995959332 4.35047862393971 P P P 3.73493682115927 3.51054552355768
3.69421866667259 P P P LNCV6_128876_PI430048170 mRNA
TACACACCCAGACACACACACACACAGTTTTTGCTTTTTCTGGAAAATCTTTCTTTCTCT NM_001270422 RefSeq
chr17 + 70075224 70135605 KCNJ16 3773 "potassium channel, inwardly rectifying subfamily J,
member 16, transcript variant 4"
GO:0005242|GO:0005886|GO:0005887|GO:0008076|GO:0010107|GO:0007268|GO:0034765|GO:0006813 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_129443_PI430048170 0.00151588906102903 3.55741350483665 4.95251738643942
5.3101900138612 5.40150583399218 P P P 3.38761303293498 3.68399656353691
3.07387951621664 P P P LNCV6_129443_PI430048170 mRNA
AACAGTTTTGCCAGAGCAAGAAACTCCCAGAGAATAAATGTATCCCCATCTGCCTCTAAA NM_182504 RefSeq
chr7 + 73861158 73865893 WBSCR28 135886 Williams-Beuren syndrome chromosome region 28
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143166_PI430048170 0.349548874757536 0.733372093288305 3.00580698712285
1.76611616258793 1.23098677133437 P A A 2.81536631856091 2.40645295046672
2.6894078991106 P A P LNCV6_143166_PI430048170 mRNA
ACCCTTCTTCATGTTCAATTATTTCCCCCATTTTTCCCAGGCAAATAAAATTCCCTAAAGNM_001887RefSeq chr22 -
26599397 26618027 CRYBB1 1414 "crystallin, beta B1" GO:0005212|GO:0007601 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_129125_PI430048170 0.0380169541334066 0.600743093120607 3.69254194997705
3.68533020903848 3.40201236344857 P P P 4.08801661669712 4.1782219748263
4.66800553483985 P P P LNCV6_129125_PI430048170 mRNA
GAACCCTGTAAGAAATAGCCCTGCTGATAGTTTTCTAGGTTTATCATGTTTGATTTTTAC NM_001284514 RefSeq
chr17 - 39757714 39864188 IKZF3 22806 "IKAROS family zinc finger 3 (Aiolos), transcript variant 14"
GO:0005515|GO:0045577|GO:0003700|GO:0046982|GO:0005886|GO:0006357|GO:0005634|GO:0030888|GO:0042
981|GO:0046872|GO:0006351|GO:0042803|GO:0043565|GO:0042113|GO:0045619|GO:0005737|GO:0007498 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137246_PI430048170 0.00510203670972751 0.467892152990769 3.59699086192961
3.86247651883063 3.85535937688948 P P P 4.69619324597722 4.74058509991062
5.13852664098577 P P P LNCV6_137246_PI430048170 mRNA
TTTCACATGTTCAAAATGAAGCGTACTATTTCCCCTCCAATAAACGAAGTCTCCTGCCAA NM_016018RefSeq chr8
+ 132775357 132848807 PHF20L1 51105 "PHD finger protein 20-like 1, transcript variant 1"
GO:0005515|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136462_PI430048170 0.0814126012956798 1.35111771575063 6.91085803694988

7.36917854407942 7.21605319832401 P P P 6.52078654326965 6.96815806472036
6.70646472911131 P P P LNCV6_136462_PI430048170 mRNA
TGGGTTTTTAACTTTACAGGGTCAGTTCCGCTTCACCTCCTTTTGTATGGAGTTCCATCCNM_033517RefSeq chr22 +
50674641 50733212 SHANK3 85358 SH3 and multiple ankyrin repeat domains 3
GO:0005515|GO:0043005|GO:0060170|GO:0017124|GO:0030054|GO:0005886|GO:0042802|GO:1900451|GO:0097
117|GO:1900452|GO:0005737|GO:0030160|GO:0097114|GO:0097113|GO:0043197|GO:0000165|GO:0045211|GO:0
097110|GO:0021773|GO:0032232|GO:0007613|GO:0030534|GO:0060997|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_52303_PI430048170 0.6689388681758290.8890339820783653.2732813145776 2.63165656931769
3.09326488021737 P A P 2.80641122832384 3.64487464221021 2.98938055680039 P P P
LNCV6_52303_PI430048170 mRNA
AGAGAAAGATGATGAACTGGAACTGAAAAGAAGTCTTTTATGTAGAGACTCTGCCTATGA NM_019073RefSeq chr1
- 48295371 48472208 SPATA6 54558 "spermatogenesis associated 6, transcript variant 1"
GO:0007275|GO:0005576|GO:0007283|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140116_PI430048170 0.0834820467890688 0.9601537571358320.434289635470761
0.3662109446502150.386799912433533A A A 0.4429850625553080.471325348904893
0.449673000336626A A A LNCV6_140116_PI430048170 mRNA
GCAGTTTATCAGGTGACTGTCCTTCACTTGCTTTCAGAAAACTTTGAAGTTAAATCGTAA NM_001009565 RefSeq
chr2 - 39178546 39229532 CDKL4 344387 cyclin-dependent kinase-like 4
GO:0005737|GO:0051726|GO:0006468|GO:0005524|GO:0004693 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139072_PI430048170 0.5576836305737071.20107322966312 0.259551165196877
0.3402530367650751.17124078032108 A A A 0.4827625963103760.378847658075975
0.296370064777222A A A LNCV6_139072_PI430048170 mRNA
CTAGTTCCAATAAAGTTAAGCAGGTTTAAATCCACTTTGTGCCTATCTTTTCACTGACAA NM_001113490 RefSeq
chrX - 112774876 112823126 AMOT 154796 "angiomotin, transcript variant 1"
GO:0005515|GO:0030036|GO:0005884|GO:0030139|GO:0005829|GO:0042074|GO:0005737|GO:0006935|GO:0008
180|GO:0040019|GO:0004872|GO:0034260|GO:0030334|GO:0051056|GO:0003365|GO:0001725|GO:0009986|GO:0
035329|GO:0001726|GO:0001701|GO:0001702|GO:0030027|GO:0045793|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126679_PI430048170 0.0182770657675862 0.7744836359184970.245893773868261
0.2637500655271460.333332942222155A A A 0.7739736861517170.607169946200371
0.560572797179874A A A LNCV6_126679_PI430048170 mRNA
ATTATGTGGCATTTGAGTAGTTTGCTTGTGCCTCACATGTCAACATTAAACTTTGTGGAG NM_001256404 RefSeq
chr1 - 114584574 114670111 DENND2C 163259 "DENN/MADD domain containing 2C, transcript variant
1" GO:0017112|GO:0032851 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95256_PI430048170 0.0111356493134574 1.34611956700555 6.25915225744122
6.15531505298841 6.08068967314161 P P P 5.87945559659529 5.67765312464395
5.64592511722384 P P P LNCV6_95256_PI430048170 mRNA
TCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTG NM_032354RefSeq chr17
- 8172978 8176396 TMEM107 84314 "transmembrane protein 107, transcript variant 1"
GO:0042384|GO:0008150|GO:0003674|GO:0021532|GO:0016021|GO:0005575|GO:0042733 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138974_PI430048170 0.1575644328516521.07761945432579 0.510353159161757
0.4539257692622360.555575358652198A A A 0.3075747885961750.399330260113142
0.485706064684969A A A LNCV6_138974_PI430048170 mRNA
GCTATCTAGGGAGGACATATTCTTAAGTTGCCTATTAAAGAAAGTGAGCTGAAGAAACTG NM_138733RefSeq chr6
- 49785650 49787340 PGK2 5232 phosphoglycerate kinase 2
GO:0016310|GO:0005737|GO:0004618|GO:0035686|GO:0005634|GO:0030317|GO:0005524|GO:0006096|GO:0070

062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133478_PI430048170 0.4779020421078441.13395944365315 10.22964702047
10.4270149148343 10.8206968725014 P P P 10.189626833528 10.1795834933868
10.5890262490371 P P P LNCV6_133478_PI430048170 mRNA
TTTTAATAATCAGGACTATTGGCTTCAGATGGCTGTTGGGGCAAATGATCACTGTCCACC NM_006638RefSeq chr6
- 4995045 5004063 RPP40 10799 "ribonuclease P/MRP 40kDa subunit, transcript variant 1"
GO:0004526|GO:0005634|GO:0005655|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135436_PI430048170 0.0638628323230746 0.8575152067750761 1.3533486563279
11.2902677249284 11.3971743976931 P P P 11.4338007514036 11.6147210384529
11.6503526790705 P P P LNCV6_135436_PI430048170 mRNA
CACTGTACCAAGGCAATGTAACTTTTGATTTTCGGTCAATTTAAGTTCTTTTGTCACCAA NM_001297549 RefSeq
chr19 + 18831934 18868232 UPF1 5976 "UPF1 regulator of nonsense transcripts homolog (yeast),
transcript variant 1"
GO:0005515|GO:0010467|GO:0003723|GO:0005634|GO:0009048|GO:0006449|GO:0005829|GO:0004004|GO:0005
737|GO:0006406|GO:0000184|GO:0044530|GO:0000932|GO:0000785|GO:0035145|GO:0004386|GO:0000956|GO:0
005524|GO:0003677|GO:0006260|GO:0006281|GO:0003682|GO:0071044|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138562_PI430048170 0.4926778795769460.8159855356617 0.97910392423045
0.3787907022612141.84043577288583 A A A 1.2302768066219 1.92226148037591
1.17743723892654 A A A LNCV6_138562_PI430048170 mRNA
TTGGAGCCTAATATAGCCAGGAGCTGCTGAATTTGTGCCCCTGGATTGGAAGCAAATAAA NM_005296RefSeq chrX
+ 78747708 78757081 LPAR4 2846 "lysophosphatidic acid receptor 4, transcript variant 2"
GO:0007186|GO:0005886|GO:0005887|GO:0004930|GO:0008289 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139424_PI430048170 0.1184178823497660.6145771665954927.75489150964413
8.74427346529479 8.45499144294227 P P P 9.17087688277535 9.08171661167356
8.97155988715874 P P P LNCV6_139424_PI430048170 mRNA
CCCTTGCTTTGTTTTCCCTGTCACCTCCCTATTATTAAATGTTTTCTACAGAAGAAAAAA NM_144641RefSeq chr3 +
52245792 52250599 PPM1M 132160 "protein phosphatase, Mg2+/Mn2+ dependent, 1M, transcript variant 1"
GO:0030145|GO:0006470|GO:0005634|GO:0008420 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144711_PI430048170 0.0307955915860917 0.2415840498722392.93096506043282
2.66710779425721 2.20132688991676 A A A 3.67696710666017 4.90154014996448
5.09662183523233 P P P LNCV6_144711_PI430048170 mRNA
GCAATTGTTAATATGACCTGGTCCTATGGGGTAGAACTTAGGAAAAATAAAGTTGGTTCT NM_080826RefSeq chr20
+ 13221770 13300650 ISM1 140862 "isthmin 1, angiogenesis inhibitor" GO:0005576 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133110_PI430048170 0.8171975088314071.01687999120991 11.2445814717893
11.2716071734842 11.2336418442458 P P P 11.591989845506 11.1560810743003
10.8268377652497 P P P LNCV6_133110_PI430048170 mRNA
CACAGATTGACTGCTCTGACTTTGACTACTCAAAATTGGCCTAAAAATTAAAAGAGATCG NM_003225RefSeq chr21
- 42362281 42366535 TFF1 7031 trefoil factor 1
GO:0005515|GO:0035902|GO:0008285|GO:0030277|GO:0005975|GO:0010039|GO:0007586|GO:0043434|GO:0032
355|GO:0008083|GO:0005615|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57742_PI430048170 0.0380608909837589 1.44665663205634 7.34180462830953
7.42346346006486 7.00072298848578 P P P 6.74930734267587 6.90984179369991
6.51560192090436 P P P LNCV6_57742_PI430048170 mRNA
ATCTGCTGGAATGATTGTCCGGGCCCTGCAGAGCAGGGGCCCCAACAGAGTTTTTAAACC NM_053054RefSeq chr11
- 66016751 66026517 CATSPER1 117144 "cation channel, sperm associated 1"
GO:0005515|GO:0035036|GO:0086010|GO:0005245|GO:0005886|GO:0031514|GO:0036128|GO:0007275|GO:0007

283|GO:0030317|GO:0030154|GO:0060296|GO:0007338|GO:0070509|GO:0007342|GO:0070588|GO:0051924|GO:0
034765|GO:0005227|GO:0032504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139138_PI430048170 0.39683330477339 0.7186178127503660.253139287669361
0.2672244939159380.368930904987899A A A 1.39572548247098 0.315888033084831
0.326832098360805A A A LNCV6_139138_PI430048170 mRNA
TCTCTGCACTCACATTTTGTGACTTATGAAGATAAATAAAGTCAAGGGAAAACAGCGTCA NM_174918RefSeq chr19
+ 7677056 7679833 MCEMP1 199675 mast cell-expressed membrane protein 1 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128348_PI430048170 0.9681682820003431.00290080729328 0.278609224713234
0.2826169307899990.437930978992075A A A 0.3514916095562880.299262185760185
0.341126438081465A A A LNCV6_128348_PI430048170 mRNA
AAACGGTATGTTGCTGTGTACCTAAGAGTATAGTAAGGTCAAGAAGAGTATCAAAGTATA NM_199321RefSeq chr17
+ 39868201 39877896 ZPBP2 124626 "zona pellucida binding protein 2, transcript variant 2"
GO:0001675|GO:0001669|GO:0005634|GO:0005576|GO:0002199|GO:0007339|GO:0044297 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133292_PI430048170 0.0504485533370183 0.3114961132095091.48813980461908
0.3877286830198972.01090119186734 A A A 2.76543159705221 3.24870769922509
3.29865061823812 P P P LNCV6_133292_PI430048170 mRNA
GCCACAAATAAATTAAGGAATTCCAGAATTTCTTCATCTACTTCTGCAGTCTTAACTCTG NM_032765RefSeq chr5
- 181256384 181261118 TRIM52 84851 tripartite motif containing 52
GO:0005622|GO:0051092|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134153_PI430048170 0.0143264940919289 0.8209015068586171 4.0087975651581
14.1620045597422 14.1702443126617 P P P 14.4083475443353 14.3315158931549
14.4581863555765 P P P LNCV6_134153_PI430048170 mRNA
TAGCCCAATATGCTGTCTTGGGTCCTATTCAAATAAAGTTATTTCTCCTGGTCTCAGCTC NM_018457RefSeq chr12
+ 53441648 53446643 PRR13 54458 "proline rich 13, transcript variant 2"
GO:0006355|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135120_PI430048170 0.4442960215861530.8910021716021179.38555053778435
8.86731436899734 8.78098631321747 P P P 9.37592103823793 9.15806911274558 9.057520311234
P P P LNCV6_135120_PI430048170 mRNA
AGACCCTCCCCAAGCCCATCCATGCACATTACTTAGCTAACAATTAGGGAGACTCGTAAG NM_018058RefSeq chr10
- 97864999 98030828 CRTAC1 55118 "cartilage acidic protein 1, transcript variant 1"
GO:0007413|GO:0021772|GO:0005509|GO:0005578|GO:1900121|GO:0070062|GO:0030426 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129255_PI430048170 0.02675221725568 0.51018115000849 2.25441344291199
2.79114086476239 2.06855020847037 A A A 3.56349030666383 3.35753532555949
3.18093173424434 P P P LNCV6_129255_PI430048170 mRNA
ACTGTCTCCTTGGGCCATGCTGGTCTGACTTATGCTTACTAATAAATTCTGTTTACTGGC NM_080746RefSeq chr14
- 46651015 46651825 RPL10L 140801 ribosomal protein L10-like
GO:0003735|GO:0016020|GO:0005634|GO:0022625|GO:0007283|GO:0006412|GO:0005844 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143411_PI430048170 0.6740262825014070.9108107089715243.14073626304377
2.94361775683035 2.22824847603988 P P A 2.87087692924403 3.30084764888394
2.60989097656604 P P P LNCV6_143411_PI430048170 mRNA
AATCACACCCACTGCCTCTCATGCCGGAGTGGGGGAAATGGAACCCGCAAAGCCTGCAGG NM_182626RefSeq
chr2 + 10141381 10211730 C2orf48 348738 chromosome 2 open reading frame 48 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128596_PI430048170 0.0906414126775602 0.4386477541940012.25889796552318
3.01507524072895 3.87938311667471 A P P 4.00585685865548 4.27353143054224

4.78060992935413 P P P LNCV6_128596_PI430048170 mRNA
CAAACAAGATTGCTGATCTGTTCTGTATTAGTGACATTCTGGTACTTCTAGATTTGCAAT NM_001174166 RefSeq
chr17 - 68267025 68291264 SLC16A6 9120 "solute carrier family 16, member 6, transcript variant 1"
GO:0015718|GO:0034220|GO:0016020|GO:0005887|GO:0008028|GO:0016021|GO:0015293 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_119002_PI430048170 0.0268231779059099 1.65388477555272 4.85265010087328
4.99182157805653 5.24739133871713 P P P 4.49530182113109 4.42573857833664
3.96628971645793 P P P LNCV6_119002_PI430048170 mRNA
CCTTCTGGAGACACCACCAGATGGGCCAGCCAGAGGCAGCAGCAGCCTCTTCCCATGGAT NM_004088 RefSeq chr10
+ 96304327 96338564 DNTT 1791 "DNA nucleotidylexotransferase, transcript variant 1"
GO:0005737|GO:0071897|GO:0003887|GO:0005654|GO:0006304|GO:0003912|GO:0003677|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130299_PI430048170 0.0342993730277649 1.39892455207684 7.34419750535977
7.38057967939993 7.56983409429712 P P P 6.75792831504803 6.89740465592231
7.16638438773055 P P P LNCV6_130299_PI430048170 mRNA
GAGCTGATAAAGACTTTAGCTGACTCGTTAAGCCTGATACATAAGCCATATTTAAAATTC NM_000288 RefSeq chr6
+ 136822563 136913934 PEX7 5191 peroxisomal biogenesis factor 7
GO:0001958|GO:0006635|GO:0005782|GO:0008611|GO:0005053|GO:0007031|GO:0019899|GO:0016558|GO:0001
764|GO:0042803|GO:0005829|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141105_PI430048170 0.190665990221246 0.969175367442482 0.451756561776988
0.465099442930083 0.394436764452753 A A A 0.507445391744717 0.493840295193907
0.44576554190074 A A A LNCV6_141105_PI430048170 mRNA
GCTTGTCTTACTCTCGCAGTTTTAAAATTATAGCTATTCTGTACACATGACATACAAGAC NM_015668 RefSeq chr8
- 99960935 100106116 RGS22 26166 "regulator of G-protein signaling 22, transcript variant 1"
GO:0043547|GO:0005737|GO:0005886|GO:0038032|GO:0005634|GO:0005096 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_96805_PI430048170 0.935540978336763 1.00319054307821 5.61748083610416 5.4987237088718
5.67522249421644 P P P 5.67227752887822 5.37398385000634 5.71372664955457 P P P
LNCV6_96805_PI430048170 mRNA
GTATCCGCTGTCAACTACGAATTTGAGGATGAATACTTCAGTAATACCAGTGCCCTAGCC NM_004938 RefSeq chr9
+ 87497680 87708634 DAPK1 1612 "death-associated protein kinase 1, transcript variant 1"
GO:0017148|GO:0005515|GO:0008625|GO:0005516|GO:0043065|GO:0005886|GO:2000310|GO:0006915|GO:0042
981|GO:0015629|GO:0097190|GO:0005524|GO:0042802|GO:0043280|GO:0035556|GO:0005737|GO:0046777|GO:0
004672|GO:0071346|GO:0004674|GO:0010506|GO:0006468|GO:0017075|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137445_PI430048170 0.142601405421314 0.814979386147804 3.23086153594695
3.25541950687926 3.05902404508807 P P P 3.28159640484388 3.71469373689117
3.40732913661701 P P P LNCV6_137445_PI430048170 mRNA
ACAGAAGACCTTCCTTTCCTCCTTTTTCCATATTGCTTTCTGTTCTAAGTGGGTGAATAA NM_001166003 RefSeq chr22
+ 39097223 39104067 APOBEC3H 164668 "apolipoprotein B mRNA editing enzyme, catalytic polypeptide-
like 3H, transcript variant SV-200"
GO:0005515|GO:0009972|GO:0045869|GO:0005634|GO:0048525|GO:0010529|GO:0005737|GO:0051607|GO:0000
932|GO:0045087|GO:0004126|GO:0008270|GO:0070383 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131739_PI430048170 0.150587013519814 0.954279119051007 0.261517195576299
0.323346470739596 0.309041129841577 A A A 0.426548166111745 0.334648378674485
0.334003462321496 A A A LNCV6_131739_PI430048170 mRNA
CCCAATATGCCCCTTTGCAGAAAGTATTGGCTTTTCCCTGAATTCTGTTATGGTAAAAAA NM_001163646 RefSeq
chr3 + 184032830 184039369 HTR3D 200909 "5-hydroxytryptamine (serotonin) receptor 3D, ionotropic,
transcript variant 3" GO:0005230|GO:0034220|GO:0005886|GO:0016021|GO:0055085 . NA - . NA NA

NA NA NA NA NA NA NA
LNCV6_34277_PI430048170 0.00117030669551413 2.67770563569951 9.56369945903716
9.87187703528731 9.5430783944439 P P P 8.31787595048851 8.28481292098126 8.1301421951038
P P P LNCV6_34277_PI430048170 mRNA
GCACCTGGCTTTATTTCTGGTGCACTCCTCTCCTGAGAGTGTAGACCAAGGTTGCCTAAT NM_001242313 RefSeq
chr22 + 18527801 18530573 TMEM191B 728229 transmembrane protein 191B GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55627_PI430048170 0.00920594830874869 2.28387797944001 1.27902559103389
1.77738233033589 1.66598429723572 A A A 0.492411599730225 0.393405399897248
0.301797412282657 A A A LNCV6_55627_PI430048170 mRNA
GGCACAAGGACCTTTACATGTTCTTTTCTGCCATTTTCTGGACTGGGGGTGGAAAGGGGG NM_001003665 RefSeq
chr1 + 226548799 226609214 C1orf95 375057 chromosome 1 open reading frame 95 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140131_PI430048170 0.704726681103355 1.0138186454974 0.462896567625119
0.530512275212799 0.532094989174486 A A A 0.569464195102333 0.416964373853686
0.476644537434373 A A A LNCV6_140131_PI430048170 mRNA
TTCTGGTAACTCACTCAGTTTATGCTGTGCTAAATATCAATCAAGCCATGTATAAATGTG NM_005233 RefSeq chr3
+ 89107523 89482134 EPHA3 2042 "EPH receptor A3, transcript variant 1"
GO:0005515|GO:0048013|GO:0005886|GO:0071300|GO:0010717|GO:0005576|GO:0018108|GO:0051893|GO:0005
524|GO:0070507|GO:0005004|GO:0016477|GO:0005887|GO:0007411|GO:0032956|GO:0010976|GO:0032319|GO:0
007155|GO:0097156|GO:0097155|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127901_PI430048170 0.672226546816952 1.02702905976233 13.0795129785503
13.0498254400584 13.032533461192 P P P 13.1657830538451 13.0065852073266
12.8580423044775 P P P LNCV6_127901_PI430048170 mRNA
TGCGTGTGGGTAATTGTGTTTTGGGGGAAAGTGGGGAATTTAATAAATTTCTGGTGCTCT NM_138774 RefSeq chr19
- 896502 913225 R3HDM4 91300 R3H domain containing 4 GO:0005634|GO:0003676 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128008_PI430048170 0.0521257673554738 0.479507634688297 2.54439850208791
1.64533844162555 1.56376486234134 A A A 3.2769403489638 2.75844247882501
3.06957237093278 P P P LNCV6_128008_PI430048170 mRNA
CAAACATGGAAAACAGAGTATTTCTGGCAGCTGTGGTACAAATGTGATAATATATTGCTA NM_001164737 RefSeq
chr7 - 93424486 93574730 CALCR 799 "calcitonin receptor, transcript variant 1"
GO:0004948|GO:0005515|GO:0032841|GO:0005886|GO:0030819|GO:0051384|GO:0045762|GO:0007202|GO:0015
031|GO:0072659|GO:0007204|GO:0031623|GO:0007190|GO:0007186|GO:0005887|GO:0008565|GO:0004872|GO:0
007189 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143870_PI430048170 0.6489855375025790 .9658069393302699.88086788088518
10.1603396952502 10.1730735138452 P P P 10.1815038786951 10.0225604138317
10.1737701902552 P P P LNCV6_143870_PI430048170 mRNA
CTGGAAACATCTGCCACATTTAGTGTGTGTATGTGTATTCATTCTTTCTCATAACTTCTT NM_001037161 RefSeq chr14
+ 73537223 73543794 ACOT1 641371 acyl-CoA thioesterase 1
GO:0052689|GO:0047617|GO:0006637|GO:0000038|GO:0001676|GO:0016290|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136413_PI430048170 0.233402040271703 0.9556445979601140.261131458895046
0.352379216978871 0.314376980442214 A A A 0.447571086049839 0.346479797151543
0.328783415112524 A A A LNCV6_136413_PI430048170 mRNA
CAAGTACCCTACCTGTATGAGCCTCTTCATTTAGCTAATAAAAAGTCTAAGCAATAAGAA NM_152467 RefSeq chr17
+ 41837790 41848347 KLHL10 317719 kelch-like family member 10
GO:0009566|GO:0000902|GO:0005737|GO:0048873|GO:0016567|GO:0007286|GO:0048808|GO:0008584 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_142422_PI430048170 0.0799147646778179 1.33752711142518 9.73497036548349
9.91130659215173 10.1185381776133 P P P 9.38272928003649 9.33079037539471
9.77596412148683 P P P LNCV6_142422_PI430048170 mRNA
GGGCAGTACTGTCAGAAATTTCTTTGAGCTGTGAGATGGATTTATTTTTAAATGCTACTT NM_182640RefSeq chr2
+ 105038024 105099960 MRPS9 64965 mitochondrial ribosomal protein S9
GO:0070124|GO:0005739|GO:0005515|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0042
769|GO:0005743|GO:0005730|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128199_PI430048170 0.3542489492617360.5995417949768860.376408565378208
0.3737617851712410.386026951939657A A A 1.89079297575383 0.347219617913724
0.609291794699071A A A LNCV6_128199_PI430048170 mRNA
CGCCATGTATTCTATTCTGTAGTAAAGCATTTCCATCAACAATGCCTAATTGTATCTGTT NM_006868RefSeq chr18
+ 9708230 9862556 RAB31 11031 "RAB31, member RAS oncogene family"
GO:0032869|GO:0005770|GO:0043001|GO:0003924|GO:0005525|GO:0032588|GO:0031623|GO:0045335|GO:0045
055|GO:0030670|GO:0032482|GO:0019003|GO:0090382|GO:0005769 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128906_PI430048170 0.0832022752195342.01450122223217 2.11914349250859
1.57921233641244 0.967049607957274A A A 1.07726339708307 0.332106348788335
0.311881874914193A A A LNCV6_128906_PI430048170 mRNA
TTGAAATCAACTTCATCAAGTCTCAGAGCAGCAACATGCTGACGCCCTATGACTACTCCT NM_001002036 RefSeq
chr2 - 96123849 96138436 ASTL 431705 astacin-like metallo-endopeptidase (M12 family)
GO:2000360|GO:0030133|GO:0005886|GO:0009566|GO:0005737|GO:0010954|GO:0070002|GO:0070001|GO:0006
508|GO:0060468|GO:0060473|GO:0008233|GO:0008270|GO:0004222|GO:0007155 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141524_PI430048170 0.54990171205964 2.9334785630029 0.309598357557226
4.25549053605316 2.7193061611045 A P A 1.4527680522989 1.66362485681883
1.71061698174382 A A A LNCV6_141524_PI430048170 mRNA
CTTTGTATGTAAGGTCTTGAGACATGTAAGGCCTGGTACTTTTTATTTAAAATGTCTGTC NM_001100164 RefSeq
chr6 + 143677964 143831185 PHACTR2 9749 "phosphatase and actin regulator 2, transcript variant
1" GO:0005515|GO:0004864|GO:0003779|GO:0043086 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144527_PI430048170 0.0273624814022179 1.41812320239954 5.61031904475354
5.80429359224293 5.7294947642102 P P P 5.19718628231826 5.40127474316239
5.01429532823032 P P P LNCV6_144527_PI430048170 mRNA
GTACATACAAGTCATCCATTAAAACAAAGAAGAAGAATATAGAGTGCCAGCAGCAACTTA NM_032120RefSeq chr7
+ 92528772 92537509 RBM48 84060 RNA binding motif protein 48 GO:0003723|GO:0005654 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135149_PI430048170 0.2868721703590720.9576801817235490.273610952266072
0.3846787068481870.300695182251546A A A 0.4570619049151810.351703345033293
0.336704155405154A A A LNCV6_135149_PI430048170 mRNA
TTGCATGGTTTGGGTAAAAGCTAGCCTACATACAAAGGAATATGAAGACTGTGGAAGAAA NM_019886RefSeq chrX
+ 46573686 46598496 CHST7 56548 carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7
GO:0006790|GO:0005976|GO:0005975|GO:0006044|GO:0008459|GO:0044281|GO:0030206|GO:0000139|GO:0009
405|GO:0001517|GO:0016021|GO:0030204|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134747_PI430048170 0.2629490190110230.8367441240220234.23430012323115
3.81184535653159 4.42519721284547 P P P 4.43906689466991 4.32362430784729 4.5384093458217
P P P LNCV6_134747_PI430048170 mRNA
ATGTGACAAGGCCTTAGACGTTGTCCTAGTTTCTGGAATCACCGAATAATTCCTACTTAC NM_178523RefSeq chr19
- 52114399 52139938 ZNF616 90317 zinc finger protein 616
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_136486_PI430048170 0.0318447169679502 1.14626941057783 0.672930668195283
0.767138075417765 0.786876510247541 A A A 0.638378489844031 0.489030091776712
0.506584171149477 A A A LNCV6_136486_PI430048170 mRNA
AAACTGCTTCACCTGGGGAAGACTTCAATATGAATGCTGAGCAGAAGTTGGAGATTTAAA NM_001005163 RefSeq
chr11 + 5488684 5489748 OR52D1 NA "olfactory receptor, family 52, subfamily D, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127485_PI430048170 0.10818042889261 0.8498312261916069.19804401881929
9.16419097291783 9.45981734454158 P P P 9.50438657768226 9.42262715338648
9.61155282790352 P P P LNCV6_127485_PI430048170 mRNA
GGGGGTCTTTCCTAAAAAAGAAAACATATGATGCTTCATTTCTACTTAATGGAACTTGTG NM_016038 RefSeq chr7
- 66987702 66995601 SBDS 51119 Shwachman-Bodian-Diamond syndrome
GO:0005515|GO:0008017|GO:0042256|GO:0008283|GO:0030595|GO:0043148|GO:0006364|GO:0001833|GO:0005
730|GO:0005634|GO:0048539|GO:0019843|GO:0030282|GO:0000922|GO:0005737|GO:0043022|GO:0042273|GO:0
005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102920_PI430048170 0.333880619985491 0.918456044300092 15.043342411377
14.7871918659034 14.9518593104834 P P P 14.8928522779702 15.1691609373149
15.0863484273834 P P P LNCV6_102920_PI430048170 mRNA
ATCGACCTGGACTCCATGAGAAATCTGAAGGCCAGCTTGGAGAACAGCCTGAGGGAGGTG NM_000224 RefSeq
chr12 + 52949058 52952901 KRT18 3875 "keratin 18, type I, transcript variant 1"
GO:0005515|GO:0005882|GO:0048471|GO:0043066|GO:0005815|GO:0045104|GO:0034451|GO:0097284|GO:0005
730|GO:0097191|GO:0009653|GO:0033209|GO:0071944|GO:0005737|GO:0007049|GO:0005198|GO:0097110|GO:0
016032|GO:0045095|GO:0043000|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145351_PI430048170 0.230740025803656 0.899984995062265 12.5149473761548
12.7542730640536 12.8255694436143 P P P 12.9058546016216 12.8135690794165 12.847954215498
P P P LNCV6_145351_PI430048170 mRNA
TTTCCCCGGGAAAGTTGACTGAGGTGACCAGTAATAGAATTGAAAAGGGAGAGTGTCTTC NM_080725 RefSeq chr20
- 646623 653370 SRXN1 140809 sulfiredoxin 1
GO:0016667|GO:0032542|GO:0006979|GO:0005524|GO:0055114|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_118204_PI430048170 0.350971807723304 1.02918493870967 0.296982624063696
0.28192377255953 0.389997353437746 A A A 0.295371837858137 0.271574260850911
0.279741306436108 A A A LNCV6_118204_PI430048170 mRNA
TTGTAAGCGCTTCCTCTGTAACTCAGGCGTAACTGTTATACATTAAAAGAAATTAAAAGC NM_001135254 RefSeq
chr1 + 18631005 18748866 PAX7 5081 "paired box 7, transcript variant 3"
GO:0014813|GO:0043066|GO:0060415|GO:0003700|GO:0000983|GO:0006366|GO:0051216|GO:0010453|GO:0048
706|GO:0043393|GO:0005634|GO:0048663|GO:0009653|GO:0021527|GO:0043565|GO:0045944|GO:0031062|GO:0
043403|GO:0006338|GO:0021904|GO:2000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139370_PI430048170 0.0647560566077345 1.16789349788994 0.605897265021414
0.784749087650994 0.823711186798867 A A A 0.625895443904201 0.45082124020989
0.468622587665265 A A A LNCV6_139370_PI430048170 mRNA
TTTGCGATCATTACGTCTTCTATTACAATGCCCTACTTTGGCAGCATGAAGAGTACTGCA NM_001128618 RefSeq
chr9 - 72051380 72060605 C9orf57 138240 chromosome 9 open reading frame 57 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134418_PI430048170 0.00845333419272553 0.222080433008356 4.42453035362668
3.52062467262235 3.30059141393761 P P P 5.51545248291405 6.26551956683763
6.13064856832848 P P P LNCV6_134418_PI430048170 mRNA
CTCCATGATGTTTGCCAAGTTTGAATGCGCAAAACTTGGAAAATGTGACAATAAAGAATA NM_007027 RefSeq chr3
- 133600604 133661893 TOPBP1 11073 topoisomerase (DNA) II binding protein 1
GO:0005515|GO:0000794|GO:0005813|GO:0005794|GO:0005694|GO:0005634|GO:0006259|GO:0015629|GO:0008

022|GO:0003677|GO:0006974|GO:0042802|GO:0000922|GO:0005737|GO:0006281|GO:0016605|GO:0010212|GO:0
001673 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59057_PI430048170 0.662069616627728 1.07830572560636 2.78952449863518 2.72484701922123
2.32549435368651 A A A 2.16666001742183 3.00439831750532 2.22554548695154 A P A
LNCV6_59057_PI430048170 mRNA
CTTAGACTAATAGACGTTTTGGAAAGTTCGGCTAGTGTTCGTGTGTTTGTCGTAGCACCC NM_017409 RefSeq chr12
+ 53985161 53990278 HOXC10 3226 homeobox C10
GO:0050905|GO:0043565|GO:0019907|GO:0008284|GO:0006355|GO:0001501|GO:0021520|GO:0009954|GO:0005
654|GO:0030326|GO:0009952|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137643_PI430048170 0.00424835612848239 1.32567905957876 6.90334918512542
7.04320613934282 7.01653401958761 P P P 6.53626734527244 6.68402958296591
6.52069022755187 P P P LNCV6_137643_PI430048170 mRNA
CCCACAAACCTGTTAACATTGTCTTAAGGTGAAATGGCTGGAAAATCAGTATTTAACTAA NM_002052 RefSeq chr8
+ 11704150 11760002 GATA4 2626 GATA binding protein 4
GO:0060045|GO:0005515|GO:0003289|GO:0000790|GO:0043627|GO:0003700|GO:0006366|GO:0044212|GO:0003
705|GO:0060290|GO:0003281|GO:0007283|GO:0060575|GO:0001947|GO:0060008|GO:0061049|GO:0003229|GO:0
001706|GO:0023019|GO:0003713|GO:0030509|GO:0000978|GO:0001701|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142048_PI430048170 0.491574440403786 1.04276173653647 0.280898624666081
0.29580286516825 0.492876085234825 A A A 0.318764472576214 0.279673110255616
0.299494689590344 A A A LNCV6_142048_PI430048170 mRNA
GCTTGCTTTGGGGTAAAATAAAAGTACGAAAAAGGTGGAAGTCAAATCAGTATTCTGTAA NM_152402 RefSeq chr4
- 117083553 117085580 TRAM1L1 133022 translocation associated membrane protein 1-like 1
GO:0005789|GO:0016021|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131512_PI430048170 0.000739719328624806 0.394826411560062 6.07688210197823
6.16119730047627 6.42559416506949 P P P 7.39798531187306 7.55778622164909
7.73379788307164 P P P LNCV6_131512_PI430048170 mRNA
GTCCTGCTTGTCTAGTTTGTATTCGCTGACTTTCTATGTGATATAGATGCATTTGTAATA NM_001334 RefSeq
chr4_GL383527v1_alt - 88740 118513 CTSO 1519 cathepsin O GO:0004197|GO:0006508|GO:0005764
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143649_PI430048170 0.577568459230156 0.819145934439623 5.70348738066156 5.8569695518851
6.10281890004713 P P P 5.51724797303856 6.1561272120508 6.66047559347817 P P P
LNCV6_143649_PI430048170 mRNA
CTGTAACAGGGCAAGTTTCCACTCTAAGCAGCTATTTAAAAATAAATATGAGGATTTTGG NM_016261 RefSeq chr17
- 59859479 59892945 TUBD1 51174 "tubulin, delta 1, transcript variant 1"
GO:0051258|GO:0005814|GO:0005874|GO:0003924|GO:0007275|GO:0007283|GO:0005525|GO:0030154|GO:0006
184|GO:0005737|GO:0005200|GO:0005654|GO:0007017 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133477_PI430048170 0.938537446263744 0.967306905126368 0.376084653101133
0.876539341929511 0.524531622991249 A A A 1.08717925308406 0.390530672545338
0.368849536226727 A A A LNCV6_133477_PI430048170 mRNA
GATCCTTGGTCACTGGTGTTTCAAACATTCTGGAAAGTCACATCGATCAAGAATATTTTT NM_001243961 RefSeq
chr6 - 32659463 32666689 HLA-DQB1 3119 "major histocompatibility complex, class II, DQ beta 1,
transcript variant 2"
GO:0050852|GO:0012507|GO:0005886|GO:0031295|GO:0019221|GO:0042613|GO:0005765|GO:0032588|GO:0030
666|GO:0019886|GO:0006955|GO:0000139|GO:0016020|GO:0002381|GO:0042605|GO:0071556|GO:0032395|GO:0
030669|GO:0010008|GO:0060333|GO:0002455|GO:0030658 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_138719_PI430048170 0.827074692140947 0.99416093702468 0.46158076935086
0.475868292334102 0.381357489865266 A A A 0.492915041901211 0.419555430726614

0.432401100957517 A A A LNCV6_138719_PI430048170 mRNA
GTTGTGTGGTTTTCCTTTGTGAAGGAGAGAGGGAAACTATTTGTAGCTTGTTTTATAAAA NM_001034852 RefSeq
chr14 + 69879396 70032366 SMOC1 64093 "SPARC related modular calcium binding 1, transcript
variant 1"
GO:0005515|GO:0007165|GO:0045667|GO:0030198|GO:0001654|GO:0010811|GO:0005509|GO:0050840|GO:0060
173|GO:0030154|GO:0005604 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121391_PI430048170 0.0118730023970956 1.41862729212524 12.8223154223769
12.8703029682938 12.8181520075661 P P P 12.4406839320128 12.3325233804524 12.215914856913
P P P LNCV6_121391_PI430048170 mRNA
TCTTTCTCAGTGACCGGGTGGTTTGCTTAGCGCAGACGGGGAAGCGGAGCCAACATGCCA NM_001013 RefSeq
chr19_GL949747v2_alt + 175839 182631 RPS9 6203 ribosomal protein S9
GO:0005515|GO:0010467|GO:0008284|GO:0019058|GO:0005634|GO:0019843|GO:0006412|GO:0045182|GO:0006
413|GO:0006414|GO:0005829|GO:0045903|GO:0005737|GO:0000184|GO:0016032|GO:0070062|GO:0003735|GO:0
006614|GO:0019083|GO:0005730|GO:0006415|GO:0016020|GO:0022627|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140913_PI430048170 0.95111888744331 1.77196893484843 0.6167579195542
3.63718558209663 0.31488392367877 A P A 2.05832313462836 1.23477045955447
1.05009985774024 A A A LNCV6_140913_PI430048170 mRNA
GGGGTATATGATTCTTTATGAAATGGGGAAAGGGAGCTAACATTAATTATGCATGTACTA NM_001017372 RefSeq
chr5 + 128965519 129033642 SLC27A6 28965 "solute carrier family 27 (fatty acid transporter),
member 6, transcript variant 2"
GO:0042383|GO:0000038|GO:0001676|GO:0005886|GO:0000166|GO:0016021|GO:0031957|GO:0015909|GO:0055
085|GO:0004467 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131774_PI430048170 0.0251115012645305 2.27123921068599 3.69367958275975
3.01858827325198 3.47271158845279 P P P 2.69657281577343 2.0661870894264
1.80014227102942 P A A LNCV6_131774_PI430048170 mRNA
CCAGGCTATTCACACAGGCCACAGCAGAAAAGAGAGCACCTGTGAAGAAATAAATACCAT NM_015077 RefSeq
chr17 + 28371661 28401038 SARM1 23098 sterile alpha and TIR motif containing 1
GO:0030424|GO:0030054|GO:0034142|GO:0005874|GO:0045202|GO:0042981|GO:0002224|GO:0030425|GO:0005
829|GO:0009749|GO:0048814|GO:0005739|GO:0002756|GO:0005737|GO:0031315|GO:0045087|GO:0034138 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128089_PI430048170 0.0524953403005477 0.45129601633722 5.50677028021725
5.62442404123519 5.54124543441577 P P P 6.13222483094149 7.01457772107375 6.8303798202134
P P P LNCV6_128089_PI430048170 mRNA
GAAATTGTTTTCCTCAACTCGGAGATTCCTGTATGGAGAGAATCAATTTCTATATTTGCA NM_052906 RefSeq chr22
- 37367959 37427470 ELFN2 114794 "extracellular leucine-rich repeat and fibronectin type III domain
containing 2, transcript variant 1" GO:0019902|GO:0010923|GO:0004864|GO:0016021|GO:0005615 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_132299_PI430048170 0.1245840763621981.34802818968957 13.3487050818052
13.7636850943339 13.2151830269063 P P P 13.0527782587073 12.9634177073882
13.0745908130156 P P P LNCV6_132299_PI430048170 mRNA
GGTGGTGCTATAATGTGGCACTGGATCTTGAGTAATAAATTTGCTGTGGTTTGTACACGG NM_001662 RefSeq chr7
+ 127588351 127591705 ARF5 381 ADP-ribosylation factor 5
GO:0005515|GO:0048471|GO:0005794|GO:0005886|GO:0007264|GO:0008152|GO:0003924|GO:0016192|GO:0015
031|GO:0005525|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137622_PI430048170 0.0643678336883001 0.7285915901264696.4586861702629
6.56137270299784 6.7781742699219 P P P 6.84384977819571 6.98639189640638 7.315768029524
P P P LNCV6_137622_PI430048170 mRNA
CTGGTTTCTCTTAGTTCTTCTCTAACATAGTACTTTCTTTCCAGCAAAAGCAAAATGTGT NM_001822 RefSeq chr2 -

174799313 175005253 CHN1 1123 "chimerin 1, transcript variant 1"
GO:0051056|GO:0048013|GO:0007264|GO:0009967|GO:0046872|GO:0005829|GO:0043547|GO:0008045|GO:0032
314|GO:0046875|GO:0005070|GO:0050770|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126978_PI430048170 0.0926360944593059 0.960563298454676 0.397764087961946
0.405675476381417 0.339478231251793 A A A 0.431589086957569 0.455991282602254
0.430235487095087 A A A LNCV6_126978_PI430048170 mRNA
TCCTACTTATACACGACGTGTTCCTAAAACATGTTTGAAAGGTGAATTTCTGAAAGTCTA NM_001145946 RefSeq
chr12 + 20695354 20753386 SLCO1C1 53919 "solute carrier organic anion transporter family,
member 1C1, transcript variant 1" GO:0005215|GO:0005886|GO:0043252|GO:0016021|GO:0055085 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134167_PI430048170 0.687363067313933 1.03330511030195 4.45838375414894
4.29939316000401 4.47036245569146 P P P 4.24282490109667 4.56925106839608
4.25630821493045 P P P LNCV6_134167_PI430048170 mRNA
TCATAAAGTCTTGCCTTGCTGAACTCCCTCTCTGCAGGCAGCCTGCCTTTAAAAATAGTT NM_002535 RefSeq chr12
+ 112978468 113010698 OAS2 4939 "2'-5'-oligoadenylate synthetase 2, 69/71kDa, transcript variant 2"
GO:0003725|GO:0048471|GO:0018377|GO:0005783|GO:0001730|GO:0019221|GO:0005634|GO:0009615|GO:0005
524|GO:0046872|GO:0043231|GO:0005829|GO:0006401|GO:0005739|GO:0051607|GO:0005737|GO:0006139|GO:0
060337|GO:0016020|GO:0006486|GO:0008270|GO:0060333|GO:0006164 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_134787_PI430048170 0.000388785352655476 2.52300109985512 8.45406125843708
8.74294005270878 8.68448646902524 P P P 7.30177159922123 7.4098381022932
7.17040097888364 P P P LNCV6_134787_PI430048170 mRNA
AGGACACACATATGCTTACACCTACCTTTATCACCATTCGTTCATGAATCATGCCTAGCT NM_173546 RefSeq chr3
+ 49171584 49176486 KLHDC8B 200942 kelch domain containing 8B GO:0005737 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139787_PI430048170 0.0012129675732512 0.335746552058437 4.40134056970223
4.31738945809751 4.64587032431377 P P P 5.81061306209303 5.97567760436506
6.28224539999608 P P P LNCV6_139787_PI430048170 mRNA
GGTCTTTTGTACTTTTCTTCAGAAGAAATGAATTAAAGGGTACAGTTGCATAAAGTGGGT NM_014946 RefSeq chr2
+ 32063610 32157637 SPAST 6683 "spastin, transcript variant 1"
GO:0005515|GO:0008017|GO:0048471|GO:0005783|GO:0001578|GO:0005634|GO:0031122|GO:0007409|GO:0007
109|GO:0034214|GO:0051013|GO:0005737|GO:0015630|GO:0051260|GO:0070062|GO:0005813|GO:0031117|GO:0
043014|GO:0005874|GO:0048487|GO:0005819|GO:0030496|GO:0031410|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129202_PI430048170 0.68075967436399 0.936671169260922 4.26714410987784
4.03088824059272 4.78226963593238 P P P 4.27348232091611 4.42662426529645
4.73014729061818 P P P LNCV6_129202_PI430048170 mRNA
GGCCTGGCCTAAAATACATCAGACCTTTTGTAAGAGAGAATTTCAATAAAGCAAAAAACA NM_173833 RefSeq chr8
- 27869881 27992852 SCARA5 286133 "scavenger receptor class A, member 5"
GO:0034605|GO:0010468|GO:0006879|GO:0070207|GO:0030193|GO:0009986|GO:0005887|GO:0006898|GO:0070
287|GO:0034755|GO:0006897|GO:0005044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140793_PI430048170 0.829279537115708 1.1056534813759 0.338696107462189
0.658210416204571 1.47491725072888 A A A 0.764538943193148 1.07808147841077
0.350606416307733 A A A LNCV6_140793_PI430048170 mRNA
TGTCAATGATTAGATCGGGTCTCGGAAGGGAAGTAGCCATCACACCATTAAAAAGCCTGT NM_032538 RefSeq chr6
+ 43243483 43288259 TTBK1 84630 tau tubulin kinase 1
GO:0005737|GO:0018105|GO:0021762|GO:0004674|GO:0008360|GO:0005634|GO:0005524 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_61214_PI430048170 0.286991369345133 1.2358747389076 0.826193417747685 0.287334796163712

0.916913781681929 A A A 0.4715709139302720.3835824674283650.331823439663183 A A A
LNCV6_61214_PI430048170 mRNA
CTTCTATTCACATCTGGGATGCAATGAACAAGCAGACTTTATCTATCCTAAGATGCTACC NM_183387 RefSeq chr14
- 88614829 88792752 EML5 NA echinoderm microtubule associated protein like 5 NA . NA -
NA NA NA NA NA NA NA NA NA
LNCV6_105211_PI430048170 0.0129533967525783 1.73593099816 5.74624562005832
5.51377643492505 5.71081382505358 P P P 5.04926728940339 4.91518193754747 4.5926237722824
P P P LNCV6_105211_PI430048170 mRNA
TCCACGTCTGGAATAATGGGTACTCTTTCCTCGTGGAATTTGAAGATTCTACAGATAAAT NM_007220 RefSeq chrX
+ 15738288 15787625 CA5B 11238 "carbonic anhydrase VB, mitochondrial"
GO:0005739|GO:0005759|GO:0015701|GO:0008270|GO:0044281|GO:0004089|GO:0006730 . NA -
NA NA NA NA NA NA NA NA NA
LNCV6_134266_PI430048170 0.00295074776123351 1.33548543799787 12.5246666681054
12.6698856840471 12.6679864909956 P P P 12.259695163248 12.2251627412294
12.1270849367144 P P P LNCV6_134266_PI430048170 mRNA
ATGCTCTGGTATTCAGTATTGCCTTAATAAACTTCACCCACAACTGCATACAGGCAAAAA NM_005817 RefSeq chr19
- 4838333 4867768 PLIN3 10226 "perilipin 3, transcript variant 1"
GO:0005811|GO:0005515|GO:0005737|GO:0005794|GO:0016020|GO:0016192|GO:0010008|GO:0043231|GO:0005
768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135315_PI430048170 0.951715183386367 1.02998229206494 0.462285505101378
0.4160738836613242.07379053380065 A A A 0.5228905493925431.87772671504557
0.685847777135093 A A A LNCV6_135315_PI430048170 mRNA
AAACCACATGCTTGTCTTCTATGTGGGAAGGCCTTCAGTCTGTCTTCCAACCTTAGATGA NM_001164457 RefSeq
chr8_KI270813v1_alt - 42257 47248 ZNF705G NA zinc finger protein 705G NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_130997_PI430048170 0.0404259682503202 0.6263797721834751 0.4241396886643
10.5037869874019 10.7620186198379 P P P 11.029072992708 11.0768566731999
11.5670841441275 P P P LNCV6_130997_PI430048170 mRNA
GCACAGGATGCTGAAAGCTATGTTACTATTCTTAGTTTGTAAATTGTCCTTTTGATACCA NM_001098504 RefSeq
chr22 - 38483437 38506340 DDX17 10521 "DEAD (Asp-Glu-Ala-Asp) box helicase 17, transcript variant
3"
GO:0005515|GO:0003724|GO:0006396|GO:0003723|GO:0003713|GO:0030331|GO:0005730|GO:0005634|GO:0005
524|GO:0006351|GO:0008186|GO:0016020|GO:0045944|GO:0033148|GO:0005654|GO:2001014 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129868_PI430048170 0.16470969498903 1.14546984400767 6.65334095976804
6.51734808864427 6.36334088873519 P P P 6.17838708991454 6.45106546098094
6.31844155012139 P P P LNCV6_129868_PI430048170 mRNA
TGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAA NM_198253 RefSeq chr5
- 1253171 1295047 TERT 7015 "telomerase reverse transcriptase, transcript variant 1"
GO:0042645|GO:0005515|GO:0030422|GO:0003721|GO:0003720|GO:0000333|GO:0030177|GO:0001172|GO:0046
872|GO:0042803|GO:0003968|GO:0000723|GO:0022616|GO:2001240|GO:0031379|GO:0000783|GO:0000781|GO:0
005697|GO:0000049|GO:0042162|GO:0005730|GO:0016779|GO:0001223|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130703_PI430048170 0.31113883839077336.4025941946892 0.265836642424669
7.06548076165828 1.95387509658628 A P A 0.3860769990455230.318807009213124
0.338936733713847 A A A LNCV6_130703_PI430048170 mRNA
CAAGCTGAAACCATACATGCAGTCTTTATGTTGGAAACTTCACCAGTAAAATTCTCTCAA NM_001171252 RefSeq
chrX - 55258415 55264846 PAGE3 NA "P antigen family, member 3 (prostate associated), transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137100_PI430048170 0.000681258803719625 0.3488550622225434.98777629816058
4.74452154485908 4.583410969937 P P P 6.13538010034949 6.48972673418297
6.25465598684217 P P P LNCV6_137100_PI430048170 mRNA
TAACAGTTTGTGTAACATTTATTATGATTTTACATAAATGAGCATCTACCATTCCAAAGC NM_014272RefSeq chr15
- 78759202 78811431 ADAMTS7 11173 "ADAM metallopeptidase with thrombospondin type 1 motif, 7"
GO:0071773|GO:0005515|GO:0009986|GO:0005578|GO:0036066|GO:0006493|GO:0051603|GO:0071356|GO:0071
347|GO:0005788|GO:0008270|GO:0032331|GO:0004222|GO:0044267|GO:0008237|GO:0043687 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143383_PI430048170 0.5896457312556750.830471302549601 2.40420244403572
2.21950083781078 1.6653855696773 A A A 2.42008224925521 2.83472324832462
1.72921644681711 A P A LNCV6_143383_PI430048170 mRNA
GAAGCTATGCCCATGTACAAAATTTTCTTCCTTCCCTAATTTTAATGGTATACTAACACC NM_153018RefSeq chr17
+ 5078458 5096374 ZFP3 124961 ZFP3 zinc finger protein
GO:0008150|GO:0003674|GO:0006355|GO:0003700|GO:0005634|GO:0005575|GO:0003677|GO:0046872|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140056_PI430048170 0.0291299652677393 0.4495907151764767.48459172237057
7.37362733281833 7.7009416840551 P P P 8.23167720190592 8.63047081736589
9.05831820947572 P P P LNCV6_140056_PI430048170 mRNA
GGGCTGTAATCTAAACAATTGGACAGATTAAATGTACATGGAAATGAGCAGTCTTACTTT NM_014755RefSeq chr2
- 64631620 64653912 SERTAD2 9792 SERTA domain containing 2
GO:0030308|GO:0005737|GO:0003713|GO:0005634|GO:0045893|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145601_PI430048170 0.8933302414390160.9970081498499426.96588223071249
7.07486575114874 7.58886514266844 P P P 7.19430542869925 7.2003058792493
7.32359449685542 P P P LNCV6_145601_PI430048170 mRNA
CTGCTTCCTTGGATGTCATTGCTTAAATATAGTCTTGAAGGGCTTGTTTTGAAATATTGTNM_002647RefSeq chr18 +
41955197 42081482 PIK3C3 5289 "phosphatidylinositol 3-kinase, catalytic subunit type 3"
GO:0005515|GO:0008286|GO:0044281|GO:0045022|GO:0005829|GO:0000910|GO:0016485|GO:0016303|GO:0007
032|GO:0000045|GO:0043201|GO:0006661|GO:0005770|GO:0036092|GO:0048015|GO:0005930|GO:0030496|GO:0
002224|GO:0005524|GO:0045335|GO:0046854|GO:0004672|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133473_PI430048170 0.00439124383072049 1.80337716605897 8.96561134325136
8.81630130069253 8.59927055120903 P P P 7.89393672295695 8.08587093233068 7.8622891678695
P P P LNCV6_133473_PI430048170 mRNA
CCTGAGTTGGGCAGCCAGGAGTGCCCCCGGGAATGGATAATAAAGATACTAGAGAACTGA NM_012391RefSeq
chr6 - 34537801 34556333 SPDEF 25803 "SAM pointed domain containing ETS transcription factor,
transcript variant 1"
GO:0060576|GO:0043065|GO:0006366|GO:0010455|GO:0010454|GO:0000981|GO:0005634|GO:0007275|GO:0000
122|GO:0030154|GO:0043565|GO:0045944|GO:0060480 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129631_PI430048170 0.00527523043393383 0.4082001800483087.27016822352876
7.20041770826713 6.96755369375292 P P P 8.65492418076879 8.5113336843636
8.11415017750535 P P P LNCV6_129631_PI430048170 mRNA
GCCAGCAATTTCACAAATCCTTGACAGAGAAAGACACAACCAAATGAAATAAAAATTCCT NM_001162997 RefSeq
chr17 + 75646565 75647977 SMIM6 100130933 small integral membrane protein 6 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143088_PI430048170 0.0663507876184166 0.8630886834769891 0.2136756948433
10.1582188790837 10.1300694363305 P P P 10.2554129814808 10.4057321804186
10.4709480957651 P P P LNCV6_143088_PI430048170 mRNA
GTAGCCTGCTGGTTTTATCTGAGTGAAATACTGTACAGGGGAATAAAAGAGATCTTATTT NM_002648RefSeq chr6

+ 37170145 37175428 PIM1 5292 "Pim-1 proto-oncogene, serine/threonine kinase, transcript variant 1"
GO:0005515|GO:0043066|GO:0030145|GO:0005886|GO:0008283|GO:0006915|GO:0005634|GO:0007275|GO:0005524|GO:0043433|GO:0007346|GO:0031659|GO:0005737|GO:0007049|GO:0046777|GO:0004674|GO:0030212|GO:0006468|GO:0043024|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144200_PI430048170 0.9114099872721990.9856322307619427.97261358694224
8.03355404956236 8.14827726040771 P P P 7.90844106008541 8.01678999857944
8.27278341545961 P P P LNCV6_144200_PI430048170 mRNA
GCTGATAGATGGTTTCCCAGTGTGAGATTTGTTATTTTGATCAGAGTATTCAAATCAGAA NM_018656RefSeq chr12
+ 68746155 68766073 SLC35E3 55508 "solute carrier family 35, member E3" GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130827_PI430048170 0.2453276396463461.04947844084549 0.353155352815313
0.3556835584269610.482647823140827A A A 0.3228699441873480.304042703203488
0.358854636802636A A A LNCV6_130827_PI430048170 mRNA
TGGAAGAGTTCAATGTACTGGAGATGGAAGTCATGAGAAGACAGCTGTATGCAGTCAACCNM_033085RefSeq chrX
+ 151716035 151723192 FATE1 89885 fetal and adult testis expressed 1
GO:0005515|GO:0005783|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88614_PI430048170 0.1885085252216351.73105458973099 0.2846209692659561.38141655950641
1.3569267482121 A A A 0.3143377453805060.27319980490544 0.30616364539173 A A A
LNCV6_88614_PI430048170 mRNA
TACAATTCCCAGCGGCATCGGGTCACAGATGAGGAGGTCCAGCAAAGCAGGTTCCAGATG NM_006725RefSeq
chr11 + 60971640 61020376 CD6 923 "CD6 molecule, transcript variant 1"
GO:0005515|GO:0005887|GO:0007155|GO:0006898|GO:0005044 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129299_PI430048170 0.3506318477388090.6422446262933370.327639656738492
1.82825765914004 0.270815778449428A A A 1.43841511169786 0.814205447883301
2.29077289510981 A A A LNCV6_129299_PI430048170 mRNA
CCAGTGATGTTCTGGAAATAATGGGAGATATTACAATAAAGCTACAGTTATGACACCCTG NM_017594RefSeq chr9
- 90609831 90643105 DIRAS2 54769 "DIRAS family, GTP-binding RAS-like 2"
GO:0006184|GO:0005886|GO:0043406|GO:0007264|GO:0005525 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137608_PI430048170 0.2449727224657441.03679977904221 0.443266977033991
0.36495915346062 0.404942348969445A A A 0.3022824310377270.346168766515491
0.407430889339725A A A LNCV6_137608_PI430048170 mRNA
TATTTTGACCCTGATTTCAATCTTCTACCCTTGGGAGTTCTGGCGTTTGGCACAAAGTCC NM_153221RefSeq chr19
+ 19538264 19546659 CILP2 148113 cartilage intermediate layer protein 2
GO:0004035|GO:0005578|GO:0004551|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129148_PI430048170 0.6022772116286120.9358651244291329.37502255635142
9.38272928003649 9.19758104843372 P P P 9.55723449879153 9.51888916009742
9.13744396524128 P P P LNCV6_129148_PI430048170 mRNA
ATCTCCTCATCACGTTCTGTGCCGTCCTTGGGAAAGGCCTGCATTCTGATCCTTCCAGGC NM_024815RefSeq chr8
- 22106871 22109419 NUDT18 79873 nudix (nucleoside diphosphate linked moiety X)-type motif 18
GO:0005515|GO:0046712|GO:0034656|GO:0000287|GO:0046057|GO:0046067|GO:0055086|GO:0044281|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134777_PI430048170 0.0141361302788567 0.38821632047067 2.22915633139019
1.49564749833033 2.28058104557766 A A A 3.65431195017606 3.03277746953026
3.47012167533414 P P P LNCV6_134777_PI430048170 mRNA
TGTATCTAACCAGATGAAAGTTGTTTATATTTGAGAGTAGTATACATATTTGATGTAGTA NM_025040RefSeq chr19
- 52013323 52028427 ZNF614 80110 zinc finger protein 614

GO:0005515|GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0005575|GO:0003677|GO:0046872|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53620_PI430048170 0.1699147581512991.1612810155004 8.39395276650767 8.30945103919066
8.36430722808383 P P P 8.23680518438991 7.91629997911685 8.24500721529689 P P P
LNCV6_53620_PI430048170 mRNA
AGTGTAGTCTCAGCTTAAAGTTGTGTAATACTAAAATCACGAGAACACCTAAACAACAAC NM_014313RefSeq chr1
+ 25338297 25362361 TMEM50A 23585 transmembrane protein 50AGO:0005783|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144189_PI430048170 0.0205672947150048 0.5272252537128079.26424229020491
9.33020599647707 9.56179240239263 P P P 10.1004979351076 10.1272246998643
10.6478243005264 P P P LNCV6_144189_PI430048170 mRNA
CTTCACAGACATGGTCTAGAATCTGTACCCTTACCCACATATGAAGAATAAAATTGATTA NM_006407RefSeq chr3
+ 69084938 69106088 ARL6IP5 10550 ADP-ribosylation factor-like 6 interacting protein 5
GO:0043065|GO:0005783|GO:0008631|GO:0032874|GO:0008022|GO:0043280|GO:0003674|GO:0015813|GO:0010
917|GO:0016020|GO:0005789|GO:0016021|GO:0070062|GO:0051051 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128799_PI430048170 0.00420610943381955 1.19981322188908 0.843147052621756
0.8789852843186160.892894699240292A A A 0.6665714152045770.574157712745945
0.58453620150933 A A A LNCV6_128799_PI430048170 mRNA
GCTCTAGTTTTGTGACCTTGTGTACTTTTGAAATAAAATCAAGAAAGCAGTTCTCTGCCT NM_001338RefSeq chr21
+ 17512905 17570111 CXADR 1525 "coxsackie virus and adenovirus receptor, transcript variant 1"
GO:0005515|GO:0043005|GO:0031594|GO:0030054|GO:0005886|GO:0008013|GO:0030175|GO:0050900|GO:0005
615|GO:0042802|GO:0030426|GO:0086067|GO:0007507|GO:0016323|GO:0051607|GO:0005912|GO:0010669|GO:0
014704|GO:0005911|GO:0001618|GO:0016032|GO:0050839|GO:0071253|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127520_PI430048170 0.00595583700701821 0.4375279400792074.68641125474751
4.45413245372129 5.01128153254124 P P P 5.79832646041407 5.71834271889997
6.21646049156684 P P P LNCV6_127520_PI430048170 mRNA
CTGGGGTTAATCCTGAAGCTAAAAGTAAATGTTTCTTGAATTGATTTTGTTCTGTGGTAC NM_001080392 RefSeq
chr7_GL383534v2_alt - 23319 68748 KIAA1147 57189 KIAA1147 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144357_PI430048170 0.00680301256976553 0.70989851924746412.2275582364639
12.2756832396371 12.1065652849587 P P P 12.6973470528509 12.7239483243555 12.676281955471
P P P LNCV6_144357_PI430048170 mRNA
GCGCTAACTCCTGATTAATACAATGGAAGTTTCTGGGCATTTACAATTTCAACACTTAAA NM_017458RefSeq chr16
+ 29820393 29848039 MVP 9961 "major vault protein, transcript variant 1"
GO:0038127|GO:0005515|GO:0048471|GO:0023057|GO:0019901|GO:0008283|GO:0019903|GO:0061099|GO:0005
634|GO:0015031|GO:0072376|GO:0031953|GO:0005737|GO:0016020|GO:0005643|GO:0030529|GO:0051028|GO:0
005856|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128745_PI430048170 0.0086060890260154 1.12607813199575 10.7695147296935
10.8373653860872 10.7641463298395 P P P 10.6147779288817 10.6401013525974
10.6031390286021 P P P LNCV6_128745_PI430048170 mRNA
GACCATGTCATGCAGAATTAACAAGGTAGCACCGAGCATATCAATAAATATTATTCTGAT NM_052839RefSeq chr22
+ 50170730 50180295 PANX2 56666 "pannexin 2, transcript variant 1"
GO:0005737|GO:0005886|GO:0002931|GO:0007268|GO:0005921|GO:0055077|GO:0016021|GO:0055085|GO:0034
214|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144772_PI430048170 0.2309188628862691.09040142120307 8.93556017702203 8.8790312851064
8.71084034868532 P P P 8.78217220290133 8.60843189014386 8.76338307839414 P P P
LNCV6_144772_PI430048170 mRNA

CAGGGATTCAGGTTCATAATGAACTTCACAGTAAAGAACACGTTTGTTCTGTAAAGCATT NM_012213 RefSeq chr16 + 83899124 83916182 MLYCD 23417 malonyl-CoA decarboxylase GO:0005782|GO:0050080|GO:0005102|GO:0046321|GO:0044281|GO:0006085|GO:2001294|GO:0010906|GO:0005739|GO:0005737|GO:0002931|GO:0005759|GO:0006633|GO:0044255|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145517_PI430048170 0.2893986944979061 .57860733452228 0.407446298925906 1.59715649761917 1.65944517834153 A A A 1.09264214350125 0.388432767620279 0.39640064893801 A A A LNCV6_145517_PI430048170 mRNA
GATGCCTTACTCTGACGGGAGCATCTGTATTTTTATGTTAAAAGCCCACAAAATAAAAAT NM_001692 RefSeq chr2 + 70935867 70965431 ATP6V1B1 525 "ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1" GO:0008286|GO:0015078|GO:0007605|GO:0045851|GO:0033180|GO:0032403|GO:0006885|GO:0055074|GO:0005829|GO:0006879|GO:0016323|GO:0033572|GO:0005737|GO:0016324|GO:0016820|GO:0090382|GO:0070062|GO:0007588|GO:0042472|GO:0046034|GO:0051701|GO:0055085|GO:0005524|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140397_PI430048170 0.00254506311141604 0.5020452152440364.81556338927631 4.74652569694275 5.00217029905073 P P P 5.91495886682968 5.63335099381629 5.98688451204692 P P P LNCV6_140397_PI430048170 mRNA
CTGATTTTTGTCTAAAGTGGCATTATTGACTGCTTCTGTGATGCTACTGTAATGTAATAC NM_001267536 RefSeq chr15 + 84235772 84245368 GOLGA6L4 643707 golgin A6 family-like 4 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133534_PI430048170 0.1314594120278471.27395579545956 3.57602732839804 3.18332452969819 3.19879038908399 P P P 3.19199116349387 2.73231949574301 2.98464157078554 P P P LNCV6_133534_PI430048170 mRNA
CAGGAAGAAGGGGCTAGGGCAGGGGAGATTCTCATAGGGGAAATAAAACTACTAAAATAT NM_024575 RefSeq chr1 + 151156628 151159749 TNFAIP8L2 79626 "tumor necrosis factor, alpha-induced protein 8-like 2" GO:0005515|GO:0005737|GO:0050868|GO:0050728|GO:0045087 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143712_PI430048170 0.6933974212323461.03693007290506 10.6273060325295 10.6179297699244 10.8960408329795 P P P 10.6536445062723 10.5366211992585 10.7996218803924 P P P LNCV6_143712_PI430048170 mRNA
GTAGCACTTAAGACTTATACTTGCCTTCTGATAGTATTCCTTTATACACAGTGGATTGAT NM_000249 RefSeq chr3 + 36993349 37050846 MLH1 4292 "mutL homolog 1, transcript variant 1" GO:0005515|GO:0032407|GO:0051257|GO:0048477|GO:0005634|GO:0007283|GO:0016446|GO:0006303|GO:0003697|GO:0006298|GO:0016887|GO:0000289|GO:0032389|GO:0000795|GO:0008630|GO:0043060|GO:0045190|GO:0005712|GO:0005524|GO:0007129|GO:0045950|GO:0006281|GO:0016020|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141115_PI430048170 0.38929483827964 1.30514380703471 0.499185975529949 0.4613163828358461.36363535672757 A A A 0.39596507025899 0.505732089067282 0.458249873559709A A A LNCV6_141115_PI430048170 mRNA
CATGCTGAGAGTGCAGAGATACCAAATACTGCTGAAAGGATGCAAAGGATGATAGGATGA NM_001143987 RefSeq chr1 + 108450281 108470638 NBPF6 NA "neuroblastoma breakpoint family, member 6, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54050_PI430048170 0.5169406800103641.57438878043774 0.5999788377786092.15547907979088 0.391012819974671A A A 0.4215308618155120.8878999328812980.52162250722767 A A A LNCV6_54050_PI430048170 mRNA
AGACCATGATAAAGAAGATTATGAGGCAGATCCAGGAGGAGCCACTGGATTCTCTCTCAA NM_001039464 RefSeq chr1 + 54641739 54710267 MROH7 374977 "maestro heat-like repeat family member 7, transcript variant 1" GO:0016021|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132707_PI430048170 0.9578065733363291.00192633944309 0.390235509276244

0.5030489695014970.40046032799071 A A A 0.5140038932886910.382452377079868
0.387799070189926A A A LNCV6_132707_PI430048170 mRNA
CTGCCTTATAGATCATGTAAACAAACAAGGTCATAGAGGACTTAAATAGCAAAGCAGAAA NM_006620RefSeq chr6
- 134960382 135054898 HBS1L 10767 "HBS1-like translational GTPase, transcript variant 1"
GO:0007165|GO:0016020|GO:0003924|GO:0005525|GO:0003746|GO:0006412|GO:0070062|GO:0006414 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142370_PI430048170 0.5080339040943651.20584658757435 1.84599678698075
2.17670302587394 1.55061390256204 A A A 0.5179327573004291.57178050879752 2.2495787829414
A A A LNCV6_142370_PI430048170 mRNA
CACTTTTGCTAAAGGAGGGGTAAAGGAGGGGGTAGGGAATAAAGCTATATTGGAACAAAA NM_032257RefSeq
chr1 - 42430329 42456267 ZMYND12 84217 "zinc finger, MYND-type containing 12, transcript
variant 1" GO:0005622|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134539_PI430048170 0.0284341561832381 0.5535912488801473.92113621419986
3.62336055807566 3.93152469226122 P P P 4.3499831364503 4.63316622692072
4.99911028919304 P P P LNCV6_134539_PI430048170 mRNA
ACACCGGCTTAAGCCTTCTGTGTTTCCTTTGAGCCTTTTCACTACAAAATCAAATATTAA NM_004496RefSeq chr14
- 37589551 37595120 FOXA1 3169 forkhead box A1
GO:0003700|GO:0006366|GO:0044212|GO:0000981|GO:2000049|GO:0005634|GO:0010719|GO:0045880|GO:0051
091|GO:0048646|GO:0045944|GO:0006338|GO:0021904|GO:0060738|GO:0032355|GO:0060528|GO:0060743|GO:0
060741|GO:0019904|GO:0060740|GO:0005730|GO:0048665|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136935_PI430048170 0.8750676395333751.08817745964344 1.28946513911631
0.3309381928056340.282543374831961A A A 0.2462021730617920.839809130999504
0.626754976405077A A A LNCV6_136935_PI430048170 mRNA
CCCTTTTACCCTCCATTTGTGTTTATTGCATATCCACTATAACAACATTAAAGGACCTTT NM_203422RefSeq chr11 -
62686401 62689899 LRRN4CL NA LRRN4 C-terminal like NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133490_PI430048170 0.5583319480644061.01599074202713 0.490720381963002
0.5390585325612750.429521432780035A A A 0.4764470156748760.453947887230585
0.462239254826283A A A LNCV6_133490_PI430048170 mRNA
TGATCTAGATATCCTTCGTCATGACACTTCTCAATAAAACGTATCCCACCGTATTGTAAA NM_000851RefSeq chr1
+ 109712241 109718268 GSTM5 2949 glutathione S-transferase mu 5
GO:0006805|GO:0006749|GO:0044281|GO:0004364|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_83098_PI430048170 0.3831667815786191.09633026034897 9.85487471905608 9.68474824061122
10.0598347631105 P P P 9.65022803731345 9.69740090698213 9.86899677346926 P P P
LNCV6_83098_PI430048170 mRNA
TGGAGCAGAGGAAGCTGAGGAAGTTGGAGTTGAACACTTGTTACGAGATATCAAAGACAC NM_002811RefSeq
chr16 + 74296774 74306288 PSMD7 5713 "proteasome (prosome, macropain) 26S subunit, non-
ATPase, 7"
GO:0005515|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0042803|GO:0005
829|GO:0034641|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0000502|GO:0
043066|GO:0005838|GO:0006521|GO:0051437|GO:0042590|GO:0006915|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128401_PI430048170 0.0053319808521633 0.5029455393115291 1.7198515329525
11.6574098620366 11.9467811721221 P P P 12.5452207925634 12.7334280313753
12.9998755433996 P P P LNCV6_128401_PI430048170 mRNA
GGTGAGAAACTGAAATCCCAAACACTGTTTTGTTGCTTGTTTTATTATGACCTCAGATTA NM_145690RefSeq chr8
- 100918575 100952129 YWHAZ 7534 "tyrosine 3-monooxygenase/tryptophan 5-monooxygenase

activation protein, zeta, transcript variant 2"
GO:0005515|GO:0010467|GO:0048471|GO:0006626|GO:0072562|GO:0005634|GO:0051683|GO:0005615|GO:0032403|GO:0090168|GO:0042629|GO:0042802|GO:0005829|GO:0005739|GO:0005737|GO:1900740|GO:0061024|GO:0031252|GO:0030659|GO:0070062|GO:0042470|GO:0043066|GO:0019901|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127532_PI430048170 0.0962933775108988 1.29156583027732 7.7994253981056 7.72183083471318 7.75537878084556 P P P 7.13999244950763 7.58978670292477 7.40550173726366 P P P LNCV6_127532_PI430048170 mRNA
TCGGAGCGGAAAAACTGGTGTGCTCTCATCACTGAGACTGCCGGATCCCTGAAAGTCCCT NM_199002RefSeq chr19 + 41884378 41907452 ARHGEF1 9138 "Rho guanine nucleotide exchange factor (GEF) 1, transcript variant 1"
GO:0005515|GO:0048011|GO:0005886|GO:0008283|GO:0038032|GO:0007266|GO:0005829|GO:0005737|GO:0032321|GO:0050771|GO:0005089|GO:0050770|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129807_PI430048170 0.865063673307895 0.971584108159529 14.4452503814486 14.2407777944125 14.3469323116233 P P P 14.0835832042834 14.4825577822017 14.5555670433998 P P P LNCV6_129807_PI430048170 mRNA
TGCTTGTCTGTTTAGTTCTGTGTATAAATGGAATGTTGTGGAGATGACCCCTCCCTGTGC NM_005507 RefSeq chr11 - 65854813 65858333 CFL1 1072 cofilin 1 (non-muscle)
GO:0005515|GO:0030036|GO:0001755|GO:0005634|GO:0030010|GO:0007266|GO:0006606|GO:0005615|GO:0016363|GO:0005737|GO:0005911|GO:0007411|GO:0030836|GO:0007010|GO:0022604|GO:0030042|GO:0061001|GO:0043200|GO:0070062|GO:0043066|GO:0048013|GO:0031258|GO:0000281|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136359_PI430048170 0.00395685239370576 0.68279460605366 8.89544789549393 8.80335987159807 8.76398613445416 P P P 9.28254706717446 9.49600714792846 9.33003501145613 P P P LNCV6_136359_PI430048170 mRNA
GTGGGGACGGGCCATCACTGTATGTATTAAAATGACTGTATCAAATAAATGTTTATTGAT NM_020713 RefSeq chr20 - 63956703 63969870 ZNF512B 57473 zinc finger protein 512B
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129157_PI430048170 0.346656901776175 0.781745810609982 5.02975065570029 3.9782862529832 3.88000580650112 P P P 4.8440297228965 4.83571316066584 4.55489638920107 P P P LNCV6_129157_PI430048170 mRNA
TTGTGGCTGTGTGTGTGACTGTGAGTGTGAGTGACAGATACATAGTTTCATTGGTCATTT NM_001447 RefSeq chr5 - 151504091 151568944 FAT2 2196 FAT atypical cadherin 2
GO:0005913|GO:0005886|GO:0005509|GO:0010631|GO:0005634|GO:0016021|GO:0007156|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138546_PI430048170 0.198436810535307 0.91459456758436 7.43410623341883 7.3574050885574 7.41523317970021 P P P 7.40302566198655 7.54404135348844 7.63756230918337 P P P LNCV6_138546_PI430048170 mRNA
TGTCCATAATCAAATCATCATCTTGCAATGCAAGGGCTACCCCATAATTATCAGACATTA NM_024758 RefSeq chr1 - 15571698 15585110 AGMAT 79814 agmatine ureohydrolase (agmatinase)
GO:0008295|GO:0005739|GO:0034641|GO:0008783|GO:0006595|GO:0033388|GO:0044281|GO:0097055|GO:0046872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64521_PI430048170 0.907554242828121 0.988167836742829 5.14432718365595 5.00202608915128 4.69449467991823 P P P 5.08783025737416 5.06458340841885 4.75212985508576 P P P LNCV6_64521_PI430048170 mRNA
AAATCCAGATCTCCCGCATCCTGGACCAAAGGAATCGGCAGGTGACGTTCACCAAGCGGA NM_005919 RefSeq chr19 - 19145566 19192591 MEF2BNB-MEF2B 4207 "MEF2BNB-MEF2B readthrough, transcript

variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126799_PI430048170 0.851474803825996 0.895515472934878 3.32854123288875
3.44919624183097 3.50335653808254 P P P 2.78500377935991 3.95307150065607
3.7758414007006 P P P LNCV6_126799_PI430048170 mRNA
CCAGACTAGTGAGTTAAGTACAAGATCTCTCTAAAAATAAACAGATGAAAATCTATCCCC NM_007175 RefSeq
chr8 + 37736578 37757801 ERLIN2 11160 "ER lipid raft associated 2, transcript variant 1"
GO:0005515|GO:0043234|GO:0005737|GO:0005886|GO:0005783|GO:0005789|GO:0016021|GO:0030433|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141622_PI430048170 0.662455598722983 1.03361257473913 11.4504091627403
11.5727200401209 11.3647334644341 P P P 11.3501699441956 11.5851229477903
11.3008181290384 P P P LNCV6_141622_PI430048170 mRNA
GCTTCGTGAGGGGTCTCTGGCCCAGTTTCCAATGAATAAAGTTCTCTTGACAGCTCTGAC NM_032015 RefSeq
chr11 + 119334499 119337314 RNF26 79102 ring finger protein 26
GO:0008150|GO:0008270|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127919_PI430048170 0.173818286365394 1.10400086525863 0.59922764228057
0.403263904237732 0.599009700179 A A A 0.290934722510106 0.404567834566089
0.480235992075562 A A A LNCV6_127919_PI430048170 mRNA
CAAGTGAAACAAGCTTTCAGTGACTCTATAAAGAGGATTGCATTTCTCTCAAAGAAGTAG NM_054105 RefSeq
chr12 + 55452213 55453152 OR6C2 NA "olfactory receptor, family 6, subfamily C, member 2" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139557_PI430048170 0.958134991027333 0.993062462268388 14.5300005525399
14.6713072879798 14.6661028483249 P P P 14.453319940684 14.6713072879798
14.7602814248759 P P P LNCV6_139557_PI430048170 mRNA
TGTCATTCAATTCCAGTCACCTCTTCTGCAATCATGACCTCTTGATGTCTCCATGGTGAC NM_004074 RefSeq
chr11 + 63974606 63976543 COX8A 1351 cytochrome c oxidase subunit VIIIA (ubiquitous)
GO:0022904|GO:0004129|GO:0005743|GO:0044281|GO:0016021|GO:0006091|GO:0055085|GO:0044237 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_136135_PI430048170 0.103091864197845 1.09801253553067 8.63635454305308
8.61275468633497 8.53388282161814 P P P 8.44240646184788 8.55519809540579
8.37702980253234 P P P LNCV6_136135_PI430048170 mRNA
GTTGGGGGCTTGGAAGCACTTGAACTTTTTATTTTATTAAAACCTTGTTATAAGCAGCAA NM_032701 RefSeq
chr19 + 55339852 55348121 SUV420H2 84787 suppressor of variegation 4-20 homolog 2
(Drosophila)
GO:0005515|GO:0000780|GO:0006355|GO:0005720|GO:0042799|GO:0005721|GO:0005654|GO:0006351|GO:0034
773 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137733_PI430048170 0.463680168453135 1.20726210442434 8.08604225434148
7.76566977170311 8.13553392922375 P P P 8.42407710636823 6.90321570297657
7.45207001535569 P P P LNCV6_137733_PI430048170 mRNA
CTGCATAGCAGACTTTTAATAACCTTGGGATTTATCTGGTAGAACAATATGTGTTCTACA NM_014822 RefSeq
chr4 - 118722822 118836171 SEC24D 9871 SEC24 family member D
GO:0002474|GO:0012507|GO:0048471|GO:0030127|GO:0048208|GO:0044281|GO:0001701|GO:0006886|GO:0005
829|GO:0006888|GO:0003674|GO:0019886|GO:0000139|GO:0005789|GO:0061024|GO:0008270|GO:0044267|GO:0
043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83545_PI430048170 0.338339702899263 1.40837212397264 0.451388203458065
1.44882185617195 0.454733030941953 A A A 0.311856092746716 0.366097614321207
0.435247558467343 A A A LNCV6_83545_PI430048170 mRNA
TTCAGCAGAGCCTATGGGGTTCAGATGATTCACATAAGAATAGAAGTTTCAGGGCTGGAC NM_006470 RefSeq
chr17 - 15627965 15682879 TRIM16 NA tripartite motif containing 16 NA . NA - . NA

NA NA NA NA NA NA NA NA
LNCV6_142656_PI430048170 0.709697033330454 1.01308970540266 6.59599671286994
6.57388410829498 6.53535400330225 P P P 6.47651278906056 6.53878826496085
6.63014784516968 P P P LNCV6_142656_PI430048170 mRNA
TGGACTGAGTAGAACTGGAGGACAGGAGTCGACGTGAGTTCCTGGGAGTCTCCAGAGATG NM_005672 RefSeq
chr8 + 142680455 142682727 PSCA 8000 "prostate stem cell antigen, transcript variant 1"
GO:0005886|GO:0031225|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_141582_PI430048170 0.00243103848476134 0.32297207345064 2.92230090795594
2.44978408928763 2.77579431948928 A A A 4.31609347503527 4.04214015229555
4.65525039747897 P P P LNCV6_141582_PI430048170 mRNA
GAAAAAGCAGAAGCCCTGCAAGAAGAGGTAGAAGAGTTACTAAGATTGCCTTCTGATTTC NM_001297756 RefSeq
chr4 - 83407342 83455883 HELQ 113510 "helicase, POLQ-like, transcript variant 3"
GO:0000724|GO:0005730|GO:0004386|GO:0005654|GO:0003676|GO:0005524 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_140598_PI430048170 0.276326712853204 0.976319455127497 0.283396934797344
0.328038243182013 0.350055299823995 A A A 0.389511378903595 0.323065471158184
0.352666880303181 A A A LNCV6_140598_PI430048170 mRNA
TTTTGCTTTCAATAATCCAACGTAGCAGCCGTGATGTCATTTTTGTATTTCAGGAAGACT NM_002785 RefSeq
chr19 - 43007656 43026479 PSG11 5680 "pregnancy specific beta-1-glycoprotein 11, transcript
variant 1" GO:0007565|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136612_PI430048170 0.375436840044979 0.697642567472633 2.01786930507095
2.25573612753222 1.28286755824549 A A A 1.67519123015358 2.97965461347638
2.33823499068127 A P A LNCV6_136612_PI430048170 mRNA
GCCCCTGAGCTGAGCAGAGTCATTATTGGAGAGTTTTGTATTTATTAAAACATTTCTTTT NM_001304473 RefSeq
chr3 + 184380072 184389835 CHRD 8646 "chordin, transcript variant 3"
GO:0005515|GO:0030336|GO:0001707|GO:0033504|GO:0021919|GO:0002053|GO:0005615|GO:0001649|GO:0001
702|GO:0045785|GO:0030514|GO:0001501|GO:0045668|GO:0019955|GO:0030900|GO:0045545|GO:0008201 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142767_PI430048170 0.000542428395662283 3.30091623527808 6.68330375297805
6.61287296847181 6.28653672359574 P P P 5.01879356972433 4.78815860959786
4.60787769416618 P P P LNCV6_142767_PI430048170 mRNA
GAGGGGGCGCTGGAGCTTCCAACCCGAGGCAATAAAAGAAATGTTGCGTAACTCAAAAAA NM_002256RefSeq
chr1 - 204190340 204196491 KISS1 3814 KiSS-1 metastasis-suppressor
GO:0005515|GO:0007010|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132200_PI430048170 0.714881455951166 0.914030087199229 1.80284254211234
0.398588428224046 0.249272126374745 A A A 1.68306355057861 0.592279696972266
0.880588232294616 A A A LNCV6_132200_PI430048170 mRNA
GGCTGTGTTAAAAAATCTATACAATAAAGCTGTGACCCTGAGATTCATGTTTTCCTAAGA NM_133170RefSeq chr20
- 42072751 43189917 PTPRT 11122 "protein tyrosine phosphatase, receptor type, T, transcript variant 1"
GO:0005515|GO:0045296|GO:0070097|GO:0045295|GO:0005886|GO:0008013|GO:0009986|GO:0045294|GO:0035
335|GO:0007165|GO:0006470|GO:0016021|GO:0007155|GO:0007156|GO:0007169|GO:0004725 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135987_PI430048170 0.0175322557773499 0.23523534833395 2.63655065213187
2.14970284908466 3.28002657435853 A A P 4.83971500375464 4.70950864120813
4.99063929305628 P P P LNCV6_135987_PI430048170 mRNA
GGCTTACTCTAATAAGTAACCTTCTGGACTATGGAATGAATATAAATGAATGGCACTTTG NM_006609RefSeq chr2
- 127298668 127343229 MAP3K2 10746 mitogen-activated protein kinase kinase kinase 2
GO:0005515|GO:0019901|GO:0007257|GO:0005524|GO:0046872|GO:0005829|GO:0000187|GO:0000186|GO:0005

737|GO:0004672|GO:0004674|GO:0005654|GO:0006468|GO:0071260|GO:0045893|GO:0004709|GO:0004708 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57816_PI430048170 0.00913446762509627 0.7284408279258194.34848384898791 4.34156715318288 4.56043209331222 P P P 4.76123854815275 4.88209887954948 4.98102096167078 P P P LNCV6_57816_PI430048170 mRNA CCAGGATAACCTGTAATGGGCAAGGAGCCACAAAGAAGAAAACATTTCTTTTAATTTTTA NM_001164160 RefSeq chr11 + 68460717 68615333 PPP6R3 55291 "protein phosphatase 6, regulatory subunit 3, transcript variant 4" GO:0005515|GO:0005737|GO:0005886|GO:0019903|GO:0043666|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128849_PI430048170 0.3118619448990331.28275492624053 1.2594744753149 0.5035619431238240.586632495251596A A A 0.3779353549652710.446280054014628 0.565868305558346A A A LNCV6_128849_PI430048170 mRNA TACATTTCTTCCAGTACGAAAGGATAAGAGAAATGGGGCCCACTTCATAAAGTGCCCCTG NM_001190452 RefSeq chr17 + 22523110 22524665 MTRNR2L1 NA MT-RNR2-like 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70127_PI430048170 0.0486494374185095 1.17547236369885 7.88091934435794 7.99893637182695 8.10294536815113 P P P 7.85655324376309 7.6977105835204 7.73247589137683 P P P LNCV6_70127_PI430048170 mRNA AATCGGTTAGACTTCTCAAGTGCAATTCAAGATATCCGAAGGTTCAATTATGTGGTCAAA NM_183421 RefSeq chr8 + 406807 469875 FBXO25 26260 "F-box protein 25, transcript variant 1" GO:0005515|GO:0004842|GO:0016567|GO:0005730|GO:0000151|GO:0005634|GO:0003779|GO:0019005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128180_PI430048170 0.1165592875748821.25057457017461 11.5192925726967 11.9105409887774 11.8746488672373 P P P 11.5165761275932 11.4774896330669 11.3701472939211 P P P LNCV6_128180_PI430048170 mRNA ATTTTCGTAGTAGATTTAAAAGTTATAATCTCTTCCCCTCCCCCCAAACTGGAGCTGTCC NM_174928 RefSeq chr13 - 20728933 20773918 N6AMT2 221143 N-6 adenine-specific DNA methyltransferase 2 (putative) GO:0008168|GO:0003676|GO:0032259|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143655_PI430048170 0.7800094856975160.8806019246504231.56683171142859 0.8713440058480260.249368010963733A A A 0.38671503946497 1.00210119714637 1.79956301298409 A A A LNCV6_143655_PI430048170 mRNA ACCTGTACGAGAAAAGGACTGTGTCAAATCACTAAATGGGCTTCTAAATAAAGCAGTCAA NM_003460 RefSeq chr16 - 21197451 21214510 ZP2 7783 "zona pellucida glycoprotein 2 (sperm receptor), transcript variant 1" GO:0060046|GO:0005794|GO:0005886|GO:0005783|GO:0005771|GO:0005578|GO:0005576|GO:0032190|GO:0007339|GO:0015026|GO:0006886|GO:0031012|GO:0007338|GO:0007165|GO:0060468|GO:0006828|GO:0016021|GO:0030141|GO:0032504. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138470_PI430048170 0.4489190120700650.285980723916939 0.445579990117072 0.42537103591283 0.456388697105551A A A 0.3452521933104573.54419924230362 0.400248086352913A P A LNCV6_138470_PI430048170 mRNA GTATAAAAGAGTCCCCTTTCTAAAATTCATACAGTGCCCTTGTATTCATTTATGCAGTGT NM_001045 RefSeq chr17 - 30194318 30235968 SLC6A4 6532 "solute carrier family 6 (neurotransmitter transporter), member 4" GO:0050998|GO:0005515|GO:0043005|GO:0005886|GO:0071300|GO:0021941|GO:0051259|GO:0042803|GO:0005829|GO:0021794|GO:0051015|GO:0042310|GO:0005335|GO:0051260|GO:0007613|GO:0017075|GO:0032355|GO:0006837|GO:0046621|GO:0001666|GO:0017137|GO:0007584|GO:0015222|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140157_PI430048170 0.4331704056220952.33570054251617 0.390263762444979 2.77947010243704 0.459791285764187A A A 0.5067545948835530.461651310800312 0.369145942208141A A A LNCV6_140157_PI430048170 mRNA ATAAACTTCAAGGAAAATGAACTCATTCTTCCTTTGATATTTGAGAGCAGATGAAAGCCG NM_021245 RefSeq chr10

- 73631611 73641757 MYOZ1 58529 myozenin 1
GO:0005515|GO:0030239|GO:0005634|GO:0051373|GO:0015629|GO:0031143 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142723_PI430048170 0.0292693462406215 0.4809535609174996.99728930227048
6.99003997505958 6.9650081368209 P P P 7.70866318063928 8.00540962588944
8.33786790474688 P P P LNCV6_142723_PI430048170 mRNA
GCTAGACATTTCTATACTCTGTTGTAACACTGAGGTATCTCATTTGCCCATGTTAATTTT NM_020338RefSeq chr10 +
79069034 79316528 ZMIZ1 57178 "zinc finger, MIZ-type containing 1"
GO:0007569|GO:0048844|GO:0048146|GO:0001701|GO:0006351|GO:0007296|GO:0043231|GO:0003007|GO:0005
737|GO:0048589|GO:0016607|GO:0045944|GO:0005654|GO:0008270|GO:0001570 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139948_PI430048170 0.0497259115065145 1.38809258599749 8.41029000656365
8.78537786568161 8.49258754836572 P P P 8.14641618875355 8.07904052891941
8.06973402665291 P P P LNCV6_139948_PI430048170 mRNA
GCATTGTGGCTGAAGAGTTCCTTAAGAATTTTTAAACCATCTGGCTGGATCTCGTGGCCT NM_005718RefSeq chr3
+ 9792547 9807105 ARPC4 10093 "actin related protein 2/3 complex, subunit 4, 20kDa, transcript
variant 1"
GO:0005515|GO:0034314|GO:0048013|GO:0005885|GO:0042995|GO:0005829|GO:0045010|GO:0051015|GO:0007
411|GO:0045087|GO:0005200|GO:0030041|GO:0019899|GO:0030674|GO:0038096|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_81143_PI430048170 0.3872261685415121.05602124592387 0.5069955569480550.283390257049498
0.324248313132172 A A A 0.2745917260403120.3217699764643270.291917522197544 A A A
LNCV6_81143_PI430048170 mRNA
GAAAGTTGCTTGACAGCTCTAATTACGAATTGAACACATTAAACACCTGGTGAAATTATC NM_001340RefSeq chr9
+ 102995310 103018488 CYLC2 1539 "cylicin, basic protein of sperm head cytoskeleton 2"
GO:0033150|GO:0005200|GO:0007275|GO:0005634|GO:0007283|GO:0030154 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131097_PI430048170 0.0479680953493631 0.866264820568387 13.3636730209095
13.5449856972557 13.380992643017 P P P 13.6255302071844 13.7003716205766
13.5899234010369 P P P LNCV6_131097_PI430048170 mRNA
GCTTCACCCTCTTGGGGATAACTTGCTTAGTTTTTTAATAAATGTTCCTGGTTGGTTTTC NM_024656RefSeq chr19 +
17555701 17583156 COLGALT1 79709 collagen beta(1-O)galactosyltransferase 1
GO:0016020|GO:0030198|GO:0050211|GO:0005788 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139850_PI430048170 0.00578260979212768 2.59710900035532 7.93287535601454
7.87258500718825 8.29485765610877 P P P 6.26087720458108 6.84664606456092
6.82623061448168 P P P LNCV6_139850_PI430048170 mRNA
CAGCATGGAGGACACAGATGACTCTTTGGTGTTGGTCTTTTTGTCTGCAGTGAATGTTCA NM_001018111 RefSeq
chr7 - 131500261 131556617 PODXL 5420 "podocalyxin-like, transcript variant 1"
GO:0005515|GO:0022408|GO:0030335|GO:0072015|GO:0005886|GO:0032534|GO:0031528|GO:0030175|GO:0050
900|GO:0033634|GO:0001726|GO:0005615|GO:0044297|GO:0030027|GO:0072175|GO:0005737|GO:0007162|GO:0
016324|GO:0016477|GO:0005887|GO:0036057|GO:0045121|GO:0007155|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133125_PI430048170 0.00831879635243328 1.7017134057895 12.4326788211697
12.4208401815429 12.4148962959885 P P P 11.5864320767679 11.5744194474011 11.795749498967
P P P LNCV6_133125_PI430048170 mRNA
GTTTCCAATGGTTCAGTCTAGCTTTCACAGTTTTTATGAATAAAAGGCATTAAAGGCTGA NM_002032RefSeq chr11
- 61964284 61967660 FTH1 2495 "ferritin, heavy polypeptide 1"
GO:0005515|GO:0008285|GO:0005506|GO:0048147|GO:0006892|GO:0005634|GO:0006880|GO:0055085|GO:0006
898|GO:0008199|GO:0005829|GO:0005739|GO:0006879|GO:0008043|GO:0004322|GO:0006955|GO:0061024|GO:0

006826|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143537_PI430048170 0.00553918134387129 0.225691095918395 0.303938406042165
0.311485774347913 0.477370452429953 A A A 2.24805724892205 2.32761465281282
2.88106960515271 A A P LNCV6_143537_PI430048170 mRNA
GATGGTCCCCAACAATGTCAACTAACAATTTCTCAGCTTTATGATGGTACAAAAGTGATA NM_001142579 RefSeq
chr19 - 40069151 40090938 ZNF780A 284323 "zinc finger protein 780A, transcript variant 4"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133366_PI430048170 0.464478274145609 1.22169414525676 0.320961935205374
1.09992780888532 0.285842092402022 A A A 0.28622305388161 0.281814828004852
0.421902704142034 A A A LNCV6_133366_PI430048170 mRNA
ATGAAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCAGACAAGCAGCTGA NM_002965 RefSeq
chr1 + 153357853 153361027 S100A9 6280 S100 calcium binding protein A9
GO:0005515|GO:0008017|GO:0035662|GO:0050544|GO:0005886|GO:0030307|GO:0045471|GO:0050832|GO:0007
267|GO:0005634|GO:0001816|GO:0005615|GO:0010043|GO:0005829|GO:0051092|GO:0006954|GO:0050786|GO:0
032602|GO:0032496|GO:0004871|GO:0005856|GO:0042742|GO:0070062|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134612_PI430048170 0.000618561723385395 0.662368541060609 9.60224563605355
9.46158097806653 9.52488577913599 P P P 10.0756171950269 10.1346090200747
10.1634289573979 P P P LNCV6_134612_PI430048170 mRNA
GTATGACTAAGTAACATGGCAACACATCTGTCTCTCCCTAAATAAATACTACCACATTAT NM_018714 RefSeq chr17
+ 73193033 73208506 COG1 9382 component of oligomeric golgi complex 1
GO:0005515|GO:0005794|GO:0000139|GO:0007030|GO:0017119|GO:0006891|GO:0015031 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139046_PI430048170 0.0095607511843402 0.168780622097108 1.63583137938527
2.09163733010034 3.08427305483436 A A P 4.27250525142178 5.26122044195943
5.17942505926269 P P P LNCV6_139046_PI430048170 mRNA
GTTCTGCATTGATAAACTCAAATGATCATGGCAGAATGAGAGTGAATCTTACATTACTAC NM_012242 RefSeq chr10
+ 52314280 52317657 DKK1 22943 dickkopf WNT signaling pathway inhibitor 1
GO:0005515|GO:0090082|GO:0005886|GO:0030178|GO:0042662|GO:0042663|GO:0030326|GO:0090244|GO:0060
394|GO:0005615|GO:0030514|GO:0031333|GO:0033137|GO:0004871|GO:0032526|GO:0090090|GO:0001942|GO:0
048019|GO:0001706|GO:0001707|GO:2000726|GO:0005576|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138982_PI430048170 0.747614861499885 0.874392943904507 0.410203595147634
1.00754931306796 0.367329499029819 A A A 1.41473035287896 0.386528264569606
0.401621911592567 A A A LNCV6_138982_PI430048170 mRNA
CTCTAGCCCCTATTAACTCTGCATTAAGCATTCCACATAATAAAATTAAAGGTTCCGGTT NM_006941 RefSeq chr22
- 37972311 37984532 SOX10 6663 SRY (sex determining region Y)-box 10
GO:0005515|GO:0001190|GO:0006366|GO:0048709|GO:0003705|GO:0001755|GO:0005634|GO:0009653|GO:0042
802|GO:0048589|GO:0031315|GO:0014015|GO:0045944|GO:0048469|GO:0090090|GO:0043066|GO:0006357|GO:0
003713|GO:0002052|GO:0030318|GO:0000978|GO:0048546|GO:0001701|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137795_PI430048170 0.0549183530194425 0.661728812252356 6.68463088609293
6.62505528203089 7.14073605857417 P P P 7.36631536507128 7.40614419193645
7.51767122512496 P P P LNCV6_137795_PI430048170 mRNA
CCCCTTTAGAAATGTACTGAAGTCTCATTTTTCACCCATTTCAGCCATGGGACATTTTTC NM_001199198 RefSeq
chr3 + 100260816 100325252 TBC1D23 55773 "TBC1 domain family, member 23, transcript variant 1"
GO:0032755|GO:0032680|GO:0050727|GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA
NA NA

LNCV6_10043_PI430048170 0.8990243153668640.9438373580030530.3631832280467141.06833270925663
1.91516960141841 A A A 0.2628402701397591.682022406272 1.6653855696773 A A A
LNCV6_10043_PI430048170 mRNA
CCCTCCTAAAGCTCTCTTGCTCTAGTATCTATGTCAACAAACTACTTATTCTATGTGTTG NM_001002905 RefSeq chr11
+ 124249675 124250611 OR8G1 26494 "olfactory receptor, family 8, subfamily G, member 1
(gene/pseudogene), transcript variant 1"
GO:0050911|GO:0007608|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144113_PI430048170 0.2103069192744555.1837289567335 0.463126129029636
3.34378955296167 3.72906598948589 A P P 0.56553023845039 0.40810060122578
0.982391402325484A A A LNCV6_144113_PI430048170 mRNA
CAGCAAATGATGCAGTTCATAGAGTATTTTGCACTTGGGGAAAAATATGTATCTGAATTG NM_152753RefSeq chr6
+ 35214061 35253079 SCUBE3 222663 "signal peptide, CUB domain, EGF-like 3, transcript variant 1"
GO:0005515|GO:0009986|GO:0005509|GO:0051260|GO:0005576|GO:0051291 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127365_PI430048170 0.0249069566910692 1.11995295340969 0.698994079517128
0.7551356956045490.719129397741916A A A 0.6285449851512080.520988570653333
0.531517873230425A A A LNCV6_127365_PI430048170 mRNA
CTGTAGCTTAAAAGGTTTTGTGAGCACTAACTATTGGCAGAAACTGCATTTGCAAATAAA NM_020341RefSeq chr20
- 9537389 9839039 PAK7 57144 "p21 protein (Cdc42/Rac)-activated kinase 7, transcript variant 1"
GO:0023014|GO:2001237|GO:0008283|GO:0006915|GO:0005634|GO:0005524|GO:0035556|GO:0005739|GO:0007
165|GO:0005737|GO:0016477|GO:0004702|GO:0007010|GO:0016049|GO:0006468|GO:0007613|GO:0007626|GO:0
007612|GO:0000278. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140706_PI430048170 0.0449448249406037 1.49913447282346 6.33911041729482
6.81494295844494 6.71905168493273 P P P 6.23986176227351 6.11443969930069
5.76875595112025 P P P LNCV6_140706_PI430048170 mRNA
TTCACATACAGTGCCCACTTTGTGTGGTAAATCTCATGGTCTCTCTCCTCTCTATGTGCT NM_001166692 RefSeq chr11
- 33698107 33700740 C11orf91 NA chromosome 11 open reading frame 91 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_144517_PI430048170 0.0503701557753738 0.9305241087051598.56907393679531
8.61256438762747 8.52148200955571 P P P 8.66837463368692 8.685175580945
8.66256590285368 P P P LNCV6_144517_PI430048170 mRNA
GAAAACTTTTAAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAATTCCAAGCCTC NM_033419RefSeq chr17
- 39671121 39688070 PGAP3 93210 "post-GPI attachment to proteins 3, transcript variant 1"
GO:0000139|GO:0016788|GO:0031227|GO:0016021|GO:0006506|GO:0006505 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129102_PI430048170 0.0171462270921787 5.01459261713525 3.82931800500371
4.88423728355628 4.54149728681204 P P P 2.19089267998367 2.19474104541796
2.07862696887521 A A A LNCV6_129102_PI430048170 mRNA
CAAAATCAAGTGGATAAACTTTTTAGCGCTTGGATGCAGCATGCTTGGTGGGTCCTTGAA NM_031916RefSeq chr5
+ 10441861 10465026 ROPN1L 83853 "rhophilin associated tail protein 1-like, transcript variant 1"
GO:0005515|GO:0005737|GO:0003351|GO:0031514|GO:0001932|GO:0030317|GO:0048240 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_119751_PI430048170 0.0853896913244926 0.3484630747065633.45422439904214
1.40324581357151 2.43528596885477 P A A 3.55491410693066 4.13056438532905 4.6609085615559
P P P LNCV6_119751_PI430048170 mRNA
CAACTTGCTCTTTCATATGAGTTGGTCATAGCATGTAAGAACCAATCTTGAAATATCGTT NM_018351RefSeq chr12
- 95076748 95217464 FGD6 55785 "FYVE, RhoGEF and PH domain containing 6"
GO:0005794|GO:0030036|GO:0031267|GO:0008360|GO:0001726|GO:0046872|GO:0030027|GO:0043088|GO:0043

547|GO:0005085|GO:0005737|GO:0032321|GO:0007010|GO:0046847|GO:0005089|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116477_PI430048170 0.5308117734351980.9436043034864161 4.4786014258378 14.4354531242016 14.3929213265161 P P P 14.3232432735039 14.5436936288784 14.6713072879798 P P P LNCV6_116477_PI430048170 mRNA
GAGTGTTGTTGGACCATGTGTGATCAGACTGCTATCTGAATAAAATAAGATTTGTCAAAA NM_006476RefSeq chr11 + 118401388 118409847 ATP5L 10632 "ATP synthase, H+ transporting, mitochondrial Fo complex, subunit G, transcript variant 1"
GO:0022904|GO:0005739|GO:0042776|GO:0015078|GO:0022857|GO:0005743|GO:0000276|GO:0044281|GO:0016887|GO:0044237|GO:0070062|GO:0005753 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144894_PI430048170 0.0118003830652785 1.30748953009349 10.8161738127137 10.6377424572674 10.6880003660698 P P P 10.2662436518773 10.4596541194283 10.2520759356298 P P P LNCV6_144894_PI430048170 mRNA
AGAGAGGCTGATCCAGGAGCTGGCCAAGTGCAAGATTGACACACACAATATAATTGTCAANM_004317RefSeq chr19 + 12737491 12748323 ASNA1 439 "arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)"
GO:0005215|GO:0005783|GO:0015698|GO:0005730|GO:0005634|GO:0045048|GO:0005524|GO:0046872|GO:0005737|GO:0015105|GO:0008152|GO:0006810|GO:0016887|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142927_PI430048170 0.6329025063596781.14144782443889 2.81120370300744 2.16298119069629 1.91499662949284 A A A 2.77575615484445 1.33359947991609 2.00271452028867 P A A LNCV6_142927_PI430048170 mRNA
TTGCCTCAAGAGAGGGACAATGTAGCTTTATTTTACAAGAAGGCATAGTTAGATTTCTAT NM_032229RefSeq chr13 - 85792786 85799348 SLITRK6 84189 "SLIT and NTRK-like family, member 6"
GO:0008344|GO:0009986|GO:0007605|GO:0007409|GO:0007416|GO:0031223|GO:0021562|GO:0060384|GO:0001964|GO:0035264|GO:0060007|GO:0002088|GO:0005887|GO:0090102|GO:0002093|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129035_PI430048170 2.8137148049587e-05 0.6354889153208490.244366387645801 0.2827311811973080.299660542674716 A A A 0.94994262740241 0.88708745684847 0.951534581710206 A A A LNCV6_129035_PI430048170 mRNA
CAGTTATGGAAGTGTGGAAAACTGTGGCTTCTCAATAAATATTCAGATGTCCTAAGAATA NM_003716RefSeq chr3 - 62398345 62875389 CADPS 8618 "Ca++-dependent secretion activator, transcript variant 1"
GO:0005515|GO:0050432|GO:0016082|GO:0030054|GO:0019901|GO:0045202|GO:0006887|GO:0015031|GO:0046872|GO:0005829|GO:0008289|GO:0016050|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68833_PI430048170 0.3542955953613721.2330553923372 3.24175869288581 3.14426036438946 3.17464951059319 P P P 2.93033575520773 3.28856589471417 2.25411457664704 P P A LNCV6_68833_PI430048170 mRNA
TGCAGATGCGGCTGGAAGCCCTGAGCCTGCTGCACACACTAGTCTGGGCATGGAGTCTCT NM_018188RefSeq chr1 + 1512142 1534687 ATAD3A 55210 "ATPase family, AAA domain containing 3A, transcript variant 1"
GO:0042645|GO:0005739|GO:0043066|GO:0005743|GO:0016049|GO:0016021|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138571_PI430048170 0.0174769982271759 0.5385848847328434.9054130003734 4.57082649374833 4.82228231620346 P P P 5.3089250306232 5.83393365003176 5.79747179087497 P P P LNCV6_138571_PI430048170 mRNA
AGCCCACGCTTGATTTTTATGTCCTTTCCTCTTGCCTTGTATTGAGTTTAAGATCTCTAC NM_001114120 RefSeq chr1 - 68474151 68497221 DEPDC1 55635 "DEP domain containing 1, transcript variant 1"
GO:0043547|GO:0035556|GO:0005515|GO:0017053|GO:0005654|GO:0005634|GO:0045892|GO:0006351|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132667_PI430048170 0.2203785238122860.3348351590394420.844118998283425 0.4692653624125360.465589259203279 A A A 2.50807008938555 2.72280490870612

0.411274555905124 A P A LNCV6_132667_PI430048170 mRNA
CATTCTTGCCACCTCCTCAATGAAAATGAAAGATGTTTTTGGGAAACTGATAGCTAATTT NM_148977 RefSeq chr10
- 89579496 89645572 PANK1 53354 "pantothenate kinase 1, transcript variant alpha"
GO:0004594|GO:0015939|GO:0006767|GO:0005634|GO:0015937|GO:0044281|GO:0005524|GO:0071944|GO:0005
829|GO:0030118|GO:0016310|GO:0006766|GO:0009108|GO:0055037 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133396_PI430048170 0.1140103349173691.04571812594042 0.474677964807967
0.5560313982642820.485244074223798 A A A 0.4104605100973730.445317775881179
0.467484869436954 A A A LNCV6_133396_PI430048170 mRNA
TCACCAAAGAAGCTGTGGGTACTTATTTTGCAACCATAGTATGTGCTCTTATTCTTTTAA NM_001293626 RefSeq
chr7_KI270803v1_alt + 73628 184204 MGAM2 NA maltase-glucoamylase (alpha-glucosidase) NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129294_PI430048170 0.5670194655107840.9626930348438941 0.4205990695301
10.7044309371938 10.565501501987 P P P 10.5444874791913 10.6594141199748
10.6620335153013 P P P LNCV6_129294_PI430048170 mRNA
GGGGCAGCCTGGCTCAGGTTTATTGATTTTCGTCTGTTTACCCTATCCATTAATCAATAC NM_017547 RefSeq chr11
+ 126269039 126278132 FOXRED1 55572 "FAD-dependent oxidoreductase domain containing 1,
transcript variant 1" GO:0005739|GO:0008150|GO:0016491|GO:0016021|GO:0055114 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_80959_PI430048170 0.0128967623376801 1.80301317662782 11.3105229417499
11.4043889766489 11.3712624451609 P P P 10.4073987836181 10.3744684326392
10.7276395723797 P P P LNCV6_80959_PI430048170 mRNA
CATTTGATCACAGTTTAGAGGCACAGTGGACCAAGTGGAAGGCGATGCACAACAGATTAT NM_001912 RefSeq chr9
+ 87726058 87731469 CTSL 1514 "cathepsin L, transcript variant 1"
GO:0005515|GO:0097067|GO:0005518|GO:0005634|GO:0005764|GO:0005615|GO:0071888|GO:0019886|GO:0042
393|GO:0022617|GO:0019882|GO:0030198|GO:0036021|GO:0051603|GO:0030574|GO:0006508|GO:0001968|GO:0
043202|GO:0070062|GO:0043394|GO:0005576|GO:0002224|GO:0004197|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_94860_PI430048170 0.4763707976958180.9341860456801314.90042149580429 5.12319741545231
4.76366598904809 P P P 5.11230570049457 5.099303831864 4.88194476271331 P P P
LNCV6_94860_PI430048170 mRNA
GAACCATCAGGAAGTAGACATGAATGTGGTGAGGATCTGCTTCCAGGCCTCATATCGGGA NM_006509 RefSeq chr19
+ 45001448 45038198 RELB 5971 v-rel avian reticuloendotheliosis viral oncogene homolog B
GO:0005515|GO:0003700|GO:0006366|GO:0000981|GO:0007249|GO:0005829|GO:0005737|GO:0006954|GO:0019
882|GO:0045944|GO:0043011|GO:0034097|GO:0033256|GO:0000977|GO:0005815|GO:0071470|GO:0003714|GO:0
001047|GO:0000122|GO:0032922|GO:0038061|GO:0045063|GO:0003682|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145537_PI430048170 0.1917736076785043.76583479857891 0.373432730513696
3.04518400449668 2.32306660518345 A P A 0.3708013999105110.339235157934355
0.385777058428597 A A A LNCV6_145537_PI430048170 mRNA
CCTTTGTTAAATCCTATCATCTACAGTCTGAGAAATAAGCAAGTCACAGTTTCATTCACA NM_001005338 RefSeq
chr3 + 98132697 98133639 OR5H1 26341 "olfactory receptor, family 5, subfamily H, member 1"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137855_PI430048170 0.31242765368774 0.9227908537816875.73896333484797
5.95539255310982 5.70220672309911 P P P 6.02809104765142 5.9114160375541
5.80972264760167 P P P LNCV6_137855_PI430048170 mRNA
AGAAATATGAGCATCTGTGGATTACACAGCCTCATCCCTCTCTACAATATTCCAGCCCAT NM_012216 RefSeq chrX
+ 107825853 107931637 MID2 11043 "midline 2, transcript variant 1"

GO:0051219|GO:0008017|GO:0016567|GO:0046982|GO:0016874|GO:0005874|GO:0032897|GO:0035372|GO:0042803|GO:0051091|GO:0005737|GO:0051092|GO:0046597|GO:0045087|GO:0008270|GO:0043123|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144578_PI430048170 0.3319215978893050.8798589851247550.254825121778597 0.2680670953972930.394615476428297A A A 0.3734451665438440.748710820555349 0.313940248935894A A A LNCV6_144578_PI430048170 mRNA TGGGTCATCCAGCCTTGGGTAGAGAAGGAATTTGAACTCAGGAAATTCAACTCCAGAACT NM_001130026 RefSeq chr7 + 143715845 143730080 TCAF2 285966 "TRPM8 channel-associated factor 2, transcript variant 3" GO:0002244 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129681_PI430048170 0.4714926020627890.6679976061802430.324254746800364 0.3269929599704160.503583482668471A A A 0.3164244239716981.74939102793574 0.341509702641059A A A LNCV6_129681_PI430048170 mRNA TAACCCTAGATAGAATCTAATGAACTCAGAGGCTTAGCTCGCCTCTTTAGGGTCCATGGT NM_000409RefSeq chr6 + 42155405 42180056 GUCA1A 2978 guanylate cyclase activator 1A (retina) GO:0007165|GO:0001917|GO:0007603|GO:0005886|GO:0005509|GO:0031284|GO:0022400|GO:0007601|GO:0016056|GO:0008048 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129808_PI430048170 0.4928038930549011.07205688700949 6.86996251741974 6.76248910037323 7.04989246478215 P P P 6.7040130111478 6.66196923329752 7.00512299918986 P P P LNCV6_129808_PI430048170 mRNA CTGAGAAGCAGAGACACCACAATGAAGGAAATGATGCATATATCCAAATTAAAAGACTTT NM_007215RefSeq chr17 - 64477784 64497066 POLG2 11232 "polymerase (DNA directed), gamma 2, accessory subunit" GO:0005515|GO:0042645|GO:0006996|GO:0003887|GO:0003677|GO:0042802|GO:0006260|GO:0006261|GO:0006281|GO:0071897|GO:0005759|GO:0000262|GO:0007005|GO:0006264|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140963_PI430048170 0.0933624409136183 1.38811934768688 4.88709759774687 4.84731447064482 4.44213901056063 P P P 4.25650762454644 4.52617369128382 3.95978081776395 P P P LNCV6_140963_PI430048170 mRNA TGCTGGGAATGGAAGCCAGGTGGGGTCATGGCACAAGTTCTGTAATCTTCAAAATAAAAC NM_005854RefSeq chr17 + 42761193 42763041 RAMP2 10266 receptor (G protein-coupled) activity modifying protein 2 GO:0005515|GO:0035924|GO:2001214|GO:0005886|GO:0034333|GO:0030819|GO:0002040|GO:0015031|GO:0006886|GO:0005764|GO:0032870|GO:0007507|GO:0031623|GO:0005737|GO:0070830|GO:0070831|GO:0006171|GO:0006816|GO:0032355|GO:0001666|GO:0007565|GO:0009986|GO:0001525|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136785_PI430048170 0.0967052035203589 1.24412070739876 4.78247339388019 4.91381970418098 4.66494527060932 P P P 4.70397691722747 4.33628945859812 4.35593539806155 P P P LNCV6_136785_PI430048170 mRNA GAACCTGCTATTTCGGATGACATTGGGCATTTTAGTTCTATATTTTTTGTGCCTCTTTTA NM_007031RefSeq chr21 - 43529191 43659493 HSF2BP 11077 heat shock transcription factor 2 binding protein GO:0006366|GO:0007283|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141436_PI430048170 0.0175969691096608 1.3487986597193 8.1703035757265 8.14109485813668 8.00461271740509 P P P 7.82242615587775 7.6571297702515 7.53203299562077 P P P LNCV6_141436_PI430048170 mRNA CACAGCCACAGCCTGCTGGACTCAGGACTGTCCTGTCAACTCCAGACAACTGAATAAACA NM_001040125 RefSeq chr1 + 19312245 19329300 PQLC2 54896 "PQ loop repeat containing 2, transcript variant 1" GO:0031301|GO:0015181|GO:0015174|GO:0015809|GO:0005765|GO:0080144|GO:0043231|GO:0015819|GO:0015189 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136353_PI430048170 0.0917321840838281.22069451438273 9.51444294400042 9.67977699436026 9.7894382228885 P P P 9.22737499282134 9.31721017753917 9.56731387935551 P P P LNCV6_136353_PI430048170 mRNA

CTAGCCAATGGAATGAAACTTCTTGGAATAACACCTGTATGTAGGATGTAATTTCCATTA NM_020320RefSeq chr6 - 87514377 87590017 RARS2 57038 "arginyl-tRNA synthetase 2, mitochondrial" GO:0005739|GO:0010467|GO:0032543|GO:0005759|GO:0006420|GO:0004814|GO:0005524|GO:0006418 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135848_PI430048170 0.0534190597347883 0.54108819599375411.7007929791118 11.4868456616092 11.4574817752686 P P P 11.9714556579997 12.4820820158407 12.7558602766667 P P P LNCV6_135848_PI430048170 mRNA
CCTCCTCACTCCTATTCTCTTTGCCTTTGTGTAAAAATAAAATGGAAATAAACAAGTTGC NM_138371RefSeq chr12 + 47079602 47236663 PCED1B91523 "PC-esterase domain containing 1B, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136471_PI430048170 0.7145905460505060.9708890482668712.1421897226367 11.9457958710045 11.8257695977841 P P P 11.8975062920714 12.1340408869008 12.0182075406664 P P P LNCV6_136471_PI430048170 mRNA
GGTGTCTGTATACACGCCAAAGGCAGATACAAATAAAATACAGATTGTCCTTTCTTAAAA NM_003124RefSeq chr2 + 72887382 72892160 SPR6697 "sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)" GO:0050661|GO:0006558|GO:0004757|GO:0006729|GO:0050999|GO:0016265|GO:0044281|GO:0005829|GO:0006809|GO:0005739|GO:0042428|GO:0042415|GO:0004033|GO:0005737|GO:0019889|GO:0042417|GO:0048667|GO:0050882|GO:0040014|GO:0046209|GO:0005654|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135794_PI430048170 0.710150734364645 1.03159394992089 0.601099984148709 0.7392570814112740.759242350288297A A A 0.6208616300818390.45698728499575 0.863070194112001A A A LNCV6_135794_PI430048170 mRNA
GACCTGTCTGTACAACTGGAAAGGCTGTATTTATTTAATGTACCTCAAGGTGTTTTAATA NM_015307RefSeq chr15_KI270905v1_alt - 1394880 1854904 FAM189A1 23359 "family with sequence similarity 189, member A1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114373_PI430048170 0.683226662978559 1.08750132949703 5.21080925153521 4.57203521469997 4.71573297068714 P P P 5.24870699091576 4.53095633573614 4.24420879753263 P P P LNCV6_114373_PI430048170 mRNA
TCCAGGCCAGTCCCTGATCCCTGACCTAATGTTATCGCGGAATGATGATATATGTATCTA NM_205839RefSeq chr6_GL000255v2_alt + 2841999 2844732 LST1 7940 "leukocyte specific transcript 1, transcript variant 4" GO:0000902|GO:0006955|GO:0005737|GO:0005794|GO:0000139|GO:0008360|GO:0016021|GO:0009653|GO:0016358|GO:0050672 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142994_PI430048170 0.3250379471612130.9783365814074820.288627092102095 0.3130267699914890.362343451597848A A A 0.3829066215934890.320873541914601 0.355319923890092A A A LNCV6_142994_PI430048170 mRNA
AGGCTCTCCAAAGTCTTGAGTTCTGTATATGGCCTGGTTTCTTGTTTTTATTAATAGATGNM_004575RefSeq chr4 + 146638892 146642471 POU4F25458 POU class 4 homeobox 2 GO:0031290|GO:0060041|GO:0007605|GO:0045597|GO:0048675|GO:0005634|GO:0000122|GO:0000978|GO:0006351|GO:0001078|GO:0001077|GO:0016607|GO:0000165|GO:0007411|GO:0045944|GO:0003682|GO:0030182|GO:0050885|GO:0030520. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53685_PI430048170 0.4060104291074880.8931704931209156.27143902947659 5.9205363096957 6.4823332309532 P P P 6.29682858744509 6.34915847931536 6.55858002596691 P P P LNCV6_53685_PI430048170 mRNA
AATACTATAGACCAAGGGATGGCAGCACTGAAGTTGGGTAGCACAGAAGTTGCAAGCAAT NM_016258RefSeq chr1 + 28736623 28769775 YTHDF251441 "YTH N(6)-methyladenosine RNA binding protein 2, transcript variant 1" GO:0043488|GO:0000932|GO:0006959 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143475_PI430048170 0.8323368464923631.0303968260204 4.18417514367173

2.35189673661564 3.04936046940298 P A P 3.37236965702077 3.62855542502195
2.98313787499728 P P P LNCV6_143475_PI430048170 mRNA
CCGGGTCTCTTCTACCTGCATTCTAAAACATTCAAAGTAATAAAAATTTCTCCACATTCA NM_018384RefSeq chr7
+ 150737347 150743649 GIMAP555340 "GTPase, IMAP family member 5"
GO:0005741|GO:0016021|GO:0005525|GO:0005764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138603_PI430048170 0.0400772576383612 0.5186000357522852.95490268569182
2.86501544558487 3.55069581695253 A A P 4.01862200921102 4.11694094881868
4.17288576448692 P P P LNCV6_138603_PI430048170 mRNA
TGTGTTTGGAGAAGGCTGCATGACTTTGTTTTTCCCTTTTAGCAAAACTAAATAAAGTTG NM_002718RefSeq chr3
+ 135965672 136147910 PPP2R3A 5523 "protein phosphatase 2, regulatory subunit B", alpha, transcript variant 1"
GO:0001754|GO:0005515|GO:0045732|GO:0008601|GO:0090263|GO:0005509|GO:0000159|GO:0090249|GO:0090244|GO:0007525|GO:0050790|GO:0061053|GO:0006470|GO:0090090 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136668_PI430048170 0.47627950503224 0.9006339209466150.369075197569612
0.3581922033327220.263223226227725A A A 0.7731508493590920.318344060647802
0.303261040872758A A A LNCV6_136668_PI430048170 mRNA
CGCATTCTCTATCCAACATTTAATTGTTTGAAAGCCTCCATATAGTTAGATTGTGCTTTGNM_016369RefSeq chr3 +
138010163 138033652 CLDN18 51208 "claudin 18, transcript variant 1"
GO:0016338|GO:0070830|GO:0005886|GO:0005198|GO:0034329|GO:0016021|GO:0005923|GO:0045216|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142643_PI430048170 0.0406322029373883 2.56026812160792 3.82098596497085
3.92062804793621 3.32012942418154 P P P 1.57149867649131 2.438327321464
2.79568685354613 A P P LNCV6_142643_PI430048170 mRNA
GAGGGGGAAATTTGTATATTAGAAACTTATTCATCCCACTCAGGACAATAAAAACGAATG NM_022468RefSeq chr16
+ 3046680 3060723 MMP25 64386 matrix metallopeptidase 25
GO:0006954|GO:0016020|GO:0005886|GO:0005509|GO:0006508|GO:0005578|GO:0008270|GO:0031225|GO:0016021|GO:0004222|GO:0060022 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131496_PI430048170 0.609160573685821 0.982560698296328 0.437089571693594
0.4440632558404660.424444872161557A A A 0.50614727318602 0.493068637102984
0.379249151264072A A A LNCV6_131496_PI430048170 mRNA
CTGAATAAGTGTCAAACTATATCTTTAAGTGTGCTGTATGCTGAGTTACAAGTTAGGTCA NM_014717RefSeq chr19
+ 30372420 30558058 ZNF536 9745 zinc finger protein 536
GO:0001078|GO:0045665|GO:0048387|GO:0044323|GO:0005634|GO:0000122|GO:0000978|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133032_PI430048170 0.18683858699245 1.06915009645576 9.59997614462067
9.42991712185614 9.53582227861382 P P P 9.37502255635142 9.44647818710907
9.45850449853449 P P P LNCV6_133032_PI430048170 mRNA
TTGAATTTTTTGATAACTGGGACAGCTTTACGTCTCCCCTGTAAAAGGGGCAAAAAGAAA NM_014140RefSeq chr2
+ 216412413 216483051 SMARCAL1 50485 "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1, transcript variant 1"
GO:0005515|GO:0006357|GO:0035861|GO:0004386|GO:0005634|GO:0006259|GO:0003677|GO:0005524|GO:0006974|GO:0000733|GO:0006281|GO:0031297|GO:0005654|GO:0005662|GO:0016568|GO:0008094 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95678_PI430048170 0.2371701806418450.8392704976999128.65364005818132 8.48060462768569
8.65548349715134 P P P 8.64103332174317 8.74618840431853 9.12231051577223 P P P
LNCV6_95678_PI430048170 mRNA
CGTCGCCATGAAAGTGAAGAAGGAGATAGTCACAGGAGACACAAACACAAAAAATCTAAA NM_030917RefSeq
chr4 + 53377652 53459936 FIP1L1 81608 "factor interacting with PAPOLA and CPSF1, transcript

variant 1" GO:0006397|GO:0005847|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139666_PI430048170 0.4417247954665440.8851555487818425.79452893801678 6.3994995088682
6.201814154114 P P P 6.48518536486497 6.07870688773882 6.39341631488398 P P P
LNCV6_139666_PI430048170 mRNA
GTTGCCACTGCTGTTTTCCAAATGTCCGATGTGTGCTATGACTAAAAATTGAAAAATTAA NM_001008391 RefSeq
chr11 - 32602079 32794658 CCDC73 493860 coiled-coil domain containing 73 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139610_PI430048170 0.9283712118505411.08250451353978 0.358444613562095
0.4462428176164421.77753544210808 A A A 1.53050561659367 0.348135575225955
0.534349182850957A A A LNCV6_139610_PI430048170 mRNA
GGTTCCCAAATCCCTCTCACAAGAATGTGCAGAAGAAATCATAAAGGATCAGAGATTCTG NM_005511RefSeq chr9
+ 5890908 5909822 MLANA 2315 melan-A
GO:0005802|GO:0005515|GO:0042470|GO:0005794|GO:0005887|GO:0005789 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134696_PI430048170 0.1029685131808550.86348320518667 12.1277389151326
12.2966949499151 12.4049998642518 P P P 12.4591975117857 12.4671579497256
12.5500238140483 P P P LNCV6_134696_PI430048170 mRNA
ATGTGGCATGCATCTGTGAGCTTTAGATCATTAAATCCAAAATGTTTGCCTAAATGAGTT NM_004394RefSeq chr5
- 10679229 10761275 DAP 1611 "death-associated protein, transcript variant 2"
GO:0070513|GO:0006919|GO:0010507|GO:0006914|GO:0006915|GO:0032088|GO:0097190|GO:0045892|GO:0034
198 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139266_PI430048170 0.1190734145446240.9274465879630130.272811925487206
0.2831977744757420.291415174234638A A A 0.4673450481117010.376408565378208
0.326157948460591A A A LNCV6_139266_PI430048170 mRNA
AGATACGGTGATTCCTGTTCTTGGCTTTGTAGATTCATCTGGTATAAACAGCACTCCTGA NM_001010919 RefSeq
chr6 + 116461369 116463771 FAM26F 441168 "family with sequence similarity 26, member F,
transcript variant 1" GO:0034220|GO:0005261|GO:0005887|GO:0006812 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144279_PI430048170 0.5185723738536440.7847032590215770.379104670960048
0.37362093001278 1.35201834674706 A A A 1.56538571130359 1.2170893355213
0.352933334367378A A A LNCV6_144279_PI430048170 mRNA
TGGAGCTTGTCAGTTAACATAAGCTAATTGGATGGTTGGTACAAAATGTATGTTTTGTCT NM_080742RefSeq chr6
- 70861365 70957085 B3GAT2135152 "beta-1,3-glucuronyltransferase 2"
GO:0015018|GO:0000139|GO:0005975|GO:0009405|GO:0006486|GO:0044281|GO:0016021|GO:0030204|GO:0030
203|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107828_PI430048170 0.00628628410964733 1.62591931635416 7.51692941534599
7.36832471268161 7.6640378554423 P P P 7.00786232083571 6.75461763951973
6.67709338665759 P P P LNCV6_107828_PI430048170 mRNA
GGAAGGAGAAAACTCTTGTCAAGAATGGCCCAGAGGAATGCCTCGCACAAAAGGTCTTCC NM_000303RefSeq
chr16 + 8797812 8849337 PMM2 5373 phosphomannomutase 2
GO:0004615|GO:0043025|GO:0019307|GO:0009298|GO:0006486|GO:0006488|GO:0044267|GO:0070062|GO:0043
687|GO:0018279|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135083_PI430048170 0.2968108749393461.64666707121732 0.848248821860311
2.27894414268268 2.08916794741217 A A A 0.9323240284104841.62516674566093
0.706206208992764A A A LNCV6_135083_PI430048170 mRNA
ATGCTTTTCTATAACTTTTAAATAAACCTTGGGGGGTGATGGAGTCATTCCTGCCTGTTA NM_005624RefSeq chr19
+ 8052761 8062663 CCL25 6370 "chemokine (C-C motif) ligand 25, transcript variant 1"
GO:0008009|GO:0005576|GO:0042379|GO:0050900|GO:0005615|GO:0031735|GO:0006955|GO:0006954|GO:0005
179|GO:0006935|GO:0007186|GO:0060326|GO:0001954|GO:0007166 . NA - . NA NA NA NA NA NA

NA NA NA
LNCV6_128589_PI430048170 0.0181659852297087 0.4830675785897664.90663994564766
4.96317206661552 4.73616521745416 P P P 5.69804864405287 5.74492055353235
6.25353696690036 P P P LNCV6_128589_PI430048170 mRNA
GGGCTTTGGCAAATCGTGTATTTTGTGTATAGAAGGAATTTAAGGAGAGGTATTACTTAT NM_016281RefSeq chr12
- 118149800 118372945 TAOK3 51347 TAO kinase 3
GO:0007095|GO:0005515|GO:0005886|GO:0046330|GO:0032874|GO:0005524|GO:0006974|GO:0000186|GO:0005
737|GO:0046777|GO:0046329|GO:0006281|GO:0000165|GO:0004674|GO:0004860|GO:0006468|GO:0043507|GO:0
006469|GO:0004709|GO:0016740 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140403_PI430048170 0.3105065460603040.9706247946545730.435153662103769
0.4068927196100690.404512430145991A A A 0.4940007919440290.484783825860195
0.394958936364128A A A LNCV6_140403_PI430048170 mRNA
GCATTGTGACAGAGTGTATTCCCTTCTCAATAAAGGAATGAAGTGGTCTTTTCCAAAAAA NM_152397RefSeq chr3
- 51894875 51903370 IQCF1 132141 IQ motif containing F1 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_145663_PI430048170 0.0251084277678264 1.27555391243293 9.69342768614133
9.44132124501 9.63202086735605 P P P 9.13152908097745 9.23709230120842 9.34843228290187 P
P P LNCV6_145663_PI430048170 mRNA
CCTGTGTGAAGGTTTGTTTTTCCAACCTGTGAAAGAAACGTGAATGTAAAAGAGACCTAA NM_001164811 RefSeq
chr20 + 18137854 18143168 PET117 NA PET117 homolog (S. cerevisiae) NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_9301_PI430048170 0.0122526878877261 0.2975572168017314.7819736463489
4.29932257451191 4.78838955540414 P P P 5.76400721832267 6.57395503056521
6.67080366200781 P P P LNCV6_9301_PI430048170 mRNA
ACCCAGCACTAGCAGTACCAGATGGTTCTGTGGAGTCCTGGGGAATGGAGAGAGCACAGT NM_001127322
RefSeq chr12 - 54230945 54259545 CBX5 23468 "chromobox homolog 5, transcript variant 1"
GO:0005515|GO:0042826|GO:0010369|GO:0005730|GO:0005634|GO:0035064|GO:0005635|GO:0042803|GO:0035
097|GO:0005720|GO:0000118|GO:0007596|GO:0017053|GO:0003682|GO:0016605|GO:0070491|GO:0000776|GO:0
016032|GO:0005654|GO:0031618|GO:0030674|GO:0045892 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_142065_PI430048170 0.8078641987804441.02709190920466 4.81313275179557
4.73594858662623 5.08299155634118 P P P 4.70156587534987 4.77562625757907
5.04024865455391 P P P LNCV6_142065_PI430048170 mRNA
CATTTGTAATGAATTTGTCGCAAAGACGTAATAAAATTAACTGGTGGCACGGTCTTTGTA NM_001204425 RefSeq
chr13 + 102807145 102876001 BIVM-ERCC5 NA BIVM-ERCC5 readthrough NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_129175_PI430048170 0.000542593727097511 0.4737444323345555.97858630668677
6.12456494559293 6.01881029448497 P P P 6.99447914386758 7.1185009317077
7.23628484130258 P P P LNCV6_129175_PI430048170 mRNA
GCTGAGTTGTCTCTGTCCACACATTATCACCTACGCGATAATAAATGACTGCGTTGGAGA NM_175732RefSeq chr11
+ 47565429 47573461 PTPMT1114971 "protein tyrosine phosphatase, mitochondrial 1, transcript variant 1"
GO:0005634|GO:0044281|GO:0035335|GO:0005739|GO:0004439|GO:0006470|GO:0046855|GO:0008962|GO:0031
305|GO:0008138|GO:0032049|GO:0006644|GO:0004725|GO:0006655|GO:0046474 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140723_PI430048170 0.0229716335189314 0.5407042339482273.15043925741993
2.86073533784678 3.52329685216899 P A P 3.87497446449169 4.35756736982491
3.99533496530798 P P P LNCV6_140723_PI430048170 mRNA
TGCTTCCCGAGAATCCATCCCTGGAGACACATCCCCAGCAGAGACAAGGCTCCAAGAACA NM_001193375 RefSeq
chr19 - 5891275 5904013 NDUFA11 126328 "NADH dehydrogenase (ubiquinone) 1 alpha

subcomplex, 11, 14.7kDa, transcript variant 2"
GO:0022904|GO:0005739|GO:0005747|GO:0005743|GO:0044281|GO:0016021|GO:0044237 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134587_PI430048170 0.3700049409531520.8267531852886460.546472400856946
0.4691130333183690.357646435887798A A A 1.12629285461342 0.497347006244596
0.481447922776922A A A LNCV6_134587_PI430048170 mRNA
GGCAGACTTCATATTCTCATCGCCCATTTTTCAAACTTGTTACATTGATCTGTACATTAT NM_020866RefSeq chr13 -
69700592 70108493 KLHL1 57626 "kelch-like family member 1, transcript variant 1"
GO:0005737|GO:0030036|GO:0021680|GO:0043025|GO:0007628|GO:0003779|GO:0005856|GO:0030425|GO:0016
358. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127150_PI430048170 0.0131318437168009 0.7122460477307717.28802489115307
7.11729539292759 7.3932241178097 P P P 7.70033648314378 7.91717533039858
7.64874177012803 P P P LNCV6_127150_PI430048170 mRNA
ATTGAGTGTATAAACCCGGCTTCTGGACCAACCCAAGATGAATAAACTGGGGCAGAAAAT NM_152374RefSeq chr1
- 35713875 35719189 C1orf216 127703 chromosome 1 open reading frame 216 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140534_PI430048170 0.3908331197005930.9800088313760270.473537740603561
0.3871119592716460.440270985977402A A A 0.4625258081361520.491434803746971
0.435124585001959A A A LNCV6_140534_PI430048170 mRNA
GAGGATGTTAAAGACTTTGTTAAATGGTTATCCAATTGCTCTTTCACAGGTAGCCTATTA NM_001287758 RefSeq
chrX - 108155606 108438430 COL4A61288 "collagen, type IV, alpha 6, transcript variant 3"
GO:0022617|GO:0030198|GO:0030574|GO:0005587|GO:0005788|GO:0005576|GO:0007155|GO:0005201 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139507_PI430048170 0.2299878249093080.6194734790039110.579000685273156
0.7289454745022710.56708362046184 A A A 0.5224902001775851.509652775767
1.67568422373527 A A A LNCV6_139507_PI430048170 mRNA
ATCTCTGGATATGGTAAGATTCCTTTTTTCCTCTCAGTTGCCTACACTTGGTTTTAATAA NM_020846RefSeq chr4 +
48341595 48426198 SLAIN2 57606 "SLAIN motif family, member 2"
GO:0005515|GO:0031116|GO:0005813|GO:0005737|GO:0007020|GO:0015630|GO:0005730|GO:0035371|GO:0031
122|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133405_PI430048170 0.0611389598220495 0.9172159108997741 1.3297537405355
11.3008181290384 11.3657524011342 P P P 11.4538306586828 11.3922523891147
11.5220516611739 P P P LNCV6_133405_PI430048170 mRNA
GCCCAGTAGAGACTCTGATTCTGGAAATTCTGACAAATAATTTAATAATACACATGTTGC NM_013248RefSeq chr20
+ 23350735 23354771 NXT1 29107 nuclear transport factor 2-like export factor 1
GO:0006405|GO:0005515|GO:0005737|GO:0016607|GO:0005643|GO:0008536|GO:0006611 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137658_PI430048170 0.2397892934474071.05153034993523 0.370742916808896
0.4474652927556870.390629902814935A A A 0.2812908061486330.418659703295867
0.288329816294728A A A LNCV6_137658_PI430048170 mRNA
CATGAATGAATCACTACATATGCTTATAATGAGGAAGAGTTATGGGTCCTGAGTGTAATT NM_032849RefSeq chr13
+ 30906174 30925572 MEDAG 84935 mesenteric estrogen-dependent adipogenesis
GO:0005737|GO:0045600 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137665_PI430048170 0.23932624789366 1.12745128033937 8.19839191655474
8.43577595053575 8.09100820072133 P P P 8.12447099802938 8.08143204075122 8.0200223603912
P P P LNCV6_137665_PI430048170 mRNA
ACCAGCCCTGTAATGGCATGGCCAGGAAGCCCAGCAGAGCTTATAAGATCTAACCCTTAT NM_001375RefSeq chr19
- 12875210 12881521 DNASE2 1777 "deoxyribonuclease II, lysosomal"
GO:0005622|GO:0006309|GO:0030218|GO:0004531|GO:0006259|GO:0005764|GO:0003677|GO:0070062 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107137_PI430048170 0.0471257608633171 1.30377901349597 12.3894483245919
12.1080154815958 12.3630488045409 P P P 11.9099250141671 11.9409226676497 11.877257864116
P P P LNCV6_107137_PI430048170 mRNA
GGCGCATGTGTGTGGGAGACAGAAGAAATTCTGGCAGATGTGCTCAAGGTGGAAGTCTTCNM_181468RefSeq chr20
- 35278905 35284717 EIF6 3692 "eukaryotic translation initiation factor 6, transcript variant 2"
GO:0005515|GO:0042256|GO:0005730|GO:0003743|GO:0005634|GO:0005638|GO:0006413|GO:0005737|GO:0043
022|GO:0005654|GO:0042273|GO:0043023|GO:0000054|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_61308_PI430048170 0.1219990571373881.40111027724207 6.796526375423 6.66750325837867
7.2838498702882 P P P 6.42912265222701 6.36591770746028 6.56168444880712 P P P
LNCV6_61308_PI430048170 mRNA
CGCAGGATTTTAATTTTGGGAAAACTAAATAACCTGGTAAAAGAGTGGATACGAGAAATC NM_001252007 RefSeq
chr14 + 96502375 96535597 PAPOLA 10914 "poly(A) polymerase alpha, transcript variant 3"
GO:0008380|GO:0006369|GO:0010467|GO:0000287|GO:0030145|GO:0006366|GO:0003723|GO:0031124|GO:0043
631|GO:0005634|GO:0005524|GO:0004652|GO:0005737|GO:0000398|GO:0005654 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127542_PI430048170 0.00999129090674263 1.12114976459906 7.77350178598753
7.72022464593952 7.72641232245807 P P P 7.59459943012661 7.52200172138844
7.60772200776389 P P P LNCV6_127542_PI430048170 mRNA
GGCTGCTATGACTCTTTGGATGGGAGTCTGGCAAGAGGAAATTGGAAGATAAAATAAATA NM_001301039 RefSeq
chr1 + 150272283 150280924 C1orf54 79630 "chromosome 1 open reading frame 54, transcript variant
1" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54163_PI430048170 0.3935332530474541.01335093788152 0.3140336326327060.336910885620697
0.371910270544924A A A 0.3358214229506750.3257686263989820.304273006696532A A A
LNCV6_54163_PI430048170 mRNA
CTGGCATTCAAGTCATGGCTAGTCTGTGTATTTAATAAATGTGTGTTATTTATGTCGTGT NM_198715RefSeq chr1
- 71005853 71047808 PTGER3 5733 "prostaglandin E receptor 3 (subtype EP3), transcript variant 5"
GO:0008219|GO:0005886|GO:0007200|GO:0005635|GO:0004957|GO:0007204|GO:0006351|GO:0031622|GO:0007
186|GO:0005887|GO:0032496|GO:0001660|GO:0015701|GO:0007188|GO:0016021|GO:0004879|GO:0035810|GO:0
030522 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134290_PI430048170 0.00892896858248395 1.36778050832365 10.0782590614092
10.3001103556246 10.2231688484415 P P P 9.81009400434845 9.6105496628445
9.82436531612776 P P P LNCV6_134290_PI430048170 mRNA
GTAGGCACGTGATGCATAATAGTCTTCAATGGTACACTTAACTAGTCTCTTCTGTGTAAC NM_001136216 RefSeq
chr1 + 15152531 15220478 TMEM51 55092 "transmembrane protein 51, transcript variant 1"
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137954_PI430048170 0.00394324416289353 0.3611551506508673.8258442972267
3.55918972112882 4.1406574719432 P P P 5.15084680605089 5.35662298529158
5.46732546074008 P P P LNCV6_137954_PI430048170 mRNA
CTACCTGGAAGATGTCTAACTTCATTTTCTACAACTCTTATGTGATTTTGCCATTGTCAT NM_001276320 RefSeq chr1
- 207043848 207052980 YOD1 55432 "YOD1 deubiquitinase, transcript variant 2"
GO:0071108|GO:0005515|GO:0004843|GO:0070536|GO:0035523|GO:0030433|GO:0046872|GO:0035871|GO:0030
968 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137272_PI430048170 0.0476449783106591.43006921881838 6.25369721316694
6.47378087872983 6.68543963963839 P P P 6.01172275657225 5.90095686797309
5.98193201455246 P P P LNCV6_137272_PI430048170 mRNA
TCTGTCTTATTTTAGGATGCAGTGTGAAACTTACCATTCAACTGAACAACTAGTTGTCAA NM_003130RefSeq chr7
- 88205116 88220084 SRI 6717 "sorcin, transcript variant 1"

GO:0005515|GO:0030018|GO:0008016|GO:0006942|GO:0042994|GO:0006880|GO:2000678|GO:0002020|GO:0005829|GO:0005739|GO:0007507|GO:0005737|GO:0010649|GO:0010880|GO:0070491|GO:0060315|GO:0051924|GO:0006508|GO:0006810|GO:0043679|GO:0006816|GO:0051281|GO:0086004|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131877_PI430048170 0.2952553625888240.9021199027025137.08799067205778 6.98671313379865 7.35435915044002 P P P 7.4001139219175 7.22587515659547 7.26852749725316 P P P LNCV6_131877_PI430048170 mRNA AATATCAAGGAAGGCAACGAAGACATAAGAGAGGCCATTAAAAACAACGCTGGCTTCCGC NM_016930RefSeq chr4 - 4418968 4542048 STX18 53407 syntaxin 18
GO:0005515|GO:0005484|GO:0000139|GO:0005783|GO:0006890|GO:0019904|GO:0005789|GO:0031201|GO:0016021|GO:0090158|GO:0006886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139376_PI430048170 0.8886983689152650.9900466227362630.278398795890409 0.5283461041813620.357383975988544A A A 0.5165595019322420.412489615346951 0.280096278576963A A A LNCV6_139376_PI430048170 mRNA ATAGTGCAGATGAAATAAAGTGTAATCCTTTATTAACATCTCTTTGCAGTGTCCCCAATG NM_145208RefSeq chr19 + 8842592 8843340 MBD3L1 85509 methyl-CpG binding domain protein 3-like 1
GO:0006355|GO:0005737|GO:0005886|GO:0005654|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140090_PI430048170 0.0690864049391438 0.82751009845690412.2134726958834 11.9631195720149 11.9861493424688 P P P 12.3014621849323 12.3470635496789 12.346692950853 P P P LNCV6_140090_PI430048170 mRNA GAGGGGTATAGGTTTGAAAGGCTGTTTGAAAGAGGAATGTTTAATAAAGGCTTTGATTTA NM_006836RefSeq chr12 - 120127209 120194710 GCN1L110985 GCN1 general control of amino-acid synthesis 1-like 1 (yeast)
GO:0005737|GO:0016020|GO:0005840|GO:0006412|GO:0008135|GO:0006417 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131653_PI430048170 0.00617380949719827 0.85712755082271611.2551922706065 11.3243602158581 11.3237136395654 P P P 11.4994601703284 11.5857036170122 11.4843605050386 P P P LNCV6_131653_PI430048170 mRNA TCAATTGTTACTGTGGACCGAATTAGGATCACAATAAACGATAATGCAGGTTCTTCAATG NM_018663RefSeq chr12 + 132687605 132704991 PXMP2 5827 "peroxisomal membrane protein 2, 22kDa"
GO:0005739|GO:0005515|GO:0043234|GO:0008150|GO:0005737|GO:0016020|GO:0016021|GO:0005778 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117008_PI430048170 0.0843812108961337 1.37175619606013 4.5496720454362 4.77003076296042 4.29456745089289 P P P 4.11694094881868 4.31239181096528 3.81253022782234 P P P LNCV6_117008_PI430048170 mRNA TACCAAAATCAAGTGTATAAAGGTCTAATAGCTTTGCTGCCCTGCGAGTCCCCAAAAGCC NM_001145636 RefSeq chr1 + 44674721 44725591 C1orf228 339541 chromosome 1 open reading frame 228 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128026_PI430048170 0.0513238383196306 2.89148371757052 1.85506732643297 2.9144524583464 3.10177850228172 A A P 1.01837127016648 1.80402126460179 0.389607742606282A A A LNCV6_128026_PI430048170 mRNA CTGCTGCAGTAGGACGGTGGTTTGGGGGTAAGGAGAAAGGAAAATAAATTTAATAAAATT NM_152358RefSeq chr19 - 50152547 50163281 IZUMO2 126123 IZUMO family member 2 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145281_PI430048170 0.2949970921105160.7246454503590093.44067255466659 3.31851841887467 4.21881887468048 P P P 3.76961783651846 3.96075711173922 4.6575150119504 P P P LNCV6_145281_PI430048170 mRNA CCTCTTTTGGTGTCTTAAGGCTTTTTGAAGCTTATTTTACTGTGAGTTTATTGGGAGTAT NM_152709RefSeq chr10 + 68827536 68893060 STOX1 219736 "storkhead box 1, transcript variant 1"

GO:0005737|GO:0005730|GO:0005654|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135205_PI430048170 0.291386743593518 0.910273821229013 6.02276919633048 5.68728049217069 5.8062073944341 P P P 5.99191097168181 6.0570241159841 5.8895337752519 P P P LNCV6_135205_PI430048170 mRNA
ATTATTCACTCTGCTAGCACCCTTCCCCTTGATGCCTGGGAATAGGTTTTGCCAATAAAC NM_000342 RefSeq chr17 - 44248389 44268134 SLC4A1 6521 "solute carrier family 4 (anion exchanger), member 1 (Diego blood group)"
GO:0006820|GO:0005515|GO:0008509|GO:0006821|GO:0030018|GO:0005886|GO:0072562|GO:0044281|GO:0042803|GO:0016323|GO:0005452|GO:0015108|GO:0015301|GO:0015106|GO:0070062|GO:0006811|GO:0030506|GO:0006873|GO:0003779|GO:0008022|GO:0055085|GO:0005887|GO:0015701|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142657_PI430048170 0.031759373446436 0.629480108107492 6.35044674008689 6.36350592039809 6.67854490661766 P P P 6.92239385429094 7.01135000975549 7.43338513986545 P P P LNCV6_142657_PI430048170 mRNA
GGTCACTAATTTTCAACTAGCATCAGGTATTTTGAAAACGTGTGTCTGGATATTAACTCT NM_173515 RefSeq chr6 - 154405298 154510619 CNKSR3 154043 CNKSR family member 3
GO:0005737|GO:0016020|GO:0033137|GO:0010765|GO:0070373 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135606_PI430048170 0.333507889067827 1.36960200347766 0.3626365219763 1.32790375220348 0.471340437791761 A A A 0.332456558413570 0.308783594483338 0.363072183457527 A A A LNCV6_135606_PI430048170 mRNA
CAACTCTTTCCTTGCCTTTTCAATATCAAATAAAACCATCAGCATCCTGCTGGATTGATA NM_130806 RefSeq chr13 + 31739541 31802872 RXFP2 122042 "relaxin/insulin-like family peptide receptor 2, transcript variant 1"
GO:0043066|GO:0008285|GO:0005886|GO:0030819|GO:0016021|GO:0007189|GO:0001556|GO:0017046|GO:0007193|GO:0008584|GO:0016500 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116625_PI430048170 0.00478034399459043 1.67375562742615 4.4280088019194 4.28330694065608 4.35873242024977 P P P 3.71673359998992 3.67148945545969 3.44134850833367 P P P LNCV6_116625_PI430048170 mRNA
AAGAAGTATTTTCCCATCCCCGTGGAGCACCTGGAGGAGGAGATCCGTATCAGATCCGCC NM_006504 RefSeq chr10 + 127907060 128085900 PTPRE 5791 "protein tyrosine phosphatase, receptor type, E, transcript variant 1"
GO:0005515|GO:0005737|GO:0006470|GO:0005886|GO:0005001|GO:0046627|GO:0007185|GO:0005634|GO:0016021|GO:0042803|GO:0035335|GO:0033003 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127802_PI430048170 0.682582759475851 1.04016571931006 6.38966770281888 6.37739012208736 6.47953844753659 P P P 6.58423312921567 6.07140880128552 6.37718536436083 P P P LNCV6_127802_PI430048170 mRNA
CTAACCAGCTTGTATTGGCCATCTGGAATATGCATTAAATGACTTTTTATAGGTCAATGC NM_001004023 RefSeq chr1 + 206635535 206649197 DYRK3 8444 "dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3, transcript variant 2"
GO:0004672|GO:0000287|GO:0004674|GO:0030218|GO:0018108|GO:0006468|GO:0005634|GO:0004712|GO:0004713|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127015_PI430048170 0.687614197421706 0.985097379375373 0.256379698583886 0.26611035659588 0.404939443315332 A A A 0.366568040194156 0.308741314539317 0.321300058854769 A A A LNCV6_127015_PI430048170 mRNA
AGAAGACAGACTGGTTCATTGAATGCCGCCTTATTTATTTCTGGTGAGGATGCATGCGTG NM_001651 RefSeq chr12 + 49961495 49965682 AQP5 362 aquaporin 5
GO:0005515|GO:0007588|GO:0005886|GO:0005783|GO:0009992|GO:0048593|GO:0030157|GO:0015670|GO:0055085|GO:0005902|GO:0016324|GO:0034220|GO:0009925|GO:0005887|GO:0015250|GO:0015793|GO:0042476|GO:0006833|GO:0015254|GO:0070062|GO:0046541 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_136748_PI430048170 0.1782483120729150.8898239995756466.7956356192979
6.72020389304835 6.52741812413438 P P P 6.79677475780134 6.9811292792289
6.77463127526027 P P P LNCV6_136748_PI430048170 mRNA
GGGCCCCTGTGTGGCCCATGAAGTTGTGAAGTCAAATAAATTAATTTTATCTTTACTGCC NM_001201552 RefSeq
chr16 - 71859679 71884190 ZNF821 55565 "zinc finger protein 821, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137064_PI430048170 0.0667575750308224 1.0719630242453 0.457288193370939
0.4941523937516220.54523942635671 A A A 0.33978259479787 0.442131909188059
0.413431788140606A A A LNCV6_137064_PI430048170 mRNA
AGACTAATTGTCCGCTCATTTCTTCAGATTCTACTCATTTGTTTTCTTCTGGGCATTAGA NM_001284223 RefSeq
chr10 - 84220490 84225589 LRIT2 340745 "leucine-rich repeat, immunoglobulin-like and
transmembrane domains 2, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_128579_PI430048170 0.0317494860161429 1.8797874920314 4.6171414338657
4.02404376871401 4.22953165448604 P P P 3.33247347963004 3.41419735822485
3.45360431829061 P P P LNCV6_128579_PI430048170 mRNA
TTAGTCTTGAGGATCCAGATGTGATTCTGTGAGCAGCATAGGCTCTGGTTGGTTAGTCTT NM_001201407 RefSeq
chr16 + 89217702 89229557 ZNF778 197320 "zinc finger protein 778, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_78697_PI430048170 0.033785033895425 0.65787795155974 8.13080202750854
7.99997661237129 8.406829931587 P P P 8.50023606605494 8.86631471594444
8.9723866518955 P P P LNCV6_78697_PI430048170 mRNA
GAAATTTGGTGAAGCTATTGGTATGGGTTTTCCTGTGAAAGTTCCCTACAGGAAAATCAC NM_032999 RefSeq
chr7 + 74657664 74760692 GTF2I 2969 "general transcription factor IIi, transcript variant 1"
GO:0005515|GO:0006355|GO:0003700|GO:0006367|GO:0006366|GO:0051481|GO:0005634|GO:0042995|GO:0003
677|GO:0007165|GO:0005737|GO:0014886|GO:0016020|GO:0016525|GO:0043025|GO:0005654|GO:0051019 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144180_PI430048170 0.428512139979964 1.11405265672705 9.66370678368342
9.46600166438041 9.82711099690339 P P P 9.23317453747228 9.47318461466161
9.75765971506482 P P P LNCV6_144180_PI430048170 mRNA
ATGGCTGGGCGGTGTAAGTCTGGCTTTGACCCTCGACATGGATCACACAATATTAAAAAA NM_032936 RefSeq
chr7 - 77793727 77798430 TMEM60 85025 transmembrane protein 60 GO:0016021 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_133652_PI430048170 0.00590008474706233 2.40288273912735 3.32221696564708
3.38093578696941 3.72349376069376 P P P 1.84911115844659 2.32939201308406
2.4239853756972 A A P LNCV6_133652_PI430048170 mRNA
ACATTCAATTCCATCACTTCTCTTCGGAGGAAGCCCTGCAGAAGGTCAAGTACTTTGTAG NM_001162530 RefSeq
chr1 + 36306392 36321347 SH3D21 79729 "SH3 domain containing 21, transcript variant 1"
GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136228_PI430048170 0.0164580567572249 1.08505430551196 0.417427326848993
0.389585808957844 0.346635722241574 A A A 0.247754764415242 0.309233242086404
0.24329341145928 A A A LNCV6_136228_PI430048170 mRNA
AATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGCTGAGGAGAGATGTTATCACCCAGTGC NM_001005276 RefSeq
chr7 - 99876061 99877033 OR2AE1 NA "olfactory receptor, family 2, subfamily AE, member 1" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133593_PI430048170 0.0109046434848712 0.945332658009314 0.367933122588644
0.35227905336544 0.328465328376627 A A A 0.453460686787701 0.431780011940759

0.406648047114871 A A A LNCV6_133593_PI430048170 mRNA
AATGTGCTCATTTGTGGTTGCCATGAGAGTGAGCTGCTTTTAAAGAAAGTGGAGCCTCCT NM_000749 RefSeq
chr8 + 42697418 42737066 CHRNB3 1142 "cholinergic receptor, nicotinic, beta 3 (neuronal)"
GO:0043005|GO:0030054|GO:0005886|GO:0007268|GO:0055085|GO:0051291|GO:0005892|GO:0007271|GO:0007
165|GO:0045211|GO:0008144|GO:0006810|GO:0042166|GO:0016021|GO:0004889|GO:0006812|GO:0015267 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57716_PI430048170 0.0172666504412565 1.28587854389067 12.1735902180749
12.2629200274865 12.2750208257555 P P P 12.0032428860616 11.7898990271024
11.8229775854584 P P P LNCV6_57716_PI430048170 mRNA
CGGCCCAGCCAGGCCATCTCACGTGTACATAATCAGAGCCACAATAAATTCTATTTCACA NM_020680 RefSeq
chr11 + 65525076 65538711 SCYL1 57410 "SCY1-like 1 (S. cerevisiae), transcript variant A"
GO:0005801|GO:0030126|GO:0005793|GO:0006355|GO:0005794|GO:0005815|GO:0006890|GO:0018108|GO:0005
634|GO:0003677|GO:0005524|GO:0006351|GO:0005737|GO:0016020|GO:0004713 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_133999_PI430048170 0.431561719710518 1.2457935132811 0.631414445922445
1.49468765288009 0.764913971076892 A A A 1.05430983975192 0.473984105416019
0.489367040802632 A A A LNCV6_133999_PI430048170 mRNA
TCCTACATTGAACCAATGCCTTGGGCTTCTCTAATTACTATACATTGTGCTCATATGAAT NM_000406 RefSeq chr4
- 67737380 67756086 GNRHR 2798 "gonadotropin-releasing hormone receptor, transcript variant 1"
GO:0042277|GO:0016020|GO:0007186|GO:0005886|GO:0005887|GO:0007275|GO:0097211|GO:0004968 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_137847_PI430048170 0.346176975391315 1.04719100283974 0.335660028000935
0.339471390029716 0.496307410694775 A A A 0.325778755935122 0.297816067580523
0.353624258842479 A A A LNCV6_137847_PI430048170 mRNA
GTCAGAGACATACATGCATTTTCCCAAATGACTCTACTTCACTATTATTTACATGGCTTA NM_181780 RefSeq chr3
- 112463965 112499561 BTLA 151888 "B and T lymphocyte associated, transcript variant 1"
GO:0002768|GO:0005886|GO:0046642|GO:0005887|GO:0031295|GO:0030889|GO:0004872|GO:0009897 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_137751_PI430048170 0.467821000780983 0.675628374088924 0.543952788226631
0.59038995670061 0.46942731384835 A A A 1.86357627794364 0.484511971556761
0.482900759393436 A A A LNCV6_137751_PI430048170 mRNA
CAGCCTAAGGAACAAAGAAGTAAAAGATGCTCTAAAGAGAACTTTAACCAATCGATTCAA NM_001002907 RefSeq
chr11_JH159136v1_alt + 156787 157747 OR8K1 NA "olfactory receptor, family 8, subfamily K, member
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136887_PI430048170 0.47607677383084 0.930580073270381 8.79971285433774
8.5232024789645 8.72285374219959 P P P 8.58502661907591 8.87731230709065
8.88870276764669 P P P LNCV6_136887_PI430048170 mRNA
ATGCAGAAGATGGGCCTCCAGAACTCCTGTTTATTCATGGAGGACACACTGCTAAGATTT NM_002893 RefSeq
chrX - 16844651 16870411 RBBP7 5931 "retinoblastoma binding protein 7, transcript variant 2"
GO:0005515|GO:0010467|GO:0030308|GO:0008283|GO:0003723|GO:0006325|GO:0006334|GO:0005634|GO:0007
275|GO:0000122|GO:0006351|GO:0034080|GO:0006260|GO:0035098|GO:0016581|GO:0045814|GO:0040029|GO:0
005654|GO:0070370 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136590_PI430048170 0.0625079626769386 0.650079912588528 4.41829329915042
4.36140331232912 4.95824715071297 P P P 5.08148755690335 5.32565468819926
5.26179781698906 P P P LNCV6_136590_PI430048170 mRNA
GTGGTCAAACCAAAATAGTGGGTTGAAGTGTATTATTCATCTTTTAGTGCATTGGCAAAA NM_152588 RefSeq
chr12 + 82687154 83134286 TMTC2 160335 transmembrane and tetratricopeptide repeat
containing 2 GO:0005515|GO:0005783|GO:0005789|GO:0016021|GO:0055074 . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_141349_PI430048170 0.00592317669754725 0.38218860890335 4.62834453275903
4.53650874886798 4.3846452792541 P P P 5.59980932138567 5.9137630694245
6.15598454987657 P P P LNCV6_141349_PI430048170 mRNA
CACTGTGCTTCTTAATGTGTAATTAAAGTGAGGAGAAATTAAATACTCTGAGGGCGTTTT NM_000462 RefSeq
chr15 - 25337248 25439028 UBE3A 7337 "ubiquitin protein ligase E3A, transcript variant 2"
GO:0005515|GO:0006511|GO:0000502|GO:0004842|GO:0060736|GO:0016874|GO:0003713|GO:2000058|GO:0005
634|GO:0014068|GO:0051865|GO:0005829|GO:0001541|GO:0005737|GO:0042787|GO:0007420|GO:0045944|GO:0
006508|GO:0042752|GO:0016032|GO:0070936|GO:0035037|GO:0030521 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127792_PI430048170 0.360057048157908 0.798699615934334 5.0562238935403
5.18284958718948 4.97188179084059 P P P 5.78423873159196 5.34152629521871
4.94350325314146 P P P LNCV6_127792_PI430048170 mRNA
TTGAAGCCCAAAGAACTTGCTGTTATGATTCGTTAACCATATTGCAATAAAAGCTGGACA NM_001989 RefSeq
chr7 + 27242544 27247819 EVX1 2128 "even-skipped homeobox 1, transcript variant 1"
GO:0043565|GO:0003700|GO:0045944|GO:0005634|GO:0009792|GO:0021913 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_142705_PI430048170 0.987366285882944 0.974200763208583 0.406294114512641
0.435400127025414 1.4219215494996 A A A 0.346564536411334 1.53743101054831
0.405502304553539 A A A LNCV6_142705_PI430048170 mRNA
GTGAATTGGGACATAGTTACAGCAGTGGAATAAGTATTCATTTAGAAATGTGAATGAGCA NM_021049 RefSeq
chrX - 152114048 152117939 MAGEA5 4104 melanoma antigen family A5
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_83507_PI430048170 0.898672901675963 0.89113118099171 1.44679517654979
2.10135676775723 1.22723401064348 A A A 2.33015139554508 1.92474695745323
0.745313212378964 A A A LNCV6_83507_PI430048170 mRNA
CAAAAAGCAGAGCAAGGAAAACACCATCACAATAAACTGTGTGACGTTCCCTCACCCAGA NM_201433 RefSeq
chr17 - 9910608 10198551 GAS7 8522 "growth arrest-specific 7, transcript variant c"
GO:0006355|GO:0005737|GO:0051015|GO:0003700|GO:0048812|GO:0008360|GO:0005884|GO:0030041|GO:0007
050|GO:0051017|GO:0001726 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140996_PI430048170 0.0448170348385359 2.71494935807633 3.60609580549238
4.02925600735404 3.85286995254467 P P P 2.25416558484987 2.97560597609226
1.67114834074537 A P A LNCV6_140996_PI430048170 mRNA
TTGCTTGGGGAATGTTGTTTTCTGACTAGGCTGATCATTATCTAAAGAATCTAATTCTGT NM_000053 RefSeq
chr13 - 51932670 52011494 ATP7B 540 "ATPase, Cu++ transporting, beta polypeptide, transcript
variant 1"
GO:0005802|GO:0005515|GO:0048471|GO:0006882|GO:0015680|GO:0005739|GO:0016323|GO:0006878|GO:0034
220|GO:0015677|GO:0060003|GO:0051208|GO:0005770|GO:0005507|GO:0005524|GO:0055085|GO:0004008|GO:0
007595|GO:0000139|GO:0016020|GO:0005887|GO:0008152|GO:0016023|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141015_PI430048170 0.526745238479297 1.40480045803602 2.21071972987016
2.00603016828313 0.631111424018567 A A A 1.54973840857084 0.293872956066493
1.63384377066799 A A A LNCV6_141015_PI430048170 mRNA
GGCCGCCTTTGAGAGTTTTACGTGAATGTGTTGTATACAACACTGGCAAAGAAATGATTA NM_175735 RefSeq
chr2 - 99242247 99255107 LYG2 254773 lysozyme G-like 2
GO:0009253|GO:0016998|GO:0003796|GO:0005576 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136178_PI430048170 0.237419646193618 1.69963110971438 0.305607326513841
1.65790481794787 1.23414484358076 A A A 0.486754354391002 0.37172872356429

0.347882639457009 A A A LNCV6_136178_PI430048170 mRNA
AGTGTTTACAACTGGCATGTGCTTTTAAACGTCAGGTAAGAGGGGAACAGCTGCTGTACA NM_014468 RefSeq
chr10 + 133237903 133241930 VENTX 27287 VENT homeobox
GO:0043565|GO:0006355|GO:0007275|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137306_PI430048170 0.513602418198755 0.658600982243781 0.290591312728514
1.50531077179631 0.516715810507846 A A A 0.322022559465903 1.19550949868104
2.26291527838755 A A A LNCV6_137306_PI430048170 mRNA
GTCATCTGATTTCCTCTGAACACTGACCTTTGAAGCTTTGTGAATCCTACGTAAAGCACT NM_005302 RefSeq chr7
- 124745600 124766025 GPR37 2861 G protein-coupled receptor 37 (endothelin receptor type B-like)
GO:0005515|GO:0042277|GO:0005886|GO:0004930|GO:0031987|GO:0000151|GO:0008528|GO:0007193|GO:0045
964|GO:0043235|GO:0042416|GO:0007186|GO:0005887|GO:0031072|GO:0005789|GO:0030544|GO:0043410|GO:0
031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143783_PI430048170 0.230954804843018 0.596906658777916 1.98693809769547
0.302715356195425 0.490912366253971 A A A 1.73341537363933 1.39508318726922
2.35231403984809 A A P LNCV6_143783_PI430048170 mRNA
AAATCCCACAGGTCCACTAACCACGATAAGGTTGTGTCAGCCTTCTATACTATGTTCACC NM_001004692 RefSeq
chr1 - 248294615 248295578 OR2T12 NA "olfactory receptor, family 2, subfamily T, member 12" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143572_PI430048170 0.0303905782067970.4754352082427764.1631970658453
3.68227719987449 4.44785091599215 P P P 4.89551097941122 4.96413813491819
5.63255813122786 P P P LNCV6_143572_PI430048170 mRNA
GTGTAACCCTGTTTGGAACTTTGCCTTCTTAAAATGATTTTTCAAAGATCTCTTTCGAACNM_024834RefSeq chr10 -
119829403 119872883 MCMBP 79892 "minichromosome maintenance complex binding protein, transcript
variant 1"
GO:0005515|GO:0042555|GO:0006261|GO:0007067|GO:0005737|GO:0005886|GO:0003682|GO:0007062|GO:0005
654|GO:0005634|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144989_PI430048170 0.401631067037909 1.09340791628867 11.1143056358752 10.942728181387
10.7534098200105 P P P 10.672415028551 10.9631942471301 10.7960296013491 P P P
LNCV6_144989_PI430048170 mRNA
TCCTGCTCCACTAAGAATGGTGCTAAAGTAAAACTAGTTTAATAAGCCCTTCTGAAAAAA NM_006332RefSeq chr19
+ 18173779 18178124 IFI30 10437 "interferon, gamma-inducible protein 30"
GO:0016667|GO:0030054|GO:0005886|GO:0019221|GO:0042590|GO:0048147|GO:0050821|GO:0005576|GO:0005
764|GO:0043231|GO:0019886|GO:0005737|GO:0060333|GO:0055114|GO:0043202 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129713_PI430048170 0.312483311884876 0.625296923557782 0.277967553841981
0.282180838022199 0.447845054620478 A A A 0.34855063458409 0.616978841263815 1.7040784114922
A A A LNCV6_129713_PI430048170 mRNA
GTATTCCAAACCTGTTCTTCTGTTTCTGTGGCACCTAGGTTTAAAATATGTATTAATGTGNM_022351RefSeq chr8 +
90791692 90959402 NECAB1 64168 N-terminal EF-hand calcium binding protein 1
GO:0005737|GO:0005509|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143543_PI430048170 0.0181313547262537 1.55093133245309 9.65713474365022
9.97902317595047 9.96603356082831 P P P 9.25051595075766 9.29917095820533 9.1727178103531
P P P LNCV6_143543_PI430048170 mRNA
CCCTGCAAAAATTCAGAGTCCTTGCAAAATTGTCTAAAATGTCAGTGTTTGGGAAATTAA NM_001127663 RefSeq
chr9 + 121268101 121332842 GSN 2934 "gelsolin, transcript variant 4"
GO:0005515|GO:0048471|GO:0045471|GO:0072562|GO:0015629|GO:0042246|GO:0030155|GO:0006921|GO:0005
829|GO:0051014|GO:0051016|GO:0030041|GO:0071276|GO:0016192|GO:0070062|GO:0048015|GO:0007568|GO:0
005509|GO:0006915|GO:0005576|GO:0003779|GO:0001726|GO:0030027|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_133873_PI430048170 0.1197736697999850.8469080723374312.3089784111789
11.9909717550661 12.1223253361306 P P P 12.5156549997291 12.2416064431413
12.3889779994718 P P P LNCV6_133873_PI430048170 mRNA
TGATATTACAGATGTGCTATTAGTGCAATAAGGTGAAGGCTGTCTGCCCAGAGAAATAAG NM_003139RefSeq chr11
- 126262918 126268982 SRPR 6734 "signal recognition particle receptor (docking protein), transcript
variant 1"
GO:0010467|GO:0005785|GO:0005783|GO:0006614|GO:0006613|GO:0003924|GO:0005525|GO:0006412|GO:0030
968|GO:0006184|GO:0016020|GO:0005789|GO:0005047|GO:0016021|GO:0006987|GO:0044267|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127768_PI430048170 0.5473708987870871.28581124749805 1.52058182670755
0.4954216044389410.333668331856612A A A 0.5252335099577540.729198751035131
0.276094243014619A A A LNCV6_127768_PI430048170 mRNA
TATGGTAAGAGGAGCCATAAGGAATGATTTCAAAGAGAGGTGTGTACAGCAAGGAAGCAA NM_025159RefSeq
chrX - 30558823 30577916 CXorf2180231 chromosome X open reading frame 21 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142169_PI430048170 0.9057075082962851.00594491484787 4.1930553423602
4.27166881904312 4.03068331935103 P P P 4.25223221202209 3.81680532797332 4.3563188531789
P P P LNCV6_142169_PI430048170 mRNA
CATGCACACCCATTAAAAATAGTACATTTTACAGTGTCCCAGTCATACTTTTAATTGGCA NM_001278346 RefSeq
chr5 - 178208473 178232822 PHYKPL 85007 "5-phosphohydroxy-L-lysine phospho-lyase, transcript
variant 3" GO:0005739|GO:0030170|GO:0008152|GO:0008483|GO:0016829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135764_PI430048170 0.00852323647248464 0.6798386621657741 0.6826543460117
10.8059667069967 10.5738516494667 P P P 11.4046202184534 11.2143622309933
11.1071972378532 P P P LNCV6_135764_PI430048170 mRNA
ACCCGCTTTGTGATCTGCATGTGTGACACTGATTCTTTGGAAATAAAGAGTGGAAGCTGC NM_173620RefSeq chr17
+ 82418375 82442640 HEXDC 284004 "hexosaminidase (glycosyl hydrolase family 20, catalytic domain)
containing" GO:0004563|GO:0005737|GO:0005975|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135344_PI430048170 0.00241681542035025 3.57382896514291 2.07770650135844
2.08355730433193 2.37872972191191 A A A 0.34435532146122 0.325338055356287
0.378369658776339A A A LNCV6_135344_PI430048170 mRNA
GGCCTTTTGTGCTTGTTTCCTATAACTTCAGTATTGTAAACTAGTTTTTGGTTTGCAGTT NM_156039RefSeq chr1 -
36466042 36483314 CSF3R 1441 "colony stimulating factor 3 receptor (granulocyte), transcript variant 3"
GO:0005515|GO:0007165|GO:0004896|GO:0097186|GO:0005887|GO:0030593|GO:0019221|GO:0006952|GO:0005
576|GO:0004872|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137344_PI430048170 0.31528728964637 3.29266243066816 0.362139744772204
3.19601303754469 0.859854286988255A P A 0.3007496451844420.294911517899529
0.340478467800686A A A LNCV6_137344_PI430048170 mRNA
GATATGAAGAGGGGACTTCAGAAAATGCTTCTCAAGTGCACAGTCTTTCAGCAGCAATAA NM_012353RefSeq chr1
- 247757461 247758406 OR1C1 26188 "olfactory receptor, family 1, subfamily C, member 1"
GO:0050911|GO:0007608|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_105208_PI430048170 0.2736231101249010.8991961648218890.253476731130662
0.3185898211373860.279884501981646A A A 0.6240959023252020.367754521796281
0.300119926199405A A A LNCV6_105208_PI430048170 mRNA
TGGGAGTTATTGTCAATTTGACAGTTGAAGATAAGGATGACCCCACCACAGGTGCATGGA NM_001220488 RefSeq
chr16 + 82626793 83796610 CDH13 1012 "cadherin 13, transcript variant 2"

GO:0043005|GO:0008285|GO:0005886|GO:0030032|GO:0002040|GO:0007266|GO:0031225|GO:0005615|GO:0042803|GO:0050927|GO:0050850|GO:0016339|GO:0005737|GO:0030100|GO:0045944|GO:0051668|GO:0007156|GO:0070062|GO:0071813|GO:0045296|GO:0030335|GO:0034329|GO:0055100|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94892_PI430048170 0.128202420935244 1.16060656777342 5.4946394539853 5.57991572257254 5.52547523722124 P P P 5.49424369072984 5.23762566477097 5.2072620551307 P P P LNCV6_94892_PI430048170 mRNA
GTGAAGGAGTTTGAGAAGCTGAACCGCATTGGAGAGGGTACCTACGGCATTGTGTATCGGNM_052988 RefSeq chr16 + 89686667 89696364 CDK10 8558 "cyclin-dependent kinase 10, transcript variant a"
GO:0005515|GO:0008285|GO:0006468|GO:0043410|GO:0007089|GO:0005524|GO:0004693 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138034_PI430048170 0.8681187882937650.9760037861354457.2143576569213 7.62611395825568 7.29680014439043 P P P 7.67878274568223 7.22377841715673 7.33354121030909 P P P LNCV6_138034_PI430048170 mRNA
TCTGGGAAATGACTTTTCTGGGAAATGACAGTTTCTTTGACATATTTTCTTTGCCCACTTNM_006235 RefSeq chr11 - 111352255 111379432 POU2AF1 5450 POU class 2 associating factor 1
GO:0005515|GO:0003712|GO:0006355|GO:0006366|GO:0006959|GO:0003713|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105376_PI430048170 0.3373051933232781.32418328517715 4.10888459771565 3.88186704570469 3.1602049542183 P P P 3.09205489367848 3.60266234720736 3.35598563108217 P P P LNCV6_105376_PI430048170 mRNA
TCTGCTTGGCCACTACAAGTTCGGCATGAGCAAGAAGGAGATGGAGCAGGTGGACGCAGT NM_014853 RefSeq chr17 + 2337511 2381054 SGSM2 9905 "small G protein signaling modulator 2, transcript variant 1"
GO:0017137|GO:0034499|GO:0033126|GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100362_PI430048170 0.9447310756712591.00230663079877 5.71094098714342 5.59001849234919 5.55468067987563 P P P 5.67273086865567 5.73815843512118 5.42033339093239 P P P LNCV6_100362_PI430048170 mRNA
TTACCACGTGGAGTCTAAGGTGTATGCTGTGGCCACCAGCACCAACACGCCGTGTGCCCG NM_013291 RefSeq chr8 - 144393230 144409349 CPSF1 29894 "cleavage and polyadenylation specific factor 1, 160kDa"
GO:0005515|GO:0006379|GO:0008380|GO:0006369|GO:0006378|GO:0010467|GO:0006366|GO:0031124|GO:0006406|GO:0000398|GO:0005847|GO:0005654|GO:0003730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143726_PI430048170 0.00957714513767343 0.62459822459442 10.9734763896252 10.8357666023921 10.9186353141922 P P P 11.417800135387 11.5904435061567 11.741800444685 P P P LNCV6_143726_PI430048170 mRNA
GCGTGTTTCCAGCAGTTGGCATTAAAGTGCCTTTTTCTAATAAAATCAGTTTATTATGAC NM_001421 RefSeq chrX - 130064919 130110500 ELF4 2000 "E74-like factor 4 (ets domain transcription factor), transcript variant 1"
GO:0005515|GO:0001077|GO:0006366|GO:0045944|GO:0016605|GO:0000981|GO:0001787|GO:0005654|GO:0045893|GO:0001866|GO:0000978|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66130_PI430048170 0.0600129899464594 0.3175843730077034.69851789714283 4.22787287025732 4.24581418984994 P P P 6.79109239126004 5.4007773911661 5.5700745270205 P P P LNCV6_66130_PI430048170 mRNA
ACTTCTCCCCGCAAACCTAGGTCAGACTTTTCCTTTCATCTTTGTGTTCATCTACTGTAA NM_001032392 RefSeq chr2 + 87748090 87759475 PLGLB1 5343 plasminogen-like B1 GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138851_PI430048170 0.1159947571798391.04117192550956 0.395448015315343 0.4224164660915810.342748608819734 A A A 0.3083206800340480.333699374735647 0.344860209433588 A A A LNCV6_138851_PI430048170 mRNA

GGGTGAGACAAAAGTCTAATGCCACTGGATCTTGTGTGATAAATAAAGAAATATATGATC NM_001031836 RefSeq chr8 + 36784323 36936126 KCNU1 NA "potassium channel, subfamily U, member 1"NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80571_PI430048170 0.801492550132495 0.9561024869522684.18860704308273 3.78687546501896 3.96166515163836 P P P 3.70124222521783 4.16220439573956 4.23976729918412 P P P LNCV6_80571_PI430048170 mRNA
CCTTAATTTTGGGGAAGATAAAAAATGTTGATTGCGTCCTCCTTGCAAGGCATGGAAGGC NM_002451 RefSeq chr9 + 21802635 21865970 MTAP 4507 methylthioadenosine phosphorylase
GO:0005634|GO:0044281|GO:0006738|GO:0004645|GO:0033574|GO:0032259|GO:0005829|GO:0034641|GO:0006166|GO:0017061|GO:0005737|GO:0006139|GO:0000096|GO:0019509|GO:0006595|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130873_PI430048170 0.00429698935574043 1.35524980020425 13.6770216490967 13.7961136485061 13.7074306754408 P P P 13.257545481516 13.2104958914577 13.3932227813297 P P P LNCV6_130873_PI430048170 mRNA
TTTCTAACCAAGCAGATGGAGAAAATCCAACCAGCTCTTCAGGAGAAGCACGCCATGAAA NM_002624 RefSeq chr12 + 53295450 53299451 PFDN5 5204 "prefoldin subunit 5, transcript variant 1"
GO:0005515|GO:0006355|GO:0060041|GO:0003714|GO:0016272|GO:0005634|GO:0005737|GO:0006457|GO:0051084|GO:0051082|GO:0044267|GO:0045892|GO:0090090 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99138_PI430048170 0.000348435981629757 3.20326672761757 6.76522774320228 6.70735496735713 7.04691481072357 P P P 5.18773812600037 5.32739994609742 4.96632409785064 P P P LNCV6_99138_PI430048170 mRNA
CTGGAAGATAAGGGAAGCCAGGAAAAGCAGGGCAAGTCCGAAGGTGAGGGCAAGCCACAA NM_001006938 RefSeq chrX - 102139960 102142416 TCEAL6 158931 transcription elongation factor A (SII)-like 6
GO:0006355|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104153_PI430048170 0.178699079823745 2.19725432784642 2.37057558997629 1.02212701822983 0.818183173727899 A A A 0.295357593461427 0.675160737157868 0.32928139887973 A A A LNCV6_104153_PI430048170 mRNA
AACAGAAAAAACTGGCAGCGTCACAAATTGAGAAACAACGGCAGCAAATGGACCTTGCTC NM_017508 RefSeq chr11 - 15966448 16402867 SOX6 55553 "SRY (sex determining region Y)-box 6, transcript variant 1"
GO:0005515|GO:0003700|GO:0044212|GO:0051216|GO:0048708|GO:0071560|GO:0016458|GO:0005634|GO:0009791|GO:0021778|GO:0045944|GO:0048821|GO:0032332|GO:0055007|GO:0006355|GO:2000741|GO:0046982|GO:0000122|GO:0003677|GO:0001701|GO:0006351|GO:0043565|GO:0000902|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66942_PI430048170 0.2031932791857381.13732614495272 8.13873069280949 7.87416743195751 7.83502958455472 P P P 7.78449896629259 7.87702190376785 7.63882661361642 P P P LNCV6_66942_PI430048170 mRNA
AGCACAGCAGCCGCTCAGAGACAGGAATAGAAATTTCATTAAAATCTATGGACTTTAAAA NM_152499 RefSeq chr1 + 43991607 43996526 CCDC24 149473 coiled-coil domain containing 24 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144971_PI430048170 0.22456304129518 1.15415976728686 7.18391686355131 7.41563572736372 7.05399283478026 P P P 7.20398302427644 6.93160326622281 6.90127132963373 P P P LNCV6_144971_PI430048170 mRNA
TTTGGGTTGGAGCTGTTCCATTGGGTCCTCTTGGTGTCGTTTCCCTCCCAACAGAGCTGG NM_000419 RefSeq chr17 - 44372181 44389505 ITGA2B 3674 "integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)"
GO:0005515|GO:0008305|GO:0009986|GO:0005886|GO:0050840|GO:0030168|GO:0072562|GO:0046872|GO:0042802|GO:0070527|GO:0007160|GO:0030198|GO:0005887|GO:0007229|GO:0007411|GO:0007596|GO:0002576|GO:0002687|GO:0031092|GO:0007155|GO:0070051|GO:0005925|GO:0009897|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_136286_PI430048170 0.0243760684598469 1.60416098023942 11.6538654755424
11.7943334126726 11.5094760610612 P P P 11.2555757732122 10.8015050741173
10.8222008821425 P P P LNCV6_136286_PI430048170 mRNA
CTTTGGCTATTATGAAAGAGGTTAGTGTGTTCCCTGCAATAAACTTGTTCCTGAGAAAAA NM_001199042 RefSeq
chr15 - 74179465 74202879 STRA6 64220 "stimulated by retinoic acid 6, transcript variant 8"
GO:0060426|GO:0007631|GO:0007603|GO:0005886|GO:0030325|GO:0030324|GO:0003184|GO:0048844|GO:0003
281|GO:0043583|GO:0050905|GO:0007507|GO:0048589|GO:0061029|GO:0048745|GO:0042573|GO:0048520|GO:0
061143|GO:0004872|GO:0097070|GO:0007612|GO:0060900|GO:0001568|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128354_PI430048170 0.52316403074934 0.923161910667412 0.307395707149971
0.311602808334923 0.371636547673613 A A A 0.312279919450777 0.700116222248415
0.286954187302922 A A A LNCV6_128354_PI430048170 mRNA
GGGGAATGACAGATTTCTGGAATGCAATGTAATGTTACTGAGACTTAAATAGATGTTATG NM_018402 RefSeq chr12
- 68201348 68225791 IL26 55801 interleukin 26
GO:0051897|GO:0007267|GO:0050680|GO:0032874|GO:0050715|GO:0005125|GO:0005615|GO:0005829|GO:0046
427|GO:0006955|GO:0006954|GO:0045944|GO:0070374 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143433_PI430048170 0.557089349745024 1.03843301303324 0.277851378604107
0.290692500425579 0.501187569864983 A A A 0.325904621000034 0.282464981520309
0.308878632479078 A A A LNCV6_143433_PI430048170 mRNA
GGCACAGGGCTGGAGAGTACTTTAATTTATTCAAGATGCTTCATTCATATGAAAATGTAT NM_006161 RefSeq chr5
- 135534281 135535949 NEUROG1 4762 neurogenin 1
GO:0003700|GO:0042472|GO:0006357|GO:0031536|GO:0070888|GO:0005634|GO:0003677|GO:0000989|GO:0006
351|GO:0007399|GO:0051091|GO:0045165|GO:0045666|GO:0045944|GO:0003682|GO:0030182|GO:0046983|GO:0
043204 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141258_PI430048170 0.0179277632010348 0.644999410695145 6.59637474724453
6.76850177099664 6.92339357152184 P P P 7.14950546478064 7.46484031729387
7.55917643137786 P P P LNCV6_141258_PI430048170 mRNA
CATGGTTACAATCATTGCTGAAAATGGTATTTTCCCCCTTTTCTGCATTTTGCTATTGTA NM_003998 RefSeq chr4 +
102501328 102617302 NFKB1 4790 "nuclear factor of kappa light polypeptide gene enhancer in B-cells 1,
transcript variant 1"
GO:0005515|GO:0003700|GO:0006366|GO:0044212|GO:0007249|GO:0042803|GO:0002756|GO:0003690|GO:0002
755|GO:0031072|GO:0006979|GO:0033256|GO:0000975|GO:0000976|GO:0038124|GO:0038123|GO:0010744|GO:0
034134|GO:0001205|GO:0000122|GO:0002224|GO:0032269|GO:0038061|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137629_PI430048170 0.506418822031986 1.33892535907167 2.48960124852634
2.59501965745982 3.73041950469109 A A P 2.26093812044065 2.47554490649719
3.04709877791116 A A P LNCV6_137629_PI430048170 mRNA
GAAAAGGGCATATCTACGTTACTTGTAGCTTGCTTTAATTAAAGTTGCCTCAAACAAGTA NM_014236 RefSeq chr1
+ 231241172 231277973 GNPAT 8443 glyceronephosphate O-acyltransferase
GO:0030913|GO:0005782|GO:0007584|GO:0008611|GO:0042493|GO:0016290|GO:0005102|GO:0021587|GO:0044
281|GO:0016287|GO:0007416|GO:0005739|GO:0070542|GO:0042594|GO:0016020|GO:0061024|GO:0006644|GO:0
006654|GO:0044255|GO:0005778|GO:0046474|GO:0005777 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_139579_PI430048170 0.876057073964311 0.992527731065987 8.14062819681762
8.02705486870957 7.91371929561587 P P P 8.09134916585846 8.06303854324638
7.96538922067316 P P P LNCV6_139579_PI430048170 mRNA
GCTCCTTGCCTTCCCCTTACCTGACCTTATTAATAAAGTCTTTCTTAGCAGTTCAAAAAA NM_001130028 RefSeq
chr15 + 74614993 74630201 CLK3 1198 "CDC-like kinase 3, transcript variant 1"
GO:0005515|GO:0001669|GO:0005634|GO:0018108|GO:0005524|GO:0046777|GO:0016020|GO:0016607|GO:0004

674|GO:0004712|GO:0005654|GO:0006468|GO:0043484|GO:0045111|GO:0004713 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131488_PI430048170 0.10314963641873 0.9258325037548970.281904994376317
0.2867978750769180.293453515752692A A A 0.46972207958622 0.385367713686562
0.337502107396322A A A LNCV6_131488_PI430048170 mRNA
CAGGATAGACGTTGCTCATCGTCTTTACCTAATAAATAAGTTTGTCTGATTGCTGAAAAA NM_001732RefSeq chr6
+ 26501266 26510424 BTN1A1696 "butyrophilin, subfamily 1, member A1"
GO:0005887|GO:0004872|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129233_PI430048170 0.5087590130378370.9685728768782290.459015100548491
0.4788532792084560.299036650846936A A A 0.4092730716248180.507714481201218
0.463088103904766A A A LNCV6_129233_PI430048170 mRNA
AATTCCCAGTGGTGTTTCTTAAGGTTCTATCTTGTGCCATGATGAATAAAAAGTTAAGCA NM_013427RefSeq chrX
- 11137542 11665701 ARHGAP6 395 "Rho GTPase activating protein 6, transcript variant 1"
GO:0051056|GO:0017124|GO:0007264|GO:0005884|GO:0010518|GO:0009967|GO:0007202|GO:0007266|GO:0015
629|GO:0043087|GO:0005100|GO:0051895|GO:0005829|GO:0051497|GO:0005737|GO:0016004|GO:0043274|GO:0
032321|GO:0048041|GO:0005070|GO:0030041 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132211_PI430048170 0.8782098692159841.0114191304582 7.40382385270977
7.61463402702652 7.41287535955235 P P P 7.46013148383425 7.65229276018599
7.25208808125281 P P P LNCV6_132211_PI430048170 mRNA
AACATATTGTATAAAAATGAAAAACACAGGAACCCTCTTCCCTTCCGCCTGGTGTGGGCT NM_002843RefSeq chr11
+ 47980557 48170842 PTPRJ 5795 "protein tyrosine phosphatase, receptor type, J, transcript variant 1"
GO:0051898|GO:0005515|GO:0051897|GO:0030308|GO:0008285|GO:0030054|GO:0008013|GO:0005886|GO:0048
709|GO:0060242|GO:0051894|GO:0030155|GO:2000272|GO:0035335|GO:0007507|GO:0016791|GO:0005911|GO:0
043407|GO:0010572|GO:0010642|GO:0004725|GO:0070062|GO:0051019|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130972_PI430048170 0.00844671659933733 0.82672656778602211.4238304258806
11.5268074701987 11.5673197268568 P P P 11.7588183841243 11.7455571055197 11.839115585704
P P P LNCV6_130972_PI430048170 mRNA
TGAACCAGGGGTATGTCATCACTTTTTTCATATCAAGTCCTCACCCTCCTTCCACATAAT NM_003904RefSeq chr11
- 116778559 116788023 ZPR1 8882 ZPR1 zinc finger
GO:0008380|GO:0005515|GO:0030424|GO:0048471|GO:0015030|GO:0001834|GO:0021510|GO:0008283|GO:0001
833|GO:2000672|GO:0005634|GO:0033120|GO:0030426|GO:0030576|GO:0005737|GO:0042023|GO:0043025|GO:0
043204|GO:0031641|GO:0045927|GO:0006397|GO:0030971|GO:0005730|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132075_PI430048170 0.0153745967200137 0.3058462038274433.08579531055322
3.95189081100522 3.58946555088091 A P P 5.32222153325948 5.38351197791047
5.16845250092101 P P P LNCV6_132075_PI430048170 mRNA
TCTCTACTACAAGAGCTGGATTTCCATTACTCACTCTTGCTCTTACATTAAAGTTGTTGANM_001143887 RefSeq chr15
- 49125273 49155657 COPS2 9318 "COP9 signalosome subunit 2, transcript variant 2"
GO:0005515|GO:0007165|GO:0005737|GO:0008180|GO:0006366|GO:0008283|GO:0030182|GO:0003714|GO:0010
388|GO:0004871|GO:0000122|GO:0035914 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128861_PI430048170 0.00144846405771191 0.6812852750647148.85150747906953
8.91574690168714 8.9976512676454 P P P 9.47318461466161 9.51444294400042
9.44107251446526 P P P LNCV6_128861_PI430048170 mRNA
GGTTTCTCTTCTAAGTCCTTGGTCTAAAGAGCGCTGTCACTTTTTTCTCTCCCACTTTTT NM_030628RefSeq chr11 -
62646847 62653302 INTS5 80789 integrator complex subunit 5
GO:0005515|GO:0016020|GO:0032039|GO:0005634|GO:0016021|GO:0016180 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_92017_PI430048170 0.1376718882994480.5400447528061883.94056410263273 4.34421055703223

4.1990075705564 P P P 4.3975043085918 5.61480778702527 4.90554914740733 P P P
LNCV6_92017_PI430048170 mRNA
CAAGCTGGTCATAGAATAGGTGAATACCTTGAGAAGATAATTCCTTTGGTGGTAAAATTT NM_018448 RefSeq chr12
+ 67269280 67314692 CAND1 55832 cullin-associated and neddylation-dissociated 1
GO:0005515|GO:0031461|GO:0016567|GO:0045899|GO:0000151|GO:0005634|GO:0010265|GO:0043086|GO:0030
154|GO:0005737|GO:0016020|GO:0017025|GO:0005654|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143609_PI430048170 0.0666780788759525 0.6983600967905479.10261133188968
8.85824872909334 8.53891135993188 P P P 9.33970030808693 9.49060308754377
9.26913377179804 P P P LNCV6_143609_PI430048170 mRNA
GGCCTGCCTCCCACCTGGAAGTCTGGGAATGAGGAGATTGAGATAAACTTTTGAAATCCC NM_001167734 RefSeq
chr6_GL000255v2_alt + 2169496 2181635 VARS2 57176 "valyl-tRNA synthetase 2, mitochondrial,
transcript variant 1"
GO:0005739|GO:0010467|GO:0004832|GO:0002161|GO:0006438|GO:0006450|GO:0005524|GO:0006418|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56458_PI430048170 0.4428438974248330.9149910593696986.57408136957347 6.62702152429092
6.44942802095094 P P P 6.66014202106081 6.88709050806378 6.46213689355048 P P P
LNCV6_56458_PI430048170 mRNA
TACTGCCATGGAACTTCTTTATCACTGCCAAGGAGTACTGGATGTTCAAACTCCGCAACT NM_001174098 RefSeq
chr10 + 71319252 71363390 SLC29A3 55315 "solute carrier family 29 (equilibrative nucleoside
transporter), member 3, transcript variant 2" GO:0005337|GO:0031902|GO:0016021|GO:0005765|GO:0055085 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139973_PI430048170 0.00273692942015059 0.0942623320860460.470193579533868
0.6160237273003971.38502085773417 A A A 4.2677060749733 4.09354242968729
4.48083349139338 P P P LNCV6_139973_PI430048170 mRNA
GCTGATCACTTCACTAAAACTGTAAATCAGTAGATTGATACGCTTATTGATTGCCTAGAA NM_018317 RefSeq chr4
+ 26583923 26756213 TBC1D19 55296 "TBC1 domain family, member 19, transcript variant 1"
GO:0005515|GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134071_PI430048170 0.43007544678568 1.03261749204471 0.449768245110814
0.2956449425569160.353889623660285 A A A 0.28433435766163 0.331296222981996
0.348212416298188 A A A LNCV6_134071_PI430048170 mRNA
GCTTCTTTATTAGAGAGGAGCGGGTGAAAAGTAGTAGTTTAATGTTCAGATATACAATCA NM_006789 RefSeq chr6
+ 41053200 41064891 APOBEC2 10930 "apolipoprotein B mRNA editing enzyme, catalytic polypeptide-
like 2" GO:0006397|GO:0009972|GO:0016556|GO:0003723|GO:0080111|GO:0004126|GO:0008270 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_65058_PI430048170 0.0122123332945147 0.5294015650829325.97748642784336
5.71372664955457 5.94972004365983 P P P 6.48511493410123 6.94932506943378
6.92766127779772 P P P LNCV6_65058_PI430048170 mRNA
CGTTTGGCACTGCAAAGACGGCAACAACCACACCTGCTACAGGGTTTTCTTTCTCCACCT NM_016553 RefSeq chr19
- 49906825 49929731 NUP62 23636 "nucleoporin 62kDa, transcript variant 2"
GO:0005515|GO:0007077|GO:0010467|GO:0008219|GO:0043130|GO:0019221|GO:0019058|GO:0030159|GO:0046
578|GO:0015031|GO:0008645|GO:0043231|GO:0031074|GO:0043069|GO:0046580|GO:0015758|GO:0017056|GO:0
043123|GO:0042169|GO:0031965|GO:0005975|GO:0045742|GO:0007569|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145104_PI430048170 0.0687224591719479 0.5379908858161533.33269349468498
4.22067484985748 3.94506531094653 P P P 4.73318556434835 4.76728295446294
4.81669509804972 P P P LNCV6_145104_PI430048170 mRNA
CCTCACTGCCAGTGAAATTGCTTTCCTATGGTATATCTCCTTACCAGAAAAATCTCTAAA NM_201269 RefSeq chr1
- 90915299 91022255 ZNF644 84146 "zinc finger protein 644, transcript variant 1"

GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131174_PI430048170 0.7786432212477770.9915831922998410.1382069819824 10.1047120725254 10.0253237641225 P P P 10.1247224603203 10.1282198614311 10.0529576752798 P P P LNCV6_131174_PI430048170 mRNA CTGACTTTTTCCCCCCAATAAAAGCTCTTCTTTTTTAATATATAAAAGCCCCTTAAAAAA NM_001270550 RefSeq chr11 + 46380783 46383837 MDK 4192 "midkine (neurite growth-promoting factor 2), transcript variant 4"
GO:0021542|GO:0030421|GO:0021987|GO:0030325|GO:0042493|GO:0007614|GO:0009611|GO:0051384|GO:0005576|GO:0042995|GO:0030154|GO:0007399|GO:0007165|GO:0043524|GO:0005737|GO:0007219|GO:0016477|GO:0050795|GO:0021681|GO:0051781|GO:0001662|GO:0045893|GO:0008083|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139979_PI430048170 0.6945635872545840.9409253834985029.8156838659983 9.74357084258793 10.2492878024047 P P P 9.81378752303138 9.96181774932493 10.3050851467493 P P P LNCV6_139979_PI430048170 mRNA AAATATACCTCAGGCTGAAATTTGGGGTGGGATAGCAGGTCAGTTGATCTTCTGCAGGAA NM_006367 RefSeq chr1 + 40040582 40072649 CAP1 10487 "CAP, adenylate cyclase-associated protein 1 (yeast), transcript variant 1"
GO:0030036|GO:0005886|GO:0001667|GO:0030168|GO:0003779|GO:0006898|GO:0007165|GO:0007190|GO:0007163|GO:0007411|GO:0007596|GO:0002576|GO:0030864|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131558_PI430048170 0.6291142269781340.9650127435269990.5713876757530310.5134925984352 0.281164450619465 A A A 0.4139668026847410.5951045010353250.52144243993528 A A A LNCV6_131558_PI430048170 mRNA CAATGATGCGCTGTTATTTATGGGTTAAAATATGCTTAATTGCTTCCTTCCTTGTAGCATNM_001031748 RefSeq chr12 + 39626169 39721916 C12orf40 283461 chromosome 12 open reading frame 40 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142910_PI430048170 0.00945669514916551 0.5011423068920317.29995924551762 7.39913476958337 7.73638434149427 P P P 8.2131175891212 8.43492945259433 8.76143593412076 P P P LNCV6_142910_PI430048170 mRNA TTGTGTACACCGGGGCTTGTACTTGGGGAATTTAATAAAAATGCTCATTACCAAGCTCCA NM_001695 RefSeq chr8 + 103021019 103073057 ATP6V1C1 528 "ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1"
GO:0005515|GO:0008286|GO:0005215|GO:0051701|GO:0005886|GO:0016469|GO:0045177|GO:0033180|GO:0031410|GO:0005765|GO:0055085|GO:0005829|GO:0006879|GO:0033572|GO:0008553|GO:0046961|GO:0015991|GO:0090382|GO:0070062|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141873_PI430048170 0.6995608465687560.9317045160219340.477370452429953 1.35668321720669 0.437796429400107 A A A 0.5519533330016681.11724066623441 1.04360476383933 A A A LNCV6_141873_PI430048170 mRNA GTCCGAAGCTGCCAGGAAGAAGAACAGAACTTTGTGTGTTTATTTCATGATAAAGTGATT NM_002183 RefSeq chrY + 1336615 1382689 IL3RA 3563 "interleukin 3 receptor, alpha (low affinity), transcript variant 1"
GO:0038156|GO:0005886|GO:0004912|GO:0016021|GO:0036016 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55363_PI430048170 0.2501852500007741.02059440996771 0.31141851983004 0.250230321725057 0.296595762410895 A A A 0.2614966555111610.2466263955374390.262541681421554 A A A LNCV6_55363_PI430048170 mRNA ATTAATGGAAATGTTTACAGATCCCCAAGCCTGGCAAGGGAATTTCTTCAACTCCCTGCC NM_001276 RefSeq chr1 - 203178930 203186794 CHI3L1 1116 chitinase 3-like 1 (cartilage glycoprotein-39)
GO:0006032|GO:0051897|GO:0048471|GO:0005783|GO:0030324|GO:0051216|GO:0005615|GO:0006955|GO:0005737|GO:0006954|GO:0071356|GO:0070374|GO:0004568|GO:0070555|GO:0070062|GO:0010800|GO:0007250|GO:0

005975|GO:0005578|GO:0006915|GO:0045766|GO:0009612|GO:0008061|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127357_PI430048170 0.0100958835440659 0.6061440894592 9.71676617006543 9.84321674793725 9.43727421531135 P P P 10.2475954734584 10.5545453655334 10.3747105868695 P P P LNCV6_127357_PI430048170 mRNA GCTGGTTACTCAGGGTTCATCTGTCCATGGCCTTTCTAATAAACTGTTGAGTTGAAGCAC NM_002953 RefSeq chr1 + 26529757 26575029 RPS6KA1 6195 "ribosomal protein S6 kinase, 90kDa, polypeptide 1, transcript variant 1"
GO:0005515|GO:2000491|GO:0034142|GO:0030307|GO:0045597|GO:0007268|GO:0005634|GO:0043620|GO:0051403|GO:0005829|GO:0043555|GO:0002756|GO:0005737|GO:0007411|GO:0045944|GO:0002755|GO:0043154|GO:0034138|GO:0043027|GO:0048011|GO:0043066|GO:0038124|GO:0000287|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52373_PI430048170 0.534821057866196 1.26543375593684 0.348505292855059 1.37588371128283 0.32631879895315 A A A 0.261899600588472 0.289088122479212 0.702171687775355 A A A LNCV6_52373_PI430048170 mRNA AAATGCAAAACCATTTATAGCATGAAGCCCTACATGATCACTGCAGGATGATCCTCCTCC NM_001040033 RefSeq chr1 + 110871198 110899936 CD53 963 "CD53 molecule, transcript variant 1"
GO:0005515|GO:0001772|GO:0007165|GO:0009986|GO:0005886|GO:0005911|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142860_PI430048170 0.285021750270101 1.21388575215565 2.81066715148598 2.99725175504319 3.04800903166825 A A P 2.28718350064774 2.61628856424234 3.02828650833239 A P P LNCV6_142860_PI430048170 mRNA TCCTTCTCTTAGAAGTGCATGTATATGTGGAGGGAGGGAAAAGGGTCCTATAGAATGAGG NM_181842 RefSeq chr6_GL000255v2_alt - 3155589 3157967 ZBTB12 221527 zinc finger and BTB domain containing 12
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138388_PI430048170 0.48244319385064 0.751815468665892 0.491975175224803 0.599816857633408 0.548194264455043 A A A 0.570930476276233 0.421945330194726 1.58794107373964 A A A LNCV6_138388_PI430048170 mRNA TCCTTGAATCAAAATTCAAAGTCCAAGACACATGTGGAGTCCACAACCTCCATGGGATGC NM_001256395 RefSeq chr1 + 156369188 156385221 RHBG 57127 "Rh family, B glycoprotein (gene/pseudogene), transcript variant 2"
GO:0016323|GO:0005886|GO:0015696|GO:0005887|GO:0072488|GO:0030506|GO:0070634|GO:0008519|GO:0014731|GO:0055085|GO:0046658|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127325_PI430048170 0.0772738764603410 0.669153201416782 0.277330140781299 0.300051192534158 0.3618248685462 A A A 0.88708745684847 1.15942402525195 0.573743878900204 A A A LNCV6_127325_PI430048170 mRNA TTGTCCCCCCAGATTTGGGGGACAAAATAAAATTAATCTTTTAAAATGTGTCAGCCATAT NM_000046 RefSeq chr5 - 78777210 78986534 ARSB 411 "arylsulfatase B, transcript variant 1"
GO:0043627|GO:0044281|GO:0005764|GO:0046872|GO:0005739|GO:0030207|GO:0003943|GO:0004065|GO:0030204|GO:0030203|GO:0009268|GO:0070062|GO:0043202|GO:0006665|GO:0005791|GO:0005794|GO:0006687|GO:0009986|GO:0005975|GO:0007584|GO:0006914|GO:0007417|GO:0051597|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69251_PI430048170 0.00011983534679437 1.47915417313545 4.1919281734618 4.17502631820182 4.26243052661986 P P P 3.62513763216635 3.62493752432744 3.68563764026673 P P P LNCV6_69251_PI430048170 mRNA ACGAGCTGAAGCAAAAGGTGGTGGCTGAGAACCCACAGCACTTTGGCGTCGCTGTTCCAC NM_001932 RefSeq chr17 - 43800798 43833179 MPP3 4356 "membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3), transcript variant 1" GO:0007165|GO:0005887|GO:0046939|GO:0004385|GO:0030165 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_135295_PI430048170 0.00352852959736753 1.39659576113046 6.47426302412701
6.63589612939291 6.65172292651665 P P P 6.00253923670122 6.13193064504063
6.18235515262116 P P P LNCV6_135295_PI430048170 mRNA
TGTTATTGCTATGTCTGGTATTTCCAAGGTTTTCGTCGGGGAGGTGGTAGAAGAAGCACT NM_005643 RefSeq chr6
- 34877777 34888071 TAF11 6882 "TAF11 RNA polymerase II, TATA box binding protein (TBP)-
associated factor, 28kDa, transcript variant 1"
GO:0005515|GO:0010467|GO:0006355|GO:0006368|GO:0005669|GO:0005794|GO:0006367|GO:0046982|GO:0006
366|GO:0003713|GO:0003677|GO:0043923|GO:0046966|GO:0047485|GO:0042809|GO:0016032|GO:0005654 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129114_PI430048170 0.0625605867120999 0.8458438235435581 3.3966697527244
13.5318401905955 13.5643813444012 P P P 13.6376931813947 13.6933528238945
13.8805214811477 P P P LNCV6_129114_PI430048170 mRNA
CGCTAAGAATTTAAAAATCACATTCTCTGTTCAGCTGTTAATGCTGGGATCCATATTTAG NM_006196 RefSeq chr2
+ 70087452 70089202 PCBP1 5093 poly(rC) binding protein 1
GO:0008380|GO:0005515|GO:0010467|GO:0005737|GO:0016020|GO:0003697|GO:0000398|GO:0030529|GO:0003
723|GO:0005654|GO:0070062|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128302_PI430048170 0.141211412295988 0.737087920034136 6.090108537177
5.65384322343215 5.4093203837963 P P P 6.20733995982706 6.21403175137193
6.13462403975002 P P P LNCV6_128302_PI430048170 mRNA
CTCCCCTTCCCATGTATCAGTGAAAACCATTATGCAAATAAAGAGCTGGGCCCCAAAAAA NM_002251 RefSeq chr20
- 45092308 45101112 KCNS1 3787 "potassium voltage-gated channel, modifier subfamily S, member
1"
GO:0005515|GO:0005251|GO:0005886|GO:0008076|GO:0015459|GO:0007268|GO:0051260|GO:0034765|GO:0006
813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139766_PI430048170 0.304745730953746 0.787385010336432 2.81022207247794
2.14748650881872 3.11461117404161 A A P 2.90104051651708 3.06277706916826
3.27941793029406 P P P LNCV6_139766_PI430048170 mRNA
AAGTCAATGCTGTTCTCTGCCTGCAGAGACAAAAACATGGTGAATTCTCGTCACAAGGCA NM_015703 RefSeq chr22
- 42508334 42519823 RRP7A 27341 ribosomal RNA processing 7 homolog A (S. cerevisiae)
GO:0000166|GO:0032545|GO:0006364|GO:0034456|GO:0000028 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142362_PI430048170 0.0534072656715692 0.433948401545229 1.86073129937939
0.792949585930629 1.698403045429 A A A 2.32679114925381 2.40939672953674
3.24967881831421 A A P LNCV6_142362_PI430048170 mRNA
GCTGCTAGACTGGTTTTCTGTGTTGGTAAATTGCCTATATAAATCTGAATAAAAAGGATC NM_005160 RefSeq chr22
+ 25564893 25729291 ADRBK2 157 "adrenergic, beta, receptor kinase 2"
GO:0031623|GO:0007165|GO:0004703|GO:0004672|GO:0047696|GO:0038032|GO:0006468|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129417_PI430048170 0.6291607389813 0.943327444847635 1.62634965178441
1.17094980578566 3.12714390742817 A A P 2.36041625196214 2.41937627578683
2.14958639567936 A A A LNCV6_129417_PI430048170 mRNA
ACCTCAGATGAGGGCTCATATGATTGAGTTGTGCACTGGCTGTTATTAAACTGTAAAGGA NM_138283 RefSeq chr20
+ 23439684 23444930 CSTL1 128817 cystatin-like 1 GO:0010951|GO:0004869|GO:0005576 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_127824_PI430048170 0.0651017492638802 0.547566447307042 2.61976951217261
1.72941086855432 2.49413954748198 A A A 3.05424381304551 3.08097467467531
3.43316580031641 P P P LNCV6_127824_PI430048170 mRNA
ATTAGACATCAGAGAATTCATACTGGACAGATGCCTTACAAATGTAAGGGTGGCAAGGTC NM_001031665 RefSeq

chr19 - 52949378 52962911 ZNF816 NA "zinc finger protein 816, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139681_PI430048170 0.0320630479275713 1.56331157614783 5.49126751048108 5.95263025293717 5.77577579027654 P P P 5.22314693384474 5.25751538512612 4.79853349301914 P P P LNCV6_139681_PI430048170 mRNA GTACTAGACTTTGTTCAGGCTGTTCTCATCTCAGTATTGCCCCTTCCTTTCACTTTCACA NM_014909 RefSeq chr14 + 76761891 76783020 VASH1 22846 vasohibin 1
GO:0010596|GO:0005737|GO:0005783|GO:0001937|GO:0016525|GO:0009611|GO:0045177|GO:0007050|GO:0001525|GO:2000772|GO:0005615|GO:0043537 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138150_PI430048170 0.3437442816175680.9204825297034950.347998401471298 0.3482324192392710.441032788319322A A A 0.3524732152781750.459429170425454 0.667958866777219A A A LNCV6_138150_PI430048170 mRNA GTGCTAGTAGAATATAAGATAAAAGAGGCTGAGAATTACCATACAAGGGTATTACAACTG NM_033439 RefSeq chr9 + 6215785 6257983 IL33 90865 "interleukin 33, transcript variant 1"
GO:0032755|GO:0005515|GO:0030133|GO:0032753|GO:0032754|GO:0043032|GO:0005694|GO:0032436|GO:0005634|GO:0032736|GO:0097191|GO:0005125|GO:0005615|GO:0006351|GO:0042092|GO:0051025|GO:0045944|GO:0002686|GO:0051024|GO:0050729|GO:0002826|GO:0002830|GO:0032689|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62566_PI430048170 0.0342954765443222 0.7935107413461961 1.7620195198453 11.9092318219945 11.7463027579403 P P P 12.2063489138657 12.2296689286709 11.9747249772531 P P P LNCV6_62566_PI430048170 mRNA GGGGGGCCTTATTTCTCAGGCCAGCTGAGTATTAGACACGATAAAGACTCTGTGGGTTCT NM_023933 RefSeq chr16 + 721141 722590 FAM173A 65990 "family with sequence similarity 173, member A, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133247_PI430048170 0.6121068617426680.96553422666264 0.533309836865379 0.5200773853857070.285933368245839A A A 0.4045600235799650.581657832483841 0.512575148064032A A A LNCV6_133247_PI430048170 mRNA GTGTCCGGTAGTTTCTTCTTACATTTTCCTTTGCCTTTATACTTTAGGGGTCTTACTCCA NM_012444 RefSeq chr20 + 57329774 57343993 SPO11 23626 "SPO11 meiotic protein covalently bound to DSB, transcript variant 1"
GO:0034502|GO:0000781|GO:0007286|GO:0005634|GO:0007283|GO:0007292|GO:0003677|GO:0005524|GO:0007129|GO:0001541|GO:0016787|GO:0000737|GO:0007141|GO:0007131 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73008_PI430048170 0.0475327917272942 1.3580587012163 3.7417819179702 4.11743157718098 3.8794236356252 P P P 3.6897591093491 3.39792888420729 3.32527616459716 P P P LNCV6_73008_PI430048170 mRNA AGAGTGGTAATGTCTTCCTCTTTTTGCTTTAGGAGAAAGACAGAATAATAAGCTGAATAG NM_001242829 RefSeq chr3 - 49724294 49786194 IP6K1 9807 "inositol hexakisphosphate kinase 1, transcript variant 3"
GO:0046854|GO:0008440|GO:0043647|GO:0005730|GO:0052724|GO:0052723|GO:0005654|GO:0005634|GO:0044281|GO:0005524|GO:0000832|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137477_PI430048170 0.0483453943726541.37327059587025 9.02471864560094 9.03480918564223 9.32612608476888 P P P 8.4954564656323 8.59035500248002 8.91370837688489 P P P LNCV6_137477_PI430048170 mRNA GGCTGATTTAGTCAGGGCAAAACCATTTACTTTACATATTCGTTTTCAATACTTGCTGTT NM_032970 RefSeq chr3 - 42547966 42582028 SEC22C 9117 "SEC22 vesicle trafficking protein homolog C (S. cerevisiae), transcript variant 1"
GO:0006888|GO:0005484|GO:0005783|GO:0000149|GO:0005789|GO:0031201|GO:0048280|GO:0016021|GO:0015031|GO:0006887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130328_PI430048170 0.6149464085460140.86712919917987 0.498033127562574 0.5202852855287781.21822082015158 A A A 1.37553892293073 0.440803226983254

1.00991670816594 A A A LNCV6_130328_PI430048170 mRNA
GATAGCTCTCTATAAGGGAGCTGCTTTCCATGTCTTTTAAGATTTTCCTTCTTTTACACC NM_018980 RefSeq chr7 +
141790216 141791366 TAS2R5 54429 "taste receptor, type 2, member 5"
GO:0007165|GO:0033038|GO:0050909|GO:0007186|GO:0005886|GO:0007635|GO:0008527|GO:0016021|GO:0001
580 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132621_PI430048170 0.3836749260575860.7007310787731410.364768139979266
2.02972738106742 1.72303366428821 A A A 2.51801596071092 1.99273423583298
1.41584482189964 P A A LNCV6_132621_PI430048170 mRNA
CAGGGAGATACAATCCCTTTCTTGTCATCTGCCATTTATGAACTTGATCCAAATAAAAAA NM_001145309 RefSeq
chr11 + 72080330 72110782 LRTOMT 220074 "leucine rich transmembrane and O-methyltransferase
domain containing, transcript variant 5"
GO:0005737|GO:0016206|GO:0007605|GO:0016021|GO:0005575|GO:0042135|GO:0042424|GO:0032259|GO:0060
117 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119028_PI430048170 0.2632043255413880.78346717810039 9.07927552009079
8.79953559553162 9.11426342123454 P P P 9.0826640518829 9.14191498307999
9.74718087474941 P P P LNCV6_119028_PI430048170 mRNA
TACCACCCCTACCCGGAAGAGTTCTAGCAGTGAGGATTCCTCCAGTGACGAGGAAGAGGA NM_001284388
RefSeq chr10 + 102152175 102163871 NOLC1 9221 "nucleolar and coiled-body phosphoprotein 1,
transcript variant 1"
GO:0007000|GO:0005515|GO:0007067|GO:0007049|GO:0005737|GO:0015030|GO:0006364|GO:0005730|GO:0005
654|GO:0005525|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140493_PI430048170 0.7980054666817590.9808585349931320.314430919658814
0.5072809704676540.357141066550079 A A A 0.5340684107034740.447953640377138
0.275800887610957 A A A LNCV6_140493_PI430048170 mRNA
AGCCCGACACGTTGTGTTCTGGTGCAGGTTTGTATTAAACTGTAGCTACTTCTCAAAAAA NM_020134 RefSeq chr2
+ 26848100 26950351 DPYSL5 56896 "dihydropyrimidinase-like 5, transcript variant 1"
GO:0007165|GO:0007411|GO:0016812|GO:0043025|GO:0030425|GO:0007399|GO:0006208|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136295_PI430048170 0.1080147351231840.6626970567537873.16468457699911
2.88841933460351 3.24723222002009 A A P 3.2250648557917 3.87061854581646
3.91219731520239 P P P LNCV6_136295_PI430048170 mRNA
GTACAGGTGATTGACTGGGTATTAGAAAAGACAAGCAAGAAATGATACATAATCATTCTC NM_022045 RefSeq chr8
+ 120445397 120523635 MTBP 27085 MDM2 binding protein
GO:0045839|GO:0008285|GO:0034501|GO:0000776|GO:0007050|GO:0007089|GO:0000785 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128482_PI430048170 0.8788393043746461.01248255626917 0.566760285915641
2.37115680345311 1.71741190244234 A A A 0.6066783148985570.989309310433455
2.65824374543262 A A P LNCV6_128482_PI430048170 mRNA
GTGATCATATCCATTTACATTTGTATCTCCATGTTCAAACAGCGTAGGTACCCAAATATT NM_001297645 RefSeq
chr5 + 64768917 64808561 CWC27 10283 "CWC27 spliceosome-associated protein homolog (S.
cerevisiae), transcript variant 3" GO:0000413|GO:0006457|GO:0000398|GO:0003755|GO:0071013 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_43523_PI430048170 0.0663758959059749 1.45491296527014 10.5480595891486 11.017945331193
10.5361356494347 P P P 10.4283572063471 10.1247224603203 9.9373331848131 P P P
LNCV6_43523_PI430048170 mRNA
AAAGAGCAGGACTCCAGACTCTTCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGA NM_006338 RefSeq chr1
- 204617172 204685353 LRRN2 10446 "leucine rich repeat neuronal 2, transcript variant 1"
GO:0007165|GO:0004872|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127093_PI430048170 0.0170464069086372 0.5886914244399780.280101367645085

0.3069705984377430.355790071763091A A A 1.15238149879123 1.20581923151859
0.854732437383066A A A LNCV6_127093_PI430048170 mRNA
TTTAGATAACTCCAACACTAGTCTTCATTTCTCACAGCTCTGTTTTTGTTCTTGAGTCAA NM_145054RefSeq chr17 +
9576626 9643461 CFAP52 146845 "cilia and flagella associated protein 52, transcript variant 2"
GO:0005515|GO:0005737|GO:0042995 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131416_PI430048170 0.3377312987768031.42271001134125 0.594557307606248
1.40246660875756 0.254481775304063A A A 0.3155352778313560.335453775900962
0.323871365325407A A A LNCV6_131416_PI430048170 mRNA
AGAAGAAATGGTGCAACAGCTGCAAATTGTCAGAGATACCCTGTGTAACGAACTCGACCA NM_001258024 RefSeq
chr15 + 67819703 67833836 SKOR1 NA SKI family transcriptional corepressor 1 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134356_PI430048170 0.7394945007921470.9666789547682791.35612493108461
2.23157095704704 0.937304212094365A A A 1.56996194875352 1.5672143458612
1.82993430638914 A A A LNCV6_134356_PI430048170 mRNA
AAACCCTTTGCTGCTTCTGTCTCTAGCTCTTGTCAATAAAGACGGTGACACCTGAAAAAA NM_001051RefSeq chr22
- 37204236 37212376 SSTR3 6753 "somatostatin receptor 3, transcript variant 1"
GO:0005515|GO:0043005|GO:0060170|GO:0006996|GO:0008285|GO:0005886|GO:0007267|GO:0007268|GO:0031
513|GO:0021549|GO:0007283|GO:0071385|GO:0004994|GO:0005737|GO:0042594|GO:0050796|GO:0042923|GO:0
005887|GO:0007187|GO:0007218|GO:0071392|GO:0030900|GO:0008628 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_137919_PI430048170 0.0935366819870198 0.6944543989072671 4.6019925176496
14.4889757968931 14.6134662335807 P P P 14.7331670071898 15.3008173308177 15.191343871378
P P P LNCV6_137919_PI430048170 mRNA
GCTTAACTGACAGACGTTAAAGCTTTCTGGTTAGATTGTTTTCACTTGGTGATCATGTCT NM_006082RefSeq chr12
- 49127783 49131521 TUBA1B10376 "tubulin, alpha 1b"
GO:0003725|GO:0005515|GO:0005881|GO:0051258|GO:0005874|GO:0003924|GO:0000226|GO:0005525|GO:0006
184|GO:0030705|GO:0005198|GO:0006457|GO:0005200|GO:0051084|GO:0071353|GO:0007017|GO:0044267|GO:0
031625|GO:0070062|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133980_PI430048170 0.3547321753474041.44589070197938 2.45126941202193
1.70892116436571 1.34509419726522 A A A 0.8700720406471262.18585639884899
0.508662067960382A A A LNCV6_133980_PI430048170 mRNA
AAAGGAGAAGGAAATGGACCCTTTTCATTATGATTACCAGACCCTGAGGATTGGGGGACT NM_001204268 RefSeq
chr11 - 117820074 117877031 FXYD6-FXYD2 NA "FXYD6-FXYD2 readthrough, transcript variant 1"NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138742_PI430048170 0.9015617508275841.00518419693925 0.475054437264559
0.4137659247369530.488437627836417A A A 0.3075662207052240.374527803851386
0.650531136068551A A A LNCV6_138742_PI430048170 mRNA
GATGTGTGTCAATCAGTTCTCTGAATCTTTTACTGAAACTGAGACAGGAAAATAAAACTG NM_001263RefSeq chr4
+ 84582903 84651340 CDS1 1040 CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1
GO:0006661|GO:0005783|GO:0044281|GO:0007165|GO:0004605|GO:0005789|GO:0016024|GO:0004142|GO:0016
021|GO:0006644|GO:0006657|GO:0007602|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135911_PI430048170 0.79820693535366 0.9323270529914422.14389474810965
0.3645959634405410.972213268804321A A A 1.49759712325292 1.97447797903715
0.557749738509932A A A LNCV6_135911_PI430048170 mRNA
CAGAAATACATTAAGTGGGCTGGTCTCATGTAGTCCCCACATCATTGCAAATTACAAACC NM_001204118 RefSeq
chr19 + 14583083 14611144 CLEC17A NA "C-type lectin domain family 17, member A, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140973_PI430048170 0.32820409730612 1.03070731334239 0.564872396994478
0.6133837612384390.506124756067838A A A 0.5636522888351190.495755358927244

0.494983189206645 A A A LNCV6_140973_PI430048170 mRNA
CAGCTTTGGCATGACTGTTTGTCTCGAAAACCAATAAACTCAAAGTTTAGAAAAACTCAA NM_173076 RefSeq chr2
- 214931541 215138428 ABCA1226154 "ATP-binding cassette, sub-family A (ABC1), member 12, transcript
variant 1"
GO:0005515|GO:0097209|GO:0005886|GO:0005743|GO:0031424|GO:0061436|GO:0010875|GO:0005829|GO:0045
055|GO:0005737|GO:0034191|GO:2000010|GO:0043129|GO:0019725|GO:0035627|GO:0048286|GO:0005102|GO:0
055088|GO:0005524|GO:0072659|GO:0033700|GO:0034040|GO:0008152|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_89049_PI430048170 0.0183729727928176 1.32736461247591 10.2167721457184
10.3704209630676 10.4961014495918 P P P 9.9571354234557 9.8460787438012
10.0599769040685 P P P LNCV6_89049_PI430048170 mRNA
GCTTTACTCTACAAATGGGATATGAAATGTGTCCACATTCCTCTTGAGTCTTTTGATGCA NM_001206987 RefSeq
chr17 + 76726829 76733881 METTL23 124512 "methyltransferase like 23, transcript variant 6"
GO:0005737|GO:0008168|GO:0016021|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59266_PI430048170 0.33712032014553 1.02474126049586 0.3475953054876590.259721744388339
0.337556549474402 A A A 0.2806870252061750.2741418069665770.285835544301859 A A A
LNCV6_59266_PI430048170 mRNA
CTGGCTATTTGCCTCAGAATATTCCTCTGGAGATTATCAGATACCTGTCTGAGGAGAAGG NM_013381 RefSeq chr12
+ 72272748 72665642 TRHDE 29953 thyrotropin-releasing hormone degrading enzyme
GO:0007165|GO:0005887|GO:0004177|GO:0007267|GO:0006508|GO:0008270|GO:0008237|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127348_PI430048170 0.0721690967523786 1.19633135558898 7.60925841359368
7.76296763576007 7.88150678533056 P P P 7.58830375248973 7.53646429986111
7.35577994995203 P P P LNCV6_127348_PI430048170 mRNA
TGACAAAGTTTATATTTGTAACATCAGCCTTCCTCGCCCATCTCTTTCCATCTGTCTCTT NM_001291964 RefSeq chr6
+ 167827634 167972020 MLLT4 4301 "myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog,
Drosophila); translocated to, 4, transcript variant 4"
GO:0005515|GO:0030054|GO:0005886|GO:0034329|GO:0007267|GO:0045177|GO:0032854|GO:0008022|GO:0045
216|GO:0005829|GO:0007165|GO:0005737|GO:0005913|GO:0005911|GO:0005654|GO:0007155|GO:0050839|GO:0
017016|GO:0034332. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143173_PI430048170 0.0234016035722224 0.7436003183003987.57140074224553
7.42526458687789 7.25554825569709 P P P 7.81729334825422 7.98768354079828
7.73508514618364 P P P LNCV6_143173_PI430048170 mRNA
AGCTGGTCCTACTTGGCCTCTTGAAAACCATTCCATCATTGTGCCAATCTAGCCTGAAAA NM_032317 RefSeq chr7
- 73680917 73683451 DNAJC30 84277 "DnaJ (Hsp40) homolog, subfamily C, member 30"
GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98516_PI430048170 0.3051452781320960.8231324177242617.7421395255071 7.90991107985374
8.28231979165929 P P P 8.12733182703719 8.04019719193785 8.5986484428045 P P P
LNCV6_98516_PI430048170 mRNA
GATGCTTCTGGAGCAAAACTTGATTACCGTCGATATGCAGAAACACTCTTTGACATTCTG NM_001207067 RefSeq
chr2 + 200811545 200823846 BZW1 9689 "basic leucine zipper and W2 domains 1, transcript variant
1" GO:0006355|GO:0005737|GO:0016020|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127972_PI430048170 0.3532320428134751.02426065569493 0.483097571620629
0.5444875294221950.447240015353472 A A A 0.4513127619177660.458120531361597
0.463299148134927 A A A LNCV6_127972_PI430048170 mRNA
CTTCGAATGTGGAGCCTGAAGATCTAAGATCCTAACATGTACATTTTATGTAAATATGTG NM_030916 RefSeq chr1
- 161070990 161089595 PVRL4 81607 poliovirus receptor-related 4
GO:0005515|GO:0005912|GO:0005886|GO:0034329|GO:0016032|GO:0016021|GO:0007155|GO:0045216|GO:0070
062|GO:0034332 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_138886_PI430048170 0.00183445390516416 0.32298700519868 5.911766071263
5.76301229037488 5.72275603713527 P P P 7.23102352675338 7.37258432743066
7.65884127448849 P P P LNCV6_138886_PI430048170 mRNA
GTTCTTATGTGACCATGTACCAAGCCAGCTATAAAGTATTGTATTTCTGTAGAATATGGA NM_001099666 RefSeq
chr9 - 69709521 69759960 PTAR1 375743 protein prenyltransferase alpha subunit repeat containing 1
GO:0018342|GO:0008318 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129824_PI430048170 0.1240321613617081.58550420824772 5.99646524070276
6.60105878416092 6.23403609699188 P P P 5.90454631629582 5.83429098366427
5.00053197084674 P P P LNCV6_129824_PI430048170 mRNA
ACATGTCCAGTGGGAGGTGAGACCACCTCTCAATATTCAATAAAGCTGCTGAGAATCTAG NM_000482RefSeq chr11
- 116820701 116823295 APOA4 337 apolipoprotein A-IV
GO:0005515|GO:0006695|GO:0035634|GO:0007603|GO:0006982|GO:0010898|GO:0030300|GO:0005615|GO:0042
803|GO:0034361|GO:0034364|GO:0019430|GO:0034445|GO:0042744|GO:0070062|GO:0042632|GO:0033344|GO:0
016209|GO:0032374|GO:0009986|GO:0005507|GO:0043691|GO:0065005|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_105003_PI430048170 0.0873840464929326 0.6366071782194976.09981851423878
5.41289751200257 5.39115014244532 P P P 6.25550806620009 6.4631284292559
6.24703213196391 P P P LNCV6_105003_PI430048170 mRNA
TCTGTGAGTGTGTGTGTGTCTGAGTGTTATTCTGAACAGCTTGTAAATATTGTAGTTGTT NM_014982RefSeq chr14
+ 70907404 71115382 PCNX 22990 pecanex homolog (Drosophila) GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_104423_PI430048170 0.0339087422601991 1.30539333426072 11.0095763685653
10.7574630729499 11.0568193387601 P P P 10.4270149148343 10.6665080747804
10.5842959456364 P P P LNCV6_104423_PI430048170 mRNA
ATTTTTCGCCCTTTCTACAGACACTGGGCCATCTATGTTGGCGATGGATATGTGGTTCAT NM_007069RefSeq chr11
- 63574470 63614437 PLA2G16 11145 "phospholipase A2, group XVI, transcript variant 1"
GO:0005515|GO:0052739|GO:0048471|GO:0005783|GO:0036149|GO:0052740|GO:0044281|GO:0005575|GO:0045
786|GO:0005829|GO:0016042|GO:0036150|GO:0004623|GO:0008970|GO:0016021|GO:0006644|GO:0036151|GO:0
046474|GO:0036152. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103892_PI430048170 0.533175110092356 1.18094451175336 2.33215394695108
2.61500592934095 3.21109954192322 A A P 2.61676528938307 2.28549735961341
2.65173108600561 P A P LNCV6_103892_PI430048170 mRNA
GTGCAAACCTTCATCAGTACCAGAAGTGTTACAGTATAGAGCAACCCTTAAGAAGGGATA NM_003435RefSeq chr19
+ 57614461 57622268 ZNF134 7693 zinc finger protein 134
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132808_PI430048170 0.6742116557176641.02032051304928 0.299381397623393
0.3074392700728760.466820249462391 A A A 0.3431869238016510.298658667441311
0.350440914872109 A A A LNCV6_132808_PI430048170 mRNA
TCCTGACTTTGTCTTAAGTGCATTCACGCACTTACTCTTGGCCTTATGTACACAGCCTTG NM_133369 RefSeq chr5
+ 176810558 176880898 UNC5A 90249 unc-5 homolog A (C. elegans)
GO:0043065|GO:0005886|GO:0007411|GO:0016021|GO:0097190|GO:0033564 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_126866_PI430048170 0.211917396621227 1.46455504242842 0.994670470560413
0.412962133130511 1.36401569672331 A A A 0.371701963428527 0.437662399851096
0.463526727355219 A A A LNCV6_126866_PI430048170 mRNA
TTTGGACATCTAACGAGCAGCTGTGCCAGAGGCTGGACCACACAGGAGAAGCTCGGACTT NM_015985 RefSeq
chr20 - 872653 916317 ANGPT4 51378 angiopoietin 4
GO:0030971|GO:0043066|GO:0071456|GO:0050731|GO:0005576|GO:0001525|GO:0050900|GO:0005615|GO:0045

766|GO:0010595|GO:0043536|GO:0007171|GO:0030297|GO:0007596|GO:0001935|GO:0016525|GO:0043537 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126720_PI430048170 0.00120237727230192 2.46607963940249 6.07023825206329 5.90317809674638 5.6910778069427 P P P 4.49304149431291 4.72962572812093 4.54931728352977 P P P LNCV6_126720_PI430048170 mRNA TGAGAAAGACTCCAACTTCCAGAACCCATTTAAAATCGACCGCACAGAGTTCATTCCCAG NM_024821 RefSeq chr22 + 41800621 41826299 CCDC134 79879 "coiled-coil domain containing 134, transcript variant 1" GO:0016020|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138891_PI430048170 0.525647747389457 1.20699947476214 1.31361668608791 0.523785075635868 0.422882426140278 A A A 0.430621773353736 0.617379518519748 0.564912870703822 A A A LNCV6_138891_PI430048170 mRNA CCCTAATTTGCTAGTGGGAAGAAAAATAGCTGAGCTTTCTAAAATGATAGCTCTCTATTT NM_000452 RefSeq chr13 - 103043997 103066846 SLC10A2 6555 "solute carrier family 10 (sodium/bile acid cotransporter), member 2" GO:0000502|GO:0005886|GO:0008508|GO:0005634|GO:0044281|GO:0055085|GO:0005902|GO:0016324|GO:0005887|GO:0015721|GO:0006810|GO:0008206|GO:0006814 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142297_PI430048170 0.14442131685587 0.581347756870989 7.22251446559838 7.41423590461684 7.17717682586938 P P P 7.3924489482061 8.46685180996322 8.1159373498809 P P P LNCV6_142297_PI430048170 mRNA AAGAAGTAACTACAGTTAGGGCTCCTATTCAACACACACATGCTTCCCTTTCCTGAGTCC NM_198235 RefSeq chr14 - 20801355 20802877 RNASE1 6035 "ribonuclease, RNase A family, 1 (pancreatic), transcript variant 1" GO:0005515|GO:0004522|GO:0003676|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138079_PI430048170 0.200760775734909 1.20506660844644 9.6239486557476 9.63180957427818 10.039826399496 P P P 9.32171719803421 9.54492326292566 9.64341333465847 P P P LNCV6_138079_PI430048170 mRNA TAAAACATCCTAACTTGTTTTTCAAGCTCACTCAGGCCTACGCCAAACGTTTCTGTTTTT NM_002814 RefSeq chrX - 108084204 108091644 PSMD10 5716 "proteasome (prosome, macropain) 26S subunit, non-ATPase, 10, transcript variant 1" GO:0005515|GO:0002474|GO:0010467|GO:0030307|GO:0090263|GO:0032436|GO:0045737|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0043409|GO:0034641|GO:0005737|GO:0000082|GO:0090201|GO:0031398|GO:0016032|GO:0045111|GO:0090090|GO:0006977|GO:0000209|GO:0043066|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145231_PI430048170 0.546910293650197 0.979487483338285 0.357142812355352 0.432663179106335 0.339405427582528 A A A 0.474893029809062 0.364539189231012 0.378673824846909 A A A LNCV6_145231_PI430048170 mRNA TTCTTTCTGGAATGGTTTTCTTTTCCATTTTCATTACCACCTTTGCTTGGAAAAGAATGG NM_144673 RefSeq chr16 + 66579447 66588274 CMTM2 146225 "CKLF-like MARVEL transmembrane domain containing 2, transcript variant 1" GO:0006935|GO:0005654|GO:0016021|GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51669_PI430048170 0.426177258619119 0.382988829161646 0.381199558994582 0.367440216427961 0.262666581918746 A A A 2.88529611279277 0.331242299074012 0.327539810886891 P A A LNCV6_51669_PI430048170 mRNA TATGAGTAATACCTTGCATTTGGTTAGTACAGTAGGTTGGGCAAGTGATATTATGTAGGA NM_001135036 RefSeq chr17 - 15536979 15563631 TVP23C 201158 "trans-golgi network vesicle protein 23 homolog C (S. cerevisiae), transcript variant 2" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131836_PI430048170 0.12908145452666 0.9053603677647 11.4977207146902

11.6147210384529 11.5015973791076 P P P 11.6706223203085 11.7881560423587 11.5811658168247 P P P LNCV6_131836_PI430048170 mRNA TGAGGAGACCTGTGGGCCACCTATTGTCTAATAAAGTGGGCAGTTGCCCCCATCTGGTGG NM_004461 RefSeq chr19 - 12922469 12933744 FARSA 2193 "phenylalanyl-tRNA synthetase, alpha subunit" GO:0005515|GO:0010467|GO:0005737|GO:0000049|GO:0016020|GO:0006432|GO:0004826|GO:0005524|GO:0006418|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57612_PI430048170 0.00506088084360917 1.56371818243238 5.07677427482331 4.82770014977643 4.81935149488922 P P P 4.35047862393971 4.28666384026407 4.16040863221031 P P P LNCV6_57612_PI430048170 mRNA ACCACCAGGAGGATTTCAAGAAAGCACCAAAGACCAGGGAGCTCGGATCCATACTCGGGG NM_013401 RefSeq chr11 - 61897295 61917609 RAB3IL1 5866 "RAB3A interacting protein (rabin3)-like 1, transcript variant 1" GO:0005515|GO:0017112|GO:0032851|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133274_PI430048170 0.104672050767038 0.730814301770889 13.0498254400584 12.8778508865453 13.0745908130156 P P P 13.1615329258591 13.4167395688686 13.7322547113031 P P P LNCV6_133274_PI430048170 mRNA TTTGTACAGACATTATTTCCACTCTGGTGGATAAGTTCAATAAAGGTCATATCCCAAACA NM_002106 RefSeq chr4 - 99948086 99950355 H2AFZ 3015 "H2A histone family, member Z" GO:0005515|GO:0001740|GO:0046982|GO:0005719|GO:0031492|GO:0005634|GO:0000978|GO:0000979|GO:0031490|GO:0005720|GO:0071392|GO:0045944|GO:0000980|GO:0000786|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132404_PI430048170 0.422247374913392 1.25871186239924 1.29475610470579 0.414987725441329 0.527895902836955 A A A 0.449893057301128 0.511432954017198 0.4461709892424 A A A LNCV6_132404_PI430048170 mRNA GGTGTTGTATATAGAGTGGAATCTCTTGGATGCAGCTTCAAGAATAAATTTTTCTTCTCT NM_001804 RefSeq chr5 + 150166780 150184558 CDX1 1044 caudal type homeobox 1 GO:0005515|GO:0060349|GO:0045944|GO:0009887|GO:0001205|GO:0005634|GO:0000980|GO:0009952 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68374_PI430048170 0.552042915423155 0.848892185262702 2.7114235410387 1.8808240747917 2.91350437187512 A A P 2.3308958020679 2.78196681174163 3.17321540000859 A P P LNCV6_68374_PI430048170 mRNA TTTAGACCCACCATCTTCAGATCTGCAACTTTAAAATGGAAAGAAAGCCTAATGAGTCGG NM_001244949 RefSeq chr10 - 112149863 112183779 GPAM 57678 "glycerol-3-phosphate acyltransferase, mitochondrial, transcript variant 1" GO:0006637|GO:0070970|GO:0005886|GO:0070236|GO:0005743|GO:0055089|GO:0004366|GO:0005741|GO:0044281|GO:0009749|GO:0042104|GO:0051607|GO:0006631|GO:0016024|GO:0019432|GO:0055091|GO:0050707|GO:0016021|GO:0040018|GO:0006644|GO:0006654|GO:0044255|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136675_PI430048170 0.358770209656757 1.03549667224331 0.294844672089444 0.270618082731766 0.405806702821454 A A A 0.288420777383424 0.256016063415761 0.279301648902389 A A A LNCV6_136675_PI430048170 mRNA GTCCGATATGAATCACAACGTGGGTGAATGTAGTATTTTCCTGAAGTGTGAAAGACTTAA NM_182848 RefSeq chr13 + 95433598 95579756 CLDN10 9071 "claudin 10, transcript variant a" GO:0005737|GO:0016338|GO:0005886|GO:0005198|GO:0016021|GO:0005923|GO:0007155|GO:0042802|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132885_PI430048170 0.625525251728088 1.01477771587606 0.366933158025846 0.248590686866874 0.287229638742671 A A A 0.26801264257604 0.304261245088673 0.269229084259783 A A A LNCV6_132885_PI430048170 mRNA CTCTGTAATTATTGTGTATTCTACCCTGTTGCAAAGGAAATAAAGCATAGGGTAGTTTGC NM_017534 RefSeq

chr17 - 10521147 10549700 MYH2 4620 "myosin, heavy chain 2, skeletal muscle, adult, transcript variant 1"
GO:0005515|GO:0014823|GO:0005516|GO:0005826|GO:0030049|GO:0005794|GO:0003779|GO:0030016|GO:0030017|GO:0005524|GO:0005829|GO:0043234|GO:0032982|GO:0000146|GO:0006936|GO:0005911|GO:0045087|GO:0008152|GO:0061024|GO:0001778|GO:0005859|GO:0038096|GO:0031672 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136293_PI430048170 0.05049695268182 0.817679994793359 12.4475053284403 12.5914207403609 12.7356116223045 P P P 12.9918311727402 12.8211820699785 12.8409638532931 P P P LNCV6_136293_PI430048170 mRNA
ATCGTAGCTTATGTTTTCCTCCTCTTGGCTCCATTGCTGTTAGCATAGAGTTTTAAAAAA NM_032575 RefSeq
chr16_KI270855v1_alt + 32587 39961 GLIS2 84662 GLIS family zinc finger 2
GO:0005515|GO:0044212|GO:0005634|GO:0045879|GO:0000122|GO:0046872|GO:0006351|GO:0030154|GO:0043433|GO:0007399|GO:0001077|GO:0005737|GO:0016607|GO:0045944|GO:0045893|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128608_PI430048170 0.342348216050983 1.4809597144261 1.48826716906443 0.281842932670297 0.465639232883197 A A A 0.29677215710066 0.25910368309827 0.289996997696202 A A A LNCV6_128608_PI430048170 mRNA
TTATTAATTAAGGTAAAATTTACATATGGTGAGATGCATGCTCTTCAGTGGAGACCCAGC NM_000744 RefSeq
chr20 - 63343309 63361396 CHRNA4 1137 "cholinergic receptor, nicotinic, alpha 4 (neuronal), transcript variant 1"
GO:0051899|GO:0030054|GO:0005886|GO:0007268|GO:0014059|GO:0030425|GO:0045211|GO:0015464|GO:0042391|GO:0043025|GO:0042166|GO:0006816|GO:0007626|GO:0006979|GO:0035640|GO:0006811|GO:0015276|GO:0001666|GO:0007585|GO:0007271|GO:0005892|GO:0019233|GO:0035095|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136442_PI430048170 0.00662120534267327 0.527748067872226 5.21289774674008 5.31580808413885 5.58008919087647 P P P 6.04779621314597 6.30819718090925 6.50775402749743 P P P LNCV6_136442_PI430048170 mRNA
ACTATGAGTGACTTACATGTGTTTTAAAATGTCAGTGTGTTTCCCAGAGGCAGAAATAAA NM_152707 RefSeq
chr10 - 68482332 68527523 SLC25A16 8034 "solute carrier family 25 (mitochondrial carrier), member 16"
GO:0015297|GO:0015939|GO:0006766|GO:0006810|GO:0005743|GO:0006767|GO:0009108|GO:0044281|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129293_PI430048170 0.1229919731028 1.41773584876111 5.7176019447254 6.03587445360687 5.90201390808117 P P P 5.65984860756418 5.47731693255887 4.92922778865113 P P P LNCV6_129293_PI430048170 mRNA
TTGTTTACTTGACTGAATCCCTTCCTTTTCCAGAAACCTTGAGCCTCCTCCACTGGTTTG NM_018958 RefSeq chr15 + 24675393 24683446 NPAP1 23742 nuclear pore associated protein 1
GO:0003674|GO:0005637|GO:0007275|GO:0005654|GO:0007283|GO:0030154|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128244_PI430048170 0.00682369766955609 0.157161071296839 4.7917472299515 4.22494373431233 4.3556627142648 P P P 6.40766197620124 7.263458260467 7.54653849976801 P P P LNCV6_128244_PI430048170 mRNA
ACACAGTAGCAAAAGAGAAGATCTCATTTACAAATATCTATGGTGTTTCCTTGTTCTGTG NM_002867 RefSeq
chr1 - 51907955 51990764 RAB3B 5865 "RAB3B, member RAS oncogene family"
GO:0005515|GO:0048471|GO:0009306|GO:0005886|GO:0003924|GO:0006886|GO:0006904|GO:0005829|GO:0005737|GO:0019882|GO:0051586|GO:0017157|GO:0032482|GO:0070062|GO:0005525|GO:0016079|GO:0031982|GO:0072659|GO:0008021|GO:0006184|GO:0018125|GO:0031489|GO:0019003|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137772_PI430048170 0.776316152376747 1.05974618198814 4.15484983112062

3.78781351428894 4.44451788258891 P P P 4.00438678106717 4.28955551225232
3.88585399364992 P P P LNCV6_137772_PI430048170 mRNA
CTGACCACTATGGGAGGTGAAATTCTGGCCTACCTTCTCACCAACAAACCTGTCAAAAAA NM_001205119 RefSeq
chr11 + 46617275 46676018 ATG13 9776 "autophagy related 13, transcript variant 3"
GO:0005739|GO:0005515|GO:0070969|GO:0019901|GO:0000407|GO:0000045|GO:0034273|GO:0005829 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_144770_PI430048170 0.361360269256247 0.576387343978169 0.6318988072531
2.73478045729676 1.00914087051381 A A A 1.1851672236345 2.88283203818399
3.01423854541831 A P P LNCV6_144770_PI430048170 mRNA
TAGCACTGGTACCGCAAACATTTTACTTAAACTCTTAATAGCATTTCTTTCGCCAGATAC NM_001129993 RefSeq
chr2 + 61065870 61124278 KIAA1841 84542 "KIAA1841, transcript variant 1" NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_59252_PI430048170 0.0357672345458268 0.710287841066457 5.05371870487716
5.44155042931322 5.39060601297179 P P P 5.73022452129368 5.66138202065027
5.98436160438766 P P P LNCV6_59252_PI430048170 mRNA
AAAGTTAAAGATGGAGCAAAACCACTTTCCCTGAAATCCGACACTACTGATTCTAGTCAA NM_144982 RefSeq
chr12 - 71609600 71663969 ZFC3H1 196441 "zinc finger, C3H1-type containing"
GO:0005622|GO:0005515|GO:0006396|GO:0005615|GO:0046872 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129780_PI430048170 0.0235047127408709 0.43994626339108 2.90767838051537
3.2197324491254 2.3798046601821 A P A 3.75551769755855 3.84825436457102
4.46951071391675 P P P LNCV6_129780_PI430048170 mRNA
CTTAATGTCTTTGATTGCTGGACATGAAACAAACTGCCAATTAAATTTTGCGGAGACAAA NM_005544 RefSeq
chr2 - 226731316 226798790 IRS1 3667 insulin receptor substrate 1
GO:0005515|GO:0008286|GO:0010468|GO:0034504|GO:0008284|GO:0005886|GO:0005159|GO:0005158|GO:0043
434|GO:0005634|GO:0030879|GO:0060397|GO:0036064|GO:0043231|GO:0005829|GO:0010907|GO:0005737|GO:0
043552|GO:0007173|GO:0046326|GO:0005899|GO:0005080|GO:0005068|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_105805_PI430048170 0.400723224202751 0.90654806285708 5.13173955148634
4.96360389903791 5.43491245781528 P P P 5.24308802231644 5.27366731251709
5.46774226001688 P P P LNCV6_105805_PI430048170 mRNA
CTTTCTAGCAGCAGATCTGTAGTTTGTATAGCCTCAACAACAATTTTAAATAAGATGGAG NM_001024956 RefSeq
chr11 + 121292867 121313410 SC5D 6309 "sterol-C5-desaturase, transcript variant 2"
GO:0006629|GO:0006695|GO:0050046|GO:0033490|GO:0005506|GO:0000248|GO:0005789|GO:0006633|GO:0044
281|GO:0016021|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129446_PI430048170 0.740308232810084 0.838111911639844 2.06179255379703
1.09626871337866 0.311549964514317 A A A 2.36635583593483 0.701988267248239
1.15711972458571 A A A LNCV6_129446_PI430048170 mRNA
CTCGATGCCCCTCAACGGATGTACAGTGAAATCATAGCTTTAATGAAGGCATATTCCTAA NM_001102469 RefSeq
chr10 + 88761405 88778242 LIPN NA "lipase, family member N" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_68255_PI430048170 0.47885288464714 0.904256180931128 6.57850634282947
6.18685053196175 6.33168010978524 P P P 6.29232807544493 6.76654816648909
6.46061823900332 P P P LNCV6_68255_PI430048170 mRNA
TGGCACTGTTGGAGTCAGTGCTGCGCCATGTTGGACTCAATGAAGTGCACAAGGCTGTGG NM_014856 RefSeq
chr1 - 153929500 153946678 DENND4B 9909 DENN/MADD domain containing 4B
GO:0017112|GO:0005794|GO:0032483|GO:0032851|GO:0005654|GO:0005634 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_134929_PI430048170 0.137411704614538 1.07480981692618 10.7450354588186

10.6925499759907 10.7368220219594 P P P 10.531075830243 10.685361445733
10.6419216820101 P P P LNCV6_134929_PI430048170 mRNA
AAACAGTTGGGGAACTAGGGAGAAAACCAGACCATTAAAACTGTTTGTGGTCGAATCTCC NM_001304763 RefSeq
chr1 + 151282311 151291905 ZNF687 57592 "zinc finger protein 687, transcript variant 1"
GO:0006355|GO:0005730|GO:0005634|GO:0003677|GO:0046872|GO:0006351|GO:0043231 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144783_PI430048170 0.447915277942545 1.10872747227402 13.6841713027404
13.823194556154 14.1091284479871 P P P 13.7271362297053 13.5048731621478
13.938311218317 P P P LNCV6_144783_PI430048170 mRNA
CGGTGGTCAGACATGGAAATGGTGGGGAGACAAAAATATACATGTGAAATAAAACTCAGT NM_002520 RefSeq
chr5 + 171387703 171410884 NPM1 4869 "nucleophosmin (nucleolar phosphoprotein B23,
numatrin), transcript variant 1"
GO:0060735|GO:0005515|GO:0008285|GO:0007098|GO:0003723|GO:0060699|GO:0032071|GO:0005634|GO:0046
599|GO:0051259|GO:0006886|GO:0042803|GO:0005829|GO:0042393|GO:0005737|GO:0051092|GO:0008104|GO:0
016032|GO:0043023|GO:0043024|GO:0043066|GO:0005813|GO:0051059|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127514_PI430048170 0.84034577301721 1.14079279841572 1.59142275011383
0.451220960596858 0.252163480254873 A A A 0.391173347196458 1.14970680475886
0.437089571693594 A A A LNCV6_127514_PI430048170 mRNA
CATGACATTGGAAGAAGGTGGTCATAGCTCTACCTTTAATATACCAATAAAATAAACAGC NM_006249 RefSeq
chr12_KI270904v1_alt - 460876 464670 PRB3 5544 proline-rich protein BstNI subfamily 3
GO:0050829|GO:0008150|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72417_PI430048170 0.140429231736357 0.762080656345414 11.0881409341775 11.0883797043218
10.8478427040201 P P P 11.6068362294097 11.4945514500511 11.0552139600984 P P P
LNCV6_72417_PI430048170 mRNA
TCTTTGGGGCTTCTCCCTCCCGTTTCAGGGGAAAGGTCTGAGTCTCCACGTTTCAGACCA NM_001195072 RefSeq
chr22 - 38219290 38273034 TMEM184B 25829 "transmembrane protein 184B, transcript variant 3"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140210_PI430048170 0.0808793525567014 0.666573826588812 2.8706627306902
2.49090197203677 3.09623891011106 A A P 3.25689197329083 3.75798223454325
3.19330440795784 P P P LNCV6_140210_PI430048170 mRNA
CAGCTTAACAATAGAACAGTTGAAACAAAAAGCAGATAAGAGAGTCAGAAGTGTTCGCTANM_022494 RefSeq chr10
- 112430289 112446959 ZDHHC6 64429 "zinc finger, DHHC-type containing 6, transcript variant 1"
GO:0018345|GO:0005783|GO:0016409|GO:0005789|GO:0008270|GO:0016021|GO:0019706 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_54463_PI430048170 0.3287152884370091.26072872335143 4.84466049283604 5.37903005642357
4.88297491255726 P P P 5.2039718367491 4.31913787116166 4.48435202700882 P P P
LNCV6_54463_PI430048170 mRNA
CTGCAGTACCTGAGCTCCAAGTTCCAGATGCATGTGCTACTCAATGAGATGAAGGAGCTG NM_001257360 RefSeq
chr1 + 109619812 109632055 AMPD2 271 "adenosine monophosphate deaminase 2, transcript variant 4"
GO:0097009|GO:0003876|GO:0006144|GO:0032264|GO:0043101|GO:0055086|GO:0052652|GO:0044281|GO:0005
575|GO:0006188|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130469_PI430048170 0.0298874238650319 0.3684812076970478.64087563091209
8.22982213659816 8.55343628174905 P P P 9.29656168237122 9.97665994191385
10.3232726685449 P P P LNCV6_130469_PI430048170 mRNA
TTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCACTCCCTGTTTTAATTCAACCCAGCNM_002483 RefSeq chr19 +
41755519 41772208 CEACAM6 4680 carcinoembryonic antigen-related cell adhesion molecule 6 (non-
specific cross reacting antigen)
GO:0005515|GO:0007165|GO:0005886|GO:0007596|GO:0005887|GO:0007267|GO:0031225|GO:0050900 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131861_PI430048170 0.0739168319479071 0.2869878565931221.27079483223791
0.29378054333252 2.39797518984179 A A A 3.42790924992157 3.14749524637518
3.51363953426468 P P P LNCV6_131861_PI430048170 mRNA
CTTCTTCAGGATTAAAAACGATGATGACCTCATCTTAGAGCCCTAAAGGGAAATGCTTAT NM_005151RefSeq chr18
+ 158482 213739 USP14 9097 "ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase), transcript variant 1"
GO:0005515|GO:0016579|GO:0000502|GO:0004843|GO:0004866|GO:0005886|GO:0009986|GO:0045202|GO:0007268|GO:0008193|GO:0005634|GO:0004197|GO:0010951|GO:0005737|GO:0061136|GO:0050920|GO:0070628|GO:0016023|GO:0043161|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135689_PI430048170 0.1775353150573370.8021597013297371 0.8130325321556
11.0233672960127 11.282384201608 P P P 11.2060109809689 11.2305028550459 11.633682085314
P P P LNCV6_135689_PI430048170 mRNA
ACTGTTATGTTTTATCTGCCCATTTATCTTTCTTAGTTACCAGGAGAAATGTGTGACACCNM_017549RefSeq chr7 +
37920560 37951940 EPDR1 54749 "ependymin related 1, transcript variant 1"
GO:0007160|GO:0005509|GO:0005764|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132034_PI430048170 0.0129562928304556 0.72348886570491111.8212845649708
11.7555617989258 11.6946440180306 P P P 12.0703579631563 12.3076913502227
12.2853970168275 P P P LNCV6_132034_PI430048170 mRNA
GCTGGCGTGTTACATCTCCATTTAAGGTTTCCTTTGAACAAAAGGTCTGTGGCTAAAAAA NM_001304372 RefSeq
chr22 - 41938720 41946754 CENPM 79019 "centromere protein M, transcript variant 6"
GO:0034080|GO:0006334|GO:0000777|GO:0005654|GO:0000278|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130231_PI430048170 0.00961741615594566 0.53767057775173511.5277784320189
11.6724509778688 11.732320790441 P P P 12.2978494135479 12.5530809800155
12.7408838987212 P P P LNCV6_130231_PI430048170 mRNA
CCGTGTGAATGTGAAGAAAAGCAGTATGTTACTGGTTGTTGTTGTTGTTCTTGTTTTTTA NM_004419RefSeq chr10
+ 110497866 110511544 DUSP5 1847 dual specificity phosphatase 5
GO:0005515|GO:0000188|GO:0001706|GO:0006470|GO:0005634|GO:0008138|GO:0035335|GO:0017017|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143798_PI430048170 0.0661689680783764 0.7856124203423618.9522368223309
8.66426083920464 8.94958633881159 P P P 9.12231051577223 9.08404951132736
9.40137621974967 P P P LNCV6_143798_PI430048170 mRNA
GGTTAGAGCTAGTGTATGTTACTGTGAATTGTAATGTAGTTGGATTGTACAAATTACTGC NM_021826RefSeq chr20
- 3146518 3159886 FASTKD5 60493 FAST kinase domains 5
GO:0005739|GO:0045333|GO:0004672|GO:0006468 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141029_PI430048170 0.1989333944377821.15989816958575 3.80945543320601
3.96979271172866 3.80059692371532 P P P 3.61527791856232 3.85712955385357
3.44141046210315 P P P LNCV6_141029_PI430048170 mRNA
TATGTCGGGCCACTGATTATCTGACTGACCATGAGATTGCTCATAACTTGTTTGTCACCC NM_001013657 RefSeq
chr15 + 90234254 90242080 GDPGP1 NA GDP-D-glucose phosphorylase 1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_111981_PI430048170 0.3902732194942750.8733289585195159.40037572116032
9.42262715338648 9.50940402502799 P P P 9.507712759647 9.41408481586987
9.94241705171208 P P P LNCV6_111981_PI430048170 mRNA
GCTCAGTTGCTTACAAGTTTCAGTGAGAAGAATTGAGAACTTTTCAGAGAAGATTTATGA NM_016033RefSeq chr8
- 86472348 86508780 RMDN1 51115 "regulator of microtubule dynamics 1, transcript variant 1"
GO:0005739|GO:0005813|GO:0000922|GO:0005874 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135941_PI430048170 0.0104088154930427 0.2405025282137670.437900271549177

0.3587228007412680.334691889084887A A A 1.96444576624878 2.58429995121031
2.65717812406364 A P P LNCV6_135941_PI430048170 mRNA
ATTTCCAACTAGTTCATCTGGAGGTAGGGAGGCTCCACTGGAAAAATAAATATTTTTGTC NM_018717RefSeq chr4
- 139716390 140154079 MAML3 55534 mastermind-like 3 (Drosophila)
GO:0010467|GO:0006367|GO:0016607|GO:0007219|GO:0045944|GO:0003713|GO:0005654|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138857_PI430048170 0.2663576191001 1.1740155843285 6.82896218680352
6.69289707433982 6.45501135471214 P P P 6.67638498075092 6.17193138962521
6.41461116499115 P P P LNCV6_138857_PI430048170 mRNA
GACCTCCGGTCACCTGCTTCCCCTTCTGTGCAAATAAACCAGGCTGTTATCTGGAAAAAA NM_001177317 RefSeq
chr9 + 137230756 137236554 SLC34A3 142680 "solute carrier family 34 (type II sodium/phosphate
cotransporter), member 3, transcript variant 2"
GO:0005886|GO:0035435|GO:0031526|GO:0055085|GO:0005436|GO:0016324|GO:0044341|GO:0015321|GO:0030
643|GO:0006817|GO:0035725|GO:0016021|GO:0006814|GO:0006811 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129386_PI430048170 0.8454576442218971.00429516281731 0.301224878786157
0.3388292349293690.387947551964036A A A 0.3543495264134980.337061890283627
0.319137919344591A A A LNCV6_129386_PI430048170 mRNA
GACATGAAACTCGCTCTGAGAAATGTCCTGTTTGGAATGAGAATTCGTCAAAATTCGTGA NM_001004479 RefSeq
chr14 + 20242791 20243766 OR11H4 NA "olfactory receptor, family 11, subfamily H, member 4"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63146_PI430048170 0.0133382153567736 1.12639867692502 12.6452247857505
12.6246455290004 12.7228445584443 P P P 12.439672566606 12.5280221085361
12.5102315051663 P P P LNCV6_63146_PI430048170 mRNA
CAGGCAGGGAGGAGGCGGAGGTGGCAAATAAACCTGGGCAATTTTGTTTATACAAAAAAT NM_007241RefSeq
chr17 - 48930095 48944792 SNF8 11267 "SNF8, ESCRT-II complex subunit"
GO:0005515|GO:0005667|GO:0000814|GO:0006357|GO:0043328|GO:0006351|GO:0042803|GO:0005829|GO:0005
737|GO:0016197|GO:0031902|GO:0061024|GO:0005654|GO:0070062|GO:0008134 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136300_PI430048170 0.3693122852270850.94410287326821 0.303959207646587
0.3437629705736550.374818409760294A A A 0.3703285393670580.557785348759793
0.334124615913456A A A LNCV6_136300_PI430048170 mRNA
CCTGAGCACTGGCTCTGTACAACTCAATTATAATTTTTTAAGAATCATACCTCTGTATAG NM_032812RefSeq chr10
+ 19816442 20289855 PLXDC284898 "plexin domain containing 2, transcript variant 1"
GO:0005515|GO:0007275|GO:0004872|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143331_PI430048170 0.1800251352326380.4439059361244811.11877632622608
0.6440546909557830.601778274805795A A A 1.47590710586583 2.785682505048
1.10698989580123 A P A LNCV6_143331_PI430048170 mRNA
GCCAGAGTGCTTGGCTCCTTGTTTATTAAAGTTCAGAAAGTGGTGGGAGAGTGTAAAAAA NM_152607RefSeq chr1
+ 54806062 54842264 C1orf177 163747 "chromosome 1 open reading frame 177, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140370_PI430048170 0.00820108861928012 0.2775945573030443.79792898860758
3.10741704568568 3.79282533927468 P P P 5.34594753602174 5.37724246457798
5.61012195107061 P P P LNCV6_140370_PI430048170 mRNA
CTCTTTACAAAATGGACCCATCGAGAATGTTGAAAAGCTTGGAAGTATCACTTTTGAAAA NM_031892RefSeq chrX
- 19533964 19887626 SH3KBP1 30011 "SH3-domain kinase binding protein 1, transcript variant 1"
GO:0005515|GO:0043005|GO:0017124|GO:0005886|GO:0008360|GO:0042059|GO:0007267|GO:0045202|GO:0006
915|GO:0005829|GO:0006897|GO:0007173|GO:0016477|GO:0005911|GO:0007010|GO:0005856|GO:0005925|GO:0

030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131073_PI430048170 0.3807363499291920.9606755347512516.81267360993715
6.75909201302255 6.81909385204403 P P P 6.95219354996711 6.8167121193966
6.79109239126004 P P P LNCV6_131073_PI430048170 mRNA
GCAGTGGGGCCAAGAAACAATATATATGAATGTGATACATGTGTTTAGTAAAATCTAGCT NM_032178RefSeq chr16
- 68300614 68310965 SLC7A6OS 84138 "solute carrier family 7, member 6 opposite strand"
GO:0005737|GO:0002244|GO:0005634|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52310_PI430048170 0.1268010990890281.20426081311348 10.6870253929378 10.8803306946298
11.0710604033699 P P P 10.6701380839921 10.5024650351749 10.6800718642905 P P P
LNCV6_52310_PI430048170 mRNA
ATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGCAGTATGTTCCCTCTGA NM_004872RefSeq chr1
- 54026680 54053438 TMEM59 9528 transmembrane protein 59
GO:0005515|GO:0005886|GO:0005770|GO:0005797|GO:0006914|GO:0090285|GO:0005765|GO:0005764|GO:0000
137|GO:0000139|GO:0004175|GO:0000138|GO:0031902|GO:0090005|GO:0006508|GO:0016021|GO:0010955|GO:0
070062|GO:0010508. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130746_PI430048170 0.9664784748224621.00417267713833 0.289184024029553
0.54726785613126 0.387098077655915A A A 0.5047191956232920.392791647999071
0.31343411556038 A A A LNCV6_130746_PI430048170 mRNA
CAATCATCTCTGAAGAGTTGCTGTTTCTTACTGACAATAAAAAATGTTCTCTTGGTTCGA NM_004946RefSeq chr5
+ 169637246 170083382 DOCK2 1794 dedicator of cytokinesis 2
GO:0005515|GO:0001771|GO:0030036|GO:0046633|GO:0007264|GO:0032855|GO:0045059|GO:0050690|GO:0005
829|GO:0012505|GO:0050766|GO:0042608|GO:0044351|GO:0006935|GO:0016020|GO:0001768|GO:0045060|GO:0
016032|GO:0001766|GO:0002277|GO:0005856|GO:0030675|GO:0030676|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128653_PI430048170 0.2686601518621391.11470138640947 5.60338906580694
5.48521013828343 5.75820646648385 P P P 5.43160490919903 5.30831287631401
5.63138875672922 P P P LNCV6_128653_PI430048170 mRNA
ACCATCTATAGTGAGCCTCTCCATAATTAGTGCCAACCATTAGTCTCGTTCATATTTTTA NM_007147RefSeq chr19
+ 51571277 51589738 ZNF175 7728 zinc finger protein 175
GO:0051607|GO:0006355|GO:0005737|GO:0003700|GO:0005654|GO:0045111|GO:0003677|GO:0046872|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139810_PI430048170 0.1356070756118070.7265623996525331 0.7986350164902
10.7201702829939 10.6131176769258 P P P 10.7798127689481 11.3911342820697
11.2791098646767 P P P LNCV6_139810_PI430048170 mRNA
ACAGCTGATCCTCGGGAAGAACAAAGCTAAAGCTGCCTTTTGTCTGTTATTTTATTTTTT NM_000937RefSeq chr17
+ 7484378 7514618 POLR2A5430 "polymerase (RNA) II (DNA directed) polypeptide A, 220kDa"
GO:0005515|GO:0008380|GO:0010467|GO:0006368|GO:0006367|GO:0006366|GO:0005634|GO:0001172|GO:0046
872|GO:0033120|GO:0003968|GO:0034587|GO:0005665|GO:0016032|GO:0035019|GO:0031625|GO:0000974|GO:0
006355|GO:0003899|GO:0005730|GO:0006370|GO:0003677|GO:0050434|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138304_PI430048170 0.3286938390353660.7089572612632312.41055087176863
0.7640281116235520.924938014593609A A A 1.63719180475937 2.26611117638061
2.21784727194819 A A A LNCV6_138304_PI430048170 mRNA
ATTTTAATCGGCTCCTGGAAACCTCACCCCAAATTGGAGATAGGCACTCCTCTTGTAGAA NM_001138RefSeq chr16
- 67482570 67483813 AGRP 181 agouti related neuropeptide
GO:0008343|GO:0007631|GO:0032868|GO:0060259|GO:0005796|GO:0060135|GO:0005102|GO:0009648|GO:0005
615|GO:2000253|GO:0009755|GO:0007218|GO:0043025|GO:0042755|GO:0005184|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135863_PI430048170 0.0682201219349164 1.16044497178849 12.193778569657

12.226696418664 12.0486107828698 P P P 11.8095229702841 12.0217278219742
11.9909717550661 P P P LNCV6_135863_PI430048170 mRNA
GCCTCGGACCCGGATTGCGTTTGCCTTAGCGGATATGTTTATACAGATGAATATAAAATG NM_024329RefSeq chr1
+ 15409894 15430343 EFHD2 79180 "EF-hand domain family, member D2" GO:0005509|GO:0045121
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144613_PI430048170 0.0206738119903023 0.1996605003101021.62574359394319
0.3916876290981610.387248653876926A A A 3.44955393552581 3.04053454647043
3.23646001387031 P P P LNCV6_144613_PI430048170 mRNA
AGATCACAGTTTCACAAATTGTGGTGTTGTTAGGTGACATTTAATATTTCTTGAGACCTC NM_006252RefSeq chr1
+ 56645316 56715335 PRKAA25563 "protein kinase, AMP-activated, alpha 2 catalytic subunit"
GO:0050405|GO:0005515|GO:0008286|GO:0006695|GO:0032007|GO:0004679|GO:0047322|GO:0044281|GO:0046
872|GO:0005829|GO:0031669|GO:0061024|GO:0006633|GO:0007050|GO:0042149|GO:0045821|GO:0016055|GO:0
044255|GO:0043066|GO:0006355|GO:0008610|GO:0006996|GO:0006853|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133607_PI430048170 0.2458560200357681.02102794394145 0.321205893375263
0.2610701423797160.273334678609794A A A 0.2544735513998780.255476320426799
0.25629555243276 A A A LNCV6_133607_PI430048170 mRNA
GGGTGTCCATATGCCACTTATGAGGAAGAAAGCACCATGACTTTTTTATTTTCAATAAAA NM_178013RefSeq
chr14_KI270847v1_alt - 832859 902982 PRIMA1 145270 proline rich membrane anchor 1
GO:0030054|GO:0031226|GO:0051649|GO:0045202|GO:0016021|GO:0043495|GO:0042135|GO:0019899 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135934_PI430048170 0.0144627364996875 1.54918640458066 6.23764733265553
6.29700418795132 6.11546150721773 P P P 5.7270762310048 5.64351225837429 5.3667534427451
P P P LNCV6_135934_PI430048170 mRNA
AGTTCACCTAAATGGGGGTCTCTATATGTTCAGGCCCAGGGGCCCCCATTGACAGGAGCT NM_016938RefSeq chr11
- 65866440 65872934 EFEMP230008 "EGF containing fibulin-like extracellular matrix protein 2, transcript
variant 1"
GO:0005515|GO:0007165|GO:0005886|GO:0030198|GO:0007596|GO:0005509|GO:0005576|GO:0031982|GO:0070
062|GO:0005604|GO:0005201|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129873_PI430048170 0.3186117247601481.03633608283045 0.38674253407196
0.2604932663636240.287759071945858A A A 0.2642733090717650.255681036101082
0.263629434888453A A A LNCV6_129873_PI430048170 mRNA
TTGTTTTACGCTAAAGATGGAAAAGAACTAGGACTGAACTATTTTAAATAAAATATTGGC NM_001140RefSeq chr17
- 4630918 4641665 ALOX15246 arachidonate 15-lipoxygenase
GO:0005515|GO:0019369|GO:0006646|GO:0034976|GO:0005886|GO:0010811|GO:0035358|GO:0044281|GO:0030
282|GO:0006691|GO:0035963|GO:0005829|GO:0006954|GO:0030838|GO:0071277|GO:0034116|GO:0070374|GO:2
001303|GO:0002820|GO:0005811|GO:0005506|GO:0019372|GO:0005546|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_76073_PI430048170 0.4247080450363610.9245445722176934.15971757563081 4.04483305447948
4.37435987204498 P P P 4.22421023068687 4.22041031735969 4.47803417993433 P P P
LNCV6_76073_PI430048170 mRNA
GTATGAAGGTGTAGGAAGAATCAGAAAAAGTCCTACCTGGAGCGAAGCGTTAAGGAAGCT NM_002622RefSeq
chr5 - 140245049 140303104 PFDN1 5201 prefoldin subunit 1
GO:0042113|GO:0007049|GO:0006355|GO:0030036|GO:0003700|GO:0006457|GO:0016272|GO:0051084|GO:0021
549|GO:0051082|GO:0044267|GO:0021537 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129918_PI430048170 0.0155449835317465 0.6858824732734567.34050900961956
7.45531310840371 7.34587638362576 P P P 8.03840371436018 7.74397603653011
7.97770570378335 P P P LNCV6_129918_PI430048170 mRNA
TCATATGCTGCCCTCCCTCAGATAATGAGGGAACCTGGGGTACTTAAAATGCCAAATGAA NM_001287525 RefSeq

chr7 - 101313366 101321823 IFT22 64792 "intraflagellar transport 22, transcript variant 5"
GO:0006184|GO:0005813|GO:0006996|GO:0003924|GO:0030992|GO:0072372|GO:0032482|GO:0019003|GO:0005
525|GO:0006886|GO:0012505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101643_PI430048170 0.542046573837965 1.12657843932868 11.2993265206129
10.9316911816506 11.286902319355 P P P 11.5481760182213 10.5453940872068
10.7310052814602 P P P LNCV6_101643_PI430048170 mRNA
TCCAGCTAGATTGCCTCTCCTGGACATGGCAATGATGAGTTTTTAAAAAACAGTGTGGAT NM_014685 RefSeq chr16
+ 56932089 56943881 HERPUD1 9709 "homocysteine-inducible, endoplasmic reticulum stress-
inducible, ubiquitin-like domain member 1, transcript variant 1"
GO:0006986|GO:0006511|GO:0034976|GO:0005783|GO:0032469|GO:2001243|GO:0034704|GO:0044325|GO:0030
968|GO:0032092|GO:0003674|GO:0016020|GO:0005789|GO:0031396|GO:0043154|GO:0006987|GO:0044267 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130991_PI430048170 0.587495970434188 0.965837472736752 0.511231872038777
0.505193458557746 0.278218752295894 A A A 0.406175815267221 0.552830352735851
0.494320537032693 A A A LNCV6_130991_PI430048170 mRNA
TAGCTTAAGGTATTGTGCAATGGCCTAGCCTAGTAGAAATGGGGGAAAAGCATTGCTGTG NM_015463 RefSeq chr2
- 68293009 68320051 CNRIP1 25927 "cannabinoid receptor interacting protein 1, transcript variant
CRIP1a" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52113_PI430048170 0.00188484047132551 0.539401673031312 4.08489184737961
4.02908605477511 3.96947593448356 P P P 4.81706662115023 4.87657759987299
5.05324249117644 P P P LNCV6_52113_PI430048170 mRNA
GAAGTTTGCGTGAAGTTCTCCAGGACTATGGAAACCTTACAGGATACTGACTTAGAACCT NM_153260 RefSeq chr15
- 42542521 42548804 LRRC57 255252 leucine rich repeat containing 57 GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135340_PI430048170 0.000627824390851581 0.117608410804668 3.51290264118106
3.0629610821118 2.92553097283236 P P P 5.78443702029404 6.51642042768734
6.42720516358903 P P P LNCV6_135340_PI430048170 mRNA
CAGAACAACACTGTGTTGATCTAGTAGGTTTCTATTTTTCCTTTCTCTTTACAATGCACA NM_004385 RefSeq chr5 +
83471673 83582303 VCAN 1462 "versican, transcript variant 1"
GO:0005515|GO:0008037|GO:0008347|GO:0044281|GO:0005539|GO:0005615|GO:0043231|GO:0030208|GO:0007
507|GO:0030207|GO:0030206|GO:0005540|GO:0030198|GO:0007155|GO:0030204|GO:0030203|GO:0043202|GO:0
005975|GO:0005796|GO:0005509|GO:0005578|GO:0005576|GO:0007275|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136130_PI430048170 0.142171241256641 1.05807913207557 0.379577528999339
0.501210588874214 0.455144385142855 A A A 0.347821198218162 0.332674120004747
0.412449328575178 A A A LNCV6_136130_PI430048170 mRNA
TAACCTACATTTTTGTCACATTAAGTTTTTCCCCATTCCAGGACAGGTCAGGCCCTTTAA NM_005141 RefSeq chr4
+ 154562979 154572763 FGB2244 "fibrinogen beta chain, transcript variant 1"
GO:0005515|GO:0051258|GO:0005886|GO:0051087|GO:0050714|GO:0072562|GO:0005615|GO:0043623|GO:0045
921|GO:1900026|GO:0045907|GO:0030198|GO:0044320|GO:0031091|GO:0034116|GO:0031093|GO:0070374|GO:0
030674|GO:0050839|GO:0005938|GO:0070062|GO:0009986|GO:0090277|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137092_PI430048170 0.00128171475693451 0.473013005681293 5.38118668192812
5.21199799683097 5.47924597729677 P P P 6.29518779118554 6.38390622685041
6.62548442261462 P P P LNCV6_137092_PI430048170 mRNA
CAGTATAATGGCATTGCTGTGTCTGGCACTTCATTGTACAGACTTTTATAATAAAAGAAC NM_016603 RefSeq chr5
- 137937952 138033113 FAM13B 51306 "family with sequence similarity 13, member B, transcript
variant 1" GO:0043547|GO:0051056|GO:0007264|GO:0005829|GO:0005096 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_139197_PI430048170 0.766435110982341 0.932772409044839 4.07277752939954
4.06726153176309 4.65313876301545 P P P 4.06147351663811 4.22587682711366
4.78549859006842 P P P LNCV6_139197_PI430048170 mRNA
GGAGAACTAGAACTTATAAACCTCTACTTCAAGTGTGTATCACGTAATTGTTTCCATGAA NM_213603 RefSeq chr7
+ 99472891 99487594 ZNF789 285989 "zinc finger protein 789, transcript variant 1"
GO:0006355|GO:0003700|GO:0005654|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_80292_PI430048170 0.287407550837211 1.03689497976278 0.453172502713867 0.349639418337565
0.401402012681773 A A A 0.297967552827784 0.346136685597811 0.403231177238354 A A A
LNCV6_80292_PI430048170 mRNA
ATTTCTCTTAGCACTGGTCGAGAGAGTTACATCCCTGGAATATGTGTGGCCAGAGTTTAC NM_001045556 RefSeq
chr8 - 133036727 133103066 SLA 6503 "Src-like-adaptor, transcript variant 1"
GO:0005515|GO:0005070|GO:0009967|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136426_PI430048170 0.115131832691686 1.05318595793854 0.433044719682583
0.464911657700123 0.475927938533493 A A A 0.332275895751802 0.379140538182182
0.436634485313946 A A A LNCV6_136426_PI430048170 mRNA
CTTGGCAATGGTACACTACAAATGTGCTGAGTTAGAATTACTCTGAAGTTATGAAACATA NM_000233 RefSeq chr2
- 48686773 48755741 LHCGR 3973 luteinizing hormone/choriogonadotropin receptor
GO:0038106|GO:0005886|GO:0042700|GO:0007200|GO:0004964|GO:0007190|GO:0030539|GO:0071371|GO:0050
890|GO:0007186|GO:0005887|GO:0007187|GO:0043950|GO:0032962|GO:0035472|GO:0008584|GO:0005768 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120467_PI430048170 0.0366412573499019 0.443904247391092 1.25294865850385
1.55547400602598 2.19186570694627 A A A 2.71042515373869 3.03099217587698
2.91918633298701 P P P LNCV6_120467_PI430048170 mRNA
AAACCAGCAGTGCTGCTATCAGATAAGTAGATGTCAATGTATACTTACAAGGAAAAACTA NM_001040450 RefSeq
chr15 + 58771193 58857535 FAM63B 54629 "family with sequence similarity 63, member B,
transcript variant 1" GO:0008150|GO:0003674|GO:0005654|GO:0005575 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_131837_PI430048170 0.304799381563068 1.11439865462625 6.8000080430872
6.82941966331169 7.13840509715835 P P P 6.67854490661766 6.77386561449953
6.86548784234471 P P P LNCV6_131837_PI430048170 mRNA
TCCTCTCAATTTCCCAGAAATTGGGTTCTATGCTGGCTGGAAATGTTGGGGGAAAGAGAA NM_144576 RefSeq chr12
+ 56266857 56270966 COQ10A 93058 "coenzyme Q10 homolog A (S. cerevisiae), transcript variant 1"
GO:0005743 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139689_PI430048170 0.108097529694947 0.727569119631748 7.50194317763739
7.91577333834676 7.7653752852725 P P P 7.83164272508861 8.35188225881657 8.3468104413101
P P P LNCV6_139689_PI430048170 mRNA
AATCTCAACACCCAAGTTGAAGACTTTGTTTTTAAAATGGTTTGTCCTGATGCTTTTGTC NM_001262 RefSeq chr1
+ 50968694 50974634 CDKN2C 1031 "cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4),
transcript variant 1"
GO:0005515|GO:0030308|GO:0008285|GO:0019901|GO:0071901|GO:0048709|GO:0005634|GO:0000079|GO:0005
829|GO:0042326|GO:0000082|GO:0005737|GO:0004861|GO:0007050|GO:0000278 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139782_PI430048170 0.239985642523533 1.12243989075531 12.0244533574671 11.996750337685
11.7149982992723 P P P 11.7512943134335 11.8167782805097 11.6850586438343 P P P
LNCV6_139782_PI430048170 mRNA
CCTGCCACACTCGGGGATTCATTCCTTAGAAACTGAAATAAATTCTAATTTTGGAAACTC NM_025204 RefSeq chr22
+ 50185930 50199598 TRABD 80305 TraB domain containing NA . NA - . NA NA NA NA NA
NA NA NA NA

LNCV6_75526_PI430048170 0.1527500666642910.7762995795772236.03265666456703 6.00464052394948
6.14354855530993 P P P 6.159641765219 6.36191220073233 6.70554175677358 P P P
LNCV6_75526_PI430048170 mRNA
CCTGGAAACTGAAGGGAGTTTTGCAAGTGAAAATTTAGATTTCTATTGACATCCTTTTGT NM_020726RefSeq chr5
+ 65722195 65829283 NLN 57486 neurolysin (metallopeptidase M3 family)
GO:0042277|GO:0005758|GO:0005886|GO:0006508|GO:0004222|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133084_PI430048170 0.0139133342126130.5466282522940796.69777379639231
6.60971148252394 6.97669362364718 P P P 7.3373702074258 7.65735596809759
7.87881830617169 P P P LNCV6_133084_PI430048170 mRNA
GGAATCATGTTTTTCTCCCCCAAAGTACAATAAAGCTGCCTTGTCTGCACCATTAAAAAA NM_016025RefSeq chr16
+ 21599475 21657473 METTL9 51108 "methyltransferase like 9, transcript variant 1" GO:0005515 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131575_PI430048170 0.3224797012122690.7625391912349930.652248454501024
0.8101440452546461.53900607384498 A A A 0.9987049608006811.81133059041648
1.41329439240427 A A A LNCV6_131575_PI430048170 mRNA
GAGTAAGCTTTGCAGTTACTGTGAACTATTGTCTCTTGGAGGAAGTTTTTTGTTTAAGAA NM_002738RefSeq chr16
+ 23835978 24220611 PRKCB 5579 "protein kinase C, beta, transcript variant 2"
GO:0050853|GO:0005515|GO:0007077|GO:0030949|GO:0005886|GO:0007268|GO:0005634|GO:0050681|GO:0005
829|GO:0035556|GO:0042393|GO:0042953|GO:0005737|GO:0051092|GO:0030374|GO:0005080|GO:0006816|GO:0
043123|GO:0070062|GO:0048010|GO:0035408|GO:0006357|GO:0005246|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_83541_PI430048170 0.7000275441381120.9521616957118744.78958302722324 4.7357914841164
4.64524800744498 P P P 4.56625917304488 5.0202206695675 4.76390336678258 P P P
LNCV6_83541_PI430048170 mRNA
ATTTTCCTGTATACCTGCTGCTACACACCACTGAAAAGGATCAGCATTGCCAACACATGG NM_001303RefSeq chr17
+ 14069401 14208679 COX10 1352 COX10 heme A:farnesyltransferase cytochrome c oxidase assembly
factor
GO:0000266|GO:0048034|GO:0004129|GO:0005743|GO:0008495|GO:0044281|GO:0006784|GO:0006783|GO:0005
739|GO:0009060|GO:0045333|GO:0006778|GO:0008535|GO:0006123|GO:0070069|GO:0016021|GO:0004311 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143728_PI430048170 0.00143877932700238 0.3512664274459173.87497446449169
3.87824256430857 4.20209821923625 P P P 5.26037254626857 5.45806106331361
5.74799591386743 P P P LNCV6_143728_PI430048170 mRNA
GGCATGATGTTTCTTCCACTTGTAATTTTATGTGCTTTCATCACAAATCCAAAGGAAAGA NM_182734RefSeq chr20
+ 8132264 8884900 PLCB1 23236 "phospholipase C, beta 1 (phosphoinositide-specific), transcript
variant 2"
GO:0005516|GO:0000790|GO:0046330|GO:0042803|GO:0045444|GO:0007613|GO:2000560|GO:0005521|GO:0070
062|GO:0031965|GO:0080154|GO:0005509|GO:0046488|GO:0005546|GO:0007215|GO:0007213|GO:0016042|GO:0
043547|GO:0008277|GO:0048639|GO:0019899|GO:0045893|GO:0045892|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127272_PI430048170 0.55816427212025 0.8667708040450010.434901107470311
0.4897271997369680.478274484888358A A A 0.35637586258447 1.10607992511986
0.437241057675664A A A LNCV6_127272_PI430048170 mRNA
GCTATATTCCAGATACAAATGACTCAAAGGCAGCTCAGTTGTACTGGTTTTGAAAACTCA NM_181645RefSeq chr11
+ 93330716 93438471 CCDC67 159989 coiled-coil domain containing 67 GO:0005737|GO:0030030
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_39393_PI430048170 0.0824949211924257 1.21484791978041 4.22007568069141
4.34308288320357 4.43244413065031 P P P 3.97640488118945 4.24153895521593

3.92258622621165 P P P LNCV6_39393_PI430048170 mRNA
TGACAAGACATTTCAAAGAAAGTATTAAATTCATTCACGAGTGCCGGCTCCGCGGTGAGA NM_001286555 RefSeq
chr6 + 292056 351355 DUSP2256940 "dual specificity phosphatase 22, transcript variant 1"
GO:0008283|GO:0046330|GO:0006915|GO:0005634|GO:0007275|GO:0000122|GO:0035335|GO:0000188|GO:0005
737|GO:0006470|GO:0042127|GO:0007179|GO:0008138|GO:0004725 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139461_PI430048170 0.259886647349586 1.01952149281898 0.304237176333975
0.265903985966452 0.327538163017905 A A A 0.279932666362212 0.262879047265595
0.27181078163382 A A A LNCV6_139461_PI430048170 mRNA
GGCTGTAAAGTAAGTGTAAGGTCCACATCCTTGGGGAAGTAGTTAAATAAAATAGTTATG NM_000273 RefSeq chrX
- 9725412 9765965 GPR143 4935 G protein-coupled receptor 143
GO:0005515|GO:0033162|GO:0072544|GO:0072545|GO:0006726|GO:0035584|GO:0005886|GO:0032438|GO:0032
400|GO:0005765|GO:0032402|GO:0005737|GO:0016324|GO:0007218|GO:0050848|GO:0042470|GO:0005794|GO:0
004930|GO:0048015|GO:0035240|GO:0007165|GO:0016020|GO:0007186|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127881_PI430048170 0.409083975670362 0.821435519086276 0.486795192576516
0.502253363945055 0.324839341849833 A A A 0.401407474153316 1.15297730494227
0.496267522743375 A A A LNCV6_127881_PI430048170 mRNA
TGTACACTGAAATTTGCCATCACGTGTTTGTGTAAACTCAATGTGCACATTTTGTATTTC NM_001035003 RefSeq
chr4 - 20728615 21697695 KCNIP4 80333 "Kv channel interacting protein 4, transcript variant 5"
GO:0005244|GO:0005886|GO:0005509|GO:0043025|GO:0005267|GO:0034765|GO:0071805|GO:0030425 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142305_PI430048170 0.00290753688614715 0.768380249348508 9.02418663508379
9.08154899145976 8.93219004234325 P P P 9.40236888292601 9.44405852790623
9.33358973369515 P P P LNCV6_142305_PI430048170 mRNA
TCCTGTTGGATATCATACTTCCATCTGGCTGCCTTTGCTTAAGCCATCTTTGTGGTAGAG NM_022171 RefSeq chr3
+ 49412205 49416476 TCTA 6988 T-cell leukemia translocation altered GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127962_PI430048170 0.0165028297585969 0.434451069778919 4.49817692219231
3.94280442272259 4.47906442351283 P P P 5.43672092413506 5.58816513268951
5.56457876605912 P P P LNCV6_127962_PI430048170 mRNA
CCTGCTAGTACCTGTTGTAAAGCTTCTTTTATTAAAGAAGAGCAGGAGATTGAAGTGTCA NM_001243650 RefSeq
chr16 - 67680715 67719370 GFOD2 81577 "glucose-fructose oxidoreductase domain containing 2,
transcript variant 3" GO:0030198|GO:0016491|GO:0005578|GO:0055114 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_138197_PI430048170 0.00919803654027986 1.42780386613946 8.56313893197494
8.58358351709478 8.73594796628092 P P P 8.04867122928452 8.01107813194998
8.27357983918633 P P P LNCV6_138197_PI430048170 mRNA
GAGGGTTGTATATTTTCCCGTTGGAGACACATCTGGAATTTGCTGCAATAAAATAATAAT NM_001033575 RefSeq
chr2 + 240560053 240564014 DUSP28NA dual specificity phosphatase 28 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_126787_PI430048170 0.552088647495643 1.30543554454231 1.71942580457436
0.444841695514384 1.70841740129074 A A A 0.392148319849838 0.90703870469658
1.52662841536457 A A A LNCV6_126787_PI430048170 mRNA
CAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTG NM_015424 RefSeq chr11
- 74696427 74731385 CHRDL2 25884 "chordin-like 2, transcript variant 1"
GO:0030514|GO:0005737|GO:0001503|GO:0051216|GO:0005615|GO:0030154 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145018_PI430048170 0.14477185260247 0.516237404952119 5.86310386199697

4.22931514863904 4.55091964195321 P P P 6.28287402471745 5.97129453824158
5.75187951084086 P P P LNCV6_145018_PI430048170 mRNA
TGTGCCCTGGCTATGTCCTTTGTTCTGCTGCTGCCCAAGGTCAACAAGAAGGCTGGATCC NM_001080483 RefSeq
chr9 - 133514585 133524946 TMEM8C NA transmembrane protein 8C NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_105633_PI430048170 0.1198578550841280.6296751893250533.51750094185025
3.36408339719325 2.5888199147535 P P A 3.82153165261834 4.16752198268401 3.583140449072
P P P LNCV6_105633_PI430048170 mRNA
TTGTGAACATTCAAGTGAAGCAAAAGCCTTTCATGATTATAGTGCAGCAGCTGCCCCGAG NM_145716RefSeq chr1
- 54225430 54406395 SSBP3 23648 "single stranded DNA binding protein 3, transcript variant 1"
GO:2000744|GO:0021501|GO:0043234|GO:0008284|GO:0006461|GO:0021547|GO:0003697|GO:0002244|GO:0060
323|GO:0045944|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143442_PI430048170 0.195065659604001 1.23656542625305 13.6490278375369
13.7742654431356 13.989426137547 P P P 13.2205961868164 13.4341730788582
13.7994684905107 P P P LNCV6_143442_PI430048170 mRNA
TGTGGAAATCAGCACACAACCACAATGACATTTAAGCACAGGATCATTATTAGTCTATGT NM_001134484 RefSeq
chr9 - 37588414 37592639 TOMM5 401505 "translocase of outer mitochondrial membrane 5 homolog
(yeast), transcript variant 3" GO:0005739|GO:0008565|GO:0006626|GO:0005742|GO:0016021|GO:0044267 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59510_PI430048170 0.5859208566328141.36912677193158 1.70096284068877 0.247604333807575
0.331893981110566 A A A 0.8219236446516240.2480008308611720.269967941395642 A A A
LNCV6_59510_PI430048170 mRNA
TGAAAACCGGAGGGCTCGTCATCCACCACTACCATGTAAGGGCCATGAGAAGGGCTCATCNM_018711RefSeq chr12
- 108908128 109021240 SVOP 55530 SV2 related protein homolog (rat)
GO:0034220|GO:0030054|GO:0015075|GO:0030672|GO:0016021|GO:0008021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141864_PI430048170 0.0221514289924612 0.6093883261316410.6543024636964
10.6463443449662 10.395089226971 P P P 11.0103078035906 11.5177276130548
11.2817608335198 P P P LNCV6_141864_PI430048170 mRNA
CAGAGCTCTCCCTTGGTAAGACTTATTTTGTTAATAAATGGAATACTTGGCTATATTCAC NM_025069RefSeq chr8
+ 37695750 37700021 ZNF703 80139 zinc finger protein 703
GO:0005515|GO:0006355|GO:0008284|GO:0030335|GO:0034333|GO:0010718|GO:0005634|GO:0034111|GO:0003
676|GO:0046872|GO:0006351|GO:0016363|GO:0060828|GO:0043234|GO:0005737|GO:0060644|GO:0071392|GO:0
070491|GO:0051726|GO:0017015|GO:0045892|GO:0033601 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_141392_PI430048170 0.10026033316532 0.7966413096901447.70905405055355 7.3551842774608
7.63562647167601 P P P 8.03486130839426 7.67796787891713 7.97019775221723 P P P
LNCV6_141392_PI430048170 mRNA
CCTTTCCATTTAGCTCATAAGCACGGCTATCTTTTTAAGAGAAAAATAAAGCCATGGTAT NM_017996RefSeq chr15
- 88512482 88546681 DET1 55070 "de-etiolated homolog 1 (Arabidopsis), transcript variant 1"
GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136825_PI430048170 0.8193794200212740.9593215625062967.05001295287618
6.95013330557774 7.12794120200415 P P P 6.75800507251877 7.2522473845046 7.2492560160259
P P P LNCV6_136825_PI430048170 mRNA
CAAGGAGCAATATTGGTTTACTCTCGTATCCTTAAAAAGTTACAGAACTGTGTCTTAAGA NM_173854RefSeq chr1
- 205789092 205813196 SLC41A1 254428 "solute carrier family 41 (magnesium transporter), member 1"
GO:0005886|GO:0008324|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135631_PI430048170 0.0233870561137473 1.28809338477784 10.6573985474539
10.4481977150374 10.4033579163684 P P P 10.0812418591004 10.2510099167092

10.0874220659751 P P P LNCV6_135631_PI430048170 mRNA
ACCTTTCCACAGGCTTCTTGTCCACAGTAGAGTTTAATAAAAATATTCACTGAAAGACCC NM_006234RefSeq chr7
- 102473100 102478934 POLR2J 5439 "polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa"
GO:0008380|GO:0005515|GO:0010467|GO:0006368|GO:0006367|GO:0006366|GO:0003899|GO:0006370|GO:0005
634|GO:0003677|GO:0050434|GO:0006281|GO:0000398|GO:0006283|GO:0030275|GO:0001055|GO:0034587|GO:0
046983|GO:0005665|GO:0016032|GO:0005654|GO:0006289|GO:0035019 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142570_PI430048170 0.0954071773454364 1.08541020795556 12.6298490469805
12.6219999068274 12.5055990781119 P P P 12.3988000628098 12.4826835260548
12.5218425860689 P P P LNCV6_142570_PI430048170 mRNA
TTTGTTCAGCTTTTACTGGAAACTGCTGTCTAGGACCACCTGCCCTAACCAGGAATAAAG NM_153339RefSeq chr1
+ 1308613 1311677 PUSL1 126789 pseudouridylate synthase-like 1
GO:0009982|GO:0003723|GO:0001522|GO:0008033|GO:0043231 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_94229_PI430048170 0.3486818245372781.18562948006408 4.39295676139639 4.80178275749529
4.65271162955913 P P P 4.56979344455274 4.55146136439262 3.93193388393319 P P P
LNCV6_94229_PI430048170 mRNA
TTGCTCTTGAACAATAAGCTGAGTGCCCTGCCAAGCTGGGCTTTCGCCAACCTCTCCAGC NM_001163925 RefSeq
chr12 + 1820266 1836752 LRTM2 654429 "leucine-rich repeats and transmembrane domains 2,
transcript variant 2" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131629_PI430048170 0.5729076106822570.8415744624235250.32231980073593
0.59893048363891 0.45014291329523 A A A 1.22140620836906 0.391913411603107
0.339039263113837A A A LNCV6_131629_PI430048170 mRNA
CTCATGTCTGTGTCCCATGGTCATAGTCAAAGATTTTGTACTGCTAAAATTACCAAATAA NM_001801RefSeq chr5
- 115804732 115816708 CDO1 1036 cysteine dioxygenase type 1
GO:0045471|GO:0006534|GO:0051384|GO:0044281|GO:0051591|GO:0008198|GO:0005829|GO:0034641|GO:0000
096|GO:0006954|GO:0000097|GO:0007595|GO:0000098|GO:0033762|GO:0017172|GO:0042412|GO:0043200|GO:0
019448|GO:0055114. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142640_PI430048170 0.4097388082062781.06800242632148 0.365727433163111
0.3827922901180890.633897385546958A A A 0.3642709755864670.390451246727942
0.358669582886181A A A LNCV6_142640_PI430048170 mRNA
TCTGTCAGCAGGAGAGTTTTACCTATTGCATGGAAAGATGCTCATTATATATTGTGAAGT NM_001168399 RefSeq
chrX - 103309345 103310955 BEX2 84707 "brain expressed X-linked 2, transcript variant 1"
GO:0007049|GO:0005737|GO:0051726|GO:0006915|GO:0042981|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_116681_PI430048170 0.1833443088866820.7581733618668099.2004056102243
8.92626085368256 8.67265970194557 P P P 9.61114864483931 9.39167783650591
8.97169969376916 P P P LNCV6_116681_PI430048170 mRNA
CAGGCATGCAGCCCCAGCCTTCTCTCTGCTCCTCAGCCTGCGAAAACAGGAGATCATTAA NM_172171RefSeq chr10
- 73812500 73874591 CAMK2G 818 "calcium/calmodulin-dependent protein kinase II gamma, transcript
variant 1"
GO:0005515|GO:0005516|GO:0005886|GO:0019221|GO:0007268|GO:0051259|GO:0030154|GO:0042803|GO:0005
829|GO:0034605|GO:0000082|GO:0046777|GO:0004723|GO:0051924|GO:0006816|GO:0004683|GO:0060333|GO:0
014733|GO:0033017|GO:0005524|GO:0007399|GO:0030666|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128380_PI430048170 0.2302134123404053.88112694052078 0.318443744706675
3.31611556512365 1.79302736909149 A P A 0.3413576160752320.302357385813066
0.356468492781925A A A LNCV6_128380_PI430048170 mRNA
GCTTAACAATCAGACTTCTTCTATTTTTGCTGCTATGGTGGTTGTATTAGAGAACTGATG NM_015070RefSeq chr13

- 45962178 46052761 ZC3H13 23091 zinc finger CCCH-type containing 13 GO:0005515|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126830_PI430048170 0.0308470449544479 0.5884784764914244.86085291187627 4.32168954958698 4.74058509991062 P P P 5.07974055285085 5.50148442108087 5.63420606815359 P P P LNCV6_126830_PI430048170 mRNA TAACGTCACCTACTCTCCACTAATAGATGCTATGCTAAGAGAAGTGAATAATCTTTCTTT NM_001304364 RefSeq chr9 - 122918028 122931265 ZBTB26 57684 "zinc finger and BTB domain containing 26, transcript variant 3"
GO:0008150|GO:0003674|GO:0006355|GO:0005737|GO:0005654|GO:0005575|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135811_PI430048170 0.0484720578495731.57911836974262 6.00373620891886 6.01293164798885 5.86887123012451 P P P 4.95045604947276 5.41330263019807 5.49186693544906 P P P LNCV6_135811_PI430048170 mRNA AAATAAGGAGCCAGAGGAGTTACCTGTGTCCTGCATTATGATTAAAGCCTTTTAAAGTTG NM_145038RefSeq chr2 + 26401915 26456711 DRC1 92749 dynein regulatory complex subunit 1
GO:0071973|GO:0060285|GO:0005930|GO:0070286|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57149_PI430048170 0.0425349531395896 2.50169449296748 4.01497175863544 3.65298201236646 3.73573950387335 P P P 1.79154800741394 2.50604865237932 2.9398684060171 A P P LNCV6_57149_PI430048170 mRNA TGACTTATCTCCTGCAACTGACTCATCTGCAACATTCACACCATTGCTTCCTTGTGGTTTNM_021616RefSeq chr11 + 5624976 5644395 TRIM34 53840 "tripartite motif containing 34, transcript variant 1"
GO:0003674|GO:0070206|GO:0051091|GO:0005737|GO:0019221|GO:0008270|GO:0060333|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121070_PI430048170 0.4196053978132090.8183478104543433.17381620123912 3.33027934683674 3.75218892124854 P P P 3.30535786549016 3.62635224139534 4.13331061548506 P P P LNCV6_121070_PI430048170 mRNA AATTTGCCCAGAACTCTGTGAAGGAAAATCTCATGAAGAAAGAACTGGAGGAGGAGCGAT NM_001080467 RefSeq chr18 - 49822785 50195081 MYO5B 4645 myosin VB
GO:0005515|GO:0005516|GO:0017137|GO:0032439|GO:0003779|GO:0016459|GO:0015031|GO:0055085|GO:0005524|GO:0003091|GO:0043234|GO:0000146|GO:0045179|GO:0008152|GO:0006833|GO:0055037|GO:0016192|GO:0030659|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134235_PI430048170 0.00457319628808875 0.4730647531603355.47411513825611 5.80972264760167 5.70543577580949 P P P 6.70344829730992 6.73215123165285 6.81131562503132 P P P LNCV6_134235_PI430048170 mRNA CTTCTCAACTTCCTAGGAATGTTTAGCAGCAACCTAATATACCAGGCAAAACTCAAAAAA NM_001260477 RefSeq chr21 - 42849225 42879275 WDR4 10785 "WD repeat domain 4, transcript variant 6"
GO:0005515|GO:0005737|GO:0030488|GO:0008176|GO:0005654|GO:0005634|GO:0006400 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129083_PI430048170 0.0969929355044937 0.3913073258398173.09946729620058 1.41779185854912 2.36261627828202 A A A 2.8538132534526 4.19774628862878 4.02635302015422 P P P LNCV6_129083_PI430048170 mRNA GGGAGAAAAGGCTGCTTGAAAATATCTTTTGATTCAGTGATTTTTAACATTGGGAAGTTG NM_016422RefSeq chr11 - 10511677 10541227 RNF141 50862 ring finger protein 141
GO:0006355|GO:0004842|GO:0008270|GO:0003677|GO:0051865 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138479_PI430048170 0.5031519053970161.03068826496889 0.283823801989425 0.3079478796357330.448672286118193 A A A 0.3254767385887750.294490477756115 0.294986229445357 A A A LNCV6_138479_PI430048170 mRNA

AGACATGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGAGACATG NM_053017 RefSeq chr11 - 3638505 3642316 ART5 116969 "ADP-ribosyltransferase 5, transcript variant 1" GO:0006471|GO:0003953|GO:0016020|GO:0003956|GO:0005576|GO:0003950 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130927_PI430048170 0.396029229788695 0.86021278923171 0.531254352184223 0.472286559961427 0.263423480277558 A A A 0.403277358455471 0.979454813982978 0.479159321636396 A A A LNCV6_130927_PI430048170 mRNA
GTGCTTTGTCTTTCTCCAGATTAATATCGGTTACACTGCTGATGTTTGTAAATTAAACAG NM_004787 RefSeq chr4 + 20253563 20620561 SLIT2 9353 "slit homolog 2 (Drosophila), transcript variant 1" GO:0001656|GO:0005515|GO:0001657|GO:0090260|GO:0071676|GO:0030308|GO:0048846|GO:0005615|GO:0048495|GO:0071672|GO:0042803|GO:0042802|GO:0016337|GO:0070100|GO:0007411|GO:0030837|GO:0070062|GO:0021972|GO:0030336|GO:0009986|GO:0005509|GO:0043394|GO:0060763|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132664_PI430048170 0.640967788125797 1.02601299961062 3.14499441787803 0.396186347507415 0.319048739620492 P A A 1.49976400982362 2.47692941018944 1.44625570046009 A A A LNCV6_132664_PI430048170 mRNA
CTCCCTTCTTCAACCCCATTATCTATAGCCTGAGGAATAAAGAAATAAAAGAAGCTATAA NM_001005279 RefSeq chr1 - 158699677 158700652 OR6K2 81448 "olfactory receptor, family 6, subfamily K, member 2" GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93431_PI430048170 0.220809743294217 1.27480343377062 6.97362369204096 7.52836242134174 7.46928662771632 P P P 6.91800551278074 6.72456330635768 7.28291003138087 P P P LNCV6_93431_PI430048170 mRNA
GACCACCAAATATCGGAACCCCTCCTTGAAGCTGATGGTGAATGTGTGCGGACACACTCT NM_002431 RefSeq chr14 + 60734740 60968680 MNAT1 4331 "MNAT CDK-activating kinase assembly factor 1, transcript variant 1" GO:0005515|GO:0010467|GO:0006368|GO:0006367|GO:0006366|GO:0008283|GO:0006363|GO:0006362|GO:0006361|GO:0006360|GO:0000079|GO:0007512|GO:0005737|GO:0000082|GO:0045944|GO:0000086|GO:0016032|GO:0008094|GO:0043066|GO:0006357|GO:0006370|GO:0048661|GO:0008353|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138707_PI430048170 0.0127249194246954 0.462716339880295 4.41442760630635 3.86846371369497 3.77413921655657 P P P 4.87986044913585 5.17904712906316 5.37664682187361 P P P LNCV6_138707_PI430048170 mRNA
CCTTTCAGTGCATTACTATGGGAGGAGCAACTAAAAAATAAAGACTTACAAAAAGGAGTA NM_001164000 RefSeq chr3 - 169083498 169147734 MECOM 2122 "MDS1 and EVI1 complex locus, transcript variant 6" GO:0005515|GO:0001780|GO:0003700|GO:0005634|GO:0009791|GO:0046872|GO:0030154|GO:0042803|GO:0043231|GO:0043069|GO:0009617|GO:0005737|GO:0046329|GO:0006954|GO:0045944|GO:0042127|GO:0051726|GO:0030512|GO:0006355|GO:0005794|GO:0016235|GO:0006915|GO:0060039|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127429_PI430048170 0.0111179698376565 2.73205175340643 8.59899177662692 9.32219534441714 8.62448934179145 P M P 7.69894550092992 7.3759456111086 7.19766475196843 P P P LNCV6_127429_PI430048170 mRNA
CAGATTACTGAGATTGGGGATTGTAACTCTGACTTGCCAAACAAACTGCTGCCTCATAAA NM_001035235 RefSeq chr5 - 140550066 140558093 SRA1 10011 "steroid receptor RNA activator 1, transcript variant 1" GO:0005515|GO:0006355|GO:0005886|GO:0008283|GO:0003713|GO:0006915|GO:0042981|GO:0005634|GO:2000273|GO:0006351|GO:0030154|GO:0045171|GO:0005737|GO:0030374|GO:0030529|GO:0015630|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53831_PI430048170 0.764148384941721 0.970693569949416 13.2597147762623 13.1355535735034 13.205020184511 P P P 13.0360559594107 13.2949930285512 13.3789397559517 P P P

LNCV6_53831_PI430048170 mRNA
AGGTTGTTTACGACAAACCTCCTTGTCAAAGTGTGTAAAAATAAAGGATTGCTCCATCCT NM_004552 RefSeq chr1
+ 39026294 39034636 NDUFS5 4725 "NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa
(NADH-coenzyme Q reductase), transcript variant 1"
GO:0022904|GO:0005739|GO:0032981|GO:0005758|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0008
137|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141166_PI430048170 0.0365065781627604 1.08636323072603 0.674800193328596
0.741066535764695 0.638734505877662 A A A 0.606937571037178 0.545926701626262
0.544201468361365 A A A LNCV6_141166_PI430048170 mRNA
GGATGTGTTGGTAACTCCGAGTTGTAATGAGTTCATGAAATGTGCTGTTATTTTTGTAAT NM_207163 RefSeq chr7
+ 123655806 123664093 LMOD2 442721 leiomodin 2 (cardiac)
GO:0006936|GO:0030239|GO:0005865|GO:0007015|GO:0003779|GO:0005523|GO:0051694 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_57662_PI430048170 1.57079835722026e-05 1.33222895288243 12.9948482176203
12.9868582710726 13.0124270800368 P P P 12.5702548252712 12.6051886501879
12.5770443807314 P P P LNCV6_57662_PI430048170 mRNA
AATGGGATTTGGGCTTTGGTACAAGAACTGTGACCCCCAACCCTGATAAAAGAGATGGAA NM_003377 RefSeq
chr11 + 64234583 64239264 VEGFB 7423 "vascular endothelial growth factor B, transcript variant
VEGFB-186"
GO:0005515|GO:0051897|GO:0030949|GO:0050731|GO:0060754|GO:0060048|GO:0005615|GO:0042803|GO:0060
976|GO:0043524|GO:0006493|GO:0051781|GO:0031093|GO:0070374|GO:0008201|GO:0048010|GO:0043066|GO:0
046982|GO:0042493|GO:0030168|GO:0005576|GO:0001525|GO:0042056|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_108008_PI430048170 0.368204170221553 1.06780829277499 10.2337498409634
10.2512266912695 10.2006915423996 P P P 10.2922948840216 10.0963632872303
9.99777673938204 P P P LNCV6_108008_PI430048170 mRNA
CTGCCCATCCTGCCTTCCGGACCCCTCTACCCAGGCCTCTTTGACATCCGTGGCTCCCCA NM_016148 RefSeq
chr19 - 50661826 50716938 SHANK1 50944 SH3 and multiple ankyrin repeat domains 1
GO:0005515|GO:0043005|GO:0017124|GO:0008328|GO:0030054|GO:0005886|GO:0017146|GO:2000311|GO:0035
418|GO:0031877|GO:0032403|GO:0030425|GO:0042802|GO:0005622|GO:0005737|GO:0030160|GO:0043197|GO:0
042048|GO:0045211|GO:0097110|GO:0032232|GO:0050885|GO:0030534|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_65222_PI430048170 0.00300829513320329 0.540756480063693 12.3575241016145
12.0431463067234 12.0577066969219 P P P 12.9530588489798 13.2197379619599
12.9519118716641 P P P LNCV6_65222_PI430048170 mRNA
TGCGTTTGTGCCGAGCTTCTATTTCATATTGCAAATATAAATAAAGGAAGGCAGTTTACG NM_014931 RefSeq
chr19 - 55229778 55258670 PPP6R1 22870 "protein phosphatase 6, regulatory subunit 1"
GO:0005515|GO:0005737|GO:0019903|GO:0043666 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139643_PI430048170 0.842185882051199 0.96774686877796 9.21743123818805
9.4112747211748 9.55305069207007 P P P 9.36118619650937 9.21714547382405
9.71787996235489 P P P LNCV6_139643_PI430048170 mRNA
GGTATTTCAGAAGGTCATCAGATTGTGAGACTGCTTCCTTGAAACATTTTTGTGCTATTG NM_006310 RefSeq
chr17 + 47531077 47623276 NPEPPS 9520 aminopeptidase puromycin sensitive
GO:0000209|GO:0002474|GO:0004177|GO:0006508|GO:0071456|GO:0008270|GO:0005634|GO:0008237|GO:0070
062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141961_PI430048170 0.0176464509072561 1.88323962384964 2.68700460733398
3.30028121628382 3.02633817548683 A P P 2.06129193519469 1.90959877995775
2.33515302449501 A A A LNCV6_141961_PI430048170 mRNA

AGAAGAAGCGCAAGCACGAGAAGAAGCTGCTGAAGAGCCAGGGCCGCCACTTGCACTCGC NM_001080461 RefSeq chr7 + 1233017 1236977 UNCX NA UNC homeobox NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100110_PI430048170 0.0752747005102887 1.35190231266842 1.30091218236587 0.901477850057273 0.92675815252954 A A A 0.676562748326266 0.585406461877667 0.596096784438896 A A A LNCV6_100110_PI430048170 mRNA
GAATGGACCTAAAAAACATGGGTGCTAAAAATGTGTGCTTGATGACAGACAAGAACCTCT NM_144650 RefSeq chr8 + 66432482 66468809 ADHFE1 137872 "alcohol dehydrogenase, iron containing, 1" GO:0005739|GO:0047988|GO:0005759|GO:0006103|GO:0044281|GO:0046872|GO:0044237|GO:0015993|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134370_PI430048170 0.380454182232426 0.930665514652523 11.9437810113294 12.0871015697574 11.7541001224227 P P P 12.0984461182651 11.9671347963736 12.0465918940965 P P P LNCV6_134370_PI430048170 mRNA
TTTAAGGCCACAGAGGCTCCAATACCTGGGAATGTTCACAAAGTCATCAACTGGAAAAAA NM_018114 RefSeq chr3 - 49015488 49021071 DALRD3 55152 "DALR anticodon binding domain containing 3, transcript variant 2" GO:0006420|GO:0004814|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100121_PI430048170 0.540130868639951 1.35346658918651 3.49852195382008 1.92348554819536 2.76659894248281 P A A 1.62889154071049 2.34614156587776 3.00066396780562 A A P LNCV6_100121_PI430048170 mRNA
CACCAGAAGAACTCAAGGCAGCAAGTAGAGGAAATGGTGAATATGCATGGTATTATGAAG NM_001242844 RefSeq chr6 + 127266737 127288560 RNF146 81847 "ring finger protein 146, transcript variant 1" GO:0005515|GO:0072572|GO:0004842|GO:0042787|GO:0016874|GO:0090263|GO:0008270|GO:0005634|GO:0070936|GO:0016055|GO:0051865|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138073_PI430048170 0.0585126871825992 0.460281433095918 4.59146290468985 3.67536243070993 4.56337079629351 P P P 5.40904742067198 5.50055112082391 5.45087543321712 P P P LNCV6_138073_PI430048170 mRNA
CAGTGTGAAAATAGCACTTTACCAAAAGATTAGCCATGAAATGGTTATTTTGCCAGTTAC NM_018348RefSeq chr16 - 71282299 71289606 CMTR2 55783 "cap methyltransferase 2, transcript variant 1" GO:0005737|GO:0097310|GO:0004483|GO:0006370|GO:0005634|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128047_PI430048170 0.000506821206403446 0.3160167146362586.91954392539498 6.96458007442942 7.18434278604418 P P P 8.69932460885864 8.47390512941789 8.86824088484561 P P P LNCV6_128047_PI430048170 mRNA
AGAGATTTCTTGGTGGTAGCTATTTGGGTAAAGGTATATGGGTATTTTTCTGTACATGTG NM_005908RefSeq chr4 - 102631485 102760994 MANBA 4126 "mannosidase, beta A, lysosomal" GO:0005975|GO:0046355|GO:0006516|GO:0005764|GO:0006464|GO:0043231|GO:0004567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136305_PI430048170 0.571067121088842 1.0866187162474 3.38187523602369 3.75773392598257 3.58667818706118 P P P 3.63773121919632 3.07514281125241 3.61158781324845 P P P LNCV6_136305_PI430048170 mRNA
GGGTGGGGGTCAGGGGCGTCTGACTATGGCTGGGGAACTCATTTGGTTTTTCTCCTCTCT NM_001039211 RefSeq chr1 + 1449688 1470158 ATAD3C 219293 "ATPase family, AAA domain containing 3C" GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141950_PI430048170 0.0636477304969616 0.675732790656871 8.40999794258543 8.39552242534367 8.52305215294931 P P P 8.68638082288357 9.09793857679374 9.19521051806239 P P P LNCV6_141950_PI430048170 mRNA
CTGTTTTCCAAACACCACCTTTTTGCCTCAAGGTCTCTGTAAATGAAATAAACTGTAATT NM_024605RefSeq chr4

+ 147732301 148072776 ARHGAP10 79658 Rho GTPase activating protein 10
GO:0005515|GO:0051056|GO:0048471|GO:0043066|GO:0005886|GO:0032321|GO:0007264|GO:0007010|GO:0006
915|GO:0042981|GO:0005100|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140163_PI430048170 0.1783488625750130.646262097548595 0.406473540712045
0.4183581850787750.351423480507263 A A A 0.4644032258528210.995010597884034
1.44368382298821 A A A LNCV6_140163_PI430048170 mRNA
TTTCTATAGAATGGAAAAGATTCCAGCCCGATCCTTGATATGTTTGTGTTAAACATGCTT NM_001297619 RefSeq
chr19 - 36334452 36379203 ZFP14 57677 "ZFP14 zinc finger protein, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131283_PI430048170 0.2768723300134890.9475591057982510.40186307012153
0.4232792928511130.367004007777818 A A A 0.5074651819312420.541150030870739
0.371706980991792 A A A LNCV6_131283_PI430048170 mRNA
GCCCTGACTGAGACATAGGGCTGAGTTTATTGTTTTACTTTTATACATTATGCACAAATA NM_172140 RefSeq chr19
+ 39296324 39298672 IFNL1 282618 "interferon, lambda 1"
GO:0032729|GO:0008285|GO:0042531|GO:0032002|GO:0032003|GO:0032714|GO:0005102|GO:0005576|GO:0005
125|GO:0005615|GO:0007259|GO:0046427|GO:0051607|GO:0043381|GO:0002829|GO:0050778|GO:0045345|GO:0
032696|GO:0045581|GO:0045893|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145368_PI430048170 0.1707208621194571.04917667726778 0.589175424985192
0.6310067797452860.560391819806744 A A A 0.5921383832534320.488720652895284
0.490365948123377 A A A LNCV6_145368_PI430048170 mRNA
GCACAAAATGTGCTATTTTTGGTCACTTGCTTTATGACGTTTATTTTCCTGTTAAAGCTG NM_002472 RefSeq chr17 -
10390324 10421950 MYH8 4626 "myosin, heavy chain 8, skeletal muscle, perinatal"
GO:0005516|GO:0030049|GO:0006200|GO:0005524|GO:0030017|GO:0005829|GO:0032982|GO:0000146|GO:0005
737|GO:0051015|GO:0006936|GO:0003009|GO:0005859|GO:0008307|GO:0016887|GO:0032027 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142028_PI430048170 0.77131662154479 1.06838151800067 0.283959137724042
0.9832111904435170.499859915430869 A A A 0.3127679319126560.470948595880336
0.753087178312612 A A A LNCV6_142028_PI430048170 mRNA
CCTAATCCCTCCTACTTATACTTCCCCAAAAAACAAGCTTTACTGGAATTAATGGAAAAT NM_178171 RefSeq chr17
+ 39962972 39977766 GSDMA 284110 gasdermin A GO:0048471|GO:0006915 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_74541_PI430048170 0.6324953131796370.9226670716303862.93644742001536 3.41315989530388
3.68928741762149 A P P 3.48032484529039 3.24680491315651 3.71924186278824 P P P
LNCV6_74541_PI430048170 mRNA
CACACGCATGACAAAATGTAGACAAGATGCCTCAAGGTATTGGTAGCAAGCAAGATTTTG NM_058172 RefSeq chr4
- 79901616 80073323 ANTXR2 118429 "anthrax toxin receptor 2, transcript variant 1"
GO:0005515|GO:0022414|GO:0005886|GO:0009405|GO:0005789|GO:0005576|GO:0004872|GO:0016021|GO:0046
872|GO:0010008|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129996_PI430048170 0.2487564013450251.08899184998227 8.72710275239498
8.86086505518509 8.75719080201794 P P P 8.79777012914542 8.52685841733611 8.6421268651917
P P P LNCV6_129996_PI430048170 mRNA
ACGCAGGTCACCATAATTTGTATTATGTTCCCTGAGTCAATGAAGGTTTTCTTTAGACTT NM_013319 RefSeq chr1
+ 11273197 11288434 UBIAD1 29914 UbiA prenyltransferase domain containing 1
GO:0005515|GO:0009234|GO:0016209|GO:0031966|GO:0005783|GO:0005634|GO:0004659|GO:0006744|GO:0005
737|GO:0030173|GO:0016020|GO:0005789|GO:0042371 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_42936_PI430048170 0.86909754250191 0.9737486643710870.5066791167461640.421666398359118
0.534091658254723 A A A 0.3037276268024810.7708194632643730.465883591438674 A A A
LNCV6_42936_PI430048170 mRNA

CCCCTTTGTAAGAAAGAGATGCTTGCCATAGAGAAGGACATGAGTACATTAAAAATAATT NM_004163 RefSeq chr18 + 54828476 54895516 RAB27B 5874 "RAB27B, member RAS oncogene family" GO:0005515|GO:0042470|GO:0009306|GO:0005795|GO:0019904|GO:0032585|GO:0003924|GO:0005525|GO:0006886|GO:0032402|GO:0006904|GO:0006184|GO:0045921|GO:0031489|GO:0016324|GO:0071985|GO:0042589|GO:0032482|GO:0019003|GO:0030141|GO:0030140|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141393_PI430048170 0.1382239023548130.8407241745118678.02165276196649 8.15154107528362 8.03736684606048 P P P 8.1714836557385 8.24633983379194 8.52293652197823 P P P LNCV6_141393_PI430048170 mRNA
ACTTACCTGTGGTTCATTCATCACTGGTTCCTTAGGAATAAAATTGTTGAGCAATGCACT NM_017863 RefSeq chrX - 135156535 135171827 CT55 54967 "cancer/testis antigen 55, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138773_PI430048170 0.0424438065668893 0.6736337375544169.02017723098188 8.9647321283123 8.96146088476768 P P P 9.31672600193246 9.56721023678271 9.74177299293461 P P P LNCV6_138773_PI430048170 mRNA
GTTGGGGATGGTTTTCTGACCCTACGGTAACTAGATCTAATATATATCATCAGAAAATAT NM_001127 RefSeq chr22 - 29327679 29388583 AP1B1 162 "adaptor-related protein complex 1, beta 1 subunit, transcript variant 1" GO:0005515|GO:0005215|GO:0030131|GO:0019901|GO:0006892|GO:0005765|GO:0032588|GO:0006886|GO:0050690|GO:0005829|GO:0030665|GO:0019886|GO:0000139|GO:0008565|GO:0061024|GO:0016032|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101014_PI430048170 0.0865113629345629 0.52956815648945 3.22395877549774 3.1122245209491 2.15219521156474 P P A 3.38555693963052 4.05153785420454 3.938580480635 P P P LNCV6_101014_PI430048170 mRNA
TACATTTGCCATGCTTTTTCTGCTCCTTATGCAAGCCTTGCCTCTGAGCTTTTTCAGAGA NM_019093 RefSeq chr2 + 233729126 233773299 UGT1A3 NA "UDP glucuronosyltransferase 1 family, polypeptide A3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129302_PI430048170 0.4037934661286780.8348499963308970.4007570495757550.4028485799128 0.365528496188823 A A A 0.4319687728679370.3706266873913561.04701284122902 A A A LNCV6_129302_PI430048170 mRNA
CTGTTAGCAACAATGCAGAAGAATCTGCATGTAATAAACTGAGTTGCTGTATTTCTTTGT NM_001017969 RefSeq chr9 - 5919007 6008003 KIAA2026 158358 KIAA2026 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126996_PI430048170 0.2142762282677960.8902160645221610.7584114524916 10.7278702655962 10.9675619118149 P P P 10.8679187228679 10.9385396685009 11.1478024255306 P P P LNCV6_126996_PI430048170 mRNA
GAGTAACAAGCTGTACAAGAACCCCTTTTATCCCTGGAAGAGGCTGTGTATGAAACCAAT NM_000984 RefSeq chr17 + 28719981 28724356 RPL23A 6147 ribosomal protein L23a GO:0005515|GO:0010467|GO:0003735|GO:0008283|GO:0019083|GO:0006614|GO:0019058|GO:0005634|GO:0019843|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0000166|GO:0000184|GO:0016032|GO:0031932|GO:0022625|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68621_PI430048170 0.0153155889585878 1.33826186926564 11.5940504564896 11.3778208348411 11.6187157761497 P P P 11.0939426054302 11.2360378179314 11.0017835981341 P P P LNCV6_68621_PI430048170 mRNA
CAAGAAGTGAGCTGCTGTTGACGGAGGCAAGTTGGATGTCGGGAATGCTGAGGTGAAGTT NM_001139457 RefSeq chrX - 153700491 153724101 BCAP31 10134 "B-cell receptor-associated protein 31, transcript variant 1" GO:0005515|GO:0002474|GO:0035584|GO:0042288|GO:0005783|GO:0030136|GO:0007283|GO:0007204|GO:0006886|GO:0032403|GO:0006921|GO:0005829|GO:0051561|GO:0032580|GO:0033116|GO:0071556|GO:0005811|GO:0006915|GO:2001244|GO:0070973|GO:0006888|GO:0043280|GO:0016020|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_131573_PI430048170 0.00196308813890505 0.5410526281686897.40945670455956
7.16303221632839 7.26951742433478 P P P 7.98328664581458 8.24263275228885
8.26832147586261 P P P LNCV6_131573_PI430048170 mRNA
GCTCTGTTTGTAAGGGCTGATTCCTTGAAAATGTAATTTTCCAGAAAAACACCTAAAGAA NM_005999RefSeq chr1
+ 231528652 231566523 TSNAX 7257 translin-associated factor X
GO:0010467|GO:0048471|GO:0005794|GO:0005634|GO:0007275|GO:0004521|GO:0007283|GO:0015031|GO:0003
677|GO:0046872|GO:0030154|GO:0005829|GO:0043565|GO:0005737|GO:0003697|GO:0008565 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141388_PI430048170 0.6673953083663221.0437481859376 8.73285979835042
8.48933760961338 8.77064748667495 P P P 8.38971335671428 8.67714039223328 8.7334924679837
P P P LNCV6_141388_PI430048170 mRNA
TTTCAGCTTTGCACCTGGAACTCTGTAGTAATAATAAAAGTTATTGCTTATTGGGCATTC NM_006809RefSeq chr20
- 44942129 44960473 TOMM34 10953 translocase of outer mitochondrial membrane 34
GO:0005737|GO:0016020|GO:0031072|GO:0006626|GO:0005741|GO:0005654|GO:0005634|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133701_PI430048170 0.42199156176085 0.85272652013585 6.46987056834804
6.06167141121487 5.83505184562286 P P P 6.61619218753702 6.44064346678459 6.0058842857669
P P P LNCV6_133701_PI430048170 mRNA
GTCCCTGTTCTCCAGAATTTGCAAAACCATTAAAAAAGCACCTACTTTAAGCCATTTTTT NM_054114RefSeq chr6
- 159034468 159045152 TAGAP 117289 "T-cell activation RhoGTPase activating protein, transcript variant 2"
GO:0043547|GO:0005085|GO:0051056|GO:0007264|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131860_PI430048170 0.3944991664662040.8025446724172683.7937188719742
4.59037227009061 4.28016536064953 P P P 4.06909418554989 4.7036211419949
4.84121745121614 P P P LNCV6_131860_PI430048170 mRNA
GGGAGATTATTTGCCTGAGATGGAAAGAGAGATGGATGATTTATTGCTTCAATTGTTTTA NM_003940RefSeq chr3
+ 179653144 179789401 USP13 8975 ubiquitin specific peptidase 13 (isopeptidase T-3)
GO:0005515|GO:0043130|GO:0006355|GO:0004843|GO:0008283|GO:0050821|GO:0006914|GO:0030318|GO:0005
764|GO:0004197|GO:0070536|GO:0061136|GO:0010506|GO:0043161|GO:0008270|GO:0008242|GO:0031625 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132283_PI430048170 0.0957962882457588 0.9614346265841790.405192576476423
0.4098923411080680.344853753406084A A A 0.4308072967273110.462217787213642
0.437850392748881A A A LNCV6_132283_PI430048170 mRNA
TGGAAGCAGCCGCTGATTACCCTTGCAAAGAAATCTGTAAAATGTGCACGTGAATGTCTG NM_033223RefSeq chr15
+ 26971281 27533227 GABRG3 2567 "gamma-aminobutyric acid (GABA) A receptor, gamma 3,
transcript variant 1"
GO:0005230|GO:0034220|GO:0030054|GO:0005886|GO:0004890|GO:0045211|GO:0042493|GO:0034707|GO:0007
268|GO:0007214|GO:0055085|GO:0005254 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143929_PI430048170 0.54457249380783 0.7627175861387791.54832473956274
0.4013122595377240.242670079074555A A A 1.88861643225677 0.424412084633497
1.05151201373178 A A A LNCV6_143929_PI430048170 mRNA
GGACAAGTAAGTGGATAGGTCATAGAATTCCTACACAAGAATACCTGGACTAATAACTAT NM_021954RefSeq chr13
- 20138255 20161044 GJA3 2700 "gap junction protein, alpha 3, 46kDa"
GO:0005243|GO:0007267|GO:0006810|GO:0005922|GO:0016021|GO:0055085|GO:0007601 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130647_PI430048170 0.4807208776242651.01410536914503 0.307591185959886
0.3353084442138350.384339422245243A A A 0.33828773143621 0.32476525812122
0.304411354174155A A A LNCV6_130647_PI430048170 mRNA

CTGAGGCTAGGCTGAGTACTTATTATACGGCTACATTTACACATTTACACTTATCTAATA NM_005894 RefSeq chr1
- 157830913 157841844 CD5L 922 CD5 molecule-like
GO:0006968|GO:0016020|GO:0006915|GO:0072562|GO:0005576|GO:0005615|GO:0006898|GO:0070062|GO:0005
044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128811_PI430048170 0.7242885279839891.14673157817689 1.13426333268226
2.15769773458354 2.06318779291782 A A A 1.81434943701892 1.56207712820913
1.57522518540203 A A A LNCV6_128811_PI430048170 mRNA
TCCTCTACTGCATATCCGGAGTACTTGTTTGGTTGTCATTGTATAATAAAGGCTTCTTCT NM_001258031 RefSeq chr15
- 43794173 43800097 SERINC4 619189 "serine incorporator 4, transcript variant 1"
GO:0016021|GO:0008654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136929_PI430048170 0.0293559088599380.3426129374416931.45087999593574
2.72609889615486 1.98536113307423 A A A 3.80431175018104 3.25698073781102
3.93717660160579 P P P LNCV6_136929_PI430048170 mRNA
ATTGTATGAAATAAACCTGGTCTTGTGTTTTTCTCTAGATAAAATACCCCTCTGTACCTC NM_015317 RefSeq chr2
- 20248691 20350850 PUM2 23369 "pumilio RNA-binding family member 2, transcript variant 1"
GO:0005515|GO:0048471|GO:0034063|GO:0031965|GO:0005737|GO:0010494|GO:0006417 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_64245_PI430048170 0.3364703593299150.5974347491524520.5947779930651720.8527861765324
0.791407489843473 A A A 1.50296472871911 0.4494131138482292.08679519988514 A A A
LNCV6_64245_PI430048170 mRNA
CGTCGTCTCCATGAGCTTTGGGGGGACTTTTATGTGGAATAAAGAAACTATCACTGAGAA NM_033064 RefSeq chr19
+ 3880619 3928082 ATCAY 85300 "ataxia, cerebellar, Cayman type"
GO:0048311|GO:0005515|GO:0030424|GO:0043005|GO:0030054|GO:0031966|GO:0045202|GO:0006915|GO:0030
425|GO:0031175|GO:0005739|GO:0032880|GO:0005737|GO:2000212|GO:0006810|GO:0019894 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136316_PI430048170 0.6744992039021020.8495314815202721.92689778593894
1.62904010567404 0.321121152661046 A A A 0.9839861419013881.46075383275322
2.28003177258762 A A A LNCV6_136316_PI430048170 mRNA
GAAGCCTCTGTACCCAACCCTGACCTATGTGGACCAGTCCCATAAACATTCAATAAATGT NM_001042693 RefSeq
chr1 + 52633393 52657065 FAM159A 348378 "family with sequence similarity 159, member A"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100658_PI430048170 0.2344154529313 0.7520156543053684.52393439511202
4.20214067558583 4.55201118616276 P P P 4.34860022369826 5.0493759213648
5.03451338430256 P P P LNCV6_100658_PI430048170 mRNA
TTTGAGCTCAGATATCGGGCTGAACGGTCAAAGACATTCACAACATGGATGAATCCAGGA NM_000565 RefSeq chr1
+ 154405192 154469450 IL6R 3570 "interleukin 6 receptor, transcript variant 1"
GO:0005515|GO:0005138|GO:0032755|GO:0008284|GO:0032717|GO:0070119|GO:0005886|GO:0050830|GO:0019
221|GO:0050731|GO:0019981|GO:0005615|GO:0042803|GO:0070110|GO:0016323|GO:0016324|GO:0051092|GO:0
002384|GO:0070102|GO:0004897|GO:0034097|GO:0010536|GO:0002446|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128701_PI430048170 0.1509229471883471.07689658124626 0.510922603192599
0.3414074910008290.427951788240531 A A A 0.2759475926279740.360956030055003
0.326451213376737 A A A LNCV6_128701_PI430048170 mRNA
ACATCTCTGCTAAACAGTTGATGGGGTATCTCTTGATTAGGGGGATCCCTAATATCCCCA NM_001300837 RefSeq
chr12 - 53326575 53344793 SP7 121340 "Sp7 transcription factor, transcript variant 3"
GO:0005737|GO:0006357|GO:0045944|GO:2000738|GO:0017151|GO:0005634|GO:0060218|GO:0003677|GO:0046
872|GO:0006351|GO:0001649 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126969_PI430048170 0.7754874939787721.04104623696479 9.66465157039821
9.86093779394749 10.1302569795736 P P P 9.69992832621995 9.67515227382558

10.1035144030327 P P P LNCV6_126969_PI430048170 mRNA
ATACTGGGAACCTATTTTCTCAATCTTCCTCCATGTTGTGTTCTTTGTATTCTTGAGATG NM_015509RefSeq chr12 +
8082210 8097777 NECAP125977 "NECAP endocytosis associated 1, transcript variant 1"
GO:0030125|GO:0005905|GO:0005886|GO:0015031|GO:0006897 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_65694_PI430048170 0.2765580510709760.6904436300190993.38979673443429 3.74623177829059
3.90186672994286 P P P 4.74783868599937 3.64121338865233 4.080731700464 P P P
LNCV6_65694_PI430048170 mRNA
CATGCTAGGGAAAGTGCAGTGTTGCCCTTCTGAATGAGACAGAATCAGTATTGTCATATC NM_001282755 RefSeq
chr2 + 42494568 42756947 MTA3 57504 "metastasis associated 1 family, member 3, transcript
variant 1"
GO:0043565|GO:0005515|GO:0006355|GO:0003700|GO:0003682|GO:0006325|GO:0008270|GO:0005654|GO:0005
634|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135522_PI430048170 0.7657986819778041.70917162482273 0.410100092535711
3.01496893277712 0.305396966100529A P A 1.74370869309566 0.729226019854593
0.290665304779339A A A LNCV6_135522_PI430048170 mRNA
CCTGACTGGTCTAGAGAACTGATGTTTCAATTTACCCCTCTGCTAAATAAATATTAAAAC NM_001920RefSeq chr12
- 91145257 91183029 DCN 1634 "decorin, transcript variant A1"
GO:0019800|GO:0005518|GO:0005589|GO:0044281|GO:0005539|GO:0005615|GO:0030208|GO:0030207|GO:0030
206|GO:0022617|GO:0030198|GO:0032496|GO:0009887|GO:0030204|GO:0030203|GO:0043202|GO:0005975|GO:0
005796|GO:0001822|GO:0007568|GO:0050840|GO:0005578|GO:0005576|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143158_PI430048170 0.5601700496039160.9701554763556440.477399467617217
0.4935216391591050.303234149327865A A A 0.406425466113061 0.524309120395753
0.479717931790948A A A LNCV6_143158_PI430048170 mRNA
TGTGGGTGTCGTTTATGTTTATGGAATGAAACGGTTCTGCGATGACATTGCGTGGATGAC NM_182632RefSeq chr5
+ 1225354 1246189 SLC6A18 348932 "solute carrier family 6 (neutral amino acid transporter),
member 18"
GO:0005886|GO:0005887|GO:0005328|GO:0006865|GO:0006836|GO:0031526|GO:0055085|GO:0003333|GO:0006
811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126189_PI430048170 0.0324984526105707 1.19099842939741 7.74805684960039
7.78708512706797 7.94526707345941 P P P 7.5031421174949 7.62547872398467
7.60005127973391 P P P LNCV6_126189_PI430048170 mRNA
TTTGTGGCTATCAGTGACTTGTATGAGCCCATTGATGATGGTTGTGAGAGCCAGTGTTCT NM_001493RefSeq chrX
+ 154436912 154443467 GDI1 2664 GDP dissociation inhibitor 1
GO:0005515|GO:0051056|GO:0043005|GO:0017137|GO:0005794|GO:0007264|GO:0030496|GO:0090315|GO:0015
031|GO:0005829|GO:0043547|GO:0051592|GO:0043234|GO:0007165|GO:0005737|GO:0050771|GO:0005093|GO:0
005092|GO:0032482|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128483_PI430048170 0.2404012341112461.02072026501632 0.319737402436572
0.2611109334014540.274010250052021A A A 0.2550533024212210.254876326527549
0.256825530894715A A A LNCV6_128483_PI430048170 mRNA
CACCCTATTTACACCTATGTTGAACCCTTTAATCTACACTGTCAAAAATAAAGCAGTGAA NM_001005513 RefSeq
chr11 + 50032873 50033794 OR4C45NA "olfactory receptor, family 4, subfamily C, member 45" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109643_PI430048170 0.3014945486512770.8280174760711333.44527903564668
2.93976286465779 2.74367440896004 P A A 3.49857467153863 3.11773908741053
3.39611554613477 P P P LNCV6_109643_PI430048170 mRNA
CATCCTTTGAACAAGAGCATGCTATGTGTAGGGCTAATGGTGAATTTTACAGTCTTTTTT NM_015336RefSeq chr12
+ 76764073 76853694 ZDHHC17 23390 "zinc finger, DHHC-type containing 17"

GO:0005515|GO:0015693|GO:0018345|GO:0005794|GO:0015095|GO:0043231|GO:0042802|GO:0007165|GO:0042953|GO:0005737|GO:0000139|GO:0030660|GO:0016409|GO:0008270|GO:0004871|GO:0016021|GO:0043123|GO:0019706 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130787_PI430048170 0.0021958668169619 2.19955839196797 9.31721017753917 9.36207020499458 9.15533013273621 P P P 8.30312727849471 8.17289866207604 7.93061011068967 P P P LNCV6_130787_PI430048170 mRNA CGTCCTCCTGGGGTGGACCCTAGTTTAATAAAGATTCACCAAGTTTCACGCATCAAAAAA NM_001302688 RefSeq chr19 + 44905748 44909395 APOE 348 "apolipoprotein E, transcript variant 1"
GO:0005515|GO:0010468|GO:0006707|GO:0007603|GO:0005764|GO:0002021|GO:0005615|GO:0034361|GO:0034365|GO:0034364|GO:0034363|GO:0034362|GO:0019433|GO:0034447|GO:0033344|GO:0032868|GO:0005794|GO:0016209|GO:0007568|GO:0031232|GO:0006898|GO:0007271|GO:0034372|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142351_PI430048170 0.14133268501271 1.13959381337538 11.6061884991231 11.6823103698874 11.5057611149375 P P P 11.3942374122316 11.5595214484142 11.2652268768784 P P P LNCV6_142351_PI430048170 mRNA AGGGTGGGACCCAGTTTTGCGTGGTTGGTTTTTATTAATTATCTGGATAACAGCAAAAAA NM_006411 RefSeq chr6_GL000256v2_alt - 3484412 3492346 AGPAT1 10554 "1-acylglycerol-3-phosphate O-acyltransferase 1, transcript variant 1"
GO:0005783|GO:0044281|GO:0001819|GO:0003841|GO:0006112|GO:0031325|GO:0016020|GO:0001961|GO:0005789|GO:0016024|GO:0019432|GO:0016021|GO:0006644|GO:0006654|GO:0044255|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127884_PI430048170 0.2032547734538590.611067364259398 4.28461888177535 3.81868340223283 4.15166943163571 P P P 4.11939408394876 5.33777387867676 4.71421483144526 P P P LNCV6_127884_PI430048170 mRNA GAGGGTGGTTCCTGTTCTCAGCATCCACTAATATTCAGTCCTGTATATTTTAATAAAATA NM_013434 RefSeq chr2 + 95297323 95386077 KCNIP3 30818 "Kv channel interacting protein 3, calsenilin, transcript variant 1"
GO:0005886|GO:0005783|GO:0015459|GO:0005634|GO:0006886|GO:0030425|GO:0005829|GO:0043523|GO:0032993|GO:0034765|GO:0043679|GO:0071805|GO:0005794|GO:0005244|GO:0006357|GO:0003714|GO:0005509|GO:0005267|GO:0006915|GO:0000122|GO:0008022|GO:0003677|GO:0006351|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143948_PI430048170 0.4215135742300760.9739527177244430.431065384276998 0.4234195061390920.407145691640135 A A A 0.5020419998935340.486833970623841 0.384265734261007 A A A LNCV6_143948_PI430048170 mRNA TGTAAAGAAGCATCGTGTTTACCTGTGCAGGCACTAGTCCTTTACAGATGACCATGCTGA NM_002173 RefSeq chr9 - 21216372 21217311 IFNA16 3449 "interferon, alpha 16"
GO:0005132|GO:0019221|GO:0005576|GO:0033141|GO:0045343|GO:0005125|GO:0005615|GO:0002250|GO:0051607|GO:0060337|GO:0060338|GO:0007596|GO:0042100|GO:0045087|GO:0006959|GO:0030183|GO:0043330|GO:0002286|GO:0002323. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122051_PI430048170 0.3080647784560280.8557915687501249.43651771251055 8.86442347839303 9.188847197264 P P P 9.59650600223441 9.36824987469469 9.23164696496251 P P P LNCV6_122051_PI430048170 mRNA GCAAAGCAGTCTGTAAAATTTCAGTCTCAAAGCAAACAAAAGAGTATTGAAGAGTGAAGT NM_018848 RefSeq chr20 - 10404779 10431925 MKKS 8195 "McKusick-Kaufman syndrome, transcript variant 1"
GO:0005515|GO:0008406|GO:0007608|GO:0038108|GO:0007368|GO:0021987|GO:0051216|GO:0007286|GO:0045776|GO:0045494|GO:0051877|GO:0032402|GO:0005829|GO:0007507|GO:0005622|GO:0001947|GO:0060027|GO:0006457|GO:0042311|GO:0045444|GO:0040018|GO:0051131|GO:0001103|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145659_PI430048170 0.1937381186029140.91406861644194 0.282277110838395 0.3417459420882170.317908827573125 A A A 0.4225093113311280.334708762839209

0.564811765578464 A A A LNCV6_145659_PI430048170 mRNA
AAGTTCAAGTCAACTGTTTTTCCCATATGGGCACCAAATTGTATCTTTCCTGTTTTCTTT NM_006219 RefSeq chr3 - 138652697 138759359 PIK3CB 5291 "phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit beta, transcript variant 1"
GO:0005515|GO:0008286|GO:0050852|GO:0005886|GO:0043560|GO:0005634|GO:0044281|GO:0050900|GO:0005829|GO:0000187|GO:0006935|GO:0007173|GO:0040016|GO:0016303|GO:2000369|GO:0007156|GO:0048010|GO:0048011|GO:0006661|GO:0036092|GO:0048015|GO:0006914|GO:0006874|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135822_PI430048170 0.000246215928716133 0.346009249358289 5.56390323885289 5.27854064791389 5.43179442833589 P P P 6.89400669629849 6.83793662111625 7.13249527408238 P P P LNCV6_135822_PI430048170 mRNA
GCAGACAAGGGCTAAGATTTCCTTAGCAGTAATAATGACATACACTGAATTGAAAATCTA NM_003758 RefSeq chr15 + 44537067 44562803 EIF3J 8669 "eukaryotic translation initiation factor 3, subunit J, transcript variant 1"
GO:0005515|GO:0010467|GO:0005852|GO:0016282|GO:0033290|GO:0001731|GO:0003743|GO:0006412|GO:0006413|GO:0005829|GO:0002181|GO:0006446|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69209_PI430048170 0.0901591272581430 0.389429451317356 0.794222870234771 0.813502935837317 1.35903484888958 A A A 3.05231769387085 2.12670342673836 1.53120219127063 P A A LNCV6_69209_PI430048170 mRNA
CGAGAACAGGGAGATAAACATCATCATCTTCTAAGAGCTGGTCAAGAAATTTAAAACAAC NM_001164404 RefSeq chr15 + 75258557 75273455 GOLGA6C 653641 "golgin A6 family, member C" GO:0005794 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127528_PI430048170 0.873054449101136 1.04243385767091 4.0205851687186 3.33674964106943 3.87876538854325 P P P 3.68491184783655 3.92650743617058 3.49910352915599 P P P LNCV6_127528_PI430048170 mRNA
TTTTTCCAGGTTCAATTTTTAAATCACAGTCAGGACAGGCCCATCCACCCCAGTATGACC NM_178160 RefSeq chr17 + 74924274 74933911 OTOP2 92736 otopetrin 2 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126862_PI430048170 0.521715869555225 0.952472050900245 4.99037834772293 5.10055441752549 5.27271288430549 P P P 5.08583974528828 5.19744947173045 5.29747684528246 P P P LNCV6_126862_PI430048170 mRNA
AATCAAATCATTTCCAACCATACTGGAGTCGCGTATATACATATTCAAGACACCTGTGCA NM_001123040 RefSeq chr3 - 48917787 48919385 ARIH2OS 646450 ariadne homolog 2 opposite strand GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61109_PI430048170 0.0850954638360715 0.839878456117243 9.64598703887114 9.4728390268368 9.68078752109114 P P P 9.74955281520933 9.77896202873273 10.0193634419733 P P P LNCV6_61109_PI430048170 mRNA
TGTTACATTCTCCCTTTAGCAACCTGAGTAAGAGACTCTCTGCCACTGGGCTGCAAAAAA NM_001242924 RefSeq chr14 + 73886614 73932288 ZNF410 57862 "zinc finger protein 410, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142341_PI430048170 0.00393715999033262 0.477070598262168 8.37310759237574 7.93191732235382 8.02988663770832 P P P 8.99487737946489 9.38342990955718 9.17152197713674 P P P LNCV6_142341_PI430048170 mRNA
GGACAAAGATGGGGAAGGTGTGTGAACTTTTTAAAATAAACACAAAAACACAGGCCTGTT NM_001282662 RefSeq chr22 - 40410280 40636719 MKL1 57591 "megakaryoblastic leukemia (translocation) 1, transcript variant 4"
GO:0005515|GO:0000976|GO:0003700|GO:2001234|GO:0003713|GO:0010735|GO:0003779|GO:0005634|GO:0006351|GO:0003785|GO:0043522|GO:0005737|GO:0045944|GO:0005654|GO:0043154|GO:0051145 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_141328_PI430048170 0.7511396721293821.0570475891597 1.01048912252298
0.5912720158617120.457288193370939A A A 0.5152389431732860.388217830420359
0.919904844682965A A A LNCV6_141328_PI430048170 mRNA
CTCTAACAGATCCTCAATTCTTAACAGACATAAGCTAATTCATACTAGAGAGAAACTGCA NM_001267716 RefSeq
chr19 - 22974882 23003208 ZNF728 388523 zinc finger protein 728
GO:0005622|GO:0006355|GO:0003676|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55287_PI430048170 0.0395869787064652 0.3459329781424113.17778207151619
2.72311345252072 3.88429688042899 A A P 4.92613213406785 4.79254174549394
4.89804054438286 P P P LNCV6_55287_PI430048170 mRNA
TGTTTGGGGATGAAGAAGTGATGTGTTTAAATGGAAACTGGACAGAACCACCTCAATGCA NM_002113 RefSeq chr1
+ 196819730 196832189 CFHR1 3078 complement factor H-related 1
GO:0006956|GO:0072562|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129082_PI430048170 0.411063375316088 1.03922921347645 0.338917523492262
0.3420674122696240.494904874563328A A A 0.36228771099072 0.298103807505063
0.353693168445413A A A LNCV6_129082_PI430048170 mRNA
ATCTGGTTAATTGTGATTTCCCAACAAACATCACCTGCGTTGTGTACAGCCACGATGGCA NM_001136533 RefSeq
chrX + 27746808 27748821 DCAF8L2 NA DDB1 and CUL4 associated factor 8-like 2 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_136464_PI430048170 0.285776822663175 1.17134417986479 0.400283249571894
0.8681238517013430.453739332911256A A A 0.3365717076058360.347909146047007
0.399194796671593A A A LNCV6_136464_PI430048170 mRNA
TAAAATGCTGGCCCATGAGGCTCTACAGGATGCTTCAGTCCTGATATTTGCCAATAAGCA NM_001143968 RefSeq
chr17 - 39156893 39166161 ARL5C NA ADP-ribosylation factor-like 5C NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_130800_PI430048170 0.00343442841212613 0.4515091540065 4.54359909140754
4.29274555871975 4.16810231447249 P P P 5.21446846681968 5.67953395911493
5.53905942202622 P P P LNCV6_130800_PI430048170 mRNA
AAGCTTTGTGCTCTGATAAATTGTGTTCTGTTAAAGAGGTTAGTAGGATGAAAACAGCAA NM_022776 RefSeq chr3
- 125528857 125595537 OSBPL11 114885 oxysterol binding protein-like 11
GO:0005794|GO:0010890|GO:0031902|GO:0006869|GO:0045444|GO:0008289 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140378_PI430048170 0.3523876146480111.06730079932763 8.91044411202631
9.00242232225981 9.06950870927844 P P P 8.7456920810013 8.98690961990457
8.96036468466958 P P P LNCV6_140378_PI430048170 mRNA
TCCATACCTGAGTGCTGTACATAAGTTGTTCTGTGTATAAATAAAACAAGCCTGTTTTTG NM_152879 RefSeq chr2
+ 233354506 233472097 DGKD 8527 "diacylglycerol kinase, delta 130kDa, transcript variant 2"
GO:0005515|GO:0005886|GO:0015031|GO:0007205|GO:0042803|GO:0046872|GO:0005737|GO:0007173|GO:0004
143|GO:0051260|GO:0010033|GO:0046982|GO:0030168|GO:0007275|GO:0005524|GO:0006897|GO:0019992|GO:0
007165|GO:0016310|GO:0003951|GO:0007596|GO:0019932|GO:0016023|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139201_PI430048170 0.00257128125289594 1.16307495725703 6.90321570297657
6.86466681844156 6.9483441404914 P P P 6.67699022983844 6.65928738910424 6.726489730622
P P P LNCV6_139201_PI430048170 mRNA
GAAAAAGGAGGCATCTGCAAACGAAAACAATTTCTACGAGGTTATATGTGATTGTTAACA NM_152411 RefSeq chr7
- 149069640 149090777 ZNF786 136051 zinc finger protein 786
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143872_PI430048170 0.00320617142229986 2.05868767666996 6.91400915521306

7.04078177011564 7.22424435465735 P P P 5.77126861351123 6.09917507996421
6.16985326565544 P P P LNCV6_143872_PI430048170 mRNA
GTTCAGTAACCCTATGTGAATCAGATGTCTCCTGGATAACATTAAAGCCATGTCTTTGTC NM_152331 RefSeq chr14
+ 73591705 73595766 ACOT4 122970 acyl-CoA thioesterase 4
GO:0052689|GO:0000038|GO:0004778|GO:0006637|GO:0001676|GO:0046459|GO:0043648|GO:0016290|GO:0043
649|GO:0005102|GO:0047617|GO:0032789|GO:0032788|GO:0006104|GO:0019605|GO:0005777 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133867_PI430048170 0.000606408384862905 0.38032428401866 6.54433195468915
6.45211988830106 6.25965109771618 P P P 7.61257612077873 7.96604654278198
7.85376178890792 P P P LNCV6_133867_PI430048170 mRNA
TGACAACGAGGGGGTAGCCAGAAGAGAAGCACTGGATTCCTCAGTCCACCAGCTCAGACA NM_178493 RefSeq
chr17 - 81952506 81961181 NOTUM 147111 notum pectinacetylesterase homolog (Drosophila)
GO:0016787|GO:0008152|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128468_PI430048170 0.193466135846907 0.900805569116618 5.91982499153232
5.71973247115606 5.9626365860247 P P P 6.12664903512426 5.91559140847848
6.01582770172196 P P P LNCV6_128468_PI430048170 mRNA
ATATACAGGAATACAAATCGGTAACCAGCAGCTGTTCCTCAGGTTGTGACTCACTGAGCA NM_173079 RefSeq chr17
+ 42980564 42993690 RUNDC1 146923 RUN domain containing 1 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128384_PI430048170 7.00965711410494e-05 1.97886496568921 8.7790582009598
8.86174760209205 8.7179477453005 P P P 7.87411342105363 7.7945334866915
7.73638434149427 P P P LNCV6_128384_PI430048170 mRNA
AAAGAACTTAAGGATTTCTGCAAGTATGAGTGAAGACCCACAGTGCACCAGAGCACAGCT NM_001278535 RefSeq
chr20 - 45888471 45891287 NEURL2 140825 "neuralized E3 ubiquitin protein ligase 2, transcript variant
2" GO:0035556|GO:0016567|GO:0030891|GO:0045214|GO:0005927 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129859_PI430048170 0.197849492439353 0.85578669731909 8.41515781277413
8.48308228802247 8.77848238556897 P P P 8.78711392083119 8.62080747724316
8.95042787860923 P P P LNCV6_129859_PI430048170 mRNA
CTATGGTCAGTTGAGGAATATGACTGTTTTTATATGCACATGTAACCCAAATGTCCAATA NM_007099 RefSeq chr2
+ 264868 278282 ACP1 52 "acid phosphatase 1, soluble, transcript variant 2"
GO:0005515|GO:0005737|GO:0003993|GO:0009898|GO:0035335|GO:0070062|GO:0004726 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143600_PI430048170 0.283823527021175 1.02389595874127 0.313637406653752
0.246253259062026 0.318986482082703 A A A 0.26562170200847 0.245249148398165
0.266830048223854 A A A LNCV6_143600_PI430048170 mRNA
TTCCGATGGCTAGAAAAATGCAAAACACAGTGGATATCATTGCATCTATTTTCATGTCTT NM_021911 RefSeq chr5
- 161288428 161548124 GABRB2 2561 "gamma-aminobutyric acid (GABA) A receptor, beta 2,
transcript variant 1"
GO:0030054|GO:0005886|GO:0004890|GO:0005237|GO:0007605|GO:0034707|GO:0060119|GO:0007268|GO:0007
214|GO:0055085|GO:0005254|GO:0005829|GO:0060384|GO:0043524|GO:0034220|GO:0005887|GO:0045211|GO:0
090102|GO:0006810|GO:0051932|GO:0071420|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_137867_PI430048170 0.472226236426429 1.29083426727962 1.92203022211067
1.35628741510375 2.50971002815377 A A A 1.09490973333696 1.59190341456847
2.06371317620493 A A A LNCV6_137867_PI430048170 mRNA
CTGCCAGTATGTCTTGTTGCTAAAATAAAGGGCCTCAAAATGAAAAATAGGATAACCTAA NM_016053 RefSeq chr12
- 102012839 102062124 CCDC53 51019 "coiled-coil domain containing 53, transcript variant 1"
GO:0005515|GO:0008150|GO:0071203|GO:0015629|GO:0043231 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_62304_PI430048170 0.0204945024417149 0.67154423386916 5.97875304824609
5.81594472211213 6.22610489893687 P P P 6.41517006897224 6.62461984875071
6.71772691079802 P P P LNCV6_62304_PI430048170 mRNA
TAGAAAGCCGCTGGGGTTACAGTGGGACGAGTGATCGAATCAGATTCACAGTTAATAGAA NM_025238 RefSeq chr15
- 83016428 83067354 BTBD1 53339 "BTB (POZ) domain containing 1, transcript variant 1"
GO:0005515|GO:0043234|GO:0016567|GO:0000932|GO:0043393 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136578_PI430048170 0.000485087709908529 0.4629991575160326.72327692540911
6.60083872053535 6.8716772420077 P P P 7.83960860990318 7.72282961248679
7.96842065975297 P P P LNCV6_136578_PI430048170 mRNA
TGTTGAGGAAAGGAAAAGGGCATTTGTCTAAACATGGATTCTGAGTTGTATATATTTCCT NM_014034 RefSeq chr6
+ 118894076 118909170 ASF1A 25842 anti-silencing function 1A histone chaperone
GO:0005515|GO:0000790|GO:0006334|GO:0006335|GO:0005634|GO:0006336|GO:0001649|GO:0006351|GO:0042
692|GO:0043234|GO:0042393|GO:0006281|GO:0003682|GO:0005654|GO:0016568|GO:0031936 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133383_PI430048170 0.3469634114779551.02157196370207 0.325817028824527
0.24362235102525 0.307699493248795 A A A 0.2654644614231120.253872898252236
0.26668102399174 A A A LNCV6_133383_PI430048170 mRNA
GTCCTCACGTGTCTGATACGTGTGTGCATTCCTTGAGGAAAATTTCTTTAATTAAAATTT NM_031431 RefSeq chr13
+ 45464894 45536698 COG3 83548 component of oligomeric golgi complex 3
GO:0005515|GO:0005801|GO:0005794|GO:0033365|GO:0005886|GO:0006890|GO:0050821|GO:0006891|GO:0006
886|GO:0006888|GO:0005737|GO:0032580|GO:0008565|GO:0007030|GO:0017119|GO:0005654|GO:0006486|GO:0
000301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133572_PI430048170 0.4274689749921370.9568791134682821 1.9027772517624
11.7881560423587 11.7579130408239 P P P 11.7934276013529 11.8611266571256
11.9827334408354 P P P LNCV6_133572_PI430048170 mRNA
CGAGTCTGTTTTTCATGCGATGACACTTGTACAATTAATTATCTTTTCAAAGGTACTTGG NM_003502 RefSeq chr16
- 287439 352676 AXIN1 8312 "axin 1, transcript variant 1"
GO:0005515|GO:0008219|GO:0008013|GO:0045599|GO:0007605|GO:0046330|GO:0030877|GO:0030159|GO:0038
032|GO:0046332|GO:0031122|GO:0043621|GO:0043623|GO:0042803|GO:0042802|GO:0030163|GO:0021797|GO:0
031398|GO:0051443|GO:0051260|GO:0005938|GO:0031625|GO:0000209|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129248_PI430048170 0.751506932335332 1.08150132142709 2.75471771724568
1.66424479880129 1.82263416899707 A A A 0.6534890155602862.55319697224454
2.32181628168888 A P A LNCV6_129248_PI430048170 mRNA
GGCAGCATTTTTCTTGGTCTACTTTGGCAAAAGAACATTTAAAAGCTGGTAACAAAACAA NM_138364 RefSeq chr4
- 147637784 147684230 PRMT9 90826 "protein arginine methyltransferase 9, transcript variant 1"
GO:0005737|GO:0006479|GO:0008276 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134542_PI430048170 0.7610449317256920.9869035431520540.455833337996352
0.4139144652130250.262494636739488 A A A 0.3585584903820170.425708326310698
0.411258283105771 A A A LNCV6_134542_PI430048170 mRNA
GGAGGGTTTTCTGTAGCAAAATCAGTGACCAATGAAGTAACTTAAATTCCTATTGAAGAA NM_022093 RefSeq chr1
+ 175067857 175148066 TNN 63923 tenascin N
GO:0003674|GO:0005178|GO:0016477|GO:0009986|GO:0007160|GO:0005578|GO:0016049|GO:0007409|GO:0005
575|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_46806_PI430048170 0.7016352808653431.04749426933591 7.82753081665044 7.99045393217976
8.17499482038144 P P P 7.91484592362873 7.66034537818992 8.18942858686422 P P P
LNCV6_46806_PI430048170 mRNA

TACGAAGATTGTATTGAGAAGGCAGTTCAGTTTTTCGTACAGGCTCTCAGGATGGCTCCT NM_003315 RefSeq chr17 - 41976420 42017697 DNAJC7 7266 "DnaJ (Hsp40) homolog, subfamily C, member 7, transcript variant 1" GO:0005515|GO:0005737|GO:0016020|GO:0070389|GO:0006457|GO:0031072|GO:0005654|GO:0005856|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111393_PI430048170 0.0985778407560321 1.29087220558849 8.95694803943573 8.55386917921491 8.87972914536456 P P P 8.41029000656365 8.43728663188675 8.46824504388554 P P P LNCV6_111393_PI430048170 mRNA
AACCCAGGAAATTAGCAAGGGAAAGAGGAAAGAGGATAGCTTGACTGCCTCTCAGAGAAA NM_022978 RefSeq chr5_KI270897v1_alt + 449076 466957 SERF1B 728492 "small EDRK-rich factor 1B (centromeric), transcript variant 2" GO:0003674|GO:0005575|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142795_PI430048170 0.384333174889454 0.656910472270526 0.443982834662563 0.428935806939922 0.24755874383678 A A A 0.378945383837213 0.459223505797446 1.70143291217534 A A A LNCV6_142795_PI430048170 mRNA
TGGGGCAGGGCTTCTTGAGAGCCGTCGTTTTTCTAATAAAATGGACAGATCCAGAAAAAA NM_001165974 RefSeq chr3 - 126481164 126517773 UROC1 131669 "urocanate hydratase 1, transcript variant 2" GO:0034641|GO:0016153|GO:0019557|GO:0019556|GO:0006548|GO:0044281|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145173_PI430048170 0.113786703295607 1.05728469779258 0.440932182600478 0.479501170512026 0.491657560498043 A A A 0.334073239182194 0.388899640500358 0.446326818745674 A A A LNCV6_145173_PI430048170 mRNA
CCTGAAAACTGGTGGTGTGATTGTTGAATGGGTTAGGGGTATAGCAGAGAAACTCAGTGT NM_001271733 RefSeq chr1 - 16754633 16764480 MST1L 11223 macrophage stimulating 1-like GO:0004252|GO:0006508|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90567_PI430048170 0.0845981102222738 0.687011584230179 5.49267055218293 4.83836623590296 5.23865166427091 P P P 5.75032806783705 5.63740713680276 5.87112696812403 P P P LNCV6_90567_PI430048170 mRNA
AACTTCCACATGGAACAGCTGAAGTATGCTGAATTACGAGCACGACAGCAAATGGAACAG NM_003074 RefSeq chr3 - 47585887 47781915 SMARCC1 6599 "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1" GO:0008286|GO:0001741|GO:0005515|GO:0071565|GO:0000790|GO:0006357|GO:0043044|GO:0003713|GO:0031492|GO:0006325|GO:0006337|GO:0000978|GO:0071564|GO:0006351|GO:0007399|GO:0043234|GO:0047485|GO:0016514|GO:0045944|GO:0009887|GO:0000980|GO:0005654|GO:0006338|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138954_PI430048170 0.500494000856575 0.775995204860854 0.275985324009559 0.288606658811788 1.61322563710512 A A A 0.427601345913093 1.60882209285281 1.42323724413878 A A A LNCV6_138954_PI430048170 mRNA
GGGCCCTTCAGAGAACCCAATATGAACATGATTTATCTATTTATTCAGTTTTTATGTCCT NM_001270497 RefSeq chr20 - 46499629 46513559 ZNF334 55713 "zinc finger protein 334, transcript variant 3" GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116526_PI430048170 0.176332395286538 0.800946580101148 4.30084001202758 4.49559529175798 4.82004983755857 P P P 5.11523755754541 4.7390627396324 4.7373665175059 P P P LNCV6_116526_PI430048170 mRNA
CAAGCTGTTGCAAGAGGATTTTTTAACTATATTGAAAAACTGAAGTATGAACACCACCTG NM_024116 RefSeq chr11 - 93735930 93741537 TAF1D 79101 "TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa" GO:0005515|GO:0005668|GO:0010467|GO:0005815|GO:0006363|GO:0006362|GO:0006361|GO:0006360|GO:0003677|GO:0000183|GO:0045814|GO:0040029|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_136123_PI430048170 0.3734340924547181.88289658206757 0.305576101254579
2.08906865689414 0.390107354028505 A A A 0.2788070176625550.24651226968073
0.278024547286129 A A A LNCV6_136123_PI430048170 mRNA
GAGGCTGATTTCTAACGAAACTTGTAGAATGAAGCCTGGAAAGAGTGATGAATTATATTA NM_138294 RefSeq chr11
+ 125746292 125749848 PATE1 160065 prostate and testis expressed 1 GO:0005576 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127422_PI430048170 0.62291512562982 0.9708302261593270.270556131568874
0.4630038520073040.314658749267441 A A A 0.4926659061247080.384598958194733
0.299700159390013 A A A LNCV6_127422_PI430048170 mRNA
CTGACGAACCCAATTGTTTATTGTGTAAAAACTAAACAGATTAGAGTGAGAGTTGTAGCA NM_001005329 RefSeq
chr11 - 4946158 4947100 OR51A4 NA "olfactory receptor, family 51, subfamily A, member 4" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94753_PI430048170 0.5962452603844810.9741625341174835.2802736428028 5.2947325457679
5.3491860266046 P P P 5.40988029449844 5.38920660927129 5.23291358996204 P P P
LNCV6_94753_PI430048170 mRNA
ACTTTGGCCTCTGCAAAGAGGGCATCAGTGACGGGGCCACCATGAAAACCTTCTGTGGGA NM_001626 RefSeq chr19
- 40230316 40285395 AKT2 208 "v-akt murine thymoma viral oncogene homolog 2, transcript variant 1"
GO:0071156|GO:0005515|GO:0008286|GO:0032859|GO:0005886|GO:0008643|GO:0031340|GO:0005634|GO:2000
147|GO:0005829|GO:0010907|GO:0060644|GO:0016301|GO:0046326|GO:0061024|GO:0045444|GO:0006006|GO:0
005938|GO:0030334|GO:0032869|GO:0045725|GO:0005978|GO:0090314|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128328_PI430048170 0.0326838153617219 1.44622329516261 10.2047398970958
10.5678654685339 10.1997952222167 P P P 9.8704160453209 9.84654299080538
9.68316119188245 P P P LNCV6_128328_PI430048170 mRNA
ATGAAGGTAATTAAAACCATGGAGGCGATCAGCGAGGTTCTCCAGGACCTTAGGTTTGAT NM_001100418 RefSeq
chr19 + 18588684 18592337 C19orf60 55049 "chromosome 19 open reading frame 60, transcript
variant 1" GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130364_PI430048170 0.4075739728178371.0187096004907 0.344120740195053
0.3337436292402110.263674780213385 A A A 0.2870030030713240.296584094661746
0.278989603716268 A A A LNCV6_130364_PI430048170 mRNA
CCCTGTGTAGACTGTTGTAAAGAAACTGTTGAAAATAAAGAGAAGCAATGTGAAGCACCT NM_206953 RefSeq chr22
- 22547695 22559361 PRAME 23532 "preferentially expressed antigen in melanoma, transcript variant 2"
GO:0005515|GO:0008284|GO:0043066|GO:0005886|GO:0006915|GO:0005634|GO:0042974|GO:0006351|GO:0030
154|GO:0048387|GO:0045596|GO:0045892|GO:0040008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140922_PI430048170 0.9593651952357921.00151955357167 0.319457645113891
0.3243287895343440.407274608708062 A A A 0.3641684211202030.316457558618213
0.365028980033694 A A A LNCV6_140922_PI430048170 mRNA
CAACTGGCTACAAAGAAGGATGTCAGAATGTAAGGAAACTATAACTAATAGTCATTACCA NM_005849 RefSeq chr16
- 21641283 21652666 IGSF6 10261 "immunoglobulin superfamily, member 6"
GO:0006955|GO:0005887|GO:0007166|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141782_PI430048170 0.9831433012660840.9996926203994 0.375437629747236
0.5278748900094650.409637135082968 A A A 0.5385754100089210.481371281175786
0.286918535179292 A A A LNCV6_141782_PI430048170 mRNA
CATGGAATGTAATTACTATGTGGTTATGAATGGGATAACCACCTTGAATGTGTACTTTTG NM_001164397 RefSeq
chr11 - 89870437 89876017 TRIM64B NA tripartite motif containing 64B NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_140826_PI430048170 0.0375560550636232 1.11509117903455 0.671823999435947
0.7377548930751120.71347690151826 A A A 0.62744108209024 0.505320003985632
0.516390064477593 A A A LNCV6_140826_PI430048170 mRNA

AGGCCTGGGAGTCTCTTGACTCCACTACTTAATTCCGTTTAGTGAGAAACCTTTCAATTT NM_006167 RefSeq chr8
- 23678692 23682937 NKX3-1 4824 "NK3 homeobox 1, transcript variant 1"
GO:0001656|GO:0005515|GO:0004882|GO:0003700|GO:0000983|GO:0006366|GO:0044212|GO:0001756|GO:0050
680|GO:0043621|GO:0007507|GO:0005622|GO:0071356|GO:0045860|GO:0051781|GO:0010942|GO:0000976|GO:0
030331|GO:0007275|GO:0001047|GO:0014068|GO:0008656|GO:0060037|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140880_PI430048170 0.2124068105801261.07105976888991 0.525951754925388
0.3620102852670370.506816362170029 A A A 0.2927259443118130.375595729261313
0.43147730122075 A A A LNCV6_140880_PI430048170 mRNA
ATGTCCTCTTGGAGGATTTTTCTGCCATGTAGATGCTCCATTAGCAGTTCCAGCTAAGCT NM_033045 RefSeq chr12
- 52377811 52385633 KRT84 NA "keratin 84, type II" NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136625_PI430048170 0.0133070334713451 0.3036558868686022.87301608436034
3.18554277455795 2.45526469942461 A P A 4.59842753971053 4.5384093458217
4.62554160249306 P P P LNCV6_136625_PI430048170 mRNA
CAGACCTAACTAGTGAATGTATTAATGAAAATGCATCTATTTCAGAGCTGACATGAAGAG NM_181453 RefSeq chr2
+ 108449120 108509398 GCC2 9648 "GRIP and coiled-coil domain containing 2, transcript variant 1"
GO:0005515|GO:0005802|GO:0005794|GO:0034453|GO:0043001|GO:0090161|GO:0005634|GO:0071955|GO:0042
802|GO:0070861|GO:0005737|GO:0016020|GO:0034499|GO:0031023|GO:0034067|GO:0006622|GO:0042147|GO:0
005654|GO:0000042. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131041_PI430048170 0.0136455138180413 0.5746555055461278.48601508313106
8.60716143456151 8.88848319540611 P P P 9.23029657546304 9.41812229191323 9.7184829873544
P P P LNCV6_131041_PI430048170 mRNA
TTACATCCAGATAGGTTACCAGTAACGGAACAGTATCCAGTACTCCTGGTTCCTAGGTGA NM_000416 RefSeq chr6
- 137197483 137219430 IFNGR1 3459 interferon gamma receptor 1
GO:0005515|GO:0004896|GO:0005886|GO:0005783|GO:0019221|GO:0014069|GO:0009615|GO:0031982|GO:0030
425|GO:0060334|GO:0007165|GO:0019955|GO:0004906|GO:0005887|GO:0016021|GO:0060333 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132685_PI430048170 0.00529877783672936 0.3846857645374194.04491077396866
3.39788123119227 3.78934722912043 P P P 4.93808767827802 5.07386092631304
5.38933104676876 P P P LNCV6_132685_PI430048170 mRNA
GCAACTGGGTGAATCTGGCAGGAATCTATCCATTGAACTAAAATAATTTTATTATGCAAC NM_002439 RefSeq chr5
+ 80654647 80876815 MSH3 4437 mutS homolog 3
GO:0005515|GO:0030983|GO:0005634|GO:0042803|GO:0003697|GO:0051096|GO:0006298|GO:0032357|GO:0007
131|GO:0008094|GO:0032181|GO:0000404|GO:0000403|GO:0000406|GO:0019237|GO:0000228|GO:0005524|GO:0
032142|GO:0043570|GO:0006281|GO:0000710|GO:0016020|GO:0032302|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135983_PI430048170 0.0909826790618590.5311894183704244.82115413293309
4.63249681801236 5.19190343978163 P P P 5.22765958056924 5.70301821823208
6.30676294681387 P P P LNCV6_135983_PI430048170 mRNA
GCACATGCTTGAACTGTAGTAATGTTAGCTTGTTCTAAAGCTATCCATTGTGTCATATTT NM_005923 RefSeq chr6
- 136557048 136792518 MAP3K5 4217 mitogen-activated protein kinase kinase kinase 5
GO:0097300|GO:0005515|GO:0070301|GO:0005783|GO:0042803|GO:0005829|GO:0000186|GO:0000165|GO:0016
032|GO:0004709|GO:0000287|GO:0043065|GO:0019901|GO:0006919|GO:0019903|GO:0008631|GO:0007254|GO:0
007257|GO:0005524|GO:0008656|GO:0097190|GO:0043280|GO:0004672|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133894_PI430048170 0.2383692755175171.06371906925429 0.517463840293799
0.3490451464756140.476933599710165 A A A 0.2913204524289610.369567359428842
0.417699519229407 A A A LNCV6_133894_PI430048170 mRNA

TGCTCATGTCATAAGCTATGTTGACAGTTGCCAGTGGAAATGTTGGGTTGGTTCAAAAAA NM_183002RefSeq chr14 - 70044216 70189070 SLC8A3 6547 "solute carrier family 8 (sodium/calcium exchanger), member 3, transcript variant c"
GO:0005516|GO:0060402|GO:0005886|GO:0005874|GO:0055085|GO:0005432|GO:0021537|GO:0005739|GO:0042383|GO:0007154|GO:0043197|GO:0002244|GO:0007596|GO:0070588|GO:0043025|GO:0035725|GO:0016021|GO:0071320|GO:0006811. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141503_PI430048170 0.0381101831268484 1.10791743802413 8.28231979165929 8.16812669052266 8.27713060557391 P P P 8.06771991350767 8.13620497507473 8.08205028523217 P P P LNCV6_141503_PI430048170 mRNA
ATTGGAAGACCTTCTTTCTTTTGATTGTCTCAAGCTGCCACCCTTCAAGGACAGGGAAGA NM_017659RefSeq chr19 + 45692482 45703990 QPCTL 54814 "glutaminyl-peptide cyclotransferase-like, transcript variant 1"
GO:0016603|GO:0005794|GO:0016020|GO:0000139|GO:0008270|GO:0016021|GO:0017186 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145461_PI430048170 0.376522643886838 0.887199664745672 12.7580010389654 12.9776941796525 12.5310270793955 P P P 13.1592809174638 12.866791644938 12.7633844617118 P P P LNCV6_145461_PI430048170 mRNA
TCAGTGGGCCTTGCCCTTTGTACAGCCTCCACCCCCATTAAAACTGCTCTGGACTTGCTG NM_002779RefSeq chr10 - 102402616 102419144 PSD5662 "pleckstrin and Sec7 domain containing, transcript variant 1"
GO:0005515|GO:0005802|GO:0030054|GO:0005886|GO:0001726|GO:0043547|GO:0005086|GO:0007165|GO:0005543|GO:0030182|GO:0032012|GO:0004871|GO:0016021|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140079_PI430048170 0.490808858349176 0.769271212284626 0.322415970320468 1.68645069965132 0.268907139599405 A A A 0.480385600158056 1.47221047009174 1.68085197314169 A A A LNCV6_140079_PI430048170 mRNA
CATATCTGCAGGATCTCCACAGGATGGTGGGCAGAATTAGTCCAAATTGGACAAATCATC NM_001009613 RefSeq chrX + 143025917 143034280 SPANXN4 NA "SPANX family, member N4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133679_PI430048170 0.190740694446794 3.12419133010281 0.332415479619962 2.6642921371548 2.04373913287656 A A A 0.314808089759026 0.288393450282391 0.363671423727502 A A A LNCV6_133679_PI430048170 mRNA
GGAATGGAAGAAACATTGAAGATGAGGCCCAGATTCAGTGGTGAAAGAAAGCTGGATCTG NM_001011717 RefSeq chr2 + 100470481 100483280 NMS NA neuromedin S NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134964_PI430048170 0.0130676133294912 0.506207991400166 5.89448829011587 6.08057992738696 6.41544829891944 P P P 6.78953981784441 7.16941980275524 7.36853410744127 P P P LNCV6_134964_PI430048170 mRNA
AGGGTAAGAGATGGGTAGAAGAGTATGCCTCTGAAAATTTTATTAGTTTATTCTTGTGGA NM_152902RefSeq chr1 + 168178844 168202113 TIPRL 261726 "TOR signaling pathway regulator, transcript variant 1"
GO:0005515|GO:0005737|GO:0000077|GO:0034048|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131987_PI430048170 0.419453613188866 1.54523047583369 1.78782505651547 0.440320958365284 0.354937735405441 A A A 0.352141623146893 0.411037316485219 0.41605279924396 A A A LNCV6_131987_PI430048170 mRNA
GTCCTGCAGAGCCAAGGAGAGATGACAGAAGCAATTAAATACTTGAAAAAATTTGTGAAA NM_001300761 RefSeq chr4 - 146707026 146945882 TTC29 83894 "tetratricopeptide repeat domain 29, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140384_PI430048170 0.289693283061966 1.05354077107346 0.47438516188215 0.549246443916948 0.548341592764628 A A A 0.340304165409485 0.507820682458746 0.493479795384493 A A A LNCV6_140384_PI430048170 mRNA

GTAACCTCTATTTGGAGCTGCTACATCCAATATTGTGACTGAAAATTAACTAAAGAGAGA NM_017655 RefSeq chr1 + 78045904 78138449 GIPC2 54810 "GIPC PDZ domain containing family, member 2, transcript variant 1" GO:0008150|GO:0003674|GO:0005737|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135765_PI430048170 0.3091015050020441.03985605042738 0.312152104740714
0.27052116825178 0.409140530440184 A A A 0.28527405252685 0.254551978930816
0.286139407950869 A A A LNCV6_135765_PI430048170 mRNA
CACTCAGTATCTGCATTACTTTTATCTCTGCAAATATCTGCATGATAGCTTTATTCTCAG NM_178134 RefSeq chr1 + 47067487 47118320 CYP4Z1 199974 "cytochrome P450, family 4, subfamily Z, polypeptide 1" GO:0070330|GO:0005506|GO:0005789|GO:0016021|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140419_PI430048170 0.0194428076776672 1.45352021246419 11.9270245101952
11.8938629753474 11.9478746891128 P P P 11.4100994683818 11.2222507211149
11.5041519303676 P P P LNCV6_140419_PI430048170 mRNA
CCCCAGTCCGTGTCTTTTTAGAATGTGAATGATGATAAAGTTGTGAAATAAAGGTTTCTA NM_018622 RefSeq chr3 - 183829384 183884905 PARL 55486 "presenilin associated, rhomboid-like, transcript variant 1" GO:0005739|GO:0005515|GO:0090201|GO:0004252|GO:0004175|GO:0033619|GO:0006508|GO:0005743|GO:0005634|GO:2001243|GO:2000377|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142798_PI430048170 0.845516525482651 1.08583213809963 0.407888936997557
1.39956560443309 0.316169284875762 A A A 1.20751531786364 0.30953327531778
0.321289647645756 A A A LNCV6_142798_PI430048170 mRNA
AGGGCAAGTCTGAGAGTGAGTTACCTCATAAACTTTATGTTTTGCTGTTTGCTAAATTCT NM_001004688 RefSeq chr1 + 248179985 248181029 OR2M2 391194 "olfactory receptor, family 2, subfamily M, member 2" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129346_PI430048170 0.158414237391995 0.958861427572711 0.27151684269394
0.28604554205603 0.350073900137255 A A A 0.411898388942179 0.350337372528546
0.32709824881276 A A A LNCV6_129346_PI430048170 mRNA
CTTTACCTATACAAAATGACTGCTATGGTGGGAACACAATAAACACCAGTTTTGACTTTT NM_032107 RefSeq chr20 + 43507679 43541895 L3MBTL1 26013 "l(3)mbt-like 1 (Drosophila), transcript variant II" GO:0030097|GO:0005515|GO:0000793|GO:0007088|GO:0003700|GO:0005886|GO:0005730|GO:0031491|GO:0005634|GO:0035064|GO:0031493|GO:0032093|GO:0006351|GO:0042802|GO:0045652|GO:0042393|GO:0003682|GO:0051726|GO:0005654|GO:0008270|GO:0045892|GO:0000785|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136153_PI430048170 0.000273799783997822 0.370443869942122 5.24041502186248
5.20466595146572 5.47019003214155 P P P 6.62332619851492 6.68543963963839
6.90388548007819 P P P LNCV6_136153_PI430048170 mRNA
CCTATGGAGGTTTCTCACACTGGTGTGTCATTATACATTAATTGTACAATATGCATTTTC NM_016265 RefSeq chr7 - 6688433 6706935 ZNF12 7559 "zinc finger protein 12, transcript variant 1" GO:0005813|GO:0003700|GO:0005654|GO:0005634|GO:0045892|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128046_PI430048170 0.17302573043658 0.433486821345104 2.46302225527446
0.356449364344606 2.59664959564091 A A A 2.79114086476239 3.41827645307173
3.58667818706118 P P P LNCV6_128046_PI430048170 mRNA
GGTGGGCTTCAGAGAATCTGTGTACCCCCTAAAATTGTATGTAGAATTTTGGATATTTAC NM_138394 RefSeq chr2 - 38563185 38603036 HNRNPLL 92906 "heterogeneous nuclear ribonucleoprotein L-like, transcript variant 1" GO:0006397|GO:0005515|GO:0016020|GO:0000166|GO:0030529|GO:0005634|GO:0003729|GO:0033120 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143253_PI430048170 0.0750633854331959 0.640937575964254 11.512878784393

10.8362965708372 11.1007715005519 P P P 11.8222358759788 11.7786408973273
11.8548294980022 P P P LNCV6_143253_PI430048170 mRNA
GCTGCTGCTTTAAAGGATAAAGTACTCTTTGGGGGATGAGTCTGGTTTGTTTTGTTTTAT NM_006415 RefSeq chr9
- 92031133 92115474 SPTLC1 10558 "serine palmitoyltransferase, long chain base subunit 1, transcript variant 1"
GO:0005515|GO:0006665|GO:0004758|GO:0006686|GO:0030148|GO:0035339|GO:0044281|GO:0030170|GO:0005789|GO:0016021|GO:0046513|GO:0017059|GO:0046512|GO:0046511 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115644_PI430048170 0.2800089772826561.20469596191812 10.1032709112939
10.4357949071811 10.5619450126453 P P P 9.87575193634233 9.96139494715846
10.4317228880654 P P P LNCV6_115644_PI430048170 mRNA
GGGACAAACGCAGGTTGCAGAAAATCCTCACTCTGAGTACGGTCTCACAGACAACGTTGA NM_032574 RefSeq chr2
- 32023902 32039775 DPY30 84661 dpy-30 homolog (C. elegans)
GO:0005515|GO:0005802|GO:0006355|GO:0005794|GO:0005634|GO:0006351|GO:0042803|GO:0042802|GO:0035097|GO:0048188|GO:0016197|GO:0005654|GO:0051568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134477_PI430048170 0.2199083227547651.26674577144557 6.63137551419829
6.52603995539095 6.28274802520173 P P P 5.72459570583569 6.44011511572063
6.18524557060133 P P P LNCV6_134477_PI430048170 mRNA
ATCCTCCTGGTTCTGACCTGGGGGGTGTTTGCATCACCCCCTTTTACTTGTATTAAAAAA NM_002855 RefSeq chr11
- 119660992 119728725 PVRL1 5818 "poliovirus receptor-related 1 (herpesvirus entry mediator C), transcript variant 1"
GO:0005515|GO:0030424|GO:0060041|GO:0005886|GO:0016342|GO:0046718|GO:0042803|GO:0043231|GO:0006955|GO:0016337|GO:0005913|GO:0005912|GO:0002089|GO:0001618|GO:0007411|GO:0007155|GO:0050839|GO:0007156|GO:0007157|GO:0051963|GO:0046982|GO:0034329|GO:0070166|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140555_PI430048170 0.4093999822177021.37307874929223 2.12020317274195
2.62163063749676 1.77365051494586 A A A 2.25178492747593 2.01746492282827
0.408418401685252 A A A LNCV6_140555_PI430048170 mRNA
ATGTCTTAGTTGTACAAATAAAGTCCCAGGTTAAAGATAACAAACGGCTCCTGTGACATA NM_004931 RefSeq chr2
- 86841565 86861924 CD8B 926 "CD8b molecule, transcript variant 5"
GO:0005515|GO:0042288|GO:0005886|GO:0005576|GO:0015026|GO:0050690|GO:0006955|GO:0042110|GO:0005887|GO:0031901|GO:0042101|GO:0050776|GO:0016032|GO:0007169|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105543_PI430048170 0.0202441695775191.80052046628926 4.15773577896465
4.63920842689965 4.26695852966973 P P P 3.84333016316402 3.30653781113587
3.35027915262916 P P P LNCV6_105543_PI430048170 mRNA
CTGAGCACAGACTTTTCCTCACAAAAGGGGGTGAAGGGTGTCCCCCTGAACCTGCAGATT NM_198173 RefSeq chr1
+ 24319321 24355318 GRHL3 57822 "grainyhead-like 3 (Drosophila), transcript variant 2"
GO:0001736|GO:0005515|GO:0007389|GO:0003700|GO:0006357|GO:0006366|GO:0000981|GO:0090179|GO:0005634|GO:0007398|GO:0007417|GO:0043565|GO:0008544|GO:0032321|GO:0061029|GO:0045944|GO:0032956|GO:0042060|GO:0090103. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126993_PI430048170 0.0334028928050413 0.7133966361283524.24438603635729
4.60883900288103 4.43341919304592 P P P 4.70078176278017 5.06874310123055
4.97685033335669 P P P LNCV6_126993_PI430048170 mRNA
GGAGTAGATCATGATGGAGGGGAAATCACTGGAGATCAAATATGTAAAATCATTTCAAAT NM_016377 RefSeq chr6
+ 131135685 131283535 AKAP7 9465 "A kinase (PRKA) anchor protein 7, transcript variant gamma"
GO:0005515|GO:0034237|GO:0005886|GO:0019901|GO:0060306|GO:0005634|GO:0016328|GO:0005829|GO:0035556|GO:0008150|GO:0016324|GO:0008104|GO:0000166|GO:0001508|GO:0071320|GO:0051018|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_126732_PI430048170 0.1032250353411660.5092241511718795.90721672804718
5.83780897084223 6.10819758311342 P P P 6.26764671752776 6.89462716949161
7.40607387758192 P P P LNCV6_126732_PI430048170 mRNA
GTCCAGGAAGATTGTTCTTGCATAACCAGACCCACAATAAATATCTACAACTTTTCTTAC NM_001114118 RefSeq
chr17 - 3806750 3846251 C17orf85 55421 chromosome 17 open reading frame 85 GO:0000166
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132930_PI430048170 0.0770690772388423 0.5602158448868664.18827325616383
3.19827545404066 3.73947334206836 P P P 4.43282926942352 4.78573458213516 4.5598566216756
P P P LNCV6_132930_PI430048170 mRNA
AGAGGGAAGACATTAAGGGGATTGGGGACATTTGTTTCACACATCTGCAGTAATATGAGT NM_001042550 RefSeq
chr9 + 104094549 104141419 SMC2 10592 "structural maintenance of chromosomes 2, transcript variant 1"
GO:0000796|GO:0005515|GO:0000793|GO:0007076|GO:0010032|GO:0046982|GO:0005634|GO:0051383|GO:0000228|GO:0005524|GO:0005829|GO:0005737|GO:0045132|GO:0005654|GO:0000278|GO:0070062|GO:0051301 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140732_PI430048170 0.8104724404693481.02050494252067 0.365365743104191
0.6049757301445990.337504371892809A A A 0.29973053537519 0.439189244388459
0.489687300679347A A A LNCV6_140732_PI430048170 mRNA
AAGGTCATGAGAAGGAAATGTGGTATTCTATGGAGTACAAGTAAAAGGAAGTTCCTTTAT NM_001001959 RefSeq
chr1 - 247840927 247841896 OR11L1 NA "olfactory receptor, family 11, subfamily L, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_86560_PI430048170 0.0748994941664205 0.5043081117167272.13680129593491
3.16527988131925 2.27759253874208 A P A 3.55288134825342 3.48356773060441
3.72271610636691 P P P LNCV6_86560_PI430048170 mRNA
GCACCAGAAAATAGAAGAAAGGTGTGTGGAGACTTAGGGTATTTTATTACATGTTTTCAT NM_002374RefSeq chr2
+ 209579678 209734110 MAP2 4133 "microtubule-associated protein 2, transcript variant 1"
GO:0005515|GO:0008017|GO:0005516|GO:0002162|GO:0071310|GO:0001578|GO:0005875|GO:0005874|GO:0005730|GO:0021954|GO:0007409|GO:0031175|GO:0048813|GO:0005737|GO:0043198|GO:0034399|GO:0005198|GO:0043025 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90912_PI430048170 0.5352565421949841.15723877990608 1.97745034991404 1.99887576275159
2.40660405970476 A A A 1.10265857923175 2.08314169984797 2.3373480657174 A A P
LNCV6_90912_PI430048170 mRNA
TTGGTCCACCATCATCGTGCCTGGCATGAAGGATGCTGTGATCCACGCACTTCAGACCTC NM_001198793 RefSeq
chr3 + 9792547 9836356 ARPC4-TTLL3 100526693 ARPC4-TTLL3 readthrough NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129827_PI430048170 0.183051330352089 1.22675964157732 0.902198510970164
0.478162633813093 0.480923664573503 A A A 0.312346823999749 0.340809675470321
0.365589710487324 A A A LNCV6_129827_PI430048170 mRNA
GGAGGCTGCAGAAGCCATTTCTCTTTGTAGATAAAAAGCATTATCTATGATTGTTGTATA NM_017770 RefSeq
chr6 - 10980759 11044391 ELOVL2 54898 ELOVL fatty acid elongase 2
GO:0005515|GO:0006636|GO:0005783|GO:0044281|GO:0035338|GO:0036109|GO:0033559|GO:0043651|GO:0009922|GO:0005789|GO:0019432|GO:0016021|GO:0034626|GO:0042761|GO:0044255 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_104351_PI430048170 0.489781758352476 0.971514113280399 0.407231275001495
0.438065693517977 0.388963451865507 A A A 0.515990092991121 0.479940694651287
0.359204147498488 A A A LNCV6_104351_PI430048170 mRNA
GTCAGGAATCAACAACTTCCCACAGCAGCTCAGGTTCAACTGACACAGCACTGTCCCCTG NM_001164462 RefSeq
chr7 + 100969622 101018949 MUC12 10071 "mucin 12, cell surface associated"
GO:0003674|GO:0006493|GO:0005887|GO:0005796|GO:0016266|GO:0044267|GO:0001558|GO:0043687 . NA

- . NA NA NA NA NA NA NA NA NA
LNCV6_135359_PI430048170 0.387577776199482 0.924376259327829 6.50036598717513
6.69075712527609 6.59500262944547 P P P 6.57602739896474 6.88929710905757
6.64848260417008 P P P LNCV6_135359_PI430048170 mRNA
ATCTACAACATGCTCCGCATGTTTGTGGTGACTGGGCCTGCACTGGCCGAGATTGACCTG NM_013366 RefSeq
chr9 - 137174783 137188605 ANAPC2 29882 anaphase promoting complex subunit 2
GO:0007094|GO:0090129|GO:0051437|GO:0045773|GO:0051436|GO:0031145|GO:0051439|GO:0005829|GO:0007
067|GO:0031915|GO:0070979|GO:0005680|GO:0050775|GO:0005654|GO:0000278|GO:0031625|GO:0051301 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136587_PI430048170 0.25692057097346 0.584342687254821 0.454033722801
1.63165408620705 2.27387191941459 A A A 1.75142694275666 2.23694752496256
2.97131880555914 A A P LNCV6_136587_PI430048170 mRNA
CGGAGTATTTTATGCCTGCCTCATTTTATTATATGATTAGCTCCTGCATTTCTTTGGTTC NM_001199324 RefSeq
chr19 - 51991333 52008230 ZNF615 284370 "zinc finger protein 615, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_137346_PI430048170 0.028264322635678 0.596108342671891 7.51499434824132
7.12832674287326 6.92917400480892 P P P 7.95928649083492 8.11486099262648
7.7806367640597 P P P LNCV6_137346_PI430048170 mRNA
TGTGCCCTACAATGGGGCCAGCTGGGCCGACAGCAGAATAAAGGCAATAAGATGAAAAAA NM_004443 RefSeq
chr3 + 184561798 184582408 EPHB3 2049 EPH receptor B3
GO:0031290|GO:0005886|GO:0001655|GO:0048538|GO:0030425|GO:0005829|GO:0007413|GO:0005003|GO:0032
314|GO:0046777|GO:0007411|GO:0060021|GO:0034446|GO:0060996|GO:0060997|GO:0051965|GO:0022407|GO:0
048013|GO:0018108|GO:0005576|GO:0021952|GO:0001525|GO:0005524|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_125150_PI430048170 0.839225729180478 0.9609513708909 1.95890186627567
2.11990465105583 2.16251411123137 A A A 2.62765945974393 2.40245064561858
0.816027566394468 A A A LNCV6_125150_PI430048170 mRNA
TTCCGCTTCAGCTCCAAGCATGCACTGACGGTGGTCCTGGCTACCTGGACCATTGGTATT NM_001708 RefSeq
chr7 - 128772488 128775790 OPN1SW 611 "opsin 1 (cone pigments), short-wave-sensitive"
GO:0018298|GO:0007165|GO:0009881|GO:0007603|GO:0007186|GO:0042622|GO:0005887|GO:0004930|GO:0004
872|GO:0007602|GO:0007601|GO:0001523 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_62253_PI430048170 0.0118597668555519 1.48847208215578 7.91399657377177
7.99409891546003 7.94954524350298 P P P 7.41109852871313 7.22716569776371
7.48679212546303 P P P LNCV6_62253_PI430048170 mRNA
CGTTTGCCAGCAACTGGAGGAAGATAAACGCCCACAACAATGGGAACCACACATTTAAAA NM_004390 RefSeq
chr15 - 78921749 78945078 CTSH 1512 cathepsin H
GO:0005515|GO:0001656|GO:0030984|GO:0097067|GO:0008284|GO:0004252|GO:0097208|GO:2001235|GO:0010
813|GO:0007283|GO:0010815|GO:0043621|GO:0070324|GO:0032403|GO:0005764|GO:0005615|GO:0005829|GO:0
031648|GO:0019882|GO:0033619|GO:0006508|GO:0043129|GO:0032526|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_123575_PI430048170 0.082878481104184 0.94917826495504 7.56791045587868
7.56983409429712 7.64741837102409 P P P 7.68270800532954 7.69065535986986
7.63843434518698 P P P LNCV6_123575_PI430048170 mRNA
TTTTTTTTACTTTCTTTTTGTATTCTATCCCAGATCACAGGAAAGTTATAAAAATCAAAC NM_000943 RefSeq chr5
- 123023382 123036730 PPIC 5480 peptidylprolyl isomerase C (cyclophilin C)
GO:0000413|GO:0016018|GO:0005737|GO:0006457|GO:0003755|GO:0070062 . NA - . NA NA
NA NA NA NA NA NA NA

LNCV6_131744_PI430048170 0.456956079249089 0.700572444539857 0.519257648376744 0.549686911700747 0.428097177604756 A A A 1.72163937116036 0.463045106397948 0.463751481095548 A A A LNCV6_131744_PI430048170 mRNA ACCTCACAGTACTGGTTAATTAAACTTTATTGCTCACTGTCCACTTTTGTGCTGAAAAAA NM_004918 RefSeq chr14 + 95686416 95692643 TCL1B 9623 T-cell leukemia/lymphoma 1B NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140800_PI430048170 0.00103042746299977 0.483489505901713 5.92646896942803 5.90028659511662 6.18424808868382 P P P 6.90566907772699 7.07781516303871 7.17727683950563 P P P LNCV6_140800_PI430048170 mRNA GTCAATAATTATCGCTTTAATTGGTGTTAATATTTGGTAGTACACAGGTTCTCCCTTGTT NM_015532 RefSeq chr15 + 57706520 57717557 POLR2M 81488 "polymerase (RNA) II (DNA directed) polypeptide M, transcript variant 1" GO:0003899|GO:0032774|GO:0016591|GO:0043025|GO:0051685|GO:0005635 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129009_PI430048170 0.0363941898500052 0.416531119025894 9.779466191106 8.80284121765205 8.91671319279465 P P P 10.4344112163611 10.7213794955819 10.3108787090815 P P P LNCV6_129009_PI430048170 mRNA ATGCAAATGCTGAAATGTACAAAATCAACCATGACAACAAAGAAAAAGACCTTGTACAGC NM_006650 RefSeq chr5 + 175796606 175884020 CPLX2 10814 "complexin 2, transcript variant 1" GO:0043303|GO:0045202|GO:0016079|GO:0030154|GO:0030425|GO:0042629|GO:0005829|GO:0006904|GO:0007399|GO:0031915|GO:0017157|GO:0043025|GO:0017075|GO:0070554|GO:0070033|GO:0048306 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141744_PI430048170 0.0170141037614352 0.5807783264076984.87959640023376 4.55321569405298 4.57994181200993 P P P 5.4641120666384 5.46109429521152 5.46263417790383 P P P LNCV6_141744_PI430048170 mRNA CAGTTCCTTTTCTGTTTGGTAGTTTGTGACTCTAAGATTTCCACTGTTATGTGTGTTAAT NM_173566RefSeq chr22 - 31681347 31750134 PRR14L 253143 proline rich 14-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131772_PI430048170 0.0568204968724798 0.8375250220199771 0.6874452355849 10.548466969525 10.7343042991944 P P P 10.782207730674 10.9103747765084 11.0399278601538 P P P LNCV6_131772_PI430048170 mRNA GGATTTTTAAAGTGCCTTTCAATTGTCTGTGAACGTCTAAAGGACTGATTTGTCTCAAAA NM_024792RefSeq chr17 + 732606 742835 FAM57A 79850 "family with sequence similarity 57, member A" GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138060_PI430048170 0.562435229331435 1.05492959501604 0.276183169234917 0.286272121143496 0.585328898730964 A A A 0.332161854358906 0.285874102716922 0.319766473278112 A A A LNCV6_138060_PI430048170 mRNA GTTGGCAACTAAAGACATGAGGCAGGGATGCTAGATTAATGTCAGGACCATTTCTCTTCT NM_019841RefSeq chr7 - 142908100 142933723 TRPV5 56302 "transient receptor potential cation channel, subfamily V, member 5" GO:0005515|GO:0005516|GO:0016324|GO:0005262|GO:0060402|GO:0051262|GO:0034220|GO:0005886|GO:0005887|GO:0070588|GO:0006816|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141673_PI430048170 0.000567319637829881 0.652157208950637 11.7402902438732 11.6937040133408 11.6163720951523 P P P 12.2741000130404 12.2898000830561 12.3385123946731 P P P LNCV6_141673_PI430048170 mRNA GCACTGGACATATTCCCTACCTGTCTTATTTCATAGGTACATGAAGTATTGTGTATAAAA NM_058004RefSeq chr22 - 20707690 20858812 PI4KA 5297 "phosphatidylinositol 4-kinase, catalytic, alpha" GO:0004430|GO:0005515|GO:0005886|GO:0006661|GO:0048015|GO:0044281|GO:0005524|GO:0005829|GO:0007165|GO:0046854|GO:0016020|GO:0030660|GO:0006644|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137365_PI430048170 0.3112605168144750.9447318011607740.327400520990729
0.3989203667346930.304011015582321A A A 0.5188657711602250.43624731797388
0.315797251693785A A A LNCV6_137365_PI430048170 mRNA
ATTCCTAGAGTTCAATATTAAGCAGCAAAAGATAAGCTGGAAAAGACAAGCAAGGCTAAT NM_001206847 RefSeq
chr8 + 30638599 30645952 SMIM18NA small integral membrane protein 18 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_137349_PI430048170 0.1900015578034691.01602601680947 0.311717333770587
0.2708157784494280.292519076305279A A A 0.2725237343237480.265763445878714
0.26823503356385 A A A LNCV6_137349_PI430048170 mRNA
GCTCCTGGAACTTATTTATATGCCTCAAAATCCTCTAAACTCATTTATAGTAACCCATAG NM_080721RefSeq chr20
- 46541030 46550574 OCSTAMP NA osteoclast stimulatory transmembrane protein NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_101298_PI430048170 0.0326000602400650.5183612426678721.70011629624936
1.42532797379255 2.19434376761865 A A A 2.78090346996181 2.3798046601821
3.03588761731895 P A P LNCV6_101298_PI430048170 mRNA
CAGTTTCTGTCAGCTGCTCCTACAGAACCATGTATTCCTATGAATAAATATCAACATAAA NM_145287RefSeq chr18
- 14099942 14132490 ZNF519 162655 "zinc finger protein 519, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144346_PI430048170 0.3693691191167141.43022497587075 1.62744123773865
0.5647641364324790.502681429823243A A A 0.5665339735528370.431439502488971
0.438889858272641A A A LNCV6_144346_PI430048170 mRNA
CCTGAGGAACAAAGATATCATGGTGGCATTGAGAAAATTACTAGCTAAGTTATTAACATG NM_001005491 RefSeq
chr11 - 55967557 55968463 OR10AG1 NA "olfactory receptor, family 10, subfamily AG, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130894_PI430048170 0.2959944705375810.7589757778799333.25455257352059
4.21556781490985 4.28996144527234 P P P 4.44485101374933 4.45220334473147
4.25987317100052 P P P LNCV6_130894_PI430048170 mRNA
GTCTTTAGTACTTCAAAATTACCTTTTCATATCCATGATCTTGAGTCCATTTGGGGGATT NM_000161RefSeq chr14 -
54842005 54902824 GCH1 2643 "GTP cyclohydrolase 1, transcript variant 1"
GO:0005515|GO:0050662|GO:0014916|GO:0006729|GO:0050999|GO:0005634|GO:0045776|GO:0044281|GO:0051
291|GO:0042803|GO:0006809|GO:0005829|GO:0042416|GO:0005737|GO:0042311|GO:0050884|GO:0032496|GO:0
046654|GO:0051260|GO:0046209|GO:0034341|GO:0031965|GO:0005509|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131089_PI430048170 0.8396618723445791.01683730299271 7.3013878173066 7.5350779485083
7.50709862299274 P P P 7.28101552817232 7.33020013169399 7.64373559947448 P P P
LNCV6_131089_PI430048170 mRNA
TGGGTTAAGCTGACCAGGAACACCCATTTAACCCCTTTTTCTTTTTGCTTTCATTTTTAT NM_005650RefSeq
chr22_KI270928v1_alt - 82357 137686 TCF20 6942 "transcription factor 20 (AR1), transcript variant 1"
GO:0006355|GO:0003713|GO:0008270|GO:0005654|GO:0005634|GO:0003677|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128060_PI430048170 0.0151161116021394 0.73342176363850310.1716800473575
10.1004979351076 10.0288982681354 P P P 10.3894047633217 10.5998674473957
10.6445384532355 P P P LNCV6_128060_PI430048170 mRNA
AAAGGAATCAGTGTACACTACAGCTAATCCTAATAAATCCGATGTTTTCGGAATGGCAAA NM_007283RefSeq chr3
- 127689061 127822882 MGLL 11343 "monoglyceride lipase, transcript variant 1"
GO:0019369|GO:0006629|GO:0005886|GO:0045202|GO:0060292|GO:0044281|GO:2000124|GO:0042803|GO:0008
289|GO:0030516|GO:0006954|GO:0004622|GO:0043196|GO:0047372|GO:0006633|GO:0019433|GO:0046464|GO:0
050727|GO:0030168|GO:0009966|GO:0007596|GO:0005789|GO:0005654|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_142082_PI430048170 0.00435933635384191 1.60908229165274 13.3237492632012
13.3392690787362 13.2973983148323 P P P 12.5751506311557 12.7395915424647
12.5811704862266 P P P LNCV6_142082_PI430048170 mRNA
TCGGTCAGCGACTGGATGCTCGCCATCAAGGTCCAGTGGAAGTTCTTCAAGAGGAAAGGC NM_001958 RefSeq chr20
- 63488011 63499315 EEF1A2 1917 eukaryotic translation elongation factor 1 alpha 2
GO:0005853|GO:0043065|GO:0010035|GO:0043025|GO:0003924|GO:0005634|GO:0005525|GO:0003746|GO:0008
135|GO:0006414 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141507_PI430048170 0.5455026684945670.8601281028666280.288213645526268
0.2869283006772190.475325312087059 A A A 0.3030469663911490.266341337510056
1.01289066664671 A A A LNCV6_141507_PI430048170 mRNA
TGTGAAGTCAACATCTGTAGGGTTGCTTTTCTCCATCACATGGAGAGATCTTGGCTCTGT NM_001101372 RefSeq
chr19 + 51311847 51330848 IGLON5 402665 IgLON family member 5
GO:0043005|GO:0016337|GO:0050767|GO:0009986|GO:0005886|GO:0005911|GO:0043025|GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62192_PI430048170 0.7381327120311730.9673816858772755.8796438966646 6.04964902635517
6.14370190681652 P P P 6.16234382562505 6.17525887828762 5.87122354564547 P P P
LNCV6_62192_PI430048170 mRNA
TTCCAGGATGCTGGCGTTATCCAAGCTGCCTACAGCCTAAACTTCCCCCTGTTGGCTCTG NM_001256494 RefSeq
chr15 - 75355791 75368627 MAN2C1 4123 "mannosidase, alpha, class 2C, member 1, transcript
variant 2" GO:0030246|GO:0008270|GO:0004559|GO:0006013 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132984_PI430048170 0.0329694806432278 1.11745957398675 10.899469086214
10.768620073091 10.8086364352266 P P P 10.6557040806187 10.7172021576476
10.6247438322198 P P P LNCV6_132984_PI430048170 mRNA
TGCCTGGCCTCATCCTTGTATTTAATTAATTAAACAAGCCCCTTTTTAAACCCTAAAAAA NM_031918 RefSeq chr19
- 1852398 1863565 KLF16 83855 Kruppel-like factor 16
GO:0003700|GO:0006357|GO:0005634|GO:0007212|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127967_PI430048170 0.418672840521863 0.425957170811724 0.403328992396623
0.384519941901742 0.263306959281109 A A A 2.68327110532088 0.359308161339603
0.357711062947707 P A A LNCV6_127967_PI430048170 mRNA
CACATCTTTGTTCCATCGGCTTGATTTAAAGACAATTCCATTAGATCTTTTCTAAGCCTT NM_139199 RefSeq chr5 -
138139769 138178669 BRD8 10902 "bromodomain containing 8, transcript variant 2"
GO:0006355|GO:0003700|GO:0006357|GO:0006325|GO:0005634|GO:0000812|GO:0006351|GO:0005739|GO:0007
165|GO:0043967|GO:0043968|GO:0035267|GO:0005654|GO:0004887|GO:0030522|GO:0040008|GO:0007166 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133950_PI430048170 0.412567486084565 1.07907288694479 9.35303133909397
9.50860427749672 9.2157025377963 P P P 9.40552630780232 9.23111911622882
9.11093099129315 P P P LNCV6_133950_PI430048170 mRNA
TAGCCCATGTGGGTTACTTTGTAGCACAGCTCCTCCCTCCCAGGAAGATGAGGACCCACA NM_001293167 RefSeq
chr11 + 797510 799185 PANO1 NA proapoptotic nucleolar protein 1 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145369_PI430048170 0.781556375040209 0.993136376655055 2.56961175707548
1.05391160742037 1.14680052690398 A A A 2.09485446041449 1.75112432440917
1.41116082327708 A A A LNCV6_145369_PI430048170 mRNA
ATTAACAGCAATACAGACAACAATCTTGCAGTCTACGACCTCTCTCGGGATATTTTAAAT NM_001017978 RefSeq
chrX - 116461685 116463033 CT83 203413 cancer/testis antigen 83
GO:0005886|GO:0005634|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_140307_PI430048170 0.0133981352686647 0.48975692108615612.2227019396068
12.1650006003704 12.253841527901 P P P 13.0117290359032 13.2213042284385
13.4639403099605 P P P LNCV6_140307_PI430048170 mRNA
ACTTGAGCTTAAACTGACAACCTGGATGTAAATAGGAGCCTTTCTACTGGTTTATTTAAT NM_024923RefSeq chr3
- 13316229 13420319 NUP21023225 nucleoporin 210kDa
GO:0007077|GO:0010467|GO:0031965|GO:0005975|GO:0019083|GO:0019221|GO:0019058|GO:0044281|GO:0005
635|GO:0015031|GO:0055085|GO:0010827|GO:0008645|GO:0015758|GO:0016020|GO:0005643|GO:0046983|GO:0
005789|GO:0009405|GO:0016032|GO:0051028|GO:0000278 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_108131_PI430048170 0.2318866513081141.27728932534699 7.4855881015857
6.92266911365413 7.14546297081629 P P P 6.86689359891429 7.13862012139446
6.46777393618554 P P P LNCV6_108131_PI430048170 mRNA
AGACTGAGGAGAAGATCGAGCGAACCCAGCGGGACATCAGGAGCATCCAGGAGGCTCTCG NM_032527RefSeq
chr20 + 63708027 63736142 ZGPAT 84619 "zinc finger, CCCH-type with G patch domain, transcript
variant 1"
GO:0043565|GO:0005515|GO:0001078|GO:0003700|GO:0007175|GO:0005634|GO:0000122|GO:0000978|GO:0045
892|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131000_PI430048170 0.5120700997408010.827863818416661 1.28659110145464
2.58860774977939 1.77828940150921 A A A 2.11388165802005 1.84645553895749
2.68512896963727 A A P LNCV6_131000_PI430048170 mRNA
CCTTACAAGACCGCAGCATAAGCTATTTTGAAGTATTTACCAAATAGTCACATGTTGTAA NM_001290983 RefSeq
chr3 - 197042559 197299272 DLG1 1739 "discs, large homolog 1 (Drosophila), transcript variant 6"
GO:0005515|GO:0008092|GO:0001658|GO:0008328|GO:0030054|GO:0031594|GO:0050680|GO:0043268|GO:0015
459|GO:0048704|GO:0042130|GO:0048608|GO:0016337|GO:0070830|GO:0030838|GO:0007411|GO:0048745|GO:0
045211|GO:0070062|GO:0035748|GO:0002369|GO:0005794|GO:0019901|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_105069_PI430048170 0.2326727302975261.16096134776416 3.41030858299928
3.61922823049872 3.32521326359367 P P P 3.08725697378212 3.48330416116646 3.119901746845
P P P LNCV6_105069_PI430048170 mRNA
AAACATTATTCGAATGCAGCATACACATGGATTCAAGGCTTTTCACATCCTCCCCCAGAC NM_015072RefSeq chr14
+ 75661207 75955082 TTLL5 23093 tubulin tyrosine ligase-like family member 5
GO:0009566|GO:0018095|GO:0005929|GO:0005813|GO:0005737|GO:0016874|GO:0007288|GO:0005634|GO:0030
317|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140674_PI430048170 0.00996265315227844 1.34410912277795 10.5233177291944
10.5140186712636 10.4087261885706 P P P 9.92392048799913 10.1452483059181
10.0906242870519 P P P LNCV6_140674_PI430048170 mRNA
CCCAACATGGGAGGGATCAGCCCCGCCTGTCACAATAAAGTTTATTATGAAAACAGGAAA NM_001014795 RefSeq
chr11 + 6603809 6610874 ILK 3611 "integrin-linked kinase, transcript variant 3"
GO:0005515|GO:0001658|GO:0030054|GO:0090263|GO:0030017|GO:0010761|GO:0043524|GO:0018105|GO:0032
956|GO:0043025|GO:0034446|GO:0010667|GO:2000178|GO:0030335|GO:0019901|GO:0007569|GO:0034329|GO:0
030027|GO:0045197|GO:0043234|GO:0005178|GO:0007229|GO:0050775|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140323_PI430048170 0.0348377761947883 1.77638148859261 1.77195493041677
1.47724065413585 1.21058254083937 A A A 1.00962784816276 0.62949215904059
0.301318669619419A A A LNCV6_140323_PI430048170 mRNA
CTTCTAGTGGACATATTTTATTGGGGGGCGGGGATTTTAAAAACAGAAAACCGAAACTGC NM_173593RefSeq chr12
+ 460376 561892 B4GALNT3 283358 "beta-1,4-N-acetyl-galactosaminyl transferase 3"
GO:0032580|GO:0008152|GO:0016021|GO:0033842|GO:0008376 . NA - . NA NA NA NA NA NA NA
NA NA

LNCV6_127139_PI430048170 0.4519501713116690.9125462134738185.14154270422339
5.29053044434503 5.63523848430532 P P P 5.34187891649557 5.59683160642473
5.55714021572253 P P P LNCV6_127139_PI430048170 mRNA
CTGTAGTATGTGAGGTTGAGAAAAAGTCTGATTGTGGTGATGTAGGTATAGTCATGCCAC NM_004528RefSeq chr1
+ 165630872 165656135 MGST3 4259 microsomal glutathione S-transferase 3
GO:0006629|GO:0006805|GO:0005635|GO:0044281|GO:0004364|GO:0043231|GO:0004602|GO:0007165|GO:0004
601|GO:0016020|GO:0005789|GO:0016021|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143647_PI430048170 0.5946469070090961.03936809066007 12.2176717954567
12.1821164754165 11.9623653173708 P P P 12.0698056979458 12.1274931369952
12.0082918747129 P P P LNCV6_143647_PI430048170 mRNA
GCCCTGGGCCTCTCTGGACGTGGCCTGTTTTCTATCAATAAACAGACATTACTTCCAGAT NM_001080849 RefSeq
chr9 - 136361899 136363811 DNLZ 728489 "DNL-type zinc finger, transcript variant 1"
GO:0005739|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130271_PI430048170 0.2249424070772811.08238881991241 0.407434152559947
0.4351764254197520.615133443550598A A A 0.3545914958865440.36286222226589
0.406035730610676A A A LNCV6_130271_PI430048170 mRNA
TCCGTTTTCACACTGGTGGCCATTGCTGTGGAAAGGTTCCGCTGCATCGTGCACCCTTTC NM_022146RefSeq chr10
- 70254956 70283694 NPFFR1 64106 neuropeptide FF receptor 1
GO:0042277|GO:0008150|GO:0005886|GO:0007218|GO:0005887|GO:0004930|GO:0007268|GO:0008188|GO:0032
870 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137007_PI430048170 0.0231919655788898 0.5977802185652684.86601627728304
4.73639435418962 4.76332622842456 P P P 5.32258737608389 5.76900911640377 5.4678731981649
P P P LNCV6_137007_PI430048170 mRNA
CTTTCTTTTGTCCTAACTCTGAAAAGTATATGTCAGAGTTCTGGAATATGTCTTTAGCCA NM_001286745 RefSeq
chr8 + 91070195 91087095 OTUD6B 51633 "OTU domain containing 6B, transcript variant 2"
GO:0006508|GO:0008234 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132198_PI430048170 0.00111236819114976 0.6207808630767668.03312718201797
7.85996509775167 7.85018173167379 P P P 8.55129355935806 8.71513799498911
8.54111849767211 P P P LNCV6_132198_PI430048170 mRNA
TATTTTCCAACTATTGCTTCCAACTGAAATAAGACTATTAAATGCCTGTTCAGGAGGGAG NM_018275RefSeq chr7
- 100154419 100158721 C7orf43 55262 "chromosome 7 open reading frame 43, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123069_PI430048170 0.9831689947941650.9942045167815164.82579062974852
4.35347985695764 4.61270074429898 P P P 4.44799468842383 4.45102786418484
4.90673742135387 P P P LNCV6_123069_PI430048170 mRNA
GGTGCCTATCTTAACACTGGATGTTAATGAAGACTTTAAAGACAAATATGAAAGTCTGGT NM_000788RefSeq chr4
+ 70993547 71030912 DCK 1633 deoxycytidine kinase
GO:0009157|GO:0055086|GO:0005634|GO:0044281|GO:0043097|GO:0006220|GO:0019206|GO:0005524|GO:0009
165|GO:0042803|GO:0005829|GO:0016310|GO:0006144|GO:0008144|GO:0043101|GO:0004137|GO:0006206 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138904_PI430048170 0.4816880956194381.06072424933345 9.21038042168287
9.35098325708458 9.20519902823465 P P P 9.34152745900474 9.16367747309799
8.98955013882368 P P P LNCV6_138904_PI430048170 mRNA
AATTTATTTATTTATAAACTCTCTGCTGCTGAGCTTGGGGCCTGGAGCCCCAGGAATGAG NM_207354RefSeq chr11
+ 67289290 67302484 ANKRD13D 338692 "ankyrin repeat domain 13 family, member D, transcript variant
1" GO:0005886|GO:0005770 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142126_PI430048170 0.6341579982963821.16366695928868 0.361319856680925
1.31764424646543 0.569464195102333A A A 0.5624593159711320.808806092773983

0.370326493222641 A A A LNCV6_142126_PI430048170 mRNA
CTGTAGAGAAACCCTGTAAATGTAAGGGATGTAGGAAAACACTAGTTCTTCTCTCTCTCT NM_152476 RefSeq chr19
- 9466354 9498603 ZNF560 147741 zinc finger protein 560
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128720_PI430048170 0.3974416810064420.58246669220862 0.437816843404273
0.4544747563465610.365374049182118 A A A 0.49419541298446 2.05163683256418
0.41733532429363 A A A LNCV6_128720_PI430048170 mRNA
TCTCCACTCCGAAGCAGTTGCTATTGGTCCAAGAGGATGCTCGGGTAGTCTTCGGTGGCT NM_139022 RefSeq chr11
+ 2302012 2318200 TSPAN32 10077 tetraspanin 32
GO:0070527|GO:0050688|GO:0005622|GO:0003674|GO:0008285|GO:0030886|GO:0009986|GO:0007229|GO:0007
010|GO:0070442|GO:0007267|GO:0042832 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140117_PI430048170 0.0573303762795823.1358700262061 2.13885634488764
3.30535786549016 3.59773156441315 A P P 2.15034872657465 0.620407802351712
1.28745742088213 A A A LNCV6_140117_PI430048170 mRNA
TGTGATGTGAGTTGTTGTTAAGACAGCCATCCATGTGCATGAGCATCATCCAGCTTTTTT NM_001113575 RefSeq
chr5 - 134298423 134367074 CDKL3 51265 "cyclin-dependent kinase-like 3, transcript variant 1"
GO:0005737|GO:0004672|GO:0030517|GO:0050775|GO:0051726|GO:0006468|GO:0005634|GO:0005524|GO:0006
464|GO:0004693 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140354_PI430048170 0.9679381469542981.01769013727061 3.68163179273518
3.86421817666925 4.25311151100853 P P P 3.99846752513216 3.79944603512995
3.97716267113834 P P P LNCV6_140354_PI430048170 mRNA
CATATGGTAGGCATTTAATTACTGATTGTGTTTGGATAATTTGGGAATTTTCGACTGTGG NM_006335 RefSeq chr1
+ 201955490 201970661 TIMM17A 10440 translocase of inner mitochondrial membrane 17 homolog A
(yeast) GO:0005744|GO:0015450|GO:0006626|GO:0005743|GO:0031305|GO:0071806|GO:0044267 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_138247_PI430048170 0.00330523375064478 0.2349945049901573.22217218743443
2.3698316130806 2.93354081930878 P A P 4.5870247812593 5.04713714812123
5.21413128295613 P P P LNCV6_138247_PI430048170 mRNA
AAGCAAACAACACAATTACAAGGTTGAATCTGAGGAAAATAATCCTTGTGCCATAGAAGT NM_012089 RefSeq chr1
- 229516581 229558695 ABCB10 23456 "ATP-binding cassette, sub-family B (MDR/TAP), member 10"
GO:0005215|GO:0032592|GO:0008152|GO:0006810|GO:0005743|GO:0042626|GO:0055085|GO:0005524|GO:0042
803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139335_PI430048170 0.12266577731178 0.7211972152201081 1.2273800874154
11.0928954145872 10.9898623122975 P P P 11.1847994259012 11.762494160911
11.7188589796177 P P P LNCV6_139335_PI430048170 mRNA
GCATCCACTTCCTTTCCCCCTTTTAACAAAAGAGAAGAACGAATTCCAAACCACAAAAAA NM_145253 RefSeq chr16
- 4608882 4614926 UBALD1 124402 UBA-like domain containing 1 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_145765_PI430048170 0.4876646828201241.08038872577017 8.56454717685273
8.33301554750602 8.55386917921491 P P P 8.19736513314013 8.62806696909464
8.26482328073761 P P P LNCV6_145765_PI430048170 mRNA
TAATATATTAATATATATCTGCTGTCCAGACAGCCTGTATCTTGGGGGACAGGGCTGGCC NM_201380 RefSeq chr8
- 143915146 143950876 PLEC 5339 "plectin, transcript variant 6"
GO:0005515|GO:0030056|GO:0005886|GO:0034329|GO:0030506|GO:0006915|GO:0003779|GO:0006921|GO:0005
829|GO:0042383|GO:0005737|GO:0016528|GO:0030198|GO:0043034|GO:0031581|GO:0045111|GO:0008307|GO:0
005925|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139430_PI430048170 0.195542688251351 0.9055747772742241 0.7840581430037
10.7149965826731 10.5513979350766 P P P 10.8349842505228 10.9295211524991

10.7172021576476 P P P LNCV6_139430_PI430048170 mRNA
GTTCTCTCCGAACCGTTCTTTGTACAGTAAATGTAATTCAGCTGTGGTCCCCACAAAAAA NM_001172663 RefSeq
chr16 + 589356 629273 RAB40C 57799 "RAB40C, member RAS oncogene family, transcript variant 1"
GO:0048471|GO:0009306|GO:0016567|GO:0005886|GO:0003924|GO:0005525|GO:0072659|GO:0006886|GO:0006
904|GO:0006184|GO:0017157|GO:0032482|GO:0019003|GO:0010008 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_136099_PI430048170 0.6160494352351250.8684128632839020.474246007746291
0.5232111503369610.545118312053517A A A 0.3321689213292261.18451252476399
0.488591272004238A A A LNCV6_136099_PI430048170 mRNA
CTAAATATACCACTACAAAGTGAGAGTTACTGCCACTCTGTTCTTACTGACACCGTCCAG NM_021184RefSeq
chr6_GL000256v2_alt - 2957574 2960049 C6orf47 57827 chromosome 6 open reading frame 47
GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131787_PI430048170 0.5291627667356981.37437155320056 1.59599362575722
0.3152612362701580.308527080994232A A A 0.4661203368811150.409168234727169
0.374812661263899A A A LNCV6_131787_PI430048170 mRNA
ACTACAAATCAATTCTCCCCAAAATGACAGAAATATGAATTGCCGAATAACCAAGGCAAT NM_152613RefSeq chr22
+ 41998724 42028473 WBP2NL 164684 WBP2 N-terminal like
GO:0033011|GO:0051321|GO:0007343|GO:0050699|GO:0035039 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143725_PI430048170 0.3355458600745290.7886867705550740.435264985529115
0.4749056593394170.437136990469733A A A 0.6042829666928731.2188718692827
0.428087527135991A A A LNCV6_143725_PI430048170 mRNA
CTGAGCTTTGGGGAGAAATAATCTTAGAAAGAAATTGTAGAAAAAACCCATGCAGACATA NM_006685RefSeq chr4
+ 70383077 70390244 SMR3B 10879 submaxillary gland androgen regulated protein 3B
GO:0008150|GO:0003674|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128998_PI430048170 0.5212511924079081.27901036372301 0.372171494585873
1.38995551614913 0.332315486309562A A A 0.4484779452065910.434745817778877
0.410419623877847A A A LNCV6_128998_PI430048170 mRNA
ATTAAACCAGATTGGAGCAATTACGGGGTGACCTTATGAGAAACTGCATGTGGGCTATGG NM_033012RefSeq chr13
+ 42562735 42608013 TNFSF11 8600 "tumor necrosis factor (ligand) superfamily, member 11,
transcript variant 2"
GO:0051897|GO:0071848|GO:0045453|GO:0019221|GO:0032813|GO:0005615|GO:0055074|GO:0051091|GO:0006
955|GO:0005737|GO:0051092|GO:0043406|GO:0045780|GO:0045944|GO:0009887|GO:0071847|GO:0051260|GO:0
002158|GO:0070371|GO:0043123|GO:0051466|GO:0071812|GO:0005164|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144034_PI430048170 0.00892044289556708 2.61748951315608 1.81482027550398
2.05051005582468 1.97944572875875 A A A 0.9034667717625230.361106925811242
0.354256176960427A A A LNCV6_144034_PI430048170 mRNA
GCAATCGGCAGCATGCTCGATTAAGAGTATGCCAAAAAATAGAAAAGCTATAAATATTTC NM_014420RefSeq chr8
- 42374067 42377156 DKK4 27121 dickkopf WNT signaling pathway inhibitor 4
GO:0003674|GO:0030178|GO:0007275|GO:0005576|GO:0005575|GO:0016055 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_74589_PI430048170 0.2311152622449680.6375132148041670.3160128228200720.256630960380211
0.280440977813884A A A 0.9029860646954110.2519018880312691.41746234389262 A A A
LNCV6_74589_PI430048170 mRNA
ATATCAAGTTGCCTTTCTTGGAAGAAATTTCATTTGGTGGTTCTGTGCAGCTCACAAAAT NM_144645RefSeq chr4
- 86876204 86892422 C4orf36 132989 chromosome 4 open reading frame 36 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_137049_PI430048170 0.1991573003652641.0160753214631 0.316371804743687

0.2797185483247350.280142693381753A A A 0.2710954041617530.269073293924588
0.267347561277219A A A LNCV6_137049_PI430048170 mRNA
GCACCGCTGCAGCCAGCAGTTGTAAAATTGTTAGTAAACATAGGTATAATTACCAGATAG NM_001206741 RefSeq
chr1 + 209686179 209734950 HSD11B1 3290 "hydroxysteroid (11-beta) dehydrogenase 1, transcript variant 3"
GO:0070524|GO:0016020|GO:0030324|GO:0006704|GO:0005789|GO:0003845|GO:0044281|GO:0016021|GO:0008202|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135470_PI430048170 0.00539345358985199 1.82120985777146 4.75914926316535
5.07941381179644 4.73410017299229 P P P 4.21503307006421 3.90367364891639
3.85889209265771 P P P LNCV6_135470_PI430048170 mRNA
CATGCGCAGCGGGTGGTCGCGGAGGTCCTGCTACCCAGTAAAAATCCACTATTTCCATTG NM_004851RefSeq chr19
- 50358476 50365674 NAPSA 9476 napsin A aspartic peptidase
GO:0004175|GO:0097208|GO:0033619|GO:0006508|GO:0043129|GO:0008233|GO:0004190|GO:0005764|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143157_PI430048170 0.1852507875997370.5626603656954010.285530018719168
0.3121048104278590.407332173439138A A A 0.3622708761557331.62744123773865
1.23556389231869 A A A LNCV6_143157_PI430048170 mRNA
GAGTTGTTTCTGACAGTGACAGAGTGACAATCTATAAGTATCTCAAGATCAAATGGTTAA NM_001003841 RefSeq
chr5 + 1201594 1225115 SLC6A19 340024 "solute carrier family 6 (neutral amino acid transporter), member 19"
GO:0015804|GO:0005886|GO:0007584|GO:0005887|GO:0005328|GO:0015175|GO:0006865|GO:0006836|GO:0031526|GO:0055085|GO:0070062|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137666_PI430048170 0.2000629571908540.8250735725330815.68492320575807
5.84888992383873 5.70143543515197 P P P 6.27084451297807 5.98586652236615
5.77296455585292 P P P LNCV6_137666_PI430048170 mRNA
TGTATTTCTATAAAAGTTGTCTCCCCTTGTTTCCTTTCCATTCTGGCACATGTAGACATT NM_014322RefSeq chr1 -
241593149 241640399 OPN3 23596 opsin 3
GO:0018298|GO:0009584|GO:0009583|GO:0009881|GO:0007186|GO:0005887|GO:0004930|GO:0042752|GO:0016021|GO:0007602|GO:0008020 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132633_PI430048170 0.1617174272764960.8205982857222929.42105645516748
9.90417695561695 9.6161697112949 P P P 10.0845986326839 9.94164598786257
9.79796772834341 P P P LNCV6_132633_PI430048170 mRNA
GTTACACCTGCTCCTTCCTGGACGCTCACTCCCTTGCTCGCTAGAATAAACTGCTTTGCG NM_003963RefSeq chr17
+ 4771891 4783211 TM4SF5 9032 transmembrane 4 L six family member 5 GO:0005887 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_145063_PI430048170 0.0086299000587282 0.7200134023936319.06013603576725
9.01418849590005 8.85581750765702 P P P 9.41221154539614 9.34434351606664
9.59171955439678 P P P LNCV6_145063_PI430048170 mRNA
AGGATAAAACGTAAACACGTGCTGTTAGTAATTTCTTGTGGATTTCATTGTTTTGCCTTC NM_006387RefSeq chr19
- 16517888 16542452 CHERP 10523 calcium homeostasis endoplasmic reticulum protein
GO:0005515|GO:0006396|GO:0048471|GO:0005737|GO:0051209|GO:0008285|GO:0016020|GO:0006874|GO:0051533|GO:0033017|GO:0044325|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140085_PI430048170 0.0127419814197481 0.8491953190729351 1.9548802285759
11.8109338026635 11.866419920976 P P P 12.0742592847278 12.1751758340332
12.0919344909775 P P P LNCV6_140085_PI430048170 mRNA
ACCAGGAGAAGAACCTGAAGAACTATTTTTCGTTATTGGTTTTCCAATCATTTGACTAAG NM_001170714 RefSeq
chr16 - 75229029 75266007 BCAR1 9564 "breast cancer anti-estrogen resistance 1, transcript variant 1"
GO:0050853|GO:0005515|GO:0008286|GO:0050852|GO:0017124|GO:0005886|GO:0008283|GO:0015629|GO:0001

558|GO:0050851|GO:0005829|GO:0005737|GO:0007173|GO:0035729|GO:0007015|GO:0004871|GO:0007155|GO:0
048010|GO:0048011|GO:0048012|GO:0030335|GO:0019901|GO:0005730|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132834_PI430048170 0.09624096086439 0.6369950943625267.34678126808357
7.01121774926182 6.98866914269068 P P P 7.27788915319202 7.96455622100829
7.97985558159533 P P P LNCV6_132834_PI430048170 mRNA
CTGGGAGAAAATCATCAAGAAGGGCTGCATGATGTTTGCCCAAAATTTATTTTATAAGAA NM_003579RefSeq chr1
+ 46247694 46278473 RAD54L 8438 "RAD54-like (S. cerevisiae), transcript variant 1"
GO:0005515|GO:0051276|GO:0042493|GO:0004386|GO:0005634|GO:0006310|GO:0003677|GO:0005524|GO:0000
733|GO:0006281|GO:0007126|GO:0000724|GO:0010212|GO:0005654 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_79031_PI430048170 0.0280133019000586 1.36110710404472 7.92845856398252
8.00514750150386 8.05412673195769 P P P 7.67118956415869 7.36299566591088
7.60410617453642 P P P LNCV6_79031_PI430048170 mRNA
GACCTTTGGGAATATAAAAATATTGCACCCACATGTCTTAATGGGGCTGAATTTCAGATT NM_032549RefSeq chr7
- 110663049 111562291 IMMP2L 83943 "IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae),
transcript variant 1"
GO:0042720|GO:0001541|GO:0006627|GO:0006508|GO:0008236|GO:0008233|GO:0016021|GO:0007283|GO:0030
728 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140002_PI430048170 0.0463102547122623 0.6794102618364410.1189618091534
9.91228706494359 10.1135615140424 P P P 10.8116302401143 10.3178989890907
10.6545427992543 P P P LNCV6_140002_PI430048170 mRNA
GGGGTGACCTATATCCCATGTGAGTGGTCACTTTATTTATAGGATCTTTAAAACATTTTT NM_022818RefSeq chr16
+ 87392194 87404774 MAP1LC3B 81631 microtubule-associated protein 1 light chain 3 beta
GO:0005515|GO:0006995|GO:0008017|GO:0005776|GO:0000422|GO:0005930|GO:0000421|GO:0005874|GO:0050
811|GO:0031410|GO:0000407|GO:0005829|GO:0012505|GO:0005622|GO:0031090|GO:0061025|GO:0000045|GO:0
019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128840_PI430048170 0.0257632325386043 1.64809163044186 8.91006888589468
8.69524436002413 8.87253329685012 P P P 7.82745714132726 8.0968968743092
8.35252255204677 P P P LNCV6_128840_PI430048170 mRNA
CCAGATCACGGGAACTTGAGAGCTTTTACTGTGATTCTTCAATGTAAAAAATAAACAACA NM_201266RefSeq chr2
+ 205682499 205798133 NRP2 8828 "neuropilin 2, transcript variant 1"
GO:0048010|GO:0005886|GO:0021675|GO:0005576|GO:0001525|GO:0048846|GO:0046872|GO:0002116|GO:0010
595|GO:0019955|GO:0019838|GO:0017154|GO:0001938|GO:0016020|GO:0007411|GO:0004872|GO:0005021|GO:0
016021|GO:0038084|GO:0007155|GO:0008201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139638_PI430048170 0.152661335885967 1.63957406383506 1.03928441112495 1.3709485734423
0.379556458875442 A A A 0.2801878988572920.2563733575975520.281698823715253 A A A
LNCV6_139638_PI430048170 mRNA
ACACCTGGCATCGGGCGGCATACCTGGTCTGCAACTATGCCATTAAGGGCAACTGGATTG NM_178491RefSeq chr20
+ 44337157 44350792 R3HDML 140902 R3H domain containing-like
GO:0010466|GO:0005576|GO:0030414 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128475_PI430048170 0.4522787808137141.1029814146564 9.76415835829334
10.0015534887524 9.98926387314066 P P P 10.0853468624526 9.63293087404097
9.56779256704815 P P P LNCV6_128475_PI430048170 mRNA
GGCAATGCTTCGTTTTCTAAAGGATGCTGCTGTTGAAGCTTTGAATTTTACAATAAACTT NM_006705RefSeq chr9
+ 89605011 89606554 GADD45G 10912 "growth arrest and DNA-damage-inducible, gamma"
GO:0005515|GO:0043065|GO:0006950|GO:0046330|GO:0006915|GO:0005634|GO:0007275|GO:0030154|GO:0000
186|GO:0005737|GO:0000185|GO:1900745|GO:0051726|GO:0006469 . NA - . NA NA NA NA NA NA
NA NA NA

LNCV6_133743_PI430048170 0.1495596099993180.8861810481030588.25702531608992 7.9942103860822
8.04793257645317 P P P 8.26380047760359 8.37268066769621 8.19355731052437 P P P
LNCV6_133743_PI430048170 mRNA
TACAGCCATGCCACCAACAAGTATGAGGTAGATGACATCGATGAAGAAGGCAAAGAGAGA NM_138414RefSeq
chr16 + 28553927 28591790 CCDC101 112869 coiled-coil domain containing 101
GO:0005515|GO:0006355|GO:0071169|GO:0043966|GO:0006325|GO:0005671|GO:0035064|GO:0006351|GO:0070
461 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141827_PI430048170 0.1602507390239951.14127093617425 14.0541075358915
14.0402486180174 14.1414849205329 P P P 13.7422413563404 13.8467556108743
14.0587963320311 P P P LNCV6_141827_PI430048170 mRNA
CCAGGAGGAAGCTCTGGCCCTTGTATTACACATTCTGGACATTAAAAATAATAATTATAC NM_006356RefSeq chr17
- 75038859 75046979 ATP5H 10476 "ATP synthase, H+ transporting, mitochondrial Fo complex, subunit
d, transcript variant 1"
GO:0015078|GO:0022857|GO:0005743|GO:0044281|GO:0005753|GO:0005739|GO:0022904|GO:0005737|GO:0042
776|GO:0000276|GO:0005654|GO:0016887|GO:0044237|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143511_PI430048170 0.1889714216459361.07759004876519 0.41804850561463
0.4534512044982760.598891270635868A A A 0.3605030607832060.376819163454441
0.415521892979084A A A LNCV6_143511_PI430048170 mRNA
TGGCTATCATGGTTGTGTTAATCGATTGTGGGGATGAAATGTCATTGTGTATGGAAGGCG NM_144626RefSeq chr1
+ 43269993 43274002 TMEM125 128218 transmembrane protein 125
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139070_PI430048170 0.00237663720460126 0.4896352723550165.85363684108732
5.61259391075694 5.8434429832029 P P P 6.63741952705499 6.74313900405288
7.00692756934295 P P P LNCV6_139070_PI430048170 mRNA
GCCAGCCTTGTGCTATGTTGATAAGATTGATTTACTGCTTAAAATCACTTTACTTTATCCNM_014159RefSeq chr3 -
47016407 47163977 SETD2 29072 SET domain containing 2
GO:0005515|GO:0006355|GO:0006368|GO:0005694|GO:0006325|GO:0001843|GO:0001525|GO:0048864|GO:0060
039|GO:0048701|GO:0018024|GO:0060977|GO:0060669|GO:0097198|GO:0035441|GO:0048332|GO:0034728|GO:0
005654|GO:0006298|GO:0010793|GO:0030900|GO:0001763 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_128287_PI430048170 0.0262782367716908 1.4175206186074 10.3720315886699
10.0192620075465 10.1198829064996 P P P 9.65468307346148 9.8496854283246
9.49838764310985 P P P LNCV6_128287_PI430048170 mRNA
ACAAGAGAACCCCAACATGCGGCTGTCGCAGCTGAAACAGCTGCTCAAGAAGGAGTGGCT NM_138442RefSeq
chr19 + 17935095 17943985 CCDC124 115098 "coiled-coil domain containing 124, transcript variant 1"
GO:0007049|GO:0005737|GO:0005886|GO:0005815|GO:0030496|GO:0051301 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_118662_PI430048170 0.6199847850802420.8996596623544263.30350026586772 2.941326111083
3.43362451891469 P A P 3.77351587407322 3.14942343183488 3.16570657134835 P P P
LNCV6_118662_PI430048170 mRNA
TTCATTACTCGCCATTTCAAAATGCTGCCGAGGCCCTAGGATCTGTGACTGCCACCCCTC NM_002393RefSeq chr1
+ 204516378 204558120 MDM4 4194 "MDM4, p53 regulator, transcript variant 1"
GO:0005515|GO:0071157|GO:0008284|GO:0043066|GO:0008285|GO:0030330|GO:0008283|GO:0042177|GO:0050
821|GO:0071456|GO:0005634|GO:0000122|GO:0045023|GO:0006461|GO:0005654|GO:0008270|GO:0019899 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124272_PI430048170 0.1745257043518812.40249450656022 4.86042603134762
3.99612567468383 2.93594901818833 P P P 2.80127107981312 3.27900500643773
2.38984513695308 P P P LNCV6_124272_PI430048170 mRNA

GAGCAAGCCGGGCGACGAGGACGACGCGCCGCCCAAGATGGGGGAGCCGGCGGGCGGCCG NM_020732 RefSeq
chr6 + 156777929 157210779 ARID1B 57492 "AT rich interactive domain 1B (SWI1-like), transcript variant 2"
GO:0005515|GO:0071565|GO:0005737|GO:0016514|GO:0003713|GO:0005654|GO:0048096|GO:0003677|GO:0006351|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134095_PI430048170 0.00202261389760419 0.3891538906713715.64168888504503
5.31059927100334 5.79095896455993 P P P 6.75994165235861 6.93633490196285 7.1466615007724
P P P LNCV6_134095_PI430048170 mRNA
GTGTGTTATCTTTATATGTCAAACTGGTTGAACACTGTAATGAGAATAAACTGCACAGAG NM_001195608 RefSeq
chr10 + 122386068 122432355 PLEKHA1 59338 "pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1, transcript variant 3"
GO:0005515|GO:0050853|GO:0051898|GO:0070301|GO:0005886|GO:0001553|GO:0048705|GO:0007283|GO:0009791|GO:0031529|GO:0045184|GO:0005737|GO:0035264|GO:0060021|GO:0070062|GO:0008209|GO:0043325|GO:0032587|GO:0030165|GO:0014065|GO:0008210|GO:0060325|GO:0033327|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_88825_PI430048170 0.9964115688794630.9827505045195415.51189941911246 5.46678991158598
5.51330565943983 P P P 5.12260156233406 5.6245106530892 5.74779868277724 P P P
LNCV6_88825_PI430048170 mRNA
AGAGTACTGCAGACATCATGAAATCACCTATGTGGCCCTTGTCTCGGATAAAGAAGGAAG NM_001013703 RefSeq
chr15 + 39934123 40035596 EIF2AK4 440275 eukaryotic translation initiation factor 2 alpha kinase 4
GO:0017148|GO:0043558|GO:0022626|GO:0004674|GO:0006446|GO:0006468|GO:0005524|GO:0004694|GO:0030968|GO:0009267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143556_PI430048170 0.1848210986804820.7632787898493360.560525680031689
0.4868576487419750.283010858844171 A A A 0.7034985379105260.547897424569233
1.18389552443687 A A A LNCV6_143556_PI430048170 mRNA
TGTAAATATGAGAGGGTGGAGGGAGACCAGCTGGTAGCAATAAACATGGGTAGAACTAAA NM_018990 RefSeq
chrX + 129779915 129795200 SASH3 54440 SAM and SH3 domain containing 3
GO:0032729|GO:0032753|GO:0046622|GO:0032733|GO:0032760|GO:0030890|GO:0032743|GO:0005634|GO:0002726|GO:0005737|GO:0048873|GO:0002639|GO:0043372|GO:0042102 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138737_PI430048170 0.2943699573731110.8863060517391513.5637726470714
13.3758291848325 13.3717340206897 P P P 13.7484657755228 13.692874088506
13.3731308035999 P P P LNCV6_138737_PI430048170 mRNA
CCAGACGGACGCTCCCTGTACCCCCTCCCTCCTCACTTGGATAAAAAGCAGATTTGCCTT NM_001190764 RefSeq
chr19 - 55379243 55384259 TMEM238 388564 transmembrane protein 238 GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134108_PI430048170 0.1234990814914610.5958310715693163.61929462022789
3.13253903380397 3.09042453745772 P P P 3.40077653743975 4.32683596124325
4.24858910316066 P P P LNCV6_134108_PI430048170 mRNA
TGCTTTTAGCCTAGTCTGATAACCTAATGCCCACTTGGGAGAGGGATAGAATGACTTGAG NM_003609 RefSeq chr16
- 29992320 29996096 HIRIP3 8479 "HIRA interacting protein 3, transcript variant 1"
GO:0005515|GO:0005730|GO:0005654|GO:0005634|GO:0006333 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144184_PI430048170 0.2076512873969951.01913158580608 0.30882777550681
0.2904431992792390.342266955244322 A A A 0.2972362866680660.283498025801778
0.279200303043772 A A A LNCV6_144184_PI430048170 mRNA
CTGAGAAATAAAGATGTGAAAGAAGCTCTCAGAAAAGTGATGGGCTCCAAAATTCACTCC NM_001004738 RefSeq
chr11 + 55811466 55812402 OR5L1 NA "olfactory receptor, family 5, subfamily L, member 1 (gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_130076_PI430048170 0.00907425781683073 0.63769211054949 10.9002955023325
10.8280286880458 10.9824343982541 P P P 11.529105065083 11.3987643526081
11.7164599571709 P P P LNCV6_130076_PI430048170 mRNA
GTCCGTTTGCTGTTTCCAGGCTGTGATATATTTTCCTAGTGGTTTGACTTTAAAAATAAA NM_032822RefSeq chr2
- 70295975 70302088 FAM136A 84908 "family with sequence similarity 136, member A"
GO:0005739|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136054_PI430048170 0.2211984571160991.01509258515913 0.318300141169415
0.2837397501820540.279376222226927A A A 0.2745554689261780.273205823657118
0.269131398024929A A A LNCV6_136054_PI430048170 mRNA
GTTTGTCCCAGGAAAATGCCTGTGTATAATTACCTAACTTCAGATCTGCACATTAACTTA NM_000724RefSeq chr10
+ 18260654 18541759 CACNB2 783 "calcium channel, voltage-dependent, beta 2 subunit, transcript
variant 1"
GO:0005515|GO:0005262|GO:0005245|GO:0051928|GO:0007268|GO:0008331|GO:0005891|GO:0042383|GO:0070
509|GO:0005887|GO:0007411|GO:0007528|GO:0070588|GO:0006810|GO:0007601 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132417_PI430048170 0.1266533272006610.3885539472546040.275660166263934
0.2816588084777841.31017722649237 A A A 0.86637681566187 2.64825531272973
2.18071332583208 A P A LNCV6_132417_PI430048170 mRNA
GGAAATCAGTCTCCTTTTCCCATTGTGTTTGTCACTTTTGCTGAGACGCAAAAAATAACG NM_001297733 RefSeq
chr4 - 73054695 73069759 COX18 285521 "COX18 cytochrome c oxidase assembly factor, transcript
variant 3" GO:0008535|GO:0051204|GO:0008565|GO:0031305|GO:0015031 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143612_PI430048170 0.7130068184263890.7738172806968811.98616497346628
1.73348059802337 0.321580392340046A A A 0.46032388998844 2.11826779634803
2.40993564020396 A A P LNCV6_143612_PI430048170 mRNA
CTTTTGGTTTCTTGATCCTTAAAATGACCTTCGAGCATATTCTAATAAAGTGCATTGCCA NM_139074RefSeq chr20
+ 157469 159163 DEFB127 140850 "defensin, beta 127"
GO:0009986|GO:0045087|GO:0005576|GO:0005575|GO:0042742 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_69557_PI430048170 0.3990089763350761.08598741446278 13.692874088506 13.7737990887644
13.8754892359312 P P P 13.4274875608275 13.7304016733539 13.8059295702459 P P P
LNCV6_69557_PI430048170 mRNA
GTAGTTCTAGATGACAAGGATTATTTCCTATTTAGAGATGGTGACATTCTTGGAAAGTAC NM_002157RefSeq chr2
+ 197499996 197503463 HSPE1 3336 heat shock 10kDa protein 1
GO:0006986|GO:0005739|GO:0005515|GO:0016020|GO:0006919|GO:0006457|GO:0005759|GO:0051087|GO:0051
082|GO:0005524|GO:0001649|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138027_PI430048170 0.24794317053496 0.6692123303947299.46343834030768
9.29441378694831 9.42064187445889 P P P 9.26913377179804 10.2830845513748
10.1727602444274 P P P LNCV6_138027_PI430048170 mRNA
ATGCTGACCGGTGCTTATCCTCTAAGCCCTGATCCACAATAAAAATGGACCCAACTCAAA NM_016095RefSeq chr16
- 85677673 85688982 GINS2 51659 GINS complex subunit 2 (Psf2 homolog)
GO:0005515|GO:0006271|GO:0005654|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53715_PI430048170 0.1689308893540531.42667805159507 6.02827010674616 6.44877973060385
6.28948591929095 P P P 6.24664918137281 5.39045319573942 5.45694268198618 P P P
LNCV6_53715_PI430048170 mRNA
AATTCCCCACCTGCCTTTGGATGAAAGACTCCGTTGGGAATAAATGGCCAAAGCTTATAG NM_001856RefSeq chr1
- 31652246 31704167 COL16A1 1307 "collagen, type XVI, alpha 1"
GO:0005515|GO:0007565|GO:0005578|GO:0005576|GO:0005597|GO:0005178|GO:0022617|GO:0071230|GO:0007
229|GO:0030198|GO:0030574|GO:0005788|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_144848_PI430048170 0.0487275774756816 0.6339080693219530.319056295151246
0.3108082224729990.294251195202175A A A 0.916720576220957 1.22159005981654
0.713078872173804A A A LNCV6_144848_PI430048170 mRNA
GCAGAGAAAAACCATTCAAATATGAGAACTGTGGGAAGAGCTTTGTACATAGATCATATC NM_013359RefSeq chr19
+ 43951244 43967600 ZNF221 7638 "zinc finger protein 221, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128263_PI430048170 0.000715214250458956 2.7367732764502 7.58252125488011
7.68013620059895 7.60191573143904 P P P 6.03019182372818 6.18710162137997 6.2806940099087
P P P LNCV6_128263_PI430048170 mRNA
TGGACTGGGATATCATCTCTACAGCCTGCAAATAAACCAGACAAACTTACCAACGTCAAA NM_001185095 RefSeq
chr9 + 131096475 131123152 AIF1L 83543 "allograft inflammatory factor 1-like, transcript variant 3"
GO:0005737|GO:0051015|GO:0005884|GO:0005509|GO:0032587|GO:0015629|GO:0005925|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58786_PI430048170 0.0560352446374972 1.6237194857086 5.91875664082701
6.20207921145024 6.12728690467824 P P P 5.55673599899785 5.57466305252629
4.95056818310961 P P P LNCV6_58786_PI430048170 mRNA
TTCAAGTGAAACTCGCTCTGTAAGAAAGAGGAGGATACAAGATCAGCTTCTCCCACGATA NM_006152RefSeq chr12
+ 25052246 25108335 LRMP 4033 "lymphoid-restricted membrane protein, transcript variant 1"
GO:0005815|GO:0005694|GO:0030176|GO:0005635|GO:0006906|GO:0006903|GO:0007338|GO:0000922|GO:0016
020|GO:0005887|GO:0005789|GO:0016021|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134318_PI430048170 0.8020087917735350.9587816186796676.86384840303152
6.71665454634663 6.08683017978394 P P P 6.78185834079125 6.82556601859334
6.29661228381165 P P P LNCV6_134318_PI430048170 mRNA
GTGCCACCTGGTTGCTTATGGCTTCGTATTTTTATGTTGAGAAATTTGAAATGAGAACCT NM_133326RefSeq
chr1_GL383520v2_alt - 164627 182350 ATP6V1G3 127124 "ATPase, H+ transporting, lysosomal 13kDa, V1
subunit G3, transcript variant 2"
GO:0008286|GO:0006879|GO:0033572|GO:0051701|GO:0008553|GO:0005886|GO:0051117|GO:0090382|GO:0055
085|GO:0016471|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131786_PI430048170 0.0818823012554538 0.8156230131240111 1.2624029124554
11.1267282379727 11.053124237007 P P P 11.6347622789961 11.3132328117757
11.3630313231427 P P P LNCV6_131786_PI430048170 mRNA
CCCTCCCCAGTGAGGGACATTTTTTGGTAAACCTATTTTCATTTTGGAAAATATTTATGA NM_014516RefSeq
chr19_KI270938v1_alt + 112548 130559 CNOT3 4849 "CCR4-NOT transcription complex, subunit 3"
GO:0005515|GO:0010467|GO:0006355|GO:0005634|GO:0031047|GO:0001829|GO:2000036|GO:0006351|GO:0006
417|GO:0030014|GO:0005829|GO:0000932|GO:0000289|GO:0000288 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132873_PI430048170 0.00687408872881331 0.6363808562942396.84870755936615
6.68940540160759 6.89115339635541 P P P 7.33585435441917 7.39661334314482
7.64212018470874 P P P LNCV6_132873_PI430048170 mRNA
GTAACAAAAACCCAGGACATTTTTGGAAATTGTATGCTCTCTAGCAACTTTGTGTGAATT NM_001080450 RefSeq
chr6 - 107065180 107114432 BEND3 57673 BEN domain containing 3 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_144545_PI430048170 0.3207810897558751.02261995388238 0.305110210166111
0.3167736125364180.383444595512825A A A 0.3175280585174720.30234870888568
0.289751697149184A A A LNCV6_144545_PI430048170 mRNA
TCTCAAATGGACCACACCATTCTCAACTCGTTTATAAATAAAGGGATGCAGAATTGCAAA NM_004845RefSeq chrX
- 24558086 24647338 PCYT1B 9468 "phosphate cytidylyltransferase 1, choline, beta, transcript variant 1"
GO:0005737|GO:0001541|GO:0005789|GO:0004105|GO:0044281|GO:0007283|GO:0006657|GO:0006644|GO:0046

474|GO:0006656 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133454_PI430048170 0.4451010576411191.13631794663214 6.20870160366548
6.67302883744867 6.65937248020999 P P P 6.21470407956744 6.12295075452232 6.6421491212081
P P P LNCV6_133454_PI430048170 mRNA
GGAGGTGCTCTAAATAACTTTTAGATTTCCTCTCTCTGTGTGCATTACCAATATCTAAGT NM_018465RefSeq chr9
- 5357965 5437937 PLGRKT 55848 "plasminogen receptor, C-terminal lysine transmembrane protein"
GO:0005739|GO:0006954|GO:0006935|GO:0010756|GO:0005887 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141931_PI430048170 0.00571256383141642 0.3543218445921620.308802365760111
0.6844993498008840.849547104153035A A A 2.05715927767678 2.0779928117428
2.24290142962039 A A A LNCV6_141931_PI430048170 mRNA
AGGCCATAGGGCATAATTTGCATCTCAAATCTGAGAATAAACTGATGAACTGTGAAAAAA NM_015719RefSeq chr19
- 9959560 10010471 COL5A350509 "collagen, type V, alpha 3"
GO:0005518|GO:0043394|GO:0005576|GO:0005588|GO:0007160|GO:0022617|GO:0007411|GO:0030198|GO:0030
199|GO:0030574|GO:0005788|GO:0043588|GO:0008201|GO:0070062|GO:0005201 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140424_PI430048170 0.00215596184950833 0.671593850194107 11.8273906080072
11.9989127554576 11.9426382067371 P P P 12.3763736420906 12.5710533625573 12.542243698853
P P P LNCV6_140424_PI430048170 mRNA
TGACGTTCCTTGTGACTTAAGGGTCCGGCTTGGGAATTAAAGTTTGTTTCTGGCCTTTAG NM_030622RefSeq chr19
+ 41193206 41207539 CYP2S1 29785 "cytochrome P450, family 2, subfamily S, polypeptide 1"
GO:0008392|GO:0006805|GO:0070330|GO:0005506|GO:0005783|GO:0008395|GO:0019373|GO:0044281|GO:0043
231|GO:0005737|GO:0019825|GO:0042738|GO:0005789|GO:0016712|GO:0055114|GO:0020037 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137041_PI430048170 0.0792712604494720.6923891240936126.16480125921806
6.31551053057897 6.78303700777951 P P P 6.92391106207574 6.83315309219358
7.15236969428232 P P P LNCV6_137041_PI430048170 mRNA
GGTGCCATTTCCTGAATCACAACTGTATTTTTGTATCTCAAGCTATTTTCATATGTTGTG NM_001130158 RefSeq chr2
+ 191245380 191425389 MYO1B 4430 "myosin IB, transcript variant 1"
GO:0030048|GO:0005516|GO:0048471|GO:0005886|GO:0005884|GO:0005547|GO:0006892|GO:0005546|GO:0030
175|GO:0016459|GO:0032588|GO:0005524|GO:0071944|GO:0005903|GO:0000146|GO:0005737|GO:0051015|GO:0
008152|GO:0007015|GO:0051017|GO:0010008|GO:0005769|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129489_PI430048170 0.0726527317757937 1.23515295970722 9.19610536542558
9.23466704776349 9.10064035241051 P P P 8.70441620994573 9.04595000631672
8.84980066054245 P P P LNCV6_129489_PI430048170 mRNA
GGCACAGGAATCTCAAAATTAAACCTGACTTCATTGCACTTGTTGCAGGAGTGGCTTAAA NM_001161581 RefSeq
chr3 - 52075232 52154690 POC1A 25886 "POC1 centriolar protein A, transcript variant 3"
GO:0005515|GO:0005813|GO:0000922|GO:0005814|GO:0030030|GO:0036064 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135798_PI430048170 0.2650001715633611.89584170509916 1.92376511874474
0.3296675165795891.82113553930085 A A A 0.4744517918841030.370234413720148
0.884465724866656A A A LNCV6_135798_PI430048170 mRNA
CGTGTTGGTTGCCACCGGTCCTACTTCAAAAGAATTATTTTGTACAAAATCATCATATTA NM_174937RefSeq chr10
- 131092391 131311721 TCERG1L 256536 transcription elongation regulator 1-like NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128396_PI430048170 0.5019683984475391.03971325640747 0.481757720025166
0.4252904612514770.510307242797301A A A 0.3084083894874450.380688080310714
0.550212142810592A A A LNCV6_128396_PI430048170 mRNA

CAGAAACCTAGGCCAAATTACTGTAATTGAGAATCATATCATAATAAACCCACCCCTAAA NM_002278 RefSeq chr17 - 41459512 41467386 KRT32 3882 "keratin 32, type I"
GO:0005882|GO:0008544|GO:0005198|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134887_PI430048170 0.276099131856299 0.846847318012021 0.296114252323144
0.305877411391923 0.499288893976016 A A A 0.776267133265567 0.288969965994952
0.717481875716664 A A A LNCV6_134887_PI430048170 mRNA
TGGGTCTCTTGAGGGCAGTGGAGTGTCACACAGCTAATAAAGTACACATTTCATGTTGGA NM_030779 RefSeq chr17 + 63523333 63546728 KCNH6 81033 "potassium channel, voltage gated eag related subfamily H, member 6, transcript variant 1"
GO:0007165|GO:0005886|GO:0005887|GO:0005249|GO:0042391|GO:0007268|GO:0034765|GO:0004871|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134848_PI430048170 0.207082909582339 0.679508891868174 4.92560926866068
4.83136383138906 5.13154263658398 P P P 4.90678920264416 5.77802906080869
5.73718022417169 P P P LNCV6_134848_PI430048170 mRNA
TTGGTTGATGCCAAGGCAAAAAGATAACTTTTAACAGTTAGAGAGGATCAGTTGCTTAAA NM_133374 RefSeq chr9 + 113876281 114056595 ZNF618 114991 zinc finger protein 618
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137082_PI430048170 0.00577155826583793 0.430622333311343 5.71459350869714
5.59636962825057 6.14987499215854 P P P 6.99582853122981 6.88405892602068
7.26156262614283 P P P LNCV6_137082_PI430048170 mRNA
TGTATACCCCTTACTGTAATTTGTTCCTCTTAGAAGTCAGATCATCTGATTTATAGAGGA NM_001267578 RefSeq chr1 + 179882041 179920077 TOR1AIP1 26092 "torsin A interacting protein 1, transcript variant 1"
GO:0008092|GO:0034504|GO:0051117|GO:0005637|GO:0005634|GO:0032781|GO:0016021|GO:0071763|GO:0005521|GO:0001671 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58725_PI430048170 0.16841938933869 0.445368848994272 0.393011215144153 0.398729237842582
0.354309952851374 A A A 0.439920067268132 1.84562299021269 1.93670244467587 A A A
LNCV6_58725_PI430048170 mRNA
AGAATTCATCTCAGGATGAAGCTGCAAGGGCAAAGGAGAAGTACTTGTGACACAAGCAAA NM_021071 RefSeq chr12 - 14829310 14843479 ART4 420 ADP-ribosyltransferase 4 (Dombrock blood group)
GO:0006471|GO:0016020|GO:0005886|GO:0003956|GO:0006525|GO:0031225 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130065_PI430048170 0.0703199267447939 0.960204107046777 0.404749836734494
0.403734000198247 0.348012201610731 A A A 0.433153000398814 0.461340483481572
0.438334729941758 A A A LNCV6_130065_PI430048170 mRNA
AAGGAAGAACTTCTCTTCGATGATAATGTCGAGTGGAAATCATGCTTAATCTGAAGATTA NM_178483 RefSeq chr20 + 18813725 18814391 SCP2D1 140856 SCP2 sterol-binding domain containing 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129741_PI430048170 0.823898556430882 0.976757658838102 6.34573956724701
6.11588066477222 6.64427150593656 P P P 6.34632975380948 6.28668161168028 6.6035499431744
P P P LNCV6_129741_PI430048170 mRNA
ACAACTGTTGCATTTTGGGGTACTAATAAATGATTGCCGATGAGTTATGAGGGCAAAAAA NM_015994 RefSeq chr14 - 67337863 67360003 ATP6V1D 51382 "ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D"
GO:0005515|GO:0008286|GO:0005813|GO:0033176|GO:0051701|GO:0042626|GO:0005765|GO:0055085|GO:0005829|GO:0006879|GO:0005929|GO:0033572|GO:0042384|GO:0016020|GO:0090382|GO:0070062|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133717_PI430048170 0.0261142233868282 2.43844596986264 1.36843899156529
2.09925727066725 1.49495153968292 A A A 0.49918852731572 0.386258037311164
0.323676658421098 A A A LNCV6_133717_PI430048170 mRNA

GGAAAGCAATAAAAGTTATTGTAACTGGTCAGGTTTTAAAGAACAGTTCAGCAACCATGA NM_175067RefSeq chr6
+ 132570321 132571359 TAAR6 319100 trace amine associated receptor 6
GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0001594 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138276_PI430048170 0.00458433521435599 0.3710364435744964.74231689237535
4.61270074429898 4.55300039907259 P P P 5.83446064189483 6.00826112899381
6.32037585200883 P P P LNCV6_138276_PI430048170 mRNA
CTGTGCTAGTCAAGTTGTTGTTTTTCCTTGAACAACTTTGGAAAAATGGATTTGACAGTA NM_012158RefSeq chr13
- 77005253 77027196 FBXL3 26224 F-box and leucine-rich repeat protein 3
GO:0005515|GO:0004842|GO:0016567|GO:0000151|GO:0005634|GO:0031146|GO:0005829|GO:0031648|GO:0005
737|GO:0007623|GO:0042752|GO:0005654|GO:0043153|GO:0019005 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132955_PI430048170 0.4337729181891910.5100385818189760.312125010440762
0.4028081139490320.374051803272708A A A 2.32997307678042 0.323564817344648
0.365014604250804A A A LNCV6_132955_PI430048170 mRNA
GAAAATTCCATCAGGGATTGGATGACCATGGGGATGGACATAATTGCTACTACCAACACA NM_153325RefSeq chr20
+ 87671 96573 DEFB125 245938 "defensin, beta 125" GO:0009986|GO:0045087|GO:0005576|GO:0042742
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133445_PI430048170 0.0330854439524251 1.22962643028338 10.1187394013451
10.1332282191272 10.3244556677615 P P P 9.78048522453064 9.89350578442125
10.0080696778493 P P P LNCV6_133445_PI430048170 mRNA
CCTATGAGGTAATGCTTGTTATCTTCCATCTAATAAAAATCTGCTGCAGATGTGTATATG NM_016055RefSeq chr11
+ 73787871 73864611 MRPL4851642 mitochondrial ribosomal protein L48
GO:0070124|GO:0005515|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0005761|GO:0005743 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142786_PI430048170 0.0239699913849760.3058057407825114.37949978518407
3.29322707578021 3.85766854319684 P P P 5.4527267116067 5.7043642397156
5.68895922974117 P P P LNCV6_142786_PI430048170 mRNA
CAAGTGTACCTGCCATAACATAAAATAAACACTAGACTGTATCACACTTCGATTGATTTC NM_205842RefSeq chr2
- 182924850 183038858 NCKAP1 10787 "NCK-associated protein 1, transcript variant 2"
GO:0005515|GO:0031209|GO:0001756|GO:0030032|GO:0032403|GO:0048570|GO:0005829|GO:0032880|GO:0010
592|GO:0042074|GO:0008078|GO:0070062|GO:0048010|GO:0010172|GO:0030950|GO:0031258|GO:0035050|GO:0
007354|GO:0050821|GO:0006915|GO:0001843|GO:0045176|GO:0045175|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132860_PI430048170 0.3202837912507611.02576950945541 0.300785913624362
0.2885776717835390.377110233924958A A A 0.2986441035799520.278830682023355
0.280400046675715A A A LNCV6_132860_PI430048170 mRNA
CATTCTGTGCTGAGATCTAAGGTGAAGTCTATAAAGATTAAAGTTCCCTTTTTTCTGATG NM_021998RefSeq chrX
+ 85243990 85273362 ZNF711 7552 zinc finger protein 711
GO:0043565|GO:0005515|GO:0005634|GO:0045893|GO:0046872|GO:0006351|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134445_PI430048170 0.9397142542433750.9508214019787481.24013376487752
1.42019483154068 1.30570500565569 A A A 0.4713484157601191.52550047158445
1.86142085279561 A A A LNCV6_134445_PI430048170 mRNA
AAAGCAAGAAACGAGACCTCCGAGACCGCTGAAAAATGTCGTACAGTGTGATGCTTTCTT NM_001243237 RefSeq
chr8 - 73241423 73259502 C8orf89 NA chromosome 8 open reading frame 89 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126682_PI430048170 0.0225516638846099 0.5415426165755113.87386781504338
3.51977136977881 3.23266185671693 P P P 4.61066955295339 4.45096673981686

4.27103765808111 P P P LNCV6_126682_PI430048170 mRNA
CCCCACCTGCCAAATAACCTGTTCAAAACAAAGAAGGCATAGAATATAAATGAATTTCAA NM_001144033 RefSeq
chr13 - 38965924 38990859 STOML3 161003 "stomatin (EPB72)-like 3, transcript variant 2"
GO:0008150|GO:0007165|GO:0005929|GO:0003674|GO:0005886|GO:0045121|GO:0016021|GO:0005575 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139012_PI430048170 0.3832372123207811.4686810556549 1.56601083534238
0.3199882323477670.445433261962806A A A 0.3492693212165090.30657967938377
0.358889717303561A A A LNCV6_139012_PI430048170 mRNA
TTCCAGCCCACCAAATCTGTATGAAACTGAGATTTCTATCATTTGGTGTTAAAACTCATC NM_207374RefSeq chr11
- 58266791 58268260 OR10W1 NA "olfactory receptor, family 10, subfamily W, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143190_PI430048170 0.1263157455467151.35732483594115 5.62476183217678
6.12353035806981 5.555742853005 P P P 5.50621658942027 5.33108037428798
5.19650698460444 P P P LNCV6_143190_PI430048170 mRNA
AGGAAACATTCTTGGCAAATACAGCTCCGAGATCAGGCCTGCCTTCTTCCTCACCATCCC NM_001001524 RefSeq
chr19 - 19264364 19273265 TM6SF2 53345 transmembrane 6 superfamily member 2
GO:0008150|GO:0003674|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83353_PI430048170 0.5207939259818251.11093698312181 7.89871403766306 7.64741837102409
7.33034864904855 P P P 7.58925963402787 7.60286103152604 7.25910548134 P P P
LNCV6_83353_PI430048170 mRNA
GGAGCTCTCCCTTTGCTAGTACTTTCTCTAAAGTACTAGTCTAGTAAAATTTATTCTTGT NM_015085RefSeq chr17 +
2796437 3037741 RAP1GAP2 23108 "RAP1 GTPase activating protein 2, transcript variant 1"
GO:0043005|GO:0048471|GO:0031965|GO:0005813|GO:0005737|GO:0046582|GO:0010977|GO:0032854|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132854_PI430048170 0.00205438401023435 0.7627589138423854.88979264591829
4.79437046189981 4.80709873506825 P P P 5.27068690759348 5.25046132980297
5.14072876580595 P P P LNCV6_132854_PI430048170 mRNA
CGATGGCAGATCGGAAACGCGTTTATAAACAAGTGATGGTTTGTGAGTCGACTGTCAAGA NM_175063RefSeq chr19
+ 50476476 50483526 EMC10 284361 "ER membrane protein complex subunit 10, transcript variant 1"
GO:0072546|GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59532_PI430048170 0.8272305718814630.9593326855776943.35131583853352 3.36783241197576
3.31947496775228 P P P 3.64616684388663 3.07752589782193 3.43880584429632 P P P
LNCV6_59532_PI430048170 mRNA
GTTAGCCAGCCTAGAGAGAGAAGCATCAGTAAAGAGAAATCAGACCCGTGAATTTGATGG NM_014055RefSeq
chr12 + 110124334 110218795 IFT81 28981 "intraflagellar transport 81, transcript variant 1"
GO:0042384|GO:0005929|GO:0005813|GO:0006996|GO:0015631|GO:0031514|GO:0097225|GO:0030992|GO:0097
228|GO:0072372|GO:0035735|GO:0007283 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128780_PI430048170 0.0931130142458865 0.5340954742109686.35278285572164
5.30703986812069 5.35967478125327 P P P 6.80849439424943 6.50041116399511
6.66394744295534 P P P LNCV6_128780_PI430048170 mRNA
GCCCACACCCACACTCTCCAGCATCTGGCACAATAAACATTCTCTGTTTTGTAGAAAAAA NM_001972RefSeq chr19
+ 852290 856246 ELANE 1991 "elastase, neutrophil expressed"
GO:0006909|GO:0005515|GO:0002438|GO:0004252|GO:0050900|GO:0002020|GO:0001878|GO:0030163|GO:0005
737|GO:0050922|GO:0022617|GO:0043406|GO:0030198|GO:0017053|GO:0045079|GO:0030574|GO:0006508|GO:0
032496|GO:0044130|GO:0030141|GO:0008201|GO:0009411|GO:0070947|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132372_PI430048170 0.00250174711104854 0.1725262772782650.572121319670668
0.4707207964426711.29079132235558 A A A 3.41369331843539 3.05713191990381
3.56693131570711 P P P LNCV6_132372_PI430048170 mRNA

GTTGATTGTTGAAATGTGAAATGTAGTCACTGTTGACCTTGTAAATATCTGCCAGAGATG NM_173822RefSeq chr2 - 200973717 201071669 FAM126B 285172 "family with sequence similarity 126, member B" GO:0005622 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144308_PI430048170 0.0033043074999986 0.441411383333309 5.26022379958 4.90085843750825 5.00125046988036 P P P 6.09381057537198 6.08293540634475 6.50740466349007 P P P LNCV6_144308_PI430048170 mRNA
GCTCTTACTCCCAGGTTTCTAAATGTCTAAGAAACAATAAAATGAGAGTCATGTACAGAA NM_053055 RefSeq chr1 - 151870866 151909885 THEM4 117145 thioesterase superfamily member 4 GO:0008286|GO:0048011|GO:0005886|GO:0048015|GO:0016290|GO:0005743|GO:0032587|GO:0005829|GO:0005739|GO:0005758|GO:0007173|GO:0008543|GO:0045087|GO:0006631|GO:0043491|GO:0038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_33659_PI430048170 0.303681075232698 0.783073551125899 3.19150943296914 3.24887485050224 2.54141840050745 P P A 2.95720269965399 3.47760840722872 3.62465582960352 P P P LNCV6_33659_PI430048170 mRNA
AGATGACAGGACATCCTGGAAGCTGGGAAATGATATGTATTCATTTCCTACCACCGTAGT NM_001242480 RefSeq chrUn_GL000195v1 - 42937 86719 LOC389831 389831 uncharacterized LOC389831 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126891_PI430048170 0.362940017161316 0.54141227387865 1.73699322151171 0.391451087691736 0.67847039457886 A A A 2.783371892227 1.593916953571 0.706987987285677 P A A LNCV6_126891_PI430048170 mRNA
CACCATCCAACTCATTGAGTCTTATGGTTCACATCTTGTTTCCTATAGAAATATTCTGTA NM_021026 RefSeq chr22 + 29438582 29442455 RFPL1 5988 ret finger protein-like 1 GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144512_PI430048170 0.0110202094366338 1.63001804229195 10.6027597878309 10.7372342429254 10.7443235634463 P P P 10.1837809874983 9.82735064419598 9.93956457181618 P P P LNCV6_144512_PI430048170 mRNA
ACATTGTAAATGAATAAAACATTCTCAACTCCTCTTGAATCTATCCCCCAAGAAACCATC NM_016128 RefSeq chr3 + 129249609 129277773 COPG1 22820 "coatomer protein complex, subunit gamma 1" GO:0005515|GO:0030126|GO:0000139|GO:0005198|GO:0006890|GO:0061024|GO:0072384|GO:0051683|GO:0006886|GO:0048205|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145695_PI430048170 0.171801664586308 1.26950624138423 2.22535725410897 1.99039007236652 2.00127393821773 A A A 2.06739239605112 1.57210280116733 1.48666169203586 A A A LNCV6_145695_PI430048170 mRNA
TTTCAAAATCCCTTGGGCTCTGGATTTCATTTCTGAATGGTTTGAATGTTTGCTTTTTTG NM_001085420 RefSeq chr3 - 146585837 146606216 PLSCR5 NA "phospholipid scramblase family, member 5" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128466_PI430048170 0.379632967681052 0.688263967502907 0.312670633022052 0.298716442492489 1.21832726471461 A A A 0.745608662658619 0.67780964139614 1.88595161526202 A A A LNCV6_128466_PI430048170 mRNA
CCTTACTGCAATCAAAATAATTTACTGAGCACAACTCCTGTAAATTAATCTACAGTCAGG NM_020704 RefSeq chr7 + 129434432 129488398 STRIP2 57464 "striatin interacting protein 2, transcript variant 1" GO:0003674|GO:0005737|GO:0016477|GO:0008360|GO:0007010 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65532_PI430048170 0.549075777987432 1.21584409310665 0.446895991652978 1.26185802970904 0.286062856434648 A A A 0.406430092229039 0.493217774526151 0.447116119832765 A A A LNCV6_65532_PI430048170 mRNA
GAGCAATTTTTATTACTTCCAGAGATCCTCTTCTTTCACTGGAATTACTTGATCAACTGT NM_199346 RefSeq chr2 - 24114808 24123477 PFN4 375189 "profilin family, member 4" GO:0005737|GO:0005856|GO:0008289 . NA - . NA NA NA NA NA NA NA NA

NA
LNCV6_141546_PI430048170 0.0010008271859461 0.546433728799356 10.5166201168471
10.4054671676154 10.2725251848222 P P P 11.202931490603 11.4146798631234
11.1918622023341 P P P LNCV6_141546_PI430048170 mRNA
CAACCAGCTGCCCATTTTGTGAAATTTTTATGTAGAATAAACATTTGTATCTGTACCAGG NM_004603 RefSeq chr7
- 73699204 73719687 STX1A 6804 "syntaxin 1A (brain), transcript variant 1"
GO:0005515|GO:0030054|GO:0042641|GO:0006886|GO:0045921|GO:0001948|GO:0017156|GO:0030672|GO:0031
629|GO:0030674|GO:0032028|GO:0046982|GO:2000463|GO:0019904|GO:0010807|GO:0009629|GO:0019855|GO:0
017022|GO:0001956|GO:0044267|GO:0048306|GO:0043005|GO:0016081|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135801_PI430048170 0.960759622132493 1.00978237007744 0.249646464948748
0.611672632221598 0.320084403390115 A A A 0.427575781116441 0.423943481979888
0.310774037023077 A A A LNCV6_135801_PI430048170 mRNA
TCAGGAATGCAGAGGTGAAAATCGCCATAAGAAGATTGTGGAGCAAAAAGGAGAATCCAG NM_001005470
RefSeq chr11 + 48216809 48217739 OR4B1 NA "olfactory receptor, family 4, subfamily B, member
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135676_PI430048170 0.614180999674624 1.02338909990687 8.41570649259209
8.45973836364947 8.52394603554949 P P P 8.45046800123632 8.33075198925897
8.51419190719708 P P P LNCV6_135676_PI430048170 mRNA
TACTGGACAGCTGAACTGAATGGCTGCAAAATAAATACCTCACATGATGTCTGTGTCTGC NM_018982 RefSeq
chr1 - 53851718 53889814 YIPF1 54432 "Yip1 domain family, member 1, transcript variant 1"
GO:0030133|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130462_PI430048170 0.314096923955571 0.813710735011698 6.11761432511461
5.60566648218694 6.26369586510375 P P P 6.00249021798943 6.29878830865125
6.59637474724453 P P P LNCV6_130462_PI430048170 mRNA
CTTCATCGTAACTGCTTCTAGAGATGGGATTGTGAAGGTGTGGAAATAAAACCTACTGAT NM_014602 RefSeq
chr3 - 130678933 130746852 PIK3R4 30849 "phosphoinositide-3-kinase, regulatory subunit 4"
GO:0008286|GO:0005515|GO:0006661|GO:0005770|GO:0005930|GO:0016236|GO:0044281|GO:0002224|GO:0005
524|GO:0071561|GO:0005829|GO:0045324|GO:0004672|GO:0016020|GO:0004674|GO:0005643|GO:0045087|GO:0
006623|GO:0006468|GO:0034271|GO:0006644|GO:0030242|GO:0034162|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139493_PI430048170 0.329304795864024 1.31212871575515 0.573303100931468
0.617104260820105 1.39403252300562 A A A 0.573394725327853 0.494934051103791
0.494244234845496 A A A LNCV6_139493_PI430048170 mRNA
CAATGAGTACTCAGAGATCAAGATCCCCAAGTAAGAAAATGCAGAGGCTCGGGCTTGTTT NM_014385 RefSeq
chr19 + 51142300 51153526 SIGLEC7 27036 "sialic acid binding Ig-like lectin 7, transcript variant 1"
GO:0005887|GO:0030246|GO:0004872|GO:0007155 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134528_PI430048170 0.798188897086432 1.00894548133675 0.45619618163354
0.532981834068141 0.505910995243275 A A A 0.570056943888414 0.422405252493997
0.461037799048962 A A A LNCV6_134528_PI430048170 mRNA
GATGCCCTGAAGAAAGTCATCATCAATAGAAACCATGCTTTTATTTTTCTGAAACTGAGA NM_001013356 RefSeq
chr11_JH159136v1_alt + 186373 187333 OR8U8 NA "olfactory receptor, family 8, subfamily U, member
8" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135471_PI430048170 0.00234776344493178 0.356685121587042 4.07816490096797
4.19081355288078 4.59807305143877 P P P 5.89785674749484 5.89126970850788
5.56914907161131 P P P LNCV6_135471_PI430048170 mRNA
CTTTCTGTAACACTTAAAGAATTCCCTCATTCATTACCTTACAGTGTAAACAGGAGTCTA NM_144778 RefSeq
chr13 + 97222295 97394120 MBNL2 10150 "muscleblind-like splicing regulator 2, transcript variant

1" GO:0008380|GO:0006397|GO:0005737|GO:0000381|GO:0043484|GO:0005634|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134493_PI430048170 0.219170104203016 0.966846836285394 0.305322110707615
0.362581353735234 0.32105059254761 A A A 0.430845468769731 0.340828395367144
0.362270876155733 A A A LNCV6_134493_PI430048170 mRNA
ATGCGTAAGTCACAAGAATTTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTCAGAT NM_007191 RefSeq
chr12 - 65050623 65121566 WIF1 11197 WNT inhibitory factor 1
GO:0005515|GO:0007165|GO:0045600|GO:0007275|GO:0005576|GO:0016055|GO:0090090 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136627_PI430048170 0.0184350848380379 0.315818500727392 1.87812074095374
1.43430965429612 2.20670187655398 A A A 2.85815865125382 3.57883001389937
3.96470158791522 P P P LNCV6_136627_PI430048170 mRNA
TGCAAGATATCACTCAAGCCAGTGTTGCTTAATACCATCTCTTTGTGTAATAGATCTGAA NM_000351 RefSeq
chrX + 7219430 7354641 STS 412 "steroid sulfatase (microsomal), isozyme S"
GO:0006665|GO:0006706|GO:0007565|GO:0005794|GO:0005886|GO:0006687|GO:0005783|GO:0044281|GO:0008
484|GO:0005764|GO:0046872|GO:0043231|GO:0016020|GO:0008544|GO:0005789|GO:0004773|GO:0005788|GO:0
016021|GO:0044267|GO:0043687|GO:0005768 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131276_PI430048170 0.953000725012258 1.00419247492794 0.269675052809483
0.275461802322942 0.444470595359408 A A A 0.350319303722357 0.297511875504325
0.330098193921349 A A A LNCV6_131276_PI430048170 mRNA
GCTTCTTGTCTCTTTAGACCACATGCACATATTACTTGTATAAAATAATGCACCAGATAC NM_001039783 RefSeq
chr3 - 126571778 126608555 TXNRD3NB NA thioredoxin reductase 3 neighbor NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144232_PI430048170 0.793570912383821 1.34316075683805 2.5991441519646
0.556385841681659 2.34193210756969 A A A 1.67991137035946 1.48088024776305
1.75929824939789 A A A LNCV6_144232_PI430048170 mRNA
AAACACCGAGAGAAAGATGTCTACCTGGCAGCCATGTCAGAGAATCACCAGTATGTATGT NM_001008528 RefSeq
chr17 - 76673649 76711005 MXRA7 439921 "matrix-remodelling associated 7, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80435_PI430048170 0.108476751719823 1.15632137379636 5.66289368297732 5.60133569857245
5.84723177476426 P P P 5.63349902279147 5.41934621032024 5.43128213456578 P P P
LNCV6_80435_PI430048170 mRNA
TAAAATCAGAATCCTATGGGACAGTGGTCAGAATCTCCCCACAGGACTTTCCTCAGAATC NM_001282795 RefSeq
chr8 + 144827517 144843222 ZNF7 7553 "zinc finger protein 7, transcript variant 1"
GO:0006355|GO:0003700|GO:0007275|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131064_PI430048170 0.248180451552955 1.14761553372587 8.20433287612248
7.80332585662726 7.95797445824956 P P P 7.64593673823965 7.8683480589621
7.87258500718825 P P P LNCV6_131064_PI430048170 mRNA
AGTGTTTGGAACATAAGTCACTATGCAGACTAATAAACATCAACTAGAGAGAACTCCCAA NM_015062 RefSeq chr10
+ 102132993 102150333 PPRC1 23082 "peroxisome proliferator-activated receptor gamma, coactivator-
related 1, transcript variant 1"
GO:0051091|GO:0030374|GO:0006996|GO:0001104|GO:0006366|GO:0000166|GO:0045944|GO:0005654|GO:0007
005|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134377_PI430048170 0.411820585191484 1.32229620765623 1.44182622943911
1.24887361110429 0.372158676017468 A A A 0.857138082368828 0.696609647127906
0.48385188448718 A A A LNCV6_134377_PI430048170 mRNA
TATTTAAACTACCTACCATGCCTGTTGTGCTCAGGTGTTTGTTCATCCTGCCATCCCCAA NM_004821 RefSeq chr5

- 154474971 154478264 HAND1 9421 heart and neural crest derivatives expressed 1
GO:0005515|GO:0055010|GO:0044212|GO:0006366|GO:0005634|GO:0043433|GO:0042803|GO:0003219|GO:0003
218|GO:0042802|GO:0001947|GO:0007507|GO:0005737|GO:0045944|GO:0003144|GO:0042475|GO:0001707|GO:0
046982|GO:0035050|GO:0003714|GO:0060707|GO:0060411|GO:0003713|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_112174_PI430048170 0.1054123149310970.9050362396256296.77922872258583
6.95031515076739 6.93498837864213 P P P 7.11256999940142 6.98634192772294
7.00026217848558 P P P LNCV6_112174_PI430048170 mRNA
AGTACGGGATGCCCTCCAGCCATTCCCAGTTTATGTGGTTCTTCTCCGTCTATTCCTTCC NM_020438RefSeq chr9
+ 129081103 129090438 DOLPP1 57171 "dolichyldiphosphatase 1, transcript variant 1"
GO:0008610|GO:0005789|GO:0030176|GO:0047874|GO:0006487|GO:0006488|GO:0044267|GO:0006489|GO:0043
687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106928_PI430048170 0.1490059181154670.70463381320068 6.68387631217495
6.04787657165461 6.72421391417976 P P P 6.77378554318245 6.86015111566479
7.35974721804537 P P P LNCV6_106928_PI430048170 mRNA
TAACAACTATTCCACACCAAATGAGAGAGGAGACCACAATAGAACACTGGATCGATCGGG NM_001085458
RefSeq chr11 + 57761761 57819180 CTNND1 1500 "catenin (cadherin-associated protein), delta 1,
transcript variant 1"
GO:0005515|GO:0005886|GO:0045202|GO:0005634|GO:0005829|GO:0030426|GO:0005915|GO:0005737|GO:0016
337|GO:0043197|GO:0005911|GO:0016055|GO:0007155|GO:0090090|GO:0070062|GO:0048010|GO:0006355|GO:0
045296|GO:0019901|GO:0034329|GO:0005102|GO:0030496|GO:0006351|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131625_PI430048170 0.3673732556943162.4219711998091 0.708267444838927
0.3853927488936152.7759899369426 A A A 0.2821117485791490.415572279336525
0.57740272332805 A A A LNCV6_131625_PI430048170 mRNA
TAGAGGCTTGCTGCCTTCAGGAAATGGACAGGTCAGTTTGTTGTAGGAAATGCATATTTT NM_014482RefSeq chr2
- 68865480 68871517 BMP10 27302 bone morphogenetic protein 10
GO:0060045|GO:0005515|GO:0030018|GO:0030308|GO:0055010|GO:0060395|GO:0005615|GO:0007512|GO:0010
614|GO:0005737|GO:0030198|GO:0043408|GO:0007155|GO:0010613|GO:0055009|GO:0033612|GO:0030336|GO:0
009986|GO:0045214|GO:0010862|GO:0031433|GO:0005576|GO:0042981|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136389_PI430048170 0.2729313406443931.14608322060795 0.343261242721078
0.6993723209190310.312328214970688A A A 0.2555767886162110.283588896953666
0.258396629641212A A A LNCV6_136389_PI430048170 mRNA
ACAAACCTGGAACCTCAGCTAAGACTCTCTGTGACCAGATTCTGAACCTCTTATATCCAG NM_003037RefSeq chr1
- 160609818 160647311 SLAMF16504 "signaling lymphocytic activation molecule family member 1,
transcript variant 1"
GO:0005515|GO:0008284|GO:0046649|GO:0003823|GO:0045335|GO:0007165|GO:0050790|GO:0016032|GO:0016
021|GO:0009897|GO:0004888|GO:0031338|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135193_PI430048170 0.000104371718277517 0.1543865630984715.59582556947976
5.62456480113404 5.28982874896651 P P P 8.14418304380962 8.33730426600261
8.12862180196666 P P P LNCV6_135193_PI430048170 mRNA
ATGGCACTTTGGTGGGGTTGGAAACAAAGTCGACATTAAAGGTCATTTCTCCTGAAAAAA NM_000679RefSeq chr5
+ 159916732 159973010 ADRA1B 147 adrenoceptor alpha 1B
GO:0005886|GO:0008283|GO:0007267|GO:0048148|GO:0005634|GO:0007512|GO:0019229|GO:0035556|GO:0001
987|GO:0035265|GO:0007626|GO:0004937|GO:0031965|GO:0046982|GO:0007275|GO:0043278|GO:0042593|GO:0
001996|GO:0045818|GO:0001975|GO:0045819|GO:0007186|GO:0005887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_48215_PI430048170 0.016030811229452 0.5732682558011083.5897125603891 3.41309565547952

3.06428686395368 P P P 3.96485758452212 4.35831584428394 4.17380956671531 P P P
LNCV6_48215_PI430048170 mRNA
GAAGAGACAGTTTTCAGGAACAACAAGCAATTATTCCTACTTTCCAAGTTATTTTGATGC NM_001202519 RefSeq
chr2 + 201116153 201172688 CFLAR 8837 "CASP8 and FADD-like apoptosis regulator, transcript
variant 8"
GO:0005515|GO:2001237|GO:2001239|GO:0031265|GO:0031264|GO:0002020|GO:0032403|GO:0005829|GO:0005
737|GO:0051092|GO:0006508|GO:0016032|GO:0043403|GO:0043123|GO:0060544|GO:0043066|GO:0006919|GO:0
006915|GO:0014732|GO:0005123|GO:0004197|GO:0007519|GO:0035877|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141511_PI430048170 0.6362986727706590.8144069556767782.93761815177422
2.64777142494351 1.55041985031687 A A A 2.89846925900427 3.25541950687926
1.88489229060776 P P A LNCV6_141511_PI430048170 mRNA
AGCAAGGACATCTATGCATAGAATTCTGACAGCAGCTGGACCCTCAACTTCTTCAGAAGA NM_002235 RefSeq chr12
+ 4809175 4851112 KCNA6 3742 "potassium channel, voltage gated shaker related subfamily A,
member 6"
GO:0005251|GO:0005886|GO:0005887|GO:0008076|GO:0005249|GO:0007268|GO:0051260|GO:0034765|GO:0034
705|GO:0016021|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92618_PI430048170 0.7367575324841131.02552392403311 5.7695151374191 5.50705487118502
5.58947907388323 P P P 5.68900956729363 5.56337852530987 5.51136277039693 P P P
LNCV6_92618_PI430048170 mRNA
AGTGAAGGCCAAGAGGGTCAGCACCTTCCAGGAGTTTGAGAGCAATACCAGCGATGCCTG NM_001284304
RefSeq chr22 + 46762616 47175699 TBC1D22A 25771 "TBC1 domain family, member 22A, transcript
variant 3" GO:0032851|GO:0042803|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137444_PI430048170 0.5707988152324960.9557869144014218.3631815923509
8.17269518666938 8.26593363087693 P P P 8.1661190519428 8.44143188190595
8.38195940527661 P P P LNCV6_137444_PI430048170 mRNA
GGTGGAATGATAGAATGCATTTTAAATCACATTGTAAACTTCCAGGTGATCCATGGATAG NM_138461 RefSeq chr3
- 196323545 196338420 TM4SF19 116211 "transmembrane 4 L six family member 19, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133363_PI430048170 0.0986041013509087 0.84230392727213516.2540137565447
15.9711617394762 15.9930084236866 P P P 16.1852802952283 16.3762886647462
16.4070283520417 P P P LNCV6_133363_PI430048170 mRNA
GCTCCTTCAGACACGTGCTTGATGCTGAGCAAGTTCAATAAAGATTCTTGGAAGTTTTGA NM_019554 RefSeq chr1
- 153543618 153545806 S100A4 6275 "S100 calcium binding protein A4, transcript variant 2"
GO:0005515|GO:0043005|GO:0048471|GO:0005509|GO:0003779|GO:0005634|GO:0001837|GO:0005615|GO:0042
802|GO:0050786|GO:0043123|GO:0048306|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127513_PI430048170 0.3519863848789021.07675014422629 0.419285206568904
0.4268887586857410.676793501793149 A A A 0.4221504560680910.384188081474782
0.411471623014741 A A A LNCV6_127513_PI430048170 mRNA
GATTCAAATGCCATGACATTGGAAAAAGGTCATCATAGCTCTAACTTCTGTATACCAATA NM_006248 RefSeq chr12
- 11391539 11395564 PRB2 653247 proline-rich protein BstNI subfamily 2
GO:0008150|GO:0003674|GO:0005576|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109672_PI430048170 0.000775822970508661 1.37468205009513 12.5070604724157
12.4965331289929 12.6117735468047 P P P 12.0611580131485 12.0393108088068
12.1385458264651 P P P LNCV6_109672_PI430048170 mRNA
TACTTGCTGTTCACGTTATGACTCTCATGCAAGCAAAATACACAGTTTCATTGTTCTGAA NM_001301141 RefSeq
chr12 + 108561462 108569384 ISCU 23479 "iron-sulfur cluster assembly enzyme, transcript variant 4"
GO:0005739|GO:0005515|GO:0009399|GO:0032947|GO:0005737|GO:0051536|GO:0016226|GO:0005506|GO:0005
759|GO:0005634|GO:0044281|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_141228_PI430048170 0.2833073187614560.8596849306303034.30189610064925
4.54696317271027 4.24393058889561 P P P 4.47737910955211 4.39985125647923
4.84747884595577 P P P LNCV6_141228_PI430048170 mRNA
ACCTGTATGTATATGCATATGTGTACATGCATATCCCCTCCTGCTAAAACTCATAAAAAA NM_024911RefSeq chr1
- 68125357 68232601 WLS 79971 "wntless Wnt ligand secretion mediator, transcript variant 1"
GO:0005515|GO:0017147|GO:0001707|GO:0005886|GO:0031852|GO:0090263|GO:0032839|GO:0032590|GO:0000
139|GO:0009948|GO:0031901|GO:0004871|GO:0016021|GO:0043123|GO:0016055|GO:0030659 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131079_PI430048170 0.8431882969524180.976624688147 8.02530265236487
8.10029947352947 8.32105462432054 P P P 8.00616700158039 8.13825985233773
8.39395276650767 P P P LNCV6_131079_PI430048170 mRNA
GGTTGAGAGTGGAGTGGTTTGGCATTTCTGTTTTAAATAAACATTTAAGCTCTTAATCAG NM_033116RefSeq chr14
- 75082114 75127075 NEK9 91754 NIMA-related kinase 9
GO:0007077|GO:0005515|GO:0007067|GO:0019901|GO:0004674|GO:0006468|GO:0005634|GO:0000278|GO:0005
524|GO:0046872|GO:0051301|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137275_PI430048170 0.9261784725818441.00764112228376 10.3334649187054
10.0909866837971 10.3072041682138 P P P 10.2123881840748 10.3574480872465
10.1318068340146 P P P LNCV6_137275_PI430048170 mRNA
TTTGAGTTCATGAAACAGAATCAGGATGCCTTCGACGTGATCATCACTGACTCCTCAGAC NM_003132RefSeq chr1
- 11054591 11060034 SRM 6723 spermidine synthase
GO:0008295|GO:0034641|GO:0004766|GO:0006595|GO:0044281|GO:0042803|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_79078_PI430048170 0.5032036066178590.2653728815754820.9738873600551660.334076558172405
0.392967817115499A A A 0.3582301886712590.3364068734658913.86346341905147 A A P
LNCV6_79078_PI430048170 mRNA
TGCGAGCCATGGAAAGAAGAAACATGCTAAATAGACACCTTATTCTTGGCACTACATGTG NM_019644RefSeq chr7
+ 118224657 118242730 ANKRD7 56311 ankyrin repeat domain 7GO:0005634|GO:0008584 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_135394_PI430048170 0.1263172906748341.07553276211027 0.490047208481614
0.6161216202746730.554450673756897A A A 0.3720784180437730.462370671540239
0.510368858171714A A A LNCV6_135394_PI430048170 mRNA
GTAGAATTTAAAGTGGACAGATGCCTGTTGGAGTAAAATCAACTGCAACTTTTTGATGTT NM_001145195 RefSeq
chr10 + 17951838 18043292 SLC39A12 221074 "solute carrier family 39 (zinc transporter), member 12,
transcript variant 1"
GO:0007165|GO:0071578|GO:0048471|GO:0005886|GO:0005385|GO:0010975|GO:0031113|GO:0016021|GO:0031
982 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126846_PI430048170 0.4617224093891961.15306320136204 8.94590256777483 9.0865446432407
8.45471809083236 P P P 8.44971034086662 8.54099565543921 8.91093473736669 P P P
LNCV6_126846_PI430048170 mRNA
CTGGCGGTGGGGACCAAGATCCGGAAAGATGAATAAAGACAAACATGACAAACTAAGAAA NM_001193380
RefSeq chr3 + 9902827 9916400 IL17RE 132014 "interleukin 17 receptor E, transcript variant 6"
GO:0005515|GO:0030368|GO:0005737|GO:0006954|GO:0005887|GO:0019221|GO:0005576 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127609_PI430048170 0.2579530475759710.9654668290658360.303300305525356
0.3777673335848970.316061457084915A A A 0.4423621439860930.345841492542923
0.360243086943102A A A LNCV6_127609_PI430048170 mRNA
GACCAGGAAATCACTTGTATTTTGTTAGCCAATAAATTCCTAGCCAGTGTTGAATGAAAA NM_020683RefSeq chr1
- 111483347 111504121 TMIGD357413 "transmembrane and immunoglobulin domain containing 3,
transcript variant 1" GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_138182_PI430048170 0.2401821998960370.9650847193737980.410187129319699
0.4314136490124760.327170871209648A A A 0.4217443036687580.467110764845958
0.435448490379777A A A LNCV6_138182_PI430048170 mRNA
TAAACTGAGGATGGAAATGGGGACAAATGCTTGGTTTGCCCAAATATCTTAATAAAAGAC NM_212558RefSeq chr9
+ 32783498 32789201 TMEM215 NA transmembrane protein 215 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_60721_PI430048170 0.1583220994747481.16924233824188 13.9316333544948 14.1721454116839
14.2557818674344 P P P 13.7412399673859 13.913382029475 14.0327216165805 P P P
LNCV6_60721_PI430048170 mRNA
TCCTGTGTGCTTCCCTCTCTTATGACTGTGTCCCTGGTTGTCAATAAAATATTTCCTGGC NM_006156RefSeq chr14 -
24216850 24232370 NEDD8 4738 "neural precursor cell expressed, developmentally down-regulated 8"
GO:0005515|GO:0006511|GO:0014070|GO:0006357|GO:0045116|GO:0005634|GO:0009653|GO:0005829|GO:0008
104|GO:0006508|GO:0007179|GO:0006464|GO:0031625|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_131547_PI430048170 0.00805804911476902 0.4524513780968274.36587318933715
4.1451447007903 4.37409528704531 P P P 5.19445869946594 5.72021073469381
5.36362409728514 P P P LNCV6_131547_PI430048170 mRNA
GGTGCCCTGTTAACCCCTTAAAGCTGTGGTTTACAACTTTTCAAAAATTTAAATCATTAG NM_005558RefSeq chr1
- 201380837 201399541 LAD1 3898 ladinin 1 GO:0005198|GO:0070062|GO:0005604 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131695_PI430048170 0.179234628868484 1.23486669091369 6.83709496783584
6.68224580267476 6.48223953112521 P P P 6.54045016898224 6.47651278906056 6.044793064095
P P P LNCV6_131695_PI430048170 mRNA
ACTGGATGGAGCTGTTCATTGACACCTTTAAGCTGGTGCACAGGGACATCGTGGGGGACC NM_058175RefSeq chr21
+ 46098118 46129805 COL6A21292 "collagen, type VI, alpha 2, transcript variant 2C2a'"
GO:0005515|GO:0005581|GO:0005578|GO:0005576|GO:0031982|GO:0005615|GO:0009749|GO:0070208|GO:0042
383|GO:0031012|GO:0043234|GO:0022617|GO:0007411|GO:0030198|GO:0030574|GO:0005788|GO:0007155|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138764_PI430048170 0.6726317601370320.6420025476738580.420006410744368 1.4279040665953
0.317601897408725A A A 0.2809737883441722.48155525723158 0.501898865927282A P A
LNCV6_138764_PI430048170 mRNA
TTATTGTCTAATTCAAATCACTCCTGAGGGGAGAGAGATAAAACGAGAGAGAGTGAGAGANM_001198801 RefSeq
chr1 - 20806291 21176888 EIF4G3 8672 "eukaryotic translation initiation factor 4 gamma, 3,
transcript variant 1"
GO:0000339|GO:0016281|GO:0019221|GO:0006446|GO:0016032|GO:0003743|GO:0008135|GO:0006413|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90885_PI430048170 0.0239687322077319 1.66911653418798 9.9128041039586
10.3204498903915 10.1497824244619 P P P 9.67550325339441 9.11542931464089
9.34835098326872 P P P LNCV6_90885_PI430048170 mRNA
CCAAGGAATATACAGCTGGCAGAGAGGCTGATGACATCGTGAACTGGCTGAAGAAGCGCA NM_000918RefSeq
chr17 - 81843157 81860668 P4HB 5034 "prolyl 4-hydroxylase, beta polypeptide"
GO:0005515|GO:0016222|GO:0034976|GO:0005886|GO:0005783|GO:0004656|GO:0044281|GO:0006457|GO:0030
198|GO:0006508|GO:0070062|GO:0042470|GO:0005793|GO:0046982|GO:0003756|GO:0071456|GO:0005576|GO:0
004175|GO:0018401|GO:0042157|GO:0005788|GO:0045454|GO:0019899|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142759_PI430048170 0.0297785062883555 0.4108072066738675.09917546578113
4.82029062864773 5.36434025176624 P P P 5.80088066385819 6.44611887503317
6.77536898293515 P P P LNCV6_142759_PI430048170 mRNA
GCCACTATTCTGTTGTCTGGAATTAAAACCTGTATAACTAATTTGCATCCCTTTATCTTC NM_182620RefSeq chr17 -

59109946 59155439 SKA2 348235 "spindle and kinetochore associated complex subunit 2, transcript variant 1"
GO:0008017|GO:0005515|GO:0007067|GO:0000940|GO:0007059|GO:0031110|GO:0005876|GO:0000278|GO:0051301|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134990_PI430048170 0.36541475831121 1.46124518390774 0.478440346830034 0.3703114260698391.56137119069083 A A A 0.2992056734334340.361620433491975 0.424898446087065A A A LNCV6_134990_PI430048170 mRNA
CATGCGTCTTTTTTGCAGTTTCTCAAGCGTTTTCTAAAGATTTCAACCCGTCTTCCTGTC NM_001101391 RefSeq chr19 - 2289774 2308157 LINGO3 NA leucine rich repeat and Ig domain containing 3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128024_PI430048170 0.0224575210547413 0.5103211825526465.05695665318272 4.95574164819939 5.59433266657059 P P P 5.94768072703852 6.04934346334017 6.53552000481227 P P P LNCV6_128024_PI430048170 mRNA
CTTTGCCATGAGGCCACATTCAGCTGCTATTTAAACTTAATATCTTGAACCTAAAGAATG NM_022739RefSeq chr17 - 64544616 64662268 SMURF2 64750 SMAD specific E3 ubiquitin protein ligase 2
GO:0005515|GO:0006511|GO:0010467|GO:0004842|GO:0006367|GO:0005886|GO:0016874|GO:0090263|GO:0000151|GO:0005634|GO:0046332|GO:0005829|GO:0042802|GO:0005737|GO:0042787|GO:0007179|GO:0017015|GO:0030579|GO:0030512|GO:0000122|GO:0030509|GO:0005160|GO:0006351|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133707_PI430048170 0.3501363349620530.8837403447795260.352649725689664 0.3609029506863130.30572486750418 A A A 0.7755481450507010.403935461955757 0.335430241012749A A A LNCV6_133707_PI430048170 mRNA
CAAGGTCTTAAGGACTGATTCGTCAACAACTAATTTATTTTCTGAAGAAGTAGAGACAGA NM_175057RefSeq chr6 + 132538287 132539336 TAAR9 134860 trace amine associated receptor 9 (gene/pseudogene)
GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0001594 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128881_PI430048170 0.0445678776580385 0.2855840946469810.600083218872592 0.4988183010873051.86149959632682 A A A 2.82849469787775 2.92831567803399 3.04691424338119 P P P LNCV6_128881_PI430048170 mRNA
GCACAAGTATATGCAGACACACACACAAATCAGTAATCTATGTGAACTAGATACTAATAC NM_001286139 RefSeq chr11 - 93144170 93197455 SLC36A4 120103 "solute carrier family 36 (proton/amino acid symporter), member 4, transcript variant 2"
GO:0005774|GO:0015827|GO:0015171|GO:0015824|GO:0016021|GO:0015808|GO:0003333|GO:0015293 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133574_PI430048170 0.8468628817059431.01171468848295 0.294186113050785 0.3036170532679960.489560232808384A A A 0.3357366980928310.366013007193563 0.343567358017858A A A LNCV6_133574_PI430048170 mRNA
CTGCTTAACCCTGTGATATATAGTCTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAA NM_001005503 RefSeq chr14 + 20197335 20198373 OR11G2 390439 "olfactory receptor, family 11, subfamily G, member 2"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104602_PI430048170 0.6092327552691661.04552407854305 0.312645832951758 0.5994439644798930.359340119393694A A A 0.4939869626078930.303503909224172 0.288745965592153A A A LNCV6_104602_PI430048170 mRNA
AGGGGGCACCTACCTAGGAATAGCCACGGGGTAGAGCTACAGTGATTAAGAGGAAAGCAA NM_001174064 RefSeq chr8 - 38411137 38468834 FGFR1 2260 "fibroblast growth factor receptor 1, transcript variant 11"
GO:0060045|GO:0005515|GO:0001657|GO:0007605|GO:0048705|GO:0001759|GO:0042803|GO:0042802|GO:0046777|GO:0007173|GO:0007411|GO:0000165|GO:0002062|GO:0048339|GO:0042472|GO:0017134|GO:0010518|GO:0

014068|GO:0018108|GO:0000122|GO:0045787|GO:0001701|GO:0043235|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129242_PI430048170 0.0769579170736558 0.6391559312164322.70295074339377 2.95150439980721 3.29246243174004 A A P 3.2304499497271 3.92316931022313 3.70748632293632 P P P LNCV6_129242_PI430048170 mRNA TACAGGATAGGCTTACCTTTCCCACCTGTGTGGCTAGCACTTCACAGTTTACAAATTCCT NM_003389RefSeq chr9 - 98120974 98172892 CORO2A 7464 "coronin, actin binding protein, 2A, transcript variant 1" GO:0035556|GO:0051015|GO:0030036|GO:0017053|GO:0015629 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140441_PI430048170 0.0368393506805412 1.46628471332783 5.8051106883108 5.68492320575807 5.57795137673476 P P P 5.38945650607634 5.06355902684858 4.92769761920972 P P P LNCV6_140441_PI430048170 mRNA TCTGCCTTGTGGCCCACAATGGCTTTGATTATGATTTCCCCCTGCTGTGTGCCGAGCTGC NM_080701RefSeq chrX - 153444719 153446487 TREX2 11219 three prime repair exonuclease 2 GO:0008296|GO:0006281|GO:0000287|GO:0008853|GO:0005634|GO:0006259|GO:0003676|GO:0042803|GO:0000738 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142397_PI430048170 0.6346251084588371.14019013401967 0.283035304098003 0.2887863161812411.05350272303194 A A A 0.4718609944582110.387605175560708 0.337776979880915A A A LNCV6_142397_PI430048170 mRNA ATTCACTCTTTTTTCCTTGGCAGTTTAATCATTCAGGAATCCCTCTCTTAAAGGAAATTG NM_052904RefSeq chr6 + 96924619 97140754 KLHL32 114792 "kelch-like family member 32, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130447_PI430048170 0.0474931819123617 0.6518513270730756.2028088392626 6.10051369959699 5.90781326465363 P P P 6.34416764292584 6.84855826284615 6.83142390048469 P P P LNCV6_130447_PI430048170 mRNA CCTTTTGTATCCTCCATTGTATCTTCATACAAAGGACAGTACACACTTGGGTAATTAAAA NM_000898RefSeq chrX - 43766609 43882475 MAOB 4129 monoamine oxidase B GO:0006805|GO:0045471|GO:0050660|GO:0005743|GO:0005741|GO:0005740|GO:0044281|GO:0010044|GO:0050665|GO:0042803|GO:0005739|GO:0045964|GO:0032496|GO:0070062|GO:0051412|GO:0042493|GO:0010269|GO:0009636|GO:0009055|GO:0014063|GO:0008131|GO:0021762|GO:0042420|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144656_PI430048170 0.0141068850344562 0.4000810311490743.91394875930625 3.23649692987728 3.86346341905147 P P P 4.53173681362451 5.20650791288769 5.23110563245461 P P P LNCV6_144656_PI430048170 mRNA CTCATACTGCAGTCAATTACTGGAAGCGGATATATTTCCTATGCAAAAACTGTTTAAACA NM_001190737 RefSeq chr9 - 14081842 14314046 NFIB 4781 "nuclear factor I/B, transcript variant 1" GO:0021960|GO:0006366|GO:0000981|GO:0071679|GO:0005634|GO:0060509|GO:2000795|GO:0003690|GO:0002062|GO:0061141|GO:0021740|GO:0045944|GO:2000791|GO:0001106|GO:0044300|GO:0005730|GO:0000122|GO:0000978|GO:0003677|GO:0043392|GO:0006260|GO:0001077|GO:0010001|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136063_PI430048170 0.0878484153042282 1.01903287179854 0.414603182703612 0.4289947463538470.411297156710843A A A 0.3867230396220580.376833607267075 0.409602018096591A A A LNCV6_136063_PI430048170 mRNA GTTACCTGGGTTTGAGTTCTTGGCATTAGCCTGTATCATCTATTTGGTATTATTATACTA NM_001170402 RefSeq chr5 - 55112970 55173177 CDC20B 166979 "cell division cycle 20B, transcript variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137089_PI430048170 0.68733506397873 0.9560611474818180.382561571116842 0.2858573481767290.282051969897236A A A 0.2571516614122760.607742515446652 0.25283579852583 A A A LNCV6_137089_PI430048170 mRNA

CCTTCATTTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATCTCAGAGAATAATAATAAA NM_001008387 RefSeq chr2 + 79025685 79028504 REG3G 130120 "regenerating islet-derived 3 gamma, transcript variant 1" GO:0045617|GO:0010838|GO:0005737|GO:0050830|GO:0090303|GO:0002755|GO:0030246|GO:0005576|GO:0006953 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136237_PI430048170 0.1320587237433130.8496852308477517.54283158246375 7.73911934957702 7.71034129903594 P P P 7.84405134321652 7.75475680766526 8.08556425406775 P P P LNCV6_136237_PI430048170 mRNA
AATAGAGGTTCCCTATATGCGCGTATGACATGGTGAATAAACACAACTCTCTCCACTCAG NM_030937 RefSeq chr1 - 1385710 1399338 CCNL2 81669 "cyclin L2, transcript variant 1" GO:0006396|GO:0006355|GO:0030054|GO:0019901|GO:0016607|GO:0005730|GO:0005654|GO:0005634|GO:0000079|GO:0006351|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133898_PI430048170 0.891855636193044 1.23278287321363 2.97635428659865 0.3121199556222630.430125916413089 P A A 2.58294331905269 0.332077945765731 0.302741536154204 A A A LNCV6_133898_PI430048170 mRNA
ATTTCTTTGGCTTTTTCTCTATGGTGGTGTTTCAATAAAAGTTCTTCCTGTTGCAAGTCA NM_181537 RefSeq chr17 - 40776807 40782534 KRT27 342574 "keratin 27, type I" GO:0005882|GO:0008150|GO:0003674|GO:0005737|GO:0005198|GO:0070062|GO:0031069 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132540_PI430048170 0.211244999580845 1.03917388977239 0.585451651705886 0.63248460352695 0.533197021621844 A A A 0.5747312626628450.505585933435652 0.505095026661491 A A A LNCV6_132540_PI430048170 mRNA
CAACTATCTTTGTGTATTTTATGACTGTGTGTGTTTGCACTCATTGCAATAAAGTAGGAC NM_198511 RefSeq chrX + 37571568 37677497 LANCL3 347404 "LanC lantibiotic synthetase component C-like 3 (bacterial), transcript variant 1" GO:0008152|GO:0003824 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136906_PI430048170 0.181397285879266 1.12905720960067 9.50403003908747 9.7834619201788 9.64198957806216 P P P 9.34402287978999 9.47397278919665 9.58924721025667 P P P LNCV6_136906_PI430048170 mRNA
TTTGAACTTTAGGTCCTTCCTCTTCTTTGGGGCTGGAACAGAATTAAATTTGTTTGGAAA NM_138376 RefSeq chr14 - 20289140 20305994 TTC5 91875 tetratricopeptide repeat domain 5 GO:0005737|GO:0006281|GO:0045944|GO:0003682|GO:0005654|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133491_PI430048170 0.454394838692972 1.78534099012326 2.62326537950091 1.58605308646033 0.367402379619654 A A A 0.9449838486534040.372965280779257 1.39787532292995 A A A LNCV6_133491_PI430048170 mRNA
GGTCTTGGGAAGAATAGTGAAGAAAACTCCACCTTTCGAAATAGCTTTGGATTTAATTTT NM_018931 RefSeq chr5 + 141199774 141203045 PCDHB11 56125 protocadherin beta 11 GO:0016339|GO:0005887|GO:0005509|GO:0007268|GO:0016021|GO:0007155|GO:0007416|GO:0007156|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79083_PI430048170 0.0174225485793468 0.432608148311016 5.00064651311374 4.81237140635226 5.37765291796025 P P P 6.27299983874648 6.31338992662444 6.28901693996498 P P P LNCV6_79083_PI430048170 mRNA
TCAAATAGTCAGGTTGATTGGACTTACGACCCAAATGAACCTCGATACTGCATTTGTAAT NM_019071 RefSeq chr7 + 120950762 120975657 ING3 54556 "inhibitor of growth family, member 3, transcript variant 1" GO:0006355|GO:0043065|GO:0005730|GO:0006325|GO:0005634|GO:0035064|GO:0000812|GO:0006351|GO:0005737|GO:0032777|GO:0043967|GO:0043968|GO:0035267|GO:0005654|GO:0008270|GO:0040008|GO:0004402 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70387_PI430048170 0.585767619303774 1.07369147097721 8.33091254703605 8.46453560821001 8.79108602961617 P P P 8.35650655170186 8.39585998137244 8.5579868828404 P P P LNCV6_70387_PI430048170 mRNA

TTCAGTTTCTGGGGAAAGTGAAGCATGAAGGGAATCATAGGAAAAATGTACTGATCATAT NM_199482 RefSeq chr2 + 197515570 197553699 MOB4 25843 "MOB family member 4, phocein, transcript variant 2" GO:0005515|GO:0048471|GO:0005737|GO:0005794|GO:0043197|GO:0032580|GO:0043025|GO:0006810|GO:0019900|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_56864_PI430048170 0.103229022261962 1.85455172848151 2.37422452467664 2.48168626074838 3.08031923265347 A A P 0.996159367423165 2.00405919762016 2.12502190668358 A A A LNCV6_56864_PI430048170 mRNA

AAGAAAGTCAAAGCCCTTGAAATCTTTGCTTATGCCCTGCAGTACTTTAAGGAGCAGGCG NM_025015 RefSeq chr10 - 116671191 116742574 HSPA12A 259217 heat shock 70kDa protein 12A GO:0008150|GO:0003674|GO:0005524|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_132177_PI430048170 0.0112026405019911 1.73909927260331 10.1394015541663 10.5056283114134 10.3874375787194 P P P 9.48998279295174 9.54933398393934 9.61907224027922 P P P LNCV6_132177_PI430048170 mRNA

ACTATCAGAAGGGAGACCAGTATGATGTCTGTGCCATTTGCCTGGATGAATATGAGGATG NM_015528 RefSeq chr17 + 4940334 4945222 RNF167 26001 ring finger protein 167 GO:0005515|GO:0000209|GO:0005737|GO:0004842|GO:0016874|GO:0008270|GO:0016021|GO:0045786|GO:0012505 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_128929_PI430048170 0.104496799096423 1.23778157280212 6.51476756664629 6.42450418008493 6.2043524574916 P P P 6.00514795074027 6.292257849085 5.91270454768684 P P P LNCV6_128929_PI430048170 mRNA

AGTGTAATAGGAATCCAGATTCCCCCTGGCCTGGTTGCTGCAGGAGGCACAGTAGCCTGA NM_001282321 RefSeq chr1_KI270713v1_random + 35406 35916 FAM231A NA "family with sequence similarity 231, member A" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_56271_PI430048170 0.0696792998837943 0.78604869318414 7.84101882463771 7.91965044382947 8.21541133420962 P P P 8.34453633705409 8.23397431566975 8.45833066552842 P P P LNCV6_56271_PI430048170 mRNA

AGTATTACCACTTGAATAATTCTCTGTACAGGGGGGTTTGTGCTATACACTGGGATGTCT NM_001282866 RefSeq chr10_GL383546v1_alt - 295415 305160 MARCH8 NA "membrane-associated ring finger (C3HC4) 8, E3 ubiquitin protein ligase, transcript variant 4" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_132393_PI430048170 0.00558594277986703 3.2085472564149 1.9897312871268 2.33812329297669 1.89213141460025 A A A 0.366134552591578 0.438528756406134 0.407623406704977 A A A LNCV6_132393_PI430048170 mRNA

AATGTTGTTTTGTTGTTCTGCAAAAGTGGCAAGCATGGAGAGAGAGGTCAGACTGGCTAG NM_175741 RefSeq chr15 + 34343314 34357737 NUTM1 256646 "NUT midline carcinoma, family member 1, transcript variant 3" GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_134311_PI430048170 0.225076372531314 0.876372536451252 6.98616999188809 6.94771282780225 7.2850052689876 P P P 7.14011791674109 7.2448442570139 7.41572233507813 P P P LNCV6_134311_PI430048170 mRNA

ATCGCGGGGATTGTGGGTGTTATACATACATTTAGGACTGCAATTTTTTGGTATTTTTTG NM_139321 RefSeq chr20 + 3471017 3651122 ATRN 8455 "attractin, transcript variant 1" GO:0005886|GO:0042552|GO:0021549|GO:0005615|GO:0005737|GO:0006954|GO:0005887|GO:0040014|GO:0043473|GO:0030246|GO:0004872|GO:0006979|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_134939_PI430048170 0.806484753979039 0.990456690814008 0.369956465397951 0.470798873416317 0.366552187735662 A A A 0.493896300343386 0.373344747178717 0.380829724512584 A A A LNCV6_134939_PI430048170 mRNA

GAAATGGCGTTACCTGCCACTGTTGTTAAGTGTTTACTTTGTATCAATACTGAATTGTTA NM_052909 RefSeq chr5 + 140257 189972 PLEKHG4B 153478 "pleckstrin homology domain containing, family G (with RhoGef domain) member 4B" GO:0032321|GO:0005089 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_130464_PI430048170 0.0403260900672067 1.89022507579058 3.62476828408636

4.15691188837691 4.20593800841748 P P P 3.10427523213094 3.11177350826743 3.0844918210008
P P P LNCV6_130464_PI430048170 mRNA
TCATTAATGATAAAGACCGTTTTTTGTCATGTGGGAATAAAGAGGCTGCTTCTCCGCAAA NM_144661 RefSeq chr10
- 116663695 116669970 C10orf82 143379 chromosome 10 open reading frame 82 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143416_PI430048170 0.2905259758126051.18474834905912 5.85427369170263
6.40237724019314 6.07100616997634 P P P 5.69420663864979 5.94875999613415
5.98708619665023 P P P LNCV6_143416_PI430048170 mRNA
GTGCAGCTAAAAGACTGGGCTTCTCGCTTTTTAATCACACATTCAGAGTTTATTTTTATA NM_206827 RefSeq chr13
+ 27270326 27273690 RASL11A 387496 "RAS-like, family 11, member A"
GO:0006184|GO:0016020|GO:0045943|GO:0007264|GO:0005730|GO:0005525|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134609_PI430048170 0.1367096762897281.33234312463924 4.1254020356483 3.8333792663569
3.51884179448393 P P P 3.5893629956564 3.2401632328299 3.44838389277698 P P P
LNCV6_134609_PI430048170 mRNA
GAAACTGAATGGATTCTTCATAAGTAAGGTAATCTTTGGTCCTTTGTGTGGACTTATGTT NM_001256155 RefSeq
chrX + 101488043 101495811 ARMCX4 100131755 "armadillo repeat containing, X-linked 4, transcript
variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142168_PI430048170 0.1751514561059151.16052848717009 8.70728153048786
8.51409180909242 8.64221443082423 P P P 8.42660260214794 8.57793846507947
8.19597065302807 P P P LNCV6_142168_PI430048170 mRNA
AATCTCCATCTTTAGGGTCTCCACAGACTAACATTGAAGTCTTCCAGAAACCTCGAGGAG NM_006062 RefSeq chr2
+ 73214237 73227227 SMYD5 10322 SMYD family member 5
GO:0008150|GO:0003674|GO:0008168|GO:0005575|GO:0032259|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_100419_PI430048170 0.1812361971375070.7051525764647182.54133975771982
2.07749385335683 1.9790747710509 A A A 3.13408835799123 2.59555350789015
2.32434273153557 P P A LNCV6_100419_PI430048170 mRNA
TCTTTGTTAGACAGTGCTTCCCATGCTGACTGCTGTCCCCAGAAGCGGAGGCTCCATCAC NM_144666 RefSeq chr11
+ 6497295 6572024 DNHD1 144132 "dynein heavy chain domain 1, transcript variant 1"
GO:0030286|GO:0008152|GO:0003777|GO:0070062|GO:0007018 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_126858_PI430048170 0.0249199993625178 1.49508556182491 4.39418541899414
4.21747954672795 3.95839789168813 P P P 3.46407547286754 3.78141549665444
3.59915863613482 P P P LNCV6_126858_PI430048170 mRNA
ACTTCTCTGTATTCTTCCTCATACTTGCCTACCCCCAAATTAATATCAGTCCTAAAGAAA NM_003057 RefSeq chr6
+ 160121830 160158718 SLC22A1 6580 "solute carrier family 22 (organic cation transporter), member 1,
transcript variant 1"
GO:0005515|GO:0015874|GO:0005329|GO:0005886|GO:0015695|GO:0015872|GO:0015697|GO:0005277|GO:0044
281|GO:0010248|GO:0055085|GO:0015101|GO:0015651|GO:0042803|GO:0016323|GO:0016020|GO:0005887|GO:0
006855|GO:0072488|GO:0006836|GO:0008513|GO:0051260|GO:0005333|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137677_PI430048170 0.2656604572977640.5428458153093953.17268093398313
0.3146882126156850.299839844561096 P A A 3.17140033758666 1.89605260192848
3.07702042383254 P A P LNCV6_137677_PI430048170 mRNA
GGACTGTCTCAGCCATGCAAACCTCATGGAGCATTTTGGAAAGTTAAAAATTGATTCTTA NM_152578 RefSeq chrX
+ 147981328 148026667 FMR1NB 158521 fragile X mental retardation 1 neighbor
GO:0005730|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145029_PI430048170 0.7147404827919250.9776778601125850.575278764237836

0.4891979765731510.305558319091518A A A 0.4164778520413290.551256288635105
0.509730969462244A A A LNCV6_145029_PI430048170 mRNA
TGCCAGCACGTGAGATACTAACTTTTTAACTAGTTGTTCTTCTCTAGTCTCTACGTTATT NM_001253732 RefSeq chr4
+ 158521713 158653369 RXFP1 59350 "relaxin/insulin-like family peptide receptor 1, transcript variant 6"
GO:0005515|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141296_PI430048170 0.15957758394388 0.8422170786510661 1.0787448017571
11.1819300379717 11.1360650001584 P P P 11.2508150542175 11.2681261494626
11.5960054466041 P P P LNCV6_141296_PI430048170 mRNA
CAGCCTGTACCGGTTTGGCTGGCTTGTTTGATTTCAACATGAGTGTATTTTTTAAAATTG NM_000876 RefSeq chr6
+ 159969098 160106551 IGF2R 3482 insulin-like growth factor 2 receptor
GO:0051219|GO:0005515|GO:0005802|GO:0005215|GO:0048471|GO:0031100|GO:0031995|GO:0030139|GO:0007
283|GO:0005765|GO:0009791|GO:0005615|GO:0005537|GO:0042802|GO:0030118|GO:0001965|GO:0001948|GO:0
005641|GO:0004872|GO:0032526|GO:0030140|GO:0070062|GO:0043065|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139614_PI430048170 0.4328710914756291.04937046705489 7.11932297308932 7.0398652989212
7.2665231155066 P P P 7.01848915261851 7.07321148575642 7.1324186708104 P P P
LNCV6_139614_PI430048170 mRNA
ATATAGTGAGTCCAATGTATGCTTTAGAAGTAAAGACATTGACCGTCACAGACCACTGCA NM_020807 RefSeq chr16
- 57994667 57999858 ZNF319 57567 zinc finger protein 319
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140927_PI430048170 0.2252056990301681.11479705698103 0.339147249954714
0.6017782748057950.339978597683099A A A 0.2776063447071270.26799275390448
0.281121432604154A A A LNCV6_140927_PI430048170 mRNA
AAACTTTCCCCAACGTGCGGGAGATGTTCAACTCCCACCGGCTGGGGATTGAGAACTCGA NM_005251 RefSeq chr16
+ 86567250 86568931 FOXC2 2303 forkhead box C2
GO:0072011|GO:0001656|GO:0008286|GO:0072112|GO:0001657|GO:0003700|GO:0055010|GO:0044212|GO:0006
366|GO:0003705|GO:0001756|GO:0048844|GO:0005634|GO:0048703|GO:0007507|GO:0001946|GO:0050880|GO:0
007219|GO:0014032|GO:0045944|GO:0030199|GO:0090050|GO:0043010|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142421_PI430048170 0.0301167193094592 0.8380464137193098.65235030964713
8.50304569020505 8.61903499708621 P P P 8.72979830816342 8.88053880789291 8.9257909878519
P P P LNCV6_142421_PI430048170 mRNA
TCACAGGCCAGGGCACATCTTTTATTTATTTCATTATGTTGGCCAACAGAACTTGATTGT NM_030803 RefSeq chr2
+ 233251570 233295674 ATG16L1 55054 "autophagy related 16-like 1 (S. cerevisiae), transcript variant 1"
GO:0005515|GO:0034045|GO:0005776|GO:0005930|GO:0000421|GO:0051260|GO:0015031|GO:0000045|GO:0042
802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131535_PI430048170 0.0322744243015640.6759846984998726.25527014788386
6.50693915381553 6.72368003233637 P P P 6.97774286654071 6.93940635479382
7.27717773098855 P P P LNCV6_131535_PI430048170 mRNA
GAACAATGCAGACAGTACTTGCCAGAGTCCCAAATGCTGAATTATTGAACCATGTTTTTT NM_024525 RefSeq chr1
- 230906240 230978872 TTC13 79573 "tetratricopeptide repeat domain 13, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126461_PI430048170 0.2707368263373911.13615033260211 7.55624508144831 7.5720944768609
7.41099624316137 P P P 7.57820120583995 7.1998535699734 7.17817847665522 P P P
LNCV6_126461_PI430048170 mRNA
ATCAAGCAGCTGATGCGGAAGGAGTTCACCCTGGAGTTCTCCCGAGACCGGAAATCCATG NM_174953 RefSeq chr17
- 3923868 3964464 ATP2A3 489 "ATPase, Ca++ transporting, ubiquitous, transcript variant 5"

GO:0031965|GO:0005783|GO:0033017|GO:0055085|GO:0005524|GO:0046872|GO:0005388|GO:0034220|GO:0016529|GO:0007596|GO:0008152|GO:0070588|GO:0005789|GO:0006810|GO:0006816|GO:0016021|GO:0031095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142495_PI430048170 0.0485827314686005 1.05080703583445 0.344566326779652 0.351808635871154 0.28951828658336 A A A 0.245548051595837 0.277626676527164 0.248809565663266 A A A LNCV6_142495_PI430048170 mRNA GGAAACTGTGCAGTCATAATGTTTTGAGGAGACTAGCAGGAAATTTAAGAGTGTACAATA NM_001145727 RefSeq chr12 - 25496315 25648562 LMNTD1 160492 "lamin tail domain containing 1, transcript variant 3" GO:0005882|GO:0005737|GO:0008283|GO:0005198|GO:0005635 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130000_PI430048170 0.0255799354514863 1.12471231875368 0.747852396020721 0.832139820212312 0.732012842347861 A A A 0.614239625567418 0.605242879383466 0.585728048039186 A A A LNCV6_130000_PI430048170 mRNA GTGTATGTATGTGAAGATGCTTGGTCAACTTGTACCCAGTGAACACACACAGTCAGGAAA NM_006741 RefSeq chr12 - 54579239 54588659 PPP1R1A 5502 "protein phosphatase 1, regulatory (inhibitor) subunit 1A" GO:0035556|GO:0005515|GO:0005737|GO:0005977|GO:0004865|GO:0006469|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138983_PI430048170 0.0858671140164967 0.960891635169779 0.404428865356621 0.407430889339725 0.345538347917393 A A A 0.431760760146729 0.461452598583937 0.437515929483134 A A A LNCV6_138983_PI430048170 mRNA CTCCAATGTCTCTTTTGCAAGAGTTTTTCACAGAGGATTACATTTGTTCAAAAGACTCTA NM_003108 RefSeq chr2 + 5692666 5701385 SOX11 6664 SRY (sex determining region Y)-box 11 GO:0003700|GO:0048704|GO:2001111|GO:0006412|GO:0014032|GO:0046887|GO:0060548|GO:0017015|GO:0000976|GO:0001105|GO:0000122|GO:0000979|GO:0048485|GO:0001841|GO:0050672|GO:0061053|GO:0001501|GO:0035332|GO:0021782|GO:0060174|GO:0045893|GO:0001158|GO:0003357|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145108_PI430048170 0.0668336576065866 0.547784052791615 2.07098769322942 1.63185411811204 2.60711438163149 A A A 2.84453780892925 2.95837803097669 3.24723222002009 P P P LNCV6_145108_PI430048170 mRNA GGGTCATGGATTCTGCATAGACAAGGGCAATAAAGCAATACCTTTGTAATATGCATAAAA NM_152446 RefSeq chr14 - 80496477 80939540 CEP128 145508 centrosomal protein 128kDa GO:0005737|GO:0000922|GO:0005815|GO:0005814 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142008_PI430048170 0.0220183516778517 0.555377577347828 9.79309593327418 9.68984859992078 10.1089676950671 P P P 10.4971674088258 10.5528536648668 11.0535959330612 P P P LNCV6_142008_PI430048170 mRNA GTACTGGAAGTGAAACATGAGGAATGCTTTAGTGTAATGTGGGAGAACTTTTTTGTAAAT NM_001258438 RefSeq chr5 + 33440775 33468091 TARS 6897 "threonyl-tRNA synthetase, transcript variant 3" GO:0010467|GO:0006435|GO:0005737|GO:0004829|GO:0015629|GO:0006412|GO:0005524|GO:0042803|GO:0070062|GO:0006418|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98113_PI430048170 0.0164376122793264 1.29479477606133 9.69192540009155 9.70355499535884 9.76415835829334 P P P 9.23264420982739 9.35885131104813 9.44327217591765 P P P LNCV6_98113_PI430048170 mRNA TTGGAAAACTGGGAGAAAACATGATTCTTAAACGAGCTGCATGGGTGAAGGTGCCATCTG NM_001172696 RefSeq chr12 + 57782744 57797587 TSFM 10102 "Ts translation elongation factor, mitochondrial, transcript variant 1" GO:0005739|GO:0070125|GO:0032543|GO:0006996|GO:0032784|GO:0005654|GO:0005634|GO:0003746|GO:0006414 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131499_PI430048170 0.00477641679507832 0.310291635420179 8.8332250749239 9.04954759365305 8.41346256667022 P P P 10.4448733982443 10.3419598109715

10.6300131519374 P P P LNCV6_131499_PI430048170 mRNA
AGGGAGTTGGCAGTTTCAAATCGCCCAAGTGATGAATAAAGTATCTGGCTCTGCACGAAA NM_001336RefSeq chr20
- 58995186 59007254 CTSZ 1522 cathepsin Z
GO:0060441|GO:0005886|GO:0002003|GO:0005783|GO:0006508|GO:0008234|GO:0044267|GO:0005764|GO:0005
615|GO:0070062|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127074_PI430048170 0.0437037182674646 0.7736182306392498.0200223603912
7.87550895899965 8.03327587952277 P P P 8.22545553826507 8.26603142639071
8.53366411584339 P P P LNCV6_127074_PI430048170 mRNA
GCTTCCTGTTTGTGGATTTTGTTTCCTATATATTCAAAGTAAAATGACTTACAGGAGCCA NM_015329RefSeq chr19
+ 19320820 19358754 MAU2 23383 MAU2 sister chromatid cohesion factor
GO:0005515|GO:0047485|GO:0034088|GO:0005654|GO:0005634|GO:0032116|GO:0000278|GO:0000785|GO:0051
301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127479_PI430048170 0.0765343050429372 0.7679541543883549.60741610223092
9.70644654598266 9.75391842262854 P P P 10.2559643651886 10.086437518186 9.8422812715566
P P P LNCV6_127479_PI430048170 mRNA
TGTCTTGATGTGTGAGCAGCAGCTGTGGTCATTAAACCATTAGTTTACCCCTCTAGAACT NM_013306RefSeq chr11
+ 65027407 65040572 SNX15 29907 "sorting nexin 15, transcript variant A"
GO:0005737|GO:0016020|GO:0005730|GO:0035091|GO:0006886|GO:0030659|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139641_PI430048170 0.0203626254862924 0.3402247253652016.2867988605809
5.73480371970673 6.16443607214847 P P P 6.99236354107318 7.72981433604647
8.00688789778433 P P P LNCV6_139641_PI430048170 mRNA
GTTACTTGCCAAGCAGTGCACATTTCATAGTTTCAAATCTGTAATCAGCAATAAAAATCC NM_001316RefSeq chr20
+ 49046245 49096960 CSE1L 1434 "CSE1 chromosome segregation 1-like (yeast), transcript variant 1"
GO:0005515|GO:0005737|GO:0016020|GO:0008283|GO:0008536|GO:0006611|GO:0006915|GO:0005654|GO:0005
634|GO:0008262|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131272_PI430048170 0.8137987019520481.00644605052871 0.422072572688123
0.3187477968698890.357851397282214A A A 0.3788043866556950.324158546064338
0.369202907737763A A A LNCV6_131272_PI430048170 mRNA
GGCTGTAGAGACAACACTTTGCCATATTTCTATTAAAGAGAAAATAAAGATTGAGTCCAC NM_024012RefSeq chr7
+ 155070323 155087392 HTR5A 3361 "5-hydroxytryptamine (serotonin) receptor 5A, G protein-coupled"
GO:0005791|GO:0005794|GO:0005886|GO:0007210|GO:0030425|GO:0021766|GO:0004993|GO:0007186|GO:0005
887|GO:0007187|GO:0019933|GO:0043204|GO:0032355 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128048_PI430048170 0.0280552587035866 0.6834943632708387.37191832999513
6.95307924370378 7.05105519029132 P P P 7.50010849744355 7.71387609464178
7.82441634218684 P P P LNCV6_128048_PI430048170 mRNA
CCCCCCAAACTTATCAGAATCCTCGTTCTTTTTCAGACTACTGAAAAATGACATTTACTC NM_138395RefSeq chr2
+ 197705303 197708390 MARS2 92935 "methionyl-tRNA synthetase 2, mitochondrial"
GO:0010467|GO:0006431|GO:0005759|GO:0004825|GO:0005524|GO:0006418|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_98587_PI430048170 0.2154782967674521.02355604158389 0.3260410247687280.2698054699627
0.27004111437168 A A A 0.2524066361047920.2590977358247280.25433547149763 A A A
LNCV6_98587_PI430048170 mRNA
TAACAGCAAGATGGCTTTGAACTCAAGACTAAGAAAGCACTGTGCATCACCTTGACCCTG NM_001135099 RefSeq
chr21 - 41464550 41508065 TMPRSS2 7113 "transmembrane protease, serine 2, transcript variant
1"
GO:0005515|GO:0016540|GO:0005886|GO:0004252|GO:0005887|GO:0006508|GO:0008236|GO:0046598|GO:0006
898|GO:0070062|GO:0005044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140199_PI430048170 0.0152214033659858 0.6516201462613611.4404938277957

11.2131140441956 11.0958123642229 P P P 12.0804325466492 11.7055323167199
11.8124059013418 P P P LNCV6_140199_PI430048170 mRNA
CTGGATAGCTATTTGCACGAATCATGGACATAAATCCAAGTTGAAGAAGATCAACAAAAA NM_001252385 RefSeq
chr5 - 151029942 151081084 TNIP1 10318 "TNFAIP3 interacting protein 1, transcript variant 1"
GO:0005515|GO:0004843|GO:0005634|GO:0006952|GO:0006412|GO:0005622|GO:0005737|GO:0006954|GO:0009
101|GO:0045944|GO:0002755|GO:0050729|GO:0007159|GO:0070373|GO:0085032|GO:0051019|GO:0043124|GO:0
045071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143269_PI430048170 0.19513463303339 0.5681160256531970.312026409232701
0.2467487602055570.314476059209751A A A 0.2646052463616051.31380269619804
1.47269190053529 A A A LNCV6_143269_PI430048170 mRNA
ATGAACAGCCAGAACTGCAGAAGAAACAGTTGTGCTCTTTCGAGATCTACGAAGTTCCCT NM_001899RefSeq chr20
- 23685639 23689025 CST4 NA cystatin S NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137567_PI430048170 0.0103468298392268 2.26705092166348 4.91272889483141
4.85469894752624 4.68333985311765 P P P 3.51661145960531 3.39262919441704
3.94823685746197 P P P LNCV6_137567_PI430048170 mRNA
ACTACCTCTGTGCCTTGCCACATTAAATTGATAACATGGAAATGAGATGCAACCCAACAA NM_016602RefSeq chr17
- 42679401 42681827 CCR10 2826 chemokine (C-C motif) receptor 10
GO:0006955|GO:0070098|GO:0009986|GO:0007186|GO:0006935|GO:0005886|GO:0005887|GO:0004930|GO:0016
493|GO:0007204 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136874_PI430048170 0.0225491755785397 1.09505739196015 0.441287636551365
0.3965703501617560.393214637446161A A A 0.2568026096459710.333442091711953
0.24674164720738 A A A LNCV6_136874_PI430048170 mRNA
GGTTTAGCAGTATAGTGGCGCCACTGTTTTGAATCTCATAATTTATACAGGTCATATTAA NM_000111RefSeq chr7
- 107765466 107803233 SLC26A3 1811 "solute carrier family 26 (anion exchanger), member 3"
GO:0003712|GO:0005515|GO:0006820|GO:0005215|GO:0007588|GO:0006355|GO:0003700|GO:0005886|GO:0097
225|GO:0031526|GO:0055085|GO:0060081|GO:0016324|GO:0016020|GO:0015301|GO:0005887|GO:0015108|GO:0
015106|GO:0051454|GO:0015701|GO:0008271|GO:0071320|GO:0048240|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133381_PI430048170 0.0412721466854555 1.24852400207776 5.52203476621795
5.74260783731683 5.57418311919697 P P P 5.30660268598878 5.42632341192428
5.14033483339291 P P P LNCV6_133381_PI430048170 mRNA
ATCTACTTTGCCTCAGAGAACAGCAAGTCAGCTGGATATGTTATTGGCATGAAGTGTGGG NM_005485RefSeq chr3
+ 51942304 51948867 PARP3 10039 "poly (ADP-ribose) polymerase family, member 3, transcript variant
2"
GO:0006471|GO:0006281|GO:0000723|GO:0060236|GO:0005814|GO:0035861|GO:0005634|GO:0051106|GO:0003
824|GO:0006302|GO:0003950 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139753_PI430048170 0.2025275402794130.8847750339085170.251975306629479
0.3494595668261910.278809653661654A A A 0.4755259273194480.621042996136371
0.297138815209918A A A LNCV6_139753_PI430048170 mRNA
TGATGCCTTTTCCGTCTTTGTATCACGTTACCCCAAATTAAGTATGTTTGAATGAGTTTA NM_001891RefSeq chr4 -
69955255 69961011 CSN2 1447 "casein beta, transcript variant 1"
GO:0004857|GO:0005215|GO:0007595|GO:0005509|GO:0006816|GO:0005576|GO:0043086|GO:0005615 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145096_PI430048170 0.3408828302232320.9666844734055945.35728390820405 5.2337478041179
5.33073454339356 P P P 5.35545258810289 5.31504525563545 5.39958760333667 P P P
LNCV6_145096_PI430048170 mRNA
AATTAAACCCTGAACTATTTGAGAATGAAAGCTATGCTGTTCCTCTAGTGCAAGCCTCAG NM_144607RefSeq chr17
+ 7857745 7862282 CYB5D1 124637 cytochrome b5 domain containing 1 GO:0046872|GO:0020037 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_36979_PI430048170 0.1821160961036811.3119911504941 4.77794444368955 4.13634206938069 4.60450726966104 P P P 4.00668146468363 4.28830921635561 4.10798784170647 P P P LNCV6_36979_PI430048170 mRNA TCTCCACAGCATGAATTACCCGGGCCGCGGGTCCCCACGGAGCCCCGAGCATAACGGCCG NM_001160148 RefSeq chr14 - 53036739 53153328 DDHD1 80821 "DDHD domain containing 1, transcript variant 3" GO:0016042|GO:0005737|GO:0016787|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_137614_PI430048170 0.3194018310825240.9530489180388630.259475780965124 0.3873306460403180.290791951334745A A A 0.4698387537144850.362270876155733 0.312196531319321A A A LNCV6_137614_PI430048170 mRNA CTGAAGATGCTTTTTGGAAAGCTCTGAATCTATACCTAATGCTCTTAATTATTGGCTTGT NM_012397RefSeq chr18 + 63587299 63599199 SERPINB13 5275 "serpin peptidase inhibitor, clade B (ovalbumin), member 13" GO:0030162|GO:0010951|GO:0005737|GO:0004867|GO:0009411|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_73549_PI430048170 0.1046386043144691.39227611982289 9.79054344970746 9.9866662950836 10.3488795333835 P P P 9.5888967096939 9.28207788113559 9.82789530065627 P P P LNCV6_73549_PI430048170 mRNA GGATGAAGATATTTTGGATGATTGACTGTAATGCTTTCCATTTACCTGACTAAACAGATC NM_004766RefSeq chr3 - 139357590 139389680 COPB2 9276 "coatomer protein complex, subunit beta 2 (beta prime), transcript variant 1" GO:0030126|GO:0005198|GO:0006890|GO:0061024|GO:0006891|GO:0006886|GO:0048205|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_93939_PI430048170 0.8351771379892040.9795609702695844.71870182274716 4.58552634402335 4.96885798801195 P P P 4.66805920975785 4.72898847009407 4.97354194000513 P P P LNCV6_93939_PI430048170 mRNA AACGTTTCTTCTGGAGAATTGGAACATGTGTGGCCCCAAGCTCAACAGAAACCAGTTGTT NM_001143827 RefSeq chr18 + 34978243 35143468 MAPRE2 10982 "microtubule-associated protein, RP/EB family, member 2, transcript variant 3" GO:0008017|GO:0007165|GO:0007067|GO:0005737|GO:0008283|GO:0015630|GO:0035371|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_145001_PI430048170 0.9308674656457350.9732640535442553.02575852379977 3.105395477746 3.47665717324076 A A P 3.4881531758428 3.38106265927844 2.80919037348361 P P P LNCV6_145001_PI430048170 mRNA TGAGGCGCTTAGGTTAAAACTACATTCACTATAACTCAGTAAAGCAGTCCCGCCCACTCT NM_001257190 RefSeq chr7 + 72879334 72951440 POM121 9883 "POM121 transmembrane nucleoporin, transcript variant 1" GO:0007077|GO:0010467|GO:0031965|GO:0005975|GO:0019083|GO:0019221|GO:0019058|GO:0044281|GO:0005635|GO:0015031|GO:0055085|GO:0010827|GO:0008645|GO:0015758|GO:0005643|GO:0005789|GO:0009405|GO:0016032|GO:0051028|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_129950_PI430048170 0.2585138664669320.7093922687299165.70046353166078 4.78701699949783 4.45802463300059 P P P 5.86912490785587 5.48430626392268 5.32151482379604 P P P LNCV6_129950_PI430048170 mRNA GGACGCCGCCCAGCTTGCTTGTGTATAAGTTGTATTTAATGGTTCTGTAACAATAAAAAA NM_033256RefSeq chr19 - 38251236 38256591 PPP1R14A 94274 "protein phosphatase 1, regulatory (inhibitor) subunit 14A, transcript variant 1" GO:0042325|GO:0005737|GO:0004864|GO:0043086 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_143063_PI430048170 0.3468460689106171.12426439528359 8.35323645804774 8.21846531768571 8.61047067387035 P P P 8.16418481200333 8.43577595053575 8.0785544211695 P P P LNCV6_143063_PI430048170 mRNA GCAAGATTAGACATACTGAAAATCCATGCAGGTCCCATTACAAAGCATGGTGAAATAGAT NM_002806RefSeq chr14

+ 52707177 52727998 PSMC6 5706 "proteasome (prosome, macropain) 26S subunit, ATPase, 6"
GO:0005515|GO:0006511|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005
829|GO:0034641|GO:0000082|GO:0016032|GO:0030674|GO:0090090|GO:0016887|GO:0070062|GO:0006977|GO:0
000209|GO:0043066|GO:0000502|GO:0006521|GO:0051437|GO:0042590|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135560_PI430048170 0.7179169417351771.01887492350645 0.27197856339383
0.2928568459294470.457399573105083A A A 0.3427511305401690.300268113785045
0.305148334710385A A A LNCV6_135560_PI430048170 mRNA
GGAATGTATGAGATAACAGTTGCAGTTGACTGAAATGCCACTGGAATTTGAAAACTTGAC NM_001288819 RefSeq
chr15 - 82543200 82647605 CPEB1 64506 "cytoplasmic polyadenylation element binding protein 1,
transcript variant 5"
GO:0006397|GO:0032869|GO:0030054|GO:0071456|GO:0014069|GO:0005634|GO:0035925|GO:0072687|GO:0046
872|GO:0030425|GO:0005737|GO:0071230|GO:0048168|GO:0000166|GO:0000932|GO:0045211|GO:0007130|GO:2
000766|GO:0000900. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137780_PI430048170 0.3268659802678541.15636989368947 5.67346978619481
5.73621456611733 5.96863937884934 P P P 5.23873101265739 5.67648002384861
5.79405861429472 P P P LNCV6_137780_PI430048170 mRNA
CATGAGCATAAAAATGCGTGCGTTTCAGTGTTTAAGAAGGCTTGATAAAGAATGTCACTT NM_001286813 RefSeq
chr5 + 119354772 119394604 TNFAIP8 25816 "tumor necrosis factor, alpha-induced protein 8,
transcript variant 3" GO:0043066|GO:0005737|GO:0050830|GO:0032611|GO:0043154|GO:0043027 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138928_PI430048170 0.8762985196233550.9878484959294980.34719346724085
0.3711887789713280.288684512429274A A A 0.27293650720002 0.502946488626954
0.272909860354711A A A LNCV6_138928_PI430048170 mRNA
AAGTTGGCCATGAGGAAACTGAAGAGACGGCTAGGACAATCAGAAAGGATTTTAATTCAA NM_001004711
RefSeq chr11 + 59514912 59515857 OR4D9 NA "olfactory receptor, family 4, subfamily D, member 9"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130026_PI430048170 0.0649239045602390.7962278268571246.2528551619644
6.06121013110589 6.07536711677071 P P P 6.36221708520315 6.65673629923657
6.34281454301292 P P P LNCV6_130026_PI430048170 mRNA
TGAATTTTTAACGACCTGATGAGGGCATCAGGTAAATTAAAGGATTTTGGGAAGATTCTT NM_014337RefSeq chr22
+ 21665983 21697913 PPIL2 23759 "peptidylprolyl isomerase (cyclophilin)-like 2, transcript variant 1"
GO:0000209|GO:0000413|GO:0005515|GO:0005886|GO:0005796|GO:0016874|GO:0034450|GO:0003755|GO:0005
634|GO:0050900|GO:0072659|GO:0005737|GO:0006457|GO:0007596|GO:0005654 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130292_PI430048170 0.6765207225044321.04054117324637 0.408063091079513
0.7049280190029010.399001515905977A A A 0.5201265128808530.484149820551129
0.351782483459788A A A LNCV6_130292_PI430048170 mRNA
GCATAGCAGTTTGTAAAAGTGTAACAGCTTATTGACTTAATAAAGCTTTTCCTGCATGCA NM_004675RefSeq chr1
- 68045961 68050777 DIRAS3 9077 "DIRAS family, GTP-binding RAS-like 3"
GO:0006184|GO:0005515|GO:0005886|GO:0007264|GO:0006349|GO:0003924|GO:0000079|GO:0005525 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129922_PI430048170 0.2516563002033791.24014121274946 0.359226585431069
0.3721310878426060.906446305371023A A A 0.2439214289870540.28631012568169
0.245769369629378A A A LNCV6_129922_PI430048170 mRNA
CTCATGCTGACGGGGAGAACGAAAGTGACAGGGGTTTCCTCATAAGTTTTGTATGAAATA NM_001288804
RefSeq chr7 - 93188585 93226519 HEPACAM2 253012 "HEPACAM family member 2, transcript
variant 3"
GO:0051297|GO:0005515|GO:0007067|GO:0005813|GO:0005794|GO:0000139|GO:0005819|GO:0030496|GO:0016

021|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143761_PI430048170 0.972025026082805 0.982701555624502 1.99417117430217
0.276546690111943 1.39105260965463 A A A 1.50610714845238 0.268188962828779
1.96744900182539 A A A LNCV6_143761_PI430048170 mRNA
AGAGATGTGTTTTTCTAAAGTGTTTGCAGGGCATTTTTCCCTCTTACCTCAGATTAAGTT NM_020759 RefSeq
chr15 + 42575658 42720998 STARD9 57519 StAR-related lipid transfer (START) domain containing 9
GO:0008017|GO:0005871|GO:0005794|GO:0005814|GO:0005634|GO:0003777|GO:0051225|GO:0005524|GO:0008
289|GO:0005737|GO:0008152|GO:0008574|GO:0005654|GO:0016887|GO:0007018 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_131163_PI430048170 0.48890329665011 0.955111594731279 0.294468970614931
0.440016401181124 0.305223471559534 A A A 0.52242717522428 0.426612748927679
0.284145871305827 A A A LNCV6_131163_PI430048170 mRNA
GTAACTTTCACTTGAACTGTTTTCCTGTTTGTAATGGTACTATTGCTCAATGTATACCTC NM_001282544 RefSeq
chr17 - 57744480 57745329 CCDC182 101927581 coiled-coil domain containing 182
GO:0008585|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_140236_PI430048170 0.177705055504872 0.941374335448734 0.245267060805058
0.317997499133899 0.289064920961785 A A A 0.453692456705045 0.351067442112441
0.305980148644142 A A A LNCV6_140236_PI430048170 mRNA
TACAGTTGTAGCTACATACTCAATGTATCAACTTTTAGCCTGCTCAACTTAGGCTCAGTG NM_006587 RefSeq chr4
- 47593997 47838106 CORIN 10699 "corin, serine peptidase, transcript variant 1"
GO:0007565|GO:0004252|GO:0005886|GO:0009986|GO:0005576|GO:0016486|GO:0005887|GO:0006508|GO:0008
217|GO:0035813|GO:0016021|GO:0003050|GO:0070008 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127889_PI430048170 0.989110447358084 1.02031420258729 0.330509028230472
1.12606229709678 0.326992959970416 A A A 0.565029571669142 0.259551165196877
0.944472551346771 A A A LNCV6_127889_PI430048170 mRNA
TTTCTAGAGGGAGGAATGGGTGTTTGAGTGCAGAGACACTGGTCTGGGGTGATCCATGGA NM_021250 RefSeq
chr19_KI270938v1_alt - 289466 295523 LILRA5 353514 "leukocyte immunoglobulin-like receptor,
subfamily A (with TM domain), member 5, transcript variant 1" GO:0045087|GO:0016021|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_144748_PI430048170 0.32231514870948 0.656347452608356 0.298319535686842
0.559790681574948 1.33162066991411 A A A 0.505894824323989 1.67133610159203
1.74370869309566 A A A LNCV6_144748_PI430048170 mRNA
GTTGATTCCAAAACTGAGTTATGAAGAATGATATAACAGTTCCTTCAAAATTGGCCTAGG NM_152581 RefSeq
chrX + 14873404 14921337 MOSPD2 158747 "motile sperm domain containing 2, transcript variant
1" GO:0016020|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69116_PI430048170 0.0037124330426654 1.84776318562246 7.95766149748846
7.78508045281984 7.90279203380802 P P P 7.1148252563488 7.05865724802983
6.80105817795813 P P P LNCV6_69116_PI430048170 mRNA
AACAGACCATCCCTCCTTCCACAGAGGAGAAGCGCATCTACCGGGTGCCTGTTTTCACAG NM_001304835 RefSeq
chr12 + 122974702 122980041 OGFOD2 79676 "2-oxoglutarate and iron-dependent oxygenase
domain containing 2, transcript variant 4" GO:0031418|GO:0005506|GO:0016706|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144337_PI430048170 0.092058929032838 1.31610465432862 3.64224982629343
3.79123253571797 4.07286726013438 P P P 3.18685556209986 3.59820119743642
3.53311676623327 P P P LNCV6_144337_PI430048170 mRNA
TGACTGACGCTGTTTAGTCTTTCTGTACATTAACCCCGCCAGATACCGAGAGGTTACAAA NM_001199014 RefSeq
chr1 - 24356998 24413772 STPG1 90529 "sperm-tail PG-rich repeat containing 1, transcript variant

4" GO:0005737|GO:0006915|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90456_PI430048170 0.639526635593284 1.05141010697624 0.686073015250739 0.394864941079288 0.457939012673371 A A A 0.266534642887379 0.362227104665378 0.677034896001705 A A A LNCV6_90456_PI430048170 mRNA CAACTGCTTGAAAACAAGTGGCATCAAAAGTCAAGACTGTCACAGTCATAGTAGAACAAG NM_198381 RefSeq chr11 - 34478794 34511799 ELF5 2001 "E74-like factor 5 (ets domain transcription factor), transcript variant 1" GO:0005737|GO:0060644|GO:0000977|GO:0006366|GO:0006357|GO:0008283|GO:0045944|GO:0000981|GO:0005634|GO:0007398|GO:0001228|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141332_PI430048170 0.829969901076578 1.02408985021668 12.3638977894799 12.4095971154105 12.0526637065555 P P P 12.5862831142201 12.1115472665879 11.9777783877477 P P P LNCV6_141332_PI430048170 mRNA CCTGTCCCTGCCCAGGCCTCTGGCTTTTTATATTGAAAATTTTTAAATATTCACAAATTT NM_000785 RefSeq chr12 - 57762333 57767193 CYP27B1 1594 "cytochrome P450, family 27, subfamily B, polypeptide 1" GO:0030308|GO:0043627|GO:0008285|GO:0006805|GO:0042369|GO:0005741|GO:0033280|GO:0030282|GO:0044281|GO:0055074|GO:0005739|GO:0004498|GO:0046697|GO:0010980|GO:0005737|GO:0045618|GO:0032496|GO:0006816|GO:0034341|GO:0008202|GO:0030500|GO:0005506|GO:0042359|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104841_PI430048170 0.898792239250395 1.05374655009055 4.32998249776541 3.45525479053711 4.11767163469742 P P P 4.08283782146128 3.68096997406693 4.01773265317939 P P P LNCV6_104841_PI430048170 mRNA AACGAATACGAAGCAGAAAAGATAGAGTACAATGAATCTATGAAGGCCTATCATAATTCC NM_003079 RefSeq chr17 - 40627727 40647851 SMARCE1 6605 "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1" GO:0005515|GO:0071565|GO:0000790|GO:0003723|GO:0005634|GO:0071564|GO:0016514|GO:0017053|GO:0006338|GO:0016922|GO:0008080|GO:0006357|GO:0043044|GO:0003713|GO:0031492|GO:0006337|GO:0000228|GO:0000978|GO:0007399|GO:0043234|GO:0047485|GO:0003682|GO:0008152|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123050_PI430048170 0.639912979778102 0.920852552947374 6.81806256458758 6.64752754943917 6.75877049095544 P P P 7.12570637112921 6.88340016367467 6.51234742216845 P P P LNCV6_123050_PI430048170 mRNA TTCTAGAGTTCTGCCTCGCTTCCCGGCGCGGTCGCAGCCCTCAGCCCACTTAGGATAATG NM_001079525 RefSeq chr4 + 56436102 56461368 PAICS 10606 "phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase, transcript variant 1" GO:0005515|GO:0009168|GO:0004639|GO:0004638|GO:0055086|GO:0044281|GO:0005524|GO:0005829|GO:0042802|GO:0016020|GO:0006144|GO:0009113|GO:0070062|GO:0006189 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64717_PI430048170 0.000203605731479305 8.41793722768715 9.18211170482251 9.34665973124388 9.29441378694831 P P P 6.39379216794634 6.1635342222517 6.0261953061994 P P P LNCV6_64717_PI430048170 mRNA AGCTATGTCAATGGTCTTCCCCCAGTCTGATGTGTGTAATAAATGGTCACTGTCAAAGGA NM_001039876 RefSeq chr19 - 36003099 36008770 SYNE4 163183 "spectrin repeat containing, nuclear envelope family member 4, transcript variant 1" GO:0034993|GO:0031309|GO:0045198 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131193_PI430048170 0.106285261048862 0.463690467334358 0.326324552185724 0.279739672380022 0.268500488136529 A A A 0.645339210272575 1.39861542387896 1.89500429131386 A A A LNCV6_131193_PI430048170 mRNA

GCCTGAACATCTGTGGAATAATTTAGCAATGTTTTTCAGTTAGCAAGTGAATATTGAACC NM_001039717 RefSeq
chr4 + 127965305 128031300 C4orf29 80167 chromosome 4 open reading frame 29 GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138086_PI430048170 0.500843031772282 1.03581158687212 0.281583898077301
0.302749255545027 0.468699735757522 A A A 0.323210888211675 0.28868624464909
0.295990618182507 A A A LNCV6_138086_PI430048170 mRNA
CTTACTACTCTTCTACTGTCTGAGATCAGAATATGACATTGCAGTAAAGAGCTTAAATAG NM_032623 RefSeq
chr4 - 139266162 139280338 MGARP 84709 mitochondria-localized glutamic acid-rich protein
GO:0005739|GO:0005515|GO:0008090|GO:0010822|GO:0071383|GO:0006626|GO:0071456|GO:0019896|GO:0031
307|GO:0008089|GO:0097211 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135730_PI430048170 0.088546803022226 0.871234975896161 12.3589071475956
12.3797452671529 12.156272462363 P P P 12.5401023624513 12.5522303951769
12.4049998642518 P P P LNCV6_135730_PI430048170 mRNA
AGCCCCTGGGGCTGGCAGGGAGGAGCTCCAGGCTAATAAAGTGGAGAAACTGTCAAAAAA NM_138418 RefSeq
chr16 + 641848 648474 FAM195A 84331 "family with sequence similarity 195, member A" NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_138236_PI430048170 0.932363744850495 1.03911111162806 2.61336949776958
1.01016110136913 1.67023198601471 A A A 2.43398794037995 1.93029484323108
0.74415836808467 P A A LNCV6_138236_PI430048170 mRNA
CTTTCTTCACTTTCTCTAAAACTAATTGCCCTTTGTCACAGTTCTGGTATAAAGCAAGAT NM_152394 RefSeq chr3
- 150659884 150703971 ERICH6 131831 glutamate-rich 6 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133670_PI430048170 0.0293376875047991 0.502651926824696 4.06699027040959
4.18392407353414 4.36668601897545 P P P 4.77268793808458 5.27693512718061
5.47375628702466 P P P LNCV6_133670_PI430048170 mRNA
AGTTAAAAATAGTCATTCCTTGTGGGTGTTGGACACAGCTTGAAAGGAGTGTTTAAAAAA NM_015562 RefSeq
chr3 - 196353497 196432474 UBXN7 26043 UBX domain protein 7
GO:0005515|GO:0043130|GO:0005654|GO:0034098|GO:0031625|GO:0008134 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_63832_PI430048170 0.0814647117062733 1.54431032115137 3.97594011416532
3.46366752947003 4.16302540451424 P P P 3.0073088430175 3.25685351283862
3.50253604678958 P P P LNCV6_63832_PI430048170 mRNA
TCTAGAGAAACTTGTGTAGCTTTGACTGATTGCCTTAATCTCTTCACCAAACAAGAAGGG NM_080597 RefSeq
chr18 - 24162045 24397869 OSBPL1A 114876 "oxysterol binding protein-like 1A, transcript variant 2"
GO:0005515|GO:0005770|GO:0005634|GO:0005765|GO:0005622|GO:0019886|GO:0005737|GO:0005543|GO:0015
485|GO:0006869|GO:0005654|GO:0016192|GO:0070062|GO:0008203 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129394_PI430048170 0.00552063794094925 0.646626793348047 9.31265375423444
9.09538436289022 9.33003501145613 P P P 9.77800244595129 9.79937372329904
10.0439134825049 P P P LNCV6_129394_PI430048170 mRNA
ACATTTGATGGAATAGGAGTACTGGTTTTTCATAATGGTTAAAAATGAAACCAGCTGTGG NM_012255 RefSeq
chr20 + 21303303 21389825 XRN2 22803 5'-3' exoribonuclease 2
GO:0006353|GO:0006397|GO:0006396|GO:0006355|GO:0008409|GO:0016235|GO:0016070|GO:0005730|GO:0005
634|GO:0007283|GO:0006401|GO:0004534|GO:0004518|GO:0016020|GO:0016049|GO:0008270|GO:0000738|GO:0
001147 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129820_PI430048170 0.0250096206056506 0.257651640368051 1.70906509588825
0.379504151886819 1.6105330607546 A A A 2.89895244028464 3.29979147587723
3.61869441883849 P P P LNCV6_129820_PI430048170 mRNA
CTGCTGGATGCTGCTTGTAATCCATTTGGTGTACAGAATCAACAATAAATAATATACATG NM_001135057 RefSeq

chr3 - 194355246 194369743 LRRC15 131578 "leucine rich repeat containing 15, transcript variant 1"
GO:0030335|GO:0043236|GO:0005518|GO:0090005|GO:0016021|GO:0001968|GO:0046813|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_145449_PI430048170 0.0208734248177967 0.330120031185695 1.74774629209242
0.922778362413967 1.46904884879838 A A A 2.31643208015081 3.13579086467586
3.39659683563477 A P P LNCV6_145449_PI430048170 mRNA
CCTCCAATGCATAGCAAAAATAGTGGTGTTAGAAAGAAAATAGGTTACATTTAAGGAAGG NM_003921 RefSeq
chr1 - 85265775 85276904 BCL10 8915 B-cell CLL/lymphoma 10
GO:0005515|GO:0008219|GO:0043130|GO:0016064|GO:0070231|GO:0042226|GO:0002020|GO:0043621|GO:0051
259|GO:0005764|GO:0002906|GO:0031398|GO:0051260|GO:0043123|GO:0031625|GO:0046696|GO:0032765|GO:0
019901|GO:0003713|GO:0045416|GO:0001843|GO:0002224|GO:0043280|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133100_PI430048170 0.914606153469628 0.990281870036524 0.556444130496067
0.756894194936666 0.595683628109369 A A A 0.81172296638282 0.540221070841957
0.592656519047499 A A A LNCV6_133100_PI430048170 mRNA
CTTCCTTCCCAAGGCTGTATTGTAATTATAGCAATATTTCATGGAGGATTTTTCTACATG NM_001242524 RefSeq
chr6_GL000252v2_alt - 4308099 4324309 HLA-DPA1 3113 "major histocompatibility complex,
class II, DP alpha 1, transcript variant 2"
GO:0050852|GO:0005886|GO:0019221|GO:0031295|GO:0005765|GO:0019886|GO:0006955|GO:0042102|GO:0042
605|GO:0071556|GO:0030658|GO:0060333|GO:0032729|GO:0012507|GO:0009986|GO:0042613|GO:0032588|GO:0
030666|GO:0000139|GO:0071346|GO:0005887|GO:0050870|GO:0030669|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132835_PI430048170 0.00785374773801182 3.56043064534947 3.94157101057391
4.48376623582417 4.54363177411426 P P P 2.55967694107193 2.56514138769361
2.41578867729535 A P P LNCV6_132835_PI430048170 mRNA
TGCTTTCTGGCCTCAGCTATGTAATTAAAACGCCCGAAGTAAAATGGCCTTCTCCAAAAA NM_032805RefSeq chr16
- 3088890 3099317 ZSCAN10 84891 "zinc finger and SCAN domain containing 10, transcript variant
1"
GO:0043565|GO:0006355|GO:0003700|GO:0005654|GO:0005634|GO:0045892|GO:0035019|GO:0046872|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142064_PI430048170 0.1567572401237321.10012909124319 11.6398595031704
11.6764454177666 11.7644198486825 P P P 11.4861213729025 11.4899275505989
11.6853802090356 P P P LNCV6_142064_PI430048170 mRNA
AAAGTGACTGGAAGCAAACGCCCTAAAAGTTACCCATCACGTTTCAGTGTAAATGAGTAA NM_032479RefSeq chr5
- 1798384 1799842 MRPL3664979 mitochondrial ribosomal protein L36
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0042254|GO:0005743|GO:0006
412|GO:0005762 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141216_PI430048170 0.000923073013519845 0.3848425810649678.83197749521999
8.77654406798391 9.14791324914993 P P P 10.1933855400264 10.2246264051991
10.4821163525824 P P P LNCV6_141216_PI430048170 mRNA
CAGAATGTCTGTGTATTTCTTGTCTGTTTCTATGTTGTCTTATAGCTCTGACTAAATGTG NM_002395RefSeq chr6 -
83210390 83431219 ME1 4199 "malic enzyme 1, NADP(+)-dependent, cytosolic"
GO:0050661|GO:0051262|GO:0030145|GO:0004470|GO:0005975|GO:0004473|GO:0006108|GO:0009055|GO:0004
471|GO:0044281|GO:0005829|GO:0005739|GO:0006741|GO:0009743|GO:0051287|GO:0043531|GO:0009725|GO:0
008948|GO:0044255|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130882_PI430048170 0.8906022371002480.9963456288057583.88742746310025
3.22962639922217 3.56059490828681 P P P 3.5649301814015 3.56177698203722
3.64004338355253 P P P LNCV6_130882_PI430048170 mRNA
GAGAGAGACTTTAACGCCATTGCCTGGTTACTTGTTTTATGCTGTAATCTAGTTTATTTTNM_020747RefSeq chr5 -

124636916 124745112 ZNF608 57507 zinc finger protein 608 GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129633_PI430048170 0.00270946148942763 0.2558689313071350.293995693149851 0.449844999724855 1.02821880821852 A A A 2.75049213510114 2.22178378481201 2.74558661354379 A A P LNCV6_129633_PI430048170 mRNA CTGCCTATGTGTTGATGTTTTCATCCTTTCTTTGTTGAATGAGGGTATAACCATCAAAAA NM_001042493 RefSeq chr6 + 87322587 87342328 SMIM8 57150 "small integral membrane protein 8, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131371_PI430048170 0.00386651965210139 0.4252462546075158.65986172209125 8.31827171874498 8.30588413356795 P P P 9.58397390972322 9.73778527416435 9.68757922702014 P P P LNCV6_131371_PI430048170 mRNA CCAGCACCTGTAACACTGACTTTATTTTTAAGTCTGAAAATGTCTTGGGAAAGTTTTACA NM_025077 RefSeq chr1 + 45339669 45343978 TOE1 114034 "target of EGR1, member 1 (nuclear)" GO:0005515|GO:0016607|GO:0005730|GO:0005654|GO:0005634|GO:0003676|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138735_PI430048170 0.4839799419139990.868414396446605 0.507406487167849 0.553058005406784 0.428442318133166 A A A 1.07873665695304 0.46507610175497 0.468334809738382 A A A LNCV6_138735_PI430048170 mRNA CCAGTTTTAAGAGGAGCCACTTATCAAAGAGATTTTAACAGTAGTAAGAAGGCAAAGAAT NM_012092 RefSeq chr2 + 203936747 203961575 ICOS 29851 inducible T-cell co-stimulator GO:0016337|GO:0006955|GO:0002517|GO:0005886|GO:0005887|GO:0031295|GO:0005576|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142661_PI430048170 0.7338031986360581.32518261020114 0.256696792874024 2.31932003932651 2.00256763453803 A A A 0.3656078129987041.61749483369113 1.73760175453504 A A A LNCV6_142661_PI430048170 mRNA CCTTCTGTGTGTTCAATTTGAAAGCCTCATTGTTAATTAAAGTTGTGGATTATGCCTCTANM_001003954 RefSeq chr8 - 123680793 123737407 ANXA13 312 "annexin A13, transcript variant 2" GO:0005886|GO:0042998|GO:0005509|GO:0031210|GO:0042997|GO:0005615|GO:0030154|GO:0005544|GO:0016323|GO:0016324|GO:0001786|GO:0005654|GO:0045121|GO:0070382|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140836_PI430048170 0.0922052143415808 0.8525039987636125.48774465473072 5.44074671670006 5.51261859057597 P P P 5.83028951305204 5.72738320015982 5.56246875946571 P P P LNCV6_140836_PI430048170 mRNA GGATATGGCTGCTGCCGCCCATCTTGCTATGGAAGATACTGGTCCTGTGGCTTCTACTGA NM_181616 RefSeq chr21 + 30635263 30635461 KRTAP20-2 NA keratin associated protein 20-2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145091_PI430048170 0.0972794504317909 0.9603088905285940.436750490907873 0.363335573297934 0.389325241071662 A A A 0.4457969650538890.472010086679723 0.44770737164253 A A A LNCV6_145091_PI430048170 mRNA CAGAGACAACATTACAGTTATGGTAATATTTCTCAATGGAAGTGAATATCAGCTTCTGAC NM_001252657 RefSeq chr3 - 19985343 20012273 PP2D1 151649 "protein phosphatase 2C-like domain containing 1, transcript variant 1" GO:0008152|GO:0003824 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69123_PI430048170 0.0366146913895835 0.3588023872318680.300727626009697 0.25707049786211 0.406688858976357 A A A 1.16565611584217 2.05940148603858 2.01677863879192 A A A LNCV6_69123_PI430048170 mRNA GCAGAGCACATATTCTTATCATTTAGGAAATCAAAATCACCATTTGCAGTTTGCAAGCAT NM_022459 RefSeq chr13 - 20777328 20902774 XPO4 64328 exportin 4 GO:0046827|GO:0005515|GO:0005737|GO:0005654|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_100145_PI430048170 0.1922980267501360.5053161350168451.24776359372662
1.45732015463033 1.94331174740876 A A A 3.11177350826743 2.63278780239534
1.53496914538612 P P A LNCV6_100145_PI430048170 mRNA
ATAAACATTTCCTCAGCAGCAGTCCAGTCTATTGCATTTTAATTGGTTGTGATATCATTG NM_152703RefSeq chr7
- 93130053 93148388 SAMD9L 219285 "sterile alpha motif domain containing 9-like, transcript variant
1" GO:0042176|GO:0002244|GO:0017145|GO:0034058|GO:0035726|GO:0048536|GO:0005769 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139238_PI430048170 0.4620083797696421.08286534635771 6.27075071789399
5.97148343082498 6.33794524945259 P P P 5.95132920952182 6.17958778097633
6.12083045743728 P P P LNCV6_139238_PI430048170 mRNA
ATTTTCAGTACCAACTTGTTATCTTTTTCCTTATCTGAGGCTACCTGGGGATTGTGGGCA NM_014976RefSeq chr10
+ 103396654 103446262 PDCD11 22984 programmed cell death 11
GO:0006397|GO:0005515|GO:0006364|GO:0005730|GO:0005634|GO:0008134|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145323_PI430048170 0.5264228470732410.9064239547342469.88424107458505
10.0000679299885 10.2402940929766 P P P 10.0299140303676 10.0053935544777
10.4853699676026 P P P LNCV6_145323_PI430048170 mRNA
AGTGGGCAAAGTAACCTCTTGCTTGGTGCAACTATTTGTTTCAAATAAAAACATTTAGAC NM_012245RefSeq chr14
- 77717600 77761154 SNW1 22938 SNW domain containing 1
GO:0048026|GO:0005515|GO:0010467|GO:0006367|GO:0071300|GO:0005112|GO:0035257|GO:0046332|GO:0005
634|GO:0071013|GO:0042974|GO:0016363|GO:0007219|GO:0050769|GO:0042809|GO:0045944|GO:0016032|GO:0
005681|GO:0000785|GO:0030511|GO:0008024|GO:0071146|GO:0006357|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93765_PI430048170 0.5477861247967250.9634853915782970.2663614088907680.448177484571391
0.302879445815488A A A 0.4966937894454650.3900900150426720.29075355361949 A A A
LNCV6_93765_PI430048170 mRNA
CAACTGGTGGTCTCTGAAGATCCAATGATGATGTCAGCAGTACCATCGGCAACATCATTA NM_001001872 RefSeq
chr14 - 58004089 58152129 C14orf37 145407 chromosome 14 open reading frame 37 GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129928_PI430048170 0.0121364385974557 0.7229388051522455.53182709347048
5.27604711818588 5.49204127560958 P P P 5.78958689600792 6.03507201731445
5.88159471771456 P P P LNCV6_129928_PI430048170 mRNA
TCACAGAAGAACTTAGAAACCCTTACAGAAACCTGCCTTTGGCCATTATCATCGGGATCC NM_001243036 RefSeq
chr19 - 32830510 32869777 SLC7A9 11136 "solute carrier family 7 (amino acid transporter light chain,
bo,+ system), member 9, transcript variant 3"
GO:0005515|GO:0005886|GO:0006865|GO:0031526|GO:0050900|GO:0055085|GO:0003333|GO:0015804|GO:0016
324|GO:0006461|GO:0015184|GO:0005887|GO:0007596|GO:0042605|GO:0015811|GO:0015175|GO:0006811 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90487_PI430048170 0.0112763912631136 7.88664410738221 4.38778115211085
4.99216091194971 5.08364313372701 P P P 2.541845863071 1.71908002719931
0.906092083410472P A A LNCV6_90487_PI430048170 mRNA
AATGTGGAGCTCAAATATGCCTTATTTTGCACAAAAGACTGCCAAGGACATGACCAGCAG NM_001013398 RefSeq
chr7 - 45912244 45921272 IGFBP3 3486 "insulin-like growth factor binding protein 3, transcript
variant 1"
GO:0005515|GO:0008285|GO:0031994|GO:0031995|GO:0005634|GO:0005615|GO:0001558|GO:0046872|GO:0010
906|GO:0014912|GO:0008160|GO:0044342|GO:0009968|GO:0001968|GO:0070062|GO:0005520|GO:0043065|GO:0
006915|GO:0048662|GO:0005576|GO:0043085|GO:0001649|GO:0016942|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128357_PI430048170 0.0924810408031340.8599384845776711.6180823851522

11.5960054466041 11.3735178062761 P P P 11.7989181358656 11.7471740758789
11.7055323167199 P P P LNCV6_128357_PI430048170 mRNA
TTGACCAGTTTGACCCTGGTTTGAATAAAGAGAAGTGCGTTTGGATTAGAAACCAAAAAA NM_170711 RefSeq chr19
+ 1407568 1435687 DAZAP1 26528 "DAZ associated protein 1, transcript variant 1"
GO:0048026|GO:0035613|GO:0005737|GO:0000166|GO:0008283|GO:0003723|GO:0001893|GO:0005654|GO:0007
283|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68187_PI430048170 0.1388605643868550.8041381514896926.98827281617707 6.90940434428766
7.01723936071539 P P P 7.19616128008509 7.09864343145549 7.52955288845757 P P P
LNCV6_68187_PI430048170 mRNA
CTAACCTAACGTAGTTGGGAAAGGTAGATTGAATGAGACATGTTTTCTGTGCTTCTAAGT NM_207043 RefSeq chr1
- 150623277 150629622 ENSA 2029 "endosulfine alpha, transcript variant 2"
GO:0007584|GO:0004864|GO:0008601|GO:0005102|GO:0019212|GO:0043086|GO:0009749|GO:0050790|GO:0005
737|GO:0007067|GO:0050796|GO:0000086|GO:0019870|GO:0006810|GO:0005654|GO:0000278|GO:0008200|GO:0
051721|GO:0051301. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128303_PI430048170 0.4441452878022590.9515113640782710.281994660717522
0.4271572048815140.295374874815862 A A A 0.5157492832470910.415165893424028
0.283909014126682 A A A LNCV6_128303_PI430048170 mRNA
CTGAGCTTGTTCATCCTTTGTTTTGAAAAAATTACTCAACCAATCCATTACAGCTTAACC NM_001286650 RefSeq
chr4 - 99306386 99321442 ADH1B 125 "alcohol dehydrogenase 1B (class I), beta polypeptide,
transcript variant 2" GO:0006805|GO:0006069|GO:0004024|GO:0008270|GO:0044281|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140872_PI430048170 0.0916927919191571 0.5670030850058648.11717883642837
7.90229169606019 8.33338370303399 P P P 8.35808507284213 9.03075770412527
9.29770859228126 P P P LNCV6_140872_PI430048170 mRNA
ACAAGTATTTGTACATACTCTGCTTCTCTCTGTCAGCGTCCTGCTGCTCTAGAAGACTGT NM_001008938 RefSeq
chr11 - 46743533 46846308 CKAP5 9793 "cytoskeleton associated protein 5, transcript variant 1"
GO:0005515|GO:0005813|GO:0006996|GO:0030951|GO:0050658|GO:0035371|GO:0005829|GO:0051297|GO:0043
234|GO:0000922|GO:0007067|GO:0016020|GO:0000086|GO:0000930|GO:0015630|GO:0007051|GO:0000278|GO:0
051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132822_PI430048170 0.5719597722901881.05069628206855 5.53128397782829
5.79323037656821 5.58981496096243 P P P 5.50538205504624 5.73638916744169
5.45602042420962 P P P LNCV6_132822_PI430048170 mRNA
CTTTTTCACAGTGGGTCCTAAAGACCTTCCCATGAGAGGGTCTCAATCCTAGGGGAAGGA NM_173555 RefSeq chr10
- 70137980 70146740 TYSND1 219743 "trypsin domain containing 1, transcript variant 1"
GO:0031998|GO:0016020|GO:0004252|GO:0016485|GO:0006508|GO:0051260|GO:0002020|GO:0042802|GO:0005
777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129357_PI430048170 0.6946181384755230.9787048943309050.507213132772587
0.44798862933851 0.268246833025755 A A A 0.3858889454109420.485209719581299
0.454323314343772 A A A LNCV6_129357_PI430048170 mRNA
GTGATCTGTTAGGCATGAAAGCAGTTGCAATTACTTTCTGTTATTACAGGGCTATCTATA NM_033484 RefSeq chr5
+ 41925253 41935083 FBXO4 26272 "F-box protein 4, transcript variant 2"
GO:0005515|GO:0000209|GO:0006511|GO:0005737|GO:0004842|GO:0016567|GO:0000723|GO:0031398|GO:0000
151|GO:0031146|GO:0042803|GO:0019005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130661_PI430048170 0.7005345574522320.9844881512739870.421808204422745
0.3889729085615020.246792835694383 A A A 0.3467588827345110.401233060949814
0.382646596560787 A A A LNCV6_130661_PI430048170 mRNA
CTAGCATCCAGACTTTCTAGTTTGTCCAGATTTCGATTTGATCAATTTTCTTGTCCAATA NM_176820 RefSeq chr19 -
55708431 55738402 NLRP9 338321 "NLR family, pyrin domain containing 9" GO:0005737|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_104548_PI430048170 0.1155773550709631.09095053447105 0.534397992775936
0.5536268980615330.560572797179874A A A 0.3361567108216910.427701097919987
0.503266462734102A A A LNCV6_104548_PI430048170 mRNA
TTGTTGGGGGTTTCTGTAGTCGTCTTGTTTGGATCAACTCCTAGAGGCTGGTTTAGAACA NM_003061RefSeq chr10
- 96998037 97185926 SLIT1 6585 slit homolog 1 (Drosophila)
GO:0031290|GO:0051964|GO:0021510|GO:0005509|GO:0050919|GO:0048843|GO:0043395|GO:0048846|GO:0005
615|GO:0048495|GO:0048853|GO:0033563|GO:0021834|GO:0008045|GO:0040023|GO:0007411 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137541_PI430048170 0.0440021529858765 0.9436367703015760.397967936150916
0.3456172480955150.34430562410127 A A A 0.4796867215534050.45425381767474
0.404686084096623A A A LNCV6_137541_PI430048170 mRNA
CCATGGTGGGGCCAAGAGTCACTTCTAATAAACAGACTGTTTTCTAATAATTCCAAAAAA NM_000803RefSeq chr11
+ 72216774 72221950 FOLR2 2350 "folate receptor 2 (fetal), transcript variant 1"
GO:0005542|GO:0016020|GO:0015884|GO:0005576|GO:0008517|GO:0031362 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145606_PI430048170 0.0616472347335817 1.49832130728681 3.7871468506121
3.9401326015967 3.82209617445221 P P P 2.93271161109946 3.30367906198615 3.5094914139872
P P P LNCV6_145606_PI430048170 mRNA
GGGGTCAGCTGATTTCTCATCAAGATAATAATGTATGGTTTTTACACTAAGCAACTGATA NM_001424RefSeq chr16
- 10528421 10580716 EMP2 2013 epithelial membrane protein 2
GO:0005515|GO:0008219|GO:2001212|GO:0070252|GO:0008284|GO:0005886|GO:0008283|GO:0005634|GO:0045
022|GO:0070836|GO:0032147|GO:0005737|GO:0016324|GO:0010594|GO:0007015|GO:0007155|GO:0019900|GO:2
001046|GO:0005794|GO:0019901|GO:0009986|GO:0007566|GO:0032060|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_121355_PI430048170 0.5043013576436550.96696937761972814.3667193788746
14.2881014940573 14.2526018696907 P P P 14.242784713781 14.4106097945684
14.3958647821232 P P P LNCV6_121355_PI430048170 mRNA
CGACCCCACCCTGTTTTCCACCAGAGTTCTGACACTGTGACTCTGTATAAAATGGTTGGG NM_006666RefSeq chr19
+ 48993898 49015925 RUVBL2 10856 RuvB-like AAA ATPase 2
GO:0005515|GO:0071733|GO:0006325|GO:0005634|GO:0000812|GO:0035066|GO:0016363|GO:0042802|GO:0005
622|GO:0034644|GO:0005737|GO:0004003|GO:0006457|GO:0071392|GO:0071339|GO:0045944|GO:0035267|GO:0
006338|GO:0032508|GO:0016887|GO:0070062|GO:0043141|GO:0005719|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127497_PI430048170 0.5676586677429051.02840588667813 0.309812141121165
0.2884976173148960.455216118918019A A A 0.3754639499774330.261640359627574
0.29861425209186 A A A LNCV6_127497_PI430048170 mRNA
GACTTGTGATGAAGTCATGGATATGTCTATCAAAATCTCAATAAATTTGTCTCAGCTGGT NM_175857RefSeq chr21
- 30812696 30813252 KRTAP8-1 337879 keratin associated protein 8-1 GO:0005882 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137459_PI430048170 0.2441748445825291.12528231062959 10.3167619540592
10.4057321804186 10.3940481907294 P P P 9.97509605204825 10.2823309323147
10.3252269274625 P P P LNCV6_137459_PI430048170 mRNA
GAGATTTCTCTTCCTGCCCTCACTTCTTTCACCTTGAACTTGGATAAGAACTCGTGTCTC NM_005702RefSeq chr17
+ 28855024 28861054 ERAL1 26284 Era-like 12S mitochondrial rRNA chaperone 1
GO:0005739|GO:0005737|GO:0005759|GO:0005743|GO:0045111|GO:0043024|GO:0019843|GO:0015629|GO:0005
525|GO:0000028 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135577_PI430048170 0.2487519225092052.90528857934245 0.361682281660802
2.86472656490964 1.3329334012612 A A A 0.3458130180885210.321037619581629
0.374520013991463A A A LNCV6_135577_PI430048170 mRNA

TTTAAGGCACTGTAGTGAATTATCTGAGCTAGAGTTACCTAGCTTACCATACTATATCTT NM_002667 RefSeq chr6 + 118548278 118560424 PLN 5350 phospholamban
GO:0005515|GO:0048471|GO:0005783|GO:0008015|GO:0008016|GO:0042030|GO:0086092|GO:0010043|GO:0090281|GO:0042802|GO:0005739|GO:0060314|GO:0051924|GO:0051117|GO:0051926|GO:0051260|GO:0006816|GO:0086004|GO:0010459|GO:0004857|GO:0032868|GO:0031966|GO:0005246|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131929_PI430048170 0.1937423991174973.18070702287542 0.331759954187687 1.85092040924996 2.75423386669559 A A A 0.2858116198157640.288655113586004 0.275499288165896 A A A LNCV6_131929_PI430048170 mRNA
GGTCACAACTATTCATGCTTCCTGTGATTTCATCCAACTACTTACCTTGCCTACGATATC NM_058173 RefSeq chr12 + 54854514 54858390 MUCL1 118430 mucin-like 1
GO:0016020|GO:0006493|GO:0005796|GO:0016266|GO:0005576|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95223_PI430048170 0.1569805040713950.7510957018579034.4243846715381 4.90638740804643 4.49651497217903 P P P 4.94931438769519 4.7472006500474 5.35108693423184 P P P LNCV6_95223_PI430048170 mRNA
AAGGGTGCCTGATAGGAAGAGCTTCAGCTTCACCTTCTTTAGATGTCCTTATTACTTTAT NM_016955 RefSeq chr4 - 25120004 25160582 SEPSECS 51091 Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase
GO:0005515|GO:0005737|GO:0000049|GO:0016785|GO:0001514|GO:0030170|GO:0005634|GO:0097056 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138190_PI430048170 0.3888848197376611.1156443317255 6.96162332828694 6.83953053097037 6.85666903873158 P P P 6.43365759843849 6.98579621773785 6.71518209517336 P P P LNCV6_138190_PI430048170 mRNA
AGAAGCCTGACCCCAAGTGTGTCTTCACCTATGTGCAGTCGCTCTACAACCACCTGCGAC NM_001207018 RefSeq chr22 + 31084995 31104624 SMTN 6525 "smoothelin, transcript variant 5"
GO:0006939|GO:0005737|GO:0007517|GO:0005654|GO:0003779|GO:0015629|GO:0008307|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109209_PI430048170 0.9040628855537121.0530543400525 3.50242847979682 3.24905523478341 2.62337288907566 P P A 3.27208307609046 2.90279719003121 3.08789281344554 P P P LNCV6_109209_PI430048170 mRNA
ATTTTCTTCTGGTGGAGAATCCTTAGATACTTCATTGGGTCTGTGTGCCAGATGAAGTAA NM_001301683 RefSeq chr10 + 69180203 69209098 SUPV3L1 6832 "suppressor of var1, 3-like 1 (S. cerevisiae), transcript variant 2"
GO:0005515|GO:0003725|GO:0042645|GO:0000962|GO:0000965|GO:0030307|GO:0003723|GO:0035946|GO:0035945|GO:0005634|GO:0042803|GO:0005739|GO:0004004|GO:0005759|GO:0032508|GO:0070827|GO:0043066|GO:0004386|GO:0000958|GO:0006310|GO:2000827|GO:0005524|GO:0003677|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129811_PI430048170 0.8290933029991810.99626395957418 0.431775733786509 0.4415982107085780.381086938462992 A A A 0.4466497187239460.396582040361511 0.427715041199481 A A A LNCV6_129811_PI430048170 mRNA
CGTAAGCTGAAGCACTGGGTGAATATTTTTATTGGGTAATAAATATTTTCATGAAAGCGC NM_032545 RefSeq chr2 - 130592164 130599575 CFC1 55997 "cripto, FRL-1, cryptic family 1, transcript variant 1"
GO:0003674|GO:0007368|GO:0007369|GO:0005886|GO:0038092|GO:0038100|GO:0005576|GO:0031225|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131380_PI430048170 0.7926402116380470.9414050921903669.6863235352301 9.74198251169245 9.96139494715846 P P P 9.4559324292766 10.0088255887228 10.1179302699743 P P P LNCV6_131380_PI430048170 mRNA
CCCAATATCAGTATTCTTTTTGTGTGTGCCAATTTTGTTATCACATCCCTATGAAGTTGA NM_013402 RefSeq chr11 -

61799624 61817057 FADS1 3992 fatty acid desaturase 1
GO:0046456|GO:0006355|GO:0006636|GO:0000248|GO:0005506|GO:0007267|GO:0044281|GO:0036109|GO:0008654|GO:0043651|GO:0043231|GO:0033559|GO:0005739|GO:0016020|GO:0005789|GO:0016491|GO:0045595|GO:0016021|GO:0044255|GO:0055114|GO:0009267|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71846_PI430048170 0.2812981885040421.11168128161788 12.5925394167896 12.7365076348785 12.9019142427781 P P P 12.5190612223211 12.4980863639174 12.7575633904446 P P P LNCV6_71846_PI430048170 mRNA
CAGCCTGCACTCTTTTGTAGATTACTTTTGGGGGATATATTTTGAGAATGATGAAACGGA NM_003720RefSeq chr21 - 39175445 39183514 PSMG1 8624 "proteasome (prosome, macropain) assembly chaperone 1, transcript variant 1"
GO:0043248|GO:0005515|GO:0005737|GO:0080129|GO:0005783|GO:0070628|GO:0005634|GO:0021930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62964_PI430048170 0.2227691015741331.20606453126532 4.73185500298537 4.22546607841266 4.57151977132913 P P P 4.31991786240189 4.27024336515136 4.1690579216606 P P P LNCV6_62964_PI430048170 mRNA
GAGTAATACAGATTCTTCCCTAGAAGGGGACACTGGTAACATGTCCCACTCTTGGATTAG NM_001130020 RefSeq chr17 + 42458843 42522579 ATP6V0A1 535 "ATPase, H+ transporting, lysosomal V0 subunit a1, transcript variant 1"
GO:0008286|GO:0005515|GO:0005886|GO:0043231|GO:0006879|GO:0000220|GO:0033572|GO:0005737|GO:0007035|GO:0046961|GO:0030670|GO:0051117|GO:0090382|GO:0070062|GO:0042470|GO:0015986|GO:0005794|GO:0070072|GO:0051701|GO:0055085|GO:0015991|GO:0005654|GO:0016021|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143329_PI430048170 0.3616182173671661.40874596399051 1.38622998154716 0.3936797826420180.306155108010932A A A 0.2825698048029750.301925386944416 0.282844315764264A A A LNCV6_143329_PI430048170 mRNA
GGTGTGGGTAGTAAGGGGATTTTCTGTCAGTCTCTTAATAAATCTATTTCCTTCAGCATA NM_181606RefSeq chr21 - 30829039 30829732 KRTAP7-1 337878 keratin associated protein 7-1 (gene/pseudogene)
GO:0005882 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137389_PI430048170 0.2911567026595710.83497971978283 6.07091886293966 5.58518705275407 5.43246417510008 P P P 6.17707444592639 5.92843250680988 5.81930103458335 P P P LNCV6_137389_PI430048170 mRNA
CCCCATCAGACCCTGCCCCAAGCACCATATGGAAATAAAGTTCTTTCTTACATCTAAAAA NM_014419RefSeq chr19 + 49363784 49375116 DKKL1 27120 "dickkopf-like 1, transcript variant 1"
GO:0007165|GO:0045600|GO:0004871|GO:0009653|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128687_PI430048170 0.1574688555889540.582083145619225 1.83269811452532 2.36639551877874 3.26142191950075 A A P 3.01732006584555 3.41193584468547 3.66810229011965 P P P LNCV6_128687_PI430048170 mRNA
CATTCATGCATTCACTAATTCAATATTTGATATGTGTCTGGGAGTGCTGGGAATAACATA NM_020354RefSeq chr10 + 99659505 99711245 ENTPD757089 ectonucleoside triphosphate diphosphohydrolase 7
GO:0016787|GO:0008152|GO:0016021|GO:0046872|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130808_PI430048170 0.5290481023691491.02760880804318 0.283545358533369 0.31025933518449 0.443684088175299A A A 0.3293834589663320.298823121352648 0.296325412480025A A A LNCV6_130808_PI430048170 mRNA
AGTTGAACCCTCTGAATTCTGGATTGAGAATGTGACAGAATGATCTGGAGCCCTTGCTGA NM_181684RefSeq chr21 - 44666188 44666927 KRTAP12-2 353323 keratin associated protein 12-2 GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_145202_PI430048170 0.00184250227083703 0.52511792038083 8.03867385659177 7.76017225690544 8.01302605405603 P P P 8.72426138782081 8.8406405175241 9.03383423031663 P P P LNCV6_145202_PI430048170 mRNA GCCCATCTGTCTACTAATAAAATGTGAAATAAAATACCTGTATTGCTACTTCCCCATGAA NM_017811 RefSeq chr9 + 33817183 33920403 UBE2R2 54926 ubiquitin-conjugating enzyme E2R 2 GO:0005737|GO:0004842|GO:0006513|GO:0019787|GO:0016874|GO:0043161|GO:0070936|GO:0005524|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138995_PI430048170 0.0410851261726849 0.950726587441973 0.413355599217045 0.353269102030105 0.363562285585641 A A A 0.456973096264504 0.460005434825692 0.432461858866786 A A A LNCV6_138995_PI430048170 mRNA GGAGGCTTTGGGAATCTGATGAAGCCTATCAATTTTCTTCCAGAAGATATTTATATAAGA NM_003117 RefSeq chr7 + 123925231 123971407 SPAM1 6677 "sperm adhesion molecule 1 (PH-20 hyaluronidase, zona pellucida binding), transcript variant 1" GO:0007338|GO:0035036|GO:0005886|GO:0007342|GO:0005975|GO:0004415|GO:0031225|GO:0007339|GO:0007155|GO:0032504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98290_PI430048170 0.436763209656422 1.11083293159361 10.1827285638728 10.3696026168859 10.4571494752153 P P P 10.0131694385577 9.99117662557873 10.5035017907583 P P P LNCV6_98290_PI430048170 mRNA TGCTTCAGTCAACTTCTCAGTTTTCTAAGAAGTGCTCAGAGAGGTGGAAGACCATGTCTG NM_002128 RefSeq chr13 - 30458740 30465944 HMGB1 3146 high mobility group box 1 GO:0005515|GO:0002437|GO:0000793|GO:0003700|GO:0005634|GO:0005615|GO:0031175|GO:0006921|GO:0003690|GO:0050786|GO:0003697|GO:0045944|GO:0017053|GO:0070491|GO:0017055|GO:0006338|GO:0001773|GO:0043065|GO:0033151|GO:2000426|GO:0009986|GO:0006357|GO:0008301|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130788_PI430048170 0.335129608426713 1.04488661618248 11.6541417701061 11.5924339888471 11.6717165647686 P P P 11.6683462361825 11.5610204186673 11.4947397709893 P P P LNCV6_130788_PI430048170 mRNA GGAAGGGGCATTAAGAGATGAAGGGTGATTATGTATTACTTATCCATTTCTGAATAAACA NM_001278657 RefSeq chr22 - 42583720 42614962 POLDIP3 84271 "polymerase (DNA-directed), delta interacting protein 3, transcript variant 3" GO:0005515|GO:0005737|GO:0016607|GO:0000166|GO:0016973|GO:0000346|GO:0045727|GO:0005654|GO:0035145|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78948_PI430048170 0.0247264092427257 1.3276450543172 12.3571923398271 12.4267117706234 12.6480670661894 P P P 11.9739694750624 12.0975109425083 12.144763488609 P P P LNCV6_78948_PI430048170 mRNA ATCATTAAATCACAACTCCTAAAAGACCCGCAAGTGCTATTTGCTGGCTACAAAGTCCCC NM_032959 RefSeq chr7 - 102636747 102671729 POLR2J2 246721 polymerase (RNA) II (DNA directed) polypeptide J2 GO:0003899|GO:0046983|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127747_PI430048170 0.0251031323236122 2.32954391596305 5.50055112082391 5.79543245646681 5.59233125070407 P P P 4.85809466506903 4.16298164706927 4.09336072702621 P P P LNCV6_127747_PI430048170 mRNA CAAGCATACTTCTTTTGCGTATTATGTTTAACTCACAAAACAAAGCTCATCATGCGTTTG NM_001304579 RefSeq chr1 + 27934954 27959157 SMPDL3B 27293 "sphingomyelin phosphodiesterase, acid-like 3B, transcript variant 3" GO:0008150|GO:0003674|GO:0006685|GO:0016798|GO:0004767|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141131_PI430048170 0.333476047528817 1.3646634890003 4.89398835920371 4.63390340934852 4.84731447064482 P P P 3.33205070737213 4.51958058811327 4.81087500792816 P P P LNCV6_141131_PI430048170 mRNA

GCTGCTTATTGGACCAGAAGTCCTATCGACTTTATACAGAACTGAATTAAGTTATTGATT NM_021969RefSeq chr1
- 26911483 26914076 NR0B2 8431 "nuclear receptor subfamily 0, group B, member 2"
GO:0005515|GO:0010467|GO:0006367|GO:0003700|GO:0031100|GO:0003707|GO:0005634|GO:0032403|GO:0042
975|GO:0042803|GO:0043433|GO:0046966|GO:0046965|GO:0005737|GO:0043401|GO:0032024|GO:0008203|GO:0
003714|GO:0019904|GO:0000122|GO:0003677|GO:0009749|GO:0010628|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139635_PI430048170 0.0481800949067689 1.29808044081646 4.49934268933279
4.59163384335914 4.84505123765451 P P P 4.33188551822936 4.15106593903761 4.338755276742
P P P LNCV6_139635_PI430048170 mRNA
TAGCTGTCTGAATCCTTCAATAAGAAGGAGAGGCACACACAAATACACACACTCACACAA NM_004757RefSeq chr4
+ 106315695 106349224 AIMP1 9255 "aminoacyl tRNA synthetase complex-interacting multifunctional
protein 1, transcript variant 1"
GO:0030133|GO:0005515|GO:0010467|GO:0005783|GO:0007267|GO:0005634|GO:0004825|GO:0050900|GO:0005
615|GO:0042803|GO:0017101|GO:0005829|GO:0005737|GO:0006954|GO:0006935|GO:0006431|GO:0006006|GO:0
007155|GO:0005794|GO:0000049|GO:0009986|GO:0009611|GO:0006915|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136989_PI430048170 0.91447345621525 1.00993788460129 0.597805742838933
0.4295725822786590.303972890186345A A A 0.5225384086419340.482061425507722
0.288388469133993A A A LNCV6_136989_PI430048170 mRNA
GTTCACTCATAGAAACATTATTAATTGGTAGGGTAAGCAGACACTCTGAAACAATGAGAA NM_000562RefSeq chr1
+ 56854769 56918221 C8A 731 "complement component 8, alpha polypeptide"
GO:0030449|GO:0001848|GO:0072562|GO:0005576|GO:0005615|GO:0032403|GO:0006957|GO:0006956|GO:0006
955|GO:0005579|GO:0016020|GO:0045087|GO:0006958|GO:0019835|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138796_PI430048170 0.0792807707723879 0.6643256853547356.7677238242122
6.10187579466347 6.34512234281957 P P P 7.04965581429609 6.924591550508 7.0855712468814
P P P LNCV6_138796_PI430048170 mRNA
GTCATTGATGGCGGCAAGCCATAGCTTTCAAGTTTTAATAAAATGCACAAAAGAGAAAAA NM_004862RefSeq chr16
- 11547721 11586373 LITAF 9516 "lipopolysaccharide-induced TNF factor, transcript variant 1"
GO:0005515|GO:0042347|GO:0005794|GO:0005886|GO:0006357|GO:0050699|GO:0007568|GO:0006915|GO:0005
765|GO:0001817|GO:0006351|GO:0043231|GO:0007165|GO:0005737|GO:0071222|GO:0005654|GO:0004871|GO:0
043123 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127126_PI430048170 0.6058689491881591.21268201700097 2.57558841737987
1.34228355096909 0.941171806812694A A A 0.37263437293903 0.429331726396221
2.57253101107544 A A P LNCV6_127126_PI430048170 mRNA
GTTTTAGGATGGGGATGGAGGCAAAGGCATCAGGCAAGTAATGAAGCAAAGGTTTATTTT NM_004246RefSeq chr17
+ 9825550 9892103 GLP2R 9340 glucagon-like peptide 2 receptor
GO:0008284|GO:0005886|GO:0071377|GO:0004930|GO:0007188|GO:0016021|GO:0004967 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127368_PI430048170 0.00287818217250912 0.3730555094065286.85678499037131
6.7709440254784 7.13353766818173 P P P 8.1123006607945 8.24754298080971
8.64087563091209 P P P LNCV6_127368_PI430048170 mRNA
GTAATAAGAGAAACAGTTACGTGTGGAATTCAACATCTTTGGTTGGAACGCATTGGCTTT NM_002577RefSeq chr3
+ 196739856 196832647 PAK2 5062 p21 protein (Cdc42/Rac)-activated kinase 2
GO:0005515|GO:0050852|GO:2001238|GO:0048471|GO:0005886|GO:0061098|GO:0031295|GO:0050731|GO:0006
921|GO:0042802|GO:0005829|GO:0035556|GO:0005737|GO:0046777|GO:0030296|GO:0004702|GO:0018105|GO:0
007411|GO:0016032|GO:0023014|GO:0048010|GO:0043066|GO:0019901|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_51716_PI430048170 0.0102336717546696 0.4985083471492094.13188946588488

3.79522995781787 3.64428085668686 P P P 4.56925106839608 4.8752246135655
5.12971129639662 P P P LNCV6_51716_PI430048170 mRNA
GGTGTGCTGTGGTGCACTGCAGTGATGTATTTGCATAACATTGTTTGATAGTGAAAAATT NM_015350 RefSeq chr1
+ 89558712 89597861 LRRC8B 23507 "leucine rich repeat containing 8 family, member B, transcript
variant 1" GO:0005515|GO:0005886|GO:0016021|GO:0006811 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134130_PI430048170 0.0537517999322452 0.656915770842565 0.407371062327526
0.433243465555263 0.303711360790564 A A A 1.24776359372662 0.952993998027218
0.716097134087009 A A A LNCV6_134130_PI430048170 mRNA
TTCCAGGTCTCATGCCATAGGGGTAGAAGAAGAACTGGAAAGCACAGGCATTTAGAGAAA NM_001080209
RefSeq chr18 - 5890184 5892104 TMEM200C 645369 transmembrane protein 200C GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142294_PI430048170 0.0612069563357383 0.693106939626391 9.17021730959882
9.1440602671176 9.42980898009236 P P P 10.031528634102 9.48424617081125
9.78089786789976 P P P LNCV6_142294_PI430048170 mRNA
GTATGCCAGCAAAATGTGAGCTCTGTATTTTTTGGCATTCTTATGTTTGGGTTTAATAAG NM_001282192 RefSeq
chr14 + 20684212 20700602 RNASE4 6038 "ribonuclease, RNase A family, 4, transcript variant 4"
GO:0006379|GO:0005576|GO:0004522|GO:0003676|GO:0070062|GO:0009267 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141422_PI430048170 0.0649674235629125 0.777425595290159 10.5972108377194
10.3447351231954 10.2577290869307 P P P 10.7666539588342 10.7981104745618
10.7459991808916 P P P LNCV6_141422_PI430048170 mRNA
GGTGAGGCGGCTGCTCTCATATTTTCAGATGTTGCTGTAGAAATAAAGACGGTTTAAATC NM_001134775 RefSeq
chr11 + 66257293 66267860 KLC2 64837 "kinesin light chain 2, transcript variant 3"
GO:0005515|GO:0043005|GO:0005871|GO:0005874|GO:0016938|GO:0003777|GO:0005829|GO:0043234|GO:0019
886|GO:0016020|GO:0007596|GO:0035253|GO:0008152|GO:0008088|GO:0019894|GO:0007018 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130127_PI430048170 6.31763497722134e-05 1.36489107459578 13.1053962358011
13.1512879174635 13.1249377676701 P P P 12.6458130200368 12.7070922332593
12.6820699695331 P P P LNCV6_130127_PI430048170 mRNA
GGGGAGGATGGGACTTTGTTTTTTCCAAGAATAAACTTCAACTCCTGTCATGTGAAAAAA NM_014017 RefSeq chr1
+ 156054725 156058510 LAMTOR2 28956 "late endosomal/lysosomal adaptor, MAPK and MTOR activator
2, transcript variant 1"
GO:0005515|GO:0032008|GO:0005770|GO:0005765|GO:0005085|GO:0043547|GO:0000186|GO:0032947|GO:0071
986|GO:0071230|GO:0016049|GO:0034613|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136274_PI430048170 0.162481383484183 0.61504448949155 0.663929321837709
0.405983649037973 0.305831612960816 A A A 0.560502365441171 1.62969878482138
1.11830700559478 A A A LNCV6_136274_PI430048170 mRNA
CACCCCTTAAGGAACATCAGAAAATTCATTTTTGAGATGATTGTTCCAAATGCAATGAGT NM_138374 RefSeq chr19
+ 53333748 53354869 ZNF845 91664 zinc finger protein 845
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137617_PI430048170 0.00267787330594183 1.6263295899904 1.08129474139285
1.33049482061778 1.18003930477757 A A A 0.469533679564774 0.6389823523687
0.377103939128947 A A A LNCV6_137617_PI430048170 mRNA
TTCATCAGGCACAATAAAACCAACACCATTCTTTTTTATGGAAGATTATGCTCCCCCTAA NM_005024 RefSeq chr18
+ 63915510 63935242 SERPINB10 5273 "serpin peptidase inhibitor, clade B (ovalbumin), member 10"
GO:0010951|GO:0005737|GO:0004867|GO:0005634|GO:0005615 . NA - . NA NA NA NA NA NA NA
NA NA

LNCV6_104937_PI430048170 0.6000344561906130.9651023695743980.532549700346066
0.49206971942769 0.261570931336084A A A 0.4096662779123130.549157052465633
0.492240156885481A A A LNCV6_104937_PI430048170 mRNA
CCCATCATTTTTGAGAGCTTTGGTGTCATTACATTTCAATAACAAAGGTCATTTCCCTTTNM_001242671 RefSeq chr20
- 18809350 18830203 C20orf78 100128496 "chromosome 20 open reading frame 78, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143590_PI430048170 0.1304781550019621.31742400811662 8.33205900752003
8.64799391110906 8.38782771281086 P P P 8.39580022942749 7.83862796017508
7.89260231425976 P P P LNCV6_143590_PI430048170 mRNA
AAAGATGCAGGTGCTCGTATCTCGACATTCATTCCCACCCCCCTCTTATTTAAATAGCTA NM_001307RefSeq chr17
- 7259902 7262945 CLDN7 1366 "claudin 7, transcript variant 1"
GO:0005515|GO:0016323|GO:0016338|GO:0005198|GO:0016021|GO:0005923|GO:0016328|GO:0042802 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132494_PI430048170 0.0607328518192174 1.46369866720259 9.11542931464089
9.3226725062651 9.65882214795816 P P P 8.65788719702695 8.71212376900762
9.09111313522002 P P P LNCV6_132494_PI430048170 mRNA
CAGGCGTCAACCCCATTTTATTTGTCCTTATTCCTGTGGAAGCAGTATATGTTTTCTTCC NM_006857RefSeq chr2 +
69893942 69905236 SNRNP27 11017 "small nuclear ribonucleoprotein 27kDa (U4/U6.U5), transcript
variant 1" GO:0008380|GO:0006397|GO:0005515|GO:0008150|GO:0005575|GO:0003676|GO:0071011 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129850_PI430048170 0.1707781722552320.87276631462609 7.73239041408272
7.59916601705331 7.63181645421604 P P P 7.65637969268874 7.95161868207022 7.9294197841641
P P P LNCV6_129850_PI430048170 mRNA
GTTTCCAAATGGGAAGGACAGTTGATTTCCAACATGAGGTTTTTTGTTTTTTATCCAGAA NM_016604RefSeq chr5
+ 138352595 138437027 KDM3B 51780 lysine (K)-specific demethylase 3B
GO:0006355|GO:0006325|GO:0051213|GO:0005654|GO:0046872|GO:0006351|GO:0055114|GO:0016568 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130195_PI430048170 0.00608726990978415 0.4622728161583935.8760869798414
5.94747209362568 5.45095244777453 P P P 7.07547950603911 6.81439158923849
6.75153511055846 P P P LNCV6_130195_PI430048170 mRNA
TGTTCCTTCAAATCTGCTGAGAATTAAATAAACATCTCTAAAGCCTGACCTCCCCACGTC NM_000767RefSeq chr19
+ 40991298 41018396 CYP2B6 1555 "cytochrome P450, family 2, subfamily B, polypeptide 6"
GO:0008392|GO:0006805|GO:0005506|GO:0017144|GO:0008395|GO:0019373|GO:0044281|GO:0043231|GO:0004
497|GO:0005737|GO:0019825|GO:0042738|GO:0005789|GO:0016712|GO:0042180|GO:0008202|GO:0055114|GO:0
020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131815_PI430048170 0.1703085830860620.3670396402662560.415672866514993
2.25431416368461 1.62268418178811 A A A 2.30242872962615 2.07080249780196
3.98995839137363 A A P LNCV6_131815_PI430048170 mRNA
CATGTACCCTTTCATGCCTACACACCCCTCATTAAAGCAGAGTCGTGGCATCTCAAAAAA NM_018687RefSeq chr19
+ 11239618 11241943 C19orf80 55908 chromosome 19 open reading frame 80
GO:0005515|GO:0044342|GO:0010954|GO:0005179|GO:0070328|GO:0045444|GO:0048469|GO:0005576|GO:0044
255|GO:0050746|GO:0019216 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98219_PI430048170 0.12035271193474 1.28033712644947 12.1453664594259 12.2461663252287
12.4970313577252 P P P 11.6508989350631 12.0089687728821 12.13905853928 P P P
LNCV6_98219_PI430048170 mRNA
TGGTAGCTGTAGGAGCTGAATATTACCTGGAGTCCCTGAATAAAGATAAGAAGCATCACT NM_001257102 RefSeq
chr2 + 201071738 201085751 NDUFB3 4709 "NADH dehydrogenase (ubiquinone) 1 beta
subcomplex, 3, 12kDa, transcript variant 2"
GO:0022904|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0016021|GO:0008137|GO:0044237|GO:0070

062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138913_PI430048170 0.23804057199757 0.6890584780343410.346547119978097
0.4301919453449020.336022250713809A A A 0.8267762498850440.362402743772436
1.36363535672757 A A A LNCV6_138913_PI430048170 mRNA
GGCATAGCTATTCTCTCTGTTTTAGTTTGATATATAGTAGTGGTAGGAATAGGAATGTGA NM_178550RefSeq chr1
- 162854296 162868815 C1orf110 339512 chromosome 1 open reading frame 110 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145681_PI430048170 0.2883028441374011.53789815178731 0.42039292987383
0.9987315540502651.69387296268475 A A A 0.5309881204340620.50279988081295
0.497064731569797A A A LNCV6_145681_PI430048170 mRNA
CCGTAACCATATGAAGGAGAACTCTTCATAGTAAAAACTGTAGCAAGATTATATGCTTTC NM_001146221 RefSeq
chr12 - 27762665 27771276 MANSC4 NA MANSC domain containing 4 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_93320_PI430048170 0.3788487472658220.73544848973027 2.49410924519681 0.366876662177614
0.966971315028128A A A 2.08283115238786 2.23385713472591 1.64680642563498 A A A
LNCV6_93320_PI430048170 mRNA
AGGCCAACTGCAGCCCCGAAGACCCATGCCAAGAAACAGTGTCCAAACCAGAACCAATGG NM_001256443
RefSeq chr16 + 29812087 29815881 PRRT2 112476 "proline-rich transmembrane protein 2, transcript
variant 3" GO:0009607|GO:0030054|GO:0005886|GO:0050884|GO:0045202|GO:0016021 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_144026_PI430048170 0.0228466048498959 0.5975850648910586.7265598235486
6.82922143566314 6.95407854365856 P P P 7.27899576680628 7.68730440723411
7.73848424550783 P P P LNCV6_144026_PI430048170 mRNA
TAACTTTCTGCCTTTGACATTCAACCTTGAGTCCACCTGTAAGTGTAACTGCGGCAGAAG NM_024627RefSeq chr22
- 19846137 19854848 C22orf29 79680 chromosome 22 open reading frame 29
GO:0005739|GO:0005515|GO:0051881 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144756_PI430048170 0.4996394138807961.03474996227547 0.282191159629734
0.3039843133034190.464069284844313A A A 0.3235530198247130.289954379916559
0.29558570242784 A A A LNCV6_144756_PI430048170 mRNA
TGACAAAGTAGCCAAAGACAATCAGCAGAAAGCATTTTCTGCAAAATAAACGCAATATGC NM_003181RefSeq chr6
- 166157655 166168669 T 6862 "T, brachyury homolog (mouse), transcript variant 1"
GO:0001191|GO:0000790|GO:0008284|GO:0003700|GO:0006366|GO:0001756|GO:0003705|GO:0048706|GO:0001
839|GO:0005634|GO:0061371|GO:0060395|GO:0014028|GO:0005737|GO:0007509|GO:0001085|GO:0008595|GO:0
060070|GO:0001102|GO:0090009|GO:0023019|GO:0001843|GO:0030509|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93836_PI430048170 0.19901889325291 1.12184833357229 5.86978912975571 5.6514438212512
5.61559913377534 P P P 5.45892735232051 5.6897482086933 5.49293556634455 P P P
LNCV6_93836_PI430048170 mRNA
TTGGGCTGCCTGACCTCCTTGGGTGCTTGCTATTAATTAACAGACTTTGTGGGGAAAAAA NM_004307RefSeq chr4
- 40810026 41214618 APBB2 323 "amyloid beta (A4) precursor protein-binding, family B, member 2,
transcript variant 1"
GO:0005515|GO:0043066|GO:0006355|GO:0030308|GO:0043065|GO:0045202|GO:0005634|GO:0030027|GO:0030
426|GO:0035556|GO:0005737|GO:0001540|GO:0016020|GO:0007411|GO:0030198|GO:0007050|GO:0001764|GO:0
008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139671_PI430048170 0.1921385467072950.9688670593281150.433858407025771
0.4316751935093720.367246548610209A A A 0.4202245704859910.485234540892514
0.464434768476509A A A LNCV6_139671_PI430048170 mRNA
GTTGTAGATCTTTGAAGACTCTGATTCTCTGAGACTGAGGAGAGATGTCTTACCAGCAGC NM_001014291 RefSeq
chr1 - 153149581 153150951 SPRR2G 6706 small proline-rich protein 2G

GO:0005737|GO:0008544|GO:0030216|GO:0031424|GO:0001533 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89732_PI430048170 0.000698027903327826 0.4082388266729955.4135233968341 5.1688779997969 5.30901140294587 P P P 6.59508140035911 6.41314032006661 6.75135249038899 P P P LNCV6_89732_PI430048170 mRNA GAAGCCAAGAGTGAACTGATGTTTCATTTATATTTTCATCCAAATGACATTATCTGCACG NM_017423RefSeq chr4 + 173168752 173323967 GALNT7 51809 polypeptide N-acetylgalactosaminyltransferase 7 GO:0004653|GO:0016020|GO:0006493|GO:0000139|GO:0005975|GO:0030246|GO:0016266|GO:0016021|GO:0044267|GO:0046872|GO:0070062|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109964_PI430048170 0.0866904522696431.1184678918447 4.90281934188881 4.76740541217772 4.78231428689851 P P P 4.56665494712234 4.75836003659042 4.64029700247226 P P P LNCV6_109964_PI430048170 mRNA CTATGCAAAGCTGGTGTTCATGTCCACCTCCTCGGGCAGCCTATGGAACCTGCATGCCAT NM_033510RefSeq chr15 + 40358232 40371055 DISP2 85455 dispatched homolog 2 (Drosophila) GO:0003674|GO:0005886|GO:0016021|GO:0005575|GO:0007224 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138848_PI430048170 0.1833490313536080.4072489493170280.460030256579446 3.15105097029547 2.71549805747734 A P A 3.1624435367553 3.85046557545334 4.16511549078483 P P P LNCV6_138848_PI430048170 mRNA CTCTTATGATTCCTCTAGCAGATAAATAAAAGAAACTTTTGCCATCCATGTGTTCTGTGT NM_001439RefSeq chr1 - 100872371 100895179 EXTL2 2135 "exostosin-like glycosyltransferase 2, transcript variant 1" GO:0001888|GO:0005783|GO:0019276|GO:0006044|GO:0005789|GO:0035248|GO:0016021|GO:0015012|GO:0046872|GO:0006024|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129399_PI430048170 0.2610236808913230.9113328620576811.6799765269677 11.7781254650344 11.6527333315662 P P P 11.7000195211537 11.8114283486717 11.989407450689 P P P LNCV6_129399_PI430048170 mRNA CAGGATTAGACTGGGTTTATATTTAACTCTTGCTTCATAGGTGTACCATTTAAAGAGTGT NM_013328RefSeq chr1 - 225919876 225924340 PYCR2 29920 "pyrroline-5-carboxylate reductase family, member 2, transcript variant 1" GO:0005737|GO:0055129|GO:0055114|GO:0004735 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133013_PI430048170 0.61505078971698 0.8790117593058977.40119127511518 7.15073550108839 7.03977283397905 P P P 7.61014452172989 7.59076492767587 6.8516560647397 P P P LNCV6_133013_PI430048170 mRNA GCCCCTGACACCTTTCCCCCAAAAATATATATTTTGGTGTCTTATATACAGAATATACAT NM_001007531 RefSeq chr6 + 28259296 28260958 NKAPL 222698 NFKB activating protein-like NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132261_PI430048170 0.0688529603529066 0.9764706796927740.335095584814406 0.3686288678612690.342581482874242A A A 0.3924894367323410.392676265713747 0.364224089112122A A A LNCV6_132261_PI430048170 mRNA CTTTACTTCCCAAACCTAAAAAAGCAATGAAATAGATGTAAGGAAGGAGGGATTTAAACC NM_030773RefSeq chr20 + 59019253 59026654 TUBB1 81027 "tubulin, beta 1 class VI" GO:0051258|GO:0005874|GO:0003924|GO:0005525|GO:0051225|GO:0055085|GO:0006184|GO:0005737|GO:0006457|GO:0005200|GO:0051084|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133968_PI430048170 0.0753121614766142 1.83792910066392 5.67891792538409 5.52453257369412 5.70853788677578 P P P 5.25863908148093 4.51897809752629 4.33346237682482 P P P LNCV6_133968_PI430048170 mRNA CCATTGTGCCTTATGCCAATAATTCAATTGCTGCAAACACCAATAAAGATTGATTCATGG NM_152792RefSeq chr2 - 69960090 69962265 ASPRV1 151516 "aspartic peptidase, retroviral-like 1" GO:0016485|GO:0006508|GO:0043588|GO:0016021|GO:0004190 . NA - . NA NA NA NA NA NA NA

NA NA
LNCV6_140906_PI430048170 0.00671533282630763 0.33772909376049 3.16756921527396
2.47166598111424 3.12754092117748 P A P 4.42068899349812 4.31194371827664
4.78800552453956 P P P LNCV6_140906_PI430048170 mRNA
CGAGTGTGAATATATTTTACTCAGAGACTATGTACAAATACACTAAAGTGGTGATGGTGA NM_001167741 RefSeq
chr5 - 79976715 79991265 MTX3 345778 "metaxin 3, transcript variant 1" GO:0006626|GO:0005741
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134499_PI430048170 0.4011558396507430.7319671915281171.98017029386084
0.3449890588844721.57481827635707 A A A 2.37839370585947 1.6946012819343 1.4640140272348
A A A LNCV6_134499_PI430048170 mRNA
ATGCCCTAAAATAACCTCACCCCAAATACAATAAAGGGACGAAGCACTTATAGATACCAC NM_001011700 RefSeq
chr6_GL000256v2_alt + 2828245 2829515 MCCD1 401250 mitochondrial coiled-coil domain 1
GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135103_PI430048170 0.2326030896253151.41742661280217 3.99555672719839
4.21160254937718 4.51586454313543 P P P 4.15941282992185 3.03243082044834
3.84936714987986 P P P LNCV6_135103_PI430048170 mRNA
GGATGAACATTAAGTGTTTGAATTCATGCTCTGCTTTTGTGTTACTGTAAACACAAGATC NM_000772RefSeq chr10
+ 94683493 94736191 CYP2C18 1562 "cytochrome P450, family 2, subfamily C, polypeptide 18,
transcript variant 1"
GO:0008392|GO:0006805|GO:0070330|GO:0005506|GO:0008395|GO:0019373|GO:0044281|GO:0043231|GO:0004
497|GO:0005737|GO:0019825|GO:0042738|GO:0005789|GO:0016712|GO:0055114|GO:0020037 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132442_PI430048170 0.4241866729414796.16682416419832 0.2619880324835615.0093955479585
1.70065751165988 A P A 0.3999098926763941.4747497720541 0.884185663510223A A A
LNCV6_132442_PI430048170 mRNA
CCTTGTCACGGTGACCACGATTGTATGACAATAAAATGGACCTTTTGGCCACCCAAAAAA NM_198571RefSeq chr7
- 101170492 101180276 NAT16 NA "N-acetyltransferase 16 (GCN5-related, putative)"NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140843_PI430048170 0.3993444219151880.6966985675955911.31249779806023
0.3366978341361361.74025054696045 A A A 2.1095673921628 2.00170978231113
0.889571925396994A A A LNCV6_140843_PI430048170 mRNA
CACGAGTAAAGTTTAATCTGCAGCCATCTTTTCTTGTCTTTGCCTTCCCTTTATAAGTAA NM_032135RefSeq chr14 -
44504150 44507296 FSCB 84075 fibrous sheath CABYR binding protein
GO:0035686|GO:0005509|GO:0097228 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144223_PI430048170 0.00039832973603798 0.4416324899326378.11732327503313
8.19265003250182 8.11978758598329 P P P 9.34835098326872 9.3963299508544
9.21773370540257 P P P LNCV6_144223_PI430048170 mRNA
TCCTGTGTCTGGTTGGCACAAAGATCCTGTGTAACATGAAATGAAAGGTGCATCAGCTTG NM_001134404 RefSeq
chr1 + 109494078 109500441 CYB561D1 284613 "cytochrome b561 family, member D1, transcript
variant 5" GO:0016021|GO:0046872|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127096_PI430048170 0.5600434708669520.889856348294083 3.02959915039252
3.18156309514132 2.43362948144795 A P A 2.956634296457 3.39698474643335
2.83724937078465 P P P LNCV6_127096_PI430048170 mRNA
TTAAGATTTTTGAATTTGTACTTCTGCGGTGCTGGTTTTTCTCCACAAACACCCCCGCCC NM_014246RefSeq chr22
- 46360833 46537170 CELSR1 9620 "cadherin, EGF LAG seven-pass G-type receptor 1"
GO:0001736|GO:0005886|GO:0007266|GO:0009952|GO:0042249|GO:0032956|GO:0046983|GO:0007626|GO:0007
156|GO:0001942|GO:0060490|GO:0042472|GO:0004930|GO:0090251|GO:0005509|GO:0090179|GO:0001843|GO:0
045176|GO:0007417|GO:0007186|GO:0005887|GO:0060489|GO:0042060|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_134382_PI430048170 0.00677082884473144 0.6605421986075386.01668562554242
5.98758319850511 6.13796088530587 P P P 6.47942209174396 6.7270620906035
6.72144213558347 P P P LNCV6_134382_PI430048170 mRNA
CTACTAGACTCAGACAGAAGGGCTGGGGCCATTAAAGCTGAATTTTCTAAGCAGTCCAAA NM_015512RefSeq chr3
+ 52316318 52400497 DNAH1 25981 "dynein, axonemal, heavy chain 1"
GO:0030286|GO:0001539|GO:0008152|GO:0005874|GO:0005858|GO:0003341|GO:0003777|GO:0016887|GO:0005
524|GO:0009612 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140883_PI430048170 0.7854971608670220.9910706479668140.276494561398377
0.2814193663887890.409764019749709A A A 0.3614367447065270.305396966100529
0.343096517190341A A A LNCV6_140883_PI430048170 mRNA
AGAAGAAAAAACGGCATCGAGGCATTTCAATAAAACCTAAGCGACTCCTGATCCAAAAAANM_178569RefSeq chr5
+ 2752130 2755397 C5orf38153571 "chromosome 5 open reading frame 38, transcript variant 1"
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138422_PI430048170 0.0202141635433711 1.33864045687737 5.98885836771241
5.97167919539468 5.87758357351844 P P P 5.51267731594661 5.66362503707323
5.38882295983685 P P P LNCV6_138422_PI430048170 mRNA
AGTTGCTTGGTTGAAAGTGCCTGTGCTGGAACTGGCCTGTACTCACTCATGGGAGCTGGC NM_057090RefSeq chr1
+ 43933319 43937240 ARTN 9048 "artemin, transcript variant 4"
GO:0050930|GO:0007165|GO:0061146|GO:0097021|GO:0007411|GO:0007422|GO:0005102|GO:0008083|GO:0005
615|GO:0007405 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_85055_PI430048170 0.06829672585652 1.04306829776659 0.3313030744134440.34287639572098
0.287703702732191A A A 0.2607921789481250.2578220216454670.261350439507655A A A
LNCV6_85055_PI430048170 mRNA
TGTTTATAGCACTATTTGATGTATGTTTTCAGTGCTTAACACTATGCCAGAGGATGGAAA NM_001195131 RefSeq
chr6 + 99520993 99533183 TSTD3 100130890 thiosulfate sulfurtransferase (rhodanese)-like domain
containing 3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73061_PI430048170 0.1032205363187860.7672325518819366.49980143651255 6.54565889656254
6.97396886299489 P P P 6.93949623492643 7.06445231062998 7.19941878771325 P P P
LNCV6_73061_PI430048170 mRNA
AGAACAAAGCCAAGTCGGGCAAACAGAATTCAAAGAAGCTGTACTGCCAAGAACTTAAAA NM_206825RefSeq
chr3 + 52685919 52694494 GNL3 26354 "guanine nucleotide binding protein-like 3 (nucleolar),
transcript variant 2"
GO:0005515|GO:0016020|GO:0008283|GO:0042254|GO:0042127|GO:0008152|GO:0005730|GO:0003924|GO:0005
654|GO:0005634|GO:0005525|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136405_PI430048170 0.0543403073986451 0.6780586119366359.87121459575671
9.35224106993977 9.51794182773371 P P P 10.1292471638102 10.0959144012482
10.2431801534014 P P P LNCV6_136405_PI430048170 mRNA
ATTCTCTTGCCGTGTTGCAAATGTGTAAAATAAAGATTATCTGGCAGAACCGTGAAAAAA NM_001136557 RefSeq
chr9 + 130053705 130140169 GPR107 57720 "G protein-coupled receptor 107, transcript variant 1"
GO:0005794|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129583_PI430048170 0.825245682168227 1.01038685889106 0.285292362700455
0.310281131794449 0.440498860192218 A A A 0.402076802983428 0.296835517678609
0.294663483887577 A A A LNCV6_129583_PI430048170 mRNA
GTCATGGGGGCTCTGAAGAAAATGTTAACAGTGGAACCTGCCTTTCAAAAAGCTATGGAG NM_001004696 RefSeq
chr1_KI270892v1_alt + 9554 10601 OR2T4 NA "olfactory receptor, family 2, subfamily T, member 4"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129532_PI430048170 0.541941494869644 0.91969353651182 0.374038259259315
0.327268232002205 0.381995590808408 A A A 0.299269181253853 0.756009589294714
0.3458787828223 A A A LNCV6_129532_PI430048170 mRNA

CCAAGAGTGCTTTTCTCTCTAATAAGAAAACATCTACTTTGAAACATCTACTGGGCGAGA NM_032391 RefSeq
chr17 - 48721719 48722520 PRAC1 84366 prostate cancer susceptibility candidate 1 GO:0005634
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144777_PI430048170 0.425461138287202 0.631900206629191 0.3577852754109
0.342179174909917 0.27501326737004 A A A 0.325046080410607 1.78646344661643
0.317937221583185 A A A LNCV6_144777_PI430048170 mRNA
TCTGTAAAATCCCCAAATCCATTAAAAGTGACTTCAGAGGTCCCAGATAGGGACCAACAT NM_025041 RefSeq
chr3 - 133928145 133929812 C3orf36 80111 chromosome 3 open reading frame 36 NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_141230_PI430048170 0.201070462286582 0.605295905849142 0.364050259623016
0.882512630356067 0.368020132387864 A A A 0.493917984680209 1.42043479207177
1.68673216152276 A A A LNCV6_141230_PI430048170 mRNA
TGTAGTAAAGCACTTCAATGCTTTTGCACTTAAATTTACAACACTGTTGGTGTGTGATTG NM_001166139 RefSeq
chr4 - 17880594 18021860 LCORL 254251 "ligand dependent nuclear receptor corepressor-like,
transcript variant 1" GO:0006366|GO:0006357|GO:0005634|GO:0003677 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_111623_PI430048170 0.00403810125994987 0.559429396837875 4.2264646009255
3.98359516142634 4.12799597124324 P P P 4.77489395121895 4.93331674491635
5.13180415511804 P P P LNCV6_111623_PI430048170 mRNA
TTCTCTATCAGAGGGAAGATGGCTCTTTCAGTGCTTTTGGGAATTATGACCCTTCTGGGA NM_133493 RefSeq
chr6 + 73696084 73828317 CD109 135228 "CD109 molecule, transcript variant 1"
GO:0010839|GO:0050431|GO:0072675|GO:0005886|GO:0009986|GO:0004867|GO:0031225|GO:0005615|GO:0010
951|GO:0045616|GO:0061045|GO:0001933|GO:0001942|GO:0030512 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130625_PI430048170 0.86042581543892 1.11273033506463 2.79250212988485
1.93193180439216 3.25507040343305 A A P 2.79741998875985 2.16539365443968
2.76502083617486 P A P LNCV6_130625_PI430048170 mRNA
AACCGTGGAACATCTAGAGATAAGTCTTAGTTTATGTAACATTAAAACTGTCTAGTGAGG NM_002014 RefSeq
chr12 + 2794941 2805421 FKBP4 2288 "FK506 binding protein 4, 59kDa"
GO:0051219|GO:0005515|GO:0000413|GO:0048471|GO:0046661|GO:0031503|GO:0035259|GO:0005829|GO:0034
605|GO:0005739|GO:0005737|GO:0006457|GO:0031072|GO:0043025|GO:0030850|GO:0030674|GO:0070062|GO:0
031115|GO:0032767|GO:0007566|GO:0031111|GO:0005874|GO:0048156|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131181_PI430048170 0.134033818440472 0.910777806140893 0.348141922136247
0.320065730183354 0.306739675471095 A A A 0.566304377966254 0.42478649895342
0.382149467927625 A A A LNCV6_131181_PI430048170 mRNA
GCACTTGGTATTTGAATGTGTGTGAAAATAAGGGAAGTCAAGAGATTAAATGCTGAACTT NM_001102416 RefSeq
chr3 + 186717308 186742889 KNG1 3827 "kininogen 1, transcript variant 1"
GO:0005515|GO:0004869|GO:0005886|GO:0072562|GO:0007204|GO:0005615|GO:0006939|GO:0006954|GO:0042
311|GO:0031093|GO:0008201|GO:0070062|GO:0043065|GO:0005102|GO:0030168|GO:0005576|GO:0045861|GO:0
010951|GO:0007162|GO:0007596|GO:0007597|GO:0030195|GO:0002576|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143504_PI430048170 0.0507284570672877 0.55205943570951 3.85746401970266
4.55315874950493 4.59738308330382 P P P 5.06070400067096 5.38820859842596
5.22401383331577 P P P LNCV6_143504_PI430048170 mRNA
GCTTTTGGTATTTGTTTGTAGCTTTCCTGGAAGTCAAATAAATGTTTCCCCCACTCCAAA NM_002147 RefSeq
chr17 - 48591256 48593741 HOXB5 3215 homeobox B5
GO:0045944|GO:0001205|GO:0048704|GO:0005634|GO:0000980|GO:0045446|GO:0009952|GO:0009653|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_132683_PI430048170 0.716332104223181 0.97392762490564 0.30948456600019
0.49108841495201 0.341985216058746 A A A 0.531509389401186 0.442915282869845
0.277643140132462 A A A LNCV6_132683_PI430048170 mRNA
GGAGTGTCACCGCGTGTACATACTGTAAATTATTTATTAATGGCTAAATGCAAGTAAAGT NM_020211 RefSeq
chr15 - 93043405 93089214 RGMA 56963 "repulsive guidance molecule family member a,
transcript variant 4" GO:0005886|GO:0007411|GO:0005783|GO:0031225|GO:0030509|GO:0015026|GO:0070062
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136133_PI430048170 0.26394055666746 1.33109435657362 0.385143297834708
1.19572470773473 0.611042508032904 A A A 0.351578033645836 0.33890136427553
0.388110717279668 A A A LNCV6_136133_PI430048170 mRNA
CCTGAGGATGATTTGTAGAAAATTAACTGCTAACTTCTATTGACCCACAAAGTTTCAGAA NM_021870 RefSeq
chr4 - 154604575 154612750 FGG 2266 "fibrinogen gamma chain, transcript variant gamma-B"
GO:0051258|GO:0005886|GO:0050714|GO:0072562|GO:0005615|GO:0043623|GO:0046872|GO:0045921|GO:1900
026|GO:0045907|GO:0030198|GO:0031091|GO:0034116|GO:0031093|GO:0070374|GO:0030674|GO:0005938|GO:0
050839|GO:0070062|GO:0009986|GO:0090277|GO:0005102|GO:0005577|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137227_PI430048170 0.0182471934465251 0.416818655624368 0.832195733646507
1.63270282008598 0.935289757512394 A A A 2.63022582239759 2.50833952722943
2.14333501960196 A P A LNCV6_137227_PI430048170 mRNA
GAAAACAGCACATGTTGATTACGAATGTTTTTTCCCCCATGTCTACATTTTTTACACTGA NM_024803 RefSeq
chr10 - 5393097 5404830 TUBAL3 79861 "tubulin, alpha-like 3, transcript variant 1"
GO:0006184|GO:0051258|GO:0005737|GO:0005874|GO:0005200|GO:0003924|GO:0007017|GO:0005525 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_99670_PI430048170 0.394822393710996 0.91864309991775 6.48866836106385
6.11831545787223 6.32628335254142 P P P 6.31631979188855 6.57514960983789
6.42099113626807 P P P LNCV6_99670_PI430048170 mRNA
TACAGCTGCAACCAGAGCATGAACCTCAAACGTCACATGCTGCGGCACACAGGCGAGAAG NM_144631 RefSeq
chr2 - 27377230 27380744 ZNF513 130557 "zinc finger protein 513, transcript variant 1"
GO:0006355|GO:0060041|GO:0044212|GO:0005634|GO:0007601|GO:0003677|GO:0050896|GO:0046872|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59579_PI430048170 0.548427385453067 0.93256167412224 14.0587963320311
13.8272947327016 14.1022660841903 P P P 13.860722792855 14.2484982448698
14.1678655210087 P P P LNCV6_59579_PI430048170 mRNA
CAGGAAGGTGAGATCTTCGACACAGAAAAAGAAAATATGAGATTACGGAGCAGCGCAAGA NM_001024662
RefSeq chr12 - 112405189 112409639 RPL6 6128 "ribosomal protein L6, transcript variant 1"
GO:0010467|GO:0006355|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0005634|GO:0006
415|GO:0003677|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0016020|GO:0000184|GO:0016032|GO:0
022625|GO:0044267|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128599_PI430048170 0.506701704204118 1.20020983674098 1.14522180678127
0.368554000545294 0.33474286247364 A A A 0.421321697659557 0.408470214278967
0.381709195446423 A A A LNCV6_128599_PI430048170 mRNA
GCAAAAATGGAAGATATATAAAGCAACAAGTTGTCTGCATTTGATCACTGGTCAGATTGT NM_033050 RefSeq
chr3 + 151873642 151882088 SUCNR1 56670 succinate receptor 1
GO:0008150|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0070062 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_139539_PI430048170 0.589246162931706 0.906285802133641 11.9597160685866
12.1961630632515 12.3732933532898 P P P 11.9692926171876 12.3540152510522
12.5939059345464 P P P LNCV6_139539_PI430048170 mRNA
AGACCTTGGATGAACTTCACTGACATCATTCTTCCCTAAGCAGTCACCAAAAAATTTATA NM_212552 RefSeq

chr2 - 74135400 74147912 BOLA3 388962 "bolA family member 3, transcript variant 1"
GO:0008150|GO:0003674|GO:0005576|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132455_PI430048170 0.535206774954977 1.03591748555627 0.384637820098485
0.578987486226809 0.481650788081938 A A A 0.528405120163951 0.387508126567571
0.378216580446694 A A A LNCV6_132455_PI430048170 mRNA
TGTTACTTCTTGTGCCAGAGATTACGTTTTCCCTGAGCTTCCATAAAGTGTTTTTAAACA NM_001002254 RefSeq
chrX - 70040541 70049938 AWAT2 NA acyl-CoA wax alcohol acyltransferase 2 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_140364_PI430048170 0.993087732591481 0.859004069457189 1.87605560330006
1.99084893789163 1.51312341376825 A A A 0.58118555471506 2.20365279588714
2.61366554389158 A A P LNCV6_140364_PI430048170 mRNA
CAAATTAAATACTGTGGTTGCCTCTATGTGCTGTTTTTCCTCATACAAGTAAACACAGAA NM_001304284 RefSeq
chr17 + 5116437 5175031 USP6 9098 "ubiquitin specific peptidase 6, transcript variant 1"
GO:0005515|GO:0005516|GO:0016579|GO:0004843|GO:0005886|GO:0032851|GO:0003676|GO:0005764|GO:0004
197|GO:0005737|GO:0061136|GO:0043161|GO:0060627|GO:0055037|GO:0005097|GO:0006464 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128320_PI430048170 0.166858348937838 1.03751948848877 0.412889712121319
0.389018630353213 0.409456110535621 A A A 0.312382182430048 0.338514249407858
0.39976828697231 A A A LNCV6_128320_PI430048170 mRNA
TGAAGGTAAAAGCTGTGCAAAAGGCATGAGACTCAGGCCTACTCTTTGTTTAAATGATGG NM_000921 RefSeq
chr12 + 20369244 20684107 PDE3A 5139 "phosphodiesterase 3A, cGMP-inhibited, transcript
variant 1"
GO:0006629|GO:0043066|GO:0004115|GO:0004119|GO:0042493|GO:0071560|GO:0001556|GO:0019934|GO:0051
591|GO:0046872|GO:0005829|GO:0040020|GO:0030552|GO:0060282|GO:0007596|GO:0019933|GO:0016101|GO:0
016021|GO:0043117|GO:0043116|GO:0071321|GO:0006198 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_144300_PI430048170 0.00547111848780448 0.543729752057573 10.0812418591004
9.73567239379757 10.0249554523062 P P P 10.5978447681466 10.8803306946298
10.9956121811875 P P P LNCV6_144300_PI430048170 mRNA
GGGTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAA NM_014452 RefSeq
chr6 - 47231526 47309947 TNFRSF21 27242 "tumor necrosis factor receptor superfamily,
member 21"
GO:0005515|GO:0050852|GO:0030424|GO:2000666|GO:0001783|GO:2001180|GO:0005886|GO:0042552|GO:2000
663|GO:0031226|GO:0006915|GO:0030889|GO:0044281|GO:0051402|GO:0042130|GO:0002250|GO:0048713|GO:0
005887|GO:0006959|GO:0071356|GO:0097252|GO:0044255|GO:0031642 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141006_PI430048170 0.281903197024267 0.646120365702893 1.77248034757204
3.20359613334523 3.59666817936248 A P P 3.58169283739382 3.91349789347014
3.48900229467914 P P P LNCV6_141006_PI430048170 mRNA
AAAGTCTCTAAGGAAGTATCCTCTTGCTGCTAAACTTGGTACAAGTTGACTACCAAAAAA NM_001099222 RefSeq
chr9 + 26947311 27062933 IFT74 80173 "intraflagellar transport 74, transcript variant 2"
GO:0005813|GO:0006996|GO:0031514|GO:0050680|GO:0048487|GO:0033630|GO:0005634|GO:0072372|GO:0003
334|GO:0005929|GO:0042384|GO:0007219|GO:0045944|GO:0003682|GO:0016023|GO:0030992|GO:0035735 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130433_PI430048170 0.284518796657167 1.07547532369999 0.347425394976367
0.324299839287391 0.545491015001099 A A A 0.306514898278688 0.313665865507949
0.292430356216594 A A A LNCV6_130433_PI430048170 mRNA
TAAACGACACCAGAAATTCACTCACTTTTTACCCAGGCCTGTAGATCCTTCTAAGTTGCC NM_003868 RefSeq

chrX + 77447674 77456522 FGF16 8823 fibroblast growth factor 16
GO:0008286|GO:0048011|GO:0048015|GO:0007267|GO:0005104|GO:0005576|GO:2000546|GO:0005615|GO:0070
349|GO:0009266|GO:0007165|GO:0043405|GO:0007173|GO:0008543|GO:0045087|GO:0001936|GO:0008152|GO:0
009887|GO:0008083|GO:0038095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129350_PI430048170 0.0277504264208595 0.461908885426239 6.29477888533057
6.11114054008317 6.65341641795334 P P P 7.00918305233225 7.44972519538367
7.86982144878989 P P P LNCV6_129350_PI430048170 mRNA
CTTCTCTGTATTAAATAGTCTAGAAGTTAAGGGGATGGTCACATTTACCATGTATTGTGT NM_021255 RefSeq
chr14 + 56118374 56301313 PELI2 57161 pellino E3 ubiquitin protein ligase family member 2
GO:0005515|GO:0038124|GO:0016567|GO:0034142|GO:0038123|GO:0016874|GO:0034134|GO:0002224|GO:0005
829|GO:0008063|GO:0045087|GO:0002755|GO:0001934|GO:0034166|GO:0043410|GO:0043123|GO:0034146|GO:0
034162 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114043_PI430048170 0.0815752381792666 0.774789399426716 8.53382534238662
8.16200026260069 8.13050338132944 P P P 8.67974861519019 8.77084005556802
8.50323403221738 P P P LNCV6_114043_PI430048170 mRNA
TGTCTTCCACTTTGCTAATGACTCCAGAAACATGTGACAGAAGAAGCAGATGTCACCGTG NM_012230 RefSeq
chr7_KI270809v1_alt - 96820 114138 POMZP3 22932 "POM121 and ZP3 fusion, transcript variant 1"
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_70373_PI430048170 0.959938407637723 1.17022668360421 2.6404003580528
1.05678419698934 0.285547260377147 A A A 0.709672068571417 1.79843158761079
1.60096745836311 A A A LNCV6_70373_PI430048170 mRNA
AAGCCATCTGTGCCTGGTTAACATTGAGTTTGAGTCTCTTCAATATATATTGATCATGTA NM_024989 RefSeq chr2
- 196833003 196926730 PGAP1 80055 post-GPI attachment to proteins 1
GO:0006501|GO:0090305|GO:0005783|GO:0007605|GO:0016255|GO:0006886|GO:0015798|GO:0021871|GO:0009
880|GO:0042578|GO:0004518|GO:0009948|GO:0005789|GO:0016021|GO:0044267|GO:0043687 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_55967_PI430048170 0.0020925202878046 0.500152451373582 4.78271023069581
4.757122126063 5.05644422296115 P P P 5.77984649490604 5.74435366635606
6.06793426499919 P P P LNCV6_55967_PI430048170 mRNA
CCAAACACTTAGAGGTAGATGTGTGGGTTATCGAACCACAGGGACTGAGATTTCTTCATG NM_002216 RefSeq
chr10 + 7703272 7749520 ITIH2 3698 inter-alpha-trypsin inhibitor heavy chain 2
GO:0010951|GO:0004866|GO:0004867|GO:0030212|GO:0072562|GO:0005576|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129120_PI430048170 0.0321916217812486 1.38170428230967 10.7764150740424
10.9204786577019 10.5944620857759 P P P 10.3204498903915 10.2528199620403
10.3357963812193 P P P LNCV6_129120_PI430048170 mRNA
GTGAATTGGGCAACTCCTTATAGTGTTGTGCACACAAAAGCATCAAATAAAGAACATTTA NM_001113205 RefSeq
chr1 - 161037631 161038984 TSTD1 100131187 "thiosulfate sulfurtransferase (rhodanese)-like
domain containing 1, transcript variant 3" GO:0005739|GO:0048471|GO:0005737 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_142241_PI430048170 0.376632640588939 1.74090936640166 2.18275140231374
0.66221871859975 0.551097113838851 A A A 0.578316751325082 0.519415258541296
0.518136097633175 A A A LNCV6_142241_PI430048170 mRNA
TTCTCAAAGATGCGTTTGCCTCCTGGAATCAGTATTTCCTTCCACTGTAGCTATTAGCGG NM_005430 RefSeq
chr12 + 48978452 48982613 WNT1 7471 "wingless-type MMTV integration site family, member 1"
GO:0021551|GO:0001658|GO:0044212|GO:0045599|GO:0090263|GO:0005615|GO:0005109|GO:0000578|GO:0021
797|GO:0016055|GO:0030579|GO:0061184|GO:0048018|GO:0045747|GO:0022408|GO:0033077|GO:0042472|GO:0
009986|GO:0005796|GO:0019904|GO:0007520|GO:0005125|GO:0021588|GO . NA - . NA NA NA

NA NA NA NA NA NA
LNCV6_140521_PI430048170 0.847718898293055 0.92804674814418 0.78465054827523
0.354931399521139 0.289158885786813 A A A 0.247590845321236 0.27608457268992
1.10625361091624 A A A LNCV6_140521_PI430048170 mRNA
GCAAAGCTCATTTTTCTATTAGTAACTCTGCTGAAGATCCATTTATTGCAATTCATGCTG NM_004038 RefSeq chr1
+ 103749817 103758689 AMY1A NA "amylase, alpha 1A (salivary), transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138140_PI430048170 0.204970554580339 0.881094253711336 0.47720204919649
0.443054396694542 0.246284720650968 A A A 0.385195768982646 0.634885185249811
0.687254229474586 A A A LNCV6_138140_PI430048170 mRNA
CCTAGCAGAGAACAAATATGTAGTAGTTAGCAGGATCATTTAAAGCAAACGTATCTGGTC NM_001271560 RefSeq
chrX + 140091666 140092911 LOC389895 389895 chromosome 16 open reading frame 72-like
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136012_PI430048170 0.475474150680545 0.790023644401537 0.396744597384748
0.380256783191474 0.408953829509555 A A A 1.28358846236613 0.326803505040794
0.385047924335254 A A A LNCV6_136012_PI430048170 mRNA
CCACCTACATGACAGTCCATCCCTGTTGAATTAATAAATTAATGTATCCATGCAACAAAA NM_001014435 RefSeq
chr16 + 66844937 66854146 CA7 766 "carbonic anhydrase VII, transcript variant 2"
GO:2001225|GO:0032849|GO:0015701|GO:0008270|GO:0044281|GO:0004089|GO:0006730|GO:0032230|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127433_PI430048170 0.1842855981141384.02075830908138 0.9813011583715983.7771712226644
3.30960047711873 A P P 0.3834198951416331.26220962982941 1.41344523813699 A A A
LNCV6_127433_PI430048170 mRNA
AATTAAACCCTAGTGACTTGTGAAATGTGAGTCACGAAAGGTGGCACTTAGAGGGTCCCT NM_001278559 RefSeq
chr7 + 6637321 6658279 ZNF316 NA zinc finger protein 316 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_94130_PI430048170 0.1913408684015370.8475108359506085.38425005205114 5.82110220455418
5.49126751048108 P P P 5.79339652171749 5.88601545934639 5.76726485420738 P P P
LNCV6_94130_PI430048170 mRNA
CTTGTAAATGATGTTCTGAAACACCAAGCTATATTACTAGGAAATGCAGAAGAGCAGAAA NM_018136RefSeq chr1
- 197084126 197146694 ASPM 259266 "asp (abnormal spindle) homolog, microcephaly associated
(Drosophila), transcript variant 1"
GO:0097150|GO:0005516|GO:0021987|GO:0048477|GO:0090263|GO:0005874|GO:0002052|GO:0030496|GO:0005
634|GO:0007283|GO:0045769|GO:0021873|GO:0072687|GO:0005737|GO:0007067|GO:0051661|GO:0048589|GO:0
045665|GO:0090306|GO:0001764|GO:0008584 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66878_PI430048170 0.4130679444991280.9880146404110790.3119617172913970.35048054755665
0.365384128403468A A A 0.3750043890755370.36405689186854 0.341272570416107A A A
LNCV6_66878_PI430048170 mRNA
CCTCCAGAGCCATATGTACAAACGACCAAAAGTTATCCCAGCAAACTGGCAAGAAACGAANM_001077269 RefSeq
chr2 - 174559573 174682899 WIPF1 7456 "WAS/WASL interacting protein family, member 1,
transcript variant 2"
GO:0005515|GO:0030048|GO:0005884|GO:0003779|GO:0015629|GO:0001726|GO:0005829|GO:0006461|GO:0008
154|GO:0045087|GO:0016023|GO:0005522|GO:0038096|GO:0051707 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129819_PI430048170 0.000783917125626802 2.34704601055458 7.94083174853405
7.66007221593361 7.77599143767391 P P P 6.36506182675978 6.69075712527609
6.62236720059306 P P P LNCV6_129819_PI430048170 mRNA
ATGGAAACTTGCAACTGGCATCCGAAAGAAAAACTGTTTTTATCCTGTTGTACAAATACA NM_001258376 RefSeq
chr19 - 16400630 16472012 EPS15L1 58513 "epidermal growth factor receptor pathway substrate

15-like 1, transcript variant 4"
GO:0005515|GO:0005905|GO:0016020|GO:0007173|GO:0005886|GO:0005509|GO:0042059|GO:0005634|GO:0006
897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103645_PI430048170 0.0384897413093884 1.18865742874221 5.21735746356391
5.27610585178645 5.26704682686418 P P P 4.88951637494642 5.07907397948841
5.03780045800263 P P P LNCV6_103645_PI430048170 mRNA
AAATGAAAAGCAGGGAAGGAAGCGTTCATCCACAGGTAGAGATAGCAAATCTTCTCCTCA NM_001303405 RefSeq
chr10 - 100232295 100267681 CWF19L1 55280 "CWF19-like 1, cell cycle control (S. pombe), transcript
variant 3" GO:0008150|GO:0003674|GO:0008152|GO:0005575|GO:0003824 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130599_PI430048170 0.000533394309327679 0.424671317926305 7.85315555573561
7.73239041408272 8.03096447181018 P P P 9.00226300182229 9.04374972651769
9.27744704489819 P P P LNCV6_130599_PI430048170 mRNA
AGGGTGGGTTTTATATTTTGTAGAAGTTTTCGGTCCTATTTTAATGCTCTTTGTATGGCA NM_030920 RefSeq chr1 -
150218416 150236156 ANP32E 81611 "acidic (leucine-rich) nuclear phosphoprotein 32 family, member E,
transcript variant 1" GO:0042393|GO:0043486|GO:0016023|GO:0005634|GO:0019212|GO:0000812|GO:0043086
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141629_PI430048170 0.0162401752846682 0.276032949385332 1.17934299145835
1.12050179855698 0.2931687125396 A A A 2.76318980592015 2.06341993318193
3.25574642358628 P A P LNCV6_141629_PI430048170 mRNA
CTTTCTGGGATAACATGGTGAGCTATATGGTGGTAATCCACACACACAAAAATAAAAGCC NM_002184 RefSeq chr5
- 55935096 55994993 IL6ST 3572 "interleukin 6 signal transducer, transcript variant 1"
GO:0038154|GO:0005515|GO:0005138|GO:0004921|GO:0008284|GO:0005886|GO:0004924|GO:0004923|GO:0019
221|GO:0019981|GO:0005615|GO:0042803|GO:0030425|GO:0070110|GO:0002675|GO:0019838|GO:0042102|GO:0
043025|GO:0070104|GO:0016032|GO:0070102|GO:0004897|GO:0034097|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136608_PI430048170 0.184307902415704 0.590935637781497 1.84185124595589
0.432135767375018 1.54655380991818 A A A 2.56556549470311 1.76816928890439
1.98789728299263 A A A LNCV6_136608_PI430048170 mRNA
AACAGTTTTAAGGAGAAGACTTGAATGAAGTTGGAGGGACATTGAATGATGGTCAGAGGG NM_003803 RefSeq
chr18 - 3066806 3220108 MYOM1 8736 "myomesin 1, transcript variant 1"
GO:0005515|GO:0005863|GO:0006936|GO:0008307|GO:0031430|GO:0042803|GO:0042802 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133501_PI430048170 0.316252865933395 1.36705313038355 2.07359044610328
1.84167522631119 1.22340483793849 A A A 0.588559780502144 1.54060371944437
1.58310495762471 A A A LNCV6_133501_PI430048170 mRNA
ACAAACATTAATTGGAATGGGGGGTAAGGAGGTAGGAATGGCTTACTTGCGGAAATGCAG NM_007199 RefSeq
chr12 + 66189197 66254614 IRAK3 11213 "interleukin-1 receptor-associated kinase 3, transcript
variant 1"
GO:0032715|GO:0034122|GO:0019221|GO:0005634|GO:0042803|GO:0045323|GO:0005737|GO:0051092|GO:0046
777|GO:0001960|GO:0043244|GO:0043407|GO:0002755|GO:0032496|GO:0070555|GO:0070498|GO:0045824|GO:0
000287|GO:0046982|GO:0042177|GO:0032720|GO:0032088|GO:0009615|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139633_PI430048170 0.193452068770411 1.88533657823645 2.59843544050101
1.99994830250145 1.08957622691196 A A A 0.550630811123776 1.50803813388935
1.10681194447619 A A A LNCV6_139633_PI430048170 mRNA
GAGCACAGCAGGACTGAAATTTTGGACGGGAGAGAGGGGCTATTCCATCTTGCTTCCTGG NM_003396 RefSeq
chr17_KI270908v1_alt + 1371016 1396488 WNT9B 7484 "wingless-type MMTV integration site
family, member 9B"

GO:0001658|GO:0071300|GO:0007267|GO:0005615|GO:0048701|GO:0072181|GO:0072038|GO:0005109|GO:0030539|GO:0072174|GO:0030182|GO:0060021|GO:0032526|GO:0016055|GO:0060070|GO:0060071|GO:0009267|GO:0072046|GO:0009786|GO:0072044|GO:0005578|GO:0007275|GO:0005576|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129462_PI430048170 0.0240849949656597 0.4513565218642946.08335043195256 6.01455957103581 5.97748642784336 P P P 6.7853574297062 7.25793684241282 7.40681625824496 P P P LNCV6_129462_PI430048170 mRNA AGGAGATTCCCTGTCCTTGATTTTTGGAGACACAATGGTATAGGGTTGTTTATGAAATAT NM_001955RefSeq chr6 + 12290295 12297194 EDN1 1906 "endothelin 1, transcript variant 1"
GO:0005515|GO:0019722|GO:0005615|GO:0006885|GO:0019229|GO:0007507|GO:0001516|GO:0014032|GO:0015758|GO:0032496|GO:0003100|GO:0031583|GO:0030335|GO:0043179|GO:0010193|GO:0030593|GO:0035994|GO:0044321|GO:0000122|GO:0001701|GO:0005125|GO:0014065|GO:0032269|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130518_PI430048170 0.53811889004718 1.03572972587775 0.54804494764808 0.3723903215616930.339707336445619A A A 0.3764022675199110.384564884100281 0.35589702815538 A A A LNCV6_130518_PI430048170 mRNA GTCAACACCAATAGAGATTGCTTTGTGTATTTTGTAGGGTTCTCTGTTTTGAAGACAGAA NM_003602RefSeq chr7 + 73328231 73358637 FKBP6 8468 "FK506 binding protein 6, 36kDa, transcript variant 1"
GO:0000413|GO:0005515|GO:0000795|GO:0051879|GO:0003755|GO:0005528|GO:0007283|GO:0031047|GO:0030154|GO:0005829|GO:0005737|GO:0007126|GO:0061077|GO:0006457|GO:0034587|GO:0005789|GO:0043046 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145148_PI430048170 0.150085671773682 1.28836989895839 9.9373331848131 9.99517674031585 10.0192620075465 P P P 9.28676408266213 9.87426860728401 9.6357688087258 P P P LNCV6_145148_PI430048170 mRNA GAACTCTTTTTAAACTCTATGCTCCGAGTAGAGTTCATCTTTATATTAAACTTCCCCTGT NM_001360RefSeq chr11 - 71434410 71448431 DHCR7 1717 "7-dehydrocholesterol reductase, transcript variant 1"
GO:0006695|GO:0001568|GO:0005783|GO:0030324|GO:0045540|GO:0047598|GO:0044281|GO:0009791|GO:0030154|GO:0005640|GO:0016020|GO:0035264|GO:0042127|GO:0005789|GO:0016021|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133699_PI430048170 0.00309569475606483 0.67829616494731811.0388453898543 10.9110120381093 10.816355839703 P P P 11.554105314338 11.527346593958 11.3664175710507 P P P LNCV6_133699_PI430048170 mRNA GAGCGGGGGCATGGTAGCAGGGCTGTCTGGTTTTAAATAAAGTTGGAACACTTCAAAAAA NM_022575RefSeq chr20 + 2840696 2866732 VPS16 64601 "vacuolar protein sorting 16 homolog (S. cerevisiae), transcript variant 1"
GO:0030424|GO:0030897|GO:0032889|GO:0005770|GO:0005884|GO:0035542|GO:0003779|GO:0046718|GO:0005765|GO:0005764|GO:0006886|GO:0051015|GO:0016197|GO:0031902|GO:0043025|GO:0055037|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132820_PI430048170 0.0627754721428047 1.31081341022348 8.5733132337326 8.88922472635316 8.5169422151921 P P P 8.36524532876719 8.3674938188159 8.08616170754815 P P P LNCV6_132820_PI430048170 mRNA AAACCATGGACGTGGAGCTGTGGTTTGACAGCGCTGGCTCTGCTTCTCCCCACACACTTA NM_174945RefSeq chr19 + 43533187 43536132 ZNF575 284346 zinc finger protein 575
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142446_PI430048170 0.845701976120916 0.993329062595281 0.474548183609559 0.494562731334166 0.392333361035934 A A A 0.530423879539821 0.424999459724725 0.434639791388782 A A A LNCV6_142446_PI430048170 mRNA TATATAATTTAAACACTGCCTTTTGGTTCCTTGATTCCCATATGCTAGGACAAGTAATTA NM_002262RefSeq chr12

+ 10307817 10317251 KLRD1 3824 "killer cell lectin-like receptor subfamily D, member 1, transcript variant 1"
GO:0043235|GO:0005515|GO:0005886|GO:0045087|GO:0050776|GO:0002228|GO:0030246|GO:0016021|GO:0023024|GO:0009897|GO:0007166|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135653_PI430048170 0.4081442412874451.80554313044228 0.288515355083018
2.09674525709347 0.435310686109608A A A 0.3162691289662230.407446298925906
0.290416677227669A A A LNCV6_135653_PI430048170 mRNA
AAACTTACTAAGAATAACTCAGTCCTTGTAGACTCTAAAGGACAGGGGGAGGGAGAGGGA NM_001171992
RefSeq chr6 + 44000599 44005957 C6orf223 221416 "chromosome 6 open reading frame 223, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136030_PI430048170 0.00377720196978264 0.73980553113694 10.7910905620189
10.7699689416895 10.697102519093 P P P 11.2486756581568 11.0887535729926
11.2217271751032 P P P LNCV6_136030_PI430048170 mRNA
GGGATTGTGTCTTTCCCTGTTGAAAATGTTTGGATGGGAATAAATATCTTCAGGAAACAT NM_005741RefSeq chr16
+ 3283486 3291459 ZNF263 10127 zinc finger protein 263
GO:0006355|GO:0005737|GO:0003700|GO:0015630|GO:0005654|GO:0005634|GO:0045892|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138359_PI430048170 0.0558651881197295 1.51266380115207 5.37081484650466
5.96678805114032 5.62811284042265 P P P 4.9113215142897 5.01114262974383
5.28749310401771 P P P LNCV6_138359_PI430048170 mRNA
CAGCCAAAGGGCTGTTTAAAAACAAAGCCTCCATGTAAACCATTTCTGCAAGAATATTTT NM_198582RefSeq chr2
+ 238138721 238152906 KLHL30 377007 kelch-like family member 30 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136433_PI430048170 0.0967012548799240.3997174655100820.478528534124639
1.95177588989456 2.20279204753973 A A A 3.34100436191517 3.16647411877573
2.47758196494788 P P A LNCV6_136433_PI430048170 mRNA
AAACTAAATTTTATCTCTGTATGGGCAAAGGCTACTGTCATCCTGTTGTTGGTCTGGGGC NM_024813RefSeq chr1
+ 92298964 92388175 RPAP2 79871 RNA polymerase II associated protein 2
GO:0005737|GO:0070940|GO:0009301|GO:0016591|GO:0005730|GO:0005634|GO:0046872|GO:0008420 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139308_PI430048170 0.8793269057177821.07315421132175 1.58470303273177
0.2687016876082171.65398993835493 A A A 1.83076642477993 0.393704307978371
0.984826772485417A A A LNCV6_139308_PI430048170 mRNA
AAGAGGCTGCAATAAGGTGCCATGAAATCAAAATCAAAGGGCTAGAACTCTCCAAGGTCT NM_172005RefSeq chr20
+ 45702015 45708817 WFDC13 164237 WAP four-disulfide core domain 13
GO:0010951|GO:0004867|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124598_PI430048170 0.0327521040173357 0.57465250529995 10.8841992709453
10.735417106704 10.5389770084437 P P P 11.8251400601533 11.49839598753
11.1819300379717 P P P LNCV6_124598_PI430048170 mRNA
GAAGGTCTCCTCTCCCGTTACAAGCAGCAGCGACTGTTGACAGTTCTTCCTTCCCTACTG NM_001105564 RefSeq
chr6_GL000255v2_alt - 2400453 2415821 CCHCR1 54535 "coiled-coil alpha-helical rod protein 1, transcript variant 1" GO:0005737|GO:0005814|GO:0006611|GO:0007275|GO:0005634|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135944_PI430048170 0.00348365844585215 1.17007686055003 0.826895200874453
0.8874394863239190.836177702263546A A A 0.6316644842043240.628544985151208
0.61114829557224 A A A LNCV6_135944_PI430048170 mRNA
GATTTGTAGGGTACTTGGCAGGTTAAATTAAACCAGAAGAGGTGACTTAATAAAAAAGGG NM_006902RefSeq chr1
+ 170664171 170739400 PRRX1 5396 "paired related homeobox 1, transcript variant pmx-1a"
GO:0042472|GO:0051216|GO:0003713|GO:0005730|GO:0002053|GO:0005634|GO:0048844|GO:0000122|GO:0030

326|GO:0048701|GO:0043565|GO:0045880|GO:0071837|GO:0060021|GO:0042474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130702_PI430048170 0.0171547668340230.5908322159071439.21714547382405 9.29521987129017 9.57064106215218 P P P 10.2872624193665 9.82234879337445 10.2321006125212 P P P LNCV6_130702_PI430048170 mRNA
AGAAGCCTCAATGATGATCACTTTGAATTGCTTGTGATTTCAAAAATAAAGCAGTGAAGC NM_006759RefSeq chr2 + 63841879 63891562 UGP2 7360 "UDP-glucose pyrophosphorylase 2, transcript variant 1"
GO:0032557|GO:0005515|GO:0006805|GO:0019255|GO:0052695|GO:0005975|GO:0005978|GO:0003983|GO:0005634|GO:0006065|GO:0044281|GO:0046872|GO:0005536|GO:0005829|GO:0009405|GO:0006006|GO:0006011|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144103_PI430048170 0.50391013190619 1.42725733395581 0.575251168158256 0.432435132828957 1.87573957269397 A A A 0.295699831537135 0.941087776203582 0.4990473217178 A A A LNCV6_144103_PI430048170 mRNA
CATATAAAAGGAATTTGGAGGGTGTCGCTTAAAATTTTATTCCACCTGTACATTTGTCAC NM_018602RefSeq chr15 + 78264144 78282196 DNAJA4 55466 "DnaJ (Hsp40) homolog, subfamily A, member 4, transcript variant 1"
GO:0005515|GO:0090084|GO:0042026|GO:0016020|GO:0009408|GO:0031072|GO:0051087|GO:0051082|GO:0005524|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135139_PI430048170 0.197659996639263 0.750027776483913 5.89583270790089 5.50839685288385 5.91044350238799 P P P 5.82270032514162 6.13445654291079 6.54565889656254 P P P LNCV6_135139_PI430048170 mRNA
CCTAAAATACTTAAATCGGATGTCTTGACTCTGATGTATTTTATCAGGTTGTGTGCATGA NM_002211RefSeq chr10 - 32900317 32958365 ITGB1 3688 "integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12), transcript variant 1A"
GO:0005515|GO:0030056|GO:0031594|GO:0002020|GO:0001948|GO:0001894|GO:0030198|GO:0001618|GO:0007411|GO:0034113|GO:0007179|GO:0035748|GO:0042470|GO:0008305|GO:0030335|GO:0001708|GO:0009986|GO:0019901|GO:0034329|GO:0031589|GO:0019904|GO:0034677|GO:0034678|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137742_PI430048170 0.0176712090065338 2.55905331462452 7.30684701891427 7.25312197712747 7.27979348879635 P P P 5.54340205158035 6.18507684342156 5.9729347292549 P P P LNCV6_137742_PI430048170 mRNA
GTCCGGACAGCCCTGCTCGAAGATATAGAAAGAGTGACCTGCACAAACTTGGAATTTTTT NM_005946RefSeq chr16 + 56638665 56640088 MT1A 4489 metallothionein 1A
GO:0071294|GO:0005515|GO:0048471|GO:0005737|GO:0008270|GO:0005634|GO:0071276|GO:0045926 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90550_PI430048170 0.367984209339557 1.40048376276844 0.48697346002528 0.573148926115499 1.58044444676509 A A A 0.293344977335003 0.357261709863388 0.758728857910485 A A A LNCV6_90550_PI430048170 mRNA
ACCAGCCCAGGATGTACCATCACACAATCCCCGTCATCAGCCTGTACAGCCTGAGAGAGA NM_000030RefSeq chr2 + 240868744 240879119 AGXT 189 alanine-glyoxylate aminotransferase
GO:0005515|GO:0046724|GO:0005782|GO:0005102|GO:0008483|GO:0051384|GO:0044281|GO:0051591|GO:0042803|GO:0008453|GO:0019265|GO:0034641|GO:0005759|GO:0042853|GO:0030170|GO:0046487|GO:0042866|GO:0009436|GO:0004760|GO:0016597|GO:0019448|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142268_PI430048170 0.0777415227592961 1.04136214673829 0.378678633281723 0.369090091466014 0.423905664574295 A A A 0.313842003845426 0.314082294980444 0.368246854898616 A A A LNCV6_142268_PI430048170 mRNA
TTTGAGGGAAAACAATCTTAAGAAAAATAGGATTAAGCTATTCTGTTCCAGTCCTCAGAG NM_145178RefSeq chr10 - 68230594 68232113 ATOH7 220202 atonal homolog 7 (Drosophila)

GO:0021554|GO:0006355|GO:0003407|GO:0009649|GO:0046983|GO:0007623|GO:0005634|GO:0003677|GO:0030
154|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133025_PI430048170 0.0174794747453648 1.27584758968632 14.2322701388763
14.3707803644775 14.4317719139703 P P P 13.909242137005 13.9434310182657
14.1254710522831 P P P LNCV6_133025_PI430048170 mRNA
CAGACCTGGTTGATTTTGTACTTTGGAACTGTACCTTGGATGGTTTTGTTTATTAAAAGA NM_002793 RefSeq chr6
- 170535115 170553329 PSMB1 5689 "proteasome (prosome, macropain) subunit, beta type, 1"
GO:0005515|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0004
298|GO:0034641|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0005839|GO:0
000502|GO:0043066|GO:0006521|GO:0042590|GO:0051437|GO:0006915|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145443_PI430048170 0.0144430711400950.6517454607362627.89364787768285 7.6659463867715
7.98502569658085 P P P 8.27093736784138 8.4617193990162 8.65738925751972 P P P
LNCV6_145443_PI430048170 mRNA
GAGTAAATGGTGGAGGATGGGAGTCAAAATCAGAATTATAGAAGAAGTATTTCCTGTAAC NM_018060 RefSeq chr1
+ 220094112 220148041 IARS2 55699 "isoleucyl-tRNA synthetase 2, mitochondrial"
GO:0005739|GO:0010467|GO:0005737|GO:0002161|GO:0032543|GO:0005759|GO:0006450|GO:0006428|GO:0005
524|GO:0004822|GO:0006418|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129133_PI430048170 0.2272414348895081.90316293558489 1.02414246412726 0.4166989777207
1.98053560829697 A A A 0.3303945028592970.3437006904593220.397523703538382 A A A
LNCV6_129133_PI430048170 mRNA
AACAGAGACATGAAGGAGGCTTTGGGTAAACTTTTTGTCAGTGGAAAAACATTCTTTTTA NM_001004457 RefSeq
chr9 + 122553169 122554162 OR1N2 138882 "olfactory receptor, family 1, subfamily N, member 2"
GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105726_PI430048170 0.2472072441836280.6403325531845030.6558744628056
0.7285013353973210.824009212198325 A A A 0.600269436293701 1.69068974024848
1.61763505674547 A A A LNCV6_105726_PI430048170 mRNA
TGTAAAAGTGTGGTTGAGTGTAAACAGCACAAAGGAGATTATAGTGGACTTAACCAATGT NM_015852 RefSeq chr7
- 64974451 64991036 ZNF117 51351 zinc finger protein 117
GO:0006355|GO:0003700|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133705_PI430048170 0.7130533006727280.7350490045621341.61541182414794
1.30675909541677 1.79106694017376 A A A 1.32195213960434 1.20050948006238
2.89605066382872 A A P LNCV6_133705_PI430048170 mRNA
CTGTCAGTGGTTTCCTCATTTTGCCATGCTTTGTAAAAATAAAAAGAATGATCAAGTAGG NM_001083 RefSeq chr4
- 119494394 119628826 PDE5A 8654 "phosphodiesterase 5A, cGMP-specific, transcript variant 1"
GO:0004114|GO:0047555|GO:0046069|GO:0005575|GO:0046872|GO:0005829|GO:0042130|GO:0007165|GO:0030
553|GO:0060282|GO:0007596|GO:0043406|GO:0055119|GO:0055118|GO:0010613|GO:0030823 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145034_PI430048170 0.4723863419278870.8319742447116510.525983984048699
2.23394032523093 1.16922785102399 A A A 1.64915747918789 1.8344668361919
1.75922025995414 A A A LNCV6_145034_PI430048170 mRNA
GACCCTTGAACCCCCTTACCTAACGTAACTAATAAAATGAAGCTGAGAGCTTTGGAATCC NM_133489 RefSeq chr12
+ 57619909 57626151 SLC26A10 65012 "solute carrier family 26, member 10"
GO:0015297|GO:0008271|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129369_PI430048170 0.00304143141251947 0.7674108077913549.56810581774196
9.44524206451762 9.45424702111348 P P P 9.93768120925192 9.78851810306282
9.88650145005793 P P P LNCV6_129369_PI430048170 mRNA

TCATTCTTCAGGATTGCCCTACTGGCTCTACCTCACAGCTGAAACTTTAAAAAACAGGAT NM_001287251 RefSeq
chr16 + 28752434 28772823 NPIPB9 100507607 "nuclear pore complex interacting protein family,
member B9, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129652_PI430048170 0.333336411545904 1.04054842194074 0.473056419154592
0.329258911390839 0.401369425471852 A A A 0.291747231044257 0.348414718437716
0.393280912865306 A A A LNCV6_129652_PI430048170 mRNA
GGAGATGGCATTTTCTTCTGGGCTTCAGCATGATGTTCAATAAAAGTTTTGCCATTTCAA NM_138289 RefSeq chrX
- 128050961 128052403 ACTRT1 139741 actin-related protein T1 GO:0005737|GO:0005856 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139172_PI430048170 0.314483343684192 1.33576807211807 0.554602439549921 1.3892876985296
0.582219736402994 A A A 0.472331102738118 0.543022166156389 0.419053057445355 A A A
LNCV6_139172_PI430048170 mRNA
ATCGTGACGGCCTACGGCATTGGCATCGAGTCGGCACACTCCTACAGCTTCCTGACGGAG NM_001101401 RefSeq
chr19 - 55529732 55536294 SBK2 646643 "SH3 domain binding kinase family, member 2"
GO:0035556|GO:0023014|GO:0000187|GO:0005737|GO:0004702|GO:0000165|GO:0006468|GO:0005524|GO:0004
708 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135316_PI430048170 0.0108323767850622 0.560498158971912 6.14401206304139
6.08697638007112 6.37879467236707 P P P 6.98634192772294 6.81753619864141
7.28846561593963 P P P LNCV6_135316_PI430048170 mRNA
GGTAAATGAGAAGAGCATTGTGGACATTATTGGCTGTCCCCAATAAAATGCTGTTCATTA NM_031243 RefSeq chr7
- 26189935 26200793 HNRNPA2B1 3181 "heterogeneous nuclear ribonucleoprotein A2/B1,
transcript variant B1"
GO:0005515|GO:0006397|GO:0008380|GO:0010467|GO:0048025|GO:0003723|GO:0050658|GO:0005634|GO:0000
122|GO:0071013|GO:0005737|GO:0000166|GO:0016020|GO:0000398|GO:0030529|GO:0005654|GO:0005681|GO:0
097157|GO:0043047. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145341_PI430048170 0.0441989197983294 0.734324264773408 7.84637369234713
7.56153362479023 7.627356591711 P P P 7.99121182701652 8.3553063831986
8.01114356177173 P P P LNCV6_145341_PI430048170 mRNA
TAAAAAGGGCTCAAAGGATAAGGAGGCCATTCAGGCCTATTCTGAATCCCTGATGACATC NM_005505 RefSeq chr12
- 124777627 124863973 SCARB1 949 "scavenger receptor class B, member 1, transcript variant 1"
GO:0005515|GO:0005215|GO:0006707|GO:0006702|GO:0010899|GO:0031528|GO:0005765|GO:0042803|GO:0015
914|GO:0032497|GO:0031663|GO:0070062|GO:0042632|GO:0033344|GO:0009986|GO:0043691|GO:0030169|GO:0
006898|GO:0010595|GO:0070506|GO:0070508|GO:0043534|GO:0005887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128897_PI430048170 0.47099387423002 0.97821187436089 0.268915391394693
0.28899783321968 0.381051950458819 A A A 0.382913628711825 0.334531797864066
0.318577674373941 A A A LNCV6_128897_PI430048170 mRNA
CCCAGATGAATTGAAGTGTATTGCTGTGTCTTGTAATACCTTGCTTTAACTAGCTTTTTANM_032250 RefSeq chr9 +
67859314 67902394 ANKRD20A1 NA "ankyrin repeat domain 20 family, member A1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141898_PI430048170 0.0181015509613109 0.580002626487146 5.26094166971039
4.72510099804731 5.06980511850434 P P P 5.75517320763944 5.67416613340884
6.01225403662967 P P P LNCV6_141898_PI430048170 mRNA
AGAATGCCAGTACGAGAGTGTAGCCAAAGTGAGAGGCTGAGAGCAAAGGAGACATTTTTT NM_003799 RefSeq
chr18 + 13726659 13764556 RNMT 8731 RNA (guanine-7-) methyltransferase
GO:0043235|GO:0005515|GO:0010467|GO:0006366|GO:0003723|GO:0004482|GO:0005730|GO:0016032|GO:0006
370|GO:0005654|GO:0005634|GO:0005845 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140225_PI430048170 0.508881552151833 0.900831566761639 0.363448933895125
0.356898360284104 0.265159492655639 A A A 0.29674851116733 0.789738570272425

0.294791014840498 A A A LNCV6_140225_PI430048170 mRNA
CCTCCTGACATGAGTCTGCTGGAAAGAGCATCCAAACAAACAAGTAATAAATAAATAAAT NM_207373 RefSeq chr10
+ 84173797 84185294 C10orf99 NA chromosome 10 open reading frame 99 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_130727_PI430048170 0.743600199842896 1.30820267174674 1.52300367142983 3.472470225065
2.96946832115123 A P P 2.83896201667066 2.54293655540208 1.88207733679956 P P A
LNCV6_130727_PI430048170 mRNA
TGGAACCAAAAATCACTGTCACTTTACAACTTAGGTTTTACTCTTTTCTTTCTACAGACCNM_000272 RefSeq chr2 -
110123335 110205062 NPHP1 4867 "nephronophthisis 1 (juvenile), transcript variant 1"
GO:0005515|GO:0007588|GO:0030036|GO:0006996|GO:0060041|GO:0031514|GO:0007632|GO:0048515|GO:0005
829|GO:0035845|GO:0007165|GO:0016337|GO:0005912|GO:0016020|GO:0005198|GO:0005911|GO:0035869|GO:0
030030|GO:0032391|GO:0034613|GO:0005923|GO:0005856 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_130556_PI430048170 0.138242096495955 0.587255506880044 9.2854296930014
9.16806612581127 9.59265106545721 P P P 9.59007509238512 9.93427248361853
10.6508779232893 P P P LNCV6_130556_PI430048170 mRNA
GGACATCTTTTCTGTAAACTTCTTCCCCTAGTTCCATCCTCACTAGTAAAAAATAAATAC NM_015135 RefSeq chr7
+ 135557913 135648751 NUP20523165 nucleoporin 205kDa
GO:0007077|GO:0005515|GO:0010467|GO:0000059|GO:0019221|GO:0019058|GO:0005635|GO:0044281|GO:0051
292|GO:0008645|GO:0005737|GO:0015758|GO:0005643|GO:0016032|GO:0017056|GO:0031965|GO:0005975|GO:0
019083|GO:0055085|GO:0010827|GO:0006913|GO:0016020|GO:0034399|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143230_PI430048170 0.279942550348452 1.29253722619998 6.9498697332579 6.8724986786158
6.90739817466298 P P P 7.06126065156586 6.25995741622752 6.10823954864871 P P P
LNCV6_143230_PI430048170 mRNA
GTGAATCTAGATGTTCTGACCTAAAGATGTAGTCTACATAGCCCCAGCTTGGGGTCCAAT NM_001282406 RefSeq
chr11 - 78015714 78046191 KCTD14 65987 "potassium channel tetramerization domain containing 14,
transcript variant 2" GO:0051260 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116528_PI430048170 0.23824410883011 1.39589548955305 0.384354527817154
1.30282340637712 0.805498284673166 A A A 0.535070040450554 0.323333758617257
0.326903325182952 A A A LNCV6_116528_PI430048170 mRNA
AGCCTCTGGCTTCACGAGACCCCAACCTTCAGTTGGAACAGCTTGGAACAGCGCGAGCGC NM_030792 RefSeq chr11
- 75434639 75525554 GDPD5 81544 glycerophosphodiester phosphodiesterase domain containing 5
GO:0006629|GO:0045746|GO:0048505|GO:0048471|GO:0021522|GO:0006071|GO:0031175|GO:0012505|GO:0030
426|GO:0045666|GO:0016021|GO:0008889|GO:0021895 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141290_PI430048170 0.414071198549617 0.556911472095625 2.94040717962109
2.79612574169789 3.24033534621949 A A P 3.42626705853885 4.70622367323547
2.67127068628229 P P P LNCV6_141290_PI430048170 mRNA
TGAGGCCGGTCCACAGGGTCCCAACCCCTTGTCTTCAAATAAAGTATAATGTAACATAAA NM_152784 RefSeq chr19
+ 5720676 5778731 CATSPERD 257062 catsper channel auxiliary subunit delta
GO:0007338|GO:0035036|GO:0005886|GO:0036128|GO:0097228|GO:0007275|GO:0030317|GO:0007283|GO:0048
240|GO:0032504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128031_PI430048170 0.466091924252114 0.756016336230045 1.21547317782491
0.392534864044206 0.272207292680857 A A A 1.61995555285654 1.03186425470437
0.364003833050631 A A A LNCV6_128031_PI430048170 mRNA
AATCTTATCCTGAGGGCCAAAGGCCAAGGCTGCAGGAATTGGGAGACAAGGGTCTGTTTG NM_000751 RefSeq chr2
+ 232526159 232536665 CHRND 1144 "cholinergic receptor, nicotinic, delta (muscle), transcript variant 1"
GO:0048630|GO:0030054|GO:0005886|GO:0007268|GO:0005892|GO:0050905|GO:0007165|GO:0006936|GO:0050
881|GO:0003009|GO:0045211|GO:0042391|GO:0006810|GO:0042166|GO:0004889 . NA - . NA NA NA

NA NA NA NA NA NA
LNCV6_144041_PI430048170 0.0131607914546558 0.5734136119169443.2331900827099
3.39548964793065 3.39286336809031 P P P 4.16573604533632 3.90371782899365
4.33301052180895 P P P LNCV6_144041_PI430048170 mRNA
GTGGTTGCCTGGAGTATATGCCTTTTTGTATCCTTTGAATTTCCAGCCATGTAAATGTAT NM_014844RefSeq chr14
+ 102362962 102502481 TECPR2 9895 "tectonin beta-propeller repeat containing 2, transcript variant 1"
GO:0005515|GO:0006914 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81532_PI430048170 0.85595934035003 0.9622569067512790.2690275392893410.486203097370056
0.754965156251047 A A A 0.9099869488744380.3076018324896160.427673032192393 A A A
LNCV6_81532_PI430048170 mRNA
TTGACAGCCAAGCACAGTATCCAGTTGTCAACACAAATTATGGCAAAATCCGGGGCCTAA NM_001282145 RefSeq
chrX - 5890025 6228882 NLGN4X 57502 "neuroligin 4, X-linked, transcript variant 3"
GO:0052689|GO:0005515|GO:0031404|GO:0030054|GO:0005886|GO:0045202|GO:0005615|GO:0030425|GO:0042
803|GO:0035265|GO:0030182|GO:0045211|GO:0004872|GO:0030534|GO:0007612|GO:0050839|GO:0007158|GO:0
009986|GO:0003360|GO:0050804|GO:0014069|GO:0021549|GO:0071625|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_118781_PI430048170 0.0355760643500627 1.21958259335157 5.18079075495986
5.23400728307468 5.05282450712709 P P P 4.81141939468713 5.0093955479585
4.78290152382462 P P P LNCV6_118781_PI430048170 mRNA
TGAAGAAACAGGAGAGTGAAGTGGAAATAGCCTGGCCCGCGTGACTTAAACCGGCCCGGA NM_001242339
RefSeq chr10 + 3068626 3136805 PFKP 5214 "phosphofructokinase, platelet, transcript variant 2"
GO:0005975|GO:0005634|GO:0044281|GO:0005524|GO:0032403|GO:0046872|GO:0006096|GO:0005829|GO:0016
020|GO:0009405|GO:0006006|GO:0046835|GO:0006002|GO:0070062|GO:0003872 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139388_PI430048170 0.0956406678463902 1.29724912649683 9.37941360363694
9.68396599884517 9.24454246610174 P P P 9.22644848048814 9.10946064150808
8.85702992287416 P P P LNCV6_139388_PI430048170 mRNA
GTTGTTTGAATAAACGTGAACGTGAACCCAGGCGGAAGGGACCCGGGAACTCTGAAAAAA NM_032789RefSeq
chr8 - 143977151 143986467 PARP10 84875 "poly (ADP-ribose) polymerase family, member 10"
GO:0005515|GO:0005794|GO:0010847|GO:0048147|GO:0005730|GO:0005634|GO:0032088|GO:0003950|GO:0070
213|GO:0006471|GO:0070212|GO:0005737|GO:0010629|GO:0033159|GO:0005654|GO:1900045|GO:0070530|GO:0
045071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130133_PI430048170 0.8964140605434280.99595841310476 0.265422032932944
0.2842461101755880.415092140318759 A A A 0.3625463815882030.314685303040158
0.309108553498549 A A A LNCV6_130133_PI430048170 mRNA
ATCTTGGGGTCAAAGTTCAAGTGACCATTAACCCAGGCACACAAACTGCAGTCTCAGAAT NM_001115152 RefSeq
chr17 - 74579971 74592231 CD300LD 100131439 CD300 molecule-like family member d
GO:0005515|GO:0005886|GO:0016021|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91649_PI430048170 0.7509864116194720.8538870895938010.2616589220786241.06924823165751
1.62473173587895 A A A 1.81308394671092 0.3134610304930051.44165619249052 A A A
LNCV6_91649_PI430048170 mRNA
AATCTCCAAGCCAGGCTGGTTCTCTGCATCCTTTCAATGACCTGTTTTCTTCTGTAACCA NM_000742RefSeq chr8
- 27459760 27479296 CHRNA2 1135 "cholinergic receptor, nicotinic, alpha 2 (neuronal), transcript
variant 1"
GO:0030054|GO:0005886|GO:0007268|GO:0051291|GO:0005892|GO:0007165|GO:0008144|GO:0015464|GO:0045
211|GO:0042166|GO:0016021|GO:0004889|GO:0006812|GO:0006811 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129584_PI430048170 0.4481082010046420.6986128442940683.16136066661653
2.27868505284356 2.80459797858761 P A A 2.88432176058074 4.01687304968602

2.62784847320306 P P P LNCV6_129584_PI430048170 mRNA
GGGAAAGGAAAGACCTGTGATGATTCAATAAATTTTTACATAGCACCCATCCCCAAAAAA NM_001145641 RefSeq
chr19 + 43612100 43614498 SRRM5 NA serine/arginine repetitive matrix 5 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_61060_PI430048170 0.0895813123935404 0.7442095115386575.18528294169616
5.16828581020105 5.33869437484187 P P P 5.38479192210494 5.66374945467677
5.88534483754061 P P P LNCV6_61060_PI430048170 mRNA
GTACCTGGGTGCCTATATCGACAAAGAGTGAGAAGAGCATTTTTACTTTTTTAAAAAAGC NM_018373 RefSeq chr14
- 70366495 70417090 SYNJ2BP 55333 synaptojanin 2 binding protein
GO:0005739|GO:0070699|GO:0048312|GO:0009986|GO:2000010|GO:0032926|GO:0032927|GO:0031307|GO:0008
022|GO:0002092 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_9356_PI430048170 0.3561373981889490.9003891045894796.43238360585778 6.63699645928727
6.85140187847919 P P P 6.62918958324184 6.90873012089103 6.85252143632337 P P P
LNCV6_9356_PI430048170 mRNA
TCCCAGGACTATTTTATCTTAAACTTAGCAGAGAGGATTTTCTGTCATGGAAAAAGCTTG NM_001172702 RefSeq
chr14 + 60981113 61083733 SLC38A6 145389 "solute carrier family 38, member 6, transcript variant 1"
GO:0015171|GO:0005887|GO:0006814|GO:0003333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143535_PI430048170 0.0078955108324172 0.3638623600208214.19019381520047
4.32152781171292 4.23434994613644 P P P 5.49749532950069 5.58475364547828
5.99274105524997 P P P LNCV6_143535_PI430048170 mRNA
GCTTCTACTTTAGATGATCCAATAATGATTAAAGAATACCTGTACCTGCAGATTCCAGTT NM_025137 RefSeq chr15
- 44562695 44663678 SPG11 80208 "spastic paraplegia 11 (autosomal recessive), transcript variant 1"
GO:0005515|GO:0005737|GO:0005886|GO:0005730|GO:0031410|GO:0016021|GO:0005765|GO:0070062|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133314_PI430048170 0.0309846903471469 2.03376983974034 6.85189247106577
6.92766127779772 6.94926175611615 P P P 6.15414016997377 5.93914330373208
5.48688928330243 P P P LNCV6_133314_PI430048170 mRNA
ATGTTATTGGAGCTATTTTGTAAGGTCCCACATTTGACCAAGGAGTGCCTGGTAGCGTTG NM_183239 RefSeq chr10
+ 104268872 104299418 GSTO2 119391 "glutathione S-transferase omega 2, transcript variant 1"
GO:0006805|GO:0006767|GO:0044281|GO:0004364|GO:0045174|GO:0005829|GO:0019852|GO:0050610|GO:0006
766|GO:0016491|GO:0071243|GO:0055114|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135701_PI430048170 0.2670936505599010.7786814199991180.292460463545596
0.2787050424213910.423067871350166A A A 0.2945591533813330.640127761003611
1.04795408375327 A A A LNCV6_135701_PI430048170 mRNA
TTACTGAGGGTCAGGTTTCACAGTGTCATGGGGTTTGGGCATTTAAGAATGGCAAACACT NM_001178089 RefSeq
chr5 + 178941192 178966217 ZNF454 285676 "zinc finger protein 454, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140533_PI430048170 0.0130423689589113 0.3907130288730731 1.2370286662262
11.3347926439784 11.4570944835488 P P P 12.3385123946731 12.6894912580734 13.001280750702
P P P LNCV6_140533_PI430048170 mRNA
CTGGGGGAGGTATATGATGAGCAGACTTCTCGGAATTCATAATAAATTTTCTAAAAGCCT NM_001233 RefSeq chr7
+ 116499600 116508541 CAV2 858 "caveolin 2, transcript variant 1"
GO:0005515|GO:0008286|GO:0030133|GO:0048471|GO:0005886|GO:0005634|GO:0051259|GO:0006906|GO:0042
803|GO:0070836|GO:0005622|GO:0016050|GO:0031748|GO:0060161|GO:0002080|GO:0048278|GO:0030512|GO:0
007088|GO:0005794|GO:0048741|GO:0031410|GO:0031234|GO:0043547|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141785_PI430048170 0.0662679061236225 0.6718037054517767.91694681712988
7.75750335357129 7.3653867823534 P P P 8.08651036585781 8.57287110421054

8.10163300659515 P P P LNCV6_141785_PI430048170 mRNA
AGATGCCTCAGTGTGGCCCAAATGTGGCTTGTGTGATAGCTGCAGGTTCTGCCATAACCG NM_033257 RefSeq chr22
- 20314237 20320105 DGCR6L 85359 DiGeorge syndrome critical region gene 6-like
GO:0005515|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65000_PI430048170 0.91058702311217 1.00383252480601 4.53410975787454 4.45828564189414
4.32188361110447 P P P 4.5727489280691 4.60441831178932 4.06853510382542 P P P
LNCV6_65000_PI430048170 mRNA
GCGAAGACGCCAGGTTCAGCATGGGAAAATGGGACTGTGGAAATAAAGTATATGTGTGGA NM_144577 RefSeq
chr19 - 48296451 48320075 CCDC114 93233 coiled-coil domain containing 114
GO:0005515|GO:0005929|GO:0036157|GO:0036158 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58696_PI430048170 0.3527962612444190.8809716207493740.35665307809039 0.475248603977163
0.366106102744811 A A A 0.4922302423191620.3719284797285880.842976016770865 A A A
LNCV6_58696_PI430048170 mRNA
AGTGAAATGTCAGCCAGGAAGAATCTCTCTTCCTAATATCAGAAAGCCAGAAGGACGACG NM_002723 RefSeq
chr12_KI270904v1_alt - 502043 505398 PRB4 5545 "proline-rich protein BstNI subfamily 4, transcript
variant 1" GO:0008150|GO:0003674|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145669_PI430048170 0.2868042471724860.6608734991463280.74618963399364
0.6176305905045870.571920595531836 A A A 1.44023129036479 0.447312584087281
1.60024659660856 A A A LNCV6_145669_PI430048170 mRNA
CCCCGAGGAGCTGTAGGGAGATTGGTTTTTAGTATAAATTACAATAAAATTTTGTGTATG NM_176819 RefSeq chrX
- 45148372 45200901 CXorf3679742 "chromosome X open reading frame 36, transcript variant 1"
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136256_PI430048170 0.00270787853681741 0.61550603779016 12.6748994994753
12.5831956205889 12.8211820699785 P P P 13.3354337167802 13.4639403099605
13.3875072276162 P P P LNCV6_136256_PI430048170 mRNA
AAATCTGATGGGATTAAGGGCCTGTACCAAGGCTTTAACGTGTCTGTGCAGGGTATTATC NM_001152 RefSeq chrX
+ 119468399 119471396 SLC25A5 292 "solute carrier family 25 (mitochondrial carrier; adenine nucleotide
translocator), member 5"
GO:0042645|GO:0005515|GO:0008284|GO:0005743|GO:0005634|GO:0044281|GO:0055085|GO:0005739|GO:0006
112|GO:0007059|GO:0050796|GO:0016020|GO:0005887|GO:0006810|GO:0015207|GO:0016032|GO:0015853|GO:0
071817|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141173_PI430048170 0.6279878240714761.14765278144254 1.14365724644554
0.4010227539440530.305298808814583 A A A 0.6844993498008840.3550564011894
0.340537108281455 A A A LNCV6_141173_PI430048170 mRNA
AACTGCGAGTACATCAAAGACAAGAAGTGCAAGTCTGGGCCTTGCCATCTGGATAATTCA NM_004314 RefSeq chr11
+ 3645130 3664416 ART1 417 ADP-ribosyltransferase 1
GO:0006471|GO:0009986|GO:0005886|GO:0005887|GO:0045087|GO:0003956|GO:0033017|GO:0031225|GO:0003
950 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108386_PI430048170 0.5801528206631631.05020260615147 5.89696618255921 5.9949211246612
5.91896418265214 P P P 5.68056356705886 5.79870568073048 6.090108537177 P P P
LNCV6_108386_PI430048170 mRNA
TGTATGCAAGGATGACTTGGTTACAGTCAAAACCCCAGCGTTTGCAGAATCTGTCACAGA NM_001933 RefSeq chr14
+ 74881890 74903747 DLST 1743 "dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-
glutarate complex), transcript variant 1"
GO:0004149|GO:0006099|GO:0033512|GO:0005634|GO:0006091|GO:0044281|GO:0034641|GO:0016020|GO:0005
759|GO:0006554|GO:0045252|GO:0044237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127158_PI430048170 0.0259696453640921 1.37831400468567 9.40945942716616
9.35198451730482 9.65921637688937 P P P 8.87612777569392 8.96073998980586
9.19474278028082 P P P LNCV6_127158_PI430048170 mRNA

TTTTCAGGACACAGACATATGATGTGAATGCCTACAAAGCCAGTGCGCATAGGAACAGTG NM_001003800 RefSeq chr9 - 92711362 92764801 BICD2 23299 "bicaudal D homolog 2 (Drosophila), transcript variant 1" GO:0005515|GO:0017137|GO:0005737|GO:0005794|GO:0005886|GO:0072385|GO:0031410|GO:0005856|GO:0072393 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_69268_PI430048170 0.0273252040118965 1.62578944817281 4.36217786015126 3.87105293878157 4.19334110429957 P P P 3.48022287046541 3.53971735172501 3.33816939488665 P P P LNCV6_69268_PI430048170 mRNA
TTCCTACGTTGGGCTGGTGTACATGTTTAACCTCATCGTGGGCACGGGCGCACTCACCAT NM_017728 RefSeq chr17 + 74776482 74839783 TMEM104 54868 transmembrane protein 104 GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127013_PI430048170 0.216331608464076 0.920540930104893 10.8117715071849 10.8778794451584 11.0471526611853 P P P 11.0330234977445 10.9956121811875 11.0757138970283 P P P LNCV6_127013_PI430048170 mRNA
CTGTGGTCTTCAAATTGTCTTTTGTCATGTGGCTAAATGCCTAATAAACAATTCAAGTGA NM_001082971 RefSeq chr7 - 50458435 50565457 DDC 1644 "dopa decarboxylase (aromatic L-amino acid decarboxylase), transcript variant 1" GO:0005515|GO:0030424|GO:0046684|GO:0010259|GO:0044281|GO:0005829|GO:0042416|GO:0034641|GO:0043025|GO:0070062|GO:0006520|GO:0033076|GO:0019904|GO:0071312|GO:0035690|GO:0008021|GO:0042427|GO:0071363|GO:0046219|GO:0052314|GO:0030170|GO:0004058|GO:0007623|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130733_PI430048170 0.0272529362385153 0.401967119160987 2.99305974963055 2.07306676242507 2.63268227160453 A A A 4.00989727551774 4.0135393801427 3.74869826349768 P P P LNCV6_130733_PI430048170 mRNA
AGAGTTCTCAGGAGGTGATGACCCTTTAATTTACTGGCAGAGGAAGATAAGCATATGGCC NM_001174108 RefSeq chr1 + 203797522 203800462 ZBED6 NA "zinc finger, BED-type containing 6" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137620_PI430048170 0.00668486195385573 0.509162013288613 5.18263430255208 4.78300240108152 5.15413976481634 P P P 5.93044979476694 6.14937352826652 5.98566956211503 P P P LNCV6_137620_PI430048170 mRNA
GCTATGAGGGTAACACCTGTTCTGCTTTTCATCTTGTATTTAGTTGACTGTATTATTTGA NM_001272044 RefSeq chr17 + 59893045 59950425 RPS6KB1 6198 "ribosomal protein S6 kinase, 70kDa, polypeptide 1, transcript variant 4" GO:0005515|GO:0030054|GO:0009408|GO:0045202|GO:0007281|GO:0046324|GO:0014878|GO:0032496|GO:0031929|GO:0007616|GO:0009986|GO:0007568|GO:0009636|GO:0051384|GO:0045931|GO:0048633|GO:0043491|GO:0005654|GO:0008286|GO:2001237|GO:0043005|GO:0048471|GO:0045471|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140760_PI430048170 0.135364451618467 0.944707194638636 0.243717332460313 0.288854811182729 0.306390995341032 A A A 0.431021154167359 0.337727083931275 0.314464631853609 A A A LNCV6_140760_PI430048170 mRNA
GTTGCCTTGCATTTGTGGTAATCTACACCAATGAAAACATGTACTACAGCTATATTTGAT NM_016192 RefSeq chr2 - 191949045 192194933 TMEFF2 23671 transmembrane protein with EGF-like and two follistatin-like domains 2 GO:0003674|GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135516_PI430048170 0.804333676136669 0.93768569290519 0.354119706231682 0.356508589370464 1.13399153629766 A A A 1.18049045524425 0.304397412932328 0.648570209102354 A A A LNCV6_135516_PI430048170 mRNA
TACCTCTACCTTCAAATAAAGATAGACCTGACAATTTGTGATATCTAATAATAACCCCCC NM_001129889 RefSeq chr13 - 94439585 94479682 DCT 1638 "dopachrome tautomerase, transcript variant 2" GO:0033162|GO:0042470|GO:0021847|GO:0005507|GO:0002052|GO:0005829|GO:0004167|GO:0006583|GO:0008544|GO:0016491|GO:0016021|GO:0048468|GO:0055114|GO:0048066 . NA - . NA NA NA NA NA NA

NA NA NA
LNCV6_145716_PI430048170 0.3637857282769671.36987351776765 0.309282687588169
1.28218356673022 0.314266137191808A A A 0.2648122931524090.243677386999705
0.265555775463722A A A LNCV6_145716_PI430048170 mRNA
CTTTGTATATATACTTATATCACGTAGGATGTAAAACCAGTATGACCTTGTCTAGTCTCC NM_005711RefSeq chr5
- 83940594 84384867 EDIL3 10085 "EGF-like repeats and discoidin I-like domains 3, transcript variant 1"
GO:0005178|GO:0010811|GO:0005509|GO:0007275|GO:0007155|GO:0031982|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143181_PI430048170 0.000149869418835896 2.18171891217413 6.2099063462408
6.15800966485624 6.33520322396917 P P P 5.17859852783249 5.15484551156082
4.99201887140169 P P P LNCV6_143181_PI430048170 mRNA
GAGTTGCTCCTTTGTTCCAAAATTAAATGTGTTAGATAAATTTGTGATTGTATGGGTGGC NM_002857RefSeq chr1
- 160276808 160285151 PEX19 5824 "peroxisomal biogenesis factor 19, transcript variant 1"
GO:0005515|GO:0006625|GO:0072663|GO:0005634|GO:0045046|GO:0031526|GO:0005829|GO:0043231|GO:0005
737|GO:0007031|GO:0051117|GO:0072321|GO:0016557|GO:0005778|GO:0016559|GO:0005777|GO:0050821|GO:0
055085|GO:0036105|GO:0043234|GO:1900131|GO:0047485|GO:0061077|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140567_PI430048170 0.457765728501236 1.02059439591371 0.381239066409532
0.2727578902972130.32105059254761 A A A 0.2853575710756260.295316877615241
0.308104072899118A A A LNCV6_140567_PI430048170 mRNA
TAGGATGCTTCCATCCTGGTCCCATGTATCTGGAATCTAATAAATAAGGAAAGGAAAAAA NM_004452RefSeq chr14
+ 76371346 76501837 ESRRB 2103 estrogen-related receptor beta
GO:0010467|GO:0001831|GO:0006355|GO:0006367|GO:0001834|GO:0003713|GO:0003707|GO:0001892|GO:0005
634|GO:0043565|GO:0045944|GO:0019827|GO:0043401|GO:0008270|GO:0000980|GO:0005654|GO:0004879|GO:0
030522|GO:0005496|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126778_PI430048170 0.0211022893946287 0.4312045349829665.95099851806211
6.30193690795928 6.39968873587561 P P P 6.9259474323501 7.59442874296474
7.69613365090395 P P P LNCV6_126778_PI430048170 mRNA
CCAAAAATGCTTGTTATATAAAGGGTACTTTTGGGAGGGTGAGTGCCGCCATTTAGTGGC NM_001142520 RefSeq
chr11 + 59142844 59155038 FAM111A 63901 "family with sequence similarity 111, member A,
transcript variant 3"
GO:0006260|GO:0005515|GO:0051607|GO:0005737|GO:0016032|GO:0005634|GO:0003824|GO:0000785|GO:0045
071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143021_PI430048170 0.0769033047451130.78784679613906 9.58598977333928
9.43279996869748 9.18196512296149 P P P 9.83015851641891 9.80820595768145
9.61317097704915 P P P LNCV6_143021_PI430048170 mRNA
GCAGAGGGAGTGTGCGAATCAAACCTGACCAAGCGGCTCAAGAATAAAATATGAATTGAG NM_177534 RefSeq
chr16 - 28605586 28609328 SULT1A1 6817 "sulfotransferase family, cytosolic, 1A, phenol-preferring,
member 1, transcript variant 4"
GO:0050294|GO:0047894|GO:0006805|GO:0050427|GO:0044281|GO:0005829|GO:0008210|GO:0009812|GO:0004
062|GO:0006584|GO:0008146|GO:0051923|GO:0009308 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_92065_PI430048170 0.00132525443955477 2.49409705188431 6.41173262204882
6.77005616487442 6.61312053233944 P P P 5.35099532699292 5.17111800423265
5.33275834952187 P P P LNCV6_92065_PI430048170 mRNA
AATTGATGGGTGAAGACACTGAAGAGTCATGAGCAGGCTCCATTAAAGCTCTTTTCTTGC NM_024643 RefSeq
chr14 + 75069576 75079987 ZC2HC1C 79696 "zinc finger, C2HC-type containing 1C, transcript
variant 1" GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127127_PI430048170 0.824360396686361 1.01354381517351 11.6166387414015

11.545473004192 11.6483022252033 P P P 11.3849315729018 11.6896683350025
11.6603568182569 P P P LNCV6_127127_PI430048170 mRNA
GCACCATTTATGAGTCTCAAGTTTTATTATTGCAATAAAAGTGCTTTATGCCGGCTTTTC NM_000801 RefSeq
chr20 - 1368976 1393172 FKBP1A 2280 "FK506 binding protein 1A, 12kDa, transcript variant 1"
GO:0005515|GO:0030018|GO:0055010|GO:0019221|GO:0046332|GO:0042803|GO:0042026|GO:0006936|GO:0006
458|GO:0006457|GO:0010039|GO:0031398|GO:0007179|GO:0043123|GO:0070062|GO:0051209|GO:0014802|GO:0
003755|GO:0005160|GO:0032925|GO:0044325|GO:0060347|GO:0007183|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131122_PI430048170 0.0691895208352191 0.316260380539827 0.370703771786848
1.49048173485699 2.25815498901244 A A A 2.90675311625083 3.34435528358279
3.38447246557917 P P P LNCV6_131122_PI430048170 mRNA
TGTGTAGAGAAAACTTGAAGATACTATCCCTTCTTTGGCATTCTTCTCTTAATGCTATGC NM_001185118 RefSeq
chr3 + 169773064 169789716 MYNN 55892 "myoneurin, transcript variant 2"
GO:0006355|GO:0003700|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_60733_PI430048170 0.107731776067109 1.23067981765648 6.78740331794463
6.85110940893255 6.69991930615098 P P P 6.52792720783846 6.64251862442366
6.24517646317785 P P P LNCV6_60733_PI430048170 mRNA
AGCCCTAACCCAGCTGCTGAATGCCAGAGGCCACGAAGTGACGTTGGTCTCCCGAAAGCC NM_020195 RefSeq
chr14 - 24439765 24442801 SDR39U1 56948 "short chain dehydrogenase/reductase family 39U,
member 1, transcript variant 1" GO:0016491|GO:0005634|GO:0055114 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145033_PI430048170 0.223771933199941 0.808760378533005 7.29667459065812
7.42578097933198 7.88620625914678 P P P 7.68575295680295 7.7889262267305
8.08998905734633 P P P LNCV6_145033_PI430048170 mRNA
GATTATCTCAGAAAAACCTCTCTGAATGATGACCCTTCCTTAATACTGGGTGATGTGTGA NM_020143 RefSeq
chr2 + 68157872 68175961 PNO1 56902 partner of NOB1 homolog (S. cerevisiae)
GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127655_PI430048170 0.0855363660502326 1.0896696414926 0.611598435563691
0.527615206237349 0.673475317224217 A A A 0.419429763911234 0.49517000109143
0.527983286233529 A A A LNCV6_127655_PI430048170 mRNA
CAGAGGAAGGACTTTGGCAAGTGATATTGTCTTCATGTGGGGTATTAATTCTCAAATAAT NM_020632 RefSeq
chr7 - 138706293 138798196 ATP6V0A4 50617 "ATPase, H+ transporting, lysosomal V0 subunit
a4, transcript variant 1"
GO:0008286|GO:0005515|GO:0005886|GO:0007605|GO:0031526|GO:0005765|GO:0006885|GO:0006879|GO:0000
220|GO:0033572|GO:0016324|GO:0007035|GO:0046961|GO:0030670|GO:0051117|GO:0090382|GO:0070062|GO:0
007588|GO:0070072|GO:0015986|GO:0051701|GO:0045177|GO:0055085|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136474_PI430048170 0.892583498375957 1.00677640405839 0.487664702903052
0.362264142166733 0.411573400347063 A A A 0.268743301258831 0.59679333002075
0.34891082503182 A A A LNCV6_136474_PI430048170 mRNA
TCCCCCACTCATATTGTAATTACTTTTTTCATCTTTGGAGGGGGAAGGCAATGAAATATA NM_001144937 RefSeq
chr1 + 108712933 108742745 FNDC7 163479 fibronectin type III domain containing 7
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_46897_PI430048170 0.0400577977584208 1.65158405651996 8.66038988994051
8.77372902474755 8.7798825996806 P P P 8.29939341950312 7.73093709060813
7.95793113522123 P P P LNCV6_46897_PI430048170 mRNA
GAACCATTATTTCTACTCTCCCTATCCAACGAAGACACAAACCATGCGTGTGAAGCTTGC NM_002950 RefSeq
chr3 - 128619969 128650876 RPN1 6184 ribophorin I

GO:0005515|GO:0005791|GO:0010467|GO:0042470|GO:0006614|GO:0006412|GO:0016020|GO:0004579|GO:0005789|GO:0016021|GO:0008250|GO:0044267|GO:0006464|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120196_PI430048170 0.19804922712871 0.965277758947178 0.432272093275893 0.390567540780597 0.394892189370005 A A A 0.487961509793097 0.479529797973077 0.402011749291607 A A A LNCV6_120196_PI430048170 mRNA AGATCTATCCCAGACAAGAGCTCTGGAAAAAGCCACATTGAGAAGTTGATCTTCCGGATG NM_020715 RefSeq chr14 + 67533290 67589538 PLEKHH1 57475 "pleckstrin homology domain containing, family H (with MyTH4 domain) member 1" GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132258_PI430048170 0.190517391514817 1.17496222915529 7.8617306490421 7.83727049996189 7.83925156214171 P P P 7.36259174469443 7.78215232225935 7.6640378554423 P P P LNCV6_132258_PI430048170 mRNA CCCCAATAGTAGACACATCTCCAATACAAACACAGGTTTATAATAAGTAATAGGAAGTCA NM_020062 RefSeq chr20 + 63739857 63744050 SLC2A4RG 56731 SLC2A4 regulator GO:0006355|GO:0005737|GO:0003700|GO:0005654|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132703_PI430048170 0.579717883320675 0.967018320581023 8.69103135801489 8.43941612311454 8.45908032881234 P P P 8.59068728036884 8.58606451413699 8.57167301818966 P P P LNCV6_132703_PI430048170 mRNA AAGGAGAAGAGTGTAAGATTTTGTTTGCATCTGAAAGAGAAAATGCGTCTCTCCTGGGGT NM_001278304 RefSeq chr12 - 122207661 122225850 DIABLO 56616 "diablo, IAP-binding mitochondrial protein, transcript variant 7" GO:0005515|GO:0008625|GO:0035631|GO:0008635|GO:0043065|GO:0006919|GO:0008631|GO:0006915|GO:0051402|GO:0097193|GO:0005829|GO:0005739|GO:0005758|GO:0009898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98250_PI430048170 9.48689381916344e-05 1.15398394424343 5.17812242516966 5.14883102215353 5.15750566519523 P P P 4.94275618538614 4.94808271419345 4.97371756819889 P P P LNCV6_98250_PI430048170 mRNA GAAGAACAAGAGTTCTGTGATTTGAATGACAGCAAGTGCAAAGGCACAACACTGAAAAAA NM_020234 RefSeq chr15 + 49621028 49645136 DTWD1 56986 "DTW domain containing 1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128220_PI430048170 0.871215600109239 1.00162656203076 0.38618812685234 0.38510997306215 0.381733002382077 A A A 0.397047744697764 0.355158063983746 0.39342260755368 A A A LNCV6_128220_PI430048170 mRNA CAGAGAATGTAAATTTTGTACAGTATTAGAATGTGTAAATGAAGCTTGCTTGGAAGGGGA NM_020805 RefSeq chr18 - 32672670 32773011 KLHL14 57565 kelch-like family member 14 GO:0043005|GO:0005783|GO:0043025|GO:0005789|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130295_PI430048170 0.00731502202225268 0.429386414726198 4.26371376523783 4.42519721284547 4.51083820920136 P P P 5.3007673012746 5.70245050586043 5.81697867564528 P P P LNCV6_130295_PI430048170 mRNA ATGTTGATGTTTTGCTTTGTCTTTTGGATGGCCTAACCTACATTAACATGTTGGCAGACC NM_001099269 RefSeq chr19 - 19792710 19821751 ZNF506 440515 "zinc finger protein 506, transcript variant 1" GO:0006355|GO:0005730|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145720_PI430048170 0.500204228228502 0.96252915019495 0.265666664744235 0.434256181169297 0.300729851367092 A A A 0.486077782302069 0.378005851500887 0.301414220138984 A A A LNCV6_145720_PI430048170 mRNA

AGAGAAGTCTCTACTCAAAATGTCACATCAAGTAGATACAAGCTGAAAGAGTCTTGGAAA NM_001171183 RefSeq chr5 + 172194171 172203454 EFCAB9 NA EF-hand calcium binding domain 9 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142504_PI430048170 0.7787599733745111.23181627436663 1.84618298029803 2.78510637601337 0.597504159442087 A A A 2.4077467529634 0.408390682995231 1.63656043489427 A A A LNCV6_142504_PI430048170 mRNA
TCTGAGCCATGTGAAGCACGTCTCCGTTGTGTTAATTTATTTCAATGTAGCTTATTTTCT NM_001301687 RefSeq chr2 - 236165235 236168009 GBX2 2637 "gastrulation brain homeobox 2, transcript variant 2" GO:0001569|GO:0006355|GO:0042472|GO:0003700|GO:0021555|GO:0001755|GO:0021568|GO:0005634|GO:0021549|GO:0048483|GO:0021930|GO:0006351|GO:0007399|GO:0043565|GO:0021794|GO:0007411|GO:0021884 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110422_PI430048170 0.0184990039980887 0.762901744848515 8.93454220339232 8.71837418515733 8.87558661996001 P P P 9.27154290306424 9.23428810639147 9.20167812796743 P P P LNCV6_110422_PI430048170 mRNA
AAGGAATTGCAGAAAGTGAAAGAGGAAATCATTGAAGCCTTCGTCCAGGAGCTGAGGAAG NM_003370 RefSeq chr19 + 45507429 45526982 VASP 7408 vasodilator-stimulated phosphoprotein GO:0005515|GO:0050852|GO:0017124|GO:0031258|GO:0005886|GO:0034329|GO:0031527|GO:0001843|GO:0003779|GO:0015629|GO:0005829|GO:0005737|GO:0030838|GO:0051289|GO:0007411|GO:0008154|GO:0005923|GO:0005522|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128389_PI430048170 0.0118849737412139 1.46182023512757 12.0742592847278 12.0473876889231 12.0429008997967 P P P 11.6230389862603 11.402399049874 11.4873828400482 P P P LNCV6_128389_PI430048170 mRNA
GTTAAAGATGAATTTCCACTGCTTTGGAGAGTCCCACCCACTAAGCACTGTGCATGTAAA NM_001013845 RefSeq chrX - 149932196 149938498 CXorf40B 541578 chromosome X open reading frame 40B NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115740_PI430048170 0.4134131846387 0.912891476363791 7.35814757983387 7.11943883772171 7.23232482425573 P P P 7.24602291176192 7.5920139447444 7.24803950779046 P P P LNCV6_115740_PI430048170 mRNA
ATGGAGATCTTGACAGAGCTGGGCTTGCACTTCCGGGTCCTGGATATGCCCACCCAAGAA NM_001145901 RefSeq chr19 - 38915263 38930896 SARS2 54938 "seryl-tRNA synthetase 2, mitochondrial, transcript variant 1" GO:0005739|GO:0010467|GO:0006434|GO:0005759|GO:0004828|GO:0097056|GO:0005524|GO:0006418 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109534_PI430048170 0.822730524758017 1.0376072959153 0.616556567537115 2.85562705172327 2.55946705427362 A A A 2.63290565278778 1.79731643083376 2.15583044134519 A A A LNCV6_109534_PI430048170 mRNA
TGCAGAAGGAAGTGCCGCGCCGCAGTCAAGTCTAATGTCTTCTACTGGCTGGTGATTTTC NM_199460 RefSeq chr12 + 2053284 2697949 CACNA1C 775 "calcium channel, voltage-dependent, L type, alpha 1C subunit, transcript variant 1" GO:0035585|GO:0005515|GO:0005516|GO:0030018|GO:0060402|GO:0086010|GO:0005886|GO:0007268|GO:0044281|GO:0007204|GO:0046872|GO:0019229|GO:0005737|GO:0043198|GO:0007411|GO:0017156|GO:0043025|GO:0007628|GO:0030252|GO:0034765|GO:0046620|GO:0005245|GO:0008331|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128636_PI430048170 0.732914031150285 0.967002040728582 0.455840700948245 0.468961730463596 0.528699663847003 A A A 0.732988088228998 0.415020186834478 0.428883473866388 A A A LNCV6_128636_PI430048170 mRNA
TTCGCAATAAGTACCAAGAAGCCCAAGATATCAGCCCAAAAGTCAATCTTATCATATTTC NM_001764 RefSeq chr1 - 158327949 158331531 CD1B 910 CD1b molecule GO:0071723|GO:0005515|GO:0030881|GO:0006955|GO:0009986|GO:0005886|GO:0030884|GO:0030883|GO:0048007|GO:0016021|GO:0005765|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_83413_PI430048170 0.1127405784040070.4756638289423672.72741591305656 1.79739128106146
3.08558342668855 A A P 4.31094935609227 3.09917663024611 3.41404794457141 P P P
LNCV6_83413_PI430048170 mRNA
GTCTGTAATCTGTAATTGTGATGCCTCTGATGGAATAAATTATCTTTTTCAGTCTCCTCT NM_001162371 RefSeq chr17
- 5499426 5500999 LOC728392 728392 uncharacterized LOC728392 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140687_PI430048170 0.0522372550487727 2.25171521974702 4.30889318558999
4.07144806067616 4.16582352594557 P P P 3.251164147842 3.27525194704847
2.33254091024404 P P A LNCV6_140687_PI430048170 mRNA
GTTCTGGGTTCTAGATGTCAATTCTAAATAATAATAATGACCTTAGTCTGCTGCCTCGAT NM_001129742 RefSeq
chr10 - 103472803 103479240 CALHM3 119395 calcium homeostasis modulator 3
GO:0034220|GO:0005261|GO:0005887|GO:0006812 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134303_PI430048170 0.1863114845964661.14341637584684 7.5260878575376
7.34385711393209 7.65418525015669 P P P 7.17919851211402 7.31308543254897
7.45531310840371 P P P LNCV6_134303_PI430048170 mRNA
CTCACTTGGCTGGAAACATCAATCTTAACCATTTATTCAGAACCATTAAACCAATGATTC NM_015935RefSeq chr1
+ 171781620 171797716 METTL13 51603 "methyltransferase like 13, transcript variant 1"
GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133830_PI430048170 0.2970166762331591.4976624670854 0.759004808187276
1.80906453282274 0.748894119689583A A A 0.6045647928310940.631500901055391
0.606073729236955A A A LNCV6_133830_PI430048170 mRNA
GACAAAAGTTCAGGTCTGTGTATTTATTCTTAGGGCTGCCATAAAAAATTACCACAACCT NM_001304947 RefSeq
chr17 - 8368652 8376711 KRBA2 NA "KRAB-A domain containing 2, transcript variant 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129200_PI430048170 0.4449697033420111.65738526168336 0.450629035977144
2.04658395405173 0.396095995208052A A A 0.5328335104472750.408149344837954
0.419485677107818A A A LNCV6_129200_PI430048170 mRNA
TCTTAAGATTACATCAAGCTAATTGTGCGAGCTCAATTCACTTTGTAAGAAAACTCTCGG NM_004527RefSeq chr17
- 43640389 43661563 MEOX1 4222 "mesenchyme homeobox 1, transcript variant 1"
GO:0003700|GO:0001757|GO:0005634|GO:0007275|GO:0060218|GO:0000978|GO:0006351|GO:0043565|GO:0003
674|GO:0008150|GO:0061053|GO:0001077|GO:0005737|GO:0045944|GO:0003682|GO:0061056|GO:0071837|GO:0
001046 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53632_PI430048170 0.0299384166395315 1.2604581677984 7.30186501439581
7.31435030980485 7.43380282003423 P P P 6.98129646933481 7.16020624528253
6.89780397918709 P P P LNCV6_53632_PI430048170 mRNA
CTTAGTTTAAAGGGTAAGAGAGAAGTTGTTTCTGGTTTTTCCTTGCCCCTGTGTGAAAAT NM_019557RefSeq chr1
+ 25820192 25832942 MTFR1L 56181 "mitochondrial fission regulator 1-like, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139470_PI430048170 0.0397512564893403 1.0553061083104 0.353524990862447
0.35707245285258 0.295221696413116A A A 0.2445575756983290.281984891430792
0.246818165825786A A A LNCV6_139470_PI430048170 mRNA
AAAGATGCTTCCAAGAAGTCAGCGAGTGAAAGGCCAATTTCCAAAGTGATTCGGGAACCANM_001304968 RefSeq
chr7 - 130668645 130687432 TSGA13 114960 "testis specific, 13, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128317_PI430048170 0.1478378162951871.54593621006364 5.53310786600123 5.880439994826
5.09532317179609 P P P 5.32177756585203 4.88397521536077 4.36803704000008 P P P
LNCV6_128317_PI430048170 mRNA
GTAGGTTTCCAGATTTCCTGAAAAATAAAAGTTTACAGCGTTATCTCTCCCCAACCTCAC NM_174914RefSeq chr5
- 36035016 36066921 UGT3A2 167127 "UDP glycosyltransferase 3 family, polypeptide A2, transcript

variant 1" GO:0052696|GO:0009813|GO:0071412|GO:0015020|GO:0008194|GO:0016021|GO:0043231 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137451_PI430048170 0.3987295852155370.9585313176624640.266051800767272
0.4116096443595470.29734410227235 A A A 0.4751864215804090.366774292776861
0.315835906198574A A A LNCV6_137451_PI430048170 mRNA
TTCCATAATTGCTTTTGCTCAGTAACTGTGTCATGAATTGCAAGAGTTTCCACAAACACT NM_145699RefSeq chr22
+ 38957521 38963183 APOBEC3A 200315 "apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A, transcript variant 1"
GO:0005515|GO:0009972|GO:0047844|GO:0005634|GO:0010529|GO:0071466|GO:0044356|GO:0005737|GO:0051607|GO:0045087|GO:0080111|GO:0004126|GO:0005654|GO:0008270|GO:0070383|GO:0045071 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127815_PI430048170 0.0501216659179923 1.37629108343481 5.31027915867183
5.33915134373441 5.21398021767802 P P P 4.78048386298121 5.04407967958422
4.62846896817217 P P P LNCV6_127815_PI430048170 mRNA
TTTTACAAAAGTTATTTTCCAACAGGGGCTGGAGGGCTGGGCAGGGCCCTGTGGCTCCAG NM_172107RefSeq
chr20_KI270871v1_alt - 182 33239 KCNQ2 3785 "potassium channel, voltage gated KQT-like subfamily Q, member 2, transcript variant 1"
GO:0005251|GO:0005886|GO:0030506|GO:0005267|GO:0007268|GO:0019226|GO:0007399|GO:0043194|GO:0033268|GO:0007411|GO:0005249|GO:0008076|GO:0034765|GO:0016021|GO:0006813|GO:0071805 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133698_PI430048170 0.0176985397134704 0.7162947294906947.01962742071312
7.0241979496213 7.20024064165226 P P P 7.37775857807982 7.61263853216804
7.68745768754416 P P P LNCV6_133698_PI430048170 mRNA
ATGGAAAATAGAGAACAGGAAATGAGAATGGGTGATATGGGTCCCCGTGGAGCAATAAAC NM_001042414
RefSeq chr13 - 19702868 19783019 PSPC1 55269 "paraspeckle component 1, transcript variant 1"
GO:0005515|GO:0005730|GO:0001047|GO:0006351|GO:0016363|GO:0005737|GO:0042382|GO:0000166|GO:0016607|GO:0042752|GO:0005654|GO:0048511|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138623_PI430048170 0.0451301344878974 0.4333974670390337.4982649645897
7.20543291747798 7.62122758792681 P P P 8.01430609751703 8.78941713788693
8.99713360194118 P P P LNCV6_138623_PI430048170 mRNA
CACATTGTGATAACATAAAGTGGATTCATCTTGTATCATTATAGGCAGAAGGTATTTGGC NM_005475RefSeq chr12
+ 111405947 111451623 SH2B3 10019 "SH2B adaptor protein 3, transcript variant 1"
GO:0035556|GO:0005515|GO:0007596|GO:0042301|GO:0004871|GO:0035162|GO:0032403|GO:0030154|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105670_PI430048170 0.0696373449254889 2.1425735820236 2.84242694984858
3.60922443076606 3.48430813314759 A P P 2.70945085274379 1.45428935616238
2.31776313552179 P A P LNCV6_105670_PI430048170 mRNA
CTCACAGTGCATAAAAGGATCCACACAGTTTCAGATGAACTCCCATAATGAATGATGAAT NM_152283RefSeq chr5
- 180847610 180861286 ZFP62 643836 "ZFP62 zinc finger protein, transcript variant 1"
GO:0006355|GO:0005634|GO:0003676|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133272_PI430048170 0.0588768650149044 0.3509831285493320.520833562277772
0.4544949357144351.13351946829185 A A A 1.51968992376937 1.90184813456547
2.93332650305955 A A P LNCV6_133272_PI430048170 mRNA
TATAGCAGTTAACCAAGACCAACATGGTGTCTGCTTGGTTGATGCTTGAAATAAGGTGAC NM_001300940 RefSeq
chr12 - 64186311 64222296 C12orf66 144577 "chromosome 12 open reading frame 66, transcript variant 1" GO:0015630|GO:0045171 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61725_PI430048170 0.1547408465550170.7159392570001815.91013393274952 5.78086399704562
6.14401206304139 P P P 6.08341188474859 6.31253385343865 6.81092199465208 P P P

LNCV6_61725_PI430048170 mRNA
GTTTAGCTTTGTATGAACTGAGTGTGCCAGAAATAAACCTGGAGCAATTTTTAAATAAGC NM_032499 RefSeq chr15
+ 36594868 36810260 C15orf41 84529 "chromosome 15 open reading frame 41, transcript variant 2"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133273_PI430048170 0.6577446740755550.9501967829614993.81479153606575
4.11939408394876 4.04662201785226 P P P 4.22918540902314 4.11968914273344
3.84340554501442 P P P LNCV6_133273_PI430048170 mRNA
TCAACCTCTTTGTGTTCAGCCCAGACACAGGTGCTGTCTCTGGCTCCTACCGAGTTCGAG NM_000203 RefSeq chr4
+ 986996 1004557 IDUA 3425 "iduronidase, alpha-L-, transcript variant 1"
GO:0048878|GO:0005975|GO:0030135|GO:0005102|GO:0048705|GO:0006027|GO:0044281|GO:0000902|GO:0003
940|GO:0030207|GO:0030209|GO:0009405|GO:0005984|GO:0030204|GO:0035108|GO:0007040|GO:0030203|GO:0
070062|GO:0043202. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133709_PI430048170 0.648456472120945 1.15561794802899 3.22783075381748
4.20541375807137 3.90796740594653 P P P 3.59258097913246 3.64978864870973
3.63757489130169 P P P LNCV6_133709_PI430048170 mRNA
TTAATTTATACTCTCTCAAATGCCCAGGATACTCTACCCACTTAAGAACCTTGCCAACTT NM_032554 RefSeq chr12
- 122727605 122730582 HCAR1 27198 hydroxycarboxylic acid receptor 1
GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0032355 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128751_PI430048170 0.3567055418655581.81125526648075 0.298315449040446
2.01378161242542 0.514731451837897 A A A 0.3107407231188960.272138679693468
0.321236262558204 A A A LNCV6_128751_PI430048170 mRNA
CCAACCACTTTATATGATTTAGGGTCTCGTTAAAATGGTTACCATTTGCTTCTCCTAAAA NM_001242699 RefSeq
chr10 + 116849511 116882601 ENO4 NA enolase family member 4 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145693_PI430048170 0.19681257726437 0.5501329679882320.305922381721847
0.2898041161405290.354905360060543 A A A 1.51027651853148 1.44968550047137
0.27957200838843 A A A LNCV6_145693_PI430048170 mRNA
GGAATTTTCAACACTGTCATCAATCCCATGCTGAACCCAATCATCTACAGCTTCAGAAAC NM_002550 RefSeq chr17
- 3291634 3292582 OR3A1 4994 "olfactory receptor, family 3, subfamily A, member 1"
GO:0050911|GO:0007165|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131279_PI430048170 0.2913394208667531.18159648927729 0.896923578826206
0.4140695771256680.434864554528251 A A A 0.3300637261022250.344491563751124
0.401445339787419 A A A LNCV6_131279_PI430048170 mRNA
GTATGAAAAATGAAAAGGCCCAGGGTTACCTTCTAGAGACAAATAAATGCAGTCTTGAAA NM_001004311 RefSeq
chr2 - 70777309 70790643 FIGLA NA folliculogenesis specific basic helix-loop-helix NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_143953_PI430048170 0.0302341185115838 1.28106448323268 9.34036164587545
9.27326356073873 9.3345349060452 P P P 8.8649842048171 8.90137694287625
9.09951832854533 P P P LNCV6_143953_PI430048170 mRNA
CGCAAAATAAAGTTTAAAACCCTGCTACCACAATGTTTCTGGAACAAGACTAGATCAAAA NM_053050 RefSeq chr2
- 74471957 74472815 MRPL53 116540 mitochondrial ribosomal protein L53
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0005743|GO:0005840 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145080_PI430048170 0.0221623869591865 0.8864684683782968.98649588640208
8.87464001797299 8.9812265696702 P P P 9.09920787403393 9.08559660661112
9.18005355956906 P P P LNCV6_145080_PI430048170 mRNA
GCTGGATTTGGAGCTGGTGGCAAGTTGAAATTATTAAAAATTGATTTGTGTGGGACTGTC NM_024541 RefSeq chr10

- 101845598 102056175 C10orf76 79591 chromosome 10 open reading frame 76 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100578_PI430048170 0.22477883234644 0.5914193713371040.816379479923298
0.87579722854769 1.40234972356627 A A A 0.9177522762453562.05013213908886
2.17604543148408 A A A LNCV6_100578_PI430048170 mRNA
TTAACAATTTGTAAGCTGCAAAAATGGCAATGGGCCAACCAAGAACAGCTACAATTTGAA NM_015093RefSeq chr6
+ 149318299 149411613 TAB2 23118 "TGF-beta activated kinase 1/MAP3K7 binding protein 2, transcript variant 1"
GO:0005515|GO:0050852|GO:0034142|GO:0005886|GO:0070423|GO:0007249|GO:0051403|GO:0035872|GO:0005829|GO:0007507|GO:0002756|GO:0000187|GO:0051092|GO:0002755|GO:0045860|GO:0043123|GO:0034138|GO:0070530|GO:0038124|GO:0038123|GO:0034134|GO:0007254|GO:0002224|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139083_PI430048170 0.0233504004563722 1.34604689593323 9.81628409847424
10.0114326244743 9.70954102443612 P P P 9.2722060501448 9.54725727392474
9.43482752260758 P P P LNCV6_139083_PI430048170 mRNA
TGCTCATTTTCTGTTTTCCTGTGTTAGGAAAAAACCACCTGTTTTCCAAGGGGAGAGGGC NM_015456RefSeq chr9
+ 137255306 137273548 NELFB 25920 negative elongation factor complex member B
GO:0005515|GO:0010467|GO:0006368|GO:0005737|GO:0006366|GO:0032021|GO:0016032|GO:0005654|GO:0045892|GO:0050434 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145070_PI430048170 0.0562654523239074 0.5493286725000934.51485972972768
3.87540148612658 4.51106094297272 P P P 4.69022729396357 5.29784278157964
5.48180610369452 P P P LNCV6_145070_PI430048170 mRNA
ATGCAGGTAGTTGTCACCATGGATTGAGTCCAGTCGTAGTAATTAATATGTTTAATCAGA NM_006635RefSeq chr19
+ 57280484 57294068 ZNF460 NA zinc finger protein 460 NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_117287_PI430048170 0.00184993814986094 1.31600920938524 7.82824948294461
7.95818844332169 7.9200922832449 P P P 7.45964841645975 7.58115977404684
7.47727566865656 P P P LNCV6_117287_PI430048170 mRNA
TTGGTCTCTGCGAAGTCAAAGGCCTGACAGCTCTGTGGCCTGGGAATCCATTTTCCTGCG NM_006116RefSeq chr22
+ 39399753 39431882 TAB1 10454 "TGF-beta activated kinase 1/MAP3K7 binding protein 1, transcript variant alpha"
GO:0005515|GO:0034142|GO:0030324|GO:0070423|GO:0007249|GO:0003824|GO:0051403|GO:0032403|GO:0035872|GO:0005829|GO:0002756|GO:0000187|GO:0005737|GO:0051092|GO:0000185|GO:0002755|GO:0007179|GO:0048273|GO:0034138|GO:0038124|GO:0038123|GO:0034134|GO:0007254|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132991_PI430048170 0.0141104031933635 0.4677327732651154.46762619867781
4.08869341604796 4.67756245741371 P P P 5.24662685660299 5.37390713782293
5.88165156910265 P P P LNCV6_132991_PI430048170 mRNA
TGTCATCTTACGTTCCTCTTCCTCGCATTGGATTTATTGCTAAAACCTGGTAAACACTTT NM_019041RefSeq chr6 -
152987365 153002815 MTRF1L 54516 "mitochondrial translational release factor 1-like, transcript variant 1"
GO:0005739|GO:0070126|GO:0032543|GO:0006996|GO:0016149|GO:0005759 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136518_PI430048170 0.1572574824947720.7675350068802355.45087543321712 5.7721106080131
5.72932018759892 P P P 5.84926888950956 5.84127063177215 6.36323778912299 P P P
LNCV6_136518_PI430048170 mRNA
GCTGTACACACAGAGGAAATGTATGTTTGTCATGTATGAAGAATGGCTTCAGTTTCTCTG NM_022344RefSeq chr17
- 32328440 32342209 C17orf75 64149 chromosome 17 open reading frame 75
GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145728_PI430048170 0.4498145370990650.9211923624161545.00596065237096

5.13533771970773 5.37204084202968 P P P 5.35178843515343 5.10430261907957
5.41807123674633 P P P LNCV6_145728_PI430048170 mRNA
ATGATTTTTAGGAAGCTATTGCCTAAATCAGCGTCAACATGCAGTAAAGGTTGTCTTCAA NM_032409RefSeq chr1
+ 20633454 20651511 PINK1 65018 PTEN induced putative kinase 1
GO:0005515|GO:0006511|GO:0002020|GO:0005758|GO:0043524|GO:0046329|GO:0018105|GO:0016301|GO:0051
443|GO:0031396|GO:0031932|GO:0005856|GO:0043123|GO:0006979|GO:0000785|GO:0031625|GO:0000287|GO:0
006950|GO:0016504|GO:0016310|GO:0032226|GO:2000377|GO:0007005|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139802_PI430048170 0.6369234570339571.02976102823674 13.601577557382 13.794266085547
13.8126454568399 P P P 13.7664735227878 13.6805569537952 13.6409895564352 P P P
LNCV6_139802_PI430048170 mRNA
TCACTGTGTAGTGGATGGAGTTTACTGTTTGTGGAATAAAAACGGCTGTTTCCGTGGTTC NM_015937RefSeq chr20
+ 45416066 45426245 PIGT 51604 "phosphatidylinositol glycan anchor biosynthesis, class T, transcript
variant 1"
GO:0005515|GO:0006501|GO:0016255|GO:0030176|GO:0003923|GO:0051402|GO:0016020|GO:0030182|GO:0005
789|GO:0016023|GO:0042765|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132154_PI430048170 0.5281880404816861.48709419712986 0.314371991518716
0.28003778270724 1.82699801271646 A A A 0.2895938779328290.670350896510844
0.292517554818427A A A LNCV6_132154_PI430048170 mRNA
CAGACAAGATGAGAGAAACAGCCATGTTTCTGTCACATTGTTTACTGTCATATTAAAGAT NM_015272RefSeq chr16
- 53599238 53703934 RPGRIP1L 23322 "RPGRIP1-like, transcript variant 1"
GO:0005515|GO:0001736|GO:0007368|GO:0031870|GO:0021532|GO:0036064|GO:0005829|GO:0005737|GO:0021
772|GO:0005911|GO:0035869|GO:0090102|GO:0043010|GO:0005813|GO:0045744|GO:0006996|GO:0001822|GO:0
005930|GO:0021549|GO:0060039|GO:0001701|GO:0001889|GO:0042384|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144203_PI430048170 0.6636193405782511.05909831317776 5.46215737511376
5.60399380836607 5.27424687386775 P P P 5.72374011556686 5.18526014246963
5.12331531482919 P P P LNCV6_144203_PI430048170 mRNA
TTCTCAATACAGCCTGCCCTTGCAGTCCCTATTTCAAAATAAAATTAGTGTGTCCTTGCC NM_002602RefSeq chr17
- 81650458 81656577 PDE6G 5148 "phosphodiesterase 6G, cGMP-specific, rod, gamma, transcript
variant 1"
GO:0004857|GO:0005515|GO:0045745|GO:0005886|GO:0007603|GO:0045742|GO:0047555|GO:0030507|GO:0022
400|GO:0043086|GO:0000187|GO:0030553|GO:0008152|GO:0007601|GO:0016056 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132806_PI430048170 0.11970501050954 1.13737214762218 12.2488696735584
12.3988000628098 12.5082702993847 P P P 12.2667955672692 12.1211729604108
12.2187560467929 P P P LNCV6_132806_PI430048170 mRNA
TCACCTTGTATGTCGAACTGCATAAAAGATCTGGTAGGCTGGTCAGCTACATGCAAAAAA NM_004147RefSeq chr22
+ 31399552 31434186 DRG1 4733 developmentally regulated GTP binding protein 1
GO:0005515|GO:0005737|GO:0016020|GO:0007275|GO:0005525|GO:0005844|GO:0006351|GO:0042802|GO:0008
134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140859_PI430048170 0.2372460608963750.8049765426723020.409764019749709
0.4328585932114330.323042905792052A A A 1.02952191204289 0.466084305338634
0.544591882247818A A A LNCV6_140859_PI430048170 mRNA
GCGGCTCTAAGGCTCCTTTTTCAACCCGAATATTAATAAATCATGAGAGTAATCAAGGTC NM_001130064 RefSeq
chr3 + 115623303 115721487 GAP43 2596 "growth associated protein 43, transcript variant 1"
GO:0005515|GO:0005516|GO:0030424|GO:0030054|GO:0005886|GO:0009611|GO:0031527|GO:0014069|GO:0032
584|GO:0042246|GO:0007205|GO:0051489|GO:0005737|GO:0045165|GO:0016198|GO:0010001|GO:0040008 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_134864_PI430048170 0.000724192716476489 0.478046876632281 12.3763736420906
12.2488696735584 12.1543755303263 P P P 13.3821699384506 13.3283499992198
13.2698730914297 P P P LNCV6_134864_PI430048170 mRNA
CGTGTTACTAACTCTAGTATGTTTCTGTGTCAATCGCTGTGAAATAAAGTCTGAAAACTT NM_198576 RefSeq chr1
+ 1020122 1056119 AGRN 375790 agrin
GO:0005515|GO:0007009|GO:0002162|GO:0010469|GO:0030054|GO:0005886|GO:0007603|GO:0051491|GO:0045
202|GO:0044281|GO:0005615|GO:0035374|GO:0005737|GO:0043525|GO:0030198|GO:0007411|GO:0007528|GO:0
045944|GO:0033691|GO:0030204|GO:0030203|GO:0070062|GO:0043202|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127759_PI430048170 0.0119559154036709 2.00309750765527 13.1086811268255
13.527486047312 13.3932227813297 P P P 12.4057582359052 12.3301710222188
12.3162694149429 P P P LNCV6_127759_PI430048170 mRNA
CTTGCCTTGGCTCTTTGAGCTCCCTTTTGCTTAATTACTGGGTTTTCTGGGCAGTTTTTT NM_152766 RefSeq chr17 -
7402973 7404131 TMEM256 254863 transmembrane protein 256
GO:0008150|GO:0003674|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89785_PI430048170 0.353340293084563 0.847270949393555 4.23312418650114 3.8074643222835
4.60148546431088 P P P 4.46835620824599 4.48582147479961 4.51290866538059 P P P
LNCV6_89785_PI430048170 mRNA
TTATTGCTGCTACAGAGTAGTGAAATCACGGACTATGATGTTTTCGTTGGATACCACTAG NM_001258286 RefSeq
chr5 - 55625844 55693053 SLC38A9 153129 "solute carrier family 38, member 9, transcript variant 2"
GO:0015171|GO:0016021|GO:0006814|GO:0003333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143805_PI430048170 0.194529795047496 1.10328677088572 0.601113299463705
0.363861367944071 0.56357728918171 A A A 0.285746984245049 0.395666995809777
0.428946166162843 A A A LNCV6_143805_PI430048170 mRNA
CCCACCACTTAACTGGGAGACACTGTTTTATTAAAACACACCGTGGCTTCCTTCAAAAAA NM_001286400 RefSeq
chr14_KI270845v1_alt + 138963 147670 C14orf180 NA "chromosome 14 open reading frame 180,
transcript variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134771_PI430048170 0.219104032554804 1.04671952345507 0.398298922792136
0.300854895320492 0.275804124934202 A A A 0.250419046489825 0.280453875583672
0.249165573724194 A A A LNCV6_134771_PI430048170 mRNA
GATGGATGTAATTCTCATGAAAGCAGTGAAGCAATTTCAGTTTTAAAAATGAAGATCGGC NM_001109878 RefSeq
chrX_KI270881v1_alt - 65313 82327 TBX22 50945 "T-box 22, transcript variant 1"
GO:0006355|GO:0003700|GO:0007275|GO:0005634|GO:0000122|GO:0045892|GO:0003677|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129215_PI430048170 0.529912609389033 1.50044638921672 2.22178378481201
1.13005939013899 0.421396748887991 A A A 0.853268728895858 0.807663488396098
0.928384852551034 A A A LNCV6_129215_PI430048170 mRNA
AGCAGATGGGCGAATCCTACGACACAAACTTTACAAAGAATATCCAGAAGGTGACTCAAA NM_021197 RefSeq chr16
+ 84294705 84329851 WFDC1 58189 "WAP four-disulfide core domain 1, transcript variant 1"
GO:0010951|GO:0003674|GO:0030308|GO:0004867|GO:0042493|GO:0050680|GO:0032355|GO:0005615 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139747_PI430048170 0.0240533997281694 0.428306973201326 9.13597958977151
8.24386183740005 8.59577316596217 P P P 10.1603396952502 9.84896117260317
9.74490014165707 P P P LNCV6_139747_PI430048170 mRNA
TCAAAACGAGTTACCACGTACAATTGATCCAATAATTTGACTAACGGAACAAGTTACCCT NM_001190706 RefSeq
chr6 + 61574102 61574629 MTRNR2L9 NA MT-RNR2-like 9 (pseudogene) NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_144507_PI430048170 0.37234030897933 0.8438314230525 6.90894401221713
6.68565772847704 6.37233950135197 P P P 7.23505750113822 6.82111236922429

6.62725419460783 P P P LNCV6_144507_PI430048170 mRNA
GGCCCCTTGCGTCCATTTACATGCCAGCCATCTCTGCAATTAAAGTTTCTGGATAAAAAA NM_001271049 RefSeq
chr2 + 119544431 119656661 CFAP221 200373 "cilia and flagella associated protein 221, transcript
variant 1" GO:0005929|GO:0005516|GO:0005930|GO:0060271|GO:0003341 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145367_PI430048170 0.296203992744971 0.943595883728895 0.258200964110179
0.375958199204692 0.27896140377564 A A A 0.487106073972951 0.381146757676075
0.292299474799529 A A A LNCV6_145367_PI430048170 mRNA
CTTTTATCTACAGCCTGAGAAACAAAGACCTGAAACAGGGCCTGAGGAAGCTTATGAGCA NM_001004454 RefSeq
chr9 - 122567547 122568477 OR1L8 NA "olfactory receptor, family 1, subfamily L, member 8" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128679_PI430048170 0.019024125589217 0.591274026226087 8.21739641949147
7.84337935026795 7.78498320944012 P P P 8.70149297491832 8.81507353413659
8.63700910673973 P P P LNCV6_128679_PI430048170 mRNA
TGAGAAGATCAAGAGCCGTCTGGACCCTCTGCGGGAGATGCAGAAGCATCTGGGGAAGAA NM_024316 RefSeq
chr19_KI270938v1_alt - 130490 134594 LENG1 79165 leukocyte receptor cluster (LRC) member 1
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92736_PI430048170 0.31652317082435 1.20189600140178 3.73490305031151 3.86416946791136
4.1083602450409 P P P 3.1923815666685 3.85054108545671 3.80508123013507 P P P
LNCV6_92736_PI430048170 mRNA
TTTGTTCCTTCTCCATCCTGTCTAACTCTTCCGTAACTGGTGCTATCGACTTAGCAGCTA NM_020825 RefSeq chr16 +
1614639 1677908 CRAMP1L 57585 "Crm, cramped-like (Drosophila)"
GO:0003682|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143757_PI430048170 3.31035961097602e-05 3.58855546525062 8.08733235631286
8.09798056975443 8.07389974424399 P P P 6.28581095537801 6.21923174591308
6.22308819287604 P P P LNCV6_143757_PI430048170 mRNA
CCTAAGTTAAGCAAAATGCTTCTGCACACAAAACTCTCTGGTTTACTTCAAATTAACTCT NM_018406 RefSeq
chr3_KI270936v1_alt + 3234 47967 MUC4 4585 "mucin 4, cell surface associated, transcript variant
1"
GO:0005796|GO:0005578|GO:0016266|GO:0005615|GO:0031982|GO:0005176|GO:0006493|GO:0007160|GO:0016
020|GO:0030197|GO:0030277|GO:0005887|GO:0044267|GO:0070062|GO:0043687 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133476_PI430048170 0.283161919160006 0.782847399106922 1.76357212467508
1.85488985422493 1.05799790134234 A A A 2.20648449587767 1.66993134200787
1.93354374630402 A A A LNCV6_133476_PI430048170 mRNA
AGGCTGCTCAATGAGATAATTGCTGATTTTGATGAGCTGCTCTCCAAGCCCAAGTTCAGT NM_001198568 RefSeq
chr14 - 24318348 24335071 ADCY4 196883 "adenylate cyclase 4, transcript variant 3"
GO:0005515|GO:0005886|GO:0007268|GO:0007202|GO:0044281|GO:0007193|GO:0030425|GO:0046872|GO:0035
556|GO:0005737|GO:0007173|GO:0071377|GO:0006171|GO:0006833|GO:0034199|GO:0048011|GO:0055085|GO:0
005524|GO:0003091|GO:0007165|GO:0006112|GO:0004016|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137657_PI430048170 0.0250755096743202 0.430947461478201 12.0556532874621
11.4036942300138 11.1950829216343 P P P 13.032533461192 12.7473153277223
12.6327708942297 P P P LNCV6_137657_PI430048170 mRNA
CCTCCCGTCTCCCACAACTTCTGCTATAACAATAAACTGTAGAGGAATCTGAGTACCGTT NM_001282213 RefSeq
chr14 - 21016762 21025105 NDRG2 57447 "NDRG family member 2, transcript variant 11"
GO:0005515|GO:0048471|GO:0005813|GO:0005794|GO:0005815|GO:0048662|GO:0001818|GO:0010574|GO:0030
154|GO:0030426|GO:0005829|GO:0003674|GO:0005737|GO:0021762|GO:0090361|GO:0070373|GO:0005654|GO:0
016055|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA

LNCV6_136187_PI430048170 0.2814421492624461.01906529954399 0.310879711739784
0.3238753033784470.371759571438231A A A 0.3220475450915780.31012212921153
0.293174619122706A A A LNCV6_136187_PI430048170 mRNA
CCCAACCCCAGTGTAAATGATATTTACCAGTGATCTAGCATATGTAATCTTTTTTAAAGG NM_001206955 RefSeq
chr3 + 2238828 3057961 CNTN4 152330 "contactin 4, transcript variant 4"
GO:0030424|GO:0005886|GO:0005576|GO:0007409|GO:0031225|GO:0031175|GO:0007399|GO:0007413|GO:0045
665|GO:0007411|GO:0007420|GO:0048167|GO:0007158 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126346_PI430048170 0.00204736669387834 1.76631694759951 8.47216293896891
8.38733546879468 8.18569470309605 P P P 7.56287724845929 7.63744155390731
7.38602628493985 P P P LNCV6_126346_PI430048170 mRNA
TCCTGCGCCTGCGCCGGCTCCTGCAAGTGCAAAAAGTGCAAATGCACCTCCTGCAAGAAG NM_005951 RefSeq chr16
+ 56669813 56671129 MT1H 4496 metallothionein 1H
GO:0071294|GO:0005515|GO:0048471|GO:0005737|GO:0008270|GO:0005634|GO:0071276|GO:0045926 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138270_PI430048170 0.1149824270754770.8268305130044965.90644445334094
6.29366739758755 6.04462110737959 P P P 6.29298878441897 6.31458635585496
6.47981652627225 P P P LNCV6_138270_PI430048170 mRNA
CTTAATCATGCATTCCTGTTGCTAGTTTCACATCAGTCCCCTGGTTTAATAAGAAATAAA NM_052859 RefSeq chr3
- 53088484 53130454 RFT1 91869 RFT1 homolog (S. cerevisiae)
GO:0005789|GO:0008643|GO:0034203|GO:0016021|GO:0006488|GO:0044267|GO:0005319|GO:0043687|GO:0018
279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134294_PI430048170 0.18759697890964 1.10167400512845 0.356282118225448
0.3615632613437680.567005552842571A A A 0.2883559238953020.302973372778244
0.284526668922555A A A LNCV6_134294_PI430048170 mRNA
ATAAAGAACAATATGCCTTTCTCTACAAGGAAAAGCTGGTGTCTGTGAAGAGGAGTTATC NM_004944 RefSeq chr3
- 58192625 58211003 DNASE1L3 1776 "deoxyribonuclease I-like 3, transcript variant 1"
GO:0004536|GO:0006309|GO:0005509|GO:0004520|GO:0005634|GO:0006259|GO:0016888|GO:0010623|GO:0003
677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140040_PI430048170 0.2371285693359920.72803698922451 3.31869102572979
4.15433017626876 4.13554663497774 P P P 3.95600382079548 4.60062637834516
4.49335165195011 P P P LNCV6_140040_PI430048170 mRNA
CTAGAAGTAGCTGTGTAGGTGGTGGTTGGCATTATAGTTGCATTTATATATGTTCTTATT NM_001101426 RefSeq
chr7 - 16087526 16421322 ISPD 729920 "isoprenoid synthase domain containing, transcript variant
1" GO:0007411|GO:0016779|GO:0008299|GO:0035269 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130035_PI430048170 0.00275495747337068 1.62988068037746 11.3480658450339
11.5220516611739 11.3889360827592 P P P 10.7117353644631 10.6891260069359
10.7490467505865 P P P LNCV6_130035_PI430048170 mRNA
CTTCTCCATGTTTTGTGGCCTTCGGTTGTAATAAACTTGGCTTCTTTATACATCTGTAAA NM_003434 RefSeq chr20 +
18288282 18316996 ZNF133 7692 "zinc finger protein 133, transcript variant 1"
GO:0005515|GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127389_PI430048170 0.0592449002260315 0.4071479610138182.6540648134713
1.46600814875523 2.73152949752399 A A A 4.06858597747329 3.51197859769035 3.3743837773791
P P P LNCV6_127389_PI430048170 mRNA
GTCAGGAAATTGTAGTGAAAGAACTAATGGTTTTGTTTTTTGGAATAAAGGCACCTAAGC NM_001270378 RefSeq
chr8 - 100520771 100559711 ANKRD46 157567 "ankyrin repeat domain 46, transcript variant 3"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143160_PI430048170 0.0033643322352508 0.4751563689602 8.48786588690087
8.23627431611089 8.58491246889279 P P P 9.34584379187789 9.41206462103436

9.75883031831279 P P P LNCV6_143160_PI430048170 mRNA
GATATGTTTCCAATCTTTAAATGACCTTGCCCTGTCCAATAAATAAATGATTGTCTCACC NM_173470 RefSeq chrX
- 135962071 135973975 MMGT1 93380 membrane magnesium transporter 1
GO:0072546|GO:0015693|GO:0005794|GO:0016020|GO:0000139|GO:0031901|GO:0015095|GO:0016021|GO:0005
769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134238_PI430048170 0.3379576752656560.8489701521190081 2.0024773864009
11.8918343864827 12.0462487799242 P P P 11.9868979024848 12.062081900999
12.5401023624513 P P P LNCV6_134238_PI430048170 mRNA
TCCCCTTGCACTTGTGAAAACACTTTGAGCGCTTTAAGAGATTAGCCTGAGAAATAATTA NM_017491 RefSeq chr4
- 10074338 10116949 WDR1 9948 "WD repeat domain 1, transcript variant 1"
GO:0030054|GO:0005884|GO:0007605|GO:0002102|GO:0030168|GO:0003779|GO:0005576|GO:0042995|GO:0005
829|GO:0048713|GO:0005737|GO:0007596|GO:0002576|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129250_PI430048170 0.5089278187790330.7668748641413260.344840935928618
0.3906519123011160.309611705407472 A A A 1.35663918196177 0.286628831473735
0.264324499895555 A A A LNCV6_129250_PI430048170 mRNA
GGGTGCCATTTTGTTTTCAAAAGTTATTCATTGTAATCCACTGTTTTGGCTTTCATGAAC NM_004681 RefSeq chrY +
20575710 20593154 EIF1AY 9086 "eukaryotic translation initiation factor 1A, Y-linked, transcript variant 1"
GO:0005515|GO:0003743|GO:0006413 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130794_PI430048170 0.6025454261795730.9768580596245420.426960033249062
0.4010480652411340.243811373557482 A A A 0.3612041759403290.424164093623976
0.393824732311571 A A A LNCV6_130794_PI430048170 mRNA
TACTCATTGAAAACATGGTGCTTGTTTTTCCTCACTCAACAGGAAGCCTGGAGCTAGGCA NM_201546 RefSeq chr1
- 54138994 54153006 CDCP2 200008 CUB domain containing protein 2 GO:0005576 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_97884_PI430048170 0.2107623683217690.8552620110158785.07503510368214 5.31653460917633
5.44838610649362 P P P 5.33701086075642 5.48172598350316 5.69921674708587 P P P
LNCV6_97884_PI430048170 mRNA
GGATCCTAAAAATGTACTGATAACTGATTTCTTTGGAAGTGTACGGAAAGTGGAAATTAC NM_005482 RefSeq chr1
- 77088981 77219447 PIGK 10026 "phosphatidylinositol glycan anchor biosynthesis, class K"
GO:0005515|GO:0006501|GO:0034235|GO:0016255|GO:0003756|GO:0030176|GO:0003923|GO:0004197|GO:0016
020|GO:0006457|GO:0005789|GO:0006508|GO:0042765|GO:0044267|GO:0043687 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128911_PI430048170 0.0309585700553475 2.44867655162872 3.6300480541916
3.95600382079548 3.88316102244997 P P P 1.93831157759237 2.88529611279277
2.63197507042016 A P P LNCV6_128911_PI430048170 mRNA
GATCTCCTGCTGCCTTTTCTGGAGTTTGTAAAATTGTTCCTGAATACAAGCCTATGCGTG NM_003881 RefSeq chr20
+ 44715243 44727811 WISP2 8839 WNT1 inducible signaling pathway protein 2
GO:0007165|GO:0005178|GO:0005886|GO:0060548|GO:0007267|GO:0005578|GO:0007155|GO:0008201|GO:0005
615|GO:0001558|GO:0070062|GO:0005520 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110453_PI430048170 0.1830045065770991.21178009938341 5.84317258143487
5.83843372526279 5.62879157532287 P P P 5.77852535793839 5.35322888471709 5.3095272849656
P P P LNCV6_110453_PI430048170 mRNA
AAACTGTGGGGAATGCATGAAAGGCGTGATCACCGGTATCTCTCCTAAATGTGTGATCAA NM_001136499 RefSeq
chr19 - 52064465 52095765 ZNF841 284371 zinc finger protein 841
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_57936_PI430048170 0.7124978838040510.9210257157397316.43741091661176 6.32758276259873
6.57577971378289 P P P 6.35168385888504 6.30873555748943 6.95338759280696 P P P

LNCV6_57936_PI430048170 mRNA
CCAGTCATTTGAACAACCCACATAGTAGACACAGAAAACGAATAAAAGAACTGAGTGAAG NM_004705 RefSeq
chr11 - 76349956 76380965 PRKRIR 5612 "protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor), transcript variant 1"
GO:0007165|GO:0008285|GO:0046983|GO:0006950|GO:0005634|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135792_PI430048170 0.0442143728333172 0.5761027674508285.17348646312287 4.61970234230554 4.59543115394571 P P P 5.54577113789452 5.67848267658362 5.62504517246414 P P P LNCV6_135792_PI430048170 mRNA
TGTCTGTTCATAGAGGACTTACTAAGTGCCAGCCACCATGATAAGCTAAAGTTAATTATT NM_001105206 RefSeq
chr6 - 112107930 112254715 LAMA4 3910 "laminin, alpha 4, transcript variant 1"
GO:0005515|GO:0030334|GO:0005102|GO:0005605|GO:0005606|GO:0005576|GO:0030155|GO:0005604|GO:0031012|GO:0045995|GO:0030198|GO:0007155|GO:0070062|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137756_PI430048170 0.00335892606905913 1.16065552863712 9.57921513399316 9.66159391976034 9.59413167177867 P P P 9.42444437105996 9.40286238326406 9.36349591857405 P P P LNCV6_137756_PI430048170 mRNA
TGGGTGCACCTGTTACTGTTGGGCTTTCCACTGAGATCTACTGGATAAAGAATAAAGTTC NM_001024809 RefSeq
chr17 + 40342018 40357643 RARA 5914 "retinoic acid receptor, alpha, transcript variant 2"
GO:0005515|GO:0001657|GO:0010467|GO:0032753|GO:0000790|GO:0003417|GO:0032754|GO:0006367|GO:0003700|GO:0033189|GO:0003707|GO:0003708|GO:0007283|GO:0007281|GO:0031076|GO:0002068|GO:0043551|GO:0043025|GO:0032355|GO:0032689|GO:0007565|GO:0000977|GO:0009986|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144652_PI430048170 0.4367150240649560.7907457101113461.58239229560776 0.3135253456672531.04537738163233 A A A 1.80583482623663 1.33712019393719 0.960539016781123 A A A LNCV6_144652_PI430048170 mRNA
CTAGTGGCCCTTCACACAACTTTTGAATCTCTAAAAATCCATAAAATCCTTAAAGAACTG NM_001243 RefSeq chr1 + 12063376 12144207 TNFRSF8 943 "tumor necrosis factor receptor superfamily, member 8, transcript variant 1"
GO:0007165|GO:0005737|GO:0043065|GO:0008285|GO:0005886|GO:0042535|GO:0016021|GO:0071260|GO:0070062|GO:0045556|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92373_PI430048170 0.8599959469789330.9745817437466 10.0270754478564 10.0216210713609 10.4159591419053 P P P 10.0539950514225 10.051386105497 10.4664245564839 P P P LNCV6_92373_PI430048170 mRNA
CACTGAGAGAACAAATCGATTGGTCCTCCTTGGCAGAAATTTAGATAAGGATATCCTTAA NM_172003 RefSeq chr2 + 113437690 113496204 CBWD2 150472 COBW domain containing 2 GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137562_PI430048170 0.0982032810290995 1.64645610614314 3.4598382920209 3.00614578625473 3.26935153187558 P A P 1.93538468799309 2.64438231203707 2.87612886875308 A P P LNCV6_137562_PI430048170 mRNA
GCGGTAGCTATTTGTTTACATGCAGATTTTTGTAATAAAGGCTATTTCCTGATAGTCATG NM_001128850 RefSeq
chr16 - 66921678 66925536 RRAD 6236 "Ras-related associated with diabetes, transcript variant 1"
GO:0006184|GO:0005515|GO:0005516|GO:0005886|GO:0007264|GO:0003924|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67092_PI430048170 0.4621359146851930.9049912970218770.3404469247686510.316694016719487 0.26772409019272 A A A 0.7245725692721930.3041074396096970.285142914901021 A A A LNCV6_67092_PI430048170 mRNA
ATTTTGAACTGGAGAGCAGTGGCCTGAGGGATGAGATTCGGTATCACTACATACACAATG NM_001288713 RefSeq
chr11 + 20669550 21575683 NELL1 4745 "NEL-like 1 (chicken), transcript variant 3"

GO:0005515|GO:0010468|GO:0048471|GO:0030501|GO:0033689|GO:0005509|GO:0005576|GO:0005635|GO:0030154|GO:0007399|GO:0045669|GO:2000599|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129305_PI430048170 0.34026982327398 1.02416390386249 0.360529467608475 0.2685179145577990.334308487083724A A A 0.2840728671981640.28254603366546 0.294916358979982A A A LNCV6_129305_PI430048170 mRNA
AACAGTGTTATCTGTACACGAACATACGAGAAAGTATCATCAAACTCAGTCTCAAACTCT NM_001105281 RefSeq chr8 - 81525045 81531315 FABP12 646486 fatty acid binding protein 12
GO:0005215|GO:0006810|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139313_PI430048170 0.215808643996783 1.44788963688026 6.7087857282018 7.34488248463659 7.66755345131885 P P P 7.05865724802983 6.59722236113395 6.56700285955605 P P P LNCV6_139313_PI430048170 mRNA
CGGCCATGTAATATCAGTATATCCCAAGTTAATGAAAGTGTTCATTTACATAGGTAATGG NM_016078RefSeq chr17 + 18781268 18806713 TVP23B 51030 trans-golgi network vesicle protein 23 homolog B (S. cerevisiae)
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_2690_PI430048170 0.0770868233137708 0.22559314361305 0.29934825923807 2.86631409973566 1.10790576340924 A A A 3.86693022652434 4.00057275644732 4.06488529400388 P P P LNCV6_2690_PI430048170 mRNA
CCATACATACTGCAAATGATTGACTTGTTGCATAAATGAAGATCTTCTGTTGTGTGCTTT NM_001278549 RefSeq chr2 + 172555968 172599134 PDK1 5163 "pyruvate dehydrogenase kinase, isozyme 1, transcript variant 1"
GO:0004740|GO:0005515|GO:0010510|GO:0005967|GO:0008283|GO:0008631|GO:0044281|GO:0005524|GO:0010906|GO:0005739|GO:0004672|GO:0006090|GO:0005759|GO:0006006|GO:0006468|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136451_PI430048170 0.0132863424132922 1.58160649834554 6.16046544337049 6.06362294618781 6.01668562554242 P P P 5.2130901531954 5.46489775356622 5.56043825856492 P P P LNCV6_136451_PI430048170 mRNA
TTCAAATCATTTGAGGAGAGGGTTGAGACAACTGTCACAAGCCTCAAGACGAAAGTAGGC NM_001003395 RefSeq chr6 + 125154273 125263498 TPD52L1 7164 "tumor protein D52-like 1, transcript variant 2"
GO:0005515|GO:0048471|GO:0005737|GO:0043281|GO:0046982|GO:0043406|GO:0000086|GO:2001235|GO:0046330|GO:0042803|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_84767_PI430048170 0.126649353216193 0.777852951180202 7.22416266161875 7.16810244822424 7.43917305620314 P P P 7.38216099305986 7.60890495108267 7.89592552571397 P P P LNCV6_84767_PI430048170 mRNA
GATTGAGAGGAAAGAAAGTTCTCTTAGATGTTACTGCTTTTGCTCAGACTTTGCAAAAAA NM_007202RefSeq chr17 - 19904451 19977856 AKAP10 11216 A kinase (PRKA) anchor protein 10
GO:0005739|GO:0007165|GO:0005737|GO:0008104|GO:0005886|GO:0007596|GO:0038032|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141130_PI430048170 0.396922718536194 0.735830908429115 0.491450709975806 0.473315718779203 0.254896356540896A A A 0.400815421316335 1.44452015746092 0.461462726933547A A A LNCV6_141130_PI430048170 mRNA
GATTTAATAACCAGATTTCTTTCTCCAAAACATACACAATTTGTTATTTTAGTAAATACC NM_001128423 RefSeq chr16_KI270853v1_alt + 1053716 1067665 MPV17L 255027 "MPV17 mitochondrial membrane protein-like, transcript variant 1"
GO:0003674|GO:0010730|GO:0072593|GO:0005102|GO:0016021|GO:0005778|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138822_PI430048170 0.00119495146684684 2.25587057166418 4.97239106552659 4.9465522274681 4.65544934081517 P P P 3.61321429975627 3.55735504702912 3.88238709092709 P P P LNCV6_138822_PI430048170 mRNA
CCTGGGTTTCTCTTACTCAATCCCTGGAGTGTAAGCATTTGGATTGTGTCACAGATTACC NM_024709RefSeq chr1

+ 220690285 220699157 C1orf115 79762 chromosome 1 open reading frame 115 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137774_PI430048170 0.0683238028038631 0.7192022699230999.53937274330052
9.14854682975957 9.02351868924302 P P P 9.59545246990894 9.87451174236722 9.7057038868229
P P P LNCV6_137774_PI430048170 mRNA
GGAGGCCACAGGCCAGCTATTGTAAAAGCTTTTTATTTTAGTAAAATATACAGAAGTTCT NM_000199RefSeq chr17
- 80209279 80220400 SGSH 6448 N-sulfoglucosamine sulfohydrolase
GO:0005975|GO:0009405|GO:0006027|GO:0044281|GO:0016250|GO:0008484|GO:0006029|GO:0003824|GO:0030
203|GO:0046872|GO:0070062|GO:0043202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127937_PI430048170 0.3564470413434040.8061398421554523.17053056580115
2.19214118130874 2.74241976729525 P A A 3.2075822900801 3.20460977209556
2.74027267777827 P P P LNCV6_127937_PI430048170 mRNA
TCTTCCTCTCCTTAATCCAACATAGCAGCTGTGATGTCATTTCTGTATTTCAGGAAGACT NM_031246RefSeq chr19
- 43064209 43082741 PSG2 5670 pregnancy specific beta-1-glycoprotein 2
GO:0003674|GO:0007565|GO:0016477|GO:0005576|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129727_PI430048170 0.4158475898652580.87983768681083 0.360468600085699
0.4105144202439660.333435775216881A A A 0.8598834343767780.360769916033452
0.381793256165349A A A LNCV6_129727_PI430048170 mRNA
GTGGGAGGTTATCTTGTTCTATTCAAGTTGCTATAAAAATAAAAACTACCATAGACTGGG NM_003820RefSeq
chr1_KI270762v1_alt + 107554 116812 TNFRSF14 8764 "tumor necrosis factor receptor superfamily,
member 14, transcript variant 1"
GO:0005515|GO:2000406|GO:0005886|GO:0050830|GO:0046642|GO:0031295|GO:0050731|GO:0009615|GO:0033
209|GO:0050829|GO:0006955|GO:0002741|GO:0005031|GO:0001618|GO:0005887|GO:0016032|GO:0007166|GO:0
009897|GO:0031625. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126912_PI430048170 0.8502937565742511.04822966935907 0.986032599175915
0.3897714543689640.372789066017588A A A 0.7488042616656880.471366626174785
0.387312170634421A A A LNCV6_126912_PI430048170 mRNA
GTGTGGAAGGCACAGTCAAATAATAGTTCTGTGTACTGTTCTTGTAACATTAGATCTTTT NM_014361RefSeq chr11
+ 99020975 100358885 CNTN5 53942 "contactin 5, transcript variant 1"
GO:0005737|GO:0005886|GO:0007605|GO:0031225|GO:0007155 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141895_PI430048170 0.1741166523870271.67282664139353 3.69653342409996
3.29456044236588 4.36982403041971 P P P 3.63193986806043 2.98038205953649
2.50744031729419 P P P LNCV6_141895_PI430048170 mRNA
CCTGAGCCATTCTGAATTTCTACACAATAAATGCAGTTTATGTCTTTTGGGTCTTAATAG NM_006584RefSeq chr17
- 34927858 34961509 CCT6B 10693 "chaperonin containing TCP1, subunit 6B (zeta 2), transcript variant
1" GO:0006457|GO:0005832|GO:0008565|GO:0051082|GO:0007283|GO:0051131|GO:0015031|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142746_PI430048170 0.0010360190703748 1.44001767233153 12.159552296493
12.2304523186754 12.1737417750877 P P P 11.7337182735137 11.6483022252033
11.6013097764771 P P P LNCV6_142746_PI430048170 mRNA
TTCCAGGAGCCGCTCATAGACCCCGCCTGCCGTCCGGTCAATAAAATCCGCCTGACTCCT NM_001099456 RefSeq
chr16 + 2019519 2020755 NPW 283869 neuropeptide W
GO:0005515|GO:0007631|GO:0001664|GO:0007186|GO:0007218|GO:0005576 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_99809_PI430048170 0.3751175207182271.50024928119898 2.51914498723842 1.08026481937083
1.94775797024061 A A A 0.5468380059461391.24840094345416 1.98735913110362 A A A
LNCV6_99809_PI430048170 mRNA

CAGTATCCTCATTGGAACCAATAAATTCTACGAAATCGACATGAAGCAGTACACGCTCGA NM_001206999 RefSeq chr12 - 119685789 119877291 CIT 11113 "citron rho-interacting serine/threonine kinase, transcript variant 1"
GO:0005515|GO:0017124|GO:0005886|GO:0048699|GO:0007283|GO:0015629|GO:0046872|GO:0035556|GO:0000910|GO:0005083|GO:0000086|GO:0043025|GO:0007030|GO:0007091|GO:0005773|GO:0032467|GO:0031985|GO:0030165|GO:0005524|GO:0001726|GO:0016358|GO:0050790|GO:0007067|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140855_PI430048170 0.000738988513678389 0.4351917884849524.81886223231108 4.85809466506903 4.59158786943046 P P P 5.83326224052023 5.88977378882172 6.14143527743974 P P P LNCV6_140855_PI430048170 mRNA
GTGGATTTACTAGTAATATGTGAGCCAAGGACGATAAAGCTCCTGATTCTGATGGGTATC NM_194358 RefSeq chr12 - 56202503 56221931 RNF41 10193 "ring finger protein 41, E3 ubiquitin protein ligase, transcript variant 2"
GO:0000209|GO:0005515|GO:0004842|GO:0030336|GO:0005135|GO:0008285|GO:0016881|GO:2000114|GO:0006914|GO:0097191|GO:0051896|GO:0051865|GO:0005829|GO:0051091|GO:0045619|GO:0043408|GO:0031386|GO:0045637|GO:0008270|GO:2000377|GO:2000379|GO:0017160|GO:0005128|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135136_PI430048170 0.0386092545179002 1.21568193514312 9.67007182451844 9.72827025435854 9.90375872950232 P P P 9.44539637479943 9.45850449853449 9.56050454610503 P P P LNCV6_135136_PI430048170 mRNA
ACAGACATTTAGGTATCTCAGGTCCTTTCTAAGTGTCCCTTTCCTATGTATGCATTTCCT NM_021035 RefSeq chr20 - 49245900 49278219 ZNFX1 57169 "zinc finger, NFX1-type containing 1" GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64965_PI430048170 0.0381267549755189 1.41469250319737 5.27339858203996 5.67057821756355 5.31386758370827 P P P 4.94048055343327 5.05943546357204 4.77653295933148 P P P LNCV6_64965_PI430048170 mRNA
TACGACAAGATCCTGCTTTTCAAACATGACCCCACGTCGGCCAACCTCCTGCAGCTGGTG NM_016457 RefSeq chr19 - 46674315 46717127 PRKD2 25865 "protein kinase D2, transcript variant 1"
GO:0005515|GO:0050852|GO:0008219|GO:0030949|GO:0035924|GO:0005886|GO:2000573|GO:0038033|GO:0005634|GO:0046872|GO:0032757|GO:0035556|GO:0051091|GO:0005737|GO:0033138|GO:0051092|GO:0046777|GO:0018105|GO:0045944|GO:0070374|GO:0007155|GO:0048010|GO:0005794|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137516_PI430048170 0.4123569898062381.32572360721781 1.231172888427 0.2610101475861740.269697351607611 A A A 0.2526869260811750.263864718373628 0.253296929129626 A A A LNCV6_137516_PI430048170 mRNA
GCTCCAGCCAGAGAACAATCTTTTATTTCTGTTGTTTCCTTATTAAAATGGTGTTTTTGG NM_178860 RefSeq chr17 - 28954928 29006063 SEZ6 124925 "seizure related 6 homolog (mouse), transcript variant 1"
GO:0008344|GO:0048471|GO:0005886|GO:0005783|GO:0060079|GO:0005615|GO:0060074|GO:0043197|GO:0021680|GO:0043198|GO:0090036|GO:0043025|GO:0016021|GO:2000171|GO:1900006 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_18386_PI430048170 0.1537382936918491.8691610069515 2.3215817584199 0.993669290120686 1.52568370763877 A A A 0.5508757168042630.426649243201735 1.30507914930258 A A A LNCV6_18386_PI430048170 mRNA
GACAGAAGGGAGTATTGTATCTTGCATGTCATCAATTAATTAAACTTTTCAGCATCATCC NM_001242698 RefSeq chr6 - 13279294 13295586 LOC100130357 100130357 uncharacterized LOC100130357 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136032_PI430048170 0.1236146120582020.7118567812713436.25267978049351 5.56023000110507 6.10387560873956 P P P 6.36575732499185 6.57506583409888 6.52677083799731 P P P LNCV6_136032_PI430048170 mRNA

ATGTGGCTGGAACACAAACAATCTTTGAAAGAAATAAATGTGCACACAGAACACTACAAA NM_015500 RefSeq chr21 - 41885109 41953890 C2CD2 25966 "C2 calcium-dependent domain containing 2, transcript variant 1" GO:0005634|GO:0005576|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131257_PI430048170 0.2360283447790720.8988288004701210.462916978439182
0.4793285314311080.380996466422279 A A A 0.6266190242967 0.418394888755313
0.725015737283886 A A A LNCV6_131257_PI430048170 mRNA
TGAGCAGTTTTGAGTGTGTTTGTCAGTTAAAGAGAGGAATTAGGTTAGTTTTCATTTGGG NM_001128303 RefSeq chr13 + 43879283 43893932 LACC1 144811 "laccase (multicopper oxidoreductase) domain containing 1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133596_PI430048170 0.4242286066700140.72180153628017 1.28878062780067
2.83724937078465 3.04130215862092 A A P 2.32777372212119 3.27118769744574 3.3242991143235
A P P LNCV6_133596_PI430048170 mRNA
CATATCAGTCTTTTACCATGTCATTCTTCTTTGCCACACATTAAATGTCACTCAGCTCTA NM_001080470 RefSeq chr1 - 119619376 119647767 ZNF697 90874 zinc finger protein 697
GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0005575|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133925_PI430048170 0.0865998090072912 1.23067660883482 9.6602888302405
9.71487332551337 9.95537923758614 P P P 9.47455741873878 9.31019539997611
9.64535148935323 P P P LNCV6_133925_PI430048170 mRNA
GCTGCTTTACACAATCTGTTCTATAAGGTTCAGGTGTTTTCAAGTTGGAAAGATCATAAA NM_018264 RefSeq chr7 + 66996804 67239520 TYW1 55253 tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)
GO:0005737|GO:0051539|GO:0005506|GO:0010181|GO:0016491|GO:0005654|GO:0016829|GO:0008033|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140071_PI430048170 0.0609907044053086 0.88155984228673 10.6570626425818
10.5453940872068 10.7372342429254 P P P 10.7950668006029 10.8072812557817
10.8875985053551 P P P LNCV6_140071_PI430048170 mRNA
TAAGAATTAGGGAAATAATTTGGTGGAAACCGGGAATGAGTTCTATTCTTAAACAGCCTT NM_015169 RefSeq chr8 + 66429027 66430733 RRS1 23212 RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)
GO:0000794|GO:0005783|GO:0002244|GO:0042254|GO:0005730|GO:0005634|GO:0007080 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140353_PI430048170 0.8014459362038771.00503753950526 0.448403496716605
0.48226833559503 0.418326518411417 A A A 0.4800724051145730.412780983481082
0.434285542698932 A A A LNCV6_140353_PI430048170 mRNA
CACGTCATGTGGATTCATTTTGAATTGGTGCTATTGGTATTTCCTCTGTTATTGCTAATA NM_018911 RefSeq chr5 + 140841321 141012344 PCDHA8 56140 "protocadherin alpha 8, transcript variant 1"
GO:0005887|GO:0005509|GO:0007155|GO:0007156|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143245_PI430048170 0.0133528142108999 0.2845424088400883.67097720568502
3.62678652932239 3.69642529547566 P P P 5.05476036747802 5.50141929336867
5.78660668548686 P P P LNCV6_143245_PI430048170 mRNA
GACTTTGCTATCGTGCCTAAAGCTCTAAATATAGGTGAATGTGTGATGAATACTCAAAAA NM_012343 RefSeq chr5 + 43602688 43705566 NNT 23530 "nicotinamide nucleotide transhydrogenase, transcript variant 1"
GO:0050661|GO:0006099|GO:0072593|GO:0005743|GO:0008746|GO:0044281|GO:0008750|GO:0005739|GO:0005746|GO:0051287|GO:0016020|GO:0003957|GO:0045454|GO:0016021|GO:0044237|GO:0055114|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136844_PI430048170 0.73418299984189 1.15254841805513 1.38204568570119
0.406898160335515 0.312852738824242 A A A 0.3979653813831810.331112560003591
0.936494596694452 A A A LNCV6_136844_PI430048170 mRNA
TTTTTCGTTCCTTCCCTGTTAGGGGAAGATACACCTGGACGAGAATATATCCTCACCTCA NM_001146683 RefSeq

chr14 + 21098936 21103724 TMEM253 NA transmembrane protein 253 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142858_PI430048170 0.00949998919421471 0.4817534344851094.46589710525252 4.13135186893263 4.72194422827737 P P P 5.28739496711425 5.54669925852995 5.67896805130426 P P P LNCV6_142858_PI430048170 mRNA
CGTGAATTGACATACAGCCCATAACTTTATAATGGCTGCTCATTTATCTTATCTTTCAGT NM_014415RefSeq chr3 - 101649438 101677144 ZBTB11 27107 zinc finger and BTB domain containing 11
GO:0008150|GO:0003674|GO:0006355|GO:0005654|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88644_PI430048170 0.5039815811420090.2775112110606720.9627196561709530.515609352977195 0.475628818274807A A A 3.85626465993807 0.418993710465747 0.449435653283886P A A LNCV6_88644_PI430048170 mRNA
GCTGTTCTCTGTATCGTGATCTATCCTCAACAACAACAGAAAAAAGGAATAAAATATCCT NM_001164836 RefSeq chr11 - 117836975 117877031 FXYD6 53826 "FXYD domain containing ion transport regulator 6, transcript variant 4" GO:0008150|GO:0003674|GO:0034220|GO:0005886|GO:0016021|GO:0055085|GO:0005216 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131373_PI430048170 0.0765177913330718 0.7411753565764615.5362196892575 15.191343871378 15.0796351956108 P P P 15.6844536894455 15.7788558801574 15.678121251824 P P P LNCV6_131373_PI430048170 mRNA
CCCCCCTCCCCTCCCTTTTTGTATAATTTAATAAAGAAATGGTCGCGCTTCTGTTTTTAA NM_002824RefSeq chr12 + 6766374 6770952 PTMS 5763 parathymosin GO:0006260|GO:0005634|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137611_PI430048170 0.1815971765182660.6877429518393330.391519368832633 0.4467807990188370.344946198692959A A A 1.16979098487854 1.11795652129963 0.395925050353046A A A LNCV6_137611_PI430048170 mRNA
TTTGCCTTTGCCCTTGAGCTGAGATTTCTGTTTTCCAAGTTGCTTTTCTGTTATGAAATG NM_203407RefSeq chrX + 51406914 51408837 CXorf67NA chromosome X open reading frame 67 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133510_PI430048170 0.00167682090513393 4.45414130698767 5.41870876600604 5.52751938704831 5.29277248699781 P P P 3.13344315914084 3.55288134825342 3.04416953692378 P P P LNCV6_133510_PI430048170 mRNA
GTCAAGACAATCCATTCCATTCAAGACCAATTTACTCTCAAATTTTGCCAACACAGAAAT NM_152421RefSeq chr9 + 136712571 136724718 FAM69B 138311 "family with sequence similarity 69, member B" GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144964_PI430048170 0.0253106349306982 0.5613903489643664.25647315444449 4.2310645961931 4.74540228410106 P P P 5.36798970517333 5.26365900014191 5.15227436223424 P P P LNCV6_144964_PI430048170 mRNA
GTGTGAAATCACAAATGTTTTTTCCTTCTTGGTTGCTGCAGCCTGGTGGATGTTCATGGA NM_020198RefSeq chr17 - 63745249 63773728 CCDC47 57003 coiled-coil domain containing 47
GO:0005515|GO:0006983|GO:0016020|GO:0005783|GO:0005509|GO:0016021|GO:0009791|GO:0001649|GO:0055074 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133030_PI430048170 0.3555081524456140.7017724258738490.478921255908581 2.94856652389993 0.745678213755914A A A 2.74932694804396 2.1605749044365 2.06377557900333 P A A LNCV6_133030_PI430048170 mRNA
CCCACCTGGCCTGTGTGACTGGGAGAATCTCTCTTTTTATTAAATGTGCTTCAAGTTTTA NM_001161814 RefSeq chr13 + 105465866 105491034 DAOA 267012 "D-amino acid oxidase activator, transcript variant 3" GO:0005739|GO:0048471|GO:0005794|GO:0043085|GO:0019899|GO:0008047 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127668_PI430048170 0.9107540735403410.9972082465526381 4.9324781422081

14.8231697549927 14.933810966719 P P P 14.8743766570802 14.9169687361261
14.9126044918258 P P P LNCV6_127668_PI430048170 mRNA
GCTGCTGTGTGTGGTCTCAGAGGCTCTGCTTCCTTAGGTTACAAAACAAAACAGGGAGAG NM_030662RefSeq chr19
- 4090321 4124129 MAP2K2 5605 mitogen-activated protein kinase kinase 2
GO:0005515|GO:0051403|GO:2000147|GO:0002756|GO:0007173|GO:0000165|GO:0007411|GO:0002755|GO:0070
371|GO:0005938|GO:0004708|GO:0005794|GO:0038124|GO:0038123|GO:0034134|GO:0018108|GO:0002224|GO:0
030165|GO:0008543|GO:0045087|GO:0009898|GO:0034166|GO:0035666|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143097_PI430048170 0.937473662948408 0.993051856711157 0.932827305106537
0.430932868240732 0.247133944570135 A A A 0.379885228640852 0.876984034016264
0.419310738894029 A A A LNCV6_143097_PI430048170 mRNA
AGGAGCTCTGCTGAGACTCTCAAGGGAGCCAGTGAAAGAAATAGAAATAAAGCCTGTGTT NM_152612 RefSeq
chr22 + 21632796 21637327 CCDC116 164592 coiled-coil domain containing 116 NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_132259_PI430048170 0.0236211556532063 0.406022915392548 4.83859609021488
4.39338942771333 4.50901222591265 P P P 5.33885800202402 5.9900917072812
6.21481311474063 P P P LNCV6_132259_PI430048170 mRNA
GTTTGTCCTAAGGTGTTTAAAACATGTCAACCTTATGTAAGGAAAAATTTCCTGGTCCAA NM_016513 RefSeq
chr6 - 53001299 53061802 ICK 22858 "intestinal cell (MAK-like) kinase, transcript variant 2"
GO:0005515|GO:0000287|GO:0005634|GO:0007275|GO:0005524|GO:0036064|GO:0005829|GO:0035556|GO:0042
384|GO:0007165|GO:0042073|GO:0004674|GO:0051726|GO:0006468|GO:0004693 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_139774_PI430048170 0.362179667463854 1.05222988910708 0.303750126193329
0.291879242811917 0.479382170760342 A A A 0.298040756846975 0.262502033299446
0.301539809593197 A A A LNCV6_139774_PI430048170 mRNA
ATAATAACTAGATCTCCTGTAATTTTGTAGTAGTTGATGACCAATCTCTGTGACTCGCTT NM_000817 RefSeq chr2
+ 170816689 170861149 GAD1 2571 "glutamate decarboxylase 1 (brain, 67kDa), transcript variant
GAD67"
GO:0005515|GO:0012506|GO:0046982|GO:0005886|GO:0042493|GO:0006538|GO:0007268|GO:0018352|GO:0007
269|GO:0005622|GO:0047485|GO:0004351|GO:0030170|GO:0061202|GO:0042136|GO:0016595|GO:0006540|GO:0
009449 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133364_PI430048170 0.00812012082100872 0.585544474841772 9.14245721945027
9.03777169123146 9.2722060501448 P P P 9.79447530047898 9.81220415854264
10.1442268779547 P P P LNCV6_133364_PI430048170 mRNA
TTAGTACCTTGCCACTCTTTTAAAACGCTGCTGTCATTTCCCATTTCTTAGTACTAATGA NM_001204410 RefSeq
chr17 + 77089152 77217099 SEC14L1 6397 "SEC14-like 1 (S. cerevisiae), transcript variant 7"
GO:0005794|GO:0016020|GO:0006810|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_63170_PI430048170 0.997074472449602 1.02496926192649 0.47205775826703
1.1386832095678 0.28300020714483 A A A 0.909934098517143 0.514714453846149
0.465575764271619 A A A LNCV6_63170_PI430048170 mRNA
AGGGCTTCAGCCCTAAGAAGTCAGCTTCCCAGGAATCCACTCTGAGTGATGACTCCACGC NM_174920 RefSeq
chr17 - 50111308 50129882 SAMD14 201191 "sterile alpha motif domain containing 14, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133776_PI430048170 0.954223505334187 1.10378714552239 2.44891253317421
0.579444553610161 1.01035197864582 A A A 1.37372021669979 0.916093658393884
1.86672167156595 A A A LNCV6_133776_PI430048170 mRNA
GTGCAGTCCTGAGATGATTACTCTTATTTGGTGTGCTGAAAATTTGAGTTGACAAAATAA NM_020817 RefSeq
chr3 - 113964136 114056613 KIAA1407 57577 KIAA1407 NA . NA - . NA NA

NA NA NA NA NA NA NA
LNCV6_142925_PI430048170 0.698546162991977 1.00459623367267 0.419243670623846
0.427125730763988 0.389417211581879 A A A 0.420434342912999 0.384033592506906
0.411496028535714 A A A LNCV6_142925_PI430048170 mRNA
CTGAACCATTGTGGTAAACTTTTGGAGTTGATATGGAATCACTTTAATGCTGTTTTCACA NM_001184749 RefSeq
chrX - 143622789 143636107 SLITRK4 139065 "SLIT and NTRK-like family, member 4, transcript variant
1" GO:0016021|GO:0007409 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99759_PI430048170 0.24762568107638 1.13970606831572 6.15326554153443
5.81101005315988 5.91768141264454 P P P 5.58843656210462 5.90296738729843
5.82773287520223 P P P LNCV6_99759_PI430048170 mRNA
AAGACGTCCGAATTCGAGATCCAAACCAAGGAGGAAAGGATATCACAGAGGAGATCATGT NM_182917 RefSeq
chr3 + 184315163 184335358 EIF4G1 1981 "eukaryotic translation initiation factor 4 gamma, 1,
transcript variant 1"
GO:0005515|GO:0008286|GO:0010467|GO:0016281|GO:0019221|GO:0003743|GO:0006412|GO:0006413|GO:0005
829|GO:0000184|GO:0016020|GO:0006446|GO:0016032|GO:0044267|GO:0000289|GO:0008135|GO:0000288 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140671_PI430048170 0.0632842387094311 1.26225284187883 6.60282162340139
6.94065073968674 6.69049129109898 P P P 6.51180617083189 6.37951873057118
6.35112510710702 P P P LNCV6_140671_PI430048170 mRNA
AAGAAGGCAATTTTCATATTGTTTCTACGGGATGGTTTTGGTTCCCTTCCCTTCCCACCC NM_015898 RefSeq
chr19 - 4045217 4066818 ZBTB7A 51341 zinc finger and BTB domain containing 7A
GO:0035035|GO:0005515|GO:0007275|GO:0005634|GO:0000122|GO:0045892|GO:0003677|GO:0046872|GO:0030
154|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143203_PI430048170 0.00417125762371807 1.1952698977134 12.0660743866081
12.1793246905408 12.1227815215956 P P P 11.841649386921 11.9155560679072
11.8398878953968 P P P LNCV6_143203_PI430048170 mRNA
TGACATATGAAGATTATGGTTCTGCCAGGGCTCCCCTCCCTGCCTGTCCCCAAGTCCTCA NM_022104 RefSeq
chr20 + 45934677 45948023 PCIF1 63935 PDX1 C-terminal inhibiting factor 1
GO:0010923|GO:0015630|GO:0005654|GO:0045171 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137361_PI430048170 0.0239534214307111 0.246045659759018 2.68501467349604
2.95167435516366 1.70917430363495 A P A 4.34918242838041 4.62183141935924
4.69301880715979 P P P LNCV6_137361_PI430048170 mRNA
AGTTTTCATCCTGTTCCAGCAGTGCCTCTGGTACTTAAAAAACAGTTTATTCTTTTTGAA NM_001164824 RefSeq
chr1 - 34850361 34859045 SMIM12 113444 "small integral membrane protein 12, transcript variant
1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141541_PI430048170 0.163581619884393 1.16228400113829 9.75206642541645
9.99704351016895 9.87080557845847 P P P 9.47263452464268 9.65104559021685
9.83323835975764 P P P LNCV6_141541_PI430048170 mRNA
TTGCCTCTTTCCATAATCCGTGGTTTCAGTTTGACTTTGTATATAAAGTTGGGGTTTTTT NM_021174 RefSeq chr8
+ 22605025 22620470 CCAR2 57805 "cell cycle and apoptosis regulator 2, transcript variant 1"
GO:0008380|GO:0005515|GO:0044609|GO:0000790|GO:2000003|GO:0005634|GO:0032435|GO:0034605|GO:0005
737|GO:0031647|GO:0032784|GO:0005759|GO:0005681|GO:0009411|GO:0006397|GO:0004857|GO:0043065|GO:0
000993|GO:0043086|GO:0043653|GO:0006974|GO:0007049|GO:0042752|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135318_PI430048170 0.240920650632711 0.764098577801298 4.25417236396635
3.53458489544653 3.75142444321912 P P P 4.07594629845857 4.62131891023844
4.02572043698479 P P P LNCV6_135318_PI430048170 mRNA
CTAAGTAAAGACCGAGTTGAAAAGCGCATAAAAACAAAGGCTCTTTTCAGAGCCACTTCA NM_021066 RefSeq

chr6 - 27814301 27814740 HIST1H2AJ 8331 "histone cluster 1, H2aj" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_102550_PI430048170 0.19981199557724 1.1171206665867 8.06996633296567
8.03614072789174 7.96131887639944 P P P 7.9409670793039 7.9538433498786
7.67908723417416 P P P LNCV6_102550_PI430048170 mRNA
GATTCGTCCCATTCTCGTCCTCATGGTGGACAAGAAACTGGTGGTGGTTTTCGGAGGCAC NM_020677 RefSeq
chr16_KI270855v1_alt - 163999 177218 NMRAL1 57407 NmrA-like family domain containing 1
GO:0048471|GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_113205_PI430048170 0.313341686689568 1.33982540669994 0.47991345459941
1.30376691771784 0.47260838092544 A A A 0.303027983652187 0.411902364990014
0.438291786859167 A A A LNCV6_113205_PI430048170 mRNA
TATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACG NM_013278 RefSeq
chr16 + 88638592 88640474 IL17C 27189 interleukin 17C
GO:1900017|GO:0006954|GO:0007267|GO:0030223|GO:0005615|GO:0005125|GO:0007166 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_53510_PI430048170 0.0089176765999514 0.522330098544302 6.50630205299046
6.52862697636341 6.81549044516644 P P P 7.29957574425463 7.53156016167187
7.8064901193219 P P P LNCV6_53510_PI430048170 mRNA
TCAACATATCCCTAAGCTAAGGGAAGAGGAAGGAATAACAACTCAGTGAAAAGATGGTCT NM_001412 RefSeq
chrX - 20124517 20141848 EIF1AX 1964 "eukaryotic translation initiation factor 1A, X-linked"
GO:0005515|GO:0010467|GO:0003743|GO:0044267|GO:0006412|GO:0008135|GO:0006413|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134471_PI430048170 0.0732821798263929 2.4437289995235 4.5227245317629
3.55024245929759 3.18316811244607 P P P 2.92753418626161 2.59427065271601
2.09426247959522 P P A LNCV6_134471_PI430048170 mRNA
CAACCAGAATTAAAGATTCCACAACCAAGATCTGTACAAACATAAAGACAAGTAACCTCA NM_001287580 RefSeq
chr2 - 27781363 27890396 RBKS 64080 "ribokinase, transcript variant 2"
GO:0019303|GO:0046835|GO:0004747|GO:0005524|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131464_PI430048170 0.00376877343113425 1.12425008472978 13.8287839182529
13.8484966143257 13.7804037480256 P P P 13.6337288121043 13.6884785356365
13.6286705164912 P P P LNCV6_131464_PI430048170 mRNA
TCCCTGTGTTCTATTTGAGAGGCGCCTGTCTGGATAAAGTTGTCTTGAAATTTCAAAAAA NM_006555 RefSeq chr7
+ 44200978 44214294 YKT6 10652 YKT6 v-SNARE homolog (S. cerevisiae)
GO:0005794|GO:0005783|GO:0031201|GO:0015031|GO:0006906|GO:0006903|GO:0005829|GO:0006904|GO:0005
739|GO:0006888|GO:0005484|GO:0005737|GO:0000139|GO:0005887|GO:0008152|GO:0000149|GO:0042147|GO:0
030659|GO:0019706|GO:0070062|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141657_PI430048170 0.647398497964335 0.93311282646087 8.74094537583783
8.63167727305623 8.24314819248949 P P P 8.37585346973338 8.69168275141355
8.85370555333284 P P P LNCV6_141657_PI430048170 mRNA
GCGGGAGACAAAAACCACACCTCTTTTTATATAAGGTTTCATATTTAATTTGGTCATGGA NM_015178 RefSeq chr8
+ 22999578 23020197 RHOBTB2 23221 "Rho-related BTB domain containing 2, transcript variant 3"
GO:0051056|GO:0005886|GO:0007264|GO:0005525|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144496_PI430048170 0.602000550733089 0.9642647187704040.542563645841482
0.4985265278711720.265050725406026 A A A 0.4112550285238750.562428379952516
0.501089204056517 A A A LNCV6_144496_PI430048170 mRNA
TCAGAACTCCTTCTGATCAAATGGAATCCAATTTGTACTACTGGCTAAAGGTCCTTTTAT NM_016559 RefSeq chr3

- 179794958 180037053 PEX5L 51555 "peroxisomal biogenesis factor 5-like, transcript variant 1"
GO:0043235|GO:0031267|GO:0016560|GO:0043949|GO:0005052|GO:0000268|GO:0042391|GO:0016558|GO:0045
185|GO:0030425|GO:0005778|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102724_PI430048170 0.700482159081812 0.956790608027323 7.25977966401999
7.35657756322475 7.4466996966964 P P P 7.19273517312511 7.43338513986545 7.604751752001
P P P LNCV6_102724_PI430048170 mRNA
TCATGAGAGACAGAGTAGAAGACGTGATGATGGAGCGAGAATCCCAGTTCAAGGAAAAAC NM_002291 RefSeq
chr7 - 107923800 108003359 LAMB1 3912 "laminin, beta 1"
GO:0048471|GO:0035987|GO:0005615|GO:0031175|GO:0022617|GO:0007411|GO:0030198|GO:0043208|GO:0042
476|GO:0034446|GO:0007155|GO:0070062|GO:0050679|GO:0030335|GO:0007566|GO:0005606|GO:0005607|GO:0
005576|GO:0021812|GO:0005604|GO:0031012|GO:0007162|GO:0043259|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_98746_PI430048170 0.0298709867173339 0.954851523844452 0.396435723378544
0.382073822953568 0.347161891112894 A A A 0.441563863149368 0.453206048122778
0.431216790797476 A A A LNCV6_98746_PI430048170 mRNA
CTGACAAGTAGTTTGACCAGACTTGGAGGAAGGATTCCTTCAAAGTTACCATCCTCAAAG NM_001145006 RefSeq
chr4 + 70430491 70482997 MUC7 4589 "mucin 7, secreted, transcript variant 1"
GO:0005515|GO:0006493|GO:0005796|GO:0016266|GO:0044267|GO:0070062|GO:0043687 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140763_PI430048170 0.0155228982536111 0.310299500507243 4.00315589757517
3.66137622451935 3.88763038219297 P P P 5.09657468141496 5.39372965648862 5.9976227803958
P P P LNCV6_140763_PI430048170 mRNA
AAAGGTACTGAGGAATTGAGGTATGTAAATCAGGTGACATAAACATGAAAATTATGTGCC NM_015139 RefSeq chr1
- 66999331 67054397 SLC35D1 23169 "solute carrier family 35 (UDP-GlcA/UDP-GalNAc transporter),
member D1"
GO:0030206|GO:0006805|GO:0052695|GO:0005461|GO:0048706|GO:0005789|GO:0008643|GO:0006065|GO:0044
281|GO:0016021|GO:0055085|GO:0015787 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141637_PI430048170 0.781073553366686 0.981383637979251 0.274372519599565
0.500689895726252 0.337481365204293 A A A 0.50690740063665 0.400771073579208
0.287406354785135 A A A LNCV6_141637_PI430048170 mRNA
TTTTATAATTCGCTCGTGGTCATTGAATAGAGCAATAAACGGAGCATTTTGAGCAAAACT NM_001278236 RefSeq
chr11 - 18727927 18792721 PTPN5 84867 "protein tyrosine phosphatase, non-receptor type 5
(striatum-enriched), transcript variant 4"
GO:0006470|GO:0005789|GO:0001784|GO:0016021|GO:0035335|GO:0004725 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134886_PI430048170 0.663722795705468 0.943318345561935 0.480431444690703
0.588508771420923 0.526210068641415 A A A 0.4746615265019 0.452864059153058
0.880776282583196 A A A LNCV6_134886_PI430048170 mRNA
GAAACCAAGGGATAAAACTGTTCATGGATGCAACTCAAATTCAGATGATCCTCAACTCAT NM_033272 RefSeq chr2
- 162371406 162838747 KCNH7 90134 "potassium channel, voltage gated eag related subfamily H,
member 7, transcript variant 1"
GO:0007165|GO:0005242|GO:0005886|GO:0005887|GO:0005249|GO:0042391|GO:0007623|GO:0007268|GO:0034
765|GO:0004871|GO:0051291|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110470_PI430048170 0.00115840899581286 1.96399076041504 8.39894843323899
8.56454717685273 8.4037911952066 P P P 7.48218046806077 7.62048915232504
7.33542310900827 P P P LNCV6_110470_PI430048170 mRNA
GAAAAACGCGAGAAGCGGTGTTCCTTCTACACAGAGGCTAGAGTGCGGATCGGCTGAGTC NM_001023561
RefSeq chr19 + 57435324 57445823 ZNF749 NA zinc finger protein 749 NA . NA - . NA NA
NA NA NA NA NA NA NA

LNCV6_143748_PI430048170 0.9204518492958160.9505232847705043.95748547075185
4.43493007790945 4.35955174163247 P P P 4.79104060709799 4.22789635329592
3.83523960838243 P P P LNCV6_143748_PI430048170 mRNA
TTTGTTTGTGAAAGATTGTGCCCATATCCTCAGTTCTTCTTAGCCTCTGCTCCTTCCCTG NM_000374RefSeq chr1 +
45012132 45015669 UROD 7389 "uroporphyrinogen decarboxylase, transcript variant 1"
GO:0005737|GO:0006778|GO:0004853|GO:0005654|GO:0044281|GO:0006782|GO:0006783|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105540_PI430048170 0.2845742103991650.80429505390261 9.03992619280312
9.20100605750685 9.54165641441409 P P P 9.20561166932297 9.61907224027922 9.8704160453209
P P P LNCV6_105540_PI430048170 mRNA
TGCCTTCGGGTTGTGCTTTAGTCTGTAAAATTCTAAAGGAGAGCTGCTAAATTGTTTTCT NM_001018159 RefSeq
chr16 - 66802877 66830976 NAE1 8883 "NEDD8 activating enzyme E1 subunit 1, transcript variant
2"
GO:0005515|GO:0005886|GO:0046982|GO:0045116|GO:0005634|GO:0042981|GO:0051402|GO:0005829|GO:0007
165|GO:0043523|GO:0005737|GO:0033314|GO:0019781|GO:0031625 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_131709_PI430048170 0.0153661529246395 0.4869295873036183.02847220313289
2.36015181340212 2.80759555726081 A A A 4.0369324445833 3.6983838933265
3.61857773131888 P P P LNCV6_131709_PI430048170 mRNA
GGTTAATGACATTCAATTCTAAATGATACATTGGAATTGTGCCTTTTCTACCACACTGGA NM_153605RefSeq chr3
+ 97822039 97944986 CRYBG3131544 beta-gamma crystallin domain containing 3 GO:0030246 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137066_PI430048170 0.0558798943828947 0.4807886819204342.16439037284505
1.19821187326986 1.7099060396274 A A A 2.83788533115159 2.73079640694081
2.83036699077119 P P P LNCV6_137066_PI430048170 mRNA
TGGATCTAATAACGACCACTTGAACCCAGTTTCACAGAATCCTTATTTTTCTGTTCAAAT NM_145165RefSeq chr14
+ 64914360 64935366 CHURC1 91612 "churchill domain containing 1, transcript variant 1"
GO:0008270|GO:0007275|GO:0045893|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114411_PI430048170 0.2370228840898551.18286957397726 6.34084084747636
6.49104191340841 6.50278375983164 P P P 6.37951873057118 6.30643204757057
5.87846488585291 P P P LNCV6_114411_PI430048170 mRNA
ATCAAGACAAATTGAAAGAAAGCAATAACTCACCAAAGCTCAACGCTGCCCCTGCCTCGA NM_015482RefSeq chr6
- 3268973 3456559 SLC22A23 63027 "solute carrier family 22, member 23, transcript variant 1"
GO:0022857|GO:0016021|GO:0055085|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135549_PI430048170 0.25369819632525 0.6153031731759021.94050236908931
2.54330866736841 2.93060807260321 A A P 2.35160887256315 3.42583476750864
3.61499429197975 A P P LNCV6_135549_PI430048170 mRNA
TCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAGTAATT NM_001170423 RefSeq
chr6 + 83512474 83525702 PRSS35 167681 "protease, serine, 35, transcript variant 1"
GO:0005739|GO:0008152|GO:0005576|GO:0003824 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141289_PI430048170 0.5731452285535631.40172910875071 0.3741623770364481.6621460128971
2.20512633643503 A A A 0.8308340171237080.4299826053883641.74250262244563 A A A
LNCV6_141289_PI430048170 mRNA
TTGCTTGATGTTTACTTCTCGTTCAGACTCAAATAAAGCCTTTTTTCAGGACCAGCAAAA NM_021185RefSeq chr19
+ 38335802 38370949 CATSPERG 57828 catsper channel auxiliary subunit gamma
GO:0007338|GO:0035036|GO:0005886|GO:0036128|GO:0097228|GO:0007275|GO:0007283|GO:0030154|GO:0032
504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145477_PI430048170 0.3123516860455411.19574093617653 10.696548127715
11.0150195928841 11.2950182201757 P P P 10.7264290692228 10.5621886720156

10.9756357983937 P P P LNCV6_145477_PI430048170 mRNA
GATGCTCATTCTGATACAACTATTTTTCGTGTCAAATATCTACTGTGCCCAAATGTACTC NM_001289108 RefSeq
chr15 - 64072558 64094008 FAM96A 84191 "family with sequence similarity 96, member A,
transcript variant 3"
GO:0008150|GO:0003674|GO:0005737|GO:0007059|GO:0016226|GO:0005654|GO:0005575|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135282_PI430048170 0.0299139355613486 2.24882955875571 2.37872972191191
2.41793121133212 2.95573892085818 A A P 0.8540122756541091.5060174139969
1.80371618833797 A A A LNCV6_135282_PI430048170 mRNA
AACATTCAGGTTTCTGAGAGCTGAATTCCAAGAGTGCAAAACCCCAGCATCCTGTTTCCT NM_032648RefSeq chr1
+ 32247216 32248860 FAM167B 84734 "family with sequence similarity 167, member B" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_137390_PI430048170 0.10226784013183 0.8228666302066587.06328325685321
6.77662283497801 7.13282785991275 P P P 7.22794703942605 7.19678619619259 7.4069245078917
P P P LNCV6_137390_PI430048170 mRNA
CTTGTGTGTTGTAGCTCATTTGTTTCAAGAGAGAATCAACAGATCATATTCAGTGTCTTG NM_005647RefSeq chrX
+ 9465160 9719740 TBL1X 6907 "transducin (beta)-like 1X-linked, transcript variant 1"
GO:0005515|GO:0008013|GO:0044212|GO:0007605|GO:0006325|GO:0005634|GO:0044281|GO:0042393|GO:0007
219|GO:0017053|GO:0045944|GO:0006508|GO:0005876|GO:0060070|GO:0044255|GO:0016575|GO:0003714|GO:0
019904|GO:0000122|GO:0008022|GO:0006351|GO:0000118|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132691_PI430048170 0.9052622925905060.9961851777637810.260760149111161
0.27335697065202 0.424534989233343A A A 0.3586804403881070.305822811014655
0.315967914824989A A A LNCV6_132691_PI430048170 mRNA
GCAGAACTACTGTGTGTCTGTTCACTACCTTTTCAGGTTTATTGTTTTTATTTTTGCATG NM_014431RefSeq chr10 +
70478807 70568450 PALD1 27143 "phosphatase domain containing, paladin 1" GO:0005515|GO:0005829
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143599_PI430048170 0.6633700739747911.14660353871702 0.467259653050118
0.4324508121645111.29929546290321 A A A 0.4009499132013040.847209220519589
0.495402501181732A A A LNCV6_143599_PI430048170 mRNA
CAGAAAGCCCACCAGCAACATAATTTTAAAGCCTTTCAGATTACTTTTAAAAAATGCAGC NM_013308RefSeq chr3
- 151197831 151203201 GPR171 29909 G protein-coupled receptor 171
GO:0007186|GO:0045028|GO:0005887|GO:0004930|GO:0035589|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127492_PI430048170 0.0110392245574445 0.3476417732577057.08854198361661
6.60520858449648 6.83594314336427 P P P 7.87597230313273 8.44946886474274
8.69932460885864 P P P LNCV6_127492_PI430048170 mRNA
AATTGTTACTTGTTACTGCAGCAGCAGCCCTAGAAAGTAAGCCCAGGGCTTCAGATCTAA NM_001080497 RefSeq
chr9 - 120600917 120714487 MEGF9 1955 multiple EGF-like-domains 9
GO:0008150|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_25157_PI430048170 0.9558094337409940.9847097725290554.63847617131801 4.06140035681321
3.8518289807447 P P P 3.76777643002658 4.6222472901711 4.22200026414049 P P P
LNCV6_25157_PI430048170 mRNA
CTCTGGGTCCTTCCTGAAACTATATTTTGTCATATCAAATAAAGAGAGAACAGGACTAAA NM_018953RefSeq chr12
+ 54033047 54035360 HOXC5 3222 "homeobox C5, transcript variant 1"
GO:0043565|GO:0030054|GO:0003700|GO:0006357|GO:0048706|GO:0005654|GO:0009952|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129687_PI430048170 0.7732525494708971.14024633512716 1.4527680522989
0.3629316829791470.46887000298206 A A A 0.9328519920114670.307229186342964

0.674391799496087 A A A LNCV6_129687_PI430048170 mRNA
ATCCAAAGACCAGAAGCGAGGTCGGTGGAAACTTGAAAACTCGATTCATTATTAAAGGCA NM_002776 RefSeq chr19
- 51012743 51020026 KLK10 5655 "kallikrein-related peptidase 10, transcript variant 1"
GO:0007049|GO:0004252|GO:0006508|GO:0008236|GO:0005576 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144075_PI430048170 0.9714365850536820.9954591552309283.70846684376964
3.81515492307914 4.12034419819075 P P P 3.83370950213677 3.70700198058735
4.12318168560861 P P P LNCV6_144075_PI430048170 mRNA
CTTTCAGATTTTTAATTTCACCCTTCTGTCCTGCCGTAACACTTCATTAGATCAAACAAT NM_023039 RefSeq chr5 -
73552199 73565686 ANKRA2 57763 "ankyrin repeat, family A (RFXANK-like), 2"
GO:0003712|GO:0008150|GO:0042826|GO:0016020|GO:0006357|GO:0030169|GO:0005634|GO:0005856|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133234_PI430048170 0.0554552498921089 0.77818339961057 9.7090264138639
9.81689045285655 9.97644008688198 P P P 10.1302569795736 10.0516297449113
10.3956185668885 P P P LNCV6_133234_PI430048170 mRNA
GTAATCGAGTTTTGATCATATTTTCTATTAAAGTGGCTAACACCTGGCTACTCTTACTGT NM_000983 RefSeq chr1
- 6185019 6199619 RPL22 6146 ribosomal protein L22
GO:0005515|GO:0010467|GO:0003735|GO:0046632|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0005
634|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0000184|GO:0030529|GO:0
016032|GO:0022625|GO:0044267|GO:0008201|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142455_PI430048170 0.7191291767036450.7595268181731280.261010147586174
0.2735614425388751.34860975987096 A A A 2.00340890498986 0.340147668437062
0.31826764664429 A A A LNCV6_142455_PI430048170 mRNA
TAAAATCCTTCTGGGGGCACTGGAAGCACAATACGGTGACCAATCTTGCTTTCATTTTTT NM_001282597 RefSeq
chr2 + 79512933 80648863 CTNNA2 1496 "catenin (cadherin-associated protein), alpha 2,
transcript variant 3"
GO:0005515|GO:0030424|GO:0045296|GO:0060134|GO:0007409|GO:0021942|GO:0015629|GO:0030027|GO:0048
854|GO:0005829|GO:0042692|GO:0048813|GO:0016323|GO:0051823|GO:0005737|GO:0016337|GO:0051149|GO:0
051015|GO:0005913|GO:0005912|GO:0005200 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139786_PI430048170 0.6047473764745350.9744630071558790.288115936698588
0.4590560318610420.328642732656748 A A A 0.4812723299860120.369371371060182
0.338781191057653 A A A LNCV6_139786_PI430048170 mRNA
CAGGTGCATTTTCCTACACCTCCAAATGAGGAATGGATTTTCTTTAATGTAAGAAGAATC NM_005259 RefSeq chr2
- 190055699 190062729 MSTN 2660 myostatin
GO:0005515|GO:0048632|GO:0043627|GO:0009408|GO:0045471|GO:2000818|GO:0060395|GO:0005615|GO:0042
802|GO:0005737|GO:0051602|GO:0043408|GO:0022602|GO:0007179|GO:0043403|GO:0048468|GO:0008201|GO:0
014850|GO:0010862|GO:0005102|GO:0014732|GO:0042981|GO:0033574|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128808_PI430048170 0.0592850070462195 0.5801171605200434.47523169651149
4.24072417970268 4.88737262618112 P P P 4.8607570857924 5.53613902407605
5.53884908967097 P P P LNCV6_128808_PI430048170 mRNA
GAGGAGGATTTTGTTTTGTAGTTTGCAGATGAGCATTTCTAAAGCATTTTCCCTTGCTGT NM_181861 RefSeq chr12
+ 98645299 98735433 APAF1 317 "apoptotic peptidase activating factor 1, transcript variant 3"
GO:0005515|GO:0043065|GO:0008635|GO:0006919|GO:2001235|GO:0001843|GO:0006915|GO:0042981|GO:0005
634|GO:0051402|GO:0005524|GO:0008656|GO:0097193|GO:0005829|GO:0007399|GO:0042802|GO:0072432|GO:0
043531|GO:0043293|GO:0000166|GO:0030900|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_130956_PI430048170 0.5804095902877960.9671750145732840.497531468542054

0.4989326457979710.280072377538289A A A 0.4061025084129570.538231548007102
0.484410399693168A A A LNCV6_130956_PI430048170 mRNA
CTGTTTTTTGCACTTCAGGGGTAAGGTCTGATGACATGTAAAAGATGATCGTTTAATAAA NM_175056RefSeq chr3
+ 102435014 102479841 ZPLD1 131368 zona pellucida-like domain containing 1 GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_137734_PI430048170 0.7941713502774031.0337969867338 7.38738925333374
7.31692228548985 7.70985419328212 P P P 7.61263853216804 7.20699039711725
7.45316923704421 P P P LNCV6_137734_PI430048170 mRNA
CCCAGGATATGGTGTTCATTTTATGATATTACGCAGGATGATGTATTGAGTAAAATCAGT NM_130809RefSeq chr5
+ 127517608 127555088 PRRC1 133619 "proline-rich coiled-coil 1, transcript variant 2" GO:0005794 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139045_PI430048170 0.212771426869605 1.59371088687342 1.13725835405734
2.14231529423871 2.15702327721238 A A A 1.22064921128764 0.648134375176797
1.60931598899122 A A A LNCV6_139045_PI430048170 mRNA
TCAGGTGCAGAAGGGAACCTTGTATTTCACAGGCCTCATTTTGATGGCAAAAAGACAGTG NM_001198695 RefSeq
chr17 - 19383441 19387219 MFAP4 4239 "microfibrillar-associated protein 4, transcript variant 1"
GO:0005515|GO:0009650|GO:0010712|GO:0001527|GO:0005576|GO:0071953|GO:0071493|GO:0031012|GO:0003
674|GO:0030198|GO:0043206|GO:0007155|GO:0048251|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129026_PI430048170 0.0313116655794581 0.4104572512629092.97667432249219
1.90166596440483 2.51259385673585 P A A 3.33046900562023 3.88377133352596
4.11792328511989 P P P LNCV6_129026_PI430048170 mRNA
TTTCTGTTTGACCTTGTGTTTGCTGCCAAACCTAATACAGTTGAATTGGGAAACAAAAAA NM_173500RefSeq chr15
- 42744345 42920809 TTBK2 146057 tau tubulin kinase 2
GO:0005515|GO:0006996|GO:0005814|GO:0008360|GO:0005634|GO:0005524|GO:0005615|GO:0036064|GO:0005
829|GO:0007224|GO:0042384|GO:0018105|GO:0004674|GO:0035869 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129217_PI430048170 0.106755016268491 1.29751641919788 9.33060691180779 9.3659159436708
9.16842483747841 P P P 9.17123748215992 8.65532308415417 8.87188830090508 P P P
LNCV6_129217_PI430048170 mRNA
CTGCCATTGATCCAGCTCAGAACGATTGGAAATAAATTTGAAATGTAACCGAGCATTCCG NM_001256584 RefSeq
chr2 + 126655934 126696675 GYPC 2995 "glycophorin C (Gerbich blood group), transcript variant 3"
GO:0005515|GO:0016020|GO:0005886|GO:0005887|GO:0030863 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_137374_PI430048170 0.60940801619468 1.04289672578814 11.124291619941
11.2410505369305 11.3551029168485 P P P 11.100595546022 11.0687665241372
11.3604315866942 P P P LNCV6_137374_PI430048170 mRNA
TCTTCCTCGTTTGTTACTTTAGAGCAAGTTTGCCCATAGTCTTGAATGCAATATTTGTTT NM_002095RefSeq chr8 -
30578513 30658221 GTF2E2 2961 "general transcription factor IIE, polypeptide 2, beta 34kDa"
GO:0005515|GO:0010467|GO:0006368|GO:0006355|GO:0005737|GO:0006367|GO:0006366|GO:0016032|GO:0005
654|GO:0005634|GO:0005673|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106280_PI430048170 0.324256698304285 1.36790216611293 3.10136066211717
2.15720538428615 2.23277268921215 A A A 2.27998191832371 1.78482340645295
2.22298370207041 A A A LNCV6_106280_PI430048170 mRNA
ACAATAGTGCCATATGGCAAACGGTAGAAGAACTGGATTACTTAGAAGTGGAGGCTGAGG NM_002693RefSeq
chr15 - 89316304 89334795 POLG 5428 "polymerase (DNA directed), gamma, transcript variant 1"
GO:0042645|GO:0005515|GO:0090305|GO:0003887|GO:0007568|GO:0005743|GO:0005760|GO:0006259|GO:0002
020|GO:0003677|GO:0005739|GO:0006261|GO:0004527|GO:0071897|GO:0003682|GO:0006287|GO:0006264|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_126702_PI430048170 0.0957986911071921 0.4149291380001472.22586688107682
2.20229463142423 2.7035589276763 A A A 2.7430103925406 3.71924186278824
4.18581647288374 A P P LNCV6_126702_PI430048170 mRNA
AAGAGATCACTTTGTCCGGATGAAGCAGCTGTTGGCATTATCCGCTGAGGCTTGAAAAAA NM_003048RefSeq chr2
+ 102619688 102711350 SLC9A2 6549 "solute carrier family 9, subfamily A (NHE2, cation proton antiporter
2), member 2"
GO:0015385|GO:0008104|GO:0005886|GO:0035725|GO:0016021|GO:0055085|GO:0006885|GO:0006811 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145132_PI430048170 0.00604660725189677 0.5474799519252328.34474226049533
8.29362790359986 8.6569876488826 P P P 9.16525909564914 9.20115945961457
9.53432126867346 P P P LNCV6_145132_PI430048170 mRNA
AAGCATTTTCTTTCTCCTAAGGAAAAGTGAATTTCTTATCAGAATATCTGGCTGGCCCTG NM_001130849 RefSeq
chr2 + 230713547 230821075 CAB39 51719 "calcium binding protein 39, transcript variant 2"
GO:0005515|GO:0008286|GO:0023014|GO:0010800|GO:0071476|GO:0071902|GO:0030295|GO:2000687|GO:0051
291|GO:0005829|GO:0032147|GO:0035556|GO:0033138|GO:2000681|GO:0004674|GO:0006468|GO:0007050|GO:0
043539|GO:0019900|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137138_PI430048170 0.00601913938778352 1.2243695359482 0.867668513343957
0.8994488012916220.940448557585114A A A 0.6849472206903340.560131726979121
0.584232472657799A A A LNCV6_137138_PI430048170 mRNA
CCACAGGCTTCTATACTGACATATTTCACAATCTTTTGCATGTTGTGTTTCAAGTAAATG NM_173563RefSeq chr6
- 4068358 4079223 FAM217A 222826 "family with sequence similarity 217, member A" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_143311_PI430048170 0.2182835323306990.9477090119558990.253497940378841
0.3523617952628890.289715012557111A A A 0.4575899144754070.352424239368893
0.315977514630012A A A LNCV6_143311_PI430048170 mRNA
TCCAATGAGGACTTTAAACAAGCATTCCATAAACTGATACGTTTTAAGTGCACAAGTTGA NM_000863RefSeq chr6
- 77462230 77463403 HTR1B 3351 "5-hydroxytryptamine (serotonin) receptor 1B, G protein-coupled"
GO:0005886|GO:0030818|GO:0045471|GO:0007198|GO:0007268|GO:0051378|GO:0042220|GO:0014059|GO:0007
205|GO:0005737|GO:0004993|GO:0046849|GO:0008144|GO:0042310|GO:0051967|GO:0071312|GO:0051385|GO:0
035690|GO:0002031|GO:0014063|GO:0071502|GO:0007187|GO:0005887|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136972_PI430048170 0.1807025391056530.76160330608525 7.99045393217976
8.03783400021186 8.30136350361563 P P P 8.24554834885057 8.3430559892301
8.86102609434215 P P P LNCV6_136972_PI430048170 mRNA
ATGAGCTTCGGGTTTTGATGCTTGTTTAGAGATCAGCAGTCTTGGATGGGAGGGAACAAA NM_032124RefSeq chr18
- 47107409 47150500 HDHD2 84064 haloacid dehalogenase-like hydrolase domain containing 2
GO:0008150|GO:0019899|GO:0046872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125360_PI430048170 0.6442704824939461.04103581618001 11.1191931763574
10.9751088810399 11.2638428187881 P P P 10.9110120381093 11.1834044242715
11.0909436048923 P P P LNCV6_125360_PI430048170 mRNA
TTCCTGAACCAGAGCTCGCCCTTCTACTTCTGGATGAATGGTGACCGCATCGACTCCCTG NM_001831RefSeq chr8
- 27596916 27614811 CLU 1191 "clusterin, transcript variant 1"
GO:1900221|GO:0006629|GO:0005515|GO:0048471|GO:0005783|GO:0032436|GO:0072562|GO:0005634|GO:0001
836|GO:0005615|GO:0045429|GO:0005829|GO:0051787|GO:0005739|GO:0051788|GO:0006956|GO:0005737|GO:0
032286|GO:0051092|GO:0006958|GO:0017038|GO:0031093|GO:0051131|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143144_PI430048170 0.7093804799892290.9619755730916870.48925878716411
0.5784872821495820.488110490348788A A A 0.4368695068610330.784913072399577
0.478105324038194A A A LNCV6_143144_PI430048170 mRNA

GAGCTAAAGATCTGAATTATAGTCTCATTAGAACCAGACAGATGTTGTTGAGAAGTACTA NM_007366 RefSeq chr2 - 159940748 160062615 PLA2R1 22925 "phospholipase A2 receptor 1, 180kDa, transcript variant 1"
GO:0005886|GO:0009986|GO:0072593|GO:0090403|GO:0090238|GO:0005576|GO:0001816|GO:0006898|GO:0006897|GO:0043235|GO:0005887|GO:0043274|GO:1900138|GO:0043517|GO:1900139|GO:0030246|GO:0004872|GO:0016021|GO:0090399|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142727_PI430048170 0.482291104065937 1.00775406464166 0.420163295010534 0.430181416609647 0.394554292476432 A A A 0.414780496334681 0.384488076297982 0.412237940079832 A A A LNCV6_142727_PI430048170 mRNA
GTCAGAACAAAGCAGATTCGTCTAGGAATTCTCCACAAGTTTGTCCTAAGGAGGAGGTTT NM_001004755 RefSeq chr11 + 4998982 4999930 OR51L1 NA "olfactory receptor, family 51, subfamily L, member 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131853_PI430048170 0.812601369323218 0.982222547920111 7.67732852843636 7.43371395316265 7.32293477478114 P P P 7.5717839868661 7.56694602547306 7.38850929682179 P P P LNCV6_131853_PI430048170 mRNA
CTTCTTGTTCCATAGGATTAAGGAAGACTCTGAGGAAATAAAAGTTGTTTGGAAAAATCC NM_021831 RefSeq chr2 + 27051622 27070622 AGBL5 60509 "ATP/GTP binding protein-like 5, transcript variant 1"
GO:0072686|GO:0005737|GO:0015631|GO:0035611|GO:0006508|GO:0030496|GO:0008270|GO:0005634|GO:0035608|GO:0005829|GO:0004181 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135707_PI430048170 0.0117342583848487 0.653974075776474 6.89959442183644 6.80547187834892 7.15735586269508 P P P 7.65006970236776 7.43802123933691 7.62656093804475 P P P LNCV6_135707_PI430048170 mRNA
ATTGCTTGGATTTCTAGTGAGAGCTGTTGAATTTGGTGATGTCAAATGTTTCTAGGGTTT NM_004180 RefSeq chr2 + 161136954 161236171 TANK 10010 "TRAF family member-associated NFKB activator, transcript variant 1"
GO:0005515|GO:0034142|GO:0007249|GO:0002224|GO:0046872|GO:0005829|GO:0002756|GO:0007165|GO:0005737|GO:0045087|GO:0035666|GO:0034138|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130662_PI430048170 0.00110696581477143 0.350084656884981 4.09178811365435 3.76378778056479 3.75589561150869 P P P 5.11813169101101 5.47621716601641 5.54997231838333 P P P LNCV6_130662_PI430048170 mRNA
CCAGGCCACACAATAATTCGGGGTTGTATTTTCTAAGAACTATGTATTGTTTTTAGCTTA NM_145257 RefSeq chr1 - 229321004 229342941 CCSAP 126731 "centriole, cilia and spindle-associated protein"
GO:0060296|GO:0045995|GO:0030424|GO:0005929|GO:0005813|GO:0005814|GO:0005930|GO:0035869|GO:0005819|GO:0007275|GO:0036064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94493_PI430048170 0.716361927998969 0.96617225510273 7.21458901391909 7.25977966401999 7.1182335635337 P P P 7.05483202016681 7.27051695101848 7.39905670499226 P P P LNCV6_94493_PI430048170 mRNA
TTTAATGGCACCTCATTTGGCTTTGTGAATTGTCACCTCACCTCGGGAAATGAGAAGACG NM_001567 RefSeq chr11 + 72224837 72239144 INPPL1 3636 inositol polyphosphate phosphatase-like 1
GO:0005515|GO:0017124|GO:0008285|GO:0005886|GO:0043647|GO:0044281|GO:0030175|GO:0009791|GO:0005829|GO:0005737|GO:0097178|GO:0006006|GO:0007015|GO:0005856|GO:0007155|GO:0042169|GO:0032868|GO:0005794|GO:0006661|GO:0003779|GO:0030027|GO:0006897|GO:0001958|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133564_PI430048170 0.945465637621185 1.08886067121322 2.26062499784579 3.88495374839426 2.89061773707685 A P P 3.54784691048294 2.97209260088753 2.38891368842446 P P A LNCV6_133564_PI430048170 mRNA
TATTTTAAACATACTAGCTGCCTGAACTTACTGTGCCCTTGGCCCAGATTTCAGCTCATA NM_001257999 RefSeq chr17 - 4163370 4263847 ANKFY1 51479 "ankyrin repeat and FYVE domain containing 1, transcript variant 3"
GO:0005515|GO:0017137|GO:0090160|GO:0032439|GO:0048549|GO:0034058|GO:0005765|GO:0046872|GO:0006

897|GO:0044354|GO:0016020|GO:0042147|GO:0005769|GO:0010008|GO:0070062|GO:0030904 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126898_PI430048170 0.1960519999737140.90676098620138 11.7283389824019 11.7184571004821 11.5293967965093 P P P 11.711808913321 11.9245685086971 11.763382040905 P P P LNCV6_126898_PI430048170 mRNA
TTGAGTCACTGATCTCTTGTGATGGGGCCAATGAGTCAATTGAATTCATGGGCCAAACAG NM_018135RefSeq chr6 - 43671196 43687812 MRPS18A 55168 "mitochondrial ribosomal protein S18A, transcript variant 1"
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0006412|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142072_PI430048170 0.9947979415798660.9757265939815338.44901434533735 8.63635454305308 8.33544789757455 P P P 8.92961871680168 8.34125846603601 8.15530592747164 P P P LNCV6_142072_PI430048170 mRNA
TGGTGCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAA NM_206895RefSeq chr2 + 232870283 232876397 C2orf82 389084 chromosome 2 open reading frame 82 GO:0016021|GO:0071944 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136282_PI430048170 0.00715061582840098 0.3607789291677 0.292401966206575 0.3016613109358080.704717508161146A A A 1.52550047158445 2.25757465803295 1.87488153858914 A A A LNCV6_136282_PI430048170 mRNA
CCCACCATTTGTGTATCAGTGGCCAATTCATTAGTAAAAATAAAGGAGGGGAAAGGAGAA NM_018704RefSeq chr1 + 112396177 112461164 CTTNBP2NL 55917 CTTNBP2 N-terminal like
GO:0005515|GO:0005737|GO:0006470|GO:0034763|GO:0032410|GO:0015629|GO:0051721 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138741_PI430048170 0.9231305101785140.9927655100220475.95016054881574 6.15093103204013 6.08780720822823 P P P 5.98095232398502 6.0261953061994 6.21007885277282 P P P LNCV6_138741_PI430048170 mRNA
TAGGTTCTTTTTCCACGCAATGTAAGAACATGATATACTGTACGTTGGAAAGCATTTACC NM_003818RefSeq chr20 + 5126760 5197887 CDS2 8760 CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2
GO:0016020|GO:0005783|GO:0004605|GO:0016024|GO:0005743|GO:0044281|GO:0016021|GO:0006644|GO:0006655|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140460_PI430048170 0.3907358647549890.7318611636577780.430011518596955 1.20804138121199 0.414958148869439A A A 1.50219106145532 1.40932566826923 0.411850675513416A A A LNCV6_140460_PI430048170 mRNA
CTTCAATGGAAGCCCTAAGGCAGTAGTATAACTAACTCCATAAAATACAAACAAACACAT NM_148909RefSeq chr1 + 51616873 51789219 OSBPL9 114883 "oxysterol binding protein-like 9, transcript variant 7"
GO:0005737|GO:0005794|GO:0031902|GO:0006869|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137980_PI430048170 0.1408059148610870.8493263126979557.35871273112857 7.24849878349206 7.03964033929565 P P P 7.56254085566004 7.51635888636454 7.27676835506665 P P P LNCV6_137980_PI430048170 mRNA
AGCCCATCTGCTGTGTGCCCGTCTGCTCTGGGGCTTCCTCTTCATGCTGCCAGCAGTCTA NM_198696RefSeq chr21 - 44558022 44558760 KRTAP10-3 NA keratin associated protein 10-3 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133788_PI430048170 0.4500595578535111.13720878326467 5.25326855786314 5.15509541731931 5.53590800160853 P P P 4.7283760564839 5.14234631205251 5.45426271334746 P P P LNCV6_133788_PI430048170 mRNA
CTTTGGTATTCCCAGTAAATAGATGACTACTTTTGAGTGGAAACAAAGAACATTCTAGCA NM_018051RefSeq chr7 + 158856577 158946192 WDR60 55112 WD repeat domain 60
GO:0006996|GO:0030030|GO:0072372|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_63654_PI430048170 0.0225696586130481.26217702799989 8.68169223579822 8.55372099124585 8.51565496687983 P P P 8.22060718974384 8.38129765054504 8.13585504437331 P P P LNCV6_63654_PI430048170 mRNA AAAGGCTTCTATTGCCACGAGGACTCTCAGGAAAGACCCAAGCCCCGAATCCCCATCCTG NM_001009905 RefSeq chr17_KI270860v1_alt + 51110 157631 B3GNTL1 146712 "UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1" GO:0016757|GO:0008152 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139177_PI430048170 0.00169151293643983 0.2740764606908124.96875364024669 4.53803865885451 5.12135758588235 P P P 6.39357033439072 6.97034195738522 6.86483224065177 P P P LNCV6_139177_PI430048170 mRNA CCCCTAAAGAGTGATATTGCTGACGTTTCTATCAATTTTACACATAATATGTGGCTATGA NM_004136RefSeq chr15 + 78438175 78501456 IREB2 3658 iron-responsive element binding protein 2 GO:0005515|GO:0017148|GO:0051539|GO:0003723|GO:0007568|GO:0010040|GO:0030316|GO:0071456|GO:0034101|GO:0030371|GO:0006782|GO:0009791|GO:0046872|GO:0005829|GO:0005739|GO:0006879|GO:0050892|GO:0005737|GO:0030350|GO:0006826|GO:0032526 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_128813_PI430048170 0.0635951686536636 2.8558139924755 2.88311128685037 3.09673151284477 3.11351615042833 A P P 2.19747463473717 0.640813089496785 1.30071796323383 A A A LNCV6_128813_PI430048170 mRNA AGGGGGGTGCAATGAGGAATGTTTCTGGTCTGAAAAGAATAAAGTGGGTTTGAAAGCGGA NM_181710RefSeq chr19 + 5455414 5456856 ZNRF4 148066 zinc and ring finger 4 GO:0005737|GO:0008270|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_126763_PI430048170 0.5172800774929280.862123956216068 0.376666383505183 0.3792732761239040.434335189016878 A A A 0.35843420441231 0.335523330209148 1.027296921735 A A A LNCV6_126763_PI430048170 mRNA CCACCAGAGTCACAGGCTTGGATTGTTTTATGTACAAACAGATGACTTAGATATTCTGTA NM_000510RefSeq chr11 + 30231015 30235277 FSHB 2488 "follicle stimulating hormone, beta polypeptide, transcript variant 1" GO:0005515|GO:0007565|GO:0008284|GO:0030335|GO:0006701|GO:0016913|GO:0042699|GO:0005576|GO:0045670|GO:0007292|GO:0007165|GO:0005737|GO:0005179|GO:0016486|GO:0045780|GO:0045944|GO:0007179|GO:0060011|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_143789_PI430048170 0.00676736582215163 0.203340514388673 3.27394808642953 3.43797011672189 3.07843509429958 P P P 5.04897119673395 5.96199290595838 5.55360098366805 P P P LNCV6_143789_PI430048170 mRNA CCACCAGAGAGGATGTGTGTGAGGAGCCAGAAACGCTGAATCCAATTAAGAGAGAAAAAT NM_178568RefSeq chr17 - 1934676 2025345 RTN4RL1 146760 reticulon 4 receptor-like 1 GO:0031103|GO:0009986|GO:0045121|GO:0004872|GO:0046658|GO:0009897|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_67437_PI430048170 0.3452086091013740.612884532617763 0.273599315942149 0.278886878370001 0.309251891079482 A A A 0.4491857628201531.74413109294366 0.331621252681537 A A A LNCV6_67437_PI430048170 mRNA CTGCCAGGGCTGCAAAACAGCTCGAATATCAGCAATTAGAAGACGATAAACTTTCTCAGA NM_012307RefSeq chr18 - 5392380 5544310 EPB41L3 23136 "erythrocyte membrane protein band 4.1-like 3, transcript variant 1" GO:0005515|GO:0002175|GO:0030913|GO:0005886|GO:0044224|GO:0008360|GO:0033270|GO:0006915|GO:0003779|GO:0072659|GO:0008150|GO:0005737|GO:0030865|GO:0030866|GO:0005911|GO:0048812|GO:0005200|GO:0043217|GO:0071205|GO:0030673|GO:0005856|GO:0007016|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_132108_PI430048170 0.4971423436786571.04681478119835 9.629912885496 9.52255599862856 9.54948563945549 P P P 9.43445806158964 9.66190924050863

9.39512458186121 P P P LNCV6_132108_PI430048170 mRNA
AGATGAAGGACAACCTGCTCCTGGACATGTATCTGGCCCCCCATGTCAGGACCCTGTACA NM_212492RefSeq chr17
+ 82051886 82057470 GPS1 2873 "G protein pathway suppressor 1, transcript variant 1"
GO:0005515|GO:0000188|GO:0007049|GO:0005737|GO:0008180|GO:0010388|GO:0007254|GO:0005634|GO:0005
095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139977_PI430048170 0.00541019056020539 0.5994583079695677.70998591867583
7.39777387497571 7.42206126107856 P P P 8.11774403889715 8.33800567769195
8.30073638894461 P P P LNCV6_139977_PI430048170 mRNA
TCCTATCTGCAAACTGTGTTCACCCTTTTGTAAAAATAAAGGAACTGGACCTGTAAAAAA NM_017585RefSeq chr9
- 133471093 133479154 SLC2A6 11182 "solute carrier family 2 (facilitated glucose transporter), member 6,
transcript variant 1" GO:0016020|GO:0015758|GO:0005886|GO:0016021|GO:0055085|GO:0005355 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139375_PI430048170 0.5598681512861560.7804168296183410.478646396396889
0.58183632254034 0.551953333001668A A A 0.3524081271460321.53134419431229
0.500519773798797A A A LNCV6_139375_PI430048170 mRNA
AGGGACCCGTGTCCTACAGAGTCAGAAAGAGAAGCTAAAGTTCTACAGTGATGAGAATGTNM_001291380 RefSeq
chr1 - 13196187 13201409 LOC400736 NA PRAME family member-like NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_128841_PI430048170 0.000280938096675867 0.2659979062328546.852769683701
6.46747168024759 6.60200194768764 P P P 8.4325773235798 8.44337561778775
8.77735390283485 P P P LNCV6_128841_PI430048170 mRNA
CTCAGACACTGAGTAGCATAAAAACCACATAGAACTGAACTGTAACTTAAATTCCAAACT NM_003873RefSeq chr10
- 33177490 33334905 NRP1 8829 "neuropilin 1, transcript variant 1"
GO:0005515|GO:0071679|GO:0048842|GO:0021828|GO:0050731|GO:0048843|GO:0048844|GO:0048846|GO:0060
301|GO:0005615|GO:0002116|GO:0043524|GO:0007413|GO:0017154|GO:0007411|GO:0043025|GO:0009887|GO:0
070374|GO:0038085|GO:0009986|GO:0021649|GO:0016358|GO:0010595|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145149_PI430048170 0.0335742691369544 1.3193926377204 3.94754943371338
4.02182762607441 3.90418910605397 P P P 3.41049838761302 3.52811983303835
3.72066608727833 P P P LNCV6_145149_PI430048170 mRNA
GGGTACTACATTTCCATCCCTTCCCTATTTTGACACCAAATTATGGTGTAGACAGCCCTC NM_144617RefSeq chr19
- 35754565 35757029 HSPB6 126393 "heat shock protein, alpha-crystallin-related, B6"
GO:0005515|GO:0006937|GO:0005737|GO:0005212|GO:0005634|GO:0042803 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142353_PI430048170 0.9198528757865050.8316345848106730.299963481317297
1.74204143318565 2.40958120092277 A A A 2.96290525705936 0.284326420643618
1.52443934959567 P A A LNCV6_142353_PI430048170 mRNA
GTGGAGAAAACCAAGGAACCCCTTTCTCTTCTTTATTAAAAAGCAAAACAAAAACTCTTG NM_020132RefSeq chr21
+ 43865234 43987594 AGPAT3 56894 "1-acylglycerol-3-phosphate O-acyltransferase 3, transcript
variant 1"
GO:0005886|GO:0005783|GO:0044281|GO:0005635|GO:0008654|GO:0003841|GO:0016020|GO:0005789|GO:0016
024|GO:0019432|GO:0016021|GO:0006644|GO:0006654|GO:0044255|GO:0046474 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128450_PI430048170 0.1122026046670520.8164117710825518.18614131819873
8.32508256791447 8.56042155882153 P P P 8.67748639589657 8.4771958497472
8.80151609453128 P P P LNCV6_128450_PI430048170 mRNA
ACAATCAGTGCTAGTGCTGGGGAAGGGACAGTCAAGAGCAGTCAGTTGCTTACTTATTTT NM_012084RefSeq chrX
+ 121047607 121049942 GLUD2 2747 glutamate dehydrogenase 2
GO:0005739|GO:0004352|GO:0004353|GO:0005737|GO:0043531|GO:0006536|GO:0006537|GO:0006538|GO:0070

728|GO:0005525|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133297_PI430048170 0.159209602393326 1.71874542556198 2.62760030163246
3.06918030671425 2.5545638856751 A P A 1.0995761966825 2.52698031026872
1.99653174334273 A P A LNCV6_133297_PI430048170 mRNA
GCCTCCAGGAAGAAAGAATGTTACTGCCTTAATAAAAAATGAAAAGAGAATGATGCTCAA NM_002298 RefSeq chr13
- 46125922 46182324 LCP1 3936 lymphocyte cytosolic protein 1 (L-plastin)
GO:0044319|GO:0005886|GO:0005884|GO:0031100|GO:0010737|GO:0030175|GO:0015629|GO:0032432|GO:0005
615|GO:0005829|GO:0042802|GO:0005737|GO:0051015|GO:0033157|GO:0051017|GO:0002286|GO:0070062|GO:0
001725|GO:0005509|GO:0003779|GO:0001891|GO:0032587|GO:0001726|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_50994_PI430048170 0.9484060955835331 1.00125327689027 7.65481918785931 7.53482720308402
7.59752049748658 P P P 7.42806001624398 7.58205514756326 7.75550252018985 P P P
LNCV6_50994_PI430048170 mRNA
TCAGCAGTAATAATCACTTGTGTTCTGAAAGAAAGGGCACCAGAAGTTCTAGCAAAATTC NM_015352 RefSeq chr20
+ 32207892 32238664 POFUT123509 "protein O-fucosyltransferase 1, transcript variant 1"
GO:0006355|GO:0005783|GO:0001756|GO:0008417|GO:0046922|GO:0016266|GO:0001525|GO:0009790|GO:0036
066|GO:0007399|GO:0007507|GO:0006493|GO:0007219|GO:0016020|GO:0006004 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139829_PI430048170 0.0208304056204712 1.22865618231383 0.756419436238097
0.8739450621385830.943717453746565 A A A 0.6762585305782280.4858827498045440.5196377623653
A A A LNCV6_139829_PI430048170 mRNA
TGTTTCCAATGCTTTGATCCCTTCTTACTTAACCTGAAGCTAGACGAGCAGGCTTCTTCC NM_000834 RefSeq chr12
- 13561475 13980088 GRIN2B 2904 "glutamate receptor, ionotropic, N-methyl D-aspartate 2B"
GO:0005515|GO:0043005|GO:0030054|GO:0005886|GO:0045471|GO:0005234|GO:0017146|GO:0007268|GO:0010
738|GO:0030425|GO:0001964|GO:0034220|GO:0001967|GO:0048167|GO:0004972|GO:0007411|GO:0045211|GO:0
006810|GO:0007611|GO:0050966|GO:0001662|GO:0007613|GO:0007612|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145420_PI430048170 0.3996462369596840.8822956660464545.6308093672214
5.24665440626905 5.42212656659587 P P P 5.33081788731969 5.66335420314109
5.82936667840686 P P P LNCV6_145420_PI430048170 mRNA
ATATAAATCCACTAAATCCAGCTACCAGGAACTGCCTGGAACTGTGGCCATGCATTTTTT NM_020162 RefSeq chr17
- 5440911 5469060 DHX33 56919 "DEAH (Asp-Glu-Ala-His) box polypeptide 33, transcript variant 1"
GO:0004004|GO:0006396|GO:0005737|GO:0045943|GO:0000182|GO:0005730|GO:0005654|GO:0033613|GO:0005
524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106531_PI430048170 0.0759938629995261 3.25483629954597 3.43393033929894
2.398559653583 1.60104244155297 P A A 0.4690532784036750.3626112757549081.6791695887361
A A A LNCV6_106531_PI430048170 mRNA
TTAAGGAAGGAAGGAAAACACAGGCAGCTCTAAGTGTACGACGAGGGAGGTCTCATCGGC NM_138412 RefSeq
chr19_KI270938v1_alt - 1026805 1052028 RDH13 112724 "retinol dehydrogenase 13 (all-trans/9-cis),
transcript variant 2" GO:0016491|GO:0005743|GO:0010842|GO:0042462|GO:0009644|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_110474_PI430048170 0.0201274605550987 1.14473398146725 0.783344754719074
0.8777348282363380.782340622456441 A A A 0.6118259703797340.636303044955816
0.612213137668532 A A A LNCV6_110474_PI430048170 mRNA
AGGATGTGTTTGTATACTTCTCTCGGGAAGAATGGGAGCTTCTTGATGATGCTCAGAGAC NM_024833 RefSeq chr19
- 57719750 57727627 ZNF671 79891 zinc finger protein 671
GO:0003712|GO:0006357|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_54827_PI430048170 0.00453339777333719 1.50192516973085 11.0221546298381

11.0174763310341 11.2486756581568 P P P 10.4238193983094 10.4799762471019
10.6285527737491 P P P LNCV6_54827_PI430048170 mRNA
CCAACAAATCTCAATACAGTCTGACAAGAGCACAGCAGTCCTACAAGTCCTTGGTGCAGA NM_017582 RefSeq chr1
- 154548574 154558644 UBE2Q1 55585 ubiquitin-conjugating enzyme E2Q family member 1
GO:0009566|GO:0005515|GO:0016567|GO:0001967|GO:0070459|GO:0007617|GO:0007566|GO:0016874|GO:0005
634|GO:0030175|GO:0005524|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135393_PI430048170 0.0027268261612585 0.6802433788106838.0868309934244
8.25445688802382 8.06567686887401 P P P 8.62473734487066 8.64000784229305
8.80993968803669 P P P LNCV6_135393_PI430048170 mRNA
GATGGACAAGACCTCATAACTGTGATTAATATCAATAAAAAGGGGATGTTGTGGATGAAA NM_001159770 RefSeq
chr17 - 72645945 73092714 SLC39A11 201266 "solute carrier family 39, member 11, transcript variant
1" GO:0046873|GO:0006829|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133809_PI430048170 0.29843118583031 0.8668061122844467.96850648484004
7.87085817252655 8.22112983288373 P P P 7.98415116279779 8.24417986887153
8.43818006730299 P P P LNCV6_133809_PI430048170 mRNA
GCTGAAGTTGTGTGTACAAGACTCTTGACAGTTGTGCTTCTCTAGGAGGTTGGGTTTTTT NM_001718 RefSeq chr6
+ 7726777 7881728 BMP6 654 bone morphogenetic protein 6
GO:0051216|GO:0001654|GO:0050714|GO:0060395|GO:0005615|GO:0006879|GO:0030539|GO:0005737|GO:0006
955|GO:0006954|GO:0045944|GO:0043408|GO:0010039|GO:0032026|GO:0032332|GO:0032526|GO:0050679|GO:0
014823|GO:0030501|GO:0046982|GO:0001822|GO:0031988|GO:0010862|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139285_PI430048170 0.2068857023410770.8376542498448266.5099331313971
6.78820107716217 7.0267523006269 P P P 6.98316836020088 7.02458083667388
7.12612555812438 P P P LNCV6_139285_PI430048170 mRNA
TAGGTAGCCTTTGGTCTATTGTACACAATCTCATTTCATATGTTTGCATTTTGGCAAAGA NM_001286043 RefSeq
chr1 + 75724346 75763678 ACADM 34 "acyl-CoA dehydrogenase, C-4 to C-12 straight chain, transcript
variant 5"
GO:0030424|GO:0006635|GO:0050660|GO:0005634|GO:0044281|GO:0019254|GO:0033539|GO:0042802|GO:0005
739|GO:0005759|GO:0045329|GO:0051793|GO:0003995|GO:0051791|GO:0070991|GO:0044255|GO:0070062|GO:0
055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135947_PI430048170 0.6252633019720930.9428716925489231 1.8247441893016
11.9212231355063 12.1418743560843 P P P 11.9485819892794 11.9000310302111
12.2817249063323 P P P LNCV6_135947_PI430048170 mRNA
AAGTAAAAGTAACCTTGGCTATGTTACCACCGTTTTGGTCACCCAGGAGGACATCTTAGC NM_006854 RefSeq chr7
- 6461080 6484218 KDELR2 11014 "KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention
receptor 2, transcript variant 1"
GO:0005801|GO:0005794|GO:0005783|GO:0005789|GO:0016021|GO:0006621|GO:0016192|GO:0006886|GO:0005
046|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92047_PI430048170 0.1425368953852011.55186255546942 3.53789720973865 4.10864279473526
3.84882204572741 P P P 3.56427938386588 2.56550936049365 3.34151456538909 P P P
LNCV6_92047_PI430048170 mRNA
TCTGGATGGAAAGCGTGCTGAAGTCTTGTTAAACTAGCAAGCTTTTGTTTGGAGGTCCAC NM_001287591 RefSeq
chr1 + 155135343 155138858 SLC50A1 55974 "solute carrier family 50 (sugar efflux transporter),
member 1, transcript variant 9"
GO:0005794|GO:0005886|GO:0000139|GO:0045815|GO:0042946|GO:0008643|GO:0006310|GO:0005634|GO:0016
021|GO:0042947|GO:0012505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142146_PI430048170 0.0220175592745522 1.35559643496022 8.95015153585283
9.25051595075766 9.18958338961237 P P P 8.75141239181662 8.77780718776168
8.55089624084782 P P P LNCV6_142146_PI430048170 mRNA

TGAGAGCCATAATGTGGCTGTAACTGTCTTCCTCATATTGCAAGAACACTGCTGGCAGAT NM_001039517 RefSeq chr1 - 155320459 155324147 RUSC1-AS1 NA RUSC1 antisense RNA 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53383_PI430048170 0.0899011299475073 1.1748361219432 4.10441997584346 4.20472332832286 4.34131842945755 P P P 4.0568657106453 4.06679170518015 3.82671168690856 P P P LNCV6_53383_PI430048170 mRNA
TTTGTCTCTTCCTTTCACCTCATTCTGGTAGCAGCATAAAGGTTAGGCAATCACTGGGAC NM_153812 RefSeq chr1 + 6613695 6624033 PHF13 148479 PHD finger protein 13
GO:0007076|GO:0007059|GO:0003682|GO:0008270|GO:0005654|GO:0005634|GO:0035064|GO:0000278|GO:0051301|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139411_PI430048170 0.339765913086621 1.04721758099915 0.593816506638124 0.440766557553204 0.586449793607906 A A A 0.424677946717472 0.533857671168016 0.465803681082527 A A A LNCV6_139411_PI430048170 mRNA
TATTCTGAAGACTGTAGCTCCACATTTAAGGGCATTTGCCAGAGAGATGCGATCTTGACG NM_001190765 RefSeq chr12 + 9881488 9895833 KLRF2 100431172 "killer cell lectin-like receptor subfamily F, member 2"
GO:0005515|GO:0050663|GO:0043320|GO:0005887|GO:0030246|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112496_PI430048170 0.12081383070859 0.91129751407865 16.1649968239564 15.9930084236866 16.0706075622823 P P P 16.2199643034475 16.1251750129711 16.2861217131416 P P P LNCV6_112496_PI430048170 mRNA
TAAAACTGGACAAAGACCGCAAAAAGATCCTCGAACGGAAAGCCAAATCTCGCCAAGTAG NM_000987 RefSeq chr17 - 8377515 8383247 RPL26 6154 ribosomal protein L26
GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006364|GO:0006614|GO:0019058|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0000184|GO:0016020|GO:0016032|GO:0042273|GO:0022625|GO:0044267|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131141_PI430048170 0.561283450587261 1.02781758492711 0.28019872974424 0.306716921338304 0.454114287739186 A A A 0.331905853895222 0.297939936560918 0.298319535686842 A A A LNCV6_131141_PI430048170 mRNA
TTGCTCTTGAGACATGGTAATCTCTTAATGTAACTACTAAAGGAGAGGTAGATTGAAAAG NM_145307 RefSeq chr10 - 62193085 62268863 RTKN2 219790 "rhotekin 2, transcript variant 1"
GO:0030097|GO:0007165|GO:0008284|GO:0005886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138233_PI430048170 0.862489658482309 0.983513401559817 0.953915438413156 1.26943157856872 0.403002976690875 A A A 1.72456718523879 0.304603538765622 0.293021687735212 A A A LNCV6_138233_PI430048170 mRNA
AAATAATAAACTCAGTGTCTACTTTTGCCGGCTTTGGGACCTTCGTGTTTTTCCGGGGCT NM_001272037 RefSeq chr21 - 44497891 44711580 TSPEAR 54084 "thrombospondin-type laminin G domain and EAR repeats, transcript variant 2" GO:0003674|GO:0060170|GO:0009986|GO:0007605|GO:0032420|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141252_PI430048170 0.426064628563733 0.906777984730004 0.519779398827545 0.590828419486028 0.464738483422887 A A A 0.504153231015497 0.914591948470563 0.546660071053116 A A A LNCV6_141252_PI430048170 mRNA
GGCTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGT NM_022034 RefSeq chr10 - 122832154 122846175 CUZD1 50624 "CUB and zona pellucida-like domains 1, transcript variant 1"
GO:0006931|GO:0007049|GO:0042589|GO:0008283|GO:0032023|GO:0016021|GO:0051301|GO:0030658 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131737_PI430048170 0.710285599958477 1.31418476495778 0.617463997679288 0.429618106485125 2.06813501679256 A A A 0.705613625868704 0.458020585131248 1.25016585127842 A A A LNCV6_131737_PI430048170 mRNA
AATTGTGCTGGCACTTAGGAGAGAGAGGAGGGGGAATAATAGTGGGTTAAAAAGCTTTCT NM_006028 RefSeq chr11

+ 113904795 113946561 HTR3B 9177 "5-hydroxytryptamine (serotonin) receptor 3B, ionotropic"
GO:0005232|GO:0004993|GO:0034220|GO:0005886|GO:0005887|GO:0045211|GO:0006810|GO:0007268|GO:0055
085|GO:0005216|GO:0007210 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129024_PI430048170 0.5588044985893481.02739854025214 0.313543881217128
0.3194391950227980.474294470908888A A A 0.3406725153885890.300438573660293
0.354461338430436A A A LNCV6_129024_PI430048170 mRNA
ATTTTGATGTCTACTCGCAGAAGTCAGCCATGTATGAGAAGTATGACGTCAGCAACGGTG NM_007180RefSeq chr11
- 118658231 118679672 TREH 11181 "trehalase (brush-border membrane glycoprotein), transcript
variant 1"
GO:0005886|GO:0005975|GO:0009405|GO:0005991|GO:0044245|GO:0009887|GO:0044281|GO:0004555|GO:0046
658|GO:0005993|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138875_PI430048170 0.0160516233272725 0.5694094710070094.93040003860685
5.15771536930278 5.46628375125866 P P P 5.78779701901606 6.00917784453663
6.21390824233579 P P P LNCV6_138875_PI430048170 mRNA
GCTGTTAAGAATTGTCTTTCCTAAGTATGTTAACTGTTGTATCTAACTCAACTGTGAGCT NM_018303RefSeq chr6
- 485137 693141 EXOC2 55770 "exocyst complex component 2, transcript variant 1"
GO:0005515|GO:0006996|GO:0005886|GO:0019901|GO:0006893|GO:0006887|GO:0015031|GO:0005829|GO:0043
231|GO:0047485|GO:0000145|GO:0016020|GO:0061024|GO:0017160|GO:0044267 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_92660_PI430048170 0.0106371876692749 1.25771449841811 7.06538741064426
7.21748617084978 7.04818440763349 P P P 6.80751616427365 6.8192795937419
6.71572475806378 P P P LNCV6_92660_PI430048170 mRNA
TTTCACCAACTTTGGCAACACGACCATTGTGGTGCCCAAGCCCTTCCGCCCGATACTTGG NM_001382RefSeq chr11
- 119096502 119102075 DPAGT1 1798 dolichyl-phosphate (UDP-N-acetylglucosamine) N-
acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)
GO:0016757|GO:0019408|GO:0030176|GO:0006047|GO:0051259|GO:0043231|GO:0016020|GO:0003975|GO:0005
789|GO:0006487|GO:0016021|GO:0006488|GO:0044267|GO:0043687|GO:0000271|GO:0008963|GO:0018279 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135883_PI430048170 0.6837297641752010.9319939335800377.08772748786728
7.04533120241738 7.01477817454294 P P P 6.78607372588022 7.33098826436393
7.27668601624331 P P P LNCV6_135883_PI430048170 mRNA
TCCCCTCATCCGATTCCGTTGTATCAGTCACTGACAGTTAATAAACCTTTGCAAACGTTC NM_005636RefSeq chrX
- 48402081 48411899 SSX4 NA "synovial sarcoma, X breakpoint 4, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_136931_PI430048170 0.8102610825012111.05223789409662 3.18066384326101 1.9394813623844
2.93917980380612 P A P 1.83259915102477 2.25766053971442 3.4863815238098 A A P
LNCV6_136931_PI430048170 mRNA
ATTCAGATCTTAATGTTCACCTCAGAGTCCACACAGGAGAGAGGCCCTATAAGTGTAAGG NM_001291490 RefSeq
chr19 - 44385645 44401611 ZNF285 26974 "zinc finger protein 285, transcript variant 4"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131838_PI430048170 0.00854152467717907 0.4733888797469937.93945619311783
7.96842065975297 8.35471301247721 P P P 9.08235833229783 8.91467309424879
9.48072807671078 P P P LNCV6_131838_PI430048170 mRNA
TGTCTCCAGCACTATGCATCCCTATTTTCTATTTATTGTGTACACTCACTTTCAGTAATG NM_025147RefSeq chr2 +
197453506 197475127 COQ10B 80219 coenzyme Q10 homolog B (S. cerevisiae) GO:0005743 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134540_PI430048170 0.9991100768581050.9982732234768 5.44118200131197
5.20633032223562 5.29538636866331 P P P 5.47153790121976 5.31231193429393

5.15945339912454 P P P LNCV6_134540_PI430048170 mRNA
GCACTATCACCACCTCTCTGCCTTCATGCCAATAATAAAGCTGATCTTTATTCCAAAAAA NM_153635RefSeq chr3
+ 9703825 9729908 CPNE9 151835 copine family member IX GO:0005615|GO:0070062 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_139105_PI430048170 0.000360089466602984 0.4413031264312246.17560919493624
6.1613831882315 6.07333646954745 P P P 7.40828019924822 7.20447349412762
7.33284903400964 P P P LNCV6_139105_PI430048170 mRNA
CATGCATTGTATTAGTGTTAGAAAACACAGCTGCGTAAATAAACAGCACGGGTGACCCGC NM_052813RefSeq chr9
- 136363955 136373681 CARD9 64170 "caspase recruitment domain family, member 9, transcript variant
1"
GO:0050700|GO:0032755|GO:0032760|GO:0050830|GO:0042493|GO:0042534|GO:0070423|GO:0046330|GO:0009
620|GO:0045408|GO:0032874|GO:0042981|GO:0035872|GO:0042803|GO:0051607|GO:0005737|GO:0045076|GO:0
045087|GO:0032494|GO:0032495|GO:0043123|GO:0043330 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_144682_PI430048170 0.4005381356449990.7696379384674641.41263684218676
0.3472469021907250.355820538937034A A A 0.6134467860076471.52904722138454
1.23808500522426 A A A LNCV6_144682_PI430048170 mRNA
CCACCTTAGAGAACTGAAATAAAAATAGAAGTTCTTACGCTTTTTTGTGGTACAGATGCT NM_033084RefSeq chr3
+ 10026428 10099660 FANCD2 2177 "Fanconi anemia, complementation group D2, transcript
variant 1"
GO:0007129|GO:0005515|GO:0000793|GO:0006281|GO:0005794|GO:0070182|GO:0007276|GO:0005654|GO:0010
332|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133472_PI430048170 0.7518086631381760.9925950454476740.287686880785714
0.3274621099000870.388488517467096A A A 0.36982528644605 0.342255214839162
0.325164101983241A A A LNCV6_133472_PI430048170 mRNA
ATGCAAGAATGAACAGAACAAGCAAAATGACCAGCTGCTTAGTCACCTGGCAAAGCAGGT NM_012344RefSeq
chr2 - 11658177 11670203 NTSR2 23620 neurotensin receptor 2
GO:0005886|GO:0007218|GO:0005887|GO:0004930|GO:0042391|GO:0007200|GO:0016492|GO:0007600|GO:0007
166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134992_PI430048170 0.0132340267939178 1.51454811755367 6.09235432792123
5.77638429474 6.03382935847166 P P P 5.28659552453236 5.57113635535337 5.24506789194678 P
P P LNCV6_134992_PI430048170 mRNA
AGCTTCAGTGATGTATGTTTTTGTGAACAAAGTTACAAATATTGTCCAAGTCTGGCTGTT NM_019102RefSeq chr7
- 27141051 27143668 HOXA5 3202 homeobox A5
GO:0005515|GO:0003700|GO:0005634|GO:0048704|GO:0030878|GO:0010870|GO:0009952|GO:0060574|GO:0003
016|GO:0060644|GO:0035264|GO:0045639|GO:0045944|GO:0060435|GO:0043065|GO:0048286|GO:0060764|GO:0
000978|GO:0003677|GO:0006351|GO:0033599|GO:0001077|GO:0060441|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133549_PI430048170 0.6025089496307070.97329778699344 0.551474674132963
0.5912064188022780.495863296716482A A A 0.59835694680792 0.4769678064756910.675068727225
A A A LNCV6_133549_PI430048170 mRNA
GTTCCAAACACAGTACTGAATGCGTTGTTTTTAAATAAACCATTTCGTTTTGCTTTGGGA NM_015879RefSeq chr18
+ 57352489 57368930 ST8SIA351046 "ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3"
GO:0003828|GO:0009311|GO:0006688|GO:0009100|GO:0030173|GO:0000139|GO:0006491|GO:0001574|GO:0006
486|GO:0033691|GO:0006488|GO:0044267|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_136832_PI430048170 0.8129522316639030.94718069958289 2.1374151013215
0.2903654601736970.496892136924481A A A 0.6426529036376052.04599255571146
0.795202973170586A A A LNCV6_136832_PI430048170 mRNA

GGCCTCTACCTTTTCTCAGAATGGTTTCCTGATTGTGTCAATGTGAAAGTTAAATAAAAT NM_004854RefSeq chr2 - 100391859 100417668 CHST10 9486 carbohydrate sulfotransferase 10 GO:0016051|GO:0016232|GO:0005794|GO:0016020|GO:0007616|GO:0000139|GO:0008146|GO:0016021|GO:0007612|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_127519_PI430048170 0.6953970904559520.8335042695271392.88841933460351 3.04668417492717 2.72318227588573 A P A 3.59996140714503 3.26203186040985 2.32220069040533 P P A LNCV6_127519_PI430048170 mRNA TCTAATACCTCCTGTTCTTCCTCTTCAGTGATTTTACCTAGGCAGCGAAGTAGAGAAATG NM_001001917 RefSeq chr11 - 6026670 6027741 OR56A1 NA "olfactory receptor, family 56, subfamily A, member 1" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_142308_PI430048170 0.948008822315354 0.998867594154354 0.580387360839826 0.308131806020599 0.309792316065252 A A A 0.459759116954996 0.397051214087477 0.362061920797631 A A A LNCV6_142308_PI430048170 mRNA ATCAAAATCAGTGAATGTGGGAAGTCACAAGGGAGTCCATAGGTTCTTATGGGAGTAGGA NM_001012446 RefSeq chr9 - 35817016 35828747 FAM221B 392307 "family with sequence similarity 221, member B, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_133965_PI430048170 0.647346422447408 0.967963590924001 11.9352150297459 11.8124059013418 11.6410478672216 P P P 11.8879220512356 11.9081580323993 11.7429892150763 P P P LNCV6_133965_PI430048170 mRNA TGTACATTGCACAGAAACTTGTGTGGGTGCTTTAGTAAAAAACGTGAATGGAGCAAAAAA NM_003780 RefSeq chr1 + 43979201 43991171 B4GALT2 8704 "UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2, transcript variant 2" GO:0005975|GO:0004461|GO:0003831|GO:0044281|GO:0008378|GO:0046872|GO:0042339|GO:0000139|GO:0003945|GO:0018146|GO:0032580|GO:0009405|GO:0016021|GO:0044267|GO:0030203|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_144644_PI430048170 0.0546035849372169 0.958893222237892 0.377939055656484 0.389604071726012 0.33268650188263 A A A 0.433196809037288 0.437752760212639 0.411441431910126 A A A LNCV6_144644_PI430048170 mRNA TCTGATCCTGTTAGTCACTGTGGTTCATCAAATAAAACTGTTTGTGCAACTGTTGTGTCC NM_005161 RefSeq chr11 - 57233577 57237453 APLNR 187 "apelin receptor, transcript variant 1" GO:0007507|GO:0007369|GO:0007186|GO:0005886|GO:0005887|GO:0004930|GO:0004872|GO:0050878 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_127470_PI430048170 0.0176842262772419 0.511521286850389 4.24806696722405 3.93090666691216 4.38765365166109 P P P 5.16310929161021 5.19421821338497 5.14747277826594 P P P LNCV6_127470_PI430048170 mRNA CTGCATCAAAAGTATGCTTTGAGGTATATATAGTGAAACAGAGCCTTTCTGAAGAGAATT NM_018439 RefSeq chr18 + 24426644 24453530 IMPACT 55364 impact RWD domain protein GO:0008150|GO:0003674|GO:0005737|GO:0006446|GO:0001933|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_136328_PI430048170 0.200957660666889 1.21372666783706 0.601885694398813 1.02602663833255 0.585203570950238 A A A 0.395009954586912 0.528128774516851 0.492950409542547 A A A LNCV6_136328_PI430048170 mRNA TGCATTTCTTTTTATACTAAATATGTGACTGACAATAAAAACAATTTTGACTTTAAAAAA NM_175617 RefSeq chr16 + 56625672 56627113 MT1E 4493 metallothionein 1E GO:0071294|GO:0048471|GO:0005737|GO:0008270|GO:0005634|GO:0071276|GO:0045926 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_134389_PI430048170 0.00340874292770142 0.570077965612199 5.46840758509278 5.16298641213151 5.42159826142181 P P P 5.99537880028133 6.19399919958092 6.29807589071893 P P P LNCV6_134389_PI430048170 mRNA

CCACCTGGACTATGGAACTGTGCGTAACAGCTTTGAAAGTGTATTTAAAAATTAAATCTA NM_017619 RefSeq chr1 + 103525955 103555237 RNPC3 55599 "RNA-binding region (RNP1, RRM) containing 3" GO:0008380|GO:0006397|GO:0000166|GO:0003723|GO:0005654|GO:0005634|GO:0005689 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131817_PI430048170 0.174609543534358 1.08683336136482 0.538172104716362 0.733434897877264 0.593422457725477 A A A 0.428631784206481 0.520895902783376 0.559092355312008 A A A LNCV6_131817_PI430048170 mRNA
CAAGAAAAAAGTATGTCTCACTTTTTGTTAATGTTGCTGCCTCATTGACCTGGGAAAAAT NM_198148 RefSeq chr10 - 123745635 123891984 CPXM2 119587 "carboxypeptidase X (M14 family), member 2" GO:0031012|GO:0006508|GO:0008270|GO:0005615|GO:0004181 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142571_PI430048170 0.0358393701023459 0.359789145824236 4.51306937162694 3.29448501277683 4.29260704496508 P P P 5.23811043773794 5.57544132428833 5.90150970025556 P P P LNCV6_142571_PI430048170 mRNA
CCTGTACACATACCAATTAGCGTGACCACTTCCATCTTAAAAACAAACCTAAAAAACAAA NM_002093 RefSeq chr3 - 119821954 120094417 GSK3B 2932 "glycogen synthase kinase 3 beta, transcript variant 1" GO:0005515|GO:0006983|GO:0008013|GO:0030877|GO:0035372|GO:0030010|GO:0032855|GO:0044027|GO:0034605|GO:0007173|GO:0018105|GO:0007411|GO:0016301|GO:0006611|GO:0043025|GO:0045444|GO:0009887|GO:0031625|GO:0010800|GO:0005813|GO:0019901|GO:0005977|GO:0007520|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136818_PI430048170 0.323651991095612 0.848967502334883 4.24124173244559 4.9289654402809 4.70388004729055 P P P 4.9504880107802 4.79330061771858 4.91686473452586 P P P LNCV6_136818_PI430048170 mRNA
TCCCAAGCTACTTCCTACAGTATTTTGGTCAATATTTGGAATGCGTTTTAGTTCTTCACC NM_014332 RefSeq chrX - 21705971 21758160 SMPX 23676 "small muscle protein, X-linked, transcript variant 1" GO:0043034|GO:0006941|GO:0005634|GO:0031430|GO:0005927 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91604_PI430048170 0.269929785754041 1.21694270708008 7.76117688097327 8.11563309635929 8.1499141542781 P P P 7.66566623047456 7.40607387758192 8.06031890855491 P P P LNCV6_91604_PI430048170 mRNA
AGTGAAATACTTCATACATTACAGTGGTTGGAATAAAAATTGGGATGAATGGGTTCCGGA NM_206839 RefSeq chr15 + 78872780 78897739 MORF4L1 10933 "mortality factor 4 like 1, transcript variant 2" GO:0005515|GO:0006355|GO:0016575|GO:0008283|GO:0006325|GO:0006351|GO:0047485|GO:0000724|GO:0016580|GO:0043967|GO:0043968|GO:0003682|GO:0035267|GO:0005654|GO:0040008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79313_PI430048170 0.00271466643613638 1.65609245381475 5.62711228598968 5.84233261607171 5.6029585205724 P P P 5.0539701795962 4.89871431978147 4.94415652260558 P P P LNCV6_79313_PI430048170 mRNA
ATTTGGATTCAAGGTTGGCTCTCAACAGTGCCAGCTGCACTGTCATCCTAAAGTACTTCT NM_001142928 RefSeq chr7 + 150323206 150338156 LRRC61 65999 "leucine rich repeat containing 61, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143825_PI430048170 0.0183708075194206 0.600039862112075 3.34315346861358 3.14586165195578 3.26960085895596 P P P 3.72842086499046 4.17111780402395 4.04140961042897 P P P LNCV6_143825_PI430048170 mRNA
GTTATCTCTCCAAAACACGACCCACACGAGGACCTCGCATTAAAGTATTTTCGGAAAAAA NM_001258018 RefSeq chr19 - 49889655 49929539 IL4I1 259307 "interleukin 4 induced 1, transcript variant 4" GO:0001716|GO:0005576|GO:0005764|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123642_PI430048170 0.487638116457488 0.950837471126584 11.987981805235

11.9673154937065 11.8105249097297 P P P 12.1290610137529 11.973612291899
11.8764619491632 P P P LNCV6_123642_PI430048170 mRNA
GAGAGCGCGCTCTGCCTGCCGCCTGCCTGCCTGCCACTGAGGGTTCCCAGCACCATGAGG NM_003118 RefSeq
chr5 - 151661095 151687054 SPARC 6678 "secreted protein, acidic, cysteine-rich (osteonectin)"
GO:0005515|GO:0005886|GO:0030324|GO:0045471|GO:0005518|GO:0043434|GO:0033591|GO:0051591|GO:0005
615|GO:0016363|GO:0005739|GO:0007507|GO:0005737|GO:0030198|GO:0071682|GO:0022604|GO:0032496|GO:0
031091|GO:0031092|GO:0031093|GO:0034097|GO:0010288|GO:0048839|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141360_PI430048170 0.00151140356693723 0.709553218694682 10.9186353141922
10.7875765289639 10.897077149935 P P P 11.3452067377406 11.4075952018603
11.3379107279789 P P P LNCV6_141360_PI430048170 mRNA
TTGTTTTGTTTTTCTTTCTTTTTCCTGGCCATGAGGACAAAAATTACTGAGTGGCCCTTA NM_001290189 RefSeq
chr19 + 53869390 53876435 MYADM 91663 "myeloid-associated differentiation marker, transcript
variant 6"
GO:0031579|GO:0030335|GO:0005886|GO:0072661|GO:0010810|GO:0001726|GO:0045217|GO:0003674|GO:0090
038|GO:1900026|GO:0061028|GO:0005911|GO:0010629|GO:0030837|GO:0034115|GO:0001933|GO:0045121|GO:0
016021|GO:0030864|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102862_PI430048170 0.221389003935994 0.923396319559359 6.57935772798403
6.67478928261176 6.44562974033062 P P P 6.6296606712348 6.76189192088249
6.65893041326829 P P P LNCV6_102862_PI430048170 mRNA
ATTTCGTTCACCTTTGTCCCGGGCATTCCAACTGGTGGAGGAGATCCGGAACCACGTGCT NM_012235 RefSeq
chr3 - 47413693 47475955 SCAP 22937 SREBF chaperone
GO:0005515|GO:0001666|GO:0012507|GO:0032868|GO:0005794|GO:0005783|GO:0045541|GO:0007568|GO:0045
716|GO:0044281|GO:0032403|GO:0043234|GO:0032933|GO:0042304|GO:0000139|GO:0015485|GO:0005789|GO:0
051082|GO:0016021|GO:0008203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143502_PI430048170 0.0281495484546891 0.822858195785465 9.86771240982021
9.83894110758731 9.94605100127007 P P P 10.2528199620403 10.0441837337621
10.1937589941142 P P P LNCV6_143502_PI430048170 mRNA
ATATCCTGTATATATACTGGCGTTTCTGTCCTGATGTCAAGTCTCGAGAGAAGATGATCA NM_024782 RefSeq
chr2 - 219075323 219160865 NHEJ1 79840 nonhomologous end-joining factor 1
GO:0070419|GO:0005515|GO:0051351|GO:0030217|GO:0010212|GO:0030183|GO:0006310|GO:0005634|GO:0007
417|GO:0006303|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143640_PI430048170 0.388189662522447 1.25620518439403 0.443779905917661
0.408743196061645 1.19706007068163 A A A 0.364467284476116 0.435247558467343
0.406100693839619 A A A LNCV6_143640_PI430048170 mRNA
TGTTTTTGCATCCTTATAAAAGCTTATGCCAGCTGAAATTAGCCTGTGCAACCACTAACA NM_181807 RefSeq
chr11 - 31262623 31369810 DCDC1 341019 doublecortin domain containing 1 GO:0035556 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70772_PI430048170 0.113762113203661 1.16851701648284 8.05569014714149
7.88786021573522 7.80225602107127 P P P 7.76685009747924 7.77834943032597
7.52418999280382 P P P LNCV6_70772_PI430048170 mRNA
AACCAGGATTGACAGGCCATCCATTCACAGCCAGGAGATGCTGGGCCAGTTCCTCCAAGA NM_023083 RefSeq
chr2 + 240586715 240599109 CAPN10 11132 "calpain 10, transcript variant 1"
GO:0008092|GO:0032388|GO:0032869|GO:0005886|GO:0031532|GO:0005623|GO:2000676|GO:0006921|GO:0005
829|GO:0005739|GO:0004198|GO:0097050|GO:0046326|GO:0000149|GO:0006508|GO:0032024 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143850_PI430048170 0.051086552301556 0.676392476635132 10.7825876674745
10.7933795048592 10.5624701332448 P P P 10.9563825708269 11.4252204499675
11.4129869120256 P P P LNCV6_143850_PI430048170 mRNA

GCCTCTGAACGGAACAGTGTCCCCACAGAGCGAATAAAGCCAAGGCTTCTTCCCAAAAAA NM_014601 RefSeq chr19 + 47713343 47743134 EHD2 30846 EH-domain containing 2
GO:0005515|GO:0048471|GO:0005886|GO:2001137|GO:0032456|GO:0019904|GO:0005509|GO:0005634|GO:0003676|GO:0005525|GO:0072659|GO:0005524|GO:0006897|GO:0016787|GO:0030866|GO:0007596|GO:0005901|GO:0008152|GO:0055038|GO:0010008|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118214_PI430048170 0.568437430151407 0.900893139836549 6.93027520696285 6.69656064044871 6.81633756069662 P P P 6.61156716344054 7.25816210125028 6.96275107322111 P P P LNCV6_118214_PI430048170 mRNA
CTCTTTTTGGTGGTGGTTAAAAGGGAACACAAAACATTTAAATAAAACTTTCCAAATATT NM_000478 RefSeq chr1 + 21509364 21578412 ALPL 249 "alkaline phosphatase, liver/bone/kidney, transcript variant 1"
GO:0005515|GO:0071529|GO:0005886|GO:0051384|GO:0033280|GO:0031225|GO:0005615|GO:0046872|GO:0001649|GO:0031012|GO:0003006|GO:0071407|GO:0001501|GO:0001958|GO:0016462|GO:0004035|GO:0016020|GO:0016311|GO:0032496|GO:0016021|GO:0046677|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127635_PI430048170 0.278667437765487 0.54239211948281 1.57271394797067 0.641678578311869 1.33268903170582 A A A 0.952505784800493 2.23067696680538 2.67257311163671 A A P LNCV6_127635_PI430048170 mRNA
CGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAATGCAAATAAAACTCACATTTGT NM_014553 RefSeq chr2 - 121216587 121285202 TFCP2L1 29842 transcription factor CP2-like 1
GO:0006694|GO:0007565|GO:0003700|GO:0006357|GO:0003714|GO:0005634|GO:0000122|GO:0008340|GO:0006351|GO:0043565|GO:0000902|GO:0005737|GO:0016020|GO:0002070|GO:0007431|GO:0007028|GO:0045927 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133621_PI430048170 0.0023304758202210.4035164058904366.76248910037323 6.34167661598777 6.56884559613051 P P P 7.6640378554423 7.79121249730582 8.13438131017174 P P P LNCV6_133621_PI430048170 mRNA
GCAGTACTAAGGGAACAATCCATGTGATTAATGTTTTCATTATGTTCATGTAAGAAGCCC NM_133631 RefSeq chr3 - 78597237 79019459 ROBO1 6091 "roundabout, axon guidance receptor, homolog 1 (Drosophila), transcript variant 2"
GO:0005515|GO:0005886|GO:0009986|GO:0006919|GO:0002042|GO:0060763|GO:0035385|GO:0021836|GO:0042802|GO:0007399|GO:0050925|GO:0005737|GO:0070100|GO:0005887|GO:0007411|GO:0016199|GO:0030275|GO:0050772|GO:0030673|GO:0033600|GO:0007155|GO:0007156|GO:0008046 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97317_PI430048170 0.0130966798256466 1.2345968661457 14.4354531242016 14.5591228158255 14.3833204406184 P P P 14.0982827119016 14.1952524905338 14.1761162569216 P P P LNCV6_97317_PI430048170 mRNA
CTACATCTGTCCCTTCCCATCAATCCCAGCCCATGTACTAATAAAAGAAAGTCTTTGAGT NM_080748 RefSeq chr20 + 35699309 35700980 ROMO1 140823 reactive oxygen species modulator 1
GO:0005739|GO:0003674|GO:0008284|GO:0034614|GO:0005743|GO:0001302|GO:0016021|GO:2000379|GO:0042742 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112039_PI430048170 0.46928611157069 0.6019739140336570.430384125874591 0.4402546825543960.540289688882247 A A A 2.09013579907595 0.395246370324987 0.417262402249069 A A A LNCV6_112039_PI430048170 mRNA
CAAGCCAGTTTGACTGAAGAACGACTTGGAGACGGCAAGTCGGCAGACAATACAGAGGTC NM_021240 RefSeq chr9 + 976967 991732 DMRT3 58524 doublesex and mab-3 related transcription factor 3
GO:0000987|GO:0006355|GO:0003700|GO:0046982|GO:0021521|GO:0046661|GO:0005634|GO:0019226|GO:0006351|GO:0042803|GO:0046872|GO:0007628|GO:0007548|GO:0042487 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_130341_PI430048170 0.6943878929997770.9152657567084427.30814195454933 7.0089402445341
6.74681852584837 P P P 7.4877717151701 7.17429571790731 6.7452573470088 P P P
LNCV6_130341_PI430048170 mRNA
TAGTCACCTGCCCCAGCACTCACACCCTAACTCAAAATAAATGTTAAATAAGTGCGATCA NM_003245RefSeq chr20
+ 2295966 2341079 TGM3 7053 transglutaminase 3
GO:0016746|GO:0051262|GO:0005509|GO:0031424|GO:0003824|GO:0031069|GO:0031234|GO:0005737|GO:0018
149|GO:0030216|GO:0003810|GO:0043163|GO:0006464|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130440_PI430048170 0.2071926611158020.8745170603461560.553540890381213
0.5511844160048260.324296190458823A A A 0.5268555672123530.614701992692261
0.858776745308193A A A LNCV6_130440_PI430048170 mRNA
TTAAAAGGAAAGAAGTTCCACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAAC NM_005429RefSeq chr4
- 176683533 176792745 VEGFC 7424 vascular endothelial growth factor C
GO:0005515|GO:0008284|GO:0008285|GO:0030947|GO:0006929|GO:0050714|GO:0050731|GO:0060754|GO:0045
776|GO:0005615|GO:0009887|GO:0051781|GO:0031093|GO:0031954|GO:0050679|GO:0048010|GO:0042493|GO:0
002052|GO:0030168|GO:0005576|GO:0001525|GO:0042056|GO:0045766|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132650_PI430048170 0.3341984863607311.01339272262471 0.326478605632812
0.3001199261994050.274108958631002A A A 0.2848663739429990.284601229281307
0.274108958631002A A A LNCV6_132650_PI430048170 mRNA
GCACCTGGAATCCAGTGTGTCCAAGCCAGTATTAAATTATCTCAACACATTCCACAGAAA NM_001100600 RefSeq
chr7 - 4905988 4959213 MMD2 221938 "monocyte to macrophage differentiation-associated 2,
transcript variant 1" GO:0048471|GO:0000139|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_143532_PI430048170 0.7083350061150640.9960547455399850.322924672112117
0.3560685927574320.359389601435634A A A 0.3614833475396510.358404608257176
0.335748472611826A A A LNCV6_143532_PI430048170 mRNA
AACCAACATGAAATGACTATAAATGGTTTTTTAATGAAAAAAGAAATCACTTTTAAAAAA NM_001001520 RefSeq
chr19 + 4472195 4502220 HDGFRP2 84717 "hepatoma-derived growth factor-related protein 2,
transcript variant 1" GO:0005739|GO:0003682|GO:0005654|GO:0005634|GO:0003677|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131917_PI430048170 0.2048642146735380.9702178701964360.275267503968405
0.3055346805376110.346968856254211A A A 0.3902615609192410.321873348380814
0.346560281601776A A A LNCV6_131917_PI430048170 mRNA
AACTACTAATGCACTGATATGAAACACGGCTTACACTAATGACATTCTGAATTCTTGCTT NM_000705RefSeq chr13
- 113648805 113658198 ATP4B 496 "ATPase, H+/K+ exchanging, beta polypeptide"
GO:0034220|GO:0005886|GO:0032496|GO:0010243|GO:0008900|GO:0007155|GO:0006814|GO:0005890|GO:0055
085|GO:0006813 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125507_PI430048170 0.2355684894639081.09938542995315 14.8081710040674
15.0049989504239 15.0264229396792 P P P 14.814577375878 14.687696623324
14.9271704624221 P P P LNCV6_125507_PI430048170 mRNA
CGGCCATCTTAGCGGCTGCTGTTGTTGGGGGCCGTCCCGCTCCTAAGGCAGGAAGATGGT NM_000989RefSeq chr8
- 98041709 98045590 RPL30 6156 ribosomal protein L30
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0005634|GO:0006
415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0016020|GO:0000184|GO:0016032|GO:0
022625|GO:0044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131776_PI430048170 0.00274803450833842 0.3422375074360110.538762951608972
0.6070357667390930.551766186121477A A A 2.29688489080604 1.98626310832561
2.03648838800911 A A A LNCV6_131776_PI430048170 mRNA

CTTACACTGCTACACCATTACTTTCTTGAGACATTTGTAAGTTCTTTGATACAGAAGAGT NM_014394 RefSeq chr10 + 84139428 84153555 GHITM 27069 growth hormone inducible transmembrane protein GO:0005515|GO:0008150|GO:0003674|GO:0005743|GO:0006915|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141571_PI430048170 0.198228883655606 1.04754688589473 0.462361073115112 0.393626887027173 0.445923356891592 A A A 0.305523649079904 0.362707583042401 0.430795969782093 A A A LNCV6_141571_PI430048170 mRNA
GGACACTTTCAATGGTGCCTTGAAATCTATGACCTCAACTTTTCAAAAGACTTTTTTCAA NM_005221 RefSeq chr7 - 97020389 97024831 DLX5 1749 distal-less homeobox 5 GO:0071773|GO:0000790|GO:0044212|GO:0008283|GO:0090263|GO:0030326|GO:0005737|GO:0048646|GO:0007411|GO:0030855|GO:0060166|GO:0060021|GO:0050679|GO:0042472|GO:0030509|GO:0000978|GO:0006351|GO:0001649|GO:0007399|GO:0045669|GO:0001958|GO:0001501|GO:0001077|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127060_PI430048170 0.163563278395287 4.77244549093369 0.472923027113087 2.61953324973859 3.31902837129296 A A P 0.264413664087394 0.347506412527617 0.258426641537898 A A A LNCV6_127060_PI430048170 mRNA
CAGGGATCCAGAGAGTCTGAAGACATTTCTTATGCCTTTATATATTGGAGAACCCTTCCC NM_001145112 RefSeq chr15 - 44665731 44676888 PATL2 NA protein associated with topoisomerase II homolog 2 (yeast) NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139137_PI430048170 0.336302338617348 0.637449158536584 2.79108479636592 2.44521186136695 0.303137861794704 A A A 2.85035165288314 3.00076655867114 2.61381191399535 P P P LNCV6_139137_PI430048170 mRNA
GTGTGACATATATCAGTACCTTCATTCTTCTATATTTTGTGTCTCCTCCAACCTCCAACT NM_024081 RefSeq chr11 + 32829934 32858123 PRRG4 79056 proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane) GO:0008150|GO:0003674|GO:0005509|GO:0005576|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133029_PI430048170 4.91623596626911e-05 2.42353897885248 6.2321927002734 6.34211435453411 6.3836568353776 P P P 5.13500338549431 5.02679142970033 4.9638158758286 P P P LNCV6_133029_PI430048170 mRNA
AGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACC NM_014266 RefSeq chr19 + 35902479 35904271 HCST 10870 "hematopoietic cell signal transducer, transcript variant 1" GO:0005515|GO:0009986|GO:0005886|GO:0050776|GO:0005102|GO:0014068|GO:0016021|GO:0043548 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53136_PI430048170 0.0302535502469475 0.727665536837367 9.28840555299855 9.38132180751528 9.23317453747228 P P P 9.55838808962335 9.88551111899586 9.81858177806357 P P P LNCV6_53136_PI430048170 mRNA
AGAAAATACCTGCACCTGAGCTTCCATGCCCTGGTGGGCCTGGCCACGGAAGAGCTCCTG NM_004260 RefSeq chr8 - 144511283 144517826 RECQL4 9401 RecQ protein-like 4 GO:0043140|GO:0000405|GO:0005634|GO:0006310|GO:0007275|GO:0005524|GO:0006260|GO:0000733|GO:0005737|GO:0006281|GO:0016020|GO:0008270|GO:0032508 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145416_PI430048170 0.0006010913973926 0.550585033670602 11.708756210041 11.5707618328533 11.4945514500511 P P P 12.3394668289 12.5493215805983 12.4686714277656 P P P LNCV6_145416_PI430048170 mRNA
GCTTCTGCGGCTTCGGTGGAGACAGTTATGGAATAAAATGTTCCTTGCACCCAGAAAAAA NM_032656 RefSeq chr12 - 124946823 124989121 DHX37 57647 DEAH (Asp-Glu-Ala-His) box polypeptide 37 GO:0004004|GO:0006396|GO:0005737|GO:0005730|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131907_PI430048170 0.230748559097931 1.01914173013329 0.308254637141243 0.255404771853348 0.298246658680913 A A A 0.264910432357311 0.251012915590211

0.264420069924025 A A A LNCV6_131907_PI430048170 mRNA
GGGAAGACTGTAACACAGCTGAACTATTTCAGTGTCAACTATTCAGAATTGAAAATGTAA NM_002711 RefSeq chr7
- 113876826 113919027 PPP1R3A NA "protein phosphatase 1, regulatory subunit 3A" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_138380_PI430048170 0.717130895109926 1.1624593581632 1.42065989284895
0.328319195201428 0.405192576476423 A A A 1.02482566858111 0.323164550850157
0.306183870420257 A A A LNCV6_138380_PI430048170 mRNA
TCCAAGATCATAGACTTACTAAAGAGAGTGACAAATGCTTCCTTAATGTCTTCTATACCA NM_004098 RefSeq chr10
+ 117542444 117549546 EMX2 2018 "empty spiracles homeobox 2, transcript variant 1"
GO:0043565|GO:0005515|GO:0021846|GO:0021542|GO:0021796|GO:0006355|GO:0042493|GO:0030182|GO:0072
001|GO:0005634|GO:0021885|GO:0009952 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138121_PI430048170 0.154705476366514 1.03873903057972 0.378641275020576
0.386830439734319 0.458421903467127 A A A 0.346019894439029 0.331173952426303
0.383046757494275 A A A LNCV6_138121_PI430048170 mRNA
TACCTGAGGCCAAGGAGAATTTCTGAAATGTCACTAGTAGTGAGAACTTCCTTTCATTAA NM_001005483 RefSeq
chr14 + 19920606 19921578 OR4K5 NA "olfactory receptor, family 4, subfamily K, member 5" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138229_PI430048170 0.170416322881589 0.380917628932054 0.922034029131184
0.40733425841779 1.18948860238959 A A A 1.04626345660384 1.96206051531112
3.08440816819167 A A P LNCV6_138229_PI430048170 mRNA
CCCTCCGTGAATGTAGATCATAAGCAAACAAATTGCCTGTTCTAAATGAACTTTACATAT NM_015446 RefSeq chr1
- 246839097 246931424 AHCTF1 25909 AT hook containing transcription factor 1
GO:0031965|GO:0006355|GO:0003700|GO:0005634|GO:0051292|GO:0015031|GO:0003677|GO:0016363|GO:0005
829|GO:0000910|GO:0005643|GO:0031080|GO:0000777|GO:0005654|GO:0051028|GO:0000278|GO:0000785|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143765_PI430048170 0.105076158835233 0.840654867072539 12.5186335278722
12.7070922332593 12.8203836887639 P P P 12.8813820506171 12.8247826345617
13.0930758054696 P P P LNCV6_143765_PI430048170 mRNA
CCTCAGTTTTCTCACAAGAACCCAGTTAGCTGATGTTTTATTGTAATTGTCTTAATTTGC NM_198976 RefSeq chr20 +
58981207 58995133 NELFCD 51497 negative elongation factor complex member C/D
GO:0005515|GO:0010467|GO:0006368|GO:0016020|GO:0006366|GO:0032021|GO:0016032|GO:0005654|GO:0045
892|GO:0050434 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127046_PI430048170 0.536749945951926 0.908132599616322 4.73410017299229
4.77295039642209 4.96169455072243 P P P 4.6271374384492 5.15617519003746
5.05984526535104 P P P LNCV6_127046_PI430048170 mRNA
GTGTCTATAATGTTGTGGTGGGAATCATTTCATTTGGTTTAAAAGAGTTTGCCTTGGAAA NM_138458 RefSeq chr2
- 68130148 68157560 WDR92 116143 "WD repeat domain 92, transcript variant 1"
GO:0005515|GO:0034968|GO:0006915|GO:0035064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58088_PI430048170 0.0921175973076593 1.28325709505138 6.41924737361988
6.67289204432717 6.55975184299494 P P P 6.39250204158096 6.22108806063158
5.93325445650353 P P P LNCV6_58088_PI430048170 mRNA
TTGCCTGAAGTTTCGGCCATACCTATCTCCCTGGACGGGCTACTCTTCCCTCGGCCCTGC NM_000926 RefSeq chr11
- 101029623 101129813 PGR 5241 "progesterone receptor, transcript variant 2"
GO:0060748|GO:0005515|GO:0050847|GO:0050678|GO:0010467|GO:0006367|GO:0007267|GO:0003707|GO:0005
102|GO:0001542|GO:0005741|GO:0000978|GO:0003677|GO:0007165|GO:0001077|GO:0045944|GO:0010629|GO:0
043401|GO:0008270|GO:0002070|GO:0005654|GO:0004879|GO:0019899|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137101_PI430048170 0.00810664330615313 0.611392409999797 6.06742277970977
5.71858726079429 5.79034732369618 P P P 6.60147910057379 6.66805157243543

6.45186712784385 P P P LNCV6_137101_PI430048170 mRNA
GGGGAAAGGAAAGAATTCACTAGAAATTTGTTTAGGGTCCAGTTGATTTGTGTATTTTTG NM_001252612 RefSeq
chr2 + 71331754 71435061 ZNF638 27332 "zinc finger protein 638, transcript variant 3"
GO:0008380|GO:0006355|GO:0005737|GO:0003690|GO:0016607|GO:0000166|GO:0003723|GO:0008270|GO:0005
654|GO:0006351|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95943_PI430048170 0.3715079373271831.22590966975405 5.84518638395326 6.16413624463505
6.16250875381518 P P P 6.13678349939081 5.8665369152112 5.13387891641371 P P P
LNCV6_95943_PI430048170 mRNA
TTGTGTCAGCAAAATTCTTGGCATGTCCACTGGCTCCGTGACGCAGGTGTCCTCGGTGAG NM_016734RefSeq chr9
- 36833274 37034479 PAX5 5079 "paired box 5, transcript variant 1"
GO:0005515|GO:0006366|GO:0005634|GO:0007275|GO:0000122|GO:0007283|GO:0000978|GO:0035914|GO:0007
399|GO:0001077|GO:0051573|GO:0006959|GO:0045944|GO:0009887 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133922_PI430048170 0.3838161580921720.8948980889361274.28304697819091
4.16622053818179 4.63993587470891 P P P 4.36245562771756 4.55797888244825
4.67538341530827 P P P LNCV6_133922_PI430048170 mRNA
AACCACGTATTATATGATCAGTGTTTTCAAGTCTATGTGAAATTGGGTAGGTGTGGAATA NM_152361RefSeq chr19
- 39531532 39532867 EID2B 126272 EP300 interacting inhibitor of differentiation 2B
GO:0006355|GO:0007517|GO:0005634|GO:0030154|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133525_PI430048170 0.1212945777728960.7997905978106779.58059393234201
9.35061827693133 9.44154697124208 P P P 10.0055587048486 9.55700328045528
9.75121486837406 P P P LNCV6_133525_PI430048170 mRNA
GGAAAGTGCTATGATGAATTTTATGCAATAAATGTATACATGTGTGCACATGCACCCATG NM_023928RefSeq chr12
+ 125065378 125143325 AACS 65985 acetoacetyl-CoA synthetase
GO:0007584|GO:0042493|GO:0045471|GO:0034201|GO:0005524|GO:0014074|GO:0047760|GO:0005829|GO:0001
889|GO:0071397|GO:0042594|GO:0071394|GO:0050872|GO:0006631|GO:0032024|GO:0071333|GO:0060612|GO:0
030729 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93351_PI430048170 3.83733419866557e-06 1.42433998477958 6.97137735663874
7.00535484667162 6.98339502143562 P P P 6.45760397676467 6.49346117878448
6.47816313547935 P P P LNCV6_93351_PI430048170 mRNA
AAAGGCTGGAATGAGTGTGAGCAGACAGTGGCCCTCCTGTCACTTCTGAAACGGGTCACC NM_018028RefSeq chr19
+ 39342458 39384897 SAMD4B NA "sterile alpha motif domain containing 4B, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59185_PI430048170 0.0719261414131664 0.7472258648950514.13878949014452
3.71779905264433 4.051120318735 P P P 4.27728355603853 4.27277383735707
4.62335888011499 P P P LNCV6_59185_PI430048170 mRNA
ATGTGGTACTCATTTTAAATGGAAGAGAAAAAGCAAAGATCTTTTATGCCACCCAGTGGT NM_001278237 RefSeq
chr12 + 63780125 63809558 TMEM5 10329 "transmembrane protein 5, transcript variant 2"
GO:0005794|GO:0000139|GO:0005887|GO:0035269 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132606_PI430048170 0.0143755737126219 0.74752199647442611.1215106377938
10.909466860898 11.1109036811783 P P P 11.3686504146288 11.4198982213655
11.6110397099987 P P P LNCV6_132606_PI430048170 mRNA
TTTTTATGAGGTGAAGTGCATCAAACTTGGGAAAGATTTGAGGAGGCTGGGAACCTCCTG NM_000637RefSeq chr8
- 30678062 30727969 GSR2936 "glutathione reductase, transcript variant 1"
GO:0050661|GO:0015949|GO:0050660|GO:0006749|GO:0009055|GO:0055086|GO:0044281|GO:0004362|GO:0005
829|GO:0045340|GO:0050787|GO:0005759|GO:0045454|GO:0000302|GO:0009897|GO:0016152|GO:0070062|GO:0
055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141398_PI430048170 0.00533496234724922 1.32943243054455 10.0493746279592

10.1809385084333 10.1551416034715 P P P 9.71599955816243 9.69702468247789
9.74297091968775 P P P LNCV6_141398_PI430048170 mRNA
ATGAGAGGCCAGGAAGTGTGAACATACTGATAGAAAAAGACTATATTTTATCCCTCATAA NM_024775 RefSeq chr2
+ 38778184 38781964 GEMIN6 79833 gem (nuclear organelle) associated protein 6
GO:0005515|GO:0016604|GO:0010467|GO:0000245|GO:0005737|GO:0032797|GO:0000398|GO:0005654|GO:0034
660|GO:0000387|GO:0034719|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108078_PI430048170 0.0495704993177836 1.31913266726674 11.9991853188895
12.1881347126567 12.0217278219742 P P P 11.881416211615 11.5015973791076
11.6076877064227 P P P LNCV6_108078_PI430048170 mRNA
CCAGACAGCGAGTGACATCCCATCTCCTCCTCTGCATTAAAGATGACCTGCTGAACATTG NM_001243526 RefSeq
chr1 - 43451002 43453989 HYI 81888 "hydroxypyruvate isomerase (putative), transcript variant 4"
GO:0008150|GO:0003674|GO:0008903|GO:0008152|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145573_PI430048170 0.4629602770390940.7254609796988350.407235989191666
0.2959795918448270.505021579554921 A A A 0.3294168139977461.53597935408393
0.400721533632559 A A A LNCV6_145573_PI430048170 mRNA
ATAAAGTGTCAAGCAAGATTTTAGCCGCAGCTGCTTCTTCTTTGGTGGATTTGAGGGGTG NM_012483 RefSeq chr2
+ 85694290 85698851 GNLY 10578 "granulysin, transcript variant 3"
GO:0006968|GO:0050832|GO:0031640|GO:0005615|GO:0042742 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_57133_PI430048170 0.6776264236809130.97765744459942 6.22618490826855 5.99917727900534
6.17454241052416 P P P 6.21403175137193 6.18643426356584 6.10469292095755 P P P
LNCV6_57133_PI430048170 mRNA
CTTATGTCTCCTCCTCCGAGGACTTCACCATCCACGAAAATGCTTTCATTGTGTTCATTG NM_001256236 RefSeq
chr11 + 3797818 3826371 PGAP2 27315 "post-GPI attachment to proteins 2, transcript variant 5"
GO:0042770|GO:0042771|GO:0000139|GO:0008565|GO:0005789|GO:0005634|GO:0016021|GO:0015031|GO:0006
506 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138110_PI430048170 0.8801165579194260.983316632846479 5.3683622284459 5.7172086079033
5.9827579342692 P P P 5.56652815901657 5.6387853043655 5.96825705953935 P P P
LNCV6_138110_PI430048170 mRNA
GACCATAAACTTTCAGAACTTTGTATTATGCAGAGGGATCTGTGAAACTAGTCAATTTGT NM_021632 RefSeq chr19
- 51964339 51986826 ZNF350 59348 zinc finger protein 350
GO:0005515|GO:0006355|GO:0001162|GO:0005634|GO:0000122|GO:0001227|GO:0003677|GO:0006351|GO:0016
363|GO:0046872|GO:0017053|GO:0005654|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143189_PI430048170 0.000396981051338995 0.828303767305701 11.3917561760987
11.4028116945506 11.3749599433235 P P P 11.67845570099 11.6324843793514
11.6735877812084 P P P LNCV6_143189_PI430048170 mRNA
GCTTCTGTTTGTTTTTTAAACTATGCACCAGGTTTCTGATGATGAAATAAAGCACCTGTT NM_001120 RefSeq chr4
- 2930560 2934237 MFSD10 10227 "major facilitator superfamily domain containing 10, transcript
variant 1" GO:0015904|GO:0006810|GO:0006915|GO:0016021|GO:0008493|GO:0055085 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_142568_PI430048170 0.81380716687679 1.00715254661263 0.507800220722567
0.4125380302479690.513699260169928 A A A 0.4582344721199530.507373332874369
0.438934912050331 A A A LNCV6_142568_PI430048170 mRNA
CGTGCTCATTTGTCAGACATAGCTGTAAATGAAAACAATGTGTGGCAAAATACAAAGTTA NM_001031804 RefSeq
chr16 - 79593847 79600725 MAF 4094 "v-maf avian musculoaponeurotic fibrosarcoma oncogene
homolog, transcript variant 2"
GO:0048839|GO:0006366|GO:0070306|GO:0005634|GO:0032330|GO:0000122|GO:0001228|GO:0001816|GO:0043
565|GO:0005737|GO:0045944|GO:0048468|GO:0000785 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_82594_PI430048170 0.0145883560322180.8029211044300157.7957357832384 7.9831003947993
7.84736454529049 P P P 8.22226279838087 8.09010386053071 8.26469850928276 P P P
LNCV6_82594_PI430048170 mRNA
TGTCTTTCCTGAAGACTATCTTCCCGTCTCAAAATGGACATGATGGATCCACGGATGTAC NM_006985RefSeq
chr16_KI270853v1_alt - 717600 732294 NPIPA1 9284 "nuclear pore complex interacting protein family,
member A1" GO:0031965|GO:0005643|GO:0051028|GO:0015031 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_132768_PI430048170 0.00910212511010833 0.6399173857874687.9602370509553
7.97136248723504 7.8495732622111 P P P 8.62806696909464 8.67951634236464
8.39295568843777 P P P LNCV6_132768_PI430048170 mRNA
TGCAACAGTAATTTATATCCAGGACAAATACAGTCTGGGCGTCACTATCCTACCAAAAAA NM_001347RefSeq chr4
- 958883 973560 DGKQ 1609 "diacylglycerol kinase, theta 110kDa"
GO:0005515|GO:0005886|GO:0006357|GO:0030168|GO:0005634|GO:0005524|GO:0070528|GO:0046872|GO:0007
205|GO:0005829|GO:0016310|GO:0005737|GO:0003951|GO:0016607|GO:0007186|GO:0070493|GO:0043274|GO:0
007596|GO:0019933|GO:0004143|GO:0033198|GO:0033613|GO:0019900|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145371_PI430048170 0.2241055864066890.8143300273793192.83477717435194
2.73750657550011 3.33982309607435 A A P 3.17654384126956 3.31358401334928
3.37855633685904 P P P LNCV6_145371_PI430048170 mRNA
GGCAGCAGATTGACTAGTTCTTTAAATCTGTGTGTAACGTATGTTTTATTCCTCATTTCT NM_001564RefSeq chr4 +
183505049 183512428 ING2 3622 "inhibitor of growth family, member 2, transcript variant 1"
GO:0005515|GO:0008285|GO:2001020|GO:0007286|GO:0005634|GO:0007283|GO:0035064|GO:0032403|GO:0005
737|GO:0016580|GO:2000772|GO:0030511|GO:0006355|GO:0005794|GO:0043065|GO:0048133|GO:0030317|GO:0
003677|GO:0006351|GO:0007165|GO:0016602|GO:0003682|GO:0072520|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145617_PI430048170 0.0526301264674335 0.3737864414875023.73828649794205
3.70779606215007 4.1539508140023 P P P 4.53673449552675 5.29267010779207 5.8042168702802
P P P LNCV6_145617_PI430048170 mRNA
GTAGACTTTGTCTTATGTGTGAAAAGTCCTAGGAAAGTGGTTGATGTTTCTTATAGCAAT NM_002053RefSeq chr1
- 89052303 89065360 GBP1 2633 "guanylate binding protein 1, interferon-inducible"
GO:0051607|GO:0000139|GO:0019221|GO:0008152|GO:0003924|GO:0005576|GO:0005525|GO:0060333|GO:0042
802|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132153_PI430048170 0.2756471126499881.4225208654462 2.63160481109642 1.8140282107552
1.98469773828716 A A A 2.29452880554928 1.27079483223791 1.19638304809175 A A A
LNCV6_132153_PI430048170 mRNA
TCTGGTTGCATCCCCAATTTCATACAAAAAGAAAAATAAAAGTGACCTCGTTCTAGCACC NM_005598RefSeq chr1
+ 160367070 160372848 NHLH1 4807 nescient helix loop helix 1
GO:0000977|GO:0045944|GO:0046983|GO:0005634|GO:0007417|GO:0001228|GO:0030154|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95916_PI430048170 0.4102067815005460.9042551695754 6.19753321566194 6.35439365158317
6.57104751594424 P P P 6.40982127596907 6.40017390828021 6.74560880606639 P P P
LNCV6_95916_PI430048170 mRNA
AACTCCATTTTGGATGGCTCCTGAGGTGATTCAAGAAATAGGCTATAACTGTGTGGCCGA NM_001256312 RefSeq
chr8 - 98454630 98942571 STK3 6788 "serine/threonine kinase 3, transcript variant 2"
GO:0005515|GO:0051897|GO:0008285|GO:0071902|GO:0097284|GO:0046330|GO:0005634|GO:0005829|GO:0032
092|GO:0035556|GO:0051091|GO:0005737|GO:0004702|GO:0046983|GO:0090090|GO:0023014|GO:0046621|GO:0
000287|GO:0043065|GO:0060706|GO:0050821|GO:0003157|GO:0006915|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_109979_PI430048170 0.0230492814650522.08882592932298 8.13676285949866

8.14133928821366 8.3384207747612 P P P 7.48470811842337 6.7971349487401 7.0720219910735
P P P LNCV6_109979_PI430048170 mRNA
CACTAACACCTGTAATAAATATGGAGTCAGTGGATATCCAACCCTGAAGATATTTAGAGA NM_005313 RefSeq chr15
+ 43746391 43772606 PDIA3 2923 "protein disulfide isomerase family A, member 3"
GO:0005515|GO:0002474|GO:2001238|GO:0034976|GO:0005783|GO:0005634|GO:0006606|GO:0004629|GO:0006
457|GO:0006508|GO:0018279|GO:0070062|GO:0042470|GO:0009986|GO:0042590|GO:0003756|GO:0005790|GO:0
004197|GO:0007165|GO:0005788|GO:0002479|GO:0045454|GO:0006621|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136657_PI430048170 0.3411067740041590.7658140136004348.02461832569883
7.80712035770248 7.71287086768991 P P P 7.70839545237047 8.65607496283336
8.19915324109802 P P P LNCV6_136657_PI430048170 mRNA
CTTTTCAGAACACATGGACTTGGAGGCAGATTTGAAATAAACTTTTAGTAAATGTAAGCC NM_152341 RefSeq chr16
+ 2969244 2973489 PAQR4 124222 "progestin and adipoQ receptor family member IV, transcript
variant 1" GO:0004872|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137603_PI430048170 6.53662818509722e-05 0.0829044207055902 8.97911856921158
8.59024913403447 8.4938000214734 P P P 12.0636694930893 12.4641511589323
12.3311497944488 P P P LNCV6_137603_PI430048170 mRNA
ACATTCCTTACCCATTAGTCTCAGAAATTGTCTTAAGCAACAGCCCCAAATGCTGGCTGC NM_031286 RefSeq chr1
+ 26279721 26281522 SH3BGRL3 83442 SH3 domain binding glutamate-rich protein like 3
GO:0015035|GO:0009055|GO:0005634|GO:0005100|GO:0030027|GO:0030834|GO:0043535|GO:0005737|GO:0032
321|GO:0032956|GO:0030215|GO:0045454|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_140890_PI430048170 0.0759477444088449 1.04418017148305 0.398086180449843
0.4109212140764590.441058115766339 A A A 0.3271276125446320.339956390299905
0.395294087596275 A A A LNCV6_140890_PI430048170 mRNA
CCTGAAGAAACTGATGAGATTTCACCACAAATCTACAAAAATAAAGAGGAATTGCAAGTC NM_030903 RefSeq
chr6_GL000250v2_alt - 309837 310800 OR2W1 26692 "olfactory receptor, family 2, subfamily W, member
1" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_126464_PI430048170 0.1568322878040821.10995784903857 10.6389937869763
10.4283572063471 10.5541384187878 P P P 10.3053129309195 10.5087668435829
10.3557814546056 P P P LNCV6_126464_PI430048170 mRNA
GAGCCCAGTCCGCGGCCCCAGCAGCAGCGCCGAGAGCAGCCCCAGTAGCAGCGCCATGGC NM_005022 RefSeq
chr17 - 4945649 4949086 PFN1 5216 profilin 1
GO:0005515|GO:0043005|GO:0030036|GO:0045202|GO:0072562|GO:0005634|GO:0005829|GO:1900029|GO:0030
838|GO:0045944|GO:0030837|GO:0032232|GO:0005856|GO:0070064|GO:0070062|GO:0051054|GO:0005102|GO:0
005546|GO:0001843|GO:0030168|GO:0003779|GO:0032781|GO:0050434|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128135_PI430048170 0.6700795876437440.5706411606628830.776163098746595
1.38005826930611 0.569184989077243 A A A 0.4377074919766732.86445869126608
0.609050144749668 A P A LNCV6_128135_PI430048170 mRNA
CTGTTTTGCTCGATTCTTTTCCTAAGTTAAATAAATGCAAGCCTCTGAACTCTGTCTATA NM_024600 RefSeq chr16 +
1533656 1555580 TMEM204 79652 "transmembrane protein 204, transcript variant 1"
GO:0030947|GO:0005912|GO:0005886|GO:0016021|GO:0001945|GO:0051145 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_82006_PI430048170 0.00328771799594122 1.55990136148992 5.97628560985197
5.88925850945725 6.02923402804587 P P P 5.38107873389833 5.1810329593201
5.40162483531235 P P P LNCV6_82006_PI430048170 mRNA
AAGAAGAAAATTCCCAACATGGACAAACCACGCAAAGAAAATGAAGAAGAGCCGCAGAGC NM_004780 RefSeq

chrX + 103628963 103630948 TCEAL1 9338 "transcription elongation factor A (SII)-like 1, transcript variant 1" GO:0003700|GO:0005654|GO:0005634|GO:0000122|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128023_PI430048170 0.5779789404968320.9799823722559670.254389253678992 0.2676021035881320.392423674500804A A A 0.3744302420941590.31676488674801 0.313985819697182A A A LNCV6_128023_PI430048170 mRNA
CACTTTCTTAGCTTGCCATCCTTTGTAGGATGAGTTTGGCCTTTGAATAAATGATTAAAG NM_032131RefSeq chr6 + 108848415 108974472 ARMC2 84071 "armadillo repeat containing 2, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132670_PI430048170 0.9057451029327480.9984604413210360.403516967966031 0.4048490019051820.37766258788894 A A A 0.4192479861023770.37074961133814 0.402442231927235A A A LNCV6_132670_PI430048170 mRNA
CTCCCTGTAGGGCGCTTTTACTGTTATCTTAAACTGCGTGTTTATCTATATGTAAAAACTNM_005413RefSeq chr2 + 44941897 44946077 SIX3 6496 SIX homeobox 3
GO:0005515|GO:0021846|GO:0003700|GO:0070306|GO:0042826|GO:0006366|GO:0001654|GO:0021983|GO:0030178|GO:0048512|GO:0005634|GO:0021537|GO:0001222|GO:0021798|GO:0002088|GO:0021797|GO:0045944|GO:0009946|GO:0042127|GO:0000060|GO:2000177|GO:0060235|GO:0003404|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134819_PI430048170 0.00437544360993273 1.50075243324284 9.19661437944138 9.0179723253747 8.96163451730972 P P P 8.55386917921491 8.40892658235013 8.46319274689401 P P P LNCV6_134819_PI430048170 mRNA
GGCGGGTCGGGGTCAGTATCCTGTTTGTTATTGTTAAATTTGTATGAACCTTAGAAAAGT NM_024644RefSeq chr14 + 73490933 73493401 C14orf169 79697 chromosome 14 open reading frame 169
GO:0005515|GO:0032453|GO:0005506|GO:0005730|GO:0005634|GO:0006351|GO:0051864|GO:0070544|GO:0034720|GO:0045668|GO:0016706|GO:0005654|GO:0045892|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137832_PI430048170 0.2563006026356661.26464219332809 0.333667158434131 0.98840051223556 0.868190111480063A A A 0.5126066661369950.387343973922545 0.349466124945276A A A LNCV6_137832_PI430048170 mRNA
ACTAACTACTCTGGCGTCAATGGATATTCTGTATAATACTATCAAGTCCCTTTTCTCTTGNM_005292RefSeq chr13 - 99254712 99258428 GPR18 2841 "G protein-coupled receptor 18, transcript variant 1"
GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136247_PI430048170 0.88694653909068 0.9944652879817251 1.0665760627313 11.2340731437521 11.2569801608844 P P P 11.1662177006151 11.2421978701154 11.1794765275873 P P P LNCV6_136247_PI430048170 mRNA
ACAAAATGCCCTCGTTTGTAAACCCTTAGACGCTTGAGAATAAACCCCTTCCTTTTCTTC NM_001297555 RefSeq chr19 + 7903779 7914483 MAP2K7 5609 "mitogen-activated protein kinase kinase 7, transcript variant 1"
GO:0005515|GO:0034142|GO:0009408|GO:0005634|GO:0051403|GO:0005829|GO:0005622|GO:0002756|GO:0005737|GO:0043525|GO:0002755|GO:0072709|GO:0034138|GO:0009411|GO:0004708|GO:0038124|GO:0000287|GO:0038123|GO:0019901|GO:0034134|GO:0019903|GO:0007254|GO:0006915|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62_PI430053867 0.1544426384815010.9656423556403770.2775652636383290.320889442326752 0.330413473126567A A A 0.4038286916369260.3275259380706070.348296525002325A A A LNCV6_62_PI430053867 mRNA
AGCCTCAGAATAATAATAGCCCTGAGCTTCAGGTTAAGGAAATCCTCTTATGAGATAGAG NM_001287053 RefSeq chr5 - 56511393 56606232 C5orf67 NA uncharacterized LOC101928448 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134933_PI430048170 0.0119484612442299 0.4553880304372034.77425388856858

4.73279803646807 4.99835017680795 P P P 5.87381221425572 5.69693540418469
6.28828820386856 P P P LNCV6_134933_PI430048170 mRNA
GACCCAATTTGTGTTATTCATCTTTAATCCTGTTTTCAGTCTCTATGTGTACAGCAGTAT NM_175854 RefSeq chr13 +
28138505 28295338 PAN3 255967 PAN3 poly(A) specific ribonuclease subunit
GO:0005515|GO:0010467|GO:0000290|GO:0006605|GO:0005524|GO:0046872|GO:0005829|GO:0004535|GO:0010
606|GO:0000932|GO:0031251|GO:0000289|GO:0000288|GO:0016772 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130809_PI430048170 0.7222241060296111.34778136891173 2.69041113550966
0.8120770269676912.48676881089767 A A A 2.12587180874481 1.5682077476741 1.5463805323347
A A A LNCV6_130809_PI430048170 mRNA
AATTCTGGATCGAGAATATAATAGAATGATCTGGAGCCCTGGCTGAACTTGCCTATCCCC NM_181686 RefSeq chr21
- 44681575 44682163 KRTAP12-1 353332 keratin associated protein 12-1 GO:0045095 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144008_PI430048170 0.5014570468470870.8305876618075155.89476635880415
5.53151906886411 5.75137681727466 P P P 6.48284285252011 5.65092607793342
5.71405749706093 P P P LNCV6_144008_PI430048170 mRNA
ATTCCCTCTTATCCATCTGCAGGTGAATCTTCAATAAAATGCTTTTGTCATTCATTCTGA NM_002272 RefSeq chr12 -
52806542 52814116 KRT4 3851 "keratin 4, type II"
GO:0005882|GO:0005515|GO:0009986|GO:0005198|GO:0030855|GO:0007010|GO:0050680|GO:0005634|GO:0045
111|GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143527_PI430048170 0.9514604604070150.9976287499717278.1155080824404
8.08165217538892 8.16469276859059 P P P 8.06389962171201 8.11563309635929
8.19096870900993 P P P LNCV6_143527_PI430048170 mRNA
TCAAGTATTCCCATGTGTTTTAAAAGCCTGAAGTCAGTGAGATGAAATTCAACATCAAGA NM_016065 RefSeq chr10
- 73248842 73252693 MRPS16 51021 mitochondrial ribosomal protein S16
GO:0070124|GO:0005739|GO:0005515|GO:0070125|GO:0070126|GO:0005737|GO:0032543|GO:0006996|GO:0003
735|GO:0005743|GO:0006412|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137342_PI430048170 0.0242925739185696 1.33910432458808 12.6936609314428
12.6807493399114 12.9220662166419 P P P 12.2507779040263 12.2566238115794
12.5213773527075 P P P LNCV6_137342_PI430048170 mRNA
GTGCCGTCATTCTGTTTTAAGCTCATGGATCAATGGATTTGTTTACAATGTGATATTTTC NM_005471 RefSeq chr5 -
142000668 142013055 GNPDA1 10007 glucosamine-6-phosphate deaminase 1
GO:0007338|GO:0005737|GO:0004342|GO:0016787|GO:0005975|GO:0006043|GO:0006044|GO:0006091|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60577_PI430048170 0.4949735668778380.8157606328061725.57614151088973 5.33445457743525
5.80205587859214 P P P 5.23796715101564 6.10269542989482 6.12679307929878 P P P
LNCV6_60577_PI430048170 mRNA
GTATTTCAACCACATCCATGAAAATAAAACACCTCCTGTTGTGGATGGTGAGCCCCTGAT NM_007111 RefSeq chr13
+ 113584740 113641473 TFDP1 7027 "transcription factor Dp-1, transcript variant 1"
GO:0005515|GO:0010467|GO:0005667|GO:0003700|GO:0006367|GO:0006357|GO:0008283|GO:0019904|GO:0003
713|GO:0043276|GO:0006915|GO:0003677|GO:0097193|GO:0006351|GO:0000082|GO:1900740|GO:0008544|GO:0
007219|GO:0045944|GO:0005654|GO:0007179|GO:0000278|GO:2000278|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_53447_PI430048170 0.467307368416161 1.84445164950225 0.4213470144193992.03011056239019
3.02206326125523 A A P 2.16122969565222 0.3867028092540160.645492624020132 A A A
LNCV6_53447_PI430048170 mRNA
AATGTCCTAAAAAGCTACATTGGATTGGGCCACATCTATTCGGGGACCTTTGCCCTGATT NM_001286 RefSeq chr1
+ 11806095 11843144 CLCN6 1185 "chloride channel, voltage-sensitive 6, transcript variant 1"
GO:0006821|GO:0005247|GO:0005765|GO:0005524|GO:0055085|GO:0006884|GO:0009612|GO:0007165|GO:0044

070|GO:0015297|GO:0034220|GO:0016021|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134179_PI430048170 0.7128757787238911.11459394243556 1.09508015423138
0.4583116526825541.4279040665953 A A A 0.78699412846664 0.373357183967301
1.34618346372594 A A A LNCV6_134179_PI430048170 mRNA
TCTGAGCATGTCCTTACATTTACTTCCAGCATACTATTCATTTGCCATAGTAGAGTATTA NM_152265RefSeq chr1
+ 52056184 52090716 BTF3L4 NA "basic transcription factor 3-like 4, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_142432_PI430048170 0.0835388763649026 1.31636423795586 6.1179216232908
6.22009880717529 5.77618121055847 P P P 5.47504385248164 5.80281312373225
5.66450426824704 P P P LNCV6_142432_PI430048170 mRNA
TAGTAAAATTGAGTGGGATTATGAGTGTGAGCCAGGGATGGTCAAAGGCATCCATCATGG NM_182513RefSeq chr19
- 11147154 11155808 SPC24 147841 "SPC24, NDC80 kinetochore complex component"
GO:0005515|GO:0007067|GO:0005730|GO:0000777|GO:0005634|GO:0000278|GO:0031262|GO:0051301|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132297_PI430048170 0.0235445112279656 1.28106087513445 9.40648859062355
9.60593571289556 9.52255599862856 P P P 9.20781079667801 9.25015102174576
8.99967469946578 P P P LNCV6_132297_PI430048170 mRNA
TAAAAATGTATTCATTTCCCTGGCCCCACAGATGCTTCCCTCCATACTTTTTATTTGCTC NM_001659RefSeq chr12 -
48936208 48957469 ARF3 377 ADP-ribosylation factor 3
GO:0048471|GO:0006661|GO:0000139|GO:0007264|GO:0003924|GO:0044281|GO:0016192|GO:0015031|GO:0006
644|GO:0005525|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136738_PI430048170 0.562513055261435 1.0276916207392 11.689768347474
11.6946440180306 11.5821736647636 P P P 11.7167952447661 11.5807128522445 11.548025140401
P P P LNCV6_136738_PI430048170 mRNA
TGGACAGCTGTCTCCTGGGGTGGGTTGGTATTAAAGAGGAAAGCGATTTTTTGGATAATG NM_005452RefSeq
chr6_GL000251v2_alt - 4690583 4701012 WDR46 9277 "WD repeat domain 46, transcript variant 1"
GO:0000462|GO:0008150|GO:0032040|GO:0005730|GO:0005575|GO:0030686 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138755_PI430048170 0.1637495250138950.96314031615126 0.381320108608442
0.4278850311166320.336472877936569 A A A 0.4515118205772120.44119112184308
0.416749142862709 A A A LNCV6_138755_PI430048170 mRNA
GAAGTGTTCTCTAACCACTGAGCTAAACACAGAAGAATGTATAAATATGTATGCTCTGCC NM_001243007 RefSeq
chr14 - 74853032 74863834 PROX2 283571 "prospero homeobox 2, transcript variant 1"
GO:0006355|GO:0007275|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_46916_PI430048170 0.00258568402682265 1.44680433165776 7.79271514858881
7.88423148249969 7.7841479765163 P P P 7.22530513996589 7.39472748595149
7.23836715869989 P P P LNCV6_46916_PI430048170 mRNA
CTAAGCTTGCAGCTGCCACAGAAAACACCCGATTAAAAACTTTTTATTTCAGCAAAATAA NM_002695RefSeq chr19
- 1086578 1095392 POLR2E 5434 "polymerase (RNA) II (DNA directed) polypeptide E, 25kDa"
GO:0008380|GO:0005515|GO:0010467|GO:0006386|GO:0006368|GO:0006385|GO:0006367|GO:0006366|GO:0006
363|GO:0006362|GO:0006361|GO:0005634|GO:0006360|GO:0006383|GO:0005829|GO:0005736|GO:0034587|GO:0
005665|GO:0016032|GO:0005666|GO:0032481|GO:0035019|GO:0003899|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139273_PI430048170 0.1508174411786572.04156850081023 1.50724053890874
2.58096519123315 2.93644742001536 A A P 1.37960700817378 1.94331174740876
0.700448596237104 A A A LNCV6_139273_PI430048170 mRNA
AAACCAAATAGGAAGGTGGAGTTAAGGGCAGGAGCAACCCTACTTCTCACCTAATGACTT NM_001509RefSeq
chr6_GL000251v2_alt + 15892 24832 GPX5 2880 "glutathione peroxidase 5, transcript variant 1"

GO:0006629|GO:0004602|GO:0006979|GO:0005615|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140231_PI430048170 0.0408413012253301 1.50300018774109 4.92161397486473 4.78630413427913 4.86459425197837 P P P 4.34357885088228 3.98690600872205 4.4429380788227 P P P LNCV6_140231_PI430048170 mRNA
CCTGGGTGTTACCCATGTACTGAAAATGAACTTTTACCAACATGGCTAAAAAATTAAAAC NM_025165 RefSeq chr15 - 43772599 43777304 ELL3 80237 elongation factor RNA polymerase II-like 3
GO:2000179|GO:0006368|GO:0006354|GO:0006366|GO:0005730|GO:0010717|GO:0005634|GO:0007283|GO:0008023|GO:0035326|GO:0048863|GO:0032786|GO:0050769|GO:0045944|GO:0042795|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127132_PI430048170 0.00142034244522413 0.3982484134255116.76573281603244 7.18720985885851 7.06475461877846 P P P 8.37005396386934 8.1333305341186 8.50659043864001 P P P LNCV6_127132_PI430048170 mRNA
GGATGGGGAACTAAGGGAAAACGTCTGTTGTATCACTGAAGTTTTTTGTTTTGTTTTTAT NM_001982 RefSeq chr12 + 56080024 56103507 ERBB3 2065 "erb-b2 receptor tyrosine kinase 3, transcript variant 1"
GO:0005515|GO:0005886|GO:0061098|GO:0051048|GO:0051402|GO:0005615|GO:0042803|GO:0042802|GO:0007507|GO:0014037|GO:0016323|GO:0043524|GO:0016324|GO:0030296|GO:0007173|GO:0019838|GO:0042127|GO:0009968|GO:0048011|GO:0046982|GO:0003197|GO:0048015|GO:0021545|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125558_PI430048170 0.00234738578553659 0.5992445980260531 1.0361001019334 10.8609198746426 11.1328105128563 P P P 11.6703120559643 11.7164599571709 11.8651876470149 P P P LNCV6_125558_PI430048170 mRNA
TGTTGCGGAAACGACGAGAACAGTTGAAACACAAACTTGAACAGCTACGGAACTCTTGTG NM_002467 RefSeq chr8 + 127736068 127741434 MYC 4609 v-myc avian myelocytomatosis viral oncogene homolog
GO:0005515|GO:0010468|GO:0010467|GO:0001658|GO:0006367|GO:0003700|GO:2001022|GO:0032403|GO:0006879|GO:0034644|GO:0007219|GO:0045656|GO:0000165|GO:0046983|GO:0007179|GO:0051782|GO:0010332|GO:0090096|GO:0050679|GO:0070888|GO:0000122|GO:0070848|GO:0000978|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_119446_PI430048170 0.0119788078063680.5652124640224768.00971162978754 7.6248877951336 7.64612088523109 P P P 8.61267999493499 8.67103389665826 8.494108148861 P P P LNCV6_119446_PI430048170 mRNA
TCGGAAGCTGGACGAGCAGCAGGAGTTCAGTGCCATCATCCTGGCAACAGCTGGCCTGCA NM_000190 RefSeq chr11 + 119084876 119093549 HMBS 3145 "hydroxymethylbilane synthase, transcript variant 1"
GO:0018160|GO:0006778|GO:0044281|GO:0006782|GO:0004418|GO:0006783|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139863_PI430048170 0.8270298996410710.9759357082591766.32096573684238 6.1871297045059 5.7960180142227 P P P 6.28992939399409 6.20386674151357 5.94370828129299 P P P LNCV6_139863_PI430048170 mRNA
ATGATCGTCTTCCGTCTCAGCCTGGGTCTCACCATCCTTGCTTGTGAGAGCAGAGTCAGC NM_002517 RefSeq chr19 + 47020885 47045759 NPAS1 4861 neuronal PAS domain protein 1
GO:0001964|GO:0042711|GO:0007165|GO:0003700|GO:0046983|GO:0005634|GO:0004871|GO:0000122|GO:0007417|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127943_PI430048170 0.5218160306556451.28793380039687 0.302373247881376 1.38680193534694 0.344940585503791 A A A 0.480377327305273 0.379648499784319 0.353741470948175 A A A LNCV6_127943_PI430048170 mRNA
AACTTTCCAAAGTGCAGCCACAGCTACAATGCTGTTAAATCCTCCCACATTCTTGGATGC NM_003399 RefSeq chrX + 129738969 129769549 XPNPEP2 7512 "X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound" GO:0016020|GO:0005886|GO:0004177|GO:0006508|GO:0031225|GO:0046872|GO:0008237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133250_PI430048170 0.6342944091840280.8628440780332660.613466745896654
0.3283114582139790.39884304282815 A A A 1.170729800757 0.332711981295455
0.316889147037783A A A LNCV6_133250_PI430048170 mRNA
ACTGAAATTATGTACACTCTCCAGGAACCCATAGACTGTACGTGCCAGTGGAATTAAACC NM_173591RefSeq chr12
+ 80209452 80379090 OTOGL 283310 otogelin-like GO:0046556|GO:0046373|GO:0007605|GO:0005576
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83171_PI430048170 0.89006127130387 0.7458214221580861.10265857923175 1.96888320233677
1.82807956671519 A A A 1.93106664439201 2.95959119800541 0.374577138654163A P A
LNCV6_83171_PI430048170 mRNA
AAAGCACTGTGGTTCGACCTGCAGCAGCGCCTGTCAGATGAAGATGGCACCAACATGCACNM_019065RefSeq chr16
+ 83968631 84002774 NECAB2 54550 N-terminal EF-hand calcium binding protein 2
GO:0005515|GO:0005737|GO:0005509 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110289_PI430048170 0.0342117063299782 0.76159569479716 12.8046038741268
12.7395915424647 12.4859461330942 P P P 13.0755163918879 13.1754082161513
12.9698726144795 P P P LNCV6_110289_PI430048170 mRNA
GGTGTCTCGTGGCACGCGTCACAGTGGTGCTAGTCTGTTTTTAACAAAAGAGGATGAAAA NM_024100RefSeq chr19
+ 984327 994570 WDR18 57418 WD repeat domain 18 GO:0005515|GO:0005737|GO:0007275|GO:0005654
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142903_PI430048170 0.0763676907091317 1.69133123573527 6.37785153754936
7.17632626367098 6.72860251113139 P P P 6.16638793637064 5.90435041963031
6.03721040483388 P P P LNCV6_142903_PI430048170 mRNA
TTCCTGTGGTCAACAGTTTCGCAGATCCGTTAGGCCCTTAAAGACAAGGAGGAAGTAAAA NM_080671RefSeq chr2
+ 223051929 223055637 KCNE4 23704 "potassium channel, voltage gated subfamily E regulatory beta
subunit 4" GO:0016324|GO:0005249|GO:0034765|GO:0016021|GO:0071805 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143863_PI430048170 0.1723319952902441.38159798579136 5.74815724030496
5.67924014646427 5.29398257511728 P P P 5.45928936407901 5.15757997116538
4.62640788770112 P P P LNCV6_143863_PI430048170 mRNA
CCTTCCTCTCCACAAAGGTAAATACAATCCTCAATTTTGTGTTTGTTATTCTCTTGGTTC NM_003281RefSeq chr1 -
201403766 201421746 TNNI1 7135 "troponin I type 1 (skeletal, slow)"
GO:0030049|GO:0005861|GO:0055010|GO:0006942|GO:0003779|GO:0046872|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133631_PI430048170 0.3525830061500940.7873782977781620.317855452265818
0.2465969681036360.29373435926504 A A A 0.4358540030978370.248567765965323
1.07446170728997 A A A LNCV6_133631_PI430048170 mRNA
ATGGTATGACCAGAGGAATAGATCCACTTCATGTTACTACAACAACAAAACTATCTAGGT NM_001039844 RefSeq
chr10 - 15075474 15088776 ACBD7 414149 acyl-CoA binding domain containing 7
GO:0000062|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134604_PI430048170 0.0343505103937579 0.3559949283176170.465417298210942
1.18358179111782 1.76571365774216 A A A 2.34828795002993 3.04533378010409 2.6922513142729
A P P LNCV6_134604_PI430048170 mRNA
CAGTGGCTAACATTATGAGCATTGTGTAAGATAAACACATGGTCAGTATCAATGTAAATG NM_033390RefSeq chr11
+ 110093360 110171841 ZC3H12C 85463 zinc finger CCCH-type containing 12C
GO:0008150|GO:0003674|GO:0004519|GO:0090305|GO:0005575|GO:0046872 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137333_PI430048170 0.4132855990219040.7551365136663850.561173283748845
0.4820746810368920.293888921500013A A A 0.4124722723005971.42359278161248
0.499326317045249A A A LNCV6_137333_PI430048170 mRNA
GTGCTGTTTTTCAGTAAACTCCTTGTTCATGTCAATAAAGTATCCCTGAAAACCACAAAA NM_018400RefSeq chr11

- 123629186 123654607 SCN3B 55800 "sodium channel, voltage gated, type III beta subunit, transcript variant 1"
GO:0030018|GO:0051899|GO:0005886|GO:0086010|GO:0086070|GO:0086091|GO:0060048|GO:0060371|GO:0060373|GO:0010765|GO:0086002|GO:0035725|GO:0001518|GO:0006814|GO:0086006|GO:0086005|GO:0005248|GO:2000649|GO:0072659|GO:0019233|GO:0044325|GO:0007399|GO:0086014|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144984_PI430048170 0.6613483893016790.9809643275989670.431199136438554 0.39694813313455 0.245117587835993A A A 0.3545935268591330.41518699080706 0.392735697900453A A A LNCV6_144984_PI430048170 mRNA
CAATTTGAGTGACTCAGGTGAAATTTAGAGTCATATTTCCCGAAGCAGAAGTTAAAGAAA NM_198271RefSeq chr3 - 69108671 69122595 LMOD3 56203 "leiomodin 3 (fetal), transcript variant 1"
GO:0003785|GO:0006936|GO:0030239|GO:0005865|GO:0007015|GO:0005523|GO:0051694 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128017_PI430048170 0.3783049251452071.019964420483 0.32894946708653 0.2427330361076220.293709074602674A A A 0.2621151764185340.255902637681981 0.263106679037528A A A LNCV6_128017_PI430048170 mRNA
CAGGGGATTCACATCATGACACAAAGTTGATGGATATCATTCTAGTCAATATATGAAAGC NM_001134659 RefSeq chr3 - 139003961 139006268 PRR23A NA proline rich 23A NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72298_PI430048170 0.9123874443312320.98848053710693410.3619644200591 10.3453457338578 10.1891008477107 P P P 10.4961014495918 10.2236397286678 10.2149684303088 P P P LNCV6_72298_PI430048170 mRNA
CTGCACCGAAGGTCCCGGCTCCTGTGCCCTCCCTGCAGCCGTCAGGGCCCGTCCCCCAAC NM_181832RefSeq chr22 + 29603555 29698600 NF24771 "neurofibromin 2 (merlin), transcript variant 8"
GO:0005515|GO:0048471|GO:0008285|GO:0030036|GO:0070306|GO:0005886|GO:0045597|GO:0042524|GO:0031527|GO:0005634|GO:0032154|GO:0043409|GO:0014010|GO:0005737|GO:1900180|GO:0031647|GO:0005912|GO:0042475|GO:0005856|GO:2000177|GO:0042518|GO:0022408|GO:0030336|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133321_PI430048170 0.4523773966682841.02749884479398 0.437030251629441 0.3015894609446940.351558585850336A A A 0.2886162652502140.327400520990729 0.359150891158659A A A LNCV6_133321_PI430048170 mRNA
CAAGGAAGGTGGGAAGTAAAACATCACTTTTTACATTAAACCAGGATCAGGAATAAAATG NM_001271507 RefSeq chr14 - 69569813 69574883 CCDC177 56936 coiled-coil domain containing 177 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140950_PI430048170 0.8410239484641750.7830653247069762.43626295593319 3.14660844020404 2.79363578567254 A P A 3.83149051197019 3.24942238319029 1.73526776974994 P P A LNCV6_140950_PI430048170 mRNA
TTCGGCCCATATTTTGTGTGTTTGGACAAGTACATCTCCCTTTTGCCTAATGAACTTTTG NM_020973RefSeq chr4 + 22692913 22819572 GBA3 57733 -
GO:0017042|GO:0006665|GO:0004565|GO:0006687|GO:0046477|GO:0005975|GO:0016139|GO:0044281|GO:0008422|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81689_PI430048170 0.8570673936603870.9797433235958695.09078435610364 4.42173126738785 5.10083849997195 P P P 4.65775279470584 5.04603727271025 5.06200309465198 P P P LNCV6_81689_PI430048170 mRNA
GAGCTTACATAGTGTAATTGGGGAGAATTTTGTCTTCTATTTCCATTCAACAGTAGCAAA NM_001257291 RefSeq chrX - 46599250 46759172 SLC9A7 84679 "solute carrier family 9, subfamily A (NHE7, cation proton antiporter 7), member 7, transcript variant 1"
GO:0005515|GO:0005802|GO:0015386|GO:0015385|GO:0055085|GO:0006885|GO:0042803|GO:0000139|GO:0035725|GO:0016021|GO:0055038|GO:0071805|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137119_PI430048170 0.6256600826051371.11669106910471 1.03571046883643
0.3667213338061250.390154232465379A A A 0.3817071653794690.34191047091998
0.672506206062533A A A LNCV6_137119_PI430048170 mRNA
GTTGAGTGAAGCGTATTTGAAGTAACTGAGAATTACCATGTACATCATATTTGGGATAAC NM_001142564 RefSeq
chr4 - 47935976 47981533 CNGA1 1259 "cyclic nucleotide gated channel alpha 1, transcript variant
1"
GO:0005223|GO:0005515|GO:0005886|GO:0007603|GO:0042622|GO:0005222|GO:0022400|GO:0030553|GO:0005
887|GO:0005249|GO:0042391|GO:0006810|GO:0007601|GO:0071805|GO:0016056 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129929_PI430048170 0.4246906024848260.6945121467186090.334591996230192
0.3561145427555730.33945345067109 A A A 1.55906787512884 0.352518074659859
0.330071989272642A A A LNCV6_129929_PI430048170 mRNA
GACAAACTTTTTGTAAAAAGCACCATCTCTGGACTTACTTGCATTAAATATTTTCAGGGG NM_152536RefSeq chr3
+ 14818961 14934565 FGD5 152273 "FYVE, RhoGEF and PH domain containing 5"
GO:0005515|GO:0005794|GO:0030036|GO:0031267|GO:0005783|GO:0008360|GO:0032587|GO:0001726|GO:0046
872|GO:0030027|GO:0043088|GO:0043547|GO:0005085|GO:0005737|GO:0032321|GO:0007010|GO:0046847|GO:0
005089|GO:0005856|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134572_PI430048170 0.3914249479263330.5786715652456761.55941423108038
1.44968550047137 2.06994975419226 A A A 1.17641969380825 2.93203499012275
2.84344842715388 A P P LNCV6_134572_PI430048170 mRNA
CCACAGCTGAACCATCTCCTTAAAGATTATTTTGAAAAACAAGTGGAAGAAAAACAGAAG NM_018392RefSeq chr4
- 112539332 112636995 ZGRF1 55345 "zinc finger, GRF-type containing 1" GO:0008270|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131375_PI430048170 0.19121819150497 0.80445366292485 0.460232835068192
0.48952906350808 0.406925000947424A A A 0.4521388868033160.970785689044634
0.82832462433008 A A A LNCV6_131375_PI430048170 mRNA
TAACTTTCACACAAGGTACGCATCTATGTTTTTGGGGGAGGTGATGTAGTTACAGCTGAC NM_207345RefSeq chr12
+ 10030676 10066030 CLEC9A NA "C-type lectin domain family 9, member A" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_116951_PI430048170 0.00681727215994721 0.6414620688573127.29614870613257
7.34461326591671 7.46238570712669 P P P 7.85190912380219 8.00701492892444
8.15511235508456 P P P LNCV6_116951_PI430048170 mRNA
TGCACTTATACCCATACCATTAGCAGTAATTACAACATGTATTGTGCTGTATATGAATGG NM_001144822 RefSeq
chr1 - 116518699 116571093 CD58 965 "CD58 molecule, transcript variant 2"
GO:0005515|GO:0005886|GO:0009986|GO:0005102|GO:0031225|GO:0050900|GO:0016337|GO:0071346|GO:0016
020|GO:0005887|GO:0007596|GO:0071356|GO:0034113|GO:0007155|GO:2000484|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131830_PI430048170 0.0418900410478335 1.04331398060855 0.45526680395832
0.4742641816230440.448342965941096 A A A 0.372425798869749 0.394681504628137
0.426851912737846 A A A LNCV6_131830_PI430048170 mRNA
AGTCTTAGAGGAAATCACAAACTACTACCAGAAAAAGCTGAAGGAAGGCACCTGCAAGGC NM_198546 RefSeq
chr1 - 16398642 16437424 SPATA21 NA spermatogenesis associated 21 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133997_PI430048170 0.291095370410235 1.89409088031132 0.432774872997939
1.0934249594191 2.219039259524 A A A 0.720977240495697 0.398812221530983
0.412045585770224 A A A LNCV6_133997_PI430048170 mRNA
TAAGGATGTCGTATTGTTTTACTCTCGGTCTCAGAATTTGTATTTTGCCTTTCTGCCTTT NM_018000 RefSeq chr2
- 215942590 216013623 MREG 55686 melanoregulin
GO:0043234|GO:0042470|GO:0016324|GO:0030318|GO:0032402 . NA - . NA NA NA NA NA

NA NA NA NA
LNCV6_140035_PI430048170 0.34203266919675 0.798101105788844 5.91502796744886
5.56126238189717 5.83702104322003 P P P 5.63473032957969 6.11914203271914
6.44619697118703 P P P LNCV6_140035_PI430048170 mRNA
GCCCCATGTCATAGAGAATAAAGCTGATGATTGTACCAGTCTTAAATTATTCATGATTCA NM_001244963 RefSeq
chr11 + 19713334 20121601 NAV2 89797 "neuron navigator 2, transcript variant 5"
GO:0007608|GO:0021554|GO:0007605|GO:0004386|GO:0005614|GO:0021564|GO:0003025|GO:0005524|GO:0021
563|GO:0008152|GO:0005654|GO:0007626|GO:0008201 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130825_PI430048170 0.35686764944302 0.923633250277441 0.366552933737614
0.44031006027934 0.313426327357162 A A A 0.379051792913458 0.40498139312894
0.665203704354035 A A A LNCV6_130825_PI430048170 mRNA
CGGTACCAAAGATATAATCACCTAGGTTTACAAATATTTTTAGGACTCACGTTAACTCAC NM_002609 RefSeq
chr5 - 150113838 150155859 PDGFRB 5159 "platelet-derived growth factor receptor, beta
polypeptide"
GO:0005515|GO:0042542|GO:0034405|GO:0035789|GO:0031226|GO:0046777|GO:0004992|GO:0043552|GO:0007
173|GO:0001894|GO:0032956|GO:0035441|GO:0035791|GO:0032355|GO:0035793|GO:0038085|GO:0030335|GO:0
009986|GO:0019901|GO:0046488|GO:0009636|GO:0045840|GO:0014068|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136705_PI430048170 0.0202528615667708 0.756947126178673 10.6502951545947
10.6138006659541 10.7966727789101 P P P 10.9631942471301 11.0535959330612
11.241623721767 P P P LNCV6_136705_PI430048170 mRNA
GTGTAATTTCTGTCAACCACGGACGTTTGCCTTCATGTGTAGAATTTACTGTTGTTATGC NM_001291978 RefSeq
chr4 - 2937936 2963506 NOP14 8602 "NOP14 nucleolar protein, transcript variant 1"
GO:0000462|GO:0000472|GO:0006364|GO:0032040|GO:0005730|GO:0000480|GO:0005634|GO:0005739|GO:0030
490|GO:0030515|GO:0016020|GO:0042274|GO:0030692|GO:0000447|GO:0019899|GO:0030686 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_89963_PI430048170 0.254621454466248 0.601347226191524 0.374214692541683
0.395702636401143 0.929685600136518 A A A 1.10551884974356 1.95932336979575
0.556019786418598 A A A LNCV6_89963_PI430048170 mRNA
ATCATGGGCACATATGTGTCCAGTGTCCCCAGGTAATGATCCTTCTGAGAGAAATGACTT NM_002119 RefSeq
chr6_GL000256v2_alt - 4453377 4458806 HLA-DOA 3111 "major histocompatibility complex, class II, DO
alpha"
GO:0019886|GO:0007165|GO:0006955|GO:0005886|GO:0002587|GO:0045580|GO:0023026|GO:0042613|GO:0016
021|GO:0005765|GO:0032395|GO:0010008 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_134486_PI430048170 0.0693184836352387 0.818222291390477 14.5132012089938
14.3334023021618 14.2231512568441 P P P 14.6358281582806 14.6358281582806
14.680894518958 P P P LNCV6_134486_PI430048170 mRNA
TTTCTCAAGCCCAAGGCCTTATCTTCACCCCACAAACAATAAAGCAAAGTAAAGAAAAAA NM_001398 RefSeq
chr19 - 38815421 38831857 ECH1 1891 "enoyl CoA hydratase 1, peroxisomal"
GO:0005739|GO:0005515|GO:0006635|GO:0016020|GO:0005102|GO:0016853|GO:0070062|GO:0005777 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_140897_PI430048170 0.656913808019562 0.857293348601208 1.15690989343554
0.639251615186108 0.600630382192519 A A A 0.597805742838933 0.734396175920477
1.58949593251511 A A A LNCV6_140897_PI430048170 mRNA
AGAAGTAACCCTTACAGCCAACACCATGTGATGATGAGGAGGAGTCCATCTGGGTTAAAG NM_001282471 RefSeq
chrY - 21382973 21386360 PRORY 100533178 "proline rich, Y-linked" NA . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_81605_PI430048170 0.0001319317697683 1.45102380151724 12.722470009182
12.6688794456536 12.762417648835 P P P 12.136019699307 12.1904754569838
12.2164193963538 P P P LNCV6_81605_PI430048170 mRNA
TCTGTTGATTCACAGTTTACCCATTTGGCCTGGATTAATACCCCTCGAAGACAAGGAGGA NM_006406 RefSeq
chrX + 23667527 23686397 PRDX4 10549 peroxiredoxin 4
GO:0005515|GO:0007252|GO:0072593|GO:0005634|GO:0007283|GO:0008379|GO:0005615|GO:0042803|GO:0005
790|GO:0005829|GO:0022417|GO:0005739|GO:2000255|GO:0019471|GO:0030198|GO:0045454|GO:0008584|GO:0
070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140958_PI430048170 0.00207755789789295 0.293620457570152 4.82989961028125
4.82541727606899 5.36348457335539 P P P 6.61690264355921 6.58784145970498
7.12201329985323 P P P LNCV6_140958_PI430048170 mRNA
GCTAGTAGTGTTTCTTCAAAGGTTATTCCAGGTATGGTTAAGTAGTGAGAAAAATCACTT NM_018362 RefSeq
chr11 - 27494417 27506779 LIN7C 55327 lin-7 homolog C (C. elegans)
GO:0008092|GO:0043005|GO:0005886|GO:0002011|GO:0019904|GO:0097025|GO:0045202|GO:0014069|GO:0030
165|GO:0006887|GO:0015031|GO:0045199|GO:0007269|GO:0016323|GO:0005737|GO:0008105|GO:0005911|GO:0
045211|GO:0005923|GO:0097016|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_134407_PI430048170 0.0373005177856309 0.457053416578505 2.62639431705397
3.55646483349485 2.93330169835976 A P P 4.0181277593622 4.26749459902396
4.35772875325623 P P P LNCV6_134407_PI430048170 mRNA
GCTTTATAAACTTTTATTTGGTGAAAGCCCCAGATACCCAAATGTCATTGGCAAAACTTA NM_207318 RefSeq
chrX + 104166474 104195901 FAM199X 139231 "family with sequence similarity 199, X-linked" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135684_PI430048170 0.427430498663419 1.13959103205947 10.5585273807424
10.404956326673 10.8519773719934 P P P 10.1458981472226 10.3145111549235
10.7553957233028 P P P LNCV6_135684_PI430048170 mRNA
CCACCGTTTGTGCGAGCTGGATGTCCTTTTCAGTAGAAAAGAATTTTCCTTTTGAATTTA NM_012071 RefSeq
chr10 + 22316382 22320317 COMMD3 23412 COMM domain containing 3 GO:0005515 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134942_PI430048170 0.00439940406645938 0.240403547561039 6.09155971809313
5.55832412217629 5.93643806773081 P P P 7.86998056630155 7.96871862561886
7.96561971186144 P P P LNCV6_134942_PI430048170 mRNA
GGGATCTATTTTTGCACTGGAATATCTGAGAATTGCAAAACTAGACAAAAGTTTCACAAC NM_005502 RefSeq
chr9 - 104781002 104928246 ABCA1 19 "ATP-binding cassette, sub-family A (ABC1), member 1"
GO:0005515|GO:0008509|GO:0031267|GO:0071300|GO:0071397|GO:0034364|GO:0006497|GO:0051117|GO:0044
255|GO:0019905|GO:0042632|GO:0033344|GO:0005794|GO:0010745|GO:0050702|GO:0043691|GO:0005548|GO:0
038027|GO:0055098|GO:0007186|GO:0005887|GO:0042157|GO:0055091|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138780_PI430048170 0.0163934906264 0.443740936347018 6.58303062639574
6.28361621027095 6.02798581243243 P P P 7.47376378091101 7.52919952223421
7.4609844122362 P P P LNCV6_138780_PI430048170 mRNA
TGAGCGTAACGACCCTTCTGACCTGGTCTCACGATCTGAAATAATAAAAGGCTGTGTCAT NM_152311 RefSeq
chr10 - 127877849 127892947 CLRN3 119467 clarin 3 GO:0016021|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_57050_PI430048170 0.0381078505981037 0.907112231865222 14.7047094404898
14.6474124233274 14.7629822581124 P P P 14.8217440085406 14.8531945251323
14.8640868140548 P P P LNCV6_57050_PI430048170 mRNA
CTGATGAATCTTGCGTTTTTTACAAATTGGAGCAGGGACAGATCATAGATTTCTGATTTT NM_006755 RefSeq
chr11 + 747431 765024 TALDO1 6888 transaldolase 1

GO:0005737|GO:0006112|GO:0005999|GO:0005975|GO:0009405|GO:0004801|GO:0005634|GO:0044281|GO:0006098|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144441_PI430048170 0.674287799406281 1.13148023964789 8.6944836640823 8.07982021809326 7.77943910479286 P P P 8.28601700578602 8.11380952496716 7.71629943735636 P P P LNCV6_144441_PI430048170 mRNA
AGGGGCGCTCGCTTCCGCATCCTAGTCTCTATCATTAAAGTTCTAGTGACCGAGAAAAAA NM_145867 RefSeq chr5 + 179793984 179796512 LTC4S 4056 leukotriene C4 synthase
GO:0005515|GO:0019369|GO:0019370|GO:0005783|GO:0019372|GO:0044281|GO:0005635|GO:0043085|GO:0004364|GO:0004464|GO:0006691|GO:0043231|GO:0008289|GO:0004602|GO:0005640|GO:0005789|GO:2001300|GO:0016021|GO:0008047|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130538_PI430048170 0.00919277164151814 0.534922738483164 12.9256761428179 12.9899079206258 13.3789397559517 P P P 13.9873082812843 13.7916799583624 14.2322701388763 P P P LNCV6_130538_PI430048170 mRNA
CTAGGTATTTCTAATGTTTATTCTTCCCTGTGTACTTCTACACATAGCTATGCACTATGA NM_015641 RefSeq chr7 + 116210492 116258783 TES 26136 "testin LIM domain protein, transcript variant 1"
GO:0043234|GO:0005737|GO:0030054|GO:0008285|GO:0005886|GO:0008270|GO:0005634|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102785_PI430048170 0.0160856441877903 0.616250119084468 3.55203599137877 3.61379488538671 3.93480771605743 P P P 4.57436868274504 4.15145444943099 4.46726947982679 P P P LNCV6_102785_PI430048170 mRNA
TAATAACTTCTTTACCCTGTCACCTACTGTTTATTCACACCAGCAGCTTATAGATGCACA NM_001114394 RefSeq chr5 + 79612419 79686648 PAPD4 167153 "PAP associated domain containing 4, transcript variant 1"
GO:0006397|GO:0004652|GO:0005737|GO:0031380|GO:0002244|GO:0071044|GO:0043631|GO:0005524|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83476_PI430048170 0.366552654719228 1.06027950055052 7.79640448284843 7.83804559730502 7.73618655396631 P P P 7.77521453465722 7.77966190880467 7.55278486706508 P P P LNCV6_83476_PI430048170 mRNA
TGCTTTCAAAAGAATTGGCGTCCGCTGTTCGCCTCTCCTCCCGGGAGTCTTCTGCCTACT NM_018081 RefSeq chr17 + 7688348 7703502 WRAP53 55135 "WD repeat containing, antisense to TP53, transcript variant 1"
GO:0005515|GO:0005737|GO:0005697|GO:0015030|GO:0003723|GO:0032203|GO:0005654|GO:0005634|GO:0051973 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127523_PI430048170 0.390474174652122 0.900289997025087 5.4574390508662 5.70146824268804 5.17956605263495 P P P 5.56937842764329 5.71400426972566 5.5510780157858 P P P LNCV6_127523_PI430048170 mRNA
TAACATGAAGAGAGTGTTTGAAAGATTCTGCCGAGGCCTCAAAGAGGTGGAGAGACTTAT NM_020990 RefSeq chr15 + 43593053 43599406 CKMT1B 1159 "creatine kinase, mitochondrial 1B"
GO:0005739|GO:0004111|GO:0034641|GO:0016310|GO:0006600|GO:0005743|GO:0044281|GO:0005524|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131208_PI430048170 0.25486537534483 1.44880628811456 0.485143241024939 1.14166101429527 1.54732347057243 A A A 0.869497296390089 0.383335468291871 0.459392446749245 A A A LNCV6_131208_PI430048170 mRNA
TTCCTGAGCCACGTTATCTCGGCGCTGGTTTCCGAGTACCGCTGAACTGTGGGTGGGTGG NM_005331 RefSeq chr16 + 180333 181179 HBQ1 3049 "hemoglobin, theta 1"
GO:0019825|GO:0005833|GO:0005506|GO:0005344|GO:0020037|GO:0015671 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143574_PI430048170 0.707351961035346 1.47111303806789 0.413966802684741 2.64512178213687 3.21556237914031 A A P 1.80825069492618 2.73072370768373 0.413877647371169 A P A LNCV6_143574_PI430048170 mRNA

CATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAATAAATTTATGTACTT NM_198541 RefSeq chr19 + 46229751 46231243 IGFL1 NA IGF-like family member 1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141850_PI430048170 0.131591654653556 0.639701486893424 6.36074061703699 7.37979407484305 6.70421403660994 P P P 7.26063590509682 7.51962210099683 7.74805684960039 P P P LNCV6_141850_PI430048170 mRNA
GGTCCACCATACTGGTAATTGGGGTACTCTGTATATGTGTTTCTTCTTTGTATACGAATC NM_014878 RefSeq chr9 - 2804154 2844130 KIAA0020 9933 KIAA0020 GO:0005783|GO:0005730|GO:0003729|GO:0006417 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58539_PI430048170 5.28089014817897e-05 0.634999440289563 9.23751922452851 9.16712288585226 9.16117325224896 P P P 9.81433836464651 9.8767224903858 9.84084945348429 P P P LNCV6_58539_PI430048170 mRNA
TCTGGTGGAGGCAGCTCCAGGCACTGCCCAGTCCGACACAACCTGCAAAAATCCATTAGA NM_002342 RefSeq chr12 + 6384032 6391571 LTBR 4055 "lymphotoxin beta receptor (TNFR superfamily, member 3), transcript variant 1"
GO:0005515|GO:0007165|GO:2001238|GO:0046330|GO:0016032|GO:0006915|GO:0043011|GO:0016021|GO:0071260|GO:0043123|GO:0031625|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127820_PI430048170 0.242330084431165 1.0186832824716 0.305874921644124 0.259336591999778 0.310650227932642 A A A 0.271338617717442 0.256668113541785 0.268251824308852 A A A LNCV6_127820_PI430048170 mRNA
GCTTTCTGCTTCACTGAAAAAGCAGTTTACCTGAAAAGAGCATGTAACCTATATTTTGTT NM_152625 RefSeq chr5 - 72439898 72507422 ZNF366 167465 zinc finger protein 366
GO:0005515|GO:0043627|GO:0003714|GO:0030331|GO:0005634|GO:0033147|GO:0000122|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145093_PI430048170 0.788373660417515 1.02970633224329 3.0126288888238 3.10920895422527 3.33046900562023 P P P 2.84292675307616 2.89104268245904 3.51020599373785 P P P LNCV6_145093_PI430048170 mRNA
GCAAATTCTAGCAGTATGTCTTCGATAACTTGGATGTTAGGATAGCCAATATGTACAAAA NM_006041 RefSeq chr17 + 14301049 14349404 HS3ST3B1 9953 "heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1, transcript variant 1"
GO:0000139|GO:0005975|GO:0005887|GO:0033872|GO:0009405|GO:0044281|GO:0015012|GO:0008467|GO:0030203|GO:0015015|GO:0006024 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128920_PI430048170 0.0605508166810364 0.739697929432137 6.5565257247491 6.49754421545482 6.78041507298836 P P P 6.82829400286826 7.01405153768795 7.27727484479253 P P P LNCV6_128920_PI430048170 mRNA
CCGTCTCCTCTGTTCAGATTTTGACATTCAGGAAAATATTTTTATTTTGATGCCATACTG NM_032182 RefSeq chr10 + 124801784 124836670 FAM175B 23172 "family with sequence similarity 175, member B"
GO:0005737|GO:0070552|GO:0071497|GO:0031593 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144819_PI430048170 0.0631432525603947 0.567580620265084 2.9358383819896 3.16838354023688 3.79465915440464 A P P 3.83798275572456 4.09130194518681 4.48709676737629 P P P LNCV6_144819_PI430048170 mRNA
GTAGAGTATCACATAAGTATCTTGGGCTAGAGAAATGCAGTTTATATATACCGTTGGATT NM_004289 RefSeq chr7 + 26152226 26187136 NFE2L3 9603 "nuclear factor, erythroid 2-like 3"
GO:0001078|GO:0003700|GO:0006366|GO:0003713|GO:0005634|GO:0000122|GO:0000978 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131397_PI430048170 0.0619246887481211 0.684249055893426 8.79196602573466 8.72489852051081 8.74935939510269 P P P 9.05480593299584 9.26544107658549

9.54656808072502 P P P LNCV6_131397_PI430048170 mRNA
TCGCCTCCCATTCTAAGGAGGTGAGGTGGTTGGAATAAAAACAGTTCCTGTCTGAAAAAA NM_001289394 RefSeq
chr8 - 134477787 134713049 ZFAT 57623 "zinc finger and AT hook domain containing, transcript variant 6"
GO:0001077|GO:0060712|GO:0002244|GO:0045944|GO:0005634|GO:0003677|GO:0046872|GO:0006351|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136151_PI430048170 0.161397980007078 1.11965830635678 0.626695022014304
0.426491810323044 0.646575126004725 A A A 0.289888100572807 0.414910536528803
0.507648862504162 A A A LNCV6_136151_PI430048170 mRNA
CCAGATTTCTTAATGCTTTTAAACTCATTTACTTCCTCTCAAGTCAAAGAGTACCTTCAG NM_152325 RefSeq
chr13 + 30932696 30975016 TEX26 122046 testis expressed 26 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_143770_PI430048170 0.049262446192589 1.11250989969753 12.3689476873786
12.3535601531943 12.2421612914791 P P P 12.140846648971 12.17873113379
12.1865127831714 P P P LNCV6_143770_PI430048170 mRNA
CACCCATAGGCCCTGTCCATACCCATGTAAGGTGTTCAATAAAGAACATGAACCAAAAAA NM_006899 RefSeq
chr20 - 2658394 2664219 IDH3B 3420 "isocitrate dehydrogenase 3 (NAD+) beta, transcript variant 1"
GO:0000287|GO:0006099|GO:0009055|GO:0005634|GO:0044281|GO:0006734|GO:0005739|GO:0006102|GO:0051287|GO:0004449|GO:0005759|GO:0006103|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141675_PI430048170 0.580455547711997 1.20554214310571 0.99851085133148
2.03389797748833 1.2140424077012 A A A 0.942640862688336 1.66381238512219
0.916821576106755 A A A LNCV6_141675_PI430048170 mRNA
CTGATCACCTTACACATTTAATAATAAAAGAGCTGTACCTACACGTTGCCTTTACACTGC NM_004102 RefSeq chr1
- 31365252 31373076 FABP3 2170 "fatty acid binding protein 3, muscle and heart"
GO:0005515|GO:0008092|GO:0042632|GO:0032868|GO:0008285|GO:0005324|GO:0042493|GO:0050543|GO:0046320|GO:0005615|GO:0005829|GO:0036041|GO:0016528|GO:0070542|GO:0071073|GO:0070538|GO:0006631|GO:0055091|GO:0044539|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129270_PI430048170 0.121982723064869 0.830787620846841 0.468978928717126
0.385060076521586 0.424590704924913 A A A 0.836527697648172 0.487550490569527
0.736128443934079 A A A LNCV6_129270_PI430048170 mRNA
GATGTTTCATGAGAAATACGAAGTCGTTTGGTGGAATAAATCCTGAGAAAATGCATAGAT NM_001291304 RefSeq
chr7 - 123536997 123601651 NDUFA5 4698 "NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, transcript variant 9"
GO:0022904|GO:0005747|GO:0006120|GO:0005743|GO:0044281|GO:0008137|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126909_PI430048170 0.990442237200423 1.02188280213787 3.7795101300435
2.79448601514945 3.12667843011304 P A P 3.60573652082823 3.23196453962889
2.84904992331516 P P P LNCV6_126909_PI430048170 mRNA
CCCCGGCGCGGAGAAGCCATGAAAATTAATGGGAAAAACAGTTTTTAAAAAACAAAAGAA NM_001276267
RefSeq chr15 - 45117365 45129876 DUOXA1 90527 "dual oxidase maturation factor 1, transcript variant 5"
GO:2000609|GO:0005886|GO:0045666|GO:0050727|GO:0005789|GO:0016021|GO:0015031|GO:2000379|GO:0042743 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136714_PI430048170 0.233817969850729 0.869292618261752 9.55505749156891
9.63202086735605 9.21630017036219 P P P 9.74785976107631 9.67207028215081
9.61980623642497 P P P LNCV6_136714_PI430048170 mRNA
TTGTTGTGTGTGACTCCAAAGAATGCCCGCGCTGAAATTTGGCGTGAATTAAACTGAAGC NM_001513 RefSeq chr14
+ 77321362 77331597 GSTZ1 2954 "glutathione S-transferase zeta 1, transcript variant 3"
GO:0005515|GO:0006559|GO:0006805|GO:0006749|GO:0044281|GO:0004364|GO:0042803|GO:0005829|GO:0004

602|GO:0005739|GO:0034641|GO:0006572|GO:0016034|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117787_PI430048170 0.980964990262515 1.00005048244361 0.268150238314528 0.2894812517700980.420155208609708 A A A 0.35961805900784 0.314043767533619 0.30809455650909 A A A LNCV6_117787_PI430048170 mRNA GCCTGTTGGGCCAGAAGACAGAAACTCCAACTGGCAAAAAAGCAAGCATCTAAGAAAAAA NM_001145460 RefSeq chr4 - 56647987 56681706 HOPX 84525 "HOP homeobox, transcript variant 5"
GO:0016575|GO:0048286|GO:0008016|GO:0043393|GO:0005634|GO:0000122|GO:0001829|GO:0003677|GO:0006351|GO:0007507|GO:0043415|GO:0051155|GO:0045596 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65838_PI430048170 0.0209531202684277 1.99697168845826 6.83134153445558 7.13891427724476 7.47075159397581 P P P 6.21541078410278 6.01535836567078 6.27495994427791 P P P LNCV6_65838_PI430048170 mRNA TCTAGGGAGGTAATTGTTGTGGATCTTGGGAATGAATACCCTACACCTCGAAGCTATACT NM_001143959 RefSeq chr2 + 61162493 61164829 C2orf74 339804 "chromosome 2 open reading frame 74, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132385_PI430048170 0.0596307477216196 0.23924084289387 2.01445736123089 2.5273502622752 0.524997246139901 A A A 3.91099403077805 3.82239178013713 4.15466893848477 P P P LNCV6_132385_PI430048170 mRNA TGTCAACTGGGTAAAGCCTTCCAGAGCTCTCTAAATACCTGAAAGACTTAAGCCTTTTTT NM_016516 RefSeq chr2 - 63892532 64019080 VPS54 51542 "vacuolar protein sorting 54 homolog (S. cerevisiae), transcript variant 1"
GO:0005515|GO:0019905|GO:0048471|GO:0060052|GO:0005794|GO:0006896|GO:0015031|GO:0048873|GO:0050881|GO:0042147|GO:0005654|GO:0040007|GO:0000938 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79689_PI430048170 0.0586393684065920.4930395061681221.62927423352561 2.07702680639247 1.15906766971691 A A A 2.26168094399605 3.18168605881688 2.45746528486629 A P P LNCV6_79689_PI430048170 mRNA AGTGCTTGGTCCTAGAAGAGAAATTGAAAATTGGACTACTGAGTGCAAGCAGTAAAAATA NM_001017420 RefSeq chr8 + 27774540 27804907 ESCO2 157570 establishment of sister chromatid cohesion N-acetyltransferase 2
GO:0001741|GO:0005794|GO:0010369|GO:0034421|GO:0035861|GO:0005634|GO:0046872|GO:0006302|GO:0004468|GO:0007059|GO:0002244|GO:0005654|GO:0071168|GO:0000278|GO:0031618|GO:0000785|GO:0006275 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133732_PI430048170 0.845813423271021 1.01528766044686 6.85936703680233 6.71708812219174 6.63757892431831 P P P 6.49415500246932 6.91536196688558 6.71702248158365 P P P LNCV6_133732_PI430048170 mRNA CCATGCAGACACCTCATGGCACTTCAAACTATTAAAATGCATTTTATCTTATCCAGAAAA NM_003935 RefSeq chr22 - 21957024 21982843 TOP3B 8940 "topoisomerase (DNA) III beta, transcript variant 1"
GO:0003916|GO:0000793|GO:0003917|GO:0007059|GO:0005654|GO:0005634|GO:0006265|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144145_PI430048170 0.00506471124521143 0.4780611475022683.81126773047346 3.35077875731109 3.50314713816475 P P P 4.4761922106822 4.66753339327514 4.74155219727399 P P P LNCV6_144145_PI430048170 mRNA TTGGAAGGGGACCATGAGAGATGATGTATTATGATGAACTCATGATTTAATTCTTTGGTG NM_153717 RefSeq chr4 + 5711196 5814304 EVC2 121 Ellis van Creveld syndrome
GO:0045880|GO:0005929|GO:0060170|GO:0005737|GO:0001501|GO:0007517|GO:0003416|GO:0051216|GO:0016021|GO:0036064|GO:0007224 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79591_PI430048170 0.9573979714837440.9945193696081464.33611792077626 3.94416113084665 4.47116187584771 P P P 4.13259233332607 4.12290624756976 4.53139393782487 P P P LNCV6_79591_PI430048170 mRNA

AACCAGGACTGTTCAGTCTTACACTGAATGAACGTTTCAGTATAAATGGTGGTTATCTGG NM_177924RefSeq chr8
- 18056415 18084370 ASAH1 427 "N-acylsphingosine amidohydrolase (acid ceramidase) 1, transcript
variant 1"
GO:0006665|GO:0017040|GO:0010033|GO:0006687|GO:0030324|GO:0006672|GO:0044281|GO:0003824|GO:0070
062|GO:0043202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138550_PI430048170 0.1212984448485060.7488882744597891 0.8179490954238
10.2286910464131 10.4047397719854 P P P 10.9680091276126 10.9653718553837
10.8300516637629 P P P LNCV6_138550_PI430048170 mRNA
AGAGGCTGCTGGCTTCCCTAAAAGTTGAAATAAAAGATTTTTGCCTTTGTTCTGAAAAAA NM_017916RefSeq chr19
- 49446292 49451858 PIH1D1 55011 PIH1 domain containing 1
GO:0005515|GO:0030855|GO:0070761|GO:0000492 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145095_PI430048170 0.3836440076253861.30377121348748 0.60804685680923
1.47233829531434 0.592705627836422A A A 0.6030029858574140.606435437104485
0.498372065843237A A A LNCV6_145095_PI430048170 mRNA
TTCTAACTTCAAGGACATTATATCACTTACTGTATAATAAAATAATCTTACAGTAAAAAA NM_023074RefSeq chr19
- 51889234 51905052 ZNF649 65251 zinc finger protein 649
GO:0005515|GO:0006355|GO:0005634|GO:0005615|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133389_PI430048170 0.0813327140296072 0.7997190010948225.67623444581357
5.32375315149475 5.47692502629649 P P P 5.79809169823115 5.82078655378056
5.84666923346611 P P P LNCV6_133389_PI430048170 mRNA
TTTCCCCCAACCCTTCACGCAAGGAAAAAGCAAAGTGATTCATACCTTCTATCTTGGAAA NM_001025091 RefSeq
chr6_GL000254v2_alt + 1915438 1935578 ABCF1 23 "ATP-binding cassette, sub-family F (GCN20),
member 1, transcript variant 1"
GO:0005515|GO:0042254|GO:0045727|GO:0008494|GO:0005635|GO:0005524|GO:0006412|GO:0006413|GO:0005
737|GO:0006954|GO:0016020|GO:0042788|GO:0043022|GO:0005840|GO:0005654|GO:0016887|GO:0008135 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104416_PI430048170 0.0406171168617692 0.5632973859818984.60953956997118
4.27968721324452 4.77949603470946 P P P 5.50141929336867 4.95349418310173
5.65223995369714 P P P LNCV6_104416_PI430048170 mRNA
AGAAGTGGAAACCACATACTGAGCATGGCTAGATTGGCTAAAGATGTCCTAGCTGAGATC NM_153634RefSeq chr12
- 38652199 38905618 CPNE8 144402 copine VIII GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_94006_PI430048170 0.7887527320949021.14567649557211 0.5677595158936810.779635563695782
1.78869239167495 A A A 0.4690206206020271.25684843165576 1.02429343524161 A A A
LNCV6_94006_PI430048170 mRNA
ATGGTGTGAGTGAAAACCCAGAGGAATACATTTGGTGGCTGAGCTAGTACAATGCCATCA NM_001042416 RefSeq
chr8 + 232396 247340 ZNF596 169270 "zinc finger protein 596, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_100537_PI430048170 0.0393792495931969 0.5908672265753696.15959094243299
5.99831263837385 6.39644985795434 P P P 6.70746741067875 6.76499540292858
7.30814195454933 P P P LNCV6_100537_PI430048170 mRNA
CAAAATCCTATGGTACAAGAAGCTATACGAATGGGGTTCAGTTTCAAGGACATTAAGAAA NM_001167RefSeq chrX
+ 123860166 123913979 XIAP 331 "X-linked inhibitor of apoptosis, E3 ubiquitin protein ligase, transcript
variant 1"
GO:0005515|GO:0004842|GO:0016567|GO:0055070|GO:0016874|GO:0090263|GO:0070424|GO:0005634|GO:0005
829|GO:0005737|GO:0042127|GO:0031398|GO:0005876|GO:0090307|GO:0016055|GO:0030510|GO:0043154|GO:0
043027|GO:0043066|GO:0050727|GO:0006915|GO:0097193|GO:0006974|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_135320_PI430048170 0.1628884443136110.7374312867991486.22053285185064
6.38485231874124 6.06798917400289 P P P 6.24551271270538 6.90617590385697
6.77617197479134 P P P LNCV6_135320_PI430048170 mRNA
TAAGGCCAAATAAGGAGCGAGGTTGTGAAAACTGGAAAACAAAGGCTCTTTTCAGAGCCA NM_080596RefSeq
chr6 + 27147081 27147562 HIST1H2AH 85235 "histone cluster 1, H2ah"
GO:0008150|GO:0003674|GO:0046982|GO:0005634|GO:0000786|GO:0003677|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140553_PI430048170 0.1981198329705431.03382878764438 0.416851809348969
0.3672195187915370.394561700536921A A A 0.3060011347747650.333766466666485
0.393897567683175A A A LNCV6_140553_PI430048170 mRNA
CAAGTCAAGCAAGCTTTCATTAACATGGCAAGGAAGACTGTATTTTTCACAAGCACATGA NM_001005182 RefSeq
chr12 + 55320599 55321538 OR6C1 NA "olfactory receptor, family 6, subfamily C, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131968_PI430048170 0.97388126541039 1.0074084208121 1.10473519120818
0.4098052865373580.243529333424837A A A 0.3651999848533720.436974303824951
0.990499054042653A A A LNCV6_131968_PI430048170 mRNA
AAGGTCATTTGTGGTTGTTTTTGTTTGTTTGTTTCTTAAATCCTACTATCTCCTGGCCTG NM_001146705 RefSeq chrY
- 19705414 19744939 KDM5D 8284 "lysine (K)-specific demethylase 5D, transcript variant 1"
GO:0034720|GO:0032453|GO:0016706|GO:0006325|GO:0008270|GO:0005654|GO:0005575|GO:0003677|GO:0055
114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136100_PI430048170 0.0410672878246666 0.39515173885833 0.259100709464564
0.3591508911586591.20521002701107 A A A 2.43357344611193 1.31154012207835
2.07901695833976 A A A LNCV6_136100_PI430048170 mRNA
GTACTGTGTTTTCACTCAAACCACTGACTTAACAGATACTGCTGTGTATAACATGTACTA NM_006948RefSeq chr21
- 14371115 14383188 HSPA136782 "heat shock protein 70kDa family, member 13"
GO:0005783|GO:0005524|GO:0070062|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94057_PI430048170 0.4045279016991170.842318125428678 2.77069037153684 2.51558862296988
2.73815727290916 A A A 2.8519307304412 2.55997414009696 3.2772725445188 P A P
LNCV6_94057_PI430048170 mRNA
AAGGAGAACAGCATTAAACTGACCTCGGTGGTGTTCATTCTCATCTGCTGCTTTATCATC NM_001400RefSeq chr1
+ 101236748 101241520 S1PR1 1901 sphingosine-1-phosphate receptor 1
GO:0005886|GO:0003376|GO:0030032|GO:0031226|GO:0045124|GO:0019226|GO:0038036|GO:0007193|GO:0030
155|GO:0050927|GO:0006935|GO:0051482|GO:0045944|GO:0030182|GO:0003245|GO:0045446|GO:0007155|GO:0
030500|GO:0001664|GO:0030335|GO:0046625|GO:0031532|GO:0004930|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139482_PI430048170 0.0518797155323710.784424594024138 6.80623764606603
6.65921918413876 6.96658008655221 P P P 7.12803385810033 7.02050349779861
7.33311508849187 P P P LNCV6_139482_PI430048170 mRNA
GTAGTTGCCAAAGAGGTTCTCCTAGGTGGTCTTAATAAACCTATTCACAGAATTCTCCTT NM_177424RefSeq chr1
+ 27773182 27824452 STX12 23673 syntaxin 12
GO:0005515|GO:0033344|GO:0050821|GO:0031201|GO:0006886|GO:0006906|GO:0012505|GO:0045335|GO:0005
484|GO:0000139|GO:0031083|GO:0000149|GO:0045121|GO:0016021|GO:0048278|GO:0010008|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134789_PI430048170 0.0415218447714635 1.77915034397343 4.33163177589224
4.650786861754 4.48396213487899 P P P 4.04375365378101 3.52819503143846
3.31966701543814 P P P LNCV6_134789_PI430048170 mRNA
GGCACCCACATGAATAGCTGTATGCACTGTACTTGTTTCTTAATAAACTTATTTTTAAGC NM_001123225 RefSeq
chr22 - 50551111 50562899 SYCE3 644186 synaptonemal complex central element protein 3

GO:0043065|GO:0005694|GO:0005634|GO:0000801|GO:0007283|GO:0007130|GO:0051301|GO:0007131 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73102_PI430048170 0.12901843907252 0.79184476081274 6.01732233027581 5.89880838304362 5.72732873753201 P P P 6.16426291536383 5.99366387130594 6.46950660317913 P P P LNCV6_73102_PI430048170 mRNA
AAAGGAAGTATTTCAGATTGCAAGTAATGTCATGATGCTGCGATTAATAGATATAGCCGT NM_012096 RefSeq chr3 + 57227736 57273470 APPL1 26060 "adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1"
GO:0005515|GO:0008286|GO:0012506|GO:0043065|GO:0008283|GO:0005634|GO:0043422|GO:0097190|GO:0005829|GO:0042802|GO:0007165|GO:0005737|GO:0007049|GO:0046324|GO:0016581|GO:0031901|GO:0090003|GO:0010008|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142816_PI430048170 0.242580776525736 0.754687302911852 3.46312257511834 2.68859628129311 3.57289092118044 P A P 3.5100691548311 3.83328193526231 3.73081908169452 P P P LNCV6_142816_PI430048170 mRNA
CCTCTAGCACCTCCAGTGATAAGCACTAATTGCCTATATACAACCCTTTTTTGTTTGAAA NM_001113738 RefSeq chr17 - 46334901 46361797 ARL17A 51326 "ADP-ribosylation factor-like 17A, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131363_PI430048170 0.146154785460794 1.02715689210763 0.32613238180269 0.288854811182729 0.268395975096038 A A A 0.251635401244145 0.262383002209129 0.253967993631354 A A A LNCV6_131363_PI430048170 mRNA
TCCTTTGAAAGAGAATGAAAGACCCTGTGACATTTCACTTCAAAAATAAGCCCTGTAGCT NM_015464 RefSeq chr7 - 16461480 16465849 SOSTDC1 25928 sclerostin domain containing 1
GO:0030514|GO:0007389|GO:0010454|GO:0060648|GO:0042475|GO:0016055|GO:0090090|GO:0005615|GO:0031069 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144111_PI430048170 0.00750247080321236 1.28801415565078 11.8406961764265 11.7482998594825 11.8592721837045 P P P 11.4468278555438 11.4628974003636 11.4454635053119 P P P LNCV6_144111_PI430048170 mRNA
CTCTGCTCTAATACACTACCTGGAGAAAGTCTTTTCCTTATTTTCAATAAATGTCAGACA NM_001078171 RefSeq chrX + 135032302 135033545 FAM127A 8933 "family with sequence similarity 127, member A" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141344_PI430048170 0.132917590567015 0.863300111208165 6.05027349211752 5.94330268960361 6.25643814883568 P P P 6.24921985495826 6.33090890294607 6.32242709089733 P P P LNCV6_141344_PI430048170 mRNA
CAGTGAGGAATTTTATTGGTGGAACTGAATGTTAACTGCTGTAAATCCTAGGAAATAAAC NM_198920 RefSeq chr6 - 82892397 83065841 UBE3D 90025 "ubiquitin protein ligase E3D, transcript variant 1"
GO:0005737|GO:0016567|GO:0016874 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64794_PI430048170 0.645767546685923 0.974545172313243 14.9430007739855 14.7148307781761 14.7447246258633 P P P 14.8640868140548 14.7794986187732 14.8793920358175 P P P LNCV6_64794_PI430048170 mRNA
AGAAATATGTGGATGAGGCTTCCAAGAAGGAGATCAAAGACATCCTCATCCAGTATGACC NM_001020 RefSeq chr19 - 39433206 39435978 RPS16 6217 ribosomal protein S16
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006364|GO:0006614|GO:0019058|GO:0015935|GO:0006415|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0016020|GO:0000184|GO:0022627|GO:0016032|GO:0042274|GO:0044267|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66124_PI430048170 0.672070252121358 0.929147134079672 2.91259609013564 3.93977916014602 3.90941678581908 A P P 3.56762593989636 3.75820899872403 3.94526543449658 P P P LNCV6_66124_PI430048170 mRNA
GAATCTTGGAGGAAAAGAAGATGGATAGAAGTCTACAGCCTTCTAAGGAGAGCATTTTTA NM_018433 RefSeq chr2

+ 86441147 86492716 KDM3A 55818 "lysine (K)-specific demethylase 3A, transcript variant 1"
GO:0000976|GO:0003700|GO:0005506|GO:0006325|GO:0007290|GO:0051213|GO:0001047|GO:0005634|GO:0050
681|GO:0006351|GO:0046293|GO:0005737|GO:0009755|GO:0036123|GO:0016020|GO:0051573|GO:0045944|GO:0
005654|GO:0045893|GO:0030521|GO:0055114|GO:0033169 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_135634_PI430048170 0.0554048453596084 0.74982557991191 5.30512900740494
4.88672718118805 5.01414421494218 P P P 5.3558502045903 5.63856102660954 5.4760820131358
P P P LNCV6_135634_PI430048170 mRNA
TGTGGCATCAGATAAAAACGTGGGAGTTTTTCCATATAATTCCCAGCCTTACTTATAAAT NM_024101 RefSeq chr2
+ 237487218 237555318 MLPH 79083 "melanophilin, transcript variant 1"
GO:0001725|GO:0017137|GO:0048471|GO:0005815|GO:0032400|GO:0003779|GO:0030318|GO:0035371|GO:0006
605|GO:0030425|GO:0046872|GO:0031489|GO:0051010|GO:0030864|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_111593_PI430048170 0.3830018227140951.25536702942446 3.19218130093214 3.0152382865575
2.60201488834392 P P A 2.86551322632637 2.90721519753265 1.91366399313778 P P A
LNCV6_111593_PI430048170 mRNA
AAGTCTCAAGAGAAGGAGGGGGGATTGGTGGTTGGAGGAAGCAGCACACCCAATTCTGCC NM_001171818
RefSeq chr6 + 35342557 35428191 PPARD 5467 "peroxisome proliferator-activated receptor delta,
transcript variant 3"
GO:0005515|GO:0051546|GO:0010467|GO:0030308|GO:0006367|GO:0003700|GO:0033189|GO:0070539|GO:0050
680|GO:0003707|GO:0006091|GO:0008366|GO:0030154|GO:0007507|GO:0015758|GO:0032024|GO:0004879|GO:0
006635|GO:0007566|GO:0003713|GO:0031589|GO:0014068|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129767_PI430048170 0.4601277594495831.31357941397684 0.335690894680997
1.45830351479075 0.534687663959509A A A 0.7951543371786370.266873054836187
0.28326934100203 A A A LNCV6_129767_PI430048170 mRNA
GGCGTAGTTGGGGATTGTTTTACAATAAGTAAACATTGCTAATAACTGTGTTACAAGATC NM_207468 RefSeq chr1
+ 222737215 222750660 FAM177B NA "family with sequence similarity 177, member B" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141887_PI430048170 0.6443153352250181.03126690532238 0.28487397247245
0.2955267341428620.515413646476648A A A 0.3223612038644190.32839393925787
0.323731557477687A A A LNCV6_141887_PI430048170 mRNA
GCAGCCATATAAAAGAATGAAGAAGCTCTTTGTGTAATGATATGAAGTGATCACCAAATG NM_001077657 RefSeq
chr3 - 196506878 196515366 SMCO1 NA single-pass membrane protein with coiled-coil domains 1
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120205_PI430048170 0.5102698125291620.9025806362881488.92693984959374
8.30997793191304 8.41866404862844 P P P 8.48244254869204 8.81268502128351
8.85385247844743 P P P LNCV6_120205_PI430048170 mRNA
GAGCTGATACCCAGACATACCAGCCTTATAACAAAGACTGGATTAAAGAGAAGATCTACG NM_004450 RefSeq chr14
- 69380122 69398304 ERH2079 enhancer of rudimentary homolog (Drosophila)
GO:0006213|GO:0007049|GO:0006139|GO:0016020|GO:0030496|GO:0001649 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144035_PI430048170 0.97182916353732 0.9428713737367482.17467976107793
2.01906984829947 2.1157120246728 A A A 1.79031191434271 1.64915747918789
2.82547161890139 A A P LNCV6_144035_PI430048170 mRNA
GCTGGCAGTAAAACATGGGTTTAAGGAAGAGTGTTTTTCAGAATTTACACTGTATATCTC NM_006630 RefSeq chr19
+ 44141556 44160309 ZNF234 10780 "zinc finger protein 234, transcript variant 1"
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_143751_PI430048170 0.6382068831016970.8551789105259430.36480361849135
1.44221818517897 0.274801895987174A A A 0.2943488423354681.14437295184381
1.41208308286883 A A A LNCV6_143751_PI430048170 mRNA
GGAATAAAGGCACACAGAACTCCATCAAGACGTGGATTTCATCATAATAGTCATTCATGA NM_139171RefSeq chr18
- 54324691 54354573 STARD6147323 StAR-related lipid transfer (START) domain containing 6
GO:0006869|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137503_PI430048170 0.0355721879690124 1.25933499056526 5.41242656514842
5.14593173835143 5.36045836355486 P P P 5.01317145821811 4.85251327996902
5.06060140594957 P P P LNCV6_137503_PI430048170 mRNA
GTCTGTTGTTGTACTCACAGCAGCAACATGAGTGTAAACAGTAGACAATAAACTTTTATT NM_018144RefSeq chr10
+ 12129640 12165404 SEC61A2 55176 "Sec61 alpha 2 subunit (S. cerevisiae), transcript variant 1"
GO:0008150|GO:0003674|GO:0002474|GO:0042590|GO:0005789|GO:0043022|GO:0002479|GO:0016021|GO:0015
031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_83175_PI430048170 0.460453969563946 1.13567905536883 4.01104174348302 3.55306587181162
3.55679720572782 P P P 3.72571316743977 3.65303537945503 3.18342272851349 P P P
LNCV6_83175_PI430048170 mRNA
CCCCAGTTATATGTAGCATAAATGGTTTAATCATAAATGTCTCCCTTAGGCATGATAAAC NM_178452RefSeq chr16
+ 84145259 84177918 DNAAF1 123872 "dynein, axonemal, assembly factor 1"
GO:0003356|GO:0036159|GO:0035469|GO:0005886|GO:0071910|GO:0030324|GO:0005930|GO:0003341|GO:0005
634|GO:0070286|GO:0060287|GO:0001947|GO:0044458|GO:0000922|GO:0005737|GO:0045502|GO:0060972|GO:0
060271|GO:0036158|GO:0071907 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127799_PI430048170 0.599731260270978 0.929483203534757 0.376617305300256
0.38519263917822 0.464519982392819A A A 0.790093617122513 0.327969514705575
0.380753086938313A A A LNCV6_127799_PI430048170 mRNA
CAAGCCTAATTGTGCAACCTGATTACAGAATAACTGGTACACTTCATTTATCCATCAATA NM_000605RefSeq chr9
- 21384254 21385397 IFNA2 3440 "interferon, alpha 2"
GO:0005515|GO:2000552|GO:2000666|GO:0005132|GO:0042517|GO:2000663|GO:0019221|GO:0007267|GO:0006
915|GO:0005576|GO:0005125|GO:0005615|GO:0051607|GO:0060337|GO:0006954|GO:0060338|GO:0046597|GO:0
007596|GO:0045087|GO:0010629|GO:0045581|GO:0045892|GO:0007166 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129610_PI430048170 0.0730605267267105 0.83825378691233 5.09401383433387
4.99964311425993 5.00169056903291 P P P 5.13206425490663 5.40410603953944
5.31170212380902 P P P LNCV6_129610_PI430048170 mRNA
GCAAGCTGCAGGTTTGTAATGCAAAAGGCTGATTACTGAAATTTAAGAAAAAGGTTCTTT NM_001291958 RefSeq
chr6 + 160991726 161117385 MAP3K4 4216 "mitogen-activated protein kinase kinase kinase 4,
transcript variant 3"
GO:0005515|GO:0010468|GO:0048471|GO:0001890|GO:0005524|GO:0046872|GO:0035556|GO:0000187|GO:0000
186|GO:0005737|GO:0010225|GO:1900745|GO:0000165|GO:0060718|GO:0006468|GO:0043507|GO:0004709|GO:0
004708|GO:0019100. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144432_PI430048170 0.0524191749750891.35253408058656 10.7574630729499
10.6701380839921 11.0027358011316 P P P 10.3180738293526 10.1891008477107
10.6051709755086 P P P LNCV6_144432_PI430048170 mRNA
CATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATTAAAATCAGAGACTGTAACAA NM_001097613 RefSeq
chr1 + 145607959 145670464 GPR89ANA "G protein-coupled receptor 89A, transcript variant 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126860_PI430048170 0.0956044068548394 1.32221276889231 9.54532020219409
9.39947141035774 9.07839635195121 P P P 9.0928451267805 9.02755412400992 8.7032626946165
P P P LNCV6_126860_PI430048170 mRNA
TCGGGACGCTGAATCTGAATCCACCAATAAATAAAGGTTCTGCAGAATCAGTGCAAAAAA NM_145252RefSeq chr16

+ 2830171 2832284 ZG16B 124220 zymogen granule protein 16B
GO:0003674|GO:0001895|GO:0030246|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_59710_PI430048170 0.0227736892598739 0.497295754881793 5.74053126831738
5.05184269914109 5.12260156233406 P P P 6.08568829623885 6.35580552150972 6.5615209217607
P P P LNCV6_59710_PI430048170 mRNA
GCAGAAACGTAGCAAGCGTTTCATGTCAGGGCTACAGCTGAGAGCAAAAACTGCAAAAAA NM_001167856
RefSeq chr12 - 123289108 123350441 SBNO1 55206 "strawberry notch homolog 1 (Drosophila),
transcript variant 1" GO:0008150|GO:0003674|GO:0006355|GO:0005575 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_135342_PI430048170 0.4724155490950620.8811424090354270.313801071252557
0.3359405666034870.372115575068115A A A 0.33467573966852 0.861540289828634
0.303181728861069A A A LNCV6_135342_PI430048170 mRNA
CCTGCTTGCTTACTGCTTATATTTGCTCAGGGAAGAGTAGGAAAATAAAATATATGCAAA NM_178817RefSeq chr21
+ 32291812 32312288 MRAP 56246 "melanocortin 2 receptor accessory protein, transcript variant 1"
GO:0005515|GO:0005886|GO:0005783|GO:0030819|GO:0031780|GO:0070996|GO:0031783|GO:0050873|GO:0031
781|GO:0034394|GO:0031782|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136893_PI430048170 0.1131965656162550.8836525585717816.330586438515
16.1058510952792 16.1210762960312 P P P 16.4258005408198 16.3810748251111 16.293991131477
P P P LNCV6_136893_PI430048170 mRNA
CTGCCAAATTCTCCGGTTTGCCCCGGGATATTATAGAAAATTATTTGTATGAATAATGAA NM_021103RefSeq chr2
+ 84905638 84906675 TMSB109168 thymosin beta 10
GO:0003785|GO:0042989|GO:0005737|GO:0007015|GO:0005856 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133793_PI430048170 0.2146913194445711.48710931429021 0.462525808136152
1.43841511169786 0.767400697703945A A A 0.3106481535334160.371874780557091
0.442989484474891A A A LNCV6_133793_PI430048170 mRNA
ACCAGAGGACCATCATGAAACCTCTGGAGTACCAATTCAAGTCTCAGATAATGAGCCTGT NM_001143986 RefSeq
chr19 + 2977537 2995184 TLE6 79816 "transducin-like enhancer of split 6, transcript variant 1"
GO:0043234|GO:0006355|GO:0045666|GO:0005634|GO:0005938 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145191_PI430048170 0.88103935873399 0.91741906327754 0.579037545385039
0.7925200030275711.0409551856398 A A A 0.5120657070217781.51597546393697
0.558876752218451A A A LNCV6_145191_PI430048170 mRNA
GCTTCACCATGTCTCTCTGGTAAACCACAGTTAATATTTTAAGCTATAGTGGGAAATAAA NM_001146686 RefSeq
chr3 - 190852736 190862676 GMNC NA geminin coiled-coil domain containing NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127426_PI430048170 0.0840902748714518 1.30915863282874 8.46033882404155
8.64016321734677 8.9073007035284 P P P 8.20945044124415 8.15934569985073
8.48647090038039 P P P LNCV6_127426_PI430048170 mRNA
GAGATGCAGCTTTAAACAGATTATTTCAGCAGATCTATTCAGATGGTTCTGATGAAGTGA NM_001130912 RefSeq
chr13 + 52652695 52688298 SUGT1 10910 "SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae),
transcript variant 1B"
GO:0005515|GO:0007067|GO:0005737|GO:0045087|GO:0000776|GO:0000151|GO:0005634|GO:0035872|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102296_PI430048170 0.2144680304577661.05225478969953 8.52468365958112
8.52217184315876 8.57116388105705 P P P 8.521151007843 8.38158195605547
8.49164435798873 P P P LNCV6_102296_PI430048170 mRNA
GGGTTGGATGAAGTGTCCTCTTGCTAGCACCAATAAAAGATTTCTAATTAACACAATTAA NM_001206559 RefSeq

chr13 + 27620742 27667422 POLR1D 51082 "polymerase (RNA) I polypeptide D, 16kDa, transcript variant 3"
GO:0010467|GO:0006386|GO:0006385|GO:0006363|GO:0006362|GO:0006361|GO:0006360|GO:0003677|GO:0006383|GO:0005829|GO:0001056|GO:0005736|GO:0045814|GO:0045087|GO:0001054|GO:0046983|GO:0040029|GO:0005666|GO:0032481|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140025_PI430048170 0.00742474210613018 0.4482313798537624.10898019278731
3.53095510843337 3.76345318326304 P P P 4.87714676543978 5.1688779997969
4.86893216457437 P P P LNCV6_140025_PI430048170 mRNA
GTACACTAAGATCGTTGAAGAGCAATAGAACCTTTAAGACAGTATTAAAGGTGTGAAACA NM_018105RefSeq chr8
- 42836673 42843331 THAP1 55145 "THAP domain containing, apoptosis associated protein 1, transcript variant 1"
GO:0043565|GO:0005515|GO:0007346|GO:0007049|GO:0006355|GO:0016605|GO:0001935|GO:0008270|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_41196_PI430048170 0.2083242286029540.8163841648938685.79071079499157 5.47838058867652
5.33248136857794 P P P 5.62594014271416 6.09537233588009 5.75533119623641 P P P
LNCV6_41196_PI430048170 mRNA
TGATGAGCAAGATGAACAAGAGCCGCCAGCGCGTGCGCTACGACTCCTCCAACCAGGTCA NM_001281453
RefSeq chr19 - 1576670 1592761 MBD3 53615 "methyl-CpG binding domain protein 3, transcript variant 1"
GO:0000792|GO:0005515|GO:0008327|GO:0000790|GO:0016573|GO:0043044|GO:0006346|GO:0031492|GO:0006325|GO:0000122|GO:0000978|GO:0001701|GO:0003677|GO:0006351|GO:0043234|GO:0005737|GO:0016581|GO:0009888|GO:0000980|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142726_PI430048170 0.0219350726711273 1.30330913041733 6.60251819674234
6.80480315402407 6.84518339338755 P P P 6.49312875624447 6.23955289688282
6.37368564691785 P P P LNCV6_142726_PI430048170 mRNA
CATGGATTGACTGTCAATGGTAAAGTTTGTCTATTTTCCAGTCCTTAAAACTCAATAGCA NM_006817RefSeq chr12
+ 112013347 112023220 ERP29 10961 "endoplasmic reticulum protein 29, transcript variant 1"
GO:0005515|GO:0042470|GO:0009306|GO:0009986|GO:0043335|GO:0005783|GO:0003756|GO:0006886|GO:0010628|GO:0000187|GO:0016020|GO:0006457|GO:0010629|GO:0050709|GO:0001934|GO:0005788|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128326_PI430048170 0.0340957737225564 1.63508154368624 8.60956155878336
8.7735157422041 9.05445558677176 P P P 7.82753081665044 8.02663806052563
8.42535971096834 P P P LNCV6_128326_PI430048170 mRNA
ATGGAATCATTTATCGTCCTCTGTAATAAACTGGCCAAGATACTAAAGGCTTACTATTCA NM_014672RefSeq chr14
+ 35122320 35274078 KIAA0391 9692 "KIAA0391, transcript variant 1" GO:0005739|GO:0008033 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129244_PI430048170 0.0165999155317475 0.2507915003095960.393427733198901
0.30353146789782 0.342528756631862A A A 2.48672539804434 1.78306867054342
2.62475867443408 P A P LNCV6_129244_PI430048170 mRNA
CCTAGTAATCATCGAGGATCTCAAAGATATGCACCAGTTTGAATAAATGCTGTTTAAAGA NM_006644RefSeq chr13
- 31134973 31162021 HSPH1 10808 "heat shock 105kDa/110kDa protein 1, transcript variant 1"
GO:0005515|GO:0006986|GO:0043014|GO:0005874|GO:0005576|GO:0005524|GO:0006898|GO:0005829|GO:0005737|GO:0045345|GO:0071682|GO:0051085|GO:0051135|GO:0005654|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_124305_PI430048170 0.24950084473249 0.76415493362313 4.60353832183232
4.41623511520358 4.18471853839005 P P P 4.32707090186245 5.082452525495
4.88750829298045 P P P LNCV6_124305_PI430048170 mRNA
TCAGCAGTCAACGTCCCAGCAGGCAACACAGGGAACCTCAGGCCAGGCACCACAGCTCTT NM_003194RefSeq
chr6 + 170554332 170572870 TBP 6908 "TATA box binding protein, transcript variant 1"

GO:0005515|GO:0010467|GO:0006368|GO:0003700|GO:0006367|GO:0006366|GO:0044212|GO:0006363|GO:0006
362|GO:0006361|GO:0006360|GO:0007283|GO:0006383|GO:0005737|GO:0000183|GO:0070491|GO:0016032|GO:0
001940|GO:0001103|GO:0005669|GO:0005719|GO:0001939|GO:0045814|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139668_PI430048170 0.41258168382806 0.7737803280570370.416982023171522
0.43435921081547 0.397842929710371A A A 1.31333293336707 0.483644341594311
0.368652519165969A A A LNCV6_139668_PI430048170 mRNA
TTTTGACCTCAAAATACATTGTAAGAGCAACATCCTACGTTAATAAATGTTCTAGCCCGG NM_181712RefSeq chr1
- 62236164 62319412 KANK4 163782 KN motif and ankyrin repeat domains 4 GO:0005737 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_132266_PI430048170 0.2683713012605491.05113057119275 0.471036201471963
0.3099881492896940.372026025013425A A A 0.2774910132342750.340543222857573
0.323049537047851A A A LNCV6_132266_PI430048170 mRNA
GCAAAGGCAATCAAAAACCTTTTTGTTTTGTAGCCTGCTTTTGCTTTCACAATTTGTCTT NM_003306RefSeq chr13 -
37636635 37869802 TRPC4 7223 "transient receptor potential cation channel, subfamily C, member 4,
transcript variant epsilon"
GO:0005515|GO:0045296|GO:0005886|GO:0008013|GO:0009986|GO:0048709|GO:0014051|GO:0034704|GO:0055
085|GO:0070679|GO:0016323|GO:0070509|GO:0034220|GO:0005911|GO:0007411|GO:0005901|GO:0070588|GO:0
006816|GO:0015279|GO:0030863 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136595_PI430048170 0.00237315703203528 1.25661844207844 10.0265242724496
10.0297999943617 9.98171261433525 P P P 9.63824052449297 9.74043366813571
9.66931090634292 P P P LNCV6_136595_PI430048170 mRNA
CCATCCCATTTGAGTTCAGGGGTGAGGCTTAAGATCTTAATAAATAATACCTTACTGCTT NM_058163RefSeq chrX
+ 54440419 54445297 TSR2 90121 "TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)"
GO:0005515|GO:0000462|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136603_PI430048170 0.0892382074062587 0.3249353067286812.16343657912647
0.2932202422471921.900799971623 A A A 3.29233751233088 3.26111725359922
3.27288896940122 P P P LNCV6_136603_PI430048170 mRNA
ATGCATCGTACCTCCAAACAGTACATATTCGGAAAGTCAAAGATTCCTGCAAAATAAATA NM_152787RefSeq chrX
- 30827441 30889394 TAB3 257397 TGF-beta activated kinase 1/MAP3K7 binding protein 3
GO:0005515|GO:0034142|GO:0005886|GO:0070423|GO:0007249|GO:0051403|GO:0035872|GO:0005829|GO:0002
756|GO:0000187|GO:0005737|GO:0051092|GO:0002755|GO:0034138|GO:0070062|GO:0038124|GO:0038123|GO:0
034134|GO:0007254|GO:0002224|GO:0045087|GO:0008270|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93105_PI430048170 0.6918389758052940.9627786586304447.93806530447569 7.5620976385649
7.45185056489883 P P P 7.71247185943258 7.79740030416014 7.64857485379843 P P P
LNCV6_93105_PI430048170 mRNA
CAGCTGTGCGAGCTCTGCCCTCCTCAGCTCTCAAACCTGAATAAATGCACCAAGCCCAGA NM_178536RefSeq chr9
+ 136952315 136955497 LCN12 286256 lipocalin 12
GO:0006629|GO:0005215|GO:0001972|GO:0005576|GO:0015909|GO:0055085 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_81098_PI430048170 0.6564469426709681.05577999179249 5.9900917072812 6.00316088348231
6.27344163325708 P P P 5.69391547417682 6.20802286138741 6.09871591978464 P P P
LNCV6_81098_PI430048170 mRNA
CAAACCCTAGATTGGGGTAGAGGGAAAAGGGTTCAACAAAGGCTGAACTGGATTCTTAACNM_000380RefSeq chr9
- 97674908 97697409 XPA 7507 "xeroderma pigmentosum, complementation group A, transcript
variant 1"
GO:0005515|GO:0005794|GO:0008630|GO:0019904|GO:0009636|GO:0005634|GO:0046872|GO:0042803|GO:0045
171|GO:0003684|GO:0005737|GO:0006281|GO:0035264|GO:0005654|GO:0006289|GO:0000718|GO:0005662|GO:0

006979|GO:0009411. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134504_PI430048170 0.0665316825909270.7860623188132134.82869064351505
5.00125046988036 5.16987757874258 P P P 5.33662854588089 5.38279773028875 5.3419422333344
P P P LNCV6_134504_PI430048170 mRNA
CCTAAAATATGTAGCTTTGTAAACAGTTTTATATCCTGCATCTTAGGGGGGAAAATCAGT NM_004175RefSeq chr22
+ 24555649 24574964 SNRPD3 6634 "small nuclear ribonucleoprotein D3 polypeptide 18kDa,
transcript variant 1"
GO:0005515|GO:0008380|GO:0006369|GO:0010467|GO:0006366|GO:0031124|GO:0071013|GO:0005829|GO:0005
737|GO:0005683|GO:0030532|GO:0005681|GO:0005687|GO:0005685|GO:0070062|GO:0008334|GO:0034660|GO:0
000387|GO:0034709|GO:0000398|GO:0005654|GO:0034715|GO:0019899|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133226_PI430048170 0.00890423496806187 0.5106252638224244.39698522577836
4.69555004563916 4.9030041953624 P P P 5.36307783871261 5.70999485305775
5.83530694936711 P P P LNCV6_133226_PI430048170 mRNA
GCCCTCTGGACTTTAGTAGGCTTTGGTAAATGTGAGAAAACTTTTGTAGAATTATCATAT NM_022495RefSeq chr14
+ 60091910 60134814 PCNXL464430 pecanex-like 4 (Drosophila) GO:0016021 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_100618_PI430048170 0.00631226544470015 0.65787796042016 4.39380732356427
4.38796686909125 4.6043746215816 P P P 5.20304182709748 5.08418721329097
4.90663994564766 P P P LNCV6_100618_PI430048170 mRNA
TGAGAATGTTACTCTGCACTGTGGCAACATCTCGGGACTGAGGGGCCAGGTGACCTGGTA NM_019086RefSeq chr12
- 118063592 118104005 VSIG10 54621 V-set and immunoglobulin domain containing 10 GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75103_PI430048170 0.3352024810771460.74157803850571 1.53777481494221 0.620628869632343
0.413966802684741 A A A 1.63886183171427 1.53569790383958 0.82516622767703 A A A
LNCV6_75103_PI430048170 mRNA
GCCATTGATAAATATACCTGCAAATCCTTGTCATCCTTTTCCTCCAGCGGAAGCCATACA NM_015398RefSeq chr4
+ 186144840 186172663 FAM149A 25854 "family with sequence similarity 149, member A, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129897_PI430048170 0.00654566279243341 0.5572515666488973.6418762621013
3.2437114991111 3.48865966967254 P P P 4.18797738597142 4.31767116014014
4.41785082752229 P P P LNCV6_129897_PI430048170 mRNA
GTAGGTGTATGGTCGATGGAAGTTTCTGGCATCCATGTTGGTAATAAAGAGATAAAACTG NM_152540RefSeq chr4
- 52872983 53366075 SCFD2 152579 sec1 family domain containing 2
GO:0008150|GO:0003674|GO:0005575|GO:0015031|GO:0006904 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_107326_PI430048170 0.0110922965039112 1.61017636755928 5.77370100642881
5.81843100877852 5.73882204941547 P P P 5.18079075495986 5.16210104844865
4.91224722399429 P P P LNCV6_107326_PI430048170 mRNA
ACCATGGCCATCCTCCTGCATGAGATCCCCCATGAGGTGGGCGACTTTGCCATCCTGCTC NM_152264RefSeq chr11
+ 47408494 47416500 SLC39A13 91252 "solute carrier family 39 (zinc transporter), member 13,
transcript variant 2"
GO:0071577|GO:0048471|GO:0030173|GO:0005794|GO:0005385|GO:0061448|GO:0006882|GO:0016021|GO:0042
803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130698_PI430048170 0.2396028911580790.6101312330578450.405154082761665
2.05689105088952 1.88495335778101 A A A 2.5107746942466 2.46321329522993
1.93728148475477 P P A LNCV6_130698_PI430048170 mRNA
GGTGAAGAGCTTCAGTGAAACATTTAAAGAGTATATTGTGTGTTGTTTTGCTGTTCATCA NM_012290RefSeq chr2
- 170990822 171160900 TLK1 9874 "tousled-like kinase 1, transcript variant 1"

GO:0035556|GO:0007049|GO:0004674|GO:0006468|GO:0005634|GO:0006886|GO:0005524|GO:0001672|GO:0006974|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138572_PI430048170 0.5131696892850070.9643028317060041 4.5910828326626 14.5114980804494 14.4437616028947 P P P 14.455604313934 14.644955262437 14.6001657409448 P P P LNCV6_138572_PI430048170 mRNA
CCACCCCAGGATCCTAAATCATGACTTACCTGCTAATAAAAACTCATTGGAAAAGTGAGA NM_001863RefSeq chr19 + 35648222 35658784 COX6B1 1340 cytochrome c oxidase subunit VIb polypeptide 1 (ubiquitous)
GO:0022904|GO:0005739|GO:0005758|GO:0021762|GO:0004129|GO:0005743|GO:0044281|GO:0055085|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139082_PI430048170 0.1607732164773320.96137648310789 0.277461256456069 0.3336993747356470.31842664107389 A A A 0.4190679837256990.332606700390259 0.347487854675238A A A LNCV6_139082_PI430048170 mRNA
CAGAAGTGAAAAGTGCCATGAGGAAGCTTTGGAGCAAGAAATTGATCACAGATGACAAAA NM_001004701 RefSeq chr11 + 55572127 55573060 OR4C16NA "olfactory receptor, family 4, subfamily C, member 16 (gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129258_PI430048170 0.3605931824782790.8709371091376727.01106444909928 7.06732822756236 7.16743286542779 P P P 7.07289665716699 7.14973882229103 7.57372203403466 P P P LNCV6_129258_PI430048170 mRNA
GCTTCTGTATGCTAAGAAAATAGGTGTGAAAAACTGGTGTTCTGAAATAGCCTAACATTT NM_018137RefSeq chr1 + 107056644 107059296 PRMT6 55170 protein arginine methyltransferase 6
GO:0005515|GO:0070611|GO:0019919|GO:0070612|GO:0016571|GO:0006325|GO:0035241|GO:0005634|GO:0006351|GO:0042054|GO:0005829|GO:0035242|GO:0042393|GO:0044020|GO:0043985|GO:0006284|GO:0016032|GO:0005654|GO:0045892|GO:0034970 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127065_PI430048170 0.00473355393998787 0.3093651585390261 0.6046787760748 10.729344724548 10.698986899293 P P P 12.0821546976656 12.428443708052 12.5617513838452 P P P LNCV6_127065_PI430048170 mRNA
GCTGTACCCTCTGCCGATGGCATTTGTGTTTTTGATATTTGTGTCTGTTACTACTTTTTT NM_002616RefSeq chr17 - 8140469 8152435 PER1 5187 period circadian clock 1
GO:0005634|GO:0051591|GO:0000989|GO:0005737|GO:0046329|GO:0009649|GO:0045944|GO:1900744|GO:0004871|GO:0019900|GO:0043153|GO:0031625|GO:0043124|GO:0070932|GO:0042634|GO:0070888|GO:0000122|GO:0000978|GO:2000323|GO:0006351|GO:0031490|GO:0032922|GO:0007165|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144249_PI430048170 0.1010472372359581.64415273916894 3.19330440795784 3.26294756600315 2.57217525648971 P P A 2.51121065726782 1.75905972196321 2.56881827691305 A A P LNCV6_144249_PI430048170 mRNA
TATTGTCATGGTTTATAAACAATAAACTGTGATGCCAGGCACATCTCTGCCTTCCCTGAG NM_001256599 RefSeq chr1 + 155173786 155184971 TRIM46 80128 "tripartite motif containing 46, transcript variant 2"
GO:0005622|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135901_PI430048170 0.0656173750681354 1.26796027958375 0.815505068439844 1.1306726108875 0.861421448351056A A A 0.6577139290502390.56553023845039 0.575529848172003A A A LNCV6_135901_PI430048170 mRNA
GGCAACTTCTAACGGTGGCATTTCTGAATCATAGACACTTTTTTGACTTCTACATATTTTNM_153337RefSeq chr16 - 50666299 50681353 SNX20 124460 "sorting nexin 20, transcript variant 2"
GO:0005515|GO:0005886|GO:0005634|GO:0035091|GO:0015031|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129882_PI430048170 0.0121356057611653 1.48573495596643 7.79376228145 7.91433051302949 8.08309801541674 P P P 7.29971844366093 7.2226065554892 7.54947524292951 P P P LNCV6_129882_PI430048170 mRNA
ACACCCGTGGAGAGAGAGGAAGAGTATACAGTCCTGTTTGAATCATTTGGAGGATTTTTT NM_001083965 RefSeq

chr1 - 151773479 151790534 TDRKH 11022 "tudor and KH domain containing, transcript variant 1"
GO:0009566|GO:0005739|GO:0010467|GO:0003723|GO:0034587|GO:0071546|GO:0031047|GO:0007283|GO:0071
547|GO:0030154|GO:0043046|GO:0007140 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131688_PI430048170 0.3751808071154971.25300174934951 0.445673916552517
0.3552744560791661.14750458084908 A A A 0.2626276086724490.567494176868471
0.256128775557761 A A A LNCV6_131688_PI430048170 mRNA
ATTCAAAGAAATACGTTTTCAGTTTCTCATGGGAACAATGCTGCTTGGGAATGTGTGTGA NM_001031834 RefSeq
chrX + 102937271 102938300 RAB40AL 282808 "RAB40A, member RAS oncogene family-like"
GO:0009306|GO:0016567|GO:0005886|GO:0003924|GO:0005525|GO:0072659|GO:0006886|GO:0006904|GO:0005
739|GO:0006184|GO:0005737|GO:0017157|GO:0032482|GO:0019003|GO:0010008 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127230_PI430048170 0.00114692894692303 1.48014622312346 9.39512458186121
9.51001434519313 9.33887529794871 P P P 8.92304991450303 8.84853645958801
8.77680810632881 P P P LNCV6_127230_PI430048170 mRNA
ATGCTTTTCTCAAACTTTCCTGATCCTGAAGGCAAGCTAAACCAGTTCCGGAAGAACCTG NM_001136152 RefSeq
chr3 + 130081830 130098390 ALG1L2 NA "ALG1, chitobiosyldiphosphodolichol beta-
mannosyltransferase-like 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144965_PI430048170 0.0301482594828655 0.9526803551276980.407330088457473
0.3663371365900750.358377299732632 A A A 0.4473891167799460.458075022553134
0.436789216579182 A A A LNCV6_144965_PI430048170 mRNA
CCATGCTGAATCCTATACTCTATAGCTTGAGAAATAAGGATGTAAAAGCTGCTGTAAAAT NM_001001961 RefSeq
chr9 - 104535769 104536813 OR13C3 NA "olfactory receptor, family 13, subfamily C, member 3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132539_PI430048170 0.0175200709476331 0.7166827539312557.87221027048727
7.86982144878989 8.15557056089071 P P P 8.57559905850833 8.33861665434183
8.43436808821459 P P P LNCV6_132539_PI430048170 mRNA
GTGTTTGAGGTTCTTTGGTTTTGTTAGTAAAAGCCAGTTCTGTGGTGATGACCTATGGAA NM_018697 RefSeq chr7
+ 55365447 55433742 LANCL2 55915 LanC lantibiotic synthetase component C-like 2 (bacterial)
GO:0009789|GO:0005886|GO:0070273|GO:0005634|GO:0032266|GO:0003824|GO:0005525|GO:0005524|GO:0005
829|GO:0005737|GO:0008152|GO:0030864|GO:0010314|GO:0045892 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134977_PI430048170 0.000130028150338966 1.92906686660242 11.8102762643751
11.8059360172007 11.6754574559194 P P P 10.909466860898 10.7581442197351
10.7796852979472 P P P LNCV6_134977_PI430048170 mRNA
ATACCCAGGCTTGTCTGGAAGGAGAAGGCCTTTGCTGCCTGAAAGTCTCATGTTAAAAAA NM_016086 RefSeq chr7
- 75996336 76048003 STYXL1 51657 serine/threonine/tyrosine interacting-like 1
GO:0035556|GO:0006470|GO:0008138 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99000_PI430048170 0.5107615841047231.40409152560086 2.83677563260557 2.64085276009408
1.3242693232738 A A A 1.18402093516749 2.10304218310004 2.24650786133522 A A A
LNCV6_99000_PI430048170 mRNA
TCGGACTGGAATGATGAATGGGACAATCTTATCAAAATGGCTTCCACAGACACACCCATG NM_001270508 RefSeq
chr6 + 137867187 137883314 TNFAIP3 7128 "tumor necrosis factor, alpha-induced protein 3,
transcript variant 1"
GO:0005515|GO:0043130|GO:0016579|GO:0004842|GO:0070301|GO:0004843|GO:0032715|GO:0016874|GO:0032
691|GO:0002020|GO:0043621|GO:0005764|GO:0051259|GO:0061043|GO:0070536|GO:0006508|GO:0031397|GO:0
070062|GO:0043124|GO:0045824|GO:0071108|GO:0005813|GO:0070433|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_83853_PI430048170 0.7029372161453750.8430923817824630.2573385576280811.15577491777394
1.27232394319805 A A A 1.34262443233624 1.64875395318544 0.326220990488955 A A A

LNCV6_83853_PI430048170 mRNA
GGCAAACACAAGAGACATTCAAGTTAAAGCACGGTGCTTGACAATACTATATTGAATGCA NM_033208RefSeq chr16
- 3298807 3305439 TIGD7 91151 tigger transposable element derived 7 GO:0005634|GO:0003677
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142140_PI430048170 0.0117858783897061 0.3780470220436074.01470982266742
3.87604358308727 4.50098726349968 P P P 5.4495871250043 5.64071042856991
5.58187232713999 P P P LNCV6_142140_PI430048170 mRNA
TAAATGTTCAGCTAAATCTCAGATATACTGTGGGATGAGTATCTCAGGGTAAGTAACAAA NM_152729RefSeq chr6
+ 116100835 116245690 NT5DC1 221294 5'-nucleotidase domain containing 1
GO:0016311|GO:0008253|GO:0046872 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_133961_PI430048170 0.170567303388996 0.446920577429364 1.59961820485148
0.353413990821912 0.947006773350873 A A A 1.0120632543767 2.63843989150306
2.51350796855221 A P P LNCV6_133961_PI430048170 mRNA
TATGCCGGTTGAGAGAACTAAAATGGTTATAGTATTGTTTATCAGAAAGAGGAAGTGTAC NM_004775 RefSeq
chr18 - 31622245 31684723 B4GALT6 9331 "UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase,
polypeptide 6"
GO:0005975|GO:0044281|GO:0008378|GO:0046872|GO:0042339|GO:0000139|GO:0018146|GO:0032580|GO:0009
405|GO:0016021|GO:0030203|GO:0044267|GO:0018279|GO:0043687 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_41248_PI430048170 0.00339818116005141 0.562608525196407 9.43407175151849
9.62047574216319 9.3134411732809 P P P 10.1966229441284 10.3607622387825
10.3118010009783 P P P LNCV6_41248_PI430048170 mRNA
CAGAGCTGGAATTGTGTGGGGTTTAGTGCTAAATACTTCAATAAAGTCTGTTTTTTGTGA NM_001142569 RefSeq
chr1 + 200894820 200915736 C1orf106 55765 "chromosome 1 open reading frame 106,
transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137982_PI430048170 0.305475324200227 1.0350336137859 0.523953981302585
0.61149441219098 0.49183873342755 A A A 0.494186365395188 0.4896144349604
0.497117119245393 A A A LNCV6_137982_PI430048170 mRNA
TTCTGAGGATTCCTCTTCATGCTGCCAGCATTCTAGCTGCCAGCCGACTTGCTGCACCTC NM_198694 RefSeq
chr21 - 44579454 44580604 KRTAP10-5 NA keratin associated protein 10-5 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134523_PI430048170 0.116779095855008 1.10390007525221 0.692451748693702
0.854160726209695 0.682496591273034 A A A 0.571105604841924 0.631146976502636
0.604916286662849 A A A LNCV6_134523_PI430048170 mRNA
AGTCACGCCGTGGGATGTCTCTGTCCACATTAAACTAACAGCATTAATGCAGTCAAAAAA NM_005211 RefSeq
chr5 - 150053290 150113372 CSF1R 1436 "colony stimulating factor 1 receptor, transcript variant 1"
GO:0008284|GO:0071902|GO:0005886|GO:0008283|GO:0061098|GO:0008360|GO:0019221|GO:0045124|GO:2000
147|GO:0042803|GO:0031529|GO:2000249|GO:0046777|GO:0006954|GO:0030225|GO:0030224|GO:0070374|GO:0
060603|GO:0090197|GO:0030097|GO:0038145|GO:0030335|GO:0036006|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135288_PI430048170 0.039196473093652 1.64172222830069 4.28771201021947
4.51511633542018 4.35938646200044 P P P 3.98805142809727 3.39373860156958
3.57883001389937 P P P LNCV6_135288_PI430048170 mRNA
AGGGAGCTCTTCAGTCTCCATCTGCTCAGAAAAGAGGCCTCAGCCCATCACCTTCTCCTG NM_017561 RefSeq
chr9 - 94318195 94328644 NUTM2F NA NUT family member 2F NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_135210_PI430048170 0.449554918385313 0.756499741452169 2.87954391138748
1.96082564376588 2.65882351270251 A A A 3.48728629703054 2.82338116798411

2.30130912787837 P P A LNCV6_135210_PI430048170 mRNA
CTTTCTCTCCCGGGTGATAGGCATTAACTAAAATTAAATAAAAATTCAGATCATCCTTGC NM_001099667 RefSeq
chr10 + 122454662 122457352 ARMS2 NA age-related maculopathy susceptibility 2 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140856_PI430048170 0.605630435320216 1.05469899349018 9.08196558737807
9.3134411732809 9.2424174018571 P P P 8.86963877093836 9.303648038479 9.2085714356105 P
P P LNCV6_140856_PI430048170 mRNA
AGGGGCAAAACTCTCCTCGTGGGTCTTCATACCTAATAAAAGTCGGCATCAAACCACAAA NM_014771 RefSeq
chr16 + 30761611 30776307 RNF40 9810 "ring finger protein 40, E3 ubiquitin protein ligase,
transcript variant 1"
GO:0005515|GO:0043005|GO:0006511|GO:0004842|GO:0033523|GO:0033503|GO:0016874|GO:0000151|GO:0005
634|GO:0032403|GO:0042803|GO:0016020|GO:0005654|GO:0008270|GO:0017075|GO:0010390|GO:0031625 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137961_PI430048170 0.346256974794854 0.628730610719255 2.71055931112614
1.31517009654507 0.408418401685252 A A A 3.14393177090606 1.98115694829315
1.88452759155552 P A A LNCV6_137961_PI430048170 mRNA
GAGGAGCAAAGCAGGAGGTCTTGGGCTAAAAATCTTTTTTACCAAAAATAAATCTAAGTC NM_001184739 RefSeq
chr14 + 24205719 24208248 TSSK4 283629 "testis-specific serine kinase 4, transcript variant 1"
GO:0005515|GO:0032793|GO:0000287|GO:0004674|GO:0007275|GO:0006468|GO:0009966|GO:0007283|GO:0005
524|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64654_PI430048170 0.309363533315377 0.715621317952703 1.17926251163917
2.28977708076726 2.6827347862586 A A A 2.52059284734313 2.68373492566132
2.76688501431756 A A P LNCV6_64654_PI430048170 mRNA
TACAGTTTTGAGAAAGAAGAATCAGAACCCTGACCCACTTACGGTTGCTGGGACAATTCC NM_014686 RefSeq
chr19_KI270866v1_alt + 705 4760 KIAA0355 9710 KIAA0355 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_137249_PI430048170 0.0637056298250582 0.23654887443105 1.68838113553112
3.37315521210409 3.72608334252141 A P P 5.03633364664696 5.30301890147313
5.36017854277044 P P P LNCV6_137249_PI430048170 mRNA
CCATTAGTCAGAGTTGTTTTTTAACATGCCAGAGAAAAAGTTGTAATGCCTTGGAAGTTA NM_001112706 RefSeq
chr7 + 12570576 12653603 SCIN 85477 "scinderin, transcript variant 1"
GO:0008285|GO:0043065|GO:0051047|GO:0005509|GO:0005546|GO:0003779|GO:0032330|GO:0051693|GO:0045
010|GO:0051014|GO:0005545|GO:0043234|GO:0045654|GO:0005737|GO:0051015|GO:0017156|GO:0001786|GO:0
005856|GO:0005938|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104923_PI430048170 0.0291667459665633 0.3466139057110975.74383595909225
5.04309897441234 4.80652839893464 P P P 6.80504587953019 6.72962987436202
6.81396251055906 P P P LNCV6_104923_PI430048170 mRNA
AAGAGAATGGTCATCCCGAACCAACCCCCTCTAACAGCAACCAAGAAGTCTACATTGAAA NM_005578RefSeq chr3
+ 188212932 188890671 LPP 4026 "LIM domain containing preferred translocation partner in lipoma,
transcript variant 1"
GO:0005515|GO:0008150|GO:0005737|GO:0005886|GO:0008270|GO:0005634|GO:0007155|GO:0005925 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72722_PI430048170 0.4905664477298730.94734925875826 7.3811299106949 7.3021770656109
7.46415430792144 P P P 7.31409981041284 7.45339466066376 7.60402967454205 P P P
LNCV6_72722_PI430048170 mRNA
AAGTGGTAAACGAGTATGTGTTTCGAGAGACGGTGAATAAAAAAGAAGGCCTGTGTGTGCNM_152396RefSeq chr3
- 15409759 15427547 METTL6 131965 "methyltransferase like 6, transcript variant 1"
GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145333_PI430048170 0.3881983231270620.6979272482216640.261400731139907

0.2735482244075150.349098003207242A A A 1.46465554753457 0.341598681219772
0.318826151736373A A A LNCV6_145333_PI430048170 mRNA
CAAAACCAAGAGAATCATTCATGAAGAATGACTATACCATGCCTGGTTCTGATGCTCGTT NM_152315RefSeq chr11
- 114521714 114559895 NXPE1 120400 "neurexophilin and PC-esterase domain family, member 1"
GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_5643_PI430048170 4.33083194764558e-05 1.76790165148835 11.5704349428654
11.5434451337864 11.5051392475929 P P P 10.7372342429254 10.6629110292911
10.7519356424144 P P P LNCV6_5643_PI430048170 mRNA
TTTGGACTGTGACCATGTACCTTCCTTTTTAAGAAAAATAAACTGCTTTATGGAAGTTGG NM_015227RefSeq chr21
- 45263927 45287896 POFUT223275 "protein O-fucosyltransferase 2, transcript variant 1"
GO:0010468|GO:0005794|GO:0001707|GO:0051046|GO:0006493|GO:0046922|GO:0005789|GO:0010717|GO:0006
004|GO:0036066|GO:0044267|GO:0043687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131494_PI430048170 0.7810143272377541.02452838160379 0.869784697139604
0.9028516849190790.907754671424587A A A 1.25800115001509 0.608867737649232
0.607046501555254A A A LNCV6_131494_PI430048170 mRNA
GTTTTTAACATAATTTTTGTTTTATCCACAACTTTTCAAGTATTGAAAGTAGAATAAAAANM_004079RefSeq chr1 -
150730195 150765957 CTSS 1520 "cathepsin S, transcript variant 1"
GO:0002474|GO:0097067|GO:0005518|GO:0005764|GO:0005615|GO:0043231|GO:0019886|GO:0006955|GO:0022
617|GO:0019882|GO:0030198|GO:0051603|GO:0036021|GO:0030574|GO:0006508|GO:0001968|GO:0034769|GO:0
043202|GO:0002480|GO:0042590|GO:0043394|GO:0005576|GO:0002224|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_113044_PI430048170 0.13470344645855 1.32518193279275 6.65793405867686
6.61121850885081 6.46747168024759 P P P 5.81983586661498 6.45003702240924
6.18658688724909 P P P LNCV6_113044_PI430048170 mRNA
TTCTTTACATTTTTCCAAGGAAAGGAAAACGGAAGCAGGGTTCTTGCCTGGTAGCTCCAG NM_130468RefSeq chr15
+ 40470960 40473158 CHST14 113189 carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14
GO:0005975|GO:0001537|GO:0044281|GO:0050655|GO:0016051|GO:0030208|GO:0000139|GO:0042301|GO:0009
405|GO:0016021|GO:0030204|GO:0030203|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136060_PI430048170 0.0352715785747349 0.6218822839290963.72874917636539
3.48026917262625 3.70416888499902 P P P 4.57463883513402 4.33632076413298 4.0173055140122
P P P LNCV6_136060_PI430048170 mRNA
GACTTTTGGGGTTTGTGCAAGGCACAGTTTTAAGCACATAATGTAATTCTAAAAGATGAA NM_001205301 RefSeq
chr5 + 38258408 38465480 EGFLAM 133584 "EGF-like, fibronectin type III and laminin G domains,
transcript variant 5"
GO:0019800|GO:0030054|GO:0030198|GO:0010811|GO:0045202|GO:0005539|GO:0005614|GO:0005604 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135159_PI430048170 0.6499223408244971.2743094366527 1.67139422926876
0.4148629226167950.323514782899991A A A 0.3135378833095141.00604770761381
0.35231698752645 A A A LNCV6_135159_PI430048170 mRNA
GCCAAGAAGTAGAAGATATATTCTCTAGCCTTAGTTTTTCCTCCCAATTTGCATTTTTGTNM_152866RefSeq chr11 +
60455808 60470752 MS4A1 931 "membrane-spanning 4-domains, subfamily A, member 1, transcript variant
1" GO:0005154|GO:0042100|GO:0005887|GO:0006959|GO:0023026|GO:0005615|GO:0009897|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62176_PI430048170 0.0201246330432389 1.30084365458146 9.3881425646913
9.48060206974249 9.39435704316298 P P P 9.15473972892925 9.05106833588496
8.91044411202631 P P P LNCV6_62176_PI430048170 mRNA
TAGACTAACGCTGTTTACACCCTTGTTCTGTCAAAGCAATTAAAGATCACTTGTGTTGAG NM_002435RefSeq chr15
+ 74890010 74899457 MPI 4351 "mannose phosphate isomerase, transcript variant 1"
GO:0009298|GO:0008270|GO:0006488|GO:0044267|GO:0070062|GO:0043687|GO:0018279|GO:0005829|GO:0004

476. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134660_PI430048170 0.3370195998198260.9666747671029290.420481952964147
0.4451070870879890.316835656775568A A A 0.4168044395797880.475495663877189
0.439395124968664A A A LNCV6_134660_PI430048170 mRNA
GGTCAAAATCTGGTTCCAGAATCGCAGGACCAAGTGGAAGAAGCAGAACCCGGGTGCCGA NM_001146340
RefSeq chr10 - 124447428 124449981 NKX1-2 390010 NK1 homeobox 2
GO:0043565|GO:0006355|GO:0007275|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132233_PI430048170 0.0391773207787984 1.27883307906391 10.4635860168556
10.3400368212803 10.5178196200406 P P P 9.91718045337659 10.0930291619344
10.2349771164485 P P P LNCV6_132233_PI430048170 mRNA
GCTCCTACTGTGATAAGTGTATCCCAGATCCACAATGTAAATATATGTGATTTGTAAGAA NM_005701RefSeq chr15
- 75598082 75626105 SNUPN 10073 "snurportin 1, transcript variant 1"
GO:0000339|GO:0010467|GO:0005643|GO:0008565|GO:0034660|GO:0006606|GO:0000387|GO:0061015|GO:0070
062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131458_PI430048170 0.1940000486127180.9048660975271630.403211540682369
0.3090231768398140.309877220480678A A A 0.4600722078684720.621702601054081
0.363150513778073A A A LNCV6_131458_PI430048170 mRNA
AGGTACCTTGAAGAGGAAGGCACAGAAACAGCTCAAATGCTCACAGTTACACTGAGATAA NM_001195280
RefSeq chr7 + 16526879 16581489 LRRC72 100506049 leucine rich repeat containing 72 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129977_PI430048170 0.1493774138194630.6650881539073913.6433581110254
12.8940553607465 12.699311882908 P P P 13.8216180469042 13.7258676982932
13.6276161470548 P P P LNCV6_129977_PI430048170 mRNA
CAGCCCCCTTCTCCCACAAATAAAGCCCAATAAAGCCTGAGAAGTGAGGAAAGCCATATT NM_001282474 RefSeq
chr14 - 23559562 23567836 AP1G2 8906 "adaptor-related protein complex 1, gamma 2 subunit,
transcript variant 3"
GO:0030133|GO:0005515|GO:0005794|GO:0016020|GO:0030121|GO:0008565|GO:0005798|GO:0016032|GO:0016
192|GO:0006886|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145726_PI430048170 0.0523482895443235 1.0909941063183 0.487137467211042
0.3660270931787080.413417706130832A A A 0.2681665109232910.352681097199326
0.269763807162118A A A LNCV6_145726_PI430048170 mRNA
GCAGAACACCCTTTCTGGGATTTCTTTGTCACTATCTGGATAATAGATATTTGCTTTTAA NM_001127698 RefSeq
chr5 + 148063971 148137362 SPINK5 11005 "serine peptidase inhibitor, Kazal type 5, transcript variant
1"
GO:0035315|GO:0048471|GO:0097209|GO:0042640|GO:0004867|GO:0005783|GO:0005576|GO:0005829|GO:0009
913|GO:0010951|GO:0005737|GO:0050777|GO:0030198|GO:0016525|GO:0030855|GO:0045580|GO:0005789|GO:0
005938|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143591_PI430048170 0.1016454648130540.9007573660257051 2.3113340435209
12.2643611286636 12.1270849367144 P P P 12.3248828267281 12.4707008122603 12.361844877401
P P P LNCV6_143591_PI430048170 mRNA
GCTATTCATCACTGTAATTATTATTATTTTCTACAATAAATGGGACCTGTGCACAGGAGG NM_001305RefSeq chr7
+ 73830862 73832693 CLDN4 1364 claudin 4
GO:0007565|GO:0005886|GO:0061436|GO:0016328|GO:0016327|GO:0042802|GO:0007165|GO:0016324|GO:0009
925|GO:0016338|GO:0005198|GO:0005887|GO:0032570|GO:0005923|GO:0004888. NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136968_PI430048170 0.000511185683574467 2.94703926204228 1.81096627299189
2.10403461285264 2.13035625755624 A A A 0.2806222783979720.42140195564657
0.660922990003429A A A LNCV6_136968_PI430048170 mRNA
CTCACCACTTACCCGGGATAGTAAACATGATACACATCAATAAAGGCAGACTTTATTGTG NM_178468RefSeq chr20

- 35285730 35292422 FAM83C 128876 "family with sequence similarity 83, member C" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_126901_PI430048170 0.1274246058096810.54368525105224 1.66154759012382
1.12677500058271 1.62931612689901 A A A 2.85620402654813 1.65879484209142
2.35805266193737 P A A LNCV6_126901_PI430048170 mRNA
GCTACCCACCTGTGTTTCTTAGCATTTCAGGAATTAAACCACATTCAGAACCCCAAAAAA NM_005226RefSeq chr9
+ 88991408 89005154 S1PR3 1903 sphingosine-1-phosphate receptor 3
GO:0008284|GO:0005886|GO:0004930|GO:0003376|GO:0001816|GO:0038036|GO:0007193|GO:0007204|GO:0009
653|GO:0008289|GO:0005178|GO:0006954|GO:0007186|GO:0005887|GO:0032651 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143352_PI430048170 0.0136259310972451 0.4189413016605496.03944130027527
5.80343521836112 6.29368223245766 P P P 6.90905083594871 7.25877172594745
7.67409502569237 P P P LNCV6_143352_PI430048170 mRNA
GTGGGATAAAAGTTATCTTCCCCTTGGAAAGACTAATGAGCACAATGATATTAATCACTT NM_032804RefSeq chr10
+ 62804755 62808479 ADO 84890 2-aminoethanethiol (cysteamine) dioxygenase
GO:0005739|GO:0047800|GO:0046872|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129863_PI430048170 0.8222918138900741.01435237203173 0.689895053173512
0.5287209980090530.601279889029487A A A 0.4380369412758570.564274261511828
0.743964272702131A A A LNCV6_129863_PI430048170 mRNA
CAGTTACATATTAGCCTCCTCAAGTGTCAGACATTATTACTCATAGTATCAGAAAACATG NM_025052RefSeq chr2
- 134964490 135024678 MAP3K19 80122 "mitogen-activated protein kinase kinase kinase 19, transcript
variant 1"
GO:0035556|GO:0005737|GO:0000186|GO:0030036|GO:0000165|GO:0006468|GO:0005524|GO:0004709 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140408_PI430048170 0.00105586629657678 0.3367909649576274.72945578995523
4.35772875325623 4.76507667101286 P P P 6.30830814308845 6.02189057196516
6.25083831280913 P P P LNCV6_140408_PI430048170 mRNA
CCCACATTTGTATGCCTTAGGTCTTCTTAAAATGGTATCTGTAAACATGTGTCCAATATA NM_001122964 RefSeq
chr2 - 55547291 55617725 SMEK2 57223 "SMEK homolog 2, suppressor of mek1 (Dictyostelium),
transcript variant 1" GO:0030289|GO:0005737|GO:0006470|GO:0005815|GO:0045722|GO:0005654|GO:0019216
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130570_PI430048170 0.1615297317924370.7574680161780523.98397465382057
4.25158541939254 4.44840224119138 P P P 4.34852787419624 4.55016692346782
4.95696726761789 P P P LNCV6_130570_PI430048170 mRNA
GTGTATGAGTTTCAGTAGAACTGTACCATCAACAATGTTTCCATAAATATGCAGAGTTCT NM_022350RefSeq chr5
+ 96875939 96919702 ERAP2 64167 "endoplasmic reticulum aminopeptidase 2, transcript variant 1"
GO:0002474|GO:0019885|GO:0004177|GO:0008217|GO:0006508|GO:0005789|GO:0005788|GO:0008270|GO:0016
021|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145433_PI430048170 0.3679456692030610.9603692309353641 1.5867558315488
11.4232790315914 11.4689203741491 P P P 11.6037822576511 11.5524736192645 11.500848766111
P P P LNCV6_145433_PI430048170 mRNA
ACTACTGGTCCAGCTGCCCTGGGCTCCTTTTCTATATTAATAAAGAAACGAGTAAAAATT NM_022060RefSeq chr14
+ 22598237 22612359 ABHD4 63874 abhydrolase domain containing 4 GO:0016042|GO:0016787 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142282_PI430048170 0.0547671588409654 1.65820390262484 3.80022053037533
4.37955766025043 3.88721086543727 P P P 3.68331187149388 3.16882658560895
3.00677588050242 P P P LNCV6_142282_PI430048170 mRNA
ACATTTAATGAAACTGAGAGACAGAGGCTTGTTTGCTTTGCCCTCTTTTCCTGGTCACCC NM_001014796 RefSeq
chr1 + 162632437 162780457 DDR2 4921 "discoidin domain receptor tyrosine kinase 2, transcript

variant 1"
GO:0005515|GO:0003416|GO:0005886|GO:0005518|GO:0048146|GO:0035988|GO:0010715|GO:0051091|GO:0016324|GO:0010763|GO:0046777|GO:0030198|GO:0030199|GO:0045860|GO:0090091|GO:0007155|GO:0070062|GO:0030500|GO:0018108|GO:0038063|GO:0005524|GO:0031214|GO:0038062|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127729_PI430048170 0.4579497971003590.8710250591732785.80029703367164 5.47479591497493 5.42232552130217 P P P 6.06467185407487 5.77068520974152 5.41745058537217 P P P LNCV6_127729_PI430048170 mRNA
TGTCAACAGAGCTACAGAAAAGTCAGTAAAGACCAATGGACCCAGAAAACAAAAACAGCC NM_006607RefSeq chr4 + 37960434 37961010 PTTG2 10744 pituitary tumor-transforming 2
GO:0003674|GO:0051276|GO:0017124|GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133735_PI430048170 0.8742614811192130.9947326191372280.356152601621394 0.3392194204237431.14242073574639 A A A 0.4591105176825480.848512310791018 0.68025233282888 A A A LNCV6_133735_PI430048170 mRNA
GAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTGAGAACAAACATTA NM_016509RefSeq chr12 - 9993060 9999300 CLEC1B 51266 "C-type lectin domain family 1, member B, transcript variant 1"
GO:0005515|GO:0005887|GO:0030246|GO:0006952|GO:0030220|GO:0007166|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54825_PI430048170 0.0124627841098555 1.54629263491033 8.61144475353277 8.94406964669643 8.86731436899734 P P P 8.34967628920882 8.19788258771704 7.98658377144569 P P P LNCV6_54825_PI430048170 mRNA
ATATTATCAAGCTAGAAAATAACCAGTTTGTGGCGGCGGATCTCCTCCTCCTTTCCAGCA NM_020452RefSeq chr1 + 154327799 154351304 ATP8B2 57198 "ATPase, aminophospholipid transporter, class I, type 8B, member 2, transcript variant 1"
GO:0034220|GO:0005794|GO:0000287|GO:0005886|GO:0008152|GO:0004012|GO:0007030|GO:0016021|GO:0055085|GO:0005524|GO:0045332 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133228_PI430048170 0.00335712699191904 1.85290258659776 11.2819872894174 11.4756357451826 11.5670841441275 P P P 10.7139396281664 10.3487008637293 10.5837746374969 P P P LNCV6_133228_PI430048170 mRNA
GAATGGTATCAATTCCCCTGTTTCTCTTGTAGCCAGTTACTAGAATAAAATCATCTACTT NM_001136134 RefSeq chr19 + 55385931 55392083 RPL28 6158 "ribosomal protein L28, transcript variant 1"
GO:0005515|GO:0010467|GO:0003735|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0006415|GO:0006412|GO:0044297|GO:0030425|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0000184|GO:0016020|GO:0016032|GO:0022625|GO:0044267|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89796_PI430048170 0.0968091899712680.7202848989645572.83447253323619 3.33806361271039 3.27482804086353 A P P 3.51459695606259 3.43205895586696 3.92198434672363 P P P LNCV6_89796_PI430048170 mRNA
CATCTAACACTAGCTATCTCTTGCTAGATCTCCTTGCTCAGCATATAACTATAAATACAT NM_001130105 RefSeq chr5 - 75371102 75511981 COL4A3BP 10087 "collagen, type IV, alpha 3 (Goodpasture antigen) binding protein, transcript variant 3"
GO:0005515|GO:0034976|GO:0048471|GO:0008283|GO:0006672|GO:0070273|GO:0044281|GO:0005829|GO:0005739|GO:0006955|GO:0006936|GO:0006665|GO:0035621|GO:0005794|GO:0035620|GO:0030148|GO:0055088|GO:0001701|GO:0000902|GO:0007165|GO:0003007|GO:0004672|GO:0070584|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142127_PI430048170 0.1130906110325320.4481874764719082.10519279622307 0.3794346527419580.948091703090915 A A A 2.3424326194348 2.71033437368707 2.37593832687035 A P P LNCV6_142127_PI430048170 mRNA
CCCCCTGGGCATACATAAATCGACACATGCCAAGTCCTTTTTTAAAAATGACATATTTGG NM_145276RefSeq chr19

- 12317489 12333720 ZNF563 147837 zinc finger protein 563
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140440_PI430048170 0.1110080133361050.8819543368540591 0.1052112556979
10.1521990767349 9.97733385657724 P P P 10.2298721744549 10.3888275867886
10.1554042008532 P P P LNCV6_140440_PI430048170 mRNA
CACACCTGGGGAGTAGGCCAAGAAGGAAAATCTGACGAATAAAGACCCCCGCTGCCCCAT NM_016381 RefSeq
chr3 + 48465519 48467645 TREX1 11277 "three prime repair exonuclease 1, transcript variant 1"
GO:0032407|GO:0032558|GO:0008408|GO:0032479|GO:0032405|GO:0090305|GO:0035458|GO:0005634|GO:0005
635|GO:0042803|GO:0046872|GO:0005829|GO:0003690|GO:0003697|GO:0032481|GO:0006298|GO:0008296|GO:0
005730|GO:0006310|GO:0006259|GO:0006260|GO:0006281|GO:0008853|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_63310_PI430048170 0.0317649990457733 4.62121372048478 3.64199502886905
3.94078356262698 3.82899522199955 P P P 0.581286001005405 2.03671273350732
1.80756210566798 A A A LNCV6_63310_PI430048170 mRNA
TTTAAGAGCAAAGGCAACTACGACGAGGGGTTTGGCCGCAAGCAGCACAAGGAGCTCTGG NM_030576 RefSeq
chr17 - 63695888 63700159 LIMD2 80774 LIM domain containing 2 GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138743_PI430048170 0.7840567189982690.9737752016499 9.25491164617828
9.10860364601736 9.14473063066097 P P P 9.06483090430386 9.14685243513283
9.39484643332156 P P P LNCV6_138743_PI430048170 mRNA
AAGAGAATAGATGCAAACAAGGCATGCATTTGGCCAAAATAAACAAATGCTGGTCTGTCC NM_020371 RefSeq chr15
- 33866226 34039102 AVEN 57099 "apoptosis, caspase activation inhibitor"
GO:0005622|GO:0005515|GO:0043066|GO:0016020|GO:0006915|GO:0012505 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129773_PI430048170 0.0157655552558644 1.83163516368049 6.09922018477033
5.72011864342515 6.09241532791323 P P P 5.1696664954223 5.08630687854585
5.06589825400206 P P P LNCV6_129773_PI430048170 mRNA
GTACAAGAAAATCATTAAGGAACATTTGGAGAGTTAGCTACTAGCTGCCTAAGTGTGCAC NM_002620 RefSeq chr4
+ 73853295 73854481 PF4V1 5197 platelet factor 4 variant 1
GO:0008009|GO:0006955|GO:0070098|GO:0006954|GO:0007186|GO:0060326|GO:0042127|GO:0032496|GO:0045
236|GO:0008201|GO:0005615|GO:0002690 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138490_PI430048170 0.9145515179132411.21057507382362 1.61081980935648
1.75674898033155 3.35277328236843 A A P 2.2453229468966 1.79242379779133
2.47201013001825 A A A LNCV6_138490_PI430048170 mRNA
ACTCTTAATGTAATGAGAGGGAAAGCCTTTAGCCATGGCACATTTTTACTGTTGTCACTA NM_001033719 RefSeq
chr19 - 43872362 43880136 ZNF404 342908 zinc finger protein 404
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144739_PI430048170 0.3879200247380690.3876885503788170.440950072510516
0.4757104341160930.452657280734969 A A A 0.5138067058376 0.551663499254157
2.94951311345129 A A P LNCV6_144739_PI430048170 mRNA
GCTGGTATAGAGAAGGTACTCAAAAAATCCTTAATGAATAAAGTAATGGATCGTACCCAA NM_145010 RefSeq chr10
- 24981978 25016156 ENKUR 219670 "enkurin, TRPC channel interacting protein, transcript variant 1"
GO:0005516|GO:0017124|GO:0031514 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134862_PI430048170 0.6156273112652190.910421958634111 0.299291105458398
0.2838459424214410.468646740326942 A A A 0.8371462774943330.258121749516623
0.294393389193704 A A A LNCV6_134862_PI430048170 mRNA
GACTCATGATGCTGGATATGAAGAACTATTGACTTCTTGGGAAAAAACGGAGAAATATTA NM_139249 RefSeq chr11

+ 60334881 60340968 MS4A6E 245802 "membrane-spanning 4-domains, subfamily A, member 6E"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130377_PI430048170 0.4158904948706760.6426699436537770.546630440539836
0.3649079949492050.274537856863201A A A 1.80683937562525 0.307100369474492
0.50876617157076 A A A LNCV6_130377_PI430048170 mRNA
GGGACTTAAACTGCTGAATTCACCTGTGGATGTTTTTGAGTAAATAAAAGCTAATAGCTA NM_001302678 RefSeq
chr1 - 111499428 111504121 ADORA3 140 "adenosine A3 receptor, transcript variant B"
GO:0005886|GO:0008016|GO:0009611|GO:0014068|GO:0042629|GO:0070257|GO:0050850|GO:0043306|GO:0001
609|GO:0007165|GO:0007190|GO:0006954|GO:0001973|GO:0002553|GO:0005887|GO:0050729|GO:0002687 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144552_PI430048170 0.0143732553875639 0.6439807668226676.66267354939301
6.64339647389807 6.91165866951703 P P P 7.40598853176528 7.3424252588296 7.3891049974346
P P P LNCV6_144552_PI430048170 mRNA
GCCCAGATCCCAGTTATCCTTGTATCCATGTAATTTCAGATGAATTATTAAGCAAACATT NM_013254RefSeq chr12
+ 64452059 64502119 TBK1 29110 TANK-binding kinase 1
GO:0051219|GO:0005515|GO:0034142|GO:0050830|GO:0007249|GO:0005829|GO:0002756|GO:0051607|GO:0005
737|GO:0033138|GO:0006954|GO:0045944|GO:0016032|GO:0032606|GO:0032481|GO:0043123|GO:0032480|GO:0
034138|GO:0032728|GO:0032727|GO:0009615|GO:0003676|GO:0002224|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127194_PI430048170 0.00100740939930195 0.7516272910550465.11208935987151
5.00110864573156 5.07139979078284 P P P 5.41261303174776 5.53344888114605
5.47391573337901 P P P LNCV6_127194_PI430048170 mRNA
CCACCATATTTGGCCTTACAGGAATTAAGGAGACTTCCTGTAATATTTCTTTCCAATAAA NM_004724RefSeq chr11
- 113733182 113773763 ZW10 9183 zw10 kinetochore protein
GO:0005828|GO:0005515|GO:0007093|GO:0005783|GO:0007096|GO:0034501|GO:0000132|GO:0005634|GO:0015
031|GO:0005829|GO:0005737|GO:0007030|GO:0019237|GO:0006888|GO:0000922|GO:0000070|GO:0006461|GO:0
007126|GO:0016020|GO:0005789|GO:0000777|GO:0000776|GO:0007080|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134013_PI430048170 0.1537201695755750.55139202842985 1.68752150054494
3.02565648430363 2.21519849839433 A P A 3.82148318186303 2.76377659316826
3.01837224946882 P P P LNCV6_134013_PI430048170 mRNA
GTGGGATGTGGTATATTCTGTGTCAACTTCAAGATAATCACTCATTTTCTCGTTATATTCNM_198551RefSeq chr1 +
222618101 222668012 MIA3 375056 "melanoma inhibitory activity family, member 3, transcript variant 1"
GO:0005515|GO:0030336|GO:0030501|GO:0006887|GO:0015031|GO:0043231|GO:0007162|GO:0002063|GO:0016
020|GO:0030199|GO:0002687|GO:0042060|GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138023_PI430048170 0.1440169451616051.05138362977698 0.435815963347422
0.4479402438750910.466558909599725A A A 0.3239158358850320.3722151511745
0.435316376352913A A A LNCV6_138023_PI430048170 mRNA
ACCACCTGAGTCTAACCAGCGTATAATGCAATAACAGGTAGAGTAGAACTGCTTTTGGCG NM_016564RefSeq chr11
- 787109 790126 CEND1 51286 cell cycle exit and neuronal differentiation 1
GO:0021933|GO:0021702|GO:0021686|GO:0021941|GO:0007628|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132194_PI430048170 0.0451778432842149 1.14614599908829 8.71188483818915
8.76615457646967 8.80666061904293 P P P 8.45768443559331 8.62473734487066
8.60768477859749 P P P LNCV6_132194_PI430048170 mRNA
CCCTCTTTCAGCTTCTATGTGGTGTTGGAGGTGCTGGTATCGTGTTCACACAAGAAAAAA NM_015690RefSeq chr2
+ 218672025 218702717 STK36 27148 "serine/threonine kinase 36, transcript variant 1"
GO:0005515|GO:0000287|GO:0003351|GO:0005634|GO:0007228|GO:0009791|GO:0005524|GO:0051090|GO:0045

880|GO:0042384|GO:0005737|GO:0004674|GO:0007420|GO:0006468|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133000_PI430048170 0.0214899886072951 0.1473658163117641.03504906305038 2.6380920687137 1.98931033994277 A A A 4.64905465326136 4.95955858769513 4.74873224958369 P P P LNCV6_133000_PI430048170 mRNA AGAATTCAGTGCTCTTTCATTTGTTAATGCTGTCCAGATTTTTCACACAGTTATACTCAGNM_001098402 RefSeq chr21 - 41986830 42010387 ZBTB21 49854 "zinc finger and BTB domain containing 21, transcript variant 1" GO:0005515|GO:0008327|GO:0006355|GO:0005634|GO:0045892|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134855_PI430048170 0.2232960091633951.33446745984972 3.22720314764188 3.97725679439402 3.80821032397404 P P P 3.37188172532891 3.08579531055322 3.38880733856435 P P P LNCV6_134855_PI430048170 mRNA CTGGCTATCTCTGAGTCCTATAAACAAAGATTTTAATTGAATGTTCCATCAATACCTCTC NM_001170633 RefSeq chr12 - 64266982 64390565 C12orf56 115749 "chromosome 12 open reading frame 56, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145049_PI430048170 0.3170586400687711.04839317316872 0.490063643611432 0.3187418976721330.404129445676042A A A 0.2857693515965690.351705285860916 0.374539674033247A A A LNCV6_145049_PI430048170 mRNA CCACTGAATGTGTGTATGTATGTACACACACACACACGTGTGCACACACAATGCACACAA NM_004319RefSeq chr1 - 176861063 177164904 ASTN1 460 "astrotactin 1, transcript variant 1" GO:0007626|GO:0016021|GO:0005575|GO:0001764|GO:0009897|GO:0007158|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142156_PI430048170 0.6734862743605840.9687114519906590.562313748079484 0.5435755635243630.302959963368175A A A 0.3993112996432890.616338247617376 0.536700143701688A A A LNCV6_142156_PI430048170 mRNA CCTGTTGTGCAATTTATCCATCAGAAATCTCTAGTTATCGAGTTACGGATGGAAAAATAA NM_023013RefSeq chr1 + 12791396 12796628 PRAMEF1 65121 "PRAME family member 1, transcript variant 1" GO:0043066|GO:0008284|GO:0048387|GO:0045596|GO:0042974|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131334_PI430048170 0.4531395153357 1.73394670416868 2.28948909162264 0.5305002896762360.526226764769234A A A 0.5945249821541020.745125297471332 0.375158642859897A A A LNCV6_131334_PI430048170 mRNA ATGGGGGAGGGGTTATTGTAGAATCACATGTATTTTTAAAGTATATATGTCATGAGGCCA NM_032184RefSeq chr1 - 85157672 85201045 SYDE2 84144 "synapse defective 1, Rho GTPase, homolog 2 (C. elegans)" GO:0051056|GO:0007264|GO:0032862|GO:0005100|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134406_PI430048170 0.000878023917058453 0.2661234332301278.11948613202785 8.4855023010108 8.63662866830044 P P P 10.1429649716517 10.2080008415465 10.620134428388 P P P LNCV6_134406_PI430048170 mRNA ACAATCACCCCCCTTTTCTAAGACTGCCTGATCCGAAATAAAGTATTTTGACAGAAAAAA NM_032607RefSeq chr19 + 4153600 4173054 CREB3L3 84699 "cAMP responsive element binding protein 3-like 3, transcript variant 1" GO:0005515|GO:0000977|GO:0035497|GO:0005783|GO:0045944|GO:0005789|GO:0005634|GO:0016021|GO:0001228|GO:0006351|GO:0030968 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103132_PI430048170 0.5530944147797280.9004371665365315.09758137220145 4.85158248692027 4.55243281684293 P P P 5.14252174486001 5.16160542923001 4.64576303751518 P P P LNCV6_103132_PI430048170 mRNA AGTAGTCTGTAGCTTGAGCAATCTCCCTTGTCCTCCTTCAAATAAATGCTTTGTGCGCAG NM_003571RefSeq chr3 + 133399994 133475212 BFSP2 8419 "beaded filament structural protein 2, phakinin"

GO:0005882|GO:0005737|GO:0005212|GO:0005886|GO:0070307|GO:0045104|GO:0005200|GO:0048469|GO:0007601|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142610_PI430048170 0.298259235675627 1.14550212680036 5.36203685160417 5.54529416133046 5.32839063828741 P P P 5.40972334003947 5.28691151156764 4.91626141841229 P P P LNCV6_142610_PI430048170 mRNA
TATTTTTGAACTCCTTGTTTCTGCGCTGTCCTTCTTAGCCCAGGACATTCAGGGTGCTTT NM_001017921 RefSeq chr19 + 5904840 5910252 VMAC 400673 vimentin-type intermediate filament associated coiled-coil protein
GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143199_PI430048170 0.0628900160001005 1.09500111115294 0.633420980088611 0.707209507412589 0.670397732770536 A A A 0.619408315081619 0.493413696827003 0.502909838070154 A A A LNCV6_143199_PI430048170 mRNA
CGTCAATAAATCTACCTTTACTGATATATCTGGTTGAGGGAATATCAGACTCCAGATTTC NM_001290259 RefSeq chr6 + 63635801 63715522 PHF3 23469 "PHD finger protein 3, transcript variant 2"
GO:0003674|GO:0008270|GO:0007275|GO:0005634|GO:0005575|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137731_PI430048170 0.530265353600457 0.930914384962223 15.0500057685567 15.0776476062286 15.3212657096649 P P P 15.1252748880393 15.1431183049289 15.4780459421099 P P P LNCV6_137731_PI430048170 mRNA
TCCCTCTCTACTCTTGACAGCAGGATTGGATGTTGTGTATTGTGGTTTATTTTATTTTCT NM_001271969 RefSeq chr6 + 44246957 44253888 HSP90AB1 3326 "heat shock protein 90kDa alpha (cytosolic), class B member 1, transcript variant 1"
GO:0005515|GO:0006986|GO:0009651|GO:0033160|GO:0031526|GO:0034605|GO:0060334|GO:0043524|GO:0060338|GO:0007411|GO:0006457|GO:0071353|GO:0017098|GO:0070062|GO:0042470|GO:0030911|GO:0019901|GO:0009986|GO:0032564|GO:0001890|GO:0002135|GO:0002134|GO:0044325|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108452_PI430048170 0.125509092216495 1.17566825494029 9.49145202479736 9.47433537936614 9.19559559763728 P P P 9.1440602671176 9.26782930721289 9.06013603576725 P P P LNCV6_108452_PI430048170 mRNA
TGAAATTCTGCCTCTGAGAAGCTAACAGTCTTCCTGTGGTCGCCACTCCTCCCCAGCAGC NM_001082575 RefSeq chr17 - 79089344 79516148 RBFOX3 146713 "RNA binding protein, fox-1 homolog (C. elegans) 3"
GO:0008380|GO:0006397|GO:0005737|GO:0000166|GO:0000381|GO:0003723|GO:0043204|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129867_PI430048170 0.0649847674059834 0.860128859320318 14.3550174575644 14.2161403144614 14.2089220812709 P P P 14.5722864264299 14.3469323116233 14.5084866325922 P P P LNCV6_129867_PI430048170 mRNA
ACTGCTTACACTGCACTCTGACCCTGTAGTACAGCAATAACCGTCTAATAAAGAGCCTAC NM_006623 RefSeq chr1 + 119711795 119744226 PHGDH 26227 phosphoglycerate dehydrogenase
GO:0010468|GO:0021510|GO:0019530|GO:0008652|GO:0009055|GO:0044281|GO:0070314|GO:0031175|GO:0005829|GO:0034641|GO:0004617|GO:0051287|GO:0021782|GO:0007420|GO:0021915|GO:0006544|GO:0006564|GO:0006566|GO:0070062|GO:0055114|GO:0006541|GO:0009448 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144323_PI430048170 0.275448262312249 1.9126683997125 2.06108924211125 1.4804485929291 0.259837470876095 A A A 0.848419500869562 0.311727872404888 0.292713597452412 A A A LNCV6_144323_PI430048170 mRNA
GTCAACACAGGACTTTCTGGATCATTCCAGAAAGTGTCAGACGTTTTCTCATTGTCTTGT NM_032551 RefSeq chr19 + 917341 921015 KISS1R 84634 KISS1 receptor
GO:0005515|GO:0008285|GO:0019722|GO:0005886|GO:0009986|GO:0008188|GO:0000186|GO:0007186|GO:0042923|GO:0007218|GO:0050806|GO:0051496|GO:0046887|GO:0016021|GO:0050482 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_133014_PI430048170 0.1004062482625781.09774058559002 13.2288079954774 13.137802293176
13.0545833760083 P P P 12.9471745013908 13.0516396341757 13.0220351918645 P P P
LNCV6_133014_PI430048170 mRNA
AGAGATTGCAAGGGCGGGGAGAGGAGGCTCTCAATAAATAATCGTGTAACCTTCAAAAAA NM_002004RefSeq
chr1 + 155308747 155320666 FDPS 2224 "farnesyl diphosphate synthase, transcript variant 1"
GO:0005739|GO:0006695|GO:0005737|GO:0045337|GO:0004337|GO:0016032|GO:0004161|GO:0033384|GO:0005
654|GO:0044281|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141690_PI430048170 0.00934823477556734 1.15554937627111 10.8697502359632
10.7929023820924 10.7862645899163 P P P 10.6347186481907 10.6470053394782
10.5406280668217 P P P LNCV6_141690_PI430048170 mRNA
CTCTGGGGGTTTCTATCACTGTGACAACACTAAGATAATAAACCAAAACACTACCTGAAT NM_004761RefSeq chr6
- 33291653 33299388 RGL2 5863 "ral guanine nucleotide dissociation stimulator-like 2, transcript
variant 1" GO:0005622|GO:0032320|GO:0007265|GO:0005575|GO:0005088 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_74085_PI430048170 0.9506230736432350.9911540945918654.91085591881356 4.34479181383237
4.44021682511836 P P P 5.03291668459411 4.56677020859187 4.0282858009902 P P P
LNCV6_74085_PI430048170 mRNA
CCTGGCCCCTGAAGACTTTAAAAAATTCAAAAAGCCTTTGCTCCCTCAATTACGAAGATG NM_001297435 RefSeq
chr4 - 1639880 1684127 FAM53A NA "family with sequence similarity 53, member A, transcript
variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132216_PI430048170 0.0220473962013030.6738146416083928.43185957327106
8.59122822995602 8.70838970411702 P P P 8.90699303333828 9.22189347012073
9.29579426074599 P P P LNCV6_132216_PI430048170 mRNA
AATAGGACCAGAGCGGTATCTCTGGCACCACACTAGGGACTATCAGGTAATAAAAGCTTT NM_002836RefSeq chr20
+ 2864194 3038669 PTPRA 5786 "protein tyrosine phosphatase, receptor type, A, transcript variant
1"
GO:0043235|GO:0008286|GO:0005515|GO:0005886|GO:0007411|GO:0005887|GO:0005001|GO:0006468|GO:0035
335|GO:0004725|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102013_PI430048170 0.9549212783200320.9969292299712160.281161878281102
0.53239875545359 0.369956465397951A A A 0.5056943237352570.396907318711247
0.298082060815188A A A LNCV6_102013_PI430048170 mRNA
CCTGGATCGCATTACTACCGTTGAACACTTACTCAAGTCAGTCTTGCTGTACAATATCAA NM_001288825 RefSeq
chr5 - 132861180 132866884 GDF9 2661 "growth differentiation factor 9, transcript variant 3"
GO:0008284|GO:0030308|GO:0010862|GO:0001555|GO:0042981|GO:0007292|GO:0030509|GO:0060395|GO:0005
125|GO:0005160|GO:0005615|GO:0005737|GO:2000870|GO:0043408|GO:0007179|GO:0048468|GO:0008083 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144349_PI430048170 0.4377649437340591.04852030467045 0.3079292914726
0.3148230036270740.514119734662955A A A 0.3199447770361740.282924338684807
0.338040519826959A A A LNCV6_144349_PI430048170 mRNA
CAGACAGCCTTTAATCCATTCAGCTTAGGTTTTCTTCTTCTGAGAATCTTTTAATGTCAT NM_001304964 RefSeq chr12
+ 75334638 75370389 GLIPR1L1 256710 "GLI pathogenesis-related 1 like 1, transcript variant 1"
GO:0001669|GO:0097224|GO:0005576|GO:0007339 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132150_PI430048170 0.142902813321967 1.09374570871939 0.508853876412058
0.6541205088691070.606128228145993A A A 0.3556603136669430.475628818274807
0.547296157239046A A A LNCV6_132150_PI430048170 mRNA
GATCTGAAGAAGGCACAGGTGCAAGTAAAATTCGTCAATTAAACCACTATTTTGATTACA NM_053006RefSeq chr22
+ 19130807 19132623 TSSK2 23617 testis-specific serine kinase 2
GO:0005515|GO:0005737|GO:0046777|GO:0000287|GO:0001669|GO:0005814|GO:0004674|GO:0007286|GO:0007
275|GO:0006468|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_143452_PI430048170 0.0292880167403583 2.14563906572374 2.77615649981289
3.48184637196145 3.29687326943404 A P P 2.10448097801865 2.21517540326338
2.01298151958737 A A A LNCV6_143452_PI430048170 mRNA
TTCTCTTTCAGCATTGAGAGTATTATGCAAGGGGTCAGGGGAGCGGGTACAGGGGCTGCG NM_199244 RefSeq chr9
+ 65737145 65738396 FOXD4L4 NA forkhead box D4-like 4 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_64656_PI430048170 0.5452754108744650.9840405971065713.8516607243858 13.8029454344239
13.7737990887644 P P P 13.7804037480256 13.8667991775879 13.850455787409 P P P
LNCV6_64656_PI430048170 mRNA
CCATGTTCACGTTGTTCACATCCCATGTAGAAAAATAAAGATGCCACGGAGGAGGTTGTA NM_001289789 RefSeq
chr19_KI270866v1_alt + 13931 30733 GPI 2821 "glucose-6-phosphate isomerase, transcript variant 3"
GO:0043005|GO:0019242|GO:0005886|GO:0046185|GO:0006094|GO:0004347|GO:0044281|GO:0005615|GO:0006
096|GO:0005829|GO:0005737|GO:0043524|GO:0006959|GO:0007611|GO:0016866|GO:0006006|GO:0043154|GO:0
051156|GO:0070062|GO:0005975|GO:0001525|GO:0005125|GO:0007599|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144672_PI430048170 0.0340379372318546 0.5709130627270962.11360243834808
2.42272085954153 2.75738206160361 A A A 3.10964113045458 3.58966269052548
3.02587195159777 P P P LNCV6_144672_PI430048170 mRNA
GTTTCCTCCCAATATTCCTTCTCAAACTTGGAGAGGGAAAATTAAGCTATACTTTTAAGA NM_183058 RefSeq chr10
- 30611778 30629718 LYZL2 119180 lysozyme-like 2 GO:0008152|GO:0003796|GO:0005576 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_137588_PI430048170 0.4232751155068751.14071338199897 6.40364070555973
5.87591489994304 6.00399310101703 P P P 6.16470573963254 5.73103286247111
5.83557106077436 P P P LNCV6_137588_PI430048170 mRNA
CGCACAAGTCAAACGCTAGGAAGTTTGAATAAAACCAATTTTTCTAACTTGTTGCTCATT NM_014943 RefSeq chr8
+ 122781661 122974515 ZHX2 22882 zinc fingers and homeoboxes 2
GO:0005515|GO:0003700|GO:0046982|GO:0005886|GO:0003714|GO:0005634|GO:0000122|GO:0006402|GO:0003
677|GO:0046872|GO:0006351|GO:0042803|GO:0005737|GO:0045665|GO:0005654|GO:0045892|GO:0035019 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138549_PI430048170 0.4202950751106580.3733395032126870.376412455218129
0.3567713587721870.260164798543391 A A A 0.3336980105420272.92401742093894
0.339215847148626 A P A LNCV6_138549_PI430048170 mRNA
GGCATCTAGCTTATGAGGCCAAATAATCCCAAAGTGTCACTTTATATAAATGTCTTGATT NM_020169 RefSeq chr3
- 158666413 158672693 LXN 56925 latexin
GO:0010951|GO:0005737|GO:0006954|GO:0008191|GO:0050965|GO:0008201|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134687_PI430048170 0.0567269838169269 0.8505968715157431 0.7729455977946
10.744140347708 10.6620335153013 P P P 10.9081591585146 11.0909436048923
10.8730418552118 P P P LNCV6_134687_PI430048170 mRNA
CATCATCTGTGGACACTGGAGTCTGGAATAAATGCTGTTTGTCACATCAACACCAAAAAA NM_001013257 RefSeq
chr19 + 44809058 44821421 BCAM 4059 "basal cell adhesion molecule (Lutheran blood group),
transcript variant 2"
GO:0007165|GO:0007160|GO:0005886|GO:0005887|GO:0043236|GO:0005055|GO:0007155|GO:0009897|GO:0070
062|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132391_PI430048170 0.1748274350599580.8994075540203529.13620070188488
8.98072515487839 8.8898533519294 P P P 9.03992619280312 9.22644848048814
9.20303046907856 P P P LNCV6_132391_PI430048170 mRNA
CTGGCTCAAGAATTACTCCGAAGTCAGTCTGCAGAAAATAAATATTTAGTATGACATGAC NM_001289174 RefSeq
chr6_GL000256v2_alt - 4698975 4720646 VPS52 6293 "vacuolar protein sorting 52 homolog (S.

cerevisiae), transcript variant 2"
GO:0019905|GO:0005515|GO:0048471|GO:0005794|GO:0010668|GO:0015031|GO:0048611|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142306_PI430048170 0.137114236664915 0.803297955373291 7.77282128414512 7.40237627370894 7.66034537818992 P P P 7.68197919160873 7.98178464489922 8.11138644605687 P P P LNCV6_142306_PI430048170 mRNA
CCAAAACTTGACAGATGTGGGAAATCTTCATATAGTGTATGAAAATTTCATTGTACAGGG NM_014240 RefSeq chr3 + 45594830 45681263 LIMD1 8994 LIM domains containing 1
GO:0005515|GO:0008360|GO:2000637|GO:0005634|GO:0016442|GO:0005737|GO:0005912|GO:0000932|GO:0007010|GO:0090090|GO:0001666|GO:0006355|GO:0033962|GO:0003714|GO:0007275|GO:0006351|GO:0007165|GO:0016310|GO:0035331|GO:0045668|GO:0002076|GO:0016477|GO:0035195|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60172_PI430048170 0.0567749340919309 0.766967132201698 5.84647451116212 5.78502160609578 6.1419770641975 P P P 6.40104384292882 6.40338552739737 6.12585168012647 P P P LNCV6_60172_PI430048170 mRNA
GCACTTTTTGACTGTAGATTGTTCGAAGACACATTTGTAAATTTTCAAGCAGCAATAGAG NM_001040443 RefSeq chr13 + 49495664 49528981 PHF11 51131 "PHD finger protein 11, transcript variant 1"
GO:0006355|GO:0008270|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122108_PI430048170 5.43473253716486e-05 0.574290476085917 4.26443559395075 4.35807714386017 4.34956048778847 P P P 5.16356689371963 5.12135758588235 5.08845329322096 P P P LNCV6_122108_PI430048170 mRNA
ATGCTCATGATGCAGCAGGATCCCAAATCAGTTAGGCTTCCAGTCTCTCAAAATGTCCAT NM_014071 RefSeq chr20 - 34714773 34825630 NCOA6 23054 "nuclear receptor coactivator 6, transcript variant 1"
GO:0005515|GO:0006367|GO:0005634|GO:0044281|GO:0043231|GO:0046966|GO:0007507|GO:0046965|GO:0030374|GO:0045944|GO:0060716|GO:0030099|GO:0009725|GO:0044255|GO:0006352|GO:0005667|GO:0003713|GO:0030331|GO:0006310|GO:0006974|GO:0006260|GO:0035097|GO:0006281|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130815_PI430048170 0.319660077621455 0.767411754029956 4.556715514443 4.36102904610138 5.22701335904851 P P P 4.73603295110327 5.07272008736874 5.52186417036724 P P P LNCV6_130815_PI430048170 mRNA
GGAGATCTCTAAGTGTAGCTGTAAATTTTGGGGTTAATTTGGCTTATATTGGACCTTTTA NM_001195098 RefSeq chr3 - 15667235 15798184 ANKRD28 23243 "ankyrin repeat domain 28, transcript variant 2"
GO:0005515|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99264_PI430048170 0.404524060072576 1.10296469021967 6.09342897384871 5.77180715756501 5.98963844346894 P P P 5.63115139139242 6.04407742032513 5.74165758034267 P P P LNCV6_99264_PI430048170 mRNA
AATCTCAGCACCCACCTGCTTATCCTCTATGGTGTCCAGGGACTGCTGACCTTCGGGTAC NM_001282291 RefSeq chr7 + 151028421 151047782 ABCB8 11194 "ATP-binding cassette, sub-family B (MDR/TAP), member 8, transcript variant 1"
GO:0005215|GO:0005730|GO:0005743|GO:0042626|GO:0005634|GO:0005740|GO:0055085|GO:0005524|GO:0005739|GO:0016020|GO:0008152|GO:0006810|GO:0016021|GO:0043190 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139629_PI430048170 0.103093436405156 0.661212954959227 1.05579977489135 1.75158176281205 1.78304302947851 A A A 2.01181405572674 2.3472399181454 2.11105101572813 A A A LNCV6_139629_PI430048170 mRNA
ATGAGCTTGGGCCTTGAAAGGCACCAGCTTGAGAGACATTAAAATGTTCTAAGTAAAAAA NM_001514 RefSeq chr1 - 88852637 88891618 GTF2B 2959 general transcription factor IIB
GO:0005515|GO:0010467|GO:0006355|GO:0006368|GO:0006367|GO:0006366|GO:0005730|GO:0001047|GO:0005634|GO:0046966|GO:0017025|GO:0016032|GO:0005654|GO:0008270|GO:0008134 . NA - . NA NA NA

NA NA NA NA NA NA
LNCV6_126882_PI430048170 0.4842850009512760.8123344443848653.37106366142231
0.2616800113806810.360959212882774P A A 1.30145546666176 2.41740621719228
2.99758606601174 A P P LNCV6_126882_PI430048170 mRNA
ACTGCACCTGTCAGATTTTCATCTCTTATAGTTCTCACATTTCAAATGTGCATGTTATGG NM_024949RefSeq chr4 +
183099309 183320776 WWC2 80014 WW and C2 domain containing 2
GO:0046621|GO:0035331|GO:0032947|GO:0000122|GO:0019900|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131534_PI430048170 0.36421448445605 1.55037505061264 0.359174435914595
1.66141115298188 0.402609950740911A A A 0.3003103108257860.292748144837703
0.337894307045304A A A LNCV6_131534_PI430048170 mRNA
GCTTTGTCAGTTATATACAGTATAAAGTTGCTATGCACAGAGCTTTTTGTAAAGACAGCT NM_022659RefSeq chr8
- 25841729 26045124 EBF2 64641 early B-cell factor 2
GO:0050873|GO:0001709|GO:0045944|GO:0003682|GO:0046983|GO:0005634|GO:0060612|GO:0035563|GO:0003
677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137641_PI430048170 0.5669453152239810.9009098101900444.54788934490136
4.15248563931161 4.29728656574602 P P P 4.80865027552398 4.41381384560172
4.18484017575519 P P P LNCV6_137641_PI430048170 mRNA
CCCCTTCCTTTTTGACTCATAAATTGGTCATCTTAACCATTTAAGTGTACACTTCTATAG NM_001260506 RefSeq chr11
+ 75399490 75406913 RPS3 6188 "ribosomal protein S3, transcript variant 3"
GO:0005515|GO:0003906|GO:0010467|GO:2001235|GO:0045738|GO:0019058|GO:0005743|GO:0005634|GO:0003
729|GO:0006412|GO:0006413|GO:0071159|GO:0005829|GO:0006414|GO:0005737|GO:0051092|GO:0002181|GO:0
000184|GO:0008534|GO:0016032|GO:0051018|GO:0070062|GO:0003735|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144670_PI430048170 0.00974721522625316 0.4582989574100366.79623584961101
6.34981725807438 6.68856961361421 P P P 7.43859878738471 7.67659981201722
8.06323489279671 P P P LNCV6_144670_PI430048170 mRNA
GCTGTTTCAATGTGGCATTATTGTTGTGGCTTAATACTACTACCTAAATGAGGTTTATAC NM_003298RefSeq chr3
+ 14947583 15049279 NR2C2 7182 "nuclear receptor subfamily 2, group C, member 2, transcript variant
1"
GO:0005515|GO:0010467|GO:0051321|GO:0006355|GO:0003700|GO:0006367|GO:0046982|GO:0003713|GO:0003
707|GO:0021549|GO:0007283|GO:0030154|GO:0007399|GO:0043565|GO:0048520|GO:0045944|GO:0043401|GO:0
040019|GO:0004872|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140508_PI430048170 0.88869921753706 0.8132643688425820.4445647707307462.1291469849995
0.419353621395142A A A 2.59627190665173 0.4105797248038610.400961385862293A A A
LNCV6_140508_PI430048170 mRNA
TTATCTGTCTATGCAACTGACCATGTCATTCCACCTGCTTTAAAATTTCTTCCACCATCA NM_153212RefSeq chr1 +
34759740 34763724 GJB4 127534 "gap junction protein, beta 4, 30.3kDa"
GO:0007608|GO:0007154|GO:0042048|GO:0005922|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131850_PI430048170 0.76044952487772 1.25956386577296 2.66275083254254
0.4853278961183351.30760872937844 A A A 2.28096180556099 0.405290077186667
0.940885631859168A A A LNCV6_131850_PI430048170 mRNA
CAGAGGGCAGGGATAGAAAAGGAAGGCAACTGCTTCAAATAAAATTCCTCCACGGCATTA NM_030785RefSeq
chr19 - 45795709 45815347 RSPH6A81492 radial spoke head 6 homolog A (Chlamydomonas)
GO:0005622 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124591_PI430048170 0.8385380510332171.0102825109995 8.63774650188914
8.64953965810457 8.58831843336334 P P P 8.54337962383452 8.76873587371033
8.50568295583804 P P P LNCV6_124591_PI430048170 mRNA

AGTGTGGTTAGCTACACTCTGAAGGACATTCACGATGACCAGGACTATTTGCACTCTTTG NM_005803 RefSeq chr6_GL000256v2_alt - 2028519 2043472 FLOT1 10211 flotillin 1 GO:0005515|GO:0042470|GO:0005815|GO:0035023|GO:0034451|GO:0007409|GO:0002020|GO:0005765|GO:0016600|GO:0042383|GO:0035255|GO:0008180|GO:0016020|GO:0022617|GO:0005901|GO:0045121|GO:0016021|GO:0090002|GO:0005925|GO:0070062|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143028_PI430048170 0.0729684666662505 1.29262710953874 3.91178552174676 4.25630821493045 4.28405606210501 P P P 3.83872020472075 3.63786622480008 3.88202394331358 P P P LNCV6_143028_PI430048170 mRNA
CTCCTGTCGAGGGAGACAGACATATCCCCACTGAAAAATTAATAAAATTGGTTTTACATA NM_001010978 RefSeq chr1 - 54007297 54018186 LDLRAD1 388633 "low density lipoprotein receptor class A domain containing 1, transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143898_PI430048170 0.1815203716349790.9148788045806020.277465878715882 0.3538989556052440.27660861284399 A A A 0.4988034968683930.487660072849158 0.29935167862319 A A A LNCV6_143898_PI430048170 mRNA
GTGCATTAAATATGCTTCCACAGTAAAATCTGAAAAACTGATTTGTGATTGAAAGCTGCC NM_002354 RefSeq chr2 + 47369147 47387028 EPCAM 4072 epithelial cell adhesion molecule GO:0005515|GO:0001657|GO:0008284|GO:0005886|GO:0009986|GO:0023019|GO:2000648|GO:2000048|GO:0016328|GO:0032403|GO:0048863|GO:0016323|GO:0016324|GO:0045944|GO:0005923|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137143_PI430048170 0.0556640568676089 2.62530140488237 2.34497526765878 3.50318940228741 3.32904413821243 A P P 1.2536371693846 1.23867661554213 2.41627853967495 A A P LNCV6_137143_PI430048170 mRNA
AAAGAATCTCCTGAAAGCCTGTAAAAATGTCCATGCATGTTCTGTGAGTGATCTACCAAG NM_001144875 RefSeq chr5 - 177501904 177510426 DOK3 79930 "docking protein 3, transcript variant 2" GO:0005515|GO:0005737|GO:0005886|GO:0005158|GO:0007265 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137546_PI430048170 0.0542229604043343 0.5557526915601042.8267250403281 2.02002563952216 2.5777349591088 A A A 3.22245453317338 3.49707518796107 3.34788091074944 P P P LNCV6_137546_PI430048170 mRNA
CCATGAGACCACTGTTATCAAAACTTTCTTTTCTGGAATGTAATCAATGTTTCTTCTAGG NM_000575 RefSeq chr2 - 112773914 112785394 IL1A 3552 "interleukin 1, alpha" GO:0005515|GO:0008285|GO:0008283|GO:0019221|GO:0046330|GO:0050715|GO:0005615|GO:0035234|GO:0005829|GO:0034605|GO:0006955|GO:0006954|GO:0045944|GO:2001240|GO:0001660|GO:0070374|GO:0043123|GO:0005149|GO:0005507|GO:0006915|GO:0005576|GO:0002248|GO:0045840|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139658_PI430048170 0.0465756094774227 0.36133382642758 3.37768313048887 2.16122969565222 3.10981625423905 P A P 4.29161718636604 4.43753725738141 4.57187032925285 P P P LNCV6_139658_PI430048170 mRNA
GCATTGTGAGGAACTGTGCAAAGACATTTTTGTTACAAACCTGTGGGCCTGTTGCAATAC NM_001286431 RefSeq chr6 - 111299030 111483715 REV3L 5980 "REV3-like, polymerase (DNA directed), zeta, catalytic subunit, transcript variant 2" GO:0005515|GO:0042276|GO:0051539|GO:0003887|GO:0005730|GO:0005634|GO:0003677|GO:0046872|GO:0006261|GO:0006281|GO:0000166|GO:0005654|GO:0016035 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134695_PI430048170 0.7808618567586721.00445468000349 1.87555224078254 1.98436477188687 1.89016357369672 A A A 2.58951287084732 1.61567681266176 1.13704965919827 P A A LNCV6_134695_PI430048170 mRNA
CACAGATGTCTTCTTTCCATACAAGCATGTTAGTTCGCCCCAATATACATATATATATGA NM_001284217 RefSeq chr1 + 159800510 159816257 FCRL6 NA "Fc receptor-like 6, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_65854_PI430048170 0.0848782032532133 0.8042307013122789.98317295003079
10.2442099830561 10.3593928682567 P P P 10.4312693248905 10.4522280251052
10.6602648494371 P P P LNCV6_65854_PI430048170 mRNA
CCCACTGACCTTTTCTAAGAAAATTCTTGTGCCCGCATTGGTATTAAATCCTCGCATTCA NM_152516RefSeq chr2
+ 61905667 62136070 COMMD1 150684 copper metabolism (Murr1) domain containing 1
GO:0005515|GO:0070300|GO:0055070|GO:0005507|GO:0043325|GO:0080025|GO:0005547|GO:0005546|GO:0048
227|GO:0005634|GO:0032088|GO:0032434|GO:0006893|GO:0042803|GO:2000009|GO:0042802|GO:0005737|GO:0
031398|GO:0031462|GO:0005654|GO:0055037|GO:0005769|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_130404_PI430048170 0.3174636424289760.8625331843930199.51937989290377
9.40945942716616 9.49043819424118 P P P 9.42064187445889 9.94130789416146
9.65226159407305 P P P LNCV6_130404_PI430048170 mRNA
AACATATGATGAAAAGGTGGATTTGTGGTGCATTGGAGTGCTCTGCTATGAGCTGCTGGT NM_001015878 RefSeq
chr19 + 57231059 57235548 AURKC 6795 "aurora kinase C, transcript variant 1"
GO:0051256|GO:0000780|GO:0000793|GO:0051321|GO:0032467|GO:0035404|GO:0005819|GO:0030496|GO:0016
570|GO:0009966|GO:0051233|GO:0005524|GO:0035174|GO:0032133|GO:0000910|GO:0005737|GO:0004672|GO:0
031616|GO:0004712|GO:0005876|GO:0006468|GO:0008608 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_141070_PI430048170 0.1157070723559341.41744928406633 5.02038040858002
5.34253613804254 5.04863930027139 P P P 4.91904088052 4.71125957765614 4.20344054133245 P
P P LNCV6_141070_PI430048170 mRNA
AACAACGTTGTCTACAAGCAATACGAGGACATGGTGGTGGAGGCCTGCGGCTGCAGGTAG NM_182828RefSeq
chr2 + 20666663 20671490 GDF7 151449 growth differentiation factor 7
GO:0005515|GO:0060571|GO:0060395|GO:0005615|GO:0042803|GO:0048608|GO:0007411|GO:0030855|GO:0043
408|GO:0022612|GO:0048468|GO:0021509|GO:0010862|GO:0042981|GO:0030509|GO:0032924|GO:0005160|GO:0
005125|GO:0021527|GO:0048853|GO:0045165|GO:0045666|GO:2001051|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142170_PI430048170 0.4928344195594131.04441807515198 0.297404268094968
0.3070940920668340.514625589797342A A A 0.3230826159874660.282279582329502
0.335725056847703A A A LNCV6_142170_PI430048170 mRNA
CTCCAGAAGATTCCCTGATCCAATCTTTCCTTGGCACAAACTTTTAGTTATTGTGTTTACNM_001243308 RefSeq chr6
- 79803586 79870420 C6orf7 NA chromosome 6 open reading frame 7 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_145182_PI430048170 0.0276872036588814 0.6875736883031027.3996319760754
7.25274063983797 7.12063826794737 P P P 7.9987192276587 7.80180318841498
7.57645398721046 P P P LNCV6_145182_PI430048170 mRNA
CTATGGTTGCATTTCCGTTTTCTATGAATGAATTTGCATTCAATAAACAACCAGACTCAG NM_001040455 RefSeq
chr11 + 117179222 117197445 SIDT2 51092 "SID1 transmembrane family, member 2"
GO:0000902|GO:0051033|GO:0044342|GO:0003323|GO:0042593|GO:0016021|GO:0005765|GO:0033227|GO:0061
178|GO:0009749 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132167_PI430048170 0.5223833718420480.8706444794399054.51914106533147
4.04151825157904 3.88197273328789 P P P 4.52598573742595 4.57802220001657
3.93170495888249 P P P LNCV6_132167_PI430048170 mRNA
AGAAGGTGCTGCCCTCAGACAAGTTCAAGGACTACCTAGAGACCATGGAGCTCCTGGAGG NM_001271223
RefSeq chr1 + 228208129 228378874 OBSCN 84033 "obscurin, cytoskeletal calmodulin and titin-
interacting RhoGEF, transcript variant IC"
GO:0005515|GO:0051056|GO:0005516|GO:0048011|GO:0030018|GO:0043065|GO:0007264|GO:0045214|GO:0030
506|GO:0007275|GO:0030016|GO:0097190|GO:0031430|GO:0005524|GO:0046872|GO:0031432|GO:0005829|GO:0
032321|GO:0004674|GO:0006468|GO:0005089|GO:0008307 . NA - . NA NA NA NA NA NA NA NA

NA
LNCV6_113360_PI430048170 0.7199929913762821.09633906825935 4.34805757300729
3.68816506228223 4.42934212741607 P P P 4.02245126497408 4.08462090497449
4.06765950938426 P P P LNCV6_113360_PI430048170 mRNA
ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA NM_004988RefSeq chrX
+ 153179283 153183878 MAGEA1 4100 melanoma antigen family A1
GO:0005515|GO:0045746|GO:0005737|GO:0042826|GO:0005886|GO:0005634|GO:0000122|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145431_PI430048170 0.0981867815671708 0.6313308667269714.15215894117562
4.50846055712213 3.64004338355253 P P P 4.66201270959179 4.91119046587637
4.83566634292911 P P P LNCV6_145431_PI430048170 mRNA
AGGGGCTTCGAGGCTGGCCCTGCCAGGCAGTTTTCCCGGCGTTTTAGGATCTGTACATAG NM_001303013 RefSeq
chr1_KI270762v1_alt + 27504 56720 PLCH2 9651 "phospholipase C, eta 2, transcript variant 3"
GO:0005886|GO:0043647|GO:0005509|GO:0046488|GO:0005575|GO:0044281|GO:0016042|GO:0035556|GO:0003
674|GO:0008150|GO:0005737|GO:0004435|GO:0004871 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143020_PI430048170 0.13456582732824 0.84368495393283 8.01165412934288
7.95987957784256 7.78449896629259 P P P 8.33371688554874 7.97613008018717
8.16944786471092 P P P LNCV6_143020_PI430048170 mRNA
AGAGGGAGTGTGCGAATCAAGCCTGACCAAGAGGCTCCAGAATAAAGTATGATTTGTGTT NM_177528RefSeq chr16
- 28591942 28596480 SULT1A2 6799 "sulfotransferase family, cytosolic, 1A, phenol-preferring,
member 2, transcript variant 2"
GO:0047894|GO:0006805|GO:0050427|GO:0006584|GO:0004062|GO:0008146|GO:0051923|GO:0044281|GO:0018
958|GO:0009309|GO:0008202|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133444_PI430048170 0.1360665512233090.7279881613916757.65884127448849
7.40119127511518 7.32370257002748 P P P 7.51623096236864 8.11704408330089
8.07225169586044 P P P LNCV6_133444_PI430048170 mRNA
GTTTCTCAGAATCCAAAGATCACATATTCTAGTGTAACACTGCAAGAAGTCTTGAGAAAA NM_001134851 RefSeq
chr5 + 134115606 134148229 TCF7 6932 "transcription factor 7 (T-cell specific, HMG-box), transcript
variant 3"
GO:0005515|GO:0005667|GO:0003700|GO:0044212|GO:0006357|GO:0008013|GO:0033153|GO:0046632|GO:0048
699|GO:0044336|GO:0005634|GO:0006351|GO:0043565|GO:0006955|GO:0048557|GO:0007420|GO:0048619|GO:0
042127|GO:0003682|GO:0030538|GO:0021915|GO:0071353|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127232_PI430048170 0.0354621592154859 1.53093777279196 9.94645400321192
10.4384737593848 10.3351483963825 P P P 9.80820595768145 9.58366828504753
9.51349150225536 P P P LNCV6_127232_PI430048170 mRNA
AGTCACTTCCTGTCCGGGAGCAGTAGTCATTGTTGTTTTAACCTCCCCTCTCCCCGGGAC NM_003322RefSeq chr6
- 35497873 35512902 TULP1 7287 "tubby like protein 1, transcript variant 1"
GO:0005515|GO:0006909|GO:0030054|GO:0060041|GO:0005886|GO:0045202|GO:0005546|GO:0005576|GO:0042
995|GO:0045494|GO:0008020|GO:0016358|GO:0001917|GO:0050766|GO:0005737|GO:0051015|GO:0050908|GO:0
001895|GO:0007602|GO:0042462|GO:0007601|GO:0001750 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_134215_PI430048170 0.6928737327717930.9894999092868420.279723311910392
0.3145969206789190.390567540780597A A A 0.3733794585445610.33737675531153
0.32156356636305 A A A LNCV6_134215_PI430048170 mRNA
AGTTCTCGGATTCTGTGTGTATTCTGCTCCTAGCAGAGTGACCTCAGGCAAATGACTTTA NM_022375RefSeq chr1
+ 186400571 186401455 OCLM 10896 oculomedin GO:0007601 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_137729_PI430048170 0.5355578170330391.04529680213457 12.9828288207758

12.8956071210341 12.751724942516 P P P 12.7255974213845 12.9422214586935
12.7708188965425 P P P LNCV6_137729_PI430048170 mRNA
ACTTTAGAGGCTGGTGCTGTGTCGGGAGGAAGGTCAGGGCTCCTGAGCAGCAATAAAGGA NM_031485 RefSeq
chr19 + 48445772 48453907 GRWD1 83743 glutamate-rich WD repeat containing 1
GO:0005737|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135647_PI430048170 0.735790682862339 0.9795488506447840.275613428248049
0.4859795826147110.332729508273612 A A A 0.4956944804985930.386689383489533
0.303175648743134 A A A LNCV6_135647_PI430048170 mRNA
ACGCAGACCAACACAGCTGCTCTATTAAATGTGTGCACTTCTTATTCTGAGTATGTCTGA NM_001014830 RefSeq -
- 0 0 --- NA chromosome 14 open reading frame 183 NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145466_PI430048170 0.2267445961976780.8175799891253621 0.6945618990712
10.7844150986257 10.4137731783976 P P P 11.2162352679906 10.8340704213151
10.6865998841302 P P P LNCV6_145466_PI430048170 mRNA
CCCTGCCTCTTTGTACTTTGCTCTTTATAGAAAAATAAACTGTTTGTACCTGGTCCCAGG NM_005055 RefSeq chr11
- 47437756 47449178 RAPSN 5913 "receptor-associated protein of the synapse, transcript variant 1"
GO:0005813|GO:0005794|GO:0030054|GO:0031594|GO:0005886|GO:1900075|GO:0007268|GO:0033130|GO:0007
271|GO:0005737|GO:0043525|GO:0035255|GO:0045211|GO:0008270|GO:0043495|GO:0071340 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130685_PI430048170 0.0281337046568067 0.3379570409923651.4887413870322
1.87216447451804 2.48250060070826 A A A 3.5843176522807 3.4901262580286
3.63711392291571 P P P LNCV6_130685_PI430048170 mRNA
GAAGTGTCTTTAAAATTGCTATCATGAGCAAAACTGGTTGCTGTAATGCTTGTTTTTCTG NM_006467 RefSeq chr5
+ 90474863 90514552 POLR3G10622 polymerase (RNA) III (DNA directed) polypeptide G (32kD)
GO:0032728|GO:0010467|GO:0000790|GO:0006386|GO:0006385|GO:0003899|GO:0008283|GO:0006359|GO:0006
384|GO:0006383|GO:0005829|GO:0051607|GO:0045089|GO:0001056|GO:0045087|GO:0005666|GO:0032481|GO:0
005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134727_PI430048170 0.3689517921881121.03785581939167 0.293547783728389
0.2749667866054170.41947165406596 A A A 0.29146668802588 0.258098748322362
0.281724023053034 A A A LNCV6_134727_PI430048170 mRNA
CTCAGTGTATTAGAAAAGAGGTCATGCAGCTTTCTAAACATTATTGAATTGTTTGAGCTG NM_001713 RefSeq chr5
+ 79111780 79132290 BHMT 635 betaine--homocysteine S-methyltransferase
GO:0010243|GO:0047150|GO:0044281|GO:0050666|GO:0032403|GO:0033528|GO:0005829|GO:0034641|GO:0043
234|GO:0005737|GO:0000096|GO:0046500|GO:0006479|GO:0008270|GO:0071267|GO:0006579|GO:0008898|GO:0
006577|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79642_PI430048170 0.0802458191233135 0.7126186782560721.78075347938053
1.65550250222623 1.78151806903096 A A A 2.06039279339641 2.51671761720151
2.06108924211125 A P A LNCV6_79642_PI430048170 mRNA
TCTTGCTTCCCATGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTTCCTGCACCATG NM_003841 RefSeq chr8
+ 23102813 23117437 TNFRSF10C 8794 "tumor necrosis factor receptor superfamily, member 10c,
decoy without an intracellular domain"
GO:0007165|GO:0045569|GO:0005887|GO:0006915|GO:0031225|GO:0004888 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142137_PI430048170 0.0617642037400390.9545047101002380.423405341988364
0.3571349092845140.374490894380687 A A A 0.4531575738779480.465408416630897
0.438689759929065 A A A LNCV6_142137_PI430048170 mRNA
TTTCTTCTTTTCACGATAACTTTGGGTTATGTCTCTGGTAGCAGAGATTCTTACCTATAT NM_031962 RefSeq
chr17_JH159147v1_alt - 63334 64326 KRTAP9-3 83900 keratin associated protein 9-3 GO:0045095
. NA - . NA NA NA NA NA NA NA NA NA

LNCV6_129256_PI430048170 0.0155719029757294 0.6403463856885666.24208839548201
6.15903520576729 6.54874624684698 P P P 6.96646223048934 6.85130848376112
7.08192294817955 P P P LNCV6_129256_PI430048170 mRNA
CATTAGGAGCCTATAAGCATGAAACAGAATTTGCAGAGCTTGAAGTGAAAACCAGAGAAA NM_006530RefSeq
chr12 + 69359709 69390870 YEATS4 8089 "YEATS domain containing 4, transcript variant 1"
GO:0005515|GO:0003700|GO:0005730|GO:0006325|GO:0008022|GO:0003677|GO:0006351|GO:0016363|GO:0005
737|GO:0007067|GO:0043967|GO:0043968|GO:0035267|GO:0005200|GO:0005654|GO:0045893|GO:0040008 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110325_PI430048170 0.2975974879790921.1319460124758 4.79586736228938
4.64587032431377 4.55839560939119 P P P 4.73674087691328 4.40310930809042
4.29660901086903 P P P LNCV6_110325_PI430048170 mRNA
GACGCGCCCTCAGGGCACGCGGCCCCGAGCCGCATCGTGTGGGAGCACACACGCGGCCGC NM_001146175
RefSeq chr19 - 8510577 8514164 ZNF414 84330 "zinc finger protein 414, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140375_PI430048170 0.000714506388473071 0.4509070533783393.10216648439508
2.85731607458171 2.9959468308175 P A P 4.28337843755761 3.97330482715988
4.13981353754454 P P P LNCV6_140375_PI430048170 mRNA
CCAGATTGCTTGAATTAAACTGTTTGGATTAAAGAACATATATGGAGTTTCCTCTCTGGT NM_001193513 RefSeq
chr2 + 32165840 32224112 SLC30A6 55676 "solute carrier family 30 (zinc transporter), member 6,
transcript variant 1"
GO:0005739|GO:0071577|GO:0005794|GO:0005385|GO:0000139|GO:0016021|GO:0055085|GO:0044267|GO:0006
895 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51965_PI430048170 0.7319990484417211.02746867215771 10.1933855400264 9.90563147021603
10.0971702892066 P P P 9.95649009685783 10.0429269296104 10.0909866837971 P P P
LNCV6_51965_PI430048170 mRNA
TTTGTCTGCCTTGCTTCCCCAACCTAAAAACCTGACTGTGAAAGAGACTAACAGGTTGCT NM_005973RefSeq chr1
+ 156767481 156800817 PRCC 5546 papillary renal cell carcinoma (translocation-associated)
GO:0005515|GO:0007093|GO:0005654|GO:0005634|GO:0043231 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132095_PI430048170 0.323381834791848 1.43492425164777 6.53611466948139
6.41238066458701 6.28643045076311 P P P 6.8460214502816 5.04047808569903
4.92973163363536 P P P LNCV6_132095_PI430048170 mRNA
GTTTTTTATTCTATGTTCAGCACCACTGGCACCAAATACATTTTAATTCACCGAAAGCAA NM_138433 RefSeq
chr22 + 50548032 50551023 KLHDC7B 113730 kelch domain containing 7B NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129436_PI430048170 0.384851650520342 1.94940094238889 0.361427386526411
2.16865717051417 0.284791866761387 A A A 0.247037425120096 0.283156832558397
0.246955568972945 A A A LNCV6_129436_PI430048170 mRNA
GATATCTAGTCCTTCCACAAGGTATGGAAAGCAATAAACATCTTCCTTTCTTTCTGAAAA NM_018327 RefSeq
chr20 + 13008978 13166764 SPTLC3 55304 "serine palmitoyltransferase, long chain base subunit 3"
GO:0006665|GO:0046520|GO:0004758|GO:0030148|GO:0030170|GO:0005789|GO:0044281|GO:0016021|GO:0017
059 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133803_PI430048170 0.125821532612606 0.707045900736125 5.42922020087753
5.04203549903503 4.66367811627285 P P P 5.66875302066991 5.65261469691231
5.39953627963503 P P P LNCV6_133803_PI430048170 mRNA
CATGCCACCACCTGCCCTAGCATTTATTAATAGTGTTAGAATTACAAGTTTATGAAATGA NM_001190790 RefSeq
chr17 + 20579723 20580911 CDRT15L2 NA CMT1A duplicated region transcript 15-like 2 NA
. NA - . NA NA NA NA NA NA NA NA NA

LNCV6_145636_PI430048170 0.239099195455645 0.946729784835411 0.275594835909168 0.326168075263579 0.322122528222405 A A A 0.480105503235737 0.330252160527406 0.346257874331285 A A A LNCV6_145636_PI430048170 mRNA CTGCATTGGTTTTCCAGTCCTGTTAAAAGTTTAGAAACTTCATATGTGTCATCACAGCTT NM_001283041 RefSeq chr21 + 15730024 15880071 USP25 29761 "ubiquitin specific peptidase 25, transcript variant 1" GO:0005515|GO:0071108|GO:0032183|GO:0004843|GO:0005634|GO:0004197|GO:0005737|GO:0070536|GO:0061136|GO:0006508|GO:0008233|GO:0043161|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130849_PI430048170 0.0521797955668591 0.663719490054384 5.5737005018525 5.32697140720391 5.21662035039109 P P P 5.71515293931257 6.27318728607023 5.86748842498339 P P P LNCV6_130849_PI430048170 mRNA AGCGTCCAGCGTCGTCTCACCGAGCCGTAAATAAATCAACAGATTCGCATTGTCAAAAAA NM_177477 RefSeq chr8 - 142771196 142777328 LYNX1 66004 "Ly6/neurotoxin 1, transcript variant 5" GO:0005886|GO:0031225|GO:0030425|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133692_PI430048170 0.0352187710975705 0.593343040767791 4.32452489175687 4.4733730459389 4.73155527421049 P P P 4.96845429918745 5.1843251299547 5.5943085780384 P P P LNCV6_133692_PI430048170 mRNA GTATTTTACCATGCATAGGTTAACTCTTTGCCACAGATTTATTGGTTCTTGATACACCTA NM_033132 RefSeq chr13 - 99963020 99971924 ZIC5 85416 Zic family member 5 GO:0006355|GO:0003700|GO:0001843|GO:0005634|GO:0030900|GO:0003677|GO:0046872|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100079_PI430048170 0.30713989172605 1.20634593197524 4.30340559869493 4.74540228410106 4.53410975787454 P P P 4.63693758133944 4.11414877166527 3.96443914293013 P P P LNCV6_100079_PI430048170 mRNA TTGAGTACTACGAGAACTTCCTGGAAGACAAAGCCCTTATGATCGCCATGGAATATGCAC NM_178170 RefSeq chr17 + 28728813 28742766 NEK8 284086 NIMA-related kinase 8 GO:0035330|GO:0005515|GO:0005737|GO:0004674|GO:0009887|GO:0006468|GO:0072372|GO:0007017|GO:0005856|GO:0000278|GO:0005524|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134502_PI430048170 0.384509745635435 1.05592617812676 0.405125211801559 0.61410091794814 0.536201473596177 A A A 0.542355794720512 0.393303980390849 0.386482463783982 A A A LNCV6_134502_PI430048170 mRNA CAGGCAAAGCTCAAAAGAGAGTTTGGAGGTTAAAAATAATTTATTTTTGCAGTAGTGTGC NM_004668 RefSeq chr7_KI270803v1_alt + 410 68627 MGAM 8972 maltase-glucoamylase (alpha-glucosidase) GO:0005886|GO:0005975|GO:0004339|GO:0044281|GO:0003824|GO:0016324|GO:0032450|GO:0009405|GO:0005983|GO:0030246|GO:0044245|GO:0016021|GO:0016160|GO:0070062|GO:0004558 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126729_PI430048170 0.458780834350857 1.12438996333279 0.910974241935383 0.397101062818524 0.691927465308449 A A A 0.280127505766568 0.761696460867574 0.454612847768627 A A A LNCV6_126729_PI430048170 mRNA CTAAAAGGACTGTTAATGCTTTTCTCAGACACATTGGCATTTTACAATTTTGCACATGGT NM_183075 RefSeq chr4 + 107931560 107953457 CYP2U1 113612 "cytochrome P450, family 2, subfamily U, polypeptide 1" GO:0019369|GO:0006805|GO:0070330|GO:0005506|GO:0008395|GO:0044281|GO:0006082|GO:0043231|GO:0005737|GO:0019825|GO:0042738|GO:0097267|GO:0005789|GO:0016712|GO:0016021|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129137_PI430048170 0.381777647661421 0.563666759305693 0.439284829121249 0.471157799624978 0.42030794407929 A A A 0.403637484869955 2.1332484086612 0.612672537867456 A A A LNCV6_129137_PI430048170 mRNA

TGGGGGATTGAGAGTCAGAAGGATTATACAGCTTGTTCAAATTATAAATAAAAGCCCTGA NM_207412 RefSeq chr8 - 38510833 38528662 C8orf86 NA "chromosome 8 open reading frame 86, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135977_PI430048170 0.21534572595062 0.190735500400955 0.308276114520729 0.257656668109316 0.297387226258125 A A A 0.266117454716477 2.25391163484925 3.72580803726347 A A P LNCV6_135977_PI430048170 mRNA
AAGTATCTGTTACTGTGTTTTGCAGAAGCTTCAGGCGGGGATATAAGCCCCACAAGGAAA NM_004160 RefSeq chr17 - 43952738 44004469 PYY 5697 peptide YY
GO:0005515|GO:0007631|GO:0001664|GO:0008283|GO:0007586|GO:0007267|GO:0032098|GO:0006928|GO:0005576|GO:0005615|GO:0005179|GO:0007186|GO:0007218|GO:0007010|GO:0042755|GO:0005184 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128037_PI430048170 0.746741998120364 0.85005247656662 0.418529101112307 1.8344668361919 1.86435356186659 A A A 2.18212596564368 0.659728381150605 1.97568508565776 A A A LNCV6_128037_PI430048170 mRNA
GGGGGCGATAAAATAAAATGCTAAACAACTGGGTATACATGCATAAAAACTATCCATTCA NM_001285 RefSeq chr1 + 86468842 86500291 CLCA1 1179 chloride channel accessory 1
GO:0006821|GO:0005886|GO:0071456|GO:0055085|GO:0005254|GO:0005615|GO:0046872|GO:0005902|GO:0034220|GO:0042589|GO:0005887|GO:0006508|GO:0006810|GO:0006816|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107273_PI430048170 0.780228307361643 0.890581012269191 2.98049149516747 2.10845158141419 2.1215961208308 A A A 3.24504420489788 2.20601341807358 2.16856127745961 P A A LNCV6_107273_PI430048170 mRNA
GTGGATCTAATGCCTTAAGTGTGCACAGCCCAGAGAAATAAAATACTACTTTAAAACGAA NM_001101376 RefSeq chr1 + 43147922 43156396 FAM183A 440585 "family with sequence similarity 183, member A" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135880_PI430048170 0.000655758937384825 0.398747497143713 5.70713629096764 5.91698169833524 6.00052062878975 P P P 7.27561844252705 6.99830701504735 7.3246970635085 P P P LNCV6_135880_PI430048170 mRNA
CAGCATAGGCACTGTGTTACATCATCTTTACGCTTTGGTATTTGAACTTATTACAGAATT NM_001242546 RefSeq chr10 + 72215999 72235860 ANAPC16 119504 "anaphase promoting complex subunit 16, transcript variant 1" GO:0007067|GO:0005737|GO:0016567|GO:0005680|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130387_PI430048170 0.438163015573191 1.01309685601671 0.364580182675581 0.361862851914167 0.411965257380049 A A A 0.367574594312691 0.333044671150419 0.381593200221317 A A A LNCV6_130387_PI430048170 mRNA
TTGAATTGTCACCACATAGCTTTCAATCTGTGCCAACAACTATACAATTCATCAAGTGTG NM_000128 RefSeq chr4 + 186265963 186289681 F11 2160 coagulation factor XI
GO:0005515|GO:0004252|GO:0005886|GO:0051919|GO:0005576|GO:0005615|GO:0016020|GO:0007596|GO:0007597|GO:0006508|GO:0031639|GO:0008201|GO:0070009|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95927_PI430048170 0.606638775249995 0.915176682468901 7.01204844450572 7.27239402055748 7.00855099850608 P P P 7.1420634778915 6.94745011815419 7.53910748851674 P P P LNCV6_95927_PI430048170 mRNA
GGCAGTTTTCGAGCGCTTTAATTGATTGTCTGATAAACCCACTTCAAGAACAGATGGAAG NM_001282971 RefSeq chr8 - 124550769 124728507 MTSS1 9788 "metastasis suppressor 1, transcript variant 1"
GO:0072160|GO:0007009|GO:0005515|GO:0030036|GO:0030035|GO:0034334|GO:0050680|GO:0006928|GO:0030139|GO:0030282|GO:0015629|GO:0042802|GO:0061333|GO:0005737|GO:0051015|GO:0010960|GO:0005912|GO:0032233|GO:2001013|GO:0030041|GO:0007155|GO:0072102|GO:0005102|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_109361_PI430048170 0.9506114448630311.00802489111774 3.78452780081146 3.763523649886
4.32836903457778 P P P 3.96037192527558 3.95764302333144 3.997242720978 P P P
LNCV6_109361_PI430048170 mRNA
TACTTTAAAGACAAGATCTTTAATGTTGCCATTCCCCGATTCCATATGGCATGTCCAACA NM_012175RefSeq chr11
- 33740943 33774525 FBXO3 26273 "F-box protein 3, transcript variant 1"
GO:0005515|GO:0005737|GO:0004842|GO:0016567|GO:0006508|GO:0005654 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129352_PI430048170 0.7062455063877630.98795021017564 0.276850869049425
0.2829199315117680.401723294089168A A A 0.3647593635811430.307591185959886
0.344499062953121A A A LNCV6_129352_PI430048170 mRNA
GGTTGCATTTGGTCAAGATTTTGAATGCTTCCTGACAATCAACTCTAATAGTGCTTAAAA NM_000639RefSeq chr1
+ 172659007 172666872 FASLG 356 "Fas ligand (TNF superfamily, member 6), transcript variant 1"
GO:0005515|GO:0008625|GO:0048471|GO:0008284|GO:2001239|GO:0005886|GO:0070231|GO:0007267|GO:0005
634|GO:0006925|GO:0060205|GO:0005615|GO:0006955|GO:0043525|GO:0032496|GO:0043123|GO:0070062|GO:0
043202|GO:0005164|GO:0070266|GO:0043065|GO:0045742|GO:0006919|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145707_PI430048170 0.5565717610522770.9429133327517370.336159491703125
0.2677706451114830.268475076723435A A A 0.5852583831606370.264793140820229
0.252591423292137A A A LNCV6_145707_PI430048170 mRNA
GTTGTGATGATGGAAGCAGTAAATCAAAATTATGGAAATTTGCACTGTTGAAAAGCATGC NM_207371RefSeq chr10
- 21513479 21525682 SKIDA1 387640 SKI/DACH domain containing 1 GO:0005634 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127449_PI430048170 0.94566871846232 0.9983209409121770.480762654006309
0.4993674813002290.394924740344695A A A 0.5033984356220490.435806186614036
0.444316862502257A A A LNCV6_127449_PI430048170 mRNA
CTGTGCTTTCATTGTTTTTTCATAATCTTTTCTCCTTCAGTGGAGTACTGATTGCATGAA NM_001288772 RefSeq chr12
+ 18261539 18648418 PIK3C2G 5288 "phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit
type 2 gamma, transcript variant 1"
GO:0005886|GO:0006661|GO:0036092|GO:0048015|GO:0016307|GO:0044281|GO:0005524|GO:0005829|GO:0046
854|GO:0008150|GO:0006935|GO:0016303|GO:0035005|GO:0005942|GO:0006644|GO:0035091 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139361_PI430048170 0.6591148908046631.05992251764273 12.9510852072942
12.6530638248884 12.5223812792627 P P P 12.4112200187029 12.80908117805 12.660696561751
P P P LNCV6_139361_PI430048170 mRNA
TGGTGTGGGATGCAGCCGGCCGATGAGAAAATAAAGCCATATTGAATGATCGCCAAAAAA NM_020170RefSeq
chr19 + 3185876 3209575 NCLN 56926 nicalin
GO:0005515|GO:0016020|GO:0005789|GO:0016021|GO:0009966 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130910_PI430048170 0.3344654136684941.25572186536454 1.10175830777619
0.3441955792662320.498792436145919A A A 0.2876005421118080.375096906245447
0.409005713424178A A A LNCV6_130910_PI430048170 mRNA
TTAGGTGTCAAACCCATCCCATTTGGTGGCTGTGTTGCTCAACTCTATTTCTATCACTTCNM_001005465 RefSeq chr14
- 21569802 21570744 OR10G3 NA "olfactory receptor, family 10, subfamily G, member 3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144930_PI430048170 0.2786738239779991.30364284626472 3.36011118568715
3.49741607591505 3.03766531507402 P P A 3.25761151537611 3.05376856897912
2.31346504543812 P P A LNCV6_144930_PI430048170 mRNA
GGATGGCATGATCACCTTCCACATCTCCAGCAAAAAATCAAGCACAAAAACGGATTCCCA NM_001199752 RefSeq
chr19 + 49691107 49713731 CPT1C 126129 "carnitine palmitoyltransferase 1C, transcript variant 3"

GO:0030054|GO:0006635|GO:0004095|GO:0032281|GO:0005789|GO:0045202|GO:0005741|GO:0009437 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136516_PI430048170 0.4264504552550831.05514973685471 8.03134078833047 8.0729231782772 7.87411342105363 P P P 7.88713347222798 8.03671385793075 7.82119179153413 P P P
LNCV6_136516_PI430048170 mRNA
ATGCTCAACAACTAGGTGCCTCCAGCCGGGGCAGTACCCAGCACTGTGCACTATTTTCAG NM_025161RefSeq chr17 - 81539884 81552403 C17orf70 80233 "chromosome 17 open reading frame 70, transcript variant 2"
GO:0005515|GO:0005737|GO:0006281|GO:0005654|GO:0045111|GO:0003677|GO:0043240 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141732_PI430048170 0.9130118760119111.07831125579816 0.354860518443822 1.77132698053553 1.00166979438792 A A A 0.3745396740332471.10947412050026 1.46181839646286 A A A LNCV6_141732_PI430048170 mRNA
TTTCAGAACCAAATAATGAAGCTGGAAAACTGCGTCCAGGCCAACAAGACCATCCAGAAC NM_001143980 RefSeq chr16 - 1434387 1444489 CCDC154 NA coiled-coil domain containing 154 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139465_PI430048170 0.0346443541291672 1.60565843994367 13.1456097158383 13.2410658354115 13.4422303714197 P P P 12.8857526401447 12.3059947381642 12.5443816201494 P P P LNCV6_139465_PI430048170 mRNA
AGTGACTATCTGTTCATGAGAGAAATTTTCTGTAAGCTTGCTGTTTTACAGGGGATTTAT NM_006808RefSeq chr9 + 99222287 99230619 SEC61B 10952 Sec61 beta subunit
GO:0005515|GO:0002474|GO:0010467|GO:0005783|GO:0048408|GO:0006614|GO:0030970|GO:0042590|GO:0030433|GO:0006412|GO:0031205|GO:0016020|GO:0002479|GO:0016021|GO:0044267|GO:0000060 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134000_PI430048170 0.000701625104571204 4.11521098275448 3.60264677984883 3.8894704598461 3.95316371590798 P P P 1.78877214445656 1.69466219383566 1.85791804581891 A A A LNCV6_134000_PI430048170 mRNA
CGTGTCGAGGCTGTGTAGAGTGCATTGTACAGCATATTTTCATGAATAAAATTGTTTTAA NM_001291281 RefSeq chr1 + 41361930 41383591 FOXO6 NA forkhead box O6 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136878_PI430048170 0.8787506323455381.00768712112223 10.9023122998549 10.7490467505865 10.8974651987919 P P P 10.7672871870204 10.8985586878355 10.8519773719934 P P P LNCV6_136878_PI430048170 mRNA
CCAGCGGGCAGGGACTGTGGGTTGGTGAATGCATTAAAGTGCTTTGGGGAAGACAAAAAA NM_032355RefSeq chr3 - 49908868 49930012 MON1A 84315 "MON1 secretory trafficking family member A, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145236_PI430048170 0.2049185250713091.15607587916713 11.7883805225414 11.8001004949783 11.9081580323993 P P P 11.4105959494363 11.8273906080072 11.6037822576511 P P P LNCV6_145236_PI430048170 mRNA
CTTTGTTACCAGTGTGCATGTGTTTGTGTGTTTTTTAATAAAATATTGACTCGGCCAGTT NM_138410RefSeq chr3 + 32391670 32454841 CMTM7 112616 "CKLF-like MARVEL transmembrane domain containing 7, transcript variant 1" GO:0016020|GO:0006935|GO:0002337|GO:0016021|GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141225_PI430048170 0.5559141191810830.9377215063501443.5386449753929 3.41643880249917 3.74225472549038 P P P 3.83977235409155 3.47346310213346 3.65812451847327 P P P LNCV6_141225_PI430048170 mRNA
ATCGATATCTACTTTTCCACTCTGGACTACCAGGACACAACTGTCCACAAGCTTCAAGAG NM_178019RefSeq chr5 + 134967905 135011707 CATSPER3 347732 "cation channel, sperm associated 3"
GO:0035036|GO:0086010|GO:0001669|GO:0005245|GO:0005886|GO:0005783|GO:0031514|GO:0036128|GO:0007275|GO:0030317|GO:0007338|GO:0070509|GO:0070588|GO:0034765|GO:0005227|GO:0006814|GO:0048240|GO:0

032504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74720_PI430048170 0.0964755845828843 1.05404989127718 0.433352799728342
0.4785740925720850.48211814798908 A A A 0.3401318743958030.386609653944218
0.438311838953508A A A LNCV6_74720_PI430048170 mRNA
TCTGACCACAATCAGAACCAGCACTTGAAGTCTATGTATTGTTTCAAGTAGGACATATTA NM_001977RefSeq chr4
+ 110476072 110563337 ENPEP 2028 glutamyl aminopeptidase (aminopeptidase A)
GO:0002003|GO:0005886|GO:0008283|GO:0007267|GO:0045177|GO:0031410|GO:0001525|GO:0005765|GO:0032
835|GO:0005903|GO:0003081|GO:0016324|GO:0016477|GO:0005887|GO:0004177|GO:0070006|GO:0006508|GO:0
002005|GO:0008270|GO:0044267|GO:0009897|GO:0008237|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_143237_PI430048170 0.0330060530223388 1.32602817293975 8.33544789757455
8.095682632313 8.26380047760359 P P P 7.62312379999799 7.90651514548668
7.93427184464521 P P P LNCV6_143237_PI430048170 mRNA
TTTTGAGAAACAGAAAGAGGTGATCGAGGGCTACCGCAAGAACGAAGAGTCACTGAAGAA NM_006342RefSeq
chr4 + 1721489 1745178 TACC3 10460 "transforming, acidic coiled-coil containing protein 3"
GO:0005515|GO:0030097|GO:0001666|GO:0005813|GO:0021987|GO:0008283|GO:0019904|GO:0000226|GO:0030
953|GO:0032886|GO:0042994|GO:0005737|GO:0022027|GO:0051726|GO:0022008 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_68662_PI430048170 0.8590556967808950.9930813925300621 3.7282087591897 13.938311218317
13.7855668983544 P P P 13.8193192468055 13.8216180469042 13.8492584781476 P P P
LNCV6_68662_PI430048170 mRNA
GTCACACTAACTTAAAAGACAGGGTGAGGGAGATATGTAAATTGTCCACTAGAAAATTAA NM_001190996 RefSeq
chr7 + 99325872 99366262 ARPC1A10552 "actin related protein 2/3 complex, subunit 1A, 41kDa,
transcript variant 2"
GO:0034314|GO:0051015|GO:0030036|GO:0048013|GO:0007411|GO:0005885|GO:0045087|GO:0003779|GO:0015
629|GO:0038096|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141399_PI430048170 0.1923182985932720.6404176858421340.246495011184538
0.4686957394486540.68795798658979 A A A 0.4586607512672711.51968992376937
1.19362962173758 A A A LNCV6_141399_PI430048170 mRNA
TTAAGTTCAGGATGTAAGCGAAGCCTTCCATTAAGTAAAGGTGAGTGTCGTTTCGTCTCA NM_024707RefSeq chr19
+ 45079271 45091524 GEMIN779760 "gem (nuclear organelle) associated protein 7, transcript variant 1"
GO:0005515|GO:0016604|GO:0010467|GO:0005737|GO:0032797|GO:0000398|GO:0005654|GO:0005634|GO:0034
660|GO:0000387|GO:0034719|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143775_PI430048170 0.2116275999184891.04115480325324 0.44744836510867
0.3843254218178540.421921280281936A A A 0.3056427143240210.353367710052427
0.418596022716381A A A LNCV6_143775_PI430048170 mRNA
AATACAAAGACAACATGGGGCCAGAACTCCAGAAAGGATGCTGACTTTAAGAGGACTCAG NM_001057RefSeq
chr10 - 69404201 69416918 TACR2 6865 tachykinin receptor 2
GO:0005515|GO:0007588|GO:0070459|GO:0005886|GO:0033685|GO:0007217|GO:0014057|GO:0014827|GO:0004
995|GO:0006936|GO:0070474|GO:0005887|GO:0016497|GO:0051602|GO:0035106|GO:0043117 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_60726_PI430048170 0.5703957578989 1.07153190587504 10.8555934435171 10.5507955155927
10.4147285688536 P P P 10.5340252772009 10.5285740861693 10.4950811858261 P P P
LNCV6_60726_PI430048170 mRNA
CCTTGCCCTTTAACTTATTGGGACTGAATAAAGAATGGAGAGGCCCTCTCAGGCTACCAA NM_004581RefSeq chr14
- 24265537 24271627 RABGGTA 5875 "Rab geranylgeranyltransferase, alpha subunit, transcript
variant 2" GO:0017137|GO:0018344|GO:0005968|GO:0004663|GO:0008270|GO:0007601|GO:0006464 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144511_PI430048170 0.3296123878918050.5915544145292670.28099445865862

0.2883637993984960.314960633084994A A A 1.81873353482526 0.51316932483099
0.34078949340276 A A A LNCV6_144511_PI430048170 mRNA
CGTTTGTATACTATTTTCAGAGACTTTACTTGCTTCATGATTAGTACCAAACCACTGTAC NM_003068RefSeq chr8
- 48917680 48921440 SNAI2 6591 snail family zinc finger 2
GO:0010839|GO:0033629|GO:0035921|GO:0060429|GO:0000790|GO:2000810|GO:0060693|GO:0006366|GO:0003
705|GO:0007605|GO:0005634|GO:0001837|GO:2000811|GO:0035066|GO:0035414|GO:1900387|GO:0046872|GO:0
005737|GO:0007219|GO:0014032|GO:0006933|GO:2001240|GO:0032642|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143298_PI430048170 0.87147326120224 0.9931114647564771 0.5074933867066
10.6882236408875 10.5423306083822 P P P 10.6577238063129 10.5507955155927
10.5635031182043 P P P LNCV6_143298_PI430048170 mRNA
GAGTGTCTGAAATTGTGGTGGTCCTGATTTATAGGATTTCATAATTAAAATGTCTGCTGA NM_012083RefSeq chr10
- 97332496 97334701 FRAT2 23401 frequently rearranged in advanced T-cell lymphomas 2
GO:0003674|GO:0008283|GO:0090263|GO:0007275|GO:0005575|GO:0016055|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144201_PI430048170 0.0160501684200081 0.2109201446248360.428923661549355
0.3969889464032291.46181839646286 A A A 3.08115612556353 3.26748288829286
2.92461126428753 P P P LNCV6_144201_PI430048170 mRNA
TCAGGGTAAATTTGTTTTTCTGAGTTTCTCGTAATGCTCATTTTTACATGCTGCTACTAG NM_001128304 RefSeq chr3
- 146192335 146251179 PLSCR4 57088 "phospholipid scramblase 4, transcript variant 1"
GO:0005515|GO:0017121|GO:0017124|GO:0071222|GO:0042609|GO:0005886|GO:0017128|GO:0005509|GO:0016
021|GO:0019899|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127252_PI430048170 0.3013689679722631.08698442127349 10.1578055476847
10.2647136176788 10.2978911300686 P P P 9.98013926815009 10.0812418591004
10.2848528767405 P P P LNCV6_127252_PI430048170 mRNA
TAGCAAGGGGGCTCCTCTGTTGGAGTAATGTAAATTGTAATTATAAATAAACATGCAAAC NM_144703RefSeq chr20
+ 62122460 62135378 LSM14B149986 "LSM14B, SCD6 homolog B (S. cerevisiae)"
GO:0030529|GO:0007275|GO:0006417 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100769_PI430048170 0.15230410014726 0.7542430371398121 1.0399278601538 11.116993677547
11.5041519303676 P P P 11.3391808201496 11.5867558315488 11.9368759763136 P P P
LNCV6_100769_PI430048170 mRNA
TGTATTTGAAGAAGGTGGTGATGTGGACGATTTATTGGACATGATATAGGTCGTGGATGT NM_021141RefSeq chr2
+ 216109296 216206293 XRCC5 7520 X-ray repair complementing defective repair in Chinese hamster
cells 5 (double-strand-break rejoining)
GO:0005515|GO:0044212|GO:0005886|GO:0008283|GO:0071481|GO:0005634|GO:0006303|GO:0005829|GO:0006
302|GO:0071398|GO:0003691|GO:0004003|GO:0003690|GO:0000723|GO:0050769|GO:0016032|GO:0032481|GO:0
032508|GO:0031625|GO:0000784|GO:0000783|GO:0071475|GO:0042493|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135361_PI430048170 0.1214913720768970.803805156208392 4.09309024347073
4.01177217062786 4.39096844493584 P P P 4.59268585696658 4.25602496815642 4.5949079842479
P P P LNCV6_135361_PI430048170 mRNA
ACTGTAAGTGTACAGTAGTTAATGAGCTCAGAACATCTGATAACTGCAATTTAAAATGGG NM_016238RefSeq chr12
- 110372899 110403730 ANAPC7 51434 "anaphase promoting complex subunit 7, transcript variant 1"
GO:0007094|GO:0019903|GO:0051437|GO:0005634|GO:0051436|GO:0031145|GO:0051439|GO:0005829|GO:0007
067|GO:0070979|GO:0005680|GO:0005654|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130043_PI430048170 0.0418087427786212 0.7450042054988666.44877973060385
6.60474154856406 6.83654737310941 P P P 6.93932900794774 7.10542054552142
7.13815812105328 P P P LNCV6_130043_PI430048170 mRNA

GTGCACTAAAATTTTGCCACTATGAAATGTTTCTTTATTGTGTGTGCGTGTGTGTTTTGANM_007157RefSeq chrX + 57591835 57597477 ZXDB NA "zinc finger, X-linked, duplicated B" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114593_PI430048170 0.25888345004604 0.8260291712852738.33391444805272 8.00325122663424 7.72136137983257 P P P 8.37856906114065 8.47048534709679 8.07257702605209 P P P LNCV6_114593_PI430048170 mRNA
TTGGGTGATACCCCTCACAGCCCCTGTCATTCCGGAGTCATAAGGCACCCGCGCGTCTAG NM_000919RefSeq chr5 + 102865822 103031104 PAM 5066 "peptidylglycine alpha-amidating monooxygenase, transcript variant 1"
GO:0005515|GO:0031418|GO:0016020|GO:0004598|GO:0005507|GO:0001519|GO:0008270|GO:0016021|GO:0004504|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63638_PI430048170 0.4340358897748511.14527315796051 4.88440092480581 4.27845689237867 4.5999727301403 P P P 4.57709362057307 4.43205421070639 4.20579507363359 P P P LNCV6_63638_PI430048170 mRNA
TAAAGCATCAGCCATAAATGGGGACAAACGTGGGGCCAGCAGCTTCTGTTCGGGGTCTCGNM_175902RefSeq chr17 - 82389209 82418637 OGFOD3 79701 "2-oxoglutarate and iron-dependent oxygenase domain containing 3, transcript variant 2"
GO:0031418|GO:0016020|GO:0005506|GO:0016706|GO:0016021|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135293_PI430048170 0.1284810474756360.7521158661487557.13659403870007 6.92614411582693 6.99571624352192 P P P 7.7118491127104 7.13729174899209 7.39259062159553 P P P LNCV6_135293_PI430048170 mRNA
ATAGGACAGCTTAGAATGAGTGCCTTGACACCTACATATGGCTGCATTCCATACCTCAGT NM_001290049 RefSeq chr4 + 75724521 75814289 USO1 8615 "USO1 vesicle transport factor, transcript variant 1"
GO:0012507|GO:0048471|GO:0005794|GO:0005795|GO:0005783|GO:0005730|GO:0048280|GO:0006886|GO:0005829|GO:0006888|GO:0048211|GO:0045056|GO:0000139|GO:0016020|GO:0008565|GO:0061025|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127510_PI430048170 0.6814353648574750.9851365354486910.436375793001601 0.4521875710397360.428572294003318A A A 0.5092129205992970.494534229957826 0.374555995373838A A A LNCV6_127510_PI430048170 mRNA
TAGGAATAAGGAGATTAAAACAGCCATGTGGAGACTCTTTGTGAAGATATATTTTCTGCA NM_001004734 RefSeq chr1 - 248681368 248682304 OR14I1 NA "olfactory receptor, family 14, subfamily I, member 1"NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59373_PI430048170 0.2066239975868831.15144417435539 8.51367397906656 8.73877419698201 8.83696676983543 P P P 8.40458619532587 8.39002826328128 8.68382936184465 P P P LNCV6_59373_PI430048170 mRNA
GTGTCTCATATGTAAAACATTTACCTGAATGTTGTCTGAGGACTGAACTGTGGACTTTAC NM_003805RefSeq chr12 + 93677374 93850755 CRADD 8738 CASP2 and RIPK1 domain containing adaptor with death domain
GO:0008625|GO:0005515|GO:0070513|GO:0005737|GO:0006919|GO:2001235|GO:0005634|GO:0071260|GO:0030674|GO:0002020|GO:0006977 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134116_PI430048170 0.15157912679913 0.79012806964523 7.76074500385355 7.75053058092198 7.58009710728924 P P P 7.72882695798175 8.2281787935051 8.11486099262648 P P P LNCV6_134116_PI430048170 mRNA
ACTCTGTCCCATTGTCTACTGGGAAGGTCCCAGGTCTTCACCAGTTTTACAATGAGTTAT NM_003733RefSeq chr12 - 121020291 121039242 OASL 8638 "2'-5'-oligoadenylate synthetase-like, transcript variant 1"
GO:0003725|GO:0001730|GO:0019221|GO:0005730|GO:0009615|GO:0003677|GO:0005524|GO:0005829|GO:0046966|GO:0051607|GO:0005737|GO:0060337|GO:0016020|GO:0008152|GO:0060333|GO:0045071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144269_PI430048170 0.4816229105953680.8936755062990214.13361873264795

4.21599277692352 3.58820397856447 P P P 4.36157432634304 4.12738950859699
3.98729145381377 P P P LNCV6_144269_PI430048170 mRNA
GGTATCTGTTCTTTTGCTCATCTTACAGCACAGAGCTACTCTGAAATTATGTTAAATGAA NM_001123228 RefSeq
chr3 - 152339697 152340990 TMEM14E 645843 transmembrane protein 14E GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_129770_PI430048170 0.5926751864457521.00932466305434 0.338577951774065
0.3145000350942760.268637169107716A A A 0.2974264554431160.301536512448841
0.283391501720819A A A LNCV6_129770_PI430048170 mRNA
CACAACCCAGGCCCCAAAGTCTTGGGCCTTCATTAATTCTGTCAATAAAATGTTTCAAGG NM_080720RefSeq chrX
- 155459418 155459935 H2AFB3NA "H2A histone family, member B3" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140394_PI430048170 0.3579596674116560.608203242528815 1.17661809060109
1.14032811127319 1.1887039072776 A A A 2.4370799367892 0.813502935837317
1.96934232694677 A A A LNCV6_140394_PI430048170 mRNA
ACCCATTTTGCAAGACTTAAAGCCGGAAGAACACATTTTCAGATTGTTAAATAAAGTCTG NM_001290009 RefSeq
chr12 - 51281037 51324198 BIN2 51411 "bridging integrator 2, transcript variant 4"
GO:0005515|GO:0071800|GO:0030054|GO:0005543|GO:0060326|GO:0097320|GO:0002102|GO:0001891|GO:0042
995|GO:0006911|GO:0005938 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134710_PI430048170 0.00206635103814332 1.69961204587874 7.59459943012661
7.5992486033846 7.82081154549482 P P P 6.95095014579837 6.7555595346397
7.01204844450572 P P P LNCV6_134710_PI430048170 mRNA
GTGGAAGTTATAGCCGTGTGCCTCTATTTATTCTCTGAATTGTACTGTAGAAAAAGGTGT NM_178832RefSeq chr10
- 97614552 97633587 MORN4 118812 "MORN repeat containing 4, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143874_PI430048170 0.31352486407355 1.23182742324133 0.63280625592142
0.3709849228996381.07558636756193 A A A 0.3216787371639760.403443889465122
0.533169273369258A A A LNCV6_143874_PI430048170 mRNA
GTCAAGCACAGCAAAATATAACATTGTAGCCACAGACCAGATACCATTAATAAAAATCCT NM_001037162 RefSeq
chr14 + 73616843 73619888 ACOT6 NA acyl-CoA thioesterase 6 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126917_PI430048170 0.2964920921038460.9274791858383510.7620186198379
10.6607126036283 10.486182896684 P P P 10.7450354588186 10.8025384442717
10.6986744294635 P P P LNCV6_126917_PI430048170 mRNA
GCCCCGGAGCCACAGCACAATCATCTCAGTGGCGAAGCACACCACTTGATTCTATTTTTT NM_032862RefSeq
chr8_KI270816v1_alt + 87943 90355 TIGD5 84948 tigger transposable element derived 5
GO:0008150|GO:0003674|GO:0005634|GO:0005575|GO:0003677 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_65572_PI430048170 0.0203306584360736 1.95909099448841 10.3857268945195
10.3932395654623 10.3197157699019 P P P 9.67614106182441 9.27686022476048
9.18814175113523 P P P LNCV6_65572_PI430048170 mRNA
TCACCTGGCAGCCCCTTCAGCTGCTAGTGATATCACTTGTTGGACATTTTTCCAATAAAG NM_022823RefSeq chr2
- 27491882 27495259 FNDC4 64838 fibronectin type III domain containing 4
GO:0005886|GO:0005783|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135774_PI430048170 0.3201230903754090.8116852629725790.599616776737252
0.4978737598959120.345371525923835A A A 1.17060376334429 0.567375078858512
0.52504319864026 A A A LNCV6_135774_PI430048170 mRNA
GGAAGTGGAACAGGAAATGATAACTCTACTGACATGTCTATAATAAAATGATGTGCTTTG NM_152774RefSeq chr7
- 19719314 19772781 TMEM196 256130 transmembrane protein 196 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_137464_PI430048170 0.1845938015924560.6815703760067670.573277083066781
0.4823528469034210.400122730702415A A A 1.10276214497486 1.38147433465948
0.501720225683504A A A LNCV6_137464_PI430048170 mRNA
ATTAGGTGCTGAGTAAAAGACCTGAAACTCTCAACTCTCTAGATTCACAAGTGGGACATT NM_176890RefSeq
chr12_KI270904v1_alt - 184605 185605 TAS2R50 259296 "taste receptor, type 2, member 50"
GO:0033038|GO:0007186|GO:0005886|GO:0016021|GO:0001580 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130830_PI430048170 0.8017056067827031.36583975336174 4.50833166669673
0.4848461973406662.47747450716619 P A A 3.07432251898666 3.02686767855727
2.37612610718594 P P A LNCV6_130830_PI430048170 mRNA
TCTACCCCCCTAGGAGTCATACATCTGGCTACTTATTTGTTAAAAATAAAATTCTGTACC NM_005840RefSeq chrX
+ 155767734 155782457 SPRY3 10251 "sprouty homolog 3 (Drosophila), transcript variant 1"
GO:0003674|GO:0005737|GO:0016020|GO:0007275|GO:0009966 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_110683_PI430048170 0.0346384324102921 0.6520276833629936.26742396489369
6.56798729862244 6.77531445817155 P P P 7.1906685191449 7.04105329327756
7.26561551527237 P P P LNCV6_110683_PI430048170 mRNA
CAGGAAAATTAAAGGAAGAGGACCAAGGCGTTATCGAACTCCTTCCAGATCCAGATCAAG NM_004792RefSeq
chr2 + 169584339 169637744 PPIG 9360 peptidylprolyl isomerase G (cyclophilin G)
GO:0008380|GO:0005515|GO:0000413|GO:0016018|GO:0005737|GO:0016607|GO:0006457|GO:0003755|GO:0005
654|GO:0005634|GO:0016363 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139520_PI430048170 0.0162953535902951 0.3912421992997453.305420592318
3.47232923959506 4.16494740870027 P P P 4.62379791245784 5.27601593535014
5.17328010529589 P P P LNCV6_139520_PI430048170 mRNA
TCCAAAATAACTCCAGTTGGGCACCCATGAGCTAGGATCAAACTTTCTTTATATACTTTA NM_018290RefSeq chr4
+ 37826659 37862938 PGM2 55276 phosphoglucomutase 2
GO:0005515|GO:0000287|GO:0005975|GO:0005978|GO:0019388|GO:0044281|GO:0005829|GO:0004614|GO:0009
405|GO:0006006|GO:0046386|GO:0008973|GO:0005980|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127409_PI430048170 0.0594501874209863 1.32314551487041 7.77356651092393
8.05542244967281 7.77834943032597 P P P 7.6707648159485 7.46075798761535
7.25197435005117 P P P LNCV6_127409_PI430048170 mRNA
AAGGTATAGTCTTGTTTCTCAGAATCCCAGGGAACAAAGCAATTGTCTGCCTCTCCCTCT NM_021794RefSeq chr1
- 119893532 119896524 ADAM30 11085 ADAM metallopeptidase domain 30
GO:0007338|GO:0005886|GO:0006508|GO:0008270|GO:0016021|GO:0007339|GO:0004222|GO:0008237|GO:0032
504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131395_PI430048170 0.1549838190838571.23707093017284 5.85392950550897
5.92166835861195 6.05693592254481 P P P 5.91881776980533 5.52472656665519
5.42750248093621 P P P LNCV6_131395_PI430048170 mRNA
CAGTTAGACTAAGCCTCTAAGTCTCTGACTGTTATGCTTGATTTGACCTTCAAAATTACA NM_033060RefSeq chr17
- 41184099 41184895 KRTAP4-1 85285 keratin associated protein 4-1 GO:0045095 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136253_PI430048170 0.0100565934137851 0.4329488607086574.45470485020225
3.93137151096214 4.44183789053089 P P P 5.09511559508394 5.62319224499746
5.71742327241638 P P P LNCV6_136253_PI430048170 mRNA
TAAGAATTGTGAAGTACACTGAGCTGTCACGGCAAAGTAGTATTTAATGTGCTTATAGGG NM_017613RefSeq chr21
- 33577552 33588708 DONSON 29980 downstream neighbor of SON
GO:0008150|GO:0003674|GO:0007275|GO:0005634|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA

LNCV6_139098_PI430048170 0.3755398611311521.02205414626581 0.302467178559208
0.3212029872919240.39205432449444 A A A 0.3231819059135090.306668544528943
0.292854883179886A A A LNCV6_139098_PI430048170 mRNA
CAAAGATCATGCTGGAGCTATTTGCACAAAAGAATTTAACATCTCAGAATTTCAGGCAAT NM_181609RefSeq chr21
- 30491463 30491957 KRTAP19-3 NA keratin associated protein 19-3 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141284_PI430048170 0.1079228953354361.0623095067743 0.448862196911675
0.4989404726342610.511684435735892A A A 0.3383598117875730.400569806962882
0.457257019515285A A A LNCV6_141284_PI430048170 mRNA
TTCCCAGTGTTTACAACCAGGAAATAGCTTGTCATCTTTGATACAAAACAGAAATCTTTG NM_173631RefSeq chr19
+ 57363434 57379557 ZNF547 284306 zinc finger protein 547
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_145441_PI430048170 0.5761672199295560.9118643155919718.64603031521856
8.34659048279576 8.01464327130718 P P P 8.74236979275757 8.43920935605756
8.25049984418636 P P P LNCV6_145441_PI430048170 mRNA
CTCACTTGATCCCGGCCTGTTCTCCTTCGCAAATAAAAACCCTGGTTTTGTAGCAAAAAA NM_152760RefSeq chr11
+ 65833938 65853701 SNX32 254122 sorting nexin 32
GO:0016050|GO:0035091|GO:0015031|GO:0019898|GO:0006897|GO:0005768 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132022_PI430048170 0.2396335055468151.06442825891796 8.98784959423533
8.91216067106818 8.94818931743086 P P P 8.76681035298999 8.96091033144989
8.84459593026609 P P P LNCV6_132022_PI430048170 mRNA
CTTGTACTTGGCAAGGGAAGTCCACTGTGTGATTGTCTGTATTCTTAATATAATTTGTTA NM_033446RefSeq chr9
+ 126326843 126507041 MVB12B 89853 "multivesicular body subunit 12B, transcript variant 1"
GO:0005515|GO:0043130|GO:0000813|GO:0005886|GO:0005770|GO:0005634|GO:0015031|GO:0031982|GO:0005
829|GO:0008289|GO:0042058|GO:0031902|GO:0043162|GO:0005769|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143170_PI430048170 0.4509628924937660.6904792353080992.44504341522507
2.00680235531194 2.37406418758463 A A A 1.85334459141219 2.85579330604649
3.37327659817081 A P P LNCV6_143170_PI430048170 mRNA
CACTGACCCCTTTAATTAATAACTGGATTCCTAGCATGAATGGATAATGAAGTCGAATAG NM_001300739 RefSeq
chr12 - 10603764 10612978 MAGOHB 55110 "mago-nashi homolog B (Drosophila), transcript variant
2" GO:0008380|GO:0006397|GO:0051028|GO:0071013|GO:0035145 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139988_PI430048170 0.3139563822594071.98137884392545 2.81052872383267
1.73440145113446 0.674048996882028A A A 0.3393324491917180.326491826980183
1.80988977612838 A A A LNCV6_139988_PI430048170 mRNA
GGTGGGCAGTCGGGGTTGCAGGACTGTAATAAATGGATCTCTGGTGTAAATATGAAAAAA NM_033423RefSeq chr14
- 24606479 24609720 GZMH 2999 "granzyme H (cathepsin G-like 2, protein h-CCPX), transcript variant
1"
GO:0006955|GO:0005737|GO:0016020|GO:0004252|GO:0016485|GO:0019835|GO:0006508|GO:0006915|GO:0043
231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140100_PI430048170 0.3873662087840331.12116496177013 0.71103052640135
0.2872839720190930.306754682699311A A A 0.2915315982847840.282778242618078
0.276550302923287A A A LNCV6_140100_PI430048170 mRNA
TTCAAATGAGGATGAAGACCTAGGCCCATGTGAAGGACCTTCAAAGGAGGACAAAGATCT NM_001009609
RefSeq chrX - 143508734 143517475 SPANXN3 139067 "SPANX family, member N3" NA . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_138310_PI430048170 0.5263850967854 0.9789770279448290.386322057601766
0.2987313965781310.307671431270694A A A 0.4281497179133570.335589279840884
0.320184708754517A A A LNCV6_138310_PI430048170 mRNA
CAGCCTAAATTTACAGTTACTTTAAGAAAATGGGCAGTCAGAATTAGGGACTAGAATGTA NM_004948RefSeq chr18
- 31129250 31162856 DSC1 1823 "desmocollin 1, transcript variant Dsc1b"
GO:0030057|GO:0016020|GO:0005886|GO:0005509|GO:0005921|GO:0016021|GO:0007156|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144716_PI430048170 0.00788769609936745 1.22659162382441 12.1612904762219
12.2067872283715 12.0962181405949 P P P 11.9133103102867 11.7698343319104
11.8951342021463 P P P LNCV6_144716_PI430048170 mRNA
GCCCTCATTATTCCAGTTCACTGTTAAAGCCAGTAATTCTCTATATTAAACTTTCCCTGT NM_001167867 RefSeq chr19
- 41431317 41439576 ATP5SL 55101 "ATP5S-like, transcript variant 1" NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133223_PI430048170 0.00967322141714988 1.21829363377375 7.89533342451501
7.9691473235431 7.91774690272988 P P P 7.69547933455548 7.67218935245321
7.55720430589979 P P P LNCV6_133223_PI430048170 mRNA
GGCCAGAGTACCAAAACTGAGTGACCCAGACCTCTGACCTTGACCCCTGATCTCTCTCAT NM_032223RefSeq chr11
+ 65616311 65637439 PCNXL3399909 pecanex-like 3 (Drosophila) GO:0016021 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_139909_PI430048170 0.0212898911385637 0.5804173005697336.7736074542654
6.94420352206868 7.21621232609254 P P P 7.601701591851 7.58826239535321
8.07774467841012 P P P LNCV6_139909_PI430048170 mRNA
CAGATCTGGGGTAAAGTCAATGTACACTTCCTCCTTATTGGAATATTTAAGTTGCATTTA NM_012269RefSeq chr7
+ 123845168 123877477 HYAL4 23553 hyaluronoglucosaminidase 4
GO:0030207|GO:0009986|GO:0005975|GO:0006027|GO:0004415|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136188_PI430048170 0.000269532638142524 0.1614755808066283.07600446759277
2.79336714420782 2.55044111196721 A A A 5.2396736890379 5.48940913248858
5.60664219375779 P P P LNCV6_136188_PI430048170 mRNA
CAATGCAGATGTTAGCAAAAGAATGAGACTACTTCATATGTCCTAATTGGAAAAAGTCTC NM_002940RefSeq chr4
+ 145098003 145129524 ABCE1 6059 "ATP-binding cassette, sub-family E (OABP), member 1, transcript
variant 1"
GO:0005739|GO:0005737|GO:0051536|GO:0016020|GO:0008428|GO:0016032|GO:0009615|GO:0043086|GO:0016
887|GO:0005524|GO:0006401 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145064_PI430048170 0.1666172240393761.4618237570478 7.77932692373817
7.40575302484553 7.89269175843224 P P P 7.66505955183864 6.70479691433436
6.92576371561074 P P P LNCV6_145064_PI430048170 mRNA
GATGCATTGTGATGGGCTTTGACTTACATTAAAGAAATGTGGATAGTCAACTGCAAAAAA NM_014445RefSeq chr3
- 150541992 150546641 SERP1 27230 stress-associated endoplasmic reticulum protein 1
GO:0007009|GO:0060124|GO:0005881|GO:0046622|GO:0005783|GO:0006950|GO:0045727|GO:0010259|GO:0015
031|GO:0009791|GO:0030968|GO:0048644|GO:0001501|GO:0005789|GO:0005840|GO:0006006|GO:0032024|GO:0
006486|GO:0016021|GO:0006987|GO:0044267|GO:0006464 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_126951_PI430048170 0.0295568946691438 1.68293059351219 7.00455303919369
6.46847139628208 6.53466970645222 P P P 5.96327003601083 6.07613056394958 5.7587976461555
P P P LNCV6_126951_PI430048170 mRNA
GAGCTGGCTGCTGAGGTGACCACAGCCTTCTCCTAATAAAGCTGTAAGTATTTAAAACCT NM_139055RefSeq chr11
+ 130448973 130476644 ADAMTS15 170689 "ADAM metallopeptidase with thrombospondin type 1 motif,
15" GO:0006508|GO:0005578|GO:0008270|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_59391_PI430048170 0.00558546354595206 1.52465094537796 7.13874127172908
7.12028713293558 7.26217379199409 P P P 6.40893935849945 6.60893697564417
6.66936743250145 P P P LNCV6_59391_PI430048170 mRNA
GATGAACCAATTGGGAAAGATTACTCACTGAACTAATGCTTTAAAAGCCACTGAATTTCA NM_003095 RefSeq chr12
+ 95858930 95866461 SNRPF 6636 small nuclear ribonucleoprotein polypeptide F
GO:0008380|GO:0005515|GO:0010467|GO:0006369|GO:0008334|GO:0006366|GO:0003723|GO:0031124|GO:0034
660|GO:0071013|GO:0000387|GO:0034709|GO:0005829|GO:0000398|GO:0030532|GO:0005683|GO:0034715|GO:0
005654|GO:0005681|GO:0005687|GO:0034719|GO:0005685|GO:0005689 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_133263_PI430048170 0.00790147106404404 0.638016229255369 4.23017931160678
3.94607298343799 4.081884682752 P P P 4.72909382291789 4.79974908044349
4.68601151543311 P P P LNCV6_133263_PI430048170 mRNA
GTCTGTCACCTGGGCATTTTCAAAGAGGACATTTTGAAGAATTTGCATATTCAGATTTTT NM_020733 RefSeq chr3
- 124965709 125055958 HEG1 57493 heart development protein with EGF-like domains 1
GO:0030324|GO:0005509|GO:0003281|GO:0005576|GO:0048845|GO:0009791|GO:0090271|GO:0060039|GO:0001
701|GO:0003209|GO:0003017|GO:0035264|GO:0001886|GO:0005911|GO:0003222|GO:0007043|GO:0016021|GO:0
001570|GO:0055017|GO:0050878|GO:0009897|GO:0001945 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_136147_PI430048170 0.0617054955687771 1.10371882475817 9.52532530447205
9.39244794642553 9.39764978572556 P P P 9.34843228290187 9.28567974912096
9.25662566897064 P P P LNCV6_136147_PI430048170 mRNA
CATCTGAATGATCTGTAGGGGAGGGAGTTCAAATAAAGCTTTATTTTGTTCATTTTCTCA NM_032501 RefSeq chr20
- 25006229 25058182 ACSS1 84532 "acyl-CoA synthetase short-chain family member 1, transcript
variant 1"
GO:0005515|GO:0006805|GO:0016208|GO:0019542|GO:0006069|GO:0005759|GO:0019427|GO:0019413|GO:0044
281|GO:0003987|GO:0006085|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131905_PI430048170 0.0280000537399051.82372405430179 4.42686988866979
4.71346075296233 4.42310246034186 P P P 4.01271019488547 3.52388447734282
3.36441902690531 P P P LNCV6_131905_PI430048170 mRNA
TAAACCTGGGTGAAGGGAGAGGCTGCTTGGTCACAAACACAAATAAACAAGACATTTCTG NM_001195263 RefSeq
chr10 - 101007682 101031157 PDZD7 79955 "PDZ domain containing 7, transcript variant 1"
GO:0005515|GO:0005929|GO:0005634|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137422_PI430048170 0.472904961612994 1.02461145460581 0.291726409754882
0.317466468550477 0.418198225311715 A A A 0.327196151149317 0.303453787911625
0.294430621626011 A A A LNCV6_137422_PI430048170 mRNA
TGATCACAGCTTTTGTTGTGTTGAATGAAAATATGTGGACTGTCATTTTGTTGCAGCAAA NM_020346 RefSeq chr11
+ 22338120 22379500 SLC17A6 57084 "solute carrier family 17 (vesicular glutamate transporter),
member 6"
GO:0043005|GO:0030054|GO:0005313|GO:0001504|GO:0030672|GO:0016021|GO:0006814|GO:0055085|GO:0015
293|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128242_PI430048170 0.101959080574608 1.51776415885367 8.15127519418178
8.86631471594444 8.38408075508169 P P P 7.97029440195467 7.94545242033909
7.76575539906522 P P P LNCV6_128242_PI430048170 mRNA
ATTATTGTAGCTATTTATTTATTTATTGAAGATGTCCCCCAGGGGCCCAGGCTCCCCTGC NM_002866 RefSeq chr19
- 18196800 18204064 RAB3A 5864 "RAB3A, member RAS oncogene family"
GO:0060201|GO:0005515|GO:0070083|GO:0030424|GO:0009306|GO:0048790|GO:0005886|GO:0030324|GO:0003
924|GO:0007268|GO:0007409|GO:0009791|GO:0006886|GO:0060203|GO:0007269|GO:0006904|GO:0005829|GO:0
045054|GO:0045921|GO:0003016|GO:0043195|GO:0051602|GO:0051117|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_141662_PI430048170 0.6641587269892581.01701678648497 16.5675448485282
16.5059382120727 16.4258005408198 P P P 16.4587715345757 16.4361424286601
16.5330420965288 P P P LNCV6_141662_PI430048170 mRNA
ATTATTCCCCTAGGCTGAGCCTGCTCATGTACCTCTGATTAATAAATGCTTATGAAATGA NM_005980RefSeq chr4
+ 6693838 6697170 S100P 6286 S100 calcium binding protein P
GO:0005515|GO:0005737|GO:0010033|GO:0000287|GO:0050786|GO:0043542|GO:0005509|GO:0031528|GO:0005
634|GO:0070062|GO:0048306 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129016_PI430048170 0.0058214208059019 1.62041719416395 10.1548630976565
9.9569242094885 9.98355205947439 P P P 9.34872295432394 9.35519822872948
9.31001107887546 P P P LNCV6_129016_PI430048170 mRNA
CGTTCCACTCCTCCCTGCCTCTGAGCCGAACATGATAATAAAAGCTATTATTGAGCGCTT NM_206833RefSeq chr19
- 7924495 7926166 CTXN1 404217 cortexin 1 GO:0016021 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_121105_PI430048170 0.5406192345507051.03740219277888 0.293177680332343
0.2883136809313010.490130238210693A A A 0.3598935093654270.262599046998047
0.297841339046106A A A LNCV6_121105_PI430048170 mRNA
CTGTCCCTGGAACTGAAATGTGAATTTCTAGCAGAACAGAAAATATTATAATAATGAGGC NM_152721RefSeq chr18
+ 69401047 69849086 DOK6 220164 docking protein 6 GO:0005515|GO:0005158 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_52659_PI430048170 0.2571456354787660.8722464368587946.62706973987375 7.0581759501001
6.78533782179688 P P P 7.18809855103027 6.92391106207574 6.96942750625115 P P P
LNCV6_52659_PI430048170 mRNA
ATGAACAGTGAGAAAAGTTATGATTCATTGCCCAATTTTACTGCTGCTGACTGTCTAAGG NM_144963RefSeq chr8
+ 123768641 123815450 FAM91A1 157769 "family with sequence similarity 91, member A1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_137254_PI430048170 0.0193265562158638 0.6170813348223454.22322546597894
4.2745963873192 4.34180433186058 P P P 4.74070220029894 5.06889598133787
5.09555160530647 P P P LNCV6_137254_PI430048170 mRNA
TTGATGAGATATATTCACATTTGGTGTTGGAACGACCACATAGCAACGTGTTGGTTTTTT NM_001830RefSeq chrX
+ 10156944 10237659 CLCN4 1183 "chloride channel, voltage-sensitive 4, transcript variant 1"
GO:0006821|GO:0005247|GO:0005254|GO:0005524|GO:0055085|GO:0044070|GO:0015297|GO:0034220|GO:0031
901|GO:0031902|GO:0006810|GO:0016021|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133371_PI430048170 0.4161087069087511.49601300649091 0.452384576029461
1.60474197350282 2.00088554292124 A A A 0.7453896623557 0.331810181115769
1.42655487498758 A A A LNCV6_133371_PI430048170 mRNA
TGAGATCTTGAAGAGTTTAATTGTTGTGAGAGCCCCCAAGCTATTCGCCGTAGCCTTCAA NM_001193336 RefSeq
chr22 - 30524929 30546682 SEC14L6 NA SEC14-like 6 (S. cerevisiae) NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_127026_PI430048170 0.0300002256558255 1.97764979598985 9.15172734891188
9.78931923531797 9.07882831047169 P P P 8.71435657800946 8.17012853398915
8.23073171760897 P P P LNCV6_127026_PI430048170 mRNA
TCCTTTTATATCACTGTGTTTGAATCGAGGGGGAGGGGTGGTAACCGGAAATAAAGACCT NM_006979RefSeq
chr6_GL000255v2_alt + 4395229 4398841 SLC39A7 7922 "solute carrier family 39 (zinc
transporter), member 7, transcript variant 1"
GO:0005515|GO:0005794|GO:0016020|GO:0005783|GO:0046873|GO:0005789|GO:0006829|GO:0005654|GO:0016
021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134021_PI430048170 0.00243764225618722 2.6100064165062 4.54685763340517
4.99201887140169 4.94515679052232 P P P 3.39460660537339 3.62419342461519
3.33689295246958 P P P LNCV6_134021_PI430048170 mRNA

TGAAGGAAACAACACATTTATACGGATTTCATATTTCTACCCGCCTTTCCTGACTCTGTG NM_001405RefSeq chr19
+ 1286153 1301430 EFNA2 1943 ephrin-A2
GO:0031594|GO:0048013|GO:0046875|GO:0046849|GO:0021772|GO:0005886|GO:0007411|GO:0030316|GO:0007
267|GO:0043204|GO:0005576|GO:0031225 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137458_PI430048170 0.5985355044203210.9587871759274121 0.3625770976866 10.102741338829
10.2417823378257 P P P 10.2495982408641 10.1960480137544 10.4433975485836 P P P
LNCV6_137458_PI430048170 mRNA
CCACAGGTGTTTAAGCTTCTCTGTACAGTTGAAATAAACAGACAGCAAAATGGTGCCAAA NM_006549RefSeq chr12
- 121237691 121298308 CAMKK2 10645 "calcium/calmodulin-dependent protein kinase kinase 2, beta,
transcript variant 1"
GO:0045859|GO:0005516|GO:0019722|GO:0005509|GO:0005634|GO:0018108|GO:0042995|GO:0005524|GO:0005
622|GO:0005737|GO:0046777|GO:0000165|GO:0006468|GO:0004713|GO:0045893|GO:0004683 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141818_PI430048170 0.11387791715036 1.08986948760669 7.53001896521227
7.38575313409907 7.53733761697953 P P P 7.36552049428026 7.31133175377041
7.40719849622204 P P P LNCV6_141818_PI430048170 mRNA
ACATTTTAGGAATTTGCTTCCCACCCAGTGCCCTGCATTTAATCAGCACCTGATGACTTG NM_016138RefSeq chr16
+ 19067594 19080095 COQ7 10229 "coenzyme Q7 homolog, ubiquinone (yeast), transcript variant 1"
GO:0005743|GO:0005634|GO:0044281|GO:0001701|GO:0008340|GO:0046872|GO:0001841|GO:0006744|GO:0070
584|GO:0042775|GO:0034599|GO:0001306|GO:0022008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133493_PI430048170 0.0710247912474688 0.9763233801485870.338111033757731
0.3711482517409110.340744571625458A A A 0.3928963997961930.394767281903831
0.366103584206755A A A LNCV6_133493_PI430048170 mRNA
AGGGCCCTTGTACAACCGACAGCTCTTACTTTTAAATGCAATCTCTTTTCTACATACATT NM_002196RefSeq chr20
+ 20368120 20370948 INSM1 3642 insulinoma-associated 1
GO:0010468|GO:0003700|GO:0008285|GO:0042826|GO:0061104|GO:0045597|GO:0060290|GO:0005634|GO:0003
310|GO:0071158|GO:0046872|GO:0003309|GO:0017053|GO:2000179|GO:0030332|GO:0003323|GO:0001047|GO:0
000122|GO:0000978|GO:0006351|GO:0031490|GO:0001078|GO:0007049|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127852_PI430048170 0.2634781766247120.7007949953973622.58945873939451
2.51514489575566 2.29138411182625 A A A 2.46731461256968 3.48375815428252
2.81018953879278 A P P LNCV6_127852_PI430048170 mRNA
GCTGGGATCTCCTAGTGTATCATCTTGTTGATATTACTTGCCTGCTTTTAATATTTTAAC NM_001142857 RefSeq chr8
- 48714914 48735311 EFCAB1 79645 "EF-hand calcium binding domain 1, transcript variant 2"
GO:0005509 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144040_PI430048170 0.9254292547452430.9809785908210475.19718628231826
5.45368235046943 5.81663195947019 P P P 5.17425746179249 5.54549186961925
5.82563678039162 P P P LNCV6_144040_PI430048170 mRNA
GAAATCAAGCATAAATCACTTCAACTGCTCTTCTGTAGTTCTTGGATTTCTTTTCCCTTT NM_015881RefSeq chr11 -
11962995 12009082 DKK3 27122 "dickkopf WNT signaling pathway inhibitor 3, transcript variant 1"
GO:0030325|GO:2000065|GO:0016055|GO:0090090|GO:0045892|GO:0009653|GO:0005615|GO:0032348 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105909_PI430048170 0.0514742612083325 0.4317324902817752.58535373862233
1.45113249517657 2.38309110029615 A A A 3.54517491571788 3.12464697066759
3.57551754510921 P P P LNCV6_105909_PI430048170 mRNA
GAGGTGCTTTCCCCATTGAGAATATTTACAGTGCAACTAAAATAGGAAAAGAAAGTTGCT NM_004100RefSeq chr6
+ 133241356 133532120 EYA4 2070 "EYA transcriptional coactivator and phosphatase 4, transcript
variant 1"
GO:0005515|GO:0006355|GO:0007605|GO:0005634|GO:0007275|GO:0009653|GO:0046872|GO:0006351|GO:0035

335|GO:0005737|GO:0006281|GO:0007601|GO:0004725|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_117232_PI430048170 0.3913868822872511.23531755841025 3.36647840157412 4.05526045140926 3.7690914814552 P P P 3.95350473693614 3.06313928900759 3.16877968828271 P P P LNCV6_117232_PI430048170 mRNA TCTCTTGGCCACATCTTGGTTTTCTGTGTGGGTCTCCTCACCATGGCCAAGGCAGGACTC NM_001278717 RefSeq chr19 + 35138992 35143055 FXYD1 5348 "FXYD domain containing ion transport regulator 1, transcript variant c"
GO:0006821|GO:0005886|GO:0008016|GO:0006874|GO:0034707|GO:2000649|GO:0005890|GO:0055085|GO:0005254|GO:0044325|GO:0042383|GO:0006936|GO:0034220|GO:0005887|GO:0086036|GO:0017080 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135073_PI430048170 0.0735891541293151.4127596897615 3.90634755918703 4.04864365922268 4.02125302999163 P P P 3.22094629670328 3.4456396217536 3.76567724082114 P P P LNCV6_135073_PI430048170 mRNA CACATCTGTTTAATGTGCATAAAGCCAAGGAAAGGACAGTTCCGAATTCAATAGAAAAAA NM_033266 RefSeq chr16 - 23690304 23713500 ERN2 10595 endoplasmic reticulum to nucleus signaling 2
GO:0006397|GO:0016075|GO:0000287|GO:0090305|GO:0004540|GO:0005524|GO:0006351|GO:0004519|GO:0070059|GO:0004674|GO:0005789|GO:0030263|GO:0006468|GO:0007050|GO:0016021|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132814_PI430048170 0.9389492297704481.0166382723616 5.30279865087117 4.8717631680576 4.75106455388587 P P P 5.2278834569204 4.89118455159229 4.75292338808016 P P P LNCV6_132814_PI430048170 mRNA TGAAATGAAAGCTTGGGATATAAGGACTGGCAAGGTGATGAGAAGCTACAAGGCGACCAT NM_024515 RefSeq chr14 + 100376495 100530303 WDR25 79446 "WD repeat domain 25, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129743_PI430048170 0.0270819607542784 1.31519664175978 13.7160061267276 13.8789133716974 13.8622658854985 P P P 13.5048731621478 13.2419014671353 13.5138885785469 P P P LNCV6_129743_PI430048170 mRNA TCTGCCCACGTTGTTTTCTCTCAAAATCCATTCCTTTAAAAAATAAATCTGATGCAGATG NM_001037494 RefSeq chr12 + 120469856 120498495 DYNLL1 8655 "dynein, light chain, LC8-type 1, transcript variant 1"
GO:0005515|GO:0072686|GO:0030036|GO:0005886|GO:0005634|GO:0009653|GO:0042803|GO:0005829|GO:0005739|GO:0019886|GO:0005737|GO:0003774|GO:1900740|GO:0008180|GO:0000086|GO:0006810|GO:0016032|GO:0030235|GO:0007017|GO:0070062|GO:0005813|GO:0006355|GO:0006996|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137475_PI430048170 0.0141542381568627 0.4652209709564617.33611137312704 6.90236498392729 7.31075515083811 P P P 8.29546077459916 8.26925792647196 8.33544789757455 P P P LNCV6_137475_PI430048170 mRNA CTTGGCCTCCCAAACCCCTTATTTTTAAAATACTTTGCGCCTTGCTTTGATAATTTGTAT NM_020119 RefSeq chr7 - 139043519 139109719 ZC3HAV1 56829 "zinc finger CCCH-type, antiviral 1, transcript variant 1"
GO:0005515|GO:0032728|GO:0005794|GO:0032727|GO:1900246|GO:0005634|GO:0009615|GO:0046872|GO:0003950|GO:0051607|GO:0005737|GO:0045087|GO:0008152|GO:0061014|GO:0043123|GO:0045071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130831_PI430048170 0.1842505592629440.9423375745004279.05937398146122 9.02258262912315 8.91006888589468 P P P 9.11426342123454 9.07517025399854 9.0633104047395 P P P LNCV6_130831_PI430048170 mRNA TTTAAGCAGAACCAGCGAAACCCAAGCCCCTCCTTCCTCTGGTGTTTTACAACTATAAAG NM_001143804 RefSeq chr17 - 49223369 49230766 PHOSPHO1 162466 "phosphatase, orphan 1, transcript variant 1"
GO:0006646|GO:0030500|GO:0052731|GO:0052732|GO:0044281|GO:0046872|GO:0005829|GO:0016791|GO:0001958|GO:0016462|GO:0016311|GO:0006644|GO:0035630|GO:0006656|GO:0046474 . NA - . NA NA NA

NA NA NA NA NA NA
LNCV6_129069_PI430048170 0.0733326206761423 0.7532657647436617.80753234975564
7.62480568899966 7.78401837884323 P P P 7.97491968365682 8.0458244469901 8.3931172670169
P P P LNCV6_129069_PI430048170 mRNA
TTCCTAACGTGACTCCAAACTGCATCTCTACATTTAGGAACAGAGACCCGCCTTAAGAGA NM_001078645 RefSeq
chr13 + 114234886 114272675 CDC16 8881 "cell division cycle 16, transcript variant 2"
GO:0005515|GO:0007094|GO:0005813|GO:0007088|GO:0008283|GO:0051437|GO:0005819|GO:0051436|GO:0031
145|GO:0051439|GO:0005829|GO:0005737|GO:0007067|GO:0070979|GO:0005680|GO:0005654|GO:0005876|GO:0
000278|GO:0051301. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57041_PI430048170 0.0109227173569761 1.42093850995284 12.7261760375294
12.7715525722729 12.6827284050019 P P P 12.2432601815297 12.3233487222083
12.0845381339331 P P P LNCV6_57041_PI430048170 mRNA
CCAGGCCTCTGTGGGCCCTTGTCGGGCACAGATGGGATCACAGTAAATTATTGGATGGTC NM_176795 RefSeq
chr11_KI270832v1_alt - 61882 65191 HRAS 3265 "Harvey rat sarcoma viral oncogene homolog,
transcript variant 2"
GO:0005515|GO:0034259|GO:0046330|GO:2000251|GO:0050900|GO:0032855|GO:0043524|GO:1900029|GO:0007
173|GO:0006935|GO:0007411|GO:0000165|GO:0048169|GO:0009887|GO:0070374|GO:0050679|GO:0005794|GO:0
030335|GO:0045740|GO:0006897|GO:0006184|GO:0060441|GO:0008543|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134735_PI430048170 0.3396506041981881.02614716029865 0.357627013426859
0.3577773383310280.444083758104959A A A 0.3518914424328440.322231490604387
0.374904634457716A A A LNCV6_134735_PI430048170 mRNA
CCAACATACACTGTTTTCTCTTTCTCTTCTTGCATTGTTTTTCAAAACGAGTTGCAAAAC NM_001013698 RefSeq chr12
- 14804649 14814182 SMCO3 440087 single-pass membrane protein with coiled-coil domains 3
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132714_PI430048170 0.0324649728069473 0.7096701921949745.66032916582528
5.32542341466916 5.39186817088204 P P P 5.99612744522975 5.90898795116211 5.9775900695942
P P P LNCV6_132714_PI430048170 mRNA
TTCCCCCTCACCCAAGGGCAGTGGGCATGAATCTACTTTTTAAAAATGATTAATTTTGGC NM_014182 RefSeq chr12
+ 55818021 55821175 ORMDL2 29095 ORMDL sphingolipid biosynthesis regulator 2
GO:0005783|GO:0006672|GO:0005789|GO:0016021|GO:0090155 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127192_PI430048170 0.3117475731773680.9673483938180350.258166976757027
0.2717713177243010.365158168953136A A A 0.3927178410292340.332340294310877
0.314923743106051A A A LNCV6_127192_PI430048170 mRNA
CCGGTAAGATTTTATTGGTGTTTCTTTTATAACTTTGCAGTTCTTACACCGTTTGGTGAT NM_021624 RefSeq chr18 +
24460628 24479957 HRH4 59340 "histamine receptor H4, transcript variant 1"
GO:0008150|GO:0006954|GO:0007186|GO:0005886|GO:0043408|GO:0016021|GO:0004969|GO:0007204 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138687_PI430048170 0.0221165562504854 1.81716770182009 4.13761240486348
4.68927483582142 4.1696265464324 P P P 3.52142801264136 3.66329907184234
3.26823769893297 P P P LNCV6_138687_PI430048170 mRNA
TTTACTGTGACACTTTTTACTTTTTCAATAAACGTGACTCCCAGGTGAGGGGGCCTGGGT NM_001007533 RefSeq
chr17 - 81833491 81835050 PPP1R27 NA "protein phosphatase 1, regulatory subunit 27" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139331_PI430048170 0.1606679884234051.08792462260465 0.546420046394571
0.4354963187202860.578254427665742A A A 0.2995620626845 0.402133119824599
0.491236046617727A A A LNCV6_139331_PI430048170 mRNA
GACAAAGCTGGCTCTGTATTTGCATTTTATTTTTGTGTTCTTGTCAGTTTGGGAATGATT NM_001039396 RefSeq chr11

- 59208509 59213021 MPEG1 219972 macrophage expressed 1 GO:0016021 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_53959_PI430048170 0.1273508340701031.12430226141677 5.70143543515197 5.65005634290343
5.86165121514727 P P P 5.45611113191137 5.66289368297732 5.58803547226166 P P P
LNCV6_53959_PI430048170 mRNA
ATCATGTAAGTGCTAAGCTGGAGCAGCTGAGTGCCAAGGATTTTGTGAATGAAGCCATCT NM_199044 RefSeq chr1
+ 46340176 46365152 NSUN4 387338 "NOP2/Sun domain family, member 4, transcript variant 1"
GO:0005515|GO:0031167|GO:0042256|GO:0008168|GO:0070181|GO:0070131|GO:0005762 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131280_PI430048170 0.00218079039476566 0.4176497940445015.79956946255002
5.37334619736947 5.72191598322507 P P P 6.65561718090014 6.96247886450276
7.06017747695238 P P P LNCV6_131280_PI430048170 mRNA
TCTACCATCCCTTGGGTCTTTGTGTATAAACAATGTTAAATAAAGGTAGACTCAGTCTTT NM_001185072 RefSeq
chr7 + 90403333 90415954 CLDN12 9069 "claudin 12, transcript variant 1"
GO:0016338|GO:0070830|GO:0005198|GO:0034329|GO:0016021|GO:0005923|GO:0016328|GO:0045216|GO:0042
802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134188_PI430048170 0.00200919245907702 0.4274870586083442.34535885499102
2.27037838593381 2.66769335787843 A A A 3.81383111828816 3.54678136462224 3.6191561629756
P P P LNCV6_134188_PI430048170 mRNA
GAAAGTGGAGAAAGAGAAACCTTGTGCTTTTTATAAAACATTGCCAAGGAGAATAATGGT NM_004388 RefSeq chr1
- 84553120 84574480 CTBS 1486 "chitobiase, di-N-acetyl-"
GO:0008061|GO:0009313|GO:0006032|GO:0005764|GO:0005615|GO:0004568|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140780_PI430048170 0.3930490447481262.95570624362295 3.18554277455795
0.4816313294041730.515527440379769 P A A 0.3745559953738380.446286054102625
0.459633931501182 A A A LNCV6_140780_PI430048170 mRNA
GAACCTGGAGATTACTGGAATTGTTTTCCAAGAGGAAATAAATTCAGTTTACCATTAGGA NM_015461 RefSeq chr18
- 25061923 25352250 ZNF521 25925 zinc finger protein 521
GO:0006355|GO:0019904|GO:0007275|GO:0005634|GO:0003677|GO:0046872|GO:0030154|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137247_PI430048170 0.9101070242135240.98607647550609 0.678147945159797
0.4490651166247922.11166569154653 A A A 0.3902355092762441.9507833588564
1.14638401253403 A A A LNCV6_137247_PI430048170 mRNA
CCCCAAAGGGTATGCCCCATGGTGATGGAAATAAAATGAACATGTTGTAAAATGAAAAAA NM_153478 RefSeq chrX
- 152727483 152733736 CSAG1 158511 "chondrosarcoma associated gene 1, transcript variant a" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139791_PI430048170 0.1422338215824840.9260099945878910.292030518040894
0.3280016956707220.280961795665996 A A A 0.495175801255909 0.405671664646679
0.328435934411389 A A A LNCV6_139791_PI430048170 mRNA
TGTATAAGGGTAAGTCCGAACTTTCTCAGACTGGAGGTTACATTCACATCAGTCTGTCTT NM_004488 RefSeq chr3
- 194394820 194399266 GP52814 glycoprotein V (platelet)
GO:0010544|GO:0007160|GO:0005886|GO:0007596|GO:0005887|GO:0007597|GO:0005518|GO:0030168|GO:0007
155|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127860_PI430048170 0.1284682315365740.5753794197786263.74881023568092
2.46731461256968 3.10976244082609 P A P 4.32464201518296 3.82052108314845
3.78789246266682 P P P LNCV6_127860_PI430048170 mRNA
AGCCCCCGTTTATATACATTTGCCCTAACATAGGAAGTATTGTGTAGTTTCTCATTGTCA NM_001025390 RefSeq
chr11 + 10455933 10507579 AMPD3 272 "adenosine monophosphate deaminase 3, transcript variant 3"
GO:0097009|GO:0003876|GO:0006196|GO:0046034|GO:0046031|GO:0006144|GO:0032264|GO:0043101|GO:0055

086|GO:0044281|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94982_PI430048170 5.56445583761325e-05 0.3331369870337456.12448433578538
6.06935180316165 6.17884305868633 P P P 7.62843533278303 7.69423029985793
7.80404699600516 P P P LNCV6_94982_PI430048170 mRNA
CCAACCACCTCAGGACCACTCCAATGACCCACCTAACAAATGAATGAAGTTACTTATTCT NM_001712 RefSeq chr19
- 42507305 42528509 CEACAM1 634 "carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein), transcript variant 1"
GO:0005515|GO:0005886|GO:0001525|GO:0050900|GO:0042803|GO:0003674|GO:0016020|GO:0016477|GO:0005887|GO:0007229|GO:0007596|GO:0016021|GO:0007156|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144488_PI430048170 0.4634730733654680.7184563150948390.460457578258304
0.9088757881503810.514527462717751 A A A 1.79414043694204 0.74269382506037
0.459939882366499 A A A LNCV6_144488_PI430048170 mRNA
GTTTCCACCATGGTTAAGGGATTATATGGAATAAAAGAAGAACTCTTTCTCAGTATCCCT NM_002301 RefSeq chr11
+ 18412305 18451246 LDHC 3948 "lactate dehydrogenase C, transcript variant 1"
GO:0006754|GO:0005737|GO:0044262|GO:0019516|GO:0004459|GO:0031514|GO:0005634|GO:0030317|GO:0019244|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127859_PI430048170 0.16776467427819 0.7387850927387640.439189244388459
0.4206629466483430.246210869972931 A A A 0.8330415988587861.0988562125994
0.410579724803861 A A A LNCV6_127859_PI430048170 mRNA
TTGCTTAGGACATGTTGCCCCTACCTAAAGTCCTGCAATAAAATCAGCAGTCAAAACATG NM_201653 RefSeq chr1
+ 111290851 111320566 CHIA 27159 "chitinase, acidic, transcript variant 4"
GO:0006032|GO:0006030|GO:0007586|GO:0009620|GO:0002532|GO:0003796|GO:0006915|GO:0006037|GO:0005615|GO:0008061|GO:0005737|GO:0006955|GO:0030246|GO:0019900|GO:0000272|GO:0004568|GO:0090197 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144140_PI430048170 0.0584699619423129 1.29564142495621 6.54320843966759
6.69059702540993 6.81480479950724 P P P 6.32079495405656 6.10129905155032
6.49190062433341 P P P LNCV6_144140_PI430048170 mRNA
GTTAGAGCTTTTCCACCCACTTCTCTTCCACTGAGCTTCACTAATAATATGTAATCATTT NM_001146699 RefSeq chr12
- 113816737 113966371 RBM19 9904 "RNA binding motif protein 19, transcript variant 1"
GO:0005737|GO:0016020|GO:0000166|GO:0005694|GO:0040019|GO:0005730|GO:0007275|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136025_PI430048170 0.1119923541256740.5559773497000531 0.5890262490371 9.5683815348477
9.45211666830751 P P P 11.0187367421004 10.6368060032725 10.7556591543052 P P P
LNCV6_136025_PI430048170 mRNA
GCCCCTCCCTACCTCAACCTGTAAATTATTTTAAATTATAAGGACTGCATGGTAATTTAT NM_002506 RefSeq chr1
- 115285915 115338236 NGF 4803 nerve growth factor (beta polypeptide)
GO:0005515|GO:0032455|GO:0051402|GO:0005615|GO:0043524|GO:0051602|GO:0032496|GO:0007613|GO:0005796|GO:0010193|GO:0046928|GO:0051384|GO:0045786|GO:0051388|GO:0005163|GO:0043281|GO:0007422|GO:0007623|GO:0050772|GO:0008083|GO:0050770|GO:0008625|GO:0008344|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141468_PI430048170 0.1754102956411720.829020319318492 8.37898536327625
8.30487049956948 8.07982021809326 P P P 8.55170595484463 8.72412788909923
8.2819705068267 P P P LNCV6_141468_PI430048170 mRNA
AGCACTACTGGTGCCTGAAACACCTGGCCTGCTAGGAGGCTCCAATAAAGCTAACCCGGA NM_138393 RefSeq
chr19 + 1491165 1497925 REEP6 92840 receptor accessory protein 6
GO:0008150|GO:0003674|GO:0032386|GO:0005789|GO:0045177|GO:0005634|GO:0016021|GO:0044317 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_100510_PI430048170 0.0114576844919056 3.12324146685857 5.97968729089487

5.98811431190283 5.87129834667531 P P P 4.53479963657967 4.40990670641716
3.89080221531534 P P P LNCV6_100510_PI430048170 mRNA
AGGACATGGCACATCAAGTCCAAGAGTTGTTTAGAACCCGTCAGGTGGTGAAGAAGTACT NM_032795 RefSeq
chr11 - 126202093 126211692 RPUSD4 84881 "RNA pseudouridylate synthase domain containing 4,
transcript variant 1" GO:0009982|GO:0005739|GO:0005515|GO:0001522 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_103293_PI430048170 0.228777126456201 1.20395513653561 0.402731270961173
0.815110986646107 0.344267658634564 A A A 0.249654433277374 0.311220632693757
0.243912393387136 A A A LNCV6_103293_PI430048170 mRNA
TAGTGCTCCATAGTTTGGCATTTGCACGGTTTCGAAGTCATTAAACTGGTTAGACGTGTC NM_004378 RefSeq
chr15 + 78340323 78348230 CRABP1 1381 cellular retinoic acid binding protein 1
GO:0005515|GO:0007165|GO:0005215|GO:0001972|GO:0016918|GO:0006810|GO:0005501|GO:0007275|GO:0019
841|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138053_PI430048170 0.431083977723569 1.59309530435786 0.281138252128082
0.295137345825827 1.78145309221799 A A A 0.318055556089688 0.278669661571854
0.299978549432971 A A A LNCV6_138053_PI430048170 mRNA
GAATGATGTCACCAGAGCTCTGAGAATAATATTTGTAAGTTAACTGTTTTATGGGGACAT NM_020794 RefSeq
chr1 + 69760174 70123488 LRRC7 57554 leucine rich repeat containing 7
GO:0005515|GO:0005737|GO:0030054|GO:0045211|GO:0014069 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_139178_PI430048170 0.840071977240286 1.02176376595662 3.97460838933873
4.48496678744273 4.31767116014014 P P P 4.71457450622142 3.84190101590883
4.01996383498688 P P P LNCV6_139178_PI430048170 mRNA
GACCTTGGGGTTGTGTATTATATGAATGATGCTGTTTTTAAGTAAACCATTCAACAGCAA NM_138396 RefSeq
chr12 + 57755097 57760410 MARCH9 NA membrane-associated ring finger (C3HC4) 9 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141199_PI430048170 0.309602372432941 1.15998575072326 8.71052308903443
9.12135180920598 8.97203605539507 P P P 8.467062331558 8.96409770240093
8.71729045337328 P P P LNCV6_141199_PI430048170 mRNA
AGGGGAAATGGGGTGAACGGTGCTGGCAGTTCGGCTAGATTTCTGTCTTGTTTGTTTTTT NM_004995 RefSeq
chr14 + 22836532 22847599 MMP14 4323 matrix metallopeptidase 14 (membrane-inserted)
GO:0005515|GO:0043627|GO:0048771|GO:0003700|GO:0005886|GO:0030324|GO:0030307|GO:0035987|GO:0048
701|GO:0035988|GO:0051895|GO:0005737|GO:0001541|GO:0022617|GO:0030198|GO:0030574|GO:0006508|GO:0
097094|GO:0006979|GO:0042470|GO:0001666|GO:0006355|GO:0030335|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_95749_PI430048170 0.115143502037864 0.923827132288434 0.288163610453911
0.30512616849509 0.284579396543722 A A A 0.483513988705543 0.3974172791157
0.336127301720081 A A A LNCV6_95749_PI430048170 mRNA
ACAGATGTTACAATTATGGAGAGGTTCCAGTTTCTAGTAAGATTGAATTGAATCGTAAGC NM_005732 RefSeq
chr5 + 132556923 132644621 RAD50 10111 RAD50 homolog (S. cerevisiae)
GO:0005515|GO:0008408|GO:0030870|GO:0090305|GO:0046872|GO:0006302|GO:0004003|GO:0000723|GO:0000
724|GO:0032508|GO:0030674|GO:0000784|GO:0007131|GO:0031954|GO:0033674|GO:0035861|GO:0006310|GO:0
005524|GO:0003677|GO:0006974|GO:0006281|GO:0016020|GO:0000014|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135761_PI430048170 0.922028250066997 0.996862447032668 0.469515793307064
0.427959026779175 0.295089000496743 A A A 0.360639959010767 0.429199408165678
0.421055755062211 A A A LNCV6_135761_PI430048170 mRNA
TGTTCTGTGAAGTGATGAAAGTATAACTGGTTCTAGTTTGCACACTACACACATAGTTTT NM_032136 RefSeq chr4
- 163471094 163473895 TKTL2 84076 transketolase-like 2

GO:0005737|GO:0008152|GO:0046872|GO:0004802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67287_PI430048170 0.363790318168502 0.924003131568109 5.53467100321788 5.68373205344337 5.61860021412241 P P P 5.87452957049006 5.5568694224475 5.73408445240565 P P P LNCV6_67287_PI430048170 mRNA ACTTCCCAGCCATGCTCTTCTCAAGCATGTTGACAGGCATTCTGTGGGACACCCTCCTGC NM_013382 RefSeq chr14 - 77274955 77320882 POMT2 29954 protein-O-mannosyltransferase 2
GO:0004169|GO:0005789|GO:0016021|GO:0046872|GO:0035269 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130327_PI430048170 0.0358300796246667 0.947050449065222 0.337823478118119 0.344059271134355 0.325067059743422 A A A 0.445225945487565 0.411483554654354 0.385136301537458 A A A LNCV6_130327_PI430048170 mRNA CAGGACATTCTGTTCTCATTATTATCACACATCCTAAACTGAAAACAACAGCAAAGAAGA NM_016944 RefSeq chr7 + 141778488 141779388 TAS2R4 50832 "taste receptor, type 2, member 4"
GO:0007165|GO:0060170|GO:0033038|GO:0050909|GO:0007585|GO:0007186|GO:0005886|GO:0008527|GO:0016021|GO:0001580 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54258_PI430048170 0.223634333445613 0.962174943971428 0.261877672249254 0.274962613398093 0.355670977740368 A A A 0.402048507262559 0.339397483759661 0.318434007037558 A A A LNCV6_54258_PI430048170 mRNA ATCTGCAGAGTATACAGCATTGGCCAGACAACTGGAAGCTGCTTTAGAAGAAGGAAGACA NM_001007022 RefSeq chr1 - 86350093 86396342 ODF2L 57489 "outer dense fiber of sperm tails 2-like, transcript variant 2" GO:0005813 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142027_PI430048170 0.209789367408527 0.819005377456963 5.53891922110265 5.30047544540647 5.68443585651538 P P P 5.5769507207588 5.71588618816286 6.07431115011171 P P P LNCV6_142027_PI430048170 mRNA ACAGAGAAGAGTTGTTGACGTCTAACTCCTTCCATTAAATTAATAAGTACTGACCTCCTA NM_014830 RefSeq chr12 - 56998832 57006513 ZBTB39 9880 zinc finger and BTB domain containing 39
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138987_PI430048170 0.240149608488167 2.13402566893257 2.34101000942333 1.35108683997657 0.424226453756734 A A A 0.33960864534547 0.766735643634954 0.300485568620138 A A A LNCV6_138987_PI430048170 mRNA CAGCAGCACAGACCAATTCCGTTGAACGTGGAAATAAAGGACCCTTTCACTGGGAAAAAA NM_006059 RefSeq chr9 + 131009116 131093059 LAMC3 10319 "laminin, gamma 3"
GO:0000904|GO:0060041|GO:0016020|GO:0030198|GO:0014002|GO:0005198|GO:0005578|GO:0005576|GO:0007155|GO:0007601|GO:0005604 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111430_PI430048170 0.799347309545203 0.674624701598446 1.45069923527389 2.32614042777277 1.6824888005842 A A A 0.404212119334481 2.86167086520918 2.93563537502089 A P P LNCV6_111430_PI430048170 mRNA CCTAATACCTCATCTCGGAAAAAGAATATAACTAGCAAAACAGAAACGCATGAACACAAA NM_001281471 RefSeq chr5 + 103120253 103203523 PPIP5K2 23262 "diphosphoinositol pentakisphosphate kinase 2, transcript variant 4"
GO:0000827|GO:0006020|GO:0033857|GO:0043647|GO:0003993|GO:0052724|GO:0052723|GO:0044281|GO:0000832|GO:0005524|GO:0005829|GO:0016310|GO:0016311 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127244_PI430048170 0.23507834277335 1.14916829484846 7.35734262270541 7.1420634778915 7.15954812343478 P P P 7.06017747695238 7.19801540224647 6.77780254221765 P P P LNCV6_127244_PI430048170 mRNA TTCTGTCCTCATTCTTAGAGACTGCTTCTCCCAAACATAACGCGTTAGCCATGAAGGAGT NM_001040661 RefSeq

chr7 + 5282929 5304073 SLC29A4 222962 "solute carrier family 29 (equilibrative nucleoside transporter), member 4, transcript variant 1"
GO:0016324|GO:0005886|GO:0005337|GO:0008504|GO:0016021|GO:0015844|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135233_PI430048170 0.182730483002014 2.263281422712 0.648639691043855 2.37377811531448 1.97981262875533 A A A 0.81465117959703 0.37766258788894 0.737569668365021 A A A LNCV6_135233_PI430048170 mRNA
TAGTTATTAATCCTTCTTTGGGGGAGGGACAGGGCTTTAAAACTGAAGAAAATAATTTTC NM_020459 RefSeq
chr2 - 71182737 71227103 PAIP2B 400961 poly(A) binding protein interacting protein 2B
GO:0005515|GO:0005737|GO:0045947|GO:0000900 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129496_PI430048170 0.0359761748456204 1.55529586051318 4.22117888795046 4.13810916458322 4.04880158967469 P P P 3.19407391562875 3.64265904500755 3.62207107479062 P P P LNCV6_129496_PI430048170 mRNA
GCTTTCTCTGCATGGTTTGCAGGAAAAATTTAGATAGCACAACAGTGGCAATTCACGATG NM_001321 RefSeq
chr12 - 76858714 76879040 CSRP2 1466 "cysteine and glycine-rich protein 2, transcript variant 1"
GO:0003674|GO:0008270|GO:0007275|GO:0005634|GO:0005925|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131430_PI430048170 0.437885590458687 0.992368600752989 0.328267486824053 0.361344096049011 0.352572649810207 A A A 0.366439163983499 0.366783243396768 0.342183404724395 A A A LNCV6_131430_PI430048170 mRNA
CGCCTCATCAATGCATGGAAGAACGTGCAATGCATCAGAATAAAAGACATGCAAAGTAAA NM_176791 RefSeq
chr20 - 43726160 43727002 GTSF1L 149699 "gametocyte specific factor 1-like, transcript variant 1"
GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68747_PI430048170 0.358946607231119 0.885788796859711 6.51914478799741 6.16752144746166 6.64374247687929 P P P 6.43442857151408 6.68309848206497 6.75931957945131 P P P LNCV6_68747_PI430048170 mRNA
ATTGGAGGTGTGACAGAACGCATGCCAACCCCAGTTATTAAAGCTTTTGGCATCTTGAAG NM_000143 RefSeq
chr1 - 241497556 241519785 FH 2271 fumarate hydratase
GO:0005739|GO:0005737|GO:0048873|GO:0006099|GO:0004333|GO:0006106|GO:0005759|GO:0045239|GO:0044281|GO:0044237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128148_PI430048170 0.642268794670262 1.2056797558972 1.52711947574556 0.382197620345094 1.45641165354033 A A A 0.425216328588332 0.952369726489894 1.30433677864586 A A A LNCV6_128148_PI430048170 mRNA
TTTTTGCTCCAGGTTAAAGGTGCAATGCTTTCCTCCTCTTTTCTTGTGAAGGATTTATCT NM_001270952 RefSeq
chr13 + 75549479 75606020 UCHL3 7347 "ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase), transcript variant 1"
GO:0005515|GO:0043130|GO:0030163|GO:0006511|GO:0005737|GO:0004843|GO:0008233|GO:0005654|GO:0005634|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88759_PI430048170 0.391986835422435 1.29894672136235 3.2906142390719 2.73472248024826 2.66334769377213 P A A 2.66228352007194 1.65334738067514 3.01054846991125 P A P LNCV6_88759_PI430048170 mRNA
TTTGAAAGGAAGCACAGCAAGATTCATTCTATCCGGAGCCTTGCTTCACAGCCTACAGAA NM_005766 RefSeq
chr13 + 98143097 98449773 FARP1 10160 "FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived), transcript variant 1"
GO:0008092|GO:0030054|GO:0045202|GO:0030175|GO:0032855|GO:0007416|GO:0030425|GO:0005829|GO:0031234|GO:0048813|GO:0005737|GO:0043197|GO:0032321|GO:0010923|GO:0005089|GO:0005856|GO:0030676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125249_PI430048170 0.0566901131653037 1.54564833308001 6.73302330084681

6.48549418356944 6.23043895276032 P P P 6.15903520576729 5.8592160434303 5.5192949449928
P P P LNCV6_125249_PI430048170 mRNA
GAGCTCACGGAAGCCCAGCGCCGGGGCCTGCAGGTGGCCCTGGAGGAATTTCACAAGCAC NM_002889RefSeq
chr7 - 150338317 150341674 RARRES2 5919 retinoic acid receptor responder (tazarotene induced) 2
GO:0005515|GO:0005102|GO:0005576|GO:0048566|GO:0050994|GO:0001523|GO:0001701|GO:0031012|GO:2001
275|GO:0006954|GO:0050921|GO:0006935|GO:0050873|GO:0001934|GO:0010759|GO:0045600|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64434_PI430048170 0.0918318000966331 2.11052847399919 2.33425828984285
2.12057738532551 2.74418732941336 A A A 0.96625781102319 2.04250829045439
0.63330952747964 A A A LNCV6_64434_PI430048170 mRNA
TCAACTTAAACCCGAAGAGTTGCCTTCTATGCAGGATCTTTTGGAAGAAGCATCCTCCAG NM_032433RefSeq chr19
+ 14690057 14720960 ZNF333 84449 "zinc finger protein 333, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144771_PI430048170 0.15102677216914 1.05654740487974 0.450509214249107
0.4503981811215630.485570831862959A A A 0.3199263235424980.379009636998369
0.446952437978037A A A LNCV6_144771_PI430048170 mRNA
AGGAAGGCAGCTTGTATTGAGCCTTTTAAAGTATTGAATGCTTGCAAATTGCTAACATTC NM_001286441 RefSeq
chr15 - 41182730 41230757 EXD1 161829 "exonuclease 3'-5' domain containing 1, transcript variant
1" GO:0008408|GO:0090305|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138530_PI430048170 0.4415196087161420.8192305217916312.71801084282159
3.00668774729693 2.36235242974929 A A A 3.34615658020139 3.05797015525446
2.49095445565187 P P A LNCV6_138530_PI430048170 mRNA
AGGTGGCCTCCTATGACCCTCGTAGGTGCGAGGTCAGAAGCCAGCAGGCTCTCTGAACTC NM_198698RefSeq chr21
- 44654212 44654659 KRTAP12-4 NA keratin associated protein 12-4 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140926_PI430048170 0.00887006991617063 1.35169802764723 10.214221723454
10.3520139902482 10.4151384069142 P P P 9.87080557845847 9.94695999082491
9.86508798570935 P P P LNCV6_140926_PI430048170 mRNA
CTATAGGGAGGCCATTTCCTGTCCTGGAATTAGTTTTTCTAAAATGTGAATAAACTTGTT NM_052868RefSeq chr1
- 160091338 160098649 IGSF8 93185 "immunoglobulin superfamily, member 8, transcript variant 1"
GO:0005515|GO:0030424|GO:0005886|GO:0008283|GO:2000145|GO:0006928|GO:0045202|GO:0007399|GO:0007
338|GO:0016020|GO:0007519|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141249_PI430048170 0.0285039457198164 0.3246106015687224.90213927914409
4.92418304254324 5.16421661377462 P P P 5.95932646908494 6.91761856482351
6.82011563565011 P P P LNCV6_141249_PI430048170 mRNA
GACGCTAGGTTGTTTATCTTTTGTTTATTGTAAAGGAACTATGTGGGATGCATTTGGTGA NM_001287492 RefSeq
chr7 - 50444128 50450390 FIGNL1 63979 "fidgetin-like 1, transcript variant 3"
GO:0005515|GO:0043066|GO:0046034|GO:0000287|GO:0033687|GO:0005634|GO:0031122|GO:2001243|GO:0000
228|GO:0005524|GO:0071479|GO:0001649|GO:0010569|GO:0008568|GO:0005737|GO:0016787|GO:0051726|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133636_PI430048170 0.8139219108128090.939175413268633 9.98870011708936 9.9391842310526
10.0599769040685 P P P 9.63253490885112 10.3707504234545 10.162290676495 P P P
LNCV6_133636_PI430048170 mRNA
TTGGCCAGAGAGCTGGTTGAAGATGTTTGTAATCGTTTTCAGTCTCCTGCAGGTTTCTGT NM_004526RefSeq chr3
+ 127598356 127622435 MCM2 4171 "minichromosome maintenance complex component 2, transcript
variant 1"
GO:0005515|GO:0042555|GO:0006334|GO:0005634|GO:0003688|GO:0003677|GO:0005524|GO:0046872|GO:0003
678|GO:0006260|GO:0042393|GO:0007049|GO:0006271|GO:0000082|GO:0005737|GO:0006270|GO:0015630|GO:0

006268|GO:0071353|GO:0005654|GO:0005664|GO:0000278|GO:0000785 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_112425_PI430048170 0.0786488257216201 0.8512472596279135.8273596427666 6.00619051352799 5.76278937989545 P P P 5.99668984145771 6.07351849799715 6.22490785880118 P P P LNCV6_112425_PI430048170 mRNA TTTGGAAGGTATCGGGCTAATCGAGAAAAAGTCCAAGAACAGCATCCAGTGGAAGTGAGT NM_001950RefSeq chr16 + 67192164 67198918 E2F4 1874 "E2F transcription factor 4, p107/p130-binding" GO:0005515|GO:0010467|GO:0008361|GO:0005667|GO:0003700|GO:0006367|GO:0008015|GO:0019904|GO:0000978|GO:0003677|GO:0006351|GO:0006884|GO:0044458|GO:0001077|GO:0000083|GO:0045944|GO:0042127|GO:0002064|GO:0009887|GO:0007179|GO:0005654|GO:0000278|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118980_PI430048170 0.799366070344688 1.49044793622469 3.17164895338219 0.279030109201967 1.68988335237229 P A A 2.28194349977152 1.27764490549585 0.796329040570193 A A A LNCV6_118980_PI430048170 mRNA TTTGCGCTTCACCAGACACAGAGCAACCGCCAGCCCCAAGAGCAGCTCCAGGCTGGATCT NM_001030015 RefSeq chr10 + 86654556 86666459 OPN4 94233 "opsin 4, transcript variant 2" GO:0005502|GO:0018298|GO:0005886|GO:0042752|GO:0048511|GO:0016021|GO:0007602|GO:0007601|GO:0008020|GO:0016056 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141841_PI430048170 0.0105490528683563 1.30388164184233 5.53419968180475 5.4971913850987 5.62053548515497 P P P 5.2506113390297 5.0451086593324 5.20264078265074 P P P LNCV6_141841_PI430048170 mRNA GATGATGTTTCTGTGGCTATGTGTGGTATGTGGTATAAATCTCAATCTATGGTCAAAAAA NM_012239RefSeq chr11 - 215029 236362 SIRT3 23410 "sirtuin 3, transcript variant 1" GO:0032041|GO:0005515|GO:0070932|GO:0006996|GO:0034983|GO:0007568|GO:0070403|GO:0003950|GO:0005739|GO:0006471|GO:0009060|GO:0016020|GO:0005759|GO:0008270|GO:0007005|GO:0019899|GO:0006476 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135497_PI430048170 0.00285119650676561 1.34702633293539 11.5046414944447 11.459474738317 11.5108024019611 P P P 10.9901530222205 11.0740914984227 11.1189336127254 P P P LNCV6_135497_PI430048170 mRNA ACACCATCAGGATAGCACAGGGAAACTGTAGTTTAAGTGGCAAATAAAAACATTTGCATC NM_021732RefSeq chr10 - 97677423 97687258 AVPI1 60370 arginine vasopressin-induced 1 GO:0000187|GO:0007049 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131206_PI430048170 0.000695940128486427 0.6023656645097043.91051809622007 3.90719593374503 3.76354507247355 P P P 4.5511977077885 4.51855202907394 4.70337954126454 P P P LNCV6_131206_PI430048170 mRNA ACCACTGCCAGCGGGGATAGAGGCTTCAAAAGCTTTGAAGTCACTCATATTAAGAGTGTT NM_001031672 RefSeq chr1 - 54172353 54200073 CYB5RL 606495 cytochrome b5 reductase-like GO:0004128|GO:0005654|GO:0005634|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139471_PI430048170 0.169220517163668 0.95719633015447 0.271143026001952 0.339194407312071 0.309002884826697 A A A 0.429738069278131 0.336779665772406 0.341045213307703 A A A LNCV6_139471_PI430048170 mRNA GTGTTCTCTATTCTATGTATAAGGATTACATTAGACCACGATTCTTCAGTGAGTCCAAAA NM_001109619 RefSeq chr12 + 50953998 50970506 HIGD1C NA "HIG1 hypoxia inducible domain family, member 1C" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139418_PI430048170 0.167149812471604 1.12149830610875 0.630564364220769 0.371400041256715 0.580639647480511 A A A 0.282246681492914 0.402890954289722 0.410520209133222 A A A LNCV6_139418_PI430048170 mRNA CCAGCTTCTCAGAAAGAATTAAAGAACTTGCTGTTCAAATTAAGTAGAAAGTGAGACTCA NM_015039RefSeq chr1 - 183248236 183418499 NMNAT2 23057 "nicotinamide nucleotide adenylyltransferase 2, transcript

variant 1"
GO:0005802|GO:0005794|GO:0005770|GO:0019674|GO:0006767|GO:0045202|GO:0044281|GO:0005524|GO:0000139|GO:0000309|GO:0006766|GO:0004515|GO:0009435 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144758_PI430048170 0.1887967267964960.94256799171498 0.246355020227316 0.3271012005465080.287957583935498A A A 0.4558333379963520.35203694060725 0.306586367303392A A A LNCV6_144758_PI430048170 mRNA
CTGGAAGATTCCAGGCATGTTAAAGATATGCAGTATTGAATATATGTAAGGAAGTATTGG NM_182699RefSeq chrX + 22999960 23002089 DDX53 168400 DEAD (Asp-Glu-Ala-Asp) box polypeptide 53
GO:0003723|GO:0008152|GO:0004386|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139028_PI430048170 0.2763523421388540.8334728402200340.404830295444064 0.4322058030743020.455794243598518A A A 0.3477042977135180.803936359334963 0.875398176621417A A A LNCV6_139028_PI430048170 mRNA
TGGGGCACACCTCTTCAAGGGAGCGTGAACTTTATAAATAAATCAGTTCTGTTTAAAAAA NM_005170RefSeq chr11 - 2268497 2270952 ASCL2 430 achaete-scute family bHLH transcription factor 2
GO:0001666|GO:0006355|GO:0003700|GO:0060712|GO:0060708|GO:0070888|GO:0005634|GO:0000122|GO:0001890|GO:0000978|GO:0006351|GO:0001078|GO:0005737|GO:0010626|GO:0046983|GO:0035019 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133704_PI430048170 0.0461748913181982 1.92225692818711 4.44216953942774 4.74812726698474 4.2810449952913 P P P 4.03321564970115 3.32007975677925 3.17679712959333 P P P LNCV6_133704_PI430048170 mRNA
TGTCAAACTTTGTTCCCTGGATTCATAAATATGTCCCTTCTCTTTTGTAATTGTACCAGT NM_001042575 RefSeq chr3 + 112039617 112081269 TMPRSS7 NA "transmembrane protease, serine 7, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132056_PI430048170 0.5146608181327640.9664608165568921 1.4249839167732 11.5864320767679 11.4625114747333 P P P 11.5094760610612 11.6360199726126 11.4760943128687 P P P LNCV6_132056_PI430048170 mRNA
GGGGGAAGGAGGGAGGCTGACAAGCCTTGAATAAAACACAAGCCTCCGTTTCTCAAAAAA NM_001487RefSeq chr12 + 55716033 55719707 BLOC1S1 2647 "biogenesis of lysosomal organelles complex-1, subunit 1, transcript variant 1"
GO:0005515|GO:0048490|GO:0032438|GO:0006892|GO:0005765|GO:0005615|GO:0018394|GO:0031175|GO:0005829|GO:0009060|GO:0005758|GO:0031083|GO:0005759|GO:0061024|GO:0060155|GO:0008089|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133300_PI430048170 0.0216666247210465 1.08821154095789 0.402048507262559 0.4784080734198910.474706515104928A A A 0.3055538054222540.331709649087097 0.352910374729773A A A LNCV6_133300_PI430048170 mRNA
GTAAACTGTCTTTGCTAATGTCCTGCCAGATGTTTAACTTCAAATTAAGCAAAAAGTAGG NM_001281765 RefSeq chr4 - 65319562 65670495 EPHA5 2044 "EPH receptor A5, transcript variant 3"
GO:0005791|GO:0030424|GO:0048471|GO:0048013|GO:0005886|GO:0018108|GO:0005524|GO:0030425|GO:0032793|GO:0005005|GO:0021766|GO:0005004|GO:0032314|GO:0005003|GO:0048666|GO:0005887|GO:0007411|GO:0032956|GO:0019933|GO:0043025|GO:0061178|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145370_PI430048170 0.0558927892703345 0.6203061639189383.65526524522873 3.61788962920854 4.23534961757792 P P P 4.51015545095867 4.69641620710887 4.44311086087547 P P P LNCV6_145370_PI430048170 mRNA
ATTGAGCTCTTACTGTTTTAGTTGTCTTAAAACAATGGGACATGTCATGAACTGGTTTCT NM_001282169 RefSeq chr13 - 52412601 52450244 VPS36 51028 "vacuolar protein sorting 36 homolog (S. cerevisiae), transcript variant 3"
GO:0005515|GO:0043130|GO:0006355|GO:0005770|GO:0005634|GO:0032266|GO:0015031|GO:0005764|GO:0006

351|GO:0005829|GO:0016020|GO:0016197|GO:0061024|GO:0070062|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142378_PI430048170 0.7082612745907081.00958256011414 11.3008181290384 11.2268354256163 11.2798193872467 P P P 11.3028908689138 11.2519342422845 11.2109016290441 P P P LNCV6_142378_PI430048170 mRNA AGACTCCCGGAACCCTTTATATGGTGCCTCAGTAAATATGTTATTAAATATGTAATCCGG NM_002437RefSeq chr2 - 27309491 27323102 MPV17 4358 MpV17 mitochondrial inner membrane protein GO:0005739|GO:0003674|GO:0048839|GO:0072593|GO:0034614|GO:0005743|GO:0042592|GO:2000377|GO:0016021|GO:0032836|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127029_PI430048170 0.6871342380125230.88389643472986 3.26810517321179 3.6431525216233 3.66302120080352 P P P 3.10083639793925 3.92552461150526 3.96265651928627 P P P LNCV6_127029_PI430048170 mRNA CCAGTTCAAAAGAATAGTAGATGTGATAGTGCCGTGAATGTATTCTACTGGAAATGAATG NM_031438RefSeq chr5 - 103548854 103562801 NUDT12 83594 "nudix (nucleoside diphosphate linked moiety X)-type motif 12, transcript variant 1" GO:0006742|GO:0000210|GO:0005634|GO:0035529|GO:0019677|GO:0046872|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143747_PI430048170 0.7820178248692810.9767336371509221 2.0201450100987 12.137676368259 12.1010219277538 P P P 11.9418770764884 12.1673002686497 12.2377688420344 P P P LNCV6_143747_PI430048170 mRNA AATTAACCTCCAAATAAAACATGACTGGTACGTGTGCTGATTGCCTGCCTGTCTGCCGTA NM_004889RefSeq chr7 - 99458160 99466201 ATP5J2 9551 "ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F2, transcript variant 1" GO:0022857|GO:0005743|GO:0005634|GO:0044281|GO:0005753|GO:0022904|GO:0042776|GO:0016021|GO:0016887|GO:0044237|GO:0045263|GO:0015992|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132305_PI430048170 0.0345676437266457 0.48203982313652 2.08459111520993 2.30457928103438 2.27097633271982 A A A 2.87603513285047 3.20816049566622 3.64124613005559 P P P LNCV6_132305_PI430048170 mRNA AATGTTTGGAAGCCATTTTGTGTTACTGTGTGACTTTCTTTTACTCAAAAACAGCACCAT NM_001286045 RefSeq chr11 + 114400528 114410610 RBM7 10179 "RNA binding motif protein 7, transcript variant 1" GO:0051321|GO:0000166|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145079_PI430048170 0.0890421514374864 1.17796489650148 10.8737351599536 11.0370970997471 11.1531768484403 P P P 10.7738348301968 10.6831020797635 10.9032416772203 P P P LNCV6_145079_PI430048170 mRNA CCTAGAGATCCTAGAGGATCCCTACTGTTTTCTGTTTTATGTGTTTATACATTGTATGTA NM_001297656 RefSeq chr1 + 44746361 44767766 KIF2C 11004 "kinesin family member 2C, transcript variant 3" GO:0005515|GO:0005881|GO:0008283|GO:0005634|GO:0035371|GO:0005829|GO:0019886|GO:0051010|GO:0015630|GO:0016887|GO:0007019|GO:0007018|GO:0005871|GO:0030951|GO:0051983|GO:0019237|GO:0003777|GO:0005524|GO:0007067|GO:0016020|GO:0007596|GO:0008152|GO:0000777|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140135_PI430048170 0.2801264072015241.14027770330962 0.510297451618786 0.8462069883912710.452099164873538A A A 0.3725169956944970.445163780057224 0.453523900457876A A A LNCV6_140135_PI430048170 mRNA ACGCTGTCGGTTAAGCTGATGAAGAACCGCGACGAGGTGCAGGCCATGATTTACGACGAC NM_031909RefSeq chr11 - 47589663 47594409 C1QTNF4 114900 C1q and tumor necrosis factor related protein 4 GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145722_PI430048170 0.0276997154101661 0.78604597059211 9.66144695235316 9.72337183610064 9.75005068843517 P P P 9.92086420935455 10.1582188790837 10.0889450410338 P P P LNCV6_145722_PI430048170 mRNA GACTGAGTTGATGTTGGGTTTTTCATTCAATAAATTGGTGATTTCTTACCGACTGCAAAA NM_018026RefSeq chr11

+ 66070352 66244747 PACS1 55690 phosphofurin acidic cluster sorting protein 1
GO:0005515|GO:0030137|GO:0072661|GO:0016032|GO:0050690|GO:0044325|GO:0005829|GO:0000042 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136708_PI430048170 0.9358163145504661.00457088839545 0.267241975714919
0.2860273597627750.431807106623071 A A A 0.3545311671747250.308192164501033
0.307799711531105 A A A LNCV6_136708_PI430048170 mRNA
GGTGCATAGTAATTCTTCTCTATGGCTTAATACCTATGTTCATTTACATGCTATCTCTAC NM_144972 RefSeq chr11 +
18455826 18479600 LDHAL6A 160287 "lactate dehydrogenase A-like 6A, transcript variant 1"
GO:0005737|GO:0044262|GO:0004459|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_134469_PI430048170 0.5326785397852890.7803342652878052.37652720077778
0.2998260934677451.28583698409752 A A A 1.15111314504803 1.79456593348854
2.50253818956141 A A P LNCV6_134469_PI430048170 mRNA
CTCACTAATTTGCCCTAATTGGATAGGGCAATCAGAACAAAATCTGACTTTCGAATATTT NM_152680 RefSeq chr4
- 152626113 152680165 TMEM154 201799 transmembrane protein 154 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132007_PI430048170 0.7823824707314440.9452647880226494.82880647552133
4.60658475335995 5.41546280619834 P P P 4.90267296935858 4.78466284861806
5.44338380992876 P P P LNCV6_132007_PI430048170 mRNA
CTGTATTTATCTTCAGTCTCTTGTTGGTATCTAACTTTGGTTCTGAAGTTTATGGAATGG NM_001277090 RefSeq chr19
- 57541835 57559863 ZNF550 162972 "zinc finger protein 550, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132677_PI430048170 0.3862610508894331.32677763964105 0.368431261888036
1.31512989738108 0.415757224547723 A A A 0.3663513126741580.334305359343142
0.382927827241997 A A A LNCV6_132677_PI430048170 mRNA
ACCCATCACTGGAAGTGGGATTTGAAATGCAGCCAAGAAGAGGAGACCGTCGGCAACGCC NM_001170754
RefSeq chr1 - 10946472 10982037 C1orf127 148345 chromosome 1 open reading frame 127 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122524_PI430048170 0.1333218724113 1.26237037332063 4.36646921592368
4.61161130026298 4.52132435802953 P P P 4.43511015738452 4.09964671672064 3.9185126555559
P P P LNCV6_122524_PI430048170 mRNA
TGATCGACTGAATGAGATCAAAGGTCACCTGGAAATTGCCTTATTGGAAAAACATTTCTT NM_015124 RefSeq chr22
+ 46626760 46679791 GRAMD4 23151 GRAM domain containing 4
GO:0031966|GO:0006915|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129983_PI430048170 0.0293882246983445 0.4040495389910770.319708099822571
0.24416808915754 1.22179718685653 A A A 1.58379793622232 2.03633558101643
2.23055831372298 A A A LNCV6_129983_PI430048170 mRNA
TGGGGAAAATGACTTTTAGTTCAGTGAATGACTTTGAAACAATCTGAATCTTCTCAAGCA NM_001195144 RefSeq
chr2 - 196986661 197310797 ANKRD44 91526 "ankyrin repeat domain 44, transcript variant A"
GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57057_PI430048170 0.0652069403503833 2.41643671574293 1.08188735213572
2.07369377775688 2.25600208955705 A A A 0.8778469687962060.540397156362668
0.381634819310447 A A A LNCV6_57057_PI430048170 mRNA
TTTCTGCTGTGTGACAAGGAGGCTAAGGGCTTCATCACCAAGCACGACCTGCAGGGTCTC NM_001286606 RefSeq
chr11 + 828259 831991 CRACR2B 283229 "calcium release activated channel regulator 2B, transcript
variant 1" GO:0005737|GO:0002115|GO:0005509|GO:2001256|GO:0034613 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141041_PI430048170 0.48007827320598 0.7588321326184850.488484673996195

0.3959000145049520.391850555250444A A A 0.3922639275708510.360358844770027
1.44130410538881 A A A LNCV6_141041_PI430048170 mRNA
ACCAAGCAGATCCGAGAGAGCCTTCTCCAAATACCAAGGATAGAAATGAAGATTAGATGA NM_001004137
RefSeq chr11 + 4545190 4546144 OR52M1 NA "olfactory receptor, family 52, subfamily M,
member 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94125_PI430048170 0.6233739169832730.70811103220523 0.3987737395788861.14312268387834
1.66003618033019 A A A 1.53973552563317 2.38698600859472 0.384816645035623A A A
LNCV6_94125_PI430048170 mRNA
TACGCAGACAAACACATGAACATCGACTTTGACAGTTTCATCTGCTGCTTCGTTAGGCTG NM_000070RefSeq chr15
+ 42359499 42412317 CAPN3 825 "calpain 3, (p94), transcript variant 1"
GO:0005515|GO:0030018|GO:0030016|GO:0045661|GO:0005622|GO:0001896|GO:0006508|GO:0008307|GO:0043
122|GO:0055103|GO:0014850|GO:0014718|GO:0005509|GO:0071472|GO:0045214|GO:0061061|GO:0031432|GO:0
043234|GO:0051592|GO:0007517|GO:0097264|GO:0008233|GO:0008234|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135279_PI430048170 0.9539330966709081.01678039544525 7.58222780675607
7.11409663312229 6.87375552466837 P P P 7.46917712270758 7.22279425898734 6.8264657576923
P P P LNCV6_135279_PI430048170 mRNA
CAGCCTGGTCTCCTGGAAAGAATCTTTATACAGAAATAAAGTATGTGTTTCACTCAAAAA NM_001058RefSeq chr2
- 75046462 75199519 TACR1 6869 "tachykinin receptor 1, transcript variant long"
GO:0005515|GO:0009408|GO:0010996|GO:0004995|GO:0070474|GO:0002118|GO:0046887|GO:0051602|GO:0045
760|GO:0032355|GO:0008306|GO:0050679|GO:0002526|GO:0009986|GO:0007616|GO:0010193|GO:0050671|GO:0
007217|GO:0043278|GO:0032230|GO:0060083|GO:0032224|GO:0046878|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136330_PI430048170 0.0974828245805474 1.16731970599196 10.0598347631105
10.3013043563744 10.0536405715738 P P P 9.85639891555893 9.98890462420141
9.91086924703468 P P P LNCV6_136330_PI430048170 mRNA
TGGCTTCACCCTGTCAGGCCAGCTCCACTCCAGGACTGAATAAAGGTCTTTGACAGCTCT NM_181843RefSeq chr11
- 67627937 67629937 NUDT8 254552 "nudix (nucleoside diphosphate linked moiety X)-type motif 8,
transcript variant 2" GO:0005739|GO:0016787|GO:0008152|GO:0046872 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_132228_PI430048170 0.0715090053789157 2.89814155379447 2.8005477789806
2.77325897016886 2.72870075060037 A A A 0.4876959125083052.02171352455817
0.666503321769488A A A LNCV6_132228_PI430048170 mRNA
TCAATCGGTAACAATTCCCCAAAGCTGTTGTAAGACTTTGCATTAAAGCCTTCCTTTTTC NM_020703RefSeq chr1
- 109506823 109509714 AMIGO1 57463 adhesion molecule with Ig-like domain 1
GO:0030424|GO:0007413|GO:0005886|GO:0007420|GO:0042552|GO:0050772|GO:0016021|GO:0007409|GO:0007
156|GO:0007157 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137995_PI430048170 0.0318712670805726 2.3933454361672 6.46434883063375
6.60335244181518 6.62478073950391 P P P 5.70196456202766 5.26271972123074 4.8230881433884
P P P LNCV6_137995_PI430048170 mRNA
ACACAGTCATGCTTCCTGGATTTTGGAGTCGAGGCTTTCTACAGAAAAGAAAGTTCTGAT NM_001193532 RefSeq
chr1 + 28592494 28594576 RAB42 115273 "RAB42, member RAS oncogene family, transcript variant 1"
GO:0006184|GO:0005794|GO:0016020|GO:0003924|GO:0032482|GO:0019003|GO:0005525|GO:0006886 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145163_PI430048170 0.000835738225448363 2.30133474185189 8.59173158295257
8.74694532977309 8.43156536719835 P P P 7.46899337444022 7.42927477613528
7.27454231332186 P P P LNCV6_145163_PI430048170 mRNA
CAAGCTAGGGCAGAAGAGGGGTGTCAAGCTCCTCAATAAACTTGTCTCCACTTCAAAAAA NM_003782RefSeq
chr6_GL000255v2_alt + 4471559 4473245 B3GALT4 8705 "UDP-Gal:betaGlcNAc beta 1,3-

galactosyltransferase, polypeptide 4" GO:0000139|GO:0008499|GO:0047915|GO:0006486|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139562_PI430048170 0.00106688968297489 2.10177894516923 6.8891441244404
6.84084225870277 7.14113403786979 P P P 5.74370623399892 6.02844483373391
5.88845662936335 P P P LNCV6_139562_PI430048170 mRNA
TGAATTTCCTGCTTTCCTGGTTGAATTTTCTACTGTTTCACGTGGTGTAACCCTAGACTG NM_001134647 RefSeq chr4
- 7758712 7939926 AFAP1 60312 "actin filament associated protein 1, transcript variant A"
GO:0005737|GO:0051493|GO:0003779|GO:0009966|GO:0015629|GO:0005925 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136374_PI430048170 0.00126653746034927 1.78801567768391 11.5610204186673
11.4552553749058 11.5391963808022 P P P 10.8011620250086 10.5981350261627
10.6350393832037 P P P LNCV6_136374_PI430048170 mRNA
TCATCAGGGCCTGGGGCCTGAGAGAATTGGCTCAATAAAGATTTCAAGATCCTCAAAAAA NM_170714 RefSeq chr3
- 50329785 50340936 RASSF1 11186 "Ras association (RalGDS/AF-6) domain family member 1, transcript variant D"
GO:0005515|GO:0071157|GO:0005815|GO:0005886|GO:0005874|GO:0050821|GO:0005634|GO:0007265|GO:0006974|GO:0042802|GO:0000922|GO:0005737|GO:0047485|GO:0015630|GO:0031398|GO:0007050|GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52993_PI430048170 0.1145802364814980.8862411777084658.03096447181018 7.98864710426617
7.95161868207022 P P P 8.19669793419275 8.25748818351511 8.03144868316738 P P P
LNCV6_52993_PI430048170 mRNA
TGAGCTTAGAAGTGGTGTGTGCTCTGTCTGTCTGTCTTTGTCTGTCTGTTGTATACAGTG NM_052840 RefSeq chr15
- 72284726 72320184 CELF6 60677 "CUGBP, Elav-like family member 6, transcript variant 1"
GO:0006397|GO:0005737|GO:0000166|GO:0000381|GO:0003723|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143620_PI430048170 0.00475380661395163 0.4041912274369186.30205520911117
5.91824357996737 6.43584797057583 P P P 7.25390876770119 7.48167472899877
7.83072656493535 P P P LNCV6_143620_PI430048170 mRNA
TGCGTCAGTGCCTCATTGTATCATCCTACTTGTGTTTTGCTCAATAAATGAATAAAAGAC NM_018841 RefSeq chr1
- 67701465 67833472 GNG12 55970 "guanine nucleotide binding protein (G protein), gamma 12"
GO:0021987|GO:0005886|GO:0005884|GO:0005834|GO:0007268|GO:0044281|GO:0030165|GO:0007165|GO:0006112|GO:0007186|GO:0071377|GO:0042301|GO:0032496|GO:0004871|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136572_PI430048170 0.0119343019037229 0.6336316797652378.2407525418234
8.20532709767918 8.30643785027661 P P P 8.729394607315 8.95447856816431
9.02876058168024 P P P LNCV6_136572_PI430048170 mRNA
CGACTGTATTAACACGGAGGCCTGCCTGGCTACTTTTTTAACATATTGTTAAGTAATATT NM_001256666 RefSeq
chr4 + 2625431 2732575 FAM193A 8603 "family with sequence similarity 193, member A, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92386_PI430048170 0.19511405592669 1.12753012097047 8.1940754755929 8.42277528322865
8.34700053290226 P P P 8.32317631250798 8.05359649868705 8.06019387291871 P P P
LNCV6_92386_PI430048170 mRNA
TACCAAGATAAGAGGTACACAAATAAGTACTCCTCTCAGTTTGGTGGTGGAAGTCAATAT NM_003753 RefSeq chr22
- 36510849 36529230 EIF3D 8664 "eukaryotic translation initiation factor 3, subunit D"
GO:0005515|GO:0010467|GO:0005852|GO:0016282|GO:0033290|GO:0001732|GO:0001731|GO:0003743|GO:0006412|GO:0006413|GO:0005829|GO:0016020|GO:0071541|GO:0006446|GO:0044267 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_132288_PI430048170 0.0377112205112143 0.63691108180781 11.3673833523568
11.5071506013237 11.6320889127772 P P P 11.8918343864827 12.0962181405949

12.4312083746326 P P P LNCV6_132288_PI430048170 mRNA
GCCACTTTGGTAGTTGTGTATCTGCTCATGTATGTGATTTGACAAACCAGTTTTTTAAAA NM_001159767 RefSeq
chr7 + 16646133 16706523 BZW2 28969 "basic leucine zipper and W2 domains 2, transcript variant
1" GO:0016020|GO:0030154|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130793_PI430048170 0.1605237556263860.8360077174431289.51216748422989
9.65448521784533 9.74887665357197 P P P 9.7278008771827 9.81865838427591
10.1236854210868 P P P LNCV6_130793_PI430048170 mRNA
CAAGCCTTAGAACTCCTCATTCTCATGTTGCTATTTATGTACCTAATTAAAACCCAAGTT NM_024122RefSeq chrX
- 23833347 23907940 APOO 79135 "apolipoprotein O, transcript variant 1"
GO:0034361|GO:0005739|GO:0034364|GO:0034362|GO:0006869|GO:0016021|GO:0005615 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_124719_PI430048170 0.0991127626886284 0.7899503297775384.15426994954799
4.07774361043472 4.03242209217347 P P P 4.48338499997975 4.58714382875978
4.18795047367905 P P P LNCV6_124719_PI430048170 mRNA
TTTTGGTCTCAGCTCCTTGATCTAAGCCTCCCAGAGAGACCCTAGAACGTTTCCCTCAAG NM_014068RefSeq
chr6_GL000252v2_alt + 2374194 2399422 PSORS1C1 170679 psoriasis susceptibility 1 candidate 1
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140805_PI430048170 0.35753516378038 1.94071708136131 0.858591772548033
2.31009218457621 0.297606172126293A A A 0.3142903872977990.725745372991233
0.293741656230277A A A LNCV6_140805_PI430048170 mRNA
TGGGGGAGAGCAACCTTCACATGTCATTTTGGGAAAAGGAATAAAAAATGATTGGGACAC NM_153021RefSeq chr2
+ 28496070 28643787 PLB1 151056 "phospholipase B1, transcript variant 1"
GO:0005886|GO:0007603|GO:0044281|GO:0001523|GO:2000344|GO:0016042|GO:0016324|GO:0004622|GO:0004
623|GO:0016021|GO:0006644|GO:0036151|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141167_PI430048170 0.64959476021541 1.12106093822404 5.34712141339991
4.96011788378084 4.52426807653642 P P P 4.91172209702612 5.06600011384989
4.39251675282268 P P P LNCV6_141167_PI430048170 mRNA
GACTTCTCCGGGGTGCCTGTGCCCTACATTAAACCCGGCGTTTGTTTCACAGCCAAAAAA NM_206918RefSeq chr14
- 100146415 100159675 DEGS2 123099 "delta(4)-desaturase, sphingolipid 2"
GO:0006665|GO:0000170|GO:0006667|GO:0030148|GO:0005789|GO:0044281|GO:0016021|GO:0046513|GO:0042
284|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136402_PI430048170 0.0314489896816909 1.30946514045559 4.00675146940009
4.16766541511547 3.86086970974825 P P P 3.59349713690567 3.71389171630319
3.57325795317285 P P P LNCV6_136402_PI430048170 mRNA
AAGAGGCCTTAAATGTGTCCACACACTTGAACTAATAAGTGTTAAAGCCCCTCCTGTGGA NM_181646RefSeq chr7
+ 88759367 89337057 ZNF804B 219578 zinc finger protein 804B GO:0046872 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_145222_PI430048170 0.6474590026293570.9849858418747180.271338617717442
0.2777613948697930.397638333756788A A A 0.36691059724288 0.307963146223819
0.340276303181943A A A LNCV6_145222_PI430048170 mRNA
TTGTCTTTGTCTCAGTAAAGTGTAGGTGGACAATCTTCCTGTGATATGTAGTGACATTGG NM_001164595 RefSeq
chr12 + 41188447 41574590 PDZRN4 29951 "PDZ domain containing ring finger 4, transcript variant
1" GO:0004842|GO:0016567|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132269_PI430048170 0.2717902495952011.02232888375029 0.304751023222701
0.2888861642751530.358881973792274A A A 0.2975873524214230.280696011540561
0.279523891394734A A A LNCV6_132269_PI430048170 mRNA
AGAACTTAAACAAAGACCACCTGAGGGTGAACAAGGGCAAAGACATTTAGCAGCCCACAT NM_020389RefSeq
chr5 - 136213310 136365476 TRPC7 57113 "transient receptor potential cation channel, subfamily C,
member 7, transcript variant 1"

GO:0005515|GO:0005801|GO:0005262|GO:0048471|GO:0005886|GO:0030168|GO:0005635|GO:0055085|GO:0034220|GO:0007411|GO:0007596|GO:0070588|GO:0006828|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127850_PI430048170 0.6866315512318931.0310689129188 6.733373074737 6.62604175675131 6.56987079451461 P P P 6.77569632964424 6.57377378063772 6.43133351143539 P P P LNCV6_127850_PI430048170 mRNA
AGCATAAAGGACTCAAGGACCACAGCCTCTGCCCACCAGCATGTTCCTTGAAGCCCATCG NM_016366RefSeq chr11 - 67518946 67523428 CABP2 51475 calcium binding protein 2
GO:0007165|GO:0048471|GO:0005794|GO:0005886|GO:0005509 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128714_PI430048170 0.3260213219578061.03520920068479 0.301605711880316 0.2580560624420320.387564187861867A A A 0.2783894780308430.245358729086641 0.276496695417344A A A LNCV6_128714_PI430048170 mRNA
CCCAATTTCCCAGAGGGAAAAATGTATTTAAAATGCCCAAAGAACATTAAATCAGGAGTA NM_001256737 RefSeq chr20 + 44247257 44280917 GDAP1L1 78997 "ganglioside induced differentiation associated protein 1-like 1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134630_PI430048170 0.00418896188008171 0.26155551713729 0.468512244823015 0.437796429400107 1.03395410921901 A A A 2.46447044914908 2.60822763263489 2.74002925609947 A A P LNCV6_134630_PI430048170 mRNA
CCCTGGCATTTTTGGGTCTTGAGAGAAAACAATTTGAATGACTGAATTTACTACAAAGGC NM_138326RefSeq chr2 + 134838615 134902032 ACMSD 130013 aminocarboxymuconate semialdehyde decarboxylase
GO:0034641|GO:0006569|GO:0046874|GO:0044281|GO:0001760|GO:0046872|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132104_PI430048170 0.3423358290460441.10316973263863 10.9580303991194 11.0542422987522 10.9468707060551 P P P 11.0798904014465 10.7264290692228 10.6981190498523 P P P LNCV6_132104_PI430048170 mRNA
CTCCTTTCCCCTCTCATACATAAAATCGCTTTCAAATTAAAATCGCTGTTTTCTGGACTG NM_001270401 RefSeq chr6_GL000254v2_alt - 4629540 4636649 RXRB 6257 "retinoid X receptor, beta, transcript variant 1"
GO:0005515|GO:0010467|GO:0006367|GO:0000977|GO:0003700|GO:0071300|GO:0055012|GO:0003713|GO:0001893|GO:0003707|GO:0005634|GO:0001228|GO:0055085|GO:0001701|GO:0060038|GO:0042803|GO:0048384|GO:0045944|GO:0043401|GO:0008270|GO:0000980|GO:0005654|GO:0004879|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131536_PI430048170 0.8364553820903240.9908907354936598.12658153312613 8.27478774205548 8.2496423834385 P P P 8.20851132594785 8.17379446240198 8.30917990203988 P P P LNCV6_131536_PI430048170 mRNA
CAGATGCACACCGTGTGTTGTTCCTATGCTAATAAAGACCTTTGATGTATCCACTTCAAA NM_017868RefSeq chr11 + 113314528 113366392 TTC12 54970 tetratricopeptide repeat domain 12 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129239_PI430048170 0.7058142662232471.0348794997356 0.254106572429372 0.5823584117153810.348342062162521A A A 0.4053558002044510.335536440344241 0.314010074515419A A A LNCV6_129239_PI430048170 mRNA
TAAAAATGTCTCAGGGGTTTGATGAAGTTACTATTCAATAAAAGAAACCTCTCAGGGAAG NM_182562RefSeq chr15 - 98437161 98514382 FAM169B 283777 "family with sequence similarity 169, member B" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128009_PI430048170 0.2186792493119370.62582110268576 0.415273180329477 0.4442223174953820.454850046397436A A A 1.32482797708849 0.362660645730639 1.43524293492582 A A A LNCV6_128009_PI430048170 mRNA
TAGAACTTTAGGGATTCAAATGTATGACAGCTTGGGGGAAAAAATAAAGAACTGACTCTG NM_002217RefSeq chr3

+ 52794767 52809009 ITIH3 3699 inter-alpha-trypsin inhibitor heavy chain 3
GO:0010951|GO:0004866|GO:0004867|GO:0030212|GO:0005576|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137993_PI430048170 0.00152488750356586 1.5366772429164 6.22274651442715
6.07377350629267 6.25969192511368 P P P 5.57033182157368 5.63068372612131
5.49940280805465 P P P LNCV6_137993_PI430048170 mRNA
ATTGCCTGTTAATTTGACTGTAATGAATAGGGGGTAGAAACAAAAGGATCAAGTGTGTTA NM_198567 RefSeq chr5
+ 176238358 176345991 SIMC1 375484 SUMO-interacting motifs containing 1 GO:0032184 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_132246_PI430048170 0.0338489592015041.23247892850117 12.378504307887
12.4475053284403 12.4112200187029 P P P 12.0556532874621 12.2377688420344
12.0309815134227 P P P LNCV6_132246_PI430048170 mRNA
TGACATGTATGATTACCTGCATCTGAGCCGCCTGGGCTACACACCTGTTTGCCGGGCTCT NM_001145939 RefSeq
chr19 - 42297032 42302777 PAFAH1B3 5050 "platelet-activating factor acetylhydrolase 1b, catalytic
subunit 3 (29kDa), transcript variant 1"
GO:0005515|GO:0006629|GO:0046982|GO:0047179|GO:0003847|GO:0007283|GO:0005829|GO:0007399|GO:0016
042|GO:0005737|GO:0016020|GO:0007420|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138299_PI430048170 0.0446354462872079 1.26539005571854 8.38370184478578
8.28593141824159 8.30312727849471 P P P 7.81950512181457 8.11285822289357
8.00838389316202 P P P LNCV6_138299_PI430048170 mRNA
GACGGCTTAACCACTGAGATCCCGTTCTATTGATTTAATAAAGTCAAACTATTGGAAAAA NM_152268 RefSeq chr1
- 54756897 54764553 PARS2 25973 "prolyl-tRNA synthetase 2, mitochondrial (putative)"
GO:0010467|GO:0006433|GO:0005759|GO:0004827|GO:0005524|GO:0006418 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127591_PI430048170 0.106883902253633 1.06719129756067 0.477866221048521
0.586689014386974 0.530646106940824 A A A 0.376587857575888 0.449278750374764
0.487731922752362 A A A LNCV6_127591_PI430048170 mRNA
CTTGCTTTAAAACAGTAGCGTATACTATGGTCATTGAACTTAATCTCTCTGGTGTTAGAA NM_001100420 RefSeq
chr21 - 17788966 17819386 C21orf91 54149 "chromosome 21 open reading frame 91, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135938_PI430048170 0.177140231372954 0.951018291780804 0.258866154844275
0.340331742217317 0.298293334021091 A A A 0.441644419279065 0.343056453658916
0.328664923411009 A A A LNCV6_135938_PI430048170 mRNA
TTTCTTTCCCGGTGCCGAGATGGCCTGAAAGAAAATGGCATCATCATATTGAAGGACAAT NM_001136107 RefSeq
chr1 + 170146046 170167782 METTL11B NA methyltransferase like 11B NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_143507_PI430048170 0.0255957280242074 0.854934676023929 8.29969013383154
8.19011504493619 8.12738359264571 P P P 8.4981647527676 8.42951847020443 8.3703040900766
P P P LNCV6_143507_PI430048170 mRNA
GGACCCTCGTTATCGCTGTTGCTCAAAATGTATTTTATGAATCATCCTAAATGAGAAAAT NM_015102 RefSeq chr1
- 5862807 5992473 NPHP4 261734 "nephronophthisis 4, transcript variant 1"
GO:0005515|GO:0005813|GO:0006996|GO:0030036|GO:0060041|GO:0007632|GO:0035329|GO:0030317|GO:0045
494|GO:0005829|GO:0035845|GO:0007165|GO:0016337|GO:0016020|GO:0005198|GO:0005911|GO:0035869|GO:0
032391|GO:0005923|GO:0090090 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144960_PI430048170 0.105517690869863 1.07729730522073 0.483500058478649
0.341990973550297 0.396038345839662 A A A 0.271053300363646 0.348523733759347
0.282025807293259 A A A LNCV6_144960_PI430048170 mRNA
GTCAATTCGAAAAAGCTTGGTGACCTCTGTGCGAGCTATGTCAGAGGCTGTTTATCAAGA NM_001080998 RefSeq
chr10 - 133625098 133626795 FRG2B NA "FSHD region gene 2 family, member B" NA . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_140727_PI430048170 0.4078452157049521.09476656832169 5.89947362291601
6.17942797879458 5.88339859546428 P P P 6.06645846594632 5.74957408872072
5.75032806783705 P P P LNCV6_140727_PI430048170 mRNA
TTTCCCCTTAGAAGGCTGTTTTTCAGTTTCCCCCAGTGAGGCCCAAAGAACAGTTTATTC NM_001142571 RefSeq
chr17 - 35099792 35119869 RAD51D 5892 "RAD51 paralog D, transcript variant 6"
GO:0000400|GO:0005515|GO:0000781|GO:0005813|GO:0043015|GO:0005657|GO:0005634|GO:0003677|GO:0005
524|GO:0005737|GO:0006281|GO:0000723|GO:0003697|GO:0000724|GO:0042148|GO:0033063|GO:0008094|GO:0
007131 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139351_PI430048170 0.5208782489085161.27521955326611 1.11801268870304
0.2778264288605761.48189864800809 A A A 0.2938250194771960.789405417101256
0.917503426877655 A A A LNCV6_139351_PI430048170 mRNA
GTGTTCCAGTTCAGTAATGGTGAATGTGGAAAAGTGAAATAAGACCAAGAAATACACCCA NM_001159352 RefSeq
chr1 - 119794017 119811580 REG4 83998 "regenerating islet-derived family, member 4, transcript
variant 1" GO:0005737|GO:0005509|GO:0005576|GO:2001065|GO:0008201 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_77399_PI430048170 0.8494819881868960.9809486106036480.2971601749575620.283608393996339
0.471334020698241 A A A 0.2959477853826340.2582645738990390.568566265283546 A A A
LNCV6_77399_PI430048170 mRNA
TACCTATGTGTCTTATCGTGGGCCACTGTGCCAATAAACAAAAACAACTGTTTGGTTTAC NM_001851 RefSeq chr6
- 70216039 70303083 COL9A11297 "collagen, type IX, alpha 1, transcript variant 1"
GO:0003417|GO:0005578|GO:0005576|GO:0005594|GO:0046872|GO:0001894|GO:0022617|GO:0030020|GO:0007
411|GO:0030198|GO:0030574|GO:0005788|GO:0009887 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103861_PI430048170 0.3458039978844671.13604983285116 4.30978627829229
4.04562483975859 4.21703976625695 P P P 3.91609553789832 4.29741961731531
3.76606063307103 P P P LNCV6_103861_PI430048170 mRNA
AAGGGCATTCAGATTTGGGAGAAGTAGCCCCAGAAATAAAAGCATCAGAGAGACGAACAG NM_001077663
RefSeq chr7 - 43875893 43907069 URGCP 55665 "upregulator of cell proliferation, transcript variant
3" GO:0007049|GO:0005737|GO:0005634|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115681_PI430048170 0.9582537774241 1.01011231042475 2.25024666631465 2.4036041301432
2.73269250162791 A A A 2.22215755207652 2.64018164427264 2.49279505029028 A P P
LNCV6_115681_PI430048170 mRNA
ATGTGTTTCTGTAGGAGTGTCACAGGTCACAACTTTAAAGCCAGCTTTGTCCACCCAGAA NM_006959 RefSeq chr19
+ 57411160 57421939 ZNF17 7565 zinc finger protein 17
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139013_PI430048170 0.5544037154590940.9943489782731590.342218911915677
0.3649313339111880.330034326429283 A A A 0.3562134824479390.36549975443311
0.34010210932853 A A A LNCV6_139013_PI430048170 mRNA
AACCTTGATGAGCGTTGTGCGATAATAAATTTCCGTTCTTCAGAAGAATGGGGCTGGAAT NM_130441 RefSeq chr12
- 7729414 7749473 CLEC4C 170482 "C-type lectin domain family 4, member C, transcript variant 1"
GO:0045087|GO:0030246|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132816_PI430048170 0.67204456609052 1.3191349773812 0.346547119978097
1.74094540056585 0.262715314532751 A A A 0.6239603234942770.299739169461319
0.709513567089756 A A A LNCV6_132816_PI430048170 mRNA
GTTGGAAGAAAAAAGAGAGAATTTCTTTTGGGCAGTGAAAATAAAGCAGTTAACAGTCCT NM_182552 RefSeq chr6
- 169457207 169702063 WDR27 253769 "WD repeat domain 27, transcript variant 1" GO:0005654 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142400_PI430048170 0.00661095667174968 0.5745660916797463.18351344398615

3.4078491558785 3.19774793962484 A P P 4.01047954435972 3.8896490824624
4.27166881904312 P P P LNCV6_142400_PI430048170 mRNA
AAGAATCCCAGGCTTGACCAACTGGTACCAGGTCAAAGATTTTTGTATTCTTGTGAATTT NM_014813 RefSeq chr1
+ 113073169 113125202 LRIG2 9860 leucine-rich repeats and immunoglobulin-like domains 2
GO:0060384|GO:0005737|GO:0005886|GO:0007605|GO:0010640|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140853_PI430048170 0.1891602432491580.9304885008567838.92668570209683
8.73415614231101 8.82323888861916 P P P 8.96318499726102 8.88234046940455
8.95544673425337 P P P LNCV6_140853_PI430048170 mRNA
GTTGCTGATTTCAGAGGGATATTCACTAATAAATGTATGATGTATACCAACGACCGCCCA NM_014901 RefSeq chr5
- 176526698 176537420 RNF44 22838 ring finger protein 44 GO:0008270 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_112218_PI430048170 0.0981212528918060.9361833575536720.273391775789135
0.2788582701348460.310762357374095 A A A 0.4474557709786790.367320738199526
0.331474206307683 A A A LNCV6_112218_PI430048170 mRNA
CCCGAGCAGAAGAGTGGTTAAATCTTTTGTTGAATACCAGAAACACATGGAAACTTTTGA NM_004010 RefSeq chrX
- 31119227 33128427 DMD 1756 "dystrophin, transcript variant Dp427p2"
GO:0050998|GO:0005515|GO:0030054|GO:0002162|GO:2000651|GO:0090287|GO:0005886|GO:0031527|GO:0005
634|GO:0030175|GO:0014819|GO:0015629|GO:0060048|GO:0043623|GO:0005829|GO:0044458|GO:0016010|GO:0
033137|GO:0030198|GO:0010880|GO:0060314|GO:0045211|GO:0016013|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_95841_PI430048170 0.0875592192857664 1.82617249434042 4.41396984812572
4.06001105635903 3.45904269432799 P P P 3.44906524872468 2.60007282869182 3.2993129755952
P A P LNCV6_95841_PI430048170 mRNA
GCAAAGGGGTGGTGAACAAGGATGAGTTCAAGCAGCTTCTCCTGACCCAGGCAGACAAGT NM_021223 RefSeq
chr7 - 44138863 44141317 MYL7 58498 "myosin, light chain 7, regulatory"
GO:0043197|GO:0005509|GO:0016459|GO:0031672 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71159_PI430048170 0.3820351164433481.06907799205523 7.95366712820946 7.78094575367691
7.96359530680999 P P P 7.90538008487934 7.85296253901654 7.64504496148198 P P P
LNCV6_71159_PI430048170 mRNA
AAGATTGCCCAGATCAAGCGCAACCTCTCCTATGGAGACAACAGCGACCCTGCCCTAGAG NM_014902 RefSeq chr20
+ 36306322 36528637 DLGAP4 22839 "discs, large (Drosophila) homolog-associated protein 4,
transcript variant 1" GO:0005515|GO:0016020|GO:0007267|GO:0045202 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_139499_PI430048170 0.0483042621293442 11.9161887928013 8.82652862626433
8.42472330935715 8.18598693001889 P P P 6.19791170642483 3.40032544885804
2.88887950105389 P P P LNCV6_139499_PI430048170 mRNA
GACAGCAACCTCCTGGGTAAATCTGAATGAAAAACGTGCTAGTCTCTTTCATGCAAAAAA NM_004933 RefSeq chr16
+ 89171754 89195492 CDH15 1013 "cadherin 15, type 1, M-cadherin (myotubule)"
GO:0031594|GO:0005886|GO:0034329|GO:0005509|GO:0045216|GO:0042692|GO:0051149|GO:0005901|GO:0016
021|GO:0007155|GO:0007156|GO:0034332|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113702_PI430048170 0.0285975367156922 0.5385097428601024.34452719408192
4.52627240682256 4.91066095702638 P P P 5.8020034736923 5.11385681321513
5.52203476621795 P P P LNCV6_113702_PI430048170 mRNA
TTCCTTGGGTGAAGGAGCTTCTTTATCTTGGTAACAGCATTATTTCAAGCATAACTTGTA NM_004323 RefSeq chr9
- 33252470 33264761 BAG1 573 "BCL2-associated athanogene, transcript variant 1"
GO:0035556|GO:0005515|GO:0043066|GO:0005737|GO:0070389|GO:0051087|GO:0006915|GO:0005634|GO:0005
057|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135185_PI430048170 0.3909404996636930.7897922253594360.461715214185286

0.4370435722154860.245403638130469A A A 0.3822957651238921.20743186503818
0.428821850578168A A A LNCV6_135185_PI430048170 mRNA
GAATGTGCAAATGTCCTCAGACAAGATGCACACCTTGCTCATTAGTGAGTTCATTTCAGG NM_020813RefSeq chr19
+ 56507842 56528900 ZNF471 57573 zinc finger protein 471
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144176_PI430048170 0.0081051733702622 0.2887412260365726.05080998941797
5.94239814670548 6.29183433222634 P P P 7.43208528788289 7.90643076347772
8.23505574545196 P P P LNCV6_144176_PI430048170 mRNA
GGGAAATCAGTAAAATGTCTTGATAATTGGTATCCAAATCACTTGTGTGCCTGAGAAAAT NM_001008495 RefSeq
chr8 - 90621994 90645905 TMEM64 169200 "transmembrane protein 64, transcript variant 1"
GO:0045780|GO:0005783|GO:0051480|GO:0043462|GO:0045672|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138979_PI430048170 0.0914030533600111 0.6099019497026672.85959660508422
2.65847135395285 1.96607030233952 A A A 2.9956287208739 3.27082804011291
3.46343343293631 P P P LNCV6_138979_PI430048170 mRNA
CCAGGCCTAGACTCAAGGTATTGTAAATGACAAGATACCAAATACAAGATTTTAAAAGCA NM_017847RefSeq chr1
+ 186375757 186421371 C1orf27 54953 "chromosome 1 open reading frame 27, transcript variant 1"
GO:0016491|GO:0008270|GO:0016021|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135115_PI430048170 0.120686556645407 0.7378404243864571 2.2566238115794 12.055438470441
12.5477253453609 P P P 12.4614884001531 12.6685375982546 13.0301906130374 P P P
LNCV6_135115_PI430048170 mRNA
GTCAGCAACTCTCCTGTTGGTTCATTATTGAATGTGCTGTAAATTAAGTTGTTTGCAATT NM_018407RefSeq chr8
+ 97775580 97852602 LAPTM4B 55353 lysosomal protein transmembrane 4 beta
GO:0005515|GO:0006810|GO:0016021|GO:0012505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143374_PI430048170 0.1085075841438862.15090794461219 2.51196643610953
3.22298797687201 2.68518811442854 A P A 0.731079960609925 2.38201860884347
1.63719180475937 A A A LNCV6_143374_PI430048170 mRNA
TTGTCAATTCCGCTGTAAAATAAGCATTGTCCGAGTAAAAACAGCAGCAACAACAAAAAA NM_024645RefSeq chr8
- 40530590 40897824 ZMAT4 79698 "zinc finger, matrin-type 4, transcript variant 1"
GO:0008270|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145356_PI430048170 0.0330504682515161 1.186487973649 0.681319570609406
0.8167612028878870.865123562917123A A A 0.6484708118983910.475309054113512
0.499397928485229A A A LNCV6_145356_PI430048170 mRNA
CAGCCTGAGGAACAAAGATATGAAGAGGGGTTTGAAGAAATTACAGGACAGAATTTACCG NM_001004453
RefSeq chr9 + 122749847 122750783 OR1L6 NA "olfactory receptor, family 1, subfamily L, member 6"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140861_PI430048170 0.3174349896038240.8564292557348297.94446375852132
7.75515664654799 7.74700857085609 P P P 8.3075652134647 8.00446487495906
7.76219830557029 P P P LNCV6_140861_PI430048170 mRNA
GCAGTGCTTTTGAACAAGATGACTTTGAAGAAGCCAAGGAAATTTTGACAAAGATGAGAT NM_172002RefSeq chr22
+ 28742054 28757508 HSCB 150274 HscB mitochondrial iron-sulfur cluster co-chaperone
GO:0005739|GO:0005515|GO:0003674|GO:0005813|GO:0005737|GO:0016226|GO:0005886|GO:0006457|GO:0051
087|GO:0051259|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58520_PI430048170 0.1786055890543730.9006649185575649.71915539807543 9.49669235957042
9.63958632278008 P P P 9.67717839737131 9.89681539124595 9.73388799274082 P P P
LNCV6_58520_PI430048170 mRNA
CATCTTTGGAAGAGAGGATAGATTCCTTAATTCTTTTGCAAGTATGCATCGGTTTGGTCC NM_005002RefSeq chr12
+ 4649097 4687554 NDUFA9 4704 "NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9,

39kDa"
GO:0005515|GO:0050662|GO:0031966|GO:0005743|GO:0005634|GO:0044281|GO:0032403|GO:0003954|GO:0022904|GO:0005747|GO:0005759|GO:0006120|GO:0006814|GO:0008137|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126671_PI430048170 0.3965456092762070.9230467086707660.300589393353602 0.4225146934806280.319167156450588A A A 0.6584287372183040.358130074045582 0.353686695373193A A A LNCV6_126671_PI430048170 mRNA
GTATTTATAAGGGGTGCATTTGTAGGGTGTGACATTTTACCCTAGGGTATAAAACTATTT NM_001011552 RefSeq chr2 + 102473302 102533972 SLC9A4 NA "solute carrier family 9, subfamily A (NHE4, cation proton antiporter 4), member 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62572_PI430048170 0.9755962565210991.00541948583124 8.00701492892444 7.70165486178866 7.47832309338739 P P P 7.65270637203823 7.86384668955805 7.68718016124302 P P P LNCV6_62572_PI430048170 mRNA
ACTTCTGGAGGCTTCCCTTGAAGCTCTGTGCAAAAGGTGGGAGACAGAGCTGGACCTGCA NM_001304799 RefSeq chr16 - 729754 741038 NARFL 64428 "nuclear prelamin A recognition factor-like, transcript variant 2" GO:0001666|GO:0006355|GO:0051539|GO:0016226|GO:0002244|GO:0044281|GO:0032364|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142240_PI430048170 0.0220541235959536 1.1108579318362 0.694487548073672 0.7491682379330050.697344149101848A A A 0.6242501877039320.526216246231228 0.534099130602354A A A LNCV6_142240_PI430048170 mRNA
GCAAGTGCAAAATACTCTATGGAAATCATAATTGTCATCTTCTTCATGGTGTTAGGGATA NM_052962RefSeq chr6 - 137143819 137173648 IL22RA2 116379 "interleukin 22 receptor, alpha 2, transcript variant 1" GO:0042018|GO:0042017|GO:0005886|GO:0050728|GO:0042516|GO:0019221|GO:0016021|GO:0005615|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127911_PI430048170 0.0828367839806893 0.5363026783376652.52918447979773 1.81593134536616 2.89445579138177 A A P 2.93948051610237 3.34940415660702 3.73655057931789 P P P LNCV6_127911_PI430048170 mRNA
AGCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTAC NM_012338RefSeq chr7 - 120787319 120858123 TSPAN12 23554 tetraspanin 12 GO:0042813|GO:0016020|GO:0005887|GO:0045765|GO:0010842|GO:0016021|GO:0001525|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137312_PI430048170 0.6450265549223130.7392878153216723.6716809833601 3.14695379781671 3.63498290997967 P P P 2.77562711786434 4.00509228179737 4.53101873958554 P P P LNCV6_137312_PI430048170 mRNA
CCTGGAATCAACTTGTATGAAACCTTGTCAAAATGTACTCCACAAGTATGTACAATTAAG NM_005915RefSeq chr2 - 135839625 135876477 MCM6 4175 minichromosome maintenance complex component 6 GO:0005515|GO:0042555|GO:0005634|GO:0005524|GO:0042802|GO:0006260|GO:0000082|GO:0006271|GO:0004003|GO:0003697|GO:0006270|GO:0006268|GO:0005654|GO:0000278 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142175_PI430048170 0.00224016941946739 0.2715030039455063.42151461452748 3.40322499538844 4.01306423546928 P P P 5.21858125311697 5.62530692651216 5.68095872558651 P P P LNCV6_142175_PI430048170 mRNA
CCCCACAACATGTGTAACACTTTTCAGTCTGTGGATATCTGATACATTAAGATTTCTTTT NM_001172312 RefSeq chr3 + 142656896 142713663 PLS1 5357 "plastin 1, transcript variant 3" GO:0005737|GO:0051015|GO:0005509|GO:0005200|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76014_PI430048170 0.5660323341132271.10671843772162 0.3421502107798130.463580783042996 0.891743465133173A A A 0.2581334108211760.7453654225577860.257701437308345A A A LNCV6_76014_PI430048170 mRNA

ATAAAATTGTCCAGTTGTCAGGAGCAGCGAAACAGCCAAAAGTTGGGTTCTACTCTTCTC NM_012159RefSeq chr5 + 135930316 135941678 FBXL21 26223 F-box and leucine-rich repeat protein 21 (gene/pseudogene) GO:0004842|GO:0016567|GO:0000151|GO:0005634|GO:0048511|GO:0043153|GO:0019005|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139497_PI430048170 0.0011683429574711 0.2106259198531117.36108111458232 6.97066977874633 7.64880802803994 P P P 9.42833801212405 9.46768800684989 9.86388676469233 P P P LNCV6_139497_PI430048170 mRNA
AGACATGAAAAGAGTGGTGACAAATCAAGAATAAACACTGGTTGTAGTCAGTTTTGTTTG NM_001144663 RefSeq chr8 - 94127165 94217303 CDH17 1015 "cadherin 17, LI cadherin (liver-intestine), transcript variant 2" GO:0005215|GO:0035672|GO:0005886|GO:0034329|GO:0005509|GO:0045216|GO:0016339|GO:0016323|GO:0005427|GO:0006857|GO:0006810|GO:0016021|GO:0007155|GO:0007156|GO:0034332 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137709_PI430048170 0.1492478205911740.3896399403616341.95616807275252 0.3459987635740562.88781940107648 A A P 3.40567654275779 3.54778977418531 3.31093263826533 P P P LNCV6_137709_PI430048170 mRNA
GGCATAGCCCTAACACAGTTGTTCACAAGTTTTCTTTTTTCTTGTTGCAATTTTCCTTCA NM_001010984 RefSeq chr1 + 231337935 231355027 SPRTN 83932 "SprT-like N-terminal domain, transcript variant 2" GO:0005515|GO:0043130|GO:0005694|GO:0005634|GO:0003677|GO:0019985|GO:0006974|GO:0046872|GO:0016607|GO:0031398|GO:0005654|GO:0009411|GO:0070530 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57121_PI430048170 0.0165487093829761 0.7101246382687074.07707832173533 3.95354012275872 4.03151782720016 P P P 4.34764687846826 4.55476769384974 4.62942909304044 P P P LNCV6_57121_PI430048170 mRNA
ATGTGATGTTGGAGAACTACAGAAACTTGTTCTCCGTTGGTCTCACTGTCTGTAAGCCAG NM_001242841 RefSeq chr11 - 3357926 3379222 ZNF195 7748 "zinc finger protein 195, transcript variant 4" GO:0006355|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129092_PI430048170 0.2984533901707071.01473598349727 0.316028371283984 0.3334875658436220.365690671079341 A A A 0.3304849536065860.321412980043662 0.300269685700643 A A A LNCV6_129092_PI430048170 mRNA
TGCATGTTGACTATTTGCAACGAGCTCAAATGCTATCTGATCAAAGTCTATTTTGCATAA NM_000324RefSeq chr6 - 49605176 49636874 RHAG 6005 Rh-associated glycoprotein GO:0005886|GO:0015696|GO:0030506|GO:0006873|GO:0008519|GO:0044281|GO:0015670|GO:0055085|GO:0060586|GO:0005887|GO:0048821|GO:0072488|GO:0015701 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140480_PI430048170 0.345940135054363 0.96795285049509 0.249211355711441 0.262438590028457 0.3677054190077 A A A 0.383453074647223 0.318477719980041 0.320392423457279 A A A LNCV6_140480_PI430048170 mRNA
GTTTATCTTTCATTTCTCAACCCCTTGTACTTTGGTGATACCAGACATCAGAATAAAAAG NM_001963 RefSeq chr4 + 109912883 110012962 EGF 1950 "epidermal growth factor, transcript variant 1" GO:0005515|GO:0005154|GO:0008284|GO:0005886|GO:0051048|GO:0007262|GO:0021940|GO:0035413|GO:0005765|GO:0005615|GO:2000008|GO:0007171|GO:0000186|GO:0030297|GO:0007173|GO:0043406|GO:1900127|GO:0031093|GO:0070371|GO:0070062|GO:0010800|GO:0048011|GO:0090279|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141084_PI430048170 0.23622468892123 0.964702337090147 0.266894617613271 0.281294308172146 0.35940103454486 A A A 0.3999734922596 0.342306405340436 0.321418425746719 A A A LNCV6_141084_PI430048170 mRNA
GAGATTGAAAACGTTACTTCAGTTCCTTGTGTCTGACATTGCTTGTTTGTAACTAAGAAA NM_172241 RefSeq chr18 - 22413600 22417915 CTAGE1 64693 cutaneous T-cell lymphoma-associated antigen 1

GO:0008150|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139755_PI430048170 0.434921448402891 0.900762493423129 9.73519142587209 9.40264956396043 9.144558703636 P P P 9.61854123516875 9.69269770245991 9.47625833867346 P P P LNCV6_139755_PI430048170 mRNA TTAGGCCCCTTTGGAGGGAGAATCAATAAATAACAAACACCAACTACAAACGCCAAAAAA NM_001261451 RefSeq chr9 - 131523795 131531275 UCK1 83549 "uridine-cytidine kinase 1, transcript variant 4"
GO:0016310|GO:0044211|GO:0044206|GO:0004849|GO:0055086|GO:0044281|GO:0043097|GO:0019206|GO:0006206|GO:0005524|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142637_PI430048170 0.466762879032311 1.2379586021354 0.481954688236748 0.4935966133361 1.33073220132982 A A A 0.550906737412502 0.525992834407335 0.477549542812307 A A A LNCV6_142637_PI430048170 mRNA CGTGTATTCCTGAAACTTTTTGACTTACTTATCTTACATGTGGTGTCTTCCTGTATATAG NM_018962 RefSeq chr21 + 37006562 37019658 RIPPLY3 53820 ripply transcriptional repressor 3
GO:0007507|GO:0008150|GO:0005634|GO:0000122|GO:0006351|GO:0060037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140246_PI430048170 0.0325080022823252 1.47114081465238 13.1746757216281 13.2305330259162 13.5821153171205 P P P 12.7651526056108 12.5800424061891 12.9784049502652 P P P LNCV6_140246_PI430048170 mRNA TGCCTTTCATTAAATGTAACCTTTTGCCTTCCAAATTAAAGAACTCCATGCCACTCCTCA NM_001344 RefSeq chr14 - 22564906 22589237 DAD1 1603 defender against cell death 1
GO:0004576|GO:0043066|GO:0007584|GO:0042493|GO:0001824|GO:0006915|GO:0016020|GO:0004579|GO:0005789|GO:0006486|GO:0016021|GO:0008250|GO:0044267|GO:0070062|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135141_PI430048170 0.464871310664116 0.729678362265465 1.63320868567635 1.13310469242067 0.434147983223172 A A A 2.00608386310388 1.79551124011432 0.696378925658234 A A A LNCV6_135141_PI430048170 mRNA GGGTGGGTGACAGAAAATGAAAGTCTTTTTGGTGATTGTTAAAGCAAAATGTGTATAAAG NM_014644 RefSeq chr1 + 148889451 149033019 PDE4DIP 9659 "phosphodiesterase 4D interacting protein, transcript variant 1"
GO:0005515|GO:0005813|GO:0005737|GO:0005794|GO:0005634|GO:0030016|GO:0019899|GO:0043623 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101228_PI430048170 0.754267555679276 0.932465329967785 2.18858222602546 2.02335389464771 0.373393194362443 A A A 1.26185802970904 1.65181610264808 2.34974001066989 A A A LNCV6_101228_PI430048170 mRNA CTGTTAAAAAACTGAGGTGTAACCAGGATTACACTGGCTGGAATAAACCAAGAGTGCCCC NM_020935 RefSeq chr2 - 218450250 218568361 USP37 57695 ubiquitin specific peptidase 37
GO:0005515|GO:0071108|GO:0016579|GO:0004843|GO:0019901|GO:0005634|GO:0035871|GO:0004197|GO:0000082|GO:0007067|GO:0061136|GO:0043161|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73473_PI430048170 0.0179722595410151 1.30894914281842 12.5064366442114 12.6665830782026 12.7633844617118 P P P 12.2458498700351 12.1900557256515 12.3427001540921 P P P LNCV6_73473_PI430048170 mRNA GCTTTGAAAGAACCCTTCCTTACCTGGTGTGTTTTCTATAAATCTTCATAGGTTATTTTG NM_003707 RefSeq chr3 - 128080956 128123828 RUVBL1 8607 RuvB-like AAA ATPase 1
GO:0005515|GO:0006325|GO:0005634|GO:0007283|GO:0000812|GO:0016363|GO:0043231|GO:0005737|GO:0071339|GO:0035267|GO:0032508|GO:0016887|GO:0070062|GO:0005794|GO:0005815|GO:0006357|GO:0006334|GO:0006310|GO:0005524|GO:0003678|GO:0006351|GO:0034080|GO:0031011|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137154_PI430048170 0.609814019115947 1.09255000993002 2.39484230997682 2.37717882690708 1.92156435732797 A A A 2.38922656359534 1.73776152582727 2.157784437667 A A A LNCV6_137154_PI430048170 mRNA TGCTGTGTATCCTAACTCCCTACAACAGCCCCTCAAATAAATCACATCTAGTGACTGGTA NM_005468 RefSeq chr11 - 65044822 65058537 NAALADL1 10004 N-acetylated alpha-linked acidic dipeptidase-like 1 GO:0016324|GO:0006508|GO:0004180|GO:0008233|GO:0016021|GO:0016805|GO:0046872|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_50037_PI430048170 0.0439374507917418 1.25617236084065 6.24837496425326 6.21415136334146 6.08049913155436 P P P 5.67277018030575 5.96242663388377 5.90992695621231 P P P LNCV6_50037_PI430048170 mRNA ACAATTTAGAAACAGAAAAACTGTGTGACTACTTCTCAGAGCACCTGGGTGTCTACCGGC NM_031232 RefSeq chr20 - 33657086 33674458 NECAB3 63941 "N-terminal EF-hand calcium binding protein 3, transcript variant 2" GO:0005515|GO:0005737|GO:0000137|GO:0009306|GO:0005509|GO:0005789|GO:0005634|GO:0042984|GO:0019538 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127857_PI430048170 0.00478432454263553 1.77642573884289 4.0250147632983 4.34271378777075 4.35547819482889 P P P 3.22582015691634 3.53521856987127 3.48038753910106 P P P LNCV6_127857_PI430048170 mRNA CCCTCGGCAAGCACCAATCCTTGGTGCTGCCGTTTTTAAAATCTTCCAAATGCCTTTTTT NM_001171162 RefSeq chrX - 71239623 71255197 ZMYM3 9203 "zinc finger, MYM-type 3, transcript variant 3" GO:0022604|GO:0007010|GO:0008270|GO:0007275|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128919_PI430048170 0.0830987646240407 0.955611852888378 0.421939945920724 0.365928395103825 0.375644842230358 A A A 0.480403524509676 0.469515793307064 0.409728000843097 A A A LNCV6_128919_PI430048170 mRNA ACCAGCGGGGTGCTTGCCATTCTGATGATAATAAAATGAATGTGTTGCAAATTGAAAAAA NM_001001888 RefSeq chrX + 8464829 8466510 VCX3B NA "variable charge, X-linked 3B" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143732_PI430048170 0.330112175267092 1.84608997801218 2.41366010513658 2.14358704946481 0.550757536947823 A A A 0.587548696811337 1.61739589751888 0.587183662461024 A A A LNCV6_143732_PI430048170 mRNA GGACTCCCCTGGTGATGGGGCAGGACCAGAACAATTAAAAATGTTTCTTCTGTCAAAAAA NM_001114759 RefSeq chr1 - 26361633 26372794 ZNF683 257101 "zinc finger protein 683, transcript variant 1" GO:0006355|GO:0005634|GO:0001779|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138342_PI430048170 0.89103462123617 1.00617645546978 11.713445874158 11.7112150389992 11.7474501318228 P P P 11.5015973791076 11.7252766370208 11.8924318212428 P P P LNCV6_138342_PI430048170 mRNA AAACTAAGTTTTGGGGGATCCTTTTGTAATGACTTACACTGGAAATGCGAACATTTGCAG NM_004996 RefSeq chr16 + 15949576 16143073 ABCC1 4363 "ATP-binding cassette, sub-family C (CFTR/MRP), member 1" GO:0019369|GO:0005215|GO:0009235|GO:0005886|GO:0042493|GO:0042626|GO:0006767|GO:0044281|GO:0055085|GO:0005524|GO:0006691|GO:0016020|GO:0005887|GO:0006766|GO:0006810|GO:0016887|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134763_PI430048170 0.0295940562665434 0.83976240284988 10.8159353426104 10.6156244264603 10.7510674056318 P P P 10.9226189645456 11.063948794631 10.9552580650324 P P P LNCV6_134763_PI430048170 mRNA CTTCCTCCCCTCTCAAAGTTTGTTTGTTTGTGTTCTGACAGAGGATAAAGCTATTTTACC NM_001256658 RefSeq chr19 - 49340595 49362457 TEAD2 8463 "TEA domain family member 2, transcript variant 1"

GO:0005515|GO:0005667|GO:0010467|GO:0048339|GO:0006355|GO:0003700|GO:0006367|GO:0003705|GO:0001843|GO:0005634|GO:0035329|GO:0003677|GO:0003143|GO:0048368|GO:0045944|GO:0060548|GO:0005654|GO:0030903|GO:0001570 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144048_PI430048170 0.469255408604967 1.41653857633251 1.92048774283243 0.439773294129704 1.03729494304919 A A A 0.969249236441151 0.492331777929356 0.777564337239164 A A A LNCV6_144048_PI430048170 mRNA
GGATAGGATACTTGGAACTAAGAAGATATACTTACTTAGCTAAAGCAGTGTTACGTAGAA NM_001205272 RefSeq
chr3 + 42936341 42942791 KRBOX1 100506243 KRAB box domain containing 1
GO:0005622|GO:0006355|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138650_PI430048170 0.167083655218807 1.27397699285013 12.2898000830561 12.4591975117857 12.495548771371 P P P 12.3575241016145 11.7344290689134 12.0458011195021 P P P LNCV6_138650_PI430048170 mRNA
GCACTGTAAAATGTGGGATTATGGGTCACAGGAAAAAGTGGGTTTTTTAGTTGAATTTTT NM_003299 RefSeq
chr12 + 103930333 103947930 HSP90B1 7184 "heat shock protein 90kDa beta (Grp94), member 1"
GO:0005515|GO:0048471|GO:0005886|GO:0005783|GO:0003723|GO:0031247|GO:0005634|GO:0015031|GO:0005829|GO:0030968|GO:0006457|GO:0071682|GO:0070062|GO:0042470|GO:0001666|GO:0051208|GO:0043066|GO:0019903|GO:0005509|GO:0046790|GO:0030496|GO:0005576|GO:0002224|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131918_PI430048170 0.29447624516126 0.67196473389913 0.452483859160712 0.421824179169013 0.299466604328058 A A A 0.673475317224217 1.55603908492762 0.407199725793845 A A A LNCV6_131918_PI430048170 mRNA
AAGCCAAGGGCTATCAGCTCCTAGAAGAAGAGAAAATCGTTTCCCACTATTTCCCCTTGA NM_005267 RefSeq
chr1 + 147902819 147909268 GJA8 2703 "gap junction protein, alpha 8, 50kDa"
GO:0005243|GO:0005887|GO:0002088|GO:0007267|GO:0006810|GO:0051260|GO:0005922|GO:0055085|GO:0007601|GO:0015267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132766_PI430048170 0.341376701614251 2.30018281433132 0.257693251848784 2.56983033816702 2.71078072434624 A A A 1.77860277506057 0.330484953606586 0.332115870456573 A A A LNCV6_132766_PI430048170 mRNA
AAGTTTCTTGTGAAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACTTATCTCCCATC NM_207393 RefSeq
chr19 - 46120070 46124674 IGFL3 NA IGF-like family member 3 NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_138890_PI430048170 0.289022934680767 0.824288380516949 7.65383856701152 7.14858555344142 6.95963002804143 P P P 7.61463402702652 7.71097686135215 7.33927414578455 P P P LNCV6_138890_PI430048170 mRNA
GTAGGTGGGCGCTGCCCAGAAAATATATTTCAATAAAAGAGAGAAGCAAGCTTGAAAAAA NM_019848 RefSeq
chrX - 154487305 154490690 SLC10A3 8273 "solute carrier family 10, member 3, transcript variant 1"
GO:0005887|GO:0015721|GO:0008508|GO:0032526|GO:0055085 . NA - . NA NA NA NA NA NA NA NA
LNCV6_136834_PI430048170 0.169227761245078 1.03882723389434 0.348814630733433 0.318055556089688 0.409716959691645 A A A 0.298373267166583 0.285417706172038 0.329092799328421 A A A LNCV6_136834_PI430048170 mRNA
TTGAGGGTATGGAGAGATGGTATACAGCAGGTAACTGTGAATTGCAGAATAAATTGAAAG NM_017677 RefSeq
chrX - 64268080 64395453 MTMR8 55613 myotubularin related protein 8
GO:0005635|GO:0035335|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128665_PI430048170 0.932160403189516 1.00402569737984 11.7916605270796 11.9385146749093 11.9145956032677 P P P 11.8160982614351 11.9437810113294 11.8689048451933 P P P LNCV6_128665_PI430048170 mRNA

GGGCAAACTGAAATGTACGCCTGAATTTTGTAAACAGAAGTATTAAATGTCTCTTTCTAC NM_003025 RefSeq chr19 - 4360366 4400568 SH3GL1 6455 "SH3-domain GRB2-like 1, transcript variant 1" GO:0005515|GO:0030054|GO:0019902|GO:0002102|GO:0042995|GO:0007417|GO:0006897|GO:0008289|GO:0042802|GO:0007165|GO:0005737|GO:0051020|GO:0031901 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106808_PI430048170 0.00357031604300609 2.97037417039145 2.60062495122856 2.01584055168139 2.570867104279 A A A 0.614353974707941 0.738476602744806 1.14046336575018 A A A LNCV6_106808_PI430048170 mRNA
ATGTTTTAGAACATACAGTTTCCTGAAGAACAGGAGGGATAGCTGGAGAGGGGATAGGAG NM_001291030 RefSeq chr22 - 38578119 38656629 FAM227A NA "family with sequence similarity 227, member A, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107869_PI430048170 0.0428459022760719 0.916486275962072 4.33516415096483 4.27866874978499 4.23101773276326 P P P 4.41008473388872 4.42242083937101 4.39150756879934 P P P LNCV6_107869_PI430048170 mRNA
TTCAATGACAAGAACAACTCCAACCTCTGGATGTCTTCCATGCCTGGAATCAACAACGGT NM_001159576 RefSeq chr12 - 6346842 6375224 SCNN1A 6337 "sodium channel, non voltage gated 1 alpha subunit, transcript variant 2" GO:0005515|GO:0007588|GO:0060170|GO:0005886|GO:0031514|GO:0050699|GO:0034706|GO:0003779|GO:0055078|GO:0055085|GO:0005829|GO:0015280|GO:0016324|GO:0034220|GO:0050909|GO:0050891|GO:0005887|GO:0035725|GO:0030864|GO:0006814|GO:0050896|GO:0009897|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138558_PI430048170 0.143320914305294 0.777785233978358 0.420556778416571 0.423754026536903 0.354198053858877 A A A 0.850463808505273 0.939704387409629 0.451818092185124 A A A LNCV6_138558_PI430048170 mRNA
CTTGTGGCCTCTATCTGCTACCATCTGTGTTTTATCTGAGTAAAGTTACCTTACTTCTGG NM_005856 RefSeq chr7 + 45157767 45184251 RAMP3 10268 receptor (G protein-coupled) activity modifying protein 3 GO:0005515|GO:0005886|GO:0009986|GO:0015031|GO:0015026|GO:0072659|GO:0005764|GO:0006886|GO:0043235|GO:0031623|GO:0005622|GO:0008277|GO:0005887|GO:0071392|GO:0008565|GO:0001921|GO:0004872|GO:0006816|GO:0045892|GO:0090004 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70575_PI430048170 0.0170848121494127 1.79177024577683 6.64662430043807 6.73276270079066 6.55585689385533 P P P 5.5919917117704 5.71810909815434 6.06413204277833 P P P LNCV6_70575_PI430048170 mRNA
AGATGTGTTCTGAGCTGGATGCCGGGTTCCAGAATCGCTGCACAGTTCCAACAGGACAGC NM_006736 RefSeq chr2 + 219279317 219286900 DNAJB23300 "DnaJ (Hsp40) homolog, subfamily B, member 2, transcript variant 2" GO:0005515|GO:0006986|GO:0090084|GO:0000502|GO:0030308|GO:0008285|GO:0016234|GO:0090086|GO:0051087|GO:0032436|GO:0005634|GO:0030433|GO:0005829|GO:0042026|GO:0006457|GO:0070628|GO:0031398|GO:0030544|GO:0051082|GO:0031593 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129817_PI430048170 0.4654822603402580.9429053909727370.34840004394034 0.3258714532350540.267452360042459A A A 0.5698567422381840.316391964410491 0.294587530379304A A A LNCV6_129817_PI430048170 mRNA
TTGGTAAATACTAATGGGAGTAGACAGAGTTGTATGGCCTGGACAGTGGAAACCAAGAGC NM_199461RefSeq chr10 + 119029715 119034342 NANOS1 340719 nanos homolog 1 (Drosophila) GO:0017148|GO:0005515|GO:0048471|GO:0005737|GO:0016477|GO:1900153|GO:0003723|GO:0010631|GO:0008270|GO:0030371 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132253_PI430048170 0.00572801225898946 0.6093020114487935.26122044195943 5.07282218113956 5.41007359367795 P P P 5.95188486783801 5.86564502614121 6.08230146565584 P P P LNCV6_132253_PI430048170 mRNA
GTCTGGAATTCTTACTGAAAAATTGACCCTGAGACAATACACAGATGTGATGATTGAATT NM_018393RefSeq chr11

+ 33039416 33073563 TCP11L1 55346 "t-complex 11, testis-specific-like 1, transcript variant 1"
GO:0005874 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128337_PI430048170 0.284029479909861 0.680837736385488 0.298993732490476
0.319324519766468 0.284284089143411 A A A 0.491834287738389 0.407063367260516
1.43090218984583 A A A LNCV6_128337_PI430048170 mRNA
CATTCATAGTAAGAATTCTGGTGTTTACACAACCAAATTTGATGCGATCTGCTCAGTAAT NM_003489 RefSeq chr21
- 14961234 15064805 NRIP1 8204 nuclear receptor interacting protein 1
GO:0005515|GO:0030054|GO:0042826|GO:0019915|GO:0035257|GO:0005634|GO:0035259|GO:0050681|GO:0046
965|GO:0045944|GO:0001046|GO:0003714|GO:0003713|GO:0030331|GO:0005730|GO:0001543|GO:0000122|GO:0
006351|GO:0032922|GO:0000118|GO:0016607|GO:0007623|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144958_PI430048170 0.00819473915051273 0.632742567394655 7.45059721754873
7.22909518054927 7.10187922550931 P P P 7.81501657088996 8.05115908254319
7.90825510031144 P P P LNCV6_144958_PI430048170 mRNA
CCAGCTAAGTTTCCCCTCAATAAAAAGCCCGCTTTCTGGGAAAGACAGAAACTGAAAAAA NM_001010911 RefSeq
chr10 - 21494491 21497284 CASC10 399726 cancer susceptibility candidate 10 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143349_PI430048170 0.426947639927559 1.47479263593416 0.473399543825981
0.456266986851142 1.75253017282067 A A A 0.395599916001098 0.509573226643991
0.503144148031905 A A A LNCV6_143349_PI430048170 mRNA
GGGGGCTGTTGTAAACAGAGGCTTAATTTTATTAGAAGTAGCCAGTTATTTATTAAAGCA NM_001448 RefSeq chrX
- 133301035 133415177 GPC4 2239 glypican 4
GO:0005886|GO:0007603|GO:0005796|GO:0005975|GO:0008283|GO:0005578|GO:0006027|GO:0043395|GO:0005
634|GO:0044281|GO:0031225|GO:0009653|GO:0001523|GO:0005615|GO:0006024|GO:0005887|GO:0009405|GO:0
030204|GO:0030203|GO:0009897|GO:0070062|GO:0043202 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_137981_PI430048170 0.182029478111382 0.889009104431423 9.9511133301039
10.1512713248441 10.2415687472143 P P P 10.3784635759692 10.1773520113043
10.3053129309195 P P P LNCV6_137981_PI430048170 mRNA
ACCCCAGGACCTCCTTACTTTTTAATATAAAGAGTGATGTTGTATTTCGTGTTCTGCACT NM_001081491 RefSeq
chr11 - 62792125 62805492 NXF1 10482 "nuclear RNA export factor 1, transcript variant 2"
GO:0005515|GO:0010467|GO:0000346|GO:0003729|GO:0005829|GO:0006406|GO:0000166|GO:0005487|GO:0016
607|GO:0005643|GO:0016973|GO:0016032|GO:0005654|GO:0042405 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_82584_PI430048170 0.134424937982442 1.12183545113103 9.15922891703306 9.30810076098402
9.35538571334852 P P P 9.12135180920598 8.9871748417613 9.21476538049263 P P P
LNCV6_82584_PI430048170 mRNA
GCCTACATCCAAAATATTATCTTGTGACTCCATGAACCATTCATTAACCCTTTGTATCTT NM_016561 RefSeq
chr16_KI270853v1_alt + 205666 242094 BFAR 51283 bifunctional apoptosis regulator
GO:0043066|GO:0016020|GO:0005887|GO:0005198|GO:0005789|GO:0006915|GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143701_PI430048170 0.36943832493474 0.760127390360924 0.33854163226219
0.378761853653006 0.328655541684247 A A A 0.437900271549177 0.348297441048125 1.2621340435355
A A A LNCV6_143701_PI430048170 mRNA
CCAGCAGTTAACTCATGTTTATTGTGCTTTCATGCATTGTGATATGGAATGTGTTTAGTA NM_022913 RefSeq chr5
+ 57173947 57264679 GPBP1 65056 "GC-rich promoter binding protein 1, transcript variant 1"
GO:0005737|GO:0003700|GO:0005886|GO:0005730|GO:0045893|GO:0003677|GO:0006351|GO:0043231 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135515_PI430048170 0.83758705910299 0.935610741206179 1.19137230009402 2.5321366007883

3.09095431962236 A A P 3.0856802383358 1.54732347057243 2.65945842260369 P A P
LNCV6_135515_PI430048170 mRNA
TCTCAGATGAAGTGTGTGGCTATGTATGCATGTAACTTGGTTTCTTTGAAAACCCAATTA NM_001199707 RefSeq
chr7 - 36324149 36367173 KIAA0895 23366 "KIAA0895, transcript variant 4" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_112337_PI430048170 0.0292152750622141.27578851851432 11.3233694122397
11.5535053044838 11.4509708143972 P P P 11.1050457319613 11.1139538456172
11.0633568785776 P P P LNCV6_112337_PI430048170 mRNA
CATGTTTACAGACCTGTTTTGTCATCCTGCTGCCAAGAAGTTTTTTAATCACTTGAATAA NM_016256RefSeq chr16
- 5024843 5033941 NAGPA 51172 N-acetylglucosamine-1-phosphodiester alpha-N-
acetylglucosaminidase
GO:0005975|GO:0003944|GO:0032580|GO:0006622|GO:0006486|GO:0016021|GO:0007040|GO:0006464 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131645_PI430048170 0.00808737745790109 0.7600853024135610.9125842527929
10.8448703692189 10.7239518429389 P P P 11.1301356081291 11.2060109809689
11.3316339403538 P P P LNCV6_131645_PI430048170 mRNA
GCCTTTTGCAATCATGAAACCTGGGAATCCAAATAGTTGGATAACTTAGAATAACTAAGT NM_001178014 RefSeq
chr3 + 136250324 136330171 PCCB 5096 "propionyl CoA carboxylase, beta polypeptide, transcript
variant 2"
GO:0005739|GO:0006635|GO:0006766|GO:0005759|GO:0006768|GO:0004658|GO:0019626|GO:0006767|GO:0044
281|GO:0005524|GO:0044255|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134007_PI430048170 0.0230449621706612 1.219661291447 14.4237882405893
14.3232432735039 14.212989510495 P P P 14.0418715821948 14.1123508560733
13.9494362927154 P P P LNCV6_134007_PI430048170 mRNA
CTAGTATGCAATAAGAGATGCCCTGTACTGATGCAAAATTTAATAAAGTTTGTCACAGAG NM_001270481 RefSeq
chr17 + 4796143 4798503 PSMB6 5694 "proteasome (prosome, macropain) subunit, beta type, 6,
transcript variant 2"
GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0004298|GO:0034
641|GO:0005737|GO:0000082|GO:0016032|GO:0090090|GO:0070062|GO:0006977|GO:0000209|GO:0000502|GO:0
005839|GO:0043066|GO:0005794|GO:0006521|GO:0051437|GO:0042590|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127035_PI430048170 0.0449726292676567 2.01286031807117 7.41881455320272
7.5582291065621 7.50795554721053 P P P 6.92339357152184 6.1725671874346
6.23958767816869 P P P LNCV6_127035_PI430048170 mRNA
GTTGAAGGCAAAATTGTTGTAACACTACAGCTGAGCAGATGTAATAGAAATAAACCTATG NM_000716RefSeq chr1
+ 207089238 207099992 C4BPB 725 "complement component 4 binding protein, beta, transcript variant 1"
GO:0044216|GO:0005515|GO:0030449|GO:0045732|GO:0005886|GO:0007596|GO:0045087|GO:0006958|GO:0045
959|GO:0005576|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143988_PI430048170 0.3567070440203570.8412913085515025.58848403576453
5.36500021665583 5.44544989322775 P P P 6.00732719664289 5.72480227234622
5.34929933658178 P P P LNCV6_143988_PI430048170 mRNA
GAACCCTAGCACCTGTCCCCATGAAAAACTCTGGTTCTATAAAATAGTTTTCCTAATTTT NM_005868RefSeq chr7
- 93991687 94004378 BET1 10282 Bet1 golgi vesicular membrane trafficking protein
GO:0019905|GO:0006888|GO:0005515|GO:0005801|GO:0016020|GO:0000139|GO:0031985|GO:0005789|GO:0048
280|GO:0016021|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121859_PI430048170 0.45002517225617 0.9114882694213990.377195581242487
0.3553567444363580.256533383490771 A A A 0.3118390658034790.331988664567109
0.712852823574265 A A A LNCV6_121859_PI430048170 mRNA
TGGTCTCCTTCGTTCAGACGCTTTGCAAGGGCTTATCCCAACCCACCACCAACCTGGTTG NM_002500RefSeq chr2

- 181676105 181680665 NEUROD1 4760 neuronal differentiation 1
GO:0071156|GO:0005515|GO:2000679|GO:0003700|GO:0007263|GO:0060730|GO:0045597|GO:0005634|GO:0009
952|GO:2000675|GO:0003326|GO:0051091|GO:0005737|GO:0003690|GO:0045944|GO:0003329|GO:0071333|GO:0
022008|GO:0001102|GO:0021542|GO:0048839|GO:0001105|GO:0043065|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139883_PI430048170 0.00210913811783746 1.93739941883046 5.32141861336333
5.11799938099276 5.45327414641653 P P P 4.31194371827664 4.25075785929999
4.47757436674978 P P P LNCV6_139883_PI430048170 mRNA
GGTCAGTAGAGTCCCAAGGATTTGTAGACTTTAGGGGGTCAATAAAGCTGAAATTGTATT NM_014584RefSeq chr14
- 52639914 52695931 ERO1L 30001 ERO1-like (S. cerevisiae)
GO:0005515|GO:0034976|GO:0005783|GO:0015035|GO:0022417|GO:0030968|GO:0043231|GO:0009266|GO:0006
457|GO:0030198|GO:0016671|GO:0051209|GO:0003756|GO:0019471|GO:0016020|GO:0070059|GO:0050873|GO:0
016491|GO:0005789|GO:0051085|GO:0005788|GO:0045454|GO:0000302|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129667_PI430048170 0.474592946086877 1.02339452422272 0.375752792219963
0.25416862915593 0.279950668178814 A A A 0.263772075575014 0.286070251464693
0.262685872734947 A A A LNCV6_129667_PI430048170 mRNA
GCTTTTCTTAGAAGTGATGTGTTGTTAGAAACTTCAAACCAGATACAAATATACCCAACG NM_001085382 RefSeq
chr4 - 7430293 7434973 PSAPL1 768239 prosaposin-like 1 (gene/pseudogene)
GO:0006665|GO:0005737|GO:0005576|GO:0005764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135773_PI430048170 0.0805519972235363 0.856344800504762 7.2003058792493
6.97774286654071 7.19055889477639 P P P 7.32461951526264 7.33859808517762
7.38663910473063 P P P LNCV6_135773_PI430048170 mRNA
AGCCCCACATCAGAGGGCATCCAATCTGATCTTTGTGAAAATTAAATCAACATAAGCCCC NM_152464RefSeq chr17
+ 28357580 28363683 TMEM199 NA transmembrane protein 199 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130600_PI430048170 0.541377909387056 0.834720511478318 1.97416871602851
2.73775233368977 2.84883659786189 A A A 2.27496014921286 3.21836467346294
2.84429646107846 A P P LNCV6_130600_PI430048170 mRNA
ATATTTAAAGGAGACTGCCTCGCTTTTAGAAGACATCTGGTCTGCTCTCTGCATGAGGCA NM_017839RefSeq chr16
+ 55509000 55586670 LPCAT2 54947 lysophosphatidylcholine acyltransferase 2
GO:0005811|GO:0047184|GO:0005795|GO:0005783|GO:0006663|GO:0005509|GO:0044281|GO:0003841|GO:0047
192|GO:0000139|GO:0005789|GO:0061024|GO:0016021|GO:0006644|GO:0036151|GO:0046474 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139254_PI430048170 0.560510551526311 1.17200024538731 1.64416693205465
2.33447307486466 1.96049873618442 A A A 2.47906142617433 1.79099426249652
0.328072031566912 A A A LNCV6_139254_PI430048170 mRNA
GCTCTGTATTTTTCCTGCAGCTGTAATTGCTGAGTGCCTGTTGTATACTTTATAGAGTTGNM_001098512 RefSeq chr10
+ 50991150 52298350 PRKG1 5592 "protein kinase, cGMP-dependent, type I, transcript variant 1"
GO:0005515|GO:0030036|GO:0005794|GO:0005886|GO:0005246|GO:0090331|GO:0019934|GO:0005524|GO:0043
087|GO:0016358|GO:0060087|GO:0005829|GO:0007165|GO:0005737|GO:0030553|GO:0007596|GO:0006468|GO:0
030900|GO:0001764|GO:0004692 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142500_PI430048170 0.0419386905396231 0.931440861741981 0.349994932043637
0.321058715027757 0.309198068381437 A A A 0.475868292334102 0.424898446087065
0.385765832446455 A A A LNCV6_142500_PI430048170 mRNA
GAAGCATGTTTCGCATGTAGGTAAACTGGTGGTGGTACTAGAAATACAATGTTATTTAAT NM_006194RefSeq chr14
+ 36657567 36677806 PAX9 5083 paired box 9
GO:0005515|GO:0000977|GO:0071363|GO:0060325|GO:0007492|GO:0045944|GO:0042481|GO:0042476|GO:0005
634|GO:0001228|GO:0045892|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_142062_PI430048170 0.0569540950580815 1.16114081044355 11.5605198469613
11.5347425310069 11.6147210384529 P P P 11.2421978701154 11.3591911490487
11.4552553749058 P P P LNCV6_142062_PI430048170 mRNA
TAGGAAGCATTTCGAACCTGCGCAACAGACCAAAGAACAGTACAAAGAACATCCGTGTACNM_023937RefSeq chr19
+ 17305667 17306843 MRPL3464981 mitochondrial ribosomal protein L34
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005761|GO:0005743|GO:0006
412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127946_PI430048170 0.00142224386878312 0.3958403188147964.43824094556552
4.06565129118365 4.31045997663764 P P P 5.37889201455767 5.62601181373234
5.81246831862283 P P P LNCV6_127946_PI430048170 mRNA
ACTGCAGACTGTATTAGAGCAAGACAACATCATTTAGCCATTGATTTTTATCTTCTACCT NM_021927RefSeq chr4
+ 44678415 44700680 GUF1 60558 GUF1 GTPase homolog (S. cerevisiae)
GO:0005759|GO:0005743|GO:0003924|GO:0043022|GO:0045727|GO:0005525|GO:0006412 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128581_PI430048170 0.1848969361786661.22621478201999 7.31361515645918 7.4736770712895
7.80472282432842 P P P 7.28136241663471 7.16753690192695 7.30109343403485 P P P
LNCV6_128581_PI430048170 mRNA
GCATGCCTAATGTTAGTTAGTGTAGATTCCATTTACTGCATTCTTCTGATCACTGAAATA NM_004085RefSeq chrX
- 101345655 101348969 TIMM8A 1678 "translocase of inner mitochondrial membrane 8 homolog A
(yeast), transcript variant 1"
GO:0005739|GO:0005758|GO:0006626|GO:0005743|GO:0072321|GO:0044267|GO:0046872|GO:0007399 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70827_PI430048170 0.0272770431252476 1.57424749472189 3.20829864362618 3.3683201548427
3.63479380305772 P P P 2.7193739249961 2.8326451570708 2.72505821373871 P P P
LNCV6_70827_PI430048170 mRNA
AAGGCAGGCTGCAGTGAAAACAGGAGCTGGTGAAACCGAGCCCTCTGCATCTGCGAATGT NM_032329RefSeq
chr2 + 241702040 241729481 ING5 84289 "inhibitor of growth family, member 5"
GO:0005515|GO:0070776|GO:0008285|GO:0043065|GO:2001235|GO:0006325|GO:0005634|GO:0035064|GO:0006
351|GO:0006260|GO:0043966|GO:0003682|GO:0005654|GO:0008270|GO:0045893|GO:0045926|GO:0006473 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133756_PI430048170 0.1102415696930760.8708090599398069.68584296479951
9.82627687067504 9.95381275266852 P P P 10.0411065830571 10.0525730092108
9.98241628615433 P P P LNCV6_133756_PI430048170 mRNA
GTGAGATTCCACTTGTGTAGAACTTTGTTGAGTAAAGATCAGTTTCTTGTGAACTCCTTA NM_001136195 RefSeq
chr19 - 12699193 12723996 TNPO2 30000 "transportin 2, transcript variant 3"
GO:0005515|GO:0005737|GO:0008536|GO:0008139|GO:0005634|GO:0006886 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134982_PI430048170 0.0604470548795165 0.72480569970250311.4384516669751
11.2232509799562 11.3639096952614 P P P 12.0536597908222 11.5940504564896
11.7402902438732 P P P LNCV6_134982_PI430048170 mRNA
GTGACTAGTCAATGAAGTGCGACAGCATTAAAGACTGATGCTAAACCTCAGGGGAAAAAA NM_006145RefSeq
chr19 - 14514763 14518559 DNAJB13337 "DnaJ (Hsp40) homolog, subfamily B, member 1, transcript
variant 1"
GO:0005515|GO:0006986|GO:0090084|GO:0005730|GO:0051087|GO:0005634|GO:0032781|GO:0005829|GO:0034
605|GO:0070389|GO:0051085|GO:0051117|GO:0030544|GO:0005654|GO:0051082|GO:0001671|GO:1900034|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133933_PI430048170 0.000204712688309102 0.1241345560865384.69489430403302
4.19879062477005 4.20455627707794 P P P 7.06629983726515 7.44089435400948
7.62450475565466 P P P LNCV6_133933_PI430048170 mRNA

CAGATCTTTTTCTCCTTTTTTGCACAAAACTATGCTTATGGTTTGTGTCACAGAAGTGAA NM_005012RefSeq chr1 + 63774018 64181496 ROR1 4919 "receptor tyrosine kinase-like orphan receptor 1, transcript variant 1"
GO:0043235|GO:0005515|GO:0017147|GO:0005737|GO:0005886|GO:0005887|GO:0018108|GO:0004714|GO:0007169|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143106_PI430048170 0.00484973730994894 2.84545353520937 4.04156293225843 4.11792328511989 4.43217651056663 P P P 2.89024994222657 2.28772296696861 2.84385989688691 P A P LNCV6_143106_PI430048170 mRNA
TGCCTCCTCAGGTATGGCAGTGACTCACCTGGTTTTAATAAAACAACCTGCAACATCTCA NM_203377RefSeq chr22 - 35606763 35623354 MB 4151 "myoglobin, transcript variant 2"
GO:0001666|GO:0042542|GO:0005506|GO:0043353|GO:0015671|GO:0007507|GO:0019825|GO:0050873|GO:0005344|GO:0031444|GO:0009725|GO:0020037|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135613_PI430048170 0.569223695831947 0.471160356650873 0.499629408134627 1.02003714050559 0.803702757990616 A A A 0.577076535799187 3.03009572690041 0.43228723980306 A P A LNCV6_135613_PI430048170 mRNA
GATTAAGATACAAATTTTGTGCAGTACTAAAGAAAAAGCAGTCTACCATTGTGGTCCTTG NM_001277171 RefSeq chr4 + 154781271 154828813 RBM46 166863 "RNA binding motif protein 46, transcript variant 2"
GO:0000166|GO:0003723 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75867_PI430048170 0.159681140807132 1.19850421756395 7.98554236409202 8.17232390758687 8.40359729380587 P P P 7.94794838036616 7.83502958455472 8.01932644170786 P P P LNCV6_75867_PI430048170 mRNA
AAATAAAATGTACTCTAGAGAATGGAATCGTGATGTCCAATACAGAGGCAGAGTCCGGGT NM_001204199 RefSeq chr5 + 112861187 112893079 SRP19 6728 "signal recognition particle 19kDa, transcript variant 6"
GO:0005786|GO:0010467|GO:0006614|GO:0042493|GO:0006613|GO:0008312|GO:0005730|GO:0005634|GO:0006412|GO:0005829|GO:0005739|GO:0005737|GO:0005654|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137183_PI430048170 0.0180806823783669 0.596535338084896 5.82563678039162 5.43385102002571 5.6963612583657 P P P 6.10092366475444 6.52786816187923 6.54761968830027 P P P LNCV6_137183_PI430048170 mRNA
CCATCTATCCAGTCTTACACTTATGGTTGGCCTCAAATCTATTGCATTTATGATAATGTA NM_020399RefSeq chr6 - 117560269 117602542 GOPC 57120 "golgi-associated PDZ and coiled-coil motif containing, transcript variant 1"
GO:0005515|GO:0030054|GO:0005886|GO:0007289|GO:0043004|GO:0015031|GO:0030425|GO:0042803|GO:0005109|GO:0005737|GO:0005083|GO:0045211|GO:0051260|GO:0030140|GO:0005794|GO:0014069|GO:0045176|GO:0006893|GO:0008022|GO:0044325|GO:0006888|GO:0043234|GO:0050790|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82126_PI430048170 0.0104615249430087 0.583813103527719 9.35648058173 9.20836797116059 8.92044898225362 P P P 10.0231471202339 10.0270754478564 9.78472764177789 P P P LNCV6_82126_PI430048170 mRNA
GCAAAACAGTATTTGTGGGTGGTCTGCCTGAAAATGGGACAGAGCAAATCATTGTGGAAG NM_182314RefSeq chrX - 130623380 130903317 ENOX2 10495 "ecto-NOX disulfide-thiol exchanger 2, transcript variant 2"
GO:0000166|GO:0015035|GO:0007624|GO:0016049|GO:0003676|GO:0005615|GO:0040008|GO:0009897|GO:0055114|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129441_PI430048170 0.00877424557765405 0.159976821169247 1.20315614645325 0.271053300363646 0.428149717913357 A A A 3.43772448992201 3.34595622660154 3.22374961641272 P P P LNCV6_129441_PI430048170 mRNA
CTGTGACATCCCAAATGTACAAACTACTGATTCTTGAACATGTTCCAAAATACAAAGTGA NM_001271700 RefSeq chr7 + 6031375 6036552 ANKRD61 NA ankyrin repeat domain 61 NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_129956_PI430048170 0.0384396927988319 0.5090802162672384.70278025589527
4.17896940717422 4.91111766493779 P P P 5.60948037333978 5.51331961016182
5.68204248868352 P P P LNCV6_129956_PI430048170 mRNA
CCTCTTATCTACTTGAGAGCAACATGTCTTTTCAATCATGGGATTGACACATGAAAAATA NM_014720RefSeq chr10
+ 103967184 104029233 SLK 9748 "STE20-like kinase, transcript variant 1"
GO:0035556|GO:0023014|GO:0005737|GO:0046777|GO:0004702|GO:0004674|GO:0006915|GO:0005524|GO:0042
803|GO:0070062|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136860_PI430048170 0.06155212015028 0.5402354714924893.58294081086364
2.90401664357813 2.713731112057 P A A 3.95838536276649 3.8958852051135
4.14964199536004 P P P LNCV6_136860_PI430048170 mRNA
GTGGGGAAGACATTGTTGTCTTTTTGTGAAAATAAAAATCCACACCTGGAAGTGTAAAAA NM_024755RefSeq chr15
- 58879044 58933653 SLTM 79811 "SAFB-like, transcription modulator, transcript variant 1"
GO:0006355|GO:0000166|GO:0006915|GO:0005654|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135645_PI430048170 0.1047756100771251.10438007020131 12.5228865964714
12.5128525775432 12.6650791585832 P P P 12.3745560529706 12.3778005497329
12.5190612223211 P P P LNCV6_135645_PI430048170 mRNA
GGGCTCATTGTAAAGTGCCTGCTGCATCAATAAAGCTCTTGGCTTATTAGTCTATACAAA NM_030978RefSeq chr9
+ 124869204 124877417 ARPC5L 81873 "actin related protein 2/3 complex, subunit 5-like"
GO:0034314|GO:0008150|GO:0003674|GO:0005737|GO:0005885|GO:0003779|GO:0005925|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142984_PI430048170 0.8416399972996961.01736353125616 9.55436002312084
9.75391842262854 9.81378752303138 P P P 9.52305937549215 9.59798293886567
9.90939670329395 P P P LNCV6_142984_PI430048170 mRNA
CTTTGATGTTTCTGGTAATCATGGACCCTTCTCCTGGGGCATTTGTTTTGTTTTCATAAT NM_007371RefSeq chr9 -
134030323 134068019 BRD3 8019 bromodomain containing 3
GO:0005515|GO:0006357|GO:0003682|GO:0070577|GO:0005634|GO:0006351|GO:0016568 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132507_PI430048170 0.1690461051170440.6919535889449443.80508123013507
2.95265577577068 3.75905798151985 P P P 4.04687778752812 4.16200521559297
4.04662201785226 P P P LNCV6_132507_PI430048170 mRNA
GGTTAATGCATTTAGTGAACGTGACTAACAAAGACTAATGTGCACATTAACAGATGTACT NM_016021RefSeq chr6
- 89326624 89352900 UBE2J1 51465 "ubiquitin-conjugating enzyme E2, J1"
GO:0005737|GO:0016567|GO:0019787|GO:0016874|GO:0005789|GO:0016021|GO:0030433|GO:0005524|GO:0031
625|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141502_PI430048170 0.1894132121424120.8033214931358662.86445869126608
2.83898463300548 3.36994327826599 A A P 3.37078405977867 3.32976252323482
3.38450693326846 P P P LNCV6_141502_PI430048170 mRNA
AAACCTGTCATGACAGACAGCAAATGTTTACACGTATATTTCTCCTGAGTGAACCTGATG NM_014238RefSeq chr17
+ 27472009 27623692 KSR1 8844 kinase suppressor of ras 1
GO:0005515|GO:0005783|GO:0031434|GO:0007265|GO:0005524|GO:0046872|GO:0004672|GO:0016020|GO:0004
674|GO:0005789|GO:0006468|GO:0043410|GO:0005078 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140915_PI430048170 0.1491411233550291.20886176816283 4.44623935422961
4.54207352160492 4.80278361860503 P P P 4.11166207526299 4.37182704886301 4.4856039328777
P P P LNCV6_140915_PI430048170 mRNA
GGACCATTGAATGAAACTTTATAGTCCTTAAATGTTGCTGAACTTTTGCTGTCTTGCAAT NM_003675RefSeq chr10
+ 13586938 13630868 PRPF18 8559 pre-mRNA processing factor 18
GO:0008380|GO:0006397|GO:0016607|GO:0019870|GO:0005681|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_130267_PI430048170 0.5232503897908020.97280752550162 0.402612497297135
0.3737975999026340.250674804343254A A A 0.3318122826227640.370670576719772
0.446046913627052A A A LNCV6_130267_PI430048170 mRNA
AGTAAGCCTAGCCCTGAAGCAAGCAAAGAATATGGCAGTGTAATGCAGGTCATTTAGAAA NM_205852RefSeq chr12
+ 10010631 10017949 CLEC12B 387837 "C-type lectin domain family 12, member B, transcript variant 2"
GO:0005886|GO:0030246|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60798_PI430048170 0.0590231363247077 0.7029942211612055.79136231189159
5.76459797232434 5.98905610453136 P P P 6.25082072582788 6.15016337517945
6.63360940493236 P P P LNCV6_60798_PI430048170 mRNA
GGCTGAACTTGATGAGAAAATTAGTGCCCTCAAACAAGCCCTCCTCAGAAAATCAAGAGA NM_016586RefSeq chr14
- 36298557 36320676 MBIP 51562 "MAP3K12 binding inhibitory protein 1, transcript variant 1"
GO:0005515|GO:0005737|GO:0000173|GO:0043966|GO:0006325|GO:0005730|GO:0005671|GO:0004860|GO:0005
634|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129221_PI430048170 0.8001052064596131.03268503866749 5.65501244048732
5.59922325757192 5.98500195104814 P P P 5.56098655496508 5.48979145544911
6.02069416719251 P P P LNCV6_129221_PI430048170 mRNA
TCCCTGAGCTTGCTCAACAAGAGAAACAAGGTTTCTTAAGTGTTTTGGTTAAAGTTTTCA NM_032900RefSeq chr10
- 97222172 97292673 ARHGAP19 84986 "Rho GTPase activating protein 19, transcript variant 1"
GO:0043547|GO:0051056|GO:0007264|GO:0005634|GO:0005829|GO:0005096 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145539_PI430048170 0.5532692182062471.03348759075353 8.89731445458708
9.04163410272977 8.99297071031347 P P P 8.91671319279465 9.04058069683397 8.8278372275209
P P P LNCV6_145539_PI430048170 mRNA
ATGGTAATACGTGAGGAATTTAAAGACTCATCCCCAGCCTCCACCTCCTGTGTGATACTT NM_003811RefSeq chr19
+ 6530998 6535928 TNFSF9 8744 "tumor necrosis factor (ligand) superfamily, member 9"
GO:0032755|GO:0032729|GO:0005164|GO:0005886|GO:0008283|GO:0005102|GO:0007267|GO:0006915|GO:0032
735|GO:0005125|GO:0005615|GO:0042104|GO:0007165|GO:0006955|GO:0043011|GO:0016021|GO:0045585 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59000_PI430048170 0.0352436521379442 1.0847220404726 0.668454564489771
0.7328467408609980.63569542876309 A A A 0.60804685680923 0.53863069841634
0.538927630439228A A A LNCV6_59000_PI430048170 mRNA
GCCTATTGGCTGAACATTATGCTACTTTCAGATATTAAAATGGTGTTCCTTTGAATCGTG NM_001039960 RefSeq
chr12 + 51424809 51515763 SLC4A8 9498 "solute carrier family 4, sodium bicarbonate cotransporter,
member 8, transcript variant 1"
GO:0043005|GO:0005886|GO:0005452|GO:0005887|GO:0051453|GO:0015701|GO:0035725|GO:0055085|GO:0008
510|GO:0032809|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144359_PI430048170 0.4326707330287891.55559596525196 1.86633144416044
0.4754223372474570.379313390898094A A A 0.5310659983046680.47294676140429
0.31127066900088 A A A LNCV6_144359_PI430048170 mRNA
GCATGAAACATTAATTGCAAAGGGCAGTCACATCCAACTTTAATAAAATATGGTGGTCTT NM_080387RefSeq chr12
+ 8513539 8522364 CLEC4D 338339 "C-type lectin domain family 4, member D"
GO:0045087|GO:0030246|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137583_PI430048170 0.4087900124172480.8737367834518724.90033043620442
5.17655043663703 5.6002389238207 P P P 5.37769779698597 5.31975484212205 5.6315824330446
P P P LNCV6_137583_PI430048170 mRNA
CCTTATCAGATAGTAAGTAACCTGTAAGTTTGGAGTATTACTGTTTTCTCAGCATGCATT NM_016656RefSeq chrX
+ 55717676 55758774 RRAGB 10325 "Ras-related GTP binding B, transcript variant RAGBl"
GO:0005515|GO:0005794|GO:0032008|GO:0003924|GO:0005634|GO:0005525|GO:0005765|GO:0005764|GO:0043
231|GO:0006184|GO:0005737|GO:0071230|GO:0032561|GO:0010506|GO:0034613|GO:0019003|GO:0034448|GO:0

009267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141467_PI430048170 0.4018446675127251.70811836659674 1.95769121426962 0.4114520983007
0.317449121778825 A A A 0.31268521085037 0.3401540600835080.349762577410533 A A A
LNCV6_141467_PI430048170 mRNA
GCTGACCTGAACCCTATATTTTAACATAGAGGTCACCATTATCCATTTAATGGTCTTATA NM_001010987 RefSeq
chr10 + 89378055 89385205 IFIT1B NA interferon-induced protein with tetratricopeptide repeats 1B
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131651_PI430048170 0.1019961131429220.7706579362042429.62539832585008
9.62237196580744 9.96696844354034 P P P 10.0624203486602 9.90926572997006
10.3612928062586 P P P LNCV6_131651_PI430048170 mRNA
CAAGCTGGGAGAGAGAAATGACTGAGATGAATGTCTTTACTAAAGTACCAATAAATTTGT NM_020357RefSeq chr3
+ 101574197 101594437 PCNP 57092 PEST proteolytic signal containing nuclear protein
GO:0005515|GO:0007049|GO:0016567|GO:0043161|GO:0005654|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143685_PI430048170 0.8647910319961250.9707316049206495.55360098366805
5.77435010058106 5.95609193696755 P P P 5.72265868972184 5.5737005018525
6.09354214799545 P P P LNCV6_143685_PI430048170 mRNA
CAGTGTGTTGTGTTTTCCATTCATTTCAGAAGAGCTACATTGTGTCACTGGACATTTTTA NM_003177RefSeq chr9
+ 90801679 90898560 SYK 6850 "spleen tyrosine kinase, transcript variant 1"
GO:0046638|GO:0005515|GO:0045401|GO:0043313|GO:0050731|GO:0002554|GO:0042991|GO:0019815|GO:0046
641|GO:0009887|GO:0002366|GO:0070372|GO:0038083|GO:0001945|GO:0042742|GO:0019901|GO:0045588|GO:0
030593|GO:0032928|GO:0030168|GO:0031234|GO:0043306|GO:0043234|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143656_PI430048170 0.2359703773021041.64307349409442 0.285095141220802
1.29720589725724 1.50904109742425 A A A 0.5056054104177910.39519261794523
0.304147538110772 A A A LNCV6_143656_PI430048170 mRNA
GCTCTGGGAAAGCAACAGACAGTGAATGGGCCCAATAAACAATCATTTCAAACCTACTGA NM_207341RefSeq chr11
+ 60867541 60875691 ZP1 22917 zona pellucida glycoprotein 1 (sperm receptor)
GO:0007338|GO:0005794|GO:0005886|GO:0005578|GO:0005576|GO:0016021|GO:0030141|GO:0007339|GO:0032
504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133470_PI430048170 0.3806253640189110.90438723818378 9.23029657546304
8.89195205843714 9.04163410272977 P P P 8.98358578493762 9.28418998459717
9.32735637929752 P P P LNCV6_133470_PI430048170 mRNA
ACCCTCCCCCAAATCTGTTTTCATGTAAAAGACAAATAAATGATGACTTCCCCCAAAGCT NM_001130438 RefSeq
chr9 + 128552557 128633665 SPTAN1 6709 "spectrin, alpha, non-erythrocytic 1, transcript variant 1"
GO:0005515|GO:0005516|GO:0008091|GO:0030018|GO:0046982|GO:0005509|GO:0032437|GO:0030507|GO:0006
915|GO:0003779|GO:0031982|GO:0016328|GO:0006921|GO:0051693|GO:0043231|GO:0005829|GO:0005916|GO:0
016020|GO:0007411|GO:0015630|GO:0005200|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_61137_PI430048170 0.0329566219280051 3.85321351281542 3.37049987041504
3.27107016295278 3.07217330193319 P P P 0.4657208064081521.88879993291641 1.1939986675231
A A A LNCV6_61137_PI430048170 mRNA
TCTGCACTGTGTGCCGGTGGAGACGGCCAATGTCACCATGCACTCCTAAAGATCCGTTCT NM_002632RefSeq chr14
- 74941829 74955764 PGF 5228 "placental growth factor, transcript variant 1"
GO:0005515|GO:0048010|GO:0001666|GO:0001658|GO:0007565|GO:0008284|GO:0046982|GO:0042493|GO:0031
100|GO:0007267|GO:0002040|GO:0005576|GO:0060688|GO:0005615|GO:0045766|GO:0042803|GO:0032870|GO:0
030154|GO:0007165|GO:0016020|GO:0001938|GO:0051781|GO:0008083|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131269_PI430048170 0.7036416198767761.16525206252474 0.62852569938124

1.47760756540031 0.359530728391139 A A A 0.5554222226382060.982391402325484
0.456683860970881 A A A LNCV6_131269_PI430048170 mRNA
CTACCCTCCAGAATAAAGAAATGTTATCATTTGCCATCTACCCTCTAGAATAAAGAAATC NM_006863 RefSeq
chr19_KI270938v1_alt + 576154 584960 LILRA1 11024 "leukocyte immunoglobulin-like receptor,
subfamily A (with TM domain), member 1, transcript variant 1"
GO:0005886|GO:0050776|GO:0006952|GO:0016021|GO:0003823|GO:0007166|GO:0004888|GO:0002376 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127633_PI430048170 0.00616841209095926 0.5231602201091451 0.3650013251942
10.4003685691957 10.3914115180935 P P P 11.1673638869327 11.3507533093585
11.4304583015256 P P P LNCV6_127633_PI430048170 mRNA
TACCCAACTTCCTGTACTGTTGCCCTTCTGATGTTAATAAAAGCAGCTGTTACTCCCAAA NM_178229 RefSeq chr1
- 156525404 156572604 IQGAP3 128239 IQ motif containing GTPase activating protein 3
GO:0005516|GO:0008361|GO:0071310|GO:0007265|GO:0016328|GO:0005099|GO:0010628|GO:0000187|GO:0000
082|GO:0005737|GO:0070856|GO:0032320|GO:0005911|GO:0010629|GO:0017048|GO:0070371|GO:0033601 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135770_PI430048170 0.209833056865125 0.57489420102987 2.3861952100399
0.6002224876597481.55495428813467 A A A 2.42259327057685 1.98000866069427
2.91360786284375 P A P LNCV6_135770_PI430048170 mRNA
CACACTAGCACAACTTTTTGGAGGCTGATCGTGAAACTGCAAAATTGGAAAAGTTCTGAG NM_001024611 RefSeq
chr4 - 51993699 52017620 LRRC66 NA leucine rich repeat containing 66 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_128100_PI430048170 0.208815468829209 1.08623671998799 0.562777592797211
0.3583524477758070.534605997513137 A A A 0.28873076985827 0.385024540294773
0.428813991186932 A A A LNCV6_128100_PI430048170 mRNA
AACCAATTTCTGTCATCTTACTGTATCAGAAATTAGAAACTATCACAAAGCGCTCTAGAG NM_001172285 RefSeq
chrX - 103718573 103728624 GLRA4 441509 "glycine receptor, alpha 4, transcript variant 2"
GO:0005230|GO:0030054|GO:0022824|GO:0005887|GO:0045211|GO:0034707|GO:0016594|GO:0005254 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135523_PI430048170 0.954609462888973 1.01737732642326 0.30037990102792
0.5324591020576220.873077163997546 A A A 0.5007853999440820.740712740666382
0.429126726187072 A A A LNCV6_135523_PI430048170 mRNA
CATGAAGTTGCATCCTTTGGCAGCTTCTTACAGTTTATTTTCACTTCCAATGTAGCAATA NM_194324 RefSeq chrX
- 104072872 104076236 TMSB15B 286527 thymosin beta 15B
GO:0003785|GO:0042989|GO:0005737|GO:0007015|GO:0005856 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_95978_PI430048170 0.0518136386380261 1.75270113194032 9.3656356778252
9.04489392114066 9.06969773659926 P P P 8.72819524365028 8.31157652834225 7.9219765737784
P P P LNCV6_95978_PI430048170 mRNA
ACCACTACTTTGAGAAGGGCCGGCTAGATGAGTGTCAGATGTACCTGGCACACGAGCAGG NM_175039 RefSeq
chr9 - 127907885 127917026 ST6GALNAC4 27090 "ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-
galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4, transcript variant 1"
GO:0006664|GO:0008373|GO:0006493|GO:0000139|GO:0047290|GO:0016266|GO:0016021|GO:0006488|GO:0044
267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141979_PI430048170 0.00143673221581199 0.4374513371866836.97625140775016
6.72958286027422 6.97085445941562 P P P 7.86658966512283 8.14002091925271
8.23692577642842 P P P LNCV6_141979_PI430048170 mRNA
AGTAAGGTGGTAGCCAGCTTGGTAACTGCATAGTAATCGAGAGGCTGTAAGATGGGAATT NM_001143835 RefSeq
chr11 - 129863774 129895595 NFRKB 4798 "nuclear factor related to kappaB binding protein, transcript
variant 1"

GO:0005515|GO:0031011|GO:0006355|GO:0006954|GO:0006281|GO:0006366|GO:0006310|GO:0005654|GO:0005634|GO:0002020|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82757_PI430048170 0.876000713644497 0.9908083494132791 2.022110578842 11.7689967149415 11.795749498967 P P P 11.9426382067371 11.9160584600398 11.776282572508 P P P
LNCV6_82757_PI430048170 mRNA
TGGGGCTTCTTCTGTAACATGACTTGCGAATATTTATATAAAAACGAGTGTTACAATGAG NM_001105079 RefSeq chr16 + 30659518 30670810 FBRS 64319 fibrosin NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107810_PI430048170 0.0772802733834487 1.23509469702833 8.63808578716545 8.65946859120306 8.5217531414029 P P P 8.46768658053731 8.30626064455137 8.11358903433338 P P P LNCV6_107810_PI430048170 mRNA
TGCTGGATGAGCTCCTGGCGAGCCCGGAGTTTCTGCAGCAGGCGCAACCTCTCCTAGAAA NM_001293798 RefSeq chr4 + 190173773 190175845 DUX4 100288687 double homeobox 4
GO:0031965|GO:0000976|GO:0008285|GO:0045944|GO:0006915|GO:0005654|GO:0005634|GO:0070317|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136423_PI430048170 8.90377030443253e-05 0.61173871504226 11.6937040133408 11.6180823851522 11.5948786504384 P P P 12.3233487222083 12.3871697671375 12.3241104451663 P P P LNCV6_136423_PI430048170 mRNA
CTCCCTCTCAAGGCAGGGGTCATAGATCCTAAGCCATAAAATAAATTTTATTCCAAAATA NM_001178078 RefSeq chr12 - 57095404 57111413 STAT6 6778 "signal transducer and activator of transcription 6, interleukin-4 induced, transcript variant 1"
GO:0005515|GO:0000790|GO:0070301|GO:0003700|GO:0048295|GO:0005829|GO:0042802|GO:0005737|GO:0002829|GO:0042127|GO:0045944|GO:0032481|GO:0004871|GO:0035771|GO:0006357|GO:0019903|GO:0000122|GO:0000979|GO:0006351|GO:0007165|GO:0033598|GO:0060443|GO:0045087|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134470_PI430048170 0.341915999859941 0.973180004629272 0.387152224394774 0.411508411919948 0.305476545557488 A A A 0.394924740344695 0.431807106623071 0.396895631146945 A A A LNCV6_134470_PI430048170 mRNA
CTAGTCAGAGTGACTCAGCAGAGATTATTTTGTTCTCTTGTGCAATTTATTCTGTGTCAT NM_152399 RefSeq chr4 - 121758929 121765185 TMEM155 132332 transmembrane protein 155 GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143386_PI430048170 0.00984119819580759 0.459980377393062 4.1417835849854 3.86688671825837 4.0173179870212 P P P 5.4333595438085 4.89388306297257 5.01595690214794 P P P LNCV6_143386_PI430048170 mRNA
AGAAGGCAGTGTTCCTCTATTCCCTTCTTCCGAATTAAAAATACCCCCTCAGAGCGAAAA NM_080429 RefSeq chr1 + 154321115 154325325 AQP10 89872 aquaporin 10
GO:0034220|GO:0005886|GO:0005887|GO:0015793|GO:0015250|GO:0009992|GO:0009636|GO:0015204|GO:0015254|GO:0006833|GO:0071918|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136544_PI430048170 0.0694872730559852 1.16024341027005 0.694675787238254 0.777256840913051 0.905113640311592 A A A 0.602578501191822 0.575663924585435 0.563067155562921 A A A LNCV6_136544_PI430048170 mRNA
TGATGTTGAAGATGATCCTGATGAAATGGCTGTGTGAAAAATGCTCTCGTAGGTGGCCAG NM_004224 RefSeq chrX + 151176583 151181465 GPR50 9248 G protein-coupled receptor 50
GO:0005515|GO:0007186|GO:0005887|GO:0004930|GO:0007267|GO:0008502|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127287_PI430048170 0.434086032998747 1.50068860123594 1.76218423058042 0.463382336426609 0.368805405253751 A A A 0.502198021812472 0.384178132773081 0.398464296430952 A A A LNCV6_127287_PI430048170 mRNA
AGGTTGTCACAGACTAGAGAAAAGTCTCAGTTTCACCAAATCCACATTCAAATGAGTTTT NM_005295 RefSeq chr7

+ 107470056 107475680 GPR22 2845 G protein-coupled receptor 22
GO:0042277|GO:0007186|GO:0005887|GO:0004930|GO:0032870 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_98837_PI430048170 0.2005507030854927.23722952675784 0.3265425252659774.22109482936566
2.82429580321359 A P A 0.3146134704294860.2855156373617060.340653071929712A A A
LNCV6_98837_PI430048170 mRNA
TCAAGATGCTCCACATAAGATCCAAAACCTCTCTTAGATCTGGAACCAAATGCAAGGTTA NM_002104RefSeq chr5
+ 55024278 55034132 GZMK 3003 granzyme K (granzyme 3; tryptase II)
GO:0004252|GO:0006508|GO:0008236|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137701_PI430048170 0.0318445770358839 1.06034323598597 0.362010285267037
0.3650470895822780.302933163664995A A A 0.2442812435201420.287046989058726
0.24550209236173 A A A LNCV6_137701_PI430048170 mRNA
CTCATGTGTTCAGCTCAAGACTCCACAGGAATTCAACCCCCAGAAAGACATAAACTTGGA NM_020227RefSeq chr5
+ 23507614 23528597 PRDM9 56979 PR domain containing 9
GO:0005694|GO:0010845|GO:0006325|GO:0010844|GO:0006311|GO:0007283|GO:0042800|GO:0006351|GO:0046
872|GO:0043565|GO:0045944|GO:0005654|GO:0051568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131301_PI430048170 0.3084308638681621.01648864654673 0.372607815316145
0.3713648175341540.415909525170172A A A 0.3671479339286690.337121164693065
0.384874928703848A A A LNCV6_131301_PI430048170 mRNA
CACTGATAAGGTGGTGGCAGTGTTTTATACTGTTGTATTTCCCATGTTTAATCCAATAAT NM_001001921 RefSeq
chr11 + 56030418 56031393 OR5AS1NA "olfactory receptor, family 5, subfamily AS, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132090_PI430048170 0.1390634707481911.05729169290894 0.446815375415646
0.4620385289049710.489401125314329A A A 0.3245307721555840.382541466754433
0.447749859084848A A A LNCV6_132090_PI430048170 mRNA
GACTTCACTGAAACTGACTGCATCTTGCAATTTTCTTTTTCGAATTGGCAGAAATATTGT NM_001195278 RefSeq
chr7 + 141074231 141480379 TMEM178B 100507421 transmembrane protein 178B GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136185_PI430048170 0.5151895665353981.23741264190291 0.282532008016398
0.2951141042119461.20760355499561 A A A 0.4855532291981970.276996217140062
0.297676362373747A A A LNCV6_136185_PI430048170 mRNA
TTCTTAAATAAAGATGGTTTCTCAACCTGTTGGGGAAGCTGGCACGAGCTGTGGGTGTTA NM_005076RefSeq chr1
+ 205043211 205078043 CNTN2 6900 contactin 2 (axonal)
GO:0005886|GO:0022010|GO:0045202|GO:0031225|GO:0043621|GO:0042802|GO:0031623|GO:0097090|GO:0007
413|GO:0001948|GO:0048168|GO:0007411|GO:0008076|GO:0043209|GO:0007628|GO:0043025|GO:0060168|GO:0
007612|GO:0007155|GO:0009986|GO:0044224|GO:0031133|GO:0000226|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130903_PI430048170 0.0326589098943924 0.4404646824323063.16193509978661
2.32124472078146 2.56078592598905 P A A 3.92069060602183 3.78891970331423
4.00859280916504 P P P LNCV6_130903_PI430048170 mRNA
CCTGGTACCCTTGTGAAACTGTAAAATATATCATATGGGGGGAGTTTTTTAACTCTTATT NM_004133RefSeq chr8
+ 75539967 75566826 HNF4G 3174 "hepatocyte nuclear factor 4, gamma"
GO:0010467|GO:0003700|GO:0006367|GO:0006357|GO:0003707|GO:0043565|GO:0031018|GO:0043401|GO:0005
654|GO:0008270|GO:0004879|GO:0045893|GO:0030522 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136357_PI430048170 0.7765377912552830.8783260250992332.35548289326137
2.43564686096238 3.00702660887159 A A P 3.10649238079054 3.09745685599891
1.98800505900543 P P A LNCV6_136357_PI430048170 mRNA
TGCCTGCCTTTCTTCAACATATATTCTTATATAACCTGTAGTGGAAGATTTGGGTACTGT NM_001252274 RefSeq
chr4 - 69588416 69653249 UGT2A1 10941 "UDP glucuronosyltransferase 2 family, polypeptide A1,

complex locus, transcript variant 2"
GO:0007608|GO:0052696|GO:0052695|GO:0009813|GO:0009593|GO:0008152|GO:0015020|GO:0016021|GO:0032
870|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134308_PI430048170 0.4905128583614630.9475596976319980.337483382347985
0.3284587411166150.300719895794182A A A 0.56713539270703 0.320086637610114
0.29699751784682 A A A LNCV6_134308_PI430048170 mRNA
AACAGGGTAAAATGGTAGCTGTATTTTATACCACAGTAATCCCTATGCTGAACCTTATAA NM_001005282 RefSeq
chr11 - 56490434 56491370 OR5M8 NA "olfactory receptor, family 5, subfamily M, member 8"NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141723_PI430048170 0.00191503612172549 1.64235552490265 7.63861028189978
7.76938232297959 7.75595309986855 P P P 6.99478800921264 7.12518234522709
6.89063291527416 P P P LNCV6_141723_PI430048170 mRNA
ACATTAAGCCAGAATTTGACTTGACGGGATGGCTTACAAGTCCTGCCTGATACCTACACA NM_017873RefSeq chr9
- 129634603 129642169 ASB6 140459 "ankyrin repeat and SOCS box containing 6, transcript variant 1"
GO:0035556|GO:0005737|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116705_PI430048170 0.2606982746628510.8284325338330238.81589185891302
8.95544673425337 9.26100983155348 P P P 9.11568103571671 9.1302232531965
9.58631702116832 P P P LNCV6_116705_PI430048170 mRNA
ATTCCAATTTATGCAGATAAGGATGTGTTTCACATGGTAGTTGAAGTACCACGCTGGTCT NM_021129RefSeq chr10
- 70202829 70233434 PPA1 5464 pyrophosphatase (inorganic) 1
GO:0010467|GO:0005737|GO:0000287|GO:0004427|GO:0071344|GO:0006796|GO:0070062|GO:0006418|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135766_PI430048170 0.5054803796195720.9181485154509483.83728732233397 3.9818063889095
3.77151235875979 P P P 3.7517648760659 3.95938037710249 4.2190172070609 P P P
LNCV6_135766_PI430048170 mRNA
CTTAAGCGTACAAAGTGATCTTGTTCACAAGTAATCTGTTGACAGTGCCAATAAATGATA NM_000663RefSeq chr16
+ 8712968 8784575 ABAT 18 "4-aminobutyrate aminotransferase, transcript variant 2"
GO:0043005|GO:0001666|GO:0003867|GO:0045471|GO:0042493|GO:0048148|GO:0007268|GO:0045776|GO:0047
298|GO:0042803|GO:0007269|GO:0005739|GO:0032145|GO:0032144|GO:0005759|GO:0010039|GO:0030170|GO:0
009450|GO:0007626|GO:0042135|GO:0007620|GO:0070062|GO:0035094 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_145440_PI430048170 0.4515773517531791.33916454524113 0.316249527625108
0.4293676162935781.43354358048058 A A A 0.4701935795338680.359604566210632
0.360605876124823A A A LNCV6_145440_PI430048170 mRNA
TATCTTGTGAAATTTCTTTCAGGTCTCATAAAAGCGATGAAAGAGACCAGGATAACATTC NM_138295RefSeq chr7
- 47774651 47948474 PKD1L1 168507 polycystic kidney disease 1 like 1
GO:0005515|GO:0005929|GO:0060170|GO:0016337|GO:0005262|GO:0050982|GO:0016020|GO:0070588|GO:0003
127|GO:0031513|GO:0070986|GO:0034704 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134801_PI430048170 0.0517783753675702 1.38788581740692 7.217084629488
7.64195526928627 7.41085127911549 P P P 6.89206302243378 7.03332314743276
6.95379468497794 P P P LNCV6_134801_PI430048170 mRNA
ACTGGCCTATTTACTGTTTACAGCTGGCCAGTGCAGAGCTGCTGCTCTTTTACCTTTTTA NM_032323RefSeq chr1
+ 156284278 156292443 TMEM79 84283 "transmembrane protein 79, transcript variant 1"
GO:0045055|GO:0042335|GO:0061436|GO:0045684|GO:0002070|GO:0016021|GO:0005765|GO:0070268|GO:0032
588|GO:0031069 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141291_PI430048170 0.2575869613708750.8745348132539760.34500940945714
0.3465934498736960.287064271716361A A A 0.6604029424984030.277254767185242
0.59374082827875 A A A LNCV6_141291_PI430048170 mRNA
GAGCTGATTCATAGATCAAAGTCTGAAGAGTGAACACATGGTGATCATAATTTCTCTTTA NM_024764RefSeq

chr14_KI270844v1_alt - 44909 199881 CATSPERB 79820 catsper channel auxiliary subunit beta
GO:0007338|GO:0035036|GO:0005929|GO:0005886|GO:0036128|GO:0007275|GO:0007283|GO:0030154|GO:0032
504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132161_PI430048170 0.0978825902141842 1.08745826463741 0.632142555942956
0.5306808944988180.677647750537969A A A 0.4281575809241880.509409554461223
0.541567702618245A A A LNCV6_132161_PI430048170 mRNA
TCTATCTGACGAGTTTTTCATATCTCATGAATGGTGCGCTGTTTTGCATATAAATAAAGG NM_005599RefSeq chr1
- 115836377 115841126 NHLH2 4808 "nescient helix loop helix 2, transcript variant 1"
GO:0005515|GO:0001102|GO:0005667|GO:0007617|GO:0005634|GO:0042698|GO:0007417|GO:0003677|GO:0006
351|GO:0030154|GO:0051091|GO:0045944|GO:0046983 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135183_PI430048170 0.2401361727919230.6040431988982342.04473933392068
0.7579120654897831.64533844162555 A A A 1.57210280116733 2.21828799481919
2.84441692243925 A A P LNCV6_135183_PI430048170 mRNA
GAATTAAACCCATTTGGTTTCAAATCCCAGTTATGACATCTGTTAACTTTGCAAACTCAC NM_024940RefSeq chr8
+ 25184771 25413103 DOCK5 80005 dedicator of cytokinesis 5
GO:0043547|GO:0005085|GO:0005737|GO:0007264 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58577_PI430048170 0.00291682720037163 1.8724068570389 6.27215924427011
6.54753645775612 6.20949924520118 P P P 5.51601041788193 5.53283906766462
5.27429552256498 P P P LNCV6_58577_PI430048170 mRNA
ATGGCTCTGGCACCACTAGGGTCCTGGCCCTCTTCTTATTCATGCTTTCTCCTTTTTCTA NM_002075RefSeq chr12 +
6840853 6847395 GNB3 2784 "guanine nucleotide binding protein (G protein), beta polypeptide 3,
transcript variant 1"
GO:0005515|GO:0043005|GO:0005886|GO:0003924|GO:0007268|GO:0030507|GO:0044281|GO:0044297|GO:0006
112|GO:0051020|GO:0007186|GO:0071377|GO:0008217|GO:0004871|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138566_PI430048170 0.00619823027361905 0.4134662401244164.44887056439111
4.08241732574318 3.83036249452334 P P P 5.29196448130851 5.28928665091156
5.64138215598114 P P P LNCV6_138566_PI430048170 mRNA
GGGCAAGTACAGGAGCAACTGCTGCTACCCAGAAAAATGTGTGTATTATAAATAATTAAA NM_147128RefSeq chr7
+ 30284306 30367692 ZNRF2 223082 "zinc and ring finger 2, E3 ubiquitin protein ligase"
GO:0042734|GO:0005737|GO:0030054|GO:0016567|GO:0005886|GO:0016874|GO:0008270|GO:0005765|GO:0030
659|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136391_PI430048170 0.3606493635357921.68641807159048 0.586838867438299
0.4038456845483031.95673910634525 A A A 0.3606765691258960.427106416761002
0.431246749215226A A A LNCV6_136391_PI430048170 mRNA
TGGGGCACACCCATTCCACATGCAAAGGGCAGAAGCAAACCCAGTAAAATGTTAACTGAC NM_214710RefSeq
chr19 - 685520 695461 PRSS57 400668 "protease, serine, 57" GO:0004252|GO:0006508|GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95544_PI430048170 0.18886052338944 1.02990461911975 0.3600671846983850.29709522390538
0.366986482110429A A A 0.2916285849578520.2870209365883260.318785331396481A A A
LNCV6_95544_PI430048170 mRNA
TCACTATCAGATGTGTCGTCGCCATTGTTGTGATATTTACAAACTTGTCATGGAAAATAG NM_001080504 RefSeq
chr2 + 237798744 237842808 RBM44 NA RNA binding motif protein 44 NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_143458_PI430048170 0.1155276007609981.06996183060874 0.46643083230263
0.3345243801532050.373968589071593A A A 0.2695870509684430.339675510538412
0.275120471461105A A A LNCV6_143458_PI430048170 mRNA
GGTTTTTTAAATTTTTTCAGTGAGCGTGGTGACTGCAGAGGTTAGTGCTGTGAAAAGCTG NM_014141RefSeq
chr7_KI270808v1_alt + 2412 204591 CNTNAP2 26047 contactin associated protein-like 2

GO:0030424|GO:0008038|GO:0021987|GO:0019226|GO:0030425|GO:0031175|GO:0021794|GO:0008076|GO:0043025|GO:0043204|GO:0030534|GO:0007612|GO:0030673|GO:0007155|GO:0071109|GO:0005794|GO:0009986|GO:0044224|GO:0071625|GO:0021756|GO:0016020|GO:0045163|GO:0007420|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131409_PI430048170 0.0388766627889056 0.5770077065942596.90284154565001 6.58543628311663 6.64922688014994 P P P 7.10637885695291 7.61179009590376 7.74397603653011 P P P LNCV6_131409_PI430048170 mRNA GAGAAGTACTGATAGGACCTTTATCTGGATATGGTCCTATAGGTTATTCTGAAATAAAGA NM_001033 RefSeq chr11 + 4094693 4138876 RRM1 6240 ribonucleotide reductase M1
GO:0005515|GO:0021846|GO:0015949|GO:0060041|GO:0055086|GO:0051290|GO:0044281|GO:0042995|GO:0005635|GO:0005524|GO:0005829|GO:0006260|GO:0005737|GO:0009263|GO:0010212|GO:0043025|GO:0005654|GO:0004748|GO:0000278|GO:0006206|GO:0008584|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140632_PI430048170 0.836676334299649 0.944497977491386 4.76343963840471 4.17798806540851 3.87240113978702 P P P 4.03178393280129 4.87025760269305 4.15568312922516 P P P LNCV6_140632_PI430048170 mRNA TTTAGTTATCTCATTTGTTAGAAGAAGGGCCTGGGGTCCTGAAGAACAAAGGTGCTCCAG NM_001195605 RefSeq chr19 + 55613592 55618541 ZNF865 NA zinc finger protein 865 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133892_PI430048170 0.208007057684294 0.762698927088743 0.291665358430719 0.301965565642812 0.505529194641159 A A A 0.328989933854947 0.99026304779715 0.879668914362209 A A A LNCV6_133892_PI430048170 mRNA GCAGATGACGTGAAATTGTGATGTTTGTTACAGAGCTTTTATGTTTAAAGACTTCAATGG NM_018059 RefSeq chr7 - 4799108 4883704 RADIL 55698 Ras association and DIL domains
GO:0007165|GO:0005874|GO:0034446|GO:0007275 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110341_PI430048170 0.121833244277287 0.934967246008057 16.3087404833913 16.4361424286601 16.330586438515 P P P 16.4126558449552 16.445754282268 16.5096481929429 P P P LNCV6_110341_PI430048170 mRNA AGGGCTTCCAATGTGCTGCCCCCCTCTTAATACTCACCAATAAATTCTACTTCCTGTCCA NM_001303625 RefSeq chrX + 154398064 154402339 RPL10 NA "ribosomal protein L10, transcript variant 5" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73608_PI430048170 0.456428511758364 1.56884894905659 0.346859940795774 0.249503300561461 1.8099493016134 A A A 0.272010026524509 0.470824898135241 0.274962613398093 A A A LNCV6_73608_PI430048170 mRNA GCAGATCCCAATCTTTCTTTTAAGCTTCTGGGTCTATTAAACTAGGTAGATCTTTTCGTA NM_001871 RefSeq chr3 + 148827800 148860185 CPB1 1360 carboxypeptidase B1 (tissue)
GO:0006508|GO:0004180|GO:0008270|GO:0005576|GO:0004181 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102752_PI430048170 0.981490336139921 0.99600039281903 9.55388734974896 9.58560180357351 9.46843859496794 P P P 9.37780350441894 9.62890506966649 9.60789744652491 P P P LNCV6_102752_PI430048170 mRNA ATAACCTCTGGGGACCCCAACCTCAGAGGCAGCTTCAAGTGCCTTTTGCTGCGCACCAAT NM_004357RefSeq chr11 + 832951 838835 CD151 977 "CD151 molecule (Raph blood group), transcript variant 1"
GO:0005515|GO:0005886|GO:0034329|GO:0005829|GO:0005178|GO:0016020|GO:0016477|GO:0042098|GO:0005887|GO:0030198|GO:0031581|GO:0007155|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78158_PI430048170 0.00262800477079888 0.543325150219311 4.46481581771423 4.23828931910494 4.26142863953126 P P P 5.0360179579719 5.18739153437079 5.37263879529291 P P P LNCV6_78158_PI430048170 mRNA

GGTGGATTCCTCTAGTTGGTTTGTAATTGTTCTTTGAAGGCTGTTTATGACTAGATTTTT NM_015204 RefSeq chr7 - 11370434 11832198 THSD7A 221981 "thrombospondin, type I, domain containing 7A" GO:0005886|GO:0016021|GO:0001525|GO:0030154|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137034_PI430048170 0.8621712056540020.790844985098641 1.78285493449222 0.6124563030014490.543270346744327 A A A 2.41922416090356 0.473363520435729 0.474902026198177 A A A LNCV6_137034_PI430048170 mRNA
TCTCCTTGCTTTGAAAGATCCAATAAAGTCCTGAGGCAAGGTTTGGAAAACCAACTTAAA NM_031290 RefSeq chr13 + 51861980 51866236 CCDC70 83446 coiled-coil domain containing 70 GO:0005886|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108321_PI430048170 0.0684945194954537 0.8352847895011294.15293824278082 4.17780925387293 4.0945581344267 P P P 4.24367783885464 4.4805783614321 4.46914610156235 P P P LNCV6_108321_PI430048170 mRNA
AAGCAAAAATGGCACTGAGCCTGAGTCTTTCCACAAGGTGCTCAAGGGTCTTTATGAGAA NM_001127460 RefSeq chr12 - 56316222 56333749 PAN2 9924 "PAN2 poly(A) specific ribonuclease subunit, transcript variant 1" GO:0005515|GO:0010467|GO:0004535|GO:0000175|GO:0000932|GO:0005634|GO:0031251|GO:0003676|GO:0000289|GO:0005829|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142369_PI430048170 0.0214536978849847 1.74515372578133 6.23164222938382 5.84081735986706 5.95871088606767 P P P 5.26257253173752 5.45348416177082 4.87449223364013 P P P LNCV6_142369_PI430048170 mRNA
GATGTGGGGACCCTCTTCCTCTAGCACAGTAAAGCTGGCCTCCAGAAACACGGGAAAAAA NM_015896 RefSeq chr3 - 50341105 50345746 ZMYND10 51364 "zinc finger, MYND-type containing 10" GO:0044458|GO:0005515|GO:0036159|GO:0005737|GO:0034451|GO:0036158|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67930_PI430048170 0.16332037155507 1.19676248890171 5.654059694582 5.73596212136656 5.41010678785937 P P P 5.23523580389169 5.57167524270255 5.20604106381911 P P P LNCV6_67930_PI430048170 mRNA
TTACAGACCTGAAGGAGGCAGAGAAGGCTGCAGGGAAGGCCCCAGAGTCAGAGAAGCCGG NM_017607 RefSeq chr19 - 55090912 55117600 PPP1R12C 54776 "protein phosphatase 1, regulatory subunit 12C, transcript variant 1" GO:0005515|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145686_PI430048170 0.0635139219400951.45446737170129 4.13087254050877 4.67275203297449 4.35413228634452 P P P 3.80929387160209 3.78653049822248 3.98406613044669 P P P LNCV6_145686_PI430048170 mRNA
GCTTTGAGGGTAGCCGAAACCCCTTATCTAATAAAGTCTAACTCTGTGAGAACCACAGAA NM_001243597 RefSeq chr11 - 125956817 126063292 CDON 50937 "cell adhesion associated, oncogene regulated, transcript variant 1" GO:0005515|GO:0043497|GO:2000179|GO:0010172|GO:0021987|GO:0001708|GO:0005886|GO:0051057|GO:0007520|GO:0060059|GO:0009952|GO:0048643|GO:0007224|GO:0014816|GO:0042692|GO:0031012|GO:0051149|GO:0045666|GO:0002088|GO:0045944|GO:0001934|GO:0016021|GO:0043410|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136560_PI430048170 0.2325564988537261.06051871685889 0.60751985909521 0.7362642739417120.575590030823015 A A A 0.5551016641928020.561133030929024 0.553880304215528 A A A LNCV6_136560_PI430048170 mRNA
GAGGGTTTTACTTCCTTGTTAACATATAAAGTTATAAATGAAGGACAAGGAGGAGATGGA NM_014936 RefSeq chr6 + 46129963 46146699 ENPP4 22875 ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative) GO:0016020|GO:0005886|GO:0030194|GO:0007596|GO:0046130|GO:0047710|GO:0016021|GO:0046872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145278_PI430048170 0.7888852858603970.8897709403654224.28197971506632

3.91713573861522 3.57902076529804 P P P 4.28512314752405 4.49647438690428
3.35120547891431 P P P LNCV6_145278_PI430048170 mRNA
CTGACCTGTCTCACCATGTACATAGCTTGATAAAGGGCCAATAAATATGATGTTATGGTG NM_001083116 RefSeq
chr10 - 70597347 70602775 PRF1 5551 "perforin 1 (pore forming protein), transcript variant 2"
GO:0005515|GO:0001771|GO:0002357|GO:0005886|GO:0022829|GO:0002418|GO:0005509|GO:0006915|GO:0005
576|GO:0055085|GO:0031904|GO:0051607|GO:0006968|GO:0016020|GO:0044194|GO:0019835|GO:0016023|GO:0
051260|GO:0016021. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127973_PI430048170 0.0155518146058126 1.43050088449931 5.72352657100218
5.61003506181236 5.68724367386395 P P P 5.06709255527062 5.32283634613376
5.06831152512173 P P P LNCV6_127973_PI430048170 mRNA
AAACAAAAACAAAAAACTGCAGTGAAAGACAAGCTGCAAATCAGCCATGTGCTGCGTGCC NM_001288718
RefSeq chr17 + 42287866 42311942 STAT5A 6776 "signal transducer and activator of transcription 5A,
transcript variant 1"
GO:0005515|GO:0033026|GO:0003700|GO:0006549|GO:0019530|GO:0019915|GO:0001553|GO:0048541|GO:0060
376|GO:0043029|GO:0007565|GO:0033077|GO:0046543|GO:0038161|GO:0046544|GO:0045588|GO:0018108|GO:0
032825|GO:0046449|GO:0019218|GO:0000979|GO:0045086|GO:0045931|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139450_PI430048170 0.4439984499360360.91022144065005 10.1499901939872
9.99060338278279 9.65814851226232 P P P 10.1872600974288 10.1302569795736
9.91726900838822 P P P LNCV6_139450_PI430048170 mRNA
GTATTGTTCTTGTCCATTGCTGTCACCAATAAAGGCATGGAAGAACAGAGTGACAAAAAA NM_022760RefSeq chr20
- 2835314 2840702 PCED1A 64773 "PC-esterase domain containing 1A, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133720_PI430048170 0.0179094735097695 1.43400590884321 4.52354763357863
4.71602136654141 4.83809347276568 P P P 4.21604245980176 3.98437911289936
4.31473736518912 P P P LNCV6_133720_PI430048170 mRNA
CTATGGCCTTTTGGAGTCTCATCTGACATAATGAAAAGTAATCACTTGAAGAGAATTAAC NM_024570RefSeq chr13
+ 50909677 50956765 RNASEH2B 79621 "ribonuclease H2, subunit B, transcript variant 1"
GO:0032299|GO:0010389|GO:0004523|GO:2000001|GO:0010629|GO:0005654|GO:0005634|GO:0048146|GO:0001
701|GO:0009259|GO:0006401 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143776_PI430048170 0.8366681060985110.9198506957048663.78738892946447
3.43386808571861 3.55007177964131 P P P 4.03405896871439 3.87462829741665
3.07766805272846 P P P LNCV6_143776_PI430048170 mRNA
AATTCTGTTGTAAGTCATCTGTGGCTCTGCCTCTTCCAGGGGCACAGATAGTGGAAAATT NM_130767RefSeq chr5
- 81330127 81394169 ACOT12 134526 acyl-CoA thioesterase 12
GO:0052689|GO:0006637|GO:0006090|GO:0006631|GO:0003986|GO:0006084|GO:0005524|GO:0008289|GO:0005
829. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89645_PI430048170 0.8054534824534771.15725127937533 1.96001083155703 0.615428539401224
1.00173055638031 A A A 0.9471827464856410.847004445259 1.42720575593784 A A A
LNCV6_89645_PI430048170 mRNA
TTAAAGCGTGCCATTGACCTGAAGGCTGAATTGGAGCTCGTACTGAGAAAATACAAGGAG NM_020894RefSeq chr4
+ 1347315 1388049 UVSSA 57654 UV-stimulated scaffold protein A
GO:0005515|GO:0016567|GO:0006283|GO:0005694|GO:0000993|GO:0009411 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145393_PI430048170 0.0679123436132102 0.4803948720024352.65197311391504
2.47444616739247 3.5771123773265 A A P 3.88750739940854 3.95928484839883
4.25863499895305 P P P LNCV6_145393_PI430048170 mRNA
GTCACTGTCTGGGAATTTAAGTGGCAAATACTTTCTTTGTCTCAGCTAATTAAACTCTAA NM_018292RefSeq chr6
+ 106629565 106668417 QRSL1 55278 glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1

GO:0005739|GO:0032543|GO:0050567|GO:0070681|GO:0030956|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145739_PI430048170 0.0680093537637253 0.5316601928687880.406380474093787
0.3941540177445990.253009937793654A A A 1.71525430030712 0.939238239622735
1.00366123846289 A A A LNCV6_145739_PI430048170 mRNA
AATGGTTGCCTCTTCAAATATATCCCCTTTAATTACTAATGGTTGGATCAAACTCGTTGA NM_001080525 RefSeq
chr3 - 48306845 48328341 SPINK8 NA "serine peptidase inhibitor, Kazal type 8 (putative)" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145027_PI430048170 0.8311565754886430.982175886099631 6.87680866888735
7.04743678028694 6.61020295274505 P P P 6.83669270064775 7.01439267668506
6.78422614402945 P P P LNCV6_145027_PI430048170 mRNA
CAAATTCTGCATCTCCAGAGGAAAATAAGAAATAAAGATGAATTGTTGCAACTCTTCCCA NM_001288957 RefSeq
chr14_KI270847v1_alt + 1225376 1231261 IFI27 3429 "interferon, alpha-inducible protein 27, transcript variant 6"
GO:0001102|GO:0006919|GO:0019221|GO:0005637|GO:0005741|GO:0000122|GO:0097190|GO:0005739|GO:0003674|GO:0060337|GO:0016021|GO:0005521|GO:0046825 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59583_PI430048170 0.3748313601642311.56432906695197 0.3824333779489441.74115925055047
0.450823615113478A A A 0.3503373725285460.3360669007071780.386153354336281A A A
LNCV6_59583_PI430048170 mRNA
TTTCCGAATGTCACCTGTGTGCTTCCTAGCAAAACAAAAACAAACGACAACAACAAAAAA NM_001143854 RefSeq
chr12 + 112791743 112898879 RPH3A 22895 "rabphilin 3A, transcript variant 1"
GO:0005515|GO:0043005|GO:0005215|GO:0017137|GO:0030054|GO:0005794|GO:0005509|GO:0045202|GO:0005546|GO:0032403|GO:0006886|GO:0005829|GO:0008021|GO:0005544|GO:0070679|GO:0043234|GO:0008430|GO:0042301|GO:0030672|GO:0008270|GO:0030141|GO:0019898 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_142861_PI430048170 0.00480317722188212 0.6362957292504014.47138941054847
4.46623197237815 4.50934092992292 P P P 5.02473425849911 5.1711759301159 5.2019842340871
P P P LNCV6_142861_PI430048170 mRNA
CTTTGACTAGTTTTTGTTTGTTTACTTTCTTCAGGGGGGAGGGGGGCAAGTTTGGGTAG NM_006885RefSeq chr16
- 72782886 73048375 ZFHX3 463 "zinc finger homeobox 3, transcript variant A"
GO:0005667|GO:0006355|GO:0003700|GO:0044212|GO:0006366|GO:0003705|GO:0005730|GO:0005634|GO:0000122|GO:0045662|GO:0043231|GO:0043565|GO:0005739|GO:0007517|GO:0007420|GO:0045663|GO:0045664|GO:0008270|GO:0005654|GO:0007050|GO:0019899|GO:0045892 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_145412_PI430048170 0.0116955437933137 0.71999684983899 9.0677766408934
9.01388749625912 9.01040138372332 P P P 9.37764229802518 9.57030571591018 9.5586788700782
P P P LNCV6_145412_PI430048170 mRNA
TGAAGCAGGTATCGCCTTACCTGTTGAAACTGAAAATAAAGCTTGTTTATTTCCAAGTTG NM_207310RefSeq chr2
- 130139282 130145134 CCDC74B 91409 "coiled-coil domain containing 74B, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132689_PI430048170 0.00401442869351982 0.4511546516636890.361439926473939
0.3902593593901430.323805156399709A A A 1.46271425310105 1.37676934970922
1.66621265770071 A A A LNCV6_132689_PI430048170 mRNA
GTAAGCTATCCACTAAGCAGGTGCCTGTGCAACTCTGATTTATGGCATTAACATATCAAA NM_001290326 RefSeq
chr4 + 143184916 143223874 USP38 84640 "ubiquitin specific peptidase 38, transcript variant 3"
GO:0004197|GO:0016579|GO:0004843|GO:0061136|GO:0043161 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_105441_PI430048170 0.0102717387205561.32441725554451 5.38554740299756
5.17503443797218 5.25494564198557 P P P 4.9175194347208 4.94229718547517

4.73911216935317 P P P LNCV6_105441_PI430048170 mRNA
TTCAACGACACTGTGAAGACGTGTGAGATCTTTGGCTGGTGCCCCGTGGAGGTGGATGAC NM_002558RefSeq chr17
- 3896590 3916666 P2RX1 5023 "purinergic receptor P2X, ligand gated ion channel, 1"
GO:0043005|GO:0005886|GO:0002554|GO:0051291|GO:0019228|GO:0005639|GO:0043270|GO:0045211|GO:0008
144|GO:0042310|GO:0051924|GO:0006810|GO:0001614|GO:0033198|GO:0051260|GO:0046513|GO:0006812|GO:0
006811|GO:0035590|GO:0005262|GO:0005261|GO:0004931|GO:0006919|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137874_PI430048170 0.6630805733065531.49133675644583 2.23277268921215
0.4510285457729032.59004305195841 A A A 1.46570087050829 1.64516702311056
1.14797676129794 A A A LNCV6_137874_PI430048170 mRNA
TTAGAACTTAGCTTCCTCACTTGGGAGCTGGGACTGACTGCATTTGCCCTTTGTATAAAC NM_145168RefSeq chr16
- 81997645 82011488 SDR42E1 93517 "short chain dehydrogenase/reductase family 42E, member 1"
GO:0006694|GO:0016021|GO:0003854|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141441_PI430048170 0.4618257207915760.81401733406228 7.32370257002748
7.43410623341883 7.34898539715972 P P P 7.82152453092083 7.95797445824956
7.07321148575642 P P P LNCV6_141441_PI430048170 mRNA
CCCAAACCTGTTCTGTCTCCCTCTCTGTATGTACATACATACACGTATAAAATATTGATA NM_139312RefSeq chr10
- 27110110 27154420 YME1L110730 "YME1-like 1 ATPase, transcript variant 1"
GO:0016020|GO:0008283|GO:0005743|GO:0006515|GO:0016021|GO:0007005|GO:0004222|GO:0005524|GO:0046
872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127269_PI430048170 0.6206782535350191.01654142379399 0.495102444517057
0.4813759314563740.521302055609183 A A A 0.5579155310460430.422935515405427
0.442487598521523 A A A LNCV6_127269_PI430048170 mRNA
GAAGATTCGAACATTGTCTATAGTTTGAAAAATCTATCAACACCTTCACTGCTTTCCCAA NM_001142771 RefSeq
chr10 - 53802770 54801291 PCDH15 65217 "protocadherin-related 15, transcript variant K"
GO:0005886|GO:0007605|GO:0005509|GO:0032420|GO:0045202|GO:0045494|GO:0005615|GO:0050957|GO:0016
021|GO:0007156|GO:0050953|GO:0001750|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116612_PI430048170 0.2534094064532990.90913806050407 0.298944675792561
0.2585304823055290.371563880672943 A A A 0.2781985081299830.561290613495744
0.489341005859284 A A A LNCV6_116612_PI430048170 mRNA
TATCACCGCTACCCAAGTAGTACAGGAAAAGGAAATTTGAAGAGGAAAAGAGGCACCAGG NM_001293172
RefSeq chr11 + 15643884 15705368 LOC102724957 NA uncharacterized LOC102724957 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_140127_PI430048170 0.45811387337626 1.39825579495223 1.92163080984845
2.04529874064646 3.13248630811092 A A P 2.11149410281237 2.58068470550818
0.704423892342661 A A A LNCV6_140127_PI430048170 mRNA
AACCAGATTCAGATTACAGTGTGATAAGGAAGACATAGGCTTTTGTCCTGCCTCGCCATC NM_007261RefSeq chr17
+ 74466382 74484798 CD300A 11314 "CD300a molecule, transcript variant 1"
GO:0043305|GO:0005515|GO:2000417|GO:0005886|GO:0050856|GO:0008429|GO:0050859|GO:0048147|GO:0030
889|GO:0038023|GO:0033007|GO:0060101|GO:0007165|GO:0016020|GO:0043407|GO:0001786|GO:0032516|GO:0
051134|GO:0016021|GO:0007155|GO:0070062|GO:0002376 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_128027_PI430048170 0.7930642363129970.9803873029314060.290771922144696
0.51184430876328 0.348571161587148 A A A 0.5282989230011750.432216851652761
0.274293293334868 A A A LNCV6_128027_PI430048170 mRNA
AGCTTGTTAGAAGTATCCTTTATTTCTAAAAGGTGCTGTGGATATTATGTAAAGGCGTGT NM_033360RefSeq chr12
- 25204788 25250931 KRAS 3845 "Kirsten rat sarcoma viral oncogene homolog, transcript variant a"
GO:0005515|GO:0008286|GO:0008284|GO:0030036|GO:0035022|GO:0005886|GO:0007264|GO:0019221|GO:0007
265|GO:0050900|GO:0032403|GO:0005829|GO:0005739|GO:0043524|GO:0005737|GO:0000186|GO:0051092|GO:0

007173|GO:0043406|GO:0000165|GO:0007411|GO:0030275|GO:0048169|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130497_PI430048170 0.8746968085390650.9774215279492529.58366828504753 10.0363200272203 9.85090381279553 P P P 9.90356779698427 9.59738724887912 10.0657619675216 P P P LNCV6_130497_PI430048170 mRNA GAGGCAACATCTCCTCTTTTTACAGAGGGTACATCCTTTTTTCTTACAAATTCTTCAATANM_001270896 RefSeq chr1 - 36136568 36149514 TRAPPC3 27095 "trafficking protein particle complex 3, transcript variant 4" GO:0005515|GO:0005794|GO:0005783|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138511_PI430048170 0.3038044977640221.14054652151768 7.86425858717871 8.22771741380886 8.10721568041871 P P P 7.62983816668553 7.99192436513544 8.00147622231116 P P P LNCV6_138511_PI430048170 mRNA CTTTTGGGTTTTCTCTTCTGTTGTTGTTGTTGTTGTTTTCTGTTGGCAGGACACACCCAA NM_001029882 RefSeq chr1 - 27534244 27603494 AHDC1 27245 "AT hook, DNA binding motif, containing 1" GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137841_PI430048170 0.2725796385886670.7714767583640855.65234307874022 4.85484694521352 4.73078322209589 P P P 5.64314842236465 5.55238122135805 5.32970295049356 P P P LNCV6_137841_PI430048170 mRNA GTCCAACAGATATCACTGTGAATTGAATAAATTTGTTGAAAGAGCACACAGGCACACATA NM_178858RefSeq chr10 + 102714540 102739189 SFXN2 118980 sideroflexin 2 GO:0034220|GO:0015075|GO:0005743|GO:0016021|GO:0055072 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145683_PI430048170 0.2135559752353541.05844352374259 0.498174772933068 0.3692630355789050.474510285297281A A A 0.2967777944845060.368537611161762 0.430918242575693A A A LNCV6_145683_PI430048170 mRNA GTCCAGTCTGGTGGAAAAAACATTGAACTTGCTATAATAAGAAGAAATCAACCTTTGAAG NM_144662RefSeq chr18 + 26133851 26193355 PSMA8 143471 "proteasome (prosome, macropain) subunit, alpha type, 8, transcript variant 1" GO:0000209|GO:0002474|GO:0010467|GO:0043066|GO:0006521|GO:0090263|GO:0051437|GO:0042590|GO:0006915|GO:0042981|GO:0005634|GO:0044281|GO:0031145|GO:0051439|GO:0004298|GO:0005829|GO:0034641|GO:0019773|GO:0002479|GO:0016032|GO:0000278|GO:0090090|GO:0070062|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129592_PI430048170 0.4002693601739780.8815121391648927.15555108188298 7.72240864341358 7.5589907904388 P P P 7.51944689488243 7.6112414927684 7.88405632031463 P P P LNCV6_129592_PI430048170 mRNA TGGTCAAGTTGTCAGCCCTGATCAGTTTGGACTCTGTAACTCATAGGTGCATTCTTTTTT NM_020416RefSeq chr4 - 6320577 6472599 PPP2R2C 5522 "protein phosphatase 2, regulatory subunit B, gamma, transcript variant 1" GO:0005515|GO:0007165|GO:0050790|GO:0008601|GO:0000159 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131780_PI430048170 0.6892310815431970.9672115368891717.36685081412326 7.33246298881404 7.21835479821598 P P P 7.46270743221527 7.41329521054343 7.17388563542883 P P P LNCV6_131780_PI430048170 mRNA CTGTCGGGGAGGCCTCAGGCCACCTCCAGGAACAGAACACAGTTTTAAGTTTGATTTTTT NM_001007467 RefSeq chr22 + 31496138 31618551 SFI1 9814 "Sfi1 homolog, spindle assembly associated (yeast), transcript variant 1" GO:0005515|GO:0006996|GO:0019902|GO:0005814|GO:0010923|GO:0000086|GO:0000278|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53752_PI430048170 0.9783114756927391.01537150173482 6.72368003233637 6.85902509940779 7.28532191276863 P P P 6.8799433577084 6.87320136660046 7.09840727528829 P P P LNCV6_53752_PI430048170 mRNA

ATAGGAAGTACGAGATTTGGATCATACAGCAGATGTCCGTTACACGCATGGGGAGATACT NM_178547 RefSeq chr1 - 32621215 32650590 ZBTB8OS 339487 zinc finger and BTB domain containing 8 opposite strand GO:0006388|GO:0072669|GO:0046872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143188_PI430048170 0.0202238087244212 0.5820566282078324.02763725807463 3.57527704958453 3.51366532386442 P P P 4.28816793764058 4.6062918902121 4.59851934899026 P P P LNCV6_143188_PI430048170 mRNA
TTGCCATGTAATAATGGGAAGCATATGTCATTCCCCATATGTGTTGGAGAATGACATTTA NM_001242532 RefSeq chr17 + 76737500 76779254 MFSD11 79157 "major facilitator superfamily domain containing 11, transcript variant 1" GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101106_PI430048170 0.1385353370023410.7478711079470264.32848321340183 4.07129888361122 3.99015828496078 P P P 4.26659816613567 4.87189497298346 4.46351630832452 P P P LNCV6_101106_PI430048170 mRNA
AAAGGAGACTTTATAACTATAGGAAGTCGAAAGGTGAGAAACCCCAAGCTGCACGTGGAG NM_018238 RefSeq chr7_GL383534v2_alt + 490 21001 AGK 55750 acylglycerol kinase GO:0005739|GO:0031966|GO:0003951|GO:0004143|GO:0047620|GO:0046834|GO:0046486|GO:0046513|GO:0005524|GO:0007205|GO:0001729|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137006_PI430048170 0.3270937596864890.8988102912351831 0.2353438090206 10.2136756948433 10.5184833397192 P P P 10.3001103556246 10.4942300811035 10.6358186188421 P P P LNCV6_137006_PI430048170 mRNA
TTCTGCATGGTTCACTGCTTAAGAAAATGCCTTCTGGAATATTTGTAAACTGAAATTCTG NM_001414 RefSeq chr12 - 123621022 123633776 EIF2B1 1967 "eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa" GO:0005515|GO:0010467|GO:0051716|GO:0009408|GO:0005886|GO:0003743|GO:0043434|GO:0006412|GO:0006413|GO:0005829|GO:0005085|GO:0005737|GO:0019509|GO:0030234|GO:0005851|GO:0005525|GO:0009749|GO:0043547|GO:0032057|GO:0016020|GO:0014003|GO:0006446|GO:0019003|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141190_PI430048170 0.00596093435707949 3.14340134291341 8.49571401420638 8.62130873781985 8.62463061922064 P P P 7.22832488369235 6.75035136230855 6.75577517664758 P P P LNCV6_141190_PI430048170 mRNA
TCCCCTCTACTTGGCAAGTGGTTGTCAAGTTCTAGTTGTTCAATAAATGTGTTAATAATG NM_006994 RefSeq chr6 + 26440471 26453415 BTN3A3 10384 "butyrophilin, subfamily 3, member A3, transcript variant 1" GO:0005737|GO:0005794|GO:0016020|GO:0005886|GO:0005730|GO:0016021|GO:0002456 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140625_PI430048170 0.0597925432169949 1.09792987870322 12.3526134371136 12.2701964663499 12.2871941666111 P P P 12.1418743560843 12.1132582568943 12.2482961979063 P P P LNCV6_140625_PI430048170 mRNA
TAACCTTGTAACTTTGTTTGGAGCTGGCACCTCTTGAAATAAAAAGGAGGATGCACGAGC NM_018447 RefSeq chr3 - 9963951 9986838 EMC3 55831 ER membrane protein complex subunit 3 GO:0072546|GO:0008150|GO:0003674|GO:0034975|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139121_PI430048170 0.5285806067108990.7785047417543322.1157471426046 0.4363425647344580.319375499448503 A A A 1.51399404297531 2.14518489861173 0.703765474049464 A A A LNCV6_139121_PI430048170 mRNA
GTTAGAGACATGAAATGTACTAGAGGAGCCCTTTTCCAATGGAAATATTATATACCACAT NM_012108 RefSeq chr4 + 67558727 67606898 STAP1 26228 signal transducing adaptor family member 1 GO:0005739|GO:0005515|GO:0043234|GO:0007165|GO:0005737|GO:0005070|GO:0061025|GO:0009967|GO:0005634|GO:0007169|GO:0006886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132543_PI430048170 0.1233223808009470.6176279475659550.321686105781331 0.2972752460130480.297667207317739 A A A 0.455563687824107 1.15499671545347

1.26608518297959 A A A LNCV6_132543_PI430048170 mRNA
TCTCCAAACTTGACTACTATTGGGAAGATGTGTATAAAAGCATCGCTTTGGGAATTTTTT NM_001195215 RefSeq
chr1 - 197504748 197775493 DENND1B 163486 "DENN/MADD domain containing 1B, transcript variant
3" GO:0017112|GO:0030136|GO:0032851|GO:0015031|GO:0005829 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139277_PI430048170 0.356600223101092 1.13521621957526 11.5691176994396
11.6184758208289 11.4109543343657 P P P 11.0535959330612 11.3158977992717
11.6302698556773 P P P LNCV6_139277_PI430048170 mRNA
CTGTGATGCTGCTGGTTTTATCTCTAGTGAAATAAAGTCAAAAGTTATTTAATTCCCGTC NM_007056 RefSeq chr19
+ 45039039 45070956 CLASRP 11129 "CLK4-associating serine/arginine rich protein, transcript variant 1"
GO:0008380|GO:0006397|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139898_PI430048170 0.771141238817318 0.991103472578009 0.461148715026872
0.476796073417274 0.37916882458927 A A A 0.508651251570071 0.417554428359663
0.429773770564242 A A A LNCV6_139898_PI430048170 mRNA
CAATGGGTGACATGATATCATGCTATGTGCCATTTTGTGTTAAACAAATTACACCAACAA NM_016206 RefSeq chr3
- 86937972 86991107 VGLL3 389136 vestigial-like family member 3
GO:0006355|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131016_PI430048170 0.0910531056966578 1.06367011147286 0.46613199907166
0.557633100619923 0.521323666973794 A A A 0.370224182301532 0.434269171495507
0.47304775770814 A A A LNCV6_131016_PI430048170 mRNA
TTTTGTTACTGTAATTCTGTTCACTAGAATAAAATGCAGAGCCACACCTGGTGAGGGCAC NM_004244 RefSeq chr12
- 7470815 7503818 CD163 9332 "CD163 molecule, transcript variant 1"
GO:0030666|GO:0005515|GO:0005886|GO:0005887|GO:0005576|GO:0006953|GO:0006898|GO:0005044 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131069_PI430048170 0.715611473545355 0.914860207059302 0.288538447322292
0.300334855228067 1.24708270740422 A A A 0.365883988096487 1.22687665779004
0.719260557426654 A A A LNCV6_131069_PI430048170 mRNA
GTCTCCATTTTTCAAGTGTGAGAGATAAGGGCTAATGATGACATCTCATTTATTTTGAGT NM_015230 RefSeq chr4
- 36065997 36244357 ARAP2 116984 "ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2"
GO:0043547|GO:0051056|GO:0008060|GO:0032312|GO:0007264|GO:0005547|GO:0008270|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137490_PI430048170 0.451626541091 5.74495287182659 4.48376623582417
0.432461858866786 0.427379381889055 P A A 0.80058132458481 0.372365245451217
0.408497387972353 A A A LNCV6_137490_PI430048170 mRNA
CAGGCTATTCTACTTTAAAGGAAGCCTTTTTATTTTGCTGCACACAATCTAGCAGGAATC NM_002543 RefSeq chr12
- 10158299 10172191 OLR1 4973 "oxidized low density lipoprotein (lectin-like) receptor 1, transcript
variant 1"
GO:0005515|GO:0042542|GO:0008219|GO:0005886|GO:0008015|GO:0050900|GO:0006898|GO:0043231|GO:0043
235|GO:0005041|GO:0006954|GO:0016020|GO:0005887|GO:0007596|GO:0042157|GO:0006508|GO:0007159|GO:0
030246|GO:0045121|GO:0005654|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139706_PI430048170 0.365679964043034 0.973810794099353 0.270594761660279
0.290773042528714 0.372754897545136 A A A 0.388848956656747 0.339745716605822
0.321587174625195 A A A LNCV6_139706_PI430048170 mRNA
TGAAACTACTGACACTTTTTCACCCAGGGCTATGCCAATAATGTGGCTGTTTACACACCA NM_001127258 RefSeq
chr14 + 99645142 99676674 HHIPL1 84439 "HHIP-like 1, transcript variant 1"
GO:0008150|GO:0003674|GO:0048038|GO:0016901|GO:0016020|GO:0005975|GO:0005576|GO:0005575|GO:0006
898|GO:0055114|GO:0005044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139563_PI430048170 0.000630225043007203 0.58006896798798 6.46747168024759
6.56654287289367 6.38567940326129 P P P 7.32275905826888 7.22148658825842

7.23616475387406 P P P LNCV6_139563_PI430048170 mRNA
CTGTGTATGTGTGTAACAGAATTCTGATTGTTAGACTGTAATGCTATTCCTCTATGGGAG NM_021202RefSeq chr20
+ 34704343 34713433 TP53INP2 58476 tumor protein p53 inducible nuclear protein 2
GO:0005515|GO:0005776|GO:0016605|GO:0005634|GO:0031410|GO:0045893|GO:0000045|GO:0006351|GO:0001
649|GO:0010508|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129152_PI430048170 0.0468602332727819 1.51869723735985 12.9009927804931
12.9319661597586 12.8703029682938 P P P 12.567220878714 12.148634454374 12.136636053516
P P P LNCV6_129152_PI430048170 mRNA
CCCTTTTGGACCCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCAAGTGTGGACTTGTG NM_024536RefSeq chr2
- 219538946 219543765 CHPF 79586 "chondroitin polymerizing factor, transcript variant 1"
GO:0005515|GO:0005975|GO:0044281|GO:0050510|GO:0046872|GO:0005829|GO:0030206|GO:0000139|GO:0005
759|GO:0032580|GO:0009405|GO:0016021|GO:0030204|GO:0047238|GO:0030203 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_136549_PI430048170 0.3171607568247861.04104116655013 12.0568849163231 12.17873113379
12.1545680413324 P P P 12.135146311477 12.0643013124595 12.0170639743684 P P P
LNCV6_136549_PI430048170 mRNA
ATTCCTATGGCACCAGCCAGGAAAAATGGCAGCTCTTAAAGGAGAAAATGTTTGAGCCCA NM_001005741 RefSeq
chr1 - 155234447 155244862 GBA 2629 "glucosidase, beta, acid, transcript variant 2"
GO:0005515|GO:0043627|GO:0097066|GO:0032715|GO:0004348|GO:0044281|GO:0005765|GO:0043407|GO:0071
356|GO:0046513|GO:0046512|GO:0009268|GO:0043202|GO:0070062|GO:0006665|GO:0006687|GO:0005975|GO:0
035307|GO:0005102|GO:0051384|GO:0033574|GO:0006680|GO:0050728|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93721_PI430048170 0.1246757527282271.42064797697092 8.817034857746 9.50595204612805
9.1018299938405 P P P 8.7788818346947 8.67384582670299 8.52501026181201 P P P
LNCV6_93721_PI430048170 mRNA
TCCATAGAATCATCACAGAAAAAATGATTTCAGGAGGTCTCCCCCGCTTTCTGCTCCCAA NM_001276378 RefSeq
chr3 - 45823317 45915724 LZTFL1 54585 "leucine zipper transcription factor-like 1, transcript variant
2" GO:0005515|GO:0034464|GO:0006996|GO:0072594|GO:0032403|GO:0042802|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144763_PI430048170 0.322039477625135 1.02210089812927 0.320732721294127
0.2440522459502520.30985646523627 A A A 0.2648629445422310.250180811751656
0.266117454716477A A A LNCV6_144763_PI430048170 mRNA
CAACCAGAGTTGTGTCTAACTTTAGGCATCTTTTAATAAATGTCATTGCGACTCTGAAAA NM_001756RefSeq
chr14_KI270847v1_alt - 1418809 1437913 SERPINA6 866 "serpin peptidase inhibitor, clade A (alpha-
1 antiproteinase, antitrypsin), member 6"
GO:0010951|GO:0004867|GO:0006810|GO:0005615|GO:0005496|GO:0008211|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138969_PI430048170 0.2259580157279831.03438259353592 0.368991044166253
0.3725686280006760.45523839249415 A A A 0.3476352904158390.325640907566228
0.378386029334176A A A LNCV6_138969_PI430048170 mRNA
GCTTCATCTTGCATGTTTAAGAGAACTTTGTTTTATTTTGAGGGATTATTTCTCTGGGGANM_001143837 RefSeq chr11
- 89324353 89589611 NOX4 50507 "NADPH oxidase 4, transcript variant 3"
GO:0051897|GO:0048471|GO:0008285|GO:2000573|GO:0045453|GO:0050660|GO:0071560|GO:0071480|GO:0050
667|GO:0014911|GO:0072341|GO:0005739|GO:0016324|GO:0006954|GO:0000166|GO:0016175|GO:0043406|GO:0
016174|GO:0070374|GO:0071333|GO:0055007|GO:0042554|GO:0001666|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135574_PI430048170 0.1896824774839171.28168511655054 4.61783572948577
5.14933877225007 4.88900002982057 P P P 4.85627321017003 4.41634434958251
4.29622623949371 P P P LNCV6_135574_PI430048170 mRNA

CATCTGAAGATTCGAATGAAAAGAAATGCATGTTTCCTGCTCTTCCCTCATTAAATTGCT NM_005416RefSeq chr1
+ 153001746 153003856 SPRR3 6707 "small proline-rich protein 3, transcript variant 1"
GO:0005515|GO:0005737|GO:0018149|GO:0008544|GO:0030216|GO:0005198|GO:0042060|GO:0031424|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141522_PI430048170 0.1847256218303391.49844342878177 1.58794107373964
0.7597932917021250.790416045774685A A A 0.6222994242394430.452118147171112
0.46789764588009 A A A LNCV6_141522_PI430048170 mRNA
GGCTAATTAACAGTCGTATGATTTCTAGCCCATGGGTTTAAAACTGTATCTTAAAGAGTC NM_181077RefSeq chr15
- 34379068 34389800 GOLGA8A 23015 "golgin A8 family, member A, transcript variant 1"
GO:0032580 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130128_PI430048170 0.4096035227095260.2706123435849223.82962194372717
3.93059195703291 3.42210135324026 P P P 6.91239660067277 4.07670174432763
3.48090176250654 P P P LNCV6_130128_PI430048170 mRNA
CAAACAATAAAATGGGATATTTGGGGAAGAAAGTTGTCTCAGGGCTCTCCAAAGAAGCAGNM_021970RefSeq chr4
- 99878337 99894546 LAMTOR3 8649 "late endosomal/lysosomal adaptor, MAPK and MTOR activator
3, transcript variant 1"
GO:0043547|GO:0005515|GO:0005085|GO:0071986|GO:0032947|GO:0032008|GO:0071230|GO:0034613|GO:0005
925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145204_PI430048170 0.1294832890741271.07025586969254 0.497186710987839
0.6252118762623530.546956507298353A A A 0.3913573218793990.473612548374063
0.510836120909542A A A LNCV6_145204_PI430048170 mRNA
GGGTGAACCAAGCTATAAAAGCCCATGCTTAAATAAAAATTATGTCCAAAAGCCATTGAA NM_005045RefSeq chr7
- 103471783 103989516 RELN 5649 "reelin, transcript variant 1"
GO:0090129|GO:0032008|GO:0021511|GO:0061098|GO:0021800|GO:2000310|GO:0097120|GO:0050731|GO:0070
326|GO:0070325|GO:0005615|GO:0021517|GO:0046872|GO:0030425|GO:0005737|GO:0097114|GO:0007411|GO:0
045860|GO:0006508|GO:0007155|GO:2000969|GO:0097119|GO:0061003|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144924_PI430048170 0.0466623739547946 0.90087910967124912.2435566774042
12.2102084809755 12.1150093927943 P P P 12.3147038414398 12.358262364343
12.3502842415709 P P P LNCV6_144924_PI430048170 mRNA
CCTGCTTAAGGTTTTAGGGTACCTTCAGTACTTTTTGCAATAAAAGTATTTCCTATCCAA NM_014851RefSeq chr1
- 6590723 6602898 KLHL21 9903 kelch-like family member 21
GO:0005827|GO:0007067|GO:0005813|GO:0005737|GO:0004842|GO:0032465|GO:0016567|GO:0035853|GO:0031
463|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145118_PI430048170 0.1318918048244221.03188990779966 0.388714525664684
0.3429633943025060.382906621593489A A A 0.30282512170353 0.312358481146456
0.363228652915289A A A LNCV6_145118_PI430048170 mRNA
TGTTAAGAACTATAGGATTTATGGGACCAAGTCTAGCGAGTCCAGATATCAAAATCATTA NM_001304441 RefSeq
chr11 - 102711794 102724954 MMP8 4317 "matrix metallopeptidase 8, transcript variant 2"
GO:0022617|GO:0004252|GO:0030198|GO:0030574|GO:0005509|GO:0006508|GO:0005578|GO:0008270|GO:0005
576|GO:0035987|GO:0004222|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128660_PI430048170 0.0146581775971195 0.5094747864022037.78995938095487
8.24228285602838 7.89607532999161 P P P 8.73591773822273 8.78785664483673 9.2945612862703
P P P LNCV6_128660_PI430048170 mRNA
CCTTCCTCCATTAATGTACAATCTCGAACTAACTGCTAATAAAGTGGGGTTCTGTTTGTA NM_001543RefSeq chr5
+ 150508111 150558211 NDST1 3340 "N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1,
transcript variant 1"
GO:0007585|GO:0005975|GO:0019213|GO:0048703|GO:0044281|GO:0015012|GO:0048702|GO:0006024|GO:0007
224|GO:0015016|GO:0006954|GO:0000139|GO:0000165|GO:0008543|GO:0009405|GO:0030901|GO:0030900|GO:0

016021|GO:0030203|GO:0030210|GO:0000271 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90363_PI430048170 0.2382873024316212.44097746071325 2.36090786552471 0.3283682589926
2.25305272279452 A A A 0.3402252495241290.3192978007218431.0412633116106 A A A
LNCV6_90363_PI430048170 mRNA
GTTTGACTGTGTCAAAAGCTGTGAGCAGCAAAATATAATCCATATGACCTTTTCTCTTGC NM_004726RefSeq chrX
+ 16946690 17153280 REPS2 9185 "RALBP1 associated Eps domain containing 2, transcript variant 1"
GO:0005515|GO:0005737|GO:0006461|GO:0007173|GO:0005509 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143730_PI430048170 0.8611970121721670.8199519148988751.91762677497281 1.1896834181929
0.581885801022925A A A 1.00893334443961 2.51765015732031 0.561764072437397A A A
LNCV6_143730_PI430048170 mRNA
TCACAGAGTGGCCAGTCATGAGACCATAAGAAACAGCTGCCCTTTTAGTGTCTTTCATAC NM_138286RefSeq chr19
- 23739194 23758891 ZNF681 148213 zinc finger protein 681
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134333_PI430048170 0.0116641695270971 0.7419896736608081 2.751724942516
12.7878047716002 12.8614469854027 P P P 13.1411965741849 13.183812141103
13.3602626423252 P P P LNCV6_134333_PI430048170 mRNA
TTTCGTCAGTCCTTAACATCTACCTCTCTGAATTTTCATGAATTTCTATTTCACAAGGGT NM_005274RefSeq chr1 -
84498322 84506579 GNG5 2787 "guanine nucleotide binding protein (G protein), gamma 5"
GO:0005886|GO:0005834|GO:0003924|GO:0007268|GO:0044281|GO:0030165|GO:0007165|GO:0006112|GO:0007
186|GO:0016020|GO:0071377|GO:0004871|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138829_PI430048170 0.0234806941087598 0.49864820852466 3.05713191990381
3.50980928557299 3.76920241110578 P P P 4.27743879960108 4.5758656409349
4.56293597243806 P P P LNCV6_138829_PI430048170 mRNA
AGTGGTCAGACGGCATTAGTTTTTCCCTTAGTTAAGCTAAATTAAAGGGACTCCATCCTG NM_006915RefSeq chrX
+ 46836911 46882356 RP2 6102 retinitis pigmentosa 2 (X-linked recessive)
GO:0005515|GO:0006241|GO:0005886|GO:0004550|GO:0015031|GO:0036064|GO:0005737|GO:0006457|GO:0007
010|GO:0070062|GO:0005794|GO:0006996|GO:0005814|GO:0006892|GO:0003779|GO:0072372|GO:0031410|GO:0
005525|GO:0005524|GO:0006165|GO:0006228|GO:0043547|GO:0006183|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136845_PI430048170 0.9654621043313050.9916341960633461.37868020526655
0.4299519067795860.6836924125093 A A A 0.2869944106699021.08315321923728 1.1774930512708
A A A LNCV6_136845_PI430048170 mRNA
CCTGGGAGATATGCCCTCGGAACCCATGAATGTTATTTTGTATTATTTTATTTTCATGATNM_153237RefSeq chr9 -
68536581 68540867 TMEM252 169693 transmembrane protein 252 GO:0016021 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_139846_PI430048170 0.0128378275222631 1.57200813069435 6.07759853642839
5.99495792200645 5.98166305883368 P P P 5.20950678334828 5.34093256782052
5.52977530209991 P P P LNCV6_139846_PI430048170 mRNA
CATACAGAAAAGAACGTCTCTGAGGTCCTTGCGTTTTTAATAAAATGGTAAGAGTCAAAA NM_016368RefSeq chr19
- 18434387 18438301 ISYNA1 51477 "inositol-3-phosphate synthase 1, transcript variant 1"
GO:0006021|GO:0043647|GO:0004512|GO:0044281|GO:0008654|GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135255_PI430048170 0.88274647279352 1.01090604098621 11.9043076515096
12.0458011195021 11.7966399982567 P P P 11.8592721837045 11.9138019562042
11.9364987539279 P P P LNCV6_135255_PI430048170 mRNA
GGGGGTTGGGTTCCTGAATGCACCATAATCGCTGTATGAAATATTAAAAAGTCTAAAGTG NM_033018RefSeq chrX
+ 47218128 47229995 CDK16 5127 "cyclin-dependent kinase 16, transcript variant 2"

GO:0005515|GO:0030133|GO:0043005|GO:0030054|GO:0005886|GO:0007283|GO:0006887|GO:0005524|GO:0031175|GO:0031234|GO:0008021|GO:0005737|GO:0004674|GO:0015630|GO:0051726|GO:0030252|GO:0006468|GO:0061178|GO:0004693. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143182_PI430048170 0.181123170655426 1.06452949211232 13.2180590927874 13.3414598448147 13.342294213992 P P P 13.2197379619599 13.2698730914297 13.142203685908 P P P LNCV6_143182_PI430048170 mRNA
GGCTGTTACCGTTGTTTTCTTGAATCACTCACAATGAGAAACTAACATTTTGCTTTTTGT NM_016062 RefSeq chr16 - 66932054 66934423 FAM96B 51647 "family with sequence similarity 96, member B, transcript variant 1"
GO:0005515|GO:0005737|GO:0007059|GO:0016226|GO:0005819|GO:0005654|GO:0005634|GO:0044281|GO:0071817. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134175_PI430048170 0.0444417856040917 0.593931914617752 0.499755932375888 0.622385802534092 0.916093658393884 A A A 1.79592179095635 1.31562786282032 1.1297864708793 A A A LNCV6_134175_PI430048170 mRNA
GCTCAGACTTAACCATTTATAAAGGTTGGTAAAATACTGGCAGTGACAACAAATTGACTT NM_003455 RefSeq chr11 - 123723926 123741683 ZNF202 7753 "zinc finger protein 202, transcript variant 1"
GO:0006629|GO:0005739|GO:0003700|GO:0006366|GO:0000981|GO:0005654|GO:0005634|GO:0000122|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131962_PI430048170 0.00198691743522515 0.663436975596382 9.05445558677176 8.93127455274174 9.14191498307999 P P P 9.60984839220464 9.55924581747092 9.73637002141506 P P P LNCV6_131962_PI430048170 mRNA
GTGGGAGGACCCTTCCACATCAACATTTGTGTGTATCCTTGCAATAAACTTCCATTGTGA NM_012192 RefSeq chr11 + 6481446 6484681 TIMM10B 26515 translocase of inner mitochondrial membrane 10 homolog B (yeast) GO:0005758|GO:0007160|GO:0006626|GO:0005743|GO:0042719|GO:0044267|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127829_PI430048170 0.151186674168296 0.739263732829499 4.5646869795687 5.19407903887312 4.9762709819166 P P P 5.02401265712499 5.55645000625395 5.47616649867423 P P P LNCV6_127829_PI430048170 mRNA
GTTGGGAAATAAAAGTTTCATGTGATGCCTAGGGTCAATTGTCTCATTAAAATGAGGTTT NM_007276 RefSeq chr7 + 26201210 26213607 CBX3 11335 "chromobox homolog 3, transcript variant 1"
GO:0005515|GO:0005719|GO:0019904|GO:0005819|GO:0005637|GO:0005634|GO:0005635|GO:0006351|GO:0042802|GO:0005720|GO:0000779|GO:0005654|GO:0006338|GO:0048511|GO:0031618|GO:0019899|GO:0045892|GO:0000785 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82606_PI430048170 0.49939541360671 0.78827707918238 0.278710711205151 2.50514259162201 2.15337403007403 A A A 1.98992573390735 2.69208337134532 1.98174344262027 A P A LNCV6_82606_PI430048170 mRNA
TGTTTGGTTACTGGCTTCTCTGCTTTGTCTTGCCAGCTACCAACGCTGCCCAGCAGGCCT NM_001171 RefSeq chr16_KI270853v1_alt - 1807490 1881466 ABCC6 368 "ATP-binding cassette, sub-family C (CFTR/MRP), member 6, transcript variant 1"
GO:0005215|GO:0005886|GO:0006200|GO:0042493|GO:0042626|GO:0005634|GO:0055085|GO:0005524|GO:0016328|GO:0016323|GO:0016324|GO:0005789|GO:0006810|GO:0016021|GO:0007601. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142721_PI430048170 0.78133180271894 1.0264750743914 5.16377638947136 4.95613628351056 4.98637065755696 P P P 5.46628375125866 4.62859776696338 4.76013940438708 P P P LNCV6_142721_PI430048170 mRNA
TTTTGTCTACACTTATCTACGTCCAAGATCCCTGCGATCTCCAACAGAGGACAAGGTTCT NM_001004687 RefSeq chr1 + 248060681 248061620 OR2L3 NA "olfactory receptor, family 2, subfamily L, member 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140909_PI430048170 0.0151026545353109 0.369266045677126 3.41204515658092 4.00656328662172 4.12583718431735 P P P 5.25713813111775 4.8230881433884

5.73012047407353 P P P LNCV6_140909_PI430048170 mRNA
GGAAGAGCTTTAGGATTCTAGTAGATGGATACTGAATACTCAGGCCCACTTAAATTATTA NM_002612 RefSeq chr7
- 95583496 95596613 PDK4 5166 "pyruvate dehydrogenase kinase, isozyme 4"
GO:0008286|GO:0005743|GO:0045124|GO:0010565|GO:0044281|GO:2000811|GO:0006885|GO:0010906|GO:0005
739|GO:0071398|GO:0042594|GO:0006090|GO:0005759|GO:0006006|GO:0044237|GO:0009267|GO:0004740|GO:0
010510|GO:0072593|GO:0042593|GO:0046320|GO:0005524|GO:0004672|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131940_PI430048170 0.01917970712668 0.671420763205579 9.24611925487145
9.20635177331244 9.57106168433793 P P P 9.84669584382125 9.80614038416606
10.1047120725254 P P P LNCV6_131940_PI430048170 mRNA
TTCAGAAGAACGGCATGAACAGTCTTCAGCCACAGTTGTGATGGTTGTTAAATGCTCACA NM_001025105 RefSeq
chr5 - 149495893 149551552 CSNK1A1 1452 "casein kinase 1, alpha 1, transcript variant 1"
GO:0005515|GO:0006909|GO:0005813|GO:0008360|GO:0090263|GO:0072372|GO:0005524|GO:0005829|GO:0007
165|GO:0005737|GO:0007067|GO:0004672|GO:0018105|GO:0016607|GO:0016020|GO:0004674|GO:0000777|GO:0
005847|GO:0006468|GO:0016055|GO:0007166|GO:0051301 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_145298_PI430048170 0.5522111043713191 .20021314933553 1.16845623168427
0.3396201412869370 .27480530448708 A A A 0.4864777224643730 .384204017678062
0.297420654286708 A A A LNCV6_145298_PI430048170 mRNA
CTGTATGATGTTTGTAAGACCATGTTTGTAAGACATGAATAAATTGCTGCTTTTGCCCAA NM_020783 RefSeq chr18
- 43267891 43277650 SYT4 6860 synaptotagmin IV
GO:0043005|GO:0005215|GO:0048471|GO:0030054|GO:0005886|GO:0005509|GO:0031045|GO:0006887|GO:0007
269|GO:0043231|GO:0045955|GO:0030276|GO:0000149|GO:0001786|GO:0030672|GO:0016021|GO:0031339 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88422_PI430048170 0.2078985525638880 .9497008564315751 0.5140186712636 10.5437502491631
10.4701504352744 P P P 10.5886134560185 10.650631591632 10.5095282672046 P P P
LNCV6_88422_PI430048170 mRNA
TGAGGTGGTGATTGACAGAGGCCCCTCCTCCTACCTGTCCAATGTGGATGTCTACCTGGA NM_001198994 RefSeq
chr1 - 1751231 1780069 NADK 65220 "NAD kinase, transcript variant 3"
GO:0016310|GO:0006741|GO:0046034|GO:0003951|GO:0006766|GO:0019674|GO:0006767|GO:0044281|GO:0005
524|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129029_PI430048170 0.1778620838963220 .8706128731867488 .39580022942749
8.12424963186402 8.20532709767918 P P P 8.58664184938145 8.27396021399001
8.46105796870586 P P P LNCV6_129029_PI430048170 mRNA
GCCCTGCAGTTCTCCTAAAACATAGTTGTTTGTTTTTCTTTAACAAAGTTTAAGCTAGTG NM_001012241 RefSeq
chr17 + 40122536 40136791 MSL1 339287 male-specific lethal 1 homolog (Drosophila)
GO:0043984|GO:0006325|GO:0072487|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73395_PI430048170 0.00388099296594381 1.65707496029662 10.4100417700893
10.5025986274108 10.6887344779432 P P P 9.71811359165697 9.86229076952781
9.84490117006581 P P P LNCV6_73395_PI430048170 mRNA
AAGCCATTTTGTAATTGCAGGAGCTGTCACGGGAAGTCTTTTTAGGATAAACGTAGGCCT NM_016589 RefSeq chr3
+ 119498520 119524278 TIMMDC1 51300 translocase of inner mitochondrial membrane domain
containing 1 GO:0005739|GO:0031966|GO:0005654|GO:0016021 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128177_PI430048170 0.1197519048757991 .28329734424728 4.59194066436325 4.9334514644135
4.91799314509717 P P P 4.7240358314644 4.38537730903326 4.23527289167077 P P P
LNCV6_128177_PI430048170 mRNA
TTAGATGGCAAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCTGCTCTCTTCCACCTGG NM_173619 RefSeq chr16
+ 70174172 70186895 CLEC18C NA "C-type lectin domain family 18, member C" NA . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_127549_PI430048170 0.9825047524600850.9870062559799025.16545186421325
5.57838632880604 5.74992331381499 P P P 5.27013837763582 5.31380937006208
5.92907231116989 P P P LNCV6_127549_PI430048170 mRNA
GGCTACCCAACTTGTATAGCAAAGATTTCTGATAGTTTGTGTTCATCTCATGTGAATAAT NM_001199322 RefSeq
chr6 - 8013566 8064414 BLOC1S5 63915 "biogenesis of lysosomal organelles complex-1, subunit
5, muted, transcript variant 2"
GO:0030133|GO:0005515|GO:0050942|GO:0048490|GO:0031083|GO:0032438|GO:0032474|GO:0035646|GO:0008
089|GO:0032402|GO:0031175 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136828_PI430048170 0.0523851920428691 0.9550890740741150.420717015790707
0.3624700757792090.37186511821025 A A A 0.4479056062898890.464644396127145
0.441965005806501 A A A LNCV6_136828_PI430048170 mRNA
CGTCCCACTTCATTTGTTCCATTCCTGATTCTTGGGTAATAAAGACAAACTTTGTACCTC NM_032579 RefSeq chr3
- 108755638 108757283 RETNLB 84666 resistin like beta
GO:0003674|GO:0005179|GO:0008283|GO:0005576|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129131_PI430048170 0.2561609880930670.8972983810688591 2.948586125941
12.7644833305418 12.5851342958098 P P P 12.9084292443961 12.9909930208018 12.888620768072
P P P LNCV6_129131_PI430048170 mRNA
CACCCTCCCCCCAATCAGTGTTCTTATTTCAGTGACAATAAACCATAGAGATGACTGGAG NM_024348 RefSeq chr9
- 34613544 34620523 DCTN3 11258 "dynactin 3 (p22), transcript variant 2"
GO:0005515|GO:0048471|GO:0005813|GO:0006996|GO:0005819|GO:0030496|GO:0032154|GO:0005829|GO:0019
886|GO:0000910|GO:0007067|GO:0005198|GO:0000086|GO:0000777|GO:0000278|GO:0005869|GO:0007017 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143078_PI430048170 0.0349983223930246 1.60985253114382 13.020652871286
13.143387279935 12.7413981997247 P P P 11.9813059392133 12.2504599914926
12.5793705483685 P P P LNCV6_143078_PI430048170 mRNA
GTGGGCCCACTGCTTTGGAGGTGATGGGACTATCAATAAGAACTCTGTTCACGCAAAAAA NM_024042 RefSeq chr16
+ 715172 717480 METRN 79006 "meteorin, glial cell differentiation regulator"
GO:0010001|GO:0050772|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56761_PI430048170 0.8891716438778831.0669714520658 3.14020484413338 0.977727715392486
2.43171334259546 P A A 1.92251553622854 2.79579752300854 2.14748650881872 A P A
LNCV6_56761_PI430048170 mRNA
AGAACTTCACAACTCCCTCTCACCATGGAGTTTGCATTTGATGCAGAAAGGCATGTGATC NM_017893 RefSeq chr10
+ 100972528 100985616 SEMA4G 57715 "sema domain, immunoglobulin domain (Ig), transmembrane
domain (TM) and short cytoplasmic domain, (semaphorin) 4G, transcript variant 1"
GO:0005886|GO:0004872|GO:0016021|GO:0030154|GO:0007399 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144306_PI430048170 0.5391173616684750.9504234393317020.584232472657799
0.4931796801785020.314760428139953 A A A 0.418468113398616 0.679025421755636
0.515540896567178 A A A LNCV6_144306_PI430048170 mRNA
ATACAATAGTGTTTTAAGAAGCACATGGCCTCATTTTCCTTAGAAACAAGACAAAGCCTT NM_001145313 RefSeq
chr9 + 105448033 105552433 FSD1L 83856 "fibronectin type III and SPRY domain containing 1-like,
transcript variant 3" GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_132352_PI430048170 0.2641461121262230.9249141386781 0.319382879839093
0.2444170819938920.298666389160514 A A A 0.418158817426917 0.509435060842114
0.263063379668254 A A A LNCV6_132352_PI430048170 mRNA
GTCTGTAGTTGATTGAAACGAGGGCAGTTATGAATTGATTTGGGCAATCAAATGAATTTA NM_014465 RefSeq chr4

- 69726967 69760712 SULT1B1 27284 "sulfotransferase family, cytosolic, 1B, member 1"
GO:0006805|GO:0050427|GO:0044281|GO:0005829|GO:0042403|GO:0009812|GO:0004062|GO:0030855|GO:0008
146|GO:0051923|GO:0018958|GO:0008202|GO:0006576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133533_PI430048170 0.565027255007035 1.13230087936851 5.03766503689873
5.40401677247594 5.37103529699221 P P P 4.29536438748799 5.3777595611973
5.38333202336872 P P P LNCV6_133533_PI430048170 mRNA
TGGCTTTTCAGTCATTTTGTGCTGTTTTCTCTGGTTCATTAATAAATTGAAACTGCCCTC NM_207381 RefSeq chr15 -
51056600 51105276 TNFAIP8L3 388121 "tumor necrosis factor, alpha-induced protein 8-like 3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136829_PI430048170 0.0544887407669751 0.6040975537067565 .42605560467989
5.3131462457866 5.73612718986473 P P P 6.03114865304873 5.95639439593631
6.61067334203197 P P P LNCV6_136829_PI430048170 mRNA
CATGAACCTTCCTCCAGGAAAAGCCATTCAAGCCTGATTATTTTTCTAAGTAACTTCAAT NM_018413 RefSeq chr12
+ 104456913 104762014 CHST11 50515 "carbohydrate (chondroitin 4) sulfotransferase 11, transcript variant
1"
GO:0043066|GO:0033037|GO:0005794|GO:0007585|GO:0005975|GO:0001537|GO:0050659|GO:0048703|GO:0044
281|GO:0009791|GO:0047756|GO:0016051|GO:0030206|GO:0048589|GO:0000139|GO:0002063|GO:0016020|GO:0
042127|GO:0009405|GO:0016021|GO:0030204|GO:0030203|GO:0042733|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136496_PI430048170 0.00309010911336758 2.22768392419334 5.25485565643097
5.39726533004293 4.94839472235376 P P P 4.01504909576712 4.26984331246429
3.85399265403005 P P P LNCV6_136496_PI430048170 mRNA
TAAACAACACACAGAGCACAAATATGCTCCTGACGGACTCAGGAAAATGCCAACAGCAGA NM_203297 RefSeq
chr5 - 181193923 181200930 TRIM7 81786 "tripartite motif containing 7, transcript variant 2"
GO:0005737|GO:0008270|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131848_PI430048170 0.60341630785343 0.9641128808618850.545520009955782
0.5001641694805740.265947770081084 A A A 0.41157050801756 0.565952931777966
0.503432359863785 A A A LNCV6_131848_PI430048170 mRNA
GTAAACATTTGTGGTGCTGTCAACCTGATTTCTTGACTCTCAAATGATTTTTGTATTTCC NM_025074 RefSeq chr4 +
78057569 78544269 FRAS1 80144 "Fraser extracellular matrix complex subunit 1, transcript variant 1"
GO:0031012|GO:0007154|GO:0003338|GO:0005886|GO:0060021|GO:0043588|GO:0030326|GO:0016021|GO:0015
031|GO:0002009|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142848_PI430048170 0.0367493672927793 0.7054316741786755.24770843495823
4.83995706881582 4.88857190093243 P P P 5.36708457183705 5.49768080526039
5.64372225336812 P P P LNCV6_142848_PI430048170 mRNA
ATCAAGCCATTTACGCTGCAGTGGATGATGATGATGACGATGCAGCTTAAGATGATTTAC NM_016216 RefSeq chr3
- 138160987 138174949 DBR1 51163 debranching RNA lariats 1
GO:0008419|GO:0000398|GO:0000375|GO:0005634|GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131959_PI430048170 0.2316224278930441.06090300895696 9.95156647445234
9.88882139276326 9.84463395474767 P P P 9.70964219580155 9.8422812715566
9.87400944180824 P P P LNCV6_131959_PI430048170 mRNA
GGCAATGTGAGGGTGATACTCTCTCACTCTAATAAACTTGGCACTTCTCCGAGTAAAAAA NM_005435 RefSeq chr7
+ 144355395 144380632 ARHGEF5 7984 Rho guanine nucleotide exchange factor (GEF) 5
GO:0035556|GO:0005515|GO:0071803|GO:0030036|GO:0032321|GO:0002408|GO:0032319|GO:0005525|GO:0005
089 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100008_PI430048170 0.13079806511908 0.7111061015915255.09538858287001
4.90651993567121 5.40900610956382 P P P 5.95888987518508 5.26875014194911
5.62201735059457 P P P LNCV6_100008_PI430048170 mRNA

ACTGCACCTGACAGAACCAGAACTCTTGATTTTCCTAATATTCAACACACTCTATGAAAA NM_001198784 RefSeq chr15 + 55408524 55418712 C15orf65 145788 chromosome 15 open reading frame 65 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139901_PI430048170 0.00168358399061711 0.272843258453542 3.55688606375653 3.52210508142178 3.09294430216647 P P P 4.88900002982057 5.41508370986428 5.46641661650077 P P P LNCV6_139901_PI430048170 mRNA
GCATGTTTGGCGTCATTCCTAAGAGCCATGTAATTTTAAACTTTTAATTGCAGTTAGTGA NM_007039 RefSeq chr14 - 88465777 88554779 PTPN21 11099 "protein tyrosine phosphatase, non-receptor type 21" GO:0005515|GO:0005737|GO:0006470|GO:0005856|GO:0035335|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142822_PI430048170 0.600439261069352 0.934229923116331 6.27926642880399 6.64169167844601 6.88794814748316 P P P 6.62674090778597 6.64339647389807 6.8826453519665 P P P LNCV6_142822_PI430048170 mRNA
GAAGAGAACTTTGTGCTCTGTTTTACCTTACTCTGTTTAGAAAAGTATACAAGCGTGTTT NM_016166 RefSeq chr15 + 68054233 68188066 PIAS1 8554 "protein inhibitor of activated STAT, 1" GO:0005515|GO:0016874|GO:0019221|GO:0032436|GO:0005634|GO:0007283|GO:0050681|GO:0060334|GO:0042127|GO:0033235|GO:0051152|GO:0031625|GO:0060333|GO:0003714|GO:0016925|GO:0003713|GO:0019904|GO:0000122|GO:0065004|GO:0007259|GO:0003677|GO:0006351|GO:0016607|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137071_PI430048170 0.318693962062018 1.02089779837674 0.328933387260778 0.253872898252236 0.274268967911104 A A A 0.254763778474499 0.257982992864866 0.255859141692337 A A A LNCV6_137071_PI430048170 mRNA
CTGGGACTAGTTGAGTTGTATCTTTAGTATTCAGGTTGTGAAAAATAAAGATGTTTGGCT NM_001260504 RefSeq chr7 + 23710325 23832511 STK31 56164 "serine/threonine kinase 31, transcript variant 4" GO:0001669|GO:0004674|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_29408_PI430048170 0.135330808478004 0.781371042670232 5.89039241629763 5.59990917347342 5.64610052698013 P P P 5.78584545979481 6.08371088457134 6.30524561803645 P P P LNCV6_29408_PI430048170 mRNA
TGAGCTGTCCAAATTTCATCTTAAAGTGGATCATTTGACTCTGAAACACGATTCTCATGG NM_020786 RefSeq chr16 + 66880479 66891099 PDP2 57546 pyruvate dehyrogenase phosphatase catalytic subunit 2 GO:0010510|GO:0035970|GO:0004741|GO:0006090|GO:0005759|GO:0004724|GO:0044281|GO:0046872|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52374_PI430048170 0.0452921748062775 0.418108459110025 2.34974001066989 2.50993175415954 3.44721556777394 A A P 3.84544020392415 4.1392042452856 4.31515717205623 P P P LNCV6_52374_PI430048170 mRNA
TTACCACAATTTTGGCTGTCATCTGCTGTGAATTCTTCAAGCACTGACCCTGAAAGGCTG NM_002557 RefSeq chr1 - 111414314 111427777 OVGP1 5016 "oviductal glycoprotein 1, 120kDa" GO:0030133|GO:2000360|GO:0006032|GO:0007565|GO:0005975|GO:0005576|GO:0007339|GO:0005829|GO:0007338|GO:0008061|GO:0035805|GO:0004568|GO:0032504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133483_PI430048170 0.0219387120718390 0.564413475511719 7.84214487308384 7.85145016648733 8.13864776504271 P P P 8.47877265246846 8.73002743899541 9.05988245285033 P P P LNCV6_133483_PI430048170 mRNA
GAATAAAGCAAAATACTCAGGTGAGCATCCTGCCTCCTGTTCCCATTCCTAGTAGCTAAA NM_001024847 RefSeq chr3 + 30606501 30694141 TGFBR2 7048 "transforming growth factor, beta receptor II (70/80kDa), transcript variant 1" GO:0005515|GO:0010468|GO:0060044|GO:0043627|GO:0046332|GO:0048701|GO:0002663|GO:0007224|GO:0007507|GO:0004702|GO:0018105|GO:0042127|GO:0018107|GO:0007179|GO:0023014|GO:0007566|GO:0007568|GO:0031435|GO:0001701|GO:0006898|GO:0043235|GO:0007182|GO:0002666|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137776_PI430048170 0.1226418483270591.55329339923641 4.93921615404646 5.7090896499665
5.09762996782625 P P P 4.58693643966376 4.65048148667979 4.71840884748242 P P P
LNCV6_137776_PI430048170 mRNA
TGATTCCCATAGGTGTGTCAACTGACAAATGAATGTTCCATCTCCCTACGACAATTTGCT NM_006315RefSeq chr4
+ 705783 770639 PCGF3 10336 polycomb group ring finger 3
GO:0031519|GO:0005515|GO:0006355|GO:0008270|GO:0005654|GO:0005634|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142166_PI430048170 0.0145796547577729 1.13641410253247 0.7661288163736
0.8445431315853580.759339373281201A A A 0.6195272634515420.608656135438411
0.589768759282802A A A LNCV6_142166_PI430048170 mRNA
TTCTCCCTCTATGTATGTACATAGAGTGTACATACATAGAGTGAGAAGCAAAGAAGGTCC NM_001242865 RefSeq
chr21 + 46635594 46655097 PRMT2 3275 "protein arginine methyltransferase 2, transcript variant 4"
GO:0005515|GO:0019919|GO:0005634|GO:0033142|GO:0050681|GO:0042974|GO:0008469|GO:0042975|GO:0042
803|GO:0005829|GO:0042054|GO:0046966|GO:0005737|GO:0035189|GO:0006479|GO:0004871|GO:0043065|GO:0
016571|GO:0003713|GO:0030331|GO:0060765|GO:0016274|GO:0005730|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106612_PI430048170 0.3920712849771371.28113586170467 4.98352371997556
4.03077055786698 4.3304519148816 P P P 4.12746311200883 4.30209528058884
3.99558612203505 P P P LNCV6_106612_PI430048170 mRNA
TCTTCTAGAACATTCCCCCGCCATTATTACTTCAATATGGCTACACATACTTCCTAATTGNM_005282RefSeq chr19 -
45589764 45602208 GPR4 2828 G protein-coupled receptor 4
GO:0007186|GO:0005886|GO:0005887|GO:0004930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127758_PI430048170 0.3323480234329741.47564669896396 0.267646784938231
1.38352422368103 1.45034389319366 A A A 0.3467187222428710.93776194735869
0.320249938166821A A A LNCV6_127758_PI430048170 mRNA
CTACAGCCTGAGGAATAATGATGTAAATGTTGCCTTAAAGAAATTCATGGAAAATCCATG NM_001004064 RefSeq
chr11 - 56136770 56137718 OR8J3 NA "olfactory receptor, family 8, subfamily J, member 3" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142553_PI430048170 0.3529199993043180.661922509626994 4.75469949428211
3.85482251542311 4.17580973205878 P P P 4.25742442822065 4.50524373077785
5.58833411362079 P P P LNCV6_142553_PI430048170 mRNA
GTGATGTGTTCAGTTGCGTGCTGGGTGACATGTGAAATAAACTCATCCTTGAGGAATTTA NM_000255RefSeq chr6
- 49430359 49463328 MUT 4594 methylmalonyl CoA mutase
GO:0006635|GO:0009235|GO:0031419|GO:0006767|GO:0044281|GO:0009791|GO:0050667|GO:0046872|GO:0072
341|GO:0005739|GO:0004494|GO:0006766|GO:0005759|GO:0019626|GO:0044255 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133569_PI430048170 0.00703158435546236 0.1995731543523513.08111254079005
2.6894754046062 2.87854660360613 A A P 4.62210630396614 5.36484431267086
5.51545248291405 P P P LNCV6_133569_PI430048170 mRNA
TAAGGAATGGTCATCTAAAATGAGAGATTCTGGATTTTAATGCAGTTCAAAGTTGAGCTG NM_014109RefSeq chr8
- 123319850 123396465 ATAD2 29028 "ATPase family, AAA domain containing 2"
GO:0006200|GO:0005654|GO:0045893|GO:0016887|GO:0005524|GO:0006351|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143059_PI430048170 0.0071299373733074 5.17387529213097 8.49859574053596
8.79647489410121 8.25986995483757 P P P 6.61241027519252 6.16025556710542
5.51496737295959 P P P LNCV6_143059_PI430048170 mRNA
AGGGCTCTCGGAGAAAGTGTGTGTATTCCTTTCTTAATAAAGTGTGGACTGAACAAAAAA NM_014370RefSeq chrX
+ 153781000 153785732 SRPK3 26576 "SRSF protein kinase 3, transcript variant 1"
GO:0005515|GO:0007519|GO:0004674|GO:0060537|GO:0006468|GO:0005575|GO:0005524|GO:0030154 .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128308_PI430048170 0.0525247179126303 0.6708640449619666.19004450369979
5.99787583435044 6.57432099463681 P P P 6.71440008385461 6.77683883821741
7.03859859862256 P P P LNCV6_128308_PI430048170 mRNA
TGAGCGAAGATGGCAGTAACTGTTAAATAAGCATTCTTTTCTACTTCTTGGAATCAGATG NM_001282497 RefSeq
chr20 - 2481820 2509132 ZNF343 79175 "zinc finger protein 343, transcript variant 4"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_7911_PI430048170 0.3018406312695261.12712864798508 6.15407125781153 6.29650479282329
6.00104580018728 P P P 5.73300953507145 6.10082606290058 6.08577666115056 P P P
LNCV6_7911_PI430048170 mRNA
GTGATGAAAAAAGTTTCGGTCCCAGATGATGGCCAGTGATAACAACATTTTTCTGATGTT NM_001267699 RefSeq
chr4 + 151099572 151104205 RPS3A 6189 "ribosomal protein S3A, transcript variant 2"
GO:0005515|GO:0010467|GO:0003723|GO:0019058|GO:0005634|GO:0006412|GO:0006413|GO:0030154|GO:0006
414|GO:0005829|GO:0005737|GO:0002181|GO:0000184|GO:0016032|GO:0070062|GO:0043066|GO:0003735|GO:0
006614|GO:0019083|GO:0005730|GO:0006415|GO:0022627|GO:0030529|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130345_PI430048170 0.0354990426823243 1.06005334728253 0.370308542831305
0.3597336796100610.303192427467912A A A 0.24535422593467 0.290872399440885
0.245012046697314A A A LNCV6_130345_PI430048170 mRNA
ACAGGATCTTTATTGGTGACCTTTTGTAAGACATTAGTTTGAGGTACTACCTATGTACTT NM_000702RefSeq chr1
+ 160115729 160143584 ATP1A2 477 "ATPase, Na+/K+ transporting, alpha 2 polypeptide"
GO:0008344|GO:0005886|GO:0051087|GO:0006883|GO:0045202|GO:0006942|GO:0006940|GO:0060048|GO:0046
872|GO:0019229|GO:0040011|GO:0005737|GO:0002087|GO:0034220|GO:0043197|GO:0045988|GO:0006814|GO:0
045822|GO:0006813|GO:0086004|GO:0005391|GO:0030007|GO:0051481|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_122360_PI430048170 0.9850666302843221.00989895646536 4.95659756163859
4.73268237277108 4.34460424178174 P P P 4.58707640306244 4.63861325019525
4.82004983755857 P P P LNCV6_122360_PI430048170 mRNA
GTGCTACAGGCTGTTTCAGGAAGCCAATTAATTTTGTACACATAATACTTAATTACCTTC NM_003906RefSeq chr21
- 46235124 46285394 MCM3AP 8888 minichromosome maintenance complex component 3
associated protein
GO:0006260|GO:0031965|GO:0005737|GO:0016746|GO:0005643|GO:0005654|GO:0005634|GO:0051028|GO:0006
606|GO:0003677|GO:0005829|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135272_PI430048170 0.00941643215202504 0.4476624635076717.65895632577781
7.17328287069922 7.51086884768075 P P P 8.2412270159121 8.68638082288357
8.86651460924842 P P P LNCV6_135272_PI430048170 mRNA
TACCTAAAGCTTGTTGCCTTTTCTTGTGCTGTTTATGCGTGTAGAGCACTCAAGAAAGTT NM_002745RefSeq chr22
- 21759657 21867680 MAPK1 5594 "mitogen-activated protein kinase 1, transcript variant 1"
GO:0005515|GO:0019858|GO:0034605|GO:0002756|GO:0006935|GO:0007173|GO:0018105|GO:0000165|GO:0007
411|GO:0018107|GO:0002755|GO:0009887|GO:0005856|GO:0031663|GO:0004707|GO:0038127|GO:0010800|GO:0
038124|GO:0030335|GO:0005794|GO:0038123|GO:0005815|GO:0019902|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133910_PI430048170 0.0407635305180173 0.52950540372023 6.87053353790752
7.0330984504247 6.86318373229649 P P P 7.4163107074013 8.09428261388886
7.93126622878708 P P P LNCV6_133910_PI430048170 mRNA
ATATATCAATTCTCATGAGTGTATTATAATCTCTGGTGGGGGCAAGTGTCTGGAAGGCCT NM_001142503 RefSeq
chrX + 68647668 68725842 STARD8 9754 "StAR-related lipid transfer (START) domain containing 8,
transcript variant 1" GO:0043547|GO:0051056|GO:0007264|GO:0005925|GO:0008289|GO:0005829|GO:0005096

. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140392_PI430048170 0.3530346228066360.8539659764656120.304373326977828
0.3374035698127190.349886527807461A A A 0.8812850707842370.37758559680389
0.352555776554246A A A LNCV6_140392_PI430048170 mRNA
GCAGTGAGACTTTTATCACTGAATAGACAAATCATTTGTGCCGAAAATACATCTGGAATA NM_001278393 RefSeq
chr12 - 95516559 95548272 USP44 84101 "ubiquitin specific peptidase 44, transcript variant 3"
GO:0005515|GO:0090231|GO:0016579|GO:0004843|GO:0090266|GO:0005730|GO:0060564|GO:0005634|GO:0004
197|GO:0007067|GO:0015630|GO:0008270|GO:0043161|GO:0051301 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_128925_PI430048170 0.00164698581581591 1.58236910492058 13.5694436616707
13.6834619870774 13.4621106161789 P P P 12.867549637935 13.0037248205913
12.8614469854027 P P P LNCV6_128925_PI430048170 mRNA
TAACTGTAGAGGCGCCTGCCATTAAACGTGTCCGCTGCTGTGGCGACAGATCTGAAAAAA NM_001284501 RefSeq
chr16 + 1782922 1789191 NUBP2 10101 "nucleotide binding protein 2, transcript variant 2"
GO:0005515|GO:0005737|GO:0051539|GO:0016226|GO:0000166|GO:0031616|GO:0005634|GO:0044281|GO:0005
524|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127105_PI430048170 0.2150846067749540.8854006175419538.27561890807572
8.32837603636952 8.4849547074104 P P P 8.54363049826538 8.36689582649784
8.69491013258831 P P P LNCV6_127105_PI430048170 mRNA
AGACAAGTTCCATGGGATACAACCTCCCTCTTGTTTTGTTTGTCTCTCCTTTTCTTTTGT NM_005777RefSeq chr3 +
49940043 50077252 RBM6 10180 "RNA binding motif protein 6, transcript variant 1"
GO:0006396|GO:0000166|GO:0003723|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127432_PI430048170 0.0223439931631722 0.3070173293402891.46222258691086
0.4909382017616320.406572950273094A A A 2.58444123297798 2.31464920834952
2.78591367321524 A A P LNCV6_127432_PI430048170 mRNA
GGGGTTGCTTTGCTTTGTCAGTTGGATGACTAAATTGGACAAATTTATAAAACATCCAAA NM_001291661 RefSeq
chr3 - 57293698 57544344 DNAH12 201625 "dynein, axonemal, heavy chain 12, transcript variant 3"
GO:0005929|GO:0005737|GO:0030286|GO:0008152|GO:0005874|GO:0003777|GO:0016887|GO:0005524|GO:0007
018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140475_PI430048170 0.3958127697773971.04715205593644 0.322952160240847
0.3279540944053840.504181203933835A A A 0.3237918335633240.291276930576208
0.34753653545798 A A A LNCV6_140475_PI430048170 mRNA
GAGGAATTTCTCGTACCCCTACTGCATGGTATCGATTTTTAATAAATTGTTGCAAATTTG NM_005458RefSeq chr9
- 98288081 98709197 GABBR2 9568 "gamma-aminobutyric acid (GABA) B receptor, 2"
GO:0005515|GO:0043005|GO:0030054|GO:0005886|GO:0004965|GO:0007268|GO:0007214|GO:0007194|GO:0038
039|GO:0005737|GO:0007186|GO:0005887|GO:0045211 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_137595_PI430048170 0.0130672844164137 0.759425178502579 7.90768155671361
8.03365764983451 8.14919914692915 P P P 8.31232815203652 8.45646058534195
8.51541271602941 P P P LNCV6_137595_PI430048170 mRNA
TACGTCTCTGTCCACATGTCAGTGTATTAAAACCCCAATGGGTTCCGTTTCTCCTTTTCC NM_032888 RefSeq chr9
+ 114155544 114312516 COL27A1 85301 "collagen, type XXVII, alpha 1"
GO:0003431|GO:0030198|GO:0005788|GO:0005576|GO:0005583|GO:0046872|GO:0005201 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141957_PI430048170 0.224267534028325 0.633593439170741 3.11440289752358
3.63026778523785 3.18940125353795 P P P 3.21020345000842 4.2913389463628
4.23072089568507 P P P LNCV6_141957_PI430048170 mRNA
CCAGTTTGTATCAAAGGGTATCGACTTAAGTGAAATTTCAACATGCTGTTACTTTTTCCT NM_152419 RefSeq chr8

+ 43140448 43202827 HGSNAT 138050 heparan-alpha-glucosaminide N-acetyltransferase
GO:0015019|GO:0016746|GO:0005975|GO:0009405|GO:0006027|GO:0007041|GO:0044281|GO:0016021|GO:0005
765|GO:0051259|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132889_PI430048170 0.411896916032626 1.05290863616464 0.303767346269277
0.307734198429362 0.512844125094907 A A A 0.3109782944351 0.274095139041129
0.325706552659737 A A A LNCV6_132889_PI430048170 mRNA
GTGTAACAGCTCCTTGGGAGGAAGCAGAATAAAGCAATTTTCCTTGAAGCCGAGAAAAAA NM_000257 RefSeq
chr14 - 23412737 23435686 MYH7 4625 "myosin, heavy chain 7, cardiac muscle, beta"
GO:0005515|GO:0005516|GO:0030018|GO:0001725|GO:0030049|GO:0055010|GO:0006200|GO:0006941|GO:0003
779|GO:0016459|GO:0030898|GO:0030017|GO:0005524|GO:0007512|GO:0032982|GO:0000146|GO:0005737|GO:0
006936|GO:0002027|GO:0002026|GO:0005654|GO:0005859|GO:0016887|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141352_PI430048170 0.962935252772679 0.993721541118829 0.592362150163025
0.410462319195362 0.575259237241981 A A A 0.389943221627526 0.704474062092214
0.500001381567633 A A A LNCV6_141352_PI430048170 mRNA
CCTGCATATCATTCACCCAAAACAAAGTAATAGCGCCTCTTTTATTATTTTGACTGAATG NM_006183 RefSeq
chr12 + 85874294 85882992 NTS 4922 neurotensin
GO:0030133|GO:0005515|GO:0007165|GO:0050880|GO:0005576|GO:0005184 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_131845_PI430048170 0.227937151851754 4.31920831299962 0.330310414911229
3.49845044781505 1.80459846040573 A P A 0.251660686887486 0.41478789144507
0.254329020726525 A A A LNCV6_131845_PI430048170 mRNA
CCAACAAACACTCATTCGATATATTTGTCTTCGAAGACATTCAAAGCCTGCCGAGCCATG NM_001012970 RefSeq
chr1 + 244352634 244389086 C1orf100 200159 "chromosome 1 open reading frame 100,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_91036_PI430048170 0.200999416421894 0.600355214266791 0.361442733909945
0.331573455416637 0.319017746110878 A A A 0.971578132235055 1.60189116022621
0.397797121718941 A A A LNCV6_91036_PI430048170 mRNA
CCAGTTGCCTCTCAACAGAATGCTTCAAGTGTTTGTGAAGAAAAACCTATACCTGCTGAA NM_013314RefSeq chr10
- 96191698 96271576 BLNK 29760 "B-cell linker, transcript variant 1"
GO:0035556|GO:0005622|GO:0005515|GO:0006954|GO:0005886|GO:0006959|GO:0005070|GO:0030183|GO:0005
068|GO:0009967|GO:0007169|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136065_PI430048170 0.598019670075785 1.01234462710615 0.301582359638042
0.25495910470203 0.346964281251984 A A A 0.272545889606635 0.308330272605012
0.270681745344449 A A A LNCV6_136065_PI430048170 mRNA
GTAATTTTAAGATGTATGCTTGGATGTATTGGGCAGCAGCTTCTAAGGTGTTGAAGATTA NM_001290355 RefSeq
chr19 + 16719975 16817963 NWD1 NA "NACHT and WD repeat domain containing 1, transcript variant
2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136742_PI430048170 0.391781768768079 0.635342974528443 1.27531274325362
1.56877556205436 1.73544830768635 A A A 2.67373927437553 1.102445378341
2.37627732344225 A A P LNCV6_136742_PI430048170 mRNA
CTTCTTGTTCTGCCCTCCAGAGATTTGCTCAAATGATCAATAAGCTTTAAATTAAACTCT NM_003241 RefSeq chr3
+ 44874605 44914596 TGM4 7047 transglutaminase 4
GO:0031012|GO:0005737|GO:0018149|GO:0005794|GO:0003810|GO:0046872|GO:0070062|GO:0042628 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58291_PI430048170 0.753681538153937 1.03326631042638 0.421493519709241 0.701312025927328
0.345206709940077 A A A 0.422957037523955 0.477481156051915 0.450251590228249 A A A
LNCV6_58291_PI430048170 mRNA
ACTCACAACCAACTCACCAGGAAGCTTTGGCAGAGTGGACAGCAGGTGACCTTGCTGGTG NM_001168468 RefSeq

chr11 + 119185456 119190223 PDZD3 79849 "PDZ domain containing 3, transcript variant 1"
GO:0005515|GO:0030251|GO:0045177|GO:0009636|GO:0019934|GO:0008022|GO:0005829|GO:0005903|GO:0031
283|GO:0006833|GO:0030827|GO:0035003|GO:0007168|GO:0008200|GO:0006811 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138256_PI430048170 0.2401453471040270.7578352451800590.3960383458396620.3635657429993
0.425105211992098A A A 1.14706177806618 0.7582918049712790.378200670467968A A A
LNCV6_138256_PI430048170 mRNA
CTGCTAAGCAAAGACTAGGGACAGGCAAAGATAATTTATGGCAAAGTGTTTAAATTGTTT NM_001122679 RefSeq
chr5 + 167284837 168264157 TENM2 57451 teneurin transmembrane protein 2
GO:0005515|GO:0043005|GO:0030054|GO:0035584|GO:0005886|GO:0005783|GO:0051491|GO:0045202|GO:0005
634|GO:0030175|GO:0030425|GO:0042803|GO:0030426|GO:0016337|GO:0043197|GO:0007411|GO:0005911|GO:0
045211|GO:0050839|GO:0007157|GO:0005794|GO:0046982|GO:0005102|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144465_PI430048170 0.3465453211856340.6710764616232941.08038865351739
0.71103052640135 0.56847936010456 A A A 1.91065777538965 1.36821518668051
0.544877701098825A A A LNCV6_144465_PI430048170 mRNA
TAAAATATCCCCAAGTTGTCCCTTTACAGCCATCAATATATTTTACACTCTGCGGCCAGG NM_152545RefSeq chr4
- 81426392 81471928 RASGEF1B 153020 "RasGEF domain family, member 1B, transcript variant 1"
GO:0032320|GO:0007264|GO:0005770|GO:0030496|GO:0005769|GO:0005088 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128349_PI430048170 1.22074539503819e-05 0.2099364956663515.19932697268674
5.06849024754346 5.24998536570962 P P P 7.30155548677745 7.47171869778445
7.49867012974474 P P P LNCV6_128349_PI430048170 mRNA
CAGTGCTTGAAGATACATTCACAAATACTTGGTTTGGGAAGACACCGTTTAATTTTAAGT NM_004521RefSeq chr10
- 32009009 32056443 KIF5B 3799 kinesin family member 5B
GO:0008017|GO:0005515|GO:0043005|GO:0048471|GO:0072383|GO:0043268|GO:0030139|GO:0035617|GO:0005
737|GO:0007411|GO:0047496|GO:0008574|GO:0042391|GO:0016887|GO:0007018|GO:0005871|GO:0005815|GO:0
005874|GO:0003777|GO:0005524|GO:0031982|GO:0032230|GO:0030705|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_3206_PI430048170 0.0227491439300999 0.3953749081333126.47451167513596
6.11979536572189 6.46789740140499 P P P 7.14268214815703 7.88004375624491
7.95303742298978 P P P LNCV6_3206_PI430048170 mRNA
AACACATAACAAAGGGCAGCCCTCCACTTCTGGTATAATTGTGTAGCCCCTTTTCTTTGG NM_001256574 RefSeq
chr5 - 74627405 74641424 ENC1 8507 "ectodermal-neural cortex 1 (with BTB domain), transcript
variant 2"
GO:0017148|GO:0005515|GO:0000790|GO:0016567|GO:0005730|GO:0003779|GO:0005634|GO:0007275|GO:0016
363|GO:0007399|GO:0005737|GO:0010976|GO:0043025|GO:0031463|GO:0005654|GO:0005856|GO:0010499 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129602_PI430048170 0.7548526242402810.9706438815169071 1.1314283959604
11.2476833854666 11.1672151088083 P P P 11.0506718529076 11.3965889057411
11.2096710531861 P P P LNCV6_129602_PI430048170 mRNA
AGCAGCACCCTCTTGTGGCTTGTTCTAGCGTGTATTAAAACTTGACACACACCCACACAC NM_001184975 RefSeq
chr11 - 47177521 47185881 PACSIN3 29763 "protein kinase C and casein kinase substrate in
neurons 3, transcript variant 1"
GO:0005515|GO:0008092|GO:0051044|GO:0005886|GO:0097320|GO:0031988|GO:0006897|GO:0008289|GO:0005
737|GO:0005543|GO:0016020|GO:0019855|GO:0030100|GO:0045806|GO:0007010|GO:0051926|GO:0005654|GO:0
070062|GO:0005768. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131627_PI430048170 0.519812576038054 0.971862779694536 0.464038257172712
0.484046332135545 0.325340818788726A A A 0.408115097639379 0.514380680425253

0.47756594824494 A A A LNCV6_131627_PI430048170 mRNA
TATGATTGCTGAGTCTTGTACATGCAGATGACAGCAACAGTACGGCTAGATCAGGTTTCC NM_005448RefSeq chrX
+ 50910734 50916641 BMP15 9210 bone morphogenetic protein 15
GO:0010862|GO:0042981|GO:0007292|GO:0030509|GO:0060395|GO:0005125|GO:0005160|GO:0005615|GO:0060
016|GO:0001541|GO:0005737|GO:0043408|GO:0048468|GO:0045893|GO:0008083 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_135824_PI430048170 0.1973218047856040.8379257366453051 3.7751078287006
13.9296797496943 14.2000393102928 P P P 14.2005935424798 14.0481171558856
14.4282989903537 P P P LNCV6_135824_PI430048170 mRNA
GGATTTCTTTAGTGTCATTGCCGATTTTGGCTATAACAGTGTCTTTCTAGCCATAATAAA NM_003756RefSeq chr8
- 116644815 116755823 EIF3H 8667 "eukaryotic translation initiation factor 3, subunit H"
GO:0005515|GO:0010467|GO:0005852|GO:0016282|GO:0033290|GO:0001731|GO:0003743|GO:0006412|GO:0006
413|GO:0005829|GO:0016020|GO:0071541|GO:0006446|GO:0044267|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131993_PI430048170 0.16081679832007 0.52870073179483 0.511156290357131
0.4092544224401571.52489280319536 A A A 1.83028696898744 2.34791241446664
1.00244713865546 A A A LNCV6_131993_PI430048170 mRNA
TTCAACCCTGACACCCCATTTGGAGACATTGTTGGATTGGACCTCGGAGAGGAAGCAGAA NM_001080441 RefSeq
chr11 + 118527494 118531025 TTC36 NA tetratricopeptide repeat domain 36 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_132133_PI430048170 0.8566812527771450.9002937485810930.592053843599117
0.5456959441166871.41755829883904 A A A 0.4049625067837321.72303366428821
0.711532203322223A A A LNCV6_132133_PI430048170 mRNA
CAAAAGCTTTTGATGACTGGTAACTGGTATCCTTCCAAATAAATGCATTGCTTGGTAAAA NM_003348RefSeq chr12
- 93408311 93442250 UBE2N 7334 ubiquitin-conjugating enzyme E2N
GO:0005515|GO:0050852|GO:0043130|GO:0006511|GO:0004842|GO:0034142|GO:0016567|GO:0016874|GO:0019
221|GO:0033182|GO:0070423|GO:0000151|GO:0005634|GO:0045739|GO:0035370|GO:0035872|GO:0006301|GO:0
005829|GO:0070534|GO:0005737|GO:0051092|GO:0019787|GO:0000724|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_75515_PI430048170 0.4574937089365940.8459928839651962.60930992075411 2.00287326968799
2.56047550428325 A A A 2.8292013174704 2.85028656928539 2.20326945166401 P P A
LNCV6_75515_PI430048170 mRNA
ATACCACAGAGATGCTAAAATCCATATGTCTGCTGGGGTCTCTTCAGTTTCATCGAAAAG NM_001029875 RefSeq
chr5 + 64505946 64612294 RGS7BP 401190 "regulator of G-protein signaling 7 binding protein,
transcript variant 1" GO:0005737|GO:0007186|GO:0005886|GO:0005634|GO:0009968 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_131393_PI430048170 0.4835581353979390.5886006214481320.611736754573091
0.6723794767412750.620010781511156A A A 0.60942954700608 0.488363156370725
2.31798082420425 A A A LNCV6_131393_PI430048170 mRNA
CTTCCTGATGTCGTGAAAACAGAGGCATGGACTGATTTGGAAAATATTTTATTAGTATGT NM_033187RefSeq chr17
- 41167230 41168172 KRTAP4-3 85290 keratin associated protein 4-3
GO:0042633|GO:0007568|GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134376_PI430048170 0.8431923908638590.9852751663599850.346826967718102
0.5041761179890240.374621093429467A A A 0.5365426701024660.463890605120355
0.282621131332829A A A LNCV6_134376_PI430048170 mRNA
TTTCCAACAGCCACTTGTTTTGTGCACTTCCGTCCTCTAAAACTAAATGGAATTTAATTA NM_021973RefSeq chr4
- 173526500 173530227 HAND2 9464 heart and neural crest derivatives expressed 2
GO:0005515|GO:0000790|GO:0044212|GO:0010463|GO:0048538|GO:0042803|GO:0007512|GO:0007507|GO:0001
947|GO:0014032|GO:0010667|GO:0003278|GO:0000977|GO:0046982|GO:0003713|GO:0070888|GO:0001701|GO:0

048485|GO:0043392|GO:0043234|GO:0048935|GO:0060536|GO:2000763|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139265_PI430048170 0.6250464999854651.02511280015999 0.56273217548894 0.4001657318331120.549775449042556A A A 0.3886634679893460.514294657714816 0.504601580046005A A A LNCV6_139265_PI430048170 mRNA TTTCTACGTACAATATCTTTGGGAACTTGGAGGTGCAGGGTCAGACGTCTGTGTGTGTAT NM_153711RefSeq chr6 + 116511644 116518546 FAM26E 254228 "family with sequence similarity 26, member E" GO:0034220|GO:0005261|GO:0005887|GO:0006812|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_8200_PI430048170 0.2482980491472781.40990676867623 0.5848037955377131.30587832559511 0.410893905143269A A A 0.3491705081663950.3217733334987920.306397499416199A A A LNCV6_8200_PI430048170 mRNA AGATTTGCACATTAAAGAAAGAGAAGCAGCAAGATATGCGTCGGGTAGAGAAGCTGGAGA NM_001282493 RefSeq chr15 - 32389584 32403292 GOLGA8K 653125 "golgin A8 family, member K" GO:0005794 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74362_PI430048170 0.11109398042771 0.8358842248188964.5063452986433 4.40326522239299 4.48784603499328 P P P 4.77998710149909 4.52743186085883 4.84855500802662 P P P LNCV6_74362_PI430048170 mRNA AACCTTACTGTTTAAGAGGCCAACTTCTGGAAGGAGGTAGGAGTCATAACTTTTTAGAGG NM_001287757 RefSeq chr4 + 51842999 51916837 DCUN1D4 23142 "DCN1, defective in cullin neddylation 1, domain containing 4, transcript variant 4" GO:0005515|GO:0008150|GO:0003674|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132492_PI430048170 0.3493115733260321.14442415619279 11.2131140441956 11.4590018029516 11.5782825004443 P P P 11.4599163633301 10.9269736897299 11.2540669446287 P P P LNCV6_132492_PI430048170 mRNA TTTAGTTTTGTCTCTCCAAGTCGTGAATTAGAGCAGCAGCAAGTTTCTAGCAGGGCCTTC NM_182852RefSeq chr14 - 20311367 20333312 CCNB1IP1 57820 "cyclin B1 interacting protein 1, E3 ubiquitin protein ligase, transcript variant 4" GO:0005515|GO:0016567|GO:0000795|GO:0051026|GO:0016874|GO:0007286|GO:0001825|GO:0008270|GO:0007131 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139750_PI430048170 0.1032865927796670.4672889148949422.73578296526044 1.27375915302975 1.70559372146433 A A A 3.21936264832266 3.12775867099654 3.06259193911048 P P P LNCV6_139750_PI430048170 mRNA TAACTTCCCCCGACTCATGTGTTTGTTGGTAAAACACTTGTCACTGGTGATCATAAAAAA NM_152479RefSeq chr19 - 40216057 40218399 TTC9B 148014 tetratricopeptide repeat domain 9B GO:0000413|GO:0008150|GO:0003674|GO:0061077|GO:0005789|GO:0003755|GO:0005528|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144181_PI430048170 0.000232676959865343 0.4221915353272016.08190406406943 6.13733936686445 6.22900299102987 P P P 7.42206126107856 7.26692362143824 7.48645615126779 P P P LNCV6_144181_PI430048170 mRNA GCACATTAAAATGCCCTAGCAGTATCTAATTAAAAACCATGGTCAGGTTCAATTGTACTT NM_020307RefSeq chr3 - 157147555 157160760 CCNL1 57018 cyclin L1 GO:0006396|GO:0006355|GO:0019901|GO:0016607|GO:0005634|GO:0000079|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139735_PI430048170 0.3799177647029810.2801897621738140.244491430482345 0.2795808927216340.302093057336629A A A 0.4398314379318660.345467514797713 3.36928067322412 A A P LNCV6_139735_PI430048170 mRNA AGTGTCAAGACCCAACAGATTCATACCAGAATGCTTAGACTCTTTTCTCTGAAAAGATAT NM_001004760 RefSeq chr11 - 5199734 5200700 OR51V1NA "olfactory receptor, family 51, subfamily V, member 1" NA .

NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136371_PI430048170 0.0873178811402388 0.8273271801162527.59614601485648
7.53349988630177 7.81831491597126 P P P 7.75715651446397 7.9710229019223
8.04103238762736 P P P LNCV6_136371_PI430048170 mRNA
TCAGGCCTCAACGTTCTGTCAGGTATTAATATGGTTAGAATTGTTCTTACAACTGGTAAT NM_032338RefSeq chr12
- 66123068 66130753 LLPH 84298 "LLP homolog, long-term synaptic facilitation (Aplysia)" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126947_PI430048170 0.2573365192638210.8759950832591915.20715251284003
5.10071755804277 5.4196512465655 P P P 5.29061405477799 5.36095720021309
5.64287790328497 P P P LNCV6_126947_PI430048170 mRNA
GATGGGCTGCTATGTTAACTGTAAATTGAGAACTGCTTGTTTTATGGCTTTTGCTGTTAA NM_004663RefSeq chr15
+ 65869458 65891991 RAB11A8766 "RAB11A, member RAS oncogene family, transcript variant 1"
GO:0008017|GO:0005515|GO:0005802|GO:0006887|GO:0006886|GO:0031175|GO:0032402|GO:0000910|GO:0048
169|GO:0030670|GO:0006833|GO:0070062|GO:0019905|GO:0006996|GO:0090150|GO:0030953|GO:0006184|GO:0
031489|GO:0043234|GO:0010971|GO:0000922|GO:0051650|GO:0010796|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93185_PI430048170 0.3449874041205691.47647642568497 0.3416161764687271.51372898535985
0.446677064856074A A A 0.3045252155863430.2855861223974960.334999227401928A A A
LNCV6_93185_PI430048170 mRNA
ATTTTTGGAGAGCTCGCGATCTTGGAAAAGCCTCAGACGCCATCTACAGTTAAAACGTAG NM_021643RefSeq chr2
+ 12716871 12742732 TRIB2 28951 "tribbles pseudokinase 2, transcript variant 1"
GO:0045599|GO:0032436|GO:0005737|GO:0004672|GO:0000166|GO:0043405|GO:0004860|GO:0055106|GO:0006
468|GO:0006469|GO:0005856|GO:0045081|GO:0031625|GO:0008134 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129513_PI430048170 0.1683489479427482.3751461751726 2.03559523148329
3.52388447734282 3.23911779583978 A P P 0.2924948108527262.16332928080489
2.27507823658345 A A A LNCV6_129513_PI430048170 mRNA
CATTCTGCGCAGTATCTCAACTGCCGTTCAACAATCGCAAGAGGAAGGTGGAGCAGGTTT NM_014324RefSeq chr5
- 33986985 34008115 AMACR 23600 "alpha-methylacyl-CoA racemase, transcript variant 1"
GO:0005739|GO:0005737|GO:0005782|GO:0006699|GO:0005102|GO:0008206|GO:0044281|GO:0033540|GO:0008
111|GO:0044255|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131186_PI430048170 0.0325349759774693 0.6349606413442798.81176225033449
8.36634713330858 8.58383432805599 P P P 8.94128940505195 9.3226725062651
9.45083379774317 P P P LNCV6_131186_PI430048170 mRNA
TTATTTCAGCTCAGGGCGGGTAATTAACATCATTGGAACTAGCTATTAGGAAAGAAAAAA NM_015425RefSeq chr2
- 86026327 86106155 POLR1A25885 "polymerase (RNA) I polypeptide A, 194kDa"
GO:0005515|GO:0010467|GO:0006363|GO:0005730|GO:0006362|GO:0006361|GO:0005634|GO:0006360|GO:0003
677|GO:0005737|GO:0005736|GO:0045814|GO:0001054|GO:0040029|GO:0005654|GO:0008270 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130293_PI430048170 0.5106233748128911.06307088735583 4.48906332766493
4.67680231978457 4.82827952981186 P P P 4.46762619867781 4.62194411373519 4.6530207381079
P P P LNCV6_130293_PI430048170 mRNA
GTTTGCATTTGGCTGCATAGCTACAATGATGGCATTTTAACTTATTCATGATTAGAGATG NM_001701RefSeq
chr9_KI270823v1_alt - 421208 432256 BAAT 570 "bile acid CoA:amino acid N-acyltransferase, transcript
variant 1"
GO:0052815|GO:0052689|GO:0006637|GO:0052817|GO:0052816|GO:0016410|GO:0005782|GO:0019530|GO:0006
699|GO:0002152|GO:0016290|GO:0031100|GO:0005102|GO:0044281|GO:0005829|GO:0001889|GO:0015721|GO:0
006544|GO:0006631|GO:0008206|GO:0047963|GO:0005777 . NA - . NA NA NA NA NA NA NA NA
NA

LNCV6_136041_PI430048170 0.1123144503436490.5146188880041960.308478619225813
0.3476951712532010.36712919824137 A A A 1.27261099988388 1.76916167322671
0.642418780511537A A A LNCV6_136041_PI430048170 mRNA
ATCTGACAAGTCAGTTGTCCTGATCTTCTCTTGCAGTGTCCCTGAATGGCAAGTGATGTA NM_005555RefSeq chr12
- 52446650 52452126 KRT6B 3854 "keratin 6B, type II"
GO:0005200|GO:0045095|GO:0007398|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133225_PI430048170 0.1970790173488311.11826224326828 0.577734959108805
0.2961680659973420.483035124495025A A A 0.3142287943255630.277612632725002
0.295161537479009A A A LNCV6_133225_PI430048170 mRNA
TCAGCTATATCTCTCATATTCTACCCTTTGGTTAAACCCAAGAGGAGTTTAGAATACTCT NM_001257967 RefSeq
chr7 + 31514070 31653689 CCDC129 NA "coiled-coil domain containing 129, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128893_PI430048170 0.8927038066396010.9896280040616519.5743960774626
9.50726687664546 9.59236431185444 P P P 9.47656287721694 9.5169630885437
9.71551118484535 P P P LNCV6_128893_PI430048170 mRNA
TAAGTCTGTTGGCATGAAGGACCATTTTCTACATAATATGACATGGATACTTGACCCAAA NM_018197RefSeq chr20
- 52151277 52191985 ZFP64 55734 "ZFP64 zinc finger protein, transcript variant 1"
GO:0048026|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135335_PI430048170 0.00323392888343317 0.45648278668961 7.39847464875579
7.35806154957999 7.67118956415869 P P P 8.41346256667022 8.53382534238662
8.85774949240405 P P P LNCV6_135335_PI430048170 mRNA
CTGACTGCTGTGGGGGATTGAAAAGAATATGCTTATGTTTGATGAAAGATATTTAACAAG NM_014290RefSeq chr9
+ 97412019 97496123 TDRD7 23424 "tudor domain containing 7, transcript variant 1"
GO:0005515|GO:0070306|GO:0007283|GO:0003729|GO:0007281|GO:0033391|GO:0005737|GO:0010608|GO:0047
485|GO:0002089|GO:0005759|GO:0035770|GO:0043186 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81487_PI430048170 0.1930284688373341.42613275902684 6.69637199324247 6.80637598333656
6.30210107029207 P P P 6.54838370435608 6.06255388421321 5.52661587590812 P P P
LNCV6_81487_PI430048170 mRNA
TACGCCGCTACCTGGACAGCGCGATGCAGGAGAAAGAGTTCAAATACACGTGTCCGCACA NM_004669RefSeq
chr9 - 136994607 136996572 CLIC3 9022 chloride intracellular channel 3
GO:0005515|GO:0007165|GO:0006821|GO:0005737|GO:0005244|GO:0034707|GO:0034765|GO:0005634|GO:0005
254|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141562_PI430048170 0.5384846604761751.01214571778359 0.340904183785445
0.3197664732781120.263748353175404A A A 0.2927967256986310.299033562956811
0.281379897358298A A A LNCV6_141562_PI430048170 mRNA
GAGAAGGTTCTCATAACAACTAATGTTTGTGCCCGAGGGATTGATGTGAAGCAGGTCACA NM_013264RefSeq chr11
+ 125904365 125923111 DDX25 29118 DEAD (Asp-Glu-Ala-Asp) box helicase 25
GO:0004004|GO:0033391|GO:0005737|GO:0006406|GO:0006200|GO:0003723|GO:0007286|GO:0007275|GO:0005
634|GO:0005524|GO:0006417 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137112_PI430048170 0.0269352137423254 0.7576146149567540.406203213654999
0.3916381428218360.366884866332489A A A 0.7207010684643650.924960430644011
0.710424639420214A A A LNCV6_137112_PI430048170 mRNA
ATATCGGACCTGGATTCAAGGTTTGGCATTGCTGTTTTCAAAGTATGTAATCTTTTAGAT NM_012334RefSeq chr5
- 16661906 16936276 MYO10 4651 myosin X
GO:0005515|GO:0005516|GO:0043005|GO:0005886|GO:0008360|GO:0031527|GO:0016459|GO:0030898|GO:0032
433|GO:0005829|GO:0051489|GO:0005737|GO:0051015|GO:0007411|GO:0060002|GO:0043025|GO:0005938|GO:0
022409|GO:0005730|GO:0005547|GO:0030507|GO:0005524|GO:0001726|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_128593_PI430048170 0.1629161243119010.8420974607407793.44800259824602
3.44463363147572 3.16644956079635 P P P 3.8133163761843 3.46464520199346
3.51764837278859 P P P LNCV6_128593_PI430048170 mRNA
AGAGCTCAAGACATGGGACATTTAAATCCTCAAGGAGTTTGGAACAAAATAAACAGATCT NM_006517RefSeq chrX
+ 74421492 74533929 SLC16A2 6567 "solute carrier family 16, member 2 (thyroid hormone
transporter)"
GO:0015718|GO:0005215|GO:0034220|GO:0016020|GO:0005887|GO:0008028|GO:0015349|GO:0006810|GO:0070
327|GO:0016021|GO:0015293 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64147_PI430048170 0.1417497748170861.09512608910887 8.24925277610707 8.18890825541802
8.12133302837187 P P P 7.98237064835913 8.1703035757265 8.009113669512 P P P
LNCV6_64147_PI430048170 mRNA
ATTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATTCCTGAAGAGGCATGA NM_005860RefSeq chr19
+ 676388 683392 FSTL3 10272 follistatin-like 3 (secreted glycoprotein)
GO:0005515|GO:0030325|GO:0030324|GO:0005634|GO:0007283|GO:0005615|GO:0030514|GO:0002244|GO:0048
185|GO:0045944|GO:0090101|GO:0001968|GO:0030141|GO:0044306|GO:0005794|GO:0022409|GO:0006357|GO:0
001822|GO:0005576|GO:0032926|GO:0045671|GO:0006351|GO:0071248|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_90059_PI430048170 0.0828178364264698 1.57753205990395 13.1732037068505 13.139723951753
13.2114476741016 P P P 12.9019142427781 12.193778569657 12.358262364343 P P P
LNCV6_90059_PI430048170 mRNA
GGCTGCTGATCTTGTTTGTTGAGGGAGATGGGACTATAATAAAATTGAATGCTGAAGTTG NM_182491RefSeq chr7
- 1152906 1160219 ZFAND2A 90637 "zinc finger, AN1-type domain 2A"
GO:0005737|GO:0000502|GO:0032436|GO:0008270|GO:0005634|GO:0071243 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130215_PI430048170 0.0818802191534255 1.21935265166281 6.98477783926443
6.92635362235292 7.01540204251768 P P P 6.87198747560458 6.60596887722103
6.57261994612123 P P P LNCV6_130215_PI430048170 mRNA
GGTTGACTTGACTCATGCTTGTTTCACTTTCACATGGAATTTCCCAGTTATGAAATTAAT NM_001282458 RefSeq
chr6_GL000254v2_alt + 3269563 3287710 C2 717 "complement component 2, transcript variant 5"
GO:0030449|GO:0006956|GO:0004252|GO:2000427|GO:0007584|GO:0045087|GO:0006958|GO:0006508|GO:0005
576|GO:0005615|GO:0046872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132377_PI430048170 0.0461094436135953 1.09613298020746 11.8777239312374
11.9282239214282 11.9207956581066 P P P 11.7825317685709 11.8330821366077 11.711808913321
P P P LNCV6_132377_PI430048170 mRNA
GAACCCTGTATGGTTTTTAGTTTAAATTAAAGGAGTCGTTATCGTGGTGGGAATATGAAA NM_001320RefSeq chr6
+ 31665879 31670070 CSNK2B 1460 "casein kinase 2, beta polypeptide, transcript variant 1"
GO:0005515|GO:0045859|GO:0008285|GO:0005886|GO:0033211|GO:0005634|GO:0046872|GO:0043623|GO:0005
829|GO:0042802|GO:0019887|GO:0005737|GO:0007411|GO:0016055|GO:0005956|GO:0070062|GO:0031519|GO:0
019904|GO:0005102|GO:0010862|GO:0032927|GO:0007165|GO:0061154|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_103377_PI430048170 0.1681535863044750.9012214978060260.253241088821551
0.2880231249064640.325992111948656A A A 0.4073433235073360.571253201319638
0.329034467044797A A A LNCV6_103377_PI430048170 mRNA
ATATGTGCTGAGATGGCTCTGACACGCCCTGAGGCCTTCAATGAATATGTTATCTTCGTT NM_016239RefSeq chr17
+ 18108705 18179802 MYO15A 51168 myosin XVA
GO:0005516|GO:0005737|GO:0003774|GO:0042472|GO:0007605|GO:0008152|GO:0032420|GO:0007626|GO:0003
779|GO:0016459|GO:0005524|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132708_PI430048170 0.00376631465332961 0.6078224225312273.65469391654923
3.73955669062632 3.87020786421128 P P P 4.55290574924755 4.29539892043771

4.56355180712141 P P P LNCV6_132708_PI430048170 mRNA
CTGTGTAGATGAAGGCTTGATCTAAAATAGTATAAGGTCTCCAGCTTCAGTAAAAGTTTT NM_007187 RefSeq chr13
+ 41061560 41084003 WBP4 11193 WW domain binding protein 4
GO:0005515|GO:0016607|GO:0005886|GO:0045292|GO:0008270|GO:0005681|GO:0005654|GO:0003676|GO:0070
064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129740_PI430048170 0.99984423387799 0.9954521765812177.35806154957999
7.30057327616648 7.2189088442612 P P P 7.39571206044879 7.40259968489055 7.0793053913682
P P P LNCV6_129740_PI430048170 mRNA
GTGATTTTTGCCATCAAAATAAAAATTTGAGACTCGTTAACCGAAGTCCACGCCAAAAAA NM_001033549 RefSeq
chr19 + 17267375 17279353 BABAM1 29086 "BRISC and BRCA1 A complex member 1, transcript
variant 1"
GO:0005515|GO:0070531|GO:0005737|GO:0070552|GO:0070536|GO:0010212|GO:0031572|GO:0005654|GO:0005
634|GO:0045739|GO:0016568|GO:0006302 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133515_PI430048170 0.0710985693827390.8325285142221745.36225578309152
5.27732757647715 5.12232428770847 P P P 5.67245339410234 5.47879857418588
5.40036207902391 P P P LNCV6_133515_PI430048170 mRNA
CTTGCTCTGGACGGTTCCCCCAGCCCATGCAATAAATCACCAGTGAGCATTTATTTCTAA NM_152614 RefSeq chr2
+ 231592863 231594283 C2orf57 165100 chromosome 2 open reading frame 57 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_131175_PI430048170 0.0153162592424326 1.07236026644112 0.396284458762738
0.4606368583732330.421247001651405 A A A 0.3033161085156930.328341754794289
0.344573124947983 A A A LNCV6_131175_PI430048170 mRNA
GACTTCAGCATCTGCTGCAAACTGAAGATCATTGAAATTGACGGACAAAAGAAGTGGTGA NM_001040448 RefSeq
chr4 + 9444533 9450514 DEFB131 NA "defensin, beta 131" NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141339_PI430048170 0.0622706366081004 1.13296285125003 12.2507779040263
12.2521186518855 12.2341873366608 P P P 11.9925290543879 12.156272462363
12.0431463067234 P P P LNCV6_141339_PI430048170 mRNA
GCCCTTTAACACAGTCTGGATTTAATAAATTCATATGGGTGTTTAACTTAAACTCAGCAC NM_001294 RefSeq chr19
+ 44955223 44993346 CLPTM1 1209 "cleft lip and palate associated transmembrane protein 1,
transcript variant 2" GO:0005515|GO:0016020|GO:0005887|GO:0033081|GO:0007275|GO:0030154|GO:0009897
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128802_PI430048170 0.8003137348915410.9849406993453931 0.1062421314051
9.97200299256895 10.2136756948433 P P P 10.110469215576 10.0386733536658
10.2132249050889 P P P LNCV6_128802_PI430048170 mRNA
CACCAGTGTTTAGTTTTATATTGAGGTGCTCAGGTTGGAATAAAGTGGTATAAAAAGCAA NM_004162 RefSeq chr3
+ 19947079 19985175 RAB5A 5868 "RAB5A, member RAS oncogene family, transcript variant 1"
GO:0005515|GO:0030424|GO:0048471|GO:0005886|GO:0003924|GO:0030139|GO:0045022|GO:0015629|GO:0006
886|GO:0030425|GO:0005829|GO:0014911|GO:0051489|GO:0045921|GO:0005737|GO:0051036|GO:0030100|GO:0
043195|GO:0048169|GO:0043025|GO:0043679|GO:0032482|GO:2000286|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134896_PI430048170 0.0247859326810622 2.61583721465608 5.96898190557635
6.62073079491021 6.18279950923632 P P P 5.44995258794427 4.50927525846208
4.51430461119201 P P P LNCV6_134896_PI430048170 mRNA
GGCTCTTTTGTAAGGTTTTTGTAGTGATTTTTATGCCACCTGAATAAAGAATGAATGGGC NM_001165920 RefSeq
chr17_KI270861v1_alt + 171977 184214 SERPINF2 5345 "serpin peptidase inhibitor, clade F (alpha-2
antiplasmin, pigment epithelium derived factor), member 2, transcript variant 2"
GO:0005515|GO:0004866|GO:0004867|GO:0045597|GO:0046330|GO:0048514|GO:2000049|GO:0072562|GO:0002
020|GO:0005615|GO:0042803|GO:0071636|GO:0030199|GO:0045944|GO:0031093|GO:0070374|GO:0070062|GO:0

010033|GO:0009986|GO:0051918|GO:0005577|GO:0002034|GO:0030168|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104711_PI430048170 0.0133516836639818 0.6800933994671245.74979967590167 5.42255685295706 5.67855145575596 P P P 6.09902512966754 6.13126964791048 6.30105412756936 P P P LNCV6_104711_PI430048170 mRNA GTTTGACTTTTGCCAGGGTAATCTTCAGTTGGCCCTGATTCAATTAAATGGCCTTAATTT NM_032148RefSeq chr12 - 104803496 104928694 SLC41A2 84102 "solute carrier family 41 (magnesium transporter), member 2" GO:0005886|GO:0008324|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118383_PI430048170 0.0438231031211611 0.9384640793772810.336543849368879 0.3292454187292550.316827771089204A A A 0.4587025674371650.413445147868974 0.384445342129133A A A LNCV6_118383_PI430048170 mRNA CTCTTCAGAAATATCTGATTCCTTTGTGAAAGAGTTTCTAGCCAAAGCCAAAGAAGACTT NM_001242860 RefSeq chr1 + 84164639 84238498 PRKACB5567 "protein kinase, cAMP-dependent, catalytic, beta, transcript variant 7" GO:0005515|GO:0048471|GO:0005886|GO:0070613|GO:0006094|GO:0007268|GO:0044281|GO:0007202|GO:0005829|GO:0035556|GO:0007173|GO:0071377|GO:0051447|GO:0006006|GO:0019433|GO:0006833|GO:0034199|GO:0031625|GO:0070062|GO:0048011|GO:0005952|GO:0005813|GO:0000287|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145475_PI430048170 0.4045187702343710.865991981268361 3.90113431558086 3.37934349935355 3.87034055115635 P P P 3.63820230277833 4.00138702532685 4.14484950194846 P P P LNCV6_145475_PI430048170 mRNA GCCAATTGCTCTTCATCACAGCTATCTGTCTTTTAGTGCCACAAATAAAAGAAAATCAAA NM_001287436 RefSeq chr7 - 51016211 51316818 COBL 23242 "cordon-bleu WH2 repeat protein, transcript variant 1" GO:0030424|GO:0048471|GO:0033504|GO:0005886|GO:0001757|GO:0005884|GO:0001843|GO:0048565|GO:0044294|GO:0044295|GO:0001726|GO:0030425|GO:0001889|GO:0003785|GO:1900029|GO:0000578|GO:0016020|GO:0051639|GO:0048669|GO:0043025|GO:0030041|GO:0030903|GO:0005938|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68322_PI430048170 0.5384634771130490.8931272613732237.55034380041104 7.36259174469443 8.04527222019189 P P P 7.58695222249179 7.76623029006563 8.12900217932782 P P P LNCV6_68322_PI430048170 mRNA TGAGGCTCATTTTGCAGTTGTTGAAATTGTCCCCGCAGTTTTCAATCATGTCTGAACCAA NM_005917RefSeq chr2 + 63588608 63607196 MDH1 4190 "malate dehydrogenase 1, NAD (soluble), transcript variant 2" GO:0005813|GO:0044262|GO:0006099|GO:0004470|GO:0005975|GO:0006094|GO:0006107|GO:0006108|GO:0044281|GO:0005615|GO:0005829|GO:0006734|GO:0005739|GO:0005737|GO:0051287|GO:0047860|GO:0009405|GO:0030060|GO:0006006|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131701_PI430048170 0.00186480273945688 0.2813135716283546.91125343452654 7.18754046086999 7.55547069803931 P P P 8.76838532848883 9.2004056102243 9.20549339990463 P P P LNCV6_131701_PI430048170 mRNA GCTTTCGAGTCTGAGTTTAAAACTACACATTTTGACATAGTGTTTATTAGCAGCCATCTA NM_001786RefSeq chr10 + 60778453 60794852 CDK1 983 "cyclin-dependent kinase 1, transcript variant 1" GO:0005515|GO:0007077|GO:0014070|GO:0033160|GO:0030261|GO:0034501|GO:0014075|GO:0002756|GO:0018105|GO:0007173|GO:0000165|GO:0007411|GO:0018107|GO:0002755|GO:0005813|GO:0038124|GO:0006996|GO:0038123|GO:0034134|GO:0030332|GO:0007569|GO:0030496|GO:0009636|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144835_PI430048170 0.000976614461985451 1.58441663016444 5.98766413981152 5.85751096480401 5.83864482975039 P P P 5.20819292650267 5.33723689409882 5.14440896981562 P P P LNCV6_144835_PI430048170 mRNA TAATTTTTATAGTGAATCTCAAGGGATCATCCCATCCTTGACCACAGGGACAAGAGGGGC NM_012324RefSeq chr22 + 50600684 50611551 MAPK8IP2 23542 mitogen-activated protein kinase 8 interacting protein 2

GO:0005515|GO:0010469|GO:2000311|GO:2000310|GO:0032874|GO:0032403|GO:0046328|GO:0005737|GO:0007172|GO:0001540|GO:0000165|GO:0045860|GO:0043025|GO:0001662|GO:0051966|GO:0019901|GO:0007617|GO:0007254|GO:0060079|GO:0030295|GO:0043234|GO:0048813|GO:0005198|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127179_PI430048170 0.391225808546941 0.913450005472061 0.253611232622118 0.265536172936719 0.393054428761586 A A A 0.650728567868113 0.314879526077541 0.315977514630012 A A A LNCV6_127179_PI430048170 mRNA
CACAGGCTCCCAGGGGTCTTAAGAGCTAATTACTGAATAAAACAATCTAGAACAAAGCAA NM_020663 RefSeq chr14 + 63204383 63293512 RHOJ 57381 ras homolog family member J
GO:0051056|GO:0030036|GO:0005886|GO:0007264|GO:0008360|GO:0008152|GO:0003924|GO:0061299|GO:0007266|GO:0005525|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111174_PI430048170 0.223404876718905 0.644480818453698 0.257001644091805 0.380981325649037 0.280370429031272 A A A 1.47736613464387 0.379532985655752 0.743239773451178 A A A LNCV6_111174_PI430048170 mRNA
CGAAATACAACAATGAGAACACATCCAAGCAGTATTCTCTCTTCAAAGTCACCAGGGCTT NM_014375 RefSeq chr3 + 186640359 186653008 FETUB 26998 fetuin B
GO:0010951|GO:0007338|GO:0008150|GO:0003674|GO:0004869|GO:0008191|GO:0007339|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128454_PI430048170 0.890750628198731 0.933498002591783 0.891743465133173 1.20196585191377 0.630184266137743 A A A 0.324430768513022 1.3009706381814 1.25937644773861 A A A LNCV6_128454_PI430048170 mRNA
ATCCCACCACCTTGGAGCTGTCATAGAGATTGAAACCTTCTAGTAAAATAAATAAAATCT NM_001005214 RefSeq chr1 + 165544240 165563948 LRRC52 NA leucine rich repeat containing 52 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128035_PI430048170 0.412062114300015 0.944472483931455 0.583507049308126 0.499586720705834 0.298345687994364 A A A 0.548322355435357 0.575815169120598 0.518680660043045 A A A LNCV6_128035_PI430048170 mRNA
TACGCTGGTATTGTCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAGTACCAC NM_012128 RefSeq chr1 + 86547075 86580749 CLCA4 22802 "chloride channel accessory 4, transcript variant 1"
GO:0006821|GO:0016324|GO:0034220|GO:0005886|GO:0005887|GO:0006810|GO:0006508|GO:0055085|GO:0005254|GO:0046872|GO:0008237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144405_PI430048170 0.83375648379066 1.01976578932438 3.93067947092916 4.11854370601766 3.74285867296214 P P P 4.07917697605076 4.18492835643243 3.32552332794371 P P P LNCV6_144405_PI430048170 mRNA
GAAAGGTGAATTGGCTCTAGAGGCCCTGTATGCTAGTATCATTTTCTTTTTTAATTTTTGNM_001172743 RefSeq chrX - 17800048 17861337 RAI2 10742 "retinoic acid induced 2, transcript variant 1"
GO:0005515|GO:0003674|GO:0009790|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130260_PI430048170 0.390161264341012 1.03963686916877 13.2305330259162 13.399667967402 13.3470469119297 P P P 13.279893584023 13.2597147762623 13.2744803186862 P P P LNCV6_130260_PI430048170 mRNA
ATTTTGTAACTGCCTACCAGTCGCCCTCTGTGCCTAATAAAGTCTCTTTTTCTCACAGAG NM_004493 RefSeq chrX - 53431257 53434376 HSD17B10 3028 "hydroxysteroid (17-beta) dehydrogenase 10, transcript variant 1"
GO:0005515|GO:0006629|GO:0005886|GO:0005783|GO:0005743|GO:0030283|GO:0008709|GO:0003857|GO:0009083|GO:0044281|GO:0008033|GO:0005739|GO:0034641|GO:0005737|GO:0005759|GO:0047015|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127687_PI430048170 0.0889800488878058 1.05043311081316 0.424007285402846 0.461462726933547 0.468162567348748 A A A 0.33839925476138 0.374909640894753 0.426404857073301 A A A LNCV6_127687_PI430048170 mRNA

TCGCCTTGTAAGTGCCTAGGCTGAATCTTCTAAATAAATACGATCCACACCTCCAAAAAA NM_021046 RefSeq chr11 + 71538024 71539207 KRTAP5-8 57830 keratin associated protein 5-8 GO:0008150|GO:0045095|GO:0030280 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_140831_PI430048170 0.1153459191983881 1.61281180538702 7.52018623281116 7.15595224577571 7.3190048801394 P P P 6.24082856354695 7.17461048493316 6.34258591535581 P P P LNCV6_140831_PI430048170 mRNA
AAGTTCCTGGCTTCTGTGAGCACCGTGCTGACCTCCAAATACCGTTAAGCTGGAGCCTCG NM_000558 RefSeq chr16 + 176650 177522 HBA1 3039 "hemoglobin, alpha 1" GO:0005515|GO:0042542|GO:0072562|GO:0044281|GO:0051291|GO:0005829|GO:0031838|GO:0004601|GO:0071682|GO:0042744|GO:0010942|GO:0031720|GO:0070062|GO:0005833|GO:0005506|GO:0005576|GO:0006898|GO:0015671|GO:0019825|GO:0016020|GO:0022627|GO:0005344|GO:0015701|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_70894_PI430048170 0.0949104103583482 1.90290514658645 3.69487629361814 4.09466101665516 3.76839784548917 P P P 3.20807041919384 2.14236610972898 3.21551260206956 P A P LNCV6_70894_PI430048170 mRNA
CGGGGTGCTTCAAGACATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCCTGGATGGA NM_001282447 RefSeq chr20 - 3667972 3682131 ADAM33 80332 "ADAM metallopeptidase domain 33, transcript variant 3" GO:0006508|GO:0008270|GO:0016021|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_130981_PI430048170 0.0801657763969698 0.453279526308021 1.07718921024735 1.20835223418874 2.21665636791566 A A A 2.87301608436034 1.98949521579244 3.12269966213091 P A P LNCV6_130981_PI430048170 mRNA
TGGGGGGAGAGAAGATTCAGTCAGAAAACTTATTCAAAGTACCTAAGTATTATAAAGGAG NM_004264 RefSeq chr12 + 27022521 27030673 MED21 9412 "mediator complex subunit 21, transcript variant 1" GO:0005515|GO:0006357|GO:0003899|GO:0045944|GO:0019827|GO:0016592|GO:0003713|GO:0001824|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_99408_PI430048170 0.501385027506447 1.01635830862478 0.301366260305739 0.330833413253279 0.394846653347247 A A A 0.336787452673226 0.319724186472643 0.301682828170619 A A A LNCV6_99408_PI430048170 mRNA
AAGCCAGACAGTCTGGAAGTTCTTCTTACTAATCTTAATCCTGGAACAACATATGAAATT NM_001145026 RefSeq chr12 + 80444345 80680189 PTPRQ NA "protein tyrosine phosphatase, receptor type, Q" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_143436_PI430048170 0.0776199726730043 0.912539429225171 0.257807180421392 0.388874482438229 0.288705062721246 A A A 0.473101977506826 0.365563769379169 0.492894367661011 A A A LNCV6_143436_PI430048170 mRNA
CGGATCAGCCACACACGTGTTCCCTTCTATTTATTATAAAGAAATTTTTCATGGGAAAAT NM_024019 RefSeq chr4 - 112513515 112516172 NEUROG2 63973 neurogenin 2 GO:0021954|GO:0070888|GO:0005634|GO:0006351|GO:0043565|GO:0051091|GO:0045165|GO:0007411|GO:0045666|GO:0045944|GO:0046983|GO:0048469|GO:0030900|GO:0001764 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_133744_PI430048170 0.0836232026835219 1.23774124477787 6.50306269633814 6.46957586008266 6.4605085927956 P P P 6.04155913591463 6.35876752012968 6.08937095744997 P P P LNCV6_133744_PI430048170 mRNA
AGGGCCCAAAAATCCCTTTTCTCATAGCAAAACTGAGACAGAAGGGTCTTTCCCAAAAAA NM_174923 RefSeq chr9 + 35658289 35661503 CCDC107 203260 "coiled-coil domain containing 107, transcript variant A" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_133940_PI430048170 0.0151111076830393 2.23104330685417 4.42076106896755 4.56445540291856 4.70018306206037 P P P 3.74209875746808 3.07702042383254 3.32734779753084 P P P LNCV6_133940_PI430048170 mRNA
GTGTTTGTTTCTCTTTGAATGTCTTGCCACTGGTTGCAGTAAAAGTGTTCTGTATTCATT NM_145051 RefSeq chr9 -

113297092 113299040 RNF183 138065 ring finger protein 183 GO:0008270|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129550_PI430048170 0.4941221098920921.176117144947 4.51472162752798
5.15518543487539 5.02161119855413 P P P 5.0050589617656 4.82059400735182
4.08599818688347 P P P LNCV6_129550_PI430048170 mRNA
AATTAGTTCCCAAGCACAAGAAGAAAATCCAGCCCAGGAAGATGGCCCCCGCGACGGCTC NM_153833RefSeq
chr3 + 129543213 129551467 H1FOO 132243 "H1 histone family, member O, oocyte-specific"
GO:0001674|GO:0051321|GO:0005737|GO:0044030|GO:0031492|GO:0006334|GO:0005730|GO:0016584|GO:0005
634|GO:0000786|GO:2000737|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142718_PI430048170 0.6577258803923210.94857467499216 0.496062781327618
0.6093862053070440.524890630701838A A A 0.8599116537873360.471185725856287
0.496503425198694A A A LNCV6_142718_PI430048170 mRNA
AAGAATTGGAGAAACTAGTTATCTGTGTTGCTGACTTTGGGACCCATCCAAGACTCCTGC NM_001126060 RefSeq
chr1 + 162362982 162370023 NOS1AP 9722 "nitric oxide synthase 1 (neuronal) adaptor protein,
transcript variant 2"
GO:0050998|GO:0045428|GO:0048471|GO:0030018|GO:0031965|GO:0050999|GO:0030315|GO:0033017|GO:0005
634|GO:0042981|GO:0060307|GO:0045429|GO:0005829|GO:0005739|GO:0010628|GO:0042383|GO:0010750|GO:0
051000|GO:0005901|GO:2000170|GO:0003062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129025_PI430048170 0.8670069488246670.9981157630597840.347486021554666
0.3546471209358990.309582409818415A A A 0.3405496982034060.351136784977441
0.328508374614372A A A LNCV6_129025_PI430048170 mRNA
GAGAATTTATGGACGTTGTAGAAATGTACAAATGCATTTCCAAACTGCCTTAAACGTTGT NM_002048RefSeq chr9
- 86944361 86947189 GAS1 2619 growth arrest-specific 1
GO:0005515|GO:0035924|GO:0030308|GO:0005886|GO:0060628|GO:0050680|GO:0048592|GO:0045879|GO:0048
701|GO:0045880|GO:0048589|GO:0007411|GO:2001240|GO:0042476|GO:0060021|GO:0021904|GO:0007050|GO:0
042474|GO:0043010|GO:0042473|GO:0046658|GO:0050679|GO:0021587|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135651_PI430048170 0.00295364099823988 0.6195094108425877.40874171875695
7.34130843572703 7.17801626007842 P P P 7.84425099668801 8.10525133482297
8.04778456424354 P P P LNCV6_135651_PI430048170 mRNA
TGCAATGTGACCAGCGAAAGCTGCATTTAATAAATGAAAGTACAGACTGTTTCTTCCCCA NM_004737RefSeq chr22
- 33273075 33920428 LARGE 9215 "like-glycosyltransferase, transcript variant 1"
GO:0008375|GO:0005794|GO:0030145|GO:0016757|GO:0006688|GO:0006044|GO:0015020|GO:0046716|GO:0035
269|GO:0030173|GO:0009101|GO:0060538|GO:0006486|GO:0043403|GO:0042285 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129971_PI430048170 0.00894014456749001 2.11189743098979 5.63637129295324
5.91215091844089 5.53694461848577 P P P 4.5944637528962 4.66590463911777
4.61517447411971 P P P LNCV6_129971_PI430048170 mRNA
AGGTCACACAGCCTAGAAGCTAGAGCAGTGCAGAGTCTGCAAATAAAACCTTAAGTCTGT NM_133639RefSeq chr15
- 40872213 40874289 RHOV 171177 ras homolog family member V
GO:0005515|GO:0051056|GO:0005886|GO:0007264|GO:0005525|GO:0046872|GO:0010008|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65667_PI430048170 0.1564966409568671.05975958194078 0.4504479799202320.321375157817994
0.349669147677628A A A 0.2690732939245880.3307762123737840.272811547347421A A A
LNCV6_65667_PI430048170 mRNA
GACCAAGGAACAGCTGTGTAAAACATACTTAAAGTTGTATTGTCAAGTGGTAAGATGAGG NM_001145451 RefSeq
chr2 + 38919362 38975449 ARHGEF33 NA Rho guanine nucleotide exchange factor (GEF) 33 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108063_PI430048170 0.3526674913435251.24451954394433 0.329462855304308

1.07446170728997 0.449600814341313 A A A 0.3482983570933440.309871284899212
0.363470334030625 A A A LNCV6_108063_PI430048170 mRNA
TTTCTCACAGAAGACAAGAGCACCCAGAATCGCAAGCTTCTTCAGAAACGAAGGACGCTG NM_018430 RefSeq chr16
+ 67806877 67828068 TSNAXIP1 55815 "translin-associated factor X interacting protein 1, transcript
variant 2" GO:0008150|GO:0003674|GO:0048471|GO:0007275|GO:0007283|GO:0005575|GO:0030154 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133638_PI430048170 0.1316063080513231.2566365315972 5.67940254376551
5.92591553573988 5.79737040709316 P P P 5.75260432360872 5.33675052163794
5.28872595718638 P P P LNCV6_133638_PI430048170 mRNA
AGGAGTGAAACATGTGAACTTTCTGGCGAGGAGACTCCCTCTTGAATCATCCATATGTAG NM_001282876 RefSeq
chr7 + 143284949 143288049 TMEM139 135932 "transmembrane protein 139, transcript variant 8"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97253_PI430048170 0.0751204868539238 0.8188687847669346.32104167725498
5.98896842675898 6.16722982211153 P P P 6.38509166482254 6.44204205500153
6.53033722134438 P P P LNCV6_97253_PI430048170 mRNA
ATTAATTGGACCCCGTGATTTCCAATCTCTGCTGTGTTGGACGTCATGAGCATTGCAATC NM_001292043 RefSeq
chr3 + 9397699 9478154 SETD5 55209 "SET domain containing 5, transcript variant 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138111_PI430048170 0.0190682620194556 0.6890561724969981 0.5668443221284
10.2550558414558 10.2409222617251 P P P 11.0127256729445 10.8655506673996
10.8130325321556 P P P LNCV6_138111_PI430048170 mRNA
AAGAAGGAAGATCTGGAGCTAATAATGACTGAGATGGAGATATCTCGAGCAGCAGCAGAA NM_016400 RefSeq
chr15 + 43800420 43802571 HYPK 25764 "huntingtin interacting protein K, transcript variant 1"
GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132726_PI430048170 0.7741954737548470.9576324270582757.60314759244853
7.70181621078913 7.94825401160014 P P P 7.76435588710673 7.57775799183737
8.07622254532326 P P P LNCV6_132726_PI430048170 mRNA
GCTAACCACATTTCATGGAATATGGCTACATTGCATCTTGCATTAAATATCTGGAGAAAA NM_001099858 RefSeq
chr7 - 42909272 42912090 C7orf25 79020 "chromosome 7 open reading frame 25, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103939_PI430048170 0.00719978846448894 0.3885316543284424.3645647285639
3.8039819457523 4.29452113517089 P P P 5.11589935203579 5.68903860380521
5.73358505393788 P P P LNCV6_103939_PI430048170 mRNA
AGTGTGGGGGAATCACGGACACTTAAAGTCAATCTGCGAAATAATTCTTTTATTACACAC NM_032142 RefSeq chr18
+ 12991361 13125052 CEP192 55125 centrosomal protein 192kDa
GO:0005515|GO:0005813|GO:0006996|GO:0005814|GO:0019902|GO:0051225|GO:0005829|GO:0051298|GO:0005
737|GO:0000086|GO:0010923|GO:0000278|GO:0000242 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_48453_PI430048170 0.8000626093554890.5933985615888852.74002925609947 2.90858479917285
2.34805953291368 A A A 4.57966631591121 1.82347832010322 2.33375956014797 P A P
LNCV6_48453_PI430048170 mRNA
AGAGTCAGGATTGGAAGGCGGACTCCCACCGTTTGCTGAGCTCCACATGACAACAGCAGA NM_001243538
RefSeq chr15_KI270905v1_alt - 3508555 3516630 LOC283710 NA uncharacterized LOC283710 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53645_PI430048170 0.2836306513357760.7314325967852366.32628335254142 5.49258045870781
5.33793844257149 P P P 6.4315123410532 6.44480075087426 5.73148802577881 P P P
LNCV6_53645_PI430048170 mRNA
CCCTTCTCCTTTCCCTGGGAAAATACAATGAATAAATAAAGACTTATTGGTACGCAAACT NM_024674 RefSeq chr1
+ 26410777 26429728 LIN28A 79727 lin-28 homolog A (C. elegans)
GO:0005515|GO:0006355|GO:0010494|GO:0003723|GO:0045686|GO:0005730|GO:0031123|GO:0045727|GO:0005

634|GO:0003729|GO:0003677|GO:0007281|GO:0010587|GO:0005829|GO:0060964|GO:0005737|GO:0035198|GO:0
045666|GO:0000932|GO:0031054|GO:0019827|GO:0031369|GO:0008270|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136107_PI430048170 0.4481256160438991.39147845300156 0.278649621949481
1.49015138006913 0.3691280702059 A A A 0.3786692013367810.316441203791647
0.348719600705798A A A LNCV6_136107_PI430048170 mRNA
TGAAAAGGATTCTAAAGGGAAAGTGCTAGGCCTAGAGGTTGCCTGAGGCACAGGATAAAA NM_016945RefSeq
chr7 - 122994704 122995700 TAS2R16 50833 "taste receptor, type 2, member 16"
GO:0005802|GO:0005515|GO:0033038|GO:0007186|GO:0005886|GO:0005783|GO:0016021|GO:0009897|GO:0001
580 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129624_PI430048170 0.2597871811386010.8258655861885416.18359710757688
6.20726264089599 6.48450085442655 P P P 6.25153053910235 6.58734046071136
6.82721686588428 P P P LNCV6_129624_PI430048170 mRNA
ATGCAGGAACTTATATGAATGTACTATAAAATAAAATGCGGACTGATTCCCAGGATTCTG NM_006390RefSeq chr12
- 30628980 30695995 IPO8 10526 "importin 8, transcript variant 1"
GO:0005515|GO:0010467|GO:0007165|GO:0008536|GO:0005654|GO:0006886|GO:0005829 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134465_PI430048170 0.1597348011353641.1519314223928 7.18095408497026
7.40935925307518 7.37800823948758 P P P 6.92951798161022 7.22471480365987
7.19449635797856 P P P LNCV6_134465_PI430048170 mRNA
GTGCTTCTGTTTGTTATGGTAGAACAGCCCTGTGTTAATATATTGAAGTCACTTAACCAG NM_006897RefSeq chr12
+ 54000092 54003336 HOXC9 3225 homeobox C9
GO:0043565|GO:0006355|GO:0048704|GO:0005634|GO:0009952|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131237_PI430048170 0.0179703045510870.4743263471493277.84111687253378
7.49202834641596 7.31660812847677 P P P 8.621973884967 8.68259319419221
8.62269899518645 P P P LNCV6_131237_PI430048170 mRNA
GTGGCTCAAAGGCACTTAGGACGCCTTAAATTTGTAAATAAAATGTTTACTACGGTTTGT NM_021958RefSeq chr1
+ 220879400 220885058 HLX3142 H2.0-like homeobox
GO:0005515|GO:0006355|GO:0008284|GO:0046622|GO:0005634|GO:0007275|GO:0006351|GO:0030154|GO:0048
484|GO:0001889|GO:0043565|GO:0048557|GO:0007519|GO:0045629|GO:0045627 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_134081_PI430048170 0.4154116146948511.0957798103895 0.330342448082494
0.3285870723779140.688374794063152A A A 0.3200844033901150.364791294475523
0.29624435734421 A A A LNCV6_134081_PI430048170 mRNA
CCTGAAAACTCAAATGAATTGTGACTTGCCTGTGAAGAAATGAAAATAAAAATTGAGGGC NM_003292RefSeq chr1
- 186311653 186375325 TPR 7175 "translocated promoter region, nuclear basket protein"
GO:0007077|GO:0005515|GO:0072686|GO:0005215|GO:0010467|GO:0019221|GO:0019058|GO:0090267|GO:0006
606|GO:0042803|GO:0008645|GO:0006405|GO:0034605|GO:0006404|GO:0015758|GO:0031072|GO:0006611|GO:0
031453|GO:0051019|GO:0031965|GO:0005975|GO:0090316|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106894_PI430048170 0.4402275972472990.8766509983045390.419729440517472
0.4248126505814390.373694699745702A A A 0.9251204989818370.385904586814184
0.411020317650973A A A LNCV6_106894_PI430048170 mRNA
TGACGTCCAGACCAATCTCACCCCAGAGGCAACTGGATGGTGCCTTTAGTTGGTGCGGAT NM_015194RefSeq chr17
- 32492521 32877173 MYO1D 4642 "myosin ID, transcript variant 1"
GO:0043005|GO:0005516|GO:0030424|GO:0006200|GO:0019904|GO:0031410|GO:0016459|GO:0030898|GO:0005
524|GO:0005790|GO:0005903|GO:0051641|GO:0016323|GO:0000146|GO:0051015|GO:0043209|GO:0010923|GO:0
043025|GO:0030673|GO:0070062|GO:0048306|GO:0005768 . NA - . NA NA NA NA NA NA NA NA

NA
LNCV6_137983_PI430048170 0.6154065756216050.91041727765141 4.1956767346433
4.42689794766813 4.18561220165138 P P P 4.51927014709713 4.62504882653258
4.01190393316904 P P P LNCV6_137983_PI430048170 mRNA
CCTTTAACTTGCCTGGCTCCTCCATTAGAATAAAAGCAGTCACTAATTTAATGTTAGAAT NM_006583RefSeq chr4
+ 109827993 109844705 RRH 10692 retinal pigment epithelium-derived rhodopsin homolog
GO:0018298|GO:0009881|GO:0007186|GO:0005887|GO:0004930|GO:0007602|GO:0007601 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135725_PI430048170 0.0104017351611230.5084706152497758.7377469738355
8.75546296258775 8.88012295959486 P P P 9.63985709200627 9.61737253755159
10.0125376905718 P P P LNCV6_135725_PI430048170 mRNA
CTCTCCAGGTTACAAATACCATGACCAAACTGTGTAATGTGATACTAATATGCAGAATAA NM_176818RefSeq chr12
+ 120446437 120463753 GATC 283459 "glutamyl-tRNA(Gln) amidotransferase, subunit C, transcript variant
1" GO:0005739|GO:0032543|GO:0050567|GO:0070681|GO:0030956|GO:0006450|GO:0005524 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139230_PI430048170 0.1617531252934340.4693197064294570.269906879649779
0.3451078832427020.274781703192825A A A 2.11253500560139 0.69730855988914
0.931671964211253A A A LNCV6_139230_PI430048170 mRNA
CACCTCATGGAAAGAATGAAGAGCCAGAAATAGATTCTATTCTGTAGAAAATCTTACACA NM_015111RefSeq chr5
+ 178113554 178126106 N4BP3 23138 NEDD4 binding protein 3 GO:0030659 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_129524_PI430048170 0.1750364054487780.5881532898233130.386825290596343
1.82178170182968 1.41593142269503 A A A 1.66025110620672 2.11101389085038
2.40322140444876 A A P LNCV6_129524_PI430048170 mRNA
TTTGATTGGGTGTCTGTTTCTCGCAGCCAAAAGAGCTCTGAATGAGGAAAGTGCTTCTGT NM_001164723 RefSeq
chr1 - 28147165 28176944 PTAFR 5724 "platelet-activating factor receptor, transcript variant 4"
GO:0005886|GO:0004930|GO:0048015|GO:0019221|GO:0001875|GO:0001816|GO:0043231|GO:0001530|GO:0006
955|GO:0032959|GO:0004992|GO:0005543|GO:0006954|GO:0016020|GO:0006935|GO:0007186|GO:0045028|GO:0
005887|GO:0005654|GO:0035589|GO:0016021|GO:0031663|GO:0060333 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_52115_PI430048170 0.0140999239828454 1.22076265091924 8.6973934929269
8.77680810632881 8.75434421852061 P P P 8.36430722808383 8.46524579296227
8.53188800448685 P P P LNCV6_52115_PI430048170 mRNA
ATCCTTTGCTAAATCCTGTTTGAATGTCATTGTAAATAAAGCCTCTGCTCTCAGATGTAA NM_018668RefSeq chr15
- 90998415 91022621 VPS33B 26276 "vacuolar protein sorting 33 homolog B (yeast), transcript variant 1"
GO:0005515|GO:0032418|GO:0048471|GO:0030897|GO:0005770|GO:0032400|GO:0070889|GO:0005765|GO:0015
031|GO:0005764|GO:0006904|GO:0005737|GO:0031902|GO:0031091|GO:0061025|GO:0016192 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143443_PI430048170 0.00687321077239734 0.5793043570660091 0.8580639062532
10.8936759357187 11.2035462222683 P P P 11.8588623296568 11.5591156640129
11.9021354619812 P P P LNCV6_143443_PI430048170 mRNA
CGCTGGCTACTGTCTATTAAAATTCTGATGTTTCTGTGAAATTCTCAGAGTGTTTAATTG NM_001040619 RefSeq
chr1 + 212608627 212620777 ATF3 467 "activating transcription factor 3, transcript variant 4"
GO:0005515|GO:0008284|GO:0000977|GO:0003700|GO:0003714|GO:0005730|GO:0006094|GO:0005634|GO:0000
122|GO:0035914|GO:0000978|GO:0001228|GO:0006351|GO:0042802|GO:0030968|GO:0001078|GO:0045944|GO:0
005654|GO:0006987|GO:0044267 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65185_PI430048170 0.162134144029561 1.03975402089672 0.36776188241182 0.303748285347258
0.277325141127982A A A 0.2504494269293010.2819151795191870.24900841089109 A A A
LNCV6_65185_PI430048170 mRNA

CCCAGTTCTCTGGGTTGTGCTTTACTCCACGCATCAATAAATAATTTTGAAGGCCTCACA NM_002287RefSeq chr19 - 54353623 54365114 LAIR1 3903 "leukocyte-associated immunoglobulin-like receptor 1, transcript variant a" GO:0005515|GO:0005886|GO:0016021|GO:0070062|GO:0002376 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131358_PI430048170 0.0507218191138605 0.4922883757526177.9052998489625 6.95122038002034 7.08054237245502 P P P 8.40503066784696 8.62632809504008 8.12486048210133 P P P LNCV6_131358_PI430048170 mRNA
CGCCCGGCTGTGCCCCGTCTGACCAAAGTTATAATAAAAACATTTTCACCCCGCAAAAAA NM_006688RefSeq chr17 - 44959692 44968276 C1QL1 10882 "complement component 1, q subcomponent-like 1" GO:0003674|GO:0005737|GO:0005581|GO:0007626|GO:0005576|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134589_PI430048170 0.1111595562476950.5367890920056090.328744033831626 1.32963225399668 1.58080789444861 A A A 2.14086038437733 1.66188076176022 2.32772395796863 A A P LNCV6_134589_PI430048170 mRNA
GATGGCGGCTGGCCTGCTCAGTAACATACATGTTCCAAATAAAGATTTTGCATGAAAGTA NM_020848RefSeq chr10 - 30012799 30059559 KIAA1462 57608 KIAA1462 GO:0005912|GO:0005911|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134594_PI430048170 0.6744903089070680.8035173115533231.24066541873663 0.2887938153614830.476066584807587A A A 0.3051127206954190.665591666105099 1.75300129063154 A A A LNCV6_134594_PI430048170 mRNA
TGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAAGCAAAAAA NM_014443RefSeq chr5 - 149374266 149379275 IL17B 27190 interleukin 17B GO:1900017|GO:0006955|GO:0006954|GO:0007267|GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141094_PI430048170 0.0369568690807455 0.87108525287397 11.9282239214282 11.8975062920714 11.7718872975015 P P P 12.0348779258503 12.0592078918498 12.1047110024901 P P P LNCV6_141094_PI430048170 mRNA
GAGAGCTTGCCATCCAGCTCACGAAGACAGAGTTATTAAACCATTCAAATCTCTGTGGTC NM_021138RefSeq chr9 + 136886512 136926615 TRAF2 7186 TNF receptor-associated factor 2 GO:0005515|GO:0097300|GO:0035631|GO:0004842|GO:0071732|GO:0016874|GO:0032403|GO:0043623|GO:0042802|GO:0030163|GO:0070207|GO:0070534|GO:0005938|GO:0031625|GO:0005164|GO:0019903|GO:0031435|GO:0002726|GO:0033209|GO:0097057|GO:0051865|GO:0045087|GO:0050870|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135724_PI430048170 0.9697467894667220.7153362821334955.2232000400592 5.35692200754208 5.57345501730842 P P P 5.78572695462439 6.74976084417177 3.73274386830706 P P P LNCV6_135724_PI430048170 mRNA
GGGATATTATGAAGGGCCTTGAGCATCTGGATTCTGCCTAATAAAAAACATTTATTTTCA NM_000518RefSeq chr11 - 5225465 5227071 HBB 3043 "hemoglobin, beta" GO:0005515|GO:0042542|GO:0072562|GO:0044281|GO:0051291|GO:0070293|GO:0005829|GO:0045429|GO:0030492|GO:0031838|GO:0004601|GO:0050880|GO:0030185|GO:0071682|GO:0042744|GO:0010942|GO:0031720|GO:0070062|GO:0005833|GO:0005506|GO:0005576|GO:0006898|GO:0015671|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139777_PI430048170 0.1168244096976711.24421674112821 8.49710175984452 8.39373644823514 8.31901444228973 P P P 8.01114356177173 8.33031764693991 7.89195428549418 P P P LNCV6_139777_PI430048170 mRNA
TCAAGACATTTGAGGGGCACGATGCTTCTGTGCTGAAGGTGGCCTTTGTGAGCCGTGGCA NM_006453RefSeq chr16 + 1972062 1978750 TBL3 10607 transducin (beta)-like 3 GO:0035556|GO:0005515|GO:0000462|GO:0030515|GO:0032040|GO:0007199|GO:0005730|GO:0005634|GO:0005057|GO:0034388 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_129494_PI430048170 0.2706519280662121.6182842342268 1.97359284759752
0.8759731956892610.756372606546741A A A 0.6004797347348110.640004018578045
0.613797379786007A A A LNCV6_129494_PI430048170 mRNA
GAAGGTTCATACCTTATTCAAAGGCAGAAAAGGTATACTGGAGTGAACTCCTATGATTAA NM_013250RefSeq chr11
+ 6926422 6958047 ZNF215 7762 zinc finger protein 215
GO:0003700|GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0003677|GO:0046872 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140005_PI430048170 0.0561912302433640.5909990912690871 3.7656877124374
13.1064989555555 13.0611327209578 P P P 14.1840639344908 14.2231512568441
13.8930059958907 P P P LNCV6_140005_PI430048170 mRNA
CCTCCCCGCCTTCCTTCTTCCTTTTTATATACAATTTGTTATTGTCAAATAAAAGTAGGA NM_001282167 RefSeq chrX
+ 48508958 48520814 PORCN 64840 "porcupine homolog (Drosophila), transcript variant F"
GO:0009100|GO:0016746|GO:0032281|GO:0005789|GO:0030176|GO:0016055 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127268_PI430048170 0.5226761767909 0.8814031496667820.343862656739739
0.2812191018322040.374227771121578A A A 0.8863177106576040.275920345985167
0.298640174244521A A A LNCV6_127268_PI430048170 mRNA
CCTGTTATGCTTACAAAATGGTGATGGCTTATGGAAGGCTGTTAAATTAATATTCCTGTT NM_145244RefSeq chr4
- 100185869 100190498 DDIT4L 115265 DNA-damage-inducible transcript 4-like GO:0005737|GO:0009968
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138124_PI430048170 0.00177122854186699 0.6945907501972639.41206462103436
9.25276527452921 9.31381908005596 P P P 9.89398380521985 9.74766893874405
9.91317265930123 P P P LNCV6_138124_PI430048170 mRNA
CACATTGCCCAAGTCACACAGGCTTCTGTATTATGTATTTAGATAAAATGTGTGAAAACA NM_001077665 RefSeq
chr10 + 49988317 50010499 AGAP6 414189 "ArfGAP with GTPase domain, ankyrin repeat and PH
domain 6" GO:0043547|GO:0008060|GO:0032312|GO:0008270 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132021_PI430048170 0.0842933099567981.20300612281995 12.0778513273471
12.2251627412294 12.1679558676845 P P P 12.0403520583535 11.9003135556311
11.7159420479891 P P P LNCV6_132021_PI430048170 mRNA
AGGCTGTGCGGGTGTCCTCCTGGCAATAAACACTACCCGGTTCTCGCCCTCTGGAAAAAA NM_138401RefSeq chr19
+ 17419846 17425339 MVB12A 93343 "multivesicular body subunit 12A, transcript variant 1"
GO:0005515|GO:0043130|GO:0017124|GO:0000813|GO:0005815|GO:0016235|GO:0015031|GO:0031982|GO:0043
231|GO:0005829|GO:0008289|GO:0042058|GO:0005737|GO:0031902|GO:0005654|GO:0043162|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139607_PI430048170 0.0103541248181746 1.52062369678577 11.9359647696453
12.0182075406664 11.9662662446297 P P P 11.5076749060745 11.3455538333284
11.2419123633745 P P P LNCV6_139607_PI430048170 mRNA
ATTCCCACGCTACCCCCTGCCTTGGGAGGTGTGTGGAATAAATTATTTTTGTTAAGGCAA NM_002826RefSeq chr1
+ 180154832 180198034 QSOX1 5768 "quiescin Q6 sulfhydryl oxidase 1, transcript variant 1"
GO:0030173|GO:0005794|GO:0006457|GO:0016971|GO:0003756|GO:0045454|GO:0005615|GO:0070062|GO:0055
114|GO:0045171|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143500_PI430048170 0.41389010362672 1.32872123080401 0.287028464657605
0.5524182247817081.37364190141494 A A A 0.5065616608492780.395677231146648
0.305618454604887A A A LNCV6_143500_PI430048170 mRNA
TTGAAACACTGAGCACCACTGAAGAATTTTGCAAATGGCTTGTCCAAAATGGAGAAAAAC NM_144725RefSeq chr5
+ 34839163 34899459 TTC23L 153657 tetratricopeptide repeat domain 23-like GO:0005515 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_136411_PI430048170 0.6580949639003751.05927369301423 8.48103934482755

8.58431408151318 8.80604618851876 P P P 8.27318630676866 8.42553609360284
8.87350404412422 P P P LNCV6_136411_PI430048170 mRNA
GAAATTCCATTTTTCCCTCTTTCCCTGAGTTGTATTGACCTACAGAGTTAATTTCCTTTG NM_021633 RefSeq chr1 -
202891095 202927272 KLHL12 59349 "kelch-like family member 12, transcript variant 2"
GO:0006888|GO:0005515|GO:0030134|GO:0006513|GO:0000139|GO:0031463|GO:0048208|GO:0016055|GO:0090
090|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142859_PI430048170 0.69500586151175 1.05018886231094 4.36891731281389
4.47162525428465 4.5097075582415 P P P 3.95446682912519 4.79505466984181
4.26509328487043 P P P LNCV6_142859_PI430048170 mRNA
CGCGGTATATAGAGATATGCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAA NM_023004 RefSeq chr22
- 20241414 20268293 RTN4R 65078 reticulon 4 receptor
GO:0005515|GO:0048011|GO:0009986|GO:0005886|GO:0005783|GO:0050771|GO:0004872|GO:0031225|GO:0007
409|GO:0050770|GO:0070062|GO:0030426 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141056_PI430048170 0.435797212277073 1.1335092428627 0.913596662051846
0.447140635235676 0.38612060485108 A A A 0.44387845719636 0.399531517432073
0.420324115123538 A A A LNCV6_141056_PI430048170 mRNA
GAAGAAAGCAGTAACTCTTCAGACTGCAGCAGTGGAGAAGAAATAGAAGTTGATGTCTGA NM_001143975
RefSeq chr11 + 90085949 90087131 UBTFL1 NA "upstream binding transcription factor, RNA
polymerase I-like 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123110_PI430048170 0.0748641023247818 1.5853146763917 7.12733578261434
7.66450820297846 6.95468480488343 P P P 6.78337610949659 6.67366083941077
6.36056499783785 P P P LNCV6_123110_PI430048170 mRNA
GTCCAGGGCTTAGTCAGCGGGGCCCGGAGTGGCTTCCCTGGCTGGCATCTGGACTTAGGC NM_001130679 RefSeq
chr4 - 98878455 98930635 EIF4E 1977 "eukaryotic translation initiation factor 4E, transcript variant
2"
GO:0005515|GO:0000339|GO:0008286|GO:0010467|GO:0016281|GO:0010494|GO:0030324|GO:0019221|GO:0003
743|GO:0006412|GO:0006413|GO:0005829|GO:0016442|GO:0005737|GO:0000082|GO:0006406|GO:0000932|GO:0
016032|GO:0000289|GO:0070062|GO:0000288|GO:0031370|GO:0006417|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144550_PI430048170 0.480527388867216 0.765933787427713 0.447773129684739
0.509609117184157 0.477705300555232 A A A 1.46607525379523 0.413591013610153
0.446641073709827 A A A LNCV6_144550_PI430048170 mRNA
CCCCACATGGTAATGTTTTCTTTAGAGAGAAGAAAAAACAACTGGCTGTAAACGTAAATT NM_001145077 RefSeq
chr11 + 61508799 61511018 LRRC10B 390205 leucine rich repeat containing 10B NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138153_PI430048170 0.425288520417432 1.28345628771096 0.464565288356135
0.468224705597068 1.35969948161253 A A A 0.401918212409133 0.510211185087962
0.492657532501528 A A A LNCV6_138153_PI430048170 mRNA
AGTCAGGCAGAGCTGATGGATCCAGTTTGAAAAAACAAAATGCCATTCAACCGTAAAAAA NM_145205 RefSeq chr1
+ 33860474 33864791 HMGB4 127540 "high mobility group box 4, transcript variant 1"
GO:0006355|GO:0005694|GO:0003682|GO:0006338|GO:0005634|GO:0003677 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129744_PI430048170 0.00502894172732262 2.17452152605656 6.89522059076759
6.99039105571939 7.11844417419297 P P P 5.61426558267505 5.95476458926981
6.04665457353623 P P P LNCV6_129744_PI430048170 mRNA
CTGTTGTCTCTTTTCAAACCAAATTGGGAGAATTGTTGCAAAGTAGTGAATGGCAAATAA NM_015941 RefSeq chr8
- 53715542 53843311 ATP6V1H 51606 "ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H,
transcript variant 1"
GO:0005515|GO:0008286|GO:0051701|GO:0005886|GO:0005765|GO:0055085|GO:0050690|GO:0005829|GO:0006

897|GO:0006879|GO:0033572|GO:0000221|GO:0050790|GO:0046961|GO:0007035|GO:0008152|GO:0015991|GO:0
016032|GO:0030234|GO:0090382|GO:0016887|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_145190_PI430048170 0.1285049450227080.85934550326699 8.93358812850215
8.91037135337128 9.20448172698899 P P P 9.24338739608752 9.13861730580797
9.33474929985699 P P P LNCV6_145190_PI430048170 mRNA
GCACAGAGCGGGTGCTTGAGTTGTTGTCGTTTTTTGTTTGTTTTTTAAATGTAAACTGGT NM_001005861 RefSeq
chr3 - 134157133 134250744 RYK6259 "receptor-like tyrosine kinase, transcript variant 1"
GO:0005515|GO:0005886|GO:0018108|GO:0005634|GO:0005524|GO:0031175|GO:0022038|GO:0007165|GO:0005
737|GO:0016020|GO:0005887|GO:0007411|GO:0030182|GO:0006468|GO:0016021|GO:0004713|GO:0043410|GO:0
016055|GO:0004714|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142980_PI430048170 0.187568757447581 2.62154986510303 2.62733535403034
1.58249691312562 0.583104556359717 A A A 0.342807593171294 0.448477945206591
0.524033410299529 A A A LNCV6_142980_PI430048170 mRNA
CTCAAGCAGACGGGGCTCAAGGGGGTTACATTTAATAAAAGGATGAAGATGGATAGAAAA NM_005428 RefSeq
chr19 + 6772667 6857366 VAV1 7409 "vav 1 guanine nucleotide exchange factor, transcript variant 1"
GO:0005515|GO:0003700|GO:0005886|GO:0007264|GO:0031295|GO:0032855|GO:0046872|GO:0005829|GO:0005
085|GO:0007173|GO:0005911|GO:0030676|GO:0051056|GO:0048010|GO:0048011|GO:0006355|GO:0043065|GO:0
048015|GO:0072593|GO:0030593|GO:0030168|GO:0097190|GO:0042110|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130838_PI430048170 0.329211636659872 1.10027883553883 0.637424458973727
0.307905652887858 0.359228010049927 A A A 0.27501326737004 0.337138828529045
0.300348337874382 A A A LNCV6_130838_PI430048170 mRNA
CCCTGTCATCAATCAGGGTAGTAACTTGACTTAAGAATACCACTTTTTAGAAAAATTACG NM_001184992 RefSeq
chr17 + 30970937 30999911 RNF135 84282 "ring finger protein 135, transcript variant 3"
GO:0005515|GO:0032728|GO:0005737|GO:0004842|GO:0016567|GO:0045087|GO:0016874|GO:0045088|GO:0043
021|GO:0008270|GO:0032480|GO:0005829 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_141518_PI430048170 0.865732883863059 0.993680901555362 0.457066108739462
0.491038288598771 0.393824732311571 A A A 0.532630984610337 0.412064469973025
0.423249706464888 A A A LNCV6_141518_PI430048170 mRNA
CAGTTGACTGTGTAGCTCTTGCCTGGCATTAAAGCATGTTTTTGGTTTAACATGAAAAAA NM_001040630 RefSeq
chr8 - 101686541 102124907 NCALD 83988 "neurocalcin delta, transcript variant 7"
GO:0019722|GO:0043014|GO:0005509|GO:0007268|GO:0003779|GO:0005829|GO:0003073|GO:0005622|GO:0015
631|GO:0030276|GO:0030130|GO:0016192|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_94589_PI430048170 0.153036727301484 1.67922187335761 2.22830456344908
1.2059841302026 2.06841583749788 A A A 0.935289757512394 0.745581988564752
1.61969917346927 A A A LNCV6_94589_PI430048170 mRNA
TTAGATGACTTGATTGTAACCAATACTTCTGAGGGCCACCTGTATGTGGTGTCCAACGCT NM_000481 RefSeq
chr3 - 49416777 49422678 AMT 275 "aminomethyltransferase, transcript variant 1"
GO:0005739|GO:0008483|GO:0006546|GO:0004047|GO:0032259 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_133008_PI430048170 0.953110522214344 1.00257449576848 0.422199445072338
0.286270001535367 0.332719236497426 A A A 0.37123599733596 0.318540115163127
0.343126002556335 A A A LNCV6_133008_PI430048170 mRNA
GCCAACATTTTATTGAAGAAGCCACAGAGGCTGAAATTCAATAAACACAAGTTTTATGAG NM_153320 RefSeq
chr6 + 43298259 43305538 SLC22A7 10864 "solute carrier family 22 (organic anion transporter),
member 7, transcript variant 2"

GO:0016323|GO:0035634|GO:0034220|GO:0016020|GO:0005886|GO:0015347|GO:0005887|GO:0015711|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140773_PI430048170 0.18875470676312 0.823189327372622 0.400646309799211 0.372002243151953 0.247466567087024 A A A 0.337720662496884 0.810965930351805 0.67780964139614 A A A LNCV6_140773_PI430048170 mRNA
TTGGAATTACCAATAGAGCTGGTCAGTTATCAACAGTAGAGCTCAGTATCAATTTTACTG NM_001271837 RefSeq chr15 + 76931620 76950260 RCN2 5955 "reticulocalbin 2, EF-hand calcium binding domain, transcript variant 2" GO:0005515|GO:0005783|GO:0005509|GO:0005730|GO:0005788 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128404_PI430048170 0.0309283513122665 0.582135150357944 2.48894078794946 2.92595809867233 2.30712547883199 A A A 3.14470236925342 3.29409559809442 3.64923341042415 P P P LNCV6_128404_PI430048170 mRNA
GAAGAAGCAGTTACACCCCAACAATAGGAGGAAAAATCTAGAACTATTTCAAGTTTTATC NM_001106 RefSeq chr3 + 38454298 38493142 ACVR2B 93 "activin A receptor, type IIB" GO:0005515|GO:0007368|GO:0005886|GO:0030324|GO:0061298|GO:0048705|GO:0009791|GO:0009952|GO:0060836|GO:0046872|GO:0016362|GO:0032147|GO:0007507|GO:0001946|GO:0005737|GO:0004702|GO:0019838|GO:0048185|GO:0035265|GO:0060021|GO:0042475|GO:0005024|GO:0007178|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141146_PI430048170 0.856613663142499 0.909280593041053 1.05574043835618 0.387415115156028 1.62121034863483 A A A 1.14416506611305 0.397376751799843 1.84024292700035 A A A LNCV6_141146_PI430048170 mRNA
GGGTGAAAAAGCCTTCCAAGATTCAAAGCAGATTTCTCTGGTATTATATTATATCCTTCT NM_144706 RefSeq chr2 + 99141721 99151465 C2orf15 150590 chromosome 2 open reading frame 15 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130205_PI430048170 0.263655354791386 1.24157201412169 3.48889784733067 3.56407034859118 4.08323081666756 P P P 3.3752170631016 3.64223347669876 3.22631564379591 P P P LNCV6_130205_PI430048170 mRNA
TTTAGAAAACAAGACAGACTCTCAGATGAAAGATCTGACAAGCACCGTGGCCAGTCACAG NM_006133 RefSeq chr11 + 61680432 61747002 DAGLA 747 "diacylglycerol lipase, alpha" GO:0046340|GO:0019369|GO:0005886|GO:0007596|GO:0071926|GO:0043196|GO:0030168|GO:0042136|GO:0016021|GO:0046872|GO:0016298|GO:0007405 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133348_PI430048170 0.140904769513008 0.450820421071062 2.13264785156777 0.302810570602847 0.455524060079325 A A A 2.11410672773562 1.78740167666383 2.94935056130707 A A P LNCV6_133348_PI430048170 mRNA
CCCCCTGTTGCTATTTTTGATGATAGAGAATAAATAGGGTTTTTGAAACCTTTGTAGTGT NM_020818 RefSeq chr14_KI270847v1_alt + 447780 821905 UNC79 57578 unc-79 homolog (C. elegans) GO:0034220|GO:0035264|GO:0005886|GO:0048149|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140412_PI430048170 0.149993655430897 1.90463411283052 2.97608246306263 4.31701879623134 3.5544832343492 A P P 2.46902739541952 3.02185595761591 2.82906716081815 P P P LNCV6_140412_PI430048170 mRNA
TCCACCACTGCTTTCTAGTCCTTTAACTCCTAGAGGCAAACTTTTGGGGGATAAGAAAGC NM_145057 RefSeq chr19_GL949752v1_alt - 369716 377945 CDC42EP5 148170 CDC42 effector protein (Rho GTPase binding) 5 GO:0005886|GO:0008360|GO:0007254|GO:0007266|GO:0005100|GO:0012505|GO:0005737|GO:0016020|GO:0030838|GO:0032321|GO:0031274|GO:0017049|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140501_PI430048170 0.0172267123856411 2.60019704888178 3.43081253652425 4.34078110152863 3.83501081928155 P P P 2.85945888423616 2.42162511042957 2.26708559099752 A A A LNCV6_140501_PI430048170 mRNA
GTACCACTAGCATCTATATGACTTTTGTGTAATTTTCTCTCTTGAACTCTGGTGCTGTTT NM_021221 RefSeq

chr6_GL000253v2_alt + 2975997 2977497 LY6G5B 58496 "lymphocyte antigen 6 complex, locus G5B" GO:0008150|GO:0003674|GO:0005576|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93493_PI430048170 0.347433496335062 0.8782944767109786 21453536312328 6.4940698832852 6.75458679804152 P P P 6.50780547358232 6.74125389224722 6.80909929191329 P P P LNCV6_93493_PI430048170 mRNA CTTGAGTGGTATATCTAATTGAAATGGGATCTTCGTTTGGCTTGTATGTTGATGAAATCA NM_014362 RefSeq chr2 - 190204633 190320045 HIBCH 26275 "3-hydroxyisobutyryl-CoA hydrolase, transcript variant 1" GO:0034641|GO:0003860|GO:0005759|GO:0006574|GO:0009083|GO:0044281|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145743_PI430048170 0.000511638301166917 0.3253852814351761 11.1386009667658 11.2335583649118 10.9235633341501 P P P 12.8128855072305 12.710277664254 12.64410567179 P P P LNCV6_145743_PI430048170 mRNA GCATGTCCACGCACCACCCGTTCAGGGCCCTGAATAAACAGTTGGCAACAGCACAAAAAANM_018998 RefSeq chr9 - 136940432 136944754 FBXW5 54461 F-box and WD repeat domain containing 5 GO:0005515|GO:0051298|GO:0007067|GO:0005737|GO:0016567|GO:0019901|GO:0043161|GO:0080008|GO:0031146|GO:0019005 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144010_PI430048170 0.354924251257301 1.11768761404905 1.01698486126817 0.67965109213225 0.651349176283284 A A A 0.611008660679225 0.790620811034127 0.47695674983211 A A A LNCV6_144010_PI430048170 mRNA TGACCAAGATGAGACAAAAGGCTTCCTTTCGCGATACTAGAGCCTCTGTAAACTTCTCCT NM_000226 RefSeq chr17 - 41565840 41572058 KRT9 3857 "keratin 9, type I" GO:0005882|GO:0045109|GO:0016020|GO:0008544|GO:0005200|GO:0043588|GO:0005634|GO:0007283|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95304_PI430048170 0.148128273070926 0.612438563840923 3.12170098802334 2.89766548999855 2.88335603724926 P A A 3.03773784379215 3.87100215952227 3.96206943296732 P P P LNCV6_95304_PI430048170 mRNA ACCTGAAATTCTGCGTGCTCTATCTAGCAGAGAAGGCAGAGTGCTTATTCACTTTGGAAG NM_144488 RefSeq chr9 + 113444728 113597743 RGS3 5998 "regulator of G-protein signaling 3, transcript variant 6" GO:0043547|GO:0000188|GO:0005737|GO:0008277|GO:0005886|GO:0038032|GO:0005654|GO:0005829|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135819_PI430048170 0.409530822512234 1.04959964717823 0.612234530312277 0.6439514429747 0.444420236400063 A A A 0.424617576675812 0.542374616468077 0.529099793524628 A A A LNCV6_135819_PI430048170 mRNA GTCCATGTAACAGTCAAGTTAGCATTCAAGCAATTATGGATGTGATACTATGATGTACTT NM_133459 RefSeq chr18 - 59430938 59697412 CCBE1 147372 collagen and calcium binding EGF domains 1 GO:0005581|GO:0005509|GO:0005518|GO:0005578|GO:0002040|GO:0048845|GO:1900748|GO:0002020|GO:0005615|GO:0010575|GO:0045766|GO:0010595|GO:0001946|GO:0010954 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118553_PI430048170 0.00326881300847822 1.35942522163847 3.51366532386442 3.53766069190075 3.39645403664732 P P P 2.94539523458718 3.12754092117748 3.0440239550194 P P P LNCV6_118553_PI430048170 mRNA TGACATGCTGCCTAAGAGAAGCAGAGTCTGTGACAGCCACCCCAACACGTGACGTCATGGNM_001077482 RefSeq chr1 - 161229665 161238210 NR1I3 9970 "nuclear receptor subfamily 1, group I, member 3, transcript variant 1" GO:0010467|GO:0004882|GO:0006367|GO:0000977|GO:0003700|GO:0003713|GO:0005634|GO:0001228|GO:0003677|GO:0005829|GO:0007165|GO:0005737|GO:0045944|GO:0043401|GO:0008270|GO:0005654|GO:0004879|GO:0004887|GO:0005856|GO:0045892|GO:0030522|GO:0030521 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137286_PI430048170 0.1952346485926572.59981380967341 0.48718412693659
2.29760435276845 2.34497526765878 A A A 0.4880287158149540.688609931970171
0.454329105581747 A A A LNCV6_137286_PI430048170 mRNA
CCAGCTGGGAACTATACCAGACCTGGATACTGATCCCAAAGTGTTAAATTCAACTACATG NM_006139RefSeq chr2
+ 203706474 203738912 CD28 940 "CD28 molecule, transcript variant 1"
GO:0005515|GO:0051897|GO:0050852|GO:0005886|GO:0002863|GO:0031295|GO:0042089|GO:0002020|GO:0005
829|GO:0042802|GO:0007173|GO:0045944|GO:0006959|GO:0042102|GO:0046641|GO:0016032|GO:0045070|GO:0
001772|GO:0048011|GO:0048015|GO:0045840|GO:0045727|GO:0014068|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139513_PI430048170 0.0344155541442029 0.6461087938501193.97374259060665
3.663356385576 4.06001105635903 P P P 4.56167785615433 4.24407785264752
4.76432359421165 P P P LNCV6_139513_PI430048170 mRNA
GTCAGCAGTGGACCCTGTCTTTTATTAAGTGAAAGAAGAAACTGAGTCTGAAAGTACTCT NM_018997RefSeq chr1
+ 150293841 150308979 MRPS21 54460 "mitochondrial ribosomal protein S21, transcript variant 2"
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0006412|GO:0005
763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136363_PI430048170 0.6604122715634170.8775838467422150.505561713864995
2.74771901310086 0.654604334234181 A A A 1.21659341102281 2.66055491492832
1.27393048683684 A P A LNCV6_136363_PI430048170 mRNA
CCGAATCCCTCCTGCAGGCTCATTGCCACTTTTGTAGAGAATGTTCTCTATCAGTATCGT NM_173477RefSeq chr17
- 74916083 74923263 USH1G 124590 "Usher syndrome 1G (autosomal recessive), transcript variant 1"
GO:0005515|GO:0060113|GO:0042472|GO:0005886|GO:0007605|GO:0030507|GO:0050957|GO:0045494|GO:0015
629|GO:0050953|GO:0042803|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_114369_PI430048170 0.1639233572064981.15960853222689 6.18279950923632
5.85374736120972 6.12128771158705 P P P 5.87006081736542 5.91121140245845
5.75169784910102 P P P LNCV6_114369_PI430048170 mRNA
GCCGGGCTCTGCTTTCTGTCATGGATGATCACAACGTGGATTCTTTCATCTCCCTCTCCT NM_005155RefSeq
chr6_GL000251v2_alt + 3592337 3602033 PPT2 9374 "palmitoyl-protein thioesterase 2,
transcript variant 1" GO:0008474|GO:0008152|GO:0005764|GO:0016790|GO:0070062 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_127666_PI430048170 0.00939648822429751 1.48622426800392 9.92307369140516
9.93385900872197 10.119640649097 P P P 9.30203651378626 9.35013442819539
9.59997614462067 P P P LNCV6_127666_PI430048170 mRNA
CCAAGTACCAATGCTGTTGTAAACAACGTGTATAGTGCCTAAAATTGTATGAAAATCCTT NM_002755RefSeq chr15
+ 66386872 66491544 MAP2K1 5604 mitogen-activated protein kinase kinase 1
GO:0005515|GO:0045597|GO:0046579|GO:0032402|GO:0002756|GO:0006935|GO:0007173|GO:0047496|GO:0000
165|GO:0007411|GO:0002755|GO:0005938|GO:0006979|GO:0017016|GO:0004708|GO:0038124|GO:0005794|GO:0
030335|GO:0038123|GO:0005815|GO:0034134|GO:0031435|GO:0018108|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130668_PI430048170 0.00330747640340657 0.6501034926793689.21182787687814
9.03040763009146 9.15204754298348 P P P 9.62047574216319 9.87400944180824
9.75832469403625 P P P LNCV6_130668_PI430048170 mRNA
AGAACAGCCAGTTCATAGTGGGACTTGTATTTTGATCTTAATAAAAAATAATAACCCGGG NM_145805RefSeq chr15
+ 76336723 76342475 ISL2 64843 ISL LIM homeobox 2
GO:0043565|GO:0031290|GO:0021524|GO:0006355|GO:0045665|GO:0048666|GO:0021520|GO:0048935|GO:0008
270|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142527_PI430048170 0.4844141164370420.9550121543399651 0.6456123530859
10.6910189368621 10.5820521045106 P P P 10.5596409390497 10.7598992765667
10.7897645663726 P P P LNCV6_142527_PI430048170 mRNA

AATGCTTCCTCCCAGCATAGGATTCATTGAGTTGGTTACTTCATATTGTTGCATTGCTTT NM_198175 RefSeq chr17 + 51153558 51162089 NME1 4830 "NME/NM23 nucleoside diphosphate kinase 1, transcript variant 1" GO:0005515|GO:0006241|GO:0008285|GO:0004550|GO:0005634|GO:0044281|GO:0006220|GO:0009142|GO:0030154|GO:0042802|GO:0005829|GO:0005739|GO:0005737|GO:0043024|GO:0070062|GO:0050679|GO:0000287|GO:0015949|GO:0055086|GO:0042981|GO:0032587|GO:0005525|GO:0005524|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142044_PI430048170 0.1277010038342761.08115196847799 0.487149475372856 0.6007028459450790.566591447917639 A A A 0.3522458083575590.449233137910331 0.513070930158195 A A A LNCV6_142044_PI430048170 mRNA
TGCACAACCTTGATGATAACCAGTGGAAATGTAACTAACTGAAATGAAGAATAAAAGGCA NM_001260497 RefSeq chr12 - 75040077 75209748 KCNC2 3747 "potassium channel, voltage gated Shaw related subfamily C, member 2, transcript variant 4" GO:0005251|GO:0006112|GO:0050796|GO:0005886|GO:0008076|GO:0007268|GO:0051260|GO:0034765|GO:0044281|GO:0016021|GO:0001508|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144582_PI430048170 0.0487870055725697 1.49914474549581 8.93064780688568 9.01603409360209 8.919194164688 P P P 8.59907902348511 8.37537804833265 8.09758323319122 P P P LNCV6_144582_PI430048170 mRNA
GCGGTAGCAGCTGTGGGTGGCTAATTAAGATAGATCGCGTTAGCCAGTTTTACCAGCGCA NM_000413 RefSeq chr17 + 42551965 42555214 HSD17B1 3292 hydroxysteroid (17-beta) dehydrogenase 1 GO:0004303|GO:0006694|GO:0031965|GO:0006703|GO:0044281|GO:0003824|GO:0005829|GO:0061370|GO:0060348|GO:0008210|GO:0071248|GO:0005737|GO:0047035|GO:0005654|GO:0008202|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98563_PI430048170 0.1316167065803670.8624085379014236.58794959205511 6.52737589657227 6.7248630362829 P P P 6.7491707324417 6.72020389304835 7.00170295262045 P P P LNCV6_98563_PI430048170 mRNA
AAGCGGAATACAGTGATAGGAACACCATTTTGGATGGCTCCAGAAGTGATTCAGGAAATT NM_006282 RefSeq chr20 + 44966478 45079952 STK4 6789 serine/threonine kinase 4 GO:0005515|GO:0008285|GO:0071902|GO:0097284|GO:0005634|GO:0042803|GO:0042802|GO:0005829|GO:0032092|GO:0035556|GO:0005737|GO:0046777|GO:0004702|GO:0018105|GO:0046983|GO:0090090|GO:0046621|GO:0023014|GO:0001569|GO:0043065|GO:0000287|GO:0060706|GO:0003157|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131491_PI430048170 0.65260941174475 1.0722974536372 6.28228349221979 5.81468550958333 5.89828245281577 P P P 6.20998862315856 5.74009757414276 5.73387857822389 P P P LNCV6_131491_PI430048170 mRNA
AGGTTTTTGCCCATCCTCCCAATCTCAATACAGCCTGAATAAACCAAGACAAGACCTCTG NM_001335 RefSeq chr11 + 65879812 65883741 CTSW 1521 cathepsin W GO:0006955|GO:0016020|GO:0006508|GO:0008234 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107169_PI430048170 0.00230816914887042 0.35879943282733 3.54425282132332 3.56804627620018 3.96510070848317 P P P 5.0594694258841 5.30587734088155 5.17762351084748 P P P LNCV6_107169_PI430048170 mRNA
AGCTCACCAGGACTTTGGCTACTTTTATGGCTCGAGCTATGTGGCAGCCCCTGACAGCAG NM_016327 RefSeq chr22 + 24495282 24526585 UPB1 51733 "ureidopropionase, beta" GO:0019483|GO:0046135|GO:0055086|GO:0044281|GO:0003837|GO:0006206|GO:0046872|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131656_PI430048170 0.3002985577019281.03899074610559 0.521927816491252 0.5077989524235830.56473568824027 A A A 0.48963215939292 0.53719532758926 0.399314398967898 A A A LNCV6_131656_PI430048170 mRNA
GTCACTTCTAGTTCATTACCATTTCTTGTAGCTGTTGTTTTTAGATATAGTCCACTGCAT NM_007035 RefSeq chr12 - 91050493 91058354 KERA 11081 keratocan

GO:0005796|GO:0005975|GO:0005578|GO:0005576|GO:0044281|GO:0042339|GO:0061303|GO:0003674|GO:0018146|GO:0009405|GO:0042340|GO:0007601|GO:0030203|GO:0050896|GO:0043202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140864_PI430048170 0.0333525029605763 0.636145271369978 11.7575617584747 11.8848955646722 11.7843742672671 P P P 12.1827330531416 12.6145281540025 12.5537317571411 P P P LNCV6_140864_PI430048170 mRNA
TACACCAATTTGGTAAAAATGCTGCTCTCAGCCTCCCACAATTAAACCGCATGTGATCTC NM_004104 RefSeq chr17 - 82078337 82098230 FASN 2194 fatty acid synthase
GO:0005515|GO:0005886|GO:0015939|GO:0006767|GO:0044281|GO:0035338|GO:0070402|GO:0042803|GO:0005829|GO:0005739|GO:0005737|GO:0047117|GO:0008144|GO:0019432|GO:0006631|GO:0071353|GO:0006633|GO:0004313|GO:0004312|GO:0044255|GO:0070062|GO:0042470|GO:0016295|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144305_PI430048170 0.0292173203659903 0.548967179719216 10.6375423248831 10.0713075595096 10.0949211890466 P P P 11.1424888528335 11.277482594453 11.0436510630476 P P P LNCV6_144305_PI430048170 mRNA
CCCCTTCCCTCCCCAGATATTTATGTGAAATGAACTGCAGCTTTATTTTTTGAAATAAAA NM_032673 RefSeq chr2 - 74505042 74507694 PCGF1 84759 polycomb group ring finger 1
GO:0031519|GO:0005515|GO:0035518|GO:0006355|GO:0008270|GO:0005654|GO:0005634|GO:0008022|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141535_PI430048170 0.396203219616727 0.730117447296144 0.462377477657543 0.475960094591805 0.280103179507418 A A A 0.405825033642316 1.46353797459261 0.456820689981531 A A A LNCV6_141535_PI430048170 mRNA
ATAACATCCATCGTGGCTCTGCCTTCAAAGGGAAATTTTACATATGTCACTGGGACCATC NM_004678 RefSeq chrY - 25030900 25052104 BPY2 NA "basic charge, Y-linked, 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127243_PI430048170 0.00508055510473269 0.541397373048824 2.27613006435078 2.30446932765595 2.55731127653258 A A A 3.29409559809442 3.30916670241638 3.20511799318314 P P P LNCV6_127243_PI430048170 mRNA
TCATCCATAGCTTTCTTCCTGATGGTGTTTGCATTATTGCGCCTTCCCAATCTGCATGCT NM_004562 RefSeq chr6 - 161347557 162727802 PARK2 5071 "parkin RBR E3 ubiquitin protein ligase, transcript variant 1"
GO:0005515|GO:0043130|GO:0004842|GO:0034976|GO:0006513|GO:0016874|GO:0044314|GO:0010906|GO:0042802|GO:0051583|GO:0043524|GO:0046329|GO:0042787|GO:0031072|GO:0007612|GO:0044257|GO:0043123|GO:0046676|GO:0006979|GO:0031625|GO:0031624|GO:0000209|GO:0005794|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127938_PI430048170 0.644075143154119 0.982475211422402 0.429104224389988 0.451706456506113 0.419727283499778 A A A 0.51184430876328 0.491890712776632 0.369430468172584 A A A LNCV6_127938_PI430048170 mRNA
TGGCCTTAATCCATTATAGCAGCCGTGATGTCATTTCTGTATTTCAGGAAGACTGGCAGA NM_021016 RefSeq chr19 - 42721641 42740516 PSG3 5671 pregnancy specific beta-1-glycoprotein 3
GO:0007565|GO:0006952|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65432_PI430048170 0.992978898076284 1.00187229361464 7.45160415833561 7.21912543261785 7.48179660680556 P P P 7.2739400945507 7.50028952065654 7.37531838335763 P P P LNCV6_65432_PI430048170 mRNA
GATGATGACTTTTGATAGTGAAGTTGAGTTGATGAAAGTTGCCAGAGCACATCCCAAAGC NM_002539 RefSeq chr2 - 10440370 10448554 ODC1 4953 "ornithine decarboxylase 1, transcript variant 1"
GO:0008284|GO:0042176|GO:0001822|GO:0004586|GO:0006521|GO:0033387|GO:0044281|GO:0005575|GO:0009615|GO:0042803|GO:0005829|GO:0034641|GO:0005737|GO:0006595 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142813_PI430048170 0.624573113806746 0.864135316685766 1.76929365272716

2.44395185805692 2.06204570585662 A A A 2.63428905461765 1.71352881029432
2.48172814664534 A A P LNCV6_142813_PI430048170 mRNA
GAGGGAAGTAAGCCAGGAAGAATAAAACTGCTGAATGTTTGTATGTGTAAGATATTTCCA NM_176877 RefSeq chr1
+ 61742476 62163919 INADL 10207 InaD-like (Drosophila)
GO:0035556|GO:0005515|GO:0043234|GO:0048471|GO:0016324|GO:0070830|GO:0005886|GO:0034329|GO:0005
923|GO:0045216|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_37990_PI430048170 0.4204413049861740.9162326369606610.3603925588954160.356462332645213
0.287326481578309 A A A 0.3383058184274730.6838893995264670.333073036059297 A A A
LNCV6_37990_PI430048170 mRNA
ATTTTCTGGAGCCAGTAAACAATATCACCATTGTCCAAGGCCAGACGGCAATTCTGCACT NM_004560 RefSeq chr9
- 91722595 91950162 ROR2 4920 receptor tyrosine kinase-like orphan receptor 2
GO:0005515|GO:0017147|GO:0008285|GO:0005886|GO:0001756|GO:0090263|GO:0007223|GO:0030154|GO:0005
109|GO:0030538|GO:0090090|GO:0060071|GO:0030335|GO:0042472|GO:0007254|GO:0007275|GO:0018108|GO:0
005524|GO:0007165|GO:0005887|GO:0001502|GO:0004714|GO:0045893|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135670_PI430048170 0.5280973326614791.34755080097561 0.28435741820254
1.61982584325512 0.502056176684283 A A A 0.33099500495495 0.780863131130854
0.332743579342722 A A A LNCV6_135670_PI430048170 mRNA
AGATGAATTATGGAGGATTCATTGCCTCCAGGACTTCAAGGAAGAAAAGCCACAGGAGCA NM_145653 RefSeq
chr18 - 47028201 47030078 TCEB3C 162699 transcription elongation factor B polypeptide 3C (elongin
A3) GO:0006355|GO:0005634|GO:0016021|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_69660_PI430048170 0.9567279866172071.01921068029716 3.67927515187765 3.22593899471521
3.05892072490531 P P P 3.0789109339856 3.36061809549383 3.48594378613626 P P P
LNCV6_69660_PI430048170 mRNA
GAAATGGGAATGTACACGATAATTAAAGAGTAAAGTTGTGCTCAACGCTGTTTACTTCTA NM_018169 RefSeq chr12
+ 31959418 31993107 KIAA1551 55196 KIAA1551 NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_110869_PI430048170 0.1845790437273991.40800108646451 5.36307783871261
5.75740578919144 5.70146824268804 P P P 5.53072848676376 5.11406469646632
4.56964936413003 P P P LNCV6_110869_PI430048170 mRNA
ATAGAAATTGTTAATTTTAACAATCCAGAGCAGGCCAACGAGGCTTTGCTCTCCCGACCC NM_006988 RefSeq chr21
- 26836286 26845409 ADAMTS1 9510 "ADAM metallopeptidase with thrombospondin type 1 motif, 1"
GO:0008285|GO:0001822|GO:0001542|GO:0031410|GO:0005604|GO:0060347|GO:0005737|GO:0007229|GO:0006
508|GO:0008270|GO:0004222|GO:0008201|GO:0008237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138597_PI430048170 0.0295324738826553 1.54657320322311 10.2293594995725
10.3059521346501 10.2505166415992 P P P 9.81865838427591 9.64490801184004
9.40675182176187 P P P LNCV6_138597_PI430048170 mRNA
CCGGTATCATCAGTGGCATGCGGTCCCATTGTGAAATAGCTGTGTTCATCGATGGACCCC NM_001160389 RefSeq
chr11 - 64223798 64226254 TRPT1 83707 "tRNA phosphotransferase 1, transcript variant 3"
GO:0045859|GO:0006388|GO:0000215 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133443_PI430048170 0.4646890376793570.6366216038546160.379303685813074
0.37740920510302 0.435324111491415 A A A 1.87476326656162 0.317303962224635
0.372120405410989 A A A LNCV6_133443_PI430048170 mRNA
CTGAACCTTATGAAATATATGTATTTCATGGTACGTATTCTCTAGCACAGTCTGAGCAAT NM_144646 RefSeq chr4
- 70655540 70666631 JCHAIN NA "immunoglobulin J polypeptide, linker protein for immunoglobulin
alpha and mu polypeptides" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130164_PI430048170 0.0291447234412752 0.7240276642921499.3333424784611
9.24263481632179 9.42604634182034 P P P 9.79024183167355 9.61718639859679

9.97577907898715 P P P LNCV6_130164_PI430048170 mRNA
AGTCAGGTTGTAATACAGGCCAAGCAGACGGGCTTTGAGGGCATTTAGTCTCAGAAAAAA NM_022070 RefSeq chr17
- 60043190 60078931 HEATR6 63897 HEAT repeat containing 6 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_118240_PI430048170 0.471877007918145 1.14997288128064 5.19806642859745
5.08849265688224 4.71447697150322 P P P 5.13106453800324 4.86587816190726
4.33174904025058 P P P LNCV6_118240_PI430048170 mRNA
GCATCCGGGTCACGCTAACGCCGCGGTTTCCTCCGCTCGATTGGTTCTACTGTGGGTCTG NM_001990 RefSeq chr1
- 27970343 28088637 EYA3 2140 "EYA transcriptional coactivator and phosphatase 3, transcript variant 1"
GO:0005515|GO:0005667|GO:0005813|GO:0006355|GO:0016576|GO:0005634|GO:0007275|GO:0045739|GO:0009653|GO:0046872|GO:0035335|GO:0006351|GO:0006302|GO:0005737|GO:0010212|GO:0003682|GO:0005654|GO:0008138|GO:0007601|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132213_PI430048170 0.547377976334068 0.915734937819204 0.274047336158278
0.288840521976723 0.485639265548297 A A A 0.333819275637798 0.289764295583448
0.766216894957536 A A A LNCV6_132213_PI430048170 mRNA
CGAAAGAAGTCTGTATGAAAATCAGTTCTTTGCTGACACAAGTTCCATTTGTTACAAATG NM_002839 RefSeq chr9
- 8314245 10612723 PTPRD 5789 "protein tyrosine phosphatase, receptor type, D, transcript variant 1"
GO:0005515|GO:0005102|GO:0006796|GO:0035335|GO:0097105|GO:0006470|GO:0005001|GO:0005887|GO:0030182|GO:0050775|GO:0007185|GO:0050839|GO:0007157|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_137142_PI430048170 0.608820985765289 2.9550941297955 3.72290423117973
0.270585164032901 0.348443424873574 P A A 1.36259612781001 0.339393948934466
0.556379056154719 A A A LNCV6_137142_PI430048170 mRNA
ACTGAGTATGACAATGTTGTACTAAAGAAAGGCCCAAAGTGACAGAGGCAGCAGAGGGAT NM_003974 RefSeq
chr8 - 21908872 21913694 DOK2 9046 "docking protein 2, 56kDa"
GO:0007165|GO:0007596|GO:0005158|GO:0005068|GO:0007265|GO:0005057|GO:0050900|GO:0007169|GO:0007166|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_85637_PI430048170 0.952400289850006 0.987379598557453 2.86362913621555 3.33879765106447
2.56349301160018 A P A 2.51989138158051 3.02051328373722 3.28619893370859 A P P
LNCV6_85637_PI430048170 mRNA
AAGTTGAGCCACCTTTGGAAGACGCACGGGTGGAGTTTGCCAGAAGAAAGGCTGTGCCAG NM_015259 RefSeq
chr21 - 44226826 44241004 ICOSLG 23308 "inducible T-cell co-stimulator ligand, transcript variant 1"
GO:0042113|GO:0042104|GO:0007165|GO:0042110|GO:0005886|GO:0031295|GO:0005102|GO:0006952|GO:0016021|GO:0006972|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126633_PI430048170 0.439335509724029 0.920713436241054 0.560990425870318
0.501198612239969 0.273867743038994 A A A 0.414014987574815 0.762187774814914
0.510263350788678 A A A LNCV6_126633_PI430048170 mRNA
GTGCGACAGAATGCAGTTAGAATCAGTTCATATCACCATTAAAATCATCCATTCAGAAAC NM_001097634 RefSeq
chr9 + 76441665 76507416 GCNT1 2650 "glucosaminyl (N-acetyl) transferase 1, core 2, transcript variant 1"
GO:0005515|GO:0005802|GO:0032868|GO:0003829|GO:0031985|GO:0016266|GO:0050901|GO:0005615|GO:0060352|GO:0009101|GO:0000139|GO:0006493|GO:0060993|GO:0048729|GO:0016021|GO:0044267|GO:0043687 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126649_PI430048170 0.573918348977051 0.987256170202362 0.415700806153336
0.422823236480665 0.359214382388214 A A A 0.460406900502858 0.384604852010511
0.408028298187947 A A A LNCV6_126649_PI430048170 mRNA
CATACTCTGTAACAGTTGCATTGACTGTCACATAATGCTCATACTTATCTAATGTTGAGT NM_000771 RefSeq chr10

+ 94938657 94989391 CYP2C9 1559 "cytochrome P450, family 2, subfamily C, polypeptide 9"
GO:0019369|GO:0018676|GO:0034875|GO:0006805|GO:0017144|GO:0018675|GO:0070989|GO:0044281|GO:0043
603|GO:0043231|GO:0004497|GO:0005737|GO:0032787|GO:0008144|GO:0019627|GO:0016712|GO:0008202|GO:0
008392|GO:0005506|GO:0008395|GO:0019373|GO:0016098|GO:0052741|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_115441_PI430048170 0.1413172062400550.7813924363263332.66209062647051
3.06733270252496 2.52375572416915 A A A 3.18950525974758 3.03992809129874
3.14400257673833 P P P LNCV6_115441_PI430048170 mRNA
CCTGGTGCCTTTTTAAATAAATTGCTGAAATTTGGCTGGAGAACTTTTAGAAGAAACAGG NM_199227 RefSeq chr2
+ 171999896 172080859 METAP1D 254042 methionyl aminopeptidase type 1D (mitochondrial)
GO:0070084|GO:0005739|GO:0004177|GO:0070006|GO:0008235|GO:0006508|GO:0018206|GO:0046872|GO:0031
365 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127042_PI430048170 0.0295555065372478 0.2647030592396930.410031870845016
0.4423814317823190.458503798596162A A A 1.63423057439529 2.60339153869658
2.62361410282158 A P P LNCV6_127042_PI430048170 mRNA
ATTCTTGCTGAACCGTTTGTGATTGCCATTTGAGCTCTGGAAGCCTCTATTGCCATGAGA NM_001281443 RefSeq
chr19 + 35666515 35678485 UPK1A 11045 "uroplakin 1A, transcript variant 2"
GO:0016324|GO:0005886|GO:0005783|GO:0030855|GO:0016021|GO:0048029|GO:0051259|GO:0042803|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136521_PI430048170 0.0319420069091582 0.5604534526985474.97017615855369
4.86533060017483 4.8175636555809 P P P 5.37038767866214 5.89657839297106
5.84075954760226 P P P LNCV6_136521_PI430048170 mRNA
CTAGATTGGATGTGTGTGTTCTAAGAAGTTGTCATAAATAAAACCTGAATGACCAATGTC NM_001252100 RefSeq
chr1 - 200969385 201023700 KIF21B 23046 "kinesin family member 21B, transcript variant 1"
GO:0008017|GO:0005871|GO:0005737|GO:0008152|GO:0005874|GO:0003777|GO:0016887|GO:0005524|GO:0007
018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143916_PI430048170 0.0486691487225251 0.8661317693564826.15565341541094
6.01383836857045 6.20898594120469 P P P 6.25592038809912 6.36334088873519
6.38494165739018 P P P LNCV6_143916_PI430048170 mRNA
GCTCCAAAATGACTCGGATTAAGGGCAAGTGCCAGTGATGGGTAGAAATAACGTTATCCT NM_139015 RefSeq chr12
- 120762509 120904352 SPPL3 121665 signal peptide peptidase like 3
GO:0005791|GO:0030660|GO:0071556|GO:0071458|GO:0006509|GO:0042803|GO:0042500 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_61454_PI430048170 0.1636701510814040.8372667301569131 0.3578272486793 10.047682541463
10.076262346565 P P P 10.310033372147 10.6373323522462 10.2975735078542 P P P
LNCV6_61454_PI430048170 mRNA
AAGGTGTACTTCGCTGAGAAGGTGACGTCTCTGGGCAAGGATTGGCACCGGCCCTGCCTG NM_001270837 RefSeq
chr14 + 105472937 105480170 CRIP2 1397 "cysteine-rich protein 2, transcript variant 2"
GO:0031012|GO:0030097|GO:0008284|GO:0008270|GO:0005938 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138557_PI430048170 0.7455019336697081.01426385974434 0.466397767023375
0.5177644887160370.52591100826746 A A A 0.5584152435179460.519318966564779
0.36456047982141 A A A LNCV6_138557_PI430048170 mRNA
GCTCCGTGTGTTAAAAAACAGCTGTATTTTATGTATGCTTTACTGATAAGTGTGCCAATA NM_001304435 RefSeq
chr4 - 16501533 16898809 LDB2 9079 "LIM domain binding 2, transcript variant 4"
GO:0003712|GO:0005667|GO:0044089|GO:0010669|GO:0045944|GO:0030274|GO:0005634|GO:0019899|GO:0035
019|GO:0001942 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100397_PI430048170 0.0208682953450942 0.6864073188337974.67605607814021
4.55647938468442 4.75132793990501 P P P 5.06226759487984 5.12255697558669

5.40988029449844 P P P LNCV6_100397_PI430048170 mRNA
GACTCGTGGTGGCACATTTTATGTTGAGCCAGCAGAGAGATATATTAAAGACCGAACTCT NM_001110RefSeq chr15
- 58595203 58749978 ADAM10 102 ADAM metallopeptidase domain 10
GO:0005515|GO:0017124|GO:0008284|GO:0007220|GO:0005886|GO:0030307|GO:0007267|GO:0051089|GO:0005
634|GO:0051088|GO:0042803|GO:0043231|GO:0005737|GO:0022617|GO:0007173|GO:0007219|GO:0030198|GO:0
007411|GO:0030574|GO:0006509|GO:0070062|GO:0030335|GO:0005794|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142483_PI430048170 0.0299582608089199 1.62889641519963 9.02185838701229
8.82637634930954 8.47100308707528 P P P 8.16890841164313 8.18432079855892
7.88848177477449 P P P LNCV6_142483_PI430048170 mRNA
GGACAGTCACATAGGAGCGTGTAGTCGTGACTGAATAAAGAAAGCAAAAGCCTGAAAAAA NM_004192RefSeq
chrY - 1403138 1452977 ASMTL 8623 "acetylserotonin O-methyltransferase-like, transcript variant
1" GO:0008150|GO:0003674|GO:0005737|GO:0032259|GO:0008171 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_145553_PI430048170 0.6666283049637210.7947027913201912.23557435887431
2.84662529370761 3.40652322367326 A A P 2.15314894965655 3.54827724124785
3.60573652082823 A P P LNCV6_145553_PI430048170 mRNA
GCTGATGCTTCAAAGAGCTTAGTTTGCGGTTTCCTGGACGTGGAAACAAGTATCTGAGTT NM_014314RefSeq chr9
- 32455301 32526324 DDX58 23586 DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
GO:0005515|GO:0003725|GO:0003727|GO:0015629|GO:0042993|GO:0005829|GO:0042802|GO:0051091|GO:0005
737|GO:0003690|GO:0045944|GO:0009597|GO:0016032|GO:0032480|GO:0030334|GO:0032728|GO:0034344|GO:0
032727|GO:0004386|GO:0032587|GO:0009615|GO:0005524|GO:0039529|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_95280_PI430048170 0.1585884809392761.17906864237033 8.86860173610085 8.87490329558709
9.20148969880707 P P P 8.7490289230576 8.66330879825722 8.84002543875215 P P P
LNCV6_95280_PI430048170 mRNA
ACAGCAGACTACAGGTAAATGGTATCCCTGAAGAAAGAAAACTGACTGAAGCAATGAATTNM_001099401 RefSeq
chr7 - 94585223 94656209 SGCE 8910 "sarcoglycan, epsilon, transcript variant 1"
GO:0042383|GO:0032590|GO:0007517|GO:0005794|GO:0016010|GO:0007160|GO:0005886|GO:0005887|GO:0016
012|GO:0005509|GO:0005856|GO:0030425 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134606_PI430048170 0.4646193863430790.9181677566200084.51897809752629
4.90495215523231 4.56167785615433 P P P 4.98447808326733 4.68964991273518
4.69248373824781 P P P LNCV6_134606_PI430048170 mRNA
TGAAAAAACACAGAATGAGGAGGCATGAGTCAATTTGCCCCACCCTGTCTGACTGTACTT NM_001242521 RefSeq
chr1 - 23010833 23015850 C1orf234 729059 chromosome 1 open reading frame 234 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_137482_PI430048170 0.3053530140862020.8168883361440395.33811808591232
5.15484551156082 4.66535117319 P P P 5.28279845721105 5.65343631494325 5.12643025730127 P
P P LNCV6_137482_PI430048170 mRNA
GAGCCATCCTACGCCTTCCCTCAGCTCTGCTACTCAATAAATCGGTGTCCCTTCAAAAAA NM_001146334 RefSeq
chr7 - 45080436 45088894 NACAD 23148 NAC alpha domain containing
GO:0005737|GO:0005634|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136848_PI430048170 0.5136388244330891.40837530508458 1.66486455033366
0.4445709546394760.246311519221061 A A A 0.3861953020291180.483282832724354
0.438374300328404 A A A LNCV6_136848_PI430048170 mRNA
GGACTGAATATACCTGGGGTATCCTATCTTGTACAAATGCATGCTTTTTCATTAAATTTG NM_001480RefSeq chr18
+ 77250051 77270140 GALR1 2587 galanin receptor 1
GO:0005515|GO:0005886|GO:0007586|GO:0004966|GO:0007194|GO:0007204|GO:0042923|GO:0007218|GO:0045
944|GO:0007189|GO:0016021|GO:0017046|GO:0051464 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_105455_PI430048170 0.73136201425756 1.61218818786525 0.469441988442079
3.37514865487055 3.19667053827448 A P P 2.87232505779568 1.67576031446983
1.30115926158017 P A A LNCV6_105455_PI430048170 mRNA
ATAGAACTTCATCTGCCTCCTCTGGACAGGGGATTTTTTCTTTCAGACCATCCCCAAATG NM_001282322 RefSeq
chr14 + 23237917 23274285 RNF212B NA ring finger protein 212B NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133262_PI430048170 0.3755297689363640.5239562188916811.19850714516992
0.5348355481364110.482194663857744A A A 2.59826208960043 1.22887049834756
0.497583924426484A A A LNCV6_133262_PI430048170 mRNA
GTGGTCTCCATCCTGACTCTTGAACTTACCCACAATAAGAATAAATTCTGCCTCATCTTT NM_020526RefSeq chr1
+ 22563510 22603594 EPHA8 2046 "EPH receptor A8, transcript variant 1"
GO:0043005|GO:0033628|GO:0048013|GO:0005886|GO:0006929|GO:0018108|GO:0005524|GO:0030155|GO:0031
175|GO:0016322|GO:0005004|GO:0046777|GO:0043552|GO:0005887|GO:0007411|GO:0031901|GO:0043410|GO:0
007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127659_PI430048170 0.4579165946995850.868885104613279 8.55984841500909
8.63005502871487 8.92519237317964 P P P 8.63455285422031 8.77501420580079
9.26275972599224 P P P LNCV6_127659_PI430048170 mRNA
CATCTCATTCTTCACTTCCTGTAAACCACTCCATAGATTTGTCTTTCTTCAAGAAATTAG NM_017910RefSeq chr2 -
28849820 28870309 TRMT61B 55006 tRNA methyltransferase 61B
GO:0005739|GO:0005515|GO:0070901|GO:0031515|GO:0016429|GO:0051260 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106359_PI430048170 0.6437679553843160.9559664146038791 2.4067392281493
12.4919963151085 12.8046038741268 P P P 12.6317938139444 12.5176011143707
12.7689064910944 P P P LNCV6_106359_PI430048170 mRNA
CTCACAGACTAGAACTTAACGGAACAAGTCTAGGACAGAAGTTAAGATCTGATTATTTAC NM_004708RefSeq chr19
+ 32581187 32587452 PDCD5 9141 programmed cell death 5
GO:0005515|GO:0008285|GO:0043065|GO:0048487|GO:0071560|GO:0005634|GO:0003677|GO:0010628|GO:0043
280|GO:0005737|GO:0010698|GO:0090200|GO:0008201|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_76895_PI430048170 0.0192950021237901 1.67735955167933 3.91745928504605
3.65365239816697 4.1558143888316 P P P 2.91366546098428 3.23539123424992
3.34836491519357 P P P LNCV6_76895_PI430048170 mRNA
ACAACTTTTTATCGAACAGCGAGGAATATCATGAGCATGTGTTTCAGCAAGGAGCCTGCC NM_004973RefSeq chr6
+ 15245974 15522042 JARID2 3720 "jumonji, AT rich interactive domain 2, transcript variant 1"
GO:0010467|GO:0008285|GO:0032452|GO:0048538|GO:0005634|GO:0000122|GO:0048536|GO:0007417|GO:0003
677|GO:0006351|GO:0048863|GO:0001889|GO:0031061|GO:0051574|GO:0035097|GO:0035098|GO:0045814|GO:0
003682|GO:0040029|GO:0005654|GO:0045892|GO:0016568 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_57688_PI430048170 0.0690997785940363 1.29694111242297 7.88340576441217
7.86371507632788 7.72882695798175 P P P 7.58046297407943 7.54181526639465
7.20434681625848 P P P LNCV6_57688_PI430048170 mRNA
TGCAATGGCTCCAAGATAGCGACTACAACCCCAATTGCCGCCTGTGCAACATACCCCTGG NM_006782RefSeq chr11
+ 65084221 65088402 ZFPL1 7542 zinc finger protein-like 1
GO:0006355|GO:0005794|GO:0008270|GO:0005634|GO:0016021|GO:0016192|GO:0003677 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135635_PI430048170 0.9686741641930650.997855970886298 8.35268666328785
8.25781815110213 8.07002655110869 P P P 8.0420721905734 8.50625937474045
8.11097173806707 P P P LNCV6_135635_PI430048170 mRNA
GCACCTCCATCTTTGTGGATAATAAATAAATATGCACAGGTTCTGAGACTGAGTAAAAAA NM_033025RefSeq chr19

+ 15107363 15114988 SYDE1 85360 "synapse defective 1, Rho GTPase, homolog 1 (C. elegans), transcript variant 1"
GO:0051056|GO:0016081|GO:0007264|GO:0050806|GO:0097060|GO:0044300|GO:0032862|GO:0007130|GO:0032403|GO:0005100|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137003_PI430048170 0.00569926017984221 1.28557845344803 10.8633560724635 10.8492887162469 10.9841713422882 P P P 10.4423683414906 10.6138006659541 10.5520444668236 P P P LNCV6_137003_PI430048170 mRNA
TGCAGACTGATGCCTTTGTCTCTAATGAGCTAGATGACCCTGATGATCTGCAATGTAAGC NM_001034116 RefSeq
chr2 - 27364351 27370457 EIF2B4 8890 "eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa, transcript variant 2"
GO:0005515|GO:0010467|GO:0051716|GO:0009408|GO:0003743|GO:0043434|GO:0006412|GO:0006413|GO:0005829|GO:0005085|GO:0005737|GO:0001541|GO:0019509|GO:0045947|GO:0005851|GO:0042552|GO:0006417|GO:0009749|GO:0043547|GO:0032057|GO:0014003|GO:0006446|GO:0031369|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139504_PI430048170 0.00371092669893614 3.07691751393958 2.44708931114553 2.1534688841412 1.86187419786284 A A A 0.3123047258119030.334792061001113 0.923428372482816A A A LNCV6_139504_PI430048170 mRNA
AGCTTTTAGAGTGAGCTCAAATCTTACTGGACATAAGAAAAGAAAACATCAAGTATGGAG NM_001010877 RefSeq
chr6_GL000252v2_alt - 260419 270863 ZNF311 282890 zinc finger protein 311
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140110_PI430048170 0.1309857856041421.12362053339764 11.1483923695474 10.9555908231379 10.9240654830205 P P P 10.8872336915785 10.74777409971 10.8942669234746 P P P LNCV6_140110_PI430048170 mRNA
TTGCCTCACATTTGCAGGTAATATCAAGCAGCAAACTAAATTCTGAGAAATAAACGAGTC NM_022163RefSeq chr15 - 88459477 88467402 MRPL4626589 mitochondrial ribosomal protein L46
GO:0070124|GO:0070125|GO:0070126|GO:0006996|GO:0030054|GO:0032543|GO:0005743|GO:0005575|GO:0005739|GO:0003674|GO:0008150|GO:0016787|GO:0005840|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141856_PI430048170 0.5469522742040441.21159881354448 1.00210119714637 2.0311994945486 1.3802765499471 A A A 1.38702407076156 1.35380091072558 1.00290638527442 A A A LNCV6_141856_PI430048170 mRNA
TATTAAGAAGATCCTTCAGAGCAACGATTGCATAGAAGCAGCCTTCTGATCTGAGGACCC NM_001025591 RefSeq
chr19 - 34593440 34594585 SCGB2B2 284402 "secretoglobin, family 2B, member 2" GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129381_PI430048170 0.00773102283030637 0.3847101881588273.63747865583398 2.98421491193177 3.59199380547315 P P P 4.51119707627652 4.90156516892731 4.98042698337995 P P P LNCV6_129381_PI430048170 mRNA
CCTGAAAGCATTCAGAATCTGTGACACGTATTGACTTCATGCTTTGAGATTCAAAATTTA NM_001031835 RefSeq
chr16 + 47461298 47701523 PHKB 5257 "phosphorylase kinase, beta, transcript variant 2"
GO:0005515|GO:0005516|GO:0005886|GO:0004689|GO:0005975|GO:0005964|GO:0005977|GO:0044281|GO:0006091|GO:0004553|GO:0005829|GO:0009405|GO:0006006|GO:0006468|GO:0005980 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129406_PI430048170 0.0180384694707895 1.40718978509827 11.0599505268285 11.02627571019 11.3134412488646 P P P 10.5801544371567 10.5247996075947 10.8167219577715 P P P LNCV6_129406_PI430048170 mRNA
CAGACCTAACAAATATTTGAGGTCAGAACCCTACCATGTTAAAACAAACAAAAACTTACC NM_033296RefSeq chr4 + 6640090 6642743 MRFAP1 93621 "Morf4 family associated protein 1, transcript variant 1"
GO:0005515|GO:0048471|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_132767_PI430048170 0.4673294476289050.7143475529376270.387259776405458
0.3640492320892920.404011513951203A A A 0.3096753776097361.56142585678157
0.371852296919342A A A LNCV6_132767_PI430048170 mRNA
GAGCTGAGATTGTTGGTTTTACTTTGGATACCGCTGGTTTTCCACATATATAGATAGATA NM_001080474 RefSeq
chr2 + 73784188 73817147 C2orf78 388960 chromosome 2 open reading frame 78 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_74537_PI430048170 0.8736132582386141.06027651328369 3.18141168171831 4.00114033026063
3.89030270783762 A P P 3.54559996958484 3.8358262411265 3.54695778278079 P P P
LNCV6_74537_PI430048170 mRNA
CAGGAATTTCTATTGGAATACTGGGCTGCTATGTCTCAGGAGTATTTTACGCATTTTATT NM_001040202 RefSeq
chr4 - 78917939 78939428 PAQR3 152559 progestin and adipoQ receptor family member III
GO:0005794|GO:0000139|GO:0033137|GO:0043407|GO:0034067|GO:0010977|GO:0001933|GO:0004872|GO:0016
021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144433_PI430048170 0.0305112048390542 1.4442002016706 6.92092586920707
6.88051315632832 7.22880746949081 P P P 6.55360385055392 6.42012026248274
6.48834500926019 P P P LNCV6_144433_PI430048170 mRNA
CAAGAGGTTATCTGTTCTTTTCCGGGAAAGGGGTGGTATGCACCTGAAATAGATTTTACC NM_016334 RefSeq chr1
+ 147928392 147993521 GPR89B 51463 G protein-coupled receptor 89B
GO:0005244|GO:0000139|GO:0034765|GO:0016021|GO:0015031|GO:0006811 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_109553_PI430048170 0.0982984095694046 1.06498952130375 0.456328675693133
0.5282835846173220.522650051920967A A A 0.3503713405171370.416146145010402
0.466966906156591A A A LNCV6_109553_PI430048170 mRNA
CCACAAACCATGGATTTATTCCTAAACTACTCCATGAACATGCAACCTGAAGACGTGTGA NM_024865 RefSeq chr12
+ 7789395 7796061 NANOG 79923 "Nanog homeobox, transcript variant 1"
GO:0008406|GO:0010468|GO:0008284|GO:0003700|GO:0008283|GO:0017145|GO:0001710|GO:0005634|GO:0001
714|GO:0030154|GO:0009880|GO:0030514|GO:0045944|GO:0032526|GO:0035019|GO:0006355|GO:0010454|GO:0
003714|GO:0005730|GO:0000122|GO:0003677|GO:0006351|GO:0045931|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141452_PI430048170 0.1516084896844691.05931069085609 0.458009032230874
0.4495192926430040.495526326729757A A A 0.3177011215114460.381320108608442
0.451945012337341A A A LNCV6_141452_PI430048170 mRNA
AGTCTGCATGGTTAAAAGTAGTCATGGATAACTACATTACCTGTTCTTGCCTAATAAGTT NM_001553 RefSeq chr4
- 57031070 57110385 IGFBP7 3490 "insulin-like growth factor binding protein 7, transcript variant 1"
GO:0005515|GO:0048839|GO:0008285|GO:0009408|GO:0007566|GO:0050810|GO:0005576|GO:0001558|GO:0005
615|GO:0032870|GO:0051414|GO:0031012|GO:0032526|GO:0007155|GO:0070062|GO:0005520 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143905_PI430048170 0.4610483891401591.50056066971835 1.7120511730858
0.2713933236624360.350018211668168A A A 0.4070892981335880.339366829315421
0.317186540664273A A A LNCV6_143905_PI430048170 mRNA
CAAGTGAAGCAAGCCTTCAAGAGCATGGTCCAGAAGATGATTTTTTCTTTAAATAAATGA NM_001005497 RefSeq
chr12 + 55365110 55366049 OR6C75 NA "olfactory receptor, family 6, subfamily C, member 75" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134104_PI430048170 0.3302566102208111.62722989618394 3.48913375866298
1.92582615819569 2.71808590300787 P A A 1.29816071500731 2.61170178267458
2.23506227659403 A P A LNCV6_134104_PI430048170 mRNA
AATGTAGTCAGCAAAATGGGGGTGGGGAAGCAGAGCATGTCCTAGTTCAATGTTGACTTT NM_002825 RefSeq chr7
- 137227345 137343800 PTN 5764 pleiotrophin
GO:0008284|GO:0005783|GO:0004864|GO:0007185|GO:0051781|GO:0030282|GO:0007612|GO:0043086|GO:0008

201|GO:0008083|GO:0005615|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141490_PI430048170 0.3996180321696361.10245010186543 9.7057038868229
9.95842402709382 10.0496037695745 P P P 9.7406985522976 9.58387057985679
9.96327848083854 P P P LNCV6_141490_PI430048170 mRNA
CAATGCTCTGGGGTCTTTTTATGCATTTGCATTTGCTCTTTCATCTCTGCTTGGATTATT NM_001080125 RefSeq chr2
+ 201258030 201287711 CASP8 841 "caspase 8, apoptosis-related cysteine peptidase, transcript variant G"
GO:0005515|GO:0060715|GO:0031265|GO:0009409|GO:0031264|GO:0032403|GO:0007507|GO:0002756|GO:0030
101|GO:0051603|GO:0006508|GO:0032496|GO:0032025|GO:0005856|GO:0043123|GO:0032355|GO:0060546|GO:0
046677|GO:0031625|GO:0043124|GO:0005164|GO:0046982|GO:0005815|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129522_PI430048170 0.3000904995130841.25091610454893 5.28337640013019
5.54740787537677 4.81837126976697 P P P 5.14142740915229 4.86171158696019
4.73895856252569 P P P LNCV6_129522_PI430048170 mRNA
ATTCCTGAAATTATTTAAAGGGGTTGGCCGGGCTCCCACCAGGGCCTGGGTGGGAAGGTA NM_005018RefSeq
chr2_KI270776v1_alt - 61978 71004 PDCD1 5133 programmed cell death 1
GO:0005515|GO:0007165|GO:0005886|GO:0006959|GO:0031295|GO:0006915|GO:0070234|GO:0007275|GO:0016
021|GO:0004871|GO:0009897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140938_PI430048170 0.6824585575453121.12398636813404 2.17703399703466
1.95591937915003 2.82807448771145 A A A 2.12010499983057 1.96185628898439
2.47251146959205 A A A LNCV6_140938_PI430048170 mRNA
GGCTGTGGCATTGTTGATGCTCACATATGATAAAAAAGTGTCCTATAATTCTATTGAAAG NM_003469RefSeq chr2
- 223596939 223602499 SCG2 7857 secretogranin II
GO:2001237|GO:0009306|GO:0006928|GO:0001525|GO:0005125|GO:0005615|GO:0042056|GO:0050918|GO:0050
930|GO:0035556|GO:0006954|GO:0001938|GO:0000165|GO:0001937|GO:0043542|GO:0048245|GO:2000352|GO:0
030141 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135349_PI430048170 0.0955509223149453 1.05707398200319 0.440649279978818
0.4944325078802090.494587477581497A A A 0.3441419175267850.397091933143143
0.447039396275617A A A LNCV6_135349_PI430048170 mRNA
GCTTAGTCTGAAAGGTGTGTGGCATTCATGGCAATCCTGTAACTTCAACATAGATTTTTT NM_006998RefSeq chr6
+ 25652200 25701780 SCGN 10590 "secretagogin, EF-hand calcium binding protein"
GO:0008150|GO:0005737|GO:0005509|GO:0005576|GO:0030658 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135844_PI430048170 0.2384546595903151.177437669701 0.35306267906919
0.7531328308126450.346444810734305A A A 0.2459122460198340.288117433296437
0.249962444208289A A A LNCV6_135844_PI430048170 mRNA
ACAGTCACTCTCACAGAATGTAAAAACTCTAATATTTAGCAGGAGAGCAAAGAAGTCTCA NM_001005567 RefSeq
chr11 - 5342513 5505652 OR51B5 282763 "olfactory receptor, family 51, subfamily B, member 5,
transcript variant 1" GO:0050911|GO:0007608|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123045_PI430048170 0.4278889535473490.8699139339275740.329887873850051
0.3437127601651940.339818294117753A A A 0.3358238043960360.334924586490231
0.875861433491296A A A LNCV6_123045_PI430048170 mRNA
GTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGTTCCCAGAGCTATGGGGACTTCC NM_006206RefSeq chr4
+ 54229096 54298245 PDGFRA 5156 "platelet-derived growth factor receptor, alpha polypeptide"
GO:0005515|GO:0001553|GO:0031226|GO:0048704|GO:0048701|GO:0042803|GO:2000249|GO:0030539|GO:0072
277|GO:0046777|GO:0007173|GO:0043552|GO:0030198|GO:0035790|GO:0055003|GO:0070374|GO:0038085|GO:0
030335|GO:0048407|GO:0023019|GO:0045740|GO:0014068|GO:0018108|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_72009_PI430048170 0.000343818327086298 0.7443804203657514.56631945949065

4.54622063340355 4.48604381231851 P P P 4.9289654402809 4.97609467116447
4.97192193875399 P P P LNCV6_72009_PI430048170 mRNA
TGGTTTTTGTTACAAATGCTGGGAACATCTTACAACACAGCAAAGCCCAGGAGCTGTCAG NM_033070 RefSeq chr22
- 17137519 17159279 CECR5 27440 "cat eye syndrome chromosome region, candidate 5, transcript
variant 2" GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137917_PI430048170 0.8517351169012080.986586693273 0.278500733308485
0.3026731514641560.466759877547304 A A A 0.5091701779064460.294634236036236
0.299370651178531 A A A LNCV6_137917_PI430048170 mRNA
ATTACTGACCTATGCTCTAAAACATGAATGCTTTGTTACAGACCCAAGCTGTCCATTTCT NM_001270399 RefSeq
chr12 - 49184794 49189324 TUBA1A 7846 "tubulin, alpha 1a, transcript variant 2"
GO:0005515|GO:0005881|GO:0051258|GO:0006996|GO:0019904|GO:0005874|GO:0003924|GO:0005634|GO:0005
525|GO:0005829|GO:0030705|GO:0006184|GO:0005198|GO:0006457|GO:0000086|GO:0005200|GO:0051084|GO:0
055037|GO:0007017|GO:0000278|GO:0044267|GO:0070062|GO:0051301 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_126728_PI430048170 0.0236463176483045 1.24548829948525 10.9763602940353
10.8562495256957 10.859668334317 P P P 10.4433975485836 10.6358186188421 10.656760469833
P P P LNCV6_126728_PI430048170 mRNA
TACCTGTAGCCCAGTGAAGGGTGTGTTTGGAACATTCATTAAATGATTCTAAGCATCTTG NM_032806 RefSeq chr3
- 43079228 43106083 POMGNT2 84892 "protein O-linked mannose N-acetylglucosaminyltransferase 2
(beta 1,4-)" GO:0008375|GO:0006493|GO:0005783|GO:0005789|GO:0016021|GO:0001764|GO:0035269 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138169_PI430048170 0.3456167804117310.8506829067390140.280791492834784
0.31513950276394 0.672834292763573 A A A 0.8772253098403790.746121541116503
0.322527958174039 A A A LNCV6_138169_PI430048170 mRNA
GAGTGGGGTGAAAGTCTATAAATGTAAGACATTTGGGAAAGCCTTCACACAGCCTTTTGA NM_021030 RefSeq chr19
- 19710471 19733112 ZNF14 7561 zinc finger protein 14
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_52105_PI430048170 0.00466843027783287 1.47251737290785 9.86439296255723
9.86874164843159 10.0850149910293 P P P 9.35045927123232 9.48660252953241
9.31152771298136 P P P LNCV6_52105_PI430048170 mRNA
TTCAGTGAAGGAGCGGACCATCTCTGAGAACAGCCTGATCATCCTACTGCAGGGCCTCCA NM_032881 RefSeq chr1
- 36393419 36397959 LSM10 84967 "LSM10, U7 small nuclear RNA associated"
GO:0005515|GO:0008380|GO:0006369|GO:0010467|GO:0015030|GO:0006366|GO:0008334|GO:1900087|GO:0031
124|GO:0005634|GO:0005683|GO:0005654|GO:0071208 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131217_PI430048170 0.9419773578585130.9970551267728520.472010086679723
0.5036116362340810.405505027541873 A A A 0.5417596456732430.420507014982489
0.430181416609647 A A A LNCV6_131217_PI430048170 mRNA
CCTTTGTTCACATTGCTATTTACTTTTGTGTTTGGGGGAAAATACGAGGGATTGATTTTA NM_181361 RefSeq chr3
+ 178536297 178844429 KCNMB2 10242 "potassium channel subfamily M regulatory beta subunit 2,
transcript variant 1"
GO:0005513|GO:0005886|GO:0007268|GO:0015459|GO:0019228|GO:0019229|GO:0005887|GO:0007596|GO:0008
076|GO:0001508|GO:0008200|GO:0006813|GO:0015269|GO:0071805 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133401_PI430048170 0.0482394975843549 0.7297919163902612.6578129605813
12.518044528636 12.4707008122603 P P P 13.2364795385168 12.8870362043034
12.8618179577047 P P P LNCV6_133401_PI430048170 mRNA
TGCAGCCCTGCGCCTTCCAGAAGCAGGTCCCAAATAAAGCCAGTGCCCACCTGCAAAAAA NM_182981 RefSeq chr16
+ 83953221 83966332 OSGIN1 29948 oxidative stress induced growth inhibitor 1

GO:0030308|GO:0043065|GO:0007275|GO:0005575|GO:0008083|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133866_PI430048170 0.00584931651337728 0.602239204228062 4.94671409721144 4.65573086792928 4.97039660584345 P P P 5.46188626403068 5.54648098236235 5.76307781968201 P P P LNCV6_133866_PI430048170 mRNA CATTGCACTTCTGTGTACAGTAAAACTGCTTTGTTTTACTAAAGAGAAAAATGTGAGTGG NM_024704 RefSeq chr20 - 16272103 16573434 KIF16B 55614 "kinesin family member 16B, transcript variant 2" GO:0001704|GO:0008017|GO:0017137|GO:0005871|GO:0043325|GO:0005874|GO:0080025|GO:0005547|GO:0032266|GO:0045022|GO:0005524|GO:0006895|GO:0001919|GO:0007173|GO:0007492|GO:0008543|GO:0032801|GO:0031901|GO:0008574|GO:0016887|GO:0005769|GO:0005768|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127300_PI430048170 0.48497926859932 0.845554204024129 0.545285397695365 0.44690551712523 0.555432203151377 A A A 1.18997464405842 0.524914695062856 0.438997346455732 A A A LNCV6_127300_PI430048170 mRNA CCATGGGAAAACCTGTATGCCGATTTTCCTCAAGCCATCTCACAAAATAAGAATTTCAAA NM_173557 RefSeq chr18 - 61815070 61893071 RNF152 220441 ring finger protein 152 GO:0004842|GO:0016874|GO:0006915|GO:0008270|GO:0016021|GO:0070936|GO:0005765|GO:0005764 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127208_PI430048170 0.209341977286479 0.73877515310501 0.305954319141216 0.345567641495902 0.370715580492073 A A A 1.10006073501744 0.796011531449917 0.337489890471609 A A A LNCV6_127208_PI430048170 mRNA GTGAAATCTCCCTGCATAGAGCAATTTAACATGTGAAATAGGCAATCCATTATCACATTA NM_139243 RefSeq chr4 + 122378965 122429792 ADAD1 132612 "adenosine deaminase domain containing 1 (testis-specific), transcript variant 1" GO:0006396|GO:0004000|GO:0003723|GO:0007286|GO:0007275|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110413_PI430048170 0.121688877778607 1.36250118132799 5.33662854588089 5.29650512931868 5.22324799490048 P P P 5.12618772859096 4.83506372366816 4.48879080076255 P P P LNCV6_110413_PI430048170 mRNA AAATGGACCAGACACTAATCATCAGAACCCCCAAAATAAGACCTCCCCATTCTCCGTGTC NM_001207025 RefSeq chr19 - 42086109 42132473 POU2F2 5452 "POU class 2 homeobox 2, transcript variant 1" GO:0043565|GO:0005737|GO:0003700|GO:0006366|GO:0006959|GO:0019904|GO:0002335|GO:0002380|GO:0048469|GO:0005634|GO:0045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135399_PI430048170 0.0251177261373372 0.64605262254928 8.88012295959486 8.71619635912738 9.07470638538597 P P P 9.30080608181554 9.47263452464268 9.77107789606952 P P P LNCV6_135399_PI430048170 mRNA GGGCCTTGTAAGTCTTTTCACCATTCATGAATAATAATAAATATGTACTGCTGGCATGTA NM_182796 RefSeq chr5 + 163503063 163519353 MAT2B 27430 "methionine adenosyltransferase II, beta, transcript variant 2" GO:0006805|GO:0005634|GO:0044281|GO:0032259|GO:0005829|GO:0005622|GO:0005739|GO:0050790|GO:0048270|GO:0006556|GO:0019899|GO:0006730|GO:0048269|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140514_PI430048170 0.00322091911364812 0.559246500077364 3.67022832184443 3.71707299220501 3.97563385445577 P P P 4.44640192590779 4.67741333735924 4.75591421093462 P P P LNCV6_140514_PI430048170 mRNA ATTTACTGGTTTTTCTTGTATCTGGTGCATAGCCAGAGTTCCACAGTAACAAATAATTTG NM_024685 RefSeq chr12 - 76344485 76348442 BBS10 79738 Bardet-Biedl syndrome 10 GO:0005515|GO:0001103|GO:0005929|GO:0001895|GO:0043254|GO:0051131|GO:0045494|GO:0035058|GO:0044267|GO:0007601|GO:0005524|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101581_PI430048170 0.567061369432855 0.90207344976372 3.29238848762795 3.20128555986402 3.02481027640334 P P P 2.95959119800541 3.3588160725793

3.58993512632981 P P P LNCV6_101581_PI430048170 mRNA
AGACCATACTCAGGAAGAGCCTGACTCCCTCTTGGAAGTGCCTGTGAGCTTCCCGCTGTT NM_173544RefSeq chr19
+ 17523300 17553839 FAM129C 199786 "family with sequence similarity 129, member C, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129577_PI430048170 0.0709237210452206 1.28560420192385 0.799788307639188
1.16184448147635 0.979567246519421A A A 0.827172037423176 0.492752031999502
0.533027034425672A A A LNCV6_129577_PI430048170 mRNA
CCCAGAACACTAGACACTTCAAATTGTTTTGTGAATAAAACTCAGAAATGAAGATGAGCT NM_022820RefSeq chr7
+ 99828012 99866106 CYP3A43 64816 "cytochrome P450, family 3, subfamily A, polypeptide 43,
transcript variant 1"
GO:0004497|GO:0006805|GO:0070330|GO:0005506|GO:0005789|GO:0044281|GO:0055114|GO:0020037 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103431_PI430048170 0.0976279567498754 0.922165980998026 7.06146192364551
7.18708990616585 7.143548861417 P P P 7.18612744870615 7.32170506103986
7.23449541278648 P P P LNCV6_103431_PI430048170 mRNA
TTCAATTTCAACAAACTGGTGCTGGTCAATTACCCATTCATTGATGTGGGGTTGGCTGGG NM_006494RefSeq chr19
- 42247560 42255164 ERF 2077 "Ets2 repressor factor, transcript variant 1"
GO:0060710|GO:0006366|GO:0000981|GO:0003714|GO:0060707|GO:0005634|GO:0000122|GO:0030154|GO:0005
829|GO:0043565|GO:0007049|GO:0005654|GO:0010668 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_118773_PI430048170 0.574243756111196 1.2600598684965 0.302068416061832
1.37349611602571 0.287059877171962A A A 0.510415110175721 0.419331416150129
0.311790821706316A A A LNCV6_118773_PI430048170 mRNA
TATGTTCATGTACATGAGACCAGCTTCTAAACATACGCCAGACCAGGACAAGATGGTGTC NM_017504RefSeq chr1
+ 248238928 248239864 OR2M4 NA "olfactory receptor, family 2, subfamily M, member 4"NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128914_PI430048170 0.138455924130396 0.576224107984251 5.18644218732119 5.4666615394244
4.9383617831146 P P P 5.43655087289465 6.54671700519934 5.81641982773539 P P P
LNCV6_128914_PI430048170 mRNA
AAGTAAACAGTGAGTTGGTTGCAAACTCTCAACCCTAACGGCTCTTTTAAGAGCCACCCA NM_021058RefSeq chr6
- 27132315 27132796 HIST1H2BJ 8970 "histone cluster 1, H2bj"
GO:0046982|GO:0050830|GO:0019731|GO:0006334|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0005
615|GO:0003677|GO:0002227 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134845_PI430048170 0.00333391800877781 0.454600130680961 7.82489691699081
7.52092113358314 7.84782866581344 P P P 8.83830513135586 8.64259309851505 9.1089815427088
P P P LNCV6_134845_PI430048170 mRNA
GTCTGATGGTATATTTGTGAGTTGTGTTATCTGTAATATACATCCCAGAATAAAGGAGTG NM_001304445 RefSeq
chr2 + 30447225 30644225 LCLAT1 253558 "lysocardiolipin acyltransferase 1, transcript variant 4"
GO:0035965|GO:0007275|GO:0044281|GO:0003841|GO:0016020|GO:0005789|GO:0016024|GO:0019432|GO:0016
021|GO:0006644|GO:0006654|GO:0044255|GO:0046474 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105587_PI430048170 0.0413802038228161 2.2971146982941 9.92161043449502
9.83668161962296 9.91018274345477 P P P 9.53003203973384 9.65208124768791
9.34552988308838 P P P LNCV6_105587_PI430048170 mRNA
AAACAGTCCACGTCTTTCTTGGTTTTGCAGGAAATCCTGGAGTCTGAAGAAAAAGGGGAT NM_020992RefSeq chr10
- 95237567 95291148 PDLIM1 9124 PDZ and LIM domain 1
GO:0005667|GO:0001666|GO:0006355|GO:0005737|GO:0003713|GO:0008270|GO:0005856|GO:0006979|GO:0005
925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143557_PI430048170 0.456933595328705 1.06096083032918 8.20273286038106
8.21689230249434 8.04063941459015 P P P 8.16464986612237 8.14311012632508
7.88672937568641 P P P LNCV6_143557_PI430048170 mRNA

TCAGATAATTGCTCCTGTGGGGCCCTGGCTTCCTTCTCTGTTTGTGCAGTATTTGTTTTT NM_002556 RefSeq chr11 - 59574397 59616144 OSBP 5007 oxysterol binding protein GO:0005515|GO:0005737|GO:0030054|GO:0005794|GO:0008142|GO:0000139|GO:0019904|GO:0006869|GO:0005730|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_84631_PI430048170 0.492756197489413 1.03570284770206 0.283796338296308 0.301678673008845 0.465333530546687 A A A 0.327309512527943 0.284678786126898 0.293663525783956 A A A LNCV6_84631_PI430048170 mRNA

ATTTCACTCGGAGTTACCTGGACTTGATTGTAACTTACACCTCAGTCATTTTACTTCTGT NM_005337 RefSeq chr12 + 54497710 54543115 NCKAP1L 3071 "NCK-associated protein 1-like, transcript variant 1" GO:0050853|GO:0005515|GO:0031209|GO:0001782|GO:0030890|GO:0032715|GO:0045579|GO:0043378|GO:0030011|GO:0032403|GO:0032855|GO:0060100|GO:0005829|GO:0070358|GO:0030838|GO:0006935|GO:0048821|GO:0045860|GO:0042102|GO:0043029|GO:0002262|GO:0030675|GO:0070062|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_55803_PI430048170 0.46400783362317 0.812618072306968 3.08530116864609 1.30606737814828 1.81381429374215 P A A 2.40322140444876 2.36041625196214 2.88529611279277 A A P LNCV6_55803_PI430048170 mRNA

ATGCACTAAAGGAGATTAGAGGAAACCAAGTTACTTTTCAGGATTGCTTTATTGCAGATT NM_001130957 RefSeq chr1 + 244461370 244640360 C1orf101 257044 "chromosome 1 open reading frame 101, transcript variant 1" GO:0036128 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_90422_PI430048170 0.0825845326768324 1.3505305338721 5.49314244966896 5.81748188011299 5.75630452107912 P P P 5.55162336983197 5.09210508567428 5.09245327981295 P P P LNCV6_90422_PI430048170 mRNA

AAGAAAGAAGAGAAAGAGGGCAAGCATGAGCCCGTGCAGCCATCAGCCCACCACTCTGCT NM_004992 RefSeq chrX - 154021812 154097731 MECP2 4204 "methyl CpG binding protein 2, transcript variant 1" GO:0000792|GO:0005515|GO:0008327|GO:0003700|GO:0060291|GO:0009791|GO:0005615|GO:0043524|GO:0006122|GO:0010385|GO:0001662|GO:0051965|GO:0007616|GO:0003714|GO:0019904|GO:0060079|GO:0021549|GO:0000122|GO:0007416|GO:0016358|GO:0008542|GO:0021591|GO:0035176|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_117911_PI430048170 0.00770570516043717 1.97765531016468 4.01093331830589 3.61308400226826 4.03737914682767 P P P 2.94017417540887 3.02384118402014 2.77263799171055 P P P LNCV6_117911_PI430048170 mRNA

AAAGCTGTCCCTGATGCTGGATGAGGGGAGCTCATGCCCAACACCTGCCAAGTTCAACAC NM_001040667 RefSeq chr16 + 67163384 67169945 HSF4 3299 "heat shock transcription factor 4, transcript variant 2" GO:0006355|GO:0008284|GO:0003700|GO:0003714|GO:0019903|GO:0045597|GO:0000122|GO:0006351|GO:0043565|GO:0070207|GO:0045944|GO:0005654|GO:0043010|GO:0048468|GO:0033169 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_134320_PI430048170 0.41495916059083 0.644435309994105 1.61066179761347 1.41319968825083 0.34044480731585 A A A 2.6272376352677 1.33611063502654 1.09305372430529 P A A LNCV6_134320_PI430048170 mRNA

GGACGCCCTCCAATGACATAACAACTGTTTTTGGTAATGTAATCTTGGGAAAATGTGTTA NM_005427 RefSeq chr1 + 3652564 3736201 TP73 7161 "tumor protein p73, transcript variant 1" GO:0005515|GO:0010468|GO:0060044|GO:0003700|GO:0030054|GO:0006366|GO:0044212|GO:0000981|GO:0009791|GO:0042802|GO:0043231|GO:0034644|GO:0043524|GO:0003690|GO:0006298|GO:0006978|GO:0000785|GO:0010332|GO:0005794|GO:0019901|GO:0010243|GO:0000122|GO:0000978|GO . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_128116_PI430048170 0.0264252054650046 0.168286934548544 1.58393260999558 0.321942339026081 2.09133763414177 A A A 3.72312492330956 4.2464724420703 4.19985814937511 P P P LNCV6_128116_PI430048170 mRNA

CTTCTTGTGGCCTACAGTGTTATGTTTGCTGTAAGAATAAGATATGTGAATTCCACAAAA NM_002655 RefSeq chr8

- 56160908 56211300 PLAG1 5324 "pleiomorphic adenoma gene 1, transcript variant 1"
GO:0003700|GO:0060736|GO:0006366|GO:0000981|GO:0005634|GO:0060252|GO:0000978|GO:0046872|GO:0001
077|GO:0035264|GO:0045944|GO:0010629|GO:0022612 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137118_PI430048170 0.181536001389916 1.26148866572537 0.381180174119631
0.910923473840717 0.53080772050111 A A A 0.281526906598606 0.293330006554511
0.295434143194874 A A A LNCV6_137118_PI430048170 mRNA
CCTTAACTGTTAGTTATGCCTGCATTCATATTTGCACAGGAAAAATAAAGACCTGGATTT NM_001298 RefSeq chr2
+ 98346154 98398601 CNGA3 1261 "cyclic nucleotide gated channel alpha 3, transcript variant 1"
GO:0005223|GO:0046549|GO:0007603|GO:0042622|GO:0005222|GO:0031960|GO:0008022|GO:0051591|GO:0030
425|GO:0007165|GO:0005737|GO:0030553|GO:0005887|GO:0005249|GO:0042391|GO:0032026|GO:0006810|GO:0
043204|GO:0007601|GO:0071805|GO:0006812|GO:0015276 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_141309_PI430048170 0.154318780180006 0.725141168367852 13.4670855232404 12.842552111474
12.7233561560425 P P P 13.6174892754458 13.5344034849565 13.3769537873746 P P P
LNCV6_141309_PI430048170 mRNA
TGTTTGTGCCCCTCTCCCCAATTTCATTAAAGATTTCATGAAACATTACCCCTGAAAAAA NM_021228 RefSeq chr19
+ 49642124 49658649 SCAF1 58506 SR-related CTD-associated factor 1
GO:0008380|GO:0006397|GO:0006366|GO:0003723|GO:0019904|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_125038_PI430048170 0.523568565908402 1.01799650391943 0.505842500421609
0.453523900457876 0.528683329665944 A A A 0.478096002353521 0.516659339686108
0.415313748929114 A A A LNCV6_125038_PI430048170 mRNA
CGGAAGCCAGAACATTCCTCCTGGAAATTCAACCTGTTTCGCAGTTTCTCGAGGAATCAG NM_000927 RefSeq chr7
- 87503862 87713323 ABCB1 5243 "ATP-binding cassette, sub-family B (MDR/TAP), member 1"
GO:0005515|GO:0005215|GO:0005886|GO:0009986|GO:0042493|GO:0072089|GO:0042626|GO:0042908|GO:0044
281|GO:0055085|GO:0005524|GO:0008559|GO:0016020|GO:0000086|GO:0006855|GO:0006810|GO:0016021|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134045_PI430048170 0.413010697761574 1.39271558354505 0.42222205482094
0.428076446888541 1.53060674106089 A A A 0.446749573703507 0.388501099918724
0.412092479579376 A A A LNCV6_134045_PI430048170 mRNA
CATGCTTTGTTAATATTTGTCCCACCATAATGCCTCCTTCAGAACATAAGTGTAACTTTA NM_033058 RefSeq chr8
+ 66127042 66175483 TRIM55 84675 "tripartite motif containing 55, transcript variant 2"
GO:0007165|GO:0005737|GO:0005874|GO:0008270|GO:0005634|GO:0004871|GO:0042802 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_110345_PI430048170 0.499137963898424 1.1156507932935 0.433418859195116
0.418636857761573 0.930430286771753 A A A 0.422516128717104 0.482040595144381
0.464504647744496 A A A LNCV6_110345_PI430048170 mRNA
AACTTGCTTGTTCTGATAGCTTTCTTAATCACATGGTGATATATTTTACAGTTGCGCTGC NM_017506 RefSeq
chr19 - 14826326 14828464 OR7A5 26659 "olfactory receptor, family 7, subfamily A, member 5"
GO:0050911|GO:0007608|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_81074_PI430048170 0.00608386174121472 0.678995520716183 10.2778426320501
10.1848870761192 10.4161059165751 P P P 10.9555908231379 10.697102519093
10.8985586878355 P P P LNCV6_81074_PI430048170 mRNA
GTTAACTGCCAGTAAAGTTATTTGTTAGCTTTGATGAAAGCTATGTTGGTATCTTTCCCT NM_007001 RefSeq chr9
- 96320705 96383710 SLC35D2 11046 "solute carrier family 35 (UDP-GlcNAc/UDP-glucose
transporter), member D2, transcript variant 1"
GO:0005338|GO:0005975|GO:0008643|GO:0005575|GO:0044281|GO:0055085|GO:0006024|GO:0042339|GO:0008
150|GO:0000139|GO:0018146|GO:0009405|GO:0016021|GO:0030203 . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_52654_PI430048170 0.000247178765332549 0.621159829918059 6.76226132457609
6.65308620250824 6.71162223814082 P P P 7.47588539224395 7.35416649899375
7.35648586380322 P P P LNCV6_52654_PI430048170 mRNA
GGATACTAGGAATAAAGAAAGTGATCATTGTCTACGTTGAAAGCATCTGCCGTGTAGAAA NM_144988 RefSeq
chr1 - 94982722 95072951 ALG14 199857 "ALG14, UDP-N-acetylglucosaminyltransferase subunit"
GO:0005789|GO:0016021|GO:0006488|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_142904_PI430048170 0.938617237901056 1.03425705102267 1.92030695842173
0.338734609599029 1.9120190029385 A A A 2.29359414051725 0.966344326340906
0.735075580345493 A A A LNCV6_142904_PI430048170 mRNA
CCCTGCTCTGTAACCCTGGGGAATGTCAGAGGCAGGTAATAAAGGTTGTTTAAACAATAA NM_012282 RefSeq
chrX - 109623699 109625164 KCNE5 23630 "potassium channel, voltage gated subfamily E
regulatory beta subunit 5"
GO:0008016|GO:0060306|GO:0015459|GO:2001257|GO:0060307|GO:0086091|GO:0060048|GO:0044325|GO:0071
435|GO:0086008|GO:0060372|GO:0005249|GO:0008076|GO:0086013|GO:0086014|GO:0071805|GO:0086005 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127283_PI430048170 0.564300919323532 1.74823275688895 0.29927611809257
2.42940488906028 0.377026733073033 A A A 0.293919282795204 0.272280421851765
1.06644274379172 A A A LNCV6_127283_PI430048170 mRNA
CAACCTGTTTGAATACAATGTACTAAAGGAGGGATGTACTTTCAGATCATGTAACCTATT NM_138815 RefSeq
chr3 - 109293787 109316517 DPPA2 151871 developmental pluripotency associated 2
GO:0031060|GO:0006355|GO:0019827|GO:0003682|GO:2000648|GO:0005654|GO:0005634|GO:0060484|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128771_PI430048170 0.306699108929691 1.18015699957676 10.5358251940049
11.0106215784944 10.805042772334 P P P 10.8470151820208 10.3450024704765
10.429984471044 P P P LNCV6_128771_PI430048170 mRNA
GCTCCTAACAGTGTAACTTATTGTGTCCCCGCGTATTTATTTGTTGTAAATATTTGAGTA NM_017789 RefSeq chr2
- 96859735 96869998 SEMA4C 54910 "sema domain, immunoglobulin domain (Ig), transmembrane
domain (TM) and short cytoplasmic domain, (semaphorin) 4C"
GO:0021535|GO:0030054|GO:0001843|GO:0014069|GO:0021549|GO:0032874|GO:0005615|GO:0042692|GO:0045
211|GO:0071526|GO:0004872|GO:0030672|GO:0016021 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143301_PI430048170 0.0165763477997593 0.212754288906789 1.68198463859164
0.40559796912883 1.58965148604583 A A A 3.17119780520736 3.60609580549238
3.83485984577872 P P P LNCV6_143301_PI430048170 mRNA
GCCTTCAATGAATTAAACCAGTGATATGTGTTAACGTATGAATGAAAGGATTGATGGTGA NM_003463 RefSeq
chr6 + 63572011 63583588 PTP4A1 7803 "protein tyrosine phosphatase type IVA, member 1"
GO:0007049|GO:0005737|GO:0030335|GO:0005783|GO:0005819|GO:0009898|GO:0007275|GO:0035335|GO:0005
769|GO:0004725|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135593_PI430048170 0.467248126687422 0.82134480635027 3.45280209022661
4.30299210286478 4.88778316192204 P P P 4.29775634927012 4.61747628122677
4.86761152005369 P P P LNCV6_135593_PI430048170 mRNA
CCTCCTTGTGTAAGACAGTAACTTTACACTTCAGACAGATTTTCTGTGTTATGAAATGTT NM_002114 RefSeq chr6
+ 12012490 12164999 HIVEP1 3096 human immunodeficiency virus type I enhancer binding protein
1 GO:0005739|GO:0005515|GO:0005654|GO:0005634|GO:0000122|GO:0003677|GO:0046872|GO:0006351 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_93062_PI430048170 0.361178781656356 1.19880672556425 6.73047758698517
7.198193724598 7.04368115714627 P P P 7.14748241137495 6.35759232327585

6.60510875274001 P P P LNCV6_93062_PI430048170 mRNA
CTTAATCCGGAAGAGAATCCACCTGAGACCTGAGGACGCCTTATTCTTCTTTGTCAACAA NM_031412 RefSeq
chr12 + 10212889 10223125 GABARAPL1 23710 GABA(A) receptor-associated protein like 1
GO:0005515|GO:0008017|GO:0005776|GO:0005794|GO:0000422|GO:0005783|GO:0000421|GO:0005874|GO:0048
487|GO:0032839|GO:0050811|GO:0000407|GO:0030957|GO:0044297|GO:0005829|GO:0005622|GO:0032590|GO:0
061025|GO:0000045|GO:0030659|GO:0019898 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_130059_PI430048170 0.656881191648 1.22560376925653 2.43129431584156
1.10020004192071 1.28084954253113 A A A 0.63384268595334 1.29608683556009
2.04452072122274 A A A LNCV6_130059_PI430048170 mRNA
TTGTCTTTTTTCCTTGACTCGGAAATGTCCGGTCGTGGTAAGCAGGGTGGCAAGGCGCGC NM_033445RefSeq chr1
- 228457363 228457859 HIST3H2A 92815 "histone cluster 3, H2a"
GO:0046982|GO:0070914|GO:0000788|GO:0006337|GO:0003677|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137615_PI430048170 0.0128286869176422 1.36761878143859 4.03008736715246
4.3040200817798 4.20171592518395 P P P 3.8443366048228 3.696136294473
3.64608018764818 P P P LNCV6_137615_PI430048170 mRNA
TTCATTAGACACAACAAAACCCAAACCATTCTCTTTTATGGCAGGGTCTGCTCTCCTTAA NM_080474RefSeq chr18
+ 63556159 63569327 SERPINB12 89777 "serpin peptidase inhibitor, clade B (ovalbumin), member 12"
GO:0010951|GO:0005737|GO:0042177|GO:0004867|GO:0002244|GO:0019899|GO:0005615|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132332_PI430048170 0.250303063231218 2.33308677760385 1.09059478329713
0.259848606236818 2.34024369210673 A A A 0.265191625045838 0.255445360795476
0.26418808042875 A A A LNCV6_132332_PI430048170 mRNA
GGAGATTTTCTATGGCCTCAGGCCTGAGTGCCAATATTAGTCTCCAGCTTCTGTGGATGA NM_198508RefSeq chr7
- 139453341 139483711 KLRG2 346689 "killer cell lectin-like receptor subfamily G, member 2"
GO:0030246|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130340_PI430048170 0.00223088210147264 0.650080965451241 7.20386657841756
7.16154879730462 7.30609162181115 P P P 7.85986211212624 7.7257160527012
7.94526707345941 P P P LNCV6_130340_PI430048170 mRNA
GCTTTCATGTAAAAAAGGGTTGGGGGGAGGGGTGTCTTTTTGCTTTTGGTGAACTTTTTT NM_012288RefSeq chr6
- 52497401 52577064 TRAM2 9697 translocation associated membrane protein 2
GO:0005515|GO:0032964|GO:0016021|GO:0015031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140033_PI430048170 0.000446120108765976 1.62988788673286 10.97017577021
11.1328105128563 11.0604895764177 P P P 10.4041860884315 10.3598932005087
10.2872624193665 P P P LNCV6_140033_PI430048170 mRNA
GGAGTAGATTTGGTGTGGCTAAAAGTGTTTAAGACTGGACAGATGATCATATTCTAAATT NM_016466RefSeq chr2
- 96847986 96858019 ANKRD39 51239 ankyrin repeat domain 39
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142275_PI430048170 0.00984400241093531 0.563776047319435 10.6790299201521
10.4421234555226 10.2181339559241 P P P 11.3664175710507 11.358721520948
11.1177781448293 P P P LNCV6_142275_PI430048170 mRNA
TCCCCTTGTCTGTCCTCCCCCACTTCTTGAATAAAATAATTTAAAGAGAAGTTGAAAAAA NM_001080429 RefSeq
chr19 + 7595901 7618310 CAMSAP3 57662 "calmodulin regulated spectrin-associated protein
family, member 3, transcript variant 1"
GO:0090136|GO:0070507|GO:0005915|GO:0005813|GO:0005737|GO:0034453|GO:0010923|GO:0051011|GO:0000
226|GO:0045218|GO:0033043 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141833_PI430048170 0.0598945702636767 0.889496728793679 5.66764162771276
5.5022803127579 5.53195753968777 P P P 5.73358505393788 5.67437020721873

5.80329222838043 P P P LNCV6_141833_PI430048170 mRNA
ATGACATTTTAGAAGTGGAGAGTGCATCATATGTAGAAAATAAATATTCAGACGTGGCTC NM_001003803 RefSeq
chr14 + 50312328 50326228 ATP5S 27109 "ATP synthase, H+ transporting, mitochondrial Fo complex, subunit s (factor B), transcript variant 1"
GO:0022904|GO:0042776|GO:0015078|GO:0005743|GO:0044281|GO:0046872|GO:0045263|GO:0044237|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139063_PI430048170 0.00893889006647516 1.1583866162199 7.51513408054049
7.40529707288162 7.45081795821864 P P P 7.26939134381565 7.21034437702553
7.25661143873748 P P P LNCV6_139063_PI430048170 mRNA
TCCCTGGAAACCTTGCTGTTGGTATTTCCATTTTGATACTTGAGAGCATCAAATTTTGTC NM_145039 RefSeq chr16
- 89969774 89972832 CENPBD1 92806 CENPB DNA-binding domains containing 1
GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144806_PI430048170 0.567520805021848 0.967931911062416 0.471869316290522
0.453128769569718 0.249659489300635 A A A 0.391544114220109 0.490647311710641
0.442185002716127 A A A LNCV6_144806_PI430048170 mRNA
CAGCACTTGAAATGAAGGCTTATGGAATTCTGACTGTGAAATGAATTTTTCTATTGGGAA NM_173495 RefSeq chrX
+ 23334867 23396801 PTCHD1 139411 patched domain containing 1
GO:0003674|GO:0050890|GO:0005886|GO:0008158|GO:0016021|GO:0007224 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133849_PI430048170 0.741165390165582 1.04309905116055 11.7365105240004
11.6720693389805 12.0498133890015 P P P 11.6170608943224 11.5951625887224
12.0462487799242 P P P LNCV6_133849_PI430048170 mRNA
CTTGCTCTTCAGATGGATGGTTTGTAAGGCTCTTGTTGCATTTCTTAAAAAAGAGTAATA NM_007062 RefSeq chr12
+ 107685812 107712480 PWP1 11137 PWP1 homolog (S. cerevisiae)
GO:0005794|GO:0005730|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140192_PI430048170 0.223113640020599 0.815790832639526 3.89439758286399
3.80283530602177 4.38242182617057 P P P 4.46538279470757 4.15127285989406
4.39522221399734 P P P LNCV6_140192_PI430048170 mRNA
CATAATGAGCAAAATTTCAGCTAGCTCAATTCAGTTGTTGAGGTATTCTTTCTTACCCAT NM_139076 RefSeq chr4
- 83460940 83485137 FAM175A 84142 "family with sequence similarity 175, member A"
GO:0005515|GO:0070531|GO:0010212|GO:0031572|GO:0005634|GO:0045739|GO:0031593|GO:0016568|GO:0006302 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141860_PI430048170 0.00633843345942334 1.39991892256853 10.4075908648377
10.3900005244437 10.349426652226 P P P 9.97902317595047 9.90582746874061
9.80124037027588 P P P LNCV6_141860_PI430048170 mRNA
TAAGGTGTCTGCTTATCCAGCCAGAAATAAAAATCTGCCAGTGGTGTTCCCAAGGGAAGA NM_001288805 RefSeq
chr8 + 143684451 143695385 ZNF707 286075 "zinc finger protein 707, transcript variant 4"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129504_PI430048170 0.26308732566377 0.571948423208939 2.4649260298825
0.61491051198334 1.87277183843018 A A A 3.25360043726531 1.92275267808548
2.43428887919858 P A A LNCV6_129504_PI430048170 mRNA
GAAACCCCTATAGAAAAGGAAAGCTCCAGCTAAATAGGAAGAATTAGAATATTGAGCTTT NM_052911 RefSeq chr18
- 21529300 21600732 ESCO1 114799 establishment of sister chromatid cohesion N-acetyltransferase 1
GO:0016746|GO:0034421|GO:0007062|GO:0005654|GO:0000278|GO:0000785|GO:0046872|GO:0006275 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132516_PI430048170 0.0927392308230075 0.66514785328551 9.70068323907585
9.82607783984586 10.2020920017256 P P P 10.1841662567597 10.3922880819563
10.8759955380826 P P P LNCV6_132516_PI430048170 mRNA

GTCACCTTGGGGTTTTGAATGTTTGCTTTAAGTGTTGGCTATTTCTATGTTTTATAAACC NM_001286712 RefSeq chr4
- 184755594 184808601 ACSL1 2180 "acyl-CoA synthetase long-chain family member 1, transcript
variant 5"
GO:0014070|GO:0001676|GO:0071902|GO:0005886|GO:0033211|GO:0005741|GO:0035338|GO:0044281|GO:0005
739|GO:0019432|GO:0044539|GO:0005778|GO:0044255|GO:0008610|GO:0007584|GO:0042178|GO:0042493|GO:0
034201|GO:0036109|GO:0005524|GO:0004467|GO:0033559|GO:0043651|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135447_PI430048170 0.1378263514570510.5264550654221380.493706591183796
0.5877115801896420.493474329985545A A A 1.81389013943269 0.672798093755134
1.62919425188905 A A A LNCV6_135447_PI430048170 mRNA
TGAGGAGTAGATGGGAATTTGAGGGAGAATACAGAGATACTATGAACGTATTTGACATTT NM_031451RefSeq chr19
+ 43388610 43418615 TEX101 83639 "testis expressed 101, transcript variant 1"
GO:0005886|GO:0031225|GO:0002080 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132143_PI430048170 0.3096852404533510.66981752667498 0.3778728118479
2.44937697077591 0.347142582173329A A A 1.88675569315111 2.12636813858861
1.97416871602851 A A A LNCV6_132143_PI430048170 mRNA
GGGTGTGAACTATGGTTTAGAAGGTTCAAGTTTCCAATTAAAGTCATTGAAGAAAACTTG NM_001172439 RefSeq
chr12 - 47709734 47725572 ENDOU 8909 "endonuclease, polyU-specific, transcript variant 1"
GO:0007565|GO:0030145|GO:0005886|GO:0003723|GO:0005576|GO:0004521|GO:0005615|GO:0006898|GO:0005
737|GO:0006955|GO:0006508|GO:0008236|GO:0030247|GO:0008083|GO:0005044 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_115144_PI430048170 0.0122577019723155 0.6141920433077938.24733164594142
8.36142156102863 8.64120117306648 P P P 9.02096285973767 8.99653958426068
9.34434351606664 P P P LNCV6_115144_PI430048170 mRNA
ATAGAAAAGCTGGCAATAATCAAGGACTTACTGAAGTAGTCTGTTGGTTCAGTGCATGCT NM_018297RefSeq chr3
- 25718943 25783498 NGLY1 55768 "N-glycanase 1, transcript variant 1"
GO:0005515|GO:0005737|GO:0006516|GO:0046872|GO:0000224 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_73840_PI430048170 0.00200056082714953 1.71522988866561 6.97293459526908
6.78735932487842 7.0376287638447 P P P 6.15146239852527 6.2399243100432
6.07832717676553 P P P LNCV6_73840_PI430048170 mRNA
TGAGGCGCAGCAGCAGTATCGCCAGCACATCCAGGTTTTCATTGACCGGTTTCGCTACAA NM_018358RefSeq chr3
+ 184186074 184194007 ABCF3 55324 "ATP-binding cassette, sub-family F (GCN20), member 3"
GO:0051607|GO:0016020|GO:0008152|GO:0016887|GO:0005524 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143818_PI430048170 0.0439093396978489 0.6566575002336384.94122833061092
4.8707381278689 5.40143921854733 P P P 5.84404893632374 5.5063251968497
5.72277566063122 P P P LNCV6_143818_PI430048170 mRNA
TGATTTGCTTCACCATTTCCCTTATATGTTCACCCCTGTAAAATTGTAAAGTCACTCACT NM_004703RefSeq chr17 +
5282262 5386339 RABEP1 9135 "rabaptin, RAB GTPase binding effector protein 1, transcript variant 1"
GO:0005515|GO:0006915|GO:0030139|GO:0015031|GO:0042803|GO:0006897|GO:0043231|GO:0043547|GO:0061
025|GO:0055037|GO:0008083|GO:0005769|GO:0005096|GO:0005768 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_142687_PI430048170 0.7554204326186050.9446789121413479.31848865584197
9.25463305345679 9.37084830264441 P P P 9.07568428551409 9.38041384031485
9.67465031437623 P P P LNCV6_142687_PI430048170 mRNA
ATCATATGTAACTGGGACTTTTGTAAATAAATGTTTGTGCGCTCTGCTCCCTCCAAAAAA NM_207111RefSeq chr7
- 5620040 5781730 RNF216 54476 "ring finger protein 216, transcript variant 1"
GO:0005515|GO:0032648|GO:0005737|GO:0016874|GO:0016032|GO:0006915|GO:0043161|GO:0008270|GO:0005

654|GO:0005634|GO:0070936|GO:0050691 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140832_PI430048170 0.1769632779261020.3898442663724652.88472131481487
1.15362852756074 1.01622791419165 A A A 4.18381347240332 2.17347654902722
2.83892484849146 P A P LNCV6_140832_PI430048170 mRNA
GTAAGTTAACCTGTTCTAGTTCCATCATTCTGTGTACAGTGAAGTATTGCATGATAATGT NM_015312RefSeq chr4
+ 122170602 122362759 KIAA1109 84162 KIAA1109
GO:0005515|GO:0030856|GO:0016020|GO:0005634|GO:0016021|GO:0001558 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128415_PI430048170 0.5865485425659470.9814206229826920.392936686923789
0.3859673347389160.260359174123239A A A 0.3557075168620320.400643395479773
0.367524833087908A A A LNCV6_128415_PI430048170 mRNA
GTGAATGCAACCTGTTAATGATAATGGCTTTTTCGCTGCTTGATTTTCTTCTTTTCCTCA NM_001105558 RefSeq
chr7_GL383534v2_alt + 80952 103871 WEE2 NA WEE1 homolog 2 (S. pombe)NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_134554_PI430048170 0.0997214637176132 0.8018004573000716.38002565831728
6.35794558381819 6.51299965722313 P P P 6.49780524958728 6.82103732335105
6.86590160122423 P P P LNCV6_134554_PI430048170 mRNA
GTGGTGTGTTTGTTCTAAGAGAAATGCCAAGGCTTTCAGATAAAGATAAGATGATAATGA NM_005107RefSeq chr3
+ 38496271 38526305 EXOG 9941 "endo/exonuclease (5'-3'), endonuclease G-like, transcript variant 1"
GO:0005739|GO:0008150|GO:0004519|GO:0005743|GO:0005575|GO:0003676|GO:0000737|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142230_PI430048170 0.0934241777404484 0.4526273393898870.38726308557095
0.94510636819717 0.308085195427451A A A 2.19616720264878 1.79378811846201
0.870827360031295A A A LNCV6_142230_PI430048170 mRNA
TCTCAGCGACATACTGGATACCAGAATAATGTTTCCTCTTCTCTGGTGCACCAAAACCTG NM_015367RefSeq chr22
+ 17638583 17730855 BCL2L13 23786 "BCL2-like 13 (apoptosis facilitator), transcript variant 1"
GO:0005739|GO:0031966|GO:0006919|GO:0006915|GO:0005634|GO:0016021|GO:0008656 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139088_PI430048170 0.3423513396087790.7651181413985340.96747248852276
0.4925394421500220.390018822101663A A A 1.16805245095909 1.32650158711392
0.435304640201505A A A LNCV6_139088_PI430048170 mRNA
GTGATACAGCCCCTTTTCTTATAAAGTCAGTTAGAAGGACTTCCTTAACAATGACTATTA NM_001198595 RefSeq
chr2 + 48530168 48598515 STON1 11037 "stonin 1, transcript variant 1"
GO:0030131|GO:0030100|GO:0006886|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143346_PI430048170 0.0751193101637511 0.6402418295324186.97421835463767
6.35855391916605 6.53816784610665 P P P 7.52643833492817 7.38728943797732
6.88171559560204 P P P LNCV6_143346_PI430048170 mRNA
TGACAATTTCGTGAAGCTCATTTCATGGTACGACAACGAATATGGCTACAGTCACCGGGT NM_014364RefSeq chr19
+ 35533411 35545319 GAPDHS 26330 "glyceraldehyde-3-phosphate dehydrogenase, spermatogenic"
GO:0050661|GO:0005515|GO:0005975|GO:0006094|GO:0097228|GO:0005634|GO:0004365|GO:0030317|GO:0044
281|GO:0006096|GO:0005829|GO:0051287|GO:0035686|GO:0009405|GO:0006006|GO:0045821|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142191_PI430048170 0.0923346072228951 0.6928122090945016.762122856349
6.33044091933434 6.97074279887221 P P P 6.93017477391782 7.41048159725491
7.33797134715324 P P P LNCV6_142191_PI430048170 mRNA
CTTCCCTGTCTATGTAGAAGTGCCTGTGTTTTTATTTATTGTTCAGATCAAAGACCAAAA NM_006577RefSeq chr2
+ 62196126 62224731 B3GNT210678 "UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2"
GO:0007608|GO:0030311|GO:0005975|GO:0016266|GO:0044281|GO:0008378|GO:0042339|GO:0008150|GO:0008
532|GO:0000139|GO:0006493|GO:0018146|GO:0007411|GO:0009405|GO:0016021|GO:0044267|GO:0030203|GO:0

070062|GO:0043687. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131029_PI430048170 0.00539324286735756 0.4725325779855947.1324186708104
7.04492410313242 7.3235288984958 P P P 8.05379983813302 8.15342578509079 8.5113336843636
P P P LNCV6_131029_PI430048170 mRNA
ATATACCTTTCCTTGGCCACCAAGTATTTTAAAAGTGTGCCACCTTTTAACCTTTACTTT NM_182972RefSeq chr1 -
234604268 234609525 IRF2BP2359948 "interferon regulatory factor 2 binding protein 2, transcript variant 1"
GO:0006355|GO:0005737|GO:0005654|GO:0005634|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137652_PI430048170 0.00303752977329127 0.4702392407079685.54904640438757
5.26638427872923 5.54777271920959 P P P 6.31311065326793 6.55377285876646
6.74731889328684 P P P LNCV6_137652_PI430048170 mRNA
ATGCAAATACCACAGACTCCAAGAAAACCCGAGTTGGGGTTTGTTTTGTTTTGATTTTTT NM_006706RefSeq chr5
+ 146447309 146511506 TCERG1 10915 "transcription elongation regulator 1, transcript variant 1"
GO:0005515|GO:0001103|GO:0006366|GO:0001106|GO:0003713|GO:0005730|GO:0005634|GO:0000122|GO:0015
629|GO:0070064 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141058_PI430048170 0.5667161877141690.9210457138039575.76895214596191
5.96872569004203 5.57149408534 P P P 5.87430709252564 6.13294374146546 5.64362572487991 P
P P LNCV6_141058_PI430048170 mRNA
GCAGGTGGAGGTCCCAGATCTACTCACACAATACCAGGCAAATACAGAAAACAGAACTTT NM_031925RefSeq chr7
- 75986836 75994674 TMEM120A 83862 transmembrane protein 120A
GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135145_PI430048170 0.1789685572167961.2473395462057 6.80628976848355
6.62424044298001 6.74073675748733 P P P 6.28890476078511 6.15086653479712
6.71846109057278 P P P LNCV6_135145_PI430048170 mRNA
CTGATGGCCTACTTGACTTATTTAATTAAAGATGAAATCATGCAATGAGCAAAACCTGCA NM_004273RefSeq chr10
+ 71964361 72013564 CHST3 9469 carbohydrate (chondroitin 6) sulfotransferase 3
GO:0006790|GO:0005975|GO:0050698|GO:0008459|GO:0044281|GO:0030206|GO:0000139|GO:0008146|GO:0009
405|GO:0016021|GO:0030204|GO:0043029|GO:0030203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129019_PI430048170 0.6349588828141611.06483935449534 6.11506897407242
5.72132471468272 6.13595445930789 P P P 5.73091850591991 6.00523824441744
5.98500195104814 P P P LNCV6_129019_PI430048170 mRNA
CATATACTTCTTTGCTGAATGCTAATAAACTTCTGGGTTCAAGAGGGAACCCCTCAGTCA NM_152424RefSeq chrX
- 64185116 64205744 AMER1 139285 APC membrane recruitment protein 1
GO:0005515|GO:0072161|GO:0005886|GO:0008013|GO:0090263|GO:0005546|GO:0005634|GO:0005829|GO:0060
828|GO:0060348|GO:0016055|GO:0060612|GO:0090090 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137931_PI430048170 0.0121669105902796 0.6414572362014491 2.4636114738658
12.1850793177998 12.1721092013389 P P P 12.8440074233318 13.1263131253014
12.7660103037339 P P P LNCV6_137931_PI430048170 mRNA
CGTGTGGATGTCGGTAACAGTTGTATAAAATAAATTCTATTTATCGCTATTGTACCCAGA NM_001145657 RefSeq
chr1 - 21596214 21669363 RAP1GAP 5909 "RAP1 GTPase activating protein, transcript variant 2"
GO:0005515|GO:0003924|GO:0032854|GO:0042803|GO:0005829|GO:0007165|GO:0046582|GO:0000139|GO:0016
020|GO:0008152|GO:0017016|GO:0005096|GO:0032318 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71360_PI430048170 0.0139296830002691 0.7160458495342047.00666762787928
6.92589848964912 6.72857661814727 P P P 7.29318515058869 7.43559984320016
7.38835645824708 P P P LNCV6_71360_PI430048170 mRNA
ACAAGCACAGCGACGAGTACAAGATCCGGCGCGAGCGCAACAACATCGCCGTGCGCAAGA NM_005194RefSeq
chr20 + 50190582 50192691 CEBPB 1051 "CCAAT/enhancer binding protein (C/EBP), beta, transcript
variant 1"
GO:0005515|GO:0060850|GO:0000790|GO:0034976|GO:0003700|GO:0006366|GO:0003705|GO:0045408|GO:0005

634|GO:0035259|GO:0042803|GO:0016363|GO:0043524|GO:0005737|GO:0006955|GO:0060644|GO:0006954|GO:0071230|GO:0045944|GO:0030182|GO:0032496|GO:0006355|GO:0046982|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82158_PI430048170 0.2847865015130930.8485191565430294.28706319771459 4.43235426127715 3.93805834323066 P P P 4.29819285893168 4.70974673687859 4.36982403041971 P P P LNCV6_82158_PI430048170 mRNA
TGAGAACTTATTCCTCGACCCGGACATGGCACAGGAGAAAATGAAACTAGGTTTCAAGTC NM_001170781 RefSeq chrX + 134807192 134811181 FAM122C 159091 "family with sequence similarity 122C, transcript variant 4" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140562_PI430048170 0.4602420121151591.02659573412983 0.433944912211529 0.3002959588935130.348665219491409A A A 0.2886111273884390.32575991647581 0.35729818056421 A A A LNCV6_140562_PI430048170 mRNA
TCTTCTCCTTATTCACCGGGGAGGCTGTGTCTTGTGCAAACAAGTCATAGAAACTTGATG NM_000554RefSeq chr19 + 47821841 47843329 CRX1406 cone-rod homeobox
GO:0005515|GO:0005667|GO:0046534|GO:0006355|GO:0003700|GO:0060041|GO:0035257|GO:0005634|GO:0000978|GO:0006351|GO:0043522|GO:0001077|GO:0045944|GO:0003682|GO:0007623|GO:0009887|GO:0007601|GO:0050896 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79185_PI430048170 0.00544600046917433 0.7166190833113421 5.688930146478 15.4968350051743 15.7009822614178 P P P 16.0358080620334 16.0938937759806 16.2031333047954 P P P LNCV6_79185_PI430048170 mRNA
CCTCTCATTTGGAAGACTATCCCTTCAATGCAGAATATTGAGGTTGAATCTCCTGGTGAG NM_020299RefSeq chr7 + 134527591 134541414 AKR1B10 57016 "aldo-keto reductase family 1, member B10 (aldose reductase)"
GO:0005515|GO:0044598|GO:0047718|GO:0045550|GO:0044597|GO:0001758|GO:0007603|GO:0007586|GO:0006081|GO:0001523|GO:0005764|GO:0005829|GO:0004033|GO:0016488|GO:0008202|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127725_PI430048170 0.7926678066757191.01985338397301 11.4001421609437 11.1352137688537 11.2968040056445 P P P 11.1925372504219 11.3480658450339 11.2137595834237 P P P LNCV6_127725_PI430048170 mRNA
CCCTGTAAATACTGGATCAATGAATGAATAAAACTCTCCTAAGAATCTCCTGAGAAATGA NM_004656RefSeq chr3 - 52401003 52410105 BAP1 8314 BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)
GO:0071108|GO:0005515|GO:0006511|GO:0016579|GO:0004843|GO:0008285|GO:0005634|GO:0001558|GO:0035517|GO:0005737|GO:0035522|GO:0003682|GO:0035520|GO:0051726|GO:0005654|GO:0008233|GO:0006464 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72088_PI430048170 0.0579237635687429 1.17801401667962 11.5493824730799 11.3094503002084 11.4338007514036 P P P 11.1267282379727 11.2395846073936 11.2246306052031 P P P LNCV6_72088_PI430048170 mRNA
ATCAGGCAAAAATGATCATGCCGAAAAAGTGGCGGAAAAGCTAGAAGCTCTCTCGGTGAA NM_001278639 RefSeq chr22 + 20115937 20127357 RANBP1 5902 "RAN binding protein 1, transcript variant 1"
GO:0043547|GO:0007165|GO:0050790|GO:0005737|GO:0008536|GO:0016032|GO:0046907|GO:0005634|GO:0005635|GO:0005092|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135833_PI430048170 0.00208016201447799 0.3585949421907066.45444445386345 6.27264598847721 6.79086309382012 P P P 7.95190926185852 7.83685723885477 8.19328550740047 P P P LNCV6_135833_PI430048170 mRNA
TTAAAGTTCACTTCTTGAGCATCAATAAAAAGGGAAGCTGTGTGGTTTTGGAATGGTAAA NM_024692RefSeq chr2 + 29115425 29183813 CLIP4 79745 "CAP-GLY domain containing linker protein family, member 4, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136090_PI430048170 0.105468907521 1.32997628861244 7.21403735486188 7.06654256328884 7.07644418885701 P P P 6.37463831795774 6.83106547578796 6.87118152227819 P P P LNCV6_136090_PI430048170 mRNA

GGGAGTTGGCTGTGTTAAAGAAAGACCATTAAATGCTTTAGACAGTGTATTTATACCAGT NM_144586 RefSeq chr2 - 132644763 132670908 LYPD1 116372 "LY6/PLAUR domain containing 1, transcript variant 1" GO:0005886|GO:0031225 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_138863_PI430048170 0.0305408383731255 1.34429168181851 10.288405206918 10.6323622893834 10.4519254125165 P P P 10.0887220198353 9.91363815101689 10.102741338829 P P P LNCV6_138863_PI430048170 mRNA
CAGACAAACCCTTTGTATTGTAGATAAGAGGAAAAGACTGAGCATGCTCACTTTTTTATA NM_005195 RefSeq chr8 - 47736913 47738164 CEBPD 1052 "CCAAT/enhancer binding protein (C/EBP), delta" GO:0001077|GO:0006366|GO:0045944|GO:0005634|GO:0000978 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_129941_PI430048170 0.0874767959100095 1.06015917710359 0.465841982894882 0.5542604118830690.512655880146644 A A A 0.3757069260438840.434682843312298 0.469332402960066 A A A LNCV6_129941_PI430048170 mRNA
CACGCTTAAAGTCCAGTGTTGACCTGTATAGTCATTTTCCTAGAAGACGTTTTAAAGTGA NM_173081 RefSeq chr10 + 22928023 23038523 ARMC3 219681 "armadillo repeat containing 3, transcript variant 1" GO:0005737|GO:0005634|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_128725_PI430048170 0.4828144042355041.04363350802175 0.281563889003423 0.2955727727111920.492750323202774 A A A 0.3172780162499510.278518079001512 0.29879564851304 A A A LNCV6_128725_PI430048170 mRNA
CCATTCATGTTGTTTTAGCTTGACCTGTTTATTTCAGCCCATGCAAAACTGTATCATATT NM_001297772 RefSeq chr1 - 167809387 167914226 ADCY10 55811 "adenylate cyclase 10 (soluble), transcript variant 3" GO:0030424|GO:0048471|GO:0043065|GO:0000287|GO:0030145|GO:0005886|GO:0045178|GO:0045177|GO:0007283|GO:0005524|GO:0030425|GO:0005829|GO:0030426|GO:0035556|GO:0005737|GO:0004016|GO:0043025|GO:0051117|GO:0006171|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_133695_PI430048170 0.1451049014336590.5694341880480512.74584677162872 1.55041985031687 2.25757465803295 A A A 3.34993693886575 3.2906142390719 2.41679070565815 P P P LNCV6_133695_PI430048170 mRNA
ACTGCGGATCCCAAACTGTTCCCTTTTTCATTTCTTGAAATGTTACCACTACAGACATTTNM_001127671 RefSeq chr5 - 38474962 38556646 LIFR 3977 "leukemia inhibitory factor receptor alpha, transcript variant 1" GO:0008284|GO:0004924|GO:0004923|GO:0019221|GO:0070120|GO:0005127|GO:0038165|GO:0043235|GO:0048861|GO:0019838|GO:0005887|GO:0004897|GO:0034097|GO:0007166|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_142206_PI430048170 0.77633227003977 1.00929375314049 0.513766961977709 0.4090536115772310.51979482789236 A A A 0.4516454487919350.507915546716587 0.44484690666741 A A A LNCV6_142206_PI430048170 mRNA
GTATCTGTACTCCTGGTATATTCAAGCACTGTTTTGAAAACAGATGACTTATTTCTCCAT NM_020144 RefSeq chr7 - 4857737 4861994 PAPOLB56903 poly(A) polymerase beta (testis specific) GO:0006378|GO:0006369|GO:0004652|GO:0005737|GO:0005783|GO:0000398|GO:0003723|GO:0005634|GO:0005524|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_105775_PI430048170 0.9548670078763640.9707211033661692.04518881083992 2.69604420265854 1.49842074657005 A A A 2.27143454101037 2.67850085526114 1.38297715221868 A P A LNCV6_105775_PI430048170 mRNA
TTCCAAGTCTTTAGAGGAAGGTACTAAGAAGACAGAAACAAGCAAAGCCGCCACCACAGA NM_017488 RefSeq chr2 - 70662083 70768243 ADD2 119 "adducin 2 (beta), transcript variant 4" GO:0030097|GO:0005516|GO:0030036|GO:0005886|GO:0046982|GO:0030507|GO:0003779|GO:0042803|GO:0032092|GO:0051016|GO:0051015|GO:0006461|GO:0005198|GO:0016023|GO:0008290|GO:0051017 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_139687_PI430048170 0.1450044666301061.80492987275569 1.76975552117885 2.18853032244697 2.07619278833343 A A A 0.365166009526752 0.899448801291622

1.84709006142814 A A A LNCV6_139687_PI430048170 mRNA
CTACCACCTTTGCAATTGTCACTTATCTTTCACTCCCTGAATAAAGTATCTATGCATATA NM_005988 RefSeq chr1 -
153056119 153057512 SPRR2A NA small proline-rich protein 2A NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141142_PI430048170 0.3602133412665670.75503683823965 4.97977340088264 3.4534365638966
3.84489612379212 P P P 4.64010724086165 4.89683927153885 4.36488988365453 P P P
LNCV6_141142_PI430048170 mRNA
CTCTCTTCTCTGCTGGCTTAAGGGTCTATTCTCCATGTGTCTATTTCTTTGATGACTTTA NM_001143978 RefSeq chrX
+ 104112525 104115847 ZCCHC18 644353 "zinc finger, CCHC domain containing 18, transcript variant 1"
GO:0008270|GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127599_PI430048170 0.1554474425828061.40106995456721 3.81775541323804
4.21043341543562 3.65886288151102 P P P 3.00589424620682 3.7981851669351
3.37139390737215 P P P LNCV6_127599_PI430048170 mRNA
CATAGAAAGCAACGTGGAGACTCAGAAGCAAGCACAGCATCAAGGAATGATCAATAAAAA NM_031895 RefSeq
chr19 + 53963035 53990215 CACNG8 59283 "calcium channel, voltage-dependent, gamma subunit
8"
GO:0030666|GO:0030054|GO:0005886|GO:0005245|GO:0045211|GO:0032281|GO:2000311|GO:0070588|GO:0014
069|GO:0007268|GO:0006816|GO:0005891 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134070_PI430048170 0.00306617043690937 0.45522884741448910.3162484531042
10.3148566148416 10.3068532261751 P P P 11.3405597655816 11.4355226853041
11.5595214484142 P P P LNCV6_134070_PI430048170 mRNA
TGCTGTTATCAGCGGGGAAATGTACTATTTAAGATCAGCTTTGTTGTAAAACCATTTGTT NM_022767 RefSeq chr15
+ 88621295 88632281 AEN 64782 apoptosis enhancing nuclease
GO:0042771|GO:0031965|GO:0004527|GO:0090305|GO:0010212|GO:0005730|GO:0005654|GO:0005634|GO:0003
676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138475_PI430048170 0.1562521698407650.856735697216515 6.93716543711312 6.7269260587646
6.70742675538796 P P P 6.83654737310941 7.01369011020926 7.18137707278711 P P P
LNCV6_138475_PI430048170 mRNA
CATAGCCAGAGAGTCATGCCACGTGGTCATTAAACCGATGATGATTGAGGCGTGAAAAAA NM_017970 RefSeq chr14
- 90278053 90332137 NRDE2 55051 "NRDE-2, necessary for RNA interference, domain containing"
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129054_PI430048170 0.2847716932855312.07690119092306 0.325019899003764
1.84923942677688 2.29540790866564 A A A 0.889439535283635 0.645654782139486
0.361399685957496 A A A LNCV6_129054_PI430048170 mRNA
TGGCTGACCAGATTGAAGCCCTGGGTTGTGCTAAAAATAAATGCAATGATTGATGCATGC NM_001127323 RefSeq
chr7 - 126438597 127252374 GRM8 2918 "glutamate receptor, metabotropic 8, transcript variant 2"
GO:0051966|GO:0042734|GO:0007608|GO:0005886|GO:0005887|GO:0004930|GO:0030818|GO:0008066|GO:0001
642|GO:0007196|GO:0007601 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_71441_PI430048170 0.4095224266714762.54723492909435 0.37178372895127 0.378973581620003
2.83308978406736 A A A 0.339807844700981 0.32377634933357 0.377236216640014 A A A
LNCV6_71441_PI430048170 mRNA
CATGAGGGACATGTGACAGTGTCATTCAGTATTATGTTCAAAAGACATTTTTATCCTGAT NM_080672 RefSeq chr20
+ 59604546 59847711 PHACTR3 116154 "phosphatase and actin regulator 3, transcript variant 1"
GO:0008599|GO:0004864|GO:0008157|GO:0005654|GO:0003779|GO:0043086|GO:0016363 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132681_PI430048170 0.00933608081949596 0.6174391206872777.78049427415381
7.82901379074692 8.14013521877111 P P P 8.72391863285684 8.45854879081639
8.66772539975559 P P P LNCV6_132681_PI430048170 mRNA
AAGTAAGAGCTAATTCATTCATTCCATGTGTGCCACTAAATAAAGAGATTGAGCAAGTGC NM_015938 RefSeq chr3

+ 161221310 161252007 NMD3 51068 NMD3 ribosome export adaptor
GO:0005737|GO:0016020|GO:0005730|GO:0043023|GO:0005654|GO:0005634|GO:0030674|GO:0015031|GO:0000
055 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_51173_PI430048170 0.2180047175707 0.7054594413533783.86827322829105 4.95852116428793
4.65258984133839 P P P 5.19072053019587 4.87286938092234 5.11293528121555 P P P
LNCV6_51173_PI430048170 mRNA
TAAAATCCCTTAGGTGTTCTTTGTTCATGCAGGCAGGTTTCTGCCGCATTTGATGTGGAG NM_002586RefSeq
chr6_GL000250v2_alt - 3517334 3522785 PBX2 5089 pre-B-cell leukemia homeobox 2
GO:0043565|GO:0005667|GO:0003700|GO:0045944|GO:0003682|GO:0009954|GO:0005634|GO:0030326|GO:0006
351|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103793_PI430048170 0.7450821013263141.11204072414332 1.35201834674706
2.18052758505261 2.45464311381749 A A A 2.24380970844777 1.01543893076671
2.18379053086777 A A A LNCV6_103793_PI430048170 mRNA
TAAGTATTGGTACAAGCCTGAGATCTCCAGGGAGCAGGCCATCGCGCTCCTCAAGGACCA NM_022648RefSeq chr2
- 217799788 217944073 TNS1 7145 tensin 1
GO:0005515|GO:0010761|GO:0005737|GO:0009986|GO:0007044|GO:0003779|GO:0005856|GO:0005925 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136319_PI430048170 0.1348791248138880.8869571591596013.0626690005307
12.9941124076829 12.8135690794165 P P P 13.1225950476043 13.1126688329724
13.1650725139738 P P P LNCV6_136319_PI430048170 mRNA
GAGTCCTAGCCCCTCCCCTGATGAAATATACATATACTCAGTTCCTTGTTATTCAAAAAA NM_001171155 RefSeq
chr19 + 7629784 7631624 PET100 100131801 "PET100 homolog (S. cerevisiae), transcript variant 1"
GO:0005739|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93661_PI430048170 0.8761980839541981.01072815600265 9.68338167831635 9.45722856375359
9.54790469982942 P P P 9.4281897543209 9.64225944531468 9.57270641531683 P P P
LNCV6_93661_PI430048170 mRNA
TACAAGTACCTTTTCATCTTCTCTGTGGCCAACATGAGGAACAGCAAGCTGAAGGACATC NM_016183RefSeq chr1
+ 19251580 19260128 MRTO4 51154 mRNA turnover 4 homolog (S. cerevisiae)
GO:0031965|GO:0005737|GO:0042254|GO:0005730|GO:0005654|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_110416_PI430048170 0.00247755985623545 2.37789267976241 5.55150417456041
5.82198949335324 5.50855521029782 P P P 4.51417876725057 4.50227734204732
4.09964671672064 P P P LNCV6_110416_PI430048170 mRNA
CTTGCGAGGCGTCCAATAAGCACGGCCATGCGAGGGCGCTCTACGTACTTGTGGTCTACG NM_145296RefSeq chr19
- 43622369 43639839 CADM4 199731 cell adhesion molecule 4 GO:0016021|GO:0007155|GO:0070062
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132255_PI430048170 0.3671495860071080.7976510091207753.45436341380265
3.42935377825483 3.59841906318621 P P P 3.62272248012575 4.26082195542219 3.452126144268
P P P LNCV6_132255_PI430048170 mRNA
AGTACACCAGCTCCAAGTGAGGCGTTCCTCGGCGTCCTGAACCCAAAGGCTCTTTTCAGA NM_175055RefSeq chr1
+ 228458106 228458558 HIST3H2BB 128312 "histone cluster 3, H2bb"
GO:0003674|GO:0046982|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0003677 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131637_PI430048170 0.8185928706035871.01964575569647 6.53375719474151
6.15101254620388 6.78476822598079 P P P 5.51883818641066 6.8496072465455
6.74843327872774 P P P LNCV6_131637_PI430048170 mRNA
AAGCAGATGCTTGTGTTTCATTTTCCTTCCTGGTTTGTGTGTGTTAATTCTCTCTCTCTC NM_152308RefSeq chr16 +
11345437 11351763 RMI2 116028 "RecQ mediated genome instability 2, transcript variant 1"
GO:0006260|GO:0005737|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_131340_PI430048170 0.00305163088452606 2.30090021377491 5.03015109428983
4.59181652787766 4.940804230703 P P P 3.81622302760913 3.51740254819622
3.64303194466484 P P P LNCV6_131340_PI430048170 mRNA
TGAATCCACATCCTGAAGGGAGGCTACAACTGGAATAAAAATAAGAAAGCTTTCAAAAAA NM_153608 RefSeq chr19
+ 48270098 48287608 ZNF114 163071 "zinc finger protein 114, transcript variant 1"
GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130147_PI430048170 0.0703510428831429 1.55909041554647 7.42513629931143
7.24466653541353 7.4852990828914 P P P 6.34529103900504 6.75760166690072
7.05448276561344 P P P LNCV6_130147_PI430048170 mRNA
CTTGAGTGTTGTGGTATGAAAAGCATTGTGGTCTTTCTACACTAATGAAGTGCAAATAAA NM_001025300 RefSeq
chr18 + 8609444 8639382 RAB12 201475 "RAB12, member RAS oncogene family"
GO:0032869|GO:0005776|GO:0005794|GO:0009306|GO:0008333|GO:0003924|GO:0006914|GO:0005525|GO:0005
765|GO:0072659|GO:0005764|GO:0006886|GO:0006904|GO:0006184|GO:0000139|GO:0032593|GO:0017157|GO:0
032482|GO:0044257|GO:0019003|GO:0055038|GO:0010008|GO:0016239 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_134246_PI430048170 0.1000784160219060.2202535159793154.31473736518912
1.05311400167685 1.44650680469753 P A A 5.54269027754019 5.12337263983363
4.93910211561667 P P P LNCV6_134246_PI430048170 mRNA
TGTGGAATAGCTCAAAATGTCCATTCTGTTTTAAGTAACAGAATTGATAACTGAGCAAGG NM_030979 RefSeq chr13
+ 25096137 25098566 PABPC3 5042 "poly(A) binding protein, cytoplasmic 3"
GO:0005737|GO:0000166|GO:0016071|GO:0008143|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136642_PI430048170 0.4729711988650680.9621206598830090.410322469230474
0.43569188279753 0.352701753817308 A A A 0.5717156372376050.384019036342903
0.40389838856184 A A A LNCV6_136642_PI430048170 mRNA
TGAGAATGGACATGAAATGAGCTCTTCATTAATACGCCTGTGAGTCTTCATAAATATGCC NM_176817 RefSeq chr7
- 141972630 141973773 TAS2R38 5726 "taste receptor, type 2, member 38"
GO:0033038|GO:0007186|GO:0005886|GO:0016021|GO:0001580 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139323_PI430048170 0.00208045600010882 2.40927587145923 5.33165040508293
5.69123510783455 5.40972334003947 P P P 3.95623171109905 4.24709266019896
4.41237993061783 P P P LNCV6_139323_PI430048170 mRNA
TGTGGGTGGGGGACTAACTGCGCAATGTAGTTAGGTGCTCAATAAACGGAGTTGCCGCTG NM_001301159 RefSeq
chr16 + 566994 569495 NHLRC4 283948 "NHL repeat containing 4, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_138865_PI430048170 0.1341268704331221.12374201795738 13.6878965140172
13.9217248908926 13.7331512919702 P P P 13.6081566211034 13.6692837085043
13.5694436616707 P P P LNCV6_138865_PI430048170 mRNA
GTTCTCTTCTTTTGGGGAGAACGTAGAGTCTCACTCTAGATGTTTTATGTATTATATCTA NM_004364 RefSeq chr19 -
33299933 33302564 CEBPA 1050 "CCAAT/enhancer binding protein (C/EBP), alpha, transcript variant 1"
GO:0005515|GO:0003700|GO:0008285|GO:0044212|GO:0006366|GO:0030324|GO:0003705|GO:0031100|GO:0019
221|GO:0005634|GO:0006091|GO:0032403|GO:0042803|GO:0016363|GO:0045944|GO:0045945|GO:0035189|GO:0
016032|GO:0030099|GO:0030225|GO:0048469|GO:0008203|GO:0071285|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143826_PI430048170 0.412836907396928 1.24694013248558 0.2675097304462
1.11786578472074 0.417226209939804 A A A 0.3596045662106320.303010667044639
0.333342150448926 A A A LNCV6_143826_PI430048170 mRNA
CTGTATATAAACTTCTTTCAATCTACAATAATAAAGGCTTGAGGTAAACTGCTTAAAAAA NM_001362 RefSeq chr14

+ 101561350 101563452 DIO3 1735 "deiodinase, iodothyronine, type III"
GO:0005886|GO:0004800|GO:0044281|GO:0008150|GO:0034641|GO:0042446|GO:0006590|GO:0016021|GO:0040018|GO:0033798|GO:0010008|GO:0042404|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132360_PI430048170 0.00418264937884335 0.5792880580333757.73066633263302
7.6069078011847 7.91879805619151 P P P 8.42338151811106 8.4602050838026
8.73273901884622 P P P LNCV6_132360_PI430048170 mRNA
TCCTCAACTGCCCCAAATCTCTTAATAGCTTCTAGTGCTGCTACAATCTAAGTCAGGTCA NM_003851RefSeq chr1
- 167541013 167553819 CREG1 8804 cellular repressor of E1A-stimulated genes 1
GO:0005667|GO:0006357|GO:0008283|GO:0010181|GO:0003714|GO:0016491|GO:0007275|GO:0040008|GO:0070062|GO:0055114|GO:0008134 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129543_PI430048170 0.3985088628052940.8454592621292140.260155833989282
0.2718517480729280.422622691036796A A A 0.3594520138636080.305748327866211
0.934277447940131A A A LNCV6_129543_PI430048170 mRNA
AGTGTAGCCCAGGGCAGATGTCAATAAATGCATACTCTGTATTTCGATTCTGAGAAAAAA NM_003613RefSeq chr15
- 65195998 65211502 CILP 8483 "cartilage intermediate layer protein, nucleotide pyrophosphohydrolase"
GO:0031012|GO:0043569|GO:0004035|GO:0005578|GO:0004551|GO:0005615|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136074_PI430048170 0.1473127795598 0.8352378747285886.65921918413876
6.64922688014994 6.29366739758755 P P P 6.67917508387861 6.93413165688556
6.78579170001264 P P P LNCV6_136074_PI430048170 mRNA
CAAAAGCAAATAAATGCAGACAAACAAACCAAGACCAAAGGCTCTTTTTAGAGCCACCCANM_003517RefSeq chr1
+ 149886974 149887411 HIST2H2AC 8338 "histone cluster 2, H2ac"
GO:0008150|GO:0003674|GO:0046982|GO:0005634|GO:0000786|GO:0003677|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134569_PI430048170 0.0789137433413386 0.6792670589688168.51568722450177
8.00431252240259 8.37193175747337 P P P 8.51474192822316 9.11839507195005
8.91582003694976 P P P LNCV6_134569_PI430048170 mRNA
TAAGAAGTTCATCTGCATATCTGACCTTCGGGCCCAAATTGCAGGATACCTATATGGGGT NM_006445RefSeq chr17
- 1650628 1684882 PRPF8 10594 pre-mRNA processing factor 8
GO:0000244|GO:0005515|GO:0006397|GO:0008380|GO:0010467|GO:0030623|GO:0005634|GO:0071013|GO:0016020|GO:0016607|GO:0000398|GO:0000375|GO:0005654|GO:0005682|GO:0017070|GO:0070530 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142773_PI430048170 0.0716940639707793 1.44039659839688 8.55592368611976
9.06347022531619 8.78196928732402 P P P 8.26099188216245 8.31679100543799
8.28862725819521 P P P LNCV6_142773_PI430048170 mRNA
GTAGAGCGCGGTTTTATTTTTGTACTGACATTGGTAAGAGACTGTATAGCATCTATTTAT NM_175709RefSeq chr22
- 39130773 39152533 CBX7 23492 chromobox homolog 7
GO:0035102|GO:0000792|GO:0005515|GO:0031519|GO:0000790|GO:0003727|GO:0005634|GO:0000122|GO:0035064|GO:0006351|GO:0005737|GO:0003682|GO:0048733|GO:0005654|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127904_PI430048170 0.2329301849043421.18913052733803 3.56892453173016
3.29627411594613 3.36167975538814 P P P 3.22973487635533 3.36625711371353
2.84651053259097 P P P LNCV6_127904_PI430048170 mRNA
TTGAACAACTACAATGCTGAAGTATGGGCATATCTGGCTCTGGTCTGCCTGAAAGTTGGA NM_145170RefSeq chr10
- 73253757 73358859 CFAP70 118491 cilia and flagella associated protein 70
GO:0008150|GO:0003674|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135864_PI430048170 0.0136392190879669 0.3144553204421731.40816773651648
0.6982670859287580.611409582738962A A A 2.09163733010034 2.48617031050642

3.10317515838531 A A P LNCV6_135864_PI430048170 mRNA
GCTGTATTGCAGTCATATATAAGGTAAAGTCAGTCTCTTGTTCCTATTAAAAAGCTACCA NM_006496RefSeq chr1
+ 109548563 109595832 GNAI3 2773 "guanine nucleotide binding protein (G protein), alpha inhibiting
activity polypeptide 3"
GO:0005886|GO:0003924|GO:0007268|GO:0005765|GO:0007194|GO:0006906|GO:0007193|GO:0046872|GO:0005
737|GO:0006810|GO:0004871|GO:0070062|GO:0005813|GO:0005794|GO:0005834|GO:0019904|GO:0030168|GO:0
030496|GO:0005525|GO:0031683|GO:0042588|GO:0006184|GO:0032794|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140673_PI430048170 5.31453188699559e-05 1.75099008206851 9.31617889873079
9.42674686559896 9.38574350099378 P P P 8.57751279396855 8.61297634223804
8.51409180909242 P P P LNCV6_140673_PI430048170 mRNA
ATGCTGGACCAGATCAACTCCTGTCTGGACCACCTGGAGGAGAAGAATGACCACCTCCAC NM_024112RefSeq chr9
+ 128160259 128163928 C9orf16 79095 chromosome 9 open reading frame 16
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123253_PI430048170 0.00309910325049198 1.49503049546703 5.88324575805454
6.00032870165606 5.82330944616015 P P P 5.20837243419244 5.44311036345205
5.31090204898625 P P P LNCV6_123253_PI430048170 mRNA
TGAGAGCGTCGAGCTGTCACCATGGGTGATCACGCTTGGAGCTTCCTAAAGGACTTCCTG NM_001151RefSeq chr4
+ 185143262 185150384 SLC25A4 291 "solute carrier family 25 (mitochondrial carrier; adenine nucleotide
translocator), member 4"
GO:0005515|GO:0005743|GO:0005634|GO:0006091|GO:0044281|GO:0055085|GO:0005739|GO:0006112|GO:0008
637|GO:0050796|GO:0005887|GO:0006810|GO:0015207|GO:0016032|GO:0015853|GO:0060546 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140931_PI430048170 0.00118335486117048 0.728091599458754 10.1521990767349
10.1619532922778 10.1530302956692 P P P 10.5842959456364 10.6091530304789
10.6464979590843 P P P LNCV6_140931_PI430048170 mRNA
TTTGCTGGTTTTCTTCGGTGTTTTTTCTAATGCAATAAACTCATTTCTGCCTGCTGCAAA NM_015704RefSeq chr22 -
41598027 41621057 DESI1 27351 desumoylating isopeptidase 1
GO:0005737|GO:0006508|GO:0008233|GO:0005634|GO:0042802 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131194_PI430048170 0.0125114624642631 0.480592461037623 4.10530079040476
3.74030031383507 3.90754783391939 P P P 4.62355797798876 5.02851765802648
5.23100844952616 P P P LNCV6_131194_PI430048170 mRNA
TGTCACCACTTCAAAAAATCAATTTGTTCTTAGAACCTGGTTGAAAATACCAGGAAACTG NM_177444RefSeq chr12
+ 27524111 27695564 PPFIBP18496 "PTPRF interacting protein, binding protein 1 (liprin beta 1),
transcript variant 2" GO:0005886|GO:0007155|GO:0005925 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_138249_PI430048170 0.201013860193888 2.16357466589648 0.269112003647231
1.88352026723316 1.69540355292473 A A A 0.356618450191341 0.312049225039796
0.307299288902703 A A A LNCV6_138249_PI430048170 mRNA
CAAGCCCTGTTTGCCTAATTAAATTGATTGTTACTTCAATTCTATCTGTTGAACTAGGGA NM_001206977 RefSeq
chr12 + 100473772 100563867 NR1H4 9971 "nuclear receptor subfamily 1, group H, member 4,
transcript variant 6"
GO:0005515|GO:0090181|GO:0010467|GO:0032052|GO:0003700|GO:0001190|GO:0006367|GO:0003705|GO:0003
707|GO:0070858|GO:0071417|GO:0046965|GO:2000213|GO:0003690|GO:0070857|GO:0045944|GO:0043401|GO:0
032496|GO:0001080|GO:0008206|GO:0004879|GO:0042277|GO:0016922|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142214_PI430048170 0.784363216356409 0.955191223980423 1.92287107586443
1.43494939862339 2.30588732171264 A A A 2.29809930956552 1.73286511535519

1.90107476643597 A A A LNCV6_142214_PI430048170 mRNA
TCTGCTTTGAGGTACTCCATGTACAGTCTAATGATGATCTTTCACTGATTTATAGTCAGC NM_005517RefSeq chr1
+ 26472410 26476642 HMGN2 3151 high mobility group nucleosomal binding domain 2
GO:0005737|GO:0031492|GO:0005634|GO:0000785 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129924_PI430048170 0.00771162928279442 0.3785206233124577.21698442870737
7.07558860653494 7.21156030567788 P P P 8.2932480041935 8.54608268343894
8.82485380861682 P P P LNCV6_129924_PI430048170 mRNA
ACCTTCCCTTCACAACCAATCAAGTGAATACTTGATTATTATCTCTTCCTTACTGTGCTT NM_152716RefSeq chr11 -
59636715 59669038 PATL1 219988 protein associated with topoisomerase II homolog 1 (yeast)
GO:0005515|GO:0010467|GO:0033962|GO:0003723|GO:0043928|GO:0000290|GO:0030014|GO:0043231|GO:0005
829|GO:0008266|GO:0034046|GO:0016607|GO:0000932|GO:0016605|GO:0000288 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137740_PI430048170 0.7796636585289091.27793138451981 0.2724796815240421.8813691987343
0.277093640189473 A A A 0.49888091955142 1.09626871337866 0.293073065698043 A A A
LNCV6_137740_PI430048170 mRNA
CAAAAAGCTATATTTGTTTCTGTTGCCTAAACATTTTCATTGAACAAGCCCCCAGAATTG NM_033057RefSeq chr6
- 27911184 27912396 OR2B2 81697 "olfactory receptor, family 2, subfamily B, member 2"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128193_PI430048170 0.7775396171498650.941256312568781 0.534790902322402
0.4476349109185870.575610360052077 A A A 0.3025777232820770.947974671676342
0.494542507361666 A A A LNCV6_128193_PI430048170 mRNA
TTTATCAATTAGCAGAATAATTATCATAAGATCCAAAATGTCTTCCAGACACCCCTGCAC NM_173521RefSeq chr9
- 111686518 111783499 C9orf84 158401 "chromosome 9 open reading frame 84, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128370_PI430048170 0.1524044670701841.48375485678698 3.75287879910431
4.09669646301252 3.77918406358679 P P P 2.69608728098764 3.52453705557061
3.57067328847629 A P P LNCV6_128370_PI430048170 mRNA
CGGAAGGAGAGGTATTTCTTAGAGAGATCATCATTTTATGGTGCCTTGAAATAAAAATAC NM_021220RefSeq chr20
- 18024151 18057882 OVOL2 58495 "ovo-like zinc finger 2, transcript variant 1"
GO:0008285|GO:0006366|GO:0044212|GO:0000981|GO:0010837|GO:0001755|GO:0005634|GO:0010719|GO:0009
953|GO:0046872|GO:0001947|GO:0045617|GO:0010944|GO:0060716|GO:0051726|GO:0045746|GO:0006357|GO:0
060214|GO:0001525|GO:0003677|GO:0001842|GO:0009913|GO:0060347|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128425_PI430048170 0.00607466533616898 0.6689255160271699.21887652268139
9.40932661454995 9.46576507628801 P P P 9.93255454022015 9.81291854904619
10.0870429444018 P P P LNCV6_128425_PI430048170 mRNA
TTCAAGGTCCCCAAATGGCAGCATTTTATGTTCTGACCTGTTTGTGTTATATAGTGGTTT NM_020967RefSeq chr20
- 46060986 46089941 NCOA5 57727 nuclear receptor coactivator 5
GO:0005515|GO:0006355|GO:0046627|GO:0003682|GO:0005654|GO:0005634|GO:0042593|GO:0015629|GO:0005
615|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63092_PI430048170 0.3306454210071060.7700411848421783.33075031637691 2.16958063713011
3.02185595761591 P A P 3.03323729674637 3.36356702784686 3.45638471035923 P P P
LNCV6_63092_PI430048170 mRNA
AGGTGGAAGTAAAATCTGAGAAGCTTGACTTCAAGGACAGAGTCCAGTCGAAGATTGGGT NM_001123066
RefSeq chr17_GL000258v2_alt - 760287 893837 MAPT 4137 "microtubule-associated protein tau,
transcript variant 6"
GO:0008017|GO:0005515|GO:0030424|GO:0017124|GO:0005886|GO:0048699|GO:0045773|GO:0048675|GO:0006
921|GO:0005829|GO:0030426|GO:0047497|GO:0007628|GO:0045298|GO:0071813|GO:0031116|GO:0032387|GO:0

019901|GO:0005930|GO:0005875|GO:0005874|GO:0031113|GO:0006915|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135594_PI430048170 0.0824639999559723 0.4507121931164973.20205858347333 2.13703101840356 2.64401318492457 P A A 3.10170884264752 3.87386781504338 4.37856895999418 P P P LNCV6_135594_PI430048170 mRNA AATGCGCACACAGTGAACGTTTGTTAGAACTACACACAATAAAGACACTGTTTTCCTTTT NM_030579RefSeq chr16 + 69424594 69466264 CYB5B 80777 cytochrome b5 type B (outer mitochondrial membrane)
GO:0016020|GO:0005741|GO:0016021|GO:0046872|GO:0055114|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141446_PI430048170 0.3428096592363930.7328313332302791 1.8700320084871 11.7132354923493 11.8892341458437 P P P 12.7845243628379 11.7204065915423 12.1150093927943 P P P LNCV6_141446_PI430048170 mRNA GTTGCCACCTGTTAAAATGTACACTGGATATGTTGTTAAACACGTGTCTATAATGGAAAC NM_000596RefSeq chr7 + 45888359 45893668 IGFBP1 3484 insulin-like growth factor binding protein 1
GO:0008286|GO:0030307|GO:0031994|GO:0031995|GO:0005576|GO:0042246|GO:0005615|GO:0030968|GO:0007165|GO:0043567|GO:0006987|GO:0044267|GO:0005520 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144391_PI430048170 0.00480632688272796 1.46300668158628 6.45339452347202 6.41045132323664 6.2215810959262 P P P 5.89248959051563 5.86252466488325 5.68543323850394 P P P LNCV6_144391_PI430048170 mRNA CCACGTATTTTCCAGTCTCTTTTATAAAGTCTCAGACTATAATAAACACAGCTTGCCCAG NM_002813RefSeq chr12 + 121888730 121917865 PSMD9 5715 "proteasome (prosome, macropain) 26S subunit, non-ATPase, 9, transcript variant 1"
GO:0005515|GO:0006511|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0034641|GO:0005737|GO:0000082|GO:0016032|GO:0032024|GO:0090090|GO:0046676|GO:0006977|GO:0000209|GO:0043066|GO:0005838|GO:0006521|GO:0003713|GO:0051437|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139330_PI430048170 0.2479139247928551.01988759680478 0.313695368486088 0.2528339016440350.287020936588326A A A 0.2592606742173060.249331438015757 0.260346647504984A A A LNCV6_139330_PI430048170 mRNA CATGGGGAAATCCCTGTTATTTTGTGAATTGGGACAAGATAACATAGCAGAGGAATTAAT NM_005365RefSeq chrX + 149781936 149787737 MAGEA9 4108 melanoma antigen family A9
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136457_PI430048170 0.41171757818405 0.8249144954928070.490301760786362 0.61549178879454 0.563067155562921A A A 1.24347421055823 0.459472188400136 0.685637303903621A A A LNCV6_136457_PI430048170 mRNA TGAAGGCTTTTTACCCAGCAATGTCCTCAATGAGGGTCTTTTCTTTCCCTCACCAAAACC NM_005621RefSeq chr1 - 153373707 153375599 S100A12 6283 S100 calcium binding protein A12
GO:0005515|GO:0045576|GO:0050663|GO:0006805|GO:0005886|GO:0050832|GO:0005634|GO:0005829|GO:0005737|GO:0006954|GO:0051092|GO:0050786|GO:0043406|GO:0031640|GO:0005856|GO:0043123|GO:0042742|GO:0005507|GO:0005509|GO:0030593|GO:0005576|GO:0002548|GO:0045087|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136244_PI430048170 0.179227874615026 1.12503263920953 0.649566870268793 0.3755349380633880.60126150330437 A A A 0.28366316999193 0.406917021358206 0.435958340629114A A A LNCV6_136244_PI430048170 mRNA CTGGCAACAACAGATTCTCTTGGCTCATATTTCTTTTCTTTCTCATCTTGATGATGATCG NM_006919RefSeq chr18 - 63655196 63661963 SERPINB3 6317 "serpin peptidase inhibitor, clade B (ovalbumin), member 3"
GO:0010951|GO:0005737|GO:0004867|GO:0001618|GO:0010466|GO:0005634|GO:0009615|GO:0043086|GO:0031982|GO:0005615|GO:0070062|GO:0045861 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_111718_PI430048170 0.5603412942776061.02719095828581 12.4744467328847

12.5691501050993 12.5137959299234 P P P 12.5859871374745 12.4475053284403
12.4029867619839 P P P LNCV6_111718_PI430048170 mRNA
GGCCAGCACCGTGGGGCTGTGGGAATCGCTCTTATTTATATTTAAACACCTTGGATTTTC NM_001097620 RefSeq
chr7 - 1542234 1556430 TMEM184A 202915 transmembrane protein 184A GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_55366_PI430048170 0.3561243811797260.7727606944174011.64563964302959 0.279862261060927
0.519733278356524 A A A 1.27414256254903 1.40066206523673 1.27294526333749 A A A
LNCV6_55366_PI430048170 mRNA
TTATCCACAAAGGTAGCGGCCACATGGTTTTTAAAGTATGAGAAACACAGTTTGTCCTCT NM_002023 RefSeq chr1
- 203340620 203351429 FMOD 2331 "fibromodulin, transcript variant 1"
GO:0005796|GO:0005975|GO:0005578|GO:0005576|GO:0044281|GO:0005615|GO:0042339|GO:0031012|GO:0007
181|GO:0018146|GO:0030198|GO:0009405|GO:0042340|GO:0030203|GO:0043202 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143000_PI430048170 0.0793890825619243 1.54792688675393 5.34010408482107
5.48000358832851 5.46129155045411 P P P 5.13856711918996 4.73980283779228
4.42751510760472 P P P LNCV6_143000_PI430048170 mRNA
TCAACGTGCTGGATTACAGCCTCCTGATAGCCTTCCAACGTCTCCACGAGGATGAGAGGG NM_001135219 RefSeq
chr9 - 127921528 127930797 PIP5KL1 138429 "phosphatidylinositol-4-phosphate 5-kinase-like 1,
transcript variant 1" GO:0046854|GO:0005737|GO:0016020|GO:0042995|GO:0005524|GO:0016308 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_119605_PI430048170 0.8048135281861061.010990989002 0.33486654672381
0.3378386410899290.472026035167911 A A A 0.4293495821781490.307416148078669
0.362364961658932 A A A LNCV6_119605_PI430048170 mRNA
TGTTTGCAGCGGAAGTGGGAAACCTGTAGGGTATGGTCCAGCTGTGCCGCACCGAGGCGA NM_001843 RefSeq
chr12 + 40692441 41072411 CNTN1 1272 "contactin 1, transcript variant 1"
GO:0005886|GO:0021549|GO:0031225|GO:0010628|GO:0001948|GO:0007219|GO:0016020|GO:0007411|GO:0010
765|GO:0010976|GO:0030246|GO:0007155|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141676_PI430048170 0.1591464390957250.815482970376047 7.10196411884078
6.88502310091552 6.93216556856828 P P P 7.49029481233583 7.26249799175563
7.02014360917439 P P P LNCV6_141676_PI430048170 mRNA
CCCCAACTGTTTGTTAGTATTATTATTACTACAAGAATAAAGGATTCCTGAGAGCCTGTC NM_001198773 RefSeq
chr1 - 151291796 151327657 PI4KB 5298 "phosphatidylinositol 4-kinase, catalytic, beta, transcript
variant 2"
GO:0004430|GO:0005515|GO:0048471|GO:0005886|GO:0006661|GO:0048015|GO:0005741|GO:0044281|GO:0005
524|GO:0006898|GO:0005829|GO:0046854|GO:0007165|GO:0005737|GO:0000139|GO:0030867|GO:0006644|GO:0
005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128732_PI430048170 0.5360082833690560.886114169693823 2.98660719517699
3.48701862390603 2.56378340684502 A P A 3.46157371938152 3.2332449044254
2.97278028511163 P P P LNCV6_128732_PI430048170 mRNA
GAAACCAAAATTAAAGAGAGAAAGAGAGAGCGTGCACGCTCCTGCTTTGTCTTTCCTGTG NM_052925 RefSeq chr19
+ 54449161 54462046 LENG8 114823 leukocyte receptor cluster (LRC) member 8 GO:0005515 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108178_PI430048170 0.00985555939581978 0.5515260235808815.38775111585732
5.26284597905982 5.43488077445474 P P P 5.974578678669 6.30992194022849
6.35298734079099 P P P LNCV6_108178_PI430048170 mRNA
TATTCATATAGCATAACCTGAGGTTGGAGAGGACCACTTGGGAGCCTGTAACCAAAACTA NM_001242797 RefSeq
chr6 - 26634382 26659752 ZNF322 79692 "zinc finger protein 322, transcript variant 1"
GO:0006355|GO:0005813|GO:0005737|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_71179_PI430048170 0.92449798407034 0.9942234656018234.64486610745744 4.66969143921506
4.55722759214349 P P P 4.52437904273378 4.7227974237322 4.6451929485856 P P P
LNCV6_71179_PI430048170 mRNA
CACTAGGAAAAGACTTCTGTTTGCTCTTGATGTCAGCCCTTTATCCAGTACTGGAGAAGG NM_014657 RefSeq chr20
- 37983006 38033468 TTI1 9675 "TELO2 interacting protein 1, transcript variant 1"
GO:0005515|GO:0032006|GO:0005737|GO:0031931|GO:0031932 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136634_PI430048170 0.7044508986405420.9767891379374580.569642255925067
0.4866634080594880.299474087272239 A A A 0.4150108091737030.546383660570556
0.506023001399526 A A A LNCV6_136634_PI430048170 mRNA
CACTTCGGAAGCTAATAAGATACCATGGTTTTCTATGTTACTCCCATTGTAACATTAGTA NM_021723 RefSeq chr7
+ 87934250 88202889 ADAM22 53616 "ADAM metallopeptidase domain 22, transcript variant 1"
GO:0005515|GO:0030424|GO:0008344|GO:0007162|GO:0005178|GO:0022011|GO:0006508|GO:0008270|GO:0016
021|GO:0007417|GO:0007155|GO:0004222 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134468_PI430048170 0.0019381207259985 0.2029737985930614.94048055343327
4.97439179714717 5.06416416978987 P P P 7.01548827717522 7.43440902696971
7.39777387497571 P P P LNCV6_134468_PI430048170 mRNA
GTTGTGTATGGTAGTTCTCACTGGATGCTAGAGTTTTCAAAACCACTATTCTTCTAATAA NM_032440 RefSeq chr10
+ 96832954 96964441 LCOR 84458 "ligand dependent nuclear receptor corepressor, transcript variant
1" GO:0003700|GO:0006366|GO:0005634|GO:0000122|GO:0003677|GO:0008134 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_137205_PI430048170 0.0154976952722101 0.6380678663847717.42133117466357
7.15261289769131 7.17632626367098 P P P 7.75910078160975 8.13503185122182
7.78508045281984 P P P LNCV6_137205_PI430048170 mRNA
TTACTCAGCCTAAGGAAACAAGTACACTCCACACATGCATAAAGGAAATCAAATGTTATT NM_001244950 RefSeq
chr10 - 72059033 72088773 SPOCK29806 "sparc/osteonectin, cwcv and kazal-like domains
proteoglycan (testican) 2, transcript variant 3"
GO:0019800|GO:0007165|GO:0030198|GO:0010811|GO:0005509|GO:0050840|GO:0005578|GO:0045595|GO:0005
539|GO:0007416 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143878_PI430048170 0.3799804123563940.7620452281282560.582276749870539
0.6233415540813090.545570914460919 A A A 0.5865276167686411.50045748138238
0.651312434145555 A A A LNCV6_143878_PI430048170 mRNA
GGTTGGACAATTTACCCTAAACAAATTAAACCATGGAAAGTGCAAACACATGAATGAAAC NM_017913 RefSeq chr9
+ 4679552 4708398 CDC37L1 55664 cell division cycle 37-like 1
GO:0005515|GO:0005737|GO:0006457|GO:0031072|GO:0051087|GO:0050821|GO:0051082 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_89503_PI430048170 0.1311039346073690.5028299879392481.70174975612796 3.24345257923377
2.92515462517949 A P P 3.87537265057894 3.43840590706047 3.89653762643319 P P P
LNCV6_89503_PI430048170 mRNA
GACCTTTGTATTCCTTGGAATTGGAAGAATGGAGAAGCCATTAAGTAACACAGAAATCTG NM_173826 RefSeq chr3
+ 44338451 44409448 TCAIM 285343 "T cell activation inhibitor, mitochondrial, transcript variant 1"
GO:0005739 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137695_PI430048170 0.000613313518989863 1.58350253339762 10.9072114093019
10.964465178751 10.8702665842113 P P P 10.3260007722161 10.1722146725084
10.2518386811359 P P P LNCV6_137695_PI430048170 mRNA
GATGCCTGGGCTGTCTTTGCTATATGTAAATAGAGCCATTGGATCTTTATTTTTGATTAA NM_001282651 RefSeq
chrX - 48903611 48911958 SLC35A2 7355 "solute carrier family 35 (UDP-galactose transporter),
member A2, transcript variant 8"
GO:0005515|GO:0005794|GO:0015785|GO:0000139|GO:0072334|GO:0005634|GO:0005351|GO:0016021|GO:0006

012|GO:0005459|GO:0055085|GO:0015992 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_58449_PI430048170 0.0484864258310582 1.44397904108805 6.48324992567372
6.89936046797044 6.68815494238175 P P P 6.43758458377153 6.06930471636114
5.95916411456438 P P P LNCV6_58449_PI430048170 mRNA
TGTGAGTGCTGGTAAGACCTGCTAGCCAACATTCAGCTGCTCTGTCCTCTCCATGCCTGG NM_054025 RefSeq chr11
- 134378503 134411918 B3GAT1 27087 "beta-1,3-glucuronyltransferase 1, transcript variant 2"
GO:0015018|GO:0000139|GO:0008499|GO:0005975|GO:0009405|GO:0006486|GO:0044281|GO:0016021|GO:0030
204|GO:0030203|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_56806_PI430048170 0.0454938448601988 1.76422656067562 3.53917136611992
3.90791454562829 3.62513763216635 P P P 2.39745064027478 3.05778995149312
3.08677391720162 A P P LNCV6_56806_PI430048170 mRNA
AGGAAACACCAGGCCAACCACAGCTGGGGATAAAATAGCACAACCACACCCTGCCGTCCA NM_015916 RefSeq
chr10 - 103446785 103452405 CALHM2 51063 "calcium homeostasis modulator 2, transcript variant 1"
GO:0034220|GO:0005261|GO:0005887|GO:0006812 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139851_PI430048170 0.29870563940713 0.980001160117661 0.338490460131261
0.3573423458554280.346022750960144 A A A 0.4125524821423480.34032648139315
0.375568670081014 A A A LNCV6_139851_PI430048170 mRNA
GCTTTGTGGTTCATGCAAACAATGTGCAGATGATAGCACCTCCATATTACTAATAAAAAT NM_133329 RefSeq chr2
- 42442016 42494097 KCNG3 170850 "potassium channel, voltage gated modifier subfamily G, member
3, transcript variant 1"
GO:0005515|GO:0005251|GO:0005886|GO:0005783|GO:0008076|GO:0007268|GO:0051260|GO:0034765|GO:0016
021|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134366_PI430048170 0.811163307388046 0.979657857205941 0.340823648965987
0.3474743991380750.286096814100001 A A A 0.2465574468452660.275550300721395
0.525422793853947 A A A LNCV6_134366_PI430048170 mRNA
GAGAATTTCATTCTTGAGAGAATCCTTACGAGTACAGCAAACCCTTCATCACAAGTTCAA NM_001136038 RefSeq
chr19 - 53107878 53132918 ZNF415 55786 "zinc finger protein 415, transcript variant 1"
GO:0006355|GO:0005737|GO:0003700|GO:0015630|GO:0005730|GO:0003677|GO:0046872|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138241_PI430048170 0.925348472795525 0.98667223794433 12.103124293708 12.103124293708
11.9855912694919 P P P 11.8548294980022 12.1928646927023 12.1805853502556 P P P
LNCV6_138241_PI430048170 mRNA
ATTGAAGTCGGGCCTCTATGCCAACTGGTTCCTTTTGTTCTCAATAAATGTTGGGTTTGG NM_001289413 RefSeq
chr6_GL000256v2_alt - 3180980 3190826 EHMT2 10919 "euchromatic histone-lysine N-
methyltransferase 2, transcript variant 1"
GO:0005515|GO:0000790|GO:0016571|GO:0006325|GO:0034968|GO:0018027|GO:0005634|GO:0000122|GO:0016
279|GO:0043231|GO:0018024|GO:0006306|GO:0002039|GO:0046974|GO:0070742|GO:0005654|GO:0008270|GO:0
045111|GO:0046976|GO:0006275|GO:0070734|GO:0051567 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_126976_PI430048170 0.00354870156803082 0.416369995184455 4.13390418577725
4.1320474557832 4.58666938104313 P P P 5.27683236211446 5.67477516163053
5.70410924950041 P P P LNCV6_126976_PI430048170 mRNA
GGCCTAATGTGCTGTATTATGAAGCCTTGTGACTGAAAAATATGTTTACATATGTTGTCT NM_032435 RefSeq chr1
+ 233327767 233385148 KIAA1804 84451 mixed lineage kinase 4
GO:0000186|GO:0046777|GO:0018108|GO:0006468|GO:0007257|GO:0005575|GO:0004713|GO:0005524|GO:0004
709|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141667_PI430048170 0.0660441997424455 1.05310870024378 0.375695250784416
0.339285876025956 0.29455062546976 A A A 0.248297099755395 0.291864001480854
0.246087932543527 A A A LNCV6_141667_PI430048170 mRNA

CTGTCCAGGTTGTTCATATAATAATATGCTGTGAGCATCTTTCCATGACATTAAATCATC NM_001082 RefSeq chr19 - 15878023 15898120 CYP4F2 8529 "cytochrome P450, family 4, subfamily F, polypeptide 2" GO:0005515|GO:0019369|GO:0000038|GO:0001676|GO:0052871|GO:0006805|GO:0052872|GO:0017144|GO:0055078|GO:0044281|GO:0006691|GO:0006690|GO:0043231|GO:0036101|GO:0005737|GO:0016324|GO:0042371|GO:0008392|GO:0005506|GO:0019373|GO:0050051|GO:0018685|GO:0052869|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139494_PI430048170 0.435043997559593 1.28381610432176 0.759242350288297 0.290135521366766 1.35591292297407 A A A 0.329852731436182 0.286408370906868 0.838429707927252 A A A LNCV6_139494_PI430048170 mRNA
CATTTATGAGACCCATAGGAATCCTTCCAACAGCCAAAGAGTTGAGTCTAACTCTTTCCT NM_003830 RefSeq chr19 - 51611502 51630474 SIGLEC5 8778 sialic acid binding Ig-like lectin 5 GO:0030246|GO:0016021|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_60920_PI430048170 0.0722806173969266 0.641880770771311 5.76807944983021 5.39173776658728 6.13538010034949 P P P 6.30563940952061 6.3548957643538 6.62749541209207 P P P LNCV6_60920_PI430048170 mRNA
GCTATTAGTCCGTCGTGCTTGATTTGTTTTTGTCCTTGAATAAGCATGTTATGTATATTG NM_001134999 RefSeq chr14 - 52857270 52951097 FERMT2 10979 "fermitin family member 2, transcript variant 2" GO:0005515|GO:0001725|GO:0031258|GO:0009986|GO:0034329|GO:0008360|GO:0005547|GO:0005634|GO:0072657|GO:0033622|GO:0031234|GO:0005829|GO:0005737|GO:0031941|GO:0007160|GO:0007229|GO:0048041|GO:0034446|GO:0005654|GO:0007179|GO:0016055|GO:0005925|GO:0005938|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136523_PI430048170 0.310485363619956 0.799222133777977 7.99019153482197 7.97178858054668 8.20098334198672 P P P 7.95516088712397 8.37829984192671 8.71261274567798 P P P LNCV6_136523_PI430048170 mRNA
AACCATTGTAGGTTTTTAGCAATGTGTATCTGTGTGTCCCTCACACCTTTTCCTATTCTA NM_018240 RefSeq chr1 + 157993272 158100262 KIRREL 55243 "kin of IRRE like (Drosophila), transcript variant 1" GO:0005515|GO:0007588|GO:0031253|GO:0048471|GO:0005886|GO:0016337|GO:0030838|GO:0005911|GO:0043198|GO:0001933|GO:0017022|GO:0045121|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139344_PI430048170 0.0044810203862362 1.38850564730116 9.56050454610503 9.56779256704815 9.47902291979394 P P P 9.07531307623739 9.14725704252539 8.95964638077618 P P P LNCV6_139344_PI430048170 mRNA
TGCTTTTCTCAAACTTTCCTGATCCTGCAGGCAAGCTAAACCAGTTTTGGAAGAACCTGC NM_001195223 RefSeq chr3 - 125929274 125937044 ALG1L 200810 "ALG1, chitobiosyldiphosphodolichol beta-mannosyltransferase-like, transcript variant 1" GO:0000030|GO:0005783|GO:0006486 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138395_PI430048170 0.369797707076954 1.0903565738166 0.603609967152097 0.28845350819023 0.304934501185039 A A A 0.266571741763575 0.31157256505065 0.266274044369513 A A A LNCV6_138395_PI430048170 mRNA
GTCCTACACAATGGTGCTATTCTGTGTCAAACACCTCTGTATTTTTTAAAACATCAATTG NM_001844 RefSeq chr12 - 47972964 48004502 COL2A1 1280 "collagen, type II, alpha 1, transcript variant 1" GO:0071773|GO:0010468|GO:0051216|GO:0007605|GO:0005615|GO:0046872|GO:0005585|GO:0042802|GO:0001894|GO:0022617|GO:0030020|GO:0007411|GO:0002062|GO:0030198|GO:0060351|GO:0030199|GO:0030574|GO:2001240|GO:0060021|GO:0042472|GO:0071599|GO:0048407|GO:0005576|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138600_PI430048170 0.0400170803697905 0.629090324722979 4.19908926045404 3.80914790177235 4.26722802525641 P P P 4.79954265392417 4.7686276537539 4.75387253876731 P P P LNCV6_138600_PI430048170 mRNA

AATGAGAGCCACTCATTACTTTTTAGAAGCCTCAATAAACTGTCCATTGCCTTGGTCAAA NM_005853 RefSeq chr16 + 54931198 54934483 IRX5 10265 "iroquois homeobox 5, transcript variant 1" GO:0043565|GO:0008406|GO:0006355|GO:0002027|GO:0060040|GO:0042551|GO:0005634|GO:0005499|GO:0048701|GO:0007601|GO:0050896|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136969_PI430048170 0.406401255920654 0.951613029791291 0.32886483542152 0.418697748402461 0.311977677488984 A A A 0.523394342792451 0.440905081621117 0.303717808776509 A A A LNCV6_136969_PI430048170 mRNA
GGGATGCAAAGTAGAATTGCTTTACATTGACTATATATGTGACATGTACGTTGCTGTTTT NM_001010872 RefSeq chr6 + 54846770 54945099 FAM83B 222584 "family with sequence similarity 83, member B" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132800_PI430048170 0.758672055143975 0.906293199335678 1.2014170224463 2.29928798880258 0.519415258541296 A A A 0.842860730384804 2.25648731999483 1.57444766491462 A A A LNCV6_132800_PI430048170 mRNA
TTTGTCTTTAATCCATTTGGATTTGGGGTACATGTTACGATTTGTCTACGTTAATTTCCC NM_001201377 RefSeq chr5 - 126541840 126595390 ALDH7A1 501 "aldehyde dehydrogenase 7 family, member A1, transcript variant 1" GO:0005515|GO:0007605|GO:0004029|GO:0006081|GO:0019285|GO:0005634|GO:0044281|GO:0005829|GO:0005739|GO:0034641|GO:0005737|GO:0008802|GO:0005759|GO:0006554|GO:0004043|GO:0070062|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144361_PI430048170 0.437912638810887 1.40977086374787 0.494113811919952 1.64698002957981 0.427789939330602 A A A 0.552390843774149 0.433911271922301 0.440756991461644 A A A LNCV6_144361_PI430048170 mRNA
TTGTTCTTTGATTCAGCCCTTTCAAACATGCTTACCTCGAGTGACCCAGTGACATCAGTG NM_173535 RefSeq chr2 - 70808644 70820600 CLEC4F 165530 "C-type lectin domain family 4, member F, transcript variant 1" GO:0051861|GO:0005534|GO:0005886|GO:0016021|GO:0051132|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130732_PI430048170 0.814296234851481 0.961570437687318 6.01272907576765 5.63108050894664 5.62646420354925 P P P 6.11678534972748 5.69150848203894 5.61433719791597 P P P LNCV6_130732_PI430048170 mRNA
TATACAGCTTCTCCCCTGGGTTCGTTTTGCCCAGAGGAACACAAATAAAGTGTTTTGTGC NM_032785 RefSeq chr1 - 48532854 50023954 AGBL4 84871 ATP/GTP binding protein-like 4 GO:0005794|GO:0035610|GO:0015631|GO:0005814|GO:0006508|GO:0008270|GO:0035609|GO:0036064|GO:0005829|GO:0004181 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132270_PI430048170 0.00166289969013471 0.317981362708111 3.45549056852596 3.8729218177495 3.99568183953217 P P P 5.17583028645353 5.5022803127579 5.62253981212067 P P P LNCV6_132270_PI430048170 mRNA
ACTGTATGCATGAGTTGAGTTGCTTCTGAGGTACATTTTGAATGACAGCATATTGTAAGA NM_001251845 RefSeq chr3 + 142724423 142807887 TRPC1 7220 "transient receptor potential cation channel, subfamily C, member 1, transcript variant 1" GO:0005515|GO:0005262|GO:0005261|GO:0005886|GO:0051480|GO:0055085|GO:0030017|GO:0044325|GO:0043235|GO:0070679|GO:0051592|GO:0016323|GO:0034220|GO:0005887|GO:0007411|GO:0070588|GO:0043034|GO:0045121|GO:0006816|GO:0015279|GO:0051281|GO:0046541 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141649_PI430048170 0.284238770571349 0.590963303441455 3.00295416756624 0.616170407401873 1.50662563657255 A A A 3.26506247090316 2.07586762382482 2.83539421422736 P A P LNCV6_141649_PI430048170 mRNA
CCCCCAAAGTCTCTGGTTTAATTCTTTGCAATTATAATAACCTGGCTGTGAGGTTCAGTT NM_004057RefSeq chrX + 16650157 16654668 S100G 795 S100 calcium binding protein G

GO:0016323|GO:0016324|GO:0005509|GO:0005499 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141504_PI430048170 0.30315615034408 0.827881155546739 9.22518943829661
9.23086174244063 9.13964467265017 P P P 9.08404951132736 9.65321999509627
9.61114864483931 P P P LNCV6_141504_PI430048170 mRNA
CTGAGGAAGGCTTGTGTGTCCTCAGTTAAAACTGTGCATATCGAAATATATTTTGTTATT NM_016354 RefSeq chr20
+ 62642444 62672295 SLCO4A1 28231 "solute carrier organic anion transporter family, member 4A1"
GO:0005215|GO:0005886|GO:0043252|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143787_PI430048170 0.00743781303972262 0.70359234459943 11.8879220512356
11.6927323799571 11.6378510393527 P P P 12.1462785059733 12.2944974081257
12.3059947381642 P P P LNCV6_143787_PI430048170 mRNA
CTATGGCTATTGTGTCAGGTCACTGTGGATAAAGGCAAAGACAGATATTTATTGAAAAAA NM_004053 RefSeq chr6
+ 41921226 41933046 BYSL 705 bystin-like
GO:0005515|GO:0000462|GO:0007565|GO:0005737|GO:0016020|GO:0008283|GO:0005730|GO:0045177|GO:0005
634|GO:0007155|GO:0001829|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128452_PI430048170 0.37823259235277 1.53510797335092 0.459656486665927
0.569405214698005 1.80137190529517 A A A 0.555967123072095 0.409157551437692
0.416798675851546 A A A LNCV6_128452_PI430048170 mRNA
AAAGCAAAGAGCTGTCTGGTGTTAATGATAAGTGAAATAGTTAAAGTTAGAAGATCCCAG NM_001025233 RefSeq
chr12 + 92423958 92430954 CLLU1 NA chronic lymphocytic leukemia up-regulated 1 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_141529_PI430048170 0.557050273638529 0.968082156042223 11.7216079880007 11.732320790441
11.6751476415595 P P P 11.701133154848 11.8784407914335 11.6823103698874 P P P
LNCV6_141529_PI430048170 mRNA
CAGGGGGCTGAACTGTGAACAAGTCAGACAAATAAAGCAAGGGTCTGCACCATCAAAAAA NM_012473 RefSeq
chr22 - 36467045 36481640 TXN2 25828 thioredoxin 2
GO:0001666|GO:0014070|GO:0007584|GO:0042493|GO:0006662|GO:0005730|GO:0015035|GO:0048678|GO:0032
403|GO:0030425|GO:0009749|GO:0005739|GO:0008113|GO:0005759|GO:0033743|GO:0031669|GO:0043025|GO:0
045454|GO:0009725|GO:0000302|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129484_PI430048170 0.00597600927724714 1.40078996550211 13.137802293176
13.2562968144883 13.350298309377 P P P 12.7264888521682 12.7376169845131
12.8272723674972 P P P LNCV6_129484_PI430048170 mRNA
AAAGCCATACCAAAGACACTCAAAGACAGCCAATAAATTCTGTTCAATCATTTCTTTCTG NM_031280 RefSeq chr1
- 36455760 36464439 MRPS15 64960 mitochondrial ribosomal protein S15
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0031965|GO:0032543|GO:0006996|GO:0003735|GO:0005
743|GO:0006412|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143108_PI430048170 0.497745403651995 0.899345820901871 8.15290818514678
8.18317649095349 8.25361186100419 P P P 8.05797322655034 8.3126148824807
8.62419571585148 P P P LNCV6_143108_PI430048170 mRNA
TTTGTGGTAATACATGGTCACAACCGTGGATCAAACAAGGTCAGTCTAAAGTGGCAGGTC NM_014506 RefSeq chr9
+ 129803152 129811281 TOR1B 27348 "torsin family 1, member B (torsin B)"
GO:0005515|GO:0006986|GO:0031965|GO:0006200|GO:0005783|GO:0005635|GO:0071763|GO:0005524|GO:0051
085|GO:0005788|GO:0051260|GO:0007029|GO:0016887|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134772_PI430048170 0.26096422402355 1.02551730276668 0.370141026080697
0.292412018611492 0.350956884388543 A A A 0.290682662088707 0.292062892119858
0.322614250576159 A A A LNCV6_134772_PI430048170 mRNA
GCTATTTATTGTACTGAGAGTGGTGTCTGGATATATTCCTTTTGTCTTCATCACTTTCTG NM_013351 RefSeq chr17 +
47733243 47746119 TBX21 30009 T-box 21

GO:0006355|GO:0003700|GO:0044212|GO:0071310|GO:0005634|GO:0007275|GO:0009615|GO:0072676|GO:0006351|GO:0030217|GO:0043025|GO:0045893|GO:0048304 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136307_PI430048170 0.00153874309779232 0.3281589429481952.3941658190227 2.26196731865051 2.45892754912041 A A A 4.14558901609405 3.7396907942898 4.02962573968723 P P P LNCV6_136307_PI430048170 mRNA
GATTTACTTTGCTGTACAGTAGAGTACTTTCCATTTTCTGGAATGTTAGATGAGTGATGT NM_001144989 RefSeq chr19 - 57869378 57889074 ZNF814 730051 zinc finger protein 814
GO:0005622|GO:0006355|GO:0003700|GO:0003676|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137495_PI430048170 0.0234970510928772 0.5360129263391 6.21662642881558 6.09342897384871 6.26301574585539 P P P 6.80537324804462 7.05441384522422 7.36321386779164 P P P LNCV6_137495_PI430048170 mRNA
CCACAAGATAGGAGGGAATCCCCTTTGTAAAACTATGAATCCAAATAAATGTTTACAAAG NM_024037RefSeq chr1 - 25834005 25859458 AUNIP 79000 "aurora kinase A and ninein interacting protein, transcript variant 2"
GO:0005515|GO:0005813|GO:0005737|GO:0000922|GO:0007051 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142520_PI430048170 0.14845015354887 1.43284046347048 4.34028951264184 4.4867526599245 4.45300772810764 P P P 4.13833051380669 4.09336072702621 3.37724857364671 P P P LNCV6_142520_PI430048170 mRNA
CTTTCCATCTTTAAATGGGCATATATACAATAAAGGCTCTGTCCATCTCCATCTCTTATANM_178130RefSeq chr3 - 138261436 138329886 NME9 347736 NME/NM23 family member 9
GO:0006241|GO:0006228|GO:0006165|GO:0005622|GO:0006183|GO:0005737|GO:0004550|GO:0045454|GO:0005856|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115382_PI430048170 0.164684362380876 1.14074942419364 5.64989956345772 5.75487815133197 5.45183004635997 P P P 5.48262469962996 5.39258841789377 5.42624121285839 P P P LNCV6_115382_PI430048170 mRNA
TACGAGCACCAGAGGAACATGGACAGCAAGCTGGCCCTGATTGACCGACTCATCAGTCAC NM_001282771 RefSeq chr2 - 240479421 240558021 ANKMY1 51281 "ankyrin repeat and MYND domain containing 1, transcript variant 3" GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140292_PI430048170 0.189417563402772 1.65266966199818 0.331157457769891 1.2846867606845 1.41686342641228 A A A 0.268468628980263 0.529384366341756 0.266773250352096 A A A LNCV6_140292_PI430048170 mRNA
GACCTCCTGCACTGTGAATGCTCTGTGACATGAGATTCTTAGTTTAATAAAACTGTCATT NM_153647RefSeq chr14 + 92323192 92501481 SLC24A4 123041 "solute carrier family 24 (sodium/potassium/calcium exchanger), member 4, transcript variant 2"
GO:0007608|GO:0005886|GO:0097186|GO:0006874|GO:0055085|GO:0005737|GO:0016020|GO:0005887|GO:0070588|GO:0035725|GO:0006813|GO:0050896|GO:0006811|GO:0008273|GO:0015293 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128279_PI430048170 0.480075699131413 0.857105600157063 11.4965147791087 11.439033927167 11.4524108835671 P P P 11.2146526346367 11.9231579104984 11.8216965313457 P P P LNCV6_128279_PI430048170 mRNA
CCTTGCTGCCATGTGGATGCTGTTGTGATTGCTGTTTGTATATTATCAAAATGTTTTTAT NM_018154RefSeq chr19 - 14119508 14136628 ASF1B 55723 anti-silencing function 1B histone chaperone
GO:0005515|GO:0000790|GO:0006355|GO:0006335|GO:0006336|GO:0007275|GO:0007283|GO:0006351|GO:0030154|GO:0042393|GO:0043234|GO:0005654|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139384_PI430048170 0.730430380007538 1.13655359847457 2.69628822198649 1.53014425718726 1.99917592570658 A A A 1.53627011727814 2.48009253127613 1.71430619202167 A P A LNCV6_139384_PI430048170 mRNA
GAGAGAGATGTGGGACTAAATAATGATCGTTCAACTACTAGCCAAGGAGACATTCAGCAA NM_001135995 RefSeq

chrX - 13318648 13320399 ATXN3L 92552 ataxin 3-like
GO:0070932|GO:0006355|GO:0016579|GO:0004843|GO:0031966|GO:0006351|GO:0034605|GO:0005759|GO:0035520|GO:0043161|GO:0006515|GO:0004407|GO:0008242|GO:0001012|GO:0071218|GO:0035640|GO:0031625|GO:0042405 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141335_PI430048170 0.285095801886735 1.24096070914863 5.03843537684183 4.69952525912376 5.13799321920374 P P P 4.24511404760576 5.02664169348167 4.59909587696097 P P P LNCV6_141335_PI430048170 mRNA
ACACTGTAAACGACACAAGAGAACAAGAATAAAACAATAACTGTGTGTGTTCTGGCTGAG NM_001175 RefSeq chr12 - 14942015 14961628 ARHGDIB 397 Rho GDP dissociation inhibitor (GDI) beta
GO:0051056|GO:0030036|GO:0007264|GO:0006928|GO:0007275|GO:0007266|GO:0005829|GO:0043547|GO:0050790|GO:0005737|GO:0006955|GO:0007162|GO:0016023|GO:0005856|GO:0005094|GO:0070062|GO:0005096 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143519_PI430048170 0.532709124156308 0.911305860219828 10.2569014208158 9.91394370958346 9.82280257825366 P P P 9.8451374361874 10.2686210627342 10.2781204002696 P P P LNCV6_143519_PI430048170 mRNA
AATACCAGGAACCCAGCGGCTCTAGCCACTGAGCGGCTAAATGAAATAAAGTGGAAAAAA NM_001273 RefSeq chr12 - 6570081 6607433 CHD4 1108 "chromodomain helicase DNA binding protein 4, transcript variant 1"
GO:0008017|GO:0001103|GO:0005515|GO:0000790|GO:0005813|GO:0006357|GO:0043044|GO:0031492|GO:0006325|GO:0005634|GO:0000978|GO:0051225|GO:0003677|GO:0005524|GO:0006351|GO:0043234|GO:0005737|GO:0004003|GO:0016581|GO:0016020|GO:0008270|GO:0000980|GO:0005654|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133204_PI430048170 0.0345798935985065 1.09721529222937 0.383741151277701 0.478076840923655 0.456611937318247 A A A 0.289696935463298 0.314908240721807 0.313830010483872 A A A LNCV6_133204_PI430048170 mRNA
TAAGCATTTGCAGCTGCAACTCTATAGACTTTTGACAAATTCTTTTTCACACTGATGTAG NM_000134 RefSeq chr4 - 119317249 119322161 FABP2 2169 "fatty acid binding protein 2, intestinal"
GO:0005215|GO:0005737|GO:0005504|GO:0007586|GO:0006810 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137761_PI430048170 0.724295399683661 1.01215755668331 0.441424694050976 0.423801168674233 0.317526736830561 A A A 0.341709189945734 0.393683992244315 0.397475329774024 A A A LNCV6_137761_PI430048170 mRNA
CCAGATGAAAAATGCCATCAGGAAATTGTGTAGTAGAAAGGACATTTCAGGTGACAAATA NM_001004703 RefSeq chr11 - 54603068 54603998 OR4C46 119749 "olfactory receptor, family 4, subfamily C, member 46"
GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141161_PI430048170 0.178591155448981 0.357611576467556 1.0157978617275 0.633250775003157 0.590959485364164 A A A 2.17761274817957 2.9806396709434 0.836784719827375 A P A LNCV6_141161_PI430048170 mRNA
AGGGACTAGGTTTTGTGGACAGAAACAAAGTGTTTGGGAGAGATTATGGCCAGTGGTCAA NM_001128076 RefSeq chr17 - 8753105 8758559 SPDYE4 388333 speedy/RINGO cell cycle regulator family member E4 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144401_PI430048170 0.0357182593555348 0.323031418987446 4.96596501417615 4.00163247733068 5.06259860167216 P P P 6.36583587118796 6.31383732862249 6.45563085305049 P P P LNCV6_144401_PI430048170 mRNA
CACGTAGATCTTTGTACAGTTGACTTTTTGACATAGCAAGGCCAAAAATAACTTTCTGAA NM_016107 RefSeq chr5 - 32354349 32444738 ZFR 51663 zinc finger RNA binding protein
GO:0005515|GO:0005737|GO:0005694|GO:0008270|GO:0007275|GO:0005654|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_41204_PI430048170 0.7360102672186140.90815603722551 5.50285259092204 5.5584251523235
5.98086019283983 P P P 5.40980592000955 5.6842192663476 6.27489644409244 P P P
LNCV6_41204_PI430048170 mRNA
TTACAAAGAAAGCATTAACCTGCCTCTGAGGTGACTAAAGGGGAATAATGGTGATTTTGC NM_016284RefSeq chr16
- 58519945 58629886 CNOT1 23019 "CCR4-NOT transcription complex, subunit 1, transcript variant 1"
GO:0005515|GO:0017148|GO:0010467|GO:0042974|GO:0005615|GO:0030014|GO:0005829|GO:0000932|GO:0005
778|GO:0000289|GO:0000288|GO:0019904|GO:0030331|GO:0060213|GO:0007275|GO:0000122|GO:2000036|GO:0
006351|GO:0004535|GO:0032947|GO:0010606|GO:0016020|GO:1900153|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_76898_PI430048170 0.8074220256785530.83946521258144 2.48451918958964 2.45084591262873
1.91951291579094 A A A 1.50770315035074 2.6790809127311 3.07689610075019 A P P
LNCV6_76898_PI430048170 mRNA
AAGTTCCTTACAAAGGAGATGTGGAAAACACTATCCTGGATATTCTCGGGGGACTGAGGT NM_006877RefSeq chr6
+ 16238579 16295549 GMPR 2766 guanosine monophosphate reductase
GO:0006144|GO:0009409|GO:0043101|GO:0055086|GO:0044281|GO:0003920|GO:0046872|GO:0009117|GO:0055
114|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133205_PI430048170 0.7221549388085130.9875881129366080.398334498423989
0.4586126349277580.364235110372566A A A 0.4975043882968120.380766937403727
0.395735900158722A A A LNCV6_133205_PI430048170 mRNA
GGTGGGCCTATTTTAACATACACTTTATGAGTTGCTATTTAGGATGTATGTTTACTGTTCNM_001164443 RefSeq chr5
- 75068296 75236878 ANKRD31 256006 ankyrin repeat domain 31 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143980_PI430048170 0.0914003751841839 1.41318405317685 4.73769442187668
5.04701085566461 5.32314599674961 P P P 4.28780458597545 4.77958559464483 4.5609257396431
P P P LNCV6_143980_PI430048170 mRNA
AAATCTGCTCTATTGAACGAATGTAACAAGCAAGGAGGCTTAAGACTGGCGCAGGCAAGA NM_001488RefSeq
chr17_KI270857v1_alt + 1646376 1716291 TADA2A 6871 "transcriptional adaptor 2A, transcript
variant 1"
GO:0003712|GO:0006355|GO:0003700|GO:0006366|GO:0005694|GO:0006325|GO:0005634|GO:0003677|GO:0043
966|GO:0000125|GO:0003682|GO:0008270|GO:0004402 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_53564_PI430048170 0.0347712552678180.6835199620009513.07299247376179 2.64960515132497
3.02834265251243 P A P 3.52159826226671 3.26263365164898 3.62603165896363 P P P
LNCV6_53564_PI430048170 mRNA
TTATTAAGAAAAATCAAGACAAAGACCACAGGAGGGTCCCTTCTAGGACACAGAGGCCAG NM_001013693
RefSeq chr1 + 21812264 21825221 LDLRAD2 NA low density lipoprotein receptor class A domain
containing 2 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144226_PI430048170 0.1989973994826870.6101942051762320.30669418628676
0.3378791066096951.27405099500396 A A A 1.95381619549318 1.28992100461575
0.801168039445563A A A LNCV6_144226_PI430048170 mRNA
AATAAGTGCCTAGTATTGCAGATGCAGTTTATGGTGAACTTAGAGGATTAAAAACCAAAG NM_001300942 RefSeq
chr11 + 76445024 76552899 C11orf30 56946 "chromosome 11 open reading frame 30, transcript
variant 1" GO:0006355|GO:0006281|GO:0005654|GO:0042803|GO:0006351|GO:0016568 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_144671_PI430048170 0.0724052563118323 0.8120576321874454.63390340934852
4.5510100115355 4.76512008875511 P P P 4.78466284861806 4.93487885968637
5.12003212632158 P P P LNCV6_144671_PI430048170 mRNA
ATCATTTGTTGGAATGAATTAAATAAACCCTTCCTGGGGCATCTGGCGAATCCCAAAAAA NM_000361RefSeq chr20
- 23045632 23049664 THBD 7056 thrombomodulin
GO:0005515|GO:0010544|GO:0007565|GO:0005886|GO:0009986|GO:0010165|GO:0005509|GO:0051918|GO:0050

900|GO:0051591|GO:0005615|GO:0007165|GO:0005887|GO:0007596|GO:0030195|GO:0032496|GO:0004872|GO:0
004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137768_PI430048170 0.7824151033165391.01414745682269 7.38695389286034
7.26117504952027 7.19895016230799 P P P 7.2143576569213 7.30757454817136
7.26922628480123 P P P LNCV6_137768_PI430048170 mRNA
GCTGCTGTCCTGGCCACTGCATTCAAATTCCAATGTGTACTTCATAGTGTAAAAATTTAT NM_139276RefSeq chr17
- 42313324 42388495 STAT3 6774 "signal transducer and activator of transcription 3 (acute-phase
response factor), transcript variant 1"
GO:0001754|GO:0005515|GO:0001659|GO:0003700|GO:0006366|GO:0044212|GO:0048708|GO:0019221|GO:0006
606|GO:0060548|GO:0046983|GO:0070102|GO:0004879|GO:0045820|GO:0032355|GO:0001103|GO:0045747|GO:0
019901|GO:0019903|GO:0006953|GO:0000122|GO:0016310|GO:0019953|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_99033_PI430048170 0.9401483228771470.911674736841521 2.24380970844777 2.46072605328871
2.4260815096112 A A A 2.87576777848757 2.90224592041078 1.20962429536918 P P A
LNCV6_99033_PI430048170 mRNA
TTGATGCAGATGTTTCCCCCAAGCCCACTATTTTTCTTCCTTCAATTGCTGAAACAAAGC NM_001003806 RefSeq
chr7 - 38259642 38273647 TARP 445347 "TCR gamma alternate reading frame protein, transcript
variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_101740_PI430048170 0.1622764099049470.8073794686444357.86658966512283
7.54873535700119 8.08218169238507 P P P 8.04452572284659 8.19200885098973
8.22965184671104 P P P LNCV6_101740_PI430048170 mRNA
GACCTAATGGAAATGGGAAGAGCAACAGTAACTCCAAAGTGTCAGAAAATAGTTAACATT NM_002715RefSeq chr5
- 134196456 134226259 PPP2CA 5515 "protein phosphatase 2, catalytic subunit, alpha isozyme"
GO:0005515|GO:0008380|GO:0010467|GO:0030308|GO:0010469|GO:0071902|GO:0030111|GO:0005886|GO:0006
672|GO:0000159|GO:0005634|GO:0050811|GO:0010719|GO:0030155|GO:0046872|GO:0005829|GO:0070208|GO:0
005739|GO:0000188|GO:0031952|GO:0006470|GO:0000184|GO:0015630|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129632_PI430048170 0.4721012800358671.06264436479882 0.591625645945995
0.3958196044630790.585976679379094A A A 0.2910068692540310.401138745235656
0.608579812271203A A A LNCV6_129632_PI430048170 mRNA
TGAGGAAGTATCTATCAGTTGAAATTAAATCGTCTTCCAACTTGAATCATCCTTTGCCTT NM_001162936 RefSeq
chrX - 154823347 154834662 SMIM9 100132963 small integral membrane protein 9
GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127114_PI430048170 0.1016206447275251.10246968357072 0.774801394253287
0.6769994038097370.591230678889577A A A 0.6009852137200490.510755202547308
0.51308188195196 A A A LNCV6_127114_PI430048170 mRNA
GAGAAAGCATTTCTTTTCTCTTTAATCTCCTATTCCTTCACACAGTTCAACATAAAGAGC NM_001166120 RefSeq
chr1 + 119414930 119423039 HSD3B23284 "hydroxy-delta-5-steroid dehydrogenase, 3 beta- and
steroid delta-isomerase 2, transcript variant 2"
GO:0006705|GO:0004769|GO:0006694|GO:0031966|GO:0005783|GO:0006702|GO:0006704|GO:0005743|GO:0044
281|GO:0003854|GO:0005758|GO:0030868|GO:0005789|GO:0016021|GO:0008202|GO:0055114 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_60918_PI430048170 0.0145730318351395 0.3906551077874962.64874758848536
1.94342584431197 1.91823126999001 A A A 3.53302809379207 3.77731572900819 3.3626606223551
P P P LNCV6_60918_PI430048170 mRNA
GGAGAGTTTATGCTTCATCTGAGTTTAGAAGTAATGTCAGAAAATGTTAAGCATGTCTGT NM_145251RefSeq chr14
+ 52730164 52774987 STYX 6815 "serine/threonine/tyrosine interacting protein, transcript variant 1"
GO:0005515|GO:0005737|GO:0006470|GO:0005634|GO:0045204|GO:0008138|GO:0007283|GO:0070372|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_57055_PI430048170 0.798489193240866 0.969311352184048 4.68349930993898 4.09083466287595
4.35214067657347 P P P 4.60137413200413 4.47850883914206 4.21659028121241 P P P
LNCV6_57055_PI430048170 mRNA
ATGCGAGGTCTGGGTGCGCTCTTGCTGTCTCACAACTGCCTCTCTGAGCTGCCTGAGGCT NM_145886 RefSeq chr11
- 799178 805250 PIDD1 55367 "p53-induced death domain protein 1, transcript variant 1"
GO:0005515|GO:0007165|GO:0043066|GO:0005737|GO:0051092|GO:0043065|GO:0005794|GO:0006919|GO:0005
634|GO:0005123|GO:0006974|GO:0006977 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138919_PI430048170 0.284421908461935 1.39727163686233 1.31599885803201
1.19056355645065 1.71480306879835 A A A 1.63456500280709 0.406857173032217
0.415592108905197 A A A LNCV6_138919_PI430048170 mRNA
TCTGTGTGTGAGGTCTGAGCTCTGAGGCAGCAGTGTTAGCACAATAAAGAAACATTGAGA NM_001013661 RefSeq
chr1 - 159854315 159862657 VSIG8 NA V-set and immunoglobulin domain containing 8 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_143607_PI430048170 0.483774554373056 1.54946291758187 1.88302739080681
0.441699566651074 0.265148008053655 A A A 0.391290958032168 0.46668662753775
0.421321697659557 A A A LNCV6_143607_PI430048170 mRNA
CTGCAGGAAATGGGATGGACCAGGGTTATATGCAATGTTCAGTTTTTACTTTTATACTTA NM_007136 RefSeq chr3
- 114234630 114237578 ZNF80 7634 zinc finger protein 80
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_75617_PI430048170 0.437998282517418 1.09370982918702 3.80225819708301 3.77731572900819
3.6127588065342 P P P 3.82303207972669 3.32933089404336 3.61740394980554 P P P
LNCV6_75617_PI430048170 mRNA
CCAAGTGGAATTATTAAAGTCTTCACCAGCAATCCAACTCCAGCTGTGTTGTGCTTCAGG NM_138782 RefSeq chr5
+ 72955980 73090522 FCHO2 115548 "FCH domain only 2, transcript variant 1"
GO:0072583|GO:0005515|GO:0005905|GO:0005886|GO:0030136|GO:0001786|GO:0005546|GO:0035091|GO:0072
659|GO:0010324|GO:0048268 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133093_PI430048170 0.847723673810499 1.05825064024253 0.269148816827103
1.14951702855108 0.465718194733894 A A A 1.04555503622681 0.294771883956082
0.320988344345139 A A A LNCV6_133093_PI430048170 mRNA
CTGCGACTGAAACAAACAGGTTCATAGAGATGAATTTTCTGAGAAACATATATCTACATG NM_001855 RefSeq chr9
+ 98943712 99070792 COL15A1 1306 "collagen, type XV, alpha 1"
GO:0005576|GO:0001525|GO:0005582|GO:0005615|GO:0030154|GO:0031012|GO:0007165|GO:0022617|GO:0030
198|GO:0030574|GO:0005788|GO:0016021|GO:0007155|GO:0070062|GO:0005201 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128179_PI430048170 0.0109062527909281 1.15308241098507 0.797023080125762
0.87357975023399 0.799697420467005 A A A 0.622209135430551 0.626817886905071
0.606019702199435 A A A LNCV6_128179_PI430048170 mRNA
ATCAGCTGAACCTGTGCATGCTCATTTCAAAGGGAAATTCAGATGATCCAGGATGACCCT NM_182619 RefSeq chr16
+ 69950901 69964347 CLEC18A NA "C-type lectin domain family 18, member A, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131747_PI430048170 0.82721013557977 1.00397348233267 0.348927552178631
0.331261258196799 0.277994246250275 A A A 0.316479918281796 0.324331180424291
0.301052901702711 A A A LNCV6_131747_PI430048170 mRNA
GCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAACTTGTATATTTAAATTCTTTGTAAT NM_001167890 RefSeq
chrX + 13569574 13633575 EGFL6 25975 "EGF-like-domain, multiple 6, transcript variant 2"
GO:0007049|GO:0005178|GO:0016020|GO:0030198|GO:0010811|GO:0005509|GO:0007275|GO:0007155|GO:0005
615|GO:0030154|GO:0005604 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131480_PI430048170 0.906962946493064 0.991476089642324 0.336507516697228

0.3604826466650410.288006346071253A A A 0.4747655172616260.278705042421391
0.259538209753902A A A LNCV6_131480_PI430048170 mRNA
TGCCAAGCTAAGACTGGAACTAGATGAAACAAAACATCAGAACCAGCTAAGGGAAAATAA NM_001277304
RefSeq chr15 - 21846328 21877279 POTEB NA "POTE ankyrin domain family, member B, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134404_PI430048170 0.000637243201939529 1.74908202804152 11.0106215784944
11.0765308147852 11.1272386098623 P P P 10.3532867130745 10.1645611034013
10.2729196943964 P P P LNCV6_134404_PI430048170 mRNA
AGTGGATGGATGTTGTTCCTTTTTTGAAGTTGTCATTAAAGTAGGTGCAACAACCAAGAA NM_182752RefSeq chr1
+ 3624991 3630130 TPRG1L 127262 tumor protein p63 regulated 1-like
GO:0008150|GO:0003674|GO:0030054|GO:0070062|GO:0042802|GO:0008021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132622_PI430048170 0.2501117514527960.7158664726627173.56131295802734
2.53630771240326 2.76990348668839 P A A 3.03717051747863 3.70608457978543
3.68502981629222 P P P LNCV6_132622_PI430048170 mRNA
CTTGAAAACTTGTTTGTGGAATAAATGTCTAAAATAAATGGCTCCCACTGGTTTCTGCCA NM_001012981 RefSeq
chr16 - 25236000 25257534 ZKSCAN2 342357 zinc finger with KRAB and SCAN domains 2
GO:0008150|GO:0003674|GO:0006366|GO:0006357|GO:0003682|GO:0000981|GO:0005634|GO:0005575|GO:0003
677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133054_PI430048170 0.1468513976187561.06500914758738 0.47107731354923
0.4487709441959870.515505742013209A A A 0.31458089276055 0.385519114833674
0.459802649574245A A A LNCV6_133054_PI430048170 mRNA
CCATTGTTATTTTTAGTTCATTGTTTCCTAGAACAAAGGATGGACATTTAGGATCCTCAC NM_001201366 RefSeq
chr14 + 73644874 73703728 DNAL1 83544 "dynein, axonemal, light chain 1, transcript variant 2" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143693_PI430048170 0.2070448697851130.7995683574875773.99957148599599
3.98380779280951 4.05384017683792 P P P 3.98921789313301 4.53051776855045
4.43108658482157 P P P LNCV6_143693_PI430048170 mRNA
ACTTAATCTGACTGCAGTAACTAGTACAGTTCAATAAAGGGAATCCATGCGATTAGCAAA NM_001271620 RefSeq
chr16 - 49490603 49857919 ZNF423 23090 "zinc finger protein 423, transcript variant 2"
GO:0005515|GO:0030513|GO:0007219|GO:0005634|GO:0045893|GO:0045892|GO:0003677|GO:0046872|GO:0030
154|GO:0006351|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136298_PI430048170 0.1026924140779260.9268118489560090.324170165779136
0.3229696524137160.29264929981769 A A A 0.4921782752018860.41824177067222
0.355286777076458A A A LNCV6_136298_PI430048170 mRNA
CCATGCATTTTTATCTACTGTCTGAGGACATACAATAAATCTGAGAAAGTCTATGCTGTC NM_020405RefSeq chr17
- 39063302 39151649 PLXDC157125 plexin domain containing 1
GO:0005515|GO:0005886|GO:0021510|GO:0005576|GO:0001525|GO:0005615|GO:0030425|GO:0043235|GO:0005
622|GO:0005737|GO:0043025|GO:0004872|GO:0005923|GO:0016021 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144627_PI430048170 0.3078335903153721.02723390298365 0.336761673872605
0.2581217495166230.347938278173615A A A 0.2788654841804350.267046607064579
0.28222186696416 A A A LNCV6_144627_PI430048170 mRNA
CAGACTACAGTGGATGTATTTTAGGCTGTATACATATTTAGCTCTTTTTGGTAAATAGGG NM_018176RefSeq chr4
- 24998848 25030792 LGI2 55203 "leucine-rich repeat LGI family, member 2" GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127083_PI430048170 0.7088728367049290.8424132435544650.347851730230955
0.2510861774002590.82832462433008 A A A 0.2735912002965751.38449516783716
0.276946873065407A A A LNCV6_127083_PI430048170 mRNA

CTTCCTTATTCATGGCTTTTTGCAATTGTCAAGGAATGACTAGGTACCAAGCAACTTTAA NM_001018088 RefSeq chr15 - 61864305 62060465 VPS13C 54832 "vacuolar protein sorting 13 homolog C (S. cerevisiae), transcript variant 2B" GO:0005622|GO:0045053|GO:0006623|GO:0070062|GO:0019898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129402_PI430048170 0.26508447432685 1.12413738218318 12.3845518247888 12.4791530318775 12.7020624512285 P P P 12.2566238115794 12.2718237052103 12.5325229393128 P P P LNCV6_129402_PI430048170 mRNA
ATAACTTCAGACTTGGGCCCCCTGTTCTTTCTTTCCCATTAACTTGAGTGACCTGTGTGA NM_007245 RefSeq chr16 + 28823047 28837237 ATXN2L 11273 "ataxin 2-like, transcript variant A" GO:0005515|GO:0034063|GO:0005737|GO:0016607|GO:0016020|GO:0010494|GO:0010603 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135903_PI430048170 0.569183215119013 1.24515851343028 0.474136440381546 0.368382834051874 1.44837997195709 A A A 0.624392602331705 0.608997490270874 0.35306267906919 A A A LNCV6_135903_PI430048170 mRNA
CTGGAGAGTCAAAGCCTCTTAACAAGGAATGAACAGGAATAAAAGACAGCTGTGAGTGTG NM_024798 RefSeq chr15 + 64151716 64157481 SNX22 79856 "sorting nexin 22, transcript variant 1" GO:0035091|GO:0015031|GO:0030659 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137059_PI430048170 0.426570704662065 1.05264412372363 0.299188965526961 0.304643448270571 0.515235326078279 A A A 0.31135011890523 0.27293650720002 0.322939108250619 A A A LNCV6_137059_PI430048170 mRNA
CAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATAACAAAA NM_018724 RefSeq chr1 + 206865808 206869223 IL20 50604 interleukin 20 GO:0042517|GO:0050727|GO:0045672|GO:0005576|GO:0005125|GO:0005615|GO:0046427|GO:0006955|GO:0045606|GO:0006954|GO:0045618|GO:0045518|GO:0045517 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113254_PI430048170 0.892144077411545 1.15469314589355 4.20914386784853 2.62980169813052 3.41460972186899 P A P 3.36029923439534 3.46757342462897 3.2143564004657 P P P LNCV6_113254_PI430048170 mRNA
ACTTCCTCAGGCGGTGGCTGGAGGCTGCGCATCTGGGGCTTTAAACATACAAAGGGATTG NM_004530 RefSeq chr16 + 55479168 55506691 MMP2 4313 "matrix metallopeptidase 2, transcript variant 1" GO:0005515|GO:0005886|GO:0004252|GO:0005634|GO:0035987|GO:0005615|GO:0030017|GO:0005739|GO:0071230|GO:0022617|GO:0007411|GO:0030198|GO:0030574|GO:0006508|GO:0001666|GO:0048013|GO:0007566|GO:0005578|GO:0005576|GO:0001525|GO:0060346|GO:0001957|GO:0060325|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77588_PI430048170 0.959955832765516 1.00935245512833 7.50357188612288 7.83019267061733 7.89533342451501 P P P 7.6368730230272 7.68013620059895 7.88876516308687 P P P LNCV6_77588_PI430048170 mRNA
CTGACACAACATTTTCAGAATTCCAGACGATACTGTGATAAATGACATCAAAGTCTGAAA NM_022361 RefSeq chr6 - 105157899 105179983 POPDC3 64208 "popeye domain containing 3, transcript variant 1" GO:0008150|GO:0003674|GO:0042391|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139139_PI430048170 0.315895969871132 0.965083481813767 0.474109956025662 0.358776072885886 0.363438841144644 A A A 0.481249335134583 0.464069284844313 0.40675832717877 A A A LNCV6_139139_PI430048170 mRNA
GTCTGGAGGTATACACAGTTGTTTTGTTTTTAACCACGGTATTGAAACCTTTAAAAGGTA NM_003411 RefSeq chrY + 2935476 2982506 ZFY 7544 "zinc finger protein, Y-linked, transcript variant 1" GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144546_PI430048170 0.0397192206005861 0.686957506751092 5.66281157584406 5.24089364462527 5.65330106733141 P P P 6.15936253732817 5.93637018136282 6.11569932680575 P P P LNCV6_144546_PI430048170 mRNA

CCAACACTAAACCTAAGGACAGCTACAAAGGAAAGACAACTGGGGAAAGAAGACCTAGGA NM_005017 RefSeq chr3 - 196238381 196287713 PCYT1A 5130 "phosphate cytidylyltransferase 1, choline, alpha" GO:0042587|GO:0005789|GO:0004105|GO:0044281|GO:0006657|GO:0006644|GO:0042803|GO:0046474|GO:0008289|GO:0006656|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139171_PI430048170 0.418809943232736 1.40252574914695 0.31006055197095 1.47789824761017 0.377751141063485 A A A 0.353767004574571 0.342255214839162 0.32277767862481 A A A LNCV6_139171_PI430048170 mRNA
TGAAAAAATACAGAATAAACTTCATGGTGGTTGCCATTGGGCAGAGGAGTATAGGACTGG NM_001282515 RefSeq chr9 - 113041814 113056791 ZFP37 7539 "ZFP37 zinc finger protein, transcript variant 1" GO:0006355|GO:0003700|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127600_PI430048170 0.00970725757217707 0.816818955203277 8.97999825326258 8.93993200952436 8.94353424559409 P P P 9.19716008198952 9.22061335618297 9.31885756231003 P P P LNCV6_127600_PI430048170 mRNA
AATGCCACAGTCTGAGGTTGATATCTAAAATCTATGCCTTCAAAAGAGTCTCTGTTTTTT NM_182915 RefSeq chr2 + 119223807 119265651 STEAP3 55240 "STEAP family member 3, metalloreductase, transcript variant 1" GO:0005515|GO:0052851|GO:0009306|GO:0000293|GO:0005886|GO:0005771|GO:0006915|GO:0008823|GO:0055085|GO:0046872|GO:0006879|GO:0033572|GO:0007049|GO:0015677|GO:0016021|GO:0010008|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131263_PI430048170 0.0199041966419991 1.39875823694337 10.558835061853 10.5117956375341 10.6067310701241 P P P 9.91689361321086 10.0898695896831 10.2052296412876 P P P LNCV6_131263_PI430048170 mRNA
AGAGACCATGGAAGTGTCAGAGATTCAGAATCCAAGATTGTCTTTAAGTTTTCAACTGTA NM_006347 RefSeq chr1 + 42658376 42676758 PPIH 10465 peptidylprolyl isomerase H (cyclophilin H) GO:0000413|GO:0005515|GO:0016018|GO:0003755|GO:0071001|GO:0005737|GO:0006461|GO:0016607|GO:0000398|GO:0006457|GO:0043021|GO:0005681|GO:0046540|GO:0045070 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133399_PI430048170 0.456304444087062 0.808838092490616 2.68056789892055 2.21875792331581 2.74865812311017 A A A 3.24567330133053 2.29869790116584 2.92322671809574 P A P LNCV6_133399_PI430048170 mRNA
GTGTGGAAGAAAACAGCAGTTCTTTTATAATTGCTTGAAATTAGGAAAGCGCTTATTTCC NM_004748 RefSeq chr15 - 55355222 55408376 CCPG1 9236 "cell cycle progression 1, transcript variant 1" GO:0003674|GO:0008284|GO:0007049|GO:0016021|GO:0045787 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_80258_PI430048170 0.28135618799249 0.801893728244678 3.86587939882005 4.06939111856758 4.40199173218088 P P P 4.0471567837324 4.53733800529061 4.68533955441814 P P P LNCV6_80258_PI430048170 mRNA
AATGGAATCCACTGTGTTGAAGACTCTTGATATCATGTGCTTGTCTAACCATTTTTTGTTN NM_174911 RefSeq chr8 - 126552437 126558466 FAM84B 157638 "family with sequence similarity 84, member B" GO:0005515|GO:0005737|GO:0005886 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144421_PI430048170 0.0133608562156706 0.42359166763784 5.86464166715779 5.43155593768486 5.99934541649887 P P P 6.58642892095444 7.04381455688612 7.34358133799052 P P P LNCV6_144421_PI430048170 mRNA
GGATAAAGGGGAACTAGGCTAGCAGTTCTAATGTGACATTCTTTAAGCATATCTTAAAAT NM_014962 RefSeq chr20 + 11917864 11926595 BTBD3 22903 "BTB (POZ) domain containing 3, transcript variant 1" GO:0048813|GO:0021987|GO:0005634|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141967_PI430048170 0.753833500458036 1.73746870592184 2.99317852560274 0.436431941703061 0.456142549626099 A A A 1.17573089093301 1.35958432677821 0.407013861572196 A A A LNCV6_141967_PI430048170 mRNA

GACCCATCTAGATAACAGCAATCAACCTGCTTAATTCTGAATGACAATTATATCCACAAA NM_031302 RefSeq chr12 - 103988986 104050137 GLT8D2 83468 glycosyltransferase 8 domain containing 2 GO:0016757|GO:0008152|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_129081_PI430048170 0.2455686847941161.1555092237191 5.04774500088829 4.99328608899621 4.78556205977563 P P P 4.98198793765244 4.64639703765185 4.54914608355585 P P P LNCV6_129081_PI430048170 mRNA
AGGTGCTGGGGGAGCCCTGGGTTCCGGTTGTTGATATTGTTTGCTGTTGGGTTTTTGCTG NM_033163 RefSeq chr10 - 101770129 101776002 FGF8 2253 "fibroblast growth factor 8 (androgen-induced), transcript variant F" GO:0001656|GO:0008406|GO:0014070|GO:0001658|GO:0005111|GO:0001759|GO:0030878|GO:0005615|GO:0009653|GO:0001947|GO:0030539|GO:0043524|GO:0007173|GO:0021798|GO:0000165|GO:0006979|GO:0021543|GO:0023019|GO:0021544|GO:0030916|GO:0045840|GO:0030509|GO:0042056|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_140479_PI430048170 0.3272693955475650.7347233673871990.246877801331055 0.2825839388071690.319690028617302 A A A 0.4159252049131181.25417193554729 0.321762704466033 A A A LNCV6_140479_PI430048170 mRNA
GAAGAGGTAAACATTAATAAAGGTGTGTCAGTGCTTATTTCATCCATATCACCTATGTTG NM_001005519 RefSeq chr12 + 55492377 55493316 OR6C68 NA "olfactory receptor, family 6, subfamily C, member 68" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_98334_PI430048170 0.0498018290443555 1.38966864958748 7.85420525590393 8.19226807060004 8.0618382882901 P P P 7.71952526868225 7.65866743088538 7.289453488562 P P P LNCV6_98334_PI430048170 mRNA
AATAACTGGCACAAACAGGACACGAGCATGAGACCACGCTCCTCTGCCTTCTCCTGGCCT NM_001039846 RefSeq chr19 + 2096868 2099584 IZUMO4 113177 "IZUMO family member 4, transcript variant 3" GO:0005634|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_130157_PI430048170 0.9778278481211521.00028381283508 0.478131562530937 0.4630260056745150.432210703663899 A A A 0.5269828133634750.414550868313544 0.428359681336376 A A A LNCV6_130157_PI430048170 mRNA
ACACTTCCCCAATTTTAGCTCTGTCCTGCACTGACACAGACAACACTGAAATGCTGATAT NM_001005201 RefSeq chr11 + 56122372 56123311 OR8H3 NA "olfactory receptor, family 8, subfamily H, member 3" NA . NA - . NA NA NA NA NA NA NA NA NA LNCV6_89673_PI430048170 0.2678817681035540.7201624204507092.54910364500328 3.79796615630075 3.41776557934439 A P P 3.90422218925316 3.66630762046418 3.86908767770245 P P P LNCV6_89673_PI430048170 mRNA
CTATGTGAACAATCGAATACGAACAACAAAGTACACACTTCTGAATTTTGTGCCAAGAAA NM_020453 RefSeq chr4 + 47485392 47593486 ATP10D 57205 "ATPase, class V, type 10D" GO:0005515|GO:0000287|GO:0005886|GO:0005783|GO:0055085|GO:0005524|GO:0006886|GO:0045332|GO:0034220|GO:0004012|GO:0008152|GO:0005789|GO:0005654|GO:0016021|GO:0006812 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_137644_PI430048170 0.8524640851020441.29863408155788 0.424112841611805 2.47270117056732 0.353084064398603 A A A 1.81851329287314 0.47899578505615 0.454351217367456 A A A LNCV6_137644_PI430048170 mRNA
ATCTTTTCTAAAAGAGACAAATGAAGCCACAGGGAAAGTGAAATAAAGCCTTGAACCTCA NM_080473 RefSeq chr20 - 62463496 62475970 GATA5 140628 GATA binding protein 5 GO:0071773|GO:0003700|GO:0044212|GO:0006366|GO:0007596|GO:0045944|GO:0003705|GO:0008270|GO:0005654|GO:0005634|GO:0001158|GO:0060575 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_111361_PI430048170 0.466863346235085 1.05987604808408 0.52434422826941 0.7109404821897770.633577216260644 A A A 0.3622448753023670.674674267905051 0.569030697682434 A A A LNCV6_111361_PI430048170 mRNA
CTGTTAGGCTGAGCTCAGGAATTGTCCAAAAAGGAAAAAGCAAAATAATTAATTGAGAGT NM_178140 RefSeq chr5

+ 31798923 32110932 PDZD2 23037 PDZ domain containing 2
GO:0005737|GO:0005911|GO:0005783|GO:0005634|GO:0005576|GO:0007155 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127883_PI430048170 0.3323776309518981.04722686346878 0.30902059547092
0.28566124938102 0.449666486138972A A A 0.2932482825828860.260175559950229
0.296437143420724A A A LNCV6_127883_PI430048170 mRNA
AGAAAATGGGATGAGAGCTTACTGAATCGTACAAAACCCTGAAACGCAGTAGTGCTGGTC NM_080389RefSeq
chr8_KI270813v1_alt - 153416 158192 DEFB104A NA "defensin, beta 104A" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_130865_PI430048170 0.1515780501010840.7888296410841040.323730203037909
0.3328601520128550.291656813396423A A A 0.9159390846646240.420706238050281
0.594194520345558A A A LNCV6_130865_PI430048170 mRNA
GGACCCATGGTAAAATGCAAATAGATCCGGTGTCTAAATGCATTCATATTTTTATGATTG NM_000474RefSeq chr7
- 19115467 19117672 TWIST1 7291 twist family bHLH transcription factor 1
GO:0005515|GO:0006366|GO:0003180|GO:0000981|GO:0003183|GO:0048701|GO:2000147|GO:0042803|GO:0071
639|GO:0050679|GO:0030500|GO:0032760|GO:0046982|GO:0019904|GO:0032720|GO:0001843|GO:0070888|GO:0
014067|GO:0000122|GO:0048642|GO:0001701|GO:0001649|GO:0007517|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_107718_PI430048170 0.0220645255836462 0.3734279433820441.61254657517
1.21724447088201 0.700116222248415A A A 3.1208616987679 2.15484213689574
2.48883545800957 P A P LNCV6_107718_PI430048170 mRNA
TAATGCAAGCTGCAATGCCAAATGGTACTGTTCAGCGATTCCTCTTTACCCCATTGGCAA NM_182641RefSeq chr17
+ 67825663 67984378 BPTF 2186 "bromodomain PHD finger transcription factor, transcript variant 1"
GO:0005515|GO:0006355|GO:0001892|GO:0005634|GO:0000122|GO:0009952|GO:0006351|GO:0043565|GO:0005
737|GO:0007492|GO:0007420|GO:0008270|GO:0005654|GO:0006338|GO:0045893|GO:0016589|GO:0070062|GO:0
008094|GO:0008134. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134024_PI430048170 0.0925636782584629 0.7466637954066988.0235478432644
8.04652752945839 8.50001625054053 P P P 8.4841835235956 8.54724570436814
8.83065717195843 P P P LNCV6_134024_PI430048170 mRNA
CCTGTAATAGTGTGTCTGCATTTTCAACCTGTTGCAATAACTTTGCTGAAATATTAACAC NM_001002296 RefSeq
chr8 + 41490653 41510980 GOLGA7 51125 "golgin A7, transcript variant 2"
GO:0005515|GO:0005795|GO:0043001|GO:0018230|GO:0031228|GO:0002178|GO:0050821|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98748_PI430048170 0.4678169969318180.9808287956796480.2779144451893670.309011812959453
0.379322818632456A A A 0.3826438300850810.3431727267656070.325496637109361A A A
LNCV6_98748_PI430048170 mRNA
CTGGGAAGACAACTAGGATACTTTCTACTTTTTCTAGCTACAATATCTTCATACAATGAC NM_000583RefSeq chr4
- 71741693 71784362 GC 2638 "group-specific component (vitamin D binding protein), transcript
variant 1"
GO:0051180|GO:0042359|GO:0051183|GO:0003779|GO:0005576|GO:0072562|GO:0044281|GO:0005615|GO:0005
829|GO:0005499|GO:0008202|GO:0043202|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138663_PI430048170 0.81173632712043 1.13496621317263 1.70917430363495
1.19999725158797 0.34181991787788 A A A 0.9524578241571871.39803298996213
0.537209908741987A A A LNCV6_138663_PI430048170 mRNA
AGTCAATCTATGAGATTCGTAACAAGGACCTGCCAAGGGTCAGTGTTCCCAATTTTGGCA NM_020660RefSeq chr15
- 34752440 34754581 GJD2 57369 "gap junction protein, delta 2, 36kDa"
GO:0005243|GO:0005886|GO:0007268|GO:0005922|GO:0016021|GO:0001508|GO:0055085|GO:0007601 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127623_PI430048170 0.3291637268027581.15583169648731 0.86827375516523

0.4470635602268820.389228491313001A A A 0.3386866576448930.386444203378541
0.400725904872751A A A LNCV6_127623_PI430048170 mRNA
CTTCCCTCAGATAACTATGAAGTCTATTATGAGTACTGAATGACCAAAGAACATGGAAAA NM_032504RefSeq chr2
+ 209771992 209999300 UNC80 285175 "unc-80 homolog (C. elegans), transcript variant 1"
GO:0034220|GO:0005886|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145315_PI430048170 0.3898189410798781.49488475049347 0.478864838924093
1.75643594725618 0.503935362756308A A A 0.3175822562852870.287183786367586
0.743750766335074A A A LNCV6_145315_PI430048170 mRNA
CAGGTGGTGGGGTTATGGGTAGTTTTTATTTTCTTCCTTCTACTTCTCTATACATTTCAG NM_020769RefSeq chrX +
110419056 110456334 RGAG1 57529 retrotransposon gag domain containing 1 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_104665_PI430048170 0.00873441624887525 0.3101171331277726.49387729960219
5.88655758513457 6.32715610480795 P P P 7.90209559351109 7.91381731120808
8.02199516116568 P P P LNCV6_104665_PI430048170 mRNA
CAGAGGACTTTGTGTTTCCATTGCTTCCCAATGAAGAATTGAGAGAGAAATACAGGCGCT NM_006321RefSeq chr3
+ 48918847 48985538 ARIH2 10425 ariadne RBR E3 ubiquitin protein ligase 2
GO:0000209|GO:0005515|GO:0004842|GO:0016874|GO:0005634|GO:0007275|GO:0003676|GO:0048588|GO:0071
425|GO:0005737|GO:0070534|GO:0042787|GO:0008270|GO:0070936 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_62627_PI430048170 0.00595280599338685 1.29777672388258 8.97732200149164
9.09499879807217 9.03435123130192 P P P 8.68624009488895 8.73135789840319
8.55777684188996 P P P LNCV6_62627_PI430048170 mRNA
TCTGGGACTTGAAAACAGACCACAACGAGCAGCTGATCCCTGAGCCCGAGGTCTCCATCA NM_022372RefSeq chr16
+ 2205176 2209417 MLST8 64223 "MTOR associated protein, LST8 homolog (S. cerevisiae), transcript
variant 1"
GO:0005515|GO:0008286|GO:0048010|GO:0048011|GO:0032008|GO:0048015|GO:0031295|GO:0050731|GO:0005
829|GO:0034605|GO:0005737|GO:0032314|GO:0007173|GO:0030838|GO:0008543|GO:0045087|GO:0032956|GO:0
005654|GO:0038095|GO:1900034 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136609_PI430048170 0.3002677681164680.7611203230290494.08693729337374
3.13811074869585 2.96637330719695 P P P 3.89058320557644 3.87139240726507
3.87734900860069 P P P LNCV6_136609_PI430048170 mRNA
ATGAAAATGCATTCCGAATCTGTGAGGGCCCAAAACAGAATTTAGGGGTGGGTGAAAGCA NM_016578RefSeq
chr11 - 77666228 77820834 RSF1 51773 remodeling and spacing factor 1
GO:0005515|GO:0006352|GO:0006334|GO:0005634|GO:0031213|GO:0050434|GO:0043392|GO:0034080|GO:0042
393|GO:0016584|GO:0005654|GO:0006338|GO:0008270|GO:0045893|GO:0045892|GO:0016887 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133689_PI430048170 0.9074538634693190.9999924027471143.33617432456749
4.07415159816258 3.90492960270191 P P P 3.84254428223399 3.88868951714566
3.67416928843823 P P P LNCV6_133689_PI430048170 mRNA
TATTTATCACCTACGAGGAGCTGCAGCAGGACTTACAGGGCTCCGTGGAGCGCATCTGTG NM_004605RefSeq chr19
+ 48575735 48599427 SULT2B1 6820 "sulfotransferase family, cytosolic, 2B, member 1, transcript
variant 1"
GO:0005515|GO:0050294|GO:0006805|GO:0050427|GO:0005783|GO:0005634|GO:0044281|GO:0005829|GO:0043
231|GO:0005737|GO:0004027|GO:0000103|GO:0008202|GO:0070062 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138952_PI430048170 0.0110974729892382 1.36855606446643 14.5950873734477
14.7358479180107 14.5555670433998 P P P 14.2037874339029 14.1678655210087
14.1628242716263 P P P LNCV6_138952_PI430048170 mRNA
AGCGATTCGGACACGGATGTGAAGTCCCACGCTGCTGGCTCCAAGCAGCACGAGAGCATC NM_033520RefSeq

chr19 + 38304163 38305006 C19orf33 64073 chromosome 19 open reading frame 33
GO:0008150|GO:0003690|GO:0003697|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134899_PI430048170 0.8793914490391720.8363715768768622.20765935764081
1.35311454171023 1.69969724202334 A A A 2.33720422852176 0.707640225443629
2.52978730407026 A A P LNCV6_134899_PI430048170 mRNA
GGGGAAGGGGGATATAGAGGTCACAAGGAAATAAAAATCATCTTTCATCTTTAATTTTAC NM_006536RefSeq chr1
+ 86424085 86456557 CLCA2 9635 chloride channel accessory 2
GO:0030054|GO:0005886|GO:0005576|GO:0055085|GO:0005254|GO:0046872|GO:0009925|GO:0034220|GO:0005
887|GO:0006508|GO:0006810|GO:0007155|GO:0008237|GO:0015276 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129581_PI430048170 0.0628222753659015 0.6749106149699478.30961610696982
8.19070991416847 8.10958718166731 P P P 8.48663105262668 9.04556178339377
8.73179707792369 P P P LNCV6_129581_PI430048170 mRNA
GGCATAAGTTGTACTGAGGGTGTGCGCCAACTTAAACCAAAGGCTCTTTTCAGAGCCACC NM_021018RefSeq chr6
- 26250141 26250607 HIST1H3F 8968 "histone cluster 1, H3f"
GO:0005515|GO:0010467|GO:0046982|GO:0006325|GO:0006335|GO:0005576|GO:0005634|GO:0000228|GO:0003
677|GO:0032776|GO:0043234|GO:0060968|GO:0016020|GO:0000183|GO:0007596|GO:0045814|GO:0040029|GO:0
005654|GO:0000786|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144937_PI430048170 0.1466636108842731.08835409394333 0.501084616886232
0.5729126220414330.590900579030958A A A 0.3302799110213470.437342631394967
0.525762874449612A A A LNCV6_144937_PI430048170 mRNA
CCGAAAGGATGTTAATTATGCCTACGATGTAATAACTATTGGAATGTCATGGTCATTACA NM_001114175 RefSeq
chr4 - 46249564 46389379 GABRA2 2555 "gamma-aminobutyric acid (GABA) A receptor, alpha 2,
transcript variant 2"
GO:0030424|GO:0005230|GO:0030054|GO:0005886|GO:0004890|GO:0034707|GO:0007268|GO:0007214|GO:0055
085|GO:0005254|GO:0034220|GO:0030285|GO:0045211|GO:0001505|GO:0006836|GO:0008503 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130389_PI430048170 0.000387426633139471 0.413085849396833.77535532998726
3.57243132778493 3.77977362615449 P P P 4.8609277146891 4.94201389323851
5.14555899175624 P P P LNCV6_130389_PI430048170 mRNA
ATGCCTCTTTGAAGCAATTCAGGCTAGGTAAACCGATTTTGCCATTTCAAAACGTTTTAT NM_001012754 RefSeq
chr13 + 39038310 39050107 NHLRC3 387921 "NHL repeat containing 3, transcript variant 1"
GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134732_PI430048170 0.1850779907554710.4782323084901590.285289166329133
0.2883920622566020.295154375067463A A A 1.25316020934079 0.388043468945883
1.99112464684098 A A A LNCV6_134732_PI430048170 mRNA
CTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCATGTTAAACA NM_001004742
RefSeq chr11 - 56469487 56470538 OR5M3 NA "olfactory receptor, family 5, subfamily M, member 3"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131138_PI430048170 0.0371107451355625 0.6690123535302659.71811359165697
9.72621776189549 9.86707761338423 P P P 10.1373433719546 10.294630569752 10.587409843162
P P P LNCV6_131138_PI430048170 mRNA
GATCACTTGTTGCTGTCTTAATGGAATGGTTTTCTACAGGAGCTGTAACATACTTAAAAA NM_006796RefSeq chr18
- 12328943 12377276 AFG3L2 10939 AFG3-like AAA ATPase 2
GO:0005515|GO:0034982|GO:0042552|GO:0005743|GO:0016265|GO:0021675|GO:0007409|GO:0005524|GO:0048
747|GO:0005739|GO:0008053|GO:0007528|GO:0040014|GO:0006508|GO:0008270|GO:0051082|GO:0016021|GO:0
004222|GO:0042407|GO:0060013 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145509_PI430048170 0.0244089983820486 0.5711126529856526.43909784886556
6.57529382284081 7.0203631093137 P P P 7.35648586380322 7.46634311519893

7.68288646525759 P P P LNCV6_145509_PI430048170 mRNA
GCCCTCAGCTCAGGTTTTAATTTCTATTGAATGCTAACATTCTTCTGATTTTTTGGTATC NM_006963 RefSeq chr10 +
45000824 45005329 ZNF22 7570 zinc finger protein 22
GO:0006355|GO:0042476|GO:0008270|GO:0005654|GO:0005634|GO:0003677|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135614_PI430048170 0.00567934122969661 0.3781338563589858.01932644170786
8.06567686887401 8.25592169382347 P P P 9.20072699134352 9.55419426283375
9.75300163840136 P P P LNCV6_135614_PI430048170 mRNA
GTGACATGGCCAATTAAGTATCAGTGAGCCTCCTATCTGGGACTTATCTGTTCCTATTGT NM_001098634 RefSeq
chr4 - 40423254 40629866 RBM47 54502 "RNA binding motif protein 47, transcript variant 1"
GO:0000166|GO:0002244|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129478_PI430048170 0.0831591036957192 1.19990884482215 11.3118233233597
11.3115307403386 11.075383434617 P P P 11.0750498872006 11.0280413004638
10.8054020983213 P P P LNCV6_129478_PI430048170 mRNA
CTGAGCAAAGGGCCTGCCCAGACAAGATTTTTTAATTGTTTAAAAACCGAATAAATGTTT NM_002434 RefSeq chr16
+ 78169 85851 MPG 4350 "N-methylpurine-DNA glycosylase, transcript variant 1"
GO:0005515|GO:0042645|GO:0003905|GO:0052822|GO:0052821|GO:0043916|GO:0003684|GO:0008725|GO:0006
281|GO:0006307|GO:0006284|GO:0045007|GO:0006285|GO:0005654 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144479_PI430048170 0.866943697473208 0.993311381792288 0.378055067512651
0.47848746126083 0.37499864132014 A A A 0.499564100958693 0.37621016963403
0.383895395154815 A A A LNCV6_144479_PI430048170 mRNA
CCAGCTAACAGCATGATCTTTTCTCACTTCAATCCTTACTCCTGCTCATTAAAACTTAAT NM_001828 RefSeq chr19 -
39731252 39738029 CLC 1178 Charcot-Leyden crystal galectin
GO:0005515|GO:0002667|GO:0097153|GO:0046006|GO:0004622|GO:0070231|GO:0030246|GO:0002724|GO:0007
275|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130578_PI430048170 0.346277069519839 0.758189109335682 3.57945585775528
2.67480474963459 2.62901402433992 P A A 3.54862627935972 3.72321322712246
2.89521341968876 P P P LNCV6_130578_PI430048170 mRNA
CTCTGTCTCTTCCTTTTCACATTTGTGCACATAAAATATACTGGTGTTTGTGTTCCAGGA NM_182526 RefSeq chr14 -
67470265 67515304 TMEM229B 161145 transmembrane protein 229B GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130822_PI430048170 0.605969387783028 0.931788086398374 7.57324827702641
7.48430599535568 7.91940772208536 P P P 7.8141968412399 7.51851428836326
7.95390376655249 P P P LNCV6_130822_PI430048170 mRNA
GGTGCAGATGGTGTTTGTTCTATATTATAAATCTGCTGTCTTTGCTTGGCATTTTATAGT NM_022072 RefSeq chr3 +
94063010 94126786 NSUN3 63899 "NOP2/Sun domain family, member 3"
GO:0003723|GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128639_PI430048170 0.207055161263834 0.94003819555602 0.248352504233957
0.335426258147529 0.28161665578406 A A A 0.467293046425518 0.361557272640688
0.300556009382178 A A A LNCV6_128639_PI430048170 mRNA
GATCTTCACAAGCACATTCATCTCTTCCTACTCTGAACAGTAGTTATTTAGGTTTTTGCT NM_030893 RefSeq chr1 +
158353695 158357553 CD1E 913 "CD1e molecule, transcript variant 1"
GO:0071723|GO:0030881|GO:0006955|GO:0005886|GO:0000139|GO:0005887|GO:0005770|GO:0030884|GO:0030
883|GO:0048007|GO:0005769|GO:0043202 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89682_PI430048170 0.799252930197622 1.12715800039386 0.572768266788911 1.63907468553319
0.654298582194738 A A A 1.07632752023049 0.966493100864443 0.502248440957936 A A A
LNCV6_89682_PI430048170 mRNA
TGAAAAACAAGCAGAAATAAAACATTGACGGAACGGATACGACCGCAGATTGCGGGAGCT NM_001303269

RefSeq chr4 + 56978639 57031162 POLR2B 5431 "polymerase (RNA) II (DNA directed) polypeptide B, 140kDa, transcript variant 3"
GO:0008380|GO:0005515|GO:0010467|GO:0006368|GO:0006367|GO:0006366|GO:0032549|GO:0006370|GO:0005634|GO:0003677|GO:0046872|GO:0050434|GO:0006281|GO:0016020|GO:0000398|GO:0006283|GO:0001055|GO:0003682|GO:0034587|GO:0005665|GO:0016032|GO:0005654|GO:0006289|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134060_PI430048170 0.1000420945526341.05923094323514 0.444470595359408 0.4991220092919970.502198021812472A A A 0.3431298694448830.400160630071058 0.452118147171112A A A LNCV6_134060_PI430048170 mRNA
CCTAAGAGGATTCTTTAGAGACTCTGTATTGAATTTGTGTGGTATGTCACTCAAAGAATA NM_153696RefSeq chr11 + 89659296 89698718 FOLH1B 219595 folate hydrolase 1B
GO:0005737|GO:0006508|GO:0016805|GO:0046872|GO:0008237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138333_PI430048170 0.4265115776277941.49327388520542 1.55163618594147 1.88570372608354 3.03703582817721 A A P 2.12606725452606 0.903936010539037 1.88675569315111 A A A LNCV6_138333_PI430048170 mRNA
AATGGACAACTTGAAAATGCATGTTCCTCAGGCCTATGCAGTTCCCAGAGACTCTTGACA NM_052846RefSeq chr20 - 41359965 41366858 EMILIN3 90187 elastin microfibril interfacer 3
GO:0031012|GO:0005737|GO:0005578 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97366_PI430048170 0.00749977052487107 0.63078336797241 4.49870924403308 4.5063452986433 4.73062854472445 P P P 5.13216867935602 5.1489278696414 5.43996100110472 P P P LNCV6_97366_PI430048170 mRNA
GAATTAAAGTGTTTGAGGGTCAGACAAACATAGAAACCTCAGGACTGCCCAAGAAACCAG NM_001009555 RefSeq chr4 - 151120280 151226508 SH3D19 152503 "SH3 domain containing 19, transcript variant 1"
GO:0005515|GO:0051044|GO:0005794|GO:0005886|GO:0022604|GO:0007010|GO:0006892|GO:0061024|GO:0005654|GO:0070064|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131664_PI430048170 0.00334401930162192 1.74235982569755 7.71611122685072 8.00858156765095 7.98783055542169 P P P 7.21398520593502 7.16127148375005 6.93751436024133 P P P LNCV6_131664_PI430048170 mRNA
ACTATGTTATCCATCCTGAGTTTGTGTCTGAGACCTATCCCGACTATCGTTGCTGGTAGA NM_032596RefSeq chr9 - 34379019 34397851 C9orf24 84688 "chromosome 9 open reading frame 24, transcript variant 1"
GO:0048471|GO:0043014|GO:0002177|GO:0005634|GO:0007283|GO:0043623|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138519_PI430048170 0.6518952804635870.9747632707771430.513266533525489 0.3607646730372540.302298479174956A A A 0.50732782905766 0.435205590393469 0.348342062162521A A A LNCV6_138519_PI430048170 mRNA
TTATCTTCAATGATGGTAATGACCTTTGAACTCATTTTCCTATTTTCCAGGCTCTGGTGA NM_001005226 RefSeq chr6_GL000256v2_alt - 395570 396676 OR2B3 NA "olfactory receptor, family 2, subfamily B, member 3"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65239_PI430048170 0.1608667473761850.7507927286914634.27769407198197 4.4297480657273 3.83732416264367 P P P 4.30753538753376 4.61002162181671 4.87559119655327 P P P LNCV6_65239_PI430048170 mRNA
TTACGGAAACCTGGGAAGTCGGCGAAACCCTACGTTCGGGTGTTTTCGGAAGCAGCCGAA NM_007279RefSeq chr19 + 55654049 55674716 U2AF2 11338 "U2 small nuclear RNA auxiliary factor 2, transcript variant 1"
GO:0000974|GO:0005515|GO:0006397|GO:0008380|GO:0006369|GO:0010467|GO:0048025|GO:0006366|GO:0031124|GO:0033120|GO:0006406|GO:0000166|GO:0016607|GO:0000398|GO:0070742|GO:0005654|GO:0005681|GO:0019899 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122673_PI430048170 0.0632463363686115 1.1714880723071 7.4327437104703 7.60934313320369 7.66164902125647 P P P 7.44050696071499 7.26714997911813

7.31529842922858 P P P LNCV6_122673_PI430048170 mRNA
AGAAGAAGTTGCCCAGTATGATGGGGCATACAAGTTAGTCGAGGGCTGTGGAAGAAATAT NM_000925 RefSeq
chr3 - 58427629 58433852 PDHB 5162 "pyruvate dehydrogenase (lipoamide) beta, transcript
variant 1"
GO:0005515|GO:0010510|GO:0006099|GO:0005634|GO:0044281|GO:0006086|GO:0005739|GO:0006090|GO:0005
759|GO:0006006|GO:0004738|GO:0005654|GO:0004739|GO:0045254|GO:0044237|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133913_PI430048170 0.99091297744331 0.9996283403022090.5518864156085
0.4836921461664050.411361341068551 A A A 0.4114060876286110.541433888996567
0.496123644217128 A A A LNCV6_133913_PI430048170 mRNA
CATTCGCTGGAACTCTGGCAATGATACTGACAAAAGACATATTAAAAAGAGAAAAACTGA NM_183378 RefSeq chr12
- 29427555 29497686 OVCH1 NA ovochymase 1 NA . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_138584_PI430048170 0.2197134645201771.04932590120541 0.358039088830281
0.3606255394265190.478306933886133 A A A 0.3232607217968060.306772071060609
0.361307783639091 A A A LNCV6_138584_PI430048170 mRNA
GCTTTGGAGTCATTTCTGTGTGAGACACTATTGCATAATCCTGTAAGATTGCTTTTATAT NM_134431 RefSeq chr12
- 21264599 21395437 SLCO1A2 6579 "solute carrier organic anion transporter family, member 1A2,
transcript variant 1"
GO:0005886|GO:0015721|GO:0015711|GO:0043252|GO:0008514|GO:0008206|GO:0044281|GO:0016021|GO:0055
085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136611_PI430048170 0.40150925858822 0.5946158718741730.909730484975994
0.26527601417948 0.375849430723074 A A A 0.3832595167732142.13124226730437
0.746554557045358 A A A LNCV6_136611_PI430048170 mRNA
CCCCTAGGATGGCTGCTTTCAAGTTGTTTGCAATTAAAGATTCTGTATAAAACCAAAAAA NM_207312 RefSeq chr2
- 130191744 130198461 TUBA3E NA "tubulin, alpha 3e" NA . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135381_PI430048170 0.1738820715283121.04248338754385 0.35074305006299
0.3326974135034230.429865161831081 A A A 0.3044327525500150.290735125891305
0.339487770901754 A A A LNCV6_135381_PI430048170 mRNA
ATTTGCTGTCTTTTTGTATCTAAAGTCTTCCTATTGTACTGCACAAACCATGGATTGTAC NM_000891 RefSeq chr17 +
70169534 70180042 KCNJ2 3759 "potassium channel, inwardly rectifying subfamily J, member 2"
GO:0014861|GO:0005886|GO:0060306|GO:0007268|GO:0031224|GO:0086091|GO:0042802|GO:0086008|GO:0014
704|GO:0043197|GO:0051289|GO:0008076|GO:0086002|GO:0043025|GO:0006813|GO:0071805|GO:0005791|GO:0
005242|GO:0015693|GO:0005794|GO:0030007|GO:0090076|GO:0010107|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138334_PI430048170 0.37631564492839 0.9277674053137464.80337885935324
4.90969687190062 5.14916179490719 P P P 5.07322969835419 5.04314535640049
5.09196557298528 P P P LNCV6_138334_PI430048170 mRNA
TTTACAAACTGCTTAGTTCCAACTAAGCATAAGAGGTGAGAACGTACACTGCAGGGCCAC NM_014573 RefSeq chr17
+ 28319094 28328685 TMEM97 27346 transmembrane protein 97
GO:0042632|GO:0005791|GO:0005515|GO:0031965|GO:0005886|GO:0016021|GO:0005764|GO:0001558 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99771_PI430048170 0.4776352894052220.9460353634190869.06950870927844 9.07342502293706
8.91037135337128 P P P 9.13668174083662 9.21082554767235 8.93824584390837 P P P
LNCV6_99771_PI430048170 mRNA
AACAGTGTGGCTTTGAAGTTCAAACCAAGGAAACACTGACCATCTTCAAGAGTCCCGTTC NM_012228 RefSeq
chr10 + 23095497 23122013 MSRB2 22921 methionine sulfoxide reductase B2
GO:0005739|GO:0006355|GO:0003700|GO:0030091|GO:0033743|GO:0030041|GO:0008270|GO:0003779|GO:0006

979|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127560_PI430048170 0.266711765413474 1.40491096426535 1.21681998091164
0.523056715247548 1.49468765288009 A A A 0.746883138139102 0.621796046744299
0.552049111320579 A A A LNCV6_127560_PI430048170 mRNA
ACGGGCGAATTCGATTTTTTAACCATGAACCAGAAGATGCTGAAGCCACACAGAACACCT NM_198534 RefSeq
chr19 + 7497558 7508450 C19orf45 NA chromosome 19 open reading frame 45 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_136839_PI430048170 0.144284188341022 0.300294551345263 0.363692540257154
0.351968818466853 0.275343716544272 A A A 0.65937096255405 1.92689778593894
2.84469978964947 A A P LNCV6_136839_PI430048170 mRNA
GACGCTGATCTTCATTAGTCAAGTTTTAGTTATTTTGTTGGCTTTTCCATGTAGAATTCC NM_004685 RefSeq chr13
- 25246200 25287566 MTMR6 9107 myotubularin related protein 6
GO:0005737|GO:0006470|GO:0006661|GO:0044281|GO:0005635|GO:0004722|GO:0006644|GO:0015269|GO:0071
805|GO:0035335|GO:0004725|GO:0005829 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_63190_PI430048170 0.619534848226703 0.982829810672682 0.259593164135356
0.275512438771378 0.394152645496695 A A A 0.374563043168376 0.320973503700005
0.311660009225855 A A A LNCV6_63190_PI430048170 mRNA
TGTGGAACCCAAGGATGCAGCTGCTCTGCTAACACGGCAGCCCATCCTTCAAGACTGTGA NM_017957 RefSeq
chr17 + 50532686 50543750 EPN3 55040 epsin 3
GO:0005515|GO:0048471|GO:0005905|GO:0030136|GO:0005634|GO:0019897|GO:0070062|GO:0008289 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_120503_PI430048170 0.118675072971412 1.36186898053476 9.5946125542873
9.5586788700782 9.43792871450689 P P P 9.4052490938178 9.00892180873715
8.7732314263352 P P P LNCV6_120503_PI430048170 mRNA
CTGTCCGGGCTGCTTTCGCCTCCGCCTGTGGATGCTGCGCCTCTCCGAACGCAACATGAA NM_000942 RefSeq
chr15 - 64155814 64163155 PPIB 5479 peptidylprolyl isomerase B (cyclophilin B)
GO:0000413|GO:0005515|GO:0042470|GO:0042277|GO:0048471|GO:0005783|GO:0005518|GO:0050821|GO:0003
755|GO:0005634|GO:0032403|GO:0005790|GO:0060348|GO:0061077|GO:0016020|GO:0030198|GO:0032991|GO:0
005788|GO:0051082|GO:0040018|GO:0070063|GO:0005925|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128417_PI430048170 0.00261864685636905 0.439825568276806 5.08240228042598
5.18598531174512 5.49749532950069 P P P 6.24107838004492 6.40507978199442
6.67422572462683 P P P LNCV6_128417_PI430048170 mRNA
CCCCACACTTGTTTTCTTTGTTTTTGTTTTTTATGGCAACTGGAAAGTATTTACTATGGG NM_020199 RefSeq chr5
- 133955506 133968715 C5orf15 56951 chromosome 5 open reading frame 15 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142344_PI430048170 0.0235013126471686 1.26265317458758 13.0421361499406
13.0406881596988 12.9705641815419 P P P 12.5828457472841 12.8011968928163
12.6524302505851 P P P LNCV6_142344_PI430048170 mRNA
ACGCAAGCAGATCAAGTTCGAGAAAGACCTGAGGCGCATCTGGCTGAAGGCGGGGCTAAA NM_017900 RefSeq
chr1 - 1373729 1375438 AURKAIP1 54998 "aurora kinase A interacting protein 1, transcript variant 1"
GO:0005515|GO:0070124|GO:0070125|GO:0070126|GO:0006996|GO:0032543|GO:0005743|GO:0005634|GO:0045
862|GO:0043231|GO:0005739|GO:0045839|GO:0005654 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129353_PI430048170 0.0571657704701291 0.74488702818387 5.51490821487408
5.50982023049139 5.89255143788301 P P P 6.00631425824296 5.94980115338702
6.25198987228579 P P P LNCV6_129353_PI430048170 mRNA
GACAGAAACCAATACCAGCTTCCTTTTCCTTTAAACTTTGAAGAGTGTTGATTTGTTACT NM_012180 RefSeq chr4

- 174236658 174284251 FBXO8 26269 F-box protein 8
GO:0043547|GO:0005802|GO:0006511|GO:0005086|GO:0030054|GO:0030036|GO:0032012|GO:0000151|GO:0005634|GO:0016192 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135001_PI430048170 0.000285650274822227 0.479278738416271 7.90741397854834 8.01345872378497 8.08661775086036 P P P 9.00105754169988 8.99421340377964 9.19213850772369 P P P LNCV6_135001_PI430048170 mRNA
AGATGCTCTGGGGGTTTTGTTTTTGCTTTTCCTTCAGGGTTTTATTTTTGACTGTTTTGT NM_001286035 RefSeq chr1 - 150809704 150876768 ARNT 405 "aryl hydrocarbon receptor nuclear translocator, transcript variant 5"
GO:0005515|GO:0030949|GO:0003700|GO:0003705|GO:0061418|GO:0005634|GO:0030154|GO:0005737|GO:0046886|GO:0045944|GO:0004874|GO:0033235|GO:0042789|GO:0045821|GO:0001666|GO:0046982|GO:0003713|GO:0071456|GO:0001892|GO:0043619|GO:0010575|GO:0006351|GO:0035326|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130640_PI430048170 0.0656446787523447 0.616497000715694 6.32543531803607 6.10092366475444 6.43986625329234 P P P 6.57322772257515 7.02793381838989 7.29011333344975 P P P LNCV6_130640_PI430048170 mRNA
CCCTGGCTCTTTTCCAAGAAGTGGATTTTCATTCAAAGTTTTTTATCCTTCTAATAAGAC NM_002692 RefSeq chr14 - 49643551 49688380 POLE2 5427 "polymerase (DNA directed), epsilon 2, accessory subunit, transcript variant 1"
GO:0042276|GO:0008622|GO:0003887|GO:0003677|GO:0043231|GO:0006260|GO:0006261|GO:0000082|GO:0006281|GO:0000723|GO:0006270|GO:0006283|GO:0000722|GO:0006297|GO:0005654|GO:0006289|GO:0000278|GO:0032201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103916_PI430048170 0.0548822695460879 1.14844973062863 10.4926810725123 10.4889171319493 10.5801544371567 P P P 10.2596416673959 10.2619433035227 10.4357949071811 P P P LNCV6_103916_PI430048170 mRNA
TGTGTGTAAATCTGTAATATACCATTCTCTGTGGCCTGTTTTTCCTGGAAGAAGAAAAAA NM_001284390 RefSeq chr3 - 11556066 11720768 VGLL4 9686 "vestigial-like family member 4, transcript variant 5"
GO:0006355|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129342_PI430048170 0.451874757746966 3.78591818366615 0.292337644864075 3.62672427928964 0.311409529072069 A P A 0.447554688597279 0.347318120511556 0.353947909698562 A A A LNCV6_129342_PI430048170 mRNA
TTATTAGAGATTACCTCCTGAGAAAAAAGGTTCCGCTTGGAGCAGAGGGGCTGAATAGCA NM_000609 RefSeq chr10 - 44370152 44385097 CXCL12 6387 "chemokine (C-X-C motif) ligand 12, transcript variant 2"
GO:0008344|GO:0009408|GO:0008015|GO:0031100|GO:0048842|GO:0043434|GO:0090280|GO:0005615|GO:0007281|GO:0022029|GO:0006955|GO:0042098|GO:0006935|GO:0007155|GO:0070062|GO:0009314|GO:0001666|GO:0008009|GO:2000406|GO:0001569|GO:0008354|GO:0070098|GO:0001667|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133888_PI430048170 0.0174496161529317 0.565169701943936 5.00438056333822 4.47087217517356 4.81422517374023 P P P 5.47131331670529 5.57054808759504 5.75277730945731 P P P LNCV6_133888_PI430048170 mRNA
GTCATGTGGTTAATCTTGTTTAAGCCAATTCATTAACTGTGTACTGATACTGATGCTATG NM_016530 RefSeq chr15 + 63189528 63267774 RAB8B 51762 "RAB8B, member RAS oncogene family"
GO:0005515|GO:0048471|GO:0009306|GO:0005886|GO:0003924|GO:0045046|GO:0006904|GO:0005739|GO:0051286|GO:0048210|GO:0019882|GO:0017157|GO:0030670|GO:0051461|GO:0032482|GO:0030140|GO:0005778|GO:0070062|GO:0030911|GO:0032869|GO:0005102|GO:0005525|GO:0072659|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131872_PI430048170 0.585508951947904 0.917975457112464 0.304858726408219 0.259026105418541 0.392568384087015 A A A 0.748555978317202 0.246570559916136

0.278348012825995 A A A LNCV6_131872_PI430048170 mRNA
TGAAGCAGGAAATGGCACTGTGATTTTGGCCATTCAACTCACTACCTGGAGAGAACTTAG NM_002511 RefSeq
chr6 - 142075607 142088799 NMBR 4829 neuromedin B receptor
GO:0005737|GO:0004946|GO:0031989|GO:0007186|GO:0005886|GO:0005887|GO:0007200 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126974_PI430048170 0.561108520190996 0.947640753669789 5.59738690743897
5.57585313909188 5.88538665376122 P P P 5.87574415084953 5.61610681517304
5.80827893847297 P P P LNCV6_126974_PI430048170 mRNA
CCTATGCTGCATTTATTGAAAGTTACAAGATTTAACCAGAAGTTTTTCCTCCATACTGGT NM_020205 RefSeq chr1
- 149940329 150010737 OTUD7B 56957 OTU deubiquitinase 7B
GO:0071108|GO:0005515|GO:0004843|GO:0032717|GO:0005634|GO:0000122|GO:1900181|GO:0003677|GO:0035
871|GO:0002385|GO:0005737|GO:0070536|GO:0006508|GO:0008270|GO:0008234|GO:0070530|GO:0043124 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132687_PI430048170 0.239285076208313 0.724036939884243 0.435791610270324
0.272694299332156 0.425667064388751 A A A 1.04144334262952 1.08008342693864
0.286193890752041 A A A LNCV6_132687_PI430048170 mRNA
TCTGAGACTGAATAAGCTCTGATGTTTCCCCGGCTAAATGGAAGAATAAATGAAGCAATT NM_080723 RefSeq
chr6 + 24126185 24147529 NRSN1 140767 neurensin 1
GO:0030133|GO:0043005|GO:0043025|GO:0016023|GO:0016021|GO:0030426|GO:0007399 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_60711_PI430048170 0.0671922454829073 1.42520503750512 4.73092801334209
4.26776237178706 4.75745917261486 P P P 4.22871365847369 4.14276521868757
3.87912608892477 P P P LNCV6_60711_PI430048170 mRNA
TGAAGATGATATGCTGCAGCTTTCAGAATTTGACCCCCTATTGAGAGAGATTGCTCCTGG NM_017999 RefSeq
chr14 + 24147449 24160661 RNF31 55072 ring finger protein 31
GO:0000209|GO:0005515|GO:0035631|GO:0043130|GO:0050852|GO:0004842|GO:0016874|GO:0023035|GO:0071
797|GO:0097039|GO:0005737|GO:0051092|GO:0009898|GO:0008270|GO:0043123|GO:0031625 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145165_PI430048170 0.561728740724881 1.01917612305906 0.403973533885916
0.275594835909168 0.318065874938629 A A A 0.284900951862793 0.308000632198783
0.32521761061622 A A A LNCV6_145165_PI430048170 mRNA
AAGTGCTTATCTCCATTTCAAATCAGTAGCCTAAGTGTTCTACTCTAAATCAAGTGATTC NM_003783 RefSeq chr1
- 193178729 193186613 B3GALT2 8707 "UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase,
polypeptide 2" GO:0009312|GO:0000139|GO:0008499|GO:0006486|GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_143636_PI430048170 0.228469913731771 0.608101319040145 0.508880744458396
0.532596410268266 0.421301138687283 A A A 1.71873329030478 0.451135836911311
1.17779971486374 A A A LNCV6_143636_PI430048170 mRNA
ACTCCATGTGATTTTAGCATGTTTAATCATTTTAACAATAAACCACCCCACAAATGGGGT NM_001102566 RefSeq
chr1 + 161258726 161285450 PCP4L1 654790 Purkinje cell protein 4 like 1 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137558_PI430048170 0.096691479589677 0.409109543189242 2.38125341988698
0.611695842481605 1.03456777544004 A A A 2.43315696282023 3.03408659140609
2.97910974869676 A P P LNCV6_137558_PI430048170 mRNA
ACAGAAATAAGCCATAGCTTTGAGATGAAGGCTTATATACGTGTAAACCATTGTAACCAA NM_001023563 RefSeq
chr19 + 57240684 57262738 ZNF805 NA "zinc finger protein 805, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129518_PI430048170 0.6191268938025890.9679580259288030.532173139867099
0.4808033175470180.260930565358259A A A 0.4073028927684650.534313819526758

0.484551670290692 A A A LNCV6_129518_PI430048170 mRNA
GATAGAACTACAGTTTTTATCGCCAGCTGGGCAAAGAGTATATTGCTGAAATGATATATA NM_001008783 RefSeq
chr6 + 136922240 136925660 SLC35D3 340146 "solute carrier family 35, member D3"
GO:0008643|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139995_PI430048170 0.989849214029093 1.00079826573437 11.0552139600984
10.9180861635834 11.251157106772 P P P 10.991428190681 11.0169362817376
11.2210253596936 P P P LNCV6_139995_PI430048170 mRNA
CTGGTATTGAAGAGGTGAATATGTTTACAAACCAAGGAACAGTGATCCACTTTAACAACC NM_001037637 RefSeq
chr5 + 73498424 73505623 BTF3 689 "basic transcription factor 3, transcript variant 1"
GO:0005515|GO:0006355|GO:0005737|GO:0006366|GO:0005634|GO:0015031|GO:0001701 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135096_PI430048170 0.499537149400448 1.17251924953587 1.06692545277059
0.285620091285774 0.494454866871312 A A A 0.641568994883479 0.286518102696829
0.319726055209586 A A A LNCV6_135096_PI430048170 mRNA
TGGCCCTGACCAGTATTCATTATTTCAGATAATTCCCTGTGATAGGACAACTAGTACATT NM_198578 RefSeq chr12
+ 40225010 40369284 LRRK2 120892 leucine-rich repeat kinase 2
GO:0005515|GO:0005802|GO:0010738|GO:0005764|GO:0005615|GO:0042803|GO:0042802|GO:0022028|GO:0043
068|GO:0001948|GO:0018105|GO:0000165|GO:0016301|GO:0005759|GO:0018107|GO:0043025|GO:0031398|GO:0
006979|GO:0035640|GO:0034260|GO:0004708|GO:0035641|GO:0031966|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136485_PI430048170 0.0781153048930894 0.590827015312402 10.3554904033803
10.0840231939681 10.4181372292323 P P P 10.6129134848449 10.9772758682998
11.4452005179482 P P P LNCV6_136485_PI430048170 mRNA
ACACTGTGTTATGCTCTGATGTGCTATGCTTAGCTATCTGTCAGAGATTAGTAAATTATA NM_006452 RefSeq chr4
+ 56435748 56461368 PAICS 10606 "phosphoribosylaminoimidazole carboxylase,
phosphoribosylaminoimidazole succinocarboxamide synthetase, transcript variant 2"
GO:0005515|GO:0009168|GO:0004639|GO:0004638|GO:0055086|GO:0044281|GO:0005524|GO:0005829|GO:0042
802|GO:0016020|GO:0006144|GO:0009113|GO:0070062|GO:0006189 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134434_PI430048170 0.264829438580014 1.66347128911973 0.56761018250731
1.95160345998093 0.996625560406852 A A A 0.616671203633808 0.690138363617527
0.343642197377347 A A A LNCV6_134434_PI430048170 mRNA
AACAAGATTTTGGGCACTACTGTCAAGCTGATGGAGCTAAAGCCTAACACGTGTTACTGC NM_017559 RefSeq chr17
+ 35121611 35130732 FNDC8 54752 fibronectin type III domain containing 8 GO:0005634 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_112091_PI430048170 0.402633391434154 1.04681998345985 0.352008305586128
0.47442479412427 0.362486721263088 A A A 0.252247120801274 0.289648132079922
0.444889655076605 A A A LNCV6_112091_PI430048170 mRNA
TCAGTCCTGAACTCCGGAGACAACTGGAGCAACACATAAAAAAGTGGATCATCCAACACT NM_015667 RefSeq chr9
+ 61190035 61196280 SPATA31A7 NA "SPATA31 subfamily A, member 7" NA . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_144117_PI430048170 0.0255836076633782 1.53277040200965 4.19819604968419
4.00615512387963 3.797358214619 P P P 3.35915555421309 3.46638110357572
3.35265743210961 P P P LNCV6_144117_PI430048170 mRNA
CAGAAGACTTTCCCTGCTGCCTTAAAACCAATAAAAGGTTAACTTTAAGTTTCTTGGAAA NM_003835 RefSeq chr17
+ 65137337 65227703 RGS9 8787 "regulator of G-protein signaling 9, transcript variant 1"
GO:0043627|GO:0005886|GO:0007603|GO:0005834|GO:0038032|GO:0005634|GO:0022400|GO:0007212|GO:0032
403|GO:0007399|GO:0043547|GO:0035556|GO:0005737|GO:0008277|GO:0004871|GO:0007601|GO:0005096|GO:0
016056 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_72955_PI430048170 0.57685870778962 0.8675156140404114.22883484858985 4.51868420557199
3.9431235146858 P P P 4.3133384967338 4.8763616592013 4.04562483975859 P P P
LNCV6_72955_PI430048170 mRNA
TGTGGTACTGTATGACTGTTCCGTGGGACATGGAGACTGCAGCCGCTGCCAAACTGCCAT NM_002673RefSeq chr3
- 48403853 48429463 PLXNB1 5364 "plexin B1, transcript variant 1"
GO:0005515|GO:1900220|GO:0033689|GO:0043931|GO:0005886|GO:0008360|GO:0005622|GO:0002116|GO:0035
556|GO:0017154|GO:0007411|GO:0004872|GO:0014068|GO:0005576|GO:0032794|GO:0007165|GO:0007162|GO:0
016477|GO:0051493|GO:0005887|GO:0032321|GO:0048812|GO:0071526|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140686_PI430048170 0.00464389077102384 0.6551104127280348.31827171874498
8.35383073023987 8.55034001628221 P P P 8.8898533519294 9.00287116619266 9.1586006844903
P P P LNCV6_140686_PI430048170 mRNA
TTCTTCAGGCTCCTTTAAGGCAGGTGCATTGATAGTTCCATTAGTGTGACCCTTGCATTG NM_002504RefSeq chr9
+ 33290419 33371157 NFX1 4799 "nuclear transcription factor, X-box binding 1, transcript variant 1"
GO:0000977|GO:0003700|GO:0005886|GO:0006366|GO:0016874|GO:0005634|GO:0000122|GO:0001078|GO:0005
737|GO:0006954|GO:0045347|GO:0016032|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_95852_PI430048170 0.6702895044581231.04497251629286 4.41550776375167 4.72096808667037
4.43114064368557 P P P 4.45474125478947 4.62419595959981 4.30112020694901 P P P
LNCV6_95852_PI430048170 mRNA
TTGTTATGGTAAAGCCTTAGGGACAACAGTGATGGTGCCTGTTCCCTATGAGAAGATGCT NM_173537RefSeq chr7
- 74796143 74851576 GTF2IRD2 84163 "GTF2I repeat domain containing 2, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138483_PI430048170 0.7279516374709420.9605944570638236.47378087872983
6.50911771923441 6.98061681649281 P P P 6.71914318248445 6.57013584360666
6.88804397094646 P P P LNCV6_138483_PI430048170 mRNA
CATTTGCCTAGGATATTGCTGGATTATACCCCATTGGAGGCTTTTAATTTTATTTGTATG NM_033540RefSeq chr3 +
179347691 179393220 MFN1 55669 mitofusin 1
GO:0006184|GO:0005515|GO:0008053|GO:0003924|GO:0005741|GO:0016021|GO:0005525 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133751_PI430048170 0.0127245710063287 0.4648837439213495.14842953387593
5.08801986858086 5.55953178554187 P P P 6.35817747671068 6.33595258353492
6.46088623102296 P P P LNCV6_133751_PI430048170 mRNA
TGTGCCTCTTAGATTGCTAAGTTCTGCTCTCATTCTTACTTCAAAGGACACTTTTTAAAG NM_001206651 RefSeq chr1
+ 86704569 86748184 SH3GLB1 51100 "SH3-domain GRB2-like endophilin B1, transcript variant 2"
GO:0005515|GO:0005737|GO:0000139|GO:0006915|GO:0005741|GO:0032461|GO:0051259|GO:0042803|GO:0070
062|GO:0042802|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109417_PI430048170 0.0764484057386078 1.08161009986059 15.7877927771788
15.732175553699 15.7559253095022 P P P 15.708873323373 15.6460380711362
15.5790618130709 P P P LNCV6_109417_PI430048170 mRNA
GCCCCAATGCCAACTCTTAAGTCTTTTGTAATTCTGGCTTTCTCTAATAAAAAAGCCACT NM_001997RefSeq chr11
- 65120626 65122200 FAU 2197 Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously
expressed
GO:0010467|GO:0003735|GO:0050830|GO:0019083|GO:0003723|GO:0006614|GO:0019058|GO:0015935|GO:0005
575|GO:0006415|GO:0005615|GO:0006412|GO:0006413|GO:0002227|GO:0005829|GO:0006414|GO:0008150|GO:0
000184|GO:0022627|GO:0019731|GO:0016032|GO:0044267 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_29968_PI430048170 0.0487882593192168 1.28889975827241 7.76765060537672
7.67725557937722 7.58954653718958 P P P 7.35040987534545 7.45786880918506

7.11184553805937 P P P LNCV6_29968_PI430048170 mRNA
TGAGATAATGCAGTCGGGAGAAGGGAGGGAGAGAATTTTATTAAATGTGACGAACTGCCC NM_001251 RefSeq
chr17 + 7579486 7582111 CD68 968 "CD68 molecule, transcript variant 1"
GO:0016020|GO:0005886|GO:0071310|GO:0016021|GO:0005765|GO:0010008 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129341_PI430048170 0.901754253298521 1.00107315672214 0.340859863611858
0.350322000854978 0.318856927677614 A A A 0.338315460926363 0.344856934091867
0.322311416121202 A A A LNCV6_129341_PI430048170 mRNA
GATGTACACATGTATCCTTTCACACATTTGCCTTGACAAACTTCTTTCACTCACATCTTT NM_006419 RefSeq chr4 +
77511752 77611836 CXCL13 10563 chemokine (C-X-C motif) ligand 13
GO:0035769|GO:0035768|GO:0048248|GO:0007267|GO:0033625|GO:0007204|GO:0005615|GO:0002518|GO:0048
535|GO:0006955|GO:0031724|GO:0006954|GO:0042127|GO:0032496|GO:0002920|GO:0002467|GO:0008201|GO:0
048018|GO:0042742|GO:0008009|GO:0070098|GO:0046982|GO:0017134|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135998_PI430048170 0.0234381220725319 0.575701402086645 9.14708634936594
9.05151820562685 9.19314564313789 P P P 9.64949858261949 9.96408612322054
10.1309320278111 P P P LNCV6_135998_PI430048170 mRNA
GATGTTTATTTGACAGTGACACTGCACTGGGTACTTAAAGAAATTATTTCCCGTTGTAAT NM_025222 RefSeq chr3
- 52254421 52278643 WDR82 80335 WD repeat domain 82
GO:0005515|GO:0035097|GO:0048188|GO:0003682|GO:0072357|GO:0042800|GO:0000785|GO:0051568 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144318_PI430048170 0.325852536133085 1.01106052888709 0.328079310140336
0.303728026145377 0.286177839934288 A A A 0.295954033135907 0.294584501565714
0.280092199388775 A A A LNCV6_144318_PI430048170 mRNA
GGCCAGTCTTACATGCTTATGAGTCTACTTTCCAATAAATTTACTCATAGTCCATTAACT NM_153366 RefSeq chr9
- 110365248 110579880 SVEP1 79987 "sushi, von Willebrand factor type A, EGF and pentraxin domain
containing 1" GO:0005737|GO:0016020|GO:0005509|GO:0005576|GO:0007155 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144501_PI430048170 0.0290094253866239 0.569371436567094 5.30027353981564
4.8236351594119 5.45285232215286 P P P 6.20407007527894 5.83047379789229
6.02766276310979 P P P LNCV6_144501_PI430048170 mRNA
CTGTACCAAAAAGGAGTACTATAAAATGAGGGTGCCAAATATATTGAGTCTTTTATGGGA NM_033087 RefSeq chr9
- 99216424 99221964 ALG2 85365 "ALG2, alpha-1,3/1,6-mannosyltransferase, transcript variant 1"
GO:0005515|GO:0048471|GO:0046982|GO:0000033|GO:0033164|GO:0005634|GO:0004378|GO:0033577|GO:0051
592|GO:0005737|GO:0047485|GO:0016020|GO:0005789|GO:0016021|GO:0006488|GO:0044267|GO:0048306|GO:0
018279|GO:0043687. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128353_PI430048170 0.344334950648992 1.21803100371878 6.37600608971091
6.14599632076567 5.72956169777033 P P P 5.96723921084522 6.00234990350277
5.43372307652399 P P P LNCV6_128353_PI430048170 mRNA
ATGATGGTTTATTTATTGTCTTGGGGCCCGATGGTCCTCCTCGGGCCAAGCCCCCATGCT NM_145659 RefSeq chr16
- 28499361 28506834 IL27 246778 interleukin 27
GO:0050688|GO:0009617|GO:0006954|GO:0045087|GO:0045078|GO:0042129|GO:0005102|GO:0045625|GO:0045
523|GO:0005615|GO:0005125 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138521_PI430048170 0.522487882654361 0.832622213067708 3.843550937103
2.76505886140219 2.18253679160845 P A A 3.75654173427389 3.27607327401489
2.93644742001536 P P P LNCV6_138521_PI430048170 mRNA
ATCTGAACAAACTATGCAATACCACCTGCTCCCTTCCAGGAGCATTTTAATAAAAGATTT NM_016563 RefSeq chr15
- 65053336 65068112 RASL12 51285 "RAS-like, family 12"
GO:0006184|GO:0016020|GO:0007264|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_131734_PI430048170 0.3954961012277880.9695995186141642.59501965745982
2.70849899518675 2.62443186917192 A A A 2.73930086907009 2.62803631446891
2.69448145626186 A A P LNCV6_131734_PI430048170 mRNA
CCTTCTACAGTTGCTTAGCCAATAAACCTTTCCTGGGCTGGAGAGCTGTCAGCATCAAAA NM_182577RefSeq chr19
- 463345 474983 ODF3L2284451 outer dense fiber of sperm tails 3-like 2 GO:0005881 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138488_PI430048170 0.2240248491971330.9356036795374250.310511411088174
0.3705569452458860.290128176642344A A A 0.5110359925948060.423198242638412
0.319942696695874A A A LNCV6_138488_PI430048170 mRNA
GTTGCTAAATATGTTATTGTGGAAAGATGAATGCAATAGTAGGACTGCTGACATTTTGCA NM_005408RefSeq chr17
+ 34356451 34358610 CCL13 6357 chemokine (C-C motif) ligand 13
GO:0008009|GO:0007165|GO:0006955|GO:0006954|GO:0006935|GO:0008360|GO:0007010|GO:0048245|GO:0007
267|GO:0006874|GO:0005102|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138715_PI430048170 0.0526833909768511 1.25771739828298 7.94619327734557
7.90752143637204 8.20723213197058 P P P 7.58293579447246 7.76238425355427
7.73556459826127 P P P LNCV6_138715_PI430048170 mRNA
TACAGAATATATTCTGGGGTCAGCTTCTTAAATTATACTACTGTTTACTGCTTTCTCCGT NM_022916RefSeq chr12 -
122231546 122266521 VPS33A 65082 vacuolar protein sorting 33 homolog A (S. cerevisiae)
GO:0005515|GO:0032418|GO:0048471|GO:0030897|GO:0005770|GO:0032400|GO:0005765|GO:0015031|GO:0006
904|GO:0048070|GO:0031902|GO:0016192|GO:0005769|GO:0030220 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130018_PI430048170 0.00422586259240911 0.3267261637681373.99858636819346
3.94424891893308 4.31609347503527 P P P 5.34164673097577 5.70341378126183
6.00776907098831 P P P LNCV6_130018_PI430048170 mRNA
GTGACAGATTAGGATTAAATTATGGTTTGACTTTTCCTAGCAGCGTGATCATGGGCAAGT NM_001130929 RefSeq
chr7 + 135662472 135676412 C7orf73 647087 chromosome 7 open reading frame 73 GO:0005576 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144706_PI430048170 0.0947569603417010.3602170833873952.27894414268268
0.4678487934991290.373313747552449A A A 2.06825903643243 3.24330879377216
2.85699687419316 A P P LNCV6_144706_PI430048170 mRNA
GTATGCAGGCCAGGAAATGAATGTTATTGTAATAAAGTGTGATGGAAAATCCAGGTAATT NM_194277RefSeq chrX
- 132076992 132128022 FRMD7 90167 FERM domain containing 7
GO:0043005|GO:0003674|GO:0010975|GO:0043025|GO:0005856|GO:0005615|GO:0030426 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138850_PI430048170 0.0684424932079320.6276992965076098.92557199441078
9.56870592986826 9.4393851272614 P P P 9.95950769539897 10.0532812749485
10.0117386085695 P P P LNCV6_138850_PI430048170 mRNA
CAGCTGATTTTAACAATAACTACTGTGTTCCTGGCAATAGTGTGTTCTGATTAGAAATGA NM_005252RefSeq chr14
+ 75278777 75282234 FOS2353 FBJ murine osteosarcoma viral oncogene homolog
GO:0005515|GO:0003700|GO:0044212|GO:0006366|GO:0009409|GO:0051591|GO:0051403|GO:0002756|GO:0003
690|GO:0002755|GO:0031668|GO:0032496|GO:0009416|GO:0007179|GO:0001661|GO:0051412|GO:0007565|GO:0
038124|GO:0038123|GO:0034134|GO:0007568|GO:0009636|GO:0030431|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131576_PI430048170 0.0967694359307803 0.8345820305604261 1.7989181358656
11.5957517397585 11.4657439249602 P P P 11.8330821366077 12.0173109152838
11.8028596980704 P P P LNCV6_131576_PI430048170 mRNA
CCTCTTCTAAACCATGATGTGGCACATTTTGGTGTTAATAAAACACAACACACAAAGTAA NM_198488RefSeq
chr8_KI270816v1_alt - 200979 210791 FAM83H 286077 "family with sequence similarity 83, member H"
GO:0031214 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_95062_PI430048170 0.0176257454618419 1.61033241491066 6.49610038407071
6.49878358750688 6.73493293845496 P P P 5.95751027326905 6.06591785127568
5.62126356555325 P P P LNCV6_95062_PI430048170 mRNA
AAAGGGCCTAGAAAGGCTCCTGTGAAGGAGAGTCCTGAAGTGCTGGTGGAACGCAACCCT NM_145271 RefSeq
chr16 - 30569700 30572407 ZNF688 146542 "zinc finger protein 688, transcript variant 1"
GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0005575|GO:0003677|GO:0046872|GO:0006351 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132520_PI430048170 0.00148561761392742 0.6103614138603198.57438330425929
8.3842523980607 8.50411378457042 P P P 9.06950870927844 9.22706615461238 9.2998225976855
P P P LNCV6_132520_PI430048170 mRNA
AGTGGAGAATGTCAGCTTTTCTCCCAAGTTGTATGTTAAGTCTATTCTAATATGTACTCA NM_005746 RefSeq chr7
- 106248285 106285192 NAMPT 10135 nicotinamide phosphoribosyltransferase
GO:0005515|GO:0008286|GO:0014070|GO:0008284|GO:0047280|GO:0007267|GO:0019674|GO:0006767|GO:0005
634|GO:0006769|GO:0044281|GO:0005615|GO:0042803|GO:0005829|GO:0008144|GO:0045944|GO:0009435|GO:0
070062|GO:0007565|GO:0005125|GO:0048661|GO:0032922|GO:0007165|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134271_PI430048170 0.4269006278864541.08829086292926 11.4749228693295
11.4721526471235 11.7726756149363 P P P 11.3046588622608 11.424087099417 11.627336967176
P P P LNCV6_134271_PI430048170 mRNA
AAACGCATGACCGAAAATCAGAAGACAAACTTGCCAAAGCTACAAGAGACAGCTGTAAAA NM_006837 RefSeq
chr8 - 67043079 67062327 COPS5 10987 COP9 signalosome subunit 5
GO:0005515|GO:0000338|GO:0048471|GO:0016579|GO:0030054|GO:0004843|GO:0005852|GO:0006366|GO:0010
388|GO:0003713|GO:0003743|GO:0005634|GO:0006412|GO:0046872|GO:0006413|GO:0008021|GO:0046328|GO:0
005737|GO:0008180|GO:0045944|GO:0051726|GO:0006508|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136559_PI430048170 0.0714285711052887 1.77348038385716 4.46749480336565
4.96263253764973 4.98015359504367 P P P 4.44113396261155 3.91285852647992
3.46844812045951 P P P LNCV6_136559_PI430048170 mRNA
CAAGATCTTAATTTAGGAACACTTTGAAACCCTGTAACCCTGCTGGGTGCTCTCTCCTCT NM_181708 RefSeq chr12
- 49836042 49843129 BCDIN3D 144233 BCDIN3 domain containing
GO:0005737|GO:0001510|GO:2000632|GO:0005634|GO:0008171|GO:0010586|GO:0008173 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_80416_PI430048170 0.33083962685059 0.89685344846653 10.0967382989083 9.74576946423626
9.71631464405904 P P P 10.1265409452335 10.0539950514225 9.86925668665223 P P P
LNCV6_80416_PI430048170 mRNA
ATCAAGGACTGTGTCTCCCCCAGCGAGCAGGTCCAGGGCTCAGAAATCAGCTCTATTGAC NM_183057 RefSeq chr8
- 144423600 144428563 VPS28 51160 "vacuolar protein sorting 28 homolog (S. cerevisiae), transcript
variant 2"
GO:0005515|GO:0000813|GO:0005886|GO:0019082|GO:0019058|GO:0043328|GO:0019068|GO:0032403|GO:0005
829|GO:0005737|GO:0031902|GO:0016197|GO:0061024|GO:0016032|GO:0031397|GO:0043162|GO:0010008|GO:0
070062|GO:0005768. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144949_PI430048170 0.1086055858107611.0402394742434 0.353545673039019
0.3135824800582420.276956845209327 A A A 0.2478441890711670.277927593630118
0.248377665302268 A A A LNCV6_144949_PI430048170 mRNA
CATATGAACACTGCTCTGAACTCCTCTGACTTAGCATTCAACTTAAGTCAAGAAATACTT NM_020864 RefSeq chr2
+ 225400885 225654018 NYAP2 57624 neuronal tyrosine-phosphorylated phosphoinositide-3-kinase
adaptor 2 GO:0048812|GO:0014065 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134441_PI430048170 0.0304494303373096 1.28289924313273 12.1314916866492
12.0032428860616 11.8496060477252 P P P 11.5731381942976 11.7787606593419

11.5572256261045 P P P LNCV6_134441_PI430048170 mRNA
GCACGAGGTTTTACAGGGGTGGTCAGACCTCAGGCTTTAATGAATAAAGACACTACTCCC NM_148912RefSeq chr7
- 73736096 73738854 ABHD11 83451 "abhydrolase domain containing 11, transcript variant 1"
GO:0005739|GO:0008150|GO:0003674|GO:0016787|GO:0008152|GO:0005575 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_81979_PI430048170 0.79591540193884 0.7397405567853171.71682814776235 0.32151784951009
0.356439579351273 A A A 2.41573090825492 0.3148932794099760.360420185160854 A A A
LNCV6_81979_PI430048170 mRNA
TCTTCAATGAAAATGAAGGAATGCCTTCGAATCAAGGAAAGATAGACAATGAAGAACAGCNM_080390RefSeq chrX
+ 102125687 102127712 TCEAL2 140597 transcription elongation factor A (SII)-like 2
GO:0006355|GO:0005634|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130330_PI430048170 0.96333243615614 1.03611351578345 0.395091689699345
1.52461595103279 0.248809565663266 A A A 0.64613945708305 0.368304414762096
1.22466575935966 A A A LNCV6_130330_PI430048170 mRNA
AAAGCAGCCTGTTCATAAATATACAACATGTCCCCTTCAGGCCTGTTTATCCAGCCTGAG NM_019599RefSeq chr5
- 9628996 9630351 TAS2R1 50834 "taste receptor, type 2, member 1"
GO:0033038|GO:0007186|GO:0005886|GO:0007635|GO:0008527|GO:0016021|GO:0001580 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126795_PI430048170 0.2038530959175440.7677696621931678.52136082122063 8.4657271260962
8.66128838890651 P P P 9.20814516784211 8.53825399900972 8.9748397827783 P P P
LNCV6_126795_PI430048170 mRNA
CCTAGGCAACCAACTTTTGCTTATAACTACAATTTAATTTCACGTTGACAAAACACAGTG NM_024315RefSeq chr7
- 87196161 87219715 TMEM243 79161 "transmembrane protein 243, mitochondrial" GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139130_PI430048170 0.3439230865587811.17834568219679 5.97646896206905
6.00090144028825 5.45750323959655 P P P 5.64636905034044 5.66032916582528
5.47285760420315 P P P LNCV6_139130_PI430048170 mRNA
CCAGTGTTTAGCTCCCAACTAGTAACAGACGGAAAGAAAAAATAAAATTATCCAGAATCT NM_178562RefSeq chr7
+ 129144715 129169694 TSPAN33 340348 tetraspanin 33
GO:0051604|GO:0009986|GO:0005886|GO:0097197|GO:0016021|GO:0019899|GO:0090002 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131641_PI430048170 0.1858702045466311.11362400138354 0.626728036168898
0.3786662422825230.595199526283285 A A A 0.2861752765193380.40428079846346
0.451768340658214 A A A LNCV6_131641_PI430048170 mRNA
TGACTCATCTTGCATCTACTTCTTGTGTGTCTTGCATTGGATATGCCAAAGTTCTTTCCT NM_001145121 RefSeq chr6
+ 167170592 167182908 TCP10L2 NA t-complex 10-like 2 NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141899_PI430048170 0.5551582765255350.7456071691858080.460572907204166
0.5351827093293230.528158870834514 A A A 0.3487939372649170.41936216178299
1.63803922753515 A A A LNCV6_141899_PI430048170 mRNA
CGTTCTCTGCATCTCACATTTCTCATTTAACAATGTAGGATGAGAATTTCTCTAAGTCTA NM_003162RefSeq chr2
- 36837697 36966472 STRN 6801 "striatin, calmodulin binding protein"
GO:0005515|GO:0005516|GO:0008285|GO:0030331|GO:0000159|GO:0014069|GO:0032403|GO:0016358|GO:0005
737|GO:0070830|GO:0043197|GO:0016020|GO:0045211|GO:0043025|GO:0007626|GO:0005923|GO:0016055|GO:0
051721|GO:0070016. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139718_PI430048170 0.2252490102942711.19449788436185 4.90250720724477
5.39327231966006 5.11615817521137 P P P 4.77790193606558 4.83066933973543
5.06042732405646 P P P LNCV6_139718_PI430048170 mRNA
CAGTAAGTGACTGGATTCTTGGCACATTTATGTTCACCAAAGTAGAACAAGAAGATATTA NM_012383RefSeq chr9

+ 75088481 75147198 OSTF1 26578 osteoclast stimulating factor 1
GO:0005622|GO:0005515|GO:0007165|GO:0017124|GO:0005737|GO:0001503|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143588_PI430048170 0.1498509812090530.7368410827385970.940390170772403
0.3761017906884420.869784697139604A A A 1.43781551206498 1.22600915170948
0.845997924009993A A A LNCV6_143588_PI430048170 mRNA
GGCTTGTGTAATTTCCTGCTCCTCCAGTACAATAAATAAAAGAAAGATGCTGATGAAAAA NM_024411RefSeq chr20
- 1978755 1994285 PDYN 5173 "prodynorphin, transcript variant 1"
GO:0005886|GO:0007218|GO:0001515|GO:0007268|GO:0005576 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141359_PI430048170 0.000339618014062863 1.76358824730328 9.62452900321685
9.69610988175415 9.66072062450002 P P P 8.919194164688 8.79134101620072
8.81289767077008 P P P LNCV6_141359_PI430048170 mRNA
CCCGGGATGTGATTCAGGACACTTTCCATCCTAGGAATAAAGGGTAGTGCAATCAAAAAA NM_016178RefSeq chr1
+ 151766654 151771330 OAZ3 51686 "ornithine decarboxylase antizyme 3, transcript variant 1"
GO:0005515|GO:0045732|GO:0006521|GO:0072562|GO:0005634|GO:0036126|GO:0044281|GO:0007283|GO:0043
086|GO:0005829|GO:0008073|GO:0015489|GO:0034641|GO:0006596|GO:0043666|GO:0015847|GO:0071532 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138191_PI430048170 0.3281372048432621.95988693638758 0.333674218034657
2.20822543466002 2.19826746402769 A A A 0.2709937790789790.695305994222709
1.33145614812109 A A A LNCV6_138191_PI430048170 mRNA
CAAAAGAGGGACAACGAACATGGCATGTGAAAAGTAAAACAGATTTGTTCATTCCGAAAANM_003385RefSeq chr2
+ 17540539 17656439 VSNL1 7447 visinin-like 1 GO:0019722|GO:0005509 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_104907_PI430048170 0.3914495032996041.17712167984203 10.477949972297
10.8066931325288 11.0792808765186 P P P 10.253920700986 10.5534720255061
10.8513387361905 P P P LNCV6_104907_PI430048170 mRNA
GGGACAAATTAGCTGCACATCTATCATCAAGAGATTCACAATCAAGATCTGTATCAAGAT NM_005192RefSeq chr14
+ 54396954 54420216 CDKN3 1033 "cyclin-dependent kinase inhibitor 3, transcript variant 1"
GO:0005515|GO:0048471|GO:0005737|GO:0000082|GO:0008285|GO:0007050|GO:0008138|GO:0004722|GO:0000
079|GO:0035335|GO:0004725 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54497_PI430048170 0.2531829652286390.83029655633326 10.1309320278111 9.98339935876145
10.4956653526405 P P P 10.3232726685449 10.3583079751856 10.7437157921434 P P P
LNCV6_54497_PI430048170 mRNA
TGCAATTGATACGGAGAAGTCACAACAGGCACTGGTTCAGAAGCGCCATTACCTTTTTGA NM_001688RefSeq chr1
+ 111449120 111461903 ATP5F1 515 "ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1"
GO:0005515|GO:0015986|GO:0022857|GO:0005743|GO:0005634|GO:0044281|GO:0005753|GO:0022904|GO:0005
739|GO:0016020|GO:0021762|GO:0046933|GO:0042776|GO:0005759|GO:0000276|GO:0005654|GO:0016887|GO:0
044237|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142475_PI430048170 0.00850034668739424 1.62918821777193 10.7766274075644
11.0399278601538 11.0456564943069 P P P 10.3309437603805 10.027932643804
10.3821286342446 P P P LNCV6_142475_PI430048170 mRNA
CCTTCTTTCCTAGACAATCAAAGTATCAGTGATGGGTTTTGGTTGGTGATTTTGAAAAAA NM_138801RefSeq chr2
+ 38665909 38734767 GALM 130589 galactose mutarotase (aldose 1-epimerase)
GO:0005737|GO:0004034|GO:0030246|GO:0006006|GO:0006012|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131107_PI430048170 0.4556736573086241.17212952164932 4.95763536277392
4.89671892778872 4.98072948596008 P P P 5.31475784493381 4.33363792750431
4.24024906308178 P P P LNCV6_131107_PI430048170 mRNA

TAATGCCACTGGTGTTAAGATATATTTTGAGTGGATGGAGGAGAAATAAACTTATTCCTC NM_000507 RefSeq chr9 - 94603138 94639641 FBP1 2203 "fructose-1,6-bisphosphatase 1, transcript variant 1" GO:0005515|GO:0030308|GO:0016208|GO:0005975|GO:0071286|GO:0006094|GO:0044281|GO:0035690|GO:0046872|GO:0042802|GO:0005829|GO:0006111|GO:0046580|GO:0005737|GO:0051289|GO:0016311|GO:0009405|GO:0006006|GO:0045820|GO:0048029|GO:0006002|GO:0070062|GO:0042132|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105526_PI430048170 0.0660202876291094 0.746252235188361 5.85273256998017 5.59914106661914 5.39398734868891 P P P 6.16002454352915 5.99255534111851 5.99014670974396 P P P LNCV6_105526_PI430048170 mRNA
TATTGCAGCAACGGCTACTACTACCACACACAGCGGCTGGAGTGCATCGACAATGACGAG NM_001042544 RefSeq chr19 + 40597234 40629820 LTBP4 8425 "latent transforming growth factor beta binding protein 4, transcript variant 1" GO:0005515|GO:0050431|GO:0005509|GO:0005578|GO:0005576|GO:0007275|GO:0005539|GO:0001558|GO:0005615|GO:0031012|GO:0030162|GO:0005178|GO:0030198|GO:0006457|GO:0005024|GO:0045595|GO:0030252|GO:0007179|GO:0017015|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133457_PI430048170 0.47569378211703 1.88003945796489 0.4974955317541 2.36275634199912 0.252112986716073 A A A 0.398870398457502 0.511318414949804 0.460923206027875 A A A LNCV6_133457_PI430048170 mRNA
TTGTCAGAGCATCCCGGACGATGCAGAGGGTGGGAGAACTACATGCTAAATTTCTTTTTT NM_004829 RefSeq chr19_KI270938v1_alt + 888621 895553 NCR1 9437 "natural cytotoxicity triggering receptor 1, transcript variant 1" GO:0042269|GO:0035556|GO:0007165|GO:0006968|GO:0030101|GO:0016514|GO:0005887|GO:0005057 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145340_PI430048170 0.0947946999527734 1.04828557831016 0.418605556993356 0.44788841939312 0.45728188860054 A A A 0.333622300543658 0.365594749353511 0.419438034166899 A A A LNCV6_145340_PI430048170 mRNA
TGCTGAAAGGTGACCAAAGAAATGCACAAAATGTGAAAATCTTTGTCACTCCATTTTGTA NM_005963 RefSeq chr17 - 10492309 10518542 MYH1 4619 "myosin, heavy chain 1, skeletal muscle, adult" GO:0005516|GO:0032982|GO:0003774|GO:0006936|GO:0014704|GO:0008152|GO:0003779|GO:0005859|GO:0031672|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138985_PI430048170 0.940603510928008 0.998067744880574 0.262109562350976 0.276811919862104 0.42527721076519 A A A 0.358419612720956 0.307355407360446 0.311950696129567 A A A LNCV6_138985_PI430048170 mRNA
TACCTCGTTGCTCTGTTCATTTGTTGAACAAAGACGTTTTGAATAAAGACAATCTGTCAT NM_004189 RefSeq chr3 + 137764291 137766330 SOX14 8403 SRY (sex determining region Y)-box 14 GO:0043565|GO:0046982|GO:0006366|GO:0009649|GO:0003682|GO:0000981|GO:2001222|GO:0005575|GO:0000122|GO:0045892|GO:0007601|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144767_PI430048170 0.414106811076655 0.891302357096933 0.274155268205239 0.302985788065693 0.390073685013612 A A A 0.768574214468867 0.333705909491396 0.318872696117228 A A A LNCV6_144767_PI430048170 mRNA
TGACACAAACATTTACTGCTGGATCGACCACAAAGCAGATGTGGCTTCTTAGGTTCCTCT NM_001288773 RefSeq chr19_KI270867v1_alt - 95156 132483 CEACAM21 90273 "carcinoembryonic antigen-related cell adhesion molecule 21, transcript variant 3" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141683_PI430048170 0.00657696427053018 0.396881672257985 4.98325525089982 4.40809736216346 4.97433014808585 P P P 6.35885110597141 5.94362405450399 6.10387560873956 P P P LNCV6_141683_PI430048170 mRNA
CCCATGACTGTTATTAGTTGTCAAAGTTGAAAAGTACTTTAGCTGTGAGAAATCCTTGTA NM_015012 RefSeq chr11 - 9280654 9314768 TMEM41B 440026 "transmembrane protein 41B, transcript variant 1"

GO:0016021|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144583_PI430048170 0.1016590231423242.0046841924557 4.17564129472402
4.16931038932228 4.33156919915726 P P P 2.50047192870351 3.01701563466749
3.83589107104915 A P P LNCV6_144583_PI430048170 mRNA
CTACTAAGAAATATGTTGGTGTGTTTGTCCTTACTTGAAATGGGTCTGTATTATGGTACT NM_003725RefSeq chr12
+ 56763217 56787790 HSD17B6 8630 hydroxysteroid (17-beta) dehydrogenase 6
GO:0005622|GO:0004303|GO:0006702|GO:0005783|GO:0031901|GO:0047035|GO:0016491|GO:0009055|GO:0006
710|GO:0004745|GO:0003824|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131066_PI430048170 0.1806771801789031.07952153495924 0.374143082896105
0.5072082266809280.327203472474445A A A 0.2859535238875670.291479576009406
0.305967020001273A A A LNCV6_131066_PI430048170 mRNA
TGAATCCTGCCATCTATACCCTGAGAAACAAGGAAGTGATCATGGCCATGAAGAAGCTGT NM_001001965 RefSeq
chr11 + 123939616 123940573 OR4D5 219875 "olfactory receptor, family 4, subfamily D, member 5"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127534_PI430048170 0.00421438395904665 0.4020227072118797.10187922550931
7.04301415569369 7.25545918897576 P P P 8.23844574249217 8.37246795606143
8.70169528735553 P P P LNCV6_127534_PI430048170 mRNA
CCTATGGGAAGGTGGTCAATGAATGTTTTGATGAAATGAATGTTTTTGTATAATGGCCTT NM_001128616 RefSeq
chr3 - 56727417 56775717 ARHGEF3 50650 "Rho guanine nucleotide exchange factor (GEF) 3,
transcript variant 2"
GO:0005622|GO:0051056|GO:0048011|GO:0043065|GO:0032321|GO:0007264|GO:0007266|GO:0005089|GO:0097
190|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132980_PI430048170 0.3350858726399990.87551794412471516.303113366404
15.7674287163584 15.8371862619404 P P P 16.2046404563886 16.2199643034475
16.1170857646927 P P P LNCV6_132980_PI430048170 mRNA
GCTTTCTTAACTATCCTAACAAGCCTTGGACCAAATGGAAATAAAGCTTTTTGATGCAAA NM_000146RefSeq chr19
+ 48965308 48966879 FTL 2512 "ferritin, light polypeptide"
GO:0005515|GO:0005506|GO:0006892|GO:0055072|GO:0055085|GO:0006898|GO:0005829|GO:0008199|GO:0042
802|GO:0006879|GO:0008043|GO:0016020|GO:0061024|GO:0006826|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_106836_PI430048170 0.1675406137074960.52629122479184 1.51909599409544
3.21537555741263 2.89967909991753 A P P 3.34469307231765 3.69519970415518
3.82392068715191 P P P LNCV6_106836_PI430048170 mRNA
ATTCCGATGGAATTAATCAACGAGGTTATGTCTACCATCACGGACCCTGCAGCAATGCTT NM_003884RefSeq chr3
+ 20040031 20154404 KAT2B 8850 K(lysine) acetyltransferase 2B
GO:0005515|GO:0010467|GO:0006367|GO:0008285|GO:0042826|GO:0042641|GO:0010835|GO:0045736|GO:0035
948|GO:0006325|GO:0006361|GO:0005634|GO:0006360|GO:0018076|GO:0032403|GO:0004468|GO:0007219|GO:0
000125|GO:0045944|GO:0016032|GO:0006338|GO:0007050|GO:0004402|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132475_PI430048170 0.0136129088193390.5187209063732836.44260367627429 6.2956783069118
6.38684832939786 P P P 7.06196480107681 7.3451421887137 7.52541718711399 P P P
LNCV6_132475_PI430048170 mRNA
GTTTAAAACAACACATTCATAATTGACTCTGTGCAGGATGTCACTCAATCAGTTTGGGTT NM_014734RefSeq chr14
+ 69611592 69715144 SUSD6 9766 sushi domain containing 6
GO:0008219|GO:0008150|GO:0003674|GO:0016021|GO:0005575|GO:0006974 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_57483_PI430048170 0.1298904751492341.15514002929335 6.69991930615098 6.84548858733997
6.54502195918754 P P P 6.55510526452999 6.49113501657033 6.43301857214426 P P P

LNCV6_57483_PI430048170 mRNA
GGCTGGCATGCGGGAGGAGTGTGTCCTGTCAGAAGAACAGATCCGCCTGAAGAAACTGAA NM_005693 RefSeq
chr11 + 47257916 47269033 NR1H3 10062 "nuclear receptor subfamily 1, group H, member 3,
transcript variant 1"
GO:0005515|GO:0034145|GO:2000189|GO:0010467|GO:0032376|GO:2000188|GO:0000790|GO:0006367|GO:0044
212|GO:0090341|GO:0032810|GO:0043031|GO:0090188|GO:0003707|GO:0070328|GO:0005634|GO:0010870|GO:0
010875|GO:0060336|GO:0015485|GO:0045944|GO:0043401|GO:0004879|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127336_PI430048170 0.0619737067025255 3.86058316563765 3.75654173427389
3.56619924947506 3.47980468322085 P P P 0.342224336548503 2.24276757189282
1.78999989213011 A A A LNCV6_127336_PI430048170 mRNA
TCTGGAAGACTGGCCAAGGTTGTGGAGGAGCTTGTGAACTTGATTAAAGTGTCGTAACAT NM_001012301 RefSeq
chr5 - 150296345 150302962 ARSI 340075 "arylsulfatase family, member I"
GO:0006665|GO:0006687|GO:0005788|GO:0005576|GO:0004065|GO:0044281|GO:0044267|GO:0046872|GO:0043
687 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63317_PI430048170 0.0072948381221684 1.41442316170898 8.41837571333736
8.56652299643965 8.30887777840732 P P P 8.00874896751738 7.97083371900342 7.8182171172031
P P P LNCV6_63317_PI430048170 mRNA
CCAACTGGAAAGATATAAAAGTTTGGGTCTGTCTCCTCTCCTTCAGAAATGAAATATAAA NM_001164257 RefSeq
chr17 + 63998350 64004284 PRR29 92340 "proline rich 29, transcript variant 2" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_69864_PI430048170 0.614699636314186 1.07499086429713 5.18871061869951 5.2420652376201
5.65428066890556 P P P 5.12722866863475 5.28181612100948 5.39675232523659 P P P
LNCV6_69864_PI430048170 mRNA
CTCCACACAGCTGTCTGGATTTCATATTTGTATTGACAAAGGGACTTTTGATGCCATAAG NM_001304467 RefSeq
chr10 - 124757830 124791941 METTL10 399818 "methyltransferase like 10, transcript variant 2"
GO:0008168|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_116939_PI430048170 0.00284792979235536 2.07262710833611 4.74155219727399
5.04790957150051 5.13724289975674 P P P 3.95057712543079 4.08011655124003 3.7520145709563
P P P LNCV6_116939_PI430048170 mRNA
TTGACATTTGAATAGGATCCGAGATGTTCTGCTTTTATCCCGGGCAGCCCTGATATGTCA NM_004980 RefSeq chr1
- 111775831 111989155 KCND3 3752 "potassium channel, voltage gated Shal related subfamily D,
member 3, transcript variant 1"
GO:0005251|GO:0005515|GO:0005250|GO:0005886|GO:0007268|GO:0097038|GO:0030425|GO:0046872|GO:0044
325|GO:0042383|GO:0071435|GO:0086009|GO:0008076|GO:0043025|GO:0051260|GO:0034765|GO:0006813 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139646_PI430048170 0.952506805117844 1.06897768321925 1.36035088437545
0.390134050154825 0.298849567498069 A A A 0.719467496732753 0.400620627156506
0.857496831669196 A A A LNCV6_139646_PI430048170 mRNA
GGTAGGATGCCAGCAACCTGAACTGCCCAAAAATGTGTATTTAAATTTTTTCTTTCTTTA NM_001079910 RefSeq
chr12 + 85036320 85245105 LRRIQ1 84125 leucine-rich repeats and IQ motif containing 1 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63306_PI430048170 0.00241086021143549 1.32153385437167 12.5493215805983
12.6291414673005 12.5102315051663 P P P 12.2222299379163 12.1831302567536
12.0752652586618 P P P LNCV6_63306_PI430048170 mRNA
CCCTGAGGCGCTCTGTACTAGAAACTGCTCTTAATAATAACGGTGATTATTGGTTGCTGC NM_016360 RefSeq chr17
+ 63600871 63608365 TACO1 51204 translational activator of mitochondrially encoded cytochrome c
oxidase I GO:0005739|GO:0005654|GO:0005634|GO:0006417 . NA - . NA NA NA NA NA NA NA
NA NA

LNCV6_121248_PI430048170 9.01483779616432e-05 0.3203014370850125.51261859057597
5.69217580934323 5.73848404284227 P P P 7.21205145015538 7.43913523133733
7.21748617084978 P P P LNCV6_121248_PI430048170 mRNA
GAAACCCTACAAATGTGAAGAATGTGGCAAAGCTTTCAACTGGTCCTCAAACCTTATGGA NM_007153RefSeq chr19
- 21966094 22010943 ZNF208 7757 zinc finger protein 208
GO:0006355|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142794_PI430048170 0.3233983129849 0.7528874643063945.1843251299547
4.00102425036796 4.22083540297483 P P P 5.25512118896917 4.98683169786761
4.61056266731239 P P P LNCV6_142794_PI430048170 mRNA
TAAGTGAACATGCCCCTCTCAGAGGTAACAGCAAGTTTCCAGTGAGGAAAACCAGAACTT NM_001084393 RefSeq
chr22_KI270879v1_alt + 203200 208923 DDTL NA D-dopachrome tautomerase-like NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_131031_PI430048170 0.0208935402877172 0.5906381730760881 1.6464089278944
11.7096056968168 11.9441880648426 P P P 12.2858197654711 12.4553515390331
12.8057706705676 P P P LNCV6_131031_PI430048170 mRNA
CCTTTGTCCGAAGAAACTGTTCCTCCATTATTTGAATTACTGAAGACAGCAAGATATTTG NM_001001973 RefSeq
chr10 + 7788129 7807799 ATP5C1 509 "ATP synthase, H+ transporting, mitochondrial F1 complex,
gamma polypeptide 1, transcript variant 1"
GO:0022857|GO:0005743|GO:0044281|GO:0005753|GO:0006119|GO:0005739|GO:0022904|GO:0006754|GO:0016
020|GO:0046961|GO:0046933|GO:0005759|GO:0042776|GO:0000275|GO:0016887|GO:0044237|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137809_PI430048170 0.2991713856334750.9812790475698030.359981473757089
0.38746290832992 0.319956873770337A A A 0.3795041518868190.401136560242561
0.369167351086036A A A LNCV6_137809_PI430048170 mRNA
TTAGACAAAGCTGATGGCACTATGTTTTGTATCATGTTCCTTGAAACTGTAAATTCAGTG NM_194250RefSeq chr2
+ 184598365 184939487 ZNF804A 91752 zinc finger protein 804A GO:0046872 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_130523_PI430048170 0.9249550585192211.00512904394344 11.3197421091496
11.5099021498302 11.4346518553967 P P P 11.5493824730799 11.4304583015256 11.25337546966
P P P LNCV6_130523_PI430048170 mRNA
TGCCCTCGGTCTTCTACTGGAGCCTGCAGCCCCTGCTGAACTTCCTGCTGCCCGTGTTTT NM_001164377 RefSeq
chr11 - 3217943 3218813 MRGPRG NA "MAS-related GPR, member G" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_127246_PI430048170 0.7183766027574990.9486371210685918.72979830816342
9.28443551287149 9.50424344967769 P P P 9.13233113759593 9.19213850772369
9.50042865934124 P P P LNCV6_127246_PI430048170 mRNA
GATTAATGACCTTTGCACAATCTGTTTCTTGATTGGGTTTGTTATAGTTTTGAGTTGGGT NM_016618RefSeq chr2 -
88027202 88055801 KRCC1 51315 "lysine-rich coiled-coil 1, transcript variant 1" NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_143742_PI430048170 0.1079323432972441.29373195084577 6.30369232713224
6.35910874724187 6.26194047970779 P P P 6.20297948744391 5.8228550401657
5.74296122191532 P P P LNCV6_143742_PI430048170 mRNA
ATGATTGATTTTGGGATGAAATTCTCCACTCCTCTCCTTTACCACATCACCACTATCCTT NM_001103170 RefSeq chr1
+ 12716114 12728759 AADACL3 NA "arylacetamide deacetylase-like 3, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136917_PI430048170 0.3203806846288711.04848483884131 0.339785549192357
0.3430369854328940.494289470409964A A A 0.3243311804242910.298656399789341
0.354135460748181A A A LNCV6_136917_PI430048170 mRNA

GTTTTTACACCCTTGATTCTTCTTGAAGCATCACTTAGAACAAGTAAAACTTGCTTCAGA NM_001013623 RefSeq chr6 + 143864435 143938346 ZC2HC1B NA "zinc finger, C2HC-type containing 1B" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140078_PI430048170 0.0397183991603269 2.12027040557311 5.66317129387379 5.93287563153119 6.47095593630551 P P P 4.96169455072243 4.86941025227848 5.09411527708953 P P P LNCV6_140078_PI430048170 mRNA
GCAGGGCACTTACTAGCATAAGAATTGGTTTGGGATTTAACTGTTTATGAAGCTAACTTG NM_004374 RefSeq chr8 - 99877994 99894014 COX6C 1345 cytochrome c oxidase subunit VIc
GO:0022904|GO:0005739|GO:0004129|GO:0005743|GO:0044281|GO:0016021|GO:0006091|GO:0055085|GO:0044237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138020_PI430048170 0.1086391619672781.16746716821214 9.75690416745442 9.82280257825366 9.94037370206899 P P P 9.50810590242374 9.54152713264075 9.78962360004308 P P P LNCV6_138020_PI430048170 mRNA
CTGCATATACTGGATTGTACTTTGTGTAAAGTAAACATACTCAGTTTTGCTGTTCAGACA NM_004589 RefSeq chr17 - 10680331 10697568 SCO1 6341 SCO1 cytochrome c oxidase assembly protein
GO:0005739|GO:0006878|GO:0008535|GO:0005507|GO:0005743|GO:0006091|GO:0030016|GO:0006825 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130942_PI430048170 0.4316212953203211.05099717875032 0.303805496576469 0.3102041052891660.516464027718641 A A A 0.3155263126921970.277958629821178 0.331490888431585 A A A LNCV6_130942_PI430048170 mRNA
CCACTGTTATGAAAAGATGTAGCAACATGAGAAATGCTTATGTTACAGGTTACATGAGAA NM_201563 RefSeq chr1 + 161581338 161601220 FCGR2CNA - NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143065_PI430048170 0.0294866131559214 1.46913217568087 2.28359927763076 2.69870981486187 2.52012982431565 A A A 1.93437829566384 1.75175741489601 2.15314894965655 A A A LNCV6_143065_PI430048170 mRNA
GTAAAAGACAGTAAAGAAATTCAGGTCACAGGCCTTGGGAGTTCATAGGAAGGAGATGTC NM_006503 RefSeq chr19 + 39971004 39981764 PSMC4 5704 "proteasome (prosome, macropain) 26S subunit, ATPase, 4, transcript variant 1"
GO:0005515|GO:0031597|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0034641|GO:0005737|GO:0000082|GO:0006508|GO:0016032|GO:0090090|GO:0016887|GO:0006977|GO:0000209|GO:0043066|GO:0000502|GO:0016234|GO:0006521|GO:0001824|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127459_PI430048170 0.00213657502234694 0.6785880997978 9.04835213442433 9.16597397549795 8.98367883462733 P P P 9.65972420981147 9.51194539548952 9.70355499535884 P P P LNCV6_127459_PI430048170 mRNA
CCAGTAGAAAAGACAGTACACTGCTTTTCTTTTAGTGTTTGCTTTTCCTTTGCTATATGT NM_033089 RefSeq chr20 + 297562 300319 ZCCHC3 85364 "zinc finger, CCHC domain containing 3" GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132349_PI430048170 0.0100855201976769 0.5826020424109273.82475665363232 3.9294277538324 4.22876162276336 P P P 4.69817235125882 4.61667165447599 5.00733343906512 P P P LNCV6_132349_PI430048170 mRNA
CTTTGGTTCTGCCCATGAAGCATGTAATCTTTCTTACACATTAAAATCACTGAATGTGTA NM_005800 RefSeq chr13 + 30617692 30659549 USPL1 10208 ubiquitin specific peptidase like 1
GO:0005515|GO:0043130|GO:0030576|GO:0032183|GO:0015030|GO:0016926|GO:0008283|GO:0006508|GO:0005615|GO:0070140 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_46756_PI430048170 0.1847400588758520.9700849013457890.2955202102609320.336885042394182 0.334749535497629 A A A 0.4075576056365720.3312123882577790.359174435914595 A A A LNCV6_46756_PI430048170 mRNA
TGGACATCATGAAGCATCAAAGCACTGTTTAACTGGGAGTGATATGATGTGTAGGGCTTT NM_000446 RefSeq chr7

- 95298356 95324572 PON1 5444 paraoxonase 1
GO:0032411|GO:0072562|GO:0005615|GO:0046434|GO:0010875|GO:0042803|GO:0043231|GO:0005543|GO:0004
063|GO:0034364|GO:0034445|GO:0031667|GO:0004064|GO:0070062|GO:0019439|GO:0005509|GO:0034366|GO:0
009636|GO:0051099|GO:0005576|GO:0009605|GO:0070542|GO:0016311|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140418_PI430048170 0.6550441844597280.9230545889098272.78249237021387
3.91682294522435 3.44179927801622 A P P 3.69040685172806 3.67902493366587
3.30311308245135 P P P LNCV6_140418_PI430048170 mRNA
TCAACCTTGAGACAGCTTCGGTTTCTAACTTGGAGCCGGACTTTCGGAGTTGGGGGTCCG NM_000911RefSeq chr1
+ 28812141 28863696 OPRD1 4985 "opioid receptor, delta 1"
GO:0005515|GO:0043005|GO:0008344|GO:0005886|GO:0031226|GO:0007268|GO:0007200|GO:0007193|GO:0004
985|GO:0006955|GO:0005737|GO:0033138|GO:0007218|GO:0045211|GO:0051924|GO:0043679|GO:0000060|GO:0
032460|GO:0038046|GO:0097237|GO:0051881|GO:0071456|GO:0038003|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_134416_PI430048170 0.2541248558506310.9365265430746167.56749208279986
7.60200212095657 7.55318204992892 P P P 7.55278486706508 7.74982139261596
7.69719057629642 P P P LNCV6_134416_PI430048170 mRNA
AAGCCCCAGGGGTCCATTTGTATCAATTTTCATCTTGTTTTGTTTTGATTTCATTTACGT NM_152531RefSeq chr3 -
195068283 195271166 XXYLT1 152002 xyloside xylosyltransferase 1
GO:0008152|GO:0005789|GO:0016763|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_107111_PI430048170 0.0111990352811254 0.5777283621917180.628112548717697
0.31033963583551 0.346955887408517A A A 0.9606584927946971.4154301294032
1.26870975097049 A A A LNCV6_107111_PI430048170 mRNA
AAGATTGCCAGCAATCCCTTCGCGAAAGGCTTCCGGGACTGTGACCCTGAGGACTGGCCC NM_080647RefSeq chr22
+ 19756702 19767332 TBX1 6899 "T-box 1, transcript variant C"
GO:0007389|GO:0003700|GO:0071300|GO:0007605|GO:0001755|GO:0048844|GO:0048538|GO:0048752|GO:0048
703|GO:0030878|GO:0048701|GO:0042803|GO:0042693|GO:0007507|GO:0048644|GO:0046983|GO:0001945|GO:0
050679|GO:0042471|GO:0042472|GO:0001708|GO:0021644|GO:0060037|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135871_PI430048170 0.0457090619418626 2.97521010379196 5.77126861351123
5.56547587998772 5.33903883778443 P P P 4.65401251590382 3.24205598707808
3.72692964528506 P P P LNCV6_135871_PI430048170 mRNA
TACCCCAGAGACAGACTCTTTTTGTAAGATTTTGTTAATAAAACACTGAAACTTCCTGGA NM_015193RefSeq chr8
- 142611043 142614472 ARC 23237 activity-regulated cytoskeleton-associated protein
GO:0030054|GO:0001669|GO:0005886|GO:0014069|GO:0009952|GO:0015629|GO:0006897|GO:0005737|GO:0048
168|GO:0043197|GO:0007492|GO:0016477|GO:0045211|GO:0007010|GO:0022604|GO:0007612|GO:0005768 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130088_PI430048170 0.6941197471291521.01077160868892 0.363632366676735
0.3438318601999140.258436471152658A A A 0.3036905750928560.317993853619183
0.299934106339926A A A LNCV6_130088_PI430048170 mRNA
TTGTCTAAATATTTAGAAGGCGGAGAAGTTCCCAGAGGCTTCTGTACAGTCAGGTCTGCT NM_000960RefSeq chr19
- 46620467 46625097 PTGIR 5739 prostaglandin I2 (prostacyclin) receptor (IP)
GO:0005886|GO:0004930|GO:0030819|GO:0007267|GO:0048662|GO:0005829|GO:0005085|GO:0043547|GO:0005
887|GO:0007187|GO:0007596|GO:0032496|GO:0043950|GO:0007189|GO:0010642 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_133304_PI430048170 0.3259113578506641.30911567559459 0.514518205101559
0.4028081139490321.24366623781505 A A A 0.2999294578511940.384229257316135
0.458082024001721A A A LNCV6_133304_PI430048170 mRNA
AATCCAGAATGCACCAAATTCTCATAGTGCACAGCATGTGAAGATGGGGTATGGAGCATG NM_001013736 RefSeq

chrX + 37008358 37011666 FAM47C 442444 "family with sequence similarity 47, member C" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144842_PI430048170 0.5590276632246240.7967140894594440.439505235080275 0.4922822075646060.492731184541143A A A 0.3438832789705790.395725665238077 1.40551165345869 A A A LNCV6_144842_PI430048170 mRNA
GGAAAGTAATGAAATTGTCTCTGGTTTCAGAAACTTTTCCTCTTACCTTCCTTTCTCTTT NM_007356RefSeq chr7 - 108023550 108130356 LAMB4 22798 "laminin, beta 4" GO:0007155|GO:0005604 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127592_PI430048170 0.00224098708866698 0.2650085979327425.40637623334219 4.96355850991874 5.43355278281068 P P P 6.77587613571376 7.2970391403604 7.44303345420031 P P P LNCV6_127592_PI430048170 mRNA
ATATCTGTCTCCTCTCAATTCCCCACCACACCTTATAAAATTGTAATCAAAGATATCTCA NM_006628RefSeq chr15 - 52547044 52569132 ARPP19 10776 "cAMP-regulated phosphoprotein, 19kDa"
GO:0004864|GO:0008601|GO:0045722|GO:0005102|GO:0015459|GO:0019212|GO:0043086|GO:0050790|GO:0005737|GO:0007067|GO:0000086|GO:0046326|GO:0005654|GO:0000278|GO:0051721|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128474_PI430048170 0.5874907708275370.9806704459993050.471545249485291 0.47360769983983 0.384259839059672A A A 0.3980958512369180.515177198958869 0.499629408134627A A A LNCV6_128474_PI430048170 mRNA
GTCATGTGGCCAAAAGGATTAGATTTGATTTGATGTTCACTTGGAGTTTACTTTTTGTAC NM_052867RefSeq chr13 - 101053777 101416462 NALCN 259232 "sodium leak channel, non selective"
GO:0005515|GO:0005245|GO:0005886|GO:0086010|GO:0005272|GO:0030317|GO:0055085|GO:0070509|GO:0034220|GO:0070588|GO:0034765|GO:0035725|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130052_PI430048170 0.00411555876566307 0.50212607722805 5.38511928244246 5.04755220260112 5.26019581767928 P P P 6.19900102469135 6.31098969613783 6.18101416905745 P P P LNCV6_130052_PI430048170 mRNA
TTCCAAGAAGTCAAACTGCCTGTGTCCTCATCGCCTTCCACCTTTAGGAAATGCTATCTT NM_002625RefSeq chrX - 54933133 54994078 PFKFB1 5207 "6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1, transcript variant 1"
GO:0005515|GO:0031100|GO:0006094|GO:0044281|GO:0051591|GO:0006096|GO:0005829|GO:0042802|GO:0035556|GO:0042594|GO:0004331|GO:0033762|GO:0006006|GO:0006003|GO:0019900|GO:0003873|GO:0006000|GO:0032868|GO:0005975|GO:0070095|GO:0051384|GO:0033133|GO:0005524|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128414_PI430048170 0.6677562308558030.9828012524147 0.48221979529371 0.4866402415682940.38450870613335 A A A 0.39376433838576 0.525233509957754 0.508236787533942A A A LNCV6_128414_PI430048170 mRNA
ATACTGTTCTGGACTGTGCCTGTTAAGTTGCTCAGTTTTGAGCTGTCTTCAGACAAGAAG NM_003386RefSeq chr7 + 100733625 100797797 ZAN 7455 "zonadhesin (gene/pseudogene), transcript variant 3"
GO:0016337|GO:0005886|GO:0016021|GO:0007339 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131149_PI430048170 0.56400416903226 1.08752297580905 9.38385942424359 8.8959890228226 9.26111383956726 P P P 9.05963391726583 9.25100565468205 8.88767655895268 P P P LNCV6_131149_PI430048170 mRNA
AACATTTGGCAGGTTGTGCCTCTATGACATGATTCAGTCCAGAGTAACACTGATGGCTCA NM_001113324 RefSeq chr17 + 75979216 76000586 TEN1 NA TEN1 CST complex subunit NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140502_PI430048170 0.0039957134913184 0.4549919374793786.50718583185237 6.42195456193443 6.39709430115824 P P P 7.37448672693608 7.66041502747859 7.68197919160873 P P P LNCV6_140502_PI430048170 mRNA
GATGCGCTGATAGAACATCCTCAAGACAGTTTCCTTGAAATCAATAAATACTGTGTTTTA NM_024009RefSeq chr1

+ 34781188 34786364 GJB3 2707 "gap junction protein, beta 3, 31kDa, transcript variant 1"
GO:0005737|GO:0005243|GO:0007154|GO:0007605|GO:0005921|GO:0043588|GO:0005922|GO:0016021|GO:0001
890|GO:0055085|GO:0001701 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141168_PI430048170 0.00404047709219844 1.40573066616368 10.5643703877369
10.6790299201521 10.5560001605514 P P P 10.1181451437539 10.1227028479849
10.0876450009389 P P P LNCV6_141168_PI430048170 mRNA
TTTCTACACACAGTGGCTCACAATGGCTCCCCCGAAGATGGGCCTCGAGTGGTCTTCATC NM_181718RefSeq chr16
+ 29900825 29906056 ASPHD1 253982 aspartate beta-hydroxylase domain containing 1
GO:0018193|GO:0051213|GO:0016021|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136016_PI430048170 0.0161963638253711 0.6194680330379774.51618570029985
4.85181565783085 4.91379298242502 P P P 5.66374945467677 5.24456217520494
5.44656161213585 P P P LNCV6_136016_PI430048170 mRNA
TGCTGGATTCCATTAAAACAAAGGGCAAGAGTGCTGACTTCACTAACTTCGATCCTCGTG NM_000067RefSeq chr8
+ 85463901 85481492 CA2 760 "carbonic anhydrase II, transcript variant 1"
GO:0005515|GO:0030424|GO:0043627|GO:0005886|GO:0044281|GO:0010043|GO:0005615|GO:0005829|GO:0016
323|GO:0005737|GO:0044070|GO:0045780|GO:0043209|GO:0042475|GO:0006730|GO:0009268|GO:0070062|GO:2
001225|GO:0001822|GO:0045672|GO:0032849|GO:0045177|GO:0004089|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141574_PI430048170 0.0923901254010721 0.6560205292022922.32269502004867
1.65663456977145 2.36958643569715 A A A 2.95623233073809 2.76027854664632
2.52936999742656 P P P LNCV6_141574_PI430048170 mRNA
CCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGAAGTGGAAAAAA NM_012427RefSeq chr19
- 50943302 50953088 KLK5 25818 "kallikrein-related peptidase 5, transcript variant 1"
GO:0005515|GO:0045745|GO:0097209|GO:0008544|GO:0004252|GO:0006508|GO:0008236|GO:0008233|GO:0005
615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137673_PI430048170 0.421687338928982 1.15114351366242 5.2084925487853
5.35131307022188 5.50440301844943 P P P 5.35961282353641 4.66762431453272
5.34137495055922 P P P LNCV6_137673_PI430048170 mRNA
GTCAATACCTCATTTGTAAAACAGACCCATTAGTCGTGAATTTCCAGCTCTTTCAAAAAT NM_173480RefSeq chr19
+ 2900897 2918476 ZNF57 126295 zinc finger protein 57
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140541_PI430048170 0.198730924814391 1.76230114954576 4.74240950887859
5.12302230778339 4.72531380976522 P P P 2.86193376655401 4.5156700906042
4.30953480321739 P P P LNCV6_140541_PI430048170 mRNA
TCCCCAGCTGTGTTTGTTTATAAATGCTGTTTATAGTGCAATAAAGGTGTTTCGGGAATA NM_001136263 RefSeq
chr19 - 405442 409170 C2CD4C 126567 C2 calcium-dependent domain containing 4C NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_136686_PI430048170 0.0182096907049496 1.10938229541391 0.696589321380882
0.7518264560185340.692569288221424A A A 0.6226948788777080.530795903851169
0.537149926238098A A A LNCV6_136686_PI430048170 mRNA
CTTGAAGTTCTTGCTCTGAGTTCACCACATGTTTTTGTAATTTTGTGGTTGGTGATTAAT NM_007226RefSeq chr2 -
138669156 138780241 NXPH2 11249 neurexophilin 2 GO:0003674|GO:0007218|GO:0005576 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135167_PI430048170 0.0301754309648642 0.497792763165741 7.63118687982339
7.59795309039456 7.66376408715144 P P P 8.29017432389869 8.65130940335583
8.90599705027374 P P P LNCV6_135167_PI430048170 mRNA
GGGGCAGTTTAGATGCTGTGAAATTAAACCTGTTCTAAGTGTACTTGTTTGAATTAATTG NM_014615 RefSeq
chr16 + 85613235 85676206 GSE1 23199 "Gse1 coiled-coil protein, transcript variant 1"

GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145329_PI430048170 0.0591409445008827 0.592804218670261 11.0812930190756
10.4091617840216 10.4203909914158 P P P 11.4170029589446 11.5559389078576
11.2965579734154 P P P LNCV6_145329_PI430048170 mRNA
CCCTCCCTCTTCCCCCAACAAGAATAAAGTTTATTAAATTATCTGGTTTTGGTGTAAAAA NM_014983 RefSeq chr5
+ 150000605 150053143 HMGXB3 NA HMG box domain containing 3 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_134091_PI430048170 0.891454211160807 0.994014229343852 8.62308288024084
8.90538229130401 8.51024935993027 P P P 8.71350846720726 8.71261274567798
8.66727827935705 P P P LNCV6_134091_PI430048170 mRNA
GGAATGGTTTCTATGGCCAAAGTTTGGTTTTCTCAACACTGTCTAAATTTGGATTAAAAC NM_020904 RefSeq
chr19 - 48837096 48868627 PLEKHA4 57664 "pleckstrin homology domain containing, family A
(phosphoinositide binding specific) member 4, transcript variant 1"
GO:0008150|GO:0005545|GO:0005737|GO:0016020|GO:0005575 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_130885_PI430048170 0.0186365953577873 1.12628679668929 13.5603788134128
13.6632163650127 13.5839369790752 P P P 13.4186932268042 13.4918009354489
13.3821699384506 P P P LNCV6_130885_PI430048170 mRNA
ACCTATGTCAGACACTACATGATGACTCAAGGCCAATAATAAAGACATTTCCTACCTGCA NM_005234 RefSeq
chr19 - 17231884 17245342 NR2F6 2063 "nuclear receptor subfamily 2, group F, member 6"
GO:0005515|GO:0010467|GO:0003700|GO:0006367|GO:0003707|GO:0005634|GO:0000122|GO:0001227|GO:0003
677|GO:0043565|GO:0007165|GO:0048666|GO:0043401|GO:0008270|GO:0000980|GO:0005654|GO:0004879|GO:0
004887|GO:0050965|GO:0043153|GO:0030522 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_122247_PI430048170 0.825399831826055 0.896099964277493 4.00593693088953
3.77610065337274 3.45362672650056 P P P 4.08386420741363 4.29939316000401
3.13679268473131 P P P LNCV6_122247_PI430048170 mRNA
ATTGCCTCTGGCCAGTGGTGTGCTAACAAAAGTTTAACCAGCAGCTCTCCAACAAAAAAG NM_001162495 RefSeq
chr21_GL383580v2_alt - 21594 44650 C21orf62 56245 "chromosome 21 open reading frame 62,
transcript variant 1" GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_130866_PI430048170 0.99742603597423 0.969913631070334 0.587743738682821
0.629840584940611 1.22461657834784 A A A 1.44739581760582 0.499288893976016
0.499436709444034 A A A LNCV6_130866_PI430048170 mRNA
TCCACTAACCATGACAAGGTTGTGTCAGCCTTCTATACTATGTTCACCCCTTTACTAAAC NM_001004695 RefSeq
chr1 - 248272851 248273814 OR2T33 NA "olfactory receptor, family 2, subfamily T, member 33" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136249_PI430048170 0.421861724768281 0.718774612264593 0.435834094568516
1.07889317713234 0.58316201637068 A A A 0.322656721924169 1.50775599870634
1.4909967149095 A A A LNCV6_136249_PI430048170 mRNA
TTGTTCAGACAGAGTTGTACCTGCAGCAGACAACTCTGAATTAAAGCATGAAAACACAGC NM_014723 RefSeq
chr20 + 1266315 1309327 SNPH 9751 syntaphilin
GO:0005881|GO:0043005|GO:0016081|GO:0030054|GO:0031966|GO:0007269|GO:0042734|GO:0005737|GO:0007
420|GO:0030182|GO:0043025|GO:0016021|GO:0017075 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141164_PI430048170 0.214756182043107 1.0627944799404 10.9944353522664
11.0125088486126 10.8613836879954 P P P 10.8631270830849 10.927923359851
10.8161738127137 P P P LNCV6_141164_PI430048170 mRNA
ATCATATATGGGGGCTGGGCCTCGGGACTCTCGCTCTAATAAAGGACTGTAGGCCATGGG NM_032792 RefSeq

chr19 - 58513529 58519554 ZBTB45 84878 zinc finger and BTB domain containing 45
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_105487_PI430048170 0.201353107498538 1.1255861958528 13.487531360178
13.6663223986479 13.7811855139762 P P P 13.3577463714061 13.4749561520271
13.5955638389858 P P P LNCV6_105487_PI430048170 mRNA
GAAGAGGTTGATTAAGCCAACCAAGTGTAGATGTAGCATTGTTCCACACATTTAAAACAT NM_006597 RefSeq
chr11 - 123057491 123062335 HSPA8 3312 "heat shock 70kDa protein 8, transcript variant 1"
GO:0048026|GO:0005515|GO:0006986|GO:0008380|GO:0010467|GO:0042623|GO:0005886|GO:0006200|GO:0000
151|GO:0007268|GO:0072562|GO:0005634|GO:0005615|GO:0007269|GO:0005829|GO:0034605|GO:0005622|GO:0
042026|GO:0006457|GO:0007411|GO:0031072|GO:0051726|GO:0061024|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_121358_PI430048170 0.595076524958548 1.04697830544146 11.6355372053673
11.7055323167199 11.7393612392154 P P P 11.3981262288331 11.652198154162
11.8045124888141 P P P LNCV6_121358_PI430048170 mRNA
GACATGTACATGGAGTCTGAGGGCGGCGACGGCTACCTGGCTCCGGAGAATGGGTATTTG NM_003089 RefSeq
chr19 + 49085139 49108613 SNRNP70 6625 "small nuclear ribonucleoprotein 70kDa (U1), transcript
variant 1"
GO:0048026|GO:0005515|GO:0006397|GO:0008380|GO:0010467|GO:0003723|GO:0005634|GO:0000166|GO:0016
607|GO:0000398|GO:0005654|GO:0005681|GO:0043484|GO:0005685 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138255_PI430048170 0.0797344483179298 1.16662841745047 7.36517167991505
7.61305715924877 7.48762100081879 P P P 7.38902524061285 7.21156030567788
7.20103669837926 P P P LNCV6_138255_PI430048170 mRNA
CAGTATGCTTTGTAGAGCCCTTATCCCCCTCCTGCTTTTTATTTGTTTTTAGCTCACTAA NM_016282 RefSeq chr9
- 4709555 4741309 AK3 50808 "adenylate kinase 3, transcript variant 1"
GO:0046041|GO:0046033|GO:0046051|GO:0004017|GO:0005525|GO:0005524|GO:0046899|GO:0005739|GO:0016
310|GO:0007596|GO:0005759|GO:0046039|GO:0006172 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_2421_PI430048170 0.453525253328037 1.07589675348217 12.0800582922124
11.9605445908946 12.0635103574549 P P P 11.7074935875241 12.135146311477
11.9160584600398 P P P LNCV6_2421_PI430048170 mRNA
TGTTGTACTTCACAATCCTGGACTGTTGCTTCAAGTAAACAATATCCACATTTTGAAACA NM_001288609 RefSeq
chr17 - 75135242 75154243 HN1 51155 "hematological and neurological expressed 1, transcript
variant 5" GO:0032502|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130654_PI430048170 0.410328147994006 1.53859912647156 0.289656354611627
0.561826298088455 1.77324145472562 A A A 0.507640913644894 0.395900014504952
0.308023570027463 A A A LNCV6_130654_PI430048170 mRNA
TGATCCTTATATAATAGGCCTCAGCAACCTTGGGATGTTATACTGGGAACTAATAAACTC NM_001010847 RefSeq
chr1 - 13474976 13513747 LRRC38 126755 leucine rich repeat containing 38
GO:0005886|GO:0016021|GO:0006811 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_90839_PI430048170 0.0107294355548739 1.83215388794613 7.03414471915278
6.81843241487381 6.97995825328389 P P P 6.26143566042522 6.11609817091893
5.80629642867327 P P P LNCV6_90839_PI430048170 mRNA
AAGACTGCTCGTGGGAGTCAATGCAGGTGTGAGCATGAACATCCAGCCCATGTACCTGGG NM_001282864 RefSeq
chr22_KI270879v1_alt + 93361 122474 SLC2A11 66035 "solute carrier family 2 (facilitated glucose
transporter), member 11, transcript variant 4" GO:0005886|GO:0022891|GO:0008643|GO:0016021|GO:0055085
. NA - . NA NA NA NA NA NA NA NA NA

LNCV6_71286_PI430048170 0.122308742814149 1.14739101138543 8.28862725819521 8.27859201701528 8.29061731063364 P P P 8.1833822984091 8.13786910362042 7.92899845349619 P P P LNCV6_71286_PI430048170 mRNA TGTGGCCTTTTTGTGGAAGGCGGTGTTGACCCTGGGGCTGGTGCTTCTCTACTACTGCTT NM_001281460 RefSeq chr20 - 46349527 46364458 SLC35C2 51006 "solute carrier family 35 (GDP-fucose transporter), member C2, transcript variant 7" GO:0045747|GO:0005801|GO:0005793|GO:0005794|GO:0033116|GO:0010629|GO:0006810|GO:0016021|GO:0036066 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_39349_PI430048170 0.0712795298703855 0.852116771778597 7.11138992391714 6.85140187847919 6.99300965271339 P P P 7.15131646647136 7.2690237928523 7.2372418343613 P P P LNCV6_39349_PI430048170 mRNA CATCGTGCGGGACTCTCTCATGCAGCCCGTGAGGAAGGTGCAGTCGGCCACACACTTCAA NM_013245 RefSeq chr16 + 69311383 69325043 VPS4A 27183 vacuolar protein sorting 4 homolog A (S. cerevisiae) GO:0005515|GO:0000815|GO:0048471|GO:0042623|GO:0019058|GO:0005634|GO:0031122|GO:0015031|GO:0005829|GO:0009838|GO:0000910|GO:0005737|GO:0016197|GO:0061024|GO:0016032|GO:0007033|GO:0016192|GO:0070062|GO:0032466|GO:0006997|GO:0005813|GO:0019904|GO:0030496|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144843_PI430048170 0.0457692111167924 1.44864800288163 11.5147559636728 11.2070828730086 11.0268095094816 P P P 10.8763002702415 10.6890188131323 10.6086882123362 P P P LNCV6_144843_PI430048170 mRNA GGGGAGGAATCCTGGACCAAGCACAAAAACTTAACAAAAGTGATGTAAAAATGAAAAGCC NM_001017402 RefSeq chr1 - 209614872 209651334 LAMB3 3914 "laminin, beta 3, transcript variant 2" GO:0005515|GO:0034329|GO:0005576|GO:0035987|GO:0032403|GO:0005610|GO:0008544|GO:0022617|GO:0005198|GO:0030198|GO:0050873|GO:0031581|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92030_PI430048170 0.538078372021393 0.957841030450247 8.98922952311904 9.08886026127209 9.06483090430386 P P P 9.24909511760683 8.98358578493762 9.08602473370612 P P P LNCV6_92030_PI430048170 mRNA CCTATGAGGGACCAATGTATTTAGAACCTCTCTCTATGAATCGGTTTACCACAGCCTTAA NM_001199383 RefSeq chr5 - 159157408 159209555 RNF145 153830 "ring finger protein 145, transcript variant 5" GO:0008270|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140211_PI430048170 0.0162497682309204 0.420355135724525 2.66830550236985 2.46116452204287 2.37260814032497 A A A 3.40316422093899 3.65943159142901 4.11498786660954 P P P LNCV6_140211_PI430048170 mRNA CTGCATAGTCATATCGAGTGTGCACTTACTGTATATCTTTTCATTTACATACTTGTATGG NM_001042459 RefSeq chr3 - 99847922 100114513 FILIP1L 11259 "filamin A interacting protein 1-like, transcript variant 3" GO:0008150|GO:0003674|GO:0005737|GO:0016020|GO:0005634 . NA - . NA NA NA NA NA NA NA NA
LNCV6_130476_PI430048170 0.0797664535614079 1.23296575913604 11.2713710084172 11.3261360119049 11.4751855621213 P P P 10.9170223041296 10.9763602940353 11.2573332298369 P P P LNCV6_130476_PI430048170 mRNA GCGAGCTTTCTCTCAGAGCATGCTTTTCTTTATTAAAATTACTGATGCAGAACATTTGAT NM_002097 RefSeq chr13 + 27424543 27435709 GTF3A 2971 general transcription factor IIIA GO:0010467|GO:0006355|GO:0009303|GO:0003723|GO:0005654|GO:0005634|GO:0006383|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81403_PI430048170 0.0784526697316848 1.31814432960012 2.82820995554925 3.14834468034978 2.94271001050267 A P P 2.83456135702298 2.48172814664534 2.38630338531047 P A A LNCV6_81403_PI430048170 mRNA AGGGAGTTCCCTGAGATGAATCTGGAATCGGTGACACCCATGACCCTCACGACCCTGGAA NM_002297 RefSeq

chr9 + 135521437 135526540 LCN1 3933 "lipocalin 1, transcript variant 1"
GO:0010951|GO:0004869|GO:0050909|GO:0001895|GO:0006508|GO:0005576|GO:0015909|GO:0055085|GO:0005615|GO:0050896|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126895_PI430048170 0.0533576470514709 1.18289864470869 9.24454246610174 9.18677034113832 9.41011977268376 P P P 8.97300409395706 9.15351517221558 8.9903907247834 P P P LNCV6_126895_PI430048170 mRNA
TCGAGATCACAAGTTGCATGTTGACTTTAGGAACGTGAAGCTCTTGGAGCAATTTGTCTG NM_014046 RefSeq
chr6_GL000256v2_alt + 1918466 1927155 MRPS18B 28973 mitochondrial ribosomal protein S18B
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0032543|GO:0030054|GO:0006996|GO:0003735|GO:0005743|GO:0005654|GO:0006412|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94423_PI430048170 0.0345424603227524 0.768771532037329 5.79682683394987 5.83326224052023 5.79379576415238 P P P 6.24292922830633 6.27333473332072 6.03456532516854 P P P LNCV6_94423_PI430048170 mRNA
TTCCGCCATTATGATTTCAGACAGAGCTGCTGGGTCCGTGCCATATCCCAGGAGGACCAG NM_032258 RefSeq
chr17 + 38127953 38138868 TBC1D3F 84218 "TBC1 domain family, member 3F"
GO:0005886|GO:0032851|GO:0005097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134631_PI430048170 0.00743287037077481 0.447703558943793 7.57899907563982 7.62918428787968 7.96187486743095 P P P 8.66727827935705 8.73485100418503 9.21333666887711 P P P LNCV6_134631_PI430048170 mRNA
AACCAGCTGCTGGTGTAATGTACAGTTATATTTGTCTATAAATGGAGCTGTTTATGGCAA NM_015131 RefSeq
chr2 + 28894642 28948220 WDR43 23160 WD repeat domain 43 GO:0005730 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135926_PI430048170 0.127208691643466 0.40387059647165 1.83341347406255 3.79837822135072 1.82134585622124 A P A 3.82764816012212 4.24298084938812 4.23962373144361 P P P LNCV6_135926_PI430048170 mRNA
TGCCATACAGGCTCATTTTCATGCAAATTCTTCCTAGAGCCAAATAAATAAAGACTTAGG NM_016252 RefSeq
chr2 + 32357027 32618898 BIRC6 57448 baculoviral IAP repeat containing 6
GO:0005515|GO:0005802|GO:2001237|GO:0060711|GO:0043066|GO:0004842|GO:0008284|GO:0032465|GO:0016567|GO:0004869|GO:0005815|GO:0060712|GO:0016874|GO:0030496|GO:0006915|GO:0010951|GO:0000922|GO:0007067|GO:0016020|GO:0042127|GO:0006468|GO:0051301|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136542_PI430048170 3.08796781692673e-05 1.44749639452461 11.6187157761497 11.6519739406036 11.5991788362251 P P P 11.0987264980044 11.0542422987522 11.1160132515672 P P P LNCV6_136542_PI430048170 mRNA
CTGGATTTGGATTTCTTGAAGCAGGCAGCTTCATATTATACCGATTTGTTCTCTGTCAAA NM_001129765 RefSeq
chrX + 152830966 152869363 NSDHL 50814 "NAD(P) dependent steroid dehydrogenase-like, transcript variant 2"
GO:0005811|GO:0006695|GO:0005783|GO:0044281|GO:0003854|GO:0007224|GO:0043231|GO:0047012|GO:0005789|GO:0060716|GO:0016021|GO:0001942|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138556_PI430048170 0.788397628477443 1.0428571929083 9.6357688087258 10.032192377397 10.1280323325031 P P P 10.1448520547871 9.84490117006581 9.62237196580744 P P P LNCV6_138556_PI430048170 mRNA
TGTTTCAGTGACATATGTATTGTTTATCTGGGTTAGGGATGGGGGACAGATAATAGAACG NM_022152 RefSeq
chr2 - 218274193 218292557 TMBIM1 64114 transmembrane BAX inhibitor motif containing 1
GO:0048553|GO:0005794|GO:0090005|GO:0016021|GO:0005123|GO:0005765|GO:2000504|GO:0010008|GO:0070062 . NA - . NA NA NA NA NANA NA NA NA

LNCV6_144167_PI430048170 0.0957485089185059 0.77998107628588412.404779281008
12.290337378113 12.4104494522899 P P P 12.469354538357 12.8300711461412
12.8535774039145 P P P LNCV6_144167_PI430048170 mRNA
GCTCCCACACTGGCCTTTGTAAATAAATGGCGTGGTCTTTGTTGTGAGAGTGTGAAAAAA NM_020131RefSeq chr1
- 156035293 156053825 UBQLN4 56893 "ubiquilin 4, transcript variant 1"
GO:0031597|GO:0005515|GO:0048471|GO:0031595|GO:0005737|GO:0005789|GO:0032434|GO:0005634|GO:0042
802|GO:0031593|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136850_PI430048170 0.0289380592057628 1.23083362314595 13.7422413563404
13.9018882295438 13.84338131332 P P P 13.667113945086 13.4502711002327
13.4654035950379 P P P LNCV6_136850_PI430048170 mRNA
TACTGTTGCTGGAAGTGTCCCACCTGCTGCTCATAATAAATGCAGATGTATAGCAAAAAA NM_014206RefSeq chr11
- 61789129 61792613 TMEM258 746 transmembrane protein 258 GO:0016021 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_142249_PI430048170 0.6656312981312380.9516117171958093.52553655272059
2.97701111444923 2.95548153582203 P P P 3.20087595973754 3.34347784697836
3.19863247076491 P P P LNCV6_142249_PI430048170 mRNA
CCTTCCCTCTCAGAGGATACATTTGTAACCATTACACAGTCATCAAAGGAATAATTTTTT NM_000511RefSeq chr19
+ 48695970 48705934 FUT2 2524 "fucosyltransferase 2 (secretor status included), transcript variant 1"
GO:0042355|GO:0005794|GO:0005975|GO:0032580|GO:0008417|GO:0008107|GO:0006486|GO:0016021|GO:0036
065|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65750_PI430048170 0.2493850654452340.8541816716065181 3.9276170262018 14.2860674911971
14.4337289776461 P P P 14.3899322054264 14.3833204406184 14.5921739678073 P P P
LNCV6_65750_PI430048170 mRNA
CATGTTGTTGTTGAAGTGTGGAGTTGTAACTCTGCGTGGACTATGGACAGTCAACAATAT NM_001743RefSeq chr2
- 47160081 47176623 CALM2 805 "calmodulin 2 (phosphorylase kinase, delta)"
GO:0005515|GO:0005513|GO:0007603|GO:0030017|GO:0006936|GO:0007173|GO:0043274|GO:0016056|GO:0010
800|GO:0005813|GO:0032465|GO:0006996|GO:0019901|GO:0005975|GO:0008179|GO:0005509|GO:0019904|GO:0
030168|GO:0022400|GO:0010801|GO:0044325|GO:0031432|GO:0000922|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_61800_PI430048170 0.2553735474447281.15895076337376 10.188778926079 10.429984471044
10.5507955155927 P P P 10.2834159133609 9.93186752323727 10.3091283521704 P P P
LNCV6_61800_PI430048170 mRNA
TCAGAGATTCCTAGGAAAGCTGCCTTATTCTCTTTTTGCAGTAAAGTATGTTGTTTTCATNM_012142RefSeq chr15 +
43185267 43197177 CCNDBP1 23582 "cyclin D-type binding-protein 1, transcript variant 1"
GO:0005515|GO:0007049|GO:0005737|GO:0051726|GO:0005654|GO:0005634 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_79933_PI430048170 0.0247345692481747 2.4317545274461 5.21786492308923
5.74547439983926 6.09991881349417 P P P 4.58127651917452 4.2086798217558
4.53250876558545 P P P LNCV6_79933_PI430048170 mRNA
ACAATATTTCTCAGAGGATAGCCTTTCACTTATTCATCTGTCCAGCATGACTCATCCCCG NM_019607RefSeq chr8
+ 66667551 66681142 C8orf44 56260 chromosome 8 open reading frame 44 GO:0005654 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_129997_PI430048170 0.43203330028111 0.8176177479452730.473213875185704
1.17541165075899 1.51916679871889 A A A 0.9826220072160261.61166389877284
1.55275224762901 A A A LNCV6_129997_PI430048170 mRNA
TTGTAACTTACTGTGCTGTCTTCCTTTTTTGCAACTTGGCTCTGACCTGGCATCGGAAAA NM_001136571 RefSeq
chr13 - 32303770 32311954 ZAR1L NA zygote arrest 1-like NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_140273_PI430048170 0.0105271015393990.5530295663487216.16809214930383

5.79124551820262 6.24252676816726 P P P 6.73895324992194 6.87178745638121
7.16133195642276 P P P LNCV6_140273_PI430048170 mRNA
ACAACAGTAACAGAACTTTGCAATTTTCTGGGGTTTTGTTTTTTACCTTTTTCCCCCCTT NM_015172 RefSeq chr1 +
171485526 171593511 PRRC2C 23215 proline-rich coiled-coil 2C GO:0016020|GO:0002244|GO:0008022 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138563_PI430048170 0.00903049949910269 0.5303998350349287.28075839970208
7.02450363945568 7.17968437690833 P P P 7.8198044088911 8.09585551771284
8.28744274350463 P P P LNCV6_138563_PI430048170 mRNA
GAATTGTGGGTGTGCCTATCATAACAATTGTTTTCTGTATCTTGAAAAAGTATTCTCCAC NM_001282101 RefSeq
chr11 + 102110460 102233423 YAP1 10413 "Yes-associated protein 1, transcript variant 9"
GO:0005515|GO:2001237|GO:0010467|GO:0008284|GO:0006367|GO:0030054|GO:0044212|GO:0008283|GO:0010
837|GO:0090263|GO:0060242|GO:0005634|GO:0071480|GO:2000737|GO:0005829|GO:0003143|GO:0005737|GO:0
030857|GO:0045944|GO:0072307|GO:0070064|GO:0035019|GO:0005667|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129014_PI430048170 0.2747349257142970.9442259214506460.253381996716269
0.3676289196826190.280391098093234A A A 0.4783278182273970.371549198149045
0.296598835946562A A A LNCV6_129014_PI430048170 mRNA
GAGATGATTCTGTCCTTGGTAAATGTGAGTGAGAATAGCGTTTTGTTTTTCAAGTAAAAC NM_001048252 RefSeq
chr5 + 127649020 127658630 CTXN3 613212 "cortexin 3, transcript variant 1" GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_134714_PI430048170 0.6557039832001650.8165123986945110.756568882533523
0.82561577692227 0.752842770205187A A A 0.6244227057050071.70931820990634
0.577076535799187A A A LNCV6_134714_PI430048170 mRNA
AGAAAATCAAAGAGGCCAACTGCCCAGAGCCACAGAAAATGGAGGATAATTGAGGCTAAG NM_001917 RefSeq
chr12 + 108880080 108900934 DAO 1610 D-amino-acid oxidase
GO:0070178|GO:0005515|GO:0048037|GO:0005782|GO:0005102|GO:0036088|GO:0005741|GO:0044281|GO:0005
829|GO:0042416|GO:0071949|GO:0034641|GO:0046983|GO:0006562|GO:0046487|GO:0003884|GO:0055130|GO:0
005778|GO:0006551|GO:0055114|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142253_PI430048170 0.00703107399693155 0.5257509842430046.36151987777425
6.00426819012429 6.43276319408734 P P P 7.14443782841369 7.10104578038789
7.35788067879003 P P P LNCV6_142253_PI430048170 mRNA
GTGCTGTTTTGGATAACACGTTTGTTACAAGCATTTAAACTGTTTCATTTGGTAGTACCT NM_004330 RefSeq chr15
- 59662862 59689443 BNIP2 663 BCL2/adenovirus E1B 19kDa interacting protein 2
GO:0005515|GO:0043066|GO:0048471|GO:0005509|GO:0006915|GO:0005635|GO:0005829|GO:0042802|GO:0043
231|GO:0042692|GO:0043547|GO:0005737|GO:0051149|GO:0005096 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_95049_PI430048170 0.1912030386694141.23605146884777 6.61765900378805 7.04197156485593
6.94453388098512 P P P 6.54550077615176 6.30702243682699 6.82173361782753 P P P
LNCV6_95049_PI430048170 mRNA
TACCATGAAACTCTGGGAGAAGCACTTCAAGGGGTTGAATTGGAATTTAGTGGTCTGGAT NM_020123 RefSeq chr10
- 96518109 96587052 TM9SF3 56889 transmembrane 9 superfamily member 3 GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139688_PI430048170 0.1074584684193490.4723898216682294.50854348462757
3.95591643522369 5.3481236298306 P P P 5.10465955251021 5.73002797128864 6.3179116968981
P P P LNCV6_139688_PI430048170 mRNA
AAGACATTACCAAGGTTTGTACAAATTCTACTACCTGACATTTATTCCAAGAAGATCTGG NM_078487 RefSeq chr9
- 22002902 22009313 CDKN2B 1030 "cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4),
transcript variant 2"
GO:0005515|GO:0031670|GO:0010467|GO:0014070|GO:0007093|GO:0006367|GO:0008285|GO:0071901|GO:0050

680|GO:0005634|GO:0000079|GO:0048536|GO:0005829|GO:0005737|GO:0030858|GO:0045944|GO:0000086|GO:0
031668|GO:0007050|GO:0007179|GO:0034097|GO:0030511|GO:0019901|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137814_PI430048170 0.16826696881236 0.5533994462862740.338957692619786
0.3629897357338111.6146853475343 A A A 1.02602663833255 2.11105101572813
1.92104837344746 A A A LNCV6_137814_PI430048170 mRNA
GTTTCAGTGTCCTGATTCCTTGATTACTGTGAACACTGAACATCTTTTATACCTTTATGA NM_001134224 RefSeq chr2
+ 98444857 98591033 INPP4A 3631 "inositol polyphosphate-4-phosphatase, type I, 107kDa, transcript
variant d"
GO:0007165|GO:0043647|GO:0006661|GO:0036092|GO:0016311|GO:0034597|GO:0044281|GO:0016316|GO:0006
644|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127464_PI430048170 0.0196795549395622.02397568560229 3.76180189832124
4.12100227292952 3.90965407449093 P P P 2.49290376507965 3.06663062345133
3.12384362577732 A P P LNCV6_127464_PI430048170 mRNA
TCAGCCACTGGTACTACGAGAATGTTTGTATTACCCACATTTGAAATGATTTGCTATGAT NM_006308RefSeq chr5
+ 54455600 54456384 HSPB3 8988 heat shock 27kDa protein 3 GO:0006986|GO:0005737|GO:0005634
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133282_PI430048170 0.0178892236785002 1.25854198838628 10.367786025433
10.4336751504173 10.3744684326392 P P P 10.1241523802857 9.94564361971254
10.1052112556979 P P P LNCV6_133282_PI430048170 mRNA
CCTCAGGGACAGGATTGGAGGCATTGAGCGTGTTTATTAACAAATTGTTTTTGGTAATAA NM_015517RefSeq chr11
+ 119121522 119135055 HINFP 25988 "histone H4 transcription factor, transcript variant 1"
GO:0005515|GO:0010468|GO:0003700|GO:0015030|GO:0044212|GO:0005634|GO:0046872|GO:0045184|GO:0042
393|GO:0000082|GO:0000083|GO:0045445|GO:0006355|GO:0003713|GO:0005730|GO:0003677|GO:0001701|GO:0
006351|GO:0010628|GO:0006281|GO:0003682|GO:0010629|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127956_PI430048170 0.1770357915801080.4018443839641041.66055841360456
0.5138501533808870.249907536266241A A A 1.48666169203586 1.37934315275173
3.16603048421476 A A P LNCV6_127956_PI430048170 mRNA
TTGCGAAAGAATCTTGGAAATGGGCCCCACGTTTCGAATTCATCTCCAGGTTAAGAAGCT NM_024335RefSeq chr16
+ 55324558 55330760 IRX6 79190 iroquois homeobox 6 GO:0043565|GO:0006355|GO:0005634 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128006_PI430048170 0.00919167817215138 0.3576966078031638.80912376858652
8.67941036755993 9.03660580672407 P P P 9.96299772283458 10.2503272399331
10.6901999811577 P P P LNCV6_128006_PI430048170 mRNA
CCTTTCAACTGGATTTATGTTTGTTTCTGCTGCTGTGAAACCCCAAAGTAATGCAGTAGG NM_033505RefSeq chr2
+ 26346085 26395891 EPT1 85465 ethanolaminephosphotransferase 1
GO:0006646|GO:0004307|GO:0005789|GO:0044281|GO:0016021|GO:0006644|GO:0046872|GO:0046474 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133336_PI430048170 0.3733377852026021.06285209730561 0.605430802668776
0.3640821128054850.558504552971906A A A 0.4777994032374510.395925050353046
0.400167371681369A A A LNCV6_133336_PI430048170 mRNA
GTTCCATATTTATCTTTGAACATGTAGCATCTCTTTCCGCAAATAAATGCAGACTTTGGT NM_001286054 RefSeq
chr4 + 53284 88211 ZNF595 152687 "zinc finger protein 595, transcript variant 4"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133856_PI430048170 0.1711287894530940.6915757163067848.90019062518369
8.71704729143336 8.9871748417613 P P P 8.89826464369061 9.46843859496794
9.72720440186005 P P P LNCV6_133856_PI430048170 mRNA

CACTGAAAGGCCAAACAGCAAGTCCGAGTGAGTTTTAAATATTAATTAATCACCCTTTAT NM_005723 RefSeq chr4 - 98470366 98658661 TSPAN5 10098 tetraspanin 5
GO:0045747|GO:0051604|GO:0005886|GO:0016021|GO:0019899|GO:0090002 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128422_PI430048170 0.0294728649075828 0.4548264130030691.27665239087977 0.5013538760712170.472416024844293 A A A 1.52479094315319 1.90586412169544 2.28235963657975 A A A LNCV6_128422_PI430048170 mRNA
CTTTCTTAATGAACCTTAGAAAGACTACATGTTACTAAGCAGGCCACTTTTATGGTTGTT NM_006540 RefSeq chr8 - 70112031 70403785 NCOA2 10499 nuclear receptor coactivator 2
GO:0005515|GO:0035257|GO:0005634|GO:0044281|GO:2000273|GO:0010906|GO:0032870|GO:0030375|GO:0005737|GO:0030374|GO:0045944|GO:0046983|GO:0004871|GO:0004402|GO:0044255|GO:0016922|GO:0006355|GO:0016573|GO:0003713|GO:0000122|GO:0006351|GO:0032922|GO:0003682|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145146_PI430048170 0.2334239858874671.0289165036263 0.328301116631307 0.25937058194292 0.336411805814347 A A A 0.2756686278082910.255314062015356 0.270880030201992 A A A LNCV6_145146_PI430048170 mRNA
AGTATGACATAGCTTCCTAGACAAGCAGTGTTCACTCAATGCCAAGTAAACTTTTCTAAG NM_001287497 RefSeq chr7 - 112762381 112790423 TMEM168 64418 "transmembrane protein 168, transcript variant 1"
GO:0030133|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144801_PI430048170 0.0180762411265438 0.70877989825241 5.3095272849656 5.04159425171364 5.26141315583184 P P P 5.58418173135831 5.62339399981517 5.88916925787182 P P P LNCV6_144801_PI430048170 mRNA
GCTCTTGGGTACAAAAATAAAGGGACACCAAAATATATTAGTAGCTGATCAAACTAGTTG NM_182627 RefSeq chr3 - 196554187 196568542 WDR53 348793 WD repeat domain 53 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130454_PI430048170 0.2291265261869181.55326520051633 0.30434160767408 0.747002199862287 1.42984659844855 A A A 0.2780465785952040.245702854078604 0.277163535859537 A A A LNCV6_130454_PI430048170 mRNA
AGTCCACATTTTAGGGCTTCCTTAAACAGGCTTCTGAGAGTCGTATCTTTTTTCTTTTTT NM_002333 RefSeq chr19 + 33194692 33208867 LRP3 4037 low density lipoprotein receptor-related protein 3
GO:0005905|GO:0016021|GO:0006898 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131726_PI430048170 0.0753030760447306 0.8395797105623336.99283530036966 6.83693594635513 7.12124304967393 P P P 7.20179344394821 7.21861505846367 7.29948095962869 P P P LNCV6_131726_PI430048170 mRNA
ATCTCCTTCATTTGTAACTAATTTCAGCCTGATGAAAACCTGGAATTCCTTTTTCACAGA NM_001258213 RefSeq chr13 - 113177538 113208648 PCID2 55795 "PCI domain containing 2, transcript variant 5"
GO:0043488|GO:0043066|GO:0045579|GO:2000117|GO:0090267|GO:0005575|GO:0048536|GO:0045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139612_PI430048170 0.2767548127011031.0398909633102 0.323489342294161 0.2815072627105620.40970754749582 A A A 0.2891019959818520.264718510341606 0.29438846793144 A A A LNCV6_139612_PI430048170 mRNA
CCTTCCATATTTAGATTGGGTAAGCATGAATGTGTATTTTCTACAAAAGACCTTGAGAAG NM_003058 RefSeq chr6 - 160216761 160258931 SLC22A2 6582 "solute carrier family 22 (organic cation transporter), member 2"
GO:0007589|GO:0015220|GO:0005886|GO:0015695|GO:0015697|GO:0015871|GO:0007268|GO:0044281|GO:0051608|GO:0055085|GO:0015101|GO:0015651|GO:0007269|GO:0016323|GO:0034220|GO:0016020|GO:0005887|GO:0006855|GO:0042136|GO:0005496|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131755_PI430048170 0.4450644196436291.03647817232208 9.2799416007696 9.28676408266213 9.39913313140998 P P P 9.17953335998714 9.28772065097731 9.34193839468196 P P P LNCV6_131755_PI430048170 mRNA

CCCCAAAATCACATTCCAGTTTTTATTGTCTTTGTGTCCAAAGTAAACTAGGTGACTTAT NM_001080533 RefSeq chr12 + 120710434 120723640 UNC119B 84747 unc-119 homolog B (C. elegans) GO:0005515|GO:0042953|GO:0006996|GO:0060271|GO:0035869|GO:0072372|GO:0008289|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134668_PI430048170 0.400225421798795 1.10488913994935 7.05159342705391 6.94658207259296 6.75290004592318 P P P 7.0082126778833 6.73247197943136 6.55844339312384 P P P LNCV6_134668_PI430048170 mRNA
GGGGCTGGTTCCCCCATCTTGAATTGTTTATCCCTTTTTCATAATTAAAGTTTTAAAACANM_152312RefSeq chr11 + 45921620 45929096 GYLTL1B 120071 "glycosyltransferase-like 1B, transcript variant 1" GO:0030145|GO:0000139|GO:0015020|GO:0016021|GO:0042285|GO:0046716|GO:0035269 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_75958_PI430048170 0.0835240708642788 0.466159832745447 2.42976395279863 2.40580366278657 2.47648192524979 A A A 2.84981909475861 3.64831238344879 3.91813908496066 P P P LNCV6_75958_PI430048170 mRNA
TCTGACGACCAAGAAAAAATGGAAAGACTGTAAGATCAGAGTATTCATTGGTGGAAAGATNM_001046RefSeq chr5 + 128083790 128189688 SLC12A2 6558 "solute carrier family 12 (sodium/potassium/chloride transporter), member 2, transcript variant 1" GO:0005515|GO:0030321|GO:0005886|GO:0045795|GO:0016323|GO:0016324|GO:0035264|GO:0072488|GO:0006810|GO:0070634|GO:0006814|GO:0006813|GO:0008511|GO:0006811|GO:0070062|GO:0015696|GO:0008519|GO:0007214|GO:0060763|GO:0006972|GO:0031982|GO:0055085|GO:0016020|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57102_PI430048170 0.2100719092697821 1.27616303936084 5.57423934086118 5.74074532358492 5.18328131745484 P P P 4.91470817993909 5.47792709033031 5.04338891029113 P P P LNCV6_57102_PI430048170 mRNA
ATGTATTCTGCACGAGAAGGTACACTGGTCCCAAGGTGTAAAGCTTTAAGAGTCATTTAT NM_000076RefSeq chr11_KI270831v1_alt - 115396 117975 CDKN1C 1028 "cyclin-dependent kinase inhibitor 1C (p57, Kip2), transcript variant 1" GO:0005515|GO:0055123|GO:0060065|GO:0030325|GO:0071901|GO:0050680|GO:0005634|GO:0060669|GO:0005737|GO:0035264|GO:0071514|GO:0030099|GO:0007050|GO:0043010|GO:0030511|GO:0033673|GO:0001822|GO:0042551|GO:0007568|GO:0000122|GO:0042326|GO:0007346|GO:0001501|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82264_PI430048170 0.2884247191297643 .31267640942411 0.3308730816490893 .5742463557984 2.55195579314079 A P A 0.2915375705105591 .71771553407877 0.301572878168626 A A A LNCV6_82264_PI430048170 mRNA
TCTCTGACTTTGGACTCTCCAAAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTGGGA NM_001039582 RefSeq chrX - 153669732 153674361 PNCK 139728 "pregnancy up-regulated nonubiquitous CaM kinase, transcript variant 1" GO:0005516|GO:0005737|GO:0006468|GO:0005634|GO:0004683|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_78832_PI430048170 0.1682183488834210 .7749270506618787 .39259062159553 7.37990451543412 7.96122162347452 P P P 7.88689039805432 7.89034991391105 8.12621609340663 P P P LNCV6_78832_PI430048170 mRNA
AACGATGACACAGTTTATCTCTTTGTTGTAAACCACCCAGAATTCAAGAATACAGTGGAA NM_000305RefSeq chr7 - 95404861 95435072 PON2 5445 "paraoxonase 2, transcript variant 1" GO:0005739|GO:0019439|GO:0005886|GO:0005634|GO:0005576|GO:0004064|GO:0006979|GO:0005764|GO:0046872|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145409_PI430048170 0.0084044856859398 1.33814862420825 12.2571339637835 12.3755380780297 12.4785694278587 P P P 12.0252673961946 11.9457958710045 11.8844948345935 P P P LNCV6_145409_PI430048170 mRNA
TTGCTTCTGGGGCTATTGGAGGGTCAGTGTCTGTGACTGAATAAAGTTCCATTTTGTGGT NM_177441RefSeq chr17

+ 44187205 44191731 TMUB2 79089 "transmembrane and ubiquitin-like domain containing 2, transcript variant 2" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133753_PI430048170 0.0241068038699396 0.6188841952020855.96638266739683
5.63534974930241 6.13971986161636 P P P 6.48162191208479 6.61736370261714
6.75126618243124 P P P LNCV6_133753_PI430048170 mRNA
GGAGATAGGTAAGTTTCAAATCTATGCCAGTCTTATGAATATTACATTAGGGTAATGTGC NM_178833RefSeq chr4
- 103025490 103076773 SLC9B2 133308 "solute carrier family 9, subfamily B (NHA2, cation proton antiporter 2), member 2, transcript variant 1"
GO:0034220|GO:0015299|GO:0005743|GO:0016021|GO:0006814|GO:0055085 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_106355_PI430048170 0.0188169691104612 0.6497369865311183.26999930881872
3.08396992510025 3.5102324145611 P P P 3.9331415592788 3.78676170478212
4.03183347301013 P P P LNCV6_106355_PI430048170 mRNA
TTCCTAAAAAGGCATTTTTGCGAGCCCTTGTGGACTATACCAGTGACAGTGCTGAAAAGC NM_002454RefSeq chr5
+ 7869103 7901122 MTRR 4552 "5-methyltetrahydrofolate-homocysteine methyltransferase reductase, transcript variant 1"
GO:0050661|GO:0006805|GO:0010181|GO:0050660|GO:0009086|GO:0006767|GO:0044281|GO:0032259|GO:0005
829|GO:0034641|GO:0005737|GO:0006555|GO:0046655|GO:0045111|GO:0009235|GO:0005506|GO:0006306|GO:0
030586|GO:0000096|GO:0003958|GO:0006766|GO:0016709|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138430_PI430048170 0.3224038277054741.07556043427563 0.621491310223204
0.3667063221949520.570990527375357A A A 0.3680149156741210.453997037057366
0.432939102536349A A A LNCV6_138430_PI430048170 mRNA
CGAATGAGAAAGAACTCCAGCAAATCCAATGGCTACAAACTAAAAATCAGCATTATTTCA NM_001291960 RefSeq
chr3 + 40387244 40428626 ENTPD3956 "ectonucleoside triphosphate diphosphohydrolase 3, transcript variant 1" GO:0017111|GO:0017110|GO:0005886|GO:0009143|GO:0009134|GO:0016021|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104069_PI430048170 0.5570758029738631.22051619994261 1.34735894471529
0.4006045980413970.41445399148575 A A A 0.3744474920865 0.71839816116269
0.396811258733282A A A LNCV6_104069_PI430048170 mRNA
AAAGAAAGTGGAGGAGCTTGAGGGAGAGATCACTACATTAAACCATAAGCTTCAGGACGC NM_004335RefSeq
chr19 - 17402938 17405648 BST2 684 bone marrow stromal cell antigen 2
GO:0005515|GO:0030308|GO:0005886|GO:0008283|GO:0035456|GO:0019221|GO:0035455|GO:0007267|GO:0031
225|GO:0042803|GO:0051607|GO:0005737|GO:0016324|GO:0060337|GO:0006959|GO:0002737|GO:0032956|GO:0
004871|GO:0034341|GO:0043123|GO:0070062|GO:0045071|GO:0030336|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145616_PI430048170 0.1035290058915830.6737112639623415.48154075915108
5.73853939199969 6.15056617518705 P P P 5.98193201455246 6.5480346897726
6.55822448829679 P P P LNCV6_145616_PI430048170 mRNA
CTGGGTACTGTTACTGTGATGCTATTGACTTAGTAGCCAATTATCATTTCTCCTGTATAA NM_018369RefSeq chr5
- 60596911 60700166 DEPDC1B 55789 "DEP domain containing 1B, transcript variant 1"
GO:0043547|GO:0051056|GO:0016477|GO:0007264|GO:0030177|GO:0005829|GO:0005096 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133526_PI430048170 0.7051742326732270.9331437121757315.67382290035316
5.19555390786087 5.69595494368055 P P P 5.30548650240917 5.64528379938104
5.90530472342176 P P P LNCV6_133526_PI430048170 mRNA
GGATTGTATCATAATAGCTGCCAAAGGATAGGTAAAGAGGTCATTAAAATGATGTTGAAC NM_012210RefSeq chr9
+ 116687301 116701300 TRIM32 22954 "tripartite motif containing 32, transcript variant 1"
GO:0005515|GO:0005863|GO:0043130|GO:0045732|GO:0004842|GO:0032479|GO:0016567|GO:0030307|GO:0016

874|GO:0003723|GO:0048147|GO:0005634|GO:0043621|GO:2000147|GO:0005829|GO:0051091|GO:0005737|GO:0
051092|GO:0042787|GO:0050769|GO:0045444|GO:0032481|GO:0043123|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93713_PI430048170 0.771413642925956 1.01142526853654 0.304666751017336 0.311312642349173
0.440414696225472 A A A 0.350613600933225 0.304769340923277 0.355401852553706 A A A
LNCV6_93713_PI430048170 mRNA
AGAAGAAAATTCCCAGAATGCTACTAATGAACTCACTAAACAGTCATCAAATGTGAAGAC NM_017738 RefSeq chr9
+ 17134990 17503923 CNTLN 54875 "centlein, centrosomal protein, transcript variant 1"
GO:0023014|GO:0010457|GO:0005737|GO:0000160|GO:0033365|GO:0019901|GO:0016020|GO:0005814|GO:0019
904|GO:0030674|GO:0000155|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144922_PI430048170 0.0206022088541876 0.520976524134321 2.21605472499899
1.9793989602898 2.63506785485715 A A A 2.93579284932021 3.23796120007207
3.50141164982582 P P P LNCV6_144922_PI430048170 mRNA
GTTGCTTAACTCCTTTACACCATTAGTTATCTGTGAGACCATCTATTCCACACTCTTCAT NM_144711 RefSeq chr2 +
169733845 169751886 KLHL23 151230 kelch-like family member 23 GO:0005515 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_142703_PI430048170 0.147455817839896 0.924515246173366 8.29871123357176
8.20293524423875 8.27389255252136 P P P 8.28369795391639 8.36732759716526 8.4604851799572
P P P LNCV6_142703_PI430048170 mRNA
AACCAGCTATGTGAAAGTCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCACATTTC NM_005362 RefSeq chrX
+ 152698751 152702347 MAGEA3 NA melanoma antigen family A3 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_127627_PI430048170 0.61941981779671 0.904970953274545 4.52108843749828
4.08462090497449 3.60154162245479 P P P 3.93145850480654 4.5230083986 4.26935948687032 P
P P LNCV6_127627_PI430048170 mRNA
GCACCTGACGCTGAACCAGAGCTCAGGAATGTCAAGTAACTTAATAAATGAGTGAATGTG NM_033212 RefSeq chr16
- 57512177 57536565 CCDC102A 92922 coiled-coil domain containing 102A NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_129688_PI430048170 0.399027285544184 0.942373615331294 0.387646162095101
0.359269023473829 0.250871624553099 A A A 0.326859732599895 0.356619098063676
0.563122327035929 A A A LNCV6_129688_PI430048170 mRNA
TCAGTGAGACCTGGATTCAAATTCTGCCTTGAAATATTGTGACTCTGGGAATGACAACAC NM_144947 RefSeq chr19
- 51022230 51027629 KLK11 11012 "kallikrein-related peptidase 11, transcript variant 2"
GO:0005794|GO:0004252|GO:0006508|GO:0008236|GO:0005615|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135836_PI430048170 0.0360472021092929 0.341021646865948 2.76969635893225
1.53482451128864 2.71577002985456 A A A 3.45252119839337 4.22193281111934
4.18190890376954 P P P LNCV6_135836_PI430048170 mRNA
GCTCAATCCTTAAGAATACATGGTTCATACAACATGCTTTTACTATGTCTTAAGTGTGAC NM_003619 RefSeq chr4
- 118280037 118352767 PRSS12 8492 "protease, serine, 12 (neurotrypsin, motopsin)"
GO:0030424|GO:0004252|GO:0005886|GO:0005576|GO:0043083|GO:0031410|GO:0006887|GO:0006898|GO:0030
425|GO:0043195|GO:0006508|GO:0008236|GO:0031638|GO:0005044 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138113_PI430048170 0.705399653953062 1.04802563550571 8.8406405175241
8.80058453199724 9.03383423031663 P P P 8.40910654160077 8.88319562002817 9.1057336813927
P P P LNCV6_138113_PI430048170 mRNA
GAATCCCTAGTCCCCCTGTTTTCTGTTTCTTCTTGTGATTGCTGCCATAATTCTAAGTTA NM_031966 RefSeq chr5 +
69167009 69178243 CCNB1 891 cyclin B1
GO:0007077|GO:0005515|GO:0060045|GO:0046680|GO:0090266|GO:0007283|GO:0001556|GO:0005113|GO:0071

398|GO:0005813|GO:0071283|GO:0019901|GO:0001701|GO:0000922|GO:0035173|GO:0045931|GO:0055015|GO:0
005654|GO:0007080|GO:0000278|GO:0031442|GO:0051301|GO:0043148|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129514_PI430048170 0.9399375140648470.9710007631514960.337063032395451
0.3458914397299931.2239131475857 A A A 0.4376444691260570.283307167871189
1.28923336455138 A A A LNCV6_129514_PI430048170 mRNA
TATGCCGCTAGATACATGCTTTTTAATGAGATAATGTGATATTATACATAACACATATCG NM_000242RefSeq chr10
- 52765379 52771700 MBL2 4153 "mannose-binding lectin (protein C) 2, soluble"
GO:0005515|GO:0051873|GO:0005581|GO:0009986|GO:0050830|GO:0005509|GO:0005102|GO:0048525|GO:0005
576|GO:0006953|GO:0005537|GO:0005615|GO:0001867|GO:0006956|GO:0050766|GO:0045087|GO:0006958|GO:0
044130|GO:0006979|GO:0042742|GO:0008228|GO:0048306 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_139483_PI430048170 0.0758834532619549 1.32458855046962 10.2103081893944
10.3294669207447 10.5167080913311 P P P 9.9714760158491 9.6863235352301
10.1598241079203 P P P LNCV6_139483_PI430048170 mRNA
ACCAGCAACTACTTCTTTATATTGTTCTTCATATCCCAAATTAGAGTTTACAGGGACAGT NM_014462RefSeq chr8
- 38163320 38176730 LSM1 27257 "LSM1, U6 small nuclear RNA associated, transcript variant 1"
GO:0000339|GO:0005515|GO:0006397|GO:0008380|GO:0010467|GO:0000290|GO:0043928|GO:0005634|GO:0005
829|GO:0005737|GO:0000932|GO:0000375|GO:0071044|GO:0000288 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134227_PI430048170 0.04068868832804 1.1835128918842 11.5347425310069
11.6872235902248 11.6799765269677 P P P 11.2742065184354 11.4055075874299
11.4899275505989 P P P LNCV6_134227_PI430048170 mRNA
TCTGAGAGTTGATGAGGATGTGTAACAAGTATTTTCTTCTATCGTGCCTGCCAGGGCTGA NM_001029991 RefSeq
chr14 + 20989805 20997035 METTL17 64745 "methyltransferase like 17, transcript variant 1"
GO:0005739|GO:0005515|GO:0005507|GO:0008168|GO:0005840|GO:0005654|GO:0005634|GO:0032259|GO:0006
412 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_79038_PI430048170 0.3727112155141990.895801315202853 9.99117662557873 9.85876128520367
10.3124103914907 P P P 10.1569813515597 10.1037607162784 10.3988149343787 P P P
LNCV6_79038_PI430048170 mRNA
TTTTATGAAGACATGGAGTCCTTGACGCAGATGCTTAGGGCCTTGGCAACAGATGGAAAT NM_001007245 RefSeq
chr7 + 112423143 112477203 IFRD1 3475 "interferon-related developmental regulator 1, transcript
variant 2" GO:0007518|GO:0007527|GO:0007275|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142025_PI430048170 0.6970993788586951.06069966142101 4.77836927582389
4.43389930184181 4.91085591881356 P P P 4.32848321340183 4.7116056742116 4.8236351594119
P P P LNCV6_142025_PI430048170 mRNA
CAGCAATTATATTGGTGTATGAAATTCTTACAGTGAATATTGTGCTGTTAGTGCTGCTTG NM_001128928 RefSeq
chr2 + 190343469 190371665 INPP1 3628 "inositol polyphosphate-1-phosphatase, transcript variant
1"
GO:0046854|GO:0007165|GO:0043647|GO:0016311|GO:0044281|GO:0006796|GO:0052829|GO:0046872|GO:0005
829|GO:0004441 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135985_PI430048170 0.0039593386021477 0.2383347228958850.261224993663904
0.3981162874039150.292442391370343 A A A 2.48009253127613 2.05431256064737
2.57618284903401 A A P LNCV6_135985_PI430048170 mRNA
CACTGAGTAAGCCCTAATTACATTAATTACATTTTACTCTTGACTCCAGGAAAAGAAAGC NM_145331RefSeq chr6
- 90513572 90587301 MAP3K7 6885 "mitogen-activated protein kinase kinase kinase 7, transcript
variant B"
GO:0005515|GO:0007249|GO:0051403|GO:0002756|GO:0002755|GO:0007179|GO:0043123|GO:0004709|GO:0004

708|GO:0000287|GO:0038124|GO:0038123|GO:0034134|GO:0002726|GO:0002224|GO:0001841|GO:0043966|GO:0
045087|GO:0050870|GO:0005654|GO:0034166|GO:0035666|GO:2000377|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144294_PI430048170 0.981343966309618 0.994258721064178 0.317641024507995
1.72686993536776 1.07430493394696 A A A 1.80988977612838 0.275709921816206
0.988275554668802 A A A LNCV6_144294_PI430048170 mRNA
GGCCATTGCAGCTATTTGGTAGTGTCTTGTTATTTCTAGGTGTACCTTAGTTAAAGAGGA NM_182569 RefSeq chr17
+ 59220466 59275969 GDPD1 284161 "glycerophosphodiester phosphodiesterase domain containing 1,
transcript variant 1" GO:0006629|GO:0005737|GO:0016020|GO:0016021|GO:0008889|GO:0006071|GO:0046872
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142555_PI430048170 0.137581085289828 1.05870202320672 0.501527126703443
0.619820992609557 0.53091123687406 A A A 0.425426003155196 0.477737589690215
0.503751547913446 A A A LNCV6_142555_PI430048170 mRNA
AACTTCATATGGTACTCCCATTCAGCCGCAGACTGTTGATCCCACACAAGAGTGTTTCAT NM_018654 RefSeq chr12
- 12940774 12950384 GPRC5D 55507 "G protein-coupled receptor, class C, group 5, member D"
GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131404_PI430048170 0.244386488704836 1.0195986698768 0.30512616849509
0.258077616657219 0.313624579671895 A A A 0.270787298702136 0.254441985685294
0.26815978227174 A A A LNCV6_131404_PI430048170 mRNA
GGATTTGTCTGCCTTTTCAACACTATACTGAGCAATAACAATAAATGCACACGTGGAAAT NM_001001331 RefSeq
chr3 - 10324022 10505584 ATP2B2 491 "ATPase, Ca++ transporting, plasma membrane 2, transcript
variant 1"
GO:0005515|GO:0005516|GO:0008361|GO:0030054|GO:0006200|GO:0005886|GO:0051928|GO:0005783|GO:0007
605|GO:0060088|GO:0045202|GO:0046068|GO:0030899|GO:0046872|GO:0040011|GO:0021707|GO:0005737|GO:0
016324|GO:0034220|GO:0048167|GO:0021702|GO:0030182|GO:0090102|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142106_PI430048170 0.00684786865903093 0.17141676373914 0.339864004676697
0.256942707322293 0.33991934557236 A A A 2.7484223026126 2.4861315146163
3.23503760749179 P P P LNCV6_142106_PI430048170 mRNA
TGGTTACTGAGCTCTAAATAGACAGGTTTGATGGCACTTCTCATGATACATTTTAGTTAT NM_022828 RefSeq chr5
+ 113513693 113595287 YTHDC2 64848 YTH domain containing 2
GO:0005515|GO:0004004|GO:0006396|GO:0005783|GO:0034612|GO:0005634|GO:0070063|GO:0005524|GO:0070
555|GO:0008186 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137830_PI430048170 0.417006949494501 1.04200244013352 0.288268581682648
0.287785682291776 0.456887785765741 A A A 0.303447981715066 0.269265914403343
0.288619867648132 A A A LNCV6_137830_PI430048170 mRNA
CTAGTGTGCAGATATTTCCCTAACATGTCCTTTTTTGTATTTGTTTGTACGGACCATAAA NM_001161415 RefSeq chr2
+ 127645863 127652639 GPR17 2840 "G protein-coupled receptor 17, transcript variant 1"
GO:0070098|GO:0007186|GO:0005886|GO:0005887|GO:0004950 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131998_PI430048170 0.00649003267632074 0.708517168852152 6.38528747959378
6.62826318216671 6.5523246025407 P P P 7.03842392648096 7.11273123097059
6.90940434428766 P P P LNCV6_131998_PI430048170 mRNA
AGGTTCTATCCTGTTCCGAGCAACTTTTCTAATTATAAACATCACAGAACATCCTGGATC NM_001785 RefSeq chr1
+ 20588950 20618907 CDA 978 cytidine deaminase
GO:0030308|GO:0009972|GO:0045980|GO:0019858|GO:0055086|GO:0005576|GO:0044281|GO:0043097|GO:0008
655|GO:0042803|GO:0005829|GO:0051289|GO:0001882|GO:0004126|GO:0008270|GO:0006206|GO:0007166 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145507_PI430048170 0.095206649253457 0.417117240037746 3.79137876645071

2.27736827248778 3.79543466444167 P A P 4.23014830655497 4.75139596603925
5.01801274149215 P P P LNCV6_145507_PI430048170 mRNA
ACTTTATGCACTATATAAGTTAATAAAATTAGCATGGCCTTCCATGATTTGGCCTGTGTC NM_006965 RefSeq chr18
- 35332207 35344467 ZNF24 7572 zinc finger protein 24
GO:0043565|GO:0005515|GO:0003700|GO:0042552|GO:0008270|GO:0005654|GO:0005634|GO:0045892|GO:0003
677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138493_PI430048170 0.0259677719728076 1.5279344892307 9.1626079685258
9.5910328879298 9.37502255635142 P P P 8.51409180909242 8.92438853832915
8.85471314756977 P P P LNCV6_138493_PI430048170 mRNA
GGAGATGCTTGAAGAACTCAACAAAATCCCAATCCAAGTCAAACTTTGCACATATTTATA NM_003955 RefSeq chr17
- 78356776 78360079 SOCS3 9021 suppressor of cytokine signaling 3
GO:0005515|GO:0043066|GO:0060674|GO:0016567|GO:0060708|GO:0046627|GO:0060707|GO:0060670|GO:0019
221|GO:0045597|GO:0060397|GO:0007259|GO:0046426|GO:0005829|GO:0060334|GO:0005737|GO:0060337|GO:0
060338|GO:0050728|GO:0004860|GO:0006469|GO:0040008|GO:0060333 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_141639_PI430048170 0.262747023928601 11.1946705526006 2.11721295572464
5.36917290105307 0.52743038032252 A P A 0.316431684309001 0.735489683799067
0.376487101066723 A A A LNCV6_141639_PI430048170 mRNA
GGTACAAGCTCCAGAACAGTAACCAAGTGGGAAAATAAAGACTTCTTGGATGACTGACTC NM_002832 RefSeq chr1
- 202147012 202161588 PTPN7 5778 "protein tyrosine phosphatase, non-receptor type 7, transcript
variant 1"
GO:0005515|GO:0005737|GO:0006470|GO:0009898|GO:0005856|GO:0035335|GO:0004725|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129068_PI430048170 0.55268586899739 1.02567362946796 0.282832358389531
0.311008899056932 0.441986688408094 A A A 0.332273470245747 0.301162286379446
0.297471083458288 A A A LNCV6_129068_PI430048170 mRNA
GCACTGTAATACGTGCTTAACTTTGCTTAAACTCTCTAATTCCCAATTTCTGAGTTACAT NM_000531 RefSeq chrX +
38352482 38421450 OTC 5009 ornithine carbamoyltransferase
GO:0019240|GO:0042450|GO:0032868|GO:0004585|GO:0042493|GO:0005743|GO:0097272|GO:0044281|GO:0010
043|GO:0070781|GO:0001889|GO:0005739|GO:0070207|GO:0034641|GO:0005543|GO:0005759|GO:0007494|GO:0
042301|GO:0000050|GO:0006593|GO:0016597 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_57180_PI430048170 0.112595239122078 1.04611850162928 0.416205338954856 0.435448490379777
0.446539093919219 A A A 0.32808662698503 0.358419612720956 0.415346743882263 A A A
LNCV6_57180_PI430048170 mRNA
AAAGTAGATCCTGCTCACAGAATCACAGCTAAGGAACTACTAGATAACCAGTGGTTAACA NM_030906 RefSeq chr11
- 8391865 8594008 STK33 65975 "serine/threonine kinase 33, transcript variant 1"
GO:0048471|GO:0046777|GO:0004674|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_88612_PI430048170 0.160568459409728 0.951946523893574 0.249296543160722 0.263500761771814
0.336183700382859 A A A 0.414270503017294 0.335669307127884 0.311691219322979 A A A
LNCV6_88612_PI430048170 mRNA
TTCTCCTCACATTTGGTTTCATCCTAGATCAAAACTACATTTGTGGTTATTCTCACCAAA NM_023945 RefSeq chr11 +
60429588 60447792 MS4A5 64232 "membrane-spanning 4-domains, subfamily A, member 5"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135382_PI430048170 0.618941851114118 1.01594447792909 0.44422655889946
0.428964383926172 0.33044603944525 A A A 0.34239956397816 0.394636510670375
0.400059502135833 A A A LNCV6_135382_PI430048170 mRNA
CCTTAGCACTTGTTATTGTACTTCCTGTGCAAGTTTTGTGGATTATTAAATGTCTTTCAC NM_001282402 RefSeq chr1
+ 226223617 226227055 MIXL1 83881 "Mix paired-like homeobox, transcript variant 1"
GO:0000987|GO:0001103|GO:0000790|GO:0001190|GO:0007369|GO:2000382|GO:0001205|GO:0048565|GO:0035

987|GO:0000978|GO:0042803|GO:0006351|GO:0007507|GO:0042074|GO:0001077|GO:0007492|GO:0002244|GO:0
045944|GO:0001085|GO:0000980 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143985_PI430048170 0.4822212610786361.74673743320956 0.284076362474968
2.13298996128586 0.307428797215529A A A 0.454076550909971 0.350036227651349
0.347288484439961A A A LNCV6_143985_PI430048170 mRNA
CAATGATGTGAGTAAAAGGAGCACTGCAGGAACCGGACCCAGTGTGACGTTATGAAAAAA NM_001253750
RefSeq chr12 - 9715859 9733299 CLECL1 160365 "C-type lectin-like 1, transcript variant 3"
GO:0005886|GO:0030246|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_102064_PI430048170 0.0144355660215311.58936832448321 6.20792804682968
6.51496498039076 6.14541127242481 P P P 5.51163697002019 5.68634093480787
5.68574503886681 P P P LNCV6_102064_PI430048170 mRNA
TCCATCTCCTGCCTTGTGTAAGAACCTGAGTTCCTTGTAATTAAATATCAACTGAATTAC NM_022742RefSeq chr7
+ 128791995 128822133 CCDC136 64753 "coiled-coil domain containing 136, transcript variant 1"
GO:0005739|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135179_PI430048170 0.0072962062004036 0.2871706172040495.37724246457798
4.92093358828532 5.558278605273 P P P 6.63952717058925 6.99195757431906
7.54935843730328 P P P LNCV6_135179_PI430048170 mRNA
CTTGTACAGAGGATTTTTCACTATGTGCCTAGCTTGGTGTCCATTCAGCTAAAATTGAAA NM_001287439 RefSeq
chr4 + 128809918 128875224 JADE1 79960 "jade family PHD finger 1, transcript variant 4"
GO:0005515|GO:0001105|GO:0030308|GO:0005886|GO:0006325|GO:0006950|GO:0006915|GO:2000134|GO:0005
634|GO:0006351|GO:0045171|GO:0043981|GO:0043983|GO:0005737|GO:0043982|GO:0043966|GO:0043984|GO:0
045944|GO:0000123|GO:0005654|GO:0008270 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142022_PI430048170 0.0608296912546952 0.7671416252419518.27734955519341
8.43173138339706 8.16598335191227 P P P 8.47611526235083 8.87350404412422
8.65764923398721 P P P LNCV6_142022_PI430048170 mRNA
AAACACTAGGACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTT NM_152637RefSeq chr12
+ 55681545 55684610 METTL7B 196410 methyltransferase like 7B
GO:0005737|GO:0008757|GO:0032259 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135317_PI430048170 0.0322021798662522 0.6660892330079377.75172167928417
7.91334372358116 7.63235898705462 P P P 8.11076281713734 8.58813294360128
8.33136843371371 P P P LNCV6_135317_PI430048170 mRNA
GGAGCAGTTCATTACTCATACCTCGGTCCAAACCAAAAAGGTTCTTTTCAGAGCCACCTA NM_003510RefSeq chr6
- 27837879 27838339 HIST1H2AK 8330 "histone cluster 1, H2ak"
GO:0005515|GO:0008150|GO:0003674|GO:0046982|GO:0005634|GO:0019899|GO:0000786|GO:0003677|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132948_PI430048170 0.3594377774518670.7069178110601480.27054787918616
0.3025123333000110.281193497937431A A A 1.39173619731144 0.380939041428575
0.314818383534076A A A LNCV6_132948_PI430048170 mRNA
CCTTCTGTTGAATGGTTGCCAACACAAACTTGAGTTCTAATAAATAATTGCATTTCCCTA NM_001017361 RefSeq
chr6 + 73362676 73364175 KHDC3L NA "KH domain containing 3-like, subcortical maternal
complex member" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131275_PI430048170 8.03369109928503e-06 0.2217055658215382.37698544372642
2.25917429505191 2.19346283168357 A A A 4.36023514932464 4.46400895022682
4.52639453969198 P P P LNCV6_131275_PI430048170 mRNA
CCTCCTGACTCATGTACTACTACACAAACTAGAAAATGCCCATTTATTTTTGTTGATTCA NM_019050RefSeq chr4
+ 119212626 119295518 USP53 54532 ubiquitin specific peptidase 53
GO:0008150|GO:0006511|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92332_PI430048170 0.0590660110347847 0.7019414516428478.48563096641963
8.45165875873706 8.80151609453128 P P P 8.84913076732175 9.03825906596452

9.36229077543564 P P P LNCV6_92332_PI430048170 mRNA
ATTGGAAGATCCCTTCAAAGCAAACACAGCACAGAAAATGACTCACCAACAAATGTACAG NM_002027 RefSeq chr8
+ 43056298 43085788 FNTA 2339 "farnesyltransferase, CAAX box, alpha, transcript variant 1"
GO:0005515|GO:0008017|GO:0018343|GO:0010469|GO:0018344|GO:0007603|GO:0005965|GO:0006921|GO:0005
829|GO:0004660|GO:0004661|GO:0005737|GO:0004662|GO:0004663|GO:0007179|GO:0005953|GO:0016056|GO:0
030971|GO:0043014|GO:0005875|GO:0006915|GO:0022400|GO:0045213|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130576_PI430048170 0.00137472953313576 0.398632646617516 4.08066491090849
4.48077469380756 4.3883979343531 P P P 5.4879932165956 5.68127364989137 5.7761072350109
P P P LNCV6_130576_PI430048170 mRNA
GACCGTAAGCTTTTTAAGTTTCTCATTGTAATTTACCTTCTCATGCAGATTGCTGATGTT NM_002709 RefSeq chr2 +
28751759 28802940 PPP1CB 5500 "protein phosphatase 1, catalytic subunit, beta isozyme, transcript
variant 1"
GO:0005515|GO:0005634|GO:0044281|GO:0030155|GO:0046872|GO:0016791|GO:0006470|GO:0000164|GO:0000
086|GO:0007179|GO:0019433|GO:0043153|GO:0030512|GO:0070062|GO:0017018|GO:0005979|GO:0019901|GO:0
005977|GO:0005730|GO:0050115|GO:0032922|GO:0042587|GO:0070688|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143051_PI430048170 0.134909900870829 0.589470544126292 5.7869525921443
5.94018629174096 5.82044147498191 P P P 6.11732635761792 6.43061264708417
7.10866558308589 P P P LNCV6_143051_PI430048170 mRNA
CTGCTTTGGTTTTAGAGTGATTGTGAGGCATTCAATGCAAGTATACAGTTATTTTCTCAT NM_007203 RefSeq chr9
+ 109780296 110172511 PALM2-AKAP2 445815 "PALM2-AKAP2 readthrough, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110888_PI430048170 0.407456196679621 0.9751409187305 7.91666075146933
7.86185014312314 7.8546649998184 P P P 7.92737541277226 7.85190912380219
7.96147487260749 P P P LNCV6_110888_PI430048170 mRNA
GAAATACCAAGAGGAGGCCATTCCAGCCTTAAGAGATATTTCTATTAGTGAAGTAAACCA NM_153681 RefSeq chr21
- 37065363 37072803 PIGP 51227 "phosphatidylinositol glycan anchor biosynthesis, class P, transcript
variant 1"
GO:0017176|GO:0006501|GO:0016254|GO:0005789|GO:0016021|GO:0044267|GO:0000506|GO:0043687 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138392_PI430048170 0.411154709393999 1.58585507527222 1.26741514396797
2.09539201511113 0.312821186047572 A A A 0.282471100127726 0.307367318649759
1.34609342440999 A A A LNCV6_138392_PI430048170 mRNA
GGGGATGTCAAGGGAGGCTTCATGAAATGGATGAGCAGAATGCAGACTTTTTTCTTTAGA NM_012364 RefSeq chr9
+ 122614737 122615682 OR1Q1 158131 "olfactory receptor, family 1, subfamily Q, member 1"
GO:0050911|GO:0007608|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144467_PI430048170 0.0959033747712914 0.789139685522875 9.4018251301393
9.20814516784211 9.65468307346148 P P P 9.74043366813571 9.65690615806088
9.91503868193274 P P P LNCV6_144467_PI430048170 mRNA
ACTTGTCATGTCATACAGTTTGTGAAAGGACACCTTGTAAAGAAGCCTTGAAACTAATAA NM_183005 RefSeq chr10
+ 15097179 15104257 RPP38 10557 "ribonuclease P/MRP 38kDa subunit, transcript variant 1"
GO:0005515|GO:0004526|GO:0005634|GO:0005655|GO:0008033 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131634_PI430048170 0.385724481505054 1.46756432627611 1.64502948922647
0.467421047204595 0.440730595805955 A A A 0.36589966131398 0.432533838532953
0.443408974568798 A A A LNCV6_131634_PI430048170 mRNA
CAGTCAAATCATGATTTAACAGAGTAAGTATAGACAGCAAATAGGAAAGTACCTGAATGC NM_001004700 RefSeq

chr11 - 55603353 55604398 OR4C11 NA "olfactory receptor, family 4, subfamily C, member 11" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129992_PI430048170 0.7770487569855340.9329723070174162.723463944077 1.39914711707741 2.01652395405211 A A A 2.73311868117777 2.04088068569414 1.79862270834465 A A A LNCV6_129992_PI430048170 mRNA AAAGTCAAAATGACTCGAATTGCTATGGCTGGGAATGACTGGATTAAAAGCAATGGAAAC NM_001145531 RefSeq
chr7 + 26637870 26647270 C7orf71 NA "chromosome 7 open reading frame 71, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133393_PI430048170 0.8942097795475470.99742673803871 0.440780906571614 0.4522845831031320.38155370250307 A A A 0.45902830714589 0.404355833033679 0.422843504728418 A A A LNCV6_133393_PI430048170 mRNA TAGTTTTGCAAGTGGCTTGAAGAGGAGTTTCATTCGCGTCCCATCTTTCAGAAGCCTTGT NM_182572 RefSeq chr19 + 58034065 58054631 ZSCAN1 284312 zinc finger and SCAN domain containing 1 GO:0006366|GO:0006357|GO:0000981|GO:0003713|GO:0005634|GO:0003677|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131083_PI430048170 0.0917429312961620.37941999497936 2.03648838800911 0.2494078194019640.622015885893815 A A A 1.73388879808297 2.98159882011813 2.76061416479913 A P P LNCV6_131083_PI430048170 mRNA AAATTTGTTTTCTTTATGCTTCAGGGTAGAGGGATTTCCCTTGAGTATAGGTCAGCAAAC NM_001168374 RefSeq
chr6 - 24544103 24646155 KIAA0319 9856 "KIAA0319, transcript variant 3" GO:0005515|GO:0005886|GO:0031901|GO:0016021|GO:0001764|GO:2000171|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140488_PI430048170 0.3002970258503481.19557750991276 5.091912697041 5.4883296900931 5.18508269269628 P P P 5.1850295526516 5.15727807514009 4.61100757833795 P P P LNCV6_140488_PI430048170 mRNA AATTCCTTCAAAGCCAGCCCTGAGCGACGGAACAGTGGGCGGTGTCTCCAGAAGTGGTTT NM_001199206 RefSeq
chr11 + 94305636 94307692 IZUMO1R 390243 "IZUMO1 receptor, JUNO" GO:0007338|GO:0005515|GO:0035036|GO:0005542|GO:0005886|GO:0007342|GO:0004872|GO:0031225|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134144_PI430048170 0.3785413738250481.04130993012285 0.292666073816715 0.2775069328586020.436021792643903 A A A 0.2934801978442630.25809267626759 0.284550594985737 A A A LNCV6_134144_PI430048170 mRNA ACTGAGAATAGACTAGCATTTGTGGGGCACTCAATAAATTTAAATTCATGGTGACAGTGA NM_178175 RefSeq chrX - 112630650 112680147 LHFPL1 340596 lipoma HMGIC fusion partner-like 1 GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139697_PI430048170 0.0177830221946308 0.4430588296327923.29585222957779 3.1432754479163 3.35190919482501 P P P 4.23287330843317 4.22033704966068 4.79228707953099 P P P LNCV6_139697_PI430048170 mRNA GTGTGTAATTATCTCATTCACCTTCAGTTACCATAAAGGAGAAGGGAAAATAAAGTTGAG NM_018109 RefSeq chr10 - 30309800 30349338 MTPAP 55149 mitochondrial poly(A) polymerase GO:0005515|GO:0006378|GO:0000287|GO:0030145|GO:0005524|GO:0006351|GO:0042803|GO:0002134|GO:0042802|GO:0043231|GO:0005739|GO:0004652|GO:0071044 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133951_PI430048170 0.0509166745194316 1.18486728115615 6.88583677255767 6.67527752466198 6.82432048384301 P P P 6.57782884978398 6.5169678276714 6.56380533663305 P P P LNCV6_133951_PI430048170 mRNA AAATGTGAGGATTGTGGGAGACGCTACAAGAGGCGCTTGAATCTGGATATACTTTTATCA NM_001260486 RefSeq
chr19 + 43984169 43998325 ZNF155 7711 "zinc finger protein 155, transcript variant 3" GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_125662_PI430048170 0.9579130936737060.98957864407785711.1662177006151
11.0074389393909 11.201462334919 P P P 11.3371709428643 11.1380044437111
10.9229569826851 P P P LNCV6_125662_PI430048170 mRNA
AGTACAAGCAGATCTTCCTGGGGGGCGTGGACAAGCACACGCAGTTCTGGAGGTACTTTG NM_001636RefSeq chrY
- 1386151 1392146 SLC25A6 293 "solute carrier family 25 (mitochondrial carrier; adenine nucleotide
translocator), member 6"
GO:0005515|GO:0006626|GO:0019058|GO:0005743|GO:0046732|GO:0006915|GO:0005634|GO:0044281|GO:0055
085|GO:0005739|GO:0005744|GO:0006112|GO:0050796|GO:0019048|GO:0015866|GO:0015867|GO:0016032|GO:0
016021|GO:0044267|GO:0005471 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98650_PI430048170 0.1777933403017881.13024439939276 9.36393710099333 9.52122708998789
9.28166545066617 P P P 9.06657660086866 9.35224106993977 9.21433770084453 P P P
LNCV6_98650_PI430048170 mRNA
TCTGGCAGCCCTGGCCTTTACCTGGACCTTGTAGGGGTCTCCTGCCTAGCTGCCTAGCAA NM_033158RefSeq chr3
- 50317789 50322850 HYAL2 8692 "hyaluronoglucosaminidase 2, transcript variant 2"
GO:0005515|GO:0030308|GO:0051216|GO:0071560|GO:0048705|GO:0005764|GO:0031362|GO:0051607|GO:0010
764|GO:0001618|GO:0071356|GO:0030203|GO:2000484|GO:0046677|GO:0009986|GO:0005975|GO:0019064|GO:0
060586|GO:0042117|GO:0071347|GO:0042307|GO:0004415|GO:0045121|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_114452_PI430048170 0.6174848479142340.9327033505605449.58831971402821
9.65792062301647 9.87361505713556 P P P 9.60685340572606 9.7112203887592
10.0758414045286 P P P LNCV6_114452_PI430048170 mRNA
TACCTTCCTTCTAAAAACCTGATTCATGCACAGCGTTTGACACACATGGAGTCTGCCAGT NM_001040451 RefSeq
chr5 + 179559691 179610026 RUFY1 80230 "RUN and FYVE domain containing 1, transcript variant
2"
GO:0005515|GO:0005737|GO:0030100|GO:0031901|GO:0008565|GO:0008270|GO:0005634|GO:0015031|GO:0043
231|GO:0008289|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126831_PI430048170 0.131792963567024 0.467805303320045 1.86643794622787
0.74997741268177 0.330850628515159 A A A 1.46222258691086 2.81120370300744
2.10572003298367 A P A LNCV6_126831_PI430048170 mRNA
GAACTATCAGTAGACAGCTGCTGCTTCCATGAAACGGAAAAATAAAAATCATGTTTTCTT NM_014069 RefSeq
chr6_GL000255v2_alt - 2395561 2397376 PSORS1C2 170680 psoriasis susceptibility 1 candidate 2
GO:0008150|GO:0003674|GO:0005576|GO:0005575 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_119694_PI430048170 0.00698022020856284 0.314096675369844 7.17893817785776
6.84729544683553 7.06946319402925 P P P 8.37718753386327 8.5736453573016
9.08226464752373 P P P LNCV6_119694_PI430048170 mRNA
GTACCATTACAGGCTTCAGTATACAGTCAGGTTTGTTCTTCACGGTGTATCTTTATAATA NM_020762 RefSeq
chr12 + 63844760 64147833 SRGAP1 57522 SLIT-ROBO Rho GTPase activating protein 1
GO:0005515|GO:0051056|GO:0048365|GO:0030336|GO:0005737|GO:0016477|GO:0007411|GO:0007264|GO:0007
266|GO:0032855|GO:0030675|GO:0005829 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_107095_PI430048170 0.530186734501279 1.06344665001034 10.4073987836181
10.455804614455 10.6583306608662 P P P 10.3013043563744 10.3063297482585
10.6342789393547 P P P LNCV6_107095_PI430048170 mRNA
CTACAAAGGAAATATCAAAGTGTTTTTCAAGCCTGTTATATTCAGTGTGTGCCACAGGAT NM_006765 RefSeq
chr8 + 15540086 15766649 TUSC3 7991 "tumor suppressor candidate 3, transcript variant 1"
GO:0015693|GO:0015095|GO:0005739|GO:0050890|GO:0005887|GO:0004579|GO:0005789|GO:0045454|GO:0006
487|GO:0008250|GO:0044267|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA
NA NA NA

LNCV6_127788_PI430048170 0.437362822821064 1.35550800140012 1.4847114853113
0.445826798762547 0.378767031650803 A A A 0.455616990684389 0.40009940751915
0.419790374934926 A A A LNCV6_127788_PI430048170 mRNA
GCTCGGAGAATTATTGCACAATTTTCAAAAGACTATGAAACCACCGATAACCCCAGTACC NM_001013627 RefSeq
chrX + 71911087 72143574 NHSL2 NA NHS-like 2 NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_142159_PI430048170 0.149378400503458 0.820258630856599 10.4017596882922
10.4895476185281 10.761616606545 P P P 10.7803996467376 10.6660313346624
11.0599505268285 P P P LNCV6_142159_PI430048170 mRNA
CTTGTTCTTATCTGTGTCCTAAAGATGTGTTCTCTATAAAATACAAACCAACGTGCCTAA NM_001281513 RefSeq
chr2 + 26244747 26290465 HADHB 3032 "hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA
thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit, transcript variant 3"
GO:0042645|GO:0005515|GO:0006635|GO:0005783|GO:0035965|GO:0005743|GO:0003857|GO:0005741|GO:0044
281|GO:0005740|GO:0032403|GO:0005739|GO:0051287|GO:0016508|GO:0016509|GO:0016507|GO:0003988|GO:0
004300|GO:0006644|GO:0000062|GO:0044255|GO:0070062|GO:0046474 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_137676_PI430048170 0.5704326884083470.9394680135730395.76900911640377
5.47770366017882 5.79747179087497 P P P 5.56385820262364 5.87282588727227
5.87713359247054 P P P LNCV6_137676_PI430048170 mRNA
GTGCTCAGTGAGGAGGCAGTAAATGAAGTTACAGGCTAGCACAATACCTAACTCATGTTT NM_018200RefSeq chr15
+ 77420650 77485603 HMG20A 10363 "high mobility group 20A, transcript variant 1"
GO:0005515|GO:0006355|GO:0003700|GO:0046982|GO:0045665|GO:0003682|GO:0006325|GO:0006338|GO:0005
634|GO:0000122|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65595_PI430048170 0.7008164323219930.8362240781416592.71527326637076 1.92699232172071
3.08150830700363 A A P 3.1439025009414 1.96144194598115 3.29130564237475 P A P
LNCV6_65595_PI430048170 mRNA
CCATCTTGGAGGCAGTGTAGGATCATGGAAGAACTTTGAATTAGGTTTTTAGAACTTCAG NM_001127401 RefSeq
chr2 + 30146883 30160533 YPEL5 51646 "yippee-like 5 (Drosophila), transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140461_PI430048170 0.0184913410219720.3052936554551736.04801063791841
5.42543614142839 4.98295266924316 P P P 7.06292723067132 7.47588539224395 7.2226065554892
P P P LNCV6_140461_PI430048170 mRNA
GGATATGTGGTGTATATCCTTCCAAAAAATTAAAACGAAAATAAAGTAGCTGCGATTGGG NM_001964RefSeq chr5
+ 138465491 138469315 EGR1 1958 early growth response 1
GO:0005515|GO:0003700|GO:0006366|GO:0048709|GO:0019221|GO:0060291|GO:0042220|GO:0072303|GO:0003
690|GO:0043525|GO:0060337|GO:0048169|GO:0051602|GO:0007611|GO:0031667|GO:0035035|GO:0032869|GO:0
000976|GO:0030509|GO:0000122|GO:0000979|GO:0071317|GO:0071383|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_76085_PI430048170 0.1597896000820692.15610920015643 3.01810425193921 2.84598063438032
3.03105995188733 P A P 2.62890670110157 1.71996369423992 0.488730420253104P A A
LNCV6_76085_PI430048170 mRNA
TGGTATGGTGGGGAATCCTACATCCAGAGCATGGAGCCAGGGGCTAAGTGCTTTGCAGTC NM_006051RefSeq chr5
- 140558267 140564604 APBB3 10307 "amyloid beta (A4) precursor protein-binding, family B, member 3,
transcript variant 4" GO:0005515|GO:0006355|GO:0005737|GO:0001540|GO:0005634|GO:0015629|GO:0008134
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136348_PI430048170 0.5857506061425210.655912068790757 1.02016530505521
1.77916353749685 2.76831932295066 A A A 3.60799976619349 1.6584996501598
1.74939102793574 P A A LNCV6_136348_PI430048170 mRNA
CTATCTGCCTCAACCAGACTGGGTACAAAATAAAGATCAAGTCTCCCGGAAACCAAAAAA NM_001288702 RefSeq

chr17 - 4556926 4560596 GGT6 124975 "gamma-glutamyltransferase 6, transcript variant 3"
GO:0019370|GO:0003840|GO:0006750|GO:0006508|GO:0006749|GO:0016021|GO:0031362|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99547_PI430048170 0.1364682444741490.5603828651052793.19418097451736 2.04344185959097
3.25931274130891 A A P 4.13852602663665 3.64769161812188 3.41009568174808 P P P
LNCV6_99547_PI430048170 mRNA
TCCCCATCCCTGTCATTTTTAACAGCATGCTGCTTTGCCAAGTTGCTGTCACTGTTTTTT NM_004469RefSeq chrX -
15345590 15384413 FIGF 2277 c-fos induced growth factor (vascular endothelial growth factor D)
GO:0048010|GO:0008284|GO:0008283|GO:0030168|GO:0060754|GO:0005576|GO:0001525|GO:0005161|GO:0042
056|GO:0005615|GO:0042803|GO:0030154|GO:0050918|GO:0050930|GO:0016020|GO:0007596|GO:0002576|GO:0
043185|GO:0051781|GO:0031093|GO:0005172|GO:0008083 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_138965_PI430048170 0.0547278102977762 1.76505287671776 14.392095003567
14.2433225206435 14.3232432735039 P P P 13.9026299567941 13.2604268422821
13.2371170252518 P P P LNCV6_138965_PI430048170 mRNA
CAGGGGACCTCCTTTCAGATGAACTGGGAAGAGATGAAATGTTTTTTCATATTTAAATAA NM_019107RefSeq chr19
- 4657544 4670403 MYDGF NA myeloid-derived growth factor NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136779_PI430048170 0.0422189727227122 0.6952627594913083.91381412057138
4.2810449952913 3.86285602318233 P P P 4.48167125815547 4.53281938359281 4.6482885467261
P P P LNCV6_136779_PI430048170 mRNA
TCTCCCCATTTCCATTTTATTTCTTCTGGGAAGACCCATAATAAATGATTCTGTAGAGGC NM_024323RefSeq chr19
- 13882354 13906096 C19orf57 79173 chromosome 19 open reading frame 57
GO:0005515|GO:0003674|GO:0007275|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_67807_PI430048170 0.0488179228415735 0.8208130188747977.56932715613735
7.64569145251657 7.60635178541365 P P P 7.84298668616068 7.79394095522987
8.02925473720213 P P P LNCV6_67807_PI430048170 mRNA
TGGTGGCATGAGAGGCATGAAGGGATTGGTCTATGAAACATCAGTTCTTGATCCTGATGA NM_004077RefSeq chr12
- 56271698 56300391 CS 1431 citrate synthase
GO:0005739|GO:0044262|GO:0006099|GO:0005975|GO:0005759|GO:0004108|GO:0005634|GO:0044281|GO:0044
237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128607_PI430048170 0.60907281631354 0.9231497960709964.19717448485577
4.79277485342371 4.18616007482421 P P P 4.67697923227548 4.62677056803159
4.27269721024741 P P P LNCV6_128607_PI430048170 mRNA
CAAAATTATAGAAGGCTTCTGAGCCCCTAGAGATTTTTAATTTGCTTCTAATCCCTGAGG NM_001190455 RefSeq
chr15 + 32030482 32170183 CHRNA7 1139 "cholinergic receptor, nicotinic, alpha 7 (neuronal),
transcript variant 2"
GO:0008284|GO:0030054|GO:0005886|GO:0022848|GO:0007268|GO:0042803|GO:0000187|GO:0001540|GO:0034
220|GO:0015464|GO:0045211|GO:0042166|GO:0007613|GO:0006816|GO:0006811|GO:0001666|GO:0006874|GO:0
032720|GO:0045766|GO:0005892|GO:0007165|GO:0050890|GO:0015643|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_43415_PI430048170 0.981995654192881 0.971338042679861 1.63483857544169 0.475433059770298
0.488430343685452 A A A 0.4082533498649461.73924231718066 0.492791162890706 A A A
LNCV6_43415_PI430048170 mRNA
CAACTACAAAGACCACAACTTCCCTAGGAGGAAGTGGCACCACTGGAGCAAAAATAAAAT NM_173600RefSeq
chr12 + 40393393 40570755 MUC19 283463 "mucin 19, oligomeric"
GO:0006493|GO:0005796|GO:0016266|GO:0044267|GO:0070062|GO:0043687 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132370_PI430048170 0.01301898720838 1.18872044718112 8.50702466712367

8.55089624084782 8.55541138818125 P P P 8.24515224536891 8.36401760003967
8.25334649177063 P P P LNCV6_132370_PI430048170 mRNA
CTTGGAATCAATCTTGCCAAATATTTGGAGAGATTGTGTGGATTTAAGAGACCTGGATTT NM_020313 RefSeq chr16
- 57428168 57447528 CIAPIN1 57019 cytokine induced apoptosis inhibitor 1
GO:0005515|GO:0030097|GO:0043066|GO:0016226|GO:0051537|GO:0005730|GO:0006915|GO:0009055|GO:0044
281|GO:0046872|GO:0005758|GO:0005737|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136045_PI430048170 0.00899687508793652 3.0791218472685 6.03786977404913
5.82654937705851 6.02690069782651 P P P 4.63965433485391 3.94157101057391
4.36825581967235 P P P LNCV6_136045_PI430048170 mRNA
CTGCTGTTGTGTGAAGATTGACATTTACCATGATTTTCCTTAGTTACTGCAGAACATAGA NM_014061 RefSeq chrX
+ 55452088 55453568 MAGEH1 28986 melanoma antigen family H1 GO:0005737|GO:0006915 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135003_PI430048170 0.48512102309915 1.07074681275984 0.828029656262997
0.6145341190462640.546585664387348 A A A 0.5500521958614530.397890378685825
0.740077303105156 A A A LNCV6_135003_PI430048170 mRNA
GGCCGGTAGAATTCAATTGTTTATGGACAAAAGCCACCTAATAAAAGATAGGAAAGCATT NM_013249 RefSeq chr11
- 6999317 7020355 ZNF214 7761 zinc finger protein 214
GO:0006355|GO:0008270|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_136052_PI430048170 0.3750864841050750.7304604986506575.03741399843184
3.62786080480452 3.93078069659834 P P P 5.22043430914255 4.76371865451943 4.1947279674064
P P P LNCV6_136052_PI430048170 mRNA
GCCGCCCAGTTATATTCTGTGTTTCTCCTAGTGTGAATTTCTTATGCTTTGTTGCATCTC NM_001146041 RefSeq
chr17_JH159146v1_alt + 255075 256175 KRTAP4-9 100132386 keratin associated protein 4-9
GO:0042633|GO:0007568|GO:0045095 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136773_PI430048170 0.9020346987187290.9956132431695082.29912208310998
3.13461078171834 2.22171233950459 A P A 2.93266084640188 2.30967892780521
2.55002752074147 P A P LNCV6_136773_PI430048170 mRNA
ATTAAATCTGCCATCTCAGGCCTGGCTGGCTCTTCTGTGCTTTCCACAAATAAAGTTCCT NM_003307 RefSeq chr21
+ 44353600 44443081 TRPM2 7226 "transient receptor potential cation channel, subfamily M, member
2, transcript variant 1"
GO:0005262|GO:0005886|GO:0005272|GO:0055085|GO:0034220|GO:0047631|GO:0005384|GO:0005887|GO:0008
152|GO:0070588|GO:0006816|GO:0035725|GO:0033194|GO:0071421 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_67786_PI430048170 0.1339316457991210.6976588620392923.95730220524143 4.17588755783395
3.518786791364 P P P 4.01700419868357 4.67110981541933 4.51949451845562 P P P
LNCV6_67786_PI430048170 mRNA
ATCGGTAAAGGAGGTTTTACACTTTTCTGGACCAGACTTGAAGAGACTGACCAACCTCTC NM_001100119 RefSeq
chr14 - 103697616 103715486 XRCC3 7517 "X-ray repair complementing defective repair in Chinese
hamster cells 3, transcript variant 1"
GO:0000400|GO:0005515|GO:0048471|GO:0010033|GO:0071140|GO:0005657|GO:0008821|GO:0005634|GO:0006
310|GO:0090267|GO:0010824|GO:0005524|GO:0006974|GO:0005739|GO:0005737|GO:0006281|GO:0000724|GO:0
033065|GO:0000737|GO:0008094 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144539_PI430048170 0.0136752818869427 1.1627187412574 11.5041519303676
11.5565345538443 11.4899275505989 P P P 11.259790332908 11.37380904915
11.2624029124554 P P P LNCV6_144539_PI430048170 mRNA
ACAGCTTTGCCTTTTGCTGACACAGCTCCATAAAGACTCGTGCTTTCTCACTGCAAAAAA NM_024741 RefSeq chr11
+ 46700766 46705916 ZNF408 79797 "zinc finger protein 408, transcript variant 1"
GO:0005515|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351|GO:0042802 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_138050_PI430048170 0.1875024307242911.09834197982432 0.590266345516026
0.3819289794354180.573458228770372A A A 0.2897551393552610.397366711072649
0.456750963118786A A A LNCV6_138050_PI430048170 mRNA
GTGTGGACTGAAGTGTAGGTATGTAGAGATGCTTCGCCAAACAGATGCTTAAAAATGAAA NM_030891RefSeq chr21
+ 44455485 44458856 LRRC3 81543 leucine rich repeat containing 3 GO:0005515|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126678_PI430048170 0.000937907392930893 0.5292669634389022.37347681297289
2.53726756912956 2.27468662830054 A A A 3.44618903491352 3.20581315951004
3.28909306185502 P P P LNCV6_126678_PI430048170 mRNA
TCACAACTGGGATTTGTGTACTAGTTTTCTGTAGCTGCCATAAAAATTGCCACAAATTCA NM_001195082 RefSeq
chr14 + 105398582 105413859 TEX22 NA testis expressed 22 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_143828_PI430048170 0.1494721853663191.04634101066588 0.42633113951399
0.4334696036315310.445969427140158A A A 0.3225073841343590.361991202103238
0.423481719179645A A A LNCV6_143828_PI430048170 mRNA
CCTAAAGTACACACGGCTGTGACTTGATTCAAAAGAAAATGTTATAAGATGCAGTAAACT NM_000792RefSeq chr1
+ 53894187 53911086 DIO1 1733 "deiodinase, iodothyronine, type I, transcript variant 1"
GO:0034641|GO:0008430|GO:0005886|GO:0005789|GO:0042446|GO:0004800|GO:0006590|GO:0044281|GO:0016
021|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127148_PI430048170 0.4632158194346970.7907790455611680.39301341247797
0.2585340199158630.288669729423276A A A 1.19123078425224 0.297554309746928
0.269612023931221A A A LNCV6_127148_PI430048170 mRNA
GCATTTCAAATATGCCCAGATGGTAACATTTGTGCAGGTGAAAACCAGTGCCAAGCTTCC NM_182517RefSeq chr1
- 43281885 43285579 C1orf210 149466 "chromosome 1 open reading frame 210, transcript variant 1"
GO:0005886|GO:0016021|GO:0055037|GO:0005769 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_59032_PI430048170 0.4167048825065221.42580738566329 1.88285828014604 3.27768988186264
2.60344182646068 A P A 1.92960935564878 2.30604486624495 2.29161171049176 A A A
LNCV6_59032_PI430048170 mRNA
TGCAATGCTCTGCACTTCTTCTCCAGGATACCTCGAACCTGCTCAAGCGCTGCCATGGGT NM_015989RefSeq chr12
- 53157662 53180646 CSAD 51380 "cysteine sulfinic acid decarboxylase, transcript variant 1"
GO:0034641|GO:0000096|GO:0000098|GO:0030170|GO:0004782|GO:0044281|GO:0042412 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129088_PI430048170 0.1212992041337290.7290957921033826.87026798178807
6.29271439735151 6.89122899424433 P P P 6.995099767744 7.12935583685683
7.35071587425156 P P P LNCV6_129088_PI430048170 mRNA
GCATTGTCTTCACGAAGAAGATGTAAAAATAATGAACAATAAATTGCGGTGGAAACCTCT NM_016066RefSeq chr1
- 193096464 193106114 GLRX2 51022 "glutaredoxin 2, transcript variant 1"
GO:0042542|GO:0006355|GO:0010033|GO:0008794|GO:0051537|GO:0015035|GO:0003756|GO:0006749|GO:0006
915|GO:0009055|GO:0005634|GO:0015038|GO:0009966|GO:0046872|GO:0030154|GO:0043231|GO:0005739|GO:0
009266|GO:0006457|GO:0042262|GO:0051775|GO:0045454|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137327_PI430048170 0.9479174932935621.06227409507916 0.397183044714665
0.4029018659449271.88285828014604 A A A 0.4278183602767381.71952890102768
0.398069758210075A A A LNCV6_137327_PI430048170 mRNA
ATGTTGAATCCCAAAACACTAACAGGAACAACTCAACTGCCTTGCAGTTAGCTAGCCGTC NM_152447RefSeq chr14
+ 41607560 41904551 LRFN5 145581 leucine rich repeat and fibronectin type III domain containing 5
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133425_PI430048170 0.00941897660985758 1.57445592028693 6.60378756672926

6.51878435267598 6.83554447075126 P P P 5.81930103458335 5.99752549803108
6.17387357927148 P P P LNCV6_133425_PI430048170 mRNA
GAATGCATGTTCTGTGTGCCCTGAAAATGTTACCAGTGTTAATAAATGGATACTTATCAA NM_022445 RefSeq chr7
- 144451940 144836053 TPK1 27010 "thiamin pyrophosphokinase 1, transcript variant 1"
GO:0004788|GO:0016310|GO:0009229|GO:0006772|GO:0016301|GO:0006766|GO:0006767|GO:0044281|GO:0042
723|GO:0030975|GO:0005524|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140120_PI430048170 0.369214971055751 1.06902949463171 12.9216587605353
12.7974755034614 12.7525470695989 P P P 12.5684648414082 12.8404366787835
12.7657381911357 P P P LNCV6_140120_PI430048170 mRNA
CCCTGTTGATTGGTCTGGCATTTCCGGTATTAAAATGATAAAATAAATGGCATTTTCTGA NM_001258359 RefSeq
chr2 + 10368763 10427617 HPCAL1 3241 "hippocalcin-like 1, transcript variant 5"
GO:0007165|GO:0005509|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133164_PI430048170 0.0102111332709409 1.23099070396368 12.3769753953257
12.3270857041764 12.3718948678987 P P P 12.0498133890015 11.9909717550661
12.1327083001928 P P P LNCV6_133164_PI430048170 mRNA
GGTGCCAAAAGTTCCCTCTGTGTTACTCCCATTTAGAAAATAAACACTTTTAAATGATCA NM_001170790 RefSeq
chr12 + 53251585 53254406 MFSD5 84975 "major facilitator superfamily domain containing 5,
transcript variant 1" GO:0016020|GO:0005886|GO:0015098|GO:0015689|GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_107602_PI430048170 0.906608338237014 1.17466483471224 3.58030504458694
3.66319563566651 1.98873339678714 P P A 3.25497527490822 3.04713554817077
2.70801477195965 P P P LNCV6_107602_PI430048170 mRNA
TTCAGAGAGACCAAGAGAAGGAGAGAGTTATGCGGGCTGCATGTGCTTTATTAAACTCAG NM_001104587 RefSeq
chr17 - 35350309 35373701 SLFN11 91607 "schlafen family member 11, transcript variant 1"
GO:0051607|GO:0005737|GO:0000049|GO:0016235|GO:2000134|GO:0005654|GO:0005634|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62622_PI430048170 0.184221205905179 0.787284917578567 3.64455428524903 3.74310847736498
3.32434251549319 P P P 3.85528578003117 4.21470132768241 3.6525950801642 P P P
LNCV6_62622_PI430048170 mRNA
ATTACGACGTTGGCTGGGAGAGTCCTCACAATGGCTCGGGGACGTGGGCCTATTCAGCGC NM_001009944 RefSeq
chr16 - 2088709 2135898 PKD1 5310 "polycystic kidney disease 1 (autosomal dominant),
transcript variant 1"
GO:0005515|GO:0006807|GO:0060674|GO:0072237|GO:0051216|GO:0034405|GO:0042994|GO:0009653|GO:0007
507|GO:0016337|GO:0018105|GO:0050982|GO:0072177|GO:0006611|GO:0048806|GO:0070062|GO:0005262|GO:0
006996|GO:0019901|GO:0060236|GO:0019904|GO:0001892|GO:0072372|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_64170_PI430048170 0.0216312309342934 1.37973840991357 8.99339212145518
9.16647121810378 8.93672229003238 P P P 8.72724363555983 8.57853484783779
8.38770603158794 P P P LNCV6_64170_PI430048170 mRNA
TTTTTACAAGATACCGTTCGGGAAAGGCTTTTGAAAGGACGGAAGCGTATTCACTGTGCG NM_032853 RefSeq chr19
+ 1354976 1378431 MUM1 84939 "melanoma associated antigen (mutated) 1, transcript variant 1"
GO:0005515|GO:0006281|GO:0006325|GO:0031491|GO:0005634 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143648_PI430048170 0.184768940704326 1.15692509696704 6.77313278739948
6.59955095798036 6.82903883068383 P P P 6.50311081081196 6.71553212546706
6.33693563733406 P P P LNCV6_143648_PI430048170 mRNA
TTTATTCTGTAACCTGACACTCATCTGGCCCTTTGCAGTTTGCCAGCCATATTCCCATGT NM_015488 RefSeq chr2
+ 218270391 218346793 PNKD 25953 "paroxysmal nonkinesigenic dyskinesia, transcript variant 1"
GO:0005739|GO:0005515|GO:0016020|GO:0032225|GO:0006750|GO:0050884|GO:0008270|GO:0005634|GO:0004

416|GO:0042053 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128606_PI430048170 0.00892839547727383 0.6251135019219794.89166812099839
4.5910313789609 4.55431942112735 P P P 5.39035436607444 5.49947775361607
5.18773812600037 P P P LNCV6_128606_PI430048170 mRNA
GTGCATGTCTCTGTAATGTAACTCACCCTCCTCAGCATTATTTGATACACTGATTGTTAG NM_004198RefSeq chr8
- 42752635 42768786 CHRNA6 8973 "cholinergic receptor, nicotinic, alpha 6 (neuronal), transcript
variant 1"
GO:0007165|GO:0051899|GO:0030054|GO:0005886|GO:0045211|GO:0015464|GO:0006810|GO:0007268|GO:0014
059|GO:0005892|GO:0004889 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132374_PI430048170 0.1315802228920621.16101255771892 9.76046201322104
9.77255442574807 9.91718045337659 P P P 9.47222113391063 9.53523973007654 9.7828979045582
P P P LNCV6_132374_PI430048170 mRNA
GAATTGTCATACTAATTATTGAGGGGGACTTATGTGCTTTTATTGAATGGAGTGCTTTAC NM_017755RefSeq chr5
- 6599238 6633360 NSUN2 54888 "NOP2/Sun RNA methyltransferase family, member 2, transcript
variant 1"
GO:0016428|GO:0007067|GO:0005737|GO:0000049|GO:0030488|GO:0005819|GO:0005730|GO:0005634|GO:0051
301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126879_PI430048170 0.0072890757985919 1.27499154873971 12.3630488045409
12.4303713106628 12.390826771541 P P P 12.0839165572288 11.9543202866649
12.0912709634957 P P P LNCV6_126879_PI430048170 mRNA
CTAGCCCATCATCTATCTAACCGGTCCTTGATTTAATAAACACTATAAAAAGTTCTTTGC NM_015516RefSeq chr11
+ 76783240 76798154 TSKU 25987 "tsukushi, small leucine rich proteoglycan, transcript variant 1"
GO:0010468|GO:0021960|GO:0021540|GO:0021670|GO:0030178|GO:0061073|GO:0005615 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_125020_PI430048170 0.00229105301963898 1.43831157112519 8.93731452207383
9.04835213442433 8.98270167978717 P P P 8.44901434533735 8.4758764776243
8.47236625557215 P P P LNCV6_125020_PI430048170 mRNA
ACATGGATCGGATGGCCAGCTCCATGAAGCAGGTGCCCAACCCACTGCCCAAGGTGCTGA NM_005338RefSeq
chr7 - 75533297 75738972 HIP1 3092 "huntingtin interacting protein 1, transcript variant 1"
GO:0005515|GO:0030036|GO:0030136|GO:0005634|GO:0030154|GO:0043231|GO:0005737|GO:0030276|GO:0005
856|GO:0030674|GO:0006355|GO:0005794|GO:0006919|GO:0006915|GO:0003779|GO:0042981|GO:0097190|GO:0
006351|GO:0006897|GO:0030665|GO:0016020|GO:0048260|GO:0005200|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_62188_PI430048170 0.3112322628577590.90672933713729412.6074775813517 12.3233487222083
12.2461663252287 P P P 12.4702428149741 12.6291414673005 12.5223812792627 P P P
LNCV6_62188_PI430048170 mRNA
CTTCCCTTGAAAGGCAATTGTTGGCTGTTTTCATAAGCAGGAAAAATAAACAGAAGTATA NM_017828RefSeq chr15
+ 75335995 75340277 COMMD4 54939 "COMM domain containing 4, transcript variant 1"
GO:0005515|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_93033_PI430048170 0.00402408606675822 0.4642364273223293.99867782555431
3.64439721437325 4.10120995112453 P P P 4.87892466677657 4.92909330555449
5.26491950999651 P P P LNCV6_93033_PI430048170 mRNA
ATAAATGCACGACATATACCTAGGACTTTAAGTGCTGTTCCATCATCTGCCTTAAAGCTG NM_025209RefSeq chr10
- 32267715 32347218 EPC1 80314 "enhancer of polycomb homolog 1 (Drosophila), transcript variant
1"
GO:0031965|GO:0006325|GO:0005634|GO:0000122|GO:0006351|GO:0032777|GO:0043967|GO:0045944|GO:0043
968|GO:0045814|GO:0035267|GO:0005654|GO:0045893|GO:0045892|GO:0004402|GO:0040008 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136872_PI430048170 0.5847767974910410.9662799124674410.501590646722724

0.4812674210035560.257106009992148A A A 0.4037194596956 0.524033410299529
0.470681062315981A A A LNCV6_136872_PI430048170 mRNA
GGAGCTGTGCACCTCAATTTGCTGTCTAGTTGAGAATAGAGATTGTGTGCCTTCATTTCA NM_173664RefSeq chr5
+ 176365498 176373500 ARL10 285598 ADP-ribosylation factor-like 10
GO:0005622|GO:0007264|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127434_PI430048170 0.9387246581421950.971793001745977 1.88406984550642
0.3349455084480220.259406620050537A A A 1.89509505739835 0.312325252220706
0.450786495803024A A A LNCV6_127434_PI430048170 mRNA
GAGGGGGACTGACACTGATTTTTCATTTGAAATCAGCCACTTAAATCTCTTTCCATACAA NM_207437RefSeq chr12
+ 123762494 123935720 DNAH10 196385 "dynein, axonemal, heavy chain 10"
GO:0005929|GO:0005737|GO:0030286|GO:0008152|GO:0005874|GO:0003777|GO:0016887|GO:0005524|GO:0007
018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140247_PI430048170 0.00819317264856694 0.6269253913756892.75940041771326
2.74703268008953 3.06133361683946 A A P 3.71054987055704 3.46357651097364
3.41963971934001 P P P LNCV6_140247_PI430048170 mRNA
GGAGAATAGTAACAATGTCTAACTTATGCTAATGATTTTGTGTGCTGAGCTCCCATTAAT NM_001146214 RefSeq
chr12 + 71839706 71926849 TBC1D15 64786 "TBC1 domain family, member 15, transcript variant 2"
GO:0005739|GO:0005515|GO:0032313|GO:0005737|GO:0032851|GO:0005097|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132063_PI430048170 0.0827742952100913 0.8985629719389245.24481673617194
5.1721349727775 5.06397233144512 P P P 5.34968225962206 5.36017854277044
5.23647208119697 P P P LNCV6_132063_PI430048170 mRNA
TGCAAGGTCCACACCCAAAAGTGTCAATGTTTGCCCCCCAAATAAAATTGTCTGGCTTCT NM_003717RefSeq chr12
- 53506689 53507638 NPFF 8620 neuropeptide FF-amide peptide precursor
GO:0002438|GO:0070253|GO:0021510|GO:0032099|GO:0007268|GO:0045777|GO:0007204|GO:0005615|GO:0030
425|GO:0030103|GO:0007218|GO:0043204|GO:0043679|GO:0005184|GO:0046676|GO:0010459|GO:0001664|GO:0
042493|GO:0060135|GO:0005102|GO:0060079|GO:0005576|GO:0043278|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_54446_PI430048170 0.00760463781082616 0.5133766543501843.39178952882442
3.05956845282591 3.45862429235186 P P P 4.27277383735707 4.18233820060115
4.36558791422059 P P P LNCV6_54446_PI430048170 mRNA
AAAGATAGAAAATGAGAGTGACATGATTCGTAACTGGAGTTACCTTGGTGTTCCCATTGT NM_007269RefSeq chr1
+ 108746662 108809526 STXBP3 6814 syntaxin binding protein 3
GO:0005515|GO:0005886|GO:0043312|GO:0042581|GO:0015031|GO:0051291|GO:0006904|GO:0005829|GO:0016
323|GO:0016324|GO:0015758|GO:0022615|GO:0031091|GO:0061024|GO:0017075|GO:0070062|GO:0019905|GO:0
032868|GO:0030168|GO:0070527|GO:0045955|GO:0007596|GO:0007420|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_140504_PI430048170 0.4105028190681331.00942562282645 0.332809197970756
0.3130472087109770.289214277889622A A A 0.3043297687374230.30447648291159
0.285911831769519A A A LNCV6_140504_PI430048170 mRNA
CTCTGCCTGAAATGTTACACATTAAACAGGATTTTACAGTAAATGAAGAGGTGGCTTGTG NM_000166RefSeq chrX
+ 71223205 71225215 GJB1 2705 "gap junction protein, beta 1, 32kDa, transcript variant 2"
GO:0007267|GO:0006810|GO:0005789|GO:0061024|GO:0005922|GO:0016264|GO:0016021|GO:0042803|GO:0007
399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131218_PI430048170 0.3140878710775520.6979419658985650.760920510542299
0.8305044069260912.25605373578129 A A A 2.33913177759595 1.957030452697
1.52479094315319 A A A LNCV6_131218_PI430048170 mRNA
GCAGCTCCCATTTCTAGAACACATTTACAGTATTACTATTTTCTAGGATATAAAGTGCCA NM_004137RefSeq chr5
- 170378160 170389677 KCNMB1 3779 potassium channel subfamily M regulatory beta subunit 1

GO:0005513|GO:0005886|GO:0007596|GO:0008076|GO:0015459|GO:0007268|GO:0015269|GO:0006813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63787_PI430048170 0.2148114238472890.8109867855091615.07880172872266 4.85358652626317 5.48217624533558 P P P 5.31711729085001 5.50606712842132 5.55851495095966 P P P
LNCV6_63787_PI430048170 mRNA
ACTGCCTGTAAATAAGGTGTTTAGTCTTTCTATAAAAACAGAATAGAGCAGTTACCTACC NM_001098801 RefSeq chr18 - 13663346 13726592 FAM210A 125228 "family with sequence similarity 210, member A, transcript variant 1" GO:0005739|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125485_PI430048170 0.0268704567077677 1.09290383118634 0.405704154824616 0.4837643658970140.49435348057761 A A A 0.3077945249833050.334560095413328 0.358142999108635 A A A LNCV6_125485_PI430048170 mRNA
TACAGAGGGTTTTCAGAACCACCTCAGAGAAGATGTTTAAATCGCTGACAAAAGTCAACA NM_019098 RefSeq chr8 - 86573934 86743675 CNGB3 54714 cyclic nucleotide gated channel beta 3 GO:0005223|GO:0007603|GO:0005222|GO:0007165|GO:0030553|GO:0005887|GO:0005249|GO:0042391|GO:0006810|GO:0007601|GO:0006812|GO:0071805|GO:0001750 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132785_PI430048170 0.47954214807032 0.9646641422834181 3.2452090993211 13.424946793718 13.3509792021545 P P P 13.3098933610911 13.4488610623782 13.420021780664 P P P
LNCV6_132785_PI430048170 mRNA
AACGTCCTCTTGTGTATAATAAACCTTTAATTTTGGTGTTGGACCCCTGGGGCCTTCCCA NM_004749 RefSeq chr7 - 45100099 45111747 TBRG4 9238 "transforming growth factor beta regulator 4, transcript variant 1" GO:0005739|GO:0045333|GO:0008284|GO:0004672|GO:0007050|GO:0006468 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_77896_PI430048170 0.6605196901953671.04471955952904 6.19415900510496 6.2901762595735 6.34823100260951 P P P 5.91138607522861 6.33107714874798 6.36251211577632 P P P
LNCV6_77896_PI430048170 mRNA
AGGCTTTTTCAGAAAGTCTTAAAAGACCCTGGGAAGATGATCCTCCAAATGTACATATTA NM_016020 RefSeq chr6 - 155256129 155314483 TFB1M 51106 "transcription factor B1, mitochondrial" GO:0042645|GO:0005515|GO:0031167|GO:0006355|GO:0006996|GO:0005759|GO:0007005|GO:0003677|GO:0006351|GO:0000179 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138246_PI430048170 0.6358259487359590.9489693050550840.359069887514743 0.4926313859775670.385264070670667 A A A 0.2457894859236760.629244386669637 0.563723217674891 A A A LNCV6_138246_PI430048170 mRNA
GAGATCCTACAATGGAAGAATAAAATCACCTCATTCTTCATTTCAGATCTGAACATTAGC NM_054027 RefSeq chr5 - 14704799 14871778 ANKH 56172 ANKH inorganic pyrophosphate transport regulator GO:0030500|GO:0001501|GO:0005886|GO:0005887|GO:0019867|GO:0035435|GO:0015114|GO:0007626|GO:0005315|GO:0016021|GO:0030504|GO:0030505 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_99372_PI430048170 0.5063769100600891.06799790035919 3.4866202708963 3.57681054732376 3.84421858103778 P P P 3.59359137177339 3.57107272939259 3.48015583850617 P P P
LNCV6_99372_PI430048170 mRNA
ACAGACATCTTCAAAGAGCCTTCTTGGACATTCTGCTTTTTGCTCCTCATAACAGGCTTC NM_001242804 RefSeq chr18 + 57630301 57669276 LOC100505549 NA uncharacterized LOC100505549 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139271_PI430048170 0.0587340305345796 1.15512348866452 10.8936759357187 10.9363217627672 10.7382085377315 P P P 10.6022826964931 10.7480067690721 10.5960409433611 P P P LNCV6_139271_PI430048170 mRNA
GGCTGTGTTGAGCTGACATTCAAATGGATTCTTTAATAATAATGAAACTGGCGAGTATTT NM_001193457 RefSeq chr12 - 6539527 6556083 IFFO1 25900 "intermediate filament family orphan 1, transcript variant 5" GO:0005882 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100325_PI430048170 0.5694725474229990.9212582750643550.676258530578228

0.5380956030610450.38510141160127 A A A 0.4249376703076140.924161089586644
0.573584580995789A A A LNCV6_100325_PI430048170 mRNA
AAAGACCAGGATGTGGTACCAACTTTGGAAACGAAAGGTCTCTTGCCAACAGTATCTACT NM_080862RefSeq chr3
+ 141051401 141148611 SPSB4 92369 splA/ryanodine receptor domain and SOCS box containing 4
GO:0035556|GO:0005515|GO:0005737|GO:0016567 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131179_PI430048170 0.190399477285208 1.07455377467608 0.523687904108843
0.3376902197523140.445956365226772A A A 0.2799823143921810.365892757655828
0.354767841352362A A A LNCV6_131179_PI430048170 mRNA
ATGCAGTCCTCTCAAAGTGTTAAAGCTGTTTATTGAAAGTAATAAATGCTGATTTGCCTG NM_001008537 RefSeq
chrX - 74732855 74925452 KIAA2022 340533 KIAA2022
GO:0006261|GO:0042276|GO:0003887|GO:0016035|GO:0005634|GO:0007399 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128517_PI430048170 0.3751632221665441.03524212051942 0.419007198630031
0.2783987958904090.306829463800893A A A 0.27004650822672 0.312799176125455
0.274966786605417A A A LNCV6_128517_PI430048170 mRNA
CTCGTGCCTTATATTTGTGTGCCAATTAATGCCTAATAAATACCATGTGCTTAAACAAGT NM_000192RefSeq chr12
- 114353929 114408442 TBX5 6910 "T-box 5, transcript variant 1"
GO:0060045|GO:0005515|GO:0060044|GO:0035136|GO:0007389|GO:0010467|GO:0003700|GO:0006367|GO:0008
285|GO:0030262|GO:0003181|GO:0030324|GO:0003166|GO:0007267|GO:0005634|GO:0003281|GO:0051891|GO:0
030326|GO:0010719|GO:0003218|GO:0007507|GO:0005737|GO:0045944|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_102347_PI430048170 0.641194175254565 1.0193523039064 0.489227268755246
0.4715426483336290.365378808823197A A A 0.4925748190002650.372435828945248
0.378049516918632A A A LNCV6_102347_PI430048170 mRNA
GTGAATCTGCATTCAGGTGGCCAAGTATTTGCATTTCCTTCAGACCAGGCTATAATTGAA NM_020784RefSeq chr14
- 52430589 52552583 TXNDC16 57544 "thioredoxin domain containing 16, transcript variant 1"
GO:0005515|GO:0008150|GO:0005788|GO:0045454|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139478_PI430048170 0.0304476037276931.28740041420968 7.61239206517343
7.86948537358202 7.6347891524959 P P P 7.40517948055784 7.42490361783471 7.1966024543618
P P P LNCV6_139478_PI430048170 mRNA
TTCGGAGACCTATTTTGAGAGGTGATTGGAATAAAAGGTCCCGTCCGTGAGGAACTCTTT NM_012321RefSeq chr19
- 18306229 18323191 LSM4 25804 "LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae),
transcript variant 1"
GO:0008380|GO:0006397|GO:0005515|GO:0010467|GO:0030532|GO:0043928|GO:0005681|GO:0005688|GO:0005
829|GO:0000288 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105505_PI430048170 0.29734093415166 0.4493223081905620.392113324244016
0.3658221332012010.400685015045947A A A 0.8715956886278050.422092492570257
2.47432289898866 A A P LNCV6_105505_PI430048170 mRNA
GAATTCTTTGAACTTGTCAGTAAAGGAGAATACGATTGGAACATCAAAAACCATCGTGAT NM_016953RefSeq chr2
- 177623248 178072755 PDE11A 50940 "phosphodiesterase 11A, transcript variant 4"
GO:0004114|GO:0004118|GO:0004112|GO:0047555|GO:0046069|GO:0005575|GO:0046872|GO:0005829|GO:0007
165|GO:0030552|GO:0030553|GO:0007596|GO:0043204|GO:0006198 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129875_PI430048170 0.167933865731452 1.75252427525244 4.08753087261831
3.54047992153257 2.82707154207133 P P A 3.0638883573059 2.72333731670721
2.43911693095105 P P P LNCV6_129875_PI430048170 mRNA
GAGCCGCTGTCAACAGACAGTTTATTCTATATACAAACACAATTTTGTACACTGCAATTA NM_138690RefSeq chr19
+ 1000437 1009724 GRIN3B 116444 "glutamate receptor, ionotropic, N-methyl-D-aspartate 3B"

GO:0005262|GO:0005261|GO:0030054|GO:0005234|GO:0017146|GO:0030594|GO:0051205|GO:0035249|GO:0030
425|GO:0035235|GO:0034220|GO:0004972|GO:0045211|GO:0070588|GO:0051924|GO:0043025|GO:0016594|GO:0
042165 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142706_PI430048170 0.6137174736044121.05712615736317 10.3119731392192
10.2267122212839 9.99186322933643 P P P 9.86479683884062 10.2586971659651
10.1569813515597 P P P LNCV6_142706_PI430048170 mRNA
GCTAAGCACCTGTGGCTGCATTTTAACAGTAAAGGAGGCCGTTGTTTTCAGCGCAAAAAA NM_014984RefSeq chr17
- 81189592 81222951 CEP131 22994 "centrosomal protein 131kDa, transcript variant 1"
GO:0005515|GO:0008284|GO:0034451|GO:0005634|GO:0007283|GO:0042995|GO:0032403|GO:0030154|GO:0042
803|GO:0005829|GO:0043231|GO:0003674|GO:0000086|GO:0015630|GO:0005813|GO:0031965|GO:0006996|GO:0
005815|GO:0001669|GO:0005814|GO:0007275|GO:0090316|GO:0010824|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145671_PI430048170 0.00425277049065753 1.17828924983535 0.80617665228216
0.8534589100200150.847879616023733A A A 0.6533832302145740.567837704939551
0.575105432738088A A A LNCV6_145671_PI430048170 mRNA
GCGAACATTGGAATTGGTTCACTTTTAAAGTGCAGGTGTATATTTGTGGTAAAACGAAAT NM_001304548 RefSeq
chrX + 35919733 36385319 CFAP47 NA "cilia and flagella associated protein 47, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136796_PI430048170 0.5472930858181280.9786825267768350.25655208221363
0.2659039859664520.390622933074312A A A 0.3716861672820820.31055678007372
0.327324824734608A A A LNCV6_136796_PI430048170 mRNA
TCTCATCCAAGTGGTCTGTAGAATTCATGTCCCTTACAGTGGTCATTTAAAGTCAATATT NM_000216RefSeq chrX
- 8528873 8732186 ANOS1 NA Kallmann syndrome 1 sequence NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139321_PI430048170 0.00750768874491589 1.31151609773101 12.7640464690612
12.8544791588397 12.7551727638425 P P P 12.2928851114504 12.4198319618431 12.482936072977
P P P LNCV6_139321_PI430048170 mRNA
GGCCTCATGTTTTATCTGGTTCTTAAATGTTTGTTACTACAGAAAATAAAACTGCGCTAC NM_006014RefSeq chrX
- 154477768 154479257 LAGE3 8270 "L antigen family, member 3"
GO:0008150|GO:0003674|GO:0005634|GO:0005575|GO:0008033 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_139722_PI430048170 0.000926477735863264 0.1659566587300175.06113803826274
4.30920505467522 4.63806418055509 P P P 6.92554510373971 7.28521878763975
7.59335314844191 P P P LNCV6_139722_PI430048170 mRNA
GAATGCTCCCATCGAGGAAGTGTAACAATCCATGAAATGTGAATAAATGAAAAGTAAACA NM_007172RefSeq chr22
+ 45163844 45188009 NUP50 10762 "nucleoporin 50kDa, transcript variant 2"
GO:0005515|GO:0007077|GO:0010467|GO:0031965|GO:0005975|GO:0019083|GO:0019221|GO:0019058|GO:0046
907|GO:0044281|GO:0015031|GO:0055085|GO:0010827|GO:0008645|GO:0005737|GO:0015758|GO:0005643|GO:0
009405|GO:0016032|GO:0005654|GO:0051028|GO:0000278 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_132069_PI430048170 0.1876810051811161.27547801411444 9.95842402709382
10.0404514043299 10.4687772638594 P P P 9.56456038673769 9.76400889417832
10.0902102945995 P P P LNCV6_132069_PI430048170 mRNA
GATACACTTTGTACAACTATCCTGCAGCCCATTGGTTGCTTATATTTATCGCTTGGCTCA NM_198189RefSeq chr2
+ 237085440 237098846 COPS8 10920 "COP9 signalosome subunit 8, transcript variant 2"
GO:0048471|GO:0005737|GO:0008285|GO:0008180|GO:0007250|GO:0010388|GO:0005654|GO:0005634|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_70273_PI430048170 0.2871304455570851.94198210552466 2.20982264829325 0.374177682300785
1.75029292217761 A A A 0.89516170606497 0.6992600732470950.376853976500669A A A

LNCV6_70273_PI430048170 mRNA
TGGGCTAGACCCTGATTGAAAATTTGAATTTAAAAATAGATGCTGGCTCCACGGACTAAA NM_173648 RefSeq chr2
- 178829756 179050059 CCDC141 285025 coiled-coil domain containing 141
GO:0005515|GO:0005737|GO:0005815 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143943_PI430048170 0.21971722333937 2.4203029931256 0.288669729423276
1.55836805585209 2.34136461916541 A A A 0.3027104242512780.265286137342819
0.464785698994207 A A A LNCV6_143943_PI430048170 mRNA
GTAAAAGCTTATAGTTTTCTGATCTGTGTTAGAAGTGTTGCAAATGCTGTACTGACTTTG NM_033151 RefSeq chr16
- 48166910 48232271 ABCC1185320 "ATP-binding cassette, sub-family C (CFTR/MRP), member 11,
transcript variant 2"
GO:0005886|GO:0005887|GO:0008152|GO:0015711|GO:0042626|GO:0015216|GO:0008514|GO:0015865|GO:0055
085|GO:0005524|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144139_PI430048170 0.0278544884184059 0.3093812073235172.16782429805316
2.40429955747188 3.01435422166847 A A P 3.44092775437067 4.40161829390774
4.68682936814549 P P P LNCV6_144139_PI430048170 mRNA
GTTGAGCTTGGTTTTCTTATGAAAACATTGCATGATGGGCTAAAGATATCCAGACAATAA NM_001042533 RefSeq
chr3 - 97941816 97972451 MINA 84864 "MYC induced nuclear antigen, transcript variant 1"
GO:0001191|GO:0005667|GO:0005737|GO:0042254|GO:0005730|GO:0051213|GO:0005634|GO:0000122|GO:0046
872|GO:0006351|GO:0055114|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131623_PI430048170 0.17981670316323 0.9835286964820430.323006173849214
0.3593081613396030.354011809035541 A A A 0.3808825374352760.376443203107428
0.35096888411486 A A A LNCV6_131623_PI430048170 mRNA
GCTGCAGTCATAACTGAAAAATTGTATCTGCCTATAAGAAAGACTAAAACAGAAAAGGTG NM_001009612 RefSeq
chr20 + 1203453 1208274 C20orf202 400831 chromosome 20 open reading frame 202 NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137934_PI430048170 0.0175893045978733 0.5633169061887554.18885664043488
4.15067461644948 4.1024365596109 P P P 4.89249351676895 4.80339625381211
5.20059798978219 P P P LNCV6_137934_PI430048170 mRNA
GAACATAAAAAATTTGACTCCCTTTCCATGTGTCCACTGTTTCCTTGTGCCTTTTGATTA NM_016052 RefSeq chr1 +
218285286 218337983 RRP15 51018 ribosomal RNA processing 15 homolog (S. cerevisiae)
GO:0005739|GO:0005730|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135980_PI430048170 0.0100631694655574 1.31999096060635 14.2272893999474
14.3438512396251 14.1254710522831 P P P 13.941251227715 13.8193192468055
13.7352804682294 P P P LNCV6_135980_PI430048170 mRNA
CAGGGGTCACTGCAGTTTGGGATGGTTGAATGCTGTATTTTCTAAAGAATAAAATATTTT NM_007284 RefSeq chr3
- 52228609 52239167 TWF2 11344 twinfilin actin-binding protein 2
GO:0032532|GO:0048471|GO:0042989|GO:0071300|GO:0045773|GO:0032420|GO:0005546|GO:0030175|GO:0030
016|GO:0005524|GO:0030027|GO:0030426|GO:0003785|GO:0010592|GO:0051016|GO:0005737|GO:0071363|GO:0
032956|GO:0030837|GO:0005080|GO:0010976|GO:0030030|GO:0005856|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_76113_PI430048170 0.2083829055091341.13713471516838 6.68963384001018 6.7736461768504
6.75391261899667 P P P 6.75516327991121 6.40237724019314 6.48053966798652 P P P
LNCV6_76113_PI430048170 mRNA
AACAAAAATAGAGCATCAGCAACCCTTTCCAGGTAGAAATTCCAGCGGGAGTTCAGGTTC NM_014773 RefSeq chr5
+ 141923819 141942047 KIAA0141 9812 "KIAA0141, transcript variant 1"
GO:0008625|GO:0005739|GO:0005515|GO:0043281 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132498_PI430048170 0.3041696970137890.7107757152830662.99832002577414
2.77088685836771 2.46842865667422 A A A 3.80959537003616 2.8250372939567
2.91133298844985 P P P LNCV6_132498_PI430048170 mRNA

ACCAGCCCATCCCAGATCTTCCTTTATTAAAATAATAACTCTGAAAGCAGATGGAAAAAA NM_001261463 RefSeq chr10 - 113588823 113664070 NRAP 4892 "nebulin-related anchoring protein, transcript variant 3" GO:0005916|GO:0051371|GO:0008150|GO:0008270|GO:0003779|GO:0005927 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127442_PI430048170 0.0511238657627281 0.6925535760546866.81753619864141 6.70301741047289 7.15021507283995 P P P 7.37990451543412 7.46928662771632 7.44824683397345 P P P LNCV6_127442_PI430048170 mRNA
TCTCTGTCAAAACAGCCCCACTGATAATATTAGACAGAACGAGAATGCAGGGGTCTCTTC NM_014342RefSeq chr11 - 47617305 47642654 MTCH2 23788 mitochondrial carrier 2 GO:0016020|GO:0070585|GO:0097284|GO:0005743|GO:0005741|GO:0005634|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109158_PI430048170 0.115378387488598 1.82385377195151 2.5710531656158 3.18924570466457 3.04420906363549 A P P 2.47506477330042 1.25708788181289 2.27264025973629 P A A LNCV6_109158_PI430048170 mRNA
CAAGGCTACGATATTTTCTTATTGCAAAGCTTCAGTCAGAGCCATTACCCTTTCAAGCCC NM_004412RefSeq chr10 - 17142982 17202071 TRDMT1 1787 tRNA aspartic acid methyltransferase 1 GO:0090116|GO:0005737|GO:0001975|GO:0003886|GO:0003723|GO:0030488|GO:0008175|GO:0005634|GO:0003677 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128322_PI430048170 0.00122778619751901 0.5628691931827127.30177159922123 7.06779035191732 7.19347065779052 P P P 7.96327325401147 7.99543835038996 8.09774483168491 P P P LNCV6_128322_PI430048170 mRNA
TCCTGGTACTGTAATGAAAATAAGGTCTGCTCAACACAGTAAACGTTTCCTCTCTTCTTT NM_020120RefSeq chr2 + 128091179 128195675 UGGT1 56886 "UDP-glucose glycoprotein glucosyltransferase 1, transcript variant 1" GO:0005793|GO:0006457|GO:0005783|GO:0051084|GO:0005788|GO:0003980|GO:0051082|GO:0044267|GO:0070062|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143823_PI430048170 0.139741005344063 0.937093741267748 0.249345415949913 0.276773445963706 0.300067890458188 A A A 0.445804909001076 0.351073587625318 0.307473466628679 A A A LNCV6_143823_PI430048170 mRNA
CCATCTCTACTTTATTCTGAGGTATTCCACAATCCTCTTGTTGCAGGTGCTGCTAAAAAA NM_016370RefSeq chrX - 103822324 103832282 RAB9B 51209 "RAB9B, member RAS oncogene family" GO:0005515|GO:0005774|GO:0005886|GO:0005770|GO:0003924|GO:0005525|GO:0005764|GO:0006886|GO:0045335|GO:0006184|GO:0030670|GO:0042147|GO:0032482|GO:0019003|GO:0090385 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128160_PI430048170 0.0176913081385907 2.01211240858876 6.59948286987125 7.18415381499082 6.87786150504871 P P P 6.23474932951504 5.81311680008745 5.56642936920393 P P P LNCV6_128160_PI430048170 mRNA
TGAAGAAAAAGTTTATGCGAGTACATGATGCGGAGTCCTCCGATGAAGACGGCTATGACT NM_001267560 RefSeq chr19 + 3708336 3750813 TJP3 27134 "tight junction protein 3, transcript variant 1" GO:0005515|GO:0016324|GO:0030054|GO:0005654|GO:0005634|GO:0005923|GO:2000045 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_54803_PI430048170 0.0200238779396021.15760359081144 9.32517857180918 9.35045927123232 9.44637403690219 P P P 9.10440725508319 9.24418954354315 9.13914688065952 P P P LNCV6_54803_PI430048170 mRNA
TAACAACATTCTACAGAATGCTCAGGAACGACTGAGACGGCTAAACCACAGTGTTGCCAA NM_012437RefSeq chr1 + 153658653 153661852 SNAPIN 23557 "SNAP-associated protein, transcript variant 1" GO:0005515|GO:0030133|GO:0048490|GO:0048471|GO:0030054|GO:0032438|GO:0045202|GO:0006886|GO:0007269|GO:0031175|GO:0000149|GO:0016032|GO:0030672|GO:0031629|GO:0030141|GO:0030659|GO:0005794|GO:0008333|GO:0005730|GO:0043393|GO:0072553|GO:0048489|GO:0016079|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_134744_PI430048170 0.7515124285043041.04151829350667 6.90848199203755 7.0720219910735
6.71572475806378 P P P 7.27434413855778 6.7789390931456 6.33673701556185 P P P
LNCV6_134744_PI430048170 mRNA
AGGTCTGTGGCCCTTAGACAGTGAAGTCTTAATTGTCAATATTATTTTTGTCTAATTCTG NM_022336RefSeq chr2
- 108894470 108989372 EDAR 10913 ectodysplasin A receptor
GO:0005515|GO:0042346|GO:0005886|GO:0045177|GO:0006915|GO:0030154|GO:0007165|GO:0008544|GO:0043
473|GO:0042475|GO:0004872|GO:0060662|GO:0016021|GO:0001942|GO:0004888 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_82292_PI430048170 0.0601727439656948 1.2242167907443 12.0536597908222
12.2037822858932 12.337158396138 P P P 11.9556516025367 11.9145956032677
11.8611266571256 P P P LNCV6_82292_PI430048170 mRNA
TTGTGCTAACAATAAGAAGTACACGGGTTTATTTCTGTGGCCTGAGAAGGAAGGGACCTC NM_001183RefSeq chrX
+ 154428631 154436517 ATP6AP1 537 "ATPase, H+ transporting, lysosomal accessory protein 1"
GO:0008286|GO:0005215|GO:0005774|GO:0017137|GO:2001206|GO:0045851|GO:0016469|GO:0033180|GO:0055
085|GO:0005524|GO:0045669|GO:0006879|GO:0045921|GO:0033572|GO:0046961|GO:0045780|GO:0046933|GO:0
015991|GO:0070374|GO:0016021|GO:0010008|GO:0070062|GO:0051656|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132000_PI430048170 0.2089705876389540.8369257496508218.35728477339512
7.99939264408495 7.91653367037043 P P P 8.13553392922375 8.46181746899006
8.46139390623575 P P P LNCV6_132000_PI430048170 mRNA
ACACACTTCATGGAGGGACTCCTTTTCAATAAGAATTAGGAAGATGAGAAAGTAATTTGA NM_005441RefSeq chr21
+ 36385390 36416827 CHAF1B8208 "chromatin assembly factor 1, subunit B (p60)"
GO:0000790|GO:0006355|GO:0033186|GO:0006335|GO:0005634|GO:0006351|GO:0005829|GO:0006260|GO:0043
234|GO:0042393|GO:0005737|GO:0007049|GO:0006281|GO:0006461|GO:0031497|GO:0003682|GO:0005654|GO:0
051082 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_81834_PI430048170 0.3013345725741181.21224161235054 6.08557163635357 6.62687674622548
6.28599141479496 P P P 6.30116554900865 5.71198925702875 6.142466162812 P P P
LNCV6_81834_PI430048170 mRNA
TCTCTTATGGTGACATTCTGCATGTCATTAATGCCTCTGATGATGAGTGGTGGCAGGCAA NM_021120RefSeq chrX
+ 70444854 70505489 DLG3 1741 "discs, large homolog 3 (Drosophila), transcript variant 1"
GO:0005515|GO:0001736|GO:0008328|GO:0008285|GO:0005886|GO:0097120|GO:0007268|GO:0005615|GO:0030
426|GO:0016323|GO:0005737|GO:0043198|GO:0007411|GO:0045211|GO:0010923|GO:0032281|GO:0043025|GO:0
031625|GO:0019902|GO:0019903|GO:0004385|GO:0014069|GO:0008022|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144027_PI430048170 0.6168121971720091.03263061961077 0.276821079217789
0.2871561993632880.498951532221845 A A A 0.330736350125856 0.284840400485582
0.319054078609335 A A A LNCV6_144027_PI430048170 mRNA
ATGCTGTCATTAGCAACCATGCATTGTTGAAGACATATAGTGAGAAAATATGTCAGGTAT NM_001024603 RefSeq
chr7 - 124777291 124790810 C7orf77 NA putative uncharacterized protein LOC154872 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_140970_PI430048170 0.4114407598153081.05099805381231 0.310856819277173
0.3161900653757970.513296351864255 A A A 0.31670982812263 0.280983742587141
0.336189719157568 A A A LNCV6_140970_PI430048170 mRNA
TAGCTGCTTGGAGAGTCTATGTAGTTCTTTCTGCATGCATTAAAAATGTTTAGAAATGCT NM_012152RefSeq chr1
- 84813402 84893213 LPAR3 23566 lysophosphatidic acid receptor 3
GO:0030424|GO:0005886|GO:0051928|GO:0004930|GO:0032060|GO:0007268|GO:0007204|GO:0008289|GO:0048
672|GO:0000187|GO:0001965|GO:0005543|GO:0005887|GO:0007187|GO:0051482|GO:0070915 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_126910_PI430048170 0.0199849594473757 0.5243280987590462.25717826894475
2.25178492747593 2.75599072413688 A A A 3.65557451316012 3.36895213086652
3.02700576885969 P P P LNCV6_126910_PI430048170 mRNA
AGTACATATGGGAATAGTTGCATATGGGAATTTAAACCAACATGTGGCTGAGCCTTTTTT NM_007018RefSeq chr9
+ 121088295 121177608 CNTRL 11064 centriolin
GO:0005515|GO:0005813|GO:0005737|GO:0006996|GO:0016020|GO:0000086|GO:0000278|GO:0051301|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132030_PI430048170 0.00994742556526215 1.43153870490145 6.79781253083839
6.76620698550169 6.72558362007157 P P P 6.20977374482325 6.3693933989775
6.14961273263731 P P P LNCV6_132030_PI430048170 mRNA
CTATTAAAGAAAATGAGCTGCTGCCATCTTTTGTGGGCAGTTAGTCAGGTGCTGCTCTTT NM_013247RefSeq chr2
+ 74529404 74533556 HTRA2 27429 "HtrA serine peptidase 2, transcript variant 1"
GO:0005515|GO:0035631|GO:0016540|GO:0035458|GO:0004252|GO:0071300|GO:0005783|GO:0006672|GO:0005
634|GO:0005829|GO:0034605|GO:0005739|GO:0005758|GO:0048666|GO:0040014|GO:0006508|GO:0007628|GO:0
019742|GO:2001241|GO:0044257|GO:0005856|GO:0000785|GO:0010942|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137056_PI430048170 0.4424865134580011.11587876769059 7.4122238972309 7.7741459389605
7.56364715917013 P P P 7.0920904230246 7.5355425032348 7.6175290532523 P P P
LNCV6_137056_PI430048170 mRNA
TTTACCTATTGCTGTAAGAAATGACGATCCCCTTCCCATTAAAGAGAGTGCGTTGACCCC NM_001166175 RefSeq
chr5 - 173232103 173235312 NKX2-5 1482 "NK2 homeobox 5, transcript variant 2"
GO:0005515|GO:0003700|GO:0001190|GO:0006366|GO:0044212|GO:0003705|GO:0003285|GO:0003350|GO:0010
736|GO:0010735|GO:0010832|GO:0030878|GO:0048536|GO:0030154|GO:0042803|GO:0007512|GO:0001947|GO:0
010765|GO:0010667|GO:0055005|GO:0055007|GO:0055008|GO:0045823|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_92931_PI430048170 0.1096250359377390.8191755383023985.92661128729959 5.806357615042
6.07582489134952 P P P 6.10984405844194 6.11106168130065 6.43838246269465 P P P
LNCV6_92931_PI430048170 mRNA
GGTGGTTACCACAACAGAATGCTGCTCATTTTCTACTGTCTACAAATGATAAAACTATAA NM_001291310 RefSeq
chr10 + 131900643 131959834 PPP2R2D 55844 "protein phosphatase 2, regulatory subunit B, delta,
transcript variant 3"
GO:0010458|GO:0007165|GO:0050790|GO:0007067|GO:0005737|GO:0008601|GO:0000159|GO:0000278|GO:0051
301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127781_PI430048170 0.0979192241569334 1.18050130722954 11.5171103913393
11.5913097757117 11.3419263710375 P P P 11.3473172227441 11.3033415381974
11.0785814833384 P P P LNCV6_127781_PI430048170 mRNA
GTACATCTTGTTTGTAGCACACTTGAGTTTGTGTATTCCATTGACATCAAATGTGACAAT NM_018645RefSeq chr2
- 238238266 238240124 HES6 55502 "hes family bHLH transcription factor 6, transcript variant 1"
GO:0003712|GO:0005667|GO:0006355|GO:0003700|GO:0006357|GO:0046983|GO:0005634|GO:0003677|GO:0030
154|GO:0006351|GO:0008134|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131172_PI430048170 0.2894316861760550.7936542917655140.352356822972385
0.3287823908682270.305107699632434A A A 1.04919359509814 0.466625902026178
0.374676545011929A A A LNCV6_131172_PI430048170 mRNA
CAGTAGAGGATTGTTATATTTGCCTAAAAAACACGATTCCAATATATGACAAGGGCAGAT NM_002223RefSeq chr12
- 26335336 26833198 ITPR2 3709 "inositol 1,4,5-trisphosphate receptor, type 2"
GO:0005886|GO:0007202|GO:0044281|GO:0007173|GO:0006810|GO:0031095|GO:0005938|GO:0001666|GO:0048
010|GO:0048011|GO:0005220|GO:0048016|GO:0015085|GO:0030168|GO:0033017|GO:0043235|GO:0007165|GO:0
071361|GO:0006112|GO:0050796|GO:0016020|GO:0008543|GO:0007596|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_129334_PI430048170 0.0154469310214355 0.5888150578359394.23546272020946
4.22604386916527 3.90170409270178 P P P 4.59874780467105 4.97758285765153 5.0626166609449
P P P LNCV6_129334_PI430048170 mRNA
CGCTAAAAGGCTTACAGTATCAGACACGATCATGGTTTTAGATCCCATAATAAAAATGAA NM_004849RefSeq chr6
- 106184476 106325820 ATG5 9474 "autophagy related 5, transcript variant 1"
GO:0005515|GO:0060047|GO:0051279|GO:0009620|GO:0070257|GO:0005737|GO:2000619|GO:0042311|GO:0002
739|GO:0044233|GO:0031397|GO:0000045|GO:0032480|GO:0006995|GO:0006501|GO:0043066|GO:0005776|GO:0
000422|GO:0005930|GO:0042493|GO:0006914|GO:0006915|GO:0034045|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135744_PI430048170 0.7105652924611841.26846615701046 0.271241602201416
2.12488734668131 1.34276739837508 A A A 0.4191767790558591.73703246153171
0.78147204700505 A A A LNCV6_135744_PI430048170 mRNA
GGTTACTGTTGGGAGCTTAATGGTAGAAACTTCCTTGGTTTCATGATTAAACTCTTTTTTNM_001192RefSeq chr16 +
11965106 11968068 TNFRSF17 608 "tumor necrosis factor receptor superfamily, member 17"
GO:0007165|GO:0005886|GO:0008283|GO:0007275|GO:0004872|GO:0016021|GO:0012505|GO:0002376 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137933_PI430048170 0.0242241231514279 3.2487259605287 2.50982836788413
3.28532465650547 2.0567721761527 A P A 0.4840406589679040.869629950004229
1.49005191648064 A A A LNCV6_137933_PI430048170 mRNA
GACTGTTAGTTGCCTCAAAGTACCCTGAAAGCAAAGGGGTATTTCAAGTACGGAAAAAGA NM_001017971 RefSeq
chr5 + 82279461 82318646 ATP6AP1L 92270 "ATPase, H+ transporting, lysosomal accessory protein
1-like" GO:0046961|GO:0046933|GO:0015991|GO:0033180|GO:0016021 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_127473_PI430048170 7.0382280630388e-05 0.4447033164230585.28797322600774
5.15584602155523 5.15637160330227 P P P 6.34105595986023 6.2990673144098
6.46610295220938 P P P LNCV6_127473_PI430048170 mRNA
GCTGCTGGCAACACATTTTGTTGTGGGCTCCTTAATTTAATGATAAAATTTAAGCTAAAC NM_004161RefSeq chr2
- 65086853 65130301 RAB1A 5861 "RAB1A, member RAS oncogene family, transcript variant 1"
GO:0005515|GO:0003924|GO:0006886|GO:0032402|GO:0005829|GO:0047496|GO:0007030|GO:0034446|GO:0030
252|GO:0032482|GO:0000045|GO:0016192|GO:0042742|GO:0070062|GO:0042470|GO:0090110|GO:0006914|GO:0
019068|GO:0005525|GO:0006897|GO:0006888|GO:0006184|GO:0042384|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_73200_PI430048170 0.3140061108771851.14486016763754 4.34308288320357 4.31161355123237
4.47505677260968 P P P 4.2191532865549 3.86952796046215 4.40983974249582 P P P
LNCV6_73200_PI430048170 mRNA
ACTCTATCGCCATTTCAAGCTGGTGATGAAGGCCTACAGGGACACTATAAAGATATTGCA NM_018130RefSeq chr3
- 72749276 72848447 SHQ1 55164 "SHQ1, H/ACA ribonucleoprotein assembly factor"
GO:0005515|GO:0005737|GO:0043065|GO:0015030|GO:0022618|GO:2000233|GO:0005730|GO:0005654|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126944_PI430048170 0.000740061732812546 0.1692800467995710.475858783291801
0.3962228887919261.03607154490987 A A A 2.90711541409777 3.35229108447908
3.37713786590314 P P P LNCV6_126944_PI430048170 mRNA
CAGACATCTGGAAGATTGCTCTAGTGGAGTAAAACATCTTAATGTATTTTGTCCCTAAAT NM_003620RefSeq chr17
+ 60600182 60666279 PPM1D 8493 "protein phosphatase, Mg2+/Mn2+ dependent, 1D"
GO:0009314|GO:0005515|GO:0009617|GO:0035970|GO:0008285|GO:0006470|GO:0000086|GO:0005634|GO:0004
722|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129724_PI430048170 0.1099920462589780.8063012243743044.76811761513366
4.96629648511904 5.16730874776445 P P P 5.11071749765532 5.27646211151406
5.45357047486908 P P P LNCV6_129724_PI430048170 mRNA

CTTCTGATCCTGGTGGCCTTATTTTTGCTATGTTAAGGTTGTGTTTTTTAATACTTGGAT NM_001172831 RefSeq chr5 - 150894391 150904983 ZNF300 91975 "zinc finger protein 300, transcript variant 1" GO:0005515|GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66600_PI430048170 0.0689648144851825 0.8159432020926897.16186803660536 6.9259474323501 6.85617633224626 P P P 7.21240494473438 7.29233513163985 7.33502494478606 P P P LNCV6_66600_PI430048170 mRNA
CCCCCCAATGACATCTTACCATAGGATGCTATTACACAGAGTAGCCGCTTACTTTGGATT NM_001282798 RefSeq chr2 + 135586322 135725270 R3HDM1 23518 "R3H domain containing 1, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144313_PI430048170 0.0462277613825635 0.5282774217328424.38921378092614 3.57586148710875 4.2884466667747 P P P 4.88086989049428 4.93785368722696 5.28963991687809 P P P LNCV6_144313_PI430048170 mRNA
GGTAAATGGTGCTGTTGGAGACATTTTTATCTTCATACCAGGCTCTGTTTCATCCCTGCA NM_032875RefSeq chr17 - 39252643 39401656 FBXL20 84961 "F-box and leucine-rich repeat protein 20, transcript variant 1" GO:0005737|GO:0001662 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129055_PI430048170 0.24744512266094 0.8616868322603588.68259319419221 8.44310572082514 8.70951328219781 P P P 8.5964654075821 8.83745511475925 9.02802736762763 P P P LNCV6_129055_PI430048170 mRNA
TTGGGGTTGTTTTTGTTTTTTCTTGCCAGGTAGATAAAACTGACATAGAGAAAAGGCTGG NM_001618RefSeq chr1 - 226360690 226408100 PARP1 142 poly (ADP-ribose) polymerase 1 GO:0005515|GO:0010467|GO:0016540|GO:2000679|GO:0006367|GO:0006366|GO:0005634|GO:0005635|GO:0042802|GO:0006302|GO:0003950|GO:0006471|GO:0051287|GO:0000723|GO:0042769|GO:0045944|GO:0030225|GO:0007179|GO:0005667|GO:0032869|GO:0071451|GO:0023019|GO:0005730|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130245_PI430048170 0.3005231063837011.61939341156545 0.646311681855862 1.80031935823441 0.486124647978409A A A 0.5075533041668830.414201395607352 0.296359139238699A A A LNCV6_130245_PI430048170 mRNA
AGTTGAAGAGGATTGACCTCTCCAACAACCTCATTTCCTCCATCGATAATGATGCCTTCC NM_014359RefSeq chr1 + 203494142 203508949 OPTC 26254 opticin GO:0016525|GO:0005578|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72544_PI430048170 0.9396322842649941.00731424834773 7.17968437690833 7.14149154636592 7.39191833645674 P P P 7.28339924384867 7.16667946416397 7.24187147847311 P P P LNCV6_72544_PI430048170 mRNA
TGCAGCCTCGACCTGGTCACTTTATTTCCATAGAAGACAATAAGGTTCTGGGAACACATA NM_018006RefSeq chr22 + 46335400 46357340 TRMU 55687 "tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase, transcript variant 1" GO:0016783|GO:0005739|GO:0000049|GO:0005524|GO:0008033 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131682_PI430048170 0.2309202790322730.7456980359613446.26565251778454 5.93968894507188 6.0951774280716 P P P 6.02901344327998 6.66120774647305 6.7899650305112 P P P LNCV6_131682_PI430048170 mRNA
GAGGCCTTTCTGTGAACAGCATCATAACTTCTATCATGGAAAGTGTACTATATATAATGT NM_004667RefSeq chr15 - 28111036 28322152 HERC2 8924 HECT and RLD domain containing E3 ubiquitin protein ligase 2 GO:0005515|GO:0032183|GO:0004842|GO:0016567|GO:0005814|GO:0016874|GO:0005743|GO:0005634|GO:0007283|GO:0006886|GO:0006974|GO:0043547|GO:0005085|GO:0005737|GO:0006281|GO:0042787|GO:0016020|GO:0008270|GO:0031625|GO:0020037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128767_PI430048170 0.3843935990231150.7710977471726240.297093844226426 0.3232178261953540.356649134608032A A A 0.3876936719345220.324607459960958 1.21153796987644 A A A LNCV6_128767_PI430048170 mRNA

CTGAGATCAAATATCTCATCAGATGACTGGATGCTTAGAATCGGGTTAACTTGATTAAAT NM_004263 RefSeq chr2 + 74654227 74683854 SEMA4F 10505 "sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F, transcript variant 1" GO:0031290|GO:0016020|GO:0005886|GO:0030517|GO:0007411|GO:0005887|GO:0005783|GO:0045211|GO:0007267|GO:0004872|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_140465_PI430048170 0.250784283038857 1.2155638849197 10.0960807122835 10.0649754944914 10.0974474053562 P P P 9.39845829506986 9.95570681028913 9.98726874997951 P P P LNCV6_140465_PI430048170 mRNA
GGAGTTAATTAAGAGAATGACCAAGCTCAGTTCAATGAGCAAATCTCCATACTGTTTCTT NM_001444 RefSeq chr8 + 81280482 81284777 FABP5 2171 fatty acid binding protein 5 (psoriasis-associated) GO:0005515|GO:0006629|GO:0005215|GO:0005504|GO:0005829|GO:0008289|GO:0005737|GO:0008544|GO:0015758|GO:0006006|GO:0005654|GO:0006656|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_131610_PI430048170 0.429596836140635 0.932764204105138 10.6666123684212 10.3021227129111 10.3900005244437 P P P 10.5117956375341 10.5650412902589 10.6070946234817 P P P LNCV6_131610_PI430048170 mRNA
CCAGGCGGGAGCGGCTATTTTTCCTAAATGAGAATTGTTACATTGCAAATTGTTGAATAA NM_014866 RefSeq chr9 - 136440095 136483055 SEC16A 9919 "SEC16 homolog A (S. cerevisiae), transcript variant 1" GO:0005737|GO:0005794|GO:0000139|GO:0021762|GO:0005789|GO:0048208|GO:0015031|GO:0007029|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_93590_PI430048170 0.262730112680563 0.548722993255819 2.88762440387996 0.26823503356385 1.99574487394948 A A A 2.44754922273834 3.32575546077342 2.90078184542963 P P P LNCV6_93590_PI430048170 mRNA
CTGTGTGTCCTTCTAACAGTGTGAATCATAACTCCTACAATGGAAAGGAAACTAAAAATA NM_006197 RefSeq chr8 + 17922856 18029948 PCM1 5108 pericentriolar material 1 GO:0005515|GO:0034453|GO:0034451|GO:0031122|GO:0036064|GO:0005829|GO:0042802|GO:0005737|GO:0050768|GO:0000086|GO:0022027|GO:0071539|GO:0000242|GO:0097150|GO:0031965|GO:0005813|GO:0006996|GO:0031513|GO:0090316|GO:0051297|GO:0042384|GO:0043234|GO:0016020|GO . NA - . NA NA NA NA NA NA NA NA NA LNCV6_93197_PI430048170 0.338229094163954 0.785873199733712 2.86077198145639 2.63952885396716 2.79250212988485 A A A 3.13050387211734 3.47128320324696 2.61830992704274 P P P LNCV6_93197_PI430048170 mRNA
TCTTCAAGATCTCTGAGACTGCGGGTACCCGGAAAGGGAGCATGAGCAATGGGCATGGCA NM_005967 RefSeq chr12 + 57088893 57095476 NAB2 4665 NGFI-A binding protein 2 (EGR1 binding protein 2) GO:0014037|GO:0001958|GO:0008283|GO:0042552|GO:0003714|GO:0045682|GO:0016480|GO:0005634|GO:0006351|GO:0008134|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_92423_PI430048170 0.0033758741319302 2.27672360112806 6.48617894717073 6.73031442980446 6.80662254699433 P P P 5.36147028158594 5.31819462289412 5.75945370075052 P P P LNCV6_92423_PI430048170 mRNA
GTTGCAGAAATTCCACAAGCCTCTTGCAACTTTTTCCTTTGCAAACCACACGATCCAGAT NM_001127395 RefSeq chr2 - 207609114 207625331 METTL21A 151194 "methyltransferase like 21A, transcript variant 2" GO:0005515|GO:0018022|GO:0005737|GO:0043462|GO:0006479|GO:0051117|GO:0030544|GO:0016279 . NA - . NA NA NA NA NA NA NA NA NA LNCV6_132365_PI430048170 0.83355470854239 1.14291507162901 1.98440925286777 3.39540466767687 3.03830427391901 A P P 3.05026523396335 2.69900626209446 2.34474642008267 P P P LNCV6_132365_PI430048170 mRNA
GGAACTTTCTTTGTTCTTCAGTAGTTACTTTTTTCCTTACCTAAAAGGGTTGTCTGTCAA NM_002146 RefSeq chr17 - 48548869 48574448 HOXB3 3213 homeobox B3 GO:0003700|GO:0051216|GO:0021546|GO:0060216|GO:0005634|GO:0048704|GO:0000122|GO:0001525|GO:0030878|GO:0009952|GO:0000979|GO:0006351|GO:0021615|GO:0050767|GO:0002244|GO:0060324 . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_134733_PI430048170 0.2249169467387541.19411973862468 4.96182201698637
5.35620127972047 4.89834042417829 P P P 4.73014729061818 4.79729335930131
4.95555606876291 P P P LNCV6_134733_PI430048170 mRNA
GAAAACAATGAGTAGTGACGTCACCAAGGCAGCCGTCGAAAGCCCAGTCCCAAAGCCGTC NM_178518RefSeq
chr17 + 7435442 7437679 TMEM102 284114 transmembrane protein 102
GO:0005515|GO:2000406|GO:0005886|GO:0009986|GO:0050730|GO:0010820|GO:0006915|GO:0045785|GO:0005
622|GO:0007165|GO:0043234|GO:0016021|GO:0034097 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137728_PI430048170 0.0611098961265773 1.04582667897801 0.419172643185062
0.4591105176825480.462285505101378A A A 0.3515109828726090.375934667366344
0.418785077464782A A A LNCV6_137728_PI430048170 mRNA
AAAGGGAAGAGAGTTGATGTTTTCAGTGTGTTTCCAGTGCCAGACAGTCTTGGTCCTGAA NM_001794RefSeq chr20
+ 61252425 61940617 CDH4 1002 "cadherin 4, type 1, R-cadherin (retinal), transcript variant 1"
GO:0005886|GO:0007411|GO:0005887|GO:0034329|GO:0005509|GO:0045773|GO:0007155|GO:0007156|GO:0045
216|GO:0007157|GO:0034332 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94013_PI430048170 0.82222708032364 1.08976184873016 3.10144888476408 2.11790506028962
2.91554059546037 A A P 2.37057558997629 2.58404252944822 2.92883068011753 A A P
LNCV6_94013_PI430048170 mRNA
GTGACCCTGGGTGACCCAAATGTGACCACACCATCGAGCTCAGTCGGCTTAACCAACATC NM_001282934 RefSeq
chr21 - 41798224 41879482 PRDM15 63977 "PR domain containing 15, transcript variant 3"
GO:0006355|GO:0008168|GO:0005634|GO:0032259|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_51838_PI430048170 0.1424895687975831.29065563633644 3.3869198341158 3.52400776357251
3.75604262052413 P P P 2.99699001525246 3.01667715058829 3.51220300998741 P P P
LNCV6_51838_PI430048170 mRNA
AGAGAGGAGGTGCAGTTGGTGGGTGCCAGCCACATGGAGCAAAAGGCCACGGCACCTGAA NM_153813RefSeq
chr16 + 88453605 88535166 ZFPM1 161882 "zinc finger protein, FOG family member 1"
GO:0032091|GO:0005515|GO:0071733|GO:0045599|GO:0003181|GO:0045403|GO:0005634|GO:0046872|GO:0007
507|GO:0060318|GO:0005737|GO:0060319|GO:0060377|GO:0045078|GO:0017053|GO:0001085|GO:0032642|GO:0
030851|GO:0035162|GO:0055008|GO:0030220|GO:0001102|GO:0005667|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_127837_PI430048170 0.4329723949944091.32752090208931 1.41601531507446
0.4362673985043480.386689383489533A A A 0.4325398960637990.39149773918335
0.436012461640279A A A LNCV6_127837_PI430048170 mRNA
GGGACTGTTTCAGACTTGGAAAGGTCACAGAAGGAAAATAATATTATATAAAGTGACAAC NM_015849RefSeq chr1
+ 15476100 15491400 CELA2B 51032 "chymotrypsin-like elastase family, member 2B"
GO:0004252|GO:0006508|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139095_PI430048170 0.45057476337277 0.7589309191766133.68860858928635
0.3244062657952282.20638514518094 P A A 3.45481746021323 3.04205225574396
2.46440784401485 P P P LNCV6_139095_PI430048170 mRNA
AGATACAGCTGCTGCCACCCATCATGCTATGGGGGATACTGGTCTTCTGGATTCTATTGA NM_181614 RefSeq
chr21 - 30561097 30561289 KRTAP19-7 NA keratin associated protein 19-7 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129757_PI430048170 0.00996348952043875 1.36807754190716 7.2355987092774
7.36321386779164 7.49102825349566 P P P 7.00575335683736 6.82829400286826
6.90513936374056 P P P LNCV6_129757_PI430048170 mRNA
TTCTCTGAAAAAACGAGGTAATTCCCTGAGCCCAACCCTGATCCTCAAGGACCTGTAATT NM_178820 RefSeq
chr19 - 39024020 39032596 FBXO27 126433 F-box protein 27
GO:0005515|GO:0001948|GO:0019005 . NA - . NA NA NA NA NA NA NA NA

NA
LNCV6_130456_PI430048170 0.429493799943602 1.86122553420746 2.33963539939504
0.409556581964324 0.556333109939855 A A A 0.41412993903411 0.518127198944965
0.544713205585591 A A A LNCV6_130456_PI430048170 mRNA
CAGAATGGGAAACTGGTATATCCCAGTTGTGAAGAAAAATAGAATCAATGGCATTACTAT NM_005666 RefSeq
chr1 + 196943803 196959226 CFHR2 3080 complement factor H-related 2 GO:0005576 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_140868_PI430048170 0.0554014576063737 0.314490671110796 0.40632931210889
2.02400259190196 1.25474197316315 A A A 2.86836285999259 3.20213615567696
3.04064494836432 P P P LNCV6_140868_PI430048170 mRNA
CTAGGTCAGATTTTTACATCTCTTTCTAGCAAGAAGAGACAAGATTTTGTGCATTTGTAC NM_182898 RefSeq chr7
+ 28412524 28825894 CREB5 9586 "cAMP responsive element binding protein 5, transcript variant
1"
GO:0043565|GO:0005515|GO:0001077|GO:0003700|GO:0006366|GO:0045944|GO:0045444|GO:0005634|GO:0045
893|GO:0060612|GO:0046872|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_131332_PI430048170 0.396991697590266 1.25548809183775 0.384903471189574
1.17456525325851 0.399533158001372 A A A 0.38057560453962 0.350051772151324
0.391922940607021 A A A LNCV6_131332_PI430048170 mRNA
ATATACGTTTGAGCTGAGGGACAGTGGAACATATGGGTTTGTTCTGCCAGAAGCTCAGAT NM_173077 RefSeq
chr2 + 206939553 206969474 CPO 130749 carboxypeptidase O
GO:0006508|GO:0008270|GO:0005576|GO:0004181 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_141610_PI430048170 0.601412671840454 0.906326444698663 0.346737138727634
0.331721953269189 0.281079283994585 A A A 0.246087932543527 0.814402352491793
0.248339741352156 A A A LNCV6_141610_PI430048170 mRNA
GAGGTCCGTGTGTGACTTTGAGCAAAAAGTGACTTCTTTTTGTGAATGTAAAATTTGTGA NM_016540 RefSeq
chr11 - 94377310 94401419 GPR83 10888 G protein-coupled receptor 83
GO:0004983|GO:0005886|GO:0007218|GO:0004930|GO:0051384|GO:0031513|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_69561_PI430048170 0.458699353756562 1.35794406322111 2.18980268772092
2.29592119785416 1.09841573968096 A A A 1.24227231733242 2.29585509414052
0.352416997836872 A A A LNCV6_69561_PI430048170 mRNA
CTTTGAAAACCACTCAGCCCTGGAGATCGCGGAGCAGCTGACCCTGCTAGATCACCTCGT NM_002891 RefSeq
chr15 - 78959946 79090873 RASGRF1 5923 "Ras protein-specific guanine nucleotide-releasing factor
1, transcript variant 1"
GO:0043005|GO:0035020|GO:0005886|GO:0007616|GO:0007264|GO:0008283|GO:2000310|GO:0007268|GO:0046
579|GO:0046578|GO:0032863|GO:0031175|GO:0005829|GO:0030426|GO:0005085|GO:0007165|GO:0048168|GO:0
032320|GO:0048167|GO:0035254|GO:0005089|GO:0005088 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_129227_PI430048170 0.52764972057847 0.742301557713604 3.48416542052805
3.82008941891764 3.83358976245351 P P P 4.82944368136659 3.78962301865409
3.4656971705839 P P P LNCV6_129227_PI430048170 mRNA
CTGTTATCATTCCTCCCCAACATAATAATACATAAAGTGGCATGGTATTTTTTCTGATGC NM_032496 RefSeq
chr12 - 57472254 57479850 ARHGAP9 64333 "Rho GTPase activating protein 9, transcript variant 1"
GO:0043547|GO:0051056|GO:0007264|GO:0005547|GO:0005829|GO:0005096 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_66028_PI430048170 0.0522480598320547 1.13750076693782 14.1475481178929
14.3225215816952 14.2772767436006 P P P 14.1414849205329 14.0096561704883

14.0409570528822 P P P LNCV6_66028_PI430048170 mRNA
GGTAAAAAGGGAAGGATGAGGCTCCCCCAATGTCACATTAAATTCATGGTTTTCATTCAA NM_181575 RefSeq chr2
- 74526647 74529897 AUP1 550 "ancient ubiquitous protein 1, transcript variant 2"
GO:0005515|GO:0016020|GO:0005789|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144959_PI430048170 0.0545641517442896 0.5596091000409923.72661599533744
3.15815037611809 3.97466130875877 P P P 4.34656443713259 4.45894976547035
4.66472526027099 P P P LNCV6_144959_PI430048170 mRNA
CCAAACAACATAAAAGACAATGTCCCTTCTTCAAAAGTGCCAAAAGGAATGTAAAATGCA NM_022571 RefSeq chr14
- 59463521 59465341 GPR135 64582 G protein-coupled receptor 135
GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140095_PI430048170 0.6314122733232630.9368536861081251 0.1463302220956
9.91018274345477 9.61535461904423 P P P 10.102741338829 10.1160678081774
9.75588059941678 P P P LNCV6_140095_PI430048170 mRNA
TCTACACCCAGTGAATGCCCCATGTAAAAACATGATGATAAAACAGCAAAGCACAAAAAA NM_006929 RefSeq
chr6_GL000256v2_alt + 3259992 3270944 SKIV2L 6499 superkiller viralicidic activity 2-like (S.
cerevisiae) GO:0004004|GO:0003723|GO:0008152|GO:0005654|GO:0005634|GO:0055087|GO:0005524 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134717_PI430048170 0.0704743854378256 0.5276545013217243.35794898436247
2.37839370585947 3.25360043726531 P A P 3.5855834472871 4.04265221618271
4.23840079022067 P P P LNCV6_134717_PI430048170 mRNA
TTAGAGTCTGAGTGATGACCAAGATTCTGTGTGTTACTACTGTTTGTTTAATAGGAACAA NM_020130 RefSeq chr8
+ 40153467 40155308 C8orf4 56892 chromosome 8 open reading frame 4 GO:0006915 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_111575_PI430048170 0.9516595774359161.00206990845965 8.1952178194938
8.02542733416053 7.99745914656657 P P P 7.92625576284765 8.26781152047963
8.00034663722022 P P P LNCV6_111575_PI430048170 mRNA
TTTATTCTCTGGGTCCAGCTCCATACCCTAAATTCTGAGTTTCAGCCACTGAACTCCAAG NM_007243 RefSeq
chr6_GL000255v2_alt - 1943160 1946534 NRM 11270 "nurim (nuclear envelope membrane
protein), transcript variant 1"
GO:0008150|GO:0003674|GO:0016020|GO:0005637|GO:0005654|GO:0005634|GO:0016021|GO:0005635 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89638_PI430048170 0.9495352053623790.9978133092429673.130397089211 3.59938044402847
3.65645394333083 P P P 3.36340216087816 3.37332098704574 3.68997039809819 P P P
LNCV6_89638_PI430048170 mRNA
GATAGAAATTGATTATTTTTATGATAGCAGTATTCAGGATCTCATCACCTTTGCCCGTGT NM_032288 RefSeq chr3
+ 197749752 197784446 FYTTD1 84248 "forty-two-three domain containing 1, transcript variant 1"
GO:0005515|GO:0006406|GO:0016607|GO:0005654|GO:0003729 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_126670_PI430048170 0.2396606995057340.5882198854215991.85415334394891
2.31969957478859 0.497756776911298 A A A 1.99289692640121 2.92999814148523
2.44161024986568 A P P LNCV6_126670_PI430048170 mRNA
CAGGTGTTCTTTGTTTGCCTTTGATAAAATACAGGATTTAAGAACAGAGAGTACTGCAAA NM_014498 RefSeq chr3
- 168008672 168095925 GOLIM427333 golgi integral membrane protein 4
GO:0005801|GO:0005794|GO:0016020|GO:0005796|GO:0032580|GO:0006810|GO:0030139|GO:0005654|GO:0016
021|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129538_PI430048170 0.4518587307275521.05118256673806 8.36032623028651
8.12581259964302 8.19597065302807 P P P 8.24650824453245 8.1100122091806 8.1155080824404
P P P LNCV6_129538_PI430048170 mRNA

CTTAAATGGAACAGAAGTTTATGTGTCCAAATGATGGAATCATTAAACCTGAGTGACTTG NM_024523RefSeq chr7 - 127580627 127585600 GCC1 79571 GRIP and coiled-coil domain containing 1
GO:0005515|GO:0005737|GO:0005794|GO:0005886|GO:0000139|GO:0000042 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141035_PI430048170 0.6824456722887850.9437336135650759.08536897269616 8.97496503212711 9.32950291181583 P P P 8.97960249039513 9.17982455721693 9.46299307350375 P P P LNCV6_141035_PI430048170 mRNA
GTTAGGGCTATCTCAGGCAATATGGCCACACCTGGGTCTTTATGCATGAAGATAATGTAA NM_016320RefSeq chr11 - 3675009 3797792 NUP98 4928 "nucleoporin 98kDa, transcript variant 1"
GO:0005515|GO:0007077|GO:0005215|GO:0010467|GO:0000059|GO:0019221|GO:0019058|GO:0044281|GO:0005635|GO:0051292|GO:0005829|GO:0008645|GO:0015758|GO:0005643|GO:0016032|GO:0017056|GO:0006999|GO:0042277|GO:0031965|GO:0005975|GO:0019083|GO:0055085|GO:0010827|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128507_PI430048170 0.3763123561593731.02090952010687 0.332009791511508 0.2440666608763790.305580984501699A A A 0.2666195731200640.258911810887027 0.267950379736048A A A LNCV6_128507_PI430048170 mRNA
GGCATGGGAAGACCAAAACCATGTGGCAGTTCCTGTTTTTGATTTTATTATATATATGTA NM_198074RefSeq chr1 - 247530131 247533839 OR2C3 81472 "olfactory receptor, family 2, subfamily C, member 3"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68558_PI430048170 0.5606379667079131.1876223841991 2.46321329522993 2.97608246306263 3.44271536616942 A P P 2.89198837523458 2.52070485077632 2.86048655377453 P P P LNCV6_68558_PI430048170 mRNA
GCAATATTTAATTCAGCCTTTGGAAGTTTTTTGGGCATCGTTATAACACCCCTGCTCCTG NM_001300842 RefSeq chr4 - 146253980 146521971 SLC10A7 84068 "solute carrier family 10, member 7, transcript variant 4"
GO:0016021|GO:0006814|GO:0055085|GO:0015293 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_109341_PI430048170 0.2321044065200410.8707505104818828.50638170598144 8.62724063435147 8.48252174173221 P P P 8.89622345336056 8.78702078807614 8.50902899025683 P P P LNCV6_109341_PI430048170 mRNA
GACTGGTCCAGAAATGGGGGACTGTGATAGAGAATCTTTAATAAAGTGGCTTTTCCCACC NM_012139RefSeq chr11 - 17788049 18013162 SERGEF 26297 "secretion regulating guanine nucleotide exchange factor, transcript variant 1"
GO:0005515|GO:0007165|GO:0005737|GO:0050709|GO:0005730|GO:0005634|GO:0045111|GO:0005087|GO:0032853 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_120047_PI430048170 0.5799408059215620.9014179504305150.298708105278097 0.3073006102765250.569314632953391A A A 0.3585039161502450.308504723934348 0.897514608401995A A A LNCV6_120047_PI430048170 mRNA
TCCTGTCATCCTGCCAGGAATGAAAGACATTAAAGGAGAGAAAGGAGATGAAGGGCCTAT NM_001846RefSeq chr13 + 110307283 110513026 COL4A21284 "collagen, type IV, alpha 2"
GO:0005515|GO:0005587|GO:0071560|GO:0005576|GO:0001525|GO:0035987|GO:0006351|GO:0006898|GO:0043231|GO:0031012|GO:0022617|GO:0007411|GO:0030198|GO:0016525|GO:0030574|GO:0005788|GO:0070062|GO:0005201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134810_PI430048170 0.8552156448639560.9510152291947373.25179669059876 2.4327940221987 2.29834007628683 P A A 2.18043587269107 3.16209904723895 2.8839539530568 A P P LNCV6_134810_PI430048170 mRNA
ATAAGCCCATCCATCTCTTTTATTCATGAACAGAGACAGAAAGAGTGCTTGGCATGGCAT NM_001037558 RefSeq chr11 + 124919249 124920677 HEPN1 641654 "hepatocellular carcinoma, down-regulated 1"
GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143650_PI430048170 0.00452462416132351 0.3718047057374799.34571415663999

9.40351865371566 9.41538263405198 P P P 10.7025911736448 10.6945618990712
11.0253112355429 P P P LNCV6_143650_PI430048170 mRNA
AAGTTCTATGGCTGTCACCTTAATTACTCAATAAACTTGCTGGTGTTCTGTGGACGTAAA NM_000187 RefSeq chr3
- 120628167 120682571 HGD 3081 "homogentisate 1,2-dioxygenase"
GO:0034641|GO:0006559|GO:0004411|GO:0044281|GO:0006572|GO:0046872|GO:0070062|GO:0055114|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127209_PI430048170 0.3164996960183860.8932491894844811.5439197745659
11.5825625103559 11.5531697596423 P P P 11.4925448062795 11.7620195198453
11.8863617760619 P P P LNCV6_127209_PI430048170 mRNA
GGGCCATGTAGCTGCCTTTGTTACTCTATTTATTTTAGTCACTTGTATAAAACACCAAAT NM_004422 RefSeq chr17
- 7225341 7234544 DVL2 1856 dishevelled segment polarity protein 2
GO:0005515|GO:0006366|GO:0005886|GO:0061098|GO:0090263|GO:0005634|GO:0043621|GO:0005829|GO:0042
802|GO:0007507|GO:0005109|GO:0044340|GO:0051091|GO:0005737|GO:0090103|GO:0043507|GO:0016055|GO:0
022007|GO:0090090|GO:0060070|GO:0060071|GO:0007379|GO:0019904|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141040_PI430048170 0.2277706444224090.751269770166501 5.35214208936939
5.39336191074965 5.35571938083783 P P P 5.47479591497493 6.18082114873424
5.57905636742064 P P P LNCV6_141040_PI430048170 mRNA
AACAAACAAAAGGCAATGTCTTCTGGTTGTGGTTATTTCCTTTCCTGCTTGCCTCCCCAG NM_014286 RefSeq chr9
+ 130172577 130237304 NCS1 23413 "neuronal calcium sensor 1, transcript variant 1"
GO:0005515|GO:0030424|GO:0048471|GO:0000287|GO:0030054|GO:0005245|GO:0005886|GO:0019901|GO:0048
015|GO:0005509|GO:0031045|GO:0014069|GO:0030425|GO:0043231|GO:0005829|GO:0045921|GO:0005737|GO:0
045211|GO:0032580|GO:0010975|GO:0070588|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_141129_PI430048170 0.591434170934946 0.977956795399146 13.6902670325324
13.5672399357367 13.5569047524379 P P P 13.6002397044841 13.6032105985353
13.7086221236711 P P P LNCV6_141129_PI430048170 mRNA
TAAAGTCATGTGGGCCACACAAGTGCAGTAGTGCAGTTCACCATGAGGGAAGAATAAAGA NM_000475 RefSeq
chrX - 30304421 30309378 NR0B1 190 "nuclear receptor subfamily 0, group B, member 1"
GO:0005515|GO:0008406|GO:0010467|GO:0006694|GO:0006367|GO:0030325|GO:0003723|GO:0021983|GO:0035
258|GO:0033144|GO:0003707|GO:0050682|GO:0005634|GO:0007283|GO:0043433|GO:0042803|GO:0060008|GO:0
005737|GO:0008104|GO:0042788|GO:0030238|GO:0043401|GO:0004879|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128574_PI430048170 0.952849520044807 1.01653844895508 9.48345737616767 9.7828979045582
10.1251048574503 P P P 9.61396165079071 9.66159391976034 10.0713075595096 P P P
LNCV6_128574_PI430048170 mRNA
CTGCAAATGGTCACCCTGAATCTCTTCTGACATTGGATGTTATTTGCTTATATTCTTATA NM_015957 RefSeq chr11 -
34882295 34916411 APIP 51074 APAF1 interacting protein
GO:0005515|GO:0043066|GO:0006915|GO:0019284|GO:0044281|GO:0042802|GO:0034641|GO:0005737|GO:0000
096|GO:0019509|GO:0006595|GO:0008270|GO:0070372|GO:0046570 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_69016_PI430048170 0.0922352484562978 1.25943556703489 10.7771215891122 11.070098688777
10.6800718642905 P P P 10.6617604350394 10.5108696386828 10.3707504234545 P P P
LNCV6_69016_PI430048170 mRNA
GCTGCTTCGCTTGCGTGTCCAAGCCCCCTGCCCTGCAGGCTCCGGCGGCCCCTGCCCCTG NM_001170820 RefSeq
chr11_KI270903v1_alt - 206155 209175 IFITM10 402778 interferon induced transmembrane protein 10
GO:0009607|GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137441_PI430048170 0.00870966142143965 1.62738179205412 8.0555401269945
8.12217701782238 7.88848177477449 P P P 7.50165728453904 7.31904132138072

7.12299153410603 P P P LNCV6_137441_PI430048170 mRNA
ATATGTTAGTGTTGCTGCAACAATAAAGCCTGTTGCATCTCTCATGCCAATTTGAAAAAA NM_007213 RefSeq chrX
- 49071155 49074045 PRAF2 11230 "PRA1 domain family, member 2"
GO:0015813|GO:0016021|GO:0015031|GO:0010008 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_98692_PI430048170 0.0860168519691996 0.7100958485147368.3487679826855
8.53710577661059 8.51108240248346 P P P 8.64034014854263 8.99062789186582 9.2004056102243
P P P LNCV6_98692_PI430048170 mRNA
TTTATAGTGTTATTTGTTTCACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTT NM_013363 RefSeq chr3 -
142817859 142889203 PCOLCE2 26577 procollagen C-endopeptidase enhancer 2
GO:0016504|GO:0010952|GO:0005518|GO:0008201|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131170_PI430048170 0.2636823605132290.6084264644585693.20238337128432
3.69251926070058 2.79839619466395 P P A 3.70045026087402 4.65126968195955
3.27551587539021 P P P LNCV6_131170_PI430048170 mRNA
AGTATATGTAGCCATCTCCACATCACTCATTATGACCCCTTCTTTTATAATGCTTATATC NM_033402 RefSeq chr8 +
85107087 85146079 LRRCC1 85444 leucine rich repeat and coiled-coil centrosomal protein 1
GO:0007067|GO:0005813|GO:0005737|GO:0005814|GO:0005654|GO:0051301 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128390_PI430048170 0.9707874277374010.9894190168427857.92929974064129
7.79903246120066 7.9584920097997 P P P 7.76034349492231 8.15491082664872
7.78803213500475 P P P LNCV6_128390_PI430048170 mRNA
ATTAAACCGGTTTCTGTGGGCACCTCTGTCCTTGCTGCTGGTGGGGAAGGGAAGCCAGAT NM_030928 RefSeq chr16
+ 88803777 88809258 CDT1 81620 chromatin licensing and DNA replication factor 1
GO:0006260|GO:0005515|GO:0000082|GO:0033262|GO:0030174|GO:0000083|GO:0000076|GO:0005654|GO:0005
634|GO:0000278|GO:0003677|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64357_PI430048170 0.00129419390293437 1.73108782833451 11.0715437018056
10.8658668904906 10.9349536893683 P P P 10.1100503928561 10.3091283521704
10.0745516178715 P P P LNCV6_64357_PI430048170 mRNA
ATCACCAGGAACTTCTACGTGGATGGCCATGTCCCCAAGCCCCACTGACATGAACACCTG NM_001031734 RefSeq
chr19 - 10310210 10316015 FDX1L 112812 ferredoxin 1-like
GO:0006805|GO:0051537|GO:0005759|GO:0006700|GO:0009055|GO:0044281|GO:0016125|GO:0046872|GO:0008
202|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144897_PI430048170 0.2203351443824461.87951492265613 1.64745182578022
0.2718283573147111.60138679103917 A A A 0.5155240763133060.324446898601662
0.312563434028555 A A A LNCV6_144897_PI430048170 mRNA
TATTTTAGCAACAATCATCAGAGTGACGCTGATGGTTTGGGGCACCAGCTATACATCAGC NM_001291274 RefSeq
chr19 + 16134027 16158573 HSH2D 84941 "hematopoietic SH2 domain containing, transcript variant
2"
GO:0005739|GO:0005515|GO:0042110|GO:0051902|GO:0005070|GO:0002903|GO:0009967|GO:0005634|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141800_PI430048170 0.0413255839755999 0.6192632776449744.57266324451993
4.40031169380269 4.78642420395021 P P P 4.90865505430707 5.42922020087753
5.45829362675291 P P P LNCV6_141800_PI430048170 mRNA
TTAGGCCTTTTATGACTTTATAAATAGGCAATAATGAACACCAAGGGAAGCAAAACACTG NM_174931 RefSeq chr2
+ 37084450 37099244 GPATCH11 253635 "G patch domain containing 11, transcript variant 1"
GO:0003676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143449_PI430048170 0.3520226491064080.9591557384159380.272756218457953
0.4026687022864990.300980757920968 A A A 0.4664995708526050.35854286848464
0.331549895358626 A A A LNCV6_143449_PI430048170 mRNA

CTACCAAGTGTTTCCAGAGATTCTGCTACATGTATTATCTGAAATGTTCTCCATATATTC NM_033048RefSeq chrX
+ 88747224 88754784 CPXCR1 53336 "CPX chromosome region, candidate 1, transcript variant 1"
GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132145_PI430048170 0.0180647204915478 0.7065245412682346.2206007895164
5.8895337752519 5.96958234041254 P P P 6.66020687783869 6.49543979600538
6.43942702518481 P P P LNCV6_132145_PI430048170 mRNA
GTGTAACTTTTCACATAAAGAGAATGCATCTTTGACAGTTATCTTATTTGTAAGGCAGCC NM_020368RefSeq chr4
+ 70688478 70690551 UTP3 57050 "UTP3, small subunit (SSU) processome component, homolog (S.
cerevisiae)" GO:0000462|GO:0007420|GO:0032040|GO:0005730|GO:0005634|GO:0016568 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_133048_PI430048170 0.12476852148101 1.01924766664856 0.398077057006384
0.4045869077265890.413746431048379A A A 0.3759633872748920.359034867637065
0.398666860147568A A A LNCV6_133048_PI430048170 mRNA
GTACTGCATGTAAACCATGCTCTTTTTAAACTGAGTATTTTCCATCACTAGAGCATAGTA NM_031914RefSeq chr14
+ 61995822 62101709 SYT16 83851 synaptotagmin XVI
GO:0005543|GO:0046982|GO:0006887|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142094_PI430048170 0.00286917377147647 0.2673364100839653.7670138111502
3.48733130103659 3.79825430308801 P P P 5.21117934271741 5.65728638536491
5.84302369538776 P P P LNCV6_142094_PI430048170 mRNA
GCTATTTTTGTGTGTTCCCTACCTTCTTAAGGCTATGGAAATAAACTGGAGTTTAGTTTT NM_032581RefSeq chr7 -
22941258 23014151 FAM126A 84668 "family with sequence similarity 126, member A"
GO:0008150|GO:0007165|GO:0005737|GO:0005886|GO:0004871 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_64877_PI430048170 0.0971129462800161 0.4398301678133410.326563866333789
0.3542215761275150.354399593689952A A A 2.09444564521391 0.823184805615828
1.39191185397148 A A A LNCV6_64877_PI430048170 mRNA
GTCACGAGAAATGAAACAGGACCTTATCAATGTGAAATACGGGACCGATATGGTGGCATC NM_002780RefSeq chr19
- 43192701 43205774 PSG4 5672 "pregnancy specific beta-1-glycoprotein 4, transcript variant 1"
GO:0007565|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137739_PI430048170 0.996378082003984 1.00069614691537 0.622459056022328
0.5042259594750620.408194825310567A A A 0.4272051300598470.570488513943596
0.538289995428577A A A LNCV6_137739_PI430048170 mRNA
CTGCATTTCTTTTTATATTAAATATGTGAGTGACAATAAAACAATTTTGACTTGAATCTT NM_176870RefSeq chr16 +
56632621 56633986 MT1M 4499 metallothionein 1M
GO:0071294|GO:0048471|GO:0005737|GO:0008270|GO:0005634|GO:0045926 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138028_PI430048170 0.0173265550219859 0.7963095641152651 0.2095991102702
10.0313246815308 10.1610111283459 P P P 10.3363923744776 10.5153800251472
10.5336772222553 P P P LNCV6_138028_PI430048170 mRNA
GACTGTACATATGTTAATAGCGCAAACCCGACGCCACATTTTTATAATTGTGATTAAACT NM_014712RefSeq chr16
+ 30957293 30984662 SETD1A 9739 SET domain containing 1A
GO:0005515|GO:2000179|GO:0006355|GO:0005694|GO:0003723|GO:0006325|GO:2000648|GO:0005634|GO:0042
800|GO:0006351|GO:0035097|GO:0000166|GO:0016607|GO:0048188|GO:0019827|GO:0005654|GO:0051568 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_76298_PI430048170 0.1046803585761921.24225783804239 9.06120740338282 8.83495292129439
9.24297621436031 P P P 8.69725893278822 8.64063605001549 8.88012295959486 P P P
LNCV6_76298_PI430048170 mRNA
TGCAACTTCAGACTGAAGATAGGCCAAGGTCGTCACTGATCTCAAGATTTCAACCTTGAC NM_138369RefSeq chr5
- 173607144 173616663 BOD1 91272 "biorientation of chromosomes in cell division 1, transcript variant

1" GO:0007067|GO:0005737|GO:0005815|GO:0000777|GO:0051301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133914_PI430048170 0.1605383130798 1.03426545967797 0.46032388998844
0.4515378438842420.397926329370399A A A 0.3476304151861870.402216817691742
0.414042417954428A A A LNCV6_133914_PI430048170 mRNA
CTTGAGTCATGAAATACTTAACACATGTGCACATGTACACATGTACATTTATATGCAGTG NM_001007248 RefSeq
chr19 - 34758073 34773229 ZNF599 148103 zinc finger protein 599
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_128962_PI430048170 0.0853679782775205 1.30200952651701 9.98211985241823
9.9486428456751 9.6168678248367 P P P 9.49181535867416 9.47022328860211 9.4707442403112
P P P LNCV6_128962_PI430048170 mRNA
AAATAAAGGAGCAGTCATCCCTAGGGCAGCTGCCTAACAGTACCTCTAAGTTTCAAAAAA NM_001080501 RefSeq
chr11 - 62790314 62792014 TMEM223 79064 transmembrane protein 223 GO:0016021 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_141832_PI430048170 0.9335781937999960.9645263109423820.388341101739266
1.22959028108883 0.264812293152409A A A 1.32488921520007 0.33896472637939
0.337949076748568A A A LNCV6_141832_PI430048170 mRNA
GGATGAATACGAGATGGTTGTGATTGTGCAGTGTACCAATAAAGTTCGAGAAATTTGTAA NM_001012393 RefSeq
chr11 - 132414980 133532508 OPCML 4978 "opioid binding protein/cell adhesion molecule-like,
transcript variant 2"
GO:0043005|GO:0016337|GO:0050767|GO:0008038|GO:0009986|GO:0005886|GO:0005911|GO:0043025|GO:0031
225|GO:0007155|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139237_PI430048170 0.0900803815580062 0.7827415628729127.92029250612501
8.14959589952905 8.36988752815923 P P P 8.5739030128281 8.3508974981779
8.59747741728913 P P P LNCV6_139237_PI430048170 mRNA
GGGATCTAATCCAGGATGTTGAATGGGATTATTGCCATCTTACACCATATTTTTGTAAAA NM_007217RefSeq chr3
- 167683905 167734806 PDCD10 11235 "programmed cell death 10, transcript variant 1"
GO:0005515|GO:0044319|GO:0042542|GO:0008284|GO:0071902|GO:0005886|GO:0035023|GO:0043149|GO:0032
874|GO:0051683|GO:0090168|GO:0042803|GO:0005829|GO:0005737|GO:0033138|GO:0043406|GO:0090051|GO:0
070062|GO:0045747|GO:0043066|GO:0030335|GO:0005794|GO:0019901|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139401_PI430048170 0.23298549584417 1.47196571143692 3.32447323922477
2.89316588991208 2.41901857355056 P A A 1.89191484178067 2.05603328036172
2.92907395284707 A A P LNCV6_139401_PI430048170 mRNA
GGTTCACATCTTGTTTCCTATAGAAATGTCCTGTATTCTGGGATCAATTTCCAAATGCTTNM_001098527 RefSeq chr22
- 32190434 32203477 RFPL2 10739 "ret finger protein-like 2, transcript variant 2" GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135747_PI430048170 0.000877386457754197 0.2971177847173713.54226651190185
3.12767845265056 3.11521612148093 P P P 5.03674383612806 5.18139718357286
4.84187762357404 P P P LNCV6_135747_PI430048170 mRNA
TGCATACTGGAGAGAAACCCTACAAATGTGAATAATGTGATAAAGTCCAGCCTTCAGACC NM_153363RefSeq chr7
+ 64228473 64266931 ZNF679 NA zinc finger protein 679 NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_134176_PI430048170 0.0129878112740615 1.55499109604058 11.2162352679906
11.3943376413292 11.084901929685 P P P 10.6402884755473 10.6156244264603
10.5439056817642 P P P LNCV6_134176_PI430048170 mRNA
GAGGGCGAGGGCGAGAAAGGGCAGGCACTCTGCGAATTAAAGGCCTTGGACTTGAAAAAA NM_001278158
RefSeq chr16 + 3112578 3120517 ZNF205 7755 "zinc finger protein 205, transcript variant 3"

GO:0005515|GO:0006355|GO:0003700|GO:0010729|GO:0008270|GO:0005634|GO:0000122|GO:0003677|GO:0006
351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133288_PI430048170 0.00427633014383788 1.49526984318147 10.4151384069142
10.4874550293568 10.2998895117252 P P P 9.88761041038808 9.8983304819326
9.67021319405821 P P P LNCV6_133288_PI430048170 mRNA
TCTCATTTTATTTCAGCTCCATTTTGCCCATAGATGGGCAGAGGGGTGAGATTGGCTCAT NM_004468RefSeq chr1
- 37996769 38005515 FHL3 2275 "four and a half LIM domains 3, transcript variant 1"
GO:0030018|GO:0001725|GO:0030036|GO:0007517|GO:0008270|GO:0005634|GO:0003779|GO:0005925 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106534_PI430048170 0.5592797826379561.11461005690395 7.26561551527237
6.83647737588829 7.1023048671609 P P P 6.36145829168546 7.16805362801468
7.10671699416613 P P P LNCV6_106534_PI430048170 mRNA
ACAACCTCTGCTCCTACAACTAGCACAACCTCTGGTCCTGGAACTACTCCCAGCCCTGTT NM_001304359 RefSeq
chr11 + 1157952 1201141 MUC5AC 4586 "mucin 5AC, oligomeric mucus/gel-forming"
GO:0006493|GO:0005796|GO:0016266|GO:0043205|GO:0043206|GO:0044267|GO:0070062|GO:0043687|GO:0005
201 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143565_PI430048170 0.0014964128685407 5.58231230644606 7.91797747656123
8.04167010184265 7.80682830667231 P P P 5.69217580934323 5.12078232608281
5.46409158557111 P P P LNCV6_143565_PI430048170 mRNA
GTCTCCTAAACCAATTATGCTGTGCCTGGGAACGAAATACTGTGTCTAAGTCTCAAAAAA NM_001145536 RefSeq
chr17 + 4899652 4902932 C17orf107 NA chromosome 17 open reading frame 107 NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_137642_PI430048170 0.1073870505013250.5238102072298731 1.5268074701987
10.3688125379323 10.4221522155177 P P P 11.9180718108042 11.8056976621849
11.7000195211537 P P P LNCV6_137642_PI430048170 mRNA
TTGTGTCTCCCCCACCCCCACAAAAAACTTTATATTAAAATCCTAACCCCCAGCAAAAAA NM_017457RefSeq chr19
+ 48469207 48482314 CYTH2 9266 "cytohesin 2, transcript variant 1"
GO:0005515|GO:0005802|GO:0030036|GO:0005886|GO:0030155|GO:0006897|GO:0008289|GO:0043547|GO:0070
679|GO:0005086|GO:0005737|GO:0016020|GO:0032012|GO:0016192 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130683_PI430048170 0.2043391036782770.5649753427076140.362224859937766
1.65121276638519 1.87973961172003 A A A 2.5412285187678 1.53437865162565
2.49335967993031 P A P LNCV6_130683_PI430048170 mRNA
GATCAAGGATGTACTTTGCCAAATAAGTATTTGGTAACATCACTTAACAAGTTGATCGTG NM_018119RefSeq chr16
+ 22297374 22335103 POLR3E 55718 "polymerase (RNA) III (DNA directed) polypeptide E (80kD),
transcript variant 1"
GO:0010467|GO:0005813|GO:0006386|GO:0006385|GO:0005634|GO:0006383|GO:0005829|GO:0051607|GO:0001
056|GO:0045087|GO:0005666|GO:0005654|GO:0032481 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141370_PI430048170 0.000542612222202623 0.3005873889788846.09274174504447
5.74569126317585 6.13847227007601 P P P 7.72594640062284 7.57343007269072
7.89326350348695 P P P LNCV6_141370_PI430048170 mRNA
GATCCAGTAATCAATTTGGCAACTTTAATCGAGGTTTTCAAAATTCCAAGGAGGGTTAAT NM_139246RefSeq chr9
- 97600079 97633680 TSTD2 158427 thiosulfate sulfurtransferase (rhodanese)-like domain containing 2
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129457_PI430048170 0.0246070579792478 1.34289640177441 9.70665567553586
9.50569466508833 9.4880171783966 P P P 9.15044933109634 9.1586006844903
9.12544631929813 P P P LNCV6_129457_PI430048170 mRNA
AGAACTAGACACCCTTGAAGATTTGGCCTGGGCCAGTGAGACTGAAATCAAGAAAAACAG NM_145058RefSeq
chr12 - 123415038 123436733 RILPL2 196383 "Rab interacting lysosomal protein-like 2, transcript variant

1" GO:0003382|GO:0005813|GO:0005737|GO:0072372|GO:0006886|GO:0070062|GO:0042802|GO:0005829 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_52228_PI430048170 0.0177454508131449 1.59489389998532 5.55976226768036
5.57197092071556 5.46114909710458 P P P 5.03077077853107 4.86895783773807
4.65023149050344 P P P LNCV6_52228_PI430048170 mRNA
CTCCCCCGGTGGGAGCGGTGGTTGGGCCAGGCTGCGGCAGAGCGTTCGCTCGGAGATGGC NM_003635 RefSeq
chr10 - 73801910 73811831 NDST2 8509 N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2
GO:0016787|GO:0000139|GO:0005975|GO:0009405|GO:0044281|GO:0016021|GO:0015012|GO:0030203|GO:0006
024|GO:0030210|GO:0015016 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132890_PI430048170 0.298500175337298 0.825413995547459 8.07160510543159
8.15290818514678 8.45283975061081 P P P 8.3971263973651 8.2318235781482
8.83767528642821 P P P LNCV6_132890_PI430048170 mRNA
GGAATGGACCCATCCGTGTACTTCATTCAAATGTGTAAATGTCATATTCATTCAGATTTA NM_001698 RefSeq chr9
- 91213814 91361924 AUH 549 AU RNA binding protein/enoyl-CoA hydratase
GO:0005739|GO:0034641|GO:0005759|GO:0004490|GO:0009083|GO:0044281|GO:0003730|GO:0004300|GO:0006
552 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141536_PI430048170 0.512617667970674 0.87946865366981 0.531235384797483
0.352172007352861 0.253720381697117 A A A 0.937404911247248 0.349468606642996
0.334748401085728 A A A LNCV6_141536_PI430048170 mRNA
GCCAACCTTAGGGCACGTGGGCATTATTAAAGGTCTTAAAAGCATTGAAGATTTAAAAAA NM_017688 RefSeq chr9
+ 113349531 113371233 BSPRY 54836 B-box and SPRY domain containing
GO:0048471|GO:0005737|GO:0016020|GO:0008270|GO:0006816|GO:0005654|GO:0031252|GO:0005925 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_63460_PI430048170 0.0075150112607580 0.397240362503424 6.56973522685927 6.72899300350651
6.22641980364739 P P P 7.76282870391229 7.90279203380802 7.89570785781755 P P P
LNCV6_63460_PI430048170 mRNA
TGTCAGTATTCTAGTCCAGTATTTGCCAGTTTCCAAGTAAAAGCTTTTGTGTTACGTGTT NM_001162995 RefSeq
chr17 + 75633433 75641406 SMIM5 NA "small integral membrane protein 5, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139540_PI430048170 0.149324079057533 0.650397222097518 8.45199421396542
8.27318630676866 8.23226685558869 P P P 8.42901513458868 9.32796222899344
8.93401057914433 P P P LNCV6_139540_PI430048170 mRNA
AGTACACCAGCTCCAAGTAAATTCTCAAGCTCTTGTCCAACCCAAAGGCTCTTTTCAGAG NM_003519 RefSeq chr6
- 27807478 27807931 HIST1H2BL 8340 "histone cluster 1, H2bl"
GO:0046982|GO:0006334|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0003677|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65141_PI430048170 0.612516640211809 0.972277181298729 0.497060642695572 0.509566808476817
0.31798177899143 A A A 0.400456866789558 0.547566306148943 0.50220600071716 A A A
LNCV6_65141_PI430048170 mRNA
AATGCTCACCTGGCAAATCACCGAAGAATTCATACTGGGGAGAAACCTTACAGGTGTACA NM_001102603 RefSeq
chr19 - 53066613 53103434 ZNF160 90338 "zinc finger protein 160, transcript variant 3"
GO:0030097|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_91187_PI430048170 0.0400109641526512 1.14593406491077 5.89536390386844
5.95238035844904 5.98060981005758 P P P 5.64522244809618 5.80451999076143 5.7851641074064
P P P LNCV6_91187_PI430048170 mRNA
TTGATTTGCAGCATCTTTGAGCCTCTACGACAAAAAACCGCGAAGCACGCCCAGCCCTCC NM_015326 RefSeq chr1
+ 206205428 206464443 SRGAP2 23380 "SLIT-ROBO Rho GTPase activating protein 2, transcript variant 1"
GO:0005515|GO:0030054|GO:0005886|GO:0008283|GO:0007264|GO:0005634|GO:0032855|GO:0042803|GO:0005

829|GO:0051014|GO:0005737|GO:0007411|GO:0045211|GO:0060548|GO:0034446|GO:0060996|GO:0046847|GO:0
030675|GO:0051056|GO:2001223|GO:0003363|GO:0014069|GO:0044327|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138226_PI430048170 0.0338336466678651.36910258508578 7.3021770656109
7.60005127973391 7.56702502449517 P P P 7.2448442570139 6.96258332006827
6.89596497702852 P P P LNCV6_138226_PI430048170 mRNA
TTGATTCCTGCCATATGGAGGAGGCTCTGGAGTCCTGCTCTGTGTGGTCCAGGTCCTTTC NM_003064RefSeq chr20
- 45252238 45254564 SLPI 6590 secretory leukocyte peptidase inhibitor
GO:0032091|GO:0031012|GO:0010951|GO:0005515|GO:0004866|GO:0004867|GO:0019899|GO:0070062|GO:0045
071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133184_PI430048170 0.000662467601515205 2.03139278532094 7.48075856712786
7.71429795753279 7.53801700145753 P P P 6.47962391644791 6.63102447005122
6.56143260842961 P P P LNCV6_133184_PI430048170 mRNA
GGCTCGGGACGCTCATGTAAATTTGGTTTTGGTGCTCAAGGGTTCTTTCCTCCCAGGGGC NM_005975RefSeq chr20
- 63528422 63537370 PTK6 5753 "protein tyrosine kinase 6, transcript variant 1"
GO:0005515|GO:0042506|GO:0030036|GO:0042503|GO:0071300|GO:0061099|GO:0005634|GO:0042802|GO:0060
575|GO:0005737|GO:0046777|GO:0042127|GO:0038083|GO:0045926|GO:0005102|GO:0005524|GO:0001726|GO:0
031234|GO:0016477|GO:0045087|GO:0010976|GO:0006468|GO:0005654|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143091_PI430048170 0.2761042474791590.86453365018437 0.361998311546705
0.36007842509988 0.328992163896934A A A 0.8138305711515420.427198513618757
0.402360184494518A A A LNCV6_143091_PI430048170 mRNA
GTACATGGAAGGAGCTGAGATGTCTAAAGTCACCCACATTTGTCATTTAAAAAAGTATAT NM_152775RefSeq chr4
- 185445183 185471759 CCDC110 256309 "coiled-coil domain containing 110, transcript variant 1"
GO:0005737|GO:0005794|GO:0005730|GO:0005634|GO:0043231 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138767_PI430048170 0.3620449864678750.6750895997238390.381176666352524
0.3735337005558160.337040627803405A A A 0.4439810671138 1.59625631988698
0.417317499245333A A A LNCV6_138767_PI430048170 mRNA
GGAAGAAGGGGTAATATGGTGAAAGCAAATTCCCTTTCCCAGGAGTCAAGAGAATTTATG NM_000349RefSeq chr8
- 38142699 38151082 STAR 6770 steroidogenic acute regulatory protein
GO:0042542|GO:0006694|GO:0043627|GO:0006701|GO:0018963|GO:0017143|GO:0006699|GO:0006703|GO:0071
560|GO:0005758|GO:0042747|GO:0043524|GO:0048168|GO:0060992|GO:0043025|GO:0018958|GO:0030061|GO:0
010288|GO:0051412|GO:0032869|GO:0071312|GO:0009635|GO:0044321|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141423_PI430048170 0.9219821966679520.9144294985848531.16031861723792
1.73270161753826 1.22359924608683 A A A 0.8121727522183532.38001605040662
0.740937487580192A A A LNCV6_141423_PI430048170 mRNA
AGAACAAGTATCAACAAGCGGAAGAGCTGTACAAAGAAATCCTCCACAAGGAGGACCTAC NM_177417RefSeq
chr19 + 45340739 45351520 KLC3 147700 kinesin light chain 3
GO:0008017|GO:0043005|GO:0005871|GO:0005737|GO:0031514|GO:0035253|GO:0008152|GO:0005874|GO:0008
088|GO:0019894|GO:0003777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133725_PI430048170 0.0121541103611799 0.7384891697001544.89789199250379
5.06070400067096 5.14496381032363 P P P 5.47335058513471 5.5919917117704
5.35105435688987 P P P LNCV6_133725_PI430048170 mRNA
TCATCAAAGTCCTCGGTGTTTTTTAAATTATCAGAACTGCCCAGGACCACGTTTCCCAGG NM_004943RefSeq chr19
- 45783005 45792802 DMWD 1762 "dystrophia myotonica, WD repeat containing"
GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143139_PI430048170 0.8413146297334451.01174359084103 0.27316213988256

0.2787322167032370.461698191019151A A A 0.3454150358675990.294430621626011
0.330826320620338A A A LNCV6_143139_PI430048170 mRNA
TTTACCTCGCGTGTGTTTACCTATATGGAGTAGCTCGCAGAGATCACAGAAATGCTTGCA NM_023926RefSeq chr19
- 58083841 58098363 ZSCAN18 65982 "zinc finger and SCAN domain containing 18, transcript variant
3" GO:0006366|GO:0006357|GO:0000981|GO:0005634|GO:0003677|GO:0046872 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141491_PI430048170 0.0323691769560369 1.52794340970773 8.38024401316913
8.66514093881834 8.61256438762747 P P P 7.64639430135204 8.14707438948565
8.00055104933751 P P P LNCV6_141491_PI430048170 mRNA
CAGAGCTACCCAGTGAGAGGCCTTGTCTAACTGCCTTTCCTTCTAAAGGGAATGTTTTTT NM_001278497 RefSeq
chr22 + 24432118 24442361 ADORA2A 135 "adenosine A2a receptor, transcript variant 1"
GO:0005515|GO:0006909|GO:0048011|GO:0005886|GO:0008015|GO:0007267|GO:0010579|GO:0006915|GO:0007
417|GO:0042802|GO:0001609|GO:0007190|GO:0006968|GO:0006954|GO:0016020|GO:0001973|GO:0007596|GO:0
005887|GO:0006171|GO:0007188|GO:0019899|GO:0007169|GO:0007600 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_134814_PI430048170 0.0949993119843294 1.1403324587378 8.20244172058015
8.3686350106033 8.32874253571355 P P P 8.16799402164914 8.18741220486242
7.97148674551763 P P P LNCV6_134814_PI430048170 mRNA
TTATTTTCTGGATGTGTTTGGAGCTTCCCCCTTCTCCGTTTCTTCTTCTGTTTGTTAAGG NM_002699RefSeq chr1 -
38043850 38046778 POU3F15453 POU class 3 homeobox 1
GO:0005667|GO:0001105|GO:0003700|GO:0022011|GO:0005634|GO:0008366|GO:0006351|GO:0010628|GO:0043
565|GO:0030216|GO:0045944|GO:0030900|GO:0045893 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141107_PI430048170 0.0152856245261344 1.82083440647481 8.87079566549457
9.11134458065593 8.73654055643235 P P P 8.06055201522897 8.0610285597238
8.02831249186527 P P P LNCV6_141107_PI430048170 mRNA
GTGGGGTGTTCTTTGTGTAAAATAGAAACATGGTTTTGTACAGAAATAAACAGCCTTGTA NM_001204240 RefSeq
chr22 - 30291989 30326966 TBC1D10A 83874 "TBC1 domain family, member 10A, transcript variant 1"
GO:0005515|GO:0005085|GO:0005902|GO:0005886|GO:0042147|GO:0032851|GO:0097202|GO:0030165|GO:0045
862|GO:0005097|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136091_PI430048170 0.6344994196637430.9380899696394229.39913313140998
9.59368582579321 9.82579561611789 P P P 9.62933023722073 9.51821841314374
9.94477966825284 P P P LNCV6_136091_PI430048170 mRNA
CTACTGACTTGACTGTCATCCTGTTCTTGTTAGCCATTGTGAATAAGATTTTAATGTTGANM_001139517 RefSeq chr2
- 178431413 178450757 PRKRA 8575 "protein kinase, interferon-inducible double stranded RNA
dependent activator, transcript variant 2"
GO:0005515|GO:0010467|GO:0048471|GO:0008285|GO:0030422|GO:0048705|GO:2001244|GO:0043085|GO:0009
615|GO:0042803|GO:0005829|GO:0005737|GO:0006955|GO:0016020|GO:0042474|GO:0005654|GO:0006468|GO:0
042473|GO:0034599|GO:0008047 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134208_PI430048170 0.0161914957267509 0.5253201353886464.43217651056663
4.7520552605245 4.8220455125394 P P P 5.2366797994274 5.77517330760534
5.74869486484505 P P P LNCV6_134208_PI430048170 mRNA
CCTTTTGAATGTTGTCTTCTCACTCAGCATCAGCACTTCGATCTAAATGCAGACTAGGTA NM_015036RefSeq chr11
+ 95089809 95132651 ENDOD1 23052 endonuclease domain containing 1
GO:0004519|GO:0090305|GO:0016020|GO:0003676|GO:0046872|GO:0070062 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_129307_PI430048170 0.1111955838150860.7678215919965937.29161629623094
7.66133786019681 7.56951754780887 P P P 7.66041502747859 7.83813029249573
8.14953772726549 P P P LNCV6_129307_PI430048170 mRNA
CGGCTCTGTATTATTTGAATCAGTCTGCCGAGAATCCATGTATATATTTGAACTAATATC NM_003106RefSeq chr3

+ 181711923 181714435 SOX2 6657 SRY (sex determining region Y)-box 2
GO:0010468|GO:0005515|GO:0003700|GO:0006366|GO:0044212|GO:0001654|GO:0060042|GO:0050680|GO:0006
325|GO:0001714|GO:0030539|GO:0048852|GO:0045747|GO:0030910|GO:0048839|GO:0000976|GO:0022409|GO:0
042472|GO:0060235|GO:0048286|GO:0046982|GO:0021879|GO:0000122|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144857_PI430048170 0.00598309438735383 0.3127331785440036.60673792267233
6.62316238913184 7.19490472718861 P P P 8.059443070911 8.49269235374482
8.87149767391928 P P P LNCV6_144857_PI430048170 mRNA
TTCCCTCAGCTTGCTGGTAATTGTGGTGTTTTGTTTTTTGTTTTGTTTTCAATGCAAATG NM_005921RefSeq chr5 +
56815072 56896151 MAP3K1 4214 "mitogen-activated protein kinase kinase kinase 1, E3 ubiquitin
protein ligase"
GO:0005515|GO:0030036|GO:0034142|GO:0005829|GO:0035556|GO:0000186|GO:0008637|GO:0030838|GO:0061
029|GO:0002755|GO:0007179|GO:0004709|GO:0003382|GO:0030334|GO:0038124|GO:0038123|GO:0019901|GO:0
034134|GO:0006915|GO:0007257|GO:0002224|GO:0005524|GO:0004672|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133334_PI430048170 0.9372832150213921.01184787108537 11.0928954145872
10.9235633341501 10.7177285384839 P P P 10.9356029002904 10.949237866972 10.819191958708
P P P LNCV6_133334_PI430048170 mRNA
AGCGGAGGGCCTCTTCTTGGTGCCCTGCCCCAAATAAAGGAACTGGACAAAGAGAAAAAA NM_015871RefSeq
chr1 + 26169896 26170873 ZNF593 51042 zinc finger protein 593
GO:0003714|GO:0005730|GO:0005634|GO:0000122|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138356_PI430048170 0.00196278818575172 0.3095061405355095.9705330837242
5.51291393126867 6.03971881416768 P P P 7.23488176230834 7.55117324711969
7.81055374821068 P P P LNCV6_138356_PI430048170 mRNA
AGACGAGCTGTTCACTTAACTGGTACCTGTTGGTCAGAAAAAGAATTTATTTAGAGATTA NM_152699RefSeq chr3
+ 196867855 196934713 SENP5 205564 SUMO1/sentrin specific peptidase 5
GO:0005515|GO:0007049|GO:0016925|GO:0006508|GO:0005730|GO:0005654|GO:0005634|GO:0008234|GO:0044
267|GO:0051301|GO:0043687|GO:0043231 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132499_PI430048170 0.00109445740543485 0.4681914550738276.22312936008511
6.03202922839461 6.1087955813032 P P P 7.05434311247751 7.22539415965628
7.35905417624609 P P P LNCV6_132499_PI430048170 mRNA
GCCTCCTTGGCCCTAAATGGAAGGGCCGATATTTTAAGTTGATTATTTTATTGTAAATTA NM_002524RefSeq chr1
- 114704463 114716894 NRAS 4893 neuroblastoma RAS viral (v-ras) oncogene homolog
GO:0008286|GO:0008284|GO:0030036|GO:0005886|GO:0035022|GO:0007264|GO:0007265|GO:0050900|GO:0032
403|GO:0000186|GO:0043524|GO:0007173|GO:0007411|GO:0000165|GO:0048169|GO:0070062|GO:0048010|GO:0
048011|GO:0048642|GO:0005525|GO:0006184|GO:0060441|GO:0000139|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139611_PI430048170 0.429943252698075 0.7798949533911376.52650244729553
6.49827834337196 6.10118329697977 P P P 7.15345914229432 6.79147050043428
6.10863920571146 P P P LNCV6_139611_PI430048170 mRNA
AGATGGCCGCCCTGAAGCTCTCTGGGCTCCTCAGCAATAAAGCACTTTATTTTCAAAAAA NM_199296RefSeq chr14
- 77474394 77498867 ISM2 145501 "isthmin 2, transcript variant 1" GO:0005576 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138596_PI430048170 0.168904658284903 1.06037619823343 0.576914059159475
0.63469765290957 0.586083039494967 A A A 0.5979909835745680.469137525170033
0.473770290009595 A A A LNCV6_138596_PI430048170 mRNA
GTTTATTGAACCTACAGTGATAATAATTAGCATGTGTCATAATCTGTGGCTGCCCAAAAA NM_144612RefSeq chr18
- 46477253 46657033 LOXHD1 125336 "lipoxygenase homology domains 1, transcript variant 1"

GO:0005262|GO:0050982|GO:0016020|GO:0007605|GO:0070588|GO:0032420 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49958_PI430048170 0.260737528306726 1.02879144317952 0.352458525504934 0.276318727242024 0.270712160491436 A A A 0.252202484849485 0.274626392078037 0.251140616233888 A A A
LNCV6_49958_PI430048170 mRNA
AAGCTATGTCTACCAGATGAGAAAAATGAATTCTATCTTCAGAACTGCGGTGCATTTTTT NM_001139456 RefSeq
chr7 - 138594284 138679045 SVOPL 136306 "SVOP-like, transcript variant 1"
GO:0022857|GO:0016021|GO:0055085 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134947_PI430048170 0.0405117278044839 0.63212590449916 7.51466382683394
7.44089435400948 8.00207763721717 P P P 8.14311012632508 8.28813873872457
8.54858997996023 P P P LNCV6_134947_PI430048170 mRNA
TTTACTAGAGGAGAGGGGCCACTGAAAACTTCCCAGGATTTAATTCATCAACTAGAGGTT NM_001286974 RefSeq
chr9 - 108942568 109013594 CTNNAL1 8727 "catenin (cadherin-associated protein), alpha-like 1, transcript variant 2" GO:0051015|GO:0045296|GO:0005886|GO:0007266|GO:0007155|GO:0005856|GO:0005829
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142844_PI430048170 0.229741955531552 1.15128394624925 9.67570318681928
9.99568486357401 9.84669584382125 P P P 9.75565228401244 9.41221154539614
9.73328405723556 P P P LNCV6_142844_PI430048170 mRNA
GCCAGCTCCATGCCCAAACCTTCCTGTTTGCAGAACTTTTTAATGTCTTTTCTTTTTCAT NM_016024 RefSeq chrX + 130401968 130413343 RBMX2 51634 "RNA binding motif protein, X-linked 2" GO:0005515|GO:0000166 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145151_PI430048170 0.307244189036909 1.0352100468965 0.317870865143172
0.261838116171702 0.387227787414376 A A A 0.281499290341326 0.255495596842763
0.282746084476074 A A A LNCV6_145151_PI430048170 mRNA
ATAAAGACCATCAGGAACTGGCTGAAGGAGAAGTTGCATGTCTTCTCGGAGAAGTTAGAG NM_001289970 RefSeq
chr5 + 171785871 171791088 SMIM23 644994 small integral membrane protein 23
GO:0005886|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145169_PI430048170 0.0145631087527882 5.1009713936358 3.27826953991042
4.12244053279922 3.03882917004466 P P P 0.864502074721163 0.409529971294127
1.91785504932886 A A A LNCV6_145169_PI430048170 mRNA
AGATTTGCATCTTTACAACCAGAAGCTCAGGGAGAAGTTGAAGGAGGAGGAGAACACAGT NM_022158 RefSeq
chr17 + 82735575 82751197 FN3K 64122 fructosamine 3 kinase
GO:0016310|GO:0030387|GO:0030389|GO:0030855|GO:0005575|GO:0030393 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128690_PI430048170 0.0323187964209685 4.911159684537 3.89407076310533
3.98593147427207 3.50866050465898 P P P 0.44182339712934 2.20279204753973
1.38352422368103 A A A LNCV6_128690_PI430048170 mRNA
ACCCCCAAATTTGACTCTGGGAGACTCAGCCAAATCCTATCTGGTAATAAAATTTCTTTT NM_001166215 RefSeq
chr19 - 10512741 10517992 S1PR5 53637 "sphingosine-1-phosphate receptor 5, transcript variant 2"
GO:0005886|GO:0045664|GO:0003376|GO:0016021|GO:0038036 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_63436_PI430048170 0.21843871921579 1.17742306987403 6.38245906360768 6.76488923462272
6.54011734186464 P P P 6.54594706202205 6.29062760031782 6.14031148309605 P P P
LNCV6_63436_PI430048170 mRNA
AATTGGGCAAGGAAATGAACCAAGCATCCGGATGTTCCAGAAACTTCACTTTGAGCAGGT NM_015654 RefSeq chr17
- 74770528 74776425 NAT9 26151 "N-acetyltransferase 9 (GCN5-related, putative)"
GO:0043234|GO:0008080|GO:0008152 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140415_PI430048170 0.308262111558749 0.50084574985119 0.350442046441371
0.347407913335769 0.261217931619299 A A A 2.17960844747678 0.787549062330087

0.289636447348986 A A A LNCV6_140415_PI430048170 mRNA
CCTGATGCTGGCGGGGTATTTGTGTGTTTTTGTATTGTTATTTGATTACAAAAATAAAGC NM_152412 RefSeq chr8
+ 124973296 124979388 ZNF572 137209 zinc finger protein 572
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127490_PI430048170 0.8616010629523231.04270363888909 4.02589846206699
4.30509172650286 3.45747517858309 P P P 4.31125399849915 3.89344100992241
3.37890745463882 P P P LNCV6_127490_PI430048170 mRNA
AAAGCCATCTCTTCCTCTGATCTGGGGTCTGTTTTGTTCATTACTTTGTTCACTCCTTCT NM_001011554 RefSeq chr20
- 46557822 46684485 SLC13A3 64849 "solute carrier family 13 (sodium-dependent dicarboxylate
transporter), member 3, transcript variant 2"
GO:0005886|GO:0006835|GO:0016021|GO:0006814|GO:0055085|GO:0070062|GO:0015362 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_133011_PI430048170 0.00274953896103669 0.3070053249275513.24059965957969
3.49945082681496 3.09205489367848 P P P 4.96892674284494 5.0571255931644
4.94436903312235 P P P LNCV6_133011_PI430048170 mRNA
GCCTGTATTTGTATGCAAAATGTCCTCTATCTGCTATTAAAGAAAAGCTACGTAAAACAC NM_007124 RefSeq chr6
+ 144291736 144853034 UTRN 7402 utrophin
GO:0005515|GO:0031594|GO:0030054|GO:0019901|GO:0005886|GO:0031527|GO:0003779|GO:2000649|GO:0030
175|GO:0043234|GO:0005737|GO:0005178|GO:0006936|GO:0007517|GO:0016010|GO:0016020|GO:0045211|GO:0
017166|GO:0005654|GO:0008270|GO:0005856|GO:0070938|GO:0001954|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_54835_PI430048170 0.0178999194593632 1.13131354903548 11.0733576710807
11.1881941212836 11.1650419112076 P P P 11.0121568324802 10.9580303991194
10.9235633341501 P P P LNCV6_54835_PI430048170 mRNA
CCCATGTTTAAACTTTGTGCCTTTGACCATCTCTTAGGTCTAATGATATTTTATGCAAAC NM_001130040 RefSeq chr1
- 154962297 154970747 SHC1 6464 "SHC (Src homology 2 domain containing) transforming protein 1,
transcript variant 3"
GO:0005515|GO:0008286|GO:0005154|GO:0008284|GO:0005886|GO:0005159|GO:0005158|GO:0007265|GO:0050
900|GO:0030968|GO:0005829|GO:0007507|GO:0000187|GO:0016337|GO:0005543|GO:0007173|GO:0000165|GO:0
005759|GO:0007176|GO:0005068|GO:0048011|GO:0031532|GO:0019901|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126653_PI430048170 0.0604823164975036 1.10498481990003 0.533740082066327
0.5241121661029870.659354672629225 A A A 0.37621016963403 0.437357014507956
0.473862052729551 A A A LNCV6_126653_PI430048170 mRNA
ACATGTTACTATGGTGATTTCTACGCAACACTAATTAAAGCTTGTACCTGGAAGACTAAA NM_005425 RefSeq chr16
- 11267856 11269303 TNP2 7142 transition protein 2 (during histone to protamine replacement)
GO:0007341|GO:0007275|GO:0005634|GO:0030317|GO:0007340|GO:0007283|GO:0007339|GO:0000786|GO:0003
677|GO:0046872|GO:0030154 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135575_PI430048170 0.2392859371551961.04578894643837 0.587231357419878
0.67346174873267 0.540882809530884 A A A 0.5566787334649110.527471417724066
0.526598036726521 A A A LNCV6_135575_PI430048170 mRNA
GTGATATGCAACCTGGTATACAGACATTTGTGCAATTTCATTTCATCAAATTCTATCTGC NM_006727 RefSeq chr5
- 24487099 24644976 CDH10 1008 "cadherin 10, type 2 (T2-cadherin)"
GO:0016337|GO:0005886|GO:0034329|GO:0005509|GO:0016021|GO:0007156|GO:0045216|GO:0034332 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92121_PI430048170 0.2036071931487371.88926154383184 3.18017664367727 1.71637623756893
2.75172157218311 P A A 1.85147088464992 1.60399807972587 1.78808512383476 A A A
LNCV6_92121_PI430048170 mRNA

TTAACTTTATTAAGCCCCTGGAACGTCTGAACCCTCTTTTGGGTACTGCAGGATTGTGGT NM_001242810 RefSeq chr1 + 91949370 92014428 BRDT 676 "bromodomain, testis-specific, transcript variant 7" GO:0006397|GO:0008380|GO:0003713|GO:0005634|GO:0001207|GO:0007283|GO:0006351|GO:0030154|GO:0042393|GO:0051039|GO:0070577|GO:0006338|GO:0043484|GO:0007141|GO:0007140 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137801_PI430048170 0.00251403138108285 0.1396981990742790.428895262369418 0.4568592310222831.22826294710806 A A A 3.37108680805734 3.56219029288062 3.81493044374218 P P P LNCV6_137801_PI430048170 mRNA
CTTAGATTTGGAATGGCTCTAATGATTCTTTGTACTTGAATGTGGTCTGTCAGGCCATGG NM_002264 RefSeq chr3 - 122421900 122514939 KPNA1 3836 "karyopherin alpha 1 (importin alpha 5), transcript variant 1" GO:0005515|GO:0019221|GO:0019058|GO:0006915|GO:0005634|GO:0006607|GO:0030425|GO:0006921|GO:0005829|GO:0005737|GO:0005643|GO:0006309|GO:0008565|GO:0042307|GO:0016032|GO:0005654|GO:0008139|GO:0000018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130539_PI430048170 0.4211069053987640.89419444362184 7.96228930981341 8.06729496969303 8.27721718183779 P P P 8.07225169586044 8.16285167560566 8.53165931501906 P P P LNCV6_130539_PI430048170 mRNA
CTTGCCTGTCGTTTGCAACTTCACACTTTTAGAATTTGTGTTTATATTTCCTGTAAGTGA NM_024063 RefSeq chr15 + 45402320 45421418 SPATA5L1 79029 "spermatogenesis associated 5-like 1, transcript variant 1" GO:0005737|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144344_PI430048170 0.0560075937450709 0.75676880932033 5.60402955095235 5.34326259790174 5.26451228579673 P P P 5.84063069930693 5.97504942713955 5.59990917347342 P P P LNCV6_144344_PI430048170 mRNA
TGAGAAAGCTCCAGACGGCCACCTCCCTAAATAAACAGCTTCTGGATTAAAGGCAAAAAA NM_001292025 RefSeq chr17 - 57861242 57903389 CUEDC1 404093 "CUE domain containing 1, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134339_PI430048170 0.1376260467526520.8269888467288839.18164338544748 9.23864417339221 9.05859835718598 P P P 9.23187424646361 9.63759065501963 9.40862175345375 P P P LNCV6_134339_PI430048170 mRNA
ACTCTGTTGCAAGTGCAATAAATCTGACCCAGTGCCCCCACTGACCAGAACTAGAAAAAA NM_002205 RefSeq chr12 - 54395260 54419266 ITGA5 3678 "integrin, alpha 5 (fibronectin receptor, alpha polypeptide)" GO:0005515|GO:0030949|GO:0005154|GO:0035313|GO:0005886|GO:0010811|GO:0050731|GO:0045202|GO:2000811|GO:0050900|GO:0035987|GO:0046872|GO:0005737|GO:0005911|GO:0007411|GO:0030198|GO:0007159|GO:0016032|GO:0034113|GO:0007613|GO:0007155|GO:0007157|GO:0008305|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132953_PI430048170 0.2385453025090241.09653193407778 0.537593108253064 0.2679722658898520.399887659495967 A A A 0.2864941895271470.254282856554012 0.278237132404211 A A A LNCV6_132953_PI430048170 mRNA
GTCCCTCAAATGACCCAAAGACCAATATTCAAATGCGTAATTAAAAGAATTTTCCCCAAA NM_003005 RefSeq chr1 - 169588849 169630139 SELP 6403 "selectin P (granule membrane protein 140kDa, antigen CD62)" GO:0005515|GO:0031088|GO:0005886|GO:0042806|GO:0050900|GO:0050901|GO:0005615|GO:0033623|GO:0005737|GO:0006954|GO:0001948|GO:0070492|GO:0043208|GO:0010572|GO:0007159|GO:0032496|GO:0031092|GO:0033691|GO:0007155|GO:0008201|GO:0007157|GO:0030168|GO:0014068|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144796_PI430048170 0.2126686071788050.6223258474985963.17456637175093 2.36561275849066 2.81906700343831 A A A 3.73107152253279 2.72885251550251 3.82999311201919 P P P LNCV6_144796_PI430048170 mRNA
CAGTGGTTTTGCCTAGTGTTCCAATTTTGGAACGTCACATAACAATGGAACATAATAAAT NM_170753 RefSeq chr10 - 49515104 49524281 PGBD3 267004 piggyBac transposable element derived 3 NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_139875_PI430048170 0.9104884819037950.9929231072957 0.278989603716268
0.5237387485469020.3615104850421 A A A 0.5056192981922910.397583483968613
0.294912723271282A A A LNCV6_139875_PI430048170 mRNA
TTCCTCAAGGTGGGGATTTCTGAGTTCTAAGACCAAGTCTCCATCTGAGACTCCCAAATT NM_145256RefSeq chr19
- 18391143 18397605 LRRC25 126364 leucine rich repeat containing 25 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136726_PI430048170 0.5489628672397130.7888469379809760.581469357717373
0.4678114142257910.588786181489523A A A 0.4485170621634811.50182568044135
0.443634055349088A A A LNCV6_136726_PI430048170 mRNA
CACAGTCTCTGTCCTTCAGTACAGCTTTTTTGAGATATTTTAAAAAGTCAGCTGTGTATG NM_018967RefSeq chr8
+ 49911778 50794118 SNTG1 54212 "syntrophin, gamma 1, transcript variant 1"
GO:0005737|GO:0007154|GO:0016013|GO:0032587|GO:0005634|GO:0003779|GO:0008022|GO:0005856 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_74708_PI430048170 0.8935167225679861.01716916976542 11.0577726853561 11.1850848944298
11.4633415556064 P P P 10.9817432675965 11.2732720708577 11.3790343501574 P P P
LNCV6_74708_PI430048170 mRNA
ATGACTGTTGGTATGGGCTATTCCATGTATCGGGAATTCTGGGCAAAACCTAAGCCTTAG NM_001099668 RefSeq
chr3 - 42782907 42804442 HIGD1A 25994 "HIG1 hypoxia inducible domain family, member 1A,
transcript variant 1"
GO:0043234|GO:0043066|GO:0090201|GO:0070469|GO:0005743|GO:0071456|GO:0042149|GO:0016021|GO:0055
114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138815_PI430048170 0.227412958029093 2.86120055361777 0.336151625223287
2.66635045961704 2.34200509685483 A A A 0.2678100288804550.85332329707348
0.507213132772587A A A LNCV6_138815_PI430048170 mRNA
CCCTTACCCTGGGCAGGGGTAGAGAGACAAGGAACAATAAAAGTGCTACAGCTCAAAAAA NM_015311RefSeq
chr2 - 219550727 219571546 OBSL1 23363 "obscurin-like 1, transcript variant 1"
GO:0005515|GO:0048471|GO:0005813|GO:0007088|GO:0030018|GO:0005794|GO:0000226|GO:0031430|GO:0005
737|GO:0014704|GO:0050775|GO:0034067|GO:0007010|GO:0007030|GO:0055003|GO:0008093 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129554_PI430048170 0.0894849053155122 0.3819069242461270.478445351732721
0.4815398873242280.323756907360629A A A 0.8986940071150622.28632830441162
1.94064111708417 A A A LNCV6_129554_PI430048170 mRNA
ACAGACTCTGTAGTCACCGGAAATACTTAAGGAATCATGAGGTACTATGTATTTCCTTAA NM_025180RefSeq chr3
+ 134486204 134565028 CEP63 80254 "centrosomal protein 63kDa, transcript variant 1"
GO:0005515|GO:0005813|GO:0006996|GO:0007099|GO:0005814|GO:0051225|GO:0005829|GO:0042770|GO:0000
922|GO:0007067|GO:0000086|GO:0000077|GO:0000278|GO:0051301 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_143115_PI430048170 0.0453535391489025 0.56466351171063 4.01947330654958
3.4501630433449 4.14308098598423 P P P 4.31478062000167 4.88875672210549 4.8991610455206
P P P LNCV6_143115_PI430048170 mRNA
AGACTTCCAAGTGTGCTAATTCTTTACCTCCTAAACTTTTAGTTGCAATTGTTTTGCAGT NM_194292RefSeq chr1 -
100083545 100133095 SASS6 163786 "spindle assembly 6 homolog (C. elegans), transcript variant 1"
GO:0005515|GO:0051298|GO:0005813|GO:0007099|GO:0005814 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_131154_PI430048170 0.4110443780225461.19668594686549 2.97701111444923
3.26546172591335 3.66189512349732 P P P 3.37113358822512 3.07837796249301
2.67772482758309 P P P LNCV6_131154_PI430048170 mRNA
CAGATGCTGTTTACGGATATTTATATTCTAGTCTCACTCTCTTGTCCCACCCTTCTTCTC NM_004106RefSeq chr1 +
161215296 161219248 FCER1G 2207 "Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide"

GO:0033026|GO:0005515|GO:0001812|GO:0032755|GO:0045576|GO:0016064|GO:0005886|GO:0032733|GO:0010543|GO:0050900|GO:0002554|GO:0032998|GO:0019886|GO:0050766|GO:0019863|GO:0019864|GO:0002283|GO:0001798|GO:0019767|GO:0042742|GO:0032765|GO:0009986|GO:0032760|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132523_PI430048170 0.3927175468646951.13001922598683 0.766686038407668 0.2960217774129970.350132208490031A A A 0.2784012938595520.331664386371365 0.320530061784486A A A LNCV6_132523_PI430048170 mRNA TGAAAATAAACCTCACAGAAGCCAGAGTGCAGGTTTGGTTCCAGAACAGAAGGGCCAAAT NM_001276451 RefSeq chr10 - 49366115 49396016 DRGX NA dorsal root ganglia homeobox NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131994_PI430048170 0.0767017347433415 0.8000068025402845.59394909351949 5.91551169864192 5.8160632464435 P P P 6.15517497585254 6.22759880905277 5.90790601571364 P P P LNCV6_131994_PI430048170 mRNA CACTGGGCATGGTAATTAGCCTTTCCCCATGTTAATTTATTCAGTTTTTTCAAGGGTCAA NM_022492RefSeq chr2 + 74483072 74494564 TTC31 64427 "tetratricopeptide repeat domain 31, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130516_PI430048170 0.1215399528410851.23496623692354 10.5383688938809 10.6453194823367 10.5921109607474 P P P 10.0914890731511 10.5160969189489 10.2235451104127 P P P LNCV6_130516_PI430048170 mRNA TCTCTCAGGAATTTGCTTGTTACTTGTACTGTGTAAATAAAGCTTCCTGGTTCAATACCC NM_014661RefSeq chr10 - 124619293 124744361 FAM53B 9679 "family with sequence similarity 53, member B" GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_124087_PI430048170 0.00170345798079443 1.4426918684233 7.53164385118408 7.46155611613431 7.55667222006898 P P P 6.924591550508 7.08045745277928 6.95544591084696 P P P LNCV6_124087_PI430048170 mRNA ATCGATTTGCCAAGGGCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACACAAAG NM_006586RefSeq chr6 + 42929121 42939270 CNPY3 10695 canopy FGF signaling regulator 3 GO:0045087|GO:0005102|GO:0005788|GO:0002224 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_105954_PI430048170 0.9349145557718460.9481452365748 1.7172259486072 2.3389534248219 2.41701263882299 A A A 1.36391237673999 1.99047242962908 2.97986910648423 A A P LNCV6_105954_PI430048170 mRNA ATGAAATGATTTGTATCCTGCAAGGAGATTGCAGTCAGTTCCTGGGTGCATTGTCGCTGA NM_001014283 RefSeq chr13 - 113455818 113490708 DCUN1D2 55208 "DCN1, defective in cullin neddylation 1, domain containing 2" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130629_PI430048170 0.0287706458664918 1.24385029532376 5.08532153817174 4.89757709581923 5.0872754908918 P P P 4.65743336035472 4.84568716398315 4.62046989541579 P P P LNCV6_130629_PI430048170 mRNA AACCCAACGCTTTTTTGGATCAGCTCAGACATATTTCAGTATAAAACAGTTGGAACCACA NM_001130981 RefSeq chr2 + 71453622 71686763 DYSF 8291 "dysferlin, transcript variant 14" GO:0005515|GO:0005886|GO:0005770|GO:0005509|GO:0030315|GO:0030139|GO:0006906|GO:0030027|GO:0042383|GO:0005544|GO:0005543|GO:0001778|GO:0016021|GO:0030659|GO:0005769|GO:0070062|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133041_PI430048170 0.1252014175910210.8205596568640071 1.7652497649524 11.4252204499675 11.8181697868239 P P P 12.0337163632934 11.8532016741735 12.001950451974 P P P LNCV6_133041_PI430048170 mRNA TCAGGATGTTTTTCACTGTCCATTGCTTTGTGTTTTAATAAACAATTTGCAGTGACACTC NM_014730RefSeq chr12 + 120687123 120701864 MLEC 9761 "malectin, transcript variant 1" GO:0016020|GO:0006457|GO:0005783|GO:0005789|GO:0030246|GO:0016021|GO:0019899|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137748_PI430048170 0.0461261097175652 1.57916519383531 6.39495719915274
6.90765604279254 6.80022253685876 P P P 6.2056253120378 6.21291162057069
5.69800181688052 P P P LNCV6_137748_PI430048170 mRNA
AGTATGTTATGATGGACCAATAATTCTGCCACTTCGGGTTTCTCCCTACATTCCTGCTCC NM_014232RefSeq chr17
- 8159146 8162975 VAMP2 6844 vesicle-associated membrane protein 2 (synaptobrevin 2)
GO:0005515|GO:0005802|GO:0005516|GO:0030054|GO:0043312|GO:0045202|GO:0060291|GO:0015031|GO:0006
887|GO:0043621|GO:0006906|GO:0060203|GO:0043231|GO:0017156|GO:0017157|GO:0030672|GO:0070062|GO:0
019905|GO:0032869|GO:0006892|GO:0090316|GO:0016079|GO:0043308|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145282_PI430048170 0.1647591267328521.39763067102302 0.574644405170242
1.12488855948625 1.2670186522786 A A A 0.53058635027796 0.535949254632141
0.539544801908571A A A LNCV6_145282_PI430048170 mRNA
AGTTCTGAAATGCATTTCGTAAGTCTCCTCAAAAGAGGAGGAGACTTCTGTGGCGGGTTT NM_001098272 RefSeq
chr5 - 43287469 43313512 HMGCS1 3157 "3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble),
transcript variant 1"
GO:0006629|GO:0006695|GO:0005886|GO:0009645|GO:0005634|GO:0044281|GO:0014074|GO:0042803|GO:0005
829|GO:0071372|GO:0005737|GO:0071397|GO:0008144|GO:0033197|GO:0044255|GO:0004421|GO:0043177|GO:0
042493|GO:0046690|GO:0008299|GO:0001889|GO:0007420|GO:0055094|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145142_PI430048170 0.000836625612011727 0.5912262165126576.71318231775091
6.62812759575442 6.51449772241461 P P P 7.44768071167618 7.2555794120152
7.42648072340428 P P P LNCV6_145142_PI430048170 mRNA
AGAATTGTGAGCCCGTGGACACTTCTGTACAATAAATCTGCTATTATTACTTCTAGAACT NM_020746RefSeq chr20
+ 3846798 3876123 MAVS 57506 "mitochondrial antiviral signaling protein, transcript variant 1"
GO:0005515|GO:0033160|GO:1900063|GO:0071651|GO:0005741|GO:0002218|GO:0042993|GO:0032757|GO:0005
739|GO:0051607|GO:0051091|GO:0045944|GO:0016032|GO:0004871|GO:0043123|GO:0032480|GO:0005778|GO:0
042742|GO:0045071|GO:0050700|GO:0032728|GO:0031966|GO:0019901|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_126249_PI430048170 0.7110787614568360.9770424513281420.578174707432864
0.4913333760343660.305737531478333A A A 0.4172530391516430.556192319009973
0.512117047004776A A A LNCV6_126249_PI430048170 mRNA
AAACACTGCAGGTGTATATAGATGCTTTCTGTCATACTGTGTTTTCAGATGCAGAATTTT NM_022166RefSeq chr16
- 17102323 17470881 XYLT1 64131 xylosyltransferase I
GO:0034605|GO:0008375|GO:0030206|GO:0000139|GO:0005789|GO:0030158|GO:0005576|GO:0016021|GO:0015
012|GO:0006024 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_113481_PI430048170 0.8110169773614041.02057513076969 2.5544178873017
2.78266097952794 2.68471129802001 A A A 2.84110972522462 2.66656175809985
2.40146650223893 P P A LNCV6_113481_PI430048170 mRNA
AGGAGTGGCATTAACAGACTGAGGAGTGAAATGAAACAGATGACTAGGCGGTTTAGTGCT NM_000292RefSeq
chrX - 18892297 18984362 PHKA2 5256 "phosphorylase kinase, alpha 2 (liver)"
GO:0005516|GO:0005886|GO:0004689|GO:0005975|GO:0005964|GO:0044281|GO:0006091|GO:0004553|GO:0005
829|GO:0009405|GO:0006006|GO:0006468|GO:0005980|GO:0006464 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133814_PI430048170 0.49912958931183 1.31671787607759 0.313593546803649
0.3570980590026151.43277024152516 A A A 0.5005643031545870.402147858279532
0.299435245876138A A A LNCV6_133814_PI430048170 mRNA
CTTTATCAGACCAAAGAGATTCAAGTACACAATATCTGGGGCATTTCTTTTACGTTTTAC NM_001113498 RefSeq
chr14 - 46839624 47674954 MDGA2 NA "MAM domain containing glycosylphosphatidylinositol anchor
2, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_131966_PI430048170 0.8588239622189091.01033590091257 0.266835444105216
0.2785007333084850.454076550909971A A A 0.3474336159989840.298012653044849
0.316758303762094A A A LNCV6_131966_PI430048170 mRNA
GTTGCATTGTATTGTACAGTATGCATATTATTGTTTGTGGTTGCATATGGCAATGAAGTG NM_001113511 RefSeq
chr13 + 111115276 111295195 ARHGEF7 8874 "Rho guanine nucleotide exchange factor (GEF) 7,
transcript variant 3"
GO:0005515|GO:0043005|GO:2000394|GO:0007264|GO:0030032|GO:0032855|GO:0005829|GO:0005085|GO:0010
763|GO:1900026|GO:0007173|GO:0007411|GO:0002244|GO:0048041|GO:0043025|GO:0005089|GO:0005938|GO:0
051056|GO:0048011|GO:0043065|GO:0019901|GO:0048013|GO:0042059|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_128310_PI430048170 0.1025693937080490.6863448591257354.85438079666725
4.51037480855826 4.58744350485706 P P P 4.7954175200775 5.47483825010398
5.25322531021425 P P P LNCV6_128310_PI430048170 mRNA
GATGTTGTAATGGGCTATACAGTCCAGCAGGCAGTATGCACCTAGAAATTTCTCCCTTTT NM_005897RefSeq chr1
- 45698734 45750813 IPP 3652 "intracisternal A particle-promoted polypeptide, transcript variant 1"
GO:0005737|GO:0003779|GO:0015629 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138855_PI430048170 0.9651403160437270.8775800193973172.98023550271912
3.15711751429328 3.39233645248784 A P P 2.19265636398133 3.45185788777658
3.96419421281874 A P P LNCV6_138855_PI430048170 mRNA
CGAATGAATCATCTGTTCATGCATGCTCTACTTTGATATTATAACCTATGTCACATGTGT NM_001018100 RefSeq
chr15 + 57591903 57685364 MYZAP 100820829 "myocardial zonula adherens protein, transcript
variant 1" GO:0035556|GO:0005515|GO:0030018|GO:0030054|GO:0030864|GO:0031674|GO:0031234 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_132553_PI430048170 0.000934893072364748 1.79937012965832 8.00375016754835
8.12914406498127 8.25086835542391 P P P 7.15954812343478 7.33263782578859
7.35199883070708 P P P LNCV6_132553_PI430048170 mRNA
GAAGGATTCAGGAAGAAGAAAACTCAACTCAGTGCCATTTTACGAATATATGCGTTTATA NM_001243539 RefSeq
chr10 - 5952370 5978187 IL15RA 3601 "interleukin 15 receptor, alpha, transcript variant 3"
GO:0005515|GO:0007165|GO:0031965|GO:0004896|GO:0000139|GO:0008283|GO:0019221|GO:0005789|GO:0016
021|GO:0004871|GO:0005615|GO:0030659 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_137909_PI430048170 0.655158945155125 0.970024462375549 0.571021604051632
0.496490642455852 0.285827891665209 A A A 0.416116772379919 0.567922459025537
0.511892368393487 A A A LNCV6_137909_PI430048170 mRNA
CAGATTGGTCTAGATAGACCTTACCTGTCACATATACTATGAATCAGGTTTTGTTAATGA NM_018451 RefSeq
chr13 - 24882273 24922889 CENPJ 55835 "centromere protein J, transcript variant 1"
GO:0005515|GO:0005813|GO:0006996|GO:0007099|GO:0019901|GO:0005814|GO:0019904|GO:0005874|GO:0046
599|GO:0005829|GO:0046785|GO:0015631|GO:0000086|GO:0007020|GO:0000278|GO:0008275|GO:0051301 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_121766_PI430048170 0.371454626420999 0.831398307966614 2.57503719993878
2.44844860679288 2.51273407977723 A A A 3.03239047010241 2.87603513285047
2.34308816715882 P P P LNCV6_121766_PI430048170 mRNA
TATCCTGCCTGGTATTGTCATCCTGTCCTGCTATTGCATTATCATCTCCAAGCTGTCACA NM_001008540 RefSeq
chr2 - 136114348 136116243 CXCR4 7852 "chemokine (C-X-C motif) receptor 4, transcript variant 1"
GO:0005515|GO:0043130|GO:0019722|GO:0030260|GO:0007281|GO:0005764|GO:0001618|GO:0031625|GO:0032
027|GO:0070062|GO:0030334|GO:0070098|GO:0009986|GO:0004930|GO:0008045|GO:0019955|GO:0007186|GO:0
071345|GO:0007420|GO:0016494|GO:0042119|GO:0009897|GO:0005886|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_66099_PI430048170 0.504289709440098 1.12076947787592 6.20873616145338

6.17095182145333 6.27410082472475 P P P 6.52244544793148 5.84063069930693
5.64665480262398 P P P LNCV6_66099_PI430048170 mRNA
AATTTTGAGAAAGTATTCTGTTGGGATCTGGGCTTCCTCACTTCTGGAGAAGTGGCCATC NM_001031738 RefSeq
chr2 - 85598546 85602699 TMEM150A 129303 "transmembrane protein 150A, transcript variant
1" GO:0030262|GO:0005886|GO:0009056|GO:0016021|GO:0005764 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142621_PI430048170 0.0104281425198513 1.407768127834 5.54115729118044
5.59474250813385 5.38820859842596 P P P 5.16537320542125 4.99032713638845
4.88176697787117 P P P LNCV6_142621_PI430048170 mRNA
ATTTTGTGGTTTACACGGTTGTCCTCCCTCTAAACTTACTCTCAGGGGCTTCTCTGTCAT NM_148887 RefSeq chr17
- 47823271 47831541 MRPL10 124995 "mitochondrial ribosomal protein L10, transcript variant 2"
GO:0070124|GO:0070125|GO:0070126|GO:0003735|GO:0006996|GO:0032543|GO:0042254|GO:0005743|GO:0006
412|GO:0005762|GO:0005739|GO:0030529|GO:0005654 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_133665_PI430048170 0.847199488286765 1.02917663052567 10.7547635152308
10.8428022280271 11.2850863057347 P P P 10.642646674404 10.7368220219594
11.3347926439784 P P P LNCV6_133665_PI430048170 mRNA
GTACGTACACATTGTGCTCTGGAGTGCCTATTTATTGAAATCATTGTAAGACCTGTTATA NM_000317 RefSeq
chr11 + 112226364 112233972 PTS 5805 6-pyruvoyltetrahydropterin synthase
GO:0006520|GO:0003874|GO:0006729|GO:0050999|GO:0044281|GO:0007417|GO:0042803|GO:0046872|GO:0005
829|GO:0042802|GO:0005739|GO:0005737|GO:0046209 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_89279_PI430048170 0.447755836252427 0.707556569068033 0.375804957431719
0.268167978444016 0.319912126904987 A A A 1.5083026330676 0.291282648420491
0.300516455209162 A A A LNCV6_89279_PI430048170 mRNA
CCGACATGCAGGAAGTCATCGGCACGGCCATTGCATTCAATCTGCTCTCAGCTGGACGAA NM_000578 RefSeq
chr2 + 218382028 218396894 SLC11A1 6556 "solute carrier family 11 (proton-coupled divalent metal
ion transporter), member 1"
GO:0006909|GO:0046915|GO:0001818|GO:0001819|GO:0070839|GO:0005764|GO:0042803|GO:0006879|GO:0007
035|GO:0070574|GO:0030670|GO:0032496|GO:0048255|GO:0042742|GO:0000060|GO:0032729|GO:0002369|GO:0
051701|GO:0042832|GO:0060586|GO:0015707|GO:0042116|GO:0005887|GO . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_64015_PI430048170 0.0628588444012517 0.599571010601932 0.446938679389856
0.279619450291855 0.424708578621167 A A A 0.983496753708286 1.48432068052568
0.817024636583754 A A A LNCV6_64015_PI430048170 mRNA
ATTCAGAGGATAGCAGCAACTTCAAAGATTGGTAGACTCTCTGCTCCAGGTTCTCAACGT NM_002091 RefSeq
chr18 + 59220167 59230770 GRP 2922 "gastrin-releasing peptide, transcript variant 1"
GO:0007165|GO:0007218|GO:0005102|GO:0005576|GO:0005184|GO:0005615 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_110813_PI430048170 0.419222029895199 1.26037115207632 5.77451373413029
5.85810921516987 6.58837956666304 P P P 5.24690840840325 5.84802458299122
6.13397495818359 P P P LNCV6_110813_PI430048170 mRNA
TAACAAAGTTTTCTTTAGAACGTCAGACTTGGGATCAGCTCTTGCTTCACTACCAGCAGG NM_001145316 RefSeq
chr20 - 36751790 36773751 DSN1 79980 "DSN1, MIS12 kinetochore complex component,
transcript variant 1"
GO:0005515|GO:0007067|GO:0005737|GO:0007059|GO:0005634|GO:0000444|GO:0000278|GO:0051301|GO:0005
829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145649_PI430048170 0.25911719520003 0.69908639273349 0.328540352082301
0.304608435039912 0.269977174217191 A A A 0.250617043493788 0.757777689691674

1.26734352579321 A A A LNCV6_145649_PI430048170 mRNA
AAACCACAGTCCTCACCACAGTTTATTGATTTCAAATTGTCTGGTACTATTGGAACAAAT NM_006898 RefSeq chr2
+ 176164076 176173098 HOXD3 3232 homeobox D3
GO:0005515|GO:0006355|GO:0003700|GO:0051216|GO:0048704|GO:0005634|GO:0030878|GO:0009952|GO:0006
351|GO:0010628|GO:0043565|GO:0007160|GO:0007219|GO:0045666|GO:0005654 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_138770_PI430048170 0.00122096900148422 1.7149419563444 6.76589376214094
6.89959442183644 6.94318014183586 P P P 6.2108231130022 5.96815362851804
6.09087509046934 P P P LNCV6_138770_PI430048170 mRNA
CCTGGTTAGAGGCATAAAGACCTTTTTTCACCGTTACCTAATTTTTTCCCCTTTCAAGAA NM_020993 RefSeq chr12
+ 122021885 122062044 BCL7A 605 "B-cell CLL/lymphoma 7A, transcript variant 1"
GO:0003674|GO:0005575|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141317_PI430048170 0.624864876894798 1.03059541668291 0.274500962273604
0.2876550288579460.489922654927597 A A A 0.3329403499151840.288133974537666
0.310484092066364 A A A LNCV6_141317_PI430048170 mRNA
ACAGCCTGTAGAGTTTCAACCTCTTTGAGATATAAGTATCTTAAATATCATAGAGCACTG NM_018409 RefSeq chr4
- 185363877 185378998 LRP2BP 55805 LRP2 binding protein GO:0005515|GO:0005737 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_126761_PI430048170 0.3065459656528070.9651734358794270.247796237408669
0.2612007979924080.362762933447837 A A A 0.3882599018457920.322240471868607
0.316328954860993 A A A LNCV6_126761_PI430048170 mRNA
CTTGTAAGTTGTCCTGCAAATGAAATTACTGTCTGGAAAACTGCAATTTCATCTTGAGAG NM_207372 RefSeq chr10
+ 80537901 80646560 SH2D4B387694 "SH2 domain containing 4B, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_129595_PI430048170 0.0672940808155275 0.5700249719032182.90618359801316
3.79156665639392 3.57579566954888 A P P 4.02187144055343 4.30304691766781 4.4840022140736
P P P LNCV6_129595_PI430048170 mRNA
ACATCTGGAGTTGGGACTTTGTTCACTTTCAATCTAAGAAAACTATGCGTAAAATATGTC NM_152420 RefSeq chr9
- 74982956 75028394 C9orf41 138199 chromosome 9 open reading frame 41 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_89086_PI430048170 0.00808360658065915 1.45953913084626 13.2562968144883
13.5420483953296 13.4392330561138 P P P 12.7505686480527 12.929662245069
12.9279504814549 P P P LNCV6_89086_PI430048170 mRNA
GAACCTGGAGCTTTATTATCAATAGATGAGAATCCTCATCTTCCTGCCCCGCTTTCCTCT NM_024292 RefSeq chr19
+ 9827891 9830121 UBL5 59286 "ubiquitin-like 5, transcript variant 1"
GO:0005515|GO:0008150|GO:0003674|GO:0005737|GO:0000398|GO:0031386|GO:0005634|GO:0006464 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131196_PI430048170 0.3670766405446740.6470511774340940.4399278663890770.4609598907599
0.330311208577498 A A A 1.75822918540609 0.49399652364455 0.460165282935291 A A A
LNCV6_131196_PI430048170 mRNA
ATGTAAAGCCTGAAGGCCTTTGTTGGGCAGGACGGCAATAAAGTCTCTGACATCCCCTCA NM_001080464 RefSeq
chr14 + 104085685 104112709 ASPG 374569 asparaginase
GO:0016042|GO:0004622|GO:0004067|GO:0006528|GO:0003847|GO:0006644 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142696_PI430048170 0.1777606301494760.7766512031528519.57554053889373
9.13332543887953 8.90538229130401 P P P 9.71746342991743 9.61835264661574
9.44092296494807 P P P LNCV6_142696_PI430048170 mRNA
TCAACTCTTCTGCCTTCTCCCCTGATGGCCAGATGCTGCTCACAGGCTCAGAAGATGGCT NM_001276374 RefSeq
chr9 + 124853416 124857891 WDR38 401551 "WD repeat domain 38, transcript variant 1" NA . NA -

. NA NA NA NA NA NA NA NA NA
LNCV6_127777_PI430048170 0.1382502987321330.8307468467691323.94592336742343
3.68047758347642 3.81843867837258 P P P 4.14132923929161 4.23541191448092
3.85642984477252 P P P LNCV6_127777_PI430048170 mRNA
AGTGAGGATAAAGACTGGGCTGCCAAGGAGGACTCCTCATAAACATTGACAAATTGCTCT NM_019089RefSeq chr1
- 6415233 6419919 HES2 54626 hes family bHLH transcription factor 2
GO:0003690|GO:0046983|GO:0005634|GO:0045892|GO:0006351|GO:0008134 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131398_PI430048170 0.4772057297531031.03727456003429 14.3803086342672
14.3974152667537 14.351007416131 P P P 14.4452503814486 14.2816929381094
14.2352457611523 P P P LNCV6_131398_PI430048170 mRNA
CCTTCAAATAAAAGTCACCCCTGCATGGTGAAGTCTTCCCTCTGCTTCTCTCATAAAAAA NM_001012662 RefSeq
chr11 + 62856011 62888883 SLC3A2 6520 "solute carrier family 3 (amino acid transporter heavy
chain), member 2, transcript variant 2"
GO:0005515|GO:0003725|GO:0005886|GO:0043169|GO:0006865|GO:0005634|GO:0003824|GO:0050900|GO:0005
432|GO:0005737|GO:0016324|GO:0015175|GO:0006816|GO:0035725|GO:0060356|GO:0070062|GO:0006811|GO:0
042470|GO:0009986|GO:0005975|GO:0055085|GO:0015827|GO:0016020|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131146_PI430048170 0.428113165300036 1.41498878516376 1.6689586366352
0.4746793490778230.483261159952127A A A 0.3308263206203380.716892297732188
0.396024823942708A A A LNCV6_131146_PI430048170 mRNA
CCAAATTATAGAACAAAAATAAGCCAAAGGATTGGAGTGTTTCAAACACATGCTTTCGTC NM_207103RefSeq chr17
- 5208920 5234860 SCIMP 388325 "SLP adaptor and CSK interacting membrane protein, transcript
variant 1"
GO:0005515|GO:0001772|GO:0031256|GO:0016020|GO:0031259|GO:0097197|GO:0070374|GO:0016021 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142864_PI430048170 0.2370738597144090.569092921343771 2.09950399001692
0.263334375065187 1.65109678486246 A A A 2.87930694450261 2.09909379656117
1.81398786438505 P A A LNCV6_142864_PI430048170 mRNA
ATCCCGCCCGACTGGAGGATAGAGAAGACGTACCTCTACCTGTGCTATGTGTGAAGGGAG NM_006006RefSeq chr11
+ 114059708 114250675 ZBTB16 7704 "zinc finger and BTB domain containing 16, transcript variant 1"
GO:0005515|GO:0035136|GO:0034504|GO:0008285|GO:0016567|GO:0005886|GO:0051216|GO:0005634|GO:0009
952|GO:0045778|GO:0046872|GO:0042803|GO:0042802|GO:0005829|GO:0009880|GO:0003690|GO:0051138|GO:0
045638|GO:0017053|GO:0030099|GO:0032332|GO:0030097|GO:0043065|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141915_PI430048170 0.7206760047024181.07022449283494 0.317553585167283
0.3544821200286240.878869440327866A A A 0.4462031094978850.363086578608673
0.514724888280661A A A LNCV6_141915_PI430048170 mRNA
CTGAAAACCTCACATGCATACATACACATATATACACACACAAAGAGAGTTAATCAACTG NM_001128834 RefSeq
chrX + 103776505 103792618 PLP1 5354 "proteolipid protein 1, transcript variant 3"
GO:0005886|GO:0022010|GO:0007268|GO:0008366|GO:0010628|GO:0006954|GO:0005198|GO:0007229|GO:0014
002|GO:0021762|GO:0043209|GO:0042759|GO:0048469|GO:0019911|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_139573_PI430048170 0.25314096556737 1.03488820348107 0.383100226815974
0.3936442750730190.304513105582759A A A 0.2867706354805190.358599372818242
0.287916934433475A A A LNCV6_139573_PI430048170 mRNA
CTTGCACCCAAGTAATCTTGAAGGGAACTTCTCTTGGTTTTTAAACATACTAGTTATAAG NM_148674RefSeq chr22
- 45344063 45413619 SMC1B 27127 "structural maintenance of chromosomes 1B, transcript variant 1"
GO:0005737|GO:0007126|GO:0030893|GO:0007062|GO:0034991|GO:0005654|GO:0000800|GO:0005524|GO:0003

677|GO:0000775 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143755_PI430048170 0.0182866271727551 1.46508083268317 10.5178196200406
10.7032837214814 10.8034778413587 P P P 10.1427932594419 10.0894220992271
10.1530302956692 P P P LNCV6_143755_PI430048170 mRNA
TATATATATGTATGTATTGTTCCCGGTTTTGTACGGACCATGCCCTCTGTCAGGTCGTCC NM_032595 RefSeq chr17
- 50133734 50150517 PPP1R9B 84687 "protein phosphatase 1, regulatory subunit 9B"
GO:0005515|GO:0008380|GO:0030308|GO:0019722|GO:0005886|GO:0004864|GO:0007096|GO:0045202|GO:0030
175|GO:0005737|GO:0043197|GO:0005912|GO:0001560|GO:0000164|GO:0042127|GO:0046847|GO:0007050|GO:0
007015|GO:0050804|GO:0003779|GO:0032587|GO:0071315|GO:0043086|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_135407_PI430048170 0.0842774541079022 1.5196924493846 4.3225852130284
4.81365893099033 4.13845557953635 P P P 3.6883109301966 4.01479386749795
3.82831423104885 P P P LNCV6_135407_PI430048170 mRNA
GAAGACTACGTGGTCAACACTTACTTCCGCCACTTCAAGCTCTATAAATACGTCTTCACA NM_001014979 RefSeq
chr16 - 30757422 30762244 C16orf93 90835 "chromosome 16 open reading frame 93, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_106003_PI430048170 0.9926017185535191.00357664341557 2.56455177746293
3.36224574044621 2.37659813656683 A P A 3.33816939488665 2.64202861925281
2.31053852601454 P A A LNCV6_106003_PI430048170 mRNA
TTATAATGCAATCCTGCTGGGCTTTTGACTCAAGGAAACGGCCATCCTTCCCTAATTTGA NM_004119 RefSeq chr13
- 28003273 28100592 FLT3 2322 "fms-related tyrosine kinase 3, transcript variant 1"
GO:0045578|GO:0005515|GO:0008284|GO:0008285|GO:0019221|GO:0031100|GO:0005634|GO:0035259|GO:0097
028|GO:0032403|GO:0042803|GO:0005829|GO:0046777|GO:0043552|GO:0043406|GO:0030183|GO:0005021|GO:0
002328|GO:0035726|GO:0038084|GO:0001776|GO:0030097|GO:0042531|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141257_PI430048170 0.1801474934588680.67910925559859 4.67070194258867
4.44156481480023 4.78925062075973 P P P 4.75407811916888 5.04555305593551
5.64978644565341 P P P LNCV6_141257_PI430048170 mRNA
GGATCAACTCCATCTTACTAACCATTTGATTCCCTATGTATTACACGATATATGACCAAT NM_148170 RefSeq chr11
- 88320812 88337773 CTSC 1075 "cathepsin C, transcript variant 2"
GO:0005515|GO:0031404|GO:0005794|GO:0010033|GO:0004252|GO:0019902|GO:0005783|GO:2001235|GO:0007
568|GO:0051087|GO:0006915|GO:0043621|GO:0005615|GO:0005764|GO:0042802|GO:0016505|GO:0006955|GO:0
016020|GO:0001913|GO:0006508|GO:0008234|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_61136_PI430048170 0.8130467718346 0.9649059323527392.58471305321456 3.0192957620455
2.47416123656817 A P A 2.96995331454722 2.81030671147348 2.46697482136671 P P P
LNCV6_61136_PI430048170 mRNA
ACTTTGTGAGCGAGGACTCCATCTTCCTGCACCTGGAGCATGTGCAAGGAGGCACTCTCT NM_031464 RefSeq chr14
- 74903953 74922442 RPS6KL1 83694 ribosomal protein S6 kinase-like 1
GO:0004674|GO:0005840|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141106_PI430048170 0.5733626220674451.17526515318688 0.242725720389464
1.08215540126486 0.304068313771634 A A A 0.43576459031685 0.341825552708181
0.308890104166618 A A A LNCV6_141106_PI430048170 mRNA
TTTTGAGAGTGGAAAAGAAATTTAAACTTCCCGAAAGAAGGTCCACCATCAGGAGATGAA NM_198545 RefSeq chr1
+ 11691723 11720279 DRAXIN 374946 dorsal inhibitory axon guidance protein
GO:0043524|GO:0030517|GO:0007411|GO:0005576|GO:0030900|GO:0016055|GO:0090090|GO:0021528|GO:0021
516 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130579_PI430048170 0.00881155907626783 0.47462557908714 5.28159464925448
4.89320573232475 5.02791756756417 P P P 6.19399919958092 6.11732635761792

6.14301766793162 P P P LNCV6_130579_PI430048170 mRNA
CCTCTGTTTTTTCCCCTTTAAAGGAAACTTTGAAAGGATTGTGAATACTGGAAAATGACA NM_201263 RefSeq chr1
- 119031215 119140672 WARS2 10352 "tryptophanyl tRNA synthetase 2, mitochondrial, transcript variant
2" GO:0006436|GO:0010467|GO:0004830|GO:0005759|GO:0005524|GO:0001570|GO:0006418 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128715_PI430048170 0.0769518588017176 0.89097114884713611.5264075395037
11.4667679801118 11.6017095143442 P P P 11.6834033186228 11.6095369814006
11.7984578277103 P P P LNCV6_128715_PI430048170 mRNA
AGCTGAGTTGAGACTTTGGAATAAGACACTGGTTTTCATGCGCTGTTTTTGTTTTAAAGT NM_004111 RefSeq chr11
+ 61792636 61797242 FEN1 2237 flap structure-specific endonuclease 1
GO:0005515|GO:0009650|GO:0008409|GO:0090305|GO:0005886|GO:0005634|GO:0006302|GO:0005739|GO:0004
527|GO:0006271|GO:0003690|GO:0000723|GO:0004523|GO:0000722|GO:0007613|GO:0008309|GO:0030145|GO:0
000287|GO:0005730|GO:0003677|GO:0003684|GO:0006260|GO:0004519|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133114_PI430048170 0.0420705529521391.23218730060232 5.78666640408019
5.57745511354887 5.83167143477813 P P P 5.48531609822353 5.46833671063388
5.34712141339991 P P P LNCV6_133114_PI430048170 mRNA
GCCCTACAGCTTCCCTAGGCAGTAAGTAAAAACATTCTCCTAGCATTAAAATGGTTTCCA NM_023112 RefSeq
chr14_KI270847v1_alt + 1140939 1163492 OTUB2 78990 "OTU deubiquitinase, ubiquitin aldehyde
binding 2" GO:0071108|GO:0016579|GO:0004843|GO:0070536|GO:0006508|GO:0005634|GO:0035871 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127119_PI430048170 0.349664196038605 1.13098287862187 11.1837588053909
11.4258555311605 11.1970141199172 P P P 10.8985586878355 11.3824360677304
10.9560631884475 P P P LNCV6_127119_PI430048170 mRNA
TTGTTTTTCAAAGGCCTCACCTTCAACTGTCTGTCTTAGAATTCCCCTCTGGAGGGCTAT NM_001142777 RefSeq
chr16 + 30985197 30989152 HSD3B780270 "hydroxy-delta-5-steroid dehydrogenase, 3 beta- and
steroid delta-isomerase 7, transcript variant 2"
GO:0006699|GO:0005789|GO:0008206|GO:0047016|GO:0044281|GO:0016021|GO:0005575|GO:0003854|GO:0055
114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130752_PI430048170 0.0729096187390642 0.5765848394834446.80185452305664
6.50630205299046 6.72974261130123 P P P 6.99571624352192 7.50294024240285
7.82167854307559 P P P LNCV6_130752_PI430048170 mRNA
GAACCATAAATCTTAAAGGGGGTATGTGATAATAGAGGGCTGGAATTTAAACCTGTATTT NM_006526 RefSeq chr20
- 53567070 53583097 ZNF217 7764 zinc finger protein 217
GO:0005515|GO:0001078|GO:0006355|GO:0003700|GO:0000118|GO:0044212|GO:0005654|GO:0000122|GO:0000
978|GO:0045892|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66271_PI430048170 0.0156030350485558 0.5599935468604139.34447438414677
9.19559559763728 9.68769594543424 P P P 10.1551416034715 10.2353438090206
10.3825055081817 P P P LNCV6_66271_PI430048170 mRNA
CATCCTGTCGTAGATCTTAATGTTTTTGATCGTTGCGTTAAAGTGGAAGTGCCACCCACA NM_145212 RefSeq chr2
+ 99181078 99199557 MRPL3051263 "mitochondrial ribosomal protein L30, transcript variant 1"
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0005743|GO:0005840 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137576_PI430048170 0.11863640023666 0.9635483755552920.288778876011139
0.3193408997511030.351423480507263 A A A 0.4108313277575620.366643010637982
0.342630822500123 A A A LNCV6_137576_PI430048170 mRNA
GATGGTTTCTTACCTTTGAGCACAAAATTTCCACGGTGAAATAAAGTCAACATTATAAGC NM_002521 RefSeq chr1
- 11857463 11858935 NPPB 4879 natriuretic peptide B
GO:0007589|GO:0030308|GO:0008613|GO:0005102|GO:0005576|GO:0005615|GO:0043234|GO:0042312|GO:0050

880|GO:0005179|GO:0006182|GO:0035815|GO:0016525|GO:0043114|GO:0008217|GO:0007168|GO:0035810|GO:0
007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132459_PI430048170 0.6165906555865060.9307839317642353.10292495208673
3.44625645048512 3.96544538464891 P P P 3.63309746860413 3.63428522055648
3.68924901948809 P P P LNCV6_132459_PI430048170 mRNA
CAAAACTTTGAGATAACGAAACCCCTATTCAAATGTAAATTTTACCCATTCCCACCTGAT NM_018342RefSeq chr4
+ 158210248 158255287 TMEM144 55314 transmembrane protein 144 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139673_PI430048170 0.82999278534973 1.05157285694527 2.93445686770052
3.02421934078198 2.21190791311887 A A A 3.18422672801502 2.22015796671091
2.50150568381955 P A P LNCV6_139673_PI430048170 mRNA
GAGCTTCCACCACCTGTGCAGTTGTCACTTTCCTTTCACTCCCTGAATAAAGAATCTATG NM_001014450 RefSeq
chr1 - 153112123 153113515 SPRR2F NA small proline-rich protein 2F NA . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144856_PI430048170 0.0696492943929088 0.7914832795947147.43013916705597
7.42251825353723 7.75771190586452 P P P 7.97282014769355 7.74482599065203
7.92104867504213 P P P LNCV6_144856_PI430048170 mRNA
AATTCCTGGCACTTCTTTTTACTGTCTATAAGAGAAAACCTATCATAAGCCCAATTTTTTNM_017444RefSeq chr8 +
140511297 140517153 CHRAC1 54108 "chromatin accessibility complex 1, transcript variant 1"
GO:0043565|GO:0008623|GO:0008622|GO:0071897|GO:0046982|GO:0003887|GO:0006338|GO:0003677 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_123101_PI430048170 0.0872784091435136 0.7719019747750535.37972647814317
5.44163585487127 5.6378867285524 P P P 5.67321186780043 5.77889295812038
6.10465640779999 P P P LNCV6_123101_PI430048170 mRNA
AGCTCTATTAAGCTGAAAGATAAAAACTCTCCAGATGTCTTCCAGTAATGTCGAAGTTTT NM_004827RefSeq chr4
- 88090263 88158859 ABCG2 9429 "ATP-binding cassette, sub-family G (WHITE), member 2 (Junior
blood group), transcript variant 1"
GO:0005515|GO:0005215|GO:0015886|GO:0031966|GO:0005886|GO:0015232|GO:0042493|GO:0042626|GO:0042
908|GO:0005634|GO:0044281|GO:0046415|GO:0055085|GO:0005524|GO:0042803|GO:0006879|GO:0008559|GO:0
006855|GO:0006810|GO:0005654|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129010_PI430048170 0.0167056972063760.4496030337773116.95720940271951
6.41810475354592 6.55052458041178 P P P 7.42852990797016 7.72732828366814
8.18427219345501 P P P LNCV6_129010_PI430048170 mRNA
ATGAGACTCACACCATGTATTATTATTCACTAGCACCCTAGGTGTGATAATTGAAGTAAA NM_001202543 RefSeq
chr7 + 101815903 102258233 CUX1 1523 "cut-like homeobox 1, transcript variant 4"
GO:0000977|GO:0042491|GO:0006357|GO:0001822|GO:0030324|GO:0001205|GO:0006891|GO:0005634|GO:0007
275|GO:0000122|GO:0006351|GO:0005829|GO:0043565|GO:0030173|GO:0050775|GO:0045944|GO:0003682 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_125245_PI430048170 0.0637804651099424 0.8394887169996059.16964586972325
9.27104046803787 9.01135921684125 P P P 9.45981734454158 9.38785997994451 9.3718785911854
P P P LNCV6_125245_PI430048170 mRNA
ATAAGCCCAAGAGAACTGTGAAGGTGGTAGTCCCTTGCCCTAATTGGTGCTCAATAAAGT NM_001195220 RefSeq
chr7 + 149262170 149284994 ZNF783 100289678 zinc finger family member 783
GO:0003712|GO:0006357|GO:0005634|GO:0003677|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135648_PI430048170 0.0152272446362736 0.1236444997182070.445036968402677
0.4727764548829062.18473636154959 A A A 4.54950725372155 3.60379141842541
4.55024440921909 P P P LNCV6_135648_PI430048170 mRNA
GCCTGCTCTAATTTCTTTTGCCCATATATGAGTATCTCCAGAATGTCTACAAATAGTTTT NM_003986RefSeq chr11 +

27040961 27127807 BBOX1 8424 "butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1"
GO:0005739|GO:0034641|GO:0008336|GO:0005506|GO:0045329|GO:0008270|GO:0044281|GO:0070062|GO:0055114|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127936_PI430048170 0.467540433512577 0.82656067749455 2.7726851056665 1.86224142730217 1.61630107347741 A A A 2.28454759437911 2.14973687836551 2.82088755593059 A A P LNCV6_127936_PI430048170 mRNA
TCAGGAAAACAATTGTATTCCCAGCCTGTGTCCCATGGGCACAAGCAAATCCCAAATTCT NM_006905 RefSeq chr19 - 42867205 42879719 PSG1 5669 "pregnancy specific beta-1-glycoprotein 1, transcript variant 1"
GO:0007565|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142891_PI430048170 0.656703632193088 0.995607960006167 0.343835914657376 0.362664385811473 0.324369290099008 A A A 0.351628837890129 0.361580104437902 0.33685857997352 A A A LNCV6_142891_PI430048170 mRNA
ATGAGGAAACTTTGGAGTAAAAAAGTAAGCTTAGCTGGGAAATGGCTGTATCACTCATGA NM_001005275 RefSeq chr11 + 55367883 55368918 OR4A1581328 "olfactory receptor, family 4, subfamily A, member 15"
GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144603_PI430048170 0.270717495407001 0.711436042109392 4.43992904068489 3.79732103126013 3.06918030671425 P P P 4.36452060639751 4.44578462978253 4.28209540015659 P P P LNCV6_144603_PI430048170 mRNA
GGAGTCACTCCTTCCTCAGCCCCCAGGGCAAGAGAGCTCAAATAAAAACCAGAGGACTGA NM_001144825 RefSeq chr17 + 44308558 44318670 RUNDC3A 10900 "RUN domain containing 3A, transcript variant 1" GO:0005083|GO:0030250|GO:0005886|GO:0007264|GO:0031284|GO:0051428|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131431_PI430048170 0.119221708408385 1.06549793799719 0.455719207436504 0.496631672449963 0.521446292773108 A A A 0.332527935167938 0.400775444669301 0.463692026762726 A A A LNCV6_131431_PI430048170 mRNA
ATCTTTTTCTGTATTGACAACTGCCCTGACTGTGGCAACAGGTCATTTTATGACCTGGAG NM_001010890 RefSeq chr1 + 13175280 13179132 PRAMEF9 NA PRAME family member 9 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130163_PI430048170 0.810382801015255 1.50514852857765 2.78422019707696 0.39147665912838 0.380334555498262 A A A 1.74086173653019 0.331154361417073 0.776227822858148 A A A LNCV6_130163_PI430048170 mRNA
CTGAGGAATAAGGACGTCAAAGTTGCTCTAAAGAAAATCTTGAACAAAAATGCATTCTCC NM_012378 RefSeq chr11 - 124440149 124441085 OR8B8 26493 "olfactory receptor, family 8, subfamily B, member 8"
GO:0050911|GO:0007608|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_62916_PI430048170 0.509842803953883 1.47688744754025 1.20966536123718 2.53663044303411 3.04611339904784 A A P 2.2496433504124 0.460086366153193 2.30924313908465 A A A LNCV6_62916_PI430048170 mRNA
GTATATCCCATGAAGACCTCATCCAGAACTTCCTGAATGCTGGCAGCTTTCCTGAGATCC NM_005310 RefSeq chr17 + 39737908 39747285 GRB7 2886 "growth factor receptor-bound protein 7, transcript variant 1"
GO:0005515|GO:0017148|GO:0030335|GO:0005886|GO:0019901|GO:0010494|GO:0003723|GO:0009967|GO:0042995|GO:0050900|GO:0042802|GO:0005829|GO:0034063|GO:0007173|GO:0007596|GO:0005070|GO:0035091|GO:0005925 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_23518_PI430048170 0.0325533062448044 3.46534729588279 3.81937440371138 3.64735041336243 3.6863294479582 P P P 2.45215641859037 1.85843144363673 1.20547790849918 A A A LNCV6_23518_PI430048170 mRNA
ATGCTTGGGTTTTGTCTTTAACCTTGTAACGCTTGCAATCCCAATAAAGCATTAAAAGTC NM_000612 RefSeq chr11

- 2129111 2138974 IGF2 3481 "insulin-like growth factor 2, transcript variant 1"
GO:0005515|GO:0005159|GO:0005158|GO:0050731|GO:0005615|GO:0009887|GO:0031667|GO:0007613|GO:0032
355|GO:0070062|GO:2000467|GO:0007565|GO:0030168|GO:0007275|GO:0045840|GO:0038028|GO:0043085|GO:0
001649|GO:0001501|GO:0005179|GO:0030546|GO:0043539|GO:0008083|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_39320_PI430048170 0.0132180821759652 0.6340891998370268.38940820524771
8.31529669303904 8.45812508763319 P P P 9.04115370920912 8.86314115394261
9.21266510519034 P P P LNCV6_39320_PI430048170 mRNA
TTAACTAACCCAAAGTCCAGGAGGATGTTCTTACAAAAATAGCTATATCAAGGGCTGGCA NM_017512RefSeq chr18
- 670323 712662 ENOSF155556 "enolase superfamily member 1, transcript variant 1"
GO:0005739|GO:0044275|GO:0000287|GO:0005575|GO:0016853|GO:0009063|GO:0050023 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_142445_PI430048170 0.40672056916816 0.8384490162359149.2513869773489
8.95511287707751 9.28097954376769 P P P 8.98690961990457 9.47785161031221
9.71487332551337 P P P LNCV6_142445_PI430048170 mRNA
AAGCACTGCTTCTGTATGTCTCTTGTGGTATTGGAACAATAAACCCGTACAACCTGCAAA NM_015338RefSeq chr20
+ 32358343 32439319 ASXL1 171023 "additional sex combs like transcriptional regulator 1, transcript
variant 1"
GO:0005515|GO:0000790|GO:0045599|GO:0003714|GO:0003713|GO:0035359|GO:0000122|GO:0042974|GO:0003
677|GO:0042975|GO:0046872|GO:0006351|GO:0035517|GO:0060348|GO:0048386|GO:0048387|GO:0035522|GO:0
045944|GO:0032526|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130003_PI430048170 0.6981858631355061.09535755125143 1.06297788525178
0.5511602935661090.320156098939524A A A 0.4127991355929970.676496403634201
0.541337568547285A A A LNCV6_130003_PI430048170 mRNA
ATGGTCATCACAGAGGTGTGGGACAACGTGGCTGAGATGCACATGGCCCTGAACAACCAG NM_001243537
RefSeq chr22 - 20148585 20149908 LOC388849 NA uncharacterized LOC388849 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_56335_PI430048170 0.976144078627 0.9995124458121870.3311975855190130.334204562365371
0.396391149463617A A A 0.3707800152675410.3232317597183 0.370320075750871A A A
LNCV6_56335_PI430048170 mRNA
CCCAAAAAAGACCTGTTCTGTCAGTGAATGGATAATCTAATGTGCTTCTAGTAGGCACAG NM_002443RefSeq chr10
- 46033304 46046269 MSMB 4477 "microseminoprotein, beta-, transcript variant PSP94"
GO:0008150|GO:0003674|GO:0005634|GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135582_PI430048170 0.0497588656345093 2.81451212682521 3.04487843384636
3.28823454218711 3.13058549846125 A P P 1.56496561485796 0.896479178931592
2.23102969204549 A A A LNCV6_135582_PI430048170 mRNA
GCTCAAGGTCTTTTTCATTCCTTACAGTCACATATCAGACAAGTTTTTGATGGAAGATTA NM_001029954 RefSeq
chr10 - 14819251 14837984 CDNF 441549 cerebral dopamine neurotrophic factor
GO:0005576|GO:0008083 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140817_PI430048170 0.3062234500087950.7029814607110860.282679394071492
0.5548884100139140.384288577938654A A A 1.47259919693884 0.401856336430459
0.660319571442739A A A LNCV6_140817_PI430048170 mRNA
AAAGCTCTCCTGCTGAAACTTCAGCCTGCAAAGATCCTCTGAAACCTTTAAAGATCAGGC NM_152377RefSeq chr1
- 59990393 60073770 C1orf87 127795 chromosome 1 open reading frame 87 NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_127335_PI430048170 0.1894192680142030.77543370788987 4.43755789698277
3.91024320726275 3.76743092657188 P P P 4.48262932436178 4.43329544038615
4.38772969382602 P P P LNCV6_127335_PI430048170 mRNA
ACCGCATTCCCTCCTGACTCAGACTCACCGCGATGCATTAAATTATGTTTTTAGACTATG NM_182528RefSeq chr2

- 119156242 119158895 C1QL2 165257 "complement component 1, q subcomponent-like 2"
GO:0005581|GO:0005576|GO:0051259|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133420_PI430048170 0.830082997682582 1.07497607989131 0.419849868888859
0.45096944429509 1.32543083854378 A A A 0.369626169358341 0.380402533558204
1.17227179919342 A A A LNCV6_133420_PI430048170 mRNA
TGAGGAATAAGGACATGAAAAATGCTTTTAGAAGAATGATGGGAAACACAGTTGCCTTGA NM_001004477 RefSeq
chr1 - 158578918 158579899 OR10X1 NA "olfactory receptor, family 10, subfamily X, member 1
(gene/pseudogene)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_64710_PI430048170 0.00309886667962656 0.133355936447389 0.453833782962653
1.02925733272875 1.34485594959464 A A A 4.11363757988862 4.20377553534645
3.15122265487876 P P P LNCV6_64710_PI430048170 mRNA
TTTCTCCGAGCATCCGTCTATGGGCAGTTTGTGGCTGGTGAGACAGCAGAGGAGGTGAAG NM_021232 RefSeq chr19
- 35799989 35813299 PRODH2 58510 proline dehydrogenase (oxidase) 2
GO:0010133|GO:0005743|GO:0004657|GO:0055114 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130598_PI430048170 0.555929013456812 0.912113186024507 5.71225290246836
6.07932800778111 5.99090964314571 P P P 6.26241458384048 6.14855789619573
5.74495911224509 P P P LNCV6_130598_PI430048170 mRNA
TTAGAAAACCTCGAGAGCTTAGACCTTTTCACTTGCGAGGTAACCAACCTGAACAACTAC NM_012404 RefSeq chr12
+ 48472664 48473060 ANP32D 23519 "acidic (leucine-rich) nuclear phosphoprotein 32 family,
member D" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144115_PI430048170 0.0997689427372539 0.643814452496023 5.17476513006384
5.49656157459682 5.58505587212862 P P P 5.58402735135746 6.35403123084419
6.15016337517945 P P P LNCV6_144115_PI430048170 mRNA
CTGCAGAATTTTCCGTAGACAAAGAAAGGATCTTGTGTATTTTTGTCCATATCCAATGTT NM_020440 RefSeq chr1
+ 116909922 116990358 PTGFRN 5738 prostaglandin F2 receptor inhibitor
GO:0005515|GO:0005794|GO:0009986|GO:0005789|GO:0016021|GO:0034389 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138022_PI430048170 0.00482423428175691 0.313277828999944 4.87478811498169
4.31681720207844 4.48365769006274 P P P 6.13466479870749 6.33231480833279
6.28252122922726 P P P LNCV6_138022_PI430048170 mRNA
TGATGCTATCTCAATCTAACAAATCATCACATACCCTACCCAAGAACAGGGTTTGTTAAG NM_001190708 RefSeq
chrX - 55181390 55182511 MTRNR2L10 NA MT-RNR2-like 10 NA . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138184_PI430048170 0.486807883306608 1.460251079703 0.392335742599472
1.73417293720038 0.319235496115646 A A A 0.417306155918111 0.447347676770638
0.414228281128916 A A A LNCV6_138184_PI430048170 mRNA
CGTCTGTTGTTAGCAAAGAATAGATTCACACAGTCTAAGGTTTCCTTCCTACCTAAAAAA NM_001289099 RefSeq
chr3 + 58332889 58426127 PXK 54899 "PX domain containing serine/threonine kinase, transcript
variant 5"
GO:0005815|GO:0005886|GO:0050804|GO:0003779|GO:0005634|GO:0032780|GO:0008022|GO:0005524|GO:0043
271|GO:0005737|GO:0004672|GO:0006954|GO:0000166|GO:0006468|GO:0035091 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_128168_PI430048170 0.580821967264006 1.04730858363491 10.7221991661033 10.991428190681
11.0095763685653 P P P 10.8784040052842 10.8179490954238 10.8437074046216 P P P
LNCV6_128168_PI430048170 mRNA
GGGCCATGTTTGAGTTTTGCTTTGTATGTTGTTTTGCAAGTATCTGCCTGGTACTTTGAT NM_012384 RefSeq chr20 -
63587601 63627028 GMEB2 26205 glucocorticoid modulatory element binding protein 2
GO:0006355|GO:0005737|GO:0006366|GO:0003713|GO:0005654|GO:0005634|GO:0003677|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA

LNCV6_126782_PI430048170 0.0787201945501321 0.8098889440513517.43346693291622
7.47420685199992 7.7624536871858 P P P 7.82124271732775 7.82331999870669
7.95672336908743 P P P LNCV6_126782_PI430048170 mRNA
GTGATCACGTTTCGTGTTCATACTCAACGTTAATAAAAGGAGAGAGTTTGTAGTGAAAAA NM_004128RefSeq chr13
+ 45120495 45284104 GTF2F2 2963 "general transcription factor IIF, polypeptide 2, 30kDa"
GO:0008380|GO:0005515|GO:0008026|GO:0010467|GO:0006355|GO:0006368|GO:0006367|GO:0006366|GO:0006
370|GO:0005634|GO:0003677|GO:0005524|GO:0050434|GO:0000398|GO:0015630|GO:0016032|GO:0005654|GO:0
005674 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130274_PI430048170 0.8100020988230671.00938610653076 0.522963678113695
0.3945841988578060.521367223779164A A A 0.4289222326731550.505561713864995
0.466702286997237A A A LNCV6_130274_PI430048170 mRNA
GTCTATACATACAGGAAGGTATATATTGTCTCAATGCAATCAAATCATCTTTTACTGGGG NM_001008777 RefSeq
chr17 - 38936431 38967402 FBXO47NA F-box protein 47 NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_113524_PI430048170 0.2516207102867480.8419515907608493.20993127342661
2.83196696781909 3.31093263826533 P A P 3.54158265262863 3.14396713345414
3.42626705853885 P P P LNCV6_113524_PI430048170 mRNA
TATTGGAACCAAGATCAAAGAAGGGAAGTGATGAGGCTTCGCAAACTGGCTCAGCAGATTNM_000381RefSeq chrX
- 10445309 10620634 MID1 4281 "midline 1, transcript variant 1"
GO:0051219|GO:0008017|GO:0005881|GO:0007389|GO:0046982|GO:0005875|GO:0016874|GO:0005874|GO:0019
221|GO:0005819|GO:0035372|GO:0000226|GO:0032874|GO:0042803|GO:0005829|GO:0008152|GO:0007026|GO:0
008270|GO:0031625|GO:0060333 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132176_PI430048170 0.5161933027706981.0322175440186 0.281804029022282
0.3056685299524080.459162640234424A A A 0.3263664158505480.293086586943339
0.296202158702027A A A LNCV6_132176_PI430048170 mRNA
ATTTTCTCCACCAATGAAGTGGTGGATGCTGAGAACACTCAGCAGCTTATCAATGTGGTG NM_015613RefSeq chr10
- 84231519 84241461 LRIT1 26103 "leucine-rich repeat, immunoglobulin-like and transmembrane
domains 1" GO:0008150|GO:0003674|GO:0030176 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137179_PI430048170 0.95005652738858 1.05404828229635 0.278570233766219
0.2861427404722681.64825864958795 A A A 0.3350460249312741.20287759710933
0.780783079876535A A A LNCV6_137179_PI430048170 mRNA
GAGCATGTCCTATGCAGACATAGATTTTTCTGTTCATTTATTTTTCTTCATTGCAGTGGA NM_001290294 RefSeq chr10
- 95311772 95561420 SORBS1 10580 "sorbin and SH3 domain containing 1, transcript variant 8"
GO:0005515|GO:0008092|GO:0008286|GO:0005886|GO:0005158|GO:0043149|GO:0005634|GO:0016363|GO:0005
829|GO:0046889|GO:0005915|GO:0005737|GO:0005913|GO:0006936|GO:0015758|GO:0048041|GO:0046326|GO:0
005899|GO:0005813|GO:0001725|GO:0032869|GO:0045725|GO:0019901|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_54005_PI430048170 0.7264987584086491.04046213189193 5.73231375156671 5.42443881413958
5.5671568151616 P P P 5.79618042024534 5.46409158557111 5.25651894666301 P P P
LNCV6_54005_PI430048170 mRNA
GCAGATGTTGGGGGAAAAAGTACGTGATATTTTAGAAACTTAGTGGGAAAAGTAGGATGGNM_014372RefSeq chr1
+ 51236272 51273447 RNF11 26994 ring finger protein 11
GO:0005515|GO:0004842|GO:0042787|GO:0000151|GO:0008270|GO:0005634|GO:0055037|GO:0003677|GO:0005
769|GO:0070062|GO:0051865 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134055_PI430048170 0.4952947667202761.0202042143318 0.376202574109987
0.3742727568208990.273648526011389A A A 0.3028377721728060.322154868723833
0.314857595861643A A A LNCV6_134055_PI430048170 mRNA
CAGGATGTCTTAGGATTGTTTTTCTCATCAGGATACATTAAAAATACAATACAGCACGTC NM_178813RefSeq chrX
+ 119895972 119920716 AKAP14158798 "A kinase (PRKA) anchor protein 14, transcript variant 1"

GO:0005737|GO:0035686|GO:0007283|GO:0051018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132718_PI430048170 0.0182961363212935 0.572012492285 6.71132573339618
6.38233898960096 6.92086417462705 P P P 7.27804842154556 7.4233910432268
7.74141237868622 P P P LNCV6_132718_PI430048170 mRNA
GTACTTGGCTACACACAGATTGTATTTTTATTGTTAATGCTCTTCTTATGGATACCTGCA NM_001137675 RefSeq chr16
+ 71845990 71857333 ATXN1L 342371 ataxin 1-like
GO:0005515|GO:0048286|GO:0030198|GO:0003723|GO:0005730|GO:0005634|GO:0000122|GO:0003677|GO:0030
425|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138176_PI430048170 0.0327281263001167 0.591777711991161 5.4464097010955
5.07633974982 5.57054808759504 P P P 5.76207990213774 6.27379448048424 6.31028979386779 P
P P LNCV6_138176_PI430048170 mRNA
CTGTGTTGAATTACGGAATAATGAGTTAGAACTATTAAAACAGCCAAAACTCCACAGTCA NM_000584 RefSeq chr4
+ 73740505 73743716 CXCL8 3576 chemokine (C-X-C motif) ligand 8
GO:0005515|GO:0034976|GO:0005153|GO:0008285|GO:0019722|GO:0002237|GO:0006928|GO:0005615|GO:0030
155|GO:0030968|GO:0045091|GO:0031623|GO:0035556|GO:0006955|GO:0006954|GO:0006935|GO:0071356|GO:0
007050|GO:0008009|GO:0070098|GO:0045744|GO:0030593|GO:0005576|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_93134_PI430048170 0.37188247498165 1.4325947663162 0.275285425014347 1.56601083534238
1.10681194447619 A A A 0.732058877083857 0.400710059064042 0.519786274844204 A A A
LNCV6_93134_PI430048170 mRNA
CTGGGTTTAAGCTTCAGTGCAGGTGGAATGACATTCAAATAAAGAAACACTTTCTATCAC NM_198560 RefSeq chr3
- 9498360 9553802 LHFPL4 375323 lipoma HMGIC fusion partner-like 4 GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135759_PI430048170 0.0063552843415739 0.362976306762646 3.48649570000288
3.0498302570503 3.57234004645187 P P P 4.73650791674431 4.93418834314188
4.86958553608989 P P P LNCV6_135759_PI430048170 mRNA
CCAGTTGTGTTTTGTGTAGTCTGAATTTGCTTTCTGTAGTTGAGCAAACGTCTTAAAAAG NM_025134 RefSeq chr16
+ 53055032 53327502 CHD9 80205 chromodomain helicase DNA binding protein 9
GO:0005515|GO:0006355|GO:0005886|GO:0004386|GO:0005634|GO:0044281|GO:0003677|GO:0005524|GO:0006
351|GO:0005737|GO:0005654|GO:0044255|GO:0016568 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137405_PI430048170 0.00488511056319783 0.678252907541844 4.62502592755092
4.60353832183232 4.66642276437334 P P P 5.08264121274877 5.24005019272991
5.24739133871713 P P P LNCV6_137405_PI430048170 mRNA
ATTGTGTATTTCCGTAGGCTTCTTAGTAGCAGCTTTGTACACTGAGGACACTGTAGCCAG NM_006426 RefSeq chr10
+ 132186909 132205776 DPYSL4 10570 dihydropyrimidinase-like 4
GO:0007411|GO:0016812|GO:0007399|GO:0006208|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_58234_PI430048170 0.131059546966739 1.25688978429775 9.72898764841154 9.39075641408987
9.43007994672525 P P P 9.45555919057915 9.06593961973 9.02245243015989 P P P
LNCV6_58234_PI430048170 mRNA
ACCAGCCCAGCCTGCCCCCTATCTTGTCCTGGAATATTTTTGGGGTTGGAACTCAAAAAA NM_001001522 RefSeq
chr11 + 117199323 117204792 TAGLN 6876 "transgelin, transcript variant 1"
GO:0005515|GO:0005737|GO:0051015|GO:0007517|GO:0030855 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_132730_PI430048170 0.148066005065215 1.21018655151945 6.53180679788914
6.78595704798636 6.78422614402945 P P P 6.28831724593675 6.29640322881118
6.67190566601024 P P P LNCV6_132730_PI430048170 mRNA
CAACAGTCAGCCGGGGGAAGATAAAGGTACATTATAAAACACACATTAATGCATTTAATA NM_153208 RefSeq chr16
+ 19716455 19858467 IQCK 124152 IQ motif containing K NA . NA - . NA NA NA NA NA

NA NA NA NA
LNCV6_144321_PI430048170 0.1669948528184391.142669946188 7.65418525015669
7.83685723885477 7.73935319375945 P P P 7.7385668856453 7.44694280808254
7.45386021426398 P P P LNCV6_144321_PI430048170 mRNA
TAAACTCCAAAGCTGAAGGGGAGGTGCTCCGGAAAAGCATTCTGAGCTTTTACATTCAGA NM_080659RefSeq chr11
+ 111918876 111926871 C11orf52 91894 chromosome 11 open reading frame 52 GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128385_PI430048170 0.0482622060623496 0.62972398964189710.0800989762628
9.96152238201628 10.0686489132168 P P P 10.3812337948745 10.7675396280637
10.9148926024439 P P P LNCV6_128385_PI430048170 mRNA
CATGTCTGTTTACTTTAGTGACGTTCCACAGAATAAAAGGAAACAAGTTTGCCATCAAAA NM_005956RefSeq chr14
+ 64388040 64460007 MTHFD1 4522 "methylenetetrahydrofolate dehydrogenase (NADP+
dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase"
GO:0006767|GO:0009086|GO:0044281|GO:0004329|GO:0004477|GO:0005524|GO:0035999|GO:0005829|GO:0005
739|GO:0004488|GO:0004486|GO:0016020|GO:0006766|GO:0046655|GO:0009396|GO:0006730|GO:0000105|GO:0
070062|GO:0055114|GO:0006164 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128477_PI430048170 0.00986123957860667 0.6140585958301429.41796630191527
9.3881425646913 9.38555053778435 P P P 9.97840470595138 10.0799868174536
10.2327305796861 P P P LNCV6_128477_PI430048170 mRNA
GAGGGCCTGTAAATATCTATATATAATTCTGTGTGTATTCTGTGTCATGTTGGGGTTTTT NM_033088RefSeq chr1
+ 110034600 110054641 STRIP1 85369 "striatin interacting protein 1, transcript variant 1"
GO:0005515|GO:0003674|GO:0005737|GO:0030866|GO:0022604|GO:0005634|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_115434_PI430048170 0.1344211072492580.7749174940996145.24238369710156
4.79789475890829 5.12082814246991 P P P 5.1609378642056 5.44274515310383
5.65471750448812 P P P LNCV6_115434_PI430048170 mRNA
CTCACTGGATGAACAAAGCAGTAGTACACTCAAGGGTGTGCTTGTGAGAAATGGAGGAAG NM_001130445
RefSeq chr2 + 181891715 181930737 SSFA2 6744 "sperm specific antigen 2, transcript variant 1"
GO:0005737|GO:0005886|GO:0005102|GO:0005654|GO:0005634|GO:0003779 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131984_PI430048170 0.00520094993749179 0.7378648271193141 1.4861213729025
11.6302698556773 11.5731381942976 P P P 12.0361566665122 11.8855343279304
12.0800582922124 P P P LNCV6_131984_PI430048170 mRNA
AATTCTGCTTTCCCACAAAATAAACCTAATGCCATCAGGCAAAACATTTCTGTGTCTGTA NM_001143679 RefSeq
chr7 + 143263428 143269129 GSTK1 373156 "glutathione S-transferase kappa 1, transcript variant 2"
GO:0005102|GO:0005743|GO:0015035|GO:0006749|GO:0004364|GO:0043231|GO:0004602|GO:0005622|GO:0016
020|GO:0005759|GO:0030855|GO:0070062|GO:0005777|GO:0055114 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_129708_PI430048170 0.0116360094232432.33789026323936 1.69661120492882
2.11208700997841 2.40814816703775 A A A 1.17326146034184 0.556795938914796
0.831726209592061 A A A LNCV6_129708_PI430048170 mRNA
CTTGTTCTTCTCAAGAGAAAGTTGTAACTCTCTGGTCTTCATATGTCCCTGTGCTCCTTT NM_024944RefSeq chr21 +
18244832 18267371 CHODL 140578 "chondrolectin, transcript variant 1"
GO:0048471|GO:0005737|GO:0007517|GO:0005540|GO:0030246|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_143249_PI430048170 0.2283045266877580.5509917901979060.452194601118636
0.8161148358439890.393676213621753 A A A 2.05650977332116 1.29530151580398
0.534749076737624 A A A LNCV6_143249_PI430048170 mRNA
GTACTCCCCTTGTGCCACACATTGCATTATTAAATGTTTCTCAAACATGGAGTTAAAAAA NM_021983RefSeq

chr6_GL000256v2_alt - 3851135 3866104 HLA-DRB4 3126 "major histocompatibility complex, class II, DR beta 4"
GO:0005515|GO:0002437|GO:0050852|GO:0005886|GO:0002862|GO:0019221|GO:0031295|GO:0042088|GO:0005765|GO:0042130|GO:0019886|GO:0006955|GO:0002381|GO:0042605|GO:2001179|GO:0071556|GO:0032689|GO:0060333|GO:0030658|GO:0012507|GO:0051262|GO:0035774|GO:0002503|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135049_PI430048170 0.0071169662599978 1.28657660413406 6.71077723518444 6.78516552449991 6.89130566169078 P P P 6.50643228857136 6.34167661598777 6.44942802095094 P P P LNCV6_135049_PI430048170 mRNA
ATAAACCCCTCCCAATTAATGCATTTTCATTTCCTACTGATACAAGGCCTGGAGAGGGCT NM_001164841 RefSeq chr6 - 5108418 5260950 LYRM4 57128 "LYR motif containing 4, transcript variant 3"
GO:0005759|GO:0005634|GO:0044281 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143928_PI430048170 0.0331726951719337 1.34142459909495 9.29898938390635 9.17727484594605 8.97840391937985 P P P 8.78622164593963 8.74862989761344 8.66378353364659 P P P LNCV6_143928_PI430048170 mRNA
CCCCAAGTGCACACCTGAACACTTGGAGGAATAAAGTTCTGTTTTTAATTGTGGAAAAAA NM_003086RefSeq chr9 - 136375576 136398437 SNAPC46621 "small nuclear RNA activating complex, polypeptide 4, 190kDa"
GO:0010467|GO:0006355|GO:0003700|GO:0006366|GO:0009301|GO:0005634|GO:0003677|GO:0006383|GO:0019185|GO:0042796|GO:0003682|GO:0042795|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137988_PI430048170 0.401994895364353 0.929554039373289 10.1605765380205 10.2936182100131 10.4548219145424 P P P 10.404956326673 10.2816755919131 10.5418832667296 P P P LNCV6_137988_PI430048170 mRNA
CAGTTGGTGGTCTTGAGTTTTCTCTTTCTTGCAAGATGAAATTTTATTTTCCACAGCAAANM_012260RefSeq chr3 - 15560703 15601852 HACL1 26061 "2-hydroxyacyl-CoA lyase 1, transcript variant 1"
GO:0048037|GO:0000287|GO:0005782|GO:0001561|GO:0005102|GO:0016830|GO:0044281|GO:0030976|GO:0051259|GO:0044255|GO:0042802|GO:0005777 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138937_PI430048170 0.138036704521622 1.25550728672065 10.3268685583951 10.8138056366759 10.567221393772 P P P 10.3840220967195 10.2219234289725 10.1479654894987 P P P LNCV6_138937_PI430048170 mRNA
GAAAGAAGAAAAGATAATACCCATTTGTTCTATCACCCCTCTCCCTATCATTAACTATCA NM_015058RefSeq chr13 - 41566824 41961085 VWA8 23078 "von Willebrand factor A domain containing 8, transcript variant 1"
GO:0005739|GO:0008152|GO:0005576|GO:0016887|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131587_PI430048170 0.614349396429468 1.01145213726353 0.349664147228502 0.329140592718099 0.261110933401454 A A A 0.297554309746928 0.306970598437743 0.287522925478147 A A A LNCV6_131587_PI430048170 mRNA
AATGGCTGCATCAACTATGAAGCATTTGTGAAGCACATCATGTCCAGCTAAACCTCGTGC NM_000258RefSeq chr3 - 46857866 46863483 MYL3 4634 "myosin, light chain 3, alkali; ventricular, skeletal, slow"
GO:0030049|GO:0055010|GO:0005509|GO:0006942|GO:0032781|GO:0060048|GO:0030017|GO:0005829|GO:0003785|GO:0003774|GO:0002026|GO:0007519|GO:0008152|GO:0032038|GO:0005859|GO:0008307|GO:0031672|GO:0031674 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145585_PI430048170 0.191610275420222 2.14778457834165 0.385627064732435 1.68574142322842 2.01584055168139 A A A 0.575460949668957 0.318594043559772 0.323996955107189 A A A LNCV6_145585_PI430048170 mRNA
CACAAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCA NM_007281RefSeq chr4 - 173388147 173399466 SCRG1 11341 stimulator of chondrogenesis 1 GO:0005615|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131503_PI430048170 0.000610248994843915 3.16921254854308 8.83054378066485 8.93491578617036 8.6421268651917 P P P 7.35944810730905 7.09323003485872

6.94697980569144 P P P LNCV6_131503_PI430048170 mRNA
AGGAAACTTGTAACCACCCTTTTCTAACAGCAATAAAGAGGTGTCCTTGTCCCGAAAAAA NM_003793 RefSeq chr11
- 66563463 66568576 CTSF 8722 cathepsin F
GO:0004197|GO:0019886|GO:0006508|GO:0031982|GO:0005764|GO:0070062|GO:0043202 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128516_PI430048170 0.1150913738437281.6906805174857 3.31861352149209
4.16275424805702 3.2780438172637 P P P 3.15243590916214 2.87988847648214 2.5801696095568
P P P LNCV6_128516_PI430048170 mRNA
ACGCTCATGACAGCAAAGTCTCCTTATGTATAATGAAACAAGGTCAGAGACAGATTTGAT NM_020485 RefSeq chr1
- 25362248 25420872 RHCE 6006 "Rh blood group, CcEe antigens, transcript variant 1"
GO:0005887|GO:0072488|GO:0008519 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128708_PI430048170 0.1093454881626610.8307232598254397.26951742433478
7.31394009056725 7.52393760897956 P P P 7.47310379093333 7.61186680011237 7.8171952669808
P P P LNCV6_128708_PI430048170 mRNA
GGAGTGGTTACAACTGAGCTTTTAGTAACCATTTAACCGTATGTAAACTTGGTTTCTAAT NM_001174129 RefSeq
chr12 - 50985991 51026141 SLC11A2 4891 "solute carrier family 11 (proton-coupled divalent metal
ion transporter), member 2, transcript variant 6"
GO:0005802|GO:0005515|GO:0015078|GO:0035434|GO:0005765|GO:0005764|GO:0010042|GO:0006879|GO:0070
835|GO:0006878|GO:0022890|GO:0071356|GO:0070574|GO:0010039|GO:0007611|GO:0016151|GO:0010288|GO:0
015692|GO:0005506|GO:0009986|GO:0015099|GO:0005507|GO:0015087|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_136912_PI430048170 0.2996877603922311.02216363868255 0.316573041201831
0.2447421431727360.308117920105545 A A A 0.2635804827700650.247051080866867
0.264917416316261 A A A LNCV6_136912_PI430048170 mRNA
AGTGGGAAAGATAATAAATCAAGCACTTCTTGCACTTGTTTCTGTGAAGCATATAGAACT NM_145259 RefSeq chr2
- 157526766 157628887 ACVR1C 130399 "activin A receptor, type IC, transcript variant 1"
GO:0016361|GO:0023014|GO:0032868|GO:0005886|GO:0030262|GO:0019915|GO:0002021|GO:0005524|GO:0046
872|GO:0030154|GO:0009749|GO:0043280|GO:0004702|GO:0019838|GO:0048179|GO:0038092|GO:0005024|GO:0
038100|GO:0006468|GO:0046676 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_65772_PI430048170 0.529451694330293 1.15167569007354 0.9862484219006690.343215279546247
0.2945231201609 A A A 0.44751960094906 0.34650827735988 0.323558130814249 A A A
LNCV6_65772_PI430048170 mRNA
GAGACTTCTGGAAGAGCAGGTATTCTTCAGCATCCAATTCAGCAAGTATTTCAACAGCTT NM_172311 RefSeq chr2
+ 48569019 48679609 STON1-GTF2A1L 286749 "STON1-GTF2A1L readthrough, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_49938_PI430048170 0.380532592541871 1.23349987836435 0.3225136525177140.999980403259266
0.268558635271414 A A A 0.2667609192027340.2715540228298240.264874531473138 A A A
LNCV6_49938_PI430048170 mRNA
AGTTTCACAGAATTGTATCTGCAGCATTGAAAATATGGAAAATGTCAGTTCTTCTAGAGC NM_138290 RefSeq chr7
+ 87628412 87832298 RUNDC3B 154661 "RUN domain containing 3B, transcript variant 1" NA . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_135362_PI430048170 0.1329102649743680.82427955702752 7.91807579977278
7.55383110992446 7.68270800532954 P P P 7.85576799543585 7.9386428727466
8.19801130826976 P P P LNCV6_135362_PI430048170 mRNA
CCTGTATTCCGTATCAGATTGCAAAGACGGAATGTTACTATTTTATCAGCAAGGTATTAA NM_006570 RefSeq chr9
+ 19049373 19051023 RRAGA 10670 Ras-related GTP binding A
GO:0051219|GO:0005515|GO:0008219|GO:0032008|GO:0005794|GO:0046982|GO:0003924|GO:0006915|GO:0005
634|GO:0005525|GO:0005765|GO:0005764|GO:0042803|GO:0043231|GO:0006184|GO:0005737|GO:0071230|GO:0
045919|GO:0019048|GO:0010506|GO:0034613|GO:0019003|GO:0034448|GO . NA - . NA NA NA NA

NA NA NA NA NA
LNCV6_131077_PI430048170 0.2284991620247281.04451821374928 0.363300619429266
0.3684020191198670.476204180653948A A A 0.335060340287761 0.316031210550604
0.370610879467202 A A A LNCV6_131077_PI430048170 mRNA
CAGAATAAACCAAGTGATAATCAAACCATGTCAAGATTATTAGTTCAGACTCTAGCCTGT NM_031279 RefSeq chr4
- 108742045 108763079 ETNPPL 64850 "ethanolamine-phosphate phospho-lyase, transcript variant 1"
GO:0005739|GO:0030170|GO:0008152|GO:0050459|GO:0008483|GO:0005575 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141072_PI430048170 0.000693142709038951 0.3849718856490624.83144803298828
4.770154133202 5.07292326757305 P P P 6.23606851723777 6.2027333663761
6.37915488366587 P P P LNCV6_141072_PI430048170 mRNA
TGAGAGCTGCTATAACCATTTCCCCAGTTCAACATTGCATTGAAAATTTATGGACCTTTA NM_024595 RefSeq chr1
+ 38991243 39006065 AKIRIN1 79647 "akirin 1, transcript variant 1"
GO:0031965|GO:0005654|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134368_PI430048170 0.2393721607684910.9651845507968910.301322786792896
0.3719117570175110.316551609753975A A A 0.4385043603654420.3439957156228710.359829804434
A A A LNCV6_134368_PI430048170 mRNA
GTAGGGCACAAGTTAGACGTGATAGAGATGCCATTAGTGTGTTTTGAAGCAAATCTCAAA NM_001281746 RefSeq
chr6 + 54018915 54218084 MLIP 90523 "muscular LMNA-interacting protein, transcript variant 2"
GO:0001191|GO:0010614|GO:0016605|GO:0005635|GO:0000122|GO:0031981 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_105802_PI430048170 0.8164618190251091.12238870911832 0.29841033837461
0.2606207026618542.45978368070284 A A A 0.8624901404004311.60351304138105
1.14242073574639 A A A LNCV6_105802_PI430048170 mRNA
TTCCTGAAGACACATAAATCCGGGAGCAGCTCTGTGCTGAGCCTGCTTCACCGCTATGGG NM_024637 RefSeq chr7
- 100159241 100168750 GAL3ST4 79690 galactose-3-O-sulfotransferase 4
GO:0006790|GO:0001733|GO:0009311|GO:0050698|GO:0007267|GO:0050694|GO:0050656|GO:0030166|GO:0009
100|GO:0016020|GO:0032580|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134969_PI430048170 0.000155842812671431 1.78627704160926 6.40212934420852
6.52706470388501 6.4776872023517 P P P 5.66362503707323 5.58993273010953
5.64418446172574 P P P LNCV6_134969_PI430048170 mRNA
GAACATCAAACTCCAAACCCTGGGGACAAACGACATGAAATAAATGTATTTTAAAACATC NM_003965 RefSeq chr3
+ 46407229 46409523 CCRL2 9034 "chemokine (C-C motif) receptor-like 2, transcript variant 1"
GO:0070098|GO:0006954|GO:0007186|GO:0006935|GO:0005886|GO:0005887|GO:0048020|GO:0004950|GO:0042
379 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_50197_PI430048170 0.5106296702658610.7951172400977530.4927181974475820.521265533342463
0.56770330476011 A A A 1.4236707622309 0.4184880831108770.505467880360635A A A
LNCV6_50197_PI430048170 mRNA
TACAAAACACCAGACCCTGGAACTGGAGAAAGAGTTTCTGTTCAACATGTACCTCACCAG NM_152739 RefSeq chr7
- 27162437 27165530 HOXA9 3205 homeobox A9
GO:0005515|GO:0005667|GO:0060065|GO:0006355|GO:0048706|GO:0060216|GO:0030879|GO:0005634|GO:0007
275|GO:0009954|GO:0007283|GO:0009952|GO:0006351|GO:0043565|GO:0007338|GO:0005737|GO:0045638|GO:0
042118|GO:0005654|GO:0035115|GO:0019899|GO:0008584 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_94419_PI430048170 0.4596876624078781.12395716310065 3.88645081027027 4.33922927301879
4.33217789346667 P P P 3.80774474054793 3.96628971645793 4.28197971506632 P P P
LNCV6_94419_PI430048170 mRNA
GAAGCACACATACATAGTGTTACTAGAGCTTCTGATGGACAGTCACGTGGCAAAACTCCA NM_152896 RefSeq chr9
+ 6413150 6507051 UHRF2 115426 "ubiquitin-like with PHD and ring finger domains 2, E3 ubiquitin

protein ligase, transcript variant 1"
GO:0005515|GO:0006511|GO:0004842|GO:0016567|GO:0008283|GO:0016874|GO:0005634|GO:0003677|GO:0071
158|GO:0030154|GO:0051865|GO:0042393|GO:0005720|GO:0007049|GO:0051726|GO:0005654|GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_61052_PI430048170 0.4565149304707690.9684921913169760.4271684710180650.448251151678588
0.286392046456351 A A A 0.4021837030291830.4731139298400930.429495098561362 A A A
LNCV6_61052_PI430048170 mRNA
ATACTAAGCGCACTGCAGAAGTGTGGATGGATGAATACAAGCAATACTACTATGAGGCCC NM_001168368 RefSeq
chr14 + 69259963 69354473 GALNT16 57452 "polypeptide N-acetylgalactosaminyltransferase 16,
transcript variant 1" GO:0004653|GO:0000139|GO:0030246|GO:0006486|GO:0016021|GO:0046872|GO:0070062
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133675_PI430048170 0.74979063135 0.9887421789578560.40233162143298 0.266498392605972
0.333919775233115 A A A 0.4089042075453980.3293927115724160.31486401355298 A A A
LNCV6_133675_PI430048170 mRNA
CTGAAGCCTAGTCAGGTTTCTGTAGTCATAAGAAATGTTCTTTTCCTAGAAACAAAGTAA NM_001005486 RefSeq
chr14 + 19975518 19976565 OR4K15 NA "olfactory receptor, family 4, subfamily K, member 15" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142120_PI430048170 0.4988255727965260.9808040451124780.391604784448178
0.4196016316534980.344033508283832 A A A 0.4706331716958490.372430070947468
0.395235034955758 A A A LNCV6_142120_PI430048170 mRNA
AGCATTGTTGACTGCCAGTTTATTCCCAGTAAATAAAGCAATACGCTTTTCAGGAGGAAG NM_004610 RefSeq chr6
- 167373088 167384510 TCP10 6953 t-complex 10 GO:0005829 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133317_PI430048170 0.0129725209119489 2.48008148638893 7.25594474045022
7.22016773286481 7.16515271684329 P P P 5.63555043998288 6.19144437544183
5.82847976985191 P P P LNCV6_133317_PI430048170 mRNA
TGGACAGATGGGTAGATGTGGCAGGCATGTCATCGACAGCACAGAAGGGCTGTCCTGTGT NM_002236 RefSeq
chr2 + 10911936 10914225 KCNF1 3754 "potassium channel, voltage gated modifier subfamily F,
member 1"
GO:0005251|GO:0005886|GO:0008076|GO:0007268|GO:0005267|GO:0051260|GO:0034765|GO:0016021|GO:0006
813|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135499_PI430048170 0.1957272694472892.21970961547201 0.359436457865409
2.00436307864114 1.90335409831845 A A A 0.2771801039604960.718304629652851
0.279373488203928 A A A LNCV6_135499_PI430048170 mRNA
TGTATGTGGTGTAAGGTAAGCAGCTCTGTATTCTTCCAAATAAATAGCCAGTTGTCCCTG NM_021045 RefSeq chr10
- 37828764 37857636 ZNF248 57209 "zinc finger protein 248, transcript variant 1"
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138261_PI430048170 0.0113620488792978 0.7941602245792621 5.5352477303719
15.4021258831888 15.4040888924721 P P P 15.8920469077763 15.7190915268216
15.7251301211759 P P P LNCV6_138261_PI430048170 mRNA
GCTTGTACATAGAGTGCTGTAGCTGTGTGTTCCAATAAATTATTTTGTAGGGAAAGTAAA NM_001675 RefSeq chr22
+ 39520558 39522686 ATF4 468 "activating transcription factor 4, transcript variant 1"
GO:0005515|GO:0043005|GO:0034976|GO:0003700|GO:0044212|GO:0006366|GO:0000981|GO:0043267|GO:0006
094|GO:0005634|GO:0030968|GO:0005737|GO:0043525|GO:0045943|GO:0045944|GO:0042149|GO:0001046|GO:0
006520|GO:0036091|GO:0006355|GO:0043065|GO:0005815|GO:0007214|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_132298_PI430048170 0.0636993545139727 0.3688148284513233.73368044684403
2.31471445652845 3.19251560528105 P A P 4.6676766318683 4.64809494266346

4.57632702430822 P P P LNCV6_132298_PI430048170 mRNA
CACCATCTGTAGTGTTAAATCAACTAAATTATTTCAGCAATAGGAGACAAAACAACCAGC NM_005006RefSeq chr2
- 206123078 206159519 NDUFS1 4719 "NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa
(NADH-coenzyme Q reductase), transcript variant 1"
GO:0005515|GO:0051539|GO:0046034|GO:0051537|GO:0072593|GO:0051881|GO:0005743|GO:0009055|GO:0044
281|GO:0046872|GO:0005739|GO:0022904|GO:0005758|GO:0045333|GO:0005747|GO:0008637|GO:0006120|GO:0
008137|GO:0044237. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127913_PI430048170 0.00203124297571346 3.63412955815411 4.23673470551246
4.73667026229862 4.23159036098075 P P P 2.48266477297664 2.73679361466715
2.44316294568588 A P P LNCV6_127913_PI430048170 mRNA
ATAGTAAATGTTTTATTCGGGTGTATCATTCATACAGTAAAGACACCAATCTTCAGAGGC NM_001290212 RefSeq
chr17 + 81637170 81648755 TSPAN10 83882 "tetraspanin 10, transcript variant 1"
GO:0072594|GO:0016021|GO:0019899 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137230_PI430048170 0.00291436001210156 0.242147366085161 1.20684938295917
0.402464425774625 0.774801394253287 A A A 2.64756184587382 3.17359069025797
2.75873901870471 P P P LNCV6_137230_PI430048170 mRNA
AGTGCAGCACTTCCACACCAAGAAGGCCCTCAATAAAGGCTTCCTGAGGAACGCAAAAAA NM_012205RefSeq
chr2 - 42767088 42792611 HAAO 23498 "3-hydroxyanthranilate 3,4-dioxygenase"
GO:0006569|GO:0031966|GO:0000334|GO:0009055|GO:0044281|GO:0010043|GO:0008198|GO:0043420|GO:0005
829|GO:0034641|GO:0019805|GO:0019825|GO:0034354|GO:0070050|GO:0046686|GO:0070062|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133057_PI430048170 0.0025492341036276 0.509729254477361 5.67201152146136
5.40015175888381 5.51438899203478 P P P 6.69482959546424 6.4682970628662
6.32917712813677 P P P LNCV6_133057_PI430048170 mRNA
CTGTTCGAAGATTTTTGGAAGAATACTGAGAACGGCATAAAGTGAAGATCGACATTTAAA NM_016424RefSeq chr17
+ 50719564 50752711 LUC7L3 51747 "LUC7-like 3 (S. cerevisiae), transcript variant 1"
GO:0008380|GO:0005515|GO:0016607|GO:0006376|GO:0005654|GO:0005634|GO:0003729|GO:0003677|GO:0005
685 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143276_PI430048170 0.651396202428704 0.782536584487553 1.13513151105623
0.311602808334923 0.304128462736496 A A A 1.73877028631778 0.420484198682473
0.372539561839807 A A A LNCV6_143276_PI430048170 mRNA
AATGGAATTGTGAGTAGCTTAATCTCTATGTTTCTCTCCATTTTCATTCCTCCTGCAACT NM_006198RefSeq chr21 +
39867420 39929397 PCP4 5121 Purkinje cell protein 4
GO:0005516|GO:0005634|GO:0007417|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138940_PI430048170 0.0388912149189115 1.38690058393958 5.82407955806215
5.93720795590526 5.78660668548686 P P P 5.34036215776147 5.58187232713999
5.18661445221065 P P P LNCV6_138940_PI430048170 mRNA
GAAACTGCCTGAAGGCAGGCAGGGTAGGACAATGTCTGGAGGCTCACGGTTTTATAGACTNM_016390RefSeq chr9
- 128819650 128829821 C9orf114 51490 chromosome 9 open reading frame 114
GO:0008150|GO:0007049|GO:0008168|GO:0000777|GO:0005575|GO:0032259|GO:0051301 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135784_PI430048170 0.0562632906664108 1.30985253756775 5.41109931984383
5.30103641034067 5.35835312300444 P P P 5.11018664050879 5.01866080310519
4.75199128101598 P P P LNCV6_135784_PI430048170 mRNA
GCACCCAGGCTCCAGGATGACTGCTGAGAAATTTCTGAACAGGCTCCCCAAGTTTGTGAT NM_183008RefSeq chr1
- 26282281 26306704 UBXN11 91544 "UBX domain protein 11, transcript variant 2"
GO:0043130|GO:0005737|GO:0043161|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_97941_PI430048170 0.0985573891076410.801862321174912 7.97748572186334 8.00599359614733
8.00065948773811 P P P 8.09713758050142 8.37498554654995 8.44494922969508 P P P

LNCV6_97941_PI430048170 mRNA
AGAAAAGAAAAGAAAATGCCCAAACCCAGACTAAAGGCTACAGTGACGCCAAGTCCAGTG NM_022731 RefSeq
chr1 - 205712818 205750244 NUCKS1 64710 nuclear casein kinase and cyclin-dependent kinase
substrate 1 GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127317_PI430048170 0.5802346409144670.9723815039365220.446847657731976
0.4206890833140340.243579884563472 A A A 0.37374471255112 0.452055047643107
0.413826028618647 A A A LNCV6_127317_PI430048170 mRNA
CTTTTGCTCACACTGAGTGTCTCATCTTGGTAATGATGTCCTACGATCGGTACATGGCTA NM_012365 RefSeq chr7
+ 144050401 144051337 OR2A5 NA "olfactory receptor, family 2, subfamily A, member 5" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135973_PI430048170 0.7520326194694791.05395200953684 7.73981986854275
7.44335883273297 7.18593689479658 P P P 7.46683019884208 7.52380748081407
7.18161228849446 P P P LNCV6_135973_PI430048170 mRNA
ATTTACATGTATCTGCAGCCCCCTTCCAGCTACTCCCAAGAGCAGGGCAAATTTATTTCT NM_001004492 RefSeq
chr1 - 247451028 247451982 OR2B11 NA "olfactory receptor, family 2, subfamily B, member 11" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127109_PI430048170 0.5279891760164750.7793248531877240.41427519426195
0.4182011043843920.432746727664789 A A A 0.3216496855904790.350383033920608
1.39614450660005 A A A LNCV6_127109_PI430048170 mRNA
CCAATCTAAAAGTCTCTGAGGGAACCATAGTAAAAAGTCTCTTATAAAGTTAGCTTGCTA NM_020366 RefSeq chr14
+ 21287976 21351301 RPGRIP1 57096 retinitis pigmentosa GTPase regulator interacting protein 1
GO:0005515|GO:0060041|GO:0005930|GO:0032391|GO:0042462|GO:0007601|GO:0050896 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_106185_PI430048170 0.1983836837310330.5192562499127122.00476102401632
0.2604874853983642.1932673689415 A A A 2.48544958378754 2.99328143875146 2.400644624959
P P P LNCV6_106185_PI430048170 mRNA
AAACACCAAAACCAGAGACTATCATCATACCAGAGCAATCTCAGATAAAGAAATGAAGTT NM_199464 RefSeq chr13
+ 50015253 50020922 KCNRG 283518 "potassium channel regulator, transcript variant 2"
GO:0005515|GO:0005783|GO:0051260|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130093_PI430048170 0.0563404527742282 2.40822079647917 2.06839729171571
2.18102694116032 2.12297055794975 A A A 0.3430261043430431.44199960931368
0.534091658254723 A A A LNCV6_130093_PI430048170 mRNA
CCACCCAGAAATCCACTCAAATTTGGGGATTGTCATTCCTTTTGTGAATAATTAATACAA NM_001012993 RefSeq
chr9 - 110199565 110208133 C9orf152 NA chromosome 9 open reading frame 152 NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_137910_PI430048170 0.0790831988709074 1.07258171747364 0.649326967849998
0.724952311208393 0.608367536943286 A A A 0.597114295705169 0.543544549847591
0.540452540322781 A A A LNCV6_137910_PI430048170 mRNA
CGTCTCCAATTTTAGCTCTGTCCTGCATGGACACATACGACATTGAAATCATGATACACA NM_001005199 RefSeq
chr11_JH159136v1_alt - 100875 101811 OR8H1 219469 "olfactory receptor, family 8, subfamily H,
member 1" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_140230_PI430048170 0.363214053990542 1.57000950477205 0.328311458213979
1.65719630635496 0.369836451076542 A A A 0.281022984987243 0.262304197342269
0.283608393996339 A A A LNCV6_140230_PI430048170 mRNA
AACTGCCCAAGTTTGACTAATTGCTTGGCCTGTGAATGGAAAAGACTCTGGTCTAAAAAA NM_178174 RefSeq
chr6 - 41149260 41154349 TREML1 340205 "triggering receptor expressed on myeloid cells-like 1,
transcript variant 1"
GO:0005515|GO:0019722|GO:0009986|GO:0005886|GO:0045087|GO:0031091|GO:0030168|GO:0016021 . NA

- . NA NA NA NA NA NA NA NA NA
LNCV6_140059_PI430048170 0.000746616751460127 1.41564003826905 4.72830339843743
4.66494527060932 4.79561466796592 P P P 4.16499847877308 4.29805120029154
4.22131231445024 P P P LNCV6_140059_PI430048170 mRNA
TAATATGGCTTCTGGTCAAAATCCCTGTGTAGCTGAATTCCCAAGCCCTGCATTGTACAG NM_000435 RefSeq
chr19 - 15159632 15200981 NOTCH3 4854 notch 3
GO:0005515|GO:0010467|GO:0006355|GO:0006367|GO:0007220|GO:0005886|GO:0005509|GO:0072104|GO:0005
576|GO:0048663|GO:0015629|GO:0048661|GO:0005829|GO:0043235|GO:0005737|GO:0045665|GO:0000139|GO:0
007219|GO:0005789|GO:0005654|GO:0030900|GO:0016021|GO:0019899 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_43754_PI430048170 0.750342940148885 1.29999816467224 0.293090560870147
1.84967446645212 0.315436020587747 A A A 0.466843910388427 0.862325747235227
0.557915531046043 A A A LNCV6_43754_PI430048170 mRNA
TAGGCAATAAAAATCTGGAAACTTTCTCTCTCAGGGCTGAGCCAAGATGGAGATAAACTG NM_203454 RefSeq
chr1 - 183646275 183653313 APOBEC4 NA "apolipoprotein B mRNA editing enzyme, catalytic
polypeptide-like 4 (putative)" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138339_PI430048170 0.00959988246597233 0.527536825444113 9.0003718029762
8.75485733438231 9.14708634936594 P P P 9.80043634080289 9.67717839737131
10.1724193616877 P P P LNCV6_138339_PI430048170 mRNA
GCACAAAATTCTAGCAGAAGGCCCCATGGGTTAGAAAAGGACTATAAGAATAATTTCTTA NM_000392 RefSeq
chr10 + 99782597 99852192 ABCC2 1244 "ATP-binding cassette, sub-family C (CFTR/MRP), member
2"
GO:0005515|GO:0046685|GO:0043627|GO:0005886|GO:0009408|GO:0009986|GO:0031427|GO:0019904|GO:0042
626|GO:0070327|GO:0055085|GO:0005524|GO:0046581|GO:0016324|GO:0030644|GO:0015732|GO:0005887|GO:0
006855|GO:0008152|GO:0006810|GO:0008514|GO:0006979 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142129_PI430048170 0.0198651179330992 1.53957391674266 6.38086209227727
6.45579828676221 6.05858546040161 P P P 5.55619354547112 5.78435727181075
5.70791171419882 P P P LNCV6_142129_PI430048170 mRNA
ATTCTCTCCTTTCCTCAAACACATTTGGAACTCAAGTAAATCCAATGCATGTTGGGTGAA NM_032611 RefSeq
chr8_KI270819v1_alt + 93843 104910 PTP4A3 11156 "protein tyrosine phosphatase type IVA, member 3,
transcript variant 1" GO:0005886|GO:0043542|GO:0004727|GO:0035335|GO:0005769 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_134172_PI430048170 0.273953432078836 0.891730579634389 10.6749135824695
10.532687255749 10.6223255027704 P P P 10.6172334254421 10.7132848324299
10.9748188271803 P P P LNCV6_134172_PI430048170 mRNA
CTTCCACTAAATCCAGTTGTGACAAAATCTAACGTGACATCAGATCGAAAGGTTATAGAA NM_001287810 RefSeq
chr15_KI270848v1_alt - 743 77414 CYFIP1 23191 "cytoplasmic FMR1 interacting protein 1, transcript
variant 3"
GO:0005515|GO:0031209|GO:0043005|GO:0048471|GO:0008360|GO:0030032|GO:0045202|GO:0048675|GO:0001
726|GO:0032403|GO:0030027|GO:0031529|GO:0048365|GO:0016601|GO:0051015|GO:0050890|GO:2000601|GO:0
005925|GO:0005845|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126771_PI430048170 0.0668959351888696 0.66587044835858 4.22454686807906
4.13893062126922 4.74314259538546 P P P 4.80788252563279 5.04973189512786
5.0712566163556 P P P LNCV6_126771_PI430048170 mRNA
TAGACCCTGTGAATGTAAGCACTTGGTAAAGCCTTAAGTAGTTTCAGTTTCTTTCCAGTA NM_005815 RefSeq
chr19 - 12429705 12441112 ZNF443 10224 zinc finger protein 443
GO:0006355|GO:0006950|GO:0006915|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_140966_PI430048170 0.000424422452565565 0.578241649961932 11.4774896330669
11.6037822576511 11.5220516611739 P P P 12.2809038904906 12.4267117706234
12.2637080169563 P P P LNCV6_140966_PI430048170 mRNA
AGCCACATTTGTGGATGAGTGGTTTGTGATTAAAAGGGATGTTCTTGAACTTGGAAAAAA NM_005855 RefSeq
chr2 + 237859543 237912117 RAMP1 10267 receptor (G protein-coupled) activity modifying protein
1
GO:0004948|GO:0005515|GO:0005886|GO:0009986|GO:0030819|GO:0031716|GO:0001525|GO:0015031|GO:0015
026|GO:0072659|GO:0005615|GO:0006886|GO:0043235|GO:0031623|GO:0008277|GO:0007186|GO:0005887|GO:0
008565|GO:0004872|GO:0006816|GO:0060050 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_141684_PI430048170 0.172319697749801 1.07101093102648 0.536137303722432
0.638705780727291 0.605144719642915 A A A 0.591457459052797 0.439943819005147
0.448477945206591 A A A LNCV6_141684_PI430048170 mRNA
GTTTGGAATTATGATTGTAGTCTGTTGAATAGTATTTACCATGGCATTTCATACCCATGG NM_018712 RefSeq
chr11 + 107591090 107666779 ELMOD1 55531 "ELMO/CED-12 domain containing 1, transcript
variant 1" GO:0043547|GO:0006909|GO:0005737|GO:0005654|GO:0005856|GO:0005096 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_131429_PI430048170 0.124434599754535 0.51864169602213 0.985013499284089
1.04555503622681 2.22633516992506 A A A 1.85281846265956 2.50218134236386
2.91481946000528 A P P LNCV6_131429_PI430048170 mRNA
AGGGTGACCCTCTTCTCAAGGAAATGGGTGTCATCAATTTTCTACACTATTAAAGATATA NM_005867 RefSeq
chr21 - 38054010 38121360 DSCR4 10281 Down syndrome critical region 4
GO:0008150|GO:0003674|GO:0005575 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_92189_PI430048170 0.00243590327479959 1.79508402939039 6.8537586913307
7.12410890149589 7.03345291971218 P P P 6.19290658967824 6.21610886269594
6.07946273878037 P P P LNCV6_92189_PI430048170 mRNA
TTTGATGAGGACGCGGAGCCGCGGCGGAGCCGGAGGAAGCTGATGGTCATCTTTTCCAAG NM_016547 RefSeq
chr1 - 1216907 1232067 SDF4 51150 "stromal cell derived factor 4, transcript variant 1"
GO:0005515|GO:0009650|GO:0005794|GO:0005886|GO:0005770|GO:0005796|GO:0070625|GO:0045471|GO:0005
509|GO:0021549|GO:0042802|GO:0005737|GO:0032059|GO:0016020|GO:0017156|GO:0045444|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115957_PI430048170 0.00567703517980447 0.598727681850219 10.8669505948225
11.0958123642229 10.7766274075644 P P P 11.752896927476 11.6458217244785
11.5741444087524 P P P LNCV6_115957_PI430048170 mRNA
AGTGCAAAGCGCCCCCCGTCTATATCATATCGCCTCTCGGTCCTCCTAAAAGTCGTATGA NM_001199163 RefSeq
chr17 + 63827683 63832027 PSMC5 5705 "proteasome (prosome, macropain) 26S subunit, ATPase,
5, transcript variant 2"
GO:0005515|GO:0031597|GO:0010467|GO:0002474|GO:0031595|GO:0006366|GO:0090261|GO:0090263|GO:0034
641|GO:0043069|GO:0006977|GO:0070062|GO:0000209|GO:0003712|GO:0000502|GO:0031531|GO:0017025|GO:0
005654|GO:0000278|GO:0045893|GO:0045892|GO:0008134|GO:0006200|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141625_PI430048170 0.5501143869102021.04410528710785 7.8485143430278
7.77622914345953 7.93163430855401 P P P 7.64208587903872 7.77062425335562
7.94497437200135 P P P LNCV6_141625_PI430048170 mRNA
GGAATGTTTCTGTAGGACTTTGTTCTCCACAAGCTTGAATTAAAGCAGGATTCAGTTTGC NM_019592RefSeq chr9
+ 101533848 101563344 RNF20 56254 "ring finger protein 20, E3 ubiquitin protein ligase"
GO:0000209|GO:0005515|GO:0006511|GO:0030336|GO:0004842|GO:0006355|GO:0033523|GO:0033503|GO:0016
874|GO:0003713|GO:0005730|GO:0000151|GO:0005634|GO:0042393|GO:0002039|GO:0003682|GO:0031062|GO:0

005654|GO:0008270|GO:0045893|GO:0010390|GO:0031625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66720_PI430048170 0.00718603128602707 0.5422390663514155.48293581423561 5.37946073841853 5.70818590223547 P P P 6.22670439524612 6.31944265623933 6.65692181323383 P P P LNCV6_66720_PI430048170 mRNA AGACAACAGACAGCAGCATTCATTCATAGGATCAACTAACAACCATGTGGTGAGGAATTC NM_003628 RefSeq chr2 + 158456879 158681428 PKP4 8502 "plakophilin 4, transcript variant 1" GO:0005515|GO:0030057|GO:0072686|GO:0048471|GO:0005886|GO:0032467|GO:0044291|GO:0007267|GO:0030496|GO:0014069|GO:0051233|GO:0030155|GO:0000922|GO:0005737|GO:0016337|GO:0032321|GO:0005911|GO:0007043|GO:0009898|GO:0005856 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144052_PI430048170 0.2841347826148931.02281708395163 0.336073596182173 0.3291571295895640.265913074854046 A A A 0.2762343462369720.286254365632207 0.272004510569557 A A A LNCV6_144052_PI430048170 mRNA ATGGTCAAAAGACTCTCCGACAAAAACAAATCCAGTCTCTAGCAGTTATGTTGTTAGAAT NM_001195470 RefSeq chr3 - 18347640 18425337 SATB1 6304 "SATB homeobox 1, transcript variant 3" GO:0005515|GO:0000977|GO:0016571|GO:0006325|GO:0043367|GO:0006915|GO:0005634|GO:0000122|GO:0001227|GO:0016363|GO:0006921|GO:0006351|GO:0005720|GO:0003690|GO:0043374|GO:0008544|GO:0060004|GO:0016605|GO:0003682|GO:0016032|GO:0050798|GO:0005654|GO:0006338 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133039_PI430048170 0.4360206215527040.9491289022533781 0.0150738762354 9.80288870363943 9.87953704791716 P P P 9.8521006164566 10.0297999943617 10.0419080429687 P P P LNCV6_133039_PI430048170 mRNA AAATGGTAATGTGAAGCTAAGAGCAGAGAGTGACCAACAGTAAACAACACGCGCAGACTC NM_020761 RefSeq chr17 + 80544824 80966373 RPTOR 57521 "regulatory associated protein of MTOR, complex 1, transcript variant 1" GO:0008286|GO:0005515|GO:0001156|GO:0008361|GO:0032008|GO:0071902|GO:0005765|GO:0005764|GO:0032403|GO:0030425|GO:0005829|GO:0043231|GO:0034605|GO:0071889|GO:0005737|GO:0071230|GO:0031931|GO:0045945|GO:0031669|GO:0043025|GO:0007050|GO:0031929|GO:0019901|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130189_PI430048170 0.1754010295133531.14287195919826 12.7065584313305 13.0296879678646 12.9129183320137 P P P 12.7585994575123 12.7020624512285 12.6257921228191 P P P LNCV6_130189_PI430048170 mRNA AAGATGCTGAGTGTCTGCACTGCTCCACTTGTCCCCCCGCTCTCTCCTCAGTACAAGTGA NM_001012984 RefSeq chr16 + 67666813 67668758 C16orf86 388284 chromosome 16 open reading frame 86 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132460_PI430048170 0.2419313406258790.9699076671696841 5.9023643184159 15.8394747519523 15.907804044538 P P P 15.8808654501598 15.955852083754 15.9450293236055 P P P LNCV6_132460_PI430048170 mRNA TACAACGGCAAGACCTTCAACCAGGTGGAGATCAAGCCCGAGATGATCGGCCACTACCTG NM_001018 RefSeq chr19 + 1438363 1440497 RPS15 6209 ribosomal protein S15 GO:0005515|GO:0010467|GO:0006364|GO:0019058|GO:0005634|GO:0006412|GO:0006413|GO:0005829|GO:0006414|GO:0005737|GO:0000184|GO:0016032|GO:0042274|GO:0000028|GO:0003735|GO:0006614|GO:0019083|GO:0006415|GO:0003677|GO:0001649|GO:0016020|GO:0022627|GO:0005654|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_96857_PI430048170 0.0574231693684463 1.3953489742301 12.2756832396371 12.6709347671106 12.7219101917821 P P P 11.9636631666781 12.0182075406664 12.2663933663876 P P P LNCV6_96857_PI430048170 mRNA GCTCTGTTGTAATATACTGGTGATGCATCTAATTCTCCACAAAGACCAATAAATTGAATG NM_001099670 RefSeq chr8 - 85214052 85220422 C8orf59 401466 "chromosome 8 open reading frame 59, transcript variant

1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144186_PI430048170 0.0413399891732237 0.3779017372855883.50957639349227
2.35637531790432 2.85010410616955 P A A 4.31141568115928 4.29717160322222
4.53941805924493 P P P LNCV6_144186_PI430048170 mRNA
GCAATTGACAGTCCTAATAACTCAGCTAATTTGAAACTAACAATCTTGCTGTGTAAAAGG NM_015322RefSeq chr15
+ 68277802 68295865 FEM1B 10116 fem-1 homolog b (C. elegans)
GO:0060442|GO:0005515|GO:0005737|GO:0004842|GO:0016567|GO:0060743|GO:2000001|GO:0051438|GO:0006
915|GO:0005654|GO:0005634|GO:0005123 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127351_PI430048170 0.0213298235799512 0.7606230141185784.88604965311193
4.78043784294852 4.88102820217078 P P P 5.15763904942778 5.17240763915581
5.39200961500271 P P P LNCV6_127351_PI430048170 mRNA
TGTTGAGGGGTTGAATGTTTTACTACAAACAAGCCACAATAAAGTGTCTATCAACATGTT NM_015346RefSeq chr14
- 67746519 67816589 ZFYVE26 23503 "zinc finger, FYVE domain containing 26"
GO:0005515|GO:0000910|GO:0005813|GO:0000724|GO:0030496|GO:0032266|GO:0005765|GO:0046872 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143852_PI430048170 0.1089011175937421.12518761242016 14.0731396151734 13.860722792855
13.9026299567941 P P P 13.8248294966226 13.7378175399942 13.7708894254208 P P P
LNCV6_143852_PI430048170 mRNA
GAAATATGTTACAGAACATGCACTTGCCCTAATAAAAAATCAGTGAAATGGTCTCTGGTA NM_005005RefSeq chr8
+ 124539101 124549986 NDUFB9 4715 "NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9,
22kDa, transcript variant 1"
GO:0022904|GO:0005739|GO:0005747|GO:0007605|GO:0006120|GO:0005743|GO:0044281|GO:0008137|GO:0044
237|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128826_PI430048170 0.00401958514376578 0.8731067765463199.49198647266405
9.54790469982942 9.54933398393934 P P P 9.71089824907779 9.73025823198005 9.7359970855247
P P P LNCV6_128826_PI430048170 mRNA
GGTGGCAAGATAGTCTCTGTCCCCACCCCCTTGTACTTGATTCCCCAGCTGTCTTTCACA NM_006662RefSeq chr16
+ 30699140 30740129 SRCAP 10847 Snf2-related CREBBP activator protein
GO:0005515|GO:0048471|GO:0005794|GO:0006357|GO:0016573|GO:0003713|GO:0004386|GO:0005634|GO:0003
677|GO:0005524|GO:0006351|GO:0043234|GO:0016032|GO:0005654|GO:0004402 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141896_PI430048170 0.0527609258282605 0.66088555447512311.2881299312432
11.2187182131495 11.4505128674138 P P P 11.7101532999523 11.7708985423168
12.2227019396068 P P P LNCV6_141896_PI430048170 mRNA
GATGTCAGCAGTGGCCTGAAGTGAGTTGTGCAATAAATGTTAAGTTGAAACCTCAAAAAA NM_001762RefSeq chr7
+ 56051684 56063989 CCT6A 908 "chaperonin containing TCP1, subunit 6A (zeta 1), transcript variant 1"
GO:0005515|GO:0001669|GO:0005832|GO:0005874|GO:0007339|GO:0005524|GO:0044297|GO:0005829|GO:0005
737|GO:0006457|GO:0051084|GO:0002199|GO:0051082|GO:0044267|GO:0070062 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143560_PI430048170 0.0153014349250985 2.28326120307636 6.71032802695222
7.04122947296762 7.42996585621022 P P P 5.84527513610227 5.72956169777033
6.09845549218422 P P P LNCV6_143560_PI430048170 mRNA
CCCCTGTATAGAATTGAAAGGATCCAAAGGATTATTGCACATTTTCTACATTCCAAGGAG NM_015364RefSeq chr8
+ 73991328 74029072 LY96 23643 "lymphocyte antigen 96, transcript variant 1"
GO:0005515|GO:0034142|GO:0005886|GO:0007249|GO:0001875|GO:0005615|GO:0002756|GO:0006954|GO:0002
755|GO:0031666|GO:0032496|GO:0032497|GO:0031663|GO:0034138|GO:0046696|GO:0038124|GO:0038123|GO:0
034134|GO:0015026|GO:0002224|GO:0006968|GO:0045087|GO:0035666|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130483_PI430048170 0.1741837029041860.83783969676101310.147499540512

10.2237725055228 10.5352361653737 P P P 10.6498272435555 10.3592673004485 10.672415028551
P P P LNCV6_130483_PI430048170 mRNA
CATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGGCTA NM_001164460 RefSeq
chr7 - 22438418 22500282 STEAP1B NA "STEAP family member 1B, transcript variant 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137485_PI430048170 0.0062883833993898 1.32504713083048 11.286902319355
11.4011679642215 11.4713145802265 P P P 10.9377994787231 10.9125842527929 11.090357149693
P P P LNCV6_137485_PI430048170 mRNA
TCAGCCTGTGTAACCATGTGGAAATAAAAATTGACGACCAATGTATTATATGGACAACTT NM_032476RefSeq chr21
+ 34073522 34143034 MRPS6 64968 mitochondrial ribosomal protein S6
GO:0070124|GO:0005515|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0015935|GO:0005
743|GO:0070181|GO:0006412|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141852_PI430048170 0.109680312382707 0.4074567879439822.40245064561858
0.77512613433418 0.62138737253534 A A A 2.77947010243704 3.01133506209436
2.59025971748539 P P P LNCV6_141852_PI430048170 mRNA
CCCCCAACCACAGGCATCAGGCAACCATTTGAAATAAAACTCCTTCAGCCTGTGAAAAAA NM_005608RefSeq chr11
- 67435509 67437682 PTPRCAP 5790 "protein tyrosine phosphatase, receptor type, C-associated
protein" GO:0005886|GO:0006952|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134556_PI430048170 0.6223906284476410.9525037323812239.83126437933896
9.80202391226063 9.51019689959755 P P P 9.66668020701749 9.95671330334666
9.73588339251484 P P P LNCV6_134556_PI430048170 mRNA
CCTCATCTAGAAAAGAGGTTACAAACCTACCATTAAACTATTTTTCCTAAAACGGAAGCA NM_006278RefSeq chr11
+ 126355893 126414641 ST3GAL4 6484 "ST3 beta-galactoside alpha-2,3-sialyltransferase 4, transcript
variant 1"
GO:0005975|GO:0016266|GO:0047288|GO:0044281|GO:0003836|GO:0042339|GO:0030173|GO:0050890|GO:0000
139|GO:0006493|GO:0016020|GO:0018146|GO:0032580|GO:0009405|GO:0006488|GO:0044267|GO:0030203|GO:0
070062|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141981_PI430048170 0.4229146185879591.03352864188103 0.438136151836798
0.2827763550517950.330858332780146A A A 0.27840379182437 0.323856842461277
0.310808222472999A A A LNCV6_141981_PI430048170 mRNA
CTTCACTGCAGAATGTAAAGGTTTCAACGTCTTGCTTTAATAAATCACTTGCTCTCCAAA NM_006551RefSeq chr11
+ 62242251 62244808 SCGB1D2 10647 "secretoglobin, family 1D, member 2" GO:0005615 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144453_PI430048170 0.0121587486923836 0.2177612804687340.667800710028306
0.5189330631502470.545934442316149A A A 2.61840500237124 3.22423516281334
2.34878527084275 A P A LNCV6_144453_PI430048170 mRNA
CTGTGATTTATAATGACATCCTGAGAAAAGTCAGTGAAACTCATTTCTAACGAATACCAG NM_001256141 RefSeq
chr8 - 94427711 94436952 FSBP NA fibrinogen silencer binding protein NA . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_36593_PI430048170 0.00837389444661612 1.4741460176186 11.4224055083052
11.3618411772218 11.6110397099987 P P P 10.8408118797581 10.9411162171131
10.9432193086246 P P P LNCV6_36593_PI430048170 mRNA
TCCCAGACGGTGAAGAAGGTGATAGAGATCAACCCATACCTGCTAGGCACCATGGCTGGG NM_001144932
RefSeq chr14 - 23025850 23035145 PSMB5 5693 "proteasome (prosome, macropain) subunit, beta
type, 5, transcript variant 3"
GO:0005515|GO:0002474|GO:0010467|GO:0090263|GO:0005634|GO:0044281|GO:0031145|GO:0005829|GO:0004
298|GO:0034641|GO:0000082|GO:0016032|GO:0090090|GO:0006979|GO:0070062|GO:0006977|GO:0000209|GO:0
005839|GO:0005813|GO:0000502|GO:0043066|GO:0006521|GO:0051437|GO . NA - . NA NA NA NA
NA NA NA NA NA

LNCV6_98405_PI430048170 0.0611372513986008 0.9589593762705270.4283596813363760.3691280702059
0.380827416211376 A A A 0.4419381012274 0.4691236291350120.449175547912815 A A A
LNCV6_98405_PI430048170 mRNA
CCCATGGGTTTTGATTGTGTCTAAGCTATGATGACCTTCATATAATCAGCATAAACATAA NM_080657 RefSeq chr2
+ 6877664 6898232 RSAD2 91543 radical S-adenosyl methionine domain containing 2
GO:2000553|GO:0005515|GO:0005783|GO:0019221|GO:0005743|GO:0005741|GO:0003824|GO:0043621|GO:0046
872|GO:0005739|GO:0051607|GO:0060337|GO:0030278|GO:0016032|GO:0045071|GO:0005811|GO:0005794|GO:0
051539|GO:0034157|GO:0043367|GO:0009615|GO:0035710|GO:0001503|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142226_PI430048170 0.0459906559309335 1.41332609858263 11.9395000010325
11.7649765416009 11.8056976621849 P P P 11.0652092191037 11.4760943128687
11.4424813517653 P P P LNCV6_142226_PI430048170 mRNA
CCCCGAGGTGGGGCAGCCCCTTCTCATTTTATACAATAAACATTCTCCACCTACAAAAAA NM_005052 RefSeq chr17
+ 82031655 82034204 RAC3 5881 "ras-related C3 botulinum toxin substrate 3 (rho family, small GTP
binding protein Rac3)"
GO:0005515|GO:0043005|GO:0048471|GO:0030036|GO:0005886|GO:0007264|GO:0003924|GO:0031175|GO:0030
426|GO:0005829|GO:0071944|GO:0035556|GO:1900026|GO:0043025|GO:0050885|GO:0070062|GO:0051056|GO:0
033630|GO:0005525|GO:0030027|GO:0012505|GO:0031941|GO:0030031|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141968_PI430048170 0.4322693189997391.02583722865084 0.343045534803061
0.3442343137325850.451680787868705 A A A 0.3481478345602970.314389239971634
0.368225059787792 A A A LNCV6_141968_PI430048170 mRNA
AAGTCAAGACACCTATGGGTAAAAGTTCTCTCTGATGCATGAAAACTCAGAGTGATAAAG NM_001077639 RefSeq
chr11 - 114570590 114595762 NXPE4 54827 "neurexophilin and PC-esterase domain family, member 4,
transcript variant 1" GO:0008150|GO:0003674|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_145314_PI430048170 0.0303001879853660.2273705056534981.76236703083867
0.48329315297765 2.01746492282827 A A A 3.892996474549 3.79285864855951
3.34475051457229 P P P LNCV6_145314_PI430048170 mRNA
CAGCAAGTTTCTGCTTTTTAAGGTTACTTTTAGAATAAATCATCAGGGAAACAGAGAGGA NM_002372 RefSeq chr5
+ 109689365 109869625 MAN2A1 4124 "mannosidase, alpha, class 2A, member 1"
GO:0005801|GO:0048286|GO:0004572|GO:0007585|GO:0060042|GO:0001701|GO:0016799|GO:0001889|GO:0000
139|GO:0016020|GO:0050769|GO:0006491|GO:0030246|GO:0008270|GO:0007005|GO:0007033|GO:0016021|GO:0
044267|GO:0070062|GO:0043687|GO:0018279|GO:0006013 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_141715_PI430048170 0.1573071390041951.07564886454151 0.506345848793716
0.4494270249477730.548937329717684 A A A 0.3076388810235480.396851071439414
0.481111875120432 A A A LNCV6_141715_PI430048170 mRNA
CTGAGCTGTCTAAAAGTTACATTGTGCTTGGTAGATTTAGTGTTAAGTGTGCAGTATAAT NM_001232 RefSeq chr1
- 115700004 115768805 CASQ2 845 calsequestrin 2 (cardiac muscle)
GO:0005515|GO:0005513|GO:0030018|GO:0051258|GO:0060306|GO:0006941|GO:0043267|GO:0060048|GO:0042
803|GO:0005622|GO:0014701|GO:0010649|GO:0005737|GO:0034220|GO:0010880|GO:0060315|GO:0086029|GO:0
051208|GO:0030314|GO:0005509|GO:0033018|GO:0045214|GO:0071313|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_141890_PI430048170 0.0328634394843384 1.47407982041467 9.90205827472009
10.1795834933868 10.2698169382713 P P P 9.59050945541028 9.51640128987797
9.58880559744741 P P P LNCV6_141890_PI430048170 mRNA
TGTTCACAATCTCCAAAGGGACTGTATTTCTTCTCTGTGCTTAATGTGATTTGAAATATG NM_020179 RefSeq chr11
- 93478472 93543380 SMCO4 56935 single-pass membrane protein with coiled-coil domains 4

GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141384_PI430048170 0.0269722076324012 1.92114749797614 4.09598825713866
4.23546272020946 4.3563188531789 P P P 3.58371465116709 3.30437608705001 2.9067087083885
P P P LNCV6_141384_PI430048170 mRNA
GGGGCCAACTCCAATATAGGGTGGGTAAGGCCTTATAATGTAAAGAGCATATAATGTAAA NM_006488RefSeq chr2
+ 27086742 27100751 KHK 3795 "ketohexokinase (fructokinase), transcript variant b"
GO:0005737|GO:0005975|GO:0009405|GO:0046835|GO:0005634|GO:0044281|GO:0004454|GO:0070873|GO:0005
524|GO:0006001|GO:0070062|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128961_PI430048170 0.1699497219814461.11961234687479 12.6671072536148
12.5218425860689 12.395196985258 P P P 12.3526134371136 12.4532112065109
12.2978494135479 P P P LNCV6_128961_PI430048170 mRNA
GTGGATTCCTTTGGGAAGGGCTCCCTGGGCAGGACAATAAAGAGTTTTGACTCCAAAAAA NM_032125RefSeq chr1
+ 27322144 27336400 TMEM222 84065 "transmembrane protein 222, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132290_PI430048170 0.2235041772842680.562123373231285 1.01863512359253
2.34261163296144 0.536032669202384A A A 2.83210868872587 2.3354366154799
1.60348700877892 A A A LNCV6_132290_PI430048170 mRNA
ATGTATGGTGTAAAACACACAAACACACACAAAAAAGCACAAGCCCGCTGCATGACCCGTNM_001005463 RefSeq
chr10 - 129835231 129963827 EBF3 253738 early B-cell factor 3
GO:0046983|GO:0007275|GO:0005634|GO:0045893|GO:0003677|GO:0046872|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130985_PI430048170 0.0263831085865243 0.7009606724247298.4039970671064
8.52771085488024 8.76772127551769 P P P 9.1176046203511 8.88292009967657
9.23833865409828 P P P LNCV6_130985_PI430048170 mRNA
CTATTGGTCTTCAAGTGGGTTTAGATTTGGTGACATCAGTTTGATATTCTCTTAAAGGAA NM_012229RefSeq chr10
- 103088016 103193306 NT5C2 22978 "5'-nucleotidase, cytosolic II, transcript variant 1"
GO:0005515|GO:0046040|GO:0050146|GO:0017144|GO:0046085|GO:0055086|GO:0044281|GO:0046872|GO:0005
829|GO:0016310|GO:0006195|GO:0000166|GO:0006144|GO:0016311|GO:0008253 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_142897_PI430048170 0.00812047100202032 2.12254408879363 9.14854682975957
9.20393907277711 9.08171661167356 P P P 8.22729367745512 8.10631464031321
7.81534614713887 P P P LNCV6_142897_PI430048170 mRNA
AAGTAACTTTTTGTATAAATAAAAGAAAATGGGACGTGTCCCAGCTCCAGGGGTAAAAAA NM_004444RefSeq chr7
- 100802564 100827521 EPHB4 2050 EPH receptor B4
GO:0005515|GO:0048013|GO:0005886|GO:0002042|GO:0018108|GO:0005576|GO:0001525|GO:0005524|GO:0005
829|GO:0003007|GO:0046777|GO:0005003|GO:0005887|GO:0007411|GO:0004714|GO:0007155|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132811_PI430048170 0.96978318809027 1.00952663885772 2.87360507836109
2.14836428740849 2.60403964572438 A A A 2.29795619932031 2.3685086499209
2.92448198765505 A A P LNCV6_132811_PI430048170 mRNA
CCTACTCGTGAAACGATGTGAACAAGCATTTTAAGGACAATAAAAAGTTAGCTGGTTGAA NM_000444RefSeq chrX
+ 22032443 22251310 PHEX 5251 "phosphate regulating endopeptidase homolog, X-linked,
transcript variant 1"
GO:0048471|GO:0005794|GO:0005886|GO:0005783|GO:0007267|GO:0030282|GO:0001501|GO:0005887|GO:0004
177|GO:0006508|GO:0008270|GO:0019637|GO:0004222|GO:0006464 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_136868_PI430048170 0.0622666045668092 1.14755077567123 4.94955244134573
4.82163853763417 4.76979729996887 P P P 4.55679939199931 4.63793052621826
4.75001866014085 P P P LNCV6_136868_PI430048170 mRNA

CAGAGGGGGGACAGAAGGACAATGGCTAATCTATTTTTCAAATATATATTTTGCTTAGTT NM_001080472 RefSeq chr20 - 44306556 44311249 FITM2 128486 fat storage-inducing transmembrane protein 2 GO:0005739|GO:0003674|GO:0019915|GO:0010890|GO:0022604|GO:0007010|GO:0005789|GO:0030176|GO:0035356|GO:0008654|GO:0010866|GO:0034389 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128759_PI430048170 0.00849966315304711 1.46855482141598 7.04818440763349 7.27209599403893 7.33013124672484 P P P 6.62706973987375 6.5615209217607 6.80281796940713 P P P LNCV6_128759_PI430048170 mRNA
AGGATCGGCATGGTCATTCACCAAGTGGAAACCAAACCCTCTGTGTATTTCATCAAGTTT NM_019003 RefSeq chrX - 57135649 57137625 SPIN2A NA "spindlin family, member 2A" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133991_PI430048170 0.5785768194442891.22803382194442 0.679162380729217 1.74492810394748 0.789442700694525A A A 0.7739336101039820.411047443355098 1.26372643289082 A A A LNCV6_133991_PI430048170 mRNA
TATTCTTACAGAAAGATAGTTATCCAGAAATTCTCATTCCCCGTCTGCGGTGCGGTGCGT NM_144685 RefSeq chr19 - 40379270 40390221 HIPK4 147746 homeodomain interacting protein kinase 4 GO:0005737|GO:0046777|GO:0018105|GO:0004674|GO:0016572|GO:0005634|GO:0005524 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_122765_PI430048170 0.0125711044376181 0.2666433180558720.435527432960417 0.3748977737565220.386702809254016A A A 2.66532678245662 1.91880002756501 2.23682494846579 A A A LNCV6_122765_PI430048170 mRNA
GTTTAATGAGTTTCACGGCTTTCAACACTATTGTCATATAGTTATCTTTGCCATTTGGAGNM_021964 RefSeq chr3 - 125225668 125375354 ZNF148 7707 zinc finger protein 148 GO:0005515|GO:0005794|GO:0006366|GO:0007276|GO:0000122|GO:0000978|GO:0046872|GO:0043565|GO:0001078|GO:0006968|GO:0003690|GO:0006461|GO:0021762|GO:0045944|GO:0010629|GO:0005654|GO:0045892 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126948_PI430048170 0.0923415209416657 1.213196714456 11.6500351063677 11.8821014913414 11.9498695606453 P P P 11.5782825004443 11.544376065354 11.5394321991826 P P P LNCV6_126948_PI430048170 mRNA
TCTTGGGGAAGATACCCCTTTTCTGAGGAATGAGTTTGCCTCCGTCCCCTGCCCATGCTG NM_001291163 RefSeq chr1 + 225810133 225845561 EPHX1 2052 "epoxide hydrolase 1, microsomal (xenobiotic), transcript variant 3" GO:0014070|GO:0033961|GO:0019439|GO:0005789|GO:0009636|GO:0016021|GO:0004301 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143533_PI430048170 0.4289726214656650.764274750510597 0.443992732895614 0.7731716722139990.369878875884464A A A 1.47035785655128 0.711532203322223 0.376779905181753A A A LNCV6_143533_PI430048170 mRNA
ACTCATTTATACCCTGAGAAATGAAGAGGTAAAAAATGCCATGAGAAAGCTCTTTACATG NM_001004702 RefSeq chr11 + 48324940 48325930 OR4C3 256144 "olfactory receptor, family 4, subfamily C, member 3" GO:0050911|GO:0050907|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_115797_PI430048170 0.0126735940456876 0.6354556650054139.68909256798456 9.66270450919129 9.68183446200255 P P P 10.2002301772017 10.4630847883782 10.3208336361133 P P P LNCV6_115797_PI430048170 mRNA
ACCGCTGCGGCGTCAGCTCAGCCTTGCAAGACCCCAGGCGCCCGCGCTGCACCTGCGACT NM_004864 RefSeq chr19 + 18386157 18389176 GDF15 9518 growth differentiation factor 15 GO:0007267|GO:0010862|GO:0005576|GO:0042981|GO:0005125|GO:0005160|GO:0005615|GO:0060395|GO:0007165|GO:0043408|GO:0007179|GO:0048468|GO:0008083|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132485_PI430048170 0.5073896922940710.9396347173053951 0.8244097386041 10.7908646030465 10.9798762498603 P P P 10.8821114925498 10.8237980468359

11.1451589147144 P P P LNCV6_132485_PI430048170 mRNA
GAGAAGAGAGAATGATTGAAAATGTTTTAGTATAGAACTCTTCTTGCAGTGGGTTGCTAT NM_004905RefSeq chr1
+ 173477346 173488807 PRDX6 9588 peroxiredoxin 6
GO:0005515|GO:0016209|GO:0005615|GO:0005764|GO:0005829|GO:0004602|GO:0005737|GO:0016020|GO:0004
623|GO:0016023|GO:0051920|GO:0042744|GO:0000302|GO:0006979|GO:0009395|GO:0070062|GO:0055114 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130434_PI430048170 0.4535592892027911.04942049566276 0.28565772835338
0.2921939324560390.503248311276849A A A 0.3108172363636840.270682861507966
0.301305478975033A A A LNCV6_130434_PI430048170 mRNA
GTGTTGTCTTACAGGATGTACAAAAGAAGAACTTAGCATTGCATGTCTTCCATATATTGA NM_007179RefSeq chr9
- 5163862 5185618 INSL6 11172 insulin-like 6
GO:0009566|GO:0008150|GO:0043066|GO:0005179|GO:0007286|GO:0005576|GO:0030317|GO:0005575|GO:0008
584. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139932_PI430048170 0.0553910031175623 0.81592486328225 8.30416252485852
8.2669728767704 8.48635860220393 P P P 8.52588388406969 8.60234286354329
8.80484299460337 P P P LNCV6_139932_PI430048170 mRNA
AAGGTGGCTTTGAACTGGAACCCAAGTGCAAATAAAGGTTGGTATTCGCTCCTGAAAAAA NM_014282RefSeq chr9
+ 96450154 96491336 HABP4 22927 hyaluronan binding protein 4
GO:0005515|GO:0006355|GO:0030168|GO:0005576|GO:0005634|GO:0030017|GO:0006351|GO:0005829|GO:0043
392|GO:0005737|GO:0007596|GO:0002576|GO:0005654|GO:0071260 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_144307_PI430048170 0.6510345198109921.23790946790285 1.07847616973105
2.40757446404749 2.3480154697969 A A A 2.17613353949817 0.979826954130598
1.85327125771067 A A A LNCV6_144307_PI430048170 mRNA
AAGCAGCAATTGGTGAGGCGAGGGAAAGGACCCTTTTCTCTGAGTAAATAAAGTCTCACA NM_182578RefSeq chr1
- 151847100 151853697 THEM5 284486 thioesterase superfamily member 5
GO:0016290|GO:0005759|GO:0035965|GO:0006631|GO:0035336 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133906_PI430048170 0.3519212939674180.8041694746794154.8558759444236
5.79805003940063 5.28557872241961 P P P 5.95283026158742 5.65775541428957
5.36725421473384 P P P LNCV6_133906_PI430048170 mRNA
GCCTGTGTCCTGGAGGCCTATACCTCTGTTATTTTCTGATACAAAATAAAACTTAAAAAA NM_006914RefSeq chr9
+ 74497335 74687201 RORB 6096 RAR-related orphan receptor B
GO:0005515|GO:0010467|GO:0006367|GO:0003700|GO:0060041|GO:0071300|GO:0003707|GO:0005634|GO:0043
401|GO:0004879|GO:0006355|GO:0046549|GO:0046548|GO:0035881|GO:0043565|GO:0045668|GO:0042752|GO:0
008270|GO:0005654|GO:0048511|GO:0045893|GO:0030522|GO:0007601|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_137013_PI430048170 0.2031132721550420.46192403180452 0.451884893657084
0.4713905595130610.289976033131287A A A 2.25050843753824 0.4989916863194341.285505694611
A A A LNCV6_137013_PI430048170 mRNA
TTTCTGACTGAACTGTTCAGGCACTGACTCTACATATAATTATGCTTTTCTACCCCCTCANM_181425RefSeq chr9 +
69035562 69079077 FXN 2395 "frataxin, transcript variant 2"
GO:0005515|GO:0008284|GO:0016540|GO:0070301|GO:0051353|GO:0030307|GO:0044281|GO:0009792|GO:0006
119|GO:0005829|GO:0006879|GO:0005739|GO:0009060|GO:0090201|GO:0040015|GO:0005759|GO:0010039|GO:0
007628|GO:0006811|GO:0046621|GO:0010722|GO:0034986|GO:0043066|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_61089_PI430048170 0.1782753933703641.29572980495723 5.8379726671891 5.77738039266296
5.94527718035572 P P P 5.53686610434308 5.07482958103479 5.75223884008518 P P P
LNCV6_61089_PI430048170 mRNA

TTCTATACAGTTGCTCCAATGACAGAGTTACCTGCACCGTTGTCCTACTTCCAGAATGCA NM_000021 RefSeq chr14 + 73136434 73223691 PSEN1 5663 "presenilin 1, transcript variant 1"
GO:0005515|GO:0030018|GO:0031594|GO:0007220|GO:0008013|GO:0001756|GO:0005765|GO:0009791|GO:0015031|GO:0001947|GO:0015813|GO:0043524|GO:0016337|GO:0021795|GO:0007219|GO:0048167|GO:0030198|GO:0016485|GO:0007175|GO:0043025|GO:0007613|GO:0006509|GO:0005938|GO . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_72367_PI430048170 0.1428440337564761.10316310048968 10.5095282672046 10.5379470072882 10.3371383211488 P P P 10.2987051820798 10.3903474007354 10.2761415856532 P P P LNCV6_72367_PI430048170 mRNA
TCTTGTACTGGGAGAGGTGCCTTTTGTATCCCCAATTAAAGGTAGAAAACCACCCTGCTA NM_001135732 RefSeq chr22 + 35299803 35347994 TOM1 10043 "target of myb1 (chicken), transcript variant 2"
GO:0005515|GO:0005737|GO:0016020|GO:0030276|GO:0016197|GO:0015031|GO:0006886|GO:0005769|GO:0070062|GO:0006897|GO:0005829|GO:0005768 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128331_PI430048170 0.00122545430981257 1.67293756600759 11.029072992708 11.2190100614031 11.2283653725915 P P P 10.3128612920122 10.4044674806115 10.5321607602274 P P P LNCV6_128331_PI430048170 mRNA
ATGGGGCACTCCTAGCCAGTGAGTCATGGTCATATTTCCTGAGTAAAGTCATTCTGAGTT NM_015448 RefSeq chr10 + 101588331 101609653 DPCD 25911 deleted in primary ciliary dyskinesia homolog (mouse)
GO:0007368|GO:0021670|GO:0003351|GO:0060972|GO:0005634|GO:0030317|GO:0007283|GO:0021678 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129751_PI430048170 0.438316757835497 1.64640079538259 0.628319138838931 1.88842797239598 2.5974818321374 A A A 0.316354541356831 1.36363535672757 1.6065246654929 A A A LNCV6_129751_PI430048170 mRNA
GTGTGTATTTCATACACACACAAGGACCTGGATTAAAAATCCAAAAAGTGATTCTCTTCT NM_024800 RefSeq chr3 + 131026849 131350465 NEK11 79858 "NIMA-related kinase 11, transcript variant 1"
GO:0035556|GO:0005515|GO:0004674|GO:0031573|GO:0031572|GO:0005730|GO:0006468|GO:0005654|GO:0005524|GO:0046872 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131621_PI430048170 0.141300742269521 0.4272140543334620.245959814269822 0.28610957266781 0.295334374989267 A A A 1.2945975185577 2.18052758505261 0.600505108039827 A A A LNCV6_131621_PI430048170 mRNA
ACGCTTCTTACTTAGCCAAGATTCAGAGGAAAATGACTCCAGTGTGTGCTTGGATTGGGA NM_001018082 RefSeq chr20 + 38581194 38588463 ADIG 149685 "adipogenin, transcript variant 1"
GO:0005737|GO:0050872|GO:0050873|GO:0045600|GO:0005634|GO:0016021|GO:0007283 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130137_PI430048170 0.0939714031422659 0.4931083233788170.41849276066118 1.56630226694622 1.44691680649238 A A A 1.59938540356474 2.59036699999785 2.37632683000678 A P A LNCV6_130137_PI430048170 mRNA
ATTCTTTTCCCACCGTTTCTTCCTGTTGATATTCAATGAATCCGTCAATCTCTCTGGAAA NM_174892 RefSeq chr17 - 74521173 74531474 CD300LB 124599 CD300 molecule-like family member b
GO:0005886|GO:0045087|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130210_PI430048170 0.1759498571713581.12708846816466 0.658572539851421 0.4069487580994680.647866611826408 A A A 0.286658734868389 0.423454109112357 0.491731691105557 A A A LNCV6_130210_PI430048170 mRNA
GTATTTTGTGCTTTGTAAATTAGCTGTACTGAGTTACCAAGTAATAAAGGGTTTGACTCC NM_174978 RefSeq chr14 - 60435955 60486046 C14orf39 317761 chromosome 14 open reading frame 39
GO:0051090|GO:0003674|GO:0007275|GO:0005575 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143706_PI430048170 0.0147577357125834 0.2544868255568870.401354497006946 0.4611396324641941.50296472871911 A A A 2.96933333132566 2.46895426045123 3.06491931503432 P A P LNCV6_143706_PI430048170 mRNA

CACCATTCACTTGTTGGGAAAATAATCTTTGGTTTGGAAGATATTAACATAATGGGCATC NM_001198819 RefSeq chr10 - 50799408 50885675 A1CF 29974 "APOBEC1 complementation factor, transcript variant 5" GO:0003725|GO:0005515|GO:0006397|GO:0030895|GO:0010467|GO:0003727|GO:0005783|GO:0016556|GO:0003723|GO:0016554|GO:0050821|GO:0005737|GO:0000166|GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135860_PI430048170 0.1416441924638 1.49535989831122 7.114254223225 7.48254298462664 7.13316807704867 P P P 6.08780720822823 7.01983903214671 6.75939058117598 P P P LNCV6_135860_PI430048170 mRNA
AGAGCAGAATTCTGGCCCCAGAACTCTGTGCCCAGGAGCCATGCCTTGAGCAGTATTAGC NM_013241 RefSeq chr16 - 67229388 67247522 FHOD1 29109 formin homology 2 domain containing 1 GO:0005515|GO:0005737|GO:0001725|GO:0032059|GO:0016020|GO:0045944|GO:0051496|GO:0005634|GO:0003779|GO:0042802 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129187_PI430048170 0.500456243466536 0.460896547906563 0.886225870293611 0.329443001845447 0.485895111801783 A A A 2.82244678092897 0.285196863119586 0.568449363631 6 P A A LNCV6_129187_PI430048170 mRNA
AACTGTTGCAAACCAGCTTCTTGTGACACTGTGATTTCTGGCCAACCAACTTGTGATGGA NM_001257309 RefSeq chr17_JH159148v1_alt + 4258 5284 KRTAP29-1 NA keratin associated protein 29-1 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142557_PI430048170 0.64441530125612 0.945010546470339 6.72547887404155 6.87559643862883 6.80938595278556 P P P 6.61889418588887 6.96790982766484 7.03838716033087 P P P LNCV6_142557_PI430048170 mRNA
GGTTTAAATGGTCTTATGTATATAGGGGAAACTGGGAGACTTTAGGATCTTAAAAAACCA NM_198525 RefSeq chr15 - 89627969 89655451 KIF7 374654 kinesin family member 7 GO:0005515|GO:0008017|GO:0005871|GO:0045879|GO:0003777|GO:0005524|GO:0007224|GO:0005929|GO:0045880|GO:0008152|GO:0021591|GO:0016887|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143824_PI430048170 0.027820444862846 1.43638447793011 7.92249282843748 8.08278311995912 8.32186031668449 P P P 7.66699560128357 7.39613322396425 7.70560865900833 P P P LNCV6_143824_PI430048170 mRNA
GGGACACATCCACTCTTGGAGGAATATATTTACTCAATAATGGCACCTTACATTTATAAA NM_004251 RefSeq chrX + 13689120 13709826 RAB9A 9367 "RAB9A, member RAS oncogene family, transcript variant 1" GO:0005515|GO:0005774|GO:0005886|GO:0005770|GO:0003924|GO:0005525|GO:0005764|GO:0006886|GO:0045335|GO:0045921|GO:0000139|GO:0008152|GO:0005789|GO:0030670|GO:0042147|GO:0032482|GO:0019003|GO:0090385|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133136_PI430048170 0.127330608120939 0.867418706125544 11.5595214484142 11.4346518553967 11.3272943953973 P P P 11.4831254121628 11.7402902438732 11.7096056968168 P P P LNCV6_133136_PI430048170 mRNA
TATAAGGTCAACTGTGCAAAACCTTATACTGGCCAAGAACAAACTAGTGCTGGGGGAGGA NM_001135055 RefSeq chr3 - 53224706 53256114 TKT 7086 "transketolase, transcript variant 2" GO:0048037|GO:0005999|GO:0005975|GO:0005634|GO:0044281|GO:0006098|GO:0046166|GO:0031982|GO:0046872|GO:0042803|GO:0009052|GO:0004802|GO:0005829|GO:0006112|GO:0009405|GO:0005654|GO:0040008|GO:0070062|GO:0005777. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140409_PI430048170 0.688701888566073 0.965071678235213 6.6510899711365 6.47542416397321 6.94575941944367 P P P 6.70502334360877 6.78646650478115 6.7729297066933 P P P LNCV6_140409_PI430048170 mRNA
TCATTTGCCAATTGTGTTGTTTAGTTCGGAAGTAAGAGGGTCTTGAGATTGAGGGGTAGG NM_006703 RefSeq chr6 - 34287195 34392680 NUDT3 11165 nudix (nucleoside diphosphate linked moiety X)-type motif 3 GO:0052846|GO:0052845|GO:0052844|GO:0000287|GO:0052843|GO:0043647|GO:0008486|GO:0052848|GO:0052847|GO:0007267|GO:0044281|GO:0052840|GO:0005829|GO:0015961|GO:0071544|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_82785_PI430048170 0.2349527613105081.09093736701942 4.72397423656613 4.71538246284236
4.77561146585937 P P P 4.66748428773637 4.70469963840361 4.45439131605079 P P P
LNCV6_82785_PI430048170 mRNA
TTCCCATGAGGGCCTGGCCCACCCGCTGCAGTTGCCCTAAGGAAAAATAAAGCTGCCTTT NM_003041 RefSeq chr16
+ 31483117 31490770 SLC5A2 6524 "solute carrier family 5 (sodium/glucose cotransporter), member 2,
transcript variant 1"
GO:0015758|GO:0005886|GO:0005975|GO:0006810|GO:0005362|GO:0016021|GO:0006814|GO:0055085|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138592_PI430048170 0.00273477207814714 0.68536600960825813.0755163918879
13.0161104449846 13.0626690005307 P P P 13.5247192659486 13.5821153171205
13.6790605353333 P P P LNCV6_138592_PI430048170 mRNA
CCTACCTGGGGCCTATTTCTACTTTCATTTTGTATTTCTGGTCTGTGAAAATGATTTAAT NM_003146 RefSeq chr11 -
57325984 57335877 SSRP1 6749 structure specific recognition protein 1
GO:0005515|GO:0010467|GO:0006368|GO:0006355|GO:0006366|GO:0005694|GO:0005730|GO:0005634|GO:0003
677|GO:0050434|GO:0006260|GO:0005737|GO:0006281|GO:0003682|GO:0016032|GO:0005654|GO:0006338 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_94445_PI430048170 0.1543964380318790.85243675110063911.0074389393909 11.0502092915251
11.3079841912347 P P P 11.3455538333284 11.1965438315322 11.5155275389363 P P P
LNCV6_94445_PI430048170 mRNA
ATGCCAAACCTGCAAACAAACAGGAAGATGAAGTGATGAGAGCCTATTTACAACAGCTAANM_001278556 RefSeq
chr12 - 110434890 110450411 ARPC3 10094 "actin related protein 2/3 complex, subunit 3, 21kDa,
transcript variant 1"
GO:0005515|GO:0034314|GO:0048013|GO:0005885|GO:0006928|GO:0015629|GO:0030027|GO:0005829|GO:0051
015|GO:0016020|GO:0007411|GO:0045087|GO:0005200|GO:0005925|GO:0038096|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_67993_PI430048170 0.5575424870482071.11914226128085 4.44275477236108 4.0448003484006
4.6788003948622 P P P 4.56029716449012 4.04407873215342 4.08544377761419 P P P
LNCV6_67993_PI430048170 mRNA
AAGCGTGACTTCTCTGCCTTCAAGGATGCGGACAATGAGCTCAAAGTGAAAATCTCCCCG NM_020184 RefSeq chr2
+ 96760901 96811891 CNNM4 26504 cyclin and CBS domain divalent metal cation transport mediator 4
GO:0005886|GO:0016021|GO:0031214|GO:0007601|GO:0050896|GO:0006811 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145614_PI430048170 0.0793403087724117 0.4098406075696861.79965591157876
2.21344413218732 1.89067003532476 A A A 2.39715615918304 3.64431162479474
3.47074549958657 A P P LNCV6_145614_PI430048170 mRNA
CTCCATCAGGGGCAAATGTTTACTTGTAATTTTCTTCCTACAGTTCGTGTTAAATTACTT NM_001201543 RefSeq chr2
- 61824847 61854143 FAM161A 84140 "family with sequence similarity 161, member A, transcript
variant 1"
GO:0005515|GO:0042384|GO:0005813|GO:0005737|GO:0032391|GO:0007601|GO:0050896|GO:0036064 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_6119_PI430048170 0.1072783961865640.7916512458741228.01972424328132 7.86849509527506
8.28481292098126 P P P 8.2080208448133 8.39701847994941 8.58562809081099 P P P
LNCV6_6119_PI430048170 mRNA
GTGGTAACTCTTAAGTGCTTTTGGTATCTCTTGAGATTCTAACTTTTAAAGAGCAACCAT NM_001136043 RefSeq
chr15 - 65578757 65611289 VWA9 81556 "von Willebrand factor A domain containing 9, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134628_PI430048170 0.2509362764035730.6468266024416611.2091027018183
10.9377994787231 11.0460691183525 P P P 10.924646257562 12.0450517322896
11.8887214358337 P P P LNCV6_134628_PI430048170 mRNA

TGATCTCCGTGTGTGCATGTGACTGTGCTGGGTTGGAATGTGAACAATAAAGAGGAATGT NM_001126181 RefSeq chr11 + 124739932 124747206 NRGN 4900 "neurogranin (protein kinase C substrate, RC3), transcript variant 2" GO:0035556|GO:0005622|GO:0007165|GO:0005516|GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134644_PI430048170 0.6241069486829420.5077820375596210.432129351721127 1.50191304412461 0.53728529757862 A A A 0.5508524098767033.0543609280495 0.401079749260537A P A LNCV6_134644_PI430048170 mRNA
CTTCAGCTTGCCCTTACTGCCACTGATATTGGTAATGTTCTTTTTTGTAAAATGTTTGTA NM_002353RefSeq chr1 - 58575422 58577494 TACSTD2 4070 tumor-associated calcium signal transducer 2 GO:0005515|GO:0050678|GO:0008283|GO:2000738|GO:2000146|GO:0005634|GO:0060675|GO:0005615|GO:0016328|GO:0005829|GO:0051497|GO:1900028|GO:0009925|GO:0016020|GO:0005887|GO:1900025|GO:0090191|GO:0004872|GO:0007601|GO:0007166|GO:0070062|GO:0010633 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139824_PI430048170 0.7724587694880181.03847707164368 5.98566956211503 6.08423059187053 5.70348738066156 P P P 5.46253837189963 6.17200345567691 5.91490159927564 P P P LNCV6_139824_PI430048170 mRNA
CTCTCTTATTCCACATTGCAGTGTTTGGAATAAACCATGTTTTTATGCCTCCTCAAAAAA NM_000836RefSeq chr19 + 48394874 48444931 GRIN2D 2906 "glutamate receptor, ionotropic, N-methyl D-aspartate 2D" GO:0005515|GO:0008344|GO:0030054|GO:0005886|GO:0005234|GO:0017146|GO:0035249|GO:0007268|GO:0030425|GO:0001964|GO:0007165|GO:0035235|GO:0034220|GO:0004972|GO:0045211|GO:0051930 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136022_PI430048170 0.1970417633502231.090899348347 0.562955341416745 0.7808954582629430.611376058778961A A A 0.4577169406723540.550987486344056 0.576462477881128A A A LNCV6_136022_PI430048170 mRNA
TCTGTGCTGACTGTGGTCCTATAAATTCATGAGAAATAAACTGGTTCTGTGTGCAAAAAA NM_021257RefSeq chr14 - 77265490 77271312 NGB 58157 neuroglobin GO:0005739|GO:0019825|GO:0005506|GO:0005344|GO:0043204|GO:0006915|GO:0020037|GO:0015671 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_95405_PI430048170 0.0358053222342651 1.40119902714737 6.59617800080359 6.96127490113685 6.94932506943378 P P P 6.50112735027222 6.28206589268821 6.28124271553155 P P P LNCV6_95405_PI430048170 mRNA
ATCGCCTCCAAGATTGGTTCTAACGCTTTGCGTATGATTCAATCGGCCACCCCTCCACCT NM_001097RefSeq chr22 + 50738223 50745299 ACR 49 acrosin GO:0005515|GO:0043159|GO:0004252|GO:0005507|GO:0005798|GO:0005576|GO:0005634|GO:0042806|GO:0048545|GO:0007339|GO:0003677|GO:0005537|GO:0007338|GO:0043234|GO:0004040|GO:0007190|GO:0002077|GO:0008144|GO:0008270|GO:0007341|GO:0007340|GO:0032504 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137563_PI430048170 0.00675095881487682 0.5308509359595355.87201169856893 5.69353685855173 5.97504942713955 P P P 6.52279673274256 6.76850177099664 6.96962838454114 P P P LNCV6_137563_PI430048170 mRNA
AACTCTGACAAAAAGGAGTCATCTGGGAGCCCGAGAATCCTACTCCTGGCCGGGCACAGTNM_018385RefSeq chr3 - 194640787 194672477 LSG1 55341 large 60S subunit nuclear export GTPase 1 GO:0005737|GO:0015030|GO:0016020|GO:0005783|GO:0042254|GO:0008152|GO:0003924|GO:0005634|GO:0015031|GO:0005525|GO:0051168|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127947_PI430048170 0.0613554409487489 0.5754188132557633.01383591260724 3.63376346083928 3.23921384838982 A P P 3.61298592260654 4.36328323563916 4.26319119021278 P P P LNCV6_127947_PI430048170 mRNA
GCGATCCTTTTAAGGCAAACAAGGGAGATAGTACCTGTATCTTAGTAGGAAATTAAATAA NM_001202473 RefSeq chr19 - 52927134 52962911 ZNF816-ZNF321P NA ZNF816-ZNF321P readthrough NA . NA - .

NA NA NA NA NA NA NA NA NA
LNCV6_136886_PI430048170 0.0266708973913589 1.69502092784026 3.97567787182768
4.15377278051463 4.0387991802884 P P P 3.51635108516432 2.9944036757173
3.33166793540935 P P P LNCV6_136886_PI430048170 mRNA
AAGGAAAAAGGTTGTCCACATGAATAAACTCCGGAAAACCATTGGCCGCCTGGAAGTCAA NM_174903 RefSeq
chr16 + 1966873 1968975 RNF151 146310 ring finger protein 151
GO:0005737|GO:0004842|GO:0016567|GO:0008270|GO:0005634|GO:0007283|GO:0030154 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_65763_PI430048170 0.00418336112668122 0.490553933359671 3.91938457995048
4.01396674264425 4.35066449100617 P P P 5.13652356555073 4.92998899181723
5.31133223821379 P P P LNCV6_65763_PI430048170 mRNA
CAACCGGTTTGGAGGCTTATTTTTAGCATCTGGTGTTAATGTGACAATGAAAGATAACAA NM_001190274 RefSeq
chr2 - 47806919 47905793 FBXO11 80204 "F-box protein 11, transcript variant 4"
GO:0005515|GO:0006511|GO:0004842|GO:0016567|GO:0005694|GO:0007605|GO:0005730|GO:0016274|GO:0000
151|GO:0005634|GO:0035246|GO:0005737|GO:0008270|GO:0006464 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_141681_PI430048170 0.00441725341483463 9.57963527343127 6.71389705328364
7.05573379465214 6.76351130077053 P P P 4.09116806847268 3.03257913427248
3.45432671450525 P P P LNCV6_141681_PI430048170 mRNA
AAGGTTTGAAGGTTACGGCTCAGGGCTGCCCCATTAAAGTCAGTGTTGTGTTCTAAAAAA NM_015417 RefSeq chr20
- 3777503 3781455 SPEF1 25876 sperm flagellar 1
GO:0008150|GO:0003674|GO:0031514|GO:0005930|GO:0005575|GO:0005856 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139229_PI430048170 0.0148818148490314 0.953232106848287 0.352499185677971
0.362776957706614 0.329581338893223 A A A 0.438358152902603 0.419591924188525
0.394066648690767 A A A LNCV6_139229_PI430048170 mRNA
TCTAATCTACACTCTCAGAAACAAGCATGTAAAAGGGGCAGCGAAGAGACTATTGGGGTG NM_030905 RefSeq
chr6_GL000256v2_alt + 482901 483942 OR2J2 26707 "olfactory receptor, family 2, subfamily J, member
2" GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_141233_PI430048170 0.191087182465454 0.964140308431825 0.398362775864552
0.418744516425919 0.325971318702426 A A A 0.423067871350166 0.455295039488746
0.424176995941563 A A A LNCV6_141233_PI430048170 mRNA
AGGCCTTGTTGCTGGAAGAAACTAGTGAAGAGAGGTTAAATTCTGGCAATATAATGTTTT NM_024993 RefSeq chr2
- 77516660 77522376 LRRTM4 80059 "leucine rich repeat transmembrane neuronal 4, transcript variant
2" GO:0030054|GO:0097113|GO:0045211|GO:0032281|GO:0043395 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_69633_PI430048170 0.471201209291337 0.914107039524819 4.07552293330333 3.67473802279014
4.19731093627683 P P P 4.0172213183807 4.11192075575614 4.24796079628736 P P P
LNCV6_69633_PI430048170 mRNA
TTGCTTCAGAAGCTGCTTACCATGGACCCAATAAAGCGAATTACCTCAGAACAGGCTATG NM_001260 RefSeq chr13
+ 26254618 26404432 CDK8 1024 cyclin-dependent kinase 8
GO:0005515|GO:0010467|GO:0006367|GO:0005634|GO:0005524|GO:0008353|GO:0006351|GO:0004672|GO:0007
219|GO:0045944|GO:0016592|GO:0051726|GO:0005654|GO:0006468|GO:0007179|GO:0004693 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_130121_PI430048170 0.000899918241916579 0.260934682476853 7.63098965691399
7.07083383990762 7.36796493091487 P P P 9.057520311234 9.35569399859884
9.49181535867416 P P P LNCV6_130121_PI430048170 mRNA
GTCTGTACGAATCTGCCTTGACTGTATATTTCATACTGCCCAACAAAACAATAAAAAACA NM_004101 RefSeq chr5

- 76615481 76623434 F2RL2 2151 "coagulation factor II (thrombin) receptor-like 2, transcript variant 1"
GO:0005515|GO:0016324|GO:0005886|GO:0070493|GO:0015057|GO:0007596|GO:0005887|GO:0004435|GO:0008
152|GO:0009611|GO:0030168|GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_73656_PI430048170 0.296292068159663 0.803624433792883 7.08932264786078 6.88576749980668
7.11816329545489 P P P 7.07384861144085 7.15427822074321 7.73001832202774 P P P
LNCV6_73656_PI430048170 mRNA
TCCACCCTGAAGTTGGCCTTACAGAAAATGGAAAAGTAATACTGAAGAATTTCCTTTATG NM_003875 RefSeq chr3
+ 155870535 155937731 GMPS 8833 guanine monphosphate synthase
GO:0009168|GO:0042493|GO:0055086|GO:0003922|GO:0044281|GO:0003921|GO:0005524|GO:0005829|GO:0005
737|GO:0016462|GO:0006177|GO:0006144|GO:0009113|GO:0019899|GO:0006541 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_130604_PI430048170 0.425423942049384 1.02679158355292 0.29368084705889
0.313319987571542 0.414228281128916 A A A 0.320465384189236 0.29788204238776
0.291209965269736 A A A LNCV6_130604_PI430048170 mRNA
TTTACAGCCTTAGGAACAAGGATGTCAAAGGTGCTCTGAGGAGTGCCATTATCCGTAAAG NM_001004471 RefSeq
chr11 - 58227881 58228918 OR10Q1 NA "olfactory receptor, family 10, subfamily Q, member 1"
NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142760_PI430048170 0.0741976498899353 0.507511486045512 5.8792641265256
5.59378744064307 6.09196021497783 P P P 6.18007865475655 7.03964033929565
7.14437460387691 P P P LNCV6_142760_PI430048170 mRNA
TTACCTGAAATGCATTTAGTGTACACCAGTCTGTAAACTTCAACCTGTAATGAAAGTGTA NM_001039535 RefSeq
chr18_GL383567v1_alt + 82828 101975 SKA1 220134 "spindle and kinetochore associated complex
subunit 1, transcript variant 1"
GO:0008017|GO:0005515|GO:0007067|GO:0000940|GO:0007059|GO:0031110|GO:0015630|GO:0005876|GO:0000
278|GO:0051301|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130125_PI430048170 0.00725963050127156 4.32940598785453 3.27150540858863
3.91595870994712 3.88223871206206 P P P 1.65082673762693 1.65524617977412
1.50235674279419 A A A LNCV6_130125_PI430048170 mRNA
TTTACAAGGGACGGATGGACACAAGGCTGCCAGGCATCCTCCGAAAAGACAGCTCAGGGA NM_032134 RefSeq
chr17 - 76274048 76307680 QRICH2 84074 "glutamine rich 2, transcript variant 1" NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_139620_PI430048170 0.867739770697117 0.991431806500321 3.67884939836821
3.98864931948385 3.29357035415804 P P P 3.78302641843641 3.6683651895841
3.62520262031713 P P P LNCV6_139620_PI430048170 mRNA
TTGTTCAACATTGTTTACTGGGTATACCATATGTATTAGTCCCCCAGTGCTCCAGAACAG NM_018558 RefSeq chrX
+ 152638182 152653362 GABRQ 55879 "gamma-aminobutyric acid (GABA) A receptor, theta"
GO:0005230|GO:0030054|GO:0005886|GO:0004890|GO:0005326|GO:0034707|GO:0007268|GO:0055085|GO:0005
254|GO:0043235|GO:0007165|GO:0034220|GO:0005887|GO:0045211|GO:0006836|GO:0004888 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135097_PI430048170 0.0188480143962501 0.638272855228126 7.5310949726253
7.44525368837472 7.76575539906522 P P P 8.0203953369022 8.1869258006673
8.46249504717523 P P P LNCV6_135097_PI430048170 mRNA
GCAGGATACTACAAACTGGTAAAGACTTCCACCATGTGAAGAATGTATGTAAATTAAAGT NM_001286636 RefSeq
chr6 + 36871869 36928964 C6orf89 221477 "chromosome 6 open reading frame 89, transcript variant
3"
GO:0005737|GO:0005886|GO:0000139|GO:0042060|GO:0005730|GO:0030496|GO:0016021|GO:0045787|GO:0050
673 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138381_PI430048170 0.125945593011016 1.32349933807268 0.365305079287276
0.887899328812980 0.703280139148326 A A A 0.256627317467251 0.28041218260708

0.253950108274226 A A A LNCV6_138381_PI430048170 mRNA
GTCCACATTTTATTTAGTTGACCTCTCTATCTCTATATTATAGTACCCATGGTATGCACC NM_014898 RefSeq chr19 -
37632487 37655412 ZFP30 22835 ZFP30 zinc finger protein
GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_131843_PI430048170 0.106359636586875 1.0434829535778 0.406735111023743
0.41748979882082 0.436340077025911 A A A 0.324869365890009 0.346692061412075
0.403783073312761 A A A LNCV6_131843_PI430048170 mRNA
GCAAGAACCCTCATACTCAGAAGCTTCCAAATAAACCTTTGATACAGATTGCTTAAAAAA NM_144594 RefSeq chr12
- 54455951 54473602 GTSF1 121355 gametocyte specific factor 1 GO:0005737|GO:0046872 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_129485_PI430048170 0.112609095615297 0.457449936929853 0.405290077186667 2.0518006118989
0.968468660990184 A A A 1.81538982021765 2.36150327961709 2.92178220480501 A A P
LNCV6_129485_PI430048170 mRNA
AATGGGCAAACACTTGTGTTCTAAAGTTACTTGCAAGTAGTTTATACTGCCAACTTGATA NM_022100 RefSeq chr1
- 175012957 175023455 MRPS14 63931 "mitochondrial ribosomal protein S14, transcript variant 1"
GO:0070124|GO:0005739|GO:0070125|GO:0070126|GO:0031965|GO:0032543|GO:0006996|GO:0003735|GO:0005
761|GO:0005743|GO:0006412|GO:0005763 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139043_PI430048170 0.0509176105245514 1.1112727268673 12.4343628665284
12.4524570450145 12.4178191627236 P P P 12.2435566774042 12.2421612914791
12.3593283468049 P P P LNCV6_139043_PI430048170 mRNA
CTCCCTCATTCCTAGAAATTTAACCTTAATGAAATCCCTAATAAAACTCAGTGCTGTGTT NM_001284367 RefSeq
chr10 - 100523728 100529923 NDUFB8 4714 "NADH dehydrogenase (ubiquinone) 1 beta
subcomplex, 8, 19kDa, transcript variant 2"
GO:0022904|GO:0005747|GO:0005783|GO:0006120|GO:0005743|GO:0044281|GO:0016021|GO:0008137|GO:0044
237 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_108049_PI430048170 0.756027561198273 1.03555583046204 10.1737701902552
10.2701686908395 10.5313185849367 P P P 10.1424930223468 10.189626833528
10.4907367465933 P P P LNCV6_108049_PI430048170 mRNA
TGCTCCAGACTATGTTTTCAGCATACCTTGGGTCTGAACAATATAAACTACTTATAAAGG NM_032273 RefSeq chr11
+ 85647918 85656553 TMEM126A 84233 "transmembrane protein 126A, transcript variant 1"
GO:0005739|GO:0003674|GO:0021554|GO:0005743|GO:0016021 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127225_PI430048170 0.0182872279256783 0.584517248661598 6.25735798268236
6.03944130027527 6.53274892903458 P P P 6.80579818309012 7.05140183125823
7.29718790032874 P P P LNCV6_127225_PI430048170 mRNA
GAAATGTTGCTTTGAAGCAATATTTGCAAAACACGCAGACTTCTGTATCTGTATTTGGAA NM_016436 RefSeq chr20
+ 35772000 35950366 PHF20 51230 PHD finger protein 20
GO:0005515|GO:0006355|GO:0031965|GO:0006325|GO:0003677|GO:0006351|GO:0043981|GO:0005737|GO:0043
982|GO:0043984|GO:0071339|GO:0043996|GO:0043995|GO:0000123|GO:0046972|GO:0005654|GO:0008270 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142223_PI430048170 0.00508192392854325 0.392080208680547 7.49570089139952
7.17540034592414 7.23116404789611 P P P 8.32070158345063 8.69932460885864
8.89716387114326 P P P LNCV6_142223_PI430048170 mRNA
CCCAGTTTGGGGCTTTTTCAAGGCTAATGAAGTTATTGTTGGTCTAGAAAAATAGTATTT NM_006670 RefSeq chr6
+ 82363205 82367416 TPBG 7162 "trophoblast glycoprotein, transcript variant 1"
GO:0009986|GO:0005887|GO:0005783|GO:0007155 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_128738_PI430048170 0.348953233830203 0.742014299763899 0.428724676915051
0.440554494308368 0.350038812124725 A A A 1.37270624321497 0.483817496676316

0.457086427050805 A A A LNCV6_128738_PI430048170 mRNA
GGCACAGGTATAGGTAGGTCCTGTTTCCTTAATTATTAAAACCAACAACTAAGTGTATTA NM_022474 RefSeq chr14
+ 67241294 67336061 MPP5 64398 "membrane protein, palmitoylated 5 (MAGUK p55 subfamily
member 5), transcript variant 1"
GO:0043220|GO:0005515|GO:0005886|GO:0002011|GO:0034329|GO:0019904|GO:0035750|GO:0045216|GO:0032
287|GO:0012505|GO:0032288|GO:0035749|GO:0043234|GO:0005737|GO:0070830|GO:0043219|GO:0005654|GO:0
005923|GO:0090002|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137408_PI430048170 0.0946900274799423 1.2062448869091 10.1074564367287
9.83032901520714 9.81926209164702 P P P 9.67090104396147 9.59335448689911
9.69804931564814 P P P LNCV6_137408_PI430048170 mRNA
CCACTGCACCAGCAATGCTAGAAAACCAAGCCAATAAAAGTGATTTCTTTTTTCATTAAA NM_001080400 RefSeq
chr19 - 4502179 4517704 PLIN4 729359 perilipin 4 GO:0005811|GO:0005737|GO:0005886 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139508_PI430048170 0.4478784427762320.4112137032856550.445285989098706
0.4960459029287170.45037125738024 A A A 0.3844554731888082.88807218893124
0.438821210638575 A P A LNCV6_139508_PI430048170 mRNA
GTGCATGGTCTGAGACTAAGTAAAGGAAATTTCCTAAAGCTGTGAAATTTGAATTTTGCT NM_001101421 RefSeq
chr12 + 109388718 109448371 MYO1H 283446 myosin IH
GO:0003774|GO:0008152|GO:0003779|GO:0016459|GO:0005524 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_140010_PI430048170 0.2220402079752441.14387186336376 6.29232807544493
6.31806024900525 6.52227390659266 P P P 5.98212435048863 6.37004265557055
6.18388607188883 P P P LNCV6_140010_PI430048170 mRNA
TTGCAATTGTGTGGCAGCTTGCTACTAATGATAATGATCAAGTAAGTTGTTTGATGCAAT NM_001127370 RefSeq
chr7 - 21900898 21945924 CDCA7L 55536 "cell division cycle associated 7-like, transcript variant
2" GO:0005515|GO:0008284|GO:0006355|GO:0005737|GO:0005730|GO:0005634|GO:0006351 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_128166_PI430048170 0.4345368388604681.05142415872347 11.9576121801508 12.026320729395
12.13905853928 P P P 11.9081580323993 11.8961402588532 12.0984461182651 P P P
LNCV6_128166_PI430048170 mRNA
GTCCTTGTTGCTGTTTGTGATAACTGATAGATAACTCATTGGAAACGTGCATACATTTAT NM_176812 RefSeq chr20
+ 33811303 33854367 CHMP4B 128866 charged multivesicular body protein 4B
GO:0005515|GO:0000815|GO:0019058|GO:0005634|GO:0046755|GO:0042803|GO:0005829|GO:0042802|GO:0005
737|GO:0007034|GO:0016197|GO:0060548|GO:0016032|GO:0061024|GO:0051260|GO:0070062|GO:0006997|GO:0
030496|GO:0010824|GO:0000920|GO:0050792|GO:0031902|GO:0009898|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_55393_PI430048170 0.2430223138745510.8659903013349430.3600210981366160.247545254924188
0.282896037680085 A A A 0.53773688535383 0.6823536554024510.264728587382818 A A A
LNCV6_55393_PI430048170 mRNA
CCCAAGTCATGTCAACTCTCATTAAAGGTGCTTCCATATTTGAGCAGGCGTCAAACAAGG NM_001199050 RefSeq
chr1 - 205381378 205422086 LEMD1 93273 "LEM domain containing 1, transcript variant 1"
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143897_PI430048170 0.2394842123562211.04224858704642 0.582504460066836
0.6580196439323420.533898194005062 A A A 0.5572380299780990.520613673181276
0.519874486199652 A A A LNCV6_143897_PI430048170 mRNA
ATGAAATACATGAACTTCCGTGTGAAGGCCTGTAACAAGGCAGTTGCAGGAGAGTTCTCT NM_024333 RefSeq chr19
+ 4304593 4323846 FSD1 79187 fibronectin type III and SPRY domain containing 1
GO:0007067|GO:0005737|GO:0005815|GO:0005874|GO:0005634|GO:0032154|GO:0051301 . NA - .
NA NA NA NA NA NA NA NA NA

LNCV6_59457_PI430048170 0.2708007123932441.05650704311345 0.4934384627911650.313883206085982
0.412966467439701 A A A 0.3567935904768360.3221214992382620.308630037433287 A A A
LNCV6_59457_PI430048170 mRNA
TTGGAACAACTGGTTAAAAAGCCTAACTGGGCACACTCAGTAAATCCTGTTCACCTGGAG NM_001278419 RefSeq
chr12 - 103301940 103496010 C12orf42 374470 "chromosome 12 open reading frame 42, transcript
variant 3" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_68529_PI430048170 0.00645816515746534 0.5737749566873765.11406469646632
4.99058657833965 4.97735129315591 P P P 5.69780064191517 5.75798067941504
6.01455957103581 P P P LNCV6_68529_PI430048170 mRNA
TTGTTCTATCTGTGTGAAAGGATCTTCCCAGCCCCAAGCAAGAGTTTATTTAACATTTGA NM_006379 RefSeq chr7
- 80742537 80919351 SEMA3C 10512 "sema domain, immunoglobulin domain (Ig), short basic
domain, secreted, (semaphorin) 3C"
GO:0042493|GO:0001756|GO:0001755|GO:0003350|GO:0003215|GO:0009791|GO:0005615|GO:0003151|GO:0006
955|GO:0016020|GO:0001974|GO:0007411|GO:0060666|GO:0021915|GO:0060174|GO:0030215|GO:0004872|GO:0
070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127247_PI430048170 0.3357616426736671.28846232910107 0.33551616531753
1.10036400753024 0.342948455716718 A A A 0.2768142717282130.265560616046731
0.279963283179363 A A A LNCV6_127247_PI430048170 mRNA
TCATTTATTCTGTGTGAGTAGGTAGAAAATGAGCATCACGGACGTGCTCAGTGCTGACGA NM_001097622 RefSeq
chr7 + 5880797 5886363 OCM NA oncomodulin NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_127882_PI430048170 0.1550673144643180.9577178365430260.269231957284208
0.3288431263409390.312984401306972 A A A 0.4230488616224820.333500408257421
0.340419559062955 A A A LNCV6_127882_PI430048170 mRNA
GTCCAGAATGCCTGCAAATTGCTGTAATTTTATACCATGTTCTAACCAATAAACAGAACT NM_001278340 RefSeq
chr5 + 170504035 170736632 KCNIP1 30820 "Kv channel interacting protein 1, transcript variant 4"
GO:0005515|GO:0005513|GO:0005244|GO:0046982|GO:0005886|GO:0005509|GO:0005267|GO:0007268|GO:0015
459|GO:0034705|GO:0030425|GO:0044325|GO:0007165|GO:0047485|GO:0043025|GO:0045760|GO:0034765|GO:0
071805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133243_PI430048170 0.0130102169017503 2.23187569921651 2.03645404154899
1.91748668687554 1.39408393994964 A A A 0.4295622275527370.82462381401345
0.669342490629167 A A A LNCV6_133243_PI430048170 mRNA
TGTCGGCTGTGAGGCGGGTGGCTGGTATAAATAATATTTATCTTTTCAACCAGCAAAAAA NM_001145146 RefSeq
chr17_KI270908v1_alt + 486390 537950 CRHR1 1394 "corticotropin releasing hormone receptor 1,
transcript variant 1b"
GO:0005802|GO:0005515|GO:0015056|GO:0032811|GO:0005886|GO:0030325|GO:2000852|GO:2000252|GO:0051
424|GO:0031226|GO:0048148|GO:0007200|GO:0060291|GO:0032403|GO:0007204|GO:0030425|GO:0042596|GO:0
007190|GO:0001965|GO:0006955|GO:0071376|GO:0007218|GO:0051602|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_139739_PI430048170 0.3286210551898920.9543505070963440.261863464272197
0.3923227355507160.292772680830517 A A A 0.4697580203902790.362002801703475
0.316339102616093 A A A LNCV6_139739_PI430048170 mRNA
CAGGTGACCACTGGCATCTATGCTTAGCTATGAAAGTGAATAAAGCAGAATAAAAATAAA NM_001038633 RefSeq
chr1 - 37611349 37634923 RSPO1 284654 "R-spondin 1, transcript variant 1"
GO:0005515|GO:0010468|GO:0001664|GO:0090263|GO:0005102|GO:0030177|GO:0005576|GO:0005634|GO:0005
615|GO:2000254|GO:2000052|GO:0001934|GO:0002090|GO:0008201|GO:0060070|GO:0007140 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145436_PI430048170 0.4505580475790390.7130658695296310.345978332362866
0.2514291208917520.274023334695939 A A A 1.45844710246351 0.26860862636017

0.25679868542728 A A A LNCV6_145436_PI430048170 mRNA
ATTGCCATCATCACAGCCTGGAACCTCAGCTGTGAGAGGGAAGGGAAGGTGGAGGAGTGA NM_001102614
RefSeq chr17 + 7481401 7483064 SLC35G6 NA "solute carrier family 35, member G6" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127812_PI430048170 0.5870256864439581.06378388253426 0.666623145888489
0.4252849103868990.676022875711681A A A 0.2870109844992770.419529902731633
0.764538943193148A A A LNCV6_127812_PI430048170 mRNA
CACCATATCCATTTCAAGCTATCATTAAAGTGTAATTTCCTTTGCTCTCTTTTACTGGGA NM_001160133 RefSeq chr6
+ 72621842 73198850 KCNQ5 56479 "potassium channel, voltage gated KQT-like subfamily Q, member 5,
transcript variant 4"
GO:0005251|GO:0005242|GO:0006461|GO:0005886|GO:0008076|GO:0007268|GO:0034765|GO:0016021|GO:0071
805 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143680_PI430048170 0.00626428305432314 0.4791079490535956.35264021971452
5.9906610363704 6.29703678576277 P P P 7.1059692523467 7.12742727380727
7.56859700410258 P P P LNCV6_143680_PI430048170 mRNA
GTATTCACTTTCCTGCCTTGTCATTTCTGGAAAGATTTTGGGGAGATATTTTATTGCATA NM_194356RefSeq chr12 -
130789600 130839274 STX2 2054 "syntaxin 2, transcript variant 2"
GO:0005515|GO:0005886|GO:0031201|GO:0051259|GO:0006886|GO:0005615|GO:0030154|GO:0043231|GO:0016
323|GO:0005911|GO:0000149|GO:0046983|GO:0009887|GO:0031629|GO:0033194|GO:0048278|GO:0070062|GO:0
009986|GO:0007398|GO:0030027|GO:0008021|GO:0012505|GO:0007165|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_130680_PI430048170 0.00125046965074767 0.2624055752776933.13713113468357
2.90168826234133 3.33757200067908 P A P 5.05556378783457 4.97456671010535
5.16322410835998 P P P LNCV6_130680_PI430048170 mRNA
TGGGAAATGTAGCCCTGGGTTTAATGTCAAATCAAGGCAAAAGGAATTAAATAATGTACT NM_003889RefSeq chr3
+ 119780483 119818485 NR1I2 8856 "nuclear receptor subfamily 1, group I, member 2, transcript variant
1"
GO:0005515|GO:0010467|GO:0000977|GO:0006367|GO:0006805|GO:0003713|GO:0003707|GO:0046618|GO:0042
908|GO:0001228|GO:0007165|GO:0042738|GO:0045944|GO:0008144|GO:0043401|GO:0005654|GO:0008270|GO:0
004879|GO:0045893|GO:0045892|GO:0030522|GO:0008202 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_66079_PI430048170 0.00815518199130142 0.6523067250126231 1.0247097126574
11.0787448017571 10.9890797408428 P P P 11.5223743312457 11.6320889127772
11.7772512049438 P P P LNCV6_66079_PI430048170 mRNA
GATGTCCTGAATTAAGATGTTTTCACCACATTGTATTACAGAGACAGCCAATAAATCTAC NM_003849RefSeq chr2
- 84423522 84459462 SUCLG18802 "succinate-CoA ligase, alpha subunit"
GO:0048037|GO:0004776|GO:0006099|GO:0046982|GO:0005886|GO:0003878|GO:0005743|GO:0044281|GO:0005
525|GO:0045244|GO:0005739|GO:0005737|GO:0006105|GO:0005759|GO:0006104|GO:0004775|GO:0019003|GO:0
044237|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_104199_PI430048170 0.4559850966922930.7414038919008410.395546542372098
0.2574735142324290.295742632522618A A A 0.2729992915101420.299694885038031
1.38020034484256 A A A LNCV6_104199_PI430048170 mRNA
CAGGTATGACTGGCACTATGTGATCTTGGACGAAGGACACAAAATTCGAAATCCAAATGC NM_000124RefSeq chr10
- 49454479 49539123 ERCC6 2074 excision repair cross-complementation group 6
GO:0005515|GO:0010165|GO:0006366|GO:0061098|GO:0006362|GO:0005634|GO:0045494|GO:0032403|GO:0032
786|GO:0030296|GO:0006290|GO:0035264|GO:0032784|GO:0010332|GO:0006979|GO:0009411|GO:0008094|GO:0
008630|GO:0005730|GO:0009636|GO:0007256|GO:0007257|GO:0008022|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142827_PI430048170 0.4091011952968711.37166053093223 0.494043303517604

0.31898066096195 1.45389592702151 A A A 0.4506153124071990.352765096424382
0.367126681488718A A A LNCV6_142827_PI430048170 mRNA
TGAGAAACCAGGACATGAAAGCAGCCATGAGGAGATTAGGCAAGTGCCTAGTAATTTGCA NM_012374RefSeq
chr17 + 58155153 58156086 OR4D1 NA "olfactory receptor, family 4, subfamily D, member 1" NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145643_PI430048170 0.9194302890727591.120572427467 0.263458706168813
0.2786800479728371.8792749189651 A A A 1.55073422811096 0.334713882125652
0.317327302589339A A A LNCV6_145643_PI430048170 mRNA
TTTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAAAGACCATACATTGCAGAG NM_001005189 RefSeq
chr1 - 158547127 158548105 OR6Y1 391112 "olfactory receptor, family 6, subfamily Y, member 1"
GO:0050911|GO:0004984|GO:0007186|GO:0005886|GO:0004930|GO:0016021 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_88872_PI430048170 0.2112577584217331.30642484153273 2.59693852059481 3.21877672553686
3.2050826641912 A P P 2.75018492476837 2.7373736388158 2.43820097222577 P P P
LNCV6_88872_PI430048170 mRNA
TACTGGATTCAACCAGATGCGTGAGCGCGAAGTGAAGCTGTGGGACACGCGGTTCTTCTC NM_024535RefSeq
chr16_KI270855v1_alt - 56866 119284 CORO7 79585 "coronin 7, transcript variant 1"
GO:0005515|GO:0005802|GO:0005794|GO:0030036|GO:0003779|GO:0015031|GO:0015629|GO:0006895|GO:0005
829|GO:0051015|GO:0000139|GO:0016020|GO:0030041|GO:0016023|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_145415_PI430048170 0.00855348704660856 0.4792146669175655.37795669163263
5.18402037957437 5.38255918489123 P P P 6.16985326565544 6.27926642880399
6.64418761088983 P P P LNCV6_145415_PI430048170 mRNA
CTCATAATGATTGATGATACCACCAGTAAAAATAGGATGTTTACCCCAAAACAAGTGTCA NM_020865RefSeq
chr3_KI270777v1_alt + 1178 6375 DHX36 170506 "DEAH (Asp-Glu-Ala-His) box polypeptide 36,
transcript variant 1"
GO:0005515|GO:0003725|GO:0042826|GO:0044212|GO:0005634|GO:0005829|GO:0004004|GO:0005737|GO:0045
944|GO:0032481|GO:0008094|GO:0070062|GO:0006396|GO:0000781|GO:0002151|GO:0051880|GO:0001047|GO:0
009615|GO:0005524|GO:0006351|GO:0001503|GO:0010501|GO:0045087|GO . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_69844_PI430048170 0.9010828461705241.00661452994165 5.02490642312231 4.96888424652586
5.2822849751084 P P P 4.65031977445343 5.23767091204249 5.29542108476777 P P P
LNCV6_69844_PI430048170 mRNA
TCTGTGGCCCAAGGAAGGCCACTCCACATTAAGCTGCCCAATAAACTGCTTTTAAGATAA NM_001287212 RefSeq
chr1 - 20664013 20718017 KIF17 57576 "kinesin family member 17, transcript variant 3"
GO:0008017|GO:0005871|GO:0006996|GO:0005930|GO:0031503|GO:0005874|GO:0072372|GO:0015031|GO:0005
524|GO:0036064|GO:0005829|GO:0030030|GO:0008152|GO:0008574|GO:0032391|GO:0030992|GO:0016192|GO:0
016887|GO:0022008|GO:0007018 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137796_PI430048170 0.0192133113327128 2.68983884655132 2.86491438353591
2.42704342091258 1.9158997695781 A A A 0.7567723892595150.978947661183619
1.29265720099425 A A A LNCV6_137796_PI430048170 mRNA
TTTTAGCATCTTCCCTAGCAGCCGGTTGAAGCGGAGACCAAGCCACTGTGAGCTGGACCT NM_005583RefSeq chr19
- 13099027 13103160 LYL1 4066 lymphoblastic leukemia associated hematopoiesis regulator 1
GO:0005515|GO:0006355|GO:0030183|GO:0046983|GO:0060216|GO:0005634|GO:0045893|GO:0003677|GO:0001
955|GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126667_PI430048170 0.4361161806484470.8687629641557588.47487870521434
8.36063166952307 8.72403543342605 P P P 8.48883899197729 8.56414186674212
9.06846010670638 P P P LNCV6_126667_PI430048170 mRNA
GTCATAGGACTCACATTTCTCTCAGTTATATTTAAAACCGTTGTGTACTTTGTACAAAGG NM_017969RefSeq chr2

- 127480806 127526511 IWS1 55677 IWS1 homolog (S. cerevisiae)
GO:0005515|GO:0006397|GO:0008380|GO:0006355|GO:0090239|GO:0005634|GO:0050684|GO:0003677|GO:0006
351|GO:0005737|GO:2001253|GO:0005654|GO:0010793|GO:0051028 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138826_PI430048170 0.3040186613386091.03990900274607 0.4672182581056
0.34274544244272 0.406941141345236A A A 0.29522004060632 0.349652523476018
0.403319902048059A A A LNCV6_138826_PI430048170 mRNA
GTTACACAAAGAACACTCTATATAACTGTGTTAAGTCCTTCAGACAAGTTCAGGAAATCA NM_020633RefSeq chr19
- 57455173 57456739 VN1R1 57191 vomeronasal 1 receptor 1
GO:0008150|GO:0016503|GO:0007186|GO:0005886|GO:0016021|GO:0019236 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_138936_PI430048170 0.1401521109889110.9260995748872179.519125814098 9.5801924778004
9.57554053889373 P P P 9.67465031437623 9.74802905526171 9.58037641576265 P P P
LNCV6_138936_PI430048170 mRNA
TGAAGTCCAGTGTGAGATTGAAGAACTAGGTGTCATCATCAACAAGGTGGTGTGATGGCT NM_199336RefSeq chr2
- 97083585 97094845 FAHD2B NA fumarylacetoacetate hydrolase domain containing 2B NA .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134056_PI430048170 0.00464988930174327 0.4459804906403915.59761449972226
5.20923564522004 5.55554465299395 P P P 6.33186223549809 6.65448833863759
6.85411983648972 P P P LNCV6_134056_PI430048170 mRNA
GAGTTTCAGAAAGGAATGAGAATGCCTCAGGAGTTGTTCTGTGATGGAAATTGGTCTGTT NM_017848RefSeq chrX
- 54068402 54183258 FAM120C 54954 "family with sequence similarity 120C, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA